Full wwPDB X-ray Structure Validation Report ⓘ

Aug 4, 2026 – 04:40 PM EDT

PDB ID	:	4W2F / pdb_00004w2f
Title	:	Crystal structure of the Thermus thermophilus 70S ribosome in complex with amicoumacin, mRNA and three deacylated tRNAs in the A, P and E sites
Authors	:	Polikanov, Y.S.; Osterman, I.A.; Szal, T.; Tashlitsky, V.N.; Serebryakova, M.V.; Kusochek, P.; Bulkley, D.; Malanicheva, I.A.; Efimenko, T.A.; Efremenkova, O.V.; Konevega, A.L.; Shaw, K.J.; Bogdanov, A.A.; Rodnina, M.V.; Dontsova, O.A.; Mankin, A.S.; Steitz, T.A.; Sergiev, P.V.
Deposited on	:	2014-09-12
Resolution	:	2.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

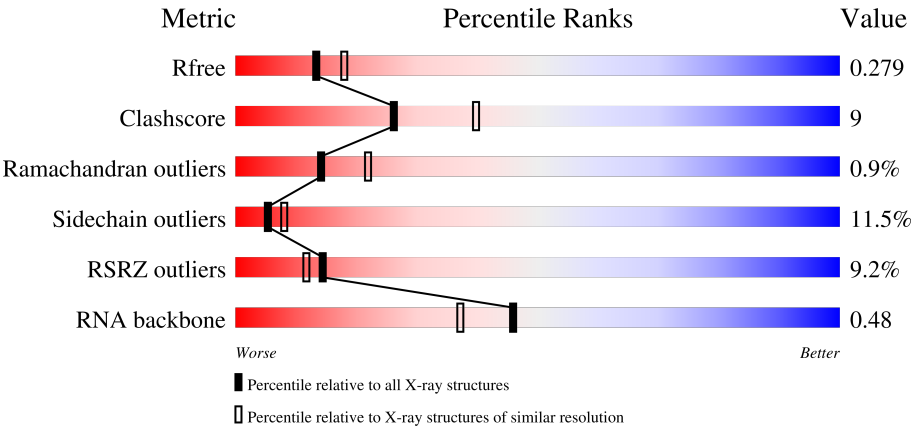
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)
RNA backbone	3983	1155 (2.70-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	1521	4% 56% 33% 9%
1	CA	1521	6% 52% 37% 10%

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Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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Mol	Chain	Length	Quality of chain
2	AB	256	23% 48% 34% 7% 10%
2	CB	256	41% 46% 33% 11% 10%
3	AC	239	13% 58% 24% 14%
3	CC	239	40% 52% 28% 6% 14%
4	AD	209	19% 70% 25%
4	CD	209	8% 67% 30%
5	AE	162	10% 56% 31% 9%
5	CE	162	17% 57% 31% 9%
6	AF	101	72% 24%
6	CF	101	2% 75% 22%
7	AG	156	12% 73% 22%
7	CG	156	17% 65% 26% 7%
8	AH	138	8% 68% 28%
8	CH	138	18% 62% 30% 8%
9	AI	128	30% 57% 36% 6%
9	CI	128	54% 55% 38% 7%
10	AJ	105	30% 52% 36% 8%
10	CJ	105	58% 50% 39% 9%
11	AK	129	9% 72% 14% 12%
11	CK	129	10% 72% 15% 12%
12	AL	132	7% 73% 15% 8%
12	CL	132	8% 64% 23% 5% 8%
13	AM	126	13% 63% 28% 7%
13	CM	126	34% 55% 36% 6%
14	AN	61	20% 48% 41% 10%

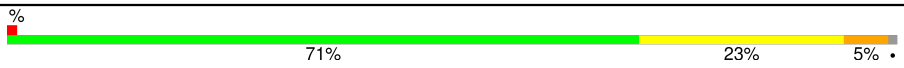
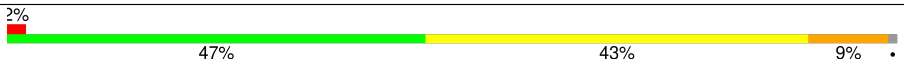
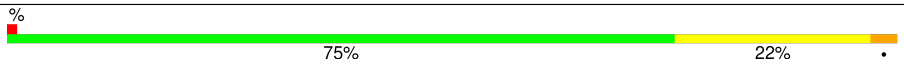
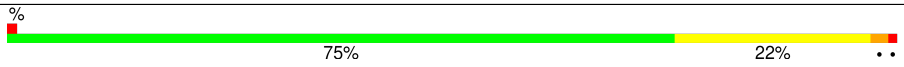
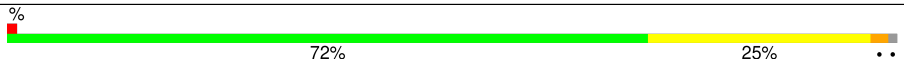
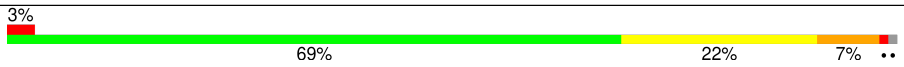
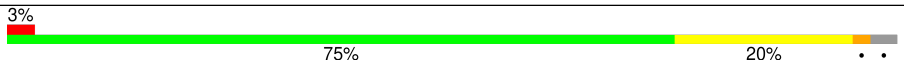
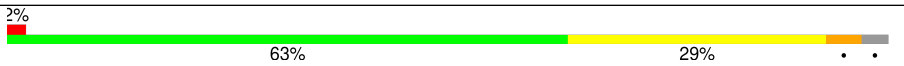
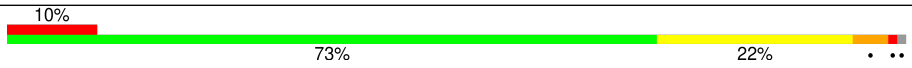
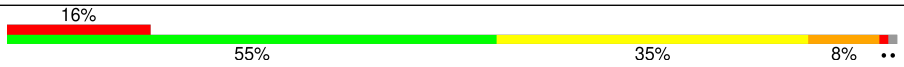
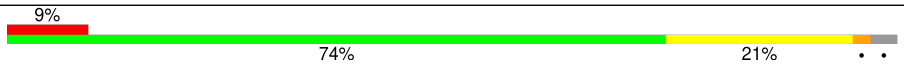
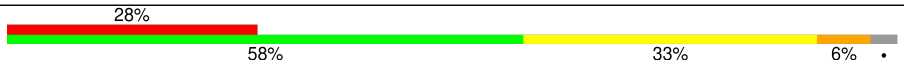
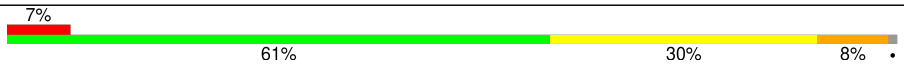
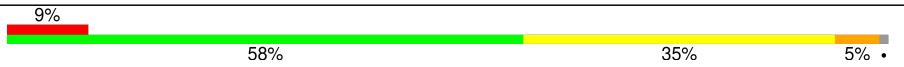
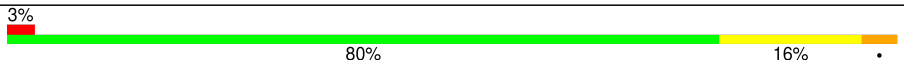
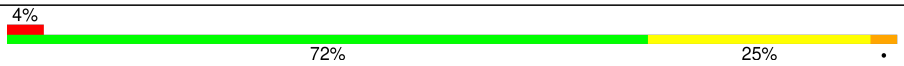
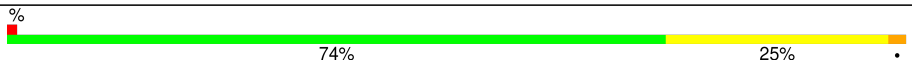
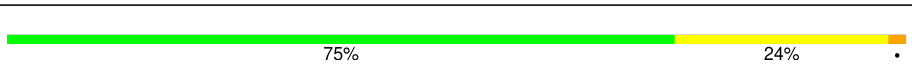
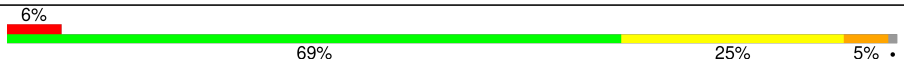
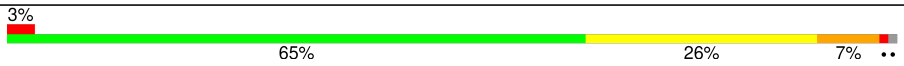
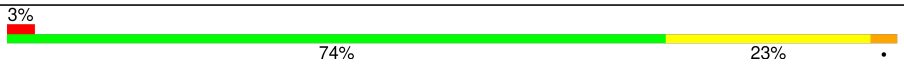
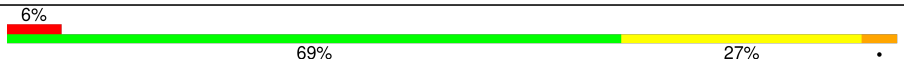
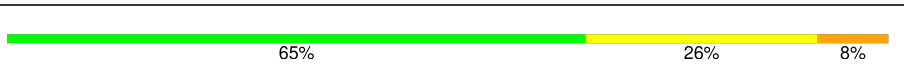
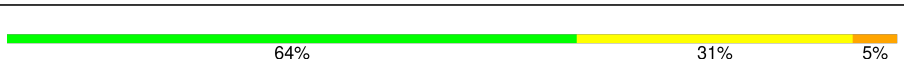
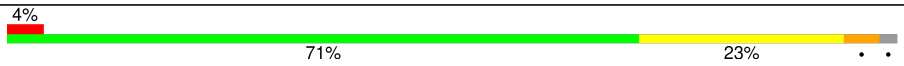
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Mol	Chain	Length	Quality of chain
14	CN	61	66% 62% 28% 8%
15	AO	89	7% 62% 34%
15	CO	89	9% 63% 33%
16	AP	88	17% 57% 31% 6% 7%
16	CP	88	16% 59% 32% 7%
17	AQ	105	7% 67% 21% 7% 6%
17	CQ	105	10% 69% 24% 6%
18	AR	88	3% 50% 22% 6% 23%
18	CR	88	8% 49% 25% 23%
19	AS	93	16% 61% 22% 6% 11%
19	CS	93	40% 56% 25% 9% 11%
20	AT	106	12% 58% 27% 5% 9%
20	CT	106	17% 59% 25% 6% 9%
21	AU	27	30% 52% 33% 15%
21	CU	27	30% 56% 26% 15%
22	AV	24	4% 46% 46%
22	CV	24	12% 33% 17% 46%
23	AW	76	16% 28% 53% 16%
23	AY	76	26% 26% 34% 36%
23	CW	76	18% 28% 38% 26% 5%
23	CY	76	22% 28% 33% 32%
24	AX	77	5% 62% 25% 12%
24	CX	77	56% 27% 16%
25	BA	2915	6% 65% 27% 7%
25	DA	2915	4% 57% 31% 8%

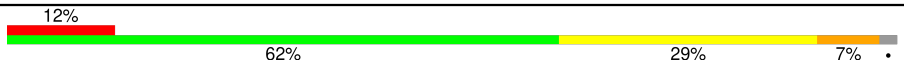
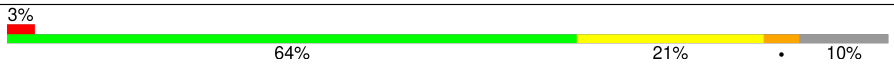
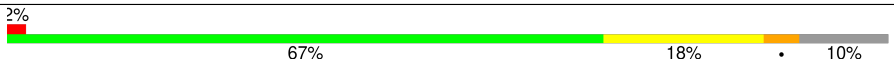
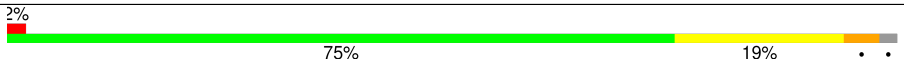
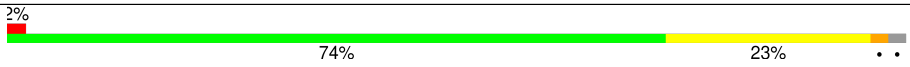
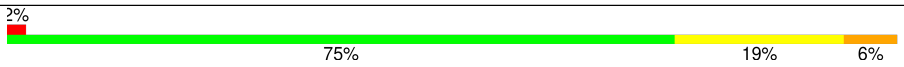
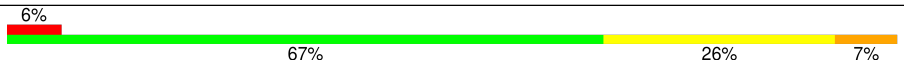
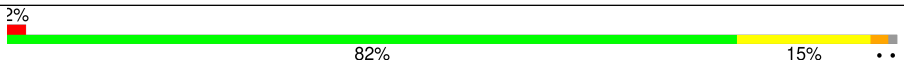
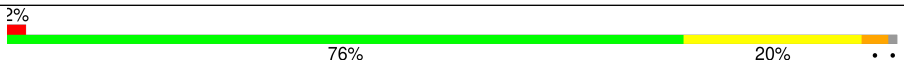
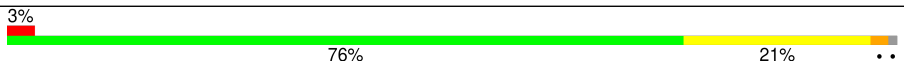
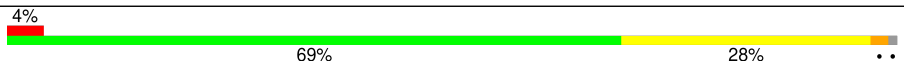
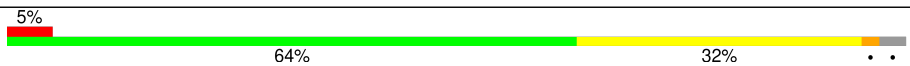
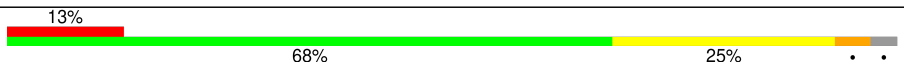
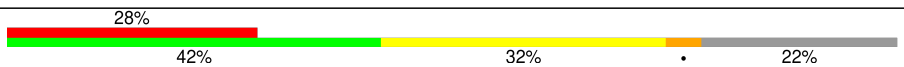
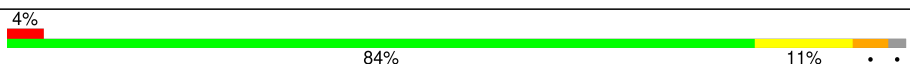
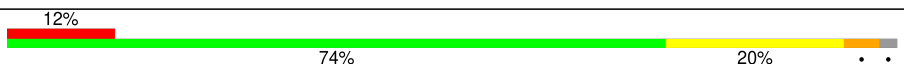
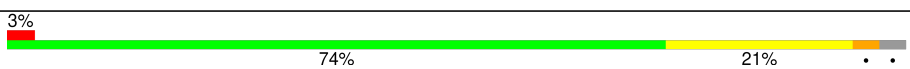
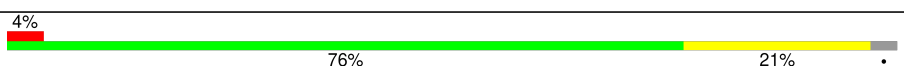
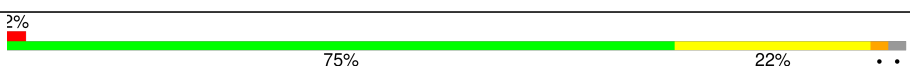
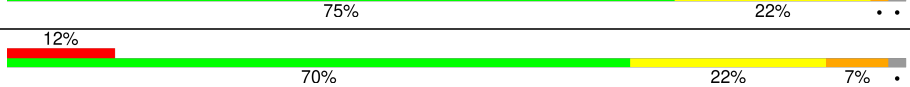
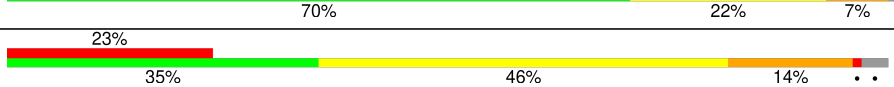
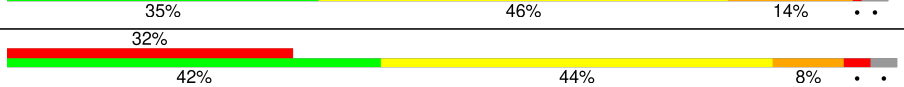
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Mol	Chain	Length	Quality of chain
26	BB	121	
26	DB	121	
27	BD	276	
27	DD	276	
28	BE	206	
28	DE	206	
29	BF	210	
29	DF	210	
30	BG	182	
30	DG	182	
31	BH	180	
31	DH	180	
32	BI	148	
32	DI	148	
33	BN	140	
33	DN	140	
34	BO	122	
34	DO	122	
35	BP	150	
35	DP	150	
36	BQ	141	
36	DQ	141	
37	BR	118	
37	DR	118	
38	BS	112	

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Mol	Chain	Length	Quality of chain
38	DS	112	
39	BT	146	
39	DT	146	
40	BU	118	
40	DU	118	
41	BV	101	
41	DV	101	
42	BW	113	
42	DW	113	
43	BX	96	
43	DX	96	
44	BY	110	
44	DY	110	
45	BZ	206	
45	DZ	206	
46	B0	85	
46	D0	85	
47	B1	98	
47	D1	98	
48	B2	72	
48	D2	72	
49	B3	60	
49	D3	60	
50	B4	71	
50	D4	71	

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Mol	Chain	Length	Quality of chain
51	B5	60	2% 85% 10%
51	D5	60	73% 22%
52	B6	54	65% 30%
52	D6	54	4% 70% 24%
53	B7	49	6% 63% 31%
53	D7	49	4% 73% 16% 6%
54	B8	65	57% 35% 6%
54	D8	65	3% 62% 32% 5%
55	B9	37	84% 14%
55	D9	37	11% 70% 27%

2 Entry composition (i)

There are 61 unique types of molecules in this entry. The entry contains 298643 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	1497	Total	C	N	O	P	0	0	0
			32185	14324	5967	10397	1497			
1	CA	1503	Total	C	N	O	P	0	0	0
			32312	14381	5990	10438	1503			

- Molecule 2 is a protein called 30S Ribosomal Protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AB	231	Total	C	N	O	S	0	0	0
			1846	1179	331	331	5			
2	CB	231	Total	C	N	O	S	0	0	0
			1825	1167	326	327	5			

- Molecule 3 is a protein called 30S Ribosomal Protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AC	206	Total	C	N	O	S	0	0	0
			1548	973	301	273	1			
3	CC	206	Total	C	N	O	S	0	0	0
			1542	968	300	273	1			

- Molecule 4 is a protein called 30S Ribosomal Protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	AD	208	Total	C	N	O	S	0	0	0
			1655	1038	326	284	7			
4	CD	208	Total	C	N	O	S	0	0	0
			1674	1050	333	284	7			

- Molecule 5 is a protein called 30S Ribosomal Protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	AE	148	Total	C	N	O	S	0	0	0
			1129	714	213	198	4			
5	CE	148	Total	C	N	O	S	0	0	0
			1133	716	214	199	4			

- Molecule 6 is a protein called 30S Ribosomal Protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AF	100	Total	C	N	O	S	0	0	0
			810	514	144	149	3			
6	CF	100	Total	C	N	O	S	0	0	0
			816	516	146	151	3			

- Molecule 7 is a protein called 30S Ribosomal Protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	AG	155	Total	C	N	O	S	0	0	0
			1231	766	243	216	6			
7	CG	155	Total	C	N	O	S	0	0	0
			1235	769	244	216	6			

- Molecule 8 is a protein called 30S Ribosomal Protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	AH	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			
8	CH	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			

- Molecule 9 is a protein called 30S Ribosomal Protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	AI	127	Total	C	N	O	0	0	0
			983	623	193	167			
9	CI	127	Total	C	N	O	0	0	0
			978	619	190	169			

- Molecule 10 is a protein called 30S Ribosomal Protein S10.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	AJ	97	Total	C	N	O	0	0	0
			709	440	138	131			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	CJ	96	Total 714	C 445	N 138	O 131	0	0	0

- Molecule 11 is a protein called 30S Ribosomal Protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	AK	114	Total 829	C 516	N 155	O 155	S 3	0	0	0
11	CK	114	Total 833	C 519	N 156	O 155	S 3	0	0	0

- Molecule 12 is a protein called 30S Ribosomal Protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	AL	122	Total 930	C 585	N 185	O 159	S 1	0	0	0
12	CL	122	Total 930	C 585	N 185	O 159	S 1	0	0	0

- Molecule 13 is a protein called 30S Ribosomal Protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	AM	123	Total 958	C 592	N 198	O 166	S 2	0	0	0
13	CM	122	Total 950	C 586	N 197	O 165	S 2	0	0	0

- Molecule 14 is a protein called 30S Ribosomal Protein S14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	AN	60	Total 492	C 312	N 104	O 72	S 4	0	0	0
14	CN	60	Total 492	C 312	N 104	O 72	S 4	0	0	0

- Molecule 15 is a protein called 30S Ribosomal Protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	AO	88	Total 728	C 456	N 144	O 126	S 2	0	0	0
15	CO	88	Total 728	C 456	N 144	O 126	S 2	0	0	0

- Molecule 16 is a protein called 30S Ribosomal Protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	AP	82	Total	C	N	O	S	0	0	0
			681	433	134	113	1			
16	CP	82	Total	C	N	O	S	0	0	0
			677	430	133	113	1			

- Molecule 17 is a protein called 30S Ribosomal Protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AQ	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			
17	CQ	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

- Molecule 18 is a protein called 30S Ribosomal Protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	AR	68	Total	C	N	O	0	0	0
			555	355	108	92			
18	CR	68	Total	C	N	O	0	0	0
			555	355	108	92			

- Molecule 19 is a protein called 30S Ribosomal Protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AS	83	Total	C	N	O	S	0	0	0
			652	417	120	113	2			
19	CS	83	Total	C	N	O	S	0	0	0
			646	412	119	113	2			

- Molecule 20 is a protein called 30S Ribosomal Protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	AT	96	Total	C	N	O	S	0	0	0
			728	446	156	124	2			
20	CT	96	Total	C	N	O	S	0	0	0
			727	446	155	124	2			

- Molecule 21 is a protein called 30S Ribosomal Protein THX.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	AU	23	Total	C	N	O	0	0	0
			199	122	48	29			
21	CU	23	Total	C	N	O	0	0	0
			199	122	48	29			

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	AV	13	Total	C	N	O	P	0	0	0
			277	125	51	88	13			
22	CV	13	Total	C	N	O	P	0	0	0
			277	125	51	88	13			

- Molecule 23 is a RNA chain called A/P-site tRNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
23	AW	74	Total	C	N	O	P	S	0	0	0
			1592	713	285	518	74	2			
23	AY	74	Total	C	N	O	P	S	0	0	0
			1585	707	285	518	74	1			
23	CW	72	Total	C	N	O	P	S	0	0	0
			1544	690	278	502	72	2			
23	CY	73	Total	C	N	O	P	S	0	0	0
			1565	698	283	510	73	1			

- Molecule 24 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
24	AX	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			
24	CX	76	Total	C	N	O	P	S	0	0	0
			1625	725	294	529	76	1			

- Molecule 25 is a RNA chain called 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	BA	2871	Total	C	N	O	P	0	0	0
			61844	27523	11572	19878	2871			
25	DA	2800	Total	C	N	O	P	0	0	0
			60314	26840	11284	19390	2800			

- Molecule 26 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	BB	120	Total	C	N	O	P	0	0	0
			2577	1146	476	835	120			
26	DB	120	Total	C	N	O	P	0	0	0
			2575	1146	476	833	120			

- Molecule 27 is a protein called 50S Ribosomal Protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	BD	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			
27	DD	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			

- Molecule 28 is a protein called 50S Ribosomal Protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	BE	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			
28	DE	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			

- Molecule 29 is a protein called 50S Ribosomal Protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	BF	203	Total	C	N	O	S	0	0	1
			1584	1009	298	275	2			
29	DF	203	Total	C	N	O	S	0	0	1
			1580	1007	297	274	2			

- Molecule 30 is a protein called 50S Ribosomal Protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	BG	181	Total	C	N	O	S	0	0	0
			1429	916	256	253	4			
30	DG	181	Total	C	N	O	S	0	0	0
			1428	913	258	253	4			

- Molecule 31 is a protein called 50S Ribosomal Protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	BH	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	DH	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			

- Molecule 32 is a protein called 50S Ribosomal Protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	BI	146	Total	C	N	O	S	0	0	0
			1097	701	191	204	1			
32	DI	146	Total	C	N	O	S	0	0	0
			1064	681	186	196	1			

- Molecule 33 is a protein called 50S Ribosomal Protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	BN	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			
33	DN	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			

- Molecule 34 is a protein called 50S Ribosomal Protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	BO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			
34	DO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

- Molecule 35 is a protein called 50S Ribosomal Protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	BP	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			
35	DP	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			

- Molecule 36 is a protein called 50S Ribosomal Protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	BQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			
36	DQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

- Molecule 37 is a protein called 50S Ribosomal Protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	BR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			
37	DR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			

- Molecule 38 is a protein called 50S Ribosomal Protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
38	BS	110	Total	C	N	O	0	0	0
			873	550	174	149			
38	DS	110	Total	C	N	O	0	0	0
			870	549	173	148			

- Molecule 39 is a protein called 50S Ribosomal Protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	BT	131	Total	C	N	O	S	0	0	0
			1091	680	225	185	1			
39	DT	131	Total	C	N	O	S	0	0	0
			1083	675	224	183	1			

- Molecule 40 is a protein called 50S Ribosomal Protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	BU	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			
40	DU	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			

- Molecule 41 is a protein called 50S Ribosomal Protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	BV	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			
41	DV	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			

- Molecule 42 is a protein called 50S Ribosomal Protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	BW	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			
42	DW	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			

- Molecule 43 is a protein called 50S Ribosomal Protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	BX	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			
43	DX	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			

- Molecule 44 is a protein called 50S Ribosomal Protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	BY	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			
44	DY	107	Total	C	N	O	S	0	0	0
			806	517	152	131	6			

- Molecule 45 is a protein called 50S Ribosomal Protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	BZ	154	Total	C	N	O	S	0	0	0
			1240	795	222	220	3			
45	DZ	160	Total	C	N	O	S	0	0	0
			1271	814	228	227	2			

- Molecule 46 is a protein called 50S Ribosomal Protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	B0	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			
46	D0	83	Total	C	N	O	S	0	0	0
			653	404	139	109	1			

- Molecule 47 is a protein called 50S Ribosomal Protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	B1	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	D1	97	Total	C	N	O	S	0	0	0
			755	475	148	131	1			

- Molecule 48 is a protein called 50S Ribosomal Protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	B2	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			
48	D2	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			

- Molecule 49 is a protein called 50S Ribosomal Protein L30.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
49	B3	59	Total	C	N	O	0	0	0
			469	298	90	81			
49	D3	59	Total	C	N	O	0	0	0
			464	296	90	78			

- Molecule 50 is a protein called 50S Ribosomal Protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	B4	69	Total	C	N	O	S	0	0	0
			552	349	99	99	5			
50	D4	69	Total	C	N	O	S	0	0	0
			532	339	97	91	5			

- Molecule 51 is a protein called 50S Ribosomal Protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	B5	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			
51	D5	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			

- Molecule 52 is a protein called 50S Ribosomal Protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	B6	53	Total	C	N	O	S	0	0	0
			453	281	91	77	4			
52	D6	53	Total	C	N	O	S	0	0	0
			449	279	91	75	4			

- Molecule 53 is a protein called 50S Ribosomal Protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	B7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			
53	D7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

- Molecule 54 is a protein called 50S Ribosomal Protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	B8	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			
54	D8	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

- Molecule 55 is a protein called 50S Ribosomal Protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	B9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			
55	D9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
56	AA	233	Total	Mg	0	0
			233	233		
56	AB	2	Total	Mg	0	0
			2	2		
56	AD	1	Total	Mg	0	0
			1	1		
56	AE	2	Total	Mg	0	0
			2	2		
56	AF	1	Total	Mg	0	0
			1	1		
56	AH	1	Total	Mg	0	0
			1	1		
56	AK	1	Total	Mg	0	0
			1	1		
56	AL	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	AM	1	Total Mg 1 1	0	0
56	AN	1	Total Mg 1 1	0	0
56	AR	1	Total Mg 1 1	0	0
56	AT	1	Total Mg 1 1	0	0
56	AW	4	Total Mg 4 4	0	0
56	AX	13	Total Mg 13 13	0	0
56	AY	2	Total Mg 2 2	0	0
56	BA	906	Total Mg 906 906	0	0
56	BB	30	Total Mg 30 30	0	0
56	BD	13	Total Mg 13 13	0	0
56	BE	12	Total Mg 12 12	0	0
56	BF	15	Total Mg 15 15	0	0
56	BG	6	Total Mg 6 6	0	0
56	BH	1	Total Mg 1 1	0	0
56	BI	1	Total Mg 1 1	0	0
56	BN	4	Total Mg 4 4	0	0
56	BO	5	Total Mg 5 5	0	0
56	BP	6	Total Mg 6 6	0	0
56	BQ	7	Total Mg 7 7	0	0
56	BR	3	Total Mg 3 3	0	0
56	BS	3	Total Mg 3 3	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	BT	2	Total Mg 2 2	0	0
56	BU	10	Total Mg 10 10	0	0
56	BV	5	Total Mg 5 5	0	0
56	BW	5	Total Mg 5 5	0	0
56	BX	6	Total Mg 6 6	0	0
56	BY	3	Total Mg 3 3	0	0
56	BZ	3	Total Mg 3 3	0	0
56	B0	7	Total Mg 7 7	0	0
56	B1	2	Total Mg 2 2	0	0
56	B2	2	Total Mg 2 2	0	0
56	B3	2	Total Mg 2 2	0	0
56	B4	1	Total Mg 1 1	0	0
56	B5	4	Total Mg 4 4	0	0
56	B6	2	Total Mg 2 2	0	0
56	B7	3	Total Mg 3 3	0	0
56	B8	3	Total Mg 3 3	0	0
56	B9	1	Total Mg 1 1	0	0
56	CA	201	Total Mg 201 201	0	0
56	CD	2	Total Mg 2 2	0	0
56	CE	1	Total Mg 1 1	0	0
56	CF	2	Total Mg 2 2	0	0

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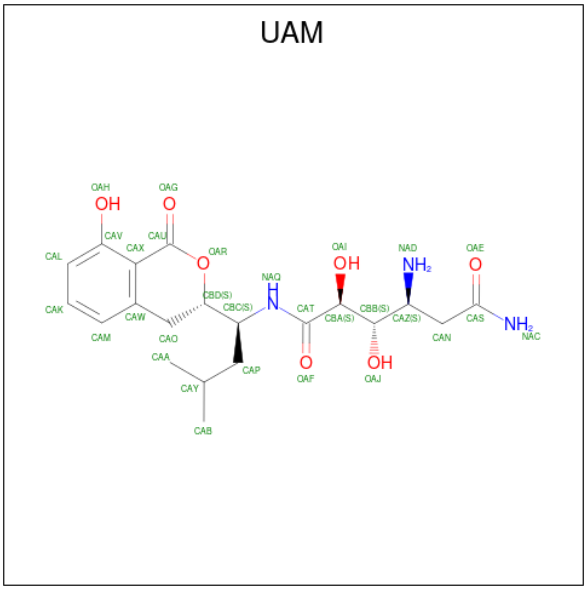
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	CG	1	Total Mg 1 1	0	0
56	CJ	2	Total Mg 2 2	0	0
56	CK	1	Total Mg 1 1	0	0
56	CL	2	Total Mg 2 2	0	0
56	CP	1	Total Mg 1 1	0	0
56	CQ	2	Total Mg 2 2	0	0
56	CR	1	Total Mg 1 1	0	0
56	CT	1	Total Mg 1 1	0	0
56	CV	1	Total Mg 1 1	0	0
56	CW	4	Total Mg 4 4	0	0
56	CX	6	Total Mg 6 6	0	0
56	DA	673	Total Mg 673 673	0	0
56	DB	21	Total Mg 21 21	0	0
56	DD	6	Total Mg 6 6	0	0
56	DE	7	Total Mg 7 7	0	0
56	DF	7	Total Mg 7 7	0	0
56	DG	1	Total Mg 1 1	0	0
56	DO	1	Total Mg 1 1	0	0
56	DP	1	Total Mg 1 1	0	0
56	DQ	3	Total Mg 3 3	0	0
56	DR	1	Total Mg 1 1	0	0

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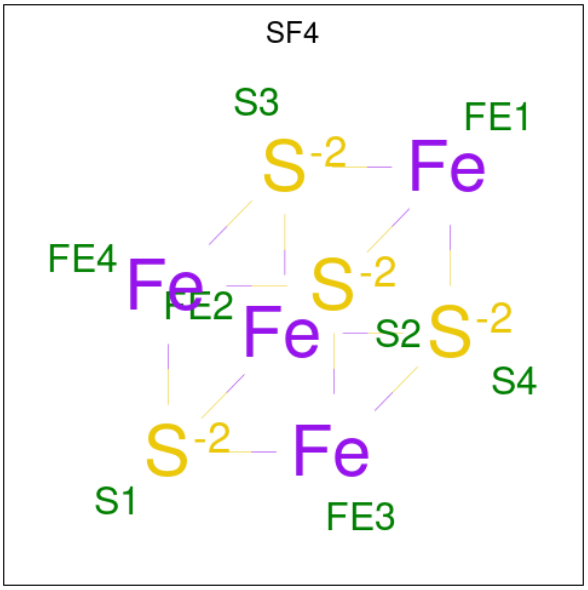
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
56	DT	1	Total Mg 1 1	0	0
56	DU	4	Total Mg 4 4	0	0
56	DV	2	Total Mg 2 2	0	0
56	DW	3	Total Mg 3 3	0	0
56	DX	1	Total Mg 1 1	0	0
56	DY	1	Total Mg 1 1	0	0
56	DZ	1	Total Mg 1 1	0	0
56	D0	1	Total Mg 1 1	0	0
56	D1	1	Total Mg 1 1	0	0
56	D3	1	Total Mg 1 1	0	0
56	D5	2	Total Mg 2 2	0	0
56	D8	2	Total Mg 2 2	0	0

- Molecule 57 is Amicoumacin A (CCD ID: UAM) (formula: $C_{20}H_{29}N_3O_7$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	AA	1	Total C N O 30 20 3 7	0	0
57	CA	1	Total C N O 30 20 3 7	0	0

- Molecule 58 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
58	AD	1	Total Fe S 8 4 4	0	0
58	CD	1	Total Fe S 8 4 4	0	0

- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	AN	1	Total Zn 1 1	0	0
59	BY	1	Total Zn 1 1	0	0
59	B4	1	Total Zn 1 1	0	0
59	B5	1	Total Zn 1 1	0	0
59	B6	1	Total Zn 1 1	0	0
59	B9	1	Total Zn 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
59	CN	1	Total Zn 1 1	0	0
59	DY	1	Total Zn 1 1	0	0
59	D4	1	Total Zn 1 1	0	0
59	D5	1	Total Zn 1 1	0	0
59	D6	1	Total Zn 1 1	0	0
59	D9	1	Total Zn 1 1	0	0

- Molecule 60 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
60	AX	1	Total K 1 1	0	0
60	CX	1	Total K 1 1	0	0

- Molecule 61 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	AA	264	Total O 264 264	0	0
61	AB	1	Total O 1 1	0	0
61	AE	2	Total O 2 2	0	0
61	AJ	1	Total O 1 1	0	0
61	AL	4	Total O 4 4	0	0
61	AM	1	Total O 1 1	0	0
61	AQ	1	Total O 1 1	0	0
61	AV	4	Total O 4 4	0	0
61	AW	2	Total O 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	AX	11	Total O 11 11	0	0
61	AY	1	Total O 1 1	0	0
61	BA	1486	Total O 1486 1486	0	0
61	BB	43	Total O 43 43	0	0
61	BD	19	Total O 19 19	0	0
61	BE	20	Total O 20 20	0	0
61	BF	14	Total O 14 14	0	0
61	BG	5	Total O 5 5	0	0
61	BH	1	Total O 1 1	0	0
61	BI	2	Total O 2 2	0	0
61	BN	2	Total O 2 2	0	0
61	BO	7	Total O 7 7	0	0
61	BP	19	Total O 19 19	0	0
61	BQ	5	Total O 5 5	0	0
61	BR	5	Total O 5 5	0	0
61	BS	5	Total O 5 5	0	0
61	BT	5	Total O 5 5	0	0
61	BU	8	Total O 8 8	0	0
61	BV	6	Total O 6 6	0	0
61	BW	1	Total O 1 1	0	0
61	BX	2	Total O 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	BY	3	Total O 3 3	0	0
61	BZ	1	Total O 1 1	0	0
61	B0	8	Total O 8 8	0	0
61	B1	3	Total O 3 3	0	0
61	B2	4	Total O 4 4	0	0
61	B3	3	Total O 3 3	0	0
61	B4	1	Total O 1 1	0	0
61	B5	4	Total O 4 4	0	0
61	B6	1	Total O 1 1	0	0
61	B7	4	Total O 4 4	0	0
61	B8	8	Total O 8 8	0	0
61	CA	204	Total O 204 204	0	0
61	CD	1	Total O 1 1	0	0
61	CG	1	Total O 1 1	0	0
61	CI	1	Total O 1 1	0	0
61	CJ	4	Total O 4 4	0	0
61	CL	4	Total O 4 4	0	0
61	CO	1	Total O 1 1	0	0
61	CP	1	Total O 1 1	0	0
61	CR	1	Total O 1 1	0	0
61	CT	1	Total O 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	CW	2	Total O 2 2	0	0
61	CX	6	Total O 6 6	0	0
61	DA	1039	Total O 1039 1039	0	0
61	DB	10	Total O 10 10	0	0
61	DD	17	Total O 17 17	0	0
61	DE	8	Total O 8 8	0	0
61	DF	6	Total O 6 6	0	0
61	DI	2	Total O 2 2	0	0
61	DN	1	Total O 1 1	0	0
61	DO	3	Total O 3 3	0	0
61	DP	12	Total O 12 12	0	0
61	DQ	1	Total O 1 1	0	0
61	DR	3	Total O 3 3	0	0
61	DT	3	Total O 3 3	0	0
61	DU	1	Total O 1 1	0	0
61	DV	1	Total O 1 1	0	0
61	DW	2	Total O 2 2	0	0
61	DX	2	Total O 2 2	0	0
61	DY	1	Total O 1 1	0	0
61	DZ	2	Total O 2 2	0	0
61	D0	4	Total O 4 4	0	0

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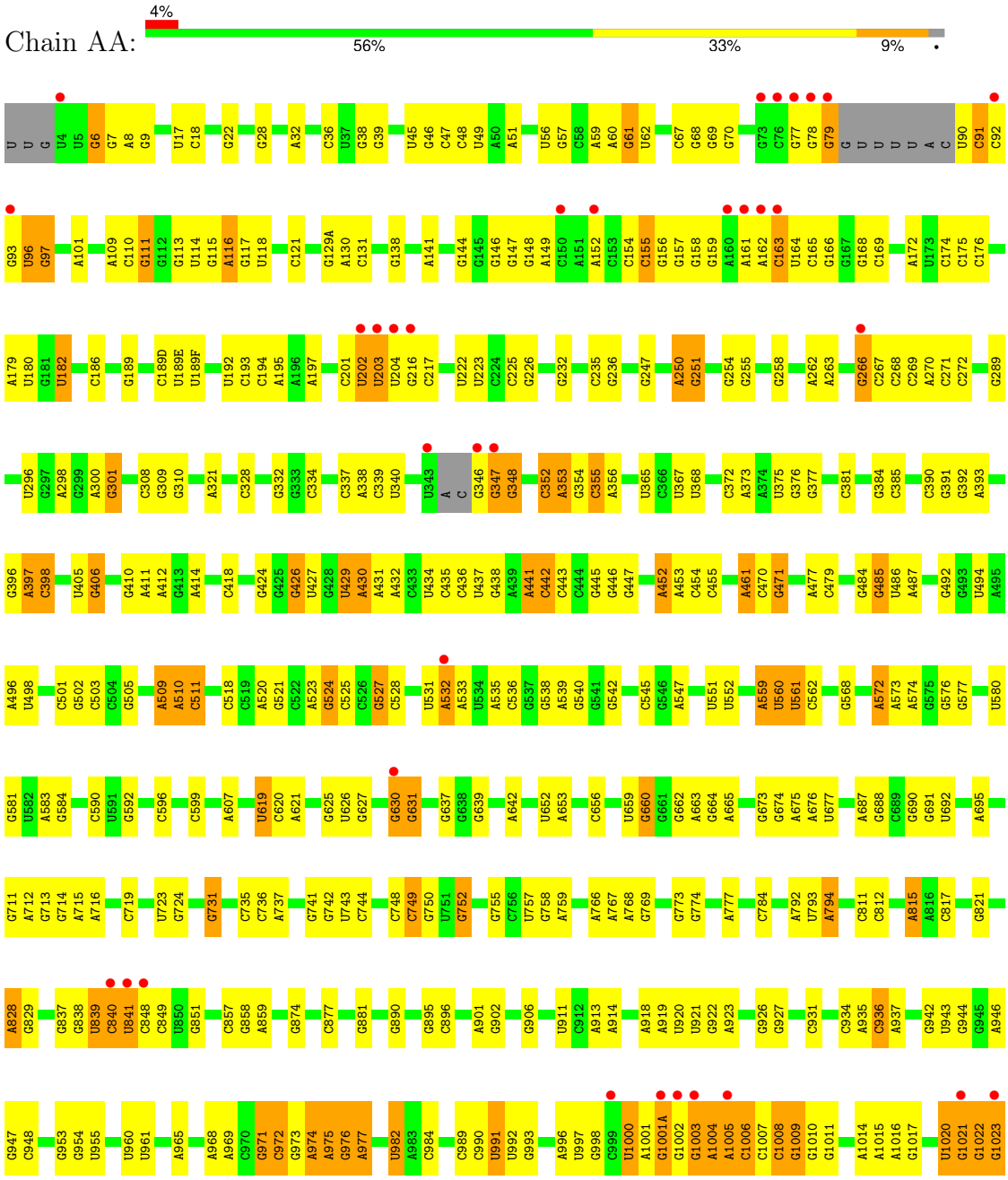
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
61	D1	4	Total O 4 4	0	0
61	D2	1	Total O 1 1	0	0
61	D3	1	Total O 1 1	0	0
61	D5	2	Total O 2 2	0	0
61	D7	5	Total O 5 5	0	0
61	D8	5	Total O 5 5	0	0
61	D9	1	Total O 1 1	0	0

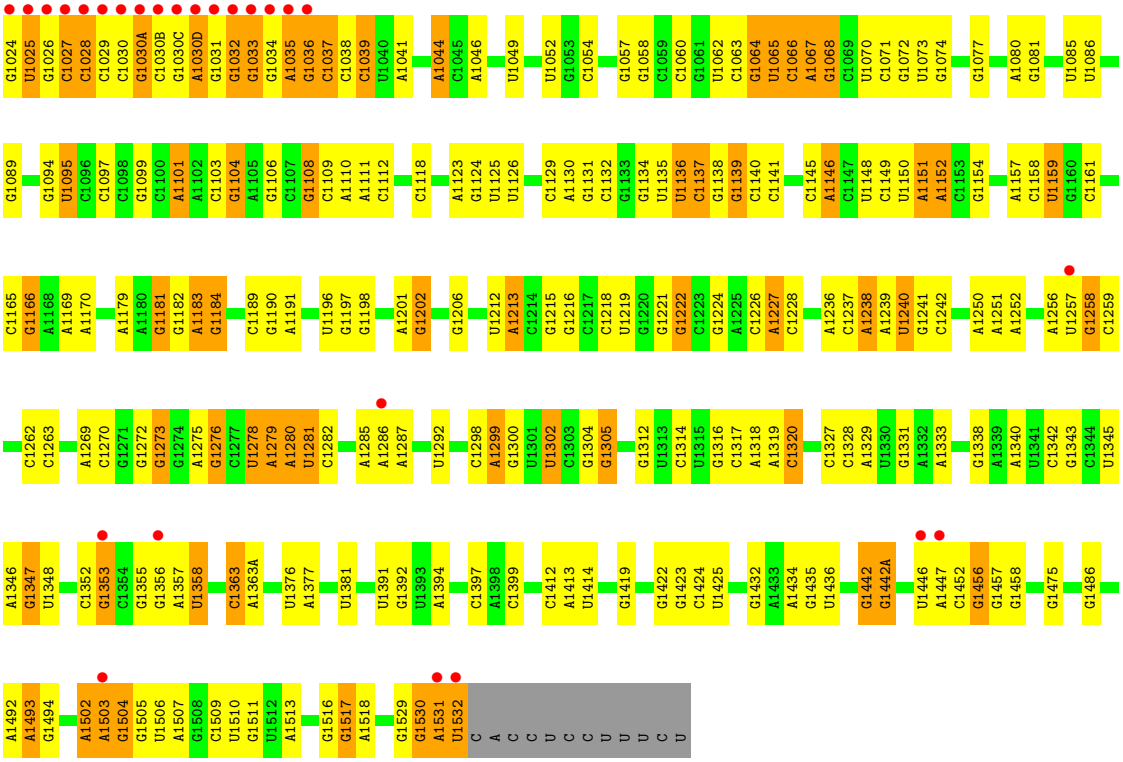
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 16S Ribosomal RNA

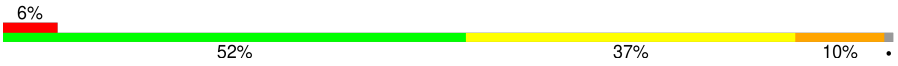
Chain AA:

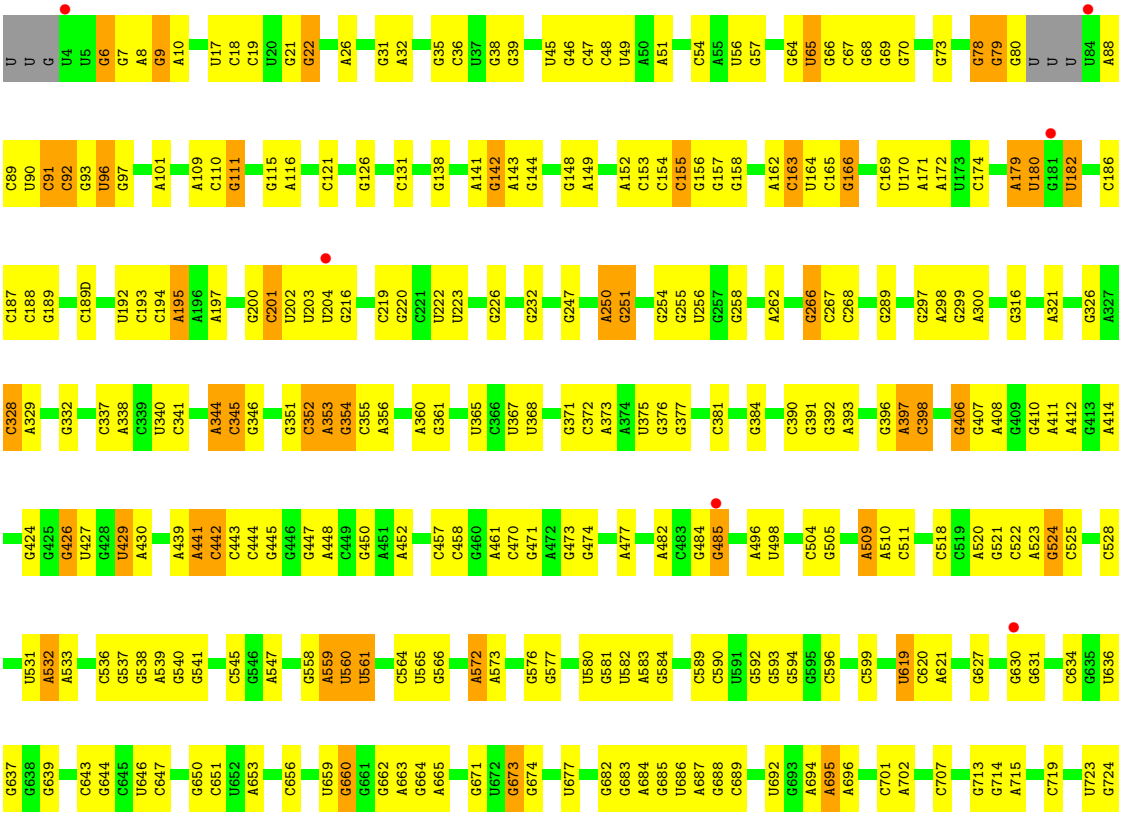


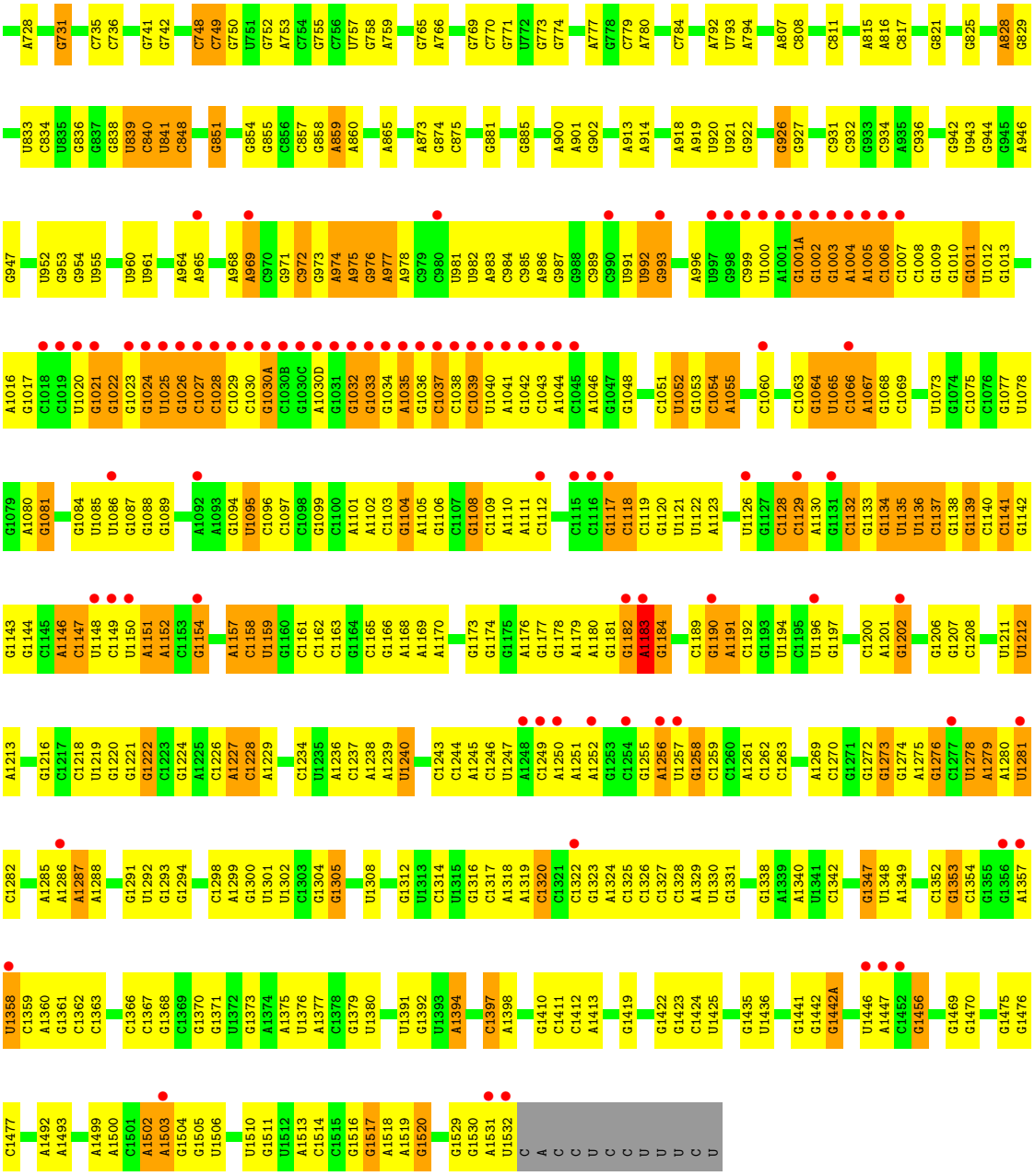


• Molecule 1: 16S Ribosomal RNA

Chain CA:



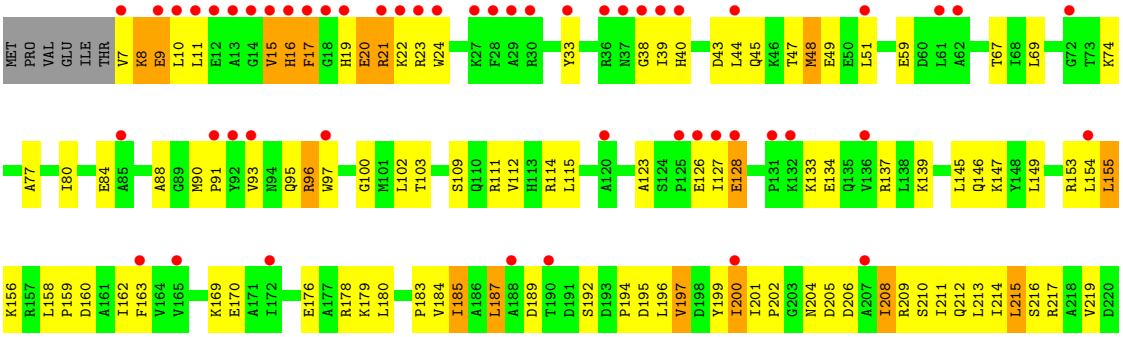


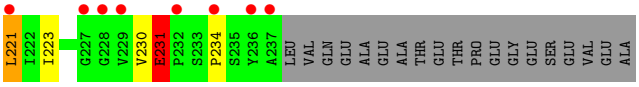


• Molecule 2: 30S Ribosomal Protein S2

Chain AB:



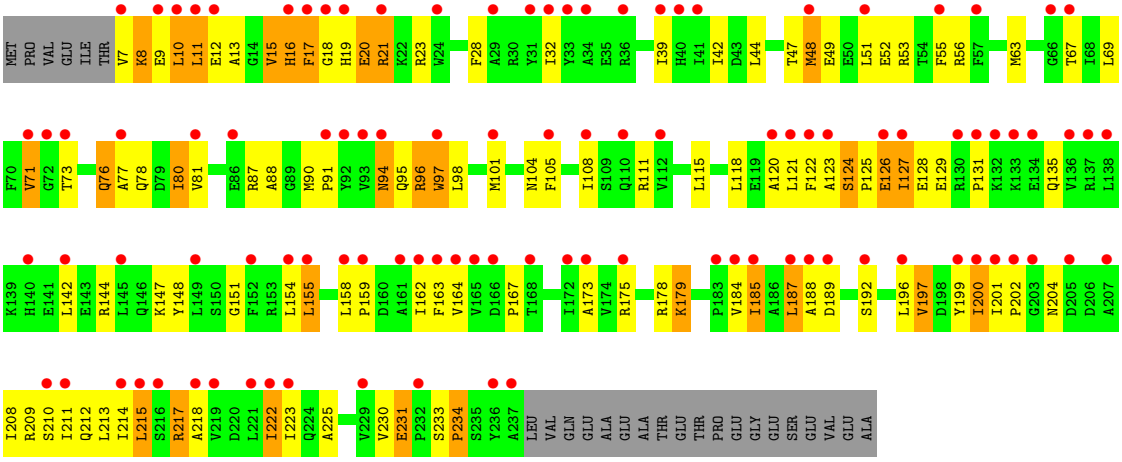




• Molecule 2: 30S Ribosomal Protein S2

Chain CB:

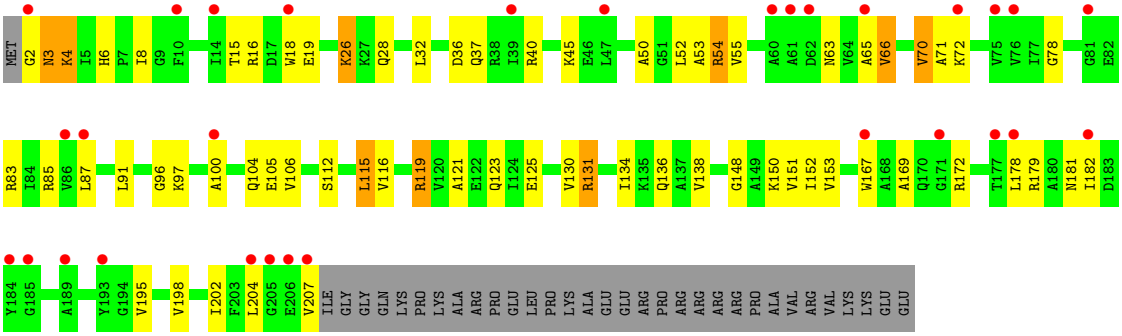




• Molecule 3: 30S Ribosomal Protein S3

Chain AC:

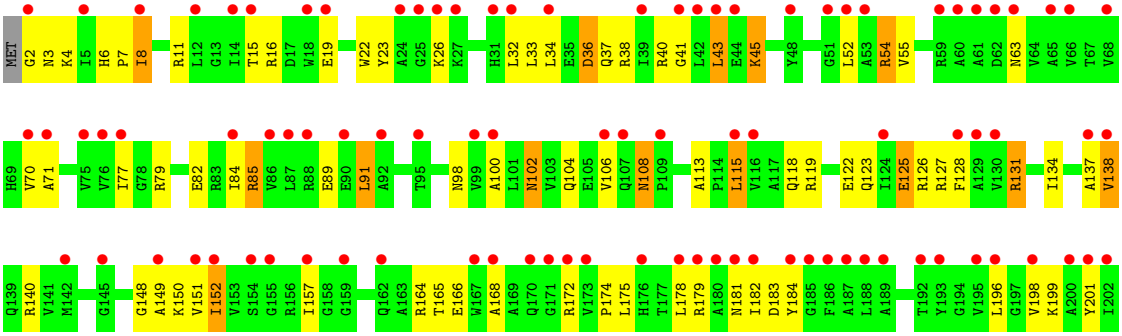


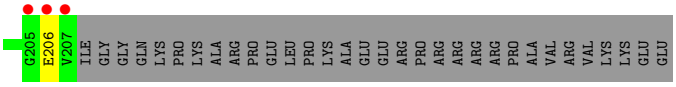


• Molecule 3: 30S Ribosomal Protein S3

Chain CC:



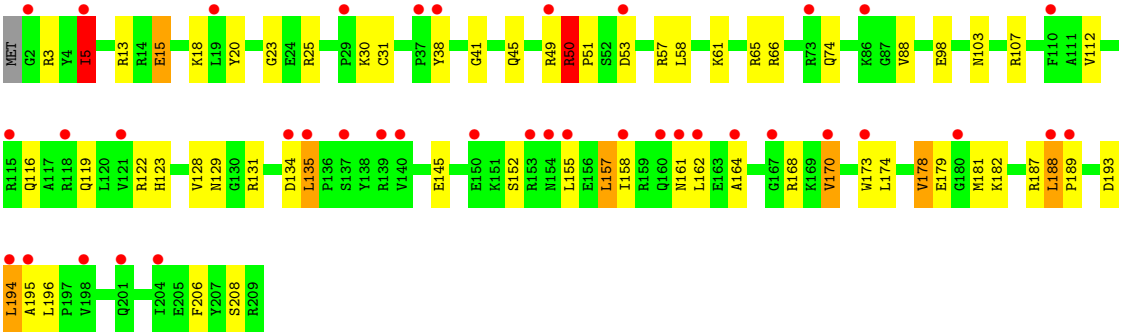




• Molecule 4: 30S Ribosomal Protein S4

Chain AD:

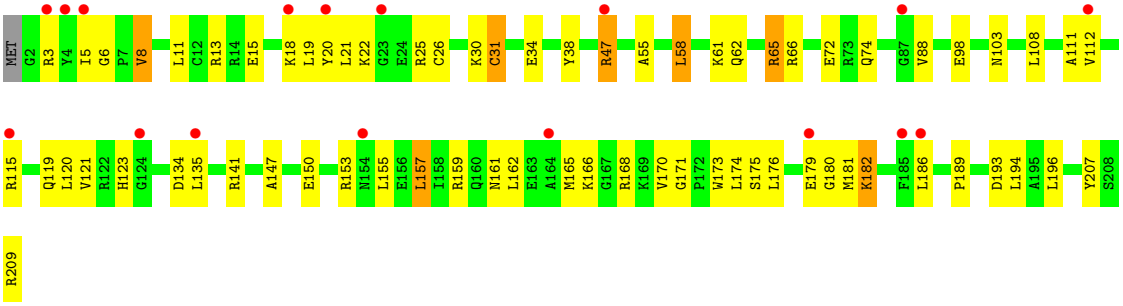




• Molecule 4: 30S Ribosomal Protein S4

Chain CD:

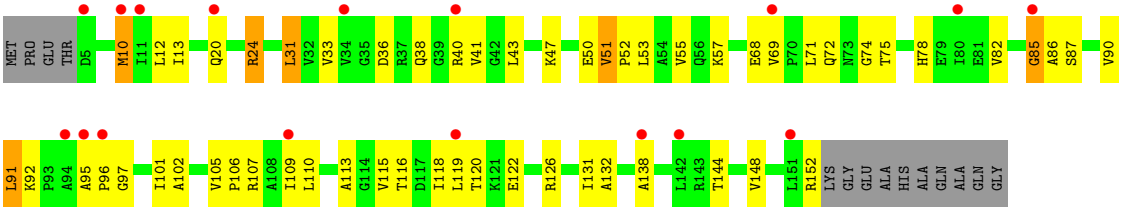




• Molecule 5: 30S Ribosomal Protein S5

Chain AE:

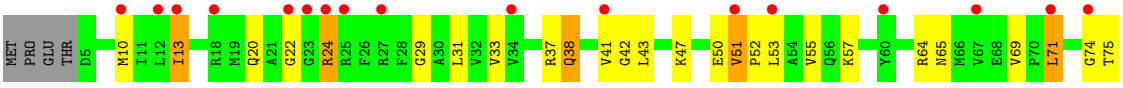


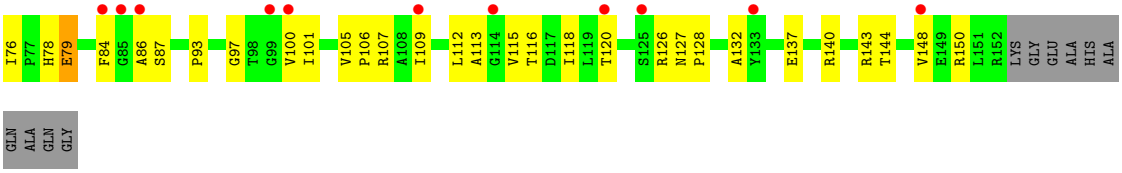


• Molecule 5: 30S Ribosomal Protein S5

Chain CE:





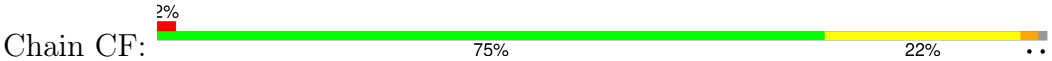


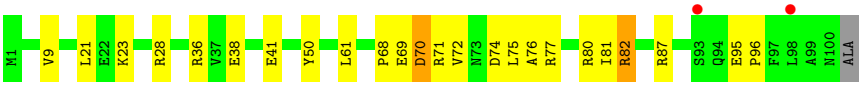
• Molecule 6: 30S Ribosomal Protein S6



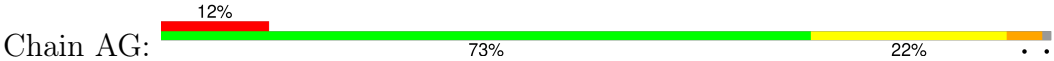


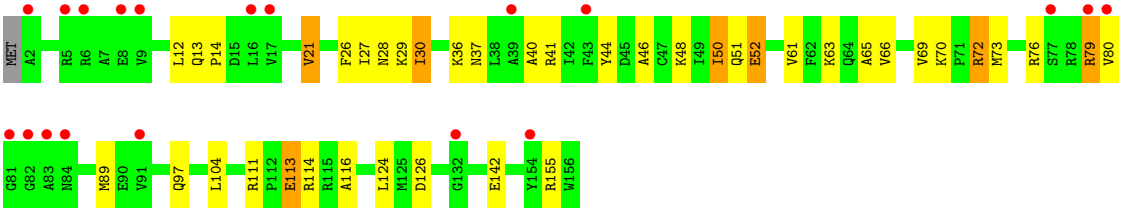
• Molecule 6: 30S Ribosomal Protein S6





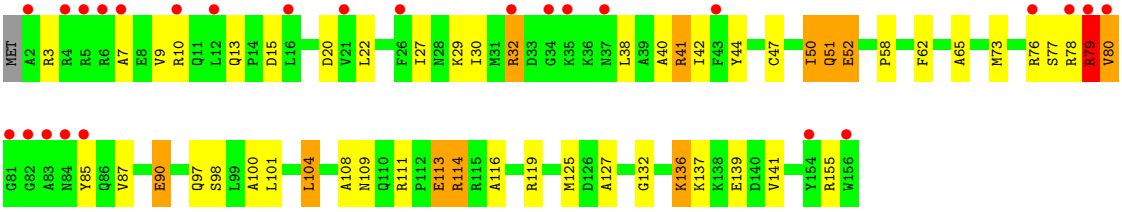
• Molecule 7: 30S Ribosomal Protein S7





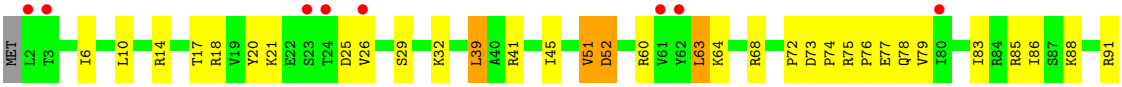
• Molecule 7: 30S Ribosomal Protein S7





• Molecule 8: 30S Ribosomal Protein S8



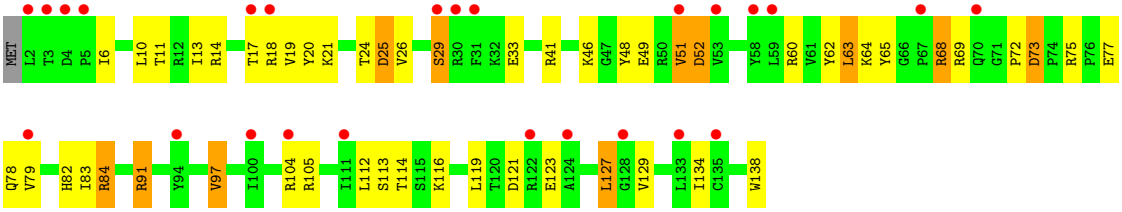




• Molecule 8: 30S Ribosomal Protein S8

Chain CH:

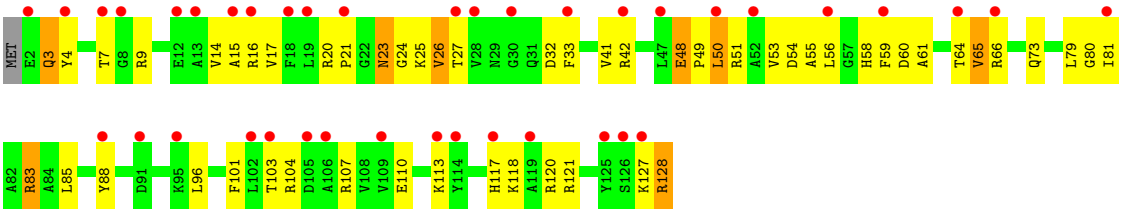




• Molecule 9: 30S Ribosomal Protein S9

Chain AI:

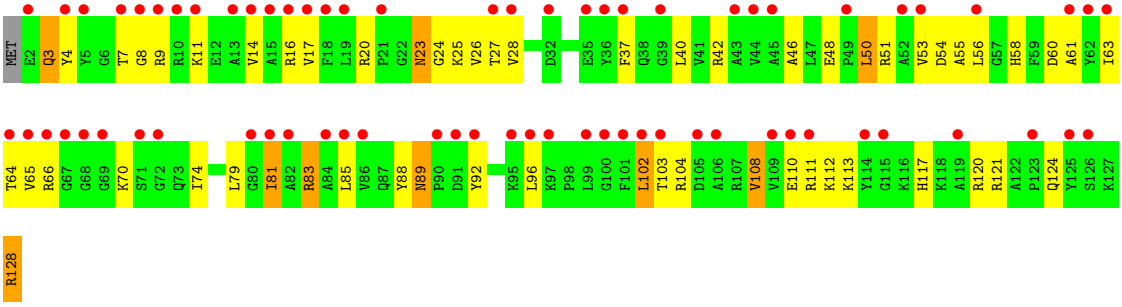




• Molecule 9: 30S Ribosomal Protein S9

Chain CI:

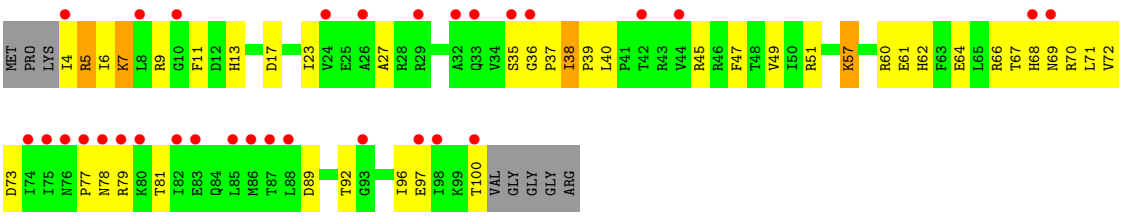




• Molecule 10: 30S Ribosomal Protein S10

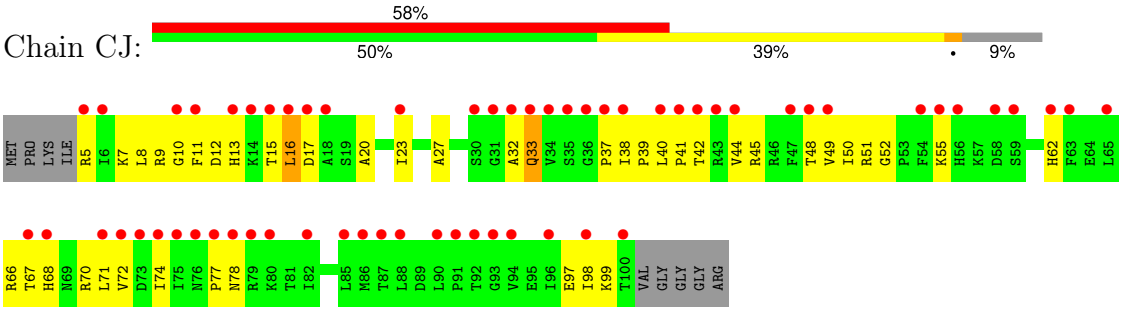
Chain AJ:





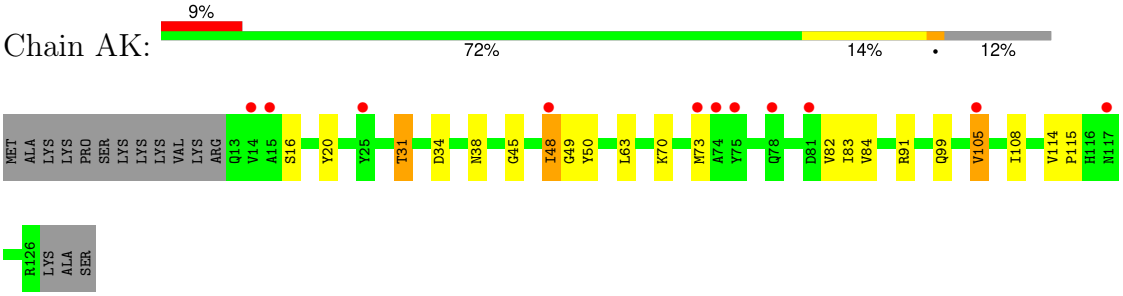
• Molecule 10: 30S Ribosomal Protein S10

Chain CJ:



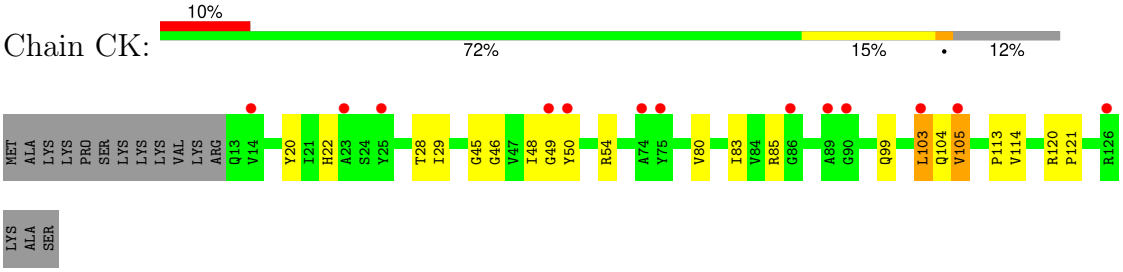
• Molecule 11: 30S Ribosomal Protein S11

Chain AK:



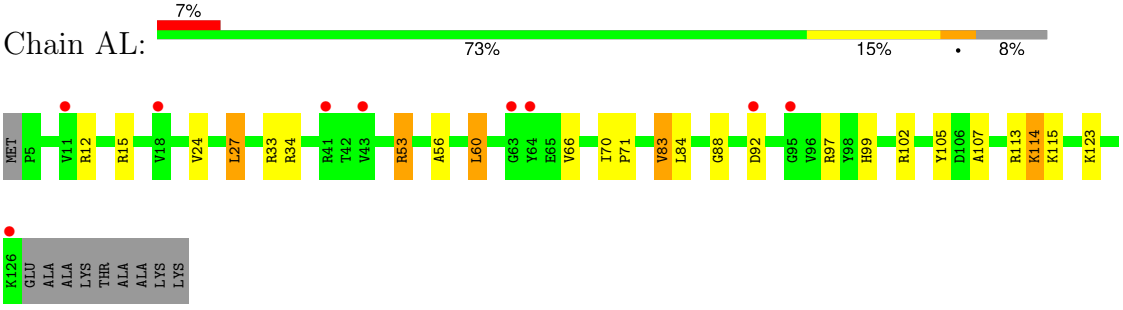
• Molecule 11: 30S Ribosomal Protein S11

Chain CK:



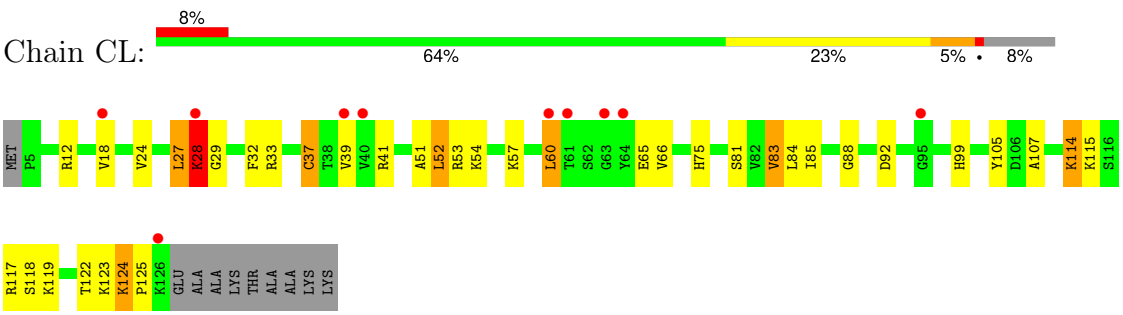
• Molecule 12: 30S Ribosomal Protein S12

Chain AL:



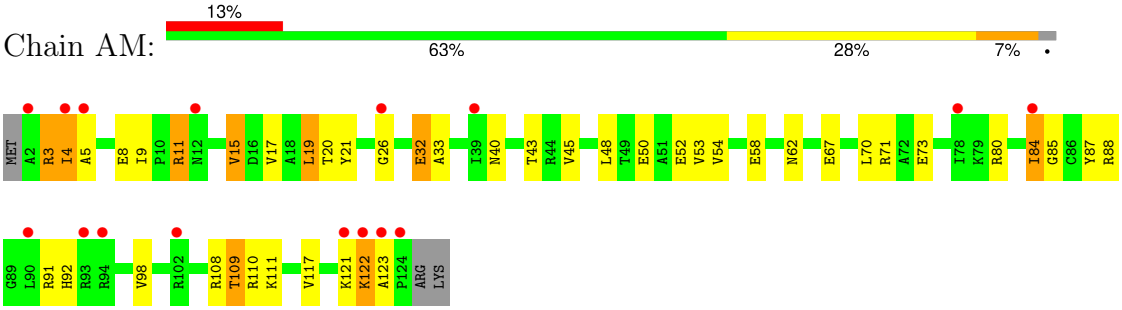
• Molecule 12: 30S Ribosomal Protein S12

Chain CL:



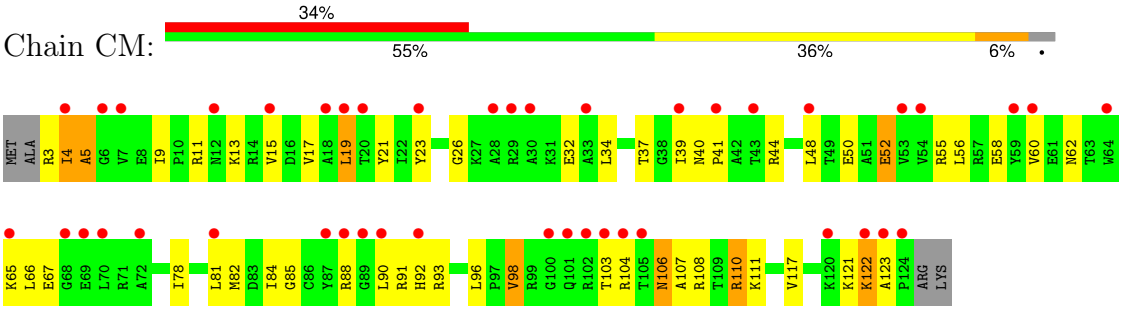
• Molecule 13: 30S Ribosomal Protein S13

Chain AM:



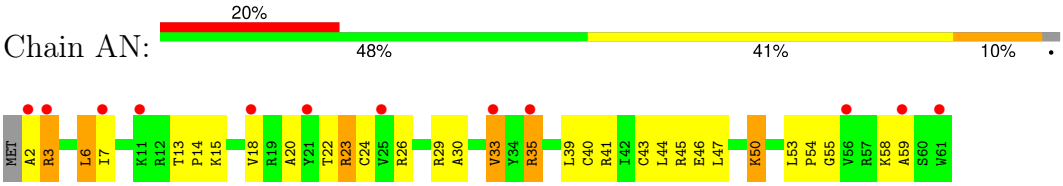
• Molecule 13: 30S Ribosomal Protein S13

Chain CM:



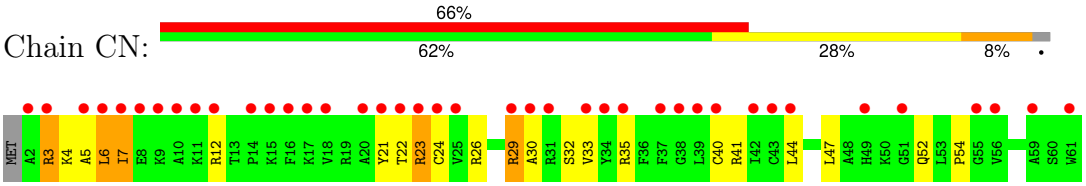
• Molecule 14: 30S Ribosomal Protein S14

Chain AN:



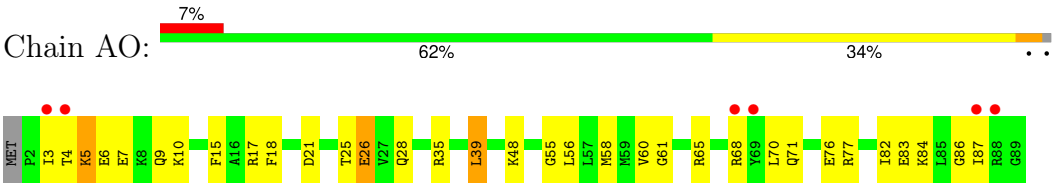
• Molecule 14: 30S Ribosomal Protein S14

Chain CN:



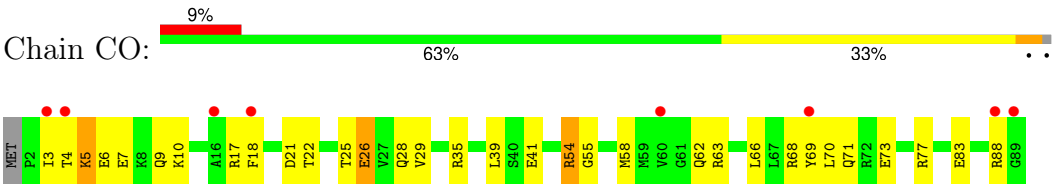
• Molecule 15: 30S Ribosomal Protein S15

Chain AO:



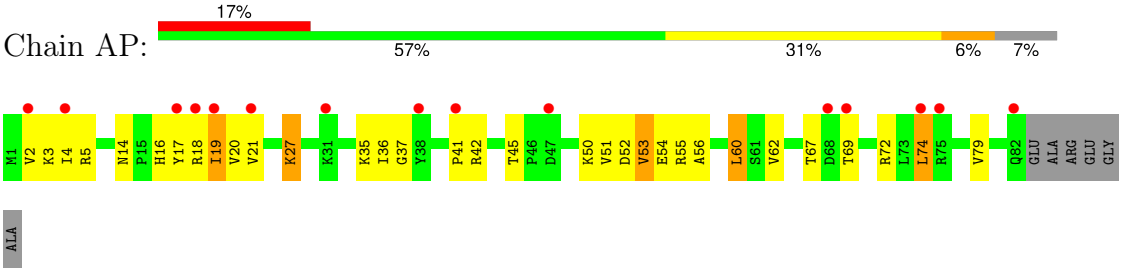
• Molecule 15: 30S Ribosomal Protein S15

Chain CO:



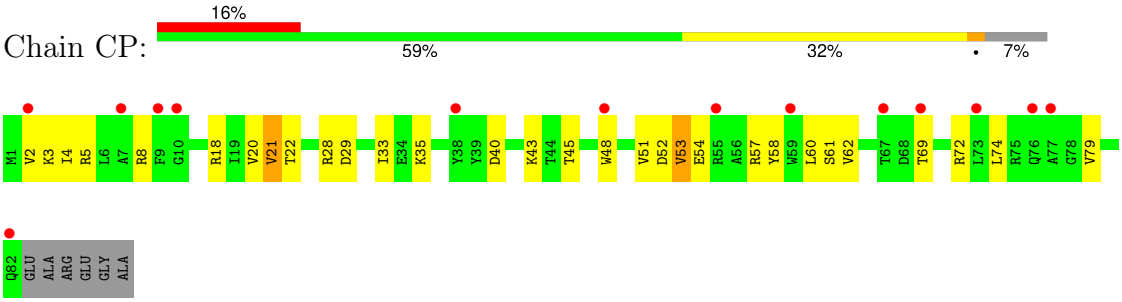
• Molecule 16: 30S Ribosomal Protein S16

Chain AP:



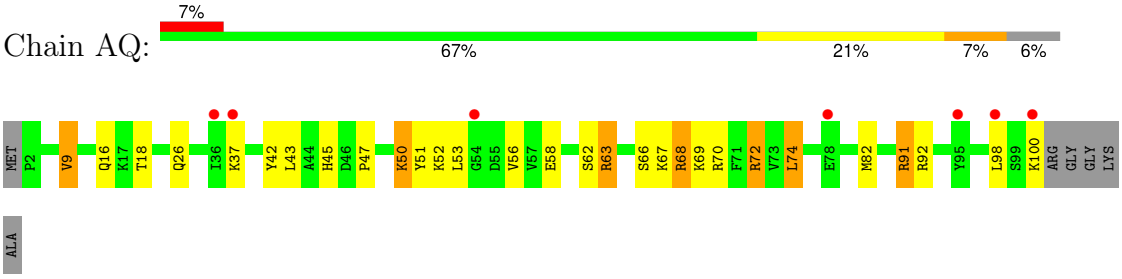
• Molecule 16: 30S Ribosomal Protein S16

Chain CP:



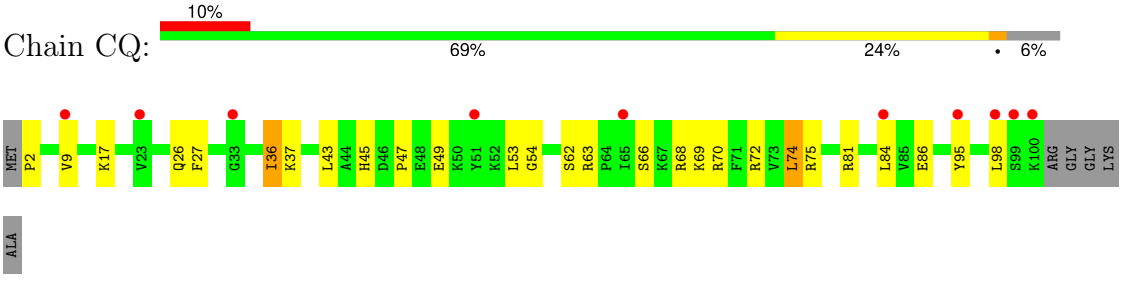
• Molecule 17: 30S Ribosomal Protein S17

Chain AQ:



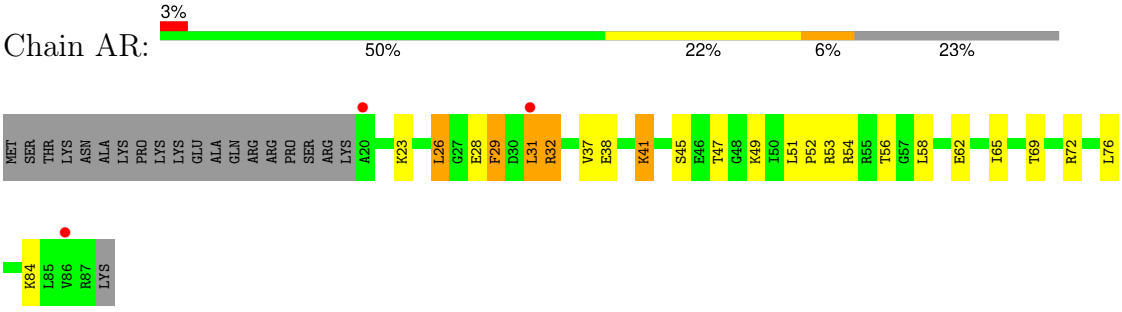
• Molecule 17: 30S Ribosomal Protein S17

Chain CQ:



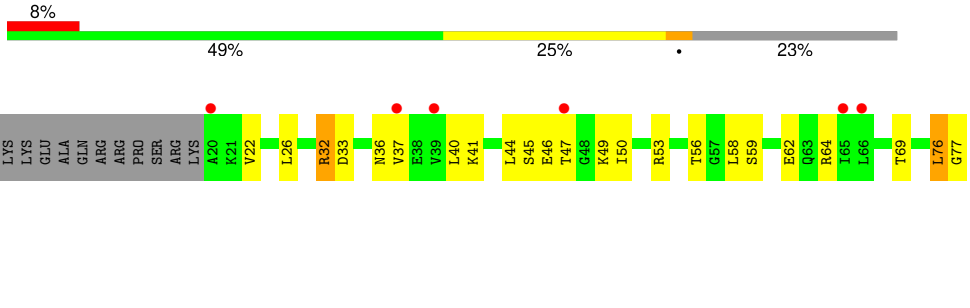
• Molecule 18: 30S Ribosomal Protein S18

Chain AR:



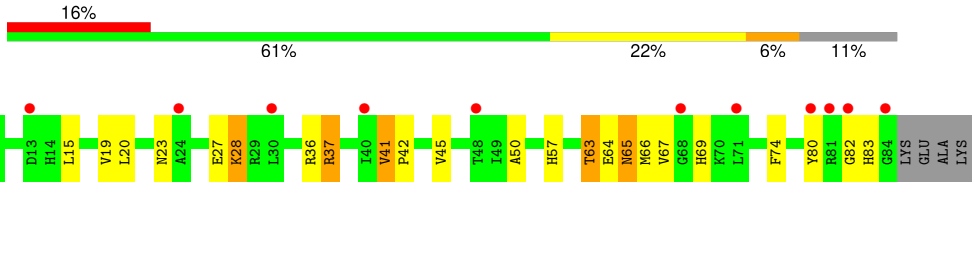
• Molecule 18: 30S Ribosomal Protein S18

Chain CR:



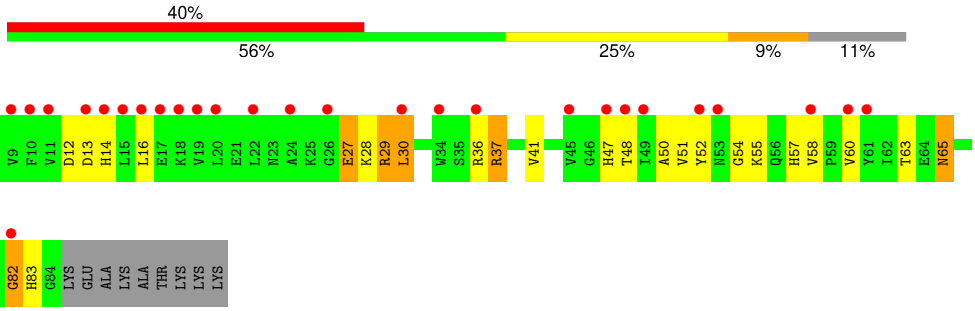
• Molecule 19: 30S Ribosomal Protein S19

Chain AS:



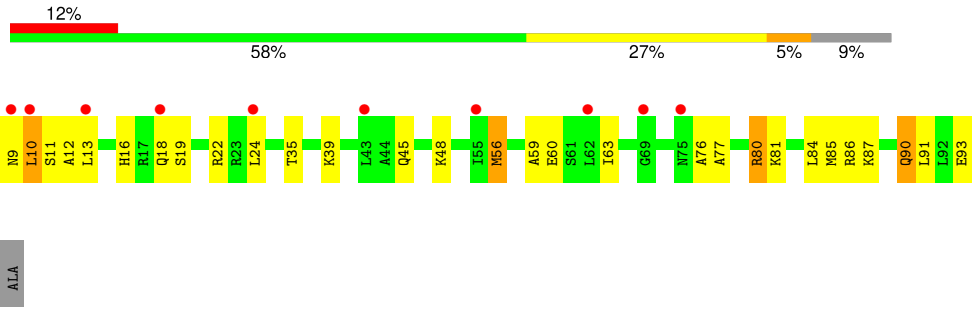
• Molecule 19: 30S Ribosomal Protein S19

Chain CS:



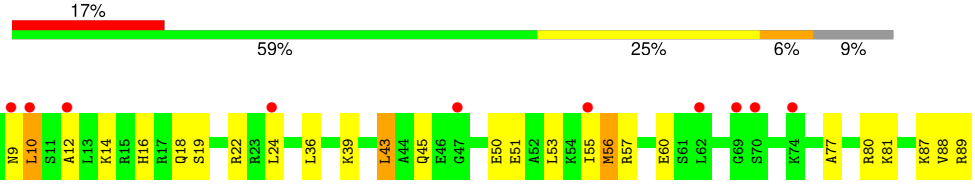
• Molecule 20: 30S Ribosomal Protein S20

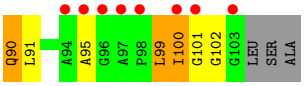
Chain AT:



• Molecule 20: 30S Ribosomal Protein S20

Chain CT:

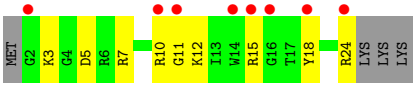




• Molecule 21: 30S Ribosomal Protein THX

Chain AU:

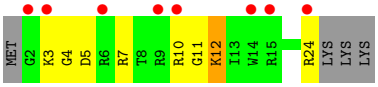




• Molecule 21: 30S Ribosomal Protein THX

Chain CU:





• Molecule 22: mRNA

Chain AV:





• Molecule 22: mRNA

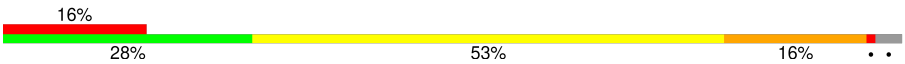
Chain CV:

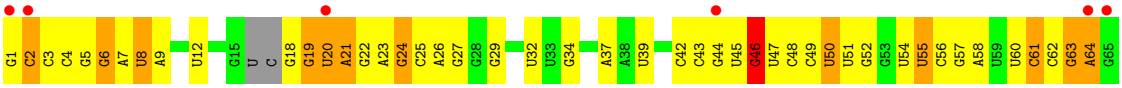


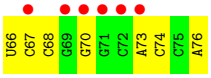


• Molecule 23: A/P-site tRNA

Chain AW:



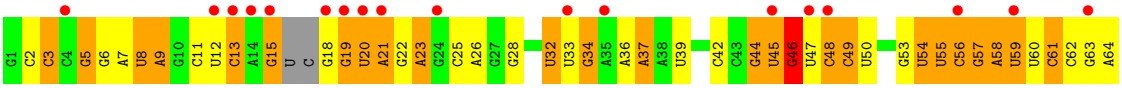


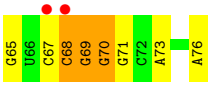


• Molecule 23: A/P-site tRNA

Chain AY:

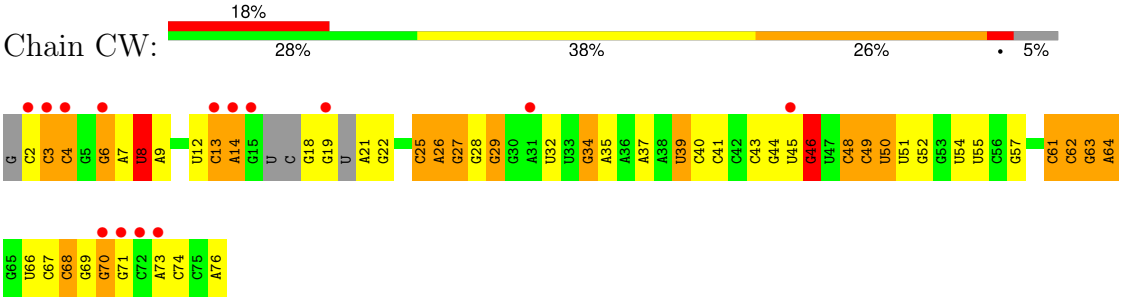






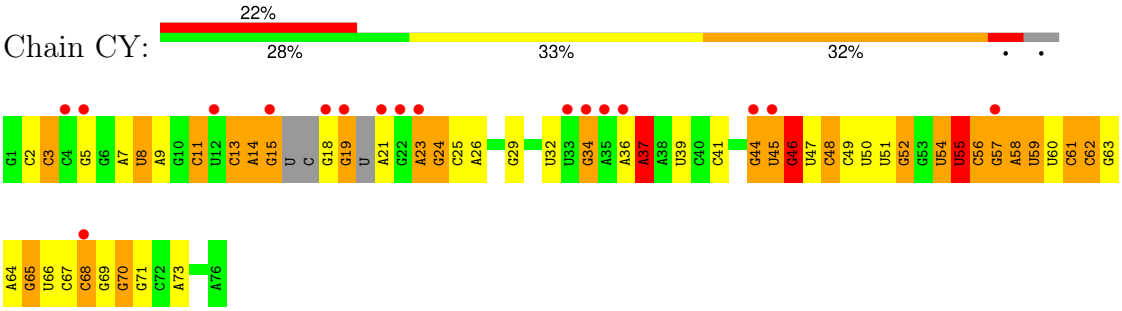
• Molecule 23: A/P-site tRNA

Chain CW:



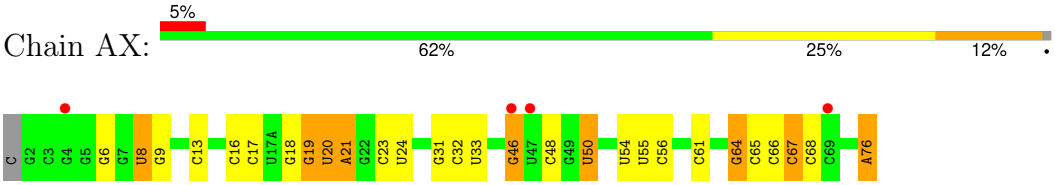
• Molecule 23: A/P-site tRNA

Chain CY:



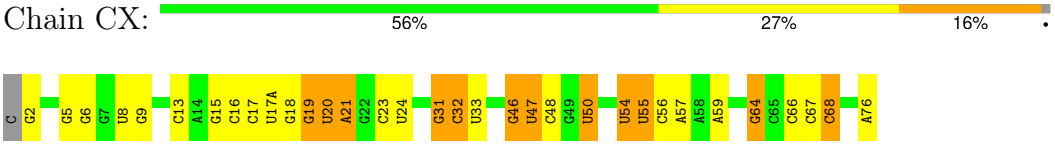
• Molecule 24: E-site tRNA

Chain AX:



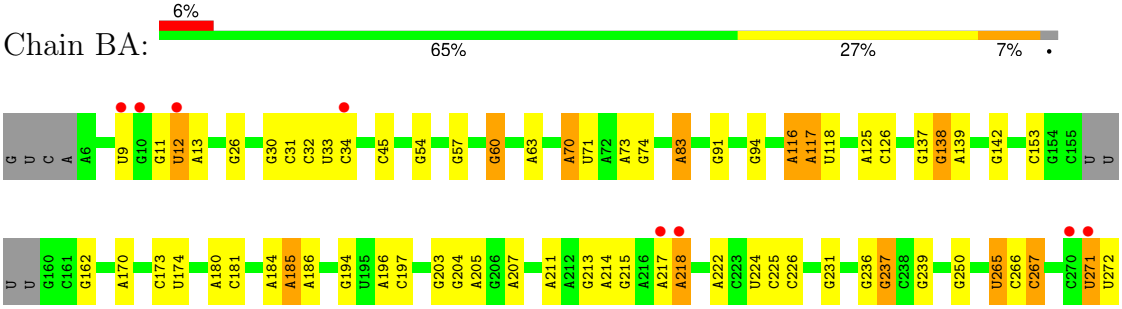
• Molecule 24: E-site tRNA

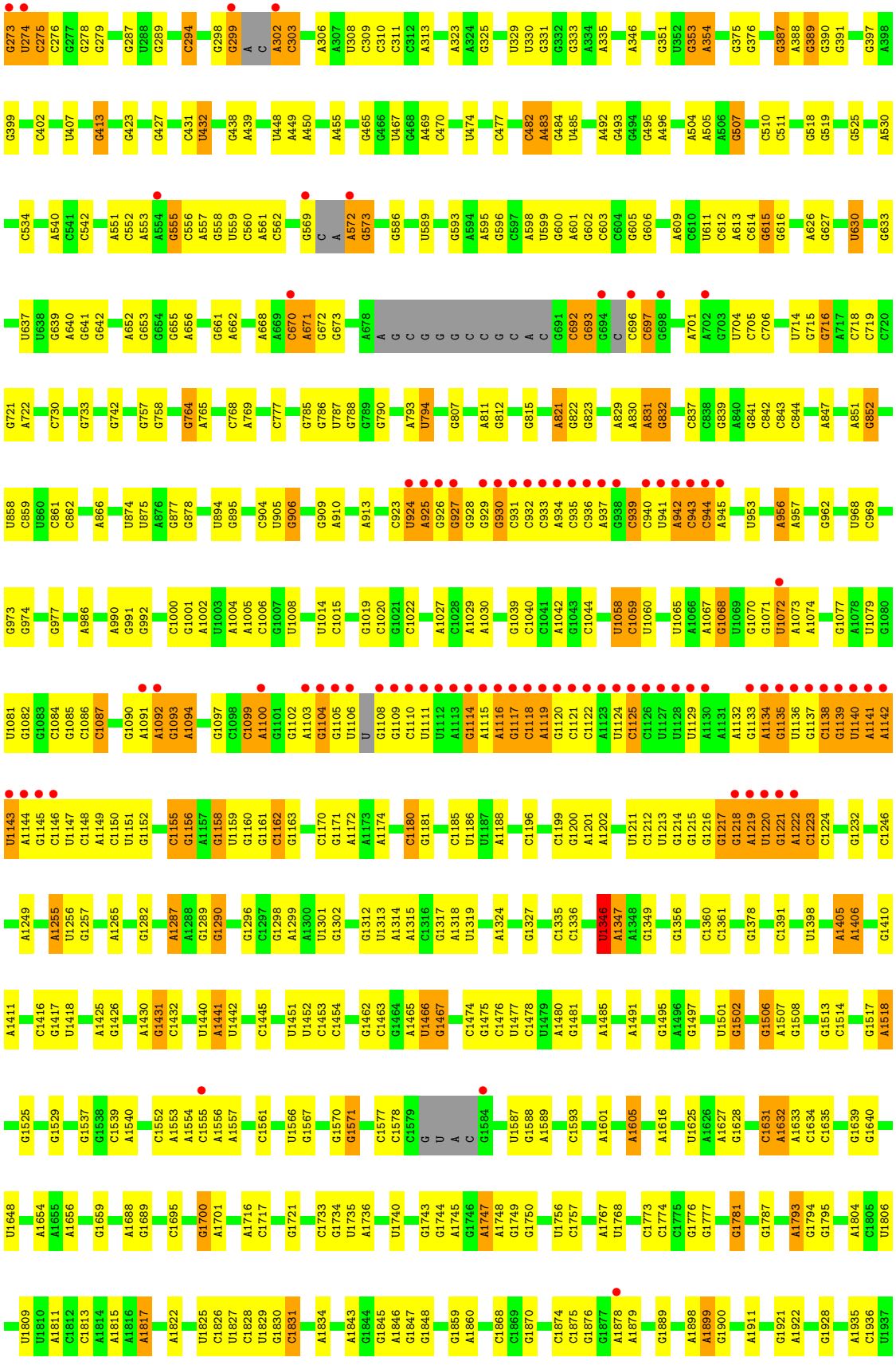
Chain CX:

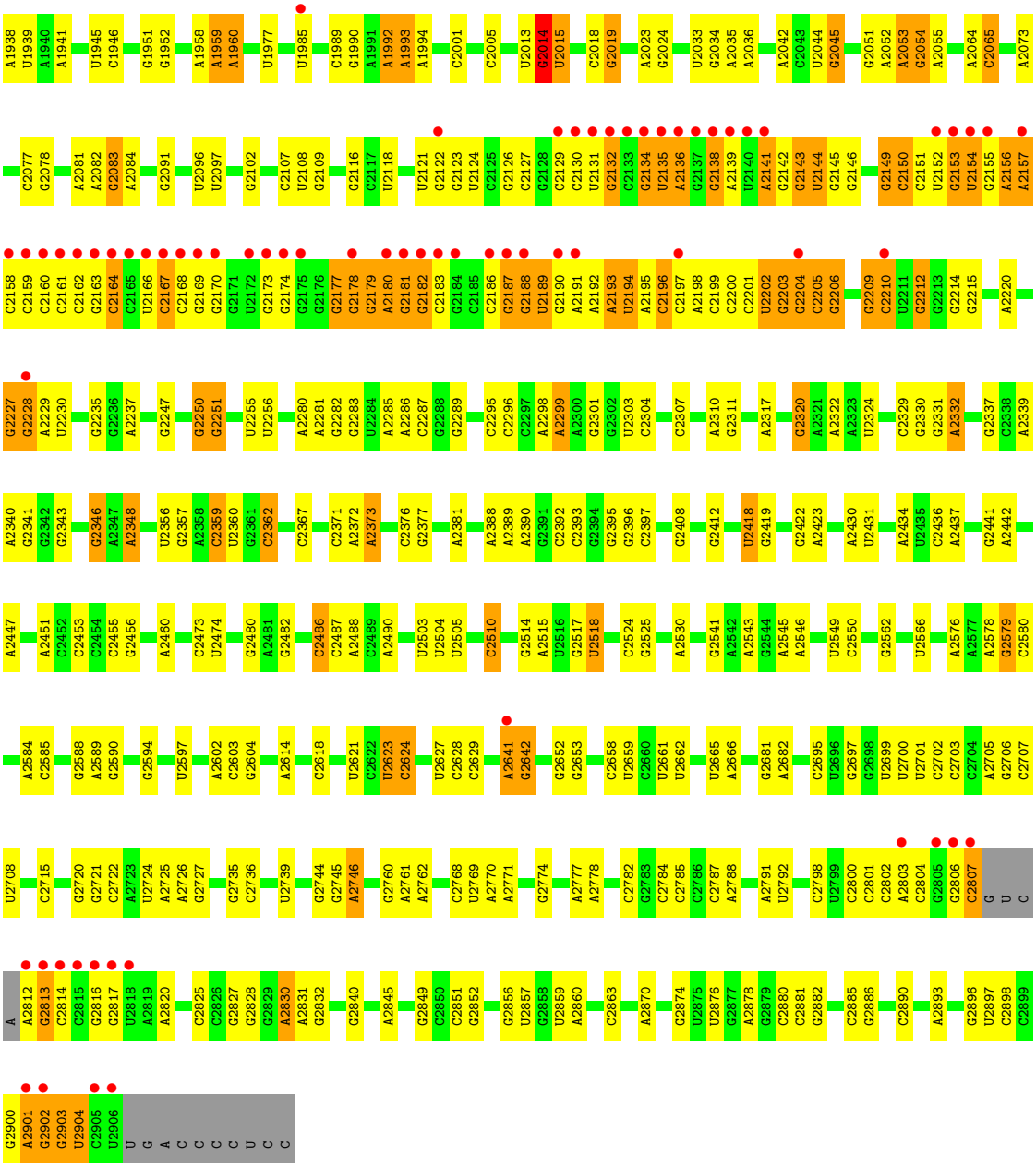


• Molecule 25: 23S Ribosomal RNA

Chain BA:



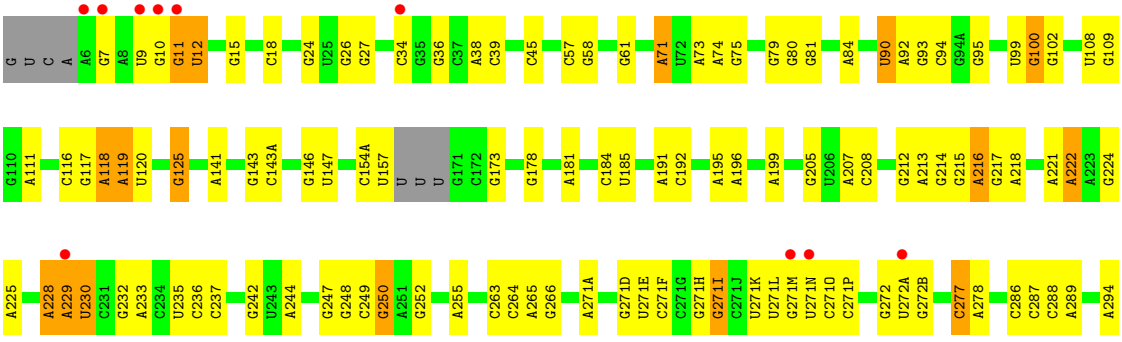


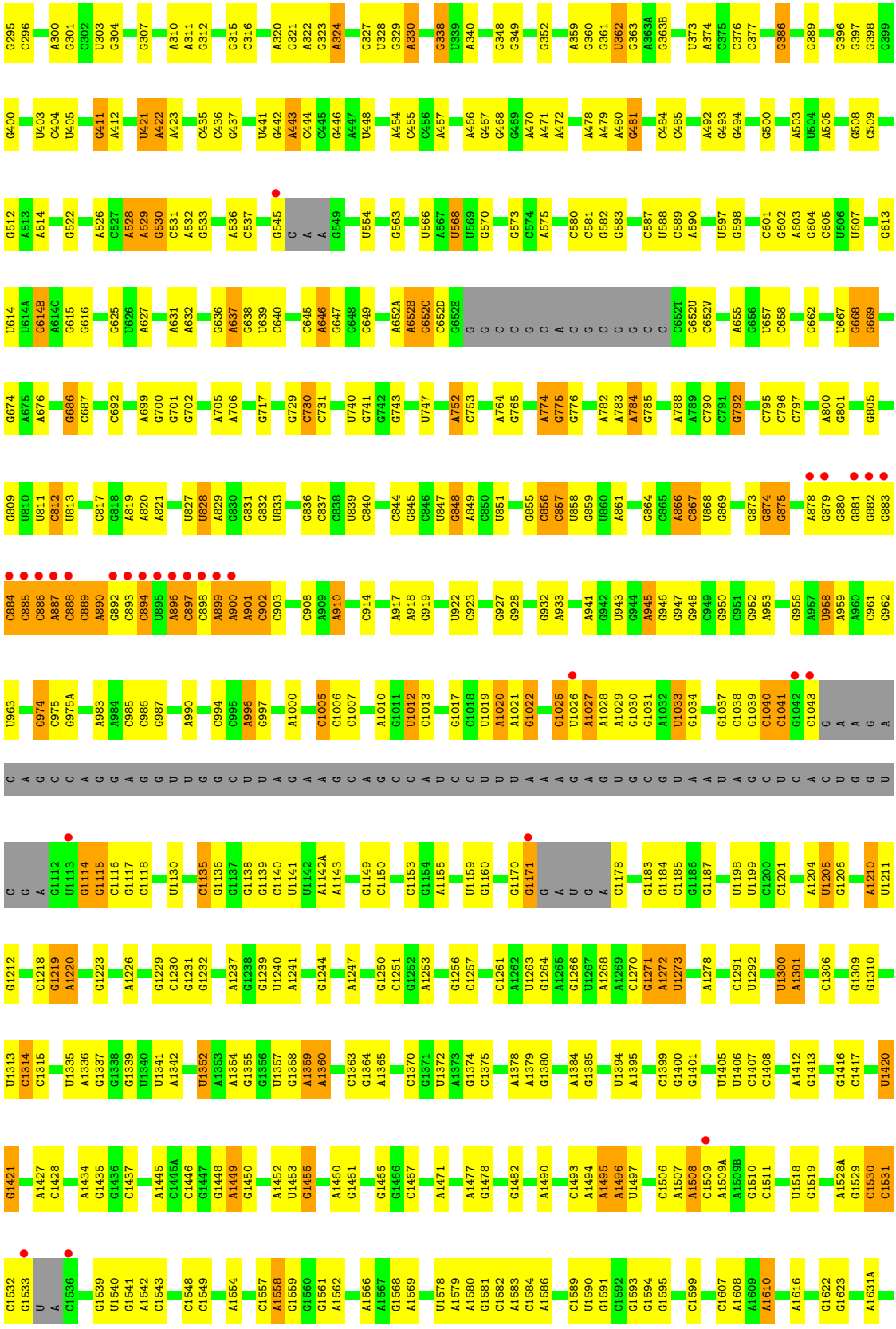


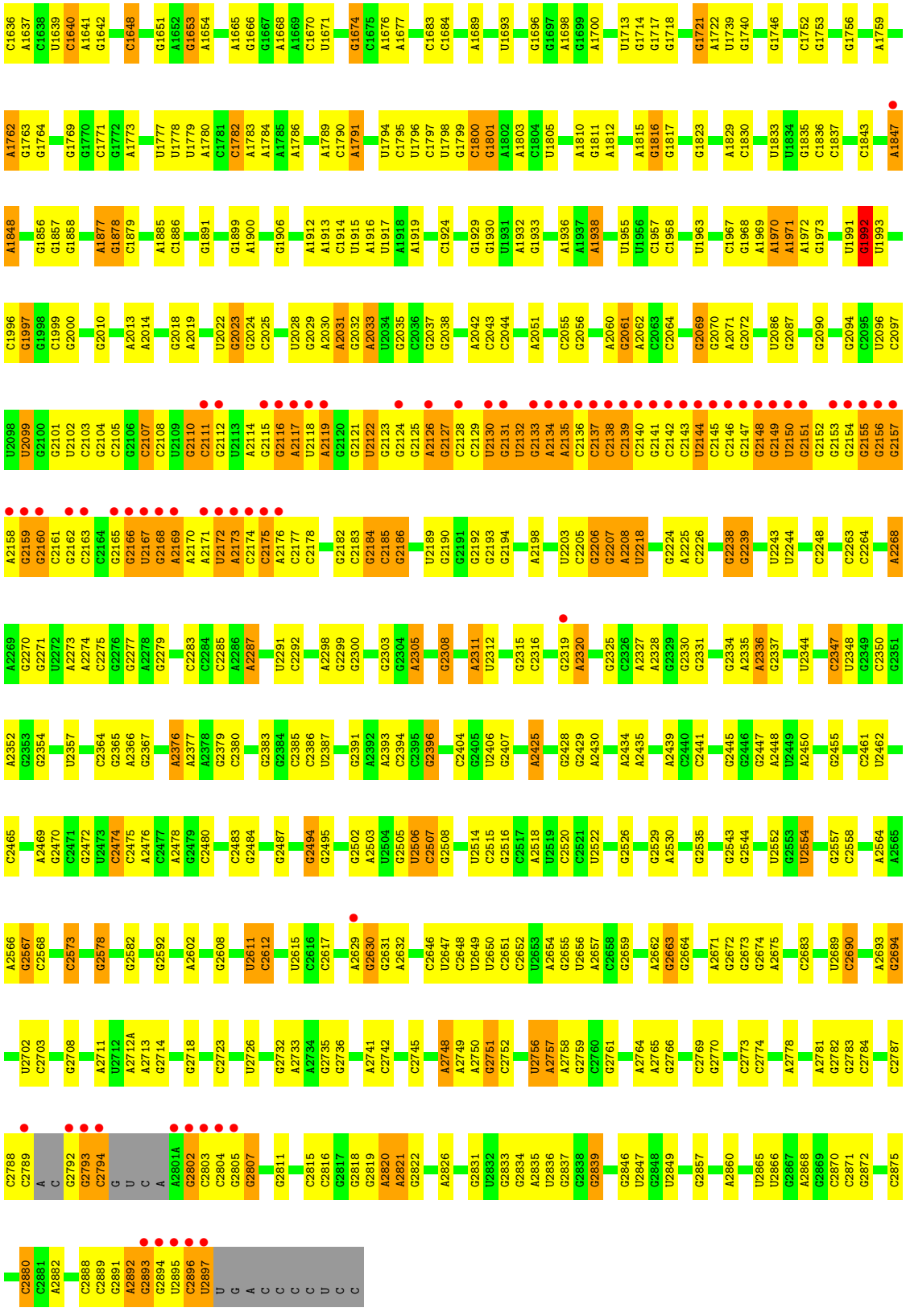
• Molecule 25: 23S Ribosomal RNA

Chain DA:





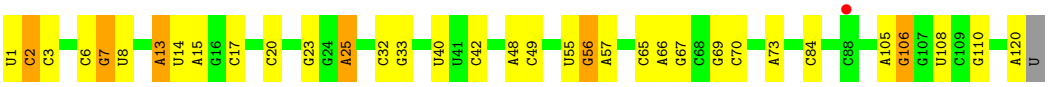

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G400 U403 C404 U405 G411 A412 U421 A422 A423 C435 C436 G437 U441 G442 A443 C444 C445 G446 A447 U448 A454 C455 C456 A457 A466 G467 G468 G469 A470 A471 A472 A478 A479 A480 G481 C484 C485 A492 G493 G494 G500 A503 U504 A505 G508 C509
G512 A513 A514 G522 A526 C527 A528 A529 G530 C531 A532 G533 A536 C537 G545 C A A G549 U554 G563 U566 A567 U568 U569 G570 G573 C574 A575 C580 C581 G582 G583 C587 U588 C589 A590 U597 G598 C601 G602 A603 G604 C605 U606 U607 G613
U614 U614A G614B A614C G615 G616 G625 U626 A627 A631 A632 G636 A637 G638 U639 C640 C645 A646 G647 G648 G649 A652A A652B G652C C652D G652E G G C C G C A C G C G G C C C652T G652U C652V A655 G656 U657 C658 G662 U667 G668 G669
G674 A675 A676 G686 C687 C692 A699 G700 G701 G702 A705 A706 G717 G729 C730 C731 U740 G741 G742 G743 U747 A752 C753 A764 G765 A774 G775 G776 A782 A783 A784 G785 A788 A789 C790 C791 G792 C795 C796 C797 A800 G801 G805
G809 U810 U811 C812 U813 C817 G818 A819 A820 A821 U827 U828 A829 G830 G831 G832 U833 G836 C837 C838 U839 C840 C844 G845 C846 U847 G848 A849 C850 U851 G855 C856 C857 U858 G859 U860 A861 G864 C865 A866 C867 U868 G869 G873 G874 G875 A878 G879 G880 G881 G882 G883
C884 C885 C886 A887 C888 C889 A890 G892 C893 C894 U895 A896 C897 C898 A899 A900 A901 C902 C903 C908 A909 A910 C914 A917 A918 G919 U922 C923 G927 G928 G932 A933 A941 G942 U943 G944 A945 G946 G947 G948 C949 G950 C951 G952 A953 G956 A957 U958 A959 A960 C961 G962
U963 G974 C975 G975A A983 A984 C985 C986 G987 A990 C994 C995 A996 G997 A1000 C1005 C1006 C1007 A1010 G1011 U1012 C1013 G1017 C1018 U1019 A1020 A1021 G1022 G1025 U1026 A1027 A1028 A1029 G1030 G1031 A1032 U1033 G1034 G1037 C1038 G1039 C1040 C1041 G1042 C1043 G A A G A
C A G C C A G G U U G C C A A G C A G C C A A U C C C A U G A A A G C U G G U
C G A G1112 U1113 G1114 G1115 C1116 G1117 C1118 U1130 C1135 G1136 G1137 G1138 G1139 C1140 U1141 U1142 A1142A A1143 G1149 C1150 C1153 G1154 A1155 U1159 G1160 G1170 G1171 G A U G A C1178 G1183 G1184 C1185 G1186 G1187 U1198 U1199 C1200 C1201 A1204 U1205 G1206 A1210 U1211
G1212 C1218 G1219 A1220 G1223 A1226 G1229 C1230 G1231 G1232 A1237 G1238 G1239 U1240 A1241 G1244 A1247 G1250 C1251 G1252 A1253 G1256 C1257 C1261 A1262 U1263 G1264 A1265 G1266 U1267 A1268 A1269 C1270 G1271 A1272 U1273 A1278 C1291 U1292 U1300 A1301 C1306 G1309 G1310
U1313 C1314 C1315 U1335 A1336 G1337 G1338 G1339 U1340 U1341 A1342 U1352 A1353 A1354 G1355 G1356 U1357 G1358 A1359 A1360 C1363 G1364 A1365 C1370 G1371 U1372 A1373 G1374 C1375 A1378 A1379 G1380 A1384 G1385 U1394 A1395 C1399 G1400 G1401 U1405 U1406 C1407 C1408 A1412 G1413 G1416 C1417 U1420
G1421 A1427 C1428 A1434 G1435 G1436 C1437 A1445 C1445A C1446 G1447 G1448 A1449 G1450 A1452 U1453 G1455 A1460 G1461 G1465 G1466 C1467 A1471 A1477 G1478 G1482 A1490 C1493 A1494 A1495 A1496 U1497 C1506 A1507 A1508 C1509 A1509A A1509B G1510 C1511 U1518 G1519 A1528A G1529 C1530 C1531
C1532 G1533 U A C1536 G1539 U1540 G1541 A1542 C1543 C1548 C1549 A1554 C1557 A1558 G1559 G1560 G1561 A1562 A1566 A1567 G1568 A1569 U1578 A1579 A1580 G1581 C1582 A1583 C1584 A1586 C1589 U1590 G1591 C1592 G1593 G1594 G1595 C1599 C1607 A1608 A1609 A1610 A1616 G1622 G1623 A1631A



• Molecule 26: 5S Ribosomal RNA

Chain BB:

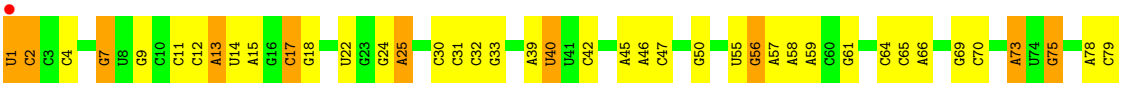




• Molecule 26: 5S Ribosomal RNA

Chain DB:







• Molecule 27: 50S Ribosomal Protein L2

Chain BD:



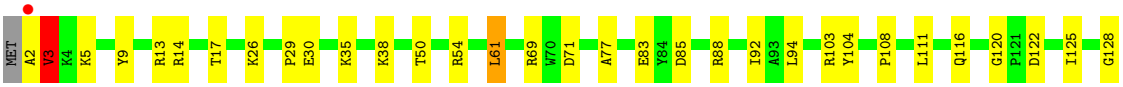


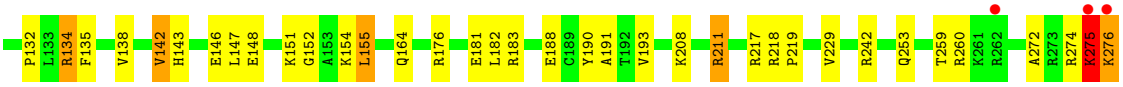


• Molecule 27: 50S Ribosomal Protein L2

Chain DD:



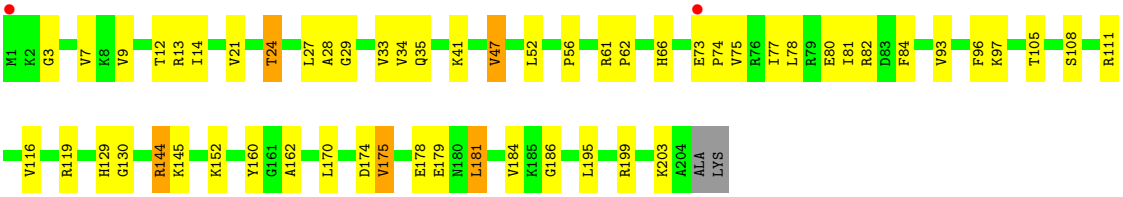




• Molecule 28: 50S Ribosomal Protein L3

Chain BE:

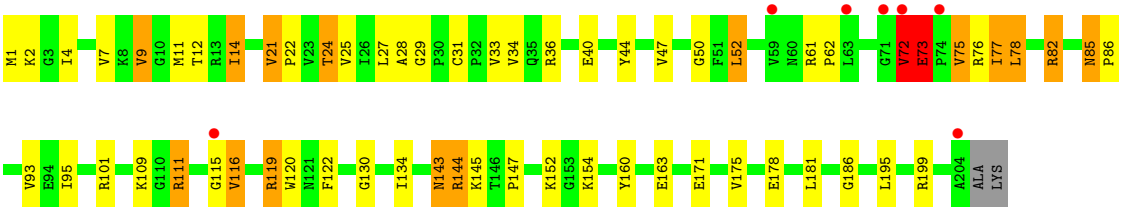




• Molecule 28: 50S Ribosomal Protein L3

Chain DE:

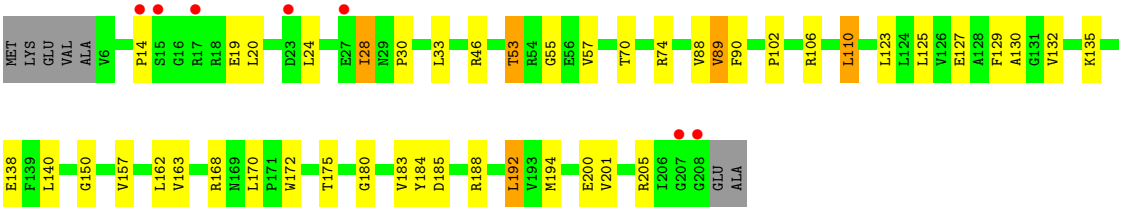




• Molecule 29: 50S Ribosomal Protein L4

Chain BF:

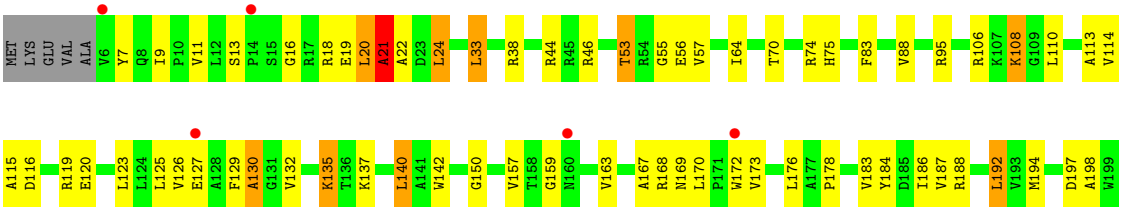




• Molecule 29: 50S Ribosomal Protein L4

Chain DF:

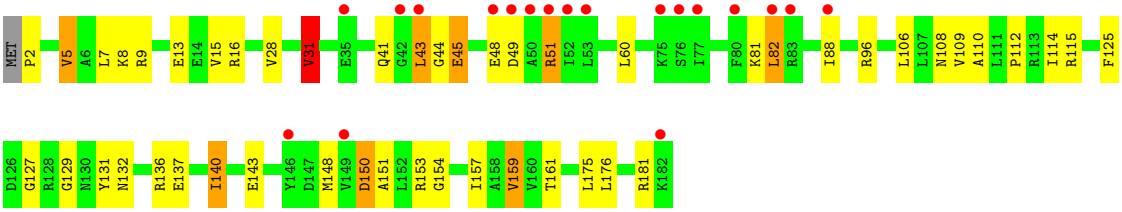




• Molecule 30: 50S Ribosomal Protein L5

Chain BG:

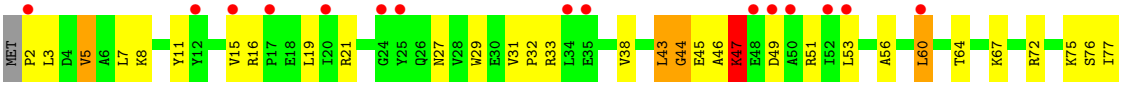


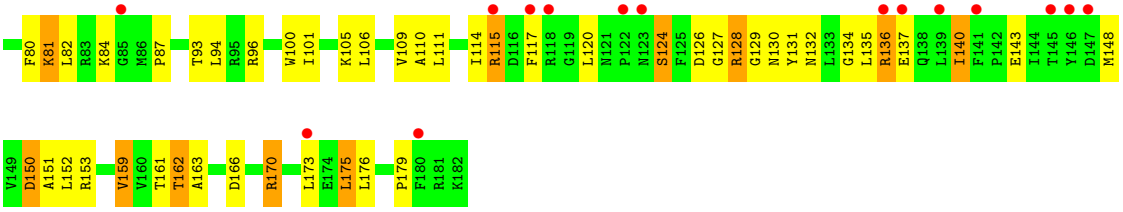


• Molecule 30: 50S Ribosomal Protein L5

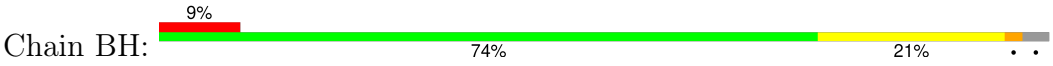
Chain DG:

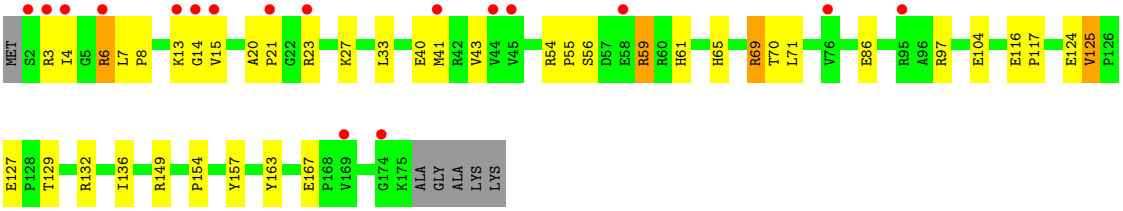






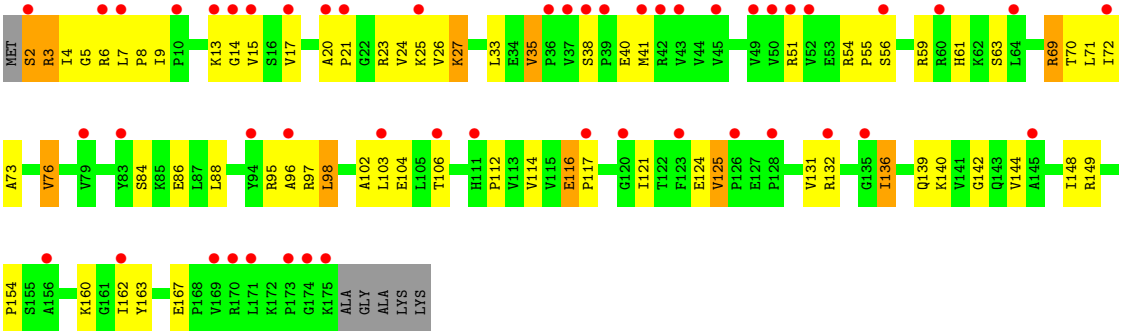
• Molecule 31: 50S Ribosomal Protein L6





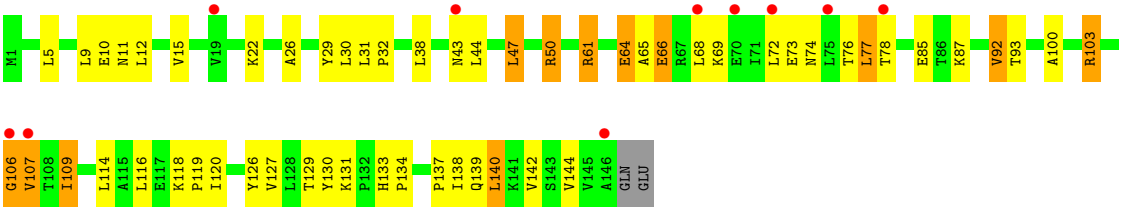
• Molecule 31: 50S Ribosomal Protein L6





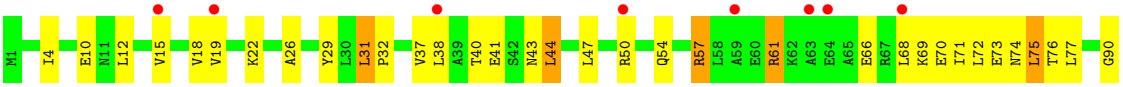
• Molecule 32: 50S Ribosomal Protein L9

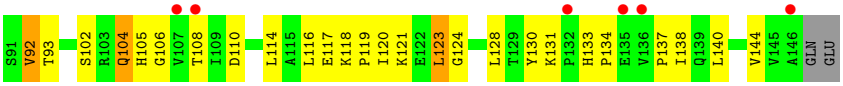




• Molecule 32: 50S Ribosomal Protein L9



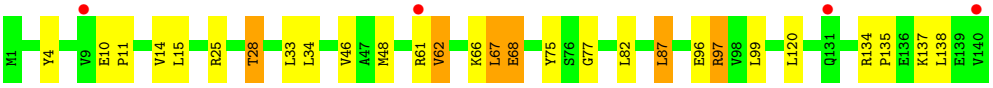




• Molecule 33: 50S Ribosomal Protein L13

Chain BN:

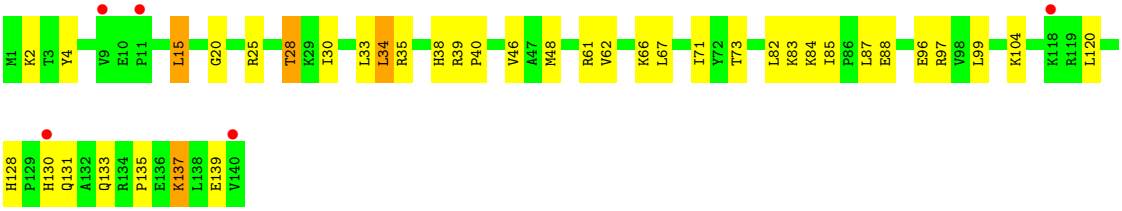




• Molecule 33: 50S Ribosomal Protein L13

Chain DN:

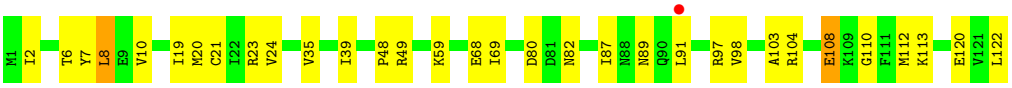




• Molecule 34: 50S Ribosomal Protein L14

Chain BO:

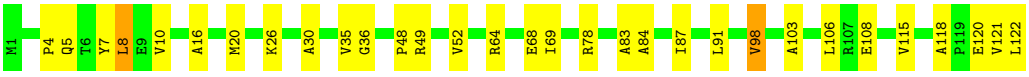




• Molecule 34: 50S Ribosomal Protein L14

Chain DO:





• Molecule 35: 50S Ribosomal Protein L15

Chain BP:

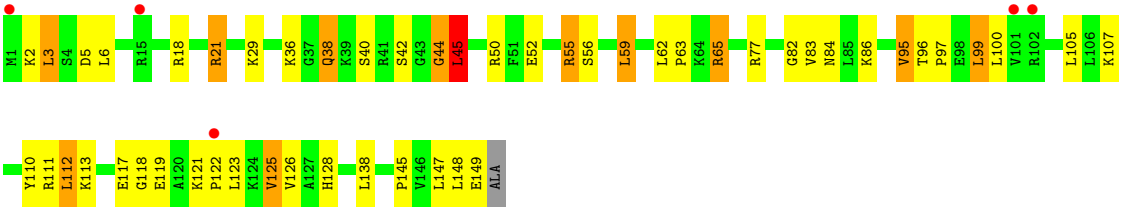




• Molecule 35: 50S Ribosomal Protein L15

Chain DP:

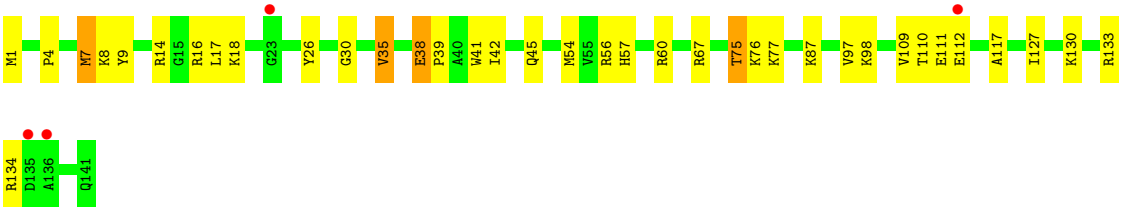




• Molecule 36: 50S Ribosomal Protein L16

Chain BQ:

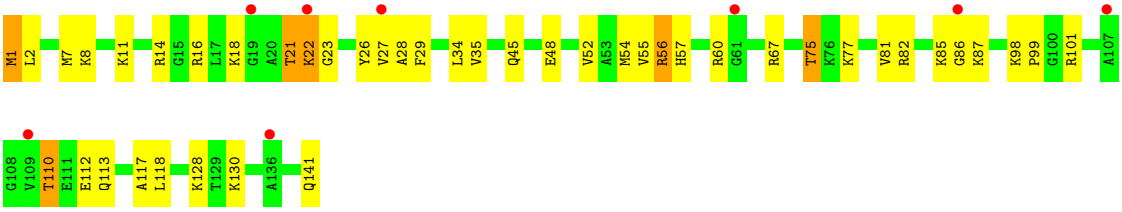




• Molecule 36: 50S Ribosomal Protein L16

Chain DQ:

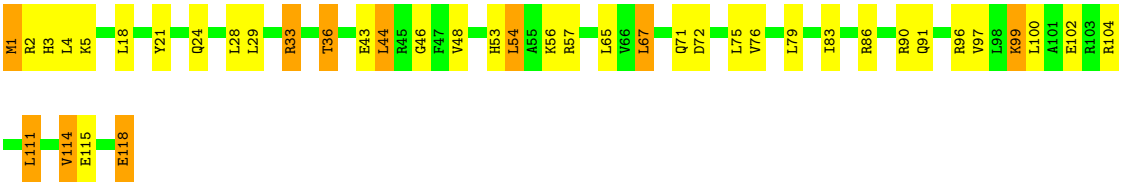




• Molecule 37: 50S Ribosomal Protein L17

Chain BR:





• Molecule 37: 50S Ribosomal Protein L17

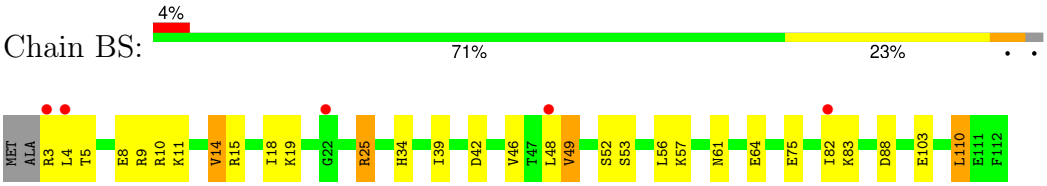
Chain DR:





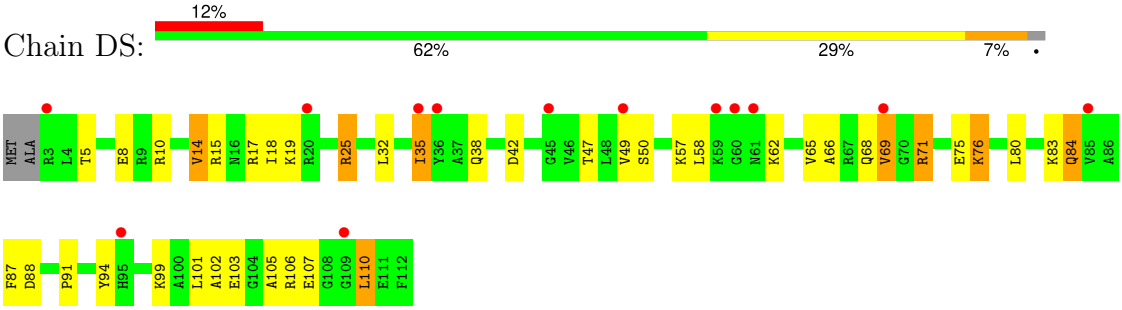
• Molecule 38: 50S Ribosomal Protein L18

Chain BS:



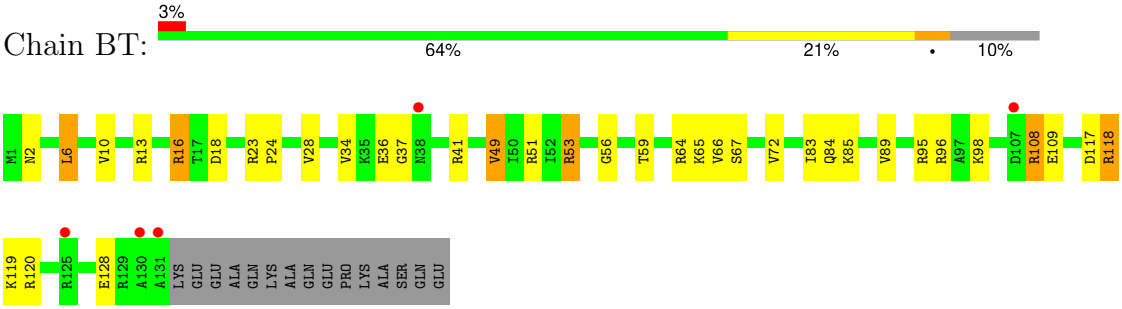
• Molecule 38: 50S Ribosomal Protein L18

Chain DS:



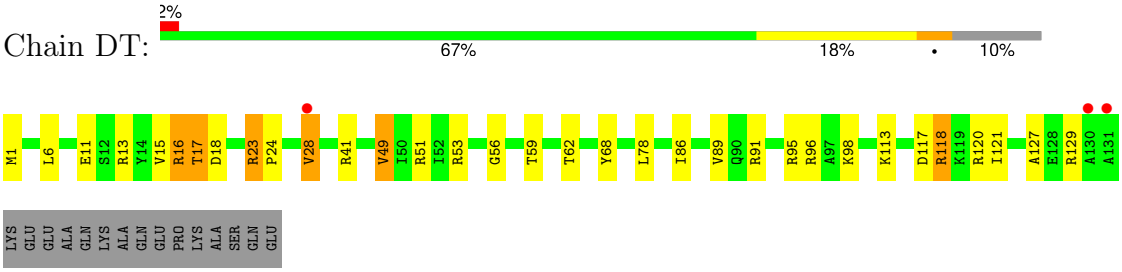
• Molecule 39: 50S Ribosomal Protein L19

Chain BT:



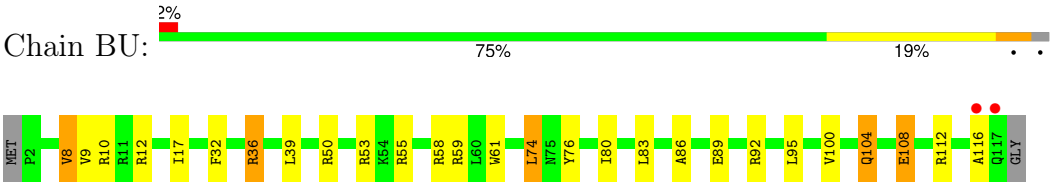
• Molecule 39: 50S Ribosomal Protein L19

Chain DT:



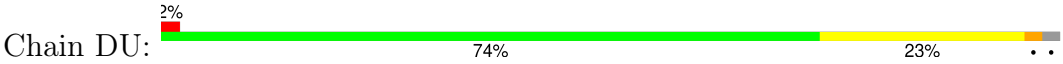
• Molecule 40: 50S Ribosomal Protein L20

Chain BU:



• Molecule 40: 50S Ribosomal Protein L20

Chain DU:





• Molecule 41: 50S Ribosomal Protein L21

Chain BV:

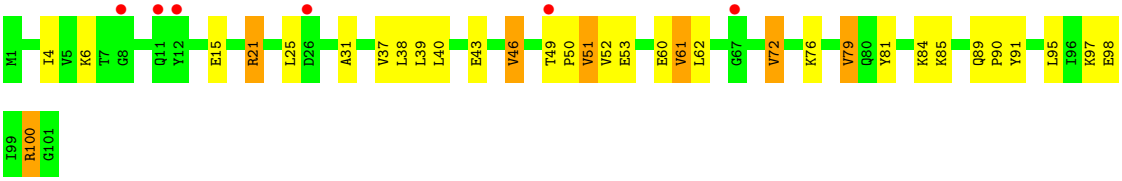




• Molecule 41: 50S Ribosomal Protein L21

Chain DV:

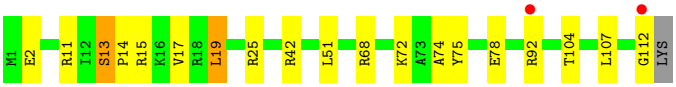




• Molecule 42: 50S Ribosomal Protein L22

Chain BW:

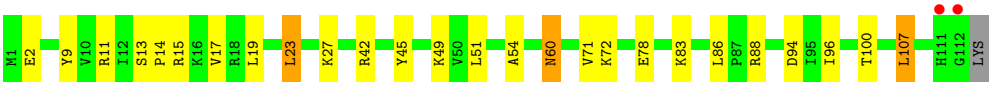




• Molecule 42: 50S Ribosomal Protein L22

Chain DW:

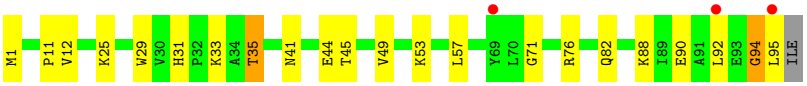




• Molecule 43: 50S Ribosomal Protein L23

Chain BX:

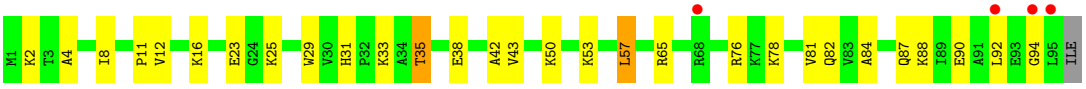




• Molecule 43: 50S Ribosomal Protein L23

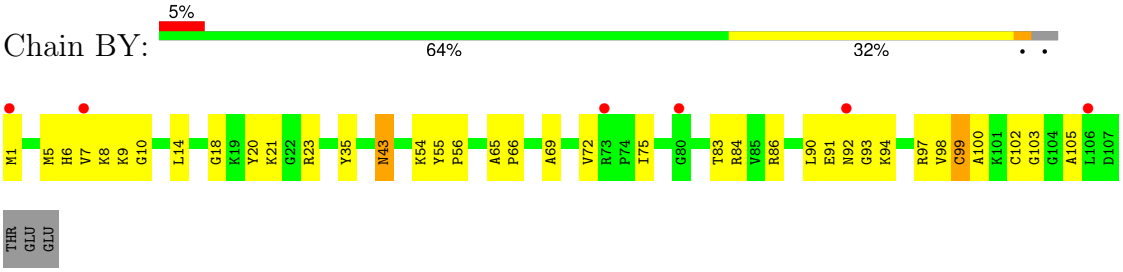
Chain DX:





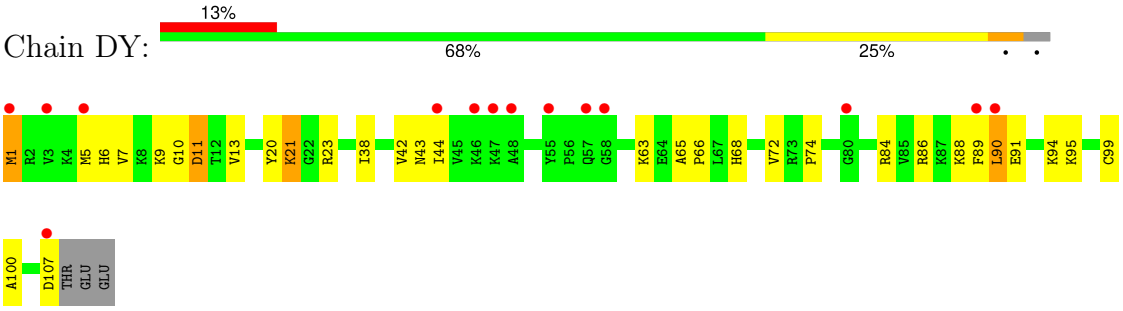
• Molecule 44: 50S Ribosomal Protein L24

Chain BY:



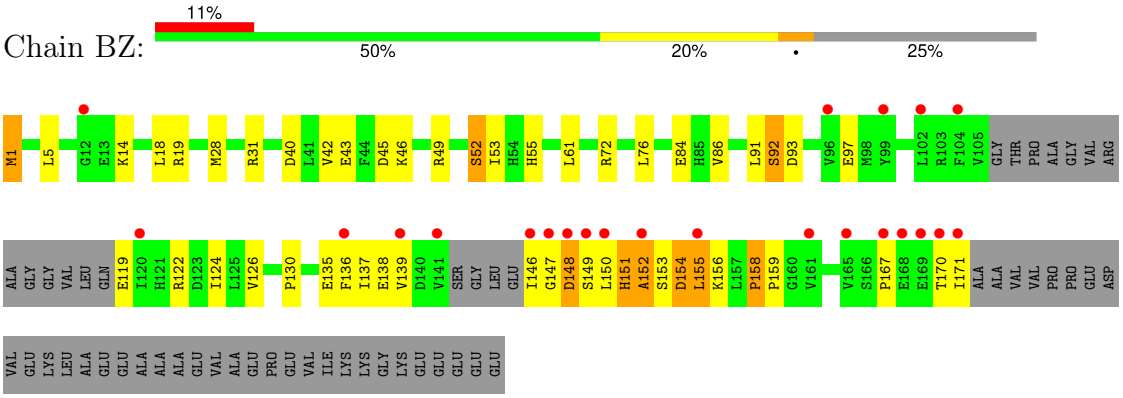
• Molecule 44: 50S Ribosomal Protein L24

Chain DY:



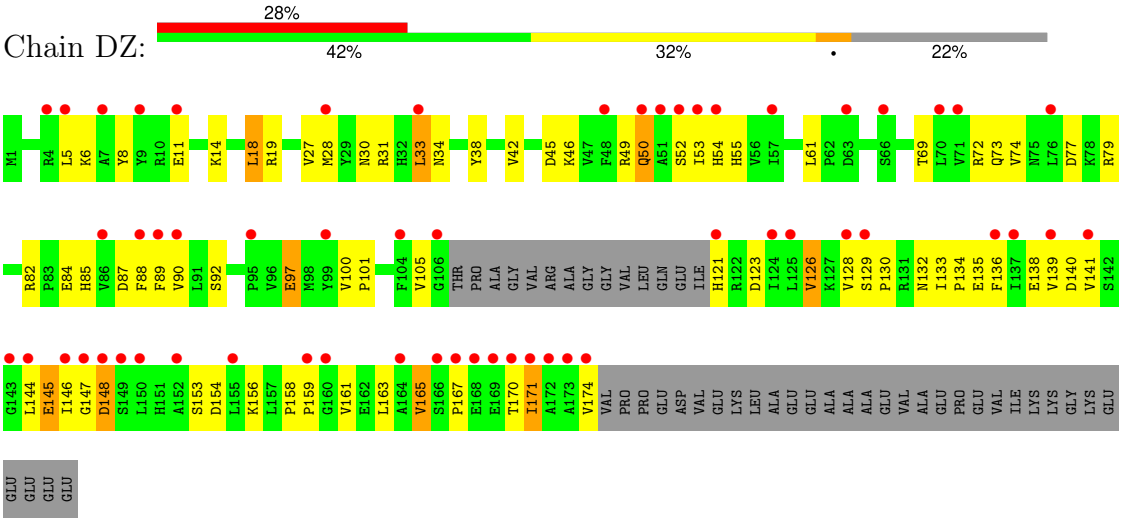
• Molecule 45: 50S Ribosomal Protein L25

Chain BZ:



• Molecule 45: 50S Ribosomal Protein L25

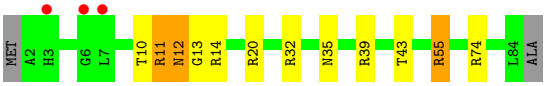
Chain DZ:



• Molecule 46: 50S Ribosomal Protein L27

Chain B0:

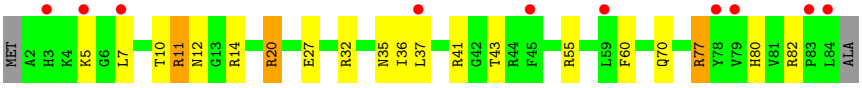




• Molecule 46: 50S Ribosomal Protein L27

Chain D0:

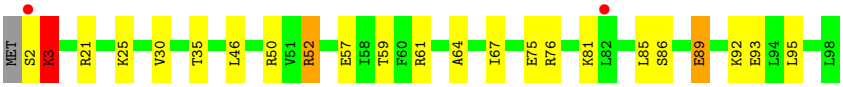




• Molecule 47: 50S Ribosomal Protein L28

Chain B1:

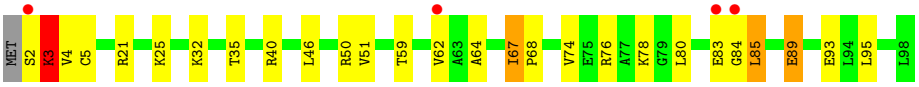




• Molecule 47: 50S Ribosomal Protein L28

Chain D1:

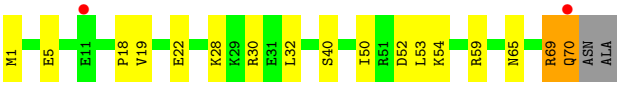




• Molecule 48: 50S Ribosomal Protein L29

Chain B2:

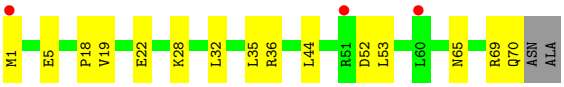




• Molecule 48: 50S Ribosomal Protein L29

Chain D2:

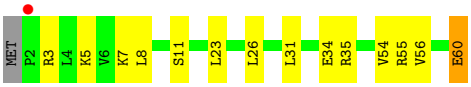




• Molecule 49: 50S Ribosomal Protein L30

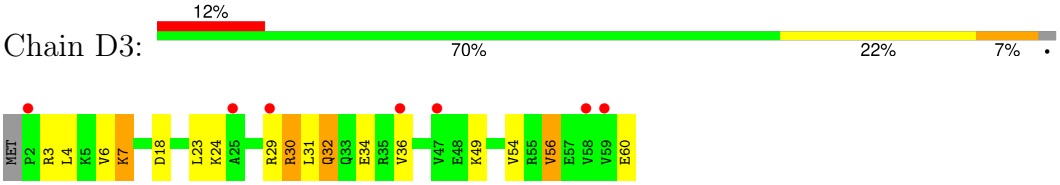
Chain B3:





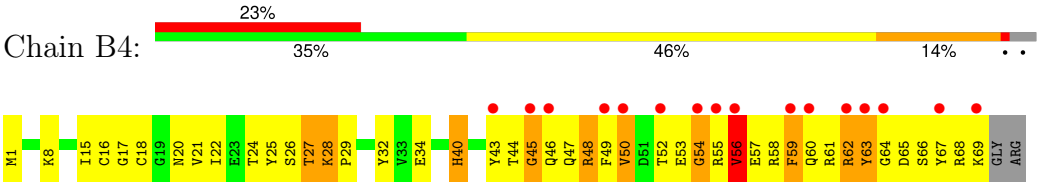
• Molecule 49: 50S Ribosomal Protein L30

Chain D3:



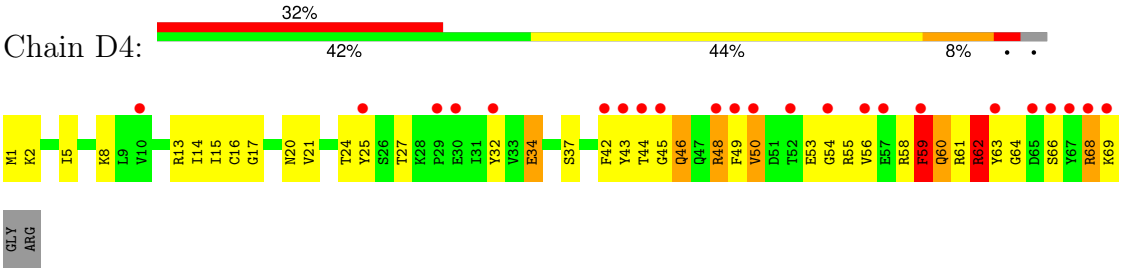
• Molecule 50: 50S Ribosomal Protein L31

Chain B4:



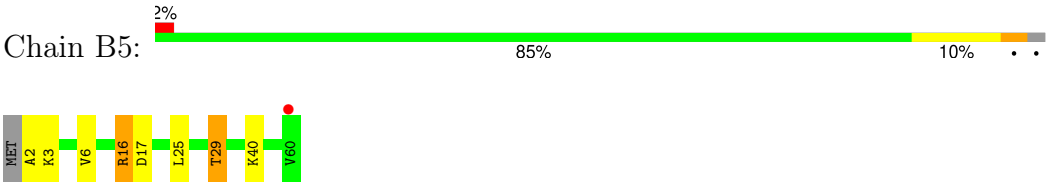
• Molecule 50: 50S Ribosomal Protein L31

Chain D4:



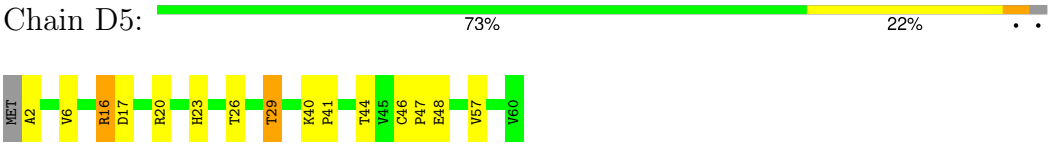
• Molecule 51: 50S Ribosomal Protein L32

Chain B5:



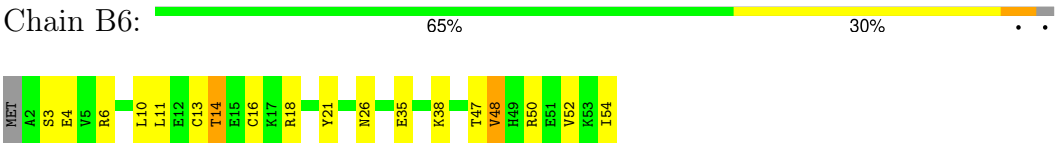
• Molecule 51: 50S Ribosomal Protein L32

Chain D5:



• Molecule 52: 50S Ribosomal Protein L33

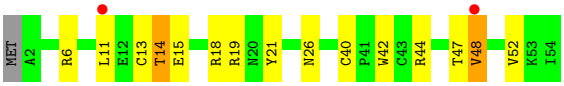
Chain B6:



• Molecule 52: 50S Ribosomal Protein L33

Chain D6:





• Molecule 53: 50S Ribosomal Protein L34

Chain B7:

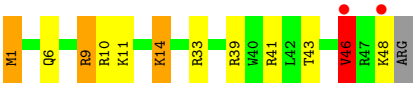




• Molecule 53: 50S Ribosomal Protein L34

Chain D7:

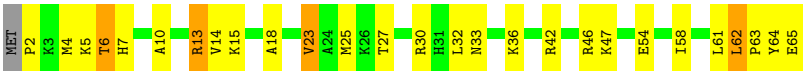




• Molecule 54: 50S Ribosomal Protein L35

Chain B8:





• Molecule 54: 50S Ribosomal Protein L35

Chain D8:

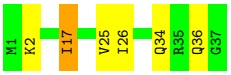




• Molecule 55: 50S Ribosomal Protein L36

Chain B9:

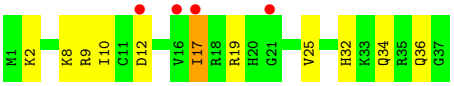




• Molecule 55: 50S Ribosomal Protein L36

Chain D9:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	210.06Å 448.57Å 623.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	256.12 – 2.40 256.12 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.7 (256.12-2.40) 99.6 (256.12-2.40)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.24 (at 2.40Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.237 , 0.277 0.239 , 0.279	Depositor DCC
R_{free} test set	113081 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	45.9	Xtriage
Anisotropy	0.221	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 65.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.38$, $< L^2 > = 0.20$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	298643	wwPDB-VP
Average B, all atoms (Å^2)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.55% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: PSU, 4SU, 5MC, UAM, MG, 5MU, SF4, 7MG, MIA, K, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	AA	0.22	0/36027	0.43	0/56227
1	CA	0.21	0/36170	0.43	1/56452 (0.0%)
2	AB	0.40	0/1881	0.95	4/2542 (0.2%)
2	CB	0.41	0/1860	0.99	3/2518 (0.1%)
3	AC	0.39	0/1572	0.85	4/2126 (0.2%)
3	CC	0.38	0/1566	0.93	3/2119 (0.1%)
4	AD	0.38	0/1685	0.84	4/2262 (0.2%)
4	CD	0.38	0/1704	0.85	2/2284 (0.1%)
5	AE	0.39	0/1145	0.85	0/1543
5	CE	0.41	0/1149	0.97	0/1548
6	AF	0.39	0/823	0.76	0/1115
6	CF	0.37	0/829	0.79	0/1123
7	AG	0.39	0/1250	0.88	0/1679
7	CG	0.37	0/1254	0.91	2/1683 (0.1%)
8	AH	0.37	0/1108	0.84	0/1494
8	CH	0.34	0/1108	0.82	2/1494 (0.1%)
9	AI	0.37	0/1002	0.88	0/1346
9	CI	0.38	0/997	0.82	0/1343
10	AJ	0.40	0/722	0.99	1/982 (0.1%)
10	CJ	0.44	0/727	0.97	1/988 (0.1%)
11	AK	0.41	0/844	0.83	0/1145
11	CK	0.39	0/848	0.82	0/1149
12	AL	0.39	0/946	0.81	1/1274 (0.1%)
12	CL	0.38	0/946	0.90	3/1274 (0.2%)
13	AM	0.40	0/969	0.89	1/1302 (0.1%)
13	CM	0.39	0/961	0.91	1/1291 (0.1%)
14	AN	0.35	0/501	0.74	0/664
14	CN	0.37	0/501	0.83	0/664
15	AO	0.36	0/739	0.83	1/985 (0.1%)
15	CO	0.38	0/739	0.83	0/985
16	AP	0.36	0/697	0.77	0/939
16	CP	0.36	0/693	0.77	0/935

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
17	AQ	0.36	0/836	0.81	1/1117 (0.1%)
17	CQ	0.33	0/836	0.77	0/1117
18	AR	0.38	0/560	0.88	2/746 (0.3%)
18	CR	0.33	0/560	0.75	0/746
19	AS	0.37	0/667	0.88	0/900
19	CS	0.43	0/661	1.06	2/893 (0.2%)
20	AT	0.37	0/730	0.88	0/965
20	CT	0.39	0/729	0.89	0/965
21	AU	0.33	0/203	0.78	0/266
21	CU	0.38	0/203	0.83	0/266
22	AV	0.20	0/310	0.32	0/480
22	CV	0.22	0/310	0.35	0/480
23	AW	0.29	0/1606	0.53	0/2497
23	AY	0.28	0/1606	0.53	0/2497
23	CW	0.30	1/1556 (0.1%)	0.53	0/2418
23	CY	0.29	1/1583 (0.1%)	0.53	0/2459
24	AX	0.27	0/1725	0.45	0/2689
24	CX	0.27	0/1725	0.46	0/2689
25	BA	0.28	0/69261	0.47	2/108110 (0.0%)
25	DA	0.23	0/67545	0.44	1/105432 (0.0%)
26	BB	0.22	0/2882	0.42	0/4494
26	DB	0.23	0/2879	0.43	0/4487
27	BD	0.47	0/2186	0.87	3/2944 (0.1%)
27	DD	0.44	0/2186	0.86	3/2944 (0.1%)
28	BE	0.48	0/1592	0.86	0/2149
28	DE	0.44	0/1592	0.95	8/2149 (0.4%)
29	BF	0.47	0/1619	0.81	1/2193 (0.0%)
29	DF	0.41	0/1615	0.89	3/2188 (0.1%)
30	BG	0.39	0/1454	0.87	4/1964 (0.2%)
30	DG	0.36	0/1453	0.89	3/1963 (0.2%)
31	BH	0.43	0/1356	0.88	0/1834
31	DH	0.43	0/1356	0.93	3/1834 (0.2%)
32	BI	0.39	0/1112	0.88	2/1514 (0.1%)
32	DI	0.37	0/1079	0.89	3/1475 (0.2%)
33	BN	0.44	0/1144	0.80	0/1543
33	DN	0.41	0/1144	0.85	0/1543
34	BO	0.46	0/943	0.81	0/1269
34	DO	0.41	0/943	0.83	0/1269
35	BP	0.44	0/1152	0.85	0/1533
35	DP	0.38	0/1152	0.90	2/1533 (0.1%)
36	BQ	0.44	0/1143	0.80	0/1527
36	DQ	0.40	0/1143	0.83	0/1527
37	BR	0.49	0/982	0.86	0/1312

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
37	DR	0.44	0/982	0.80	0/1312
38	BS	0.41	0/883	0.78	0/1176
38	DS	0.39	0/880	0.85	0/1172
39	BT	0.44	0/1105	0.83	0/1477
39	DT	0.38	0/1097	0.78	0/1468
40	BU	0.51	0/977	0.83	1/1301 (0.1%)
40	DU	0.41	0/977	0.83	0/1301
41	BV	0.53	0/782	0.92	0/1049
41	DV	0.37	0/782	0.82	1/1049 (0.1%)
42	BW	0.53	0/897	0.85	2/1205 (0.2%)
42	DW	0.43	0/897	0.85	0/1205
43	BX	0.46	0/764	0.95	3/1025 (0.3%)
43	DX	0.41	0/764	0.86	0/1025
44	BY	0.44	0/819	0.86	0/1095
44	DY	0.38	0/819	0.90	0/1095
45	BZ	0.39	0/1267	0.95	6/1717 (0.3%)
45	DZ	0.39	0/1299	0.90	2/1763 (0.1%)
46	B0	0.45	0/662	0.82	1/881 (0.1%)
46	D0	0.34	0/662	0.82	2/881 (0.2%)
47	B1	0.40	0/762	0.81	0/1014
47	D1	0.41	0/762	0.82	1/1014 (0.1%)
48	B2	0.43	0/590	0.83	0/781
48	D2	0.35	0/590	0.78	0/781
49	B3	0.49	0/474	0.92	1/635 (0.2%)
49	D3	0.36	0/469	0.87	0/630
50	B4	0.41	0/565	1.09	8/761 (1.1%)
50	D4	0.42	0/545	1.05	4/737 (0.5%)
51	B5	0.52	0/469	0.79	0/635
51	D5	0.45	0/469	0.98	4/635 (0.6%)
52	B6	0.46	0/460	0.78	0/613
52	D6	0.37	0/456	0.74	0/608
53	B7	0.53	0/426	0.77	0/561
53	D7	0.48	0/426	0.86	2/561 (0.4%)
54	B8	0.46	0/525	0.89	2/691 (0.3%)
54	D8	0.39	0/525	0.82	2/691 (0.3%)
55	B9	0.42	0/310	0.79	0/407
55	D9	0.36	0/310	0.84	0/407
All	All	0.30	2/317730 (0.0%)	0.59	119/475754 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	AB	0	1
7	AG	0	1
7	CG	0	1
50	B4	0	2
All	All	0	5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	CW	8	4SU	O3'-P	5.27	1.61	1.56
23	CY	8	4SU	O3'-P	5.08	1.61	1.56

All (119) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
43	BX	94	GLY	N-CA-C	10.18	124.81	112.49
45	BZ	158	PRO	CA-C-N	9.18	131.32	119.84
45	BZ	158	PRO	C-N-CA	9.18	131.32	119.84
28	DE	72	VAL	CA-C-N	8.47	136.95	121.70
28	DE	72	VAL	C-N-CA	8.47	136.95	121.70
13	AM	84	ILE	N-CA-C	8.17	118.97	110.72
2	AB	123	ALA	N-CA-C	-7.79	103.77	113.28
50	B4	60	GLN	N-CA-C	-7.75	103.55	113.16
50	D4	59	PHE	N-CA-C	7.51	119.46	110.44
30	BG	31	VAL	CA-C-N	7.36	127.41	119.90
30	BG	31	VAL	C-N-CA	7.36	127.41	119.90
4	CD	171	GLY	CA-C-N	7.30	126.83	119.24
4	CD	171	GLY	C-N-CA	7.30	126.83	119.24
2	AB	128	GLU	N-CA-C	-7.25	102.70	112.26
2	CB	124	SER	CA-C-N	-7.06	112.65	120.14
2	CB	124	SER	C-N-CA	-7.06	112.65	120.14
35	DP	44	GLY	CA-C-N	7.03	134.36	121.70
35	DP	44	GLY	C-N-CA	7.03	134.36	121.70
12	CL	28	LYS	N-CA-C	6.97	121.01	111.39
46	B0	12	ASN	N-CA-C	6.92	122.02	113.50
13	CM	106	ASN	N-CA-C	6.92	121.48	113.38
28	DE	85	ASN	CA-C-N	6.92	126.84	119.85
28	DE	85	ASN	C-N-CA	6.92	126.84	119.85
4	AD	188	LEU	CA-C-N	6.84	126.88	119.90
4	AD	188	LEU	C-N-CA	6.84	126.88	119.90
3	AC	72	LYS	CA-C-N	6.76	126.72	119.28
3	AC	72	LYS	C-N-CA	6.76	126.72	119.28
27	DD	120	GLY	CA-C-N	6.66	126.61	119.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
27	DD	120	GLY	C-N-CA	6.66	126.61	119.28
25	BA	2014	G	C2'-C3'-O3'	6.52	119.28	109.50
51	D5	46	CYS	CA-C-N	6.49	126.11	119.56
51	D5	46	CYS	C-N-CA	6.49	126.11	119.56
29	BF	89	VAL	N-CA-C	6.47	116.61	110.53
54	B8	62	LEU	CA-C-N	6.38	126.00	119.56
54	B8	62	LEU	C-N-CA	6.38	126.00	119.56
19	CS	82	GLY	N-CA-C	6.34	118.99	110.43
17	AQ	67	LYS	N-CA-C	-6.26	101.15	110.23
43	BX	94	GLY	CA-C-N	6.20	132.86	121.70
43	BX	94	GLY	C-N-CA	6.20	132.86	121.70
8	CH	73	ASP	CA-C-N	6.13	127.50	119.84
8	CH	73	ASP	C-N-CA	6.13	127.50	119.84
27	BD	274	ARG	N-CA-C	6.09	118.41	110.43
32	DI	72	LEU	N-CA-C	6.08	117.98	111.36
29	DF	21	ALA	CA-C-N	6.07	132.62	121.70
29	DF	21	ALA	C-N-CA	6.07	132.62	121.70
30	DG	127	GLY	N-CA-C	-6.06	107.87	115.08
25	DA	1992	G	C2'-C3'-O3'	6.03	118.54	109.50
45	BZ	151	HIS	N-CA-C	6.02	117.67	110.44
4	AD	50	ARG	CA-C-N	5.93	126.27	119.92
4	AD	50	ARG	C-N-CA	5.93	126.27	119.92
12	CL	119	LYS	N-CA-C	-5.83	101.84	110.48
15	AO	87	ILE	N-CA-C	5.83	117.21	111.67
50	B4	65	ASP	N-CA-C	-5.81	105.50	112.59
30	DG	96	ARG	CB-CA-C	-5.79	109.88	116.54
12	CL	105	TYR	CB-CA-C	-5.70	109.47	117.23
51	D5	26	THR	CA-C-N	5.69	123.81	119.66
51	D5	26	THR	C-N-CA	5.69	123.81	119.66
50	B4	40	HIS	CA-C-N	5.68	126.94	119.84
50	B4	40	HIS	C-N-CA	5.68	126.94	119.84
45	BZ	14	LYS	CA-C-N	5.67	125.34	119.05
45	BZ	14	LYS	C-N-CA	5.67	125.34	119.05
32	DI	31	LEU	CA-C-N	-5.62	114.02	119.87
32	DI	31	LEU	C-N-CA	-5.62	114.02	119.87
19	CS	30	LEU	N-CA-C	5.61	118.58	110.28
50	D4	68	ARG	N-CA-C	5.57	118.99	110.36
3	AC	96	GLY	N-CA-C	-5.56	107.59	115.43
54	D8	62	LEU	CA-C-N	5.52	125.14	119.56
54	D8	62	LEU	C-N-CA	5.52	125.14	119.56
30	BG	127	GLY	N-CA-C	-5.50	106.92	114.67
40	BU	9	VAL	N-CA-C	5.44	115.65	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	CG	79	ARG	N-CA-C	5.44	120.30	111.37
45	DZ	14	LYS	CA-C-N	5.44	125.09	119.05
45	DZ	14	LYS	C-N-CA	5.44	125.09	119.05
2	CB	129	GLU	N-CA-C	-5.41	105.94	112.54
27	DD	275	LYS	N-CA-C	-5.40	100.23	108.76
2	AB	23	ARG	N-CA-C	-5.39	105.14	112.26
49	B3	11	SER	N-CA-C	5.39	116.48	109.64
7	CG	87	VAL	N-CA-C	5.34	114.35	108.05
32	BI	118	LYS	CA-C-N	5.32	126.49	119.84
32	BI	118	LYS	C-N-CA	5.32	126.49	119.84
31	DH	35	VAL	N-CA-C	5.31	113.72	107.77
50	D4	59	PHE	CA-C-N	5.29	131.22	121.70
50	D4	59	PHE	C-N-CA	5.29	131.22	121.70
50	B4	28	LYS	CA-C-N	5.27	124.90	119.05
50	B4	28	LYS	C-N-CA	5.27	124.90	119.05
3	CC	43	LEU	N-CA-C	5.27	118.17	111.69
30	DG	44	GLY	N-CA-C	-5.24	108.39	115.36
42	BW	13	SER	CA-C-N	5.21	125.25	119.32
42	BW	13	SER	C-N-CA	5.21	125.25	119.32
53	D7	6	GLN	CA-C-N	5.21	125.21	119.90
53	D7	6	GLN	C-N-CA	5.21	125.21	119.90
18	AR	51	LEU	CA-C-N	5.20	125.18	120.03
18	AR	51	LEU	C-N-CA	5.20	125.18	120.03
50	B4	62	ARG	CB-CA-C	-5.19	110.57	116.54
46	D0	82	ARG	CA-C-N	5.18	125.18	119.89
46	D0	82	ARG	C-N-CA	5.18	125.18	119.89
45	BZ	52	SER	CB-CA-C	-5.18	110.62	116.63
30	BG	96	ARG	CB-CA-C	-5.17	110.59	116.54
12	AL	105	TYR	CB-CA-C	-5.17	110.20	117.23
25	BA	1346	U	P-O3'-C3'	5.16	127.94	120.20
28	DE	143	ASN	CB-CA-C	-5.15	109.02	116.54
28	DE	72	VAL	CA-C-O	-5.11	115.44	120.90
28	DE	31	CYS	CA-C-N	5.09	124.85	119.76
28	DE	31	CYS	C-N-CA	5.09	124.85	119.76
2	AB	38	GLY	N-CA-C	-5.09	106.11	114.76
3	AC	4	LYS	N-CA-C	5.07	117.59	110.23
3	CC	108	ASN	CA-C-N	5.07	125.14	119.87
3	CC	108	ASN	C-N-CA	5.07	125.14	119.87
27	BD	120	GLY	CA-C-N	5.06	124.85	119.28
27	BD	120	GLY	C-N-CA	5.06	124.85	119.28
31	DH	38	SER	CA-C-N	5.06	124.72	119.56
31	DH	38	SER	C-N-CA	5.06	124.72	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
47	D1	67	ILE	CB-CA-C	-5.05	109.00	114.35
50	B4	52	THR	N-CA-C	-5.04	107.18	113.38
10	AJ	57	LYS	N-CA-C	5.03	117.50	111.71
41	DV	53	GLU	N-CA-C	5.02	116.60	111.03
29	DF	159	GLY	N-CA-C	-5.01	106.97	115.34
1	CA	1183	A	P-O3'-C3'	5.00	127.71	120.20
10	CJ	98	ILE	N-CA-C	5.00	115.18	107.77

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	9	GLU	Peptide
7	AG	79	ARG	Peptide
50	B4	59	PHE	Peptide
50	B4	67	TYR	Peptide
7	CG	79	ARG	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32185	0	16243	451	0
1	CA	32312	0	16307	523	0
2	AB	1846	0	1867	73	0
2	CB	1825	0	1828	88	0
3	AC	1548	0	1535	40	0
3	CC	1542	0	1517	55	0
4	AD	1655	0	1672	51	0
4	CD	1674	0	1714	45	0
5	AE	1129	0	1185	36	0
5	CE	1133	0	1191	40	0
6	AF	810	0	804	18	0
6	CF	816	0	808	12	0
7	AG	1231	0	1238	29	0
7	CG	1235	0	1249	32	0
8	AH	1088	0	1126	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	CH	1088	0	1126	40	0
9	AI	983	0	986	40	0
9	CI	978	0	966	46	0
10	AJ	709	0	650	28	0
10	CJ	714	0	672	36	0
11	AK	829	0	825	13	0
11	CK	833	0	836	10	0
12	AL	930	0	980	15	0
12	CL	930	0	980	23	0
13	AM	958	0	1002	30	0
13	CM	950	0	988	39	0
14	AN	492	0	529	24	0
14	CN	492	0	529	17	0
15	AO	728	0	760	21	0
15	CO	728	0	760	24	0
16	AP	681	0	697	17	0
16	CP	677	0	686	18	0
17	AQ	823	0	891	22	0
17	CQ	823	0	891	14	0
18	AR	555	0	618	18	0
18	CR	555	0	618	17	0
19	AS	652	0	662	28	0
19	CS	646	0	644	29	0
20	AT	728	0	798	19	0
20	CT	727	0	796	23	0
21	AU	199	0	208	4	0
21	CU	199	0	208	6	0
22	AV	277	0	140	1	0
22	CV	277	0	140	7	0
23	AW	1592	0	819	29	0
23	AY	1585	0	804	55	0
23	CW	1544	0	788	39	0
23	CY	1565	0	795	61	0
24	AX	1625	0	828	15	0
24	CX	1625	0	828	19	0
25	BA	61844	0	31181	619	0
25	DA	60314	0	30412	746	0
26	BB	2577	0	1305	15	0
26	DB	2575	0	1303	51	0
27	BD	2136	0	2218	52	0
27	DD	2136	0	2218	56	0
28	BE	1559	0	1618	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	DE	1559	0	1617	40	0
29	BF	1584	0	1625	22	0
29	DF	1580	0	1619	44	0
30	BG	1429	0	1447	25	0
30	DG	1428	0	1438	55	0
31	BH	1330	0	1407	24	0
31	DH	1330	0	1407	43	0
32	BI	1097	0	1140	33	0
32	DI	1064	0	1082	31	0
33	BN	1117	0	1184	15	0
33	DN	1117	0	1184	21	0
34	BO	933	0	996	19	0
34	DO	933	0	996	17	0
35	BP	1135	0	1212	29	0
35	DP	1135	0	1212	48	0
36	BQ	1122	0	1179	21	0
36	DQ	1122	0	1179	32	0
37	BR	968	0	1033	24	0
37	DR	968	0	1033	34	0
38	BS	873	0	927	23	0
38	DS	870	0	923	23	0
39	BT	1091	0	1151	26	0
39	DT	1083	0	1136	22	0
40	BU	959	0	1019	19	0
40	DU	959	0	1019	21	0
41	BV	771	0	830	15	0
41	DV	771	0	830	18	0
42	BW	886	0	940	10	0
42	DW	886	0	940	15	0
43	BX	750	0	814	14	0
43	DX	750	0	814	18	0
44	BY	806	0	881	20	0
44	DY	806	0	881	21	0
45	BZ	1240	0	1240	26	0
45	DZ	1271	0	1273	54	0
46	B0	653	0	674	10	0
46	D0	653	0	674	19	0
47	B1	755	0	826	16	0
47	D1	755	0	826	15	0
48	B2	588	0	643	8	0
48	D2	588	0	643	7	0
49	B3	469	0	518	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	D3	464	0	514	9	0
50	B4	552	0	533	27	0
50	D4	532	0	503	30	0
51	B5	455	0	465	6	0
51	D5	455	0	465	8	0
52	B6	453	0	473	9	0
52	D6	449	0	469	11	0
53	B7	418	0	467	10	0
53	D7	418	0	467	11	0
54	B8	517	0	582	19	0
54	D8	517	0	582	23	0
55	B9	307	0	335	4	0
55	D9	307	0	335	9	0
56	AA	233	0	0	0	0
56	AB	2	0	0	0	0
56	AD	1	0	0	0	0
56	AE	2	0	0	0	0
56	AF	1	0	0	0	0
56	AH	1	0	0	0	0
56	AK	1	0	0	0	0
56	AL	1	0	0	0	0
56	AM	1	0	0	0	0
56	AN	1	0	0	0	0
56	AR	1	0	0	0	0
56	AT	1	0	0	0	0
56	AW	4	0	0	0	0
56	AX	13	0	0	0	0
56	AY	2	0	0	0	0
56	B0	7	0	0	0	0
56	B1	2	0	0	0	0
56	B2	2	0	0	0	0
56	B3	2	0	0	0	0
56	B4	1	0	0	0	0
56	B5	4	0	0	0	0
56	B6	2	0	0	0	0
56	B7	3	0	0	0	0
56	B8	3	0	0	0	0
56	B9	1	0	0	0	0
56	BA	906	0	0	0	0
56	BB	30	0	0	0	0
56	BD	13	0	0	0	0
56	BE	12	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	BF	15	0	0	0	0
56	BG	6	0	0	0	0
56	BH	1	0	0	0	0
56	BI	1	0	0	0	0
56	BN	4	0	0	0	0
56	BO	5	0	0	0	0
56	BP	6	0	0	0	0
56	BQ	7	0	0	0	0
56	BR	3	0	0	0	0
56	BS	3	0	0	0	0
56	BT	2	0	0	0	0
56	BU	10	0	0	0	0
56	BV	5	0	0	0	0
56	BW	5	0	0	0	0
56	BX	6	0	0	0	0
56	BY	3	0	0	0	0
56	BZ	3	0	0	0	0
56	CA	201	0	0	0	0
56	CD	2	0	0	0	0
56	CE	1	0	0	0	0
56	CF	2	0	0	0	0
56	CG	1	0	0	0	0
56	CJ	2	0	0	0	0
56	CK	1	0	0	0	0
56	CL	2	0	0	0	0
56	CP	1	0	0	0	0
56	CQ	2	0	0	0	0
56	CR	1	0	0	0	0
56	CT	1	0	0	0	0
56	CV	1	0	0	0	0
56	CW	4	0	0	0	0
56	CX	6	0	0	0	0
56	D0	1	0	0	0	0
56	D1	1	0	0	0	0
56	D3	1	0	0	0	0
56	D5	2	0	0	0	0
56	D8	2	0	0	0	0
56	DA	673	0	0	0	0
56	DB	21	0	0	0	0
56	DD	6	0	0	0	0
56	DE	7	0	0	0	0
56	DF	7	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	DG	1	0	0	0	0
56	DO	1	0	0	0	0
56	DP	1	0	0	0	0
56	DQ	3	0	0	0	0
56	DR	1	0	0	0	0
56	DT	1	0	0	0	0
56	DU	4	0	0	0	0
56	DV	2	0	0	0	0
56	DW	3	0	0	0	0
56	DX	1	0	0	0	0
56	DY	1	0	0	0	0
56	DZ	1	0	0	0	0
57	AA	30	0	28	1	0
57	CA	30	0	29	1	0
58	AD	8	0	0	0	0
58	CD	8	0	0	0	0
59	AN	1	0	0	0	0
59	B4	1	0	0	0	0
59	B5	1	0	0	0	0
59	B6	1	0	0	0	0
59	B9	1	0	0	0	0
59	BY	1	0	0	0	0
59	CN	1	0	0	0	0
59	D4	1	0	0	0	0
59	D5	1	0	0	0	0
59	D6	1	0	0	0	0
59	D9	1	0	0	0	0
59	DY	1	0	0	0	0
60	AX	1	0	0	0	0
60	CX	1	0	0	0	0
61	AA	264	0	0	16	0
61	AB	1	0	0	0	0
61	AE	2	0	0	0	0
61	AJ	1	0	0	0	0
61	AL	4	0	0	0	0
61	AM	1	0	0	0	0
61	AQ	1	0	0	0	0
61	AV	4	0	0	0	0
61	AW	2	0	0	0	0
61	AX	11	0	0	2	0
61	AY	1	0	0	0	0
61	B0	8	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	B1	3	0	0	0	0
61	B2	4	0	0	2	0
61	B3	3	0	0	0	0
61	B4	1	0	0	0	0
61	B5	4	0	0	0	0
61	B6	1	0	0	0	0
61	B7	4	0	0	1	0
61	B8	8	0	0	0	0
61	BA	1486	0	0	44	0
61	BB	43	0	0	2	0
61	BD	19	0	0	2	0
61	BE	20	0	0	1	0
61	BF	14	0	0	1	0
61	BG	5	0	0	1	0
61	BH	1	0	0	0	0
61	BI	2	0	0	0	0
61	BN	2	0	0	0	0
61	BO	7	0	0	0	0
61	BP	19	0	0	1	0
61	BQ	5	0	0	1	0
61	BR	5	0	0	0	0
61	BS	5	0	0	0	0
61	BT	5	0	0	0	0
61	BU	8	0	0	1	0
61	BV	6	0	0	0	0
61	BW	1	0	0	0	0
61	BX	2	0	0	0	0
61	BY	3	0	0	0	0
61	BZ	1	0	0	0	0
61	CA	204	0	0	12	0
61	CD	1	0	0	0	0
61	CG	1	0	0	0	0
61	CI	1	0	0	0	0
61	CJ	4	0	0	0	0
61	CL	4	0	0	0	0
61	CO	1	0	0	0	0
61	CP	1	0	0	0	0
61	CR	1	0	0	0	0
61	CT	1	0	0	0	0
61	CW	2	0	0	0	0
61	CX	6	0	0	0	0
61	D0	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	D1	4	0	0	1	0
61	D2	1	0	0	0	0
61	D3	1	0	0	0	0
61	D5	2	0	0	0	0
61	D7	5	0	0	0	0
61	D8	5	0	0	0	0
61	D9	1	0	0	0	0
61	DA	1039	0	0	58	0
61	DB	10	0	0	1	0
61	DD	17	0	0	0	0
61	DE	8	0	0	1	0
61	DF	6	0	0	0	0
61	DI	2	0	0	0	0
61	DN	1	0	0	0	0
61	DO	3	0	0	0	0
61	DP	12	0	0	3	0
61	DQ	1	0	0	0	0
61	DR	3	0	0	0	0
61	DT	3	0	0	0	0
61	DU	1	0	0	0	0
61	DV	1	0	0	0	0
61	DW	2	0	0	0	0
61	DX	2	0	0	0	0
61	DY	1	0	0	1	0
61	DZ	2	0	0	0	0
All	All	298643	0	196646	4470	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (4470) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1027:C:N3	1:AA:1034:G:C6	2.18	1.10
1:CA:1002:G:H1	1:CA:1038:C:N4	1.51	1.08
23:AW:6:G:H1	23:AW:67:C:N4	1.49	1.07
1:CA:1028:C:N3	1:CA:1033:G:C6	2.23	1.06
1:AA:78:G:C6	1:AA:91:C:N4	2.29	1.00
1:AA:1027:C:C2	1:AA:1034:G:C6	2.51	0.99
1:AA:78:G:HO2'	1:AA:79:G:H8	1.08	0.97
1:CA:1029:C:C4	1:CA:1032:G:N1	2.32	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2124:G:H1	25:DA:2174:C:H42	1.12	0.97
23:CW:50:U:H3	23:CW:64:A:N6	1.63	0.97
1:CA:947:G:H1	1:CA:1234:C:H42	0.97	0.96
1:AA:1502:A:H2	1:AA:1505:G:H1	1.12	0.96
25:BA:2121:U:H3	25:BA:2212:G:H1	1.11	0.95
1:CA:1132:C:H42	1:CA:1142:G:H1	1.14	0.95
1:CA:999:C:H42	1:CA:1042:G:H1	1.10	0.95
25:BA:2161:C:H42	25:BA:2174:G:H1	1.13	0.94
23:CW:27:G:H1	23:CW:43:C:H42	1.12	0.93
1:CA:38:G:H22	1:CA:397:A:H5”	1.32	0.93
1:CA:1030(A):G:N2	1:CA:1030(D):A:OP2	2.00	0.93
23:AY:26:A:H61	23:AY:44:G:H1	1.10	0.93
23:AW:26:A:H61	23:AW:44:G:H1	1.02	0.92
25:DA:2121:G:H1	25:DA:2177:C:H42	1.13	0.91
25:BA:2161:C:N4	25:BA:2174:G:H1	1.68	0.91
23:CY:19:G:N2	23:CY:56:C:N3	2.19	0.91
1:AA:78:G:C2	1:AA:91:C:N3	2.39	0.90
25:DA:2807:G:N1	25:DA:2893:G:O6	2.04	0.90
13:CM:122:LYS:HD3	13:CM:123:ALA:H	1.37	0.89
55:D9:25:VAL:HB	55:D9:34:GLN:HB2	1.55	0.89
26:DB:7:G:H21	38:DS:38:GLN:HE22	1.20	0.89
1:CA:1002:G:N2	1:CA:1038:C:N3	2.20	0.89
25:BA:2146:G:H1	25:BA:2196:C:H42	1.15	0.88
42:BW:14:PRO:HG2	42:BW:78:GLU:HG2	1.54	0.88
1:CA:947:G:H1	1:CA:1234:C:N4	1.70	0.88
23:CW:50:U:H3	23:CW:64:A:H61	0.89	0.88
7:AG:72:ARG:HH11	7:AG:72:ARG:HG3	1.35	0.88
25:DA:1689:A:H62	25:DA:1698:A:H2	1.22	0.88
25:BA:2143:G:H1	25:BA:2199:C:H42	1.16	0.88
42:DW:14:PRO:HG2	42:DW:78:GLU:HG2	1.57	0.87
1:CA:1353:G:OP1	21:CU:10:ARG:NH1	2.07	0.87
23:CY:29:G:H1	23:CY:41:C:H42	1.23	0.87
46:B0:11:ARG:O	46:B0:14:ARG:NH2	2.07	0.87
25:BA:2158:C:N4	25:BA:2177:G:N1	2.22	0.87
6:CF:81:ILE:HD11	27:DD:125:ILE:HB	1.55	0.87
25:DA:1315:C:OP2	61:DA:4472:HOH:O	1.90	0.87
25:BA:1829:U:H5’	27:BD:259:THR:HG22	1.56	0.87
1:CA:656:C:O2’	15:CO:28:GLN:NE2	2.07	0.86
2:CB:16:HIS:HB2	2:CB:204:ASN:HB3	1.57	0.86
15:CO:54:ARG:NH1	15:CO:58:MET:SD	2.48	0.86
1:CA:999:C:N4	1:CA:1042:G:H1	1.73	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:900:A:H2'	25:DA:901:A:H8	1.39	0.86
2:CB:18:GLY:HA2	2:CB:42:ILE:HG13	1.55	0.86
1:AA:1008:C:N4	1:AA:1021:G:N1	2.22	0.86
7:AG:72:ARG:NH1	7:AG:142:GLU:OE2	2.08	0.86
43:BX:31:HIS:HD2	43:BX:33:LYS:H	1.24	0.85
1:AA:1008:C:N3	1:AA:1021:G:N2	2.23	0.85
3:CC:41:GLY:O	3:CC:45:LYS:NZ	2.09	0.85
25:DA:2141:G:O6	25:DA:2150:U:O2	1.95	0.85
5:CE:143:ARG:NH1	8:CH:77:GLU:OE1	2.09	0.85
23:AY:26:A:N6	23:AY:44:G:H1	1.75	0.85
23:AW:26:A:N6	23:AW:44:G:H1	1.74	0.85
25:DA:2139:C:N4	25:DA:2152:G:H1	1.75	0.85
25:DA:948:G:OP1	61:DA:4588:HOH:O	1.94	0.84
44:BY:92:ASN:HB3	44:BY:94:LYS:H	1.43	0.84
25:BA:2331:G:H22	38:BS:3:ARG:HE	1.22	0.84
28:DE:72:VAL:HG13	28:DE:73:GLU:HG3	1.59	0.84
5:CE:100:VAL:O	5:CE:107:ARG:NH2	2.10	0.83
1:CA:1003:G:N2	1:CA:1025:U:O4	2.11	0.83
25:DA:2139:C:N4	25:DA:2152:G:N1	2.26	0.83
1:CA:1360:A:OP2	14:CN:35:ARG:NH2	2.12	0.83
1:CA:1029:C:N3	1:CA:1032:G:N2	2.27	0.83
1:CA:1502:A:H2	1:CA:1505:G:H1	1.27	0.82
25:DA:323:G:HO2'	25:DA:1205:U:H3	1.26	0.82
25:BA:1114:G:N2	25:BA:1141:A:O2'	2.11	0.82
1:AA:1027:C:C2	1:AA:1034:G:N1	2.47	0.82
25:BA:2299:A:H62	25:BA:2356:U:H3	1.27	0.82
45:DZ:46:LYS:O	45:DZ:50:GLN:NE2	2.11	0.81
1:CA:1028:C:C2	1:CA:1033:G:C6	2.68	0.81
23:CY:26:A:N1	23:CY:44:G:C6	2.48	0.81
25:BA:2158:C:N3	25:BA:2177:G:N2	2.29	0.81
38:DS:38:GLN:NE2	38:DS:47:THR:OG1	2.13	0.81
25:DA:1568:G:N7	61:DA:5002:HOH:O	2.13	0.81
25:DA:2139:C:N3	25:DA:2152:G:N2	2.28	0.81
1:AA:1314:C:OP2	19:AS:4:SER:OG	1.98	0.81
25:BA:181:C:OP1	61:BA:4160:HOH:O	1.97	0.80
35:BP:126:VAL:HG12	35:BP:148:LEU:HD22	1.63	0.80
1:CA:953:G:H5'	1:CA:965:A:H61	1.45	0.80
1:CA:1002:G:H1	1:CA:1038:C:H42	0.83	0.80
25:BA:1060:U:OP2	61:BA:5368:HOH:O	1.99	0.80
25:BA:2044:U:OP1	61:BA:4800:HOH:O	1.97	0.80
1:CA:1003:G:O6	1:CA:1035:A:N6	2.13	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:DX:31:HIS:HD2	43:DX:33:LYS:H	1.30	0.80
1:AA:1189:C:OP1	10:AJ:51:ARG:NH2	2.14	0.80
25:BA:2015:U:OP2	61:BA:5459:HOH:O	1.99	0.80
20:AT:86:ARG:O	20:AT:90:GLN:NE2	2.15	0.80
23:AY:50:U:O4	23:AY:64:A:N1	2.13	0.80
17:AQ:26:GLN:HG2	17:AQ:37:LYS:HG2	1.63	0.80
25:DA:1973:G:OP1	61:DA:4547:HOH:O	1.99	0.80
2:AB:16:HIS:HB2	2:AB:204:ASN:HB3	1.63	0.80
25:BA:1736:A:H62	25:BA:1745:A:H2	1.29	0.80
2:AB:16:HIS:CG	2:AB:17:PHE:H	1.99	0.80
25:BA:1111:U:O2	25:BA:1119:A:N6	2.14	0.80
25:DA:2287:A:H62	25:DA:2344:U:H3	1.28	0.80
25:BA:542:C:OP1	51:B5:16:ARG:NH2	2.15	0.80
1:AA:38:G:H22	1:AA:397:A:H5"	1.47	0.80
10:AJ:35:SER:HB3	10:AJ:73:ASP:HB2	1.63	0.80
25:DA:2206:G:H3'	25:DA:2207:G:C8	2.17	0.80
25:DA:1798:U:OP2	27:DD:274:ARG:NH2	2.14	0.79
25:DA:1648:C:OP1	61:DA:4516:HOH:O	1.98	0.79
23:AW:6:G:N2	23:AW:67:C:N3	2.28	0.79
1:AA:1002:G:H3'	1:AA:1003:G:O4'	1.83	0.79
1:AA:1414:U:H3	1:AA:1486:G:H1	1.31	0.79
45:BZ:139:VAL:HG22	45:BZ:155:LEU:HD11	1.64	0.79
1:CA:1029:C:N4	1:CA:1032:G:N1	2.31	0.79
1:AA:1025:U:O2	1:AA:1036:G:O6	1.99	0.79
25:DA:900:A:H2'	25:DA:901:A:C8	2.18	0.79
1:AA:975:A:H4'	1:AA:976:G:H5"	1.63	0.79
25:DA:2683:C:OP1	39:DT:53:ARG:NH2	2.16	0.79
24:AX:6:G:H1	24:AX:67:C:H42	1.28	0.79
1:CA:522:C:H41	12:CL:53:ARG:HH22	1.30	0.79
1:CA:992:U:H3	1:CA:1044:A:H62	1.26	0.79
30:DG:80:PHE:O	30:DG:82:LEU:N	2.16	0.79
1:AA:997:U:H3	1:AA:1044:A:H61	1.28	0.78
25:DA:994:C:OP1	40:DU:53:ARG:NH2	2.15	0.78
25:BA:894:U:OP2	61:BA:4554:HOH:O	2.01	0.78
23:CW:27:G:H1	23:CW:43:C:N4	1.80	0.78
1:AA:511:C:OP2	4:AD:49:ARG:NH1	2.16	0.78
11:AK:48:ILE:HD12	11:AK:63:LEU:HB2	1.65	0.78
25:BA:2158:C:N4	25:BA:2177:G:C6	2.52	0.78
46:B0:10:THR:HG22	46:B0:12:ASN:H	1.47	0.78
1:CA:1422:G:H5"	34:DO:48:PRO:HB3	1.64	0.78
23:CY:5:G:H1	23:CY:68:C:H42	1.28	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1027:C:O2	1:AA:1034:G:C2	2.36	0.78
1:CA:346:G:OP1	39:DT:41:ARG:NH2	2.16	0.78
26:DB:92:C:OP1	45:DZ:79:ARG:NH1	2.16	0.78
1:CA:742:G:OP2	15:CO:35:ARG:NH2	2.17	0.78
25:DA:1449:A:O2'	25:DA:1529:G:N2	2.17	0.78
25:BA:1059:C:OP2	61:BA:5368:HOH:O	2.00	0.78
25:DA:963:U:OP2	61:DA:4588:HOH:O	2.02	0.78
36:DQ:22:LYS:HD3	36:DQ:23:GLY:N	1.98	0.78
24:CX:6:G:H1	24:CX:67:C:H42	1.30	0.77
25:DA:301:G:OP2	44:DY:84:ARG:NH2	2.18	0.77
25:DA:1171:G:H1	25:DA:1178:C:H42	1.29	0.77
36:DQ:26:TYR:O	36:DQ:67:ARG:NH1	2.16	0.77
1:AA:1182:G:H4'	1:AA:1183:A:H5'	1.66	0.77
11:CK:99:GLN:HG2	11:CK:105:VAL:HG21	1.66	0.77
1:AA:1086:U:H3	1:AA:1099:G:H22	1.32	0.77
25:BA:2145:G:H1	25:BA:2197:C:H42	1.32	0.77
25:DA:2121:G:H1	25:DA:2177:C:N4	1.82	0.77
42:DW:2:GLU:OE2	42:DW:72:LYS:NZ	2.17	0.77
45:DZ:72:ARG:NH2	45:DZ:97:GLU:O	2.17	0.77
23:AY:26:A:N6	23:AY:44:G:N1	2.28	0.77
25:BA:693:G:O6	25:BA:697:C:N4	2.15	0.77
23:CY:26:A:N1	23:CY:44:G:O6	2.18	0.77
25:DA:2124:G:H1	25:DA:2174:C:N4	1.83	0.77
2:AB:16:HIS:CD2	2:AB:17:PHE:H	2.02	0.77
9:AI:9:ARG:HG2	9:AI:14:VAL:HG12	1.66	0.77
25:BA:239:G:OP2	54:B8:13:ARG:NH2	2.17	0.77
25:BA:1249:A:H2	25:BA:1287:A:H62	1.31	0.77
1:CA:148:G:H2'	1:CA:149:A:H8	1.49	0.77
1:AA:1352:C:OP1	21:AU:3:LYS:NZ	2.17	0.77
1:AA:1422:G:H5"	34:BO:48:PRO:HB3	1.67	0.77
2:AB:155:LEU:HD21	2:AB:159:PRO:HG3	1.67	0.77
23:CW:4:C:N3	23:CW:69:G:N2	2.33	0.77
1:CA:975:A:H4'	1:CA:976:G:H5"	1.67	0.77
36:BQ:111:GLU:OE1	36:BQ:133:ARG:NH2	2.18	0.77
1:AA:78:G:C2	1:AA:91:C:C4	2.73	0.76
1:AA:116:A:OP1	61:AA:4254:HOH:O	2.02	0.76
1:CA:427:U:OP1	4:CD:13:ARG:NH2	2.18	0.76
1:AA:78:G:N1	1:AA:91:C:C4	2.53	0.76
1:AA:742:G:OP2	15:AO:35:ARG:NH2	2.17	0.76
2:AB:69:LEU:HB3	2:AB:162:ILE:HG22	1.65	0.76
25:BA:2146:G:H1	25:BA:2196:C:N4	1.83	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:DB:4:C:H42	26:DB:117:G:H1	1.33	0.76
25:BA:656:A:OP1	35:BP:65:ARG:NH1	2.19	0.76
23:CY:19:G:N1	23:CY:56:C:N4	2.34	0.76
45:BZ:154:ASP:N	45:BZ:154:ASP:OD1	2.19	0.76
25:DA:1798:U:H5'	27:DD:259:THR:HG22	1.68	0.76
25:DA:2122:U:O4	25:DA:2176:A:N1	2.18	0.76
4:CD:98:GLU:OE1	4:CD:103:ASN:ND2	2.16	0.76
25:DA:7:G:N2	25:DA:2896:C:O2	2.14	0.76
1:CA:1329:A:H5"	13:CM:26:GLY:H	1.51	0.76
2:CB:88:ALA:HB1	2:CB:222:ILE:HD11	1.67	0.76
4:CD:165:MET:SD	4:CD:168:ARG:NH1	2.58	0.76
9:CI:117:HIS:HB2	9:CI:121:ARG:HG2	1.68	0.76
25:DA:2112:G:N7	25:DA:2169:A:N6	2.33	0.76
45:BZ:28:MET:HE1	45:BZ:61:LEU:HD21	1.66	0.75
1:CA:158:G:N2	1:CA:163:C:O2	2.19	0.75
25:BA:2144:U:O4	25:BA:2198:A:N1	2.19	0.75
38:BS:25:ARG:NH1	38:BS:42:ASP:OD1	2.19	0.75
13:CM:58:GLU:O	13:CM:62:ASN:ND2	2.18	0.75
25:DA:990:A:OP2	61:DA:4499:HOH:O	2.04	0.75
2:AB:201:ILE:HG21	2:AB:214:ILE:HG21	1.68	0.75
2:AB:185:ILE:HG22	2:AB:199:TYR:HB2	1.67	0.75
13:CM:3:ARG:NH2	13:CM:9:ILE:O	2.18	0.75
25:DA:397:G:N7	61:DA:4914:HOH:O	2.18	0.75
25:BA:2157:A:N6	25:BA:2178:G:O2'	2.20	0.75
1:CA:1029:C:C2	1:CA:1032:G:N2	2.55	0.75
1:CA:1256:A:N6	1:CA:1278:U:O2	2.20	0.75
8:CH:51:VAL:HG21	8:CH:60:ARG:HB2	1.67	0.75
9:CI:7:THR:O	9:CI:83:ARG:NH1	2.20	0.75
23:CY:18:G:N2	23:CY:55:PSU:N3	2.34	0.75
30:DG:115:ARG:HD2	30:DG:136:ARG:HH21	1.51	0.75
45:BZ:72:ARG:NH2	45:BZ:97:GLU:O	2.20	0.74
40:DU:76:TYR:OH	40:DU:92:ARG:NH1	2.19	0.74
1:CA:1132:C:N4	1:CA:1142:G:H1	1.86	0.74
43:DX:11:PRO:HB3	43:DX:92:LEU:HD11	1.69	0.74
1:AA:583:A:OP2	61:AA:4028:HOH:O	2.05	0.74
53:B7:34:ARG:NH1	53:B7:41:ARG:O	2.20	0.74
23:AW:5:G:H2'	23:AW:6:G:C8	2.22	0.74
1:CA:504:C:OP1	61:CA:4006:HOH:O	2.05	0.74
25:DA:2849:U:OP2	39:DT:95:ARG:NH1	2.21	0.74
25:BA:928:G:H3'	25:BA:929:G:H8	1.53	0.74
1:AA:1183:A:H3'	1:AA:1184:G:H5"	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AY:19:G:N2	23:AY:56:C:N3	2.36	0.74
25:BA:2736:C:OP1	37:BR:3:HIS:ND1	2.19	0.74
1:CA:922:G:H4'	5:CE:20:GLN:HA	1.69	0.74
1:CA:1301:U:O2'	1:CA:1302:U:H5'	1.88	0.74
22:CV:23:A:H4'	22:CV:24:A:H5'	1.70	0.74
25:DA:2646:C:OP2	25:DA:2732:G:O2'	2.06	0.74
25:BA:2143:G:H1	25:BA:2199:C:N4	1.85	0.74
25:BA:325:G:OP2	44:BY:84:ARG:NH2	2.21	0.74
13:CM:13:LYS:HA	13:CM:44:ARG:HH11	1.53	0.74
25:DA:1019:U:H3	25:DA:1142(A):A:H62	1.36	0.74
1:AA:96:U:HO2'	1:AA:97:G:H8	1.33	0.73
25:BA:2251:G:OP2	61:BA:4474:HOH:O	2.06	0.73
40:BU:104:GLN:NE2	61:BU:308:HOH:O	2.20	0.73
1:AA:90:U:H2'	1:AA:91:C:H5"	1.68	0.73
3:AC:153:VAL:HG22	3:AC:198:VAL:HG12	1.70	0.73
25:BA:1296:G:OP2	35:BP:21:ARG:NH1	2.21	0.73
31:BH:86:GLU:OE2	31:BH:132:ARG:NH2	2.20	0.73
1:CA:860:A:OP2	61:CA:4160:HOH:O	2.04	0.73
13:CM:107:ALA:HB3	13:CM:111:LYS:HD2	1.68	0.73
1:AA:1027:C:C4	1:AA:1034:G:O6	2.40	0.73
25:BA:1185:C:O3'	33:BN:25:ARG:NH1	2.21	0.73
10:CJ:11:PHE:HE1	10:CJ:67:THR:HG22	1.52	0.73
23:CY:51:U:H3	23:CY:63:G:H1	1.36	0.73
1:AA:953:G:H5'	1:AA:965:A:H61	1.52	0.73
25:BA:2161:C:N3	25:BA:2174:G:N2	2.36	0.73
1:CA:1279:A:O2'	1:CA:1281:U:OP2	2.06	0.73
25:DA:1800:C:OP2	27:DD:183:ARG:NH2	2.20	0.73
33:DN:128:HIS:O	33:DN:131:GLN:NE2	2.21	0.73
36:DQ:27:VAL:O	36:DQ:29:PHE:N	2.19	0.73
1:CA:1029:C:N4	1:CA:1032:G:C6	2.57	0.73
5:AE:74:GLY:HA3	5:AE:116:THR:HG22	1.71	0.73
25:DA:2407:G:OP1	61:DA:4203:HOH:O	2.07	0.73
1:CA:582:U:OP1	15:CO:68:ARG:NH2	2.20	0.73
2:AB:115:LEU:HD13	2:AB:145:LEU:HB3	1.71	0.73
1:CA:21:G:OP1	61:CA:4063:HOH:O	2.06	0.73
1:AA:1238:A:OP2	61:AA:4170:HOH:O	2.06	0.73
25:DA:962:G:OP1	61:DA:4588:HOH:O	2.06	0.73
45:DZ:146:ILE:HG13	45:DZ:174:VAL:HG12	1.70	0.73
47:D1:50:ARG:HG2	47:D1:59:THR:HG22	1.70	0.73
23:CY:29:G:H1	23:CY:41:C:N4	1.87	0.73
3:AC:8:ILE:HG23	3:AC:16:ARG:HG2	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:AQ:66:SER:O	17:AQ:70:ARG:NH1	2.21	0.72
1:CA:770:C:OP1	61:CA:4118:HOH:O	2.06	0.72
25:DA:467:G:OP1	53:D7:33:ARG:NH1	2.22	0.72
25:DA:2116:G:N2	25:DA:2162:G:OP1	2.22	0.72
25:BA:1361:C:OP2	61:BA:4787:HOH:O	2.07	0.72
16:CP:52:ASP:O	16:CP:54:GLU:N	2.22	0.72
26:DB:75:G:N2	45:DZ:87:ASP:OD1	2.21	0.72
1:AA:376:G:H5"	16:AP:5:ARG:HG2	1.71	0.72
25:BA:2153:G:H5"	25:BA:2154:U:H3'	1.70	0.72
26:BB:106:G:H5'	45:BZ:31:ARG:HG2	1.68	0.72
20:CT:57:ARG:HH22	20:CT:100:ILE:HD12	1.50	0.72
25:DA:649:G:H4'	54:D8:46:ARG:HH22	1.54	0.72
25:DA:1314:C:OP1	61:DA:4472:HOH:O	2.07	0.72
25:BA:2802:C:O2	25:BA:2903:G:N1	2.18	0.72
1:AA:1027:C:N3	1:AA:1034:G:C5	2.57	0.72
1:CA:1244:C:H42	1:CA:1293:G:H1	1.37	0.72
1:AA:1423:G:OP1	34:BO:49:ARG:NH2	2.16	0.72
25:BA:1312:G:O5'	42:BW:15:ARG:NH2	2.23	0.72
39:BT:95:ARG:HG2	39:BT:95:ARG:HH11	1.54	0.72
25:DA:2788:C:OP1	28:DE:61:ARG:NH2	2.22	0.72
29:DF:53:THR:HG23	29:DF:55:GLY:H	1.55	0.72
34:DO:35:VAL:HG11	34:DO:103:ALA:HB3	1.70	0.72
35:DP:96:THR:H	35:DP:99:LEU:HD21	1.55	0.72
1:AA:677:U:H3	1:AA:713:G:H22	1.38	0.72
12:CL:57:LYS:NZ	12:CL:65:GLU:OE2	2.21	0.72
25:DA:652(C):G:N2	25:DA:652(V):C:O2	2.17	0.72
1:AA:572:A:OP1	61:AA:4111:HOH:O	2.08	0.72
25:DA:125:G:H5'	53:D7:14:LYS:HD2	1.72	0.72
1:AA:78:G:N2	1:AA:91:C:N3	2.38	0.72
1:AA:427:U:OP1	4:AD:13:ARG:NH2	2.23	0.72
7:AG:79:ARG:HB3	7:AG:80:VAL:HG22	1.72	0.71
53:B7:24:THR:HG22	53:B7:27:GLY:H	1.55	0.71
1:AA:1103:C:OP1	2:AB:96:ARG:NH2	2.23	0.71
13:AM:84:ILE:HG13	13:AM:85:GLY:HA2	1.72	0.71
23:AY:26:A:N1	23:AY:44:G:N2	2.38	0.71
26:BB:25:A:OP2	61:BB:3142:HOH:O	2.08	0.71
9:CI:53:VAL:O	9:CI:55:ALA:N	2.22	0.71
25:DA:1171:G:N2	25:DA:1178:C:N3	2.34	0.71
25:DA:2033:A:OP1	61:DA:4237:HOH:O	2.08	0.71
31:DH:84:SER:HB3	31:DH:132:ARG:HH11	1.55	0.71
35:DP:44:GLY:O	61:DP:301:HOH:O	2.07	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:346:G:OP2	39:BT:41:ARG:NH2	2.22	0.71
25:DA:1968:G:OP1	61:DA:4546:HOH:O	2.08	0.71
50:D4:44:THR:O	50:D4:46:GLN:N	2.23	0.71
25:BA:1829:U:OP2	27:BD:274:ARG:NH2	2.24	0.71
16:CP:28:ARG:NH1	16:CP:29:ASP:OD1	2.24	0.71
25:DA:528:A:O2'	25:DA:529:A:H5"	1.90	0.71
25:DA:2135:A:H5'	25:DA:2159:G:O2'	1.90	0.71
1:AA:1183:A:O2'	1:AA:1184:G:OP1	2.08	0.71
24:AX:76:A:OP2	61:AX:3103:HOH:O	2.07	0.71
25:BA:572:A:O2'	25:BA:573:G:OP1	2.06	0.71
47:D1:51:VAL:HG11	47:D1:74:VAL:HG21	1.73	0.71
34:BO:35:VAL:HG11	34:BO:103:ALA:HB3	1.72	0.71
45:BZ:153:SER:HB3	45:BZ:167:PRO:HB3	1.71	0.71
25:BA:1360:C:OP1	61:BA:4787:HOH:O	2.07	0.71
2:CB:201:ILE:HG21	2:CB:214:ILE:HG21	1.73	0.71
15:CO:4:THR:OG1	15:CO:7:GLU:OE1	2.08	0.71
1:CA:64:G:H4'	1:CA:65:U:H3'	1.72	0.71
25:DA:2135:A:H61	25:DA:2157:G:N2	1.89	0.71
25:DA:2805:G:H2'	25:DA:2807:G:C8	2.25	0.71
30:DG:161:THR:HG22	30:DG:163:ALA:H	1.56	0.71
25:BA:71:U:OP1	61:BA:4786:HOH:O	2.08	0.71
13:CM:4:ILE:HG23	13:CM:5:ALA:H	1.55	0.71
31:DH:33:LEU:HD21	31:DH:136:ILE:HB	1.73	0.71
1:CA:664:G:H22	1:CA:741:G:H1	1.38	0.70
30:BG:125:PHE:O	61:BG:4004:HOH:O	2.09	0.70
1:CA:1314:C:OP2	19:CS:4:SER:OG	2.07	0.70
7:CG:136:LYS:NZ	7:CG:139:GLU:OE2	2.24	0.70
4:AD:122:ARG:HH21	4:AD:134:ASP:HB3	1.56	0.70
1:CA:1028:C:C4	1:CA:1033:G:O6	2.44	0.70
1:CA:1029:C:C4	1:CA:1032:G:C2	2.80	0.70
25:DA:775:G:O3'	61:DA:4554:HOH:O	2.08	0.70
25:DA:2116:G:N7	25:DA:2166:G:N2	2.39	0.70
25:DA:2592:G:OP1	61:DA:4546:HOH:O	2.09	0.70
3:AC:40:ARG:NH2	3:AC:55:VAL:O	2.23	0.70
7:AG:111:ARG:NH1	7:AG:113:GLU:OE2	2.21	0.70
25:BA:1151:U:H2'	25:BA:1152:G:H8	1.55	0.70
1:CA:1163:C:H42	1:CA:1173:G:H1	1.40	0.70
7:CG:80:VAL:HB	7:CG:85:TYR:HE2	1.57	0.70
25:DA:411:G:OP1	61:DA:4203:HOH:O	2.08	0.70
1:AA:1027:C:O2	1:AA:1034:G:N1	2.24	0.70
8:AH:41:ARG:NH2	8:AH:123:GLU:OE2	2.23	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AM:58:GLU:O	13:AM:62:ASN:ND2	2.23	0.70
32:BI:92:VAL:HG13	32:BI:120:ILE:HB	1.74	0.70
54:B8:33:ASN:HA	54:B8:36:LYS:HD2	1.74	0.70
1:CA:1129:C:H42	1:CA:1143:G:H1	1.40	0.70
1:AA:1348:U:H4'	9:AI:120:ARG:HD2	1.73	0.70
34:BO:7:TYR:HE1	34:BO:20:MET:HE3	1.57	0.70
2:CB:47:THR:HA	2:CB:202:PRO:HG2	1.74	0.70
10:CJ:52:GLY:O	14:CN:41:ARG:NH2	2.24	0.70
25:DA:1204:A:H2	25:DA:1241:A:H62	1.38	0.70
1:AA:664:G:H22	1:AA:741:G:H1	1.36	0.70
2:CB:120:ALA:O	2:CB:122:PHE:N	2.21	0.70
13:CM:39:ILE:HD12	13:CM:52:GLU:HG2	1.73	0.70
25:DA:958:U:OP2	36:DQ:14:ARG:NH1	2.24	0.70
45:DZ:92:SER:O	45:DZ:130:PRO:HG3	1.91	0.70
1:AA:78:G:N1	1:AA:91:C:N4	2.39	0.70
14:AN:47:LEU:HA	14:AN:50:LYS:HZ2	1.56	0.70
16:AP:51:VAL:HG12	16:AP:53:VAL:H	1.57	0.70
25:BA:2255:U:OP1	61:BA:4160:HOH:O	2.09	0.70
1:CA:1151:A:HO2'	1:CA:1152:A:H8	1.37	0.70
25:DA:1815:A:OP2	27:DD:54:ARG:NH2	2.24	0.70
29:DF:184:TYR:CE2	29:DF:188:ARG:HD2	2.27	0.70
36:DQ:1:MET:N	36:DQ:1:MET:SD	2.65	0.70
1:AA:1008:C:C4	1:AA:1021:G:N1	2.60	0.70
25:BA:2518:U:OP1	28:BE:144:ARG:NH2	2.25	0.70
1:CA:1148:U:O2'	9:CI:66:ARG:NH2	2.25	0.70
8:CH:69:ARG:NH2	8:CH:75:ARG:O	2.23	0.70
31:DH:17:VAL:HG13	31:DH:26:VAL:HG22	1.72	0.70
13:AM:3:ARG:HD2	13:AM:9:ILE:HG12	1.74	0.69
15:CO:25:THR:HG21	15:CO:70:LEU:HB2	1.74	0.69
25:DA:831:G:O2'	35:DP:38:GLN:NE2	2.24	0.69
1:CA:677:U:H3	1:CA:713:G:H22	1.39	0.69
1:CA:1104:G:O3'	2:CB:111:ARG:NH2	2.25	0.69
6:AF:99:ALA:HB3	18:AR:29:PHE:HE1	1.57	0.69
25:BA:431:C:H4'	25:BA:432:U:H5"	1.74	0.69
25:BA:1040:C:OP1	40:BU:53:ARG:NH2	2.24	0.69
1:CA:1024:G:H2'	1:CA:1025:U:H5"	1.73	0.69
10:CJ:17:ASP:OD1	10:CJ:70:ARG:NH1	2.26	0.69
25:DA:1342:A:OP2	61:DA:4187:HOH:O	2.10	0.69
35:DP:52:GLU:OE1	35:DP:55:ARG:NH1	2.24	0.69
1:CA:1027:C:C2	1:CA:1034:G:N1	2.57	0.69
30:DG:5:VAL:HG22	30:DG:8:LYS:H	1.58	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:AX:20:U:H5"	24:AX:21:A:OP2	1.92	0.69
1:CA:1228:C:OP2	13:CM:108:ARG:NH2	2.20	0.69
25:DA:741:G:OP2	61:DA:4523:HOH:O	2.11	0.69
1:AA:1008:C:N4	1:AA:1021:G:C6	2.61	0.69
25:BA:1116:A:N7	25:BA:1142:A:O2'	2.24	0.69
39:BT:16:ARG:NH2	39:BT:83:ILE:O	2.26	0.69
18:AR:38:GLU:HA	18:AR:41:LYS:HD3	1.74	0.69
25:BA:271:U:H1'	32:BI:50:ARG:NH1	2.08	0.69
25:BA:1648:U:O4	61:BA:4373:HOH:O	2.08	0.69
25:BA:2227:G:H3'	25:BA:2228:G:C8	2.28	0.69
39:BT:24:PRO:HA	39:BT:49:VAL:HG22	1.73	0.69
1:CA:1159:U:O4'	1:CA:1182:G:N2	2.26	0.69
25:DA:1378:A:OP1	53:D7:10:ARG:NH2	2.26	0.69
16:AP:52:ASP:O	16:AP:54:GLU:N	2.26	0.69
23:AY:28:G:H1	23:AY:42:C:H42	1.40	0.69
25:BA:1151:U:H2'	25:BA:1152:G:C8	2.28	0.69
25:BA:1378:G:OP1	61:BA:4787:HOH:O	2.10	0.69
9:CI:128:ARG:NH2	24:CX:33:U:OP2	2.26	0.69
25:DA:1310:G:OP2	53:D7:9:ARG:NH1	2.25	0.69
27:DD:71:ASP:HB3	27:DD:103:ARG:HH22	1.57	0.69
23:CW:4:C:N4	23:CW:69:G:N1	2.40	0.69
25:DA:2148:G:H2'	25:DA:2149:G:C8	2.28	0.69
25:BA:2801:C:OP1	28:BE:61:ARG:NH2	2.25	0.69
1:CA:254:G:OP1	17:CQ:66:SER:OG	2.09	0.69
26:DB:13:A:N1	26:DB:69:G:O2'	2.24	0.69
25:BA:331:G:H21	25:BA:354:A:H62	1.41	0.68
55:B9:25:VAL:HB	55:B9:34:GLN:HB2	1.75	0.68
25:DA:908:C:P	36:DQ:22:LYS:HD2	2.32	0.68
25:DA:1030:G:OP2	36:DQ:128:LYS:NZ	2.26	0.68
9:AI:26:VAL:HG13	9:AI:61:ALA:HB3	1.76	0.68
25:BA:2289:G:OP2	46:B0:10:THR:HG21	1.93	0.68
18:CR:32:ARG:HA	18:CR:69:THR:HG21	1.75	0.68
25:DA:2327:A:H2'	25:DA:2328:A:C8	2.28	0.68
36:BQ:18:LYS:O	36:BQ:98:LYS:NZ	2.21	0.68
1:AA:559:A:OP1	5:AE:126:ARG:NH2	2.25	0.68
25:BA:1001:G:OP2	36:BQ:14:ARG:NH2	2.23	0.68
27:BD:71:ASP:HB3	27:BD:103:ARG:HH22	1.59	0.68
1:CA:539:A:OP2	12:CL:115:LYS:NZ	2.26	0.68
1:CA:1010:G:N2	1:CA:1020:U:H1'	2.09	0.68
47:D1:21:ARG:HD3	47:D1:35:THR:HG21	1.74	0.68
1:AA:346:G:H3'	1:AA:347:G:H4'	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:BP:98:GLU:OE2	35:BP:102:ARG:NH1	2.27	0.68
36:DQ:110:THR:HG23	36:DQ:113:GLN:HB2	1.76	0.68
1:AA:310:G:OP2	16:AP:27:LYS:NZ	2.27	0.68
23:CY:7:A:H61	23:CY:66:U:H3	1.42	0.68
45:DZ:27:VAL:HG12	45:DZ:85:HIS:HE1	1.58	0.68
1:CA:1010:G:H2'	1:CA:1011:G:H8	1.59	0.68
25:DA:81:G:N7	61:DA:4466:HOH:O	2.25	0.68
23:AY:50:U:N3	23:AY:64:A:C2	2.62	0.68
25:DA:2447:G:OP2	61:DA:4723:HOH:O	2.10	0.68
41:DV:6:LYS:HB2	41:DV:38:LEU:HD21	1.74	0.68
25:BA:1039:G:OP1	40:BU:50:ARG:NH2	2.26	0.68
25:BA:1044:C:OP1	61:BA:4797:HOH:O	2.11	0.68
25:BA:1067:A:H62	25:BA:1186:U:H3	1.41	0.68
25:BA:2209:G:O2'	25:BA:2210:C:OP1	2.10	0.68
32:BI:72:LEU:O	32:BI:74:ASN:N	2.27	0.68
1:CA:1152:A:H5'	10:CJ:13:HIS:HB2	1.75	0.68
10:CJ:44:VAL:HG13	10:CJ:66:ARG:HG2	1.75	0.68
25:DA:1452:A:OP2	61:DA:4788:HOH:O	2.12	0.68
1:AA:812:C:N3	61:AA:4053:HOH:O	2.27	0.67
25:DA:2028:U:O4	61:DA:4237:HOH:O	2.10	0.67
25:BA:1846:A:N1	61:BA:4024:HOH:O	2.27	0.67
27:BD:108:PRO:HB3	27:BD:143:HIS:CE1	2.29	0.67
35:BP:42:SER:O	61:BP:303:HOH:O	2.10	0.67
2:AB:67:THR:HA	2:AB:90:MET:HE1	1.75	0.67
1:CA:1189:C:OP1	10:CJ:51:ARG:NH2	2.27	0.67
31:DH:104:GLU:HG3	31:DH:114:VAL:HG22	1.75	0.67
1:AA:347:G:H2'	1:AA:348:G:H8	1.60	0.67
36:BQ:14:ARG:HG2	36:BQ:41:TRP:HH2	1.57	0.67
1:CA:1312:G:H5'	19:CS:5:LEU:HD21	1.77	0.67
35:DP:100:LEU:HD12	35:DP:112:LEU:HD11	1.75	0.67
1:AA:503:C:OP1	61:AA:4193:HOH:O	2.13	0.67
1:CA:36:C:OP1	12:CL:123:LYS:NZ	2.28	0.67
1:CA:999:C:N3	1:CA:1042:G:N2	2.37	0.67
13:CM:88:ARG:HG3	13:CM:98:VAL:HG11	1.76	0.67
25:DA:1970:A:OP1	61:DA:4259:HOH:O	2.12	0.67
1:AA:78:G:C5	1:AA:91:C:N4	2.61	0.67
1:AA:266:G:H5"	1:AA:268:C:H41	1.58	0.67
11:CK:48:ILE:O	11:CK:50:TYR:N	2.28	0.67
19:CS:50:ALA:HB1	19:CS:57:HIS:HB3	1.76	0.67
25:DA:2379:G:O2'	38:DS:17:ARG:NH2	2.25	0.67
25:DA:2839:G:H5'	37:DR:46:GLY:HA2	1.74	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:237:G:OP1	61:BA:5132:HOH:O	2.13	0.67
25:BA:943:C:N3	25:BA:944:C:N4	2.42	0.67
45:BZ:151:HIS:O	45:BZ:153:SER:N	2.24	0.67
1:CA:148:G:H2'	1:CA:149:A:C8	2.30	0.67
1:CA:1028:C:C2	1:CA:1033:G:N1	2.62	0.67
9:CI:9:ARG:HG2	9:CI:14:VAL:HG12	1.75	0.67
28:DE:111:ARG:HD3	37:DR:1:MET:HE1	1.77	0.67
46:D0:10:THR:HG22	46:D0:12:ASN:H	1.60	0.67
23:AW:6:G:H1	23:AW:67:C:H42	0.75	0.67
25:BA:1831:C:OP2	27:BD:183:ARG:NH2	2.28	0.67
1:CA:1129:C:H2'	1:CA:1139:G:N7	2.10	0.67
2:AB:178:ARG:HG2	8:AH:72:PRO:HA	1.75	0.67
42:BW:2:GLU:OE2	42:BW:72:LYS:NZ	2.23	0.67
5:CE:50:GLU:HB2	5:CE:53:LEU:HD13	1.76	0.67
3:AC:6:HIS:HD2	3:AC:8:ILE:H	1.42	0.66
5:AE:50:GLU:HB2	5:AE:53:LEU:HD13	1.76	0.66
25:BA:1027:A:OP1	61:BA:4722:HOH:O	2.12	0.66
9:CI:23:ASN:ND2	9:CI:25:LYS:HG2	2.10	0.66
18:CR:56:THR:HB	18:CR:58:LEU:HD23	1.77	0.66
25:DA:249:C:O2	54:D8:12:LYS:NZ	2.27	0.66
25:DA:307:G:N7	61:DA:4267:HOH:O	2.27	0.66
25:DA:2148:G:H2'	25:DA:2149:G:H8	1.59	0.66
25:DA:2880:C:O3'	37:DR:90:ARG:NH1	2.27	0.66
31:DH:7:LEU:HD12	31:DH:8:PRO:HD2	1.75	0.66
54:D8:33:ASN:HA	54:D8:36:LYS:HD2	1.77	0.66
1:AA:109:A:OP1	61:AA:4230:HOH:O	2.13	0.66
3:AC:181:ASN:HD22	3:AC:204:LEU:HB2	1.60	0.66
1:CA:1129:C:N4	1:CA:1143:G:H1	1.93	0.66
25:DA:1801:G:OP2	27:DD:154:LYS:NZ	2.26	0.66
2:AB:88:ALA:HB2	2:AB:219:VAL:HG13	1.77	0.66
20:AT:10:LEU:HD13	20:AT:11:SER:H	1.61	0.66
25:BA:2081:A:OP2	61:BA:4476:HOH:O	2.11	0.66
25:DA:11:G:N7	61:DA:4575:HOH:O	2.28	0.66
3:CC:100:ALA:O	3:CC:102:ASN:ND2	2.28	0.66
25:DA:2118:U:C4	25:DA:2149:G:H1'	2.30	0.66
32:DI:93:THR:HG22	32:DI:119:PRO:HB3	1.76	0.66
1:AA:539:A:OP2	12:AL:115:LYS:NZ	2.29	0.66
27:BD:69:ARG:NH2	27:BD:128:GLY:O	2.29	0.66
47:B1:2:SER:HB3	47:B1:46:LEU:HD12	1.77	0.66
9:CI:3:GLN:OE1	9:CI:20:ARG:NH2	2.25	0.66
9:CI:102:LEU:HD13	9:CI:103:THR:H	1.59	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:570:G:OP1	61:DA:4397:HOH:O	2.12	0.66
25:DA:1783:A:OP1	61:DA:4522:HOH:O	2.12	0.66
25:BA:142:G:H4'	43:BX:35:THR:HG21	1.76	0.66
25:BA:354:A:H2	25:BA:1255:A:HO2'	1.44	0.66
1:CA:1064:G:N2	1:CA:1190:G:O2'	2.29	0.66
2:CB:125:PRO:O	2:CB:127:ILE:N	2.28	0.66
1:AA:972:C:OP1	61:AA:4182:HOH:O	2.13	0.66
1:AA:1278:U:H5'	1:AA:1279:A:O4'	1.96	0.66
61:AX:3104:HOH:O	25:BA:2597:U:OP1	2.14	0.66
25:BA:465:G:N7	61:BA:4532:HOH:O	2.28	0.66
25:BA:655:G:OP2	54:B8:15:LYS:NZ	2.24	0.66
25:DA:252:G:P	35:DP:50:ARG:HH12	2.18	0.66
4:AD:188:LEU:HD23	4:AD:188:LEU:H	1.61	0.66
1:CA:38:G:N2	1:CA:397:A:H5"	2.09	0.66
25:DA:250:G:OP2	54:D8:13:ARG:NH2	2.29	0.66
18:AR:56:THR:HB	18:AR:58:LEU:HD23	1.77	0.66
25:BA:715:G:N7	61:BA:4012:HOH:O	2.28	0.66
1:CA:79:G:H1	1:CA:90:U:H3	1.44	0.66
10:CJ:49:VAL:HG23	14:CN:41:ARG:HB2	1.77	0.66
25:DA:2819:G:N7	61:DA:4380:HOH:O	2.29	0.66
8:AH:51:VAL:HG21	8:AH:60:ARG:HB2	1.77	0.65
28:BE:12:THR:HG22	28:BE:13:ARG:H	1.62	0.65
25:DA:1912:A:OP1	61:DA:4643:HOH:O	2.13	0.65
1:AA:545:C:OP1	4:AD:61:LYS:NZ	2.29	0.65
20:CT:10:LEU:HB3	20:CT:12:ALA:H	1.60	0.65
50:D4:59:PHE:H	50:D4:59:PHE:HD1	1.45	0.65
25:BA:333:G:N3	25:BA:353:G:O2'	2.29	0.65
25:BA:1218:G:O2'	25:BA:1219:A:O4'	2.13	0.65
25:BA:2156:A:H62	25:BA:2179:G:H1'	1.59	0.65
25:BA:2362:C:OP2	61:BA:4195:HOH:O	2.13	0.65
37:BR:33:ARG:NH1	37:BR:115:GLU:OE2	2.30	0.65
49:B3:5:LYS:NZ	49:B3:34:GLU:OE2	2.29	0.65
25:DA:1670:C:OP1	61:DA:4063:HOH:O	2.13	0.65
38:BS:15:ARG:O	38:BS:19:LYS:HG2	1.95	0.65
1:CA:1166:G:N2	1:CA:1170:A:OP2	2.29	0.65
25:DA:568:U:H5'	25:DA:945:A:N1	2.12	0.65
25:DA:1434:A:H61	25:DA:1558:A:H62	1.43	0.65
25:DA:2126:A:N6	25:DA:2162:G:O2'	2.30	0.65
1:AA:1027:C:N3	1:AA:1034:G:O6	2.30	0.65
7:CG:111:ARG:NH1	7:CG:113:GLU:OE2	2.29	0.65
14:CN:4:LYS:HA	14:CN:7:ILE:HG22	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:CP:51:VAL:HG12	16:CP:53:VAL:H	1.61	0.65
25:DA:886:C:H1'	25:DA:890:A:H61	1.62	0.65
28:DE:47:VAL:HG11	28:DE:86:PRO:HD2	1.79	0.65
25:BA:467:U:O2	29:BF:46:ARG:NH2	2.27	0.65
25:DA:1530:C:O2'	25:DA:1531:C:O5'	2.15	0.65
1:AA:59:A:N1	61:AA:4123:HOH:O	2.28	0.65
1:CA:390:C:O3'	16:CP:28:ARG:NH2	2.29	0.65
1:CA:426:G:OP1	4:CD:38:TYR:OH	2.12	0.65
1:CA:947:G:N2	1:CA:1234:C:N3	2.42	0.65
24:CX:47:U:N3	24:CX:50:U:OP1	2.30	0.65
25:DA:832:G:OP1	61:DA:4580:HOH:O	2.13	0.65
25:DA:1031:G:H5"	55:D9:8:LYS:HE3	1.78	0.65
1:AA:1305:G:N2	1:AA:1331:G:H1'	2.11	0.65
1:AA:1381:U:H1'	7:AG:79:ARG:HG3	1.78	0.65
4:AD:23:GLY:HA3	4:AD:112:VAL:HG12	1.78	0.65
25:BA:807:G:OP1	61:BA:5080:HOH:O	2.13	0.65
25:BA:1219:A:H4'	25:BA:1220:U:OP1	1.97	0.65
36:BQ:38:GLU:HG3	36:BQ:127:ILE:HB	1.79	0.65
23:CW:50:U:H5'	23:CW:50:U:H6	1.62	0.65
25:DA:1816:G:O6	27:DD:35:LYS:NZ	2.20	0.65
23:AY:9:A:O3'	23:AY:45:U:O2'	2.15	0.65
38:BS:34:HIS:ND1	38:BS:53:SER:OG	2.28	0.65
1:CA:377:G:OP1	16:CP:3:LYS:HD2	1.97	0.65
1:CA:1106:G:H5"	3:CC:172:ARG:HG2	1.77	0.65
4:CD:175:SER:HB3	4:CD:186:LEU:HD11	1.79	0.65
25:DA:1021:A:H62	25:DA:1141:U:H3	1.42	0.65
25:DA:1250:G:N7	35:DP:18:ARG:NH2	2.45	0.65
25:DA:2171:A:N3	25:DA:2172:U:N3	2.45	0.65
45:DZ:28:MET:HE1	45:DZ:61:LEU:HD21	1.79	0.65
44:BY:54:LYS:H	44:BY:56:PRO:HD3	1.61	0.64
45:BZ:45:ASP:OD1	45:BZ:49:ARG:NH1	2.30	0.64
7:AG:111:ARG:NH2	7:AG:126:ASP:OD2	2.30	0.64
25:BA:2902:G:H4'	25:BA:2903:G:O5'	1.96	0.64
13:CM:78:ILE:HA	13:CM:81:LEU:HD12	1.79	0.64
23:CY:15:G:H22	23:CY:48:C:H42	1.44	0.64
1:AA:1530:G:H2'	1:AA:1531:A:O4'	1.97	0.64
3:AC:3:ASN:N	3:AC:3:ASN:OD1	2.30	0.64
25:BA:928:G:H3'	25:BA:929:G:C8	2.32	0.64
25:BA:1094:A:OP2	25:BA:1155:C:N4	2.30	0.64
27:BD:237:GLU:OE2	61:BD:409:HOH:O	2.15	0.64
1:CA:411:A:OP2	4:CD:25:ARG:NH2	2.29	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:300:A:OP1	44:DY:86:ARG:NH2	2.30	0.64
26:DB:106:G:H5'	45:DZ:31:ARG:HG2	1.79	0.64
10:AJ:38:ILE:HD11	10:AJ:71:LEU:HB3	1.78	0.64
15:AO:25:THR:HG21	15:AO:70:LEU:HB2	1.79	0.64
1:CA:954:G:H21	1:CA:1227:A:H62	1.45	0.64
1:CA:1108:G:O6	61:CA:4094:HOH:O	2.11	0.64
1:CA:1422:G:O3'	34:DO:49:ARG:NH1	2.30	0.64
2:CB:15:VAL:HG21	2:CB:213:LEU:HD12	1.79	0.64
3:CC:164:ARG:NH1	3:CC:166:GLU:OE1	2.31	0.64
29:DF:21:ALA:HB3	29:DF:22:ALA:HA	1.80	0.64
1:AA:8:A:H5'	5:AE:101:ILE:HG22	1.78	0.64
25:BA:1296:G:N7	35:BP:18:ARG:NH2	2.45	0.64
25:BA:1749:G:N7	61:BA:5142:HOH:O	2.30	0.64
27:BD:108:PRO:HB3	27:BD:143:HIS:HE1	1.62	0.64
1:CA:8:A:H5'	5:CE:101:ILE:HG22	1.79	0.64
10:CJ:38:ILE:HD11	10:CJ:71:LEU:HD23	1.79	0.64
25:DA:2291:U:OP1	25:DA:2380:C:O2'	2.16	0.64
31:DH:20:ALA:HB3	31:DH:23:ARG:HG3	1.80	0.64
34:DO:7:TYR:HE1	34:DO:20:MET:HE3	1.63	0.64
10:AJ:49:VAL:HG23	14:AN:41:ARG:HB2	1.79	0.64
13:AM:11:ARG:HA	13:AM:45:VAL:HB	1.80	0.64
35:BP:86:LYS:HD3	35:BP:117:GLU:HB3	1.80	0.64
1:CA:1027:C:N3	1:CA:1034:G:O6	2.30	0.64
1:CA:1119:C:H42	1:CA:1154:G:H1	1.44	0.64
2:CB:78:GLN:NE2	2:CB:95:GLN:OE1	2.30	0.64
28:DE:77:ILE:HD13	28:DE:195:LEU:HD22	1.79	0.64
1:AA:974:A:OP2	14:AN:29:ARG:NH2	2.30	0.64
1:CA:1028:C:N3	1:CA:1033:G:O6	2.30	0.64
1:CA:1251:A:H2'	1:CA:1252:A:C8	2.33	0.64
6:CF:70:ASP:OD1	6:CF:70:ASP:N	2.28	0.64
29:DF:157:VAL:HB	29:DF:194:MET:HG2	1.79	0.64
1:CA:559:A:OP1	5:CE:126:ARG:NH2	2.27	0.64
25:DA:2632:A:HO2'	25:DA:2811:G:HO2'	1.42	0.64
25:BA:2138:G:O6	25:BA:2187:G:N2	2.31	0.63
25:BA:2145:G:H1	25:BA:2197:C:N4	1.94	0.63
1:AA:1198:G:OP1	61:AA:4206:HOH:O	2.16	0.63
4:AD:15:GLU:OE2	4:AD:66:ARG:NH1	2.31	0.63
37:DR:21:TYR:CZ	37:DR:43:GLU:HG2	2.33	0.63
9:AI:20:ARG:O	9:AI:60:ASP:N	2.30	0.63
25:BA:139:A:H8	25:BA:1454:C:HO2'	1.44	0.63
25:BA:2798:C:OP1	28:BE:41:LYS:NZ	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:178:ARG:HH22	8:CH:68:ARG:NH1	1.96	0.63
28:DE:72:VAL:HA	28:DE:73:GLU:HB3	1.81	0.63
1:AA:1502:A:H2	1:AA:1505:G:N1	1.92	0.63
32:BI:61:ARG:NH2	32:BI:64:GLU:OE2	2.31	0.63
25:DA:1420:U:O2'	25:DA:1421:G:OP1	2.16	0.63
25:BA:929:G:H1	25:BA:940:C:H42	1.45	0.63
25:BA:1485:A:OP1	61:BA:5011:HOH:O	2.14	0.63
25:BA:2624:C:OP2	51:B5:2:ALA:N	2.30	0.63
42:BW:25:ARG:NH2	42:BW:74:ALA:O	2.29	0.63
1:CA:572:A:OP1	61:CA:4047:HOH:O	2.15	0.63
25:DA:2807:G:H22	25:DA:2892:A:H62	1.47	0.63
25:DA:1266:G:O5'	42:DW:15:ARG:NH2	2.31	0.63
24:AX:6:G:H1	24:AX:67:C:N4	1.97	0.63
36:BQ:35:VAL:HG13	36:BQ:130:LYS:HB3	1.80	0.63
1:CA:1278:U:H5'	1:CA:1279:A:O4'	1.98	0.63
29:DF:24:LEU:HD23	29:DF:115:ALA:HA	1.81	0.63
31:DH:149:ARG:NH1	31:DH:167:GLU:OE1	2.31	0.63
41:DV:43:GLU:N	41:DV:43:GLU:OE2	2.32	0.63
25:BA:1466:U:O2'	25:BA:1467:G:OP1	2.16	0.63
31:BH:59:ARG:HH11	31:BH:59:ARG:HG2	1.63	0.63
1:CA:1026:G:H5'	1:CA:1027:C:O5'	1.98	0.63
1:AA:405:U:OP2	4:AD:3:ARG:NH2	2.31	0.63
1:AA:911:U:OP2	12:AL:97:ARG:NH1	2.32	0.63
2:AB:33:TYR:HB2	2:AB:43:ASP:HB2	1.80	0.63
3:AC:78:GLY:HA3	3:AC:83:ARG:H	1.63	0.63
25:BA:553:A:N1	25:BA:2064:A:H2'	2.13	0.63
1:CA:811:C:O2'	1:CA:901:A:N1	2.30	0.63
1:CA:1027:C:O2	1:CA:1034:G:N1	2.30	0.63
1:CA:1039:C:H2'	1:CA:1040:U:O4'	1.99	0.63
26:DB:66:A:H61	26:DB:109:C:H5'	1.64	0.63
27:DD:132:PRO:HD3	27:DD:190:TYR:CZ	2.34	0.63
29:DF:24:LEU:HD21	29:DF:114:VAL:HG12	1.80	0.63
45:DZ:145:GLU:H	45:DZ:148:ASP:HB2	1.62	0.63
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.33	0.62
25:BA:1071:G:C4	25:BA:1180:C:H1'	2.34	0.62
25:BA:1125:C:H41	25:BA:1134:A:P	2.22	0.62
25:BA:2807:C:H42	25:BA:2813:G:H1	1.48	0.62
32:DI:31:LEU:HD21	32:DI:38:LEU:HG	1.81	0.62
38:DS:71:ARG:NH1	38:DS:107:GLU:OE1	2.32	0.62
23:AY:50:U:C4	23:AY:64:A:N1	2.68	0.62
1:CA:1499:A:H1'	1:CA:1520:G:H5'	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:155:LEU:HD21	2:CB:159:PRO:HG3	1.80	0.62
23:CY:44:G:H2'	23:CY:45:U:H5'	1.81	0.62
1:AA:353:A:H8	1:AA:353:A:H5'	1.63	0.62
9:CI:20:ARG:O	9:CI:60:ASP:N	2.29	0.62
23:CY:18:G:N2	23:CY:55:PSU:C4	2.66	0.62
28:DE:36:ARG:HG2	28:DE:47:VAL:HG12	1.81	0.62
1:AA:96:U:O2'	1:AA:97:G:H8	1.83	0.62
9:AI:110:GLU:OE2	9:AI:113:LYS:NZ	2.33	0.62
25:BA:2849:G:H5'	37:BR:46:GLY:HA2	1.82	0.62
15:CO:55:GLY:HA2	15:CO:58:MET:HE2	1.80	0.62
25:DA:625:G:O6	35:DP:107:LYS:NZ	2.30	0.62
25:DA:2308:G:O6	25:DA:2311:A:N6	2.20	0.62
25:DA:2316:C:O2'	30:DG:128:ARG:NH2	2.31	0.62
2:AB:51:LEU:HD23	2:AB:201:ILE:HD12	1.80	0.62
50:B4:46:GLN:O	50:B4:48:ARG:N	2.32	0.62
25:DA:2870:C:H2'	25:DA:2871:C:O4'	2.00	0.62
27:DD:85:ASP:OD2	27:DD:88:ARG:NH1	2.32	0.62
45:DZ:156:LYS:HE3	45:DZ:158:PRO:HD3	1.81	0.62
45:DZ:159:PRO:HA	45:DZ:161:VAL:H	1.63	0.62
1:AA:1030(A):G:O2'	1:AA:1031:G:N2	2.32	0.62
25:BA:1118:C:N3	25:BA:1138:C:N4	2.47	0.62
1:CA:881:G:P	12:CL:12:ARG:HH22	2.22	0.62
1:CA:1010:G:H2'	1:CA:1011:G:C8	2.35	0.62
23:CW:51:U:H2'	23:CW:52:G:C8	2.35	0.62
25:DA:692:C:O2'	27:DD:38:LYS:NZ	2.31	0.62
35:DP:50:ARG:HH21	54:D8:7:HIS:HD2	1.45	0.62
4:AD:173:TRP:CD1	4:AD:173:TRP:H	2.18	0.62
23:AY:50:U:H3	23:AY:64:A:H2	1.47	0.62
25:BA:294:C:H42	25:BA:390:G:H1	1.48	0.62
25:BA:298:G:H2'	25:BA:299:G:H8	1.65	0.62
1:CA:1221:G:OP1	1:CA:1320:C:N4	2.33	0.62
2:CB:187:LEU:HA	2:CB:201:ILE:HB	1.81	0.62
20:CT:9:ASN:O	20:CT:10:LEU:HB2	1.99	0.62
25:DA:1405:U:H2'	25:DA:1406:U:C6	2.35	0.62
25:DA:2151:G:H2'	25:DA:2152:G:H8	1.65	0.62
26:DB:24:G:N7	26:DB:56:G:H2'	2.15	0.62
36:DQ:35:VAL:HG13	36:DQ:130:LYS:HB3	1.82	0.62
1:AA:1002:G:O6	1:AA:1003:G:N2	2.32	0.62
23:AW:56:C:OP1	25:BA:943:C:H5'	1.99	0.62
25:BA:2825:C:H5'	51:B5:29:THR:HG21	1.81	0.62
1:CA:406:G:H5'	4:CD:5:ILE:HD11	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:134:ILE:HG23	3:CC:151:VAL:HB	1.82	0.62
3:AC:26:LYS:HG2	10:AJ:45:ARG:HH12	1.65	0.62
23:AY:63:G:C2	23:AY:64:A:H1'	2.35	0.62
25:BA:388:A:H2'	25:BA:389:G:C8	2.34	0.62
25:BA:2720:G:H1'	37:BR:71:GLN:HE22	1.64	0.62
1:CA:771:G:N7	61:CA:4039:HOH:O	2.30	0.62
27:DD:3:VAL:HG13	27:DD:17:THR:HB	1.82	0.62
44:DY:23:ARG:HG2	44:DY:42:VAL:HG22	1.80	0.62
1:AA:922:G:H4'	5:AE:20:GLN:HA	1.81	0.62
25:BA:2126:G:H2'	25:BA:2127:C:C6	2.35	0.62
45:BZ:138:GLU:H	45:BZ:156:LYS:HE2	1.63	0.62
1:CA:1502:A:H2	1:CA:1505:G:N1	1.94	0.62
3:CC:8:ILE:HG23	3:CC:16:ARG:HG2	1.81	0.62
23:CY:11:C:N3	23:CY:24:G:O6	2.33	0.62
25:BA:302:A:O2'	25:BA:303:C:OP1	2.15	0.61
25:BA:1105:G:N2	25:BA:1125:C:O2	2.29	0.61
50:B4:53:GLU:HG3	50:B4:55:ARG:HA	1.82	0.61
51:B5:16:ARG:HG3	51:B5:17:ASP:N	2.15	0.61
5:CE:52:PRO:HG2	5:CE:53:LEU:HD12	1.82	0.61
38:DS:25:ARG:NH1	38:DS:42:ASP:OD2	2.33	0.61
45:DZ:153:SER:HB3	45:DZ:167:PRO:HB3	1.81	0.61
24:AX:50:U:H3	24:AX:64:G:H1	1.48	0.61
23:AY:53:G:H1	23:AY:61:C:N4	1.98	0.61
1:CA:448:A:P	1:CA:485:G:H22	2.23	0.61
4:CD:166:LYS:NZ	4:CD:179:GLU:OE2	2.32	0.61
25:DA:2758:A:C2	25:DA:2759:G:H1'	2.35	0.61
32:DI:92:VAL:HG13	32:DI:120:ILE:HB	1.82	0.61
43:DX:57:LEU:HD21	43:DX:78:LYS:HE2	1.81	0.61
1:AA:159:G:O2'	1:AA:161:A:N7	2.33	0.61
1:AA:165:C:H2'	1:AA:166:G:C8	2.35	0.61
1:AA:1353:G:OP1	21:AU:10:ARG:NH1	2.33	0.61
9:AI:49:PRO:HG3	9:AI:101:PHE:HD2	1.66	0.61
25:BA:346:A:OP1	29:BF:168:ARG:HD2	2.00	0.61
8:CH:14:ARG:HG2	8:CH:18:ARG:HH22	1.66	0.61
25:DA:1639:U:H2'	25:DA:1640:C:H5"	1.80	0.61
1:AA:78:G:N2	1:AA:91:C:C2	2.68	0.61
1:AA:975:A:H5'	1:AA:975:A:H8	1.64	0.61
1:AA:997:U:H3	1:AA:1044:A:N6	1.97	0.61
1:CA:1027:C:C4	1:CA:1034:G:O6	2.53	0.61
1:CA:1240:U:N3	7:CG:30:ILE:O	2.29	0.61
27:DD:132:PRO:HG2	27:DD:135:PHE:CD2	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:DR:101:ALA:HB3	51:D5:47:PRO:HG3	1.83	0.61
1:AA:1152:A:OP1	10:AJ:68:HIS:ND1	2.33	0.61
2:AB:115:LEU:HD11	2:AB:146:GLN:HG3	1.81	0.61
1:CA:564:C:O2'	8:CH:91:ARG:NH2	2.31	0.61
25:DA:2130:U:H4'	25:DA:2133:G:H4'	1.81	0.61
37:DR:2:ARG:NH1	37:DR:5:LYS:O	2.33	0.61
44:DY:94:LYS:NZ	61:DY:601:HOH:O	2.32	0.61
1:AA:1432:G:O6	61:AA:4147:HOH:O	2.13	0.61
1:AA:1503:A:O2'	22:AV:13:A:N1	2.34	0.61
4:AD:194:LEU:HD12	4:AD:195:ALA:H	1.65	0.61
20:AT:76:ALA:O	20:AT:80:ARG:HG2	2.00	0.61
25:BA:1099:C:H2'	25:BA:1100:A:O4'	2.00	0.61
48:D2:35:LEU:HD12	48:D2:53:LEU:HD12	1.82	0.61
50:D4:24:THR:OG1	50:D4:25:TYR:N	2.29	0.61
5:AE:33:VAL:HG21	5:AE:109:ILE:HA	1.82	0.61
25:BA:2396:G:OP2	46:B0:55:ARG:NH1	2.33	0.61
45:BZ:92:SER:O	45:BZ:130:PRO:HG2	2.00	0.61
1:CA:920:U:H2'	1:CA:921:U:C6	2.36	0.61
2:CB:67:THR:HA	2:CB:90:MET:HE1	1.82	0.61
23:CY:14:A:O2'	23:CY:15:G:OP1	2.17	0.61
26:DB:75:G:O2'	45:DZ:85:HIS:NE2	2.34	0.61
25:BA:2235:G:OP1	27:BD:172:TYR:OH	2.13	0.61
45:BZ:148:ASP:OD1	45:BZ:148:ASP:N	2.33	0.61
1:CA:986:A:N3	19:CS:52:TYR:OH	2.31	0.61
1:CA:1005:A:H5"	1:CA:1006:C:C5	2.35	0.61
1:CA:1055:A:N7	1:CA:1200:C:N4	2.49	0.61
29:DF:167:ALA:HB1	29:DF:173:VAL:HG11	1.81	0.61
36:DQ:18:LYS:O	36:DQ:98:LYS:NZ	2.28	0.61
1:AA:890:G:O2'	1:AA:906:G:O6	2.19	0.61
1:AA:1320:C:O2	19:AS:36:ARG:NH2	2.34	0.61
25:BA:1834:A:O2'	27:BD:259:THR:HG21	2.01	0.61
1:CA:1028:C:O2	1:CA:1033:G:N1	2.34	0.61
10:CJ:8:LEU:HB2	10:CJ:70:ARG:HB2	1.82	0.61
25:DA:821:A:N1	61:DA:4395:HOH:O	2.31	0.61
25:DA:1019:U:H2'	25:DA:1020:A:H8	1.64	0.61
1:AA:1240:U:OP2	7:AG:116:ALA:N	2.34	0.61
23:AY:8:4SU:H4'	23:AY:48:C:H4'	1.83	0.61
25:BA:2205:C:H2'	25:BA:2206:G:H8	1.65	0.61
25:BA:2859:U:OP2	39:BT:95:ARG:NH1	2.34	0.61
1:CA:17:U:H2'	1:CA:18:C:C6	2.36	0.61
1:CA:256:U:OP1	17:CQ:17:LYS:NZ	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:854:G:O6	61:CA:4130:HOH:O	2.16	0.61
4:CD:88:VAL:HG13	5:CE:97:GLY:HA2	1.83	0.61
23:CY:5:G:H1	23:CY:68:C:N4	1.97	0.61
25:DA:1218:C:OP2	40:DU:15:LYS:NZ	2.32	0.61
41:DV:4:ILE:HD12	41:DV:39:LEU:HB3	1.83	0.61
4:AD:50:ARG:HH21	5:AE:10:MET:HE3	1.65	0.60
46:D0:11:ARG:O	46:D0:14:ARG:NH2	2.34	0.60
1:AA:538:G:H5"	12:AL:114:LYS:HB2	1.81	0.60
4:AD:128:VAL:N	4:AD:131:ARG:O	2.33	0.60
15:AO:39:LEU:HD13	15:AO:56:LEU:HB2	1.82	0.60
32:BI:72:LEU:C	32:BI:74:ASN:H	2.09	0.60
45:BZ:19:ARG:NH1	45:BZ:84:GLU:O	2.34	0.60
1:CA:1010:G:H22	1:CA:1020:U:H1'	1.65	0.60
1:CA:1216:G:H5"	14:CN:5:ALA:HB2	1.81	0.60
24:CX:6:G:H1	24:CX:67:C:N4	1.97	0.60
25:DA:1183:G:O3'	49:D3:29:ARG:NH1	2.33	0.60
1:AA:560:U:O2'	1:AA:561:U:OP2	2.16	0.60
25:BA:1513:G:O2'	25:BA:1593:C:O2'	2.18	0.60
25:BA:2227:G:H5"	25:BA:2228:G:C5	2.36	0.60
25:BA:2761:A:H5'	31:BH:4:ILE:HD13	1.82	0.60
25:DA:2364:C:OP1	46:D0:55:ARG:NH1	2.32	0.60
46:D0:32:ARG:H	46:D0:35:ASN:ND2	2.00	0.60
50:D4:59:PHE:HA	50:D4:61:ARG:N	2.16	0.60
7:AG:72:ARG:HG3	7:AG:72:ARG:NH1	2.12	0.60
29:BF:157:VAL:HB	29:BF:194:MET:HG2	1.82	0.60
25:DA:2615:U:OP1	61:DA:4305:HOH:O	2.16	0.60
50:B4:15:ILE:HB	50:B4:32:TYR:HD1	1.65	0.60
9:AI:53:VAL:O	9:AI:55:ALA:N	2.33	0.60
25:BA:1480:A:H61	25:BA:1605:A:H62	1.48	0.60
25:BA:2299:A:N6	25:BA:2356:U:H3	1.98	0.60
41:BV:72:VAL:HG13	41:BV:85:LYS:HB3	1.81	0.60
5:CE:140:ARG:O	5:CE:143:ARG:NH2	2.35	0.60
25:DA:2723:C:O3'	37:DR:1:MET:HE3	2.01	0.60
25:BA:83:A:H5'	44:BY:8:LYS:HG2	1.82	0.60
1:CA:1120:G:C5	1:CA:1154:G:N2	2.70	0.60
20:CT:10:LEU:HD23	20:CT:12:ALA:HB2	1.83	0.60
25:DA:2655:G:O2'	25:DA:2664:G:O6	2.15	0.60
1:AA:377:G:OP1	16:AP:3:LYS:HD2	2.01	0.60
1:AA:1064:G:H4'	1:AA:1065:U:OP1	2.01	0.60
1:AA:1191:A:OP1	3:AC:4:LYS:NZ	2.35	0.60
23:AY:58:A:O2'	23:AY:59:U:H5'	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1126:U:H3	10:CJ:40:LEU:HD11	1.66	0.60
8:CH:119:LEU:HB3	8:CH:123:GLU:HB3	1.82	0.60
11:CK:22:HIS:HB3	11:CK:29:ILE:HB	1.84	0.60
23:CW:13:C:O2'	23:CW:14:A:O5'	2.16	0.60
23:CY:50:U:O2	23:CY:64:A:N1	2.34	0.60
26:DB:14:U:OP2	26:DB:70:C:O2'	2.17	0.60
30:DG:150:ASP:OD1	30:DG:150:ASP:N	2.25	0.60
25:BA:2045:G:H5'	25:BA:2629:C:H4'	1.83	0.60
9:AI:9:ARG:H	9:AI:79:LEU:HD23	1.66	0.60
17:AQ:50:LYS:HD2	17:AQ:51:TYR:CZ	2.37	0.60
20:AT:87:LYS:O	20:AT:91:LEU:HG	2.01	0.60
23:AW:58:A:O2'	23:AW:60:U:OP2	2.19	0.60
36:BQ:16:ARG:HG2	36:BQ:18:LYS:HE2	1.83	0.60
1:CA:6:G:H4'	1:CA:298:A:H4'	1.84	0.60
35:DP:138:LEU:HD23	35:DP:145:PRO:HB3	1.83	0.60
4:AD:157:LEU:HD22	4:AD:161:ASN:HD21	1.67	0.59
25:BA:1587:U:O4	61:BA:5372:HOH:O	2.16	0.59
1:CA:1183:A:O2'	1:CA:1184:G:OP1	2.16	0.59
1:CA:1286:A:C8	1:CA:1287:A:H4'	2.37	0.59
25:DA:1891:G:O6	61:DA:4758:HOH:O	2.16	0.59
1:AA:17:U:H2'	1:AA:18:C:C6	2.37	0.59
1:AA:619:U:H3	4:AD:134:ASP:HB2	1.67	0.59
19:AS:23:ASN:HA	19:AS:27:GLU:CD	2.26	0.59
41:BV:40:LEU:HB2	41:BV:46:VAL:HG13	1.84	0.59
1:CA:1086:U:H3	1:CA:1099:G:H22	1.47	0.59
25:DA:848:G:N3	25:DA:933:A:H1'	2.17	0.59
25:DA:2751:G:H8	31:DH:2:SER:HA	1.66	0.59
1:AA:148:G:H2'	1:AA:149:A:H8	1.66	0.59
28:BE:7:VAL:HG12	28:BE:27:LEU:HB3	1.84	0.59
47:B1:85:LEU:HB3	47:B1:89:GLU:HG3	1.84	0.59
1:CA:1103:C:OP1	2:CB:96:ARG:NH2	2.34	0.59
25:DA:2183:C:H2'	25:DA:2184:G:C8	2.37	0.59
25:DA:2507:C:H5"	25:DA:2573:C:N4	2.17	0.59
1:AA:1126:U:O2	1:AA:1280:A:H2'	2.03	0.59
5:AE:122:GLU:O	5:AE:126:ARG:NH1	2.35	0.59
18:AR:52:PRO:HB2	18:AR:54:ARG:HG2	1.85	0.59
25:BA:1218:G:O2'	25:BA:1219:A:O5'	2.20	0.59
25:BA:1539:C:N4	25:BA:2227:G:O2'	2.35	0.59
27:BD:85:ASP:OD2	27:BD:88:ARG:NH1	2.34	0.59
25:DA:322:A:OP2	29:DF:169:ASN:HB2	2.02	0.59
25:DA:1033:U:OP1	55:D9:9:ARG:NH2	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1803:A:O2'	27:DD:259:THR:HG21	2.02	0.59
25:DA:2162:G:H4'	25:DA:2172:U:H2'	1.83	0.59
25:DA:2206:G:H8	25:DA:2207:G:N7	1.99	0.59
39:DT:117:ASP:OD2	39:DT:120:ARG:NE	2.29	0.59
40:DU:83:LEU:HD12	40:DU:88:ILE:HB	1.83	0.59
1:AA:406:G:H5'	4:AD:5:ILE:HD11	1.84	0.59
1:AA:1456:G:O3'	20:AT:39:LYS:NZ	2.36	0.59
28:BE:28:ALA:HB3	28:BE:93:VAL:HG12	1.85	0.59
25:DA:1159:U:H2'	25:DA:1160:G:H8	1.67	0.59
25:DA:1448:G:H4'	25:DA:1542:A:OP1	2.03	0.59
25:DA:2285:C:OP2	52:D6:6:ARG:NH1	2.35	0.59
28:DE:2:LYS:NZ	28:DE:95:ILE:O	2.32	0.59
37:DR:67:LEU:HD13	37:DR:76:VAL:HG21	1.83	0.59
1:AA:976:G:H5'	1:AA:1358:U:O2'	2.02	0.59
37:BR:44:LEU:HD22	37:BR:48:VAL:HG23	1.84	0.59
1:CA:67:C:H2'	1:CA:68:G:C8	2.37	0.59
1:CA:1029:C:N3	1:CA:1032:G:C2	2.70	0.59
8:AH:39:LEU:HB3	8:AH:45:ILE:HG12	1.83	0.59
25:BA:239:G:P	54:B8:13:ARG:HH22	2.25	0.59
45:BZ:155:LEU:HD12	45:BZ:156:LYS:H	1.66	0.59
1:CA:1128:C:H1'	1:CA:1147:C:H42	1.67	0.59
3:CC:19:GLU:HA	3:CC:54:ARG:HH22	1.68	0.59
25:DA:1762:A:N1	61:DA:4594:HOH:O	2.31	0.59
25:DA:2447:G:N2	25:DA:2450:A:OP2	2.35	0.59
23:AY:19:G:N1	23:AY:56:C:N4	2.50	0.59
25:BA:1740:U:O2'	27:BD:14:ARG:NH2	2.36	0.59
25:DA:1239:G:H2'	25:DA:1240:U:O4'	2.02	0.59
25:DA:1261:C:OP2	42:DW:83:LYS:NZ	2.29	0.59
30:DG:131:TYR:HB3	30:DG:159:VAL:HG13	1.85	0.59
9:AI:3:GLN:OE1	9:AI:20:ARG:NH2	2.31	0.59
19:AS:27:GLU:HB3	19:AS:28:LYS:HA	1.84	0.59
19:AS:63:THR:HG23	19:AS:66:MET:HE3	1.84	0.59
25:BA:1116:A:N6	25:BA:1142:A:N3	2.51	0.59
28:BE:29:GLY:HA3	61:BE:409:HOH:O	2.02	0.59
31:BH:7:LEU:HD12	31:BH:8:PRO:HD2	1.85	0.59
23:CW:43:C:H2'	23:CW:44:G:C8	2.36	0.59
41:DV:72:VAL:HG13	41:DV:85:LYS:HB3	1.85	0.59
2:AB:74:LYS:NZ	2:AB:206:ASP:OD1	2.34	0.59
4:AD:122:ARG:NH2	4:AD:134:ASP:HB3	2.18	0.59
4:CD:147:ALA:HB2	4:CD:182:LYS:HG3	1.85	0.59
13:CM:37:THR:O	13:CM:55:ARG:NH1	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:CW:25:C:H2'	23:CW:26:A:H5"	1.84	0.59
25:DA:324:A:N6	25:DA:338:G:O2'	2.36	0.59
26:DB:101:G:OP2	61:DB:3105:HOH:O	2.17	0.59
41:DV:76:LYS:HB2	41:DV:81:TYR:HB3	1.84	0.59
1:AA:347:G:H2'	1:AA:348:G:C8	2.38	0.58
1:CA:344:A:H5"	1:CA:345:C:H5	1.68	0.58
1:CA:942:G:H21	9:CI:124:GLN:NE2	2.01	0.58
1:CA:1286:A:H2'	1:CA:1287:A:H4'	1.85	0.58
25:DA:674:G:H1'	29:DF:74:ARG:HD3	1.84	0.58
28:DE:111:ARG:HG3	28:DE:160:TYR:CD2	2.38	0.58
32:DI:124:GLY:H	32:DI:144:VAL:HG23	1.68	0.58
1:AA:1136:U:H5"	1:AA:1137:C:N3	2.17	0.58
25:BA:1211:U:H2'	25:BA:1212:C:C6	2.38	0.58
25:BA:1990:G:OP1	61:BA:4942:HOH:O	2.17	0.58
35:BP:121:LYS:O	35:BP:123:LEU:N	2.36	0.58
1:CA:1503:A:O2'	22:CV:13:A:N1	2.35	0.58
23:CY:51:U:H2'	23:CY:52:G:O4'	2.03	0.58
30:DG:15:VAL:HG22	30:DG:175:LEU:HB3	1.85	0.58
23:AY:50:U:N3	23:AY:64:A:H2	1.99	0.58
25:BA:1346:U:H4'	25:BA:1347:A:C5'	2.32	0.58
1:CA:1147:C:H1'	9:CI:16:ARG:HH21	1.68	0.58
25:DA:631:A:OP1	35:DP:65:ARG:NH1	2.37	0.58
25:DA:2176:A:H2'	25:DA:2177:C:C6	2.38	0.58
25:DA:2299:G:H2'	25:DA:2300:G:H8	1.68	0.58
29:DF:135:LYS:HG2	29:DF:137:LYS:HZ3	1.68	0.58
38:DS:15:ARG:O	38:DS:19:LYS:HG2	2.02	0.58
1:AA:189(F):U:O2'	17:AQ:63:ARG:NH2	2.36	0.58
26:BB:23:G:O6	61:BB:3128:HOH:O	2.16	0.58
1:CA:410:G:OP1	4:CD:30:LYS:NZ	2.33	0.58
1:CA:662:G:H2'	1:CA:663:A:C8	2.38	0.58
28:DE:116:VAL:HG13	28:DE:122:PHE:HB2	1.85	0.58
32:DI:4:ILE:HD11	32:DI:44:LEU:HD13	1.84	0.58
44:DY:86:ARG:HD2	44:DY:100:ALA:HA	1.84	0.58
31:BH:33:LEU:HD21	31:BH:136:ILE:HG13	1.85	0.58
32:BI:92:VAL:HG11	32:BI:144:VAL:HG11	1.85	0.58
50:B4:24:THR:OG1	50:B4:25:TYR:N	2.36	0.58
1:CA:673:G:H2'	1:CA:674:G:C8	2.38	0.58
1:CA:1119:C:OP2	9:CI:9:ARG:NH1	2.37	0.58
25:DA:1012:U:H5	33:DN:28:THR:HG21	1.67	0.58
1:AA:1151:A:HO2'	1:AA:1152:A:H8	1.52	0.58
1:AA:1166:G:N2	1:AA:1170:A:OP2	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2130:C:H2'	25:BA:2131:U:C6	2.39	0.58
37:BR:118:GLU:CD	37:BR:118:GLU:H	2.10	0.58
15:CO:4:THR:N	15:CO:7:GLU:OE2	2.35	0.58
23:CW:44:G:H8	23:CW:44:G:O5'	1.87	0.58
23:CW:61:C:O2'	23:CW:62:C:O5'	2.12	0.58
25:DA:1010:A:OP2	61:DA:4488:HOH:O	2.17	0.58
25:DA:1693:U:O2'	27:DD:14:ARG:NH2	2.36	0.58
32:DI:102:SER:O	32:DI:106:GLY:N	2.36	0.58
1:AA:1316:G:N1	1:AA:1319:A:OP2	2.36	0.58
25:BA:2880:C:H2'	25:BA:2881:C:O4'	2.04	0.58
40:BU:108:GLU:O	40:BU:112:ARG:HG2	2.04	0.58
5:CE:71:LEU:HD11	5:CE:115:VAL:HG22	1.85	0.58
25:DA:526:A:OP1	61:DA:4494:HOH:O	2.17	0.58
25:DA:1589:C:H2'	25:DA:1590:U:H6	1.69	0.58
25:DA:2693:A:H2'	25:DA:2694:G:H8	1.68	0.58
47:D1:32:LYS:O	61:D1:202:HOH:O	2.16	0.58
1:AA:1036:G:H3'	1:AA:1037:C:C6	2.38	0.58
5:AE:36:ASP:OD2	5:AE:40:ARG:HB2	2.04	0.58
15:AO:17:ARG:HH11	15:AO:17:ARG:HG3	1.68	0.58
25:BA:1793:A:N1	61:BA:4975:HOH:O	2.32	0.58
23:CY:36:A:H2'	23:CY:37:MIA:O4'	2.03	0.58
25:DA:2136:C:HO2'	25:DA:2137:C:H6	1.52	0.58
25:DA:2836:U:H2'	25:DA:2837:G:C8	2.39	0.58
34:DO:8:LEU:HD12	34:DO:84:ALA:HB2	1.84	0.58
42:DW:60:ASN:HD22	42:DW:60:ASN:N	2.02	0.58
47:D1:85:LEU:HB3	47:D1:89:GLU:HB3	1.85	0.58
2:AB:185:ILE:CG2	2:AB:199:TYR:HB2	2.32	0.58
50:B4:63:TYR:N	50:B4:64:GLY:HA2	2.18	0.58
1:CA:976:G:H5'	1:CA:1358:U:O2'	2.04	0.58
23:CW:63:G:H2'	23:CW:64:A:O4'	2.04	0.58
25:DA:880:G:H2'	25:DA:881:G:H8	1.69	0.58
25:DA:886:C:O2'	25:DA:889:C:N4	2.37	0.58
25:DA:1769:G:O2'	25:DA:1958:C:OP1	2.22	0.58
1:AA:232:G:H1'	1:AA:262:A:N1	2.19	0.58
25:BA:721:G:H1'	29:BF:74:ARG:HD3	1.85	0.58
25:BA:1502:G:O2'	25:BA:2863:C:OP1	2.13	0.58
45:BZ:1:MET:HG2	45:BZ:55:HIS:ND1	2.18	0.58
45:BZ:52:SER:OG	45:BZ:53:ILE:N	2.26	0.58
1:CA:1133:G:H2'	1:CA:1134:G:O4'	2.04	0.58
1:CA:1348:U:H4'	9:CI:120:ARG:HD2	1.86	0.58
25:DA:1823:G:OP1	27:DD:54:ARG:NH1	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:DG:114:ILE:HA	30:DG:140:ILE:HD11	1.86	0.58
1:AA:8:A:N7	4:AD:208:SER:OG	2.37	0.57
2:AB:93:VAL:HG21	2:AB:97:TRP:HD1	1.69	0.57
5:AE:95:ALA:HB1	5:AE:96:PRO:HD2	1.86	0.57
25:BA:70:A:N7	43:BX:31:HIS:HE1	2.02	0.57
25:BA:1139:G:H3'	25:BA:1140:U:H5"	1.86	0.57
50:B4:55:ARG:N	50:B4:56:VAL:HA	2.19	0.57
1:CA:1244:C:N4	1:CA:1293:G:H1	2.00	0.57
2:CB:185:ILE:HG22	2:CB:199:TYR:HD2	1.69	0.57
7:CG:27:ILE:HD12	7:CG:40:ALA:HA	1.85	0.57
25:DA:974:G:OP1	25:DA:1187:G:O2'	2.14	0.57
25:DA:2141:G:H2'	25:DA:2142:C:O4'	2.03	0.57
25:DA:2478:A:OP2	55:D9:2:LYS:NZ	2.28	0.57
35:DP:95:VAL:HA	35:DP:99:LEU:HD21	1.85	0.57
45:DZ:55:HIS:CE1	45:DZ:135:GLU:HB2	2.39	0.57
8:AH:73:ASP:OD1	8:AH:75:ARG:HD3	2.03	0.57
9:AI:24:GLY:HA2	9:AI:59:PHE:O	2.05	0.57
25:DA:2114:A:N6	25:DA:2115:G:H21	2.02	0.57
1:AA:1002:G:C4	1:AA:1003:G:H1'	2.38	0.57
2:AB:213:LEU:HD22	2:AB:214:ILE:HD13	1.86	0.57
25:BA:2340:A:H2'	25:BA:2341:G:C8	2.40	0.57
5:CE:43:LEU:HD21	5:CE:132:ALA:HB1	1.86	0.57
30:DG:137:GLU:HG2	30:DG:152:LEU:HD13	1.86	0.57
40:DU:49:HIS:HA	40:DU:52:ARG:HB3	1.86	0.57
23:AW:51:U:H2'	23:AW:52:G:C8	2.39	0.57
31:BH:41:MET:HE2	31:BH:65:HIS:HA	1.87	0.57
39:BT:51:ARG:HG3	39:BT:98:LYS:HD2	1.85	0.57
1:CA:1327:C:P	21:CU:12:LYS:HZ1	2.27	0.57
15:CO:5:LYS:HD3	15:CO:5:LYS:N	2.19	0.57
23:CW:2:C:N3	23:CW:71:G:O6	2.37	0.57
23:CW:4:C:N4	23:CW:69:G:H1	2.02	0.57
48:D2:65:ASN:OD1	48:D2:69:ARG:NH1	2.38	0.57
1:AA:1118:C:OP1	9:AI:104:ARG:NH1	2.37	0.57
3:AC:6:HIS:CD2	3:AC:8:ILE:H	2.22	0.57
25:BA:555:G:N1	25:BA:2045:G:OP1	2.24	0.57
25:BA:2735:G:OP2	61:BA:4257:HOH:O	2.17	0.57
10:CJ:5:ARG:N	10:CJ:99:LYS:O	2.37	0.57
25:DA:1037:G:H1	25:DA:1118:C:H42	1.52	0.57
17:AQ:45:HIS:NE2	17:AQ:47:PRO:HG3	2.20	0.57
25:BA:1114:G:O2'	25:BA:1142:A:O2'	2.18	0.57
25:BA:1633:A:H2'	25:BA:1634:C:C6	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2146:G:N2	25:BA:2196:C:N3	2.43	0.57
25:BA:2699:U:OP2	61:BA:4996:HOH:O	2.17	0.57
37:DR:44:LEU:HD22	37:DR:48:VAL:HG23	1.85	0.57
49:D3:7:LYS:HG3	49:D3:34:GLU:HG3	1.87	0.57
1:AA:838:G:H2'	1:AA:839:U:H2'	1.85	0.57
2:AB:100:GLY:N	2:AB:176:GLU:OE2	2.28	0.57
5:AE:43:LEU:HD21	5:AE:132:ALA:HB1	1.87	0.57
23:AW:19:G:H1	23:AW:56:C:H42	1.53	0.57
36:BQ:30:GLY:O	36:BQ:134:ARG:NH1	2.36	0.57
36:BQ:42:ILE:HD13	36:BQ:97:VAL:HB	1.85	0.57
1:CA:978:A:O2'	1:CA:1322:C:N3	2.31	0.57
23:CY:50:U:C2	23:CY:64:A:N1	2.73	0.57
25:DA:403:U:H4'	25:DA:404:C:H5'	1.87	0.57
25:DA:2128:C:H1'	25:DA:2173:A:O2'	2.05	0.57
29:DF:11:VAL:HG22	29:DF:125:LEU:HD13	1.86	0.57
29:DF:21:ALA:CB	29:DF:22:ALA:HA	2.35	0.57
45:DZ:19:ARG:NH1	45:DZ:84:GLU:O	2.37	0.57
1:AA:346:G:N1	1:AA:347:G:N3	2.53	0.57
8:AH:119:LEU:HB3	8:AH:123:GLU:HB3	1.86	0.57
23:AW:66:U:H2'	23:AW:67:C:C6	2.39	0.57
25:BA:1140:U:H3	25:BA:1142:A:H3'	1.69	0.57
25:BA:2490:A:OP2	55:B9:2:LYS:NZ	2.32	0.57
28:BE:179:GLU:HB3	28:BE:181:LEU:HD22	1.87	0.57
30:BG:131:TYR:HB3	30:BG:159:VAL:HG13	1.86	0.57
24:CX:5:G:H1	24:CX:68:C:H42	1.52	0.57
25:DA:1364:G:N7	47:D1:3:LYS:HE2	2.20	0.57
25:DA:2103:C:H42	25:DA:2186:G:H1	1.52	0.57
36:DQ:34:LEU:HB2	36:DQ:118:LEU:HD22	1.87	0.57
5:AE:110:LEU:HD13	5:AE:118:ILE:HG21	1.85	0.57
11:AK:70:LYS:HA	11:AK:73:MET:HE3	1.86	0.57
13:AM:4:ILE:HG12	13:AM:5:ALA:HA	1.85	0.57
25:BA:1221:G:H1'	25:BA:1222:A:H5'	1.86	0.57
1:CA:1054:C:C4	23:CW:34:G:H1'	2.40	0.57
4:CD:162:LEU:HD13	4:CD:181:MET:HG2	1.85	0.57
25:DA:2023:G:H5'	25:DA:2617:C:H4'	1.86	0.57
25:DA:2122:U:H3	25:DA:2176:A:H2	1.51	0.57
25:DA:2693:A:H2'	25:DA:2694:G:C8	2.40	0.57
45:DZ:105:VAL:N	45:DZ:139:VAL:O	2.37	0.57
1:AA:1000:U:O4	1:AA:1041:A:N1	2.38	0.57
2:AB:19:HIS:NE2	2:AB:206:ASP:OD2	2.30	0.57
2:AB:97:TRP:HZ2	2:AB:102:LEU:HD13	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:AM:122:LYS:HD3	13:AM:123:ALA:H	1.69	0.57
25:BA:1065:U:O2'	25:BA:1067:A:H2	1.88	0.57
27:BD:2:ALA:N	27:BD:200:ASP:OD2	2.38	0.57
29:DF:135:LYS:HG2	29:DF:137:LYS:NZ	2.20	0.57
33:DN:20:GLY:HA2	33:DN:61:ARG:HE	1.70	0.57
1:AA:36:C:OP1	12:AL:123:LYS:NZ	2.29	0.56
1:AA:60:A:H4'	1:AA:61:G:H5'	1.86	0.56
6:AF:82:ARG:HB3	6:AF:85:VAL:HG23	1.86	0.56
23:AY:12:U:H2'	23:AY:13:C:O4'	2.04	0.56
25:BA:2367:C:H1'	46:B0:39:ARG:HH21	1.70	0.56
25:BA:2807:C:N4	25:BA:2813:G:H1	2.02	0.56
35:BP:59:LEU:HD21	54:B8:10:ALA:HA	1.86	0.56
2:CB:131:PRO:O	2:CB:135:GLN:HB2	2.05	0.56
19:CS:30:LEU:HD11	19:CS:50:ALA:HB2	1.87	0.56
39:DT:16:ARG:NH1	39:DT:18:ASP:OD1	2.38	0.56
1:AA:67:C:H2'	1:AA:68:G:C8	2.40	0.56
25:BA:794:U:H4'	42:BW:92:ARG:HH22	1.71	0.56
25:DA:2892:A:H2'	25:DA:2893:G:H5'	1.85	0.56
26:DB:57:A:H1'	30:DG:29:TRP:HB2	1.87	0.56
26:DB:66:A:N6	26:DB:108:U:H3'	2.20	0.56
31:DH:56:SER:HB3	31:DH:61:HIS:ND1	2.19	0.56
8:AH:10:LEU:HD22	8:AH:83:ILE:HD11	1.87	0.56
10:AJ:17:ASP:OD1	10:AJ:70:ARG:NH1	2.38	0.56
25:BA:1100:A:OP1	25:BA:1100:A:H4'	2.05	0.56
25:BA:1117:G:O2'	25:BA:1135:G:H2'	2.06	0.56
28:BE:56:PRO:HG3	28:BE:74:PRO:HG2	1.86	0.56
29:BF:53:THR:HG22	29:BF:55:GLY:H	1.69	0.56
29:BF:185:ASP:HA	29:BF:188:ARG:HD3	1.87	0.56
32:BI:131:LYS:HA	32:BI:137:PRO:HA	1.87	0.56
48:B2:59:ARG:NH2	61:B2:4003:HOH:O	2.38	0.56
1:CA:828:A:OP1	8:CH:21:LYS:NZ	2.38	0.56
1:CA:1004:A:N6	1:CA:1037:C:C2	2.74	0.56
1:CA:1239:A:H4'	1:CA:1240:U:H5"	1.88	0.56
1:CA:1348:U:H2'	1:CA:1349:A:H8	1.70	0.56
9:CI:110:GLU:OE2	9:CI:113:LYS:NZ	2.38	0.56
17:CQ:95:TYR:HA	17:CQ:98:LEU:HD12	1.85	0.56
25:DA:1019:U:H2'	25:DA:1020:A:C8	2.40	0.56
39:DT:24:PRO:HA	39:DT:49:VAL:HG22	1.87	0.56
25:BA:611:U:H2'	25:BA:612:C:C6	2.41	0.56
44:BY:18:GLY:O	44:BY:21:LYS:NZ	2.32	0.56
47:B1:3:LYS:HB2	47:B1:61:ARG:HH12	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1255:G:OP1	10:CJ:45:ARG:NH2	2.35	0.56
3:CC:71:ALA:HA	3:CC:106:VAL:HB	1.88	0.56
9:CI:9:ARG:O	9:CI:104:ARG:HG3	2.06	0.56
12:CL:117:ARG:HB3	12:CL:122:THR:O	2.04	0.56
25:DA:2291:U:H2'	25:DA:2292:C:C6	2.40	0.56
7:AG:28:ASN:HD21	7:AG:36:LYS:HZ1	1.54	0.56
17:AQ:43:LEU:HD12	17:AQ:68:ARG:HG2	1.88	0.56
23:AW:5:G:H2'	23:AW:6:G:H8	1.66	0.56
23:AW:50:U:H6	23:AW:50:U:H5'	1.70	0.56
23:AY:19:G:H4'	23:AY:57:G:H22	1.69	0.56
23:AY:56:C:H2'	23:AY:57:G:O4'	2.06	0.56
26:BB:33:G:H5'	30:BG:2:PRO:HD3	1.87	0.56
1:CA:1064:G:O6	1:CA:1191:A:N6	2.39	0.56
25:DA:108:U:H2'	25:DA:109:G:C8	2.40	0.56
25:DA:1183:G:H5"	49:D3:30:ARG:HH22	1.71	0.56
7:AG:79:ARG:HB3	7:AG:80:VAL:CG2	2.35	0.56
25:BA:1817:A:H1'	25:BA:1960:A:N6	2.21	0.56
1:CA:1305:G:N2	1:CA:1331:G:H1'	2.20	0.56
4:CD:157:LEU:O	4:CD:161:ASN:ND2	2.38	0.56
7:CG:113:GLU:CG	7:CG:119:ARG:HG2	2.36	0.56
19:CS:28:LYS:HB3	19:CS:29:ARG:HA	1.88	0.56
25:DA:400:G:N7	61:DA:4696:HOH:O	2.32	0.56
27:DD:17:THR:O	27:DD:211:ARG:NH2	2.35	0.56
50:D4:16:CYS:SG	50:D4:17:GLY:N	2.79	0.56
1:AA:532:A:H2	1:AA:1206:G:H21	1.54	0.56
29:BF:14:PRO:HD2	29:BF:127:GLU:OE2	2.06	0.56
41:BV:10:LYS:NZ	41:BV:23:GLU:OE2	2.38	0.56
1:CA:1151:A:O2'	1:CA:1152:A:H8	1.88	0.56
2:CB:73:THR:HA	2:CB:94:ASN:O	2.06	0.56
2:CB:76:GLN:CD	2:CB:76:GLN:H	2.14	0.56
3:CC:43:LEU:HD21	3:CC:91:LEU:HD13	1.88	0.56
8:CH:14:ARG:HG2	8:CH:18:ARG:NH2	2.20	0.56
11:CK:85:ARG:HD3	11:CK:113:PRO:HD3	1.88	0.56
25:DA:1005:C:H2'	25:DA:1006:C:C6	2.40	0.56
38:DS:87:PHE:CE1	38:DS:102:ALA:HB2	2.41	0.56
7:AG:26:PHE:O	7:AG:30:ILE:HD12	2.05	0.56
23:AY:2:C:H42	23:AY:71:G:H1	1.53	0.56
25:BA:1159:U:H2'	25:BA:1160:G:C8	2.40	0.56
30:BG:16:ARG:HH21	30:BG:31:VAL:HG11	1.71	0.56
35:BP:91:PHE:O	35:BP:121:LYS:NZ	2.35	0.56
52:B6:6:ARG:NH1	52:B6:26:ASN:HB2	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:152:ILE:HG23	3:CC:199:LYS:HB2	1.87	0.56
13:CM:91:ARG:HB2	13:CM:98:VAL:HG13	1.87	0.56
25:DA:2165:G:H2'	25:DA:2166:G:H5"	1.88	0.56
26:DB:103:G:N3	45:DZ:73:GLN:NE2	2.43	0.56
30:DG:32:PRO:HB3	30:DG:163:ALA:HB2	1.88	0.56
41:DV:40:LEU:HB2	41:DV:46:VAL:HG13	1.88	0.56
38:BS:10:ARG:O	38:BS:14:VAL:HG13	2.06	0.56
23:CY:19:G:C6	23:CY:56:C:N4	2.73	0.56
23:CY:19:G:C2	23:CY:56:C:N3	2.74	0.56
25:DA:1717:G:H2'	25:DA:1718:G:H8	1.70	0.56
25:DA:1799:G:O2'	27:DD:181:GLU:OE2	2.20	0.56
1:AA:438:G:O2'	1:AA:494:U:O4	2.20	0.56
25:BA:2298:A:H4'	25:BA:2299:A:O4'	2.06	0.56
2:CB:233:SER:HB2	2:CB:234:PRO:HD2	1.86	0.56
19:CS:27:GLU:HG2	19:CS:47:HIS:CE1	2.40	0.56
25:DA:1507:A:O2'	25:DA:1508:A:O5'	2.24	0.56
52:D6:6:ARG:NH1	52:D6:26:ASN:HB2	2.20	0.56
37:BR:96:ARG:NH2	37:BR:118:GLU:OE2	2.35	0.55
1:CA:1028:C:O2	1:CA:1033:G:C2	2.60	0.55
25:DA:2166:G:H3'	25:DA:2167:U:H5"	1.88	0.55
25:DA:2472:G:H2'	25:DA:2475:C:H42	1.70	0.55
1:AA:38:G:N2	1:AA:397:A:H5"	2.19	0.55
1:AA:356:A:N3	1:AA:368:U:O2'	2.34	0.55
2:AB:178:ARG:HH22	8:AH:68:ARG:NH1	2.04	0.55
25:BA:742:G:OP1	25:BA:1426:G:O2'	2.23	0.55
25:BA:2307:C:OP1	38:BS:10:ARG:NH1	2.39	0.55
36:BQ:57:HIS:HD2	36:BQ:117:ALA:HB2	1.71	0.55
8:CH:41:ARG:NH2	8:CH:123:GLU:OE2	2.38	0.55
25:DA:143:G:H4'	43:DX:35:THR:HG21	1.88	0.55
25:DA:307:G:N1	25:DA:310:A:OP2	2.35	0.55
25:DA:2376:A:N3	38:DS:106:ARG:NH2	2.52	0.55
25:DA:2815:C:H5'	51:D5:29:THR:HG21	1.88	0.55
2:AB:16:HIS:CG	2:AB:17:PHE:N	2.70	0.55
17:AQ:53:LEU:HD23	17:AQ:82:MET:HE1	1.88	0.55
23:AY:36:A:H2'	23:AY:37:MIA:O4'	2.06	0.55
25:BA:1475:G:H2'	25:BA:1476:C:C6	2.40	0.55
25:BA:2482:G:OP1	36:BQ:56:ARG:NH2	2.39	0.55
38:BS:14:VAL:O	38:BS:18:ILE:HG12	2.07	0.55
1:CA:646:U:H2'	1:CA:647:C:C6	2.42	0.55
1:CA:1221:G:O3'	19:CS:77:THR:OG1	2.24	0.55
1:CA:1239:A:H62	1:CA:1299:A:H62	1.52	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:26:LYS:HG3	10:CJ:45:ARG:HH12	1.72	0.55
25:DA:902:C:H2'	25:DA:903:C:H6	1.71	0.55
38:DS:15:ARG:NE	38:DS:88:ASP:OD2	2.31	0.55
1:AA:346:G:C3'	1:AA:347:G:H4'	2.35	0.55
8:AH:29:SER:HB3	8:AH:32:LYS:HG3	1.88	0.55
9:AI:17:VAL:HG11	9:AI:80:GLY:C	2.31	0.55
19:AS:20:LEU:HD23	19:AS:23:ASN:HD22	1.70	0.55
20:AT:10:LEU:HB3	20:AT:12:ALA:H	1.70	0.55
23:AY:19:G:O4'	23:AY:57:G:N1	2.40	0.55
25:BA:1148:C:H2'	25:BA:1149:A:H8	1.72	0.55
25:BA:1298:G:OP1	40:BU:36:ARG:NH2	2.39	0.55
1:CA:450:G:OP1	16:CP:43:LYS:NZ	2.38	0.55
1:CA:532:A:H2	1:CA:1206:G:H21	1.54	0.55
1:CA:1318:A:OP1	19:CS:3:ARG:NH2	2.38	0.55
15:CO:17:ARG:HH11	15:CO:17:ARG:HG3	1.71	0.55
25:DA:108:U:H2'	25:DA:109:G:H8	1.70	0.55
25:DA:897:C:H3'	25:DA:898:C:C6	2.41	0.55
25:DA:1012:U:C5	33:DN:28:THR:HG21	2.40	0.55
31:DH:6:ARG:HH21	31:DH:54:ARG:HH12	1.54	0.55
1:AA:130:A:OP2	17:AQ:63:ARG:NE	2.39	0.55
1:AA:662:G:H2'	1:AA:663:A:C8	2.41	0.55
3:CC:52:LEU:HD11	3:CC:55:VAL:HG23	1.88	0.55
23:CY:9:A:H5'	23:CY:46:7MG:N3	2.22	0.55
25:DA:1359:A:H61	25:DA:1372:U:H3	1.55	0.55
17:AQ:9:VAL:HG13	17:AQ:56:VAL:HG22	1.87	0.55
23:AY:8:4SU:H1'	23:AY:48:C:H1'	1.88	0.55
25:BA:1217:G:O6	25:BA:1223:C:N4	2.22	0.55
2:CB:144:ARG:NH2	2:CB:148:TYR:OH	2.39	0.55
25:DA:1352:U:OP1	61:DA:4122:HOH:O	2.18	0.55
25:DA:2769:C:H2'	25:DA:2770:G:O4'	2.07	0.55
1:AA:1002:G:N1	1:AA:1004:A:O2'	2.38	0.55
11:AK:20:TYR:HB2	11:AK:31:THR:HG23	1.88	0.55
25:BA:2138:G:H8	25:BA:2188:G:H22	1.55	0.55
25:BA:2695:C:OP1	39:BT:53:ARG:NH2	2.40	0.55
49:B3:3:ARG:NH1	49:B3:60:GLU:OE2	2.34	0.55
50:B4:16:CYS:SG	50:B4:17:GLY:N	2.79	0.55
1:CA:538:G:H5"	12:CL:114:LYS:HB2	1.88	0.55
1:CA:1075:C:OP1	2:CB:179:LYS:NZ	2.31	0.55
1:CA:1299:A:H2'	1:CA:1299:A:N3	2.22	0.55
15:CO:5:LYS:O	15:CO:9:GLN:HG2	2.07	0.55
25:DA:1796:U:H2'	25:DA:1797:C:C6	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:154:C:C2'	1:AA:155:C:H5'	2.37	0.55
2:AB:195:ASP:O	8:AH:68:ARG:NH2	2.30	0.55
32:BI:109:ILE:HG13	32:BI:130:TYR:CZ	2.42	0.55
44:BY:92:ASN:N	44:BY:93:GLY:HA2	2.21	0.55
1:CA:942:G:H21	9:CI:124:GLN:HE22	1.54	0.55
23:CW:27:G:N2	23:CW:43:C:N3	2.48	0.55
25:DA:1778:U:H2'	25:DA:1784:A:N6	2.22	0.55
25:DA:1847:A:H3'	25:DA:1848:A:H5'	1.88	0.55
1:AA:652:U:O4	1:AA:752:G:O2'	2.23	0.55
1:AA:1003:G:H21	1:AA:1038:C:H42	1.54	0.55
4:AD:107:ARG:HH22	4:AD:194:LEU:HD11	1.72	0.55
4:AD:173:TRP:CE3	4:AD:174:LEU:HG	2.42	0.55
5:AE:78:HIS:HD2	8:AH:107:LEU:HD12	1.72	0.55
23:AY:58:A:H2'	23:AY:60:U:OP2	2.06	0.55
25:BA:298:G:H2'	25:BA:299:G:C8	2.40	0.55
25:BA:493:G:OP1	53:B7:33:ARG:NH1	2.40	0.55
28:BE:111:ARG:HG3	28:BE:160:TYR:CD2	2.42	0.55
29:BF:89:VAL:O	61:BF:406:HOH:O	2.18	0.55
1:CA:1028:C:C4	1:CA:1033:G:C6	2.94	0.55
1:CA:1060:C:N4	3:CC:2:GLY:HA2	2.22	0.55
3:CC:79:ARG:O	3:CC:82:GLU:HB2	2.06	0.55
25:DA:271(H):G:O2'	25:DA:271(I):G:OP2	2.25	0.55
41:DV:60:GLU:HB2	41:DV:97:LYS:HE2	1.87	0.55
43:DX:31:HIS:CD2	43:DX:33:LYS:H	2.16	0.55
1:AA:757:U:H2'	1:AA:758:G:O4'	2.07	0.55
1:AA:984:C:H42	1:AA:1221:G:H1	1.55	0.55
1:AA:1272:G:H2'	1:AA:1273:G:O4'	2.06	0.55
10:AJ:61:GLU:OE1	14:AN:58:LYS:NZ	2.36	0.55
23:AY:33:U:H2'	23:AY:34:G:H5"	1.87	0.55
26:BB:105:A:OP1	45:BZ:72:ARG:NH1	2.40	0.55
1:CA:953:G:H5'	1:CA:965:A:N6	2.19	0.55
1:CA:973:G:H3'	1:CA:974:A:H5"	1.88	0.55
12:CL:117:ARG:NH2	12:CL:124:LYS:HG2	2.22	0.55
25:DA:471:A:H2'	25:DA:472:A:O4'	2.07	0.55
39:DT:95:ARG:HG2	39:DT:95:ARG:HH11	1.72	0.55
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.42	0.54
1:AA:1457:G:OP1	20:AT:39:LYS:NZ	2.40	0.54
5:AE:102:ALA:O	5:AE:107:ARG:NH1	2.39	0.54
8:AH:51:VAL:HG12	8:AH:52:ASP:H	1.71	0.54
23:AW:76:A:H4'	25:BA:2518:U:O2'	2.06	0.54
25:BA:139:A:H8	25:BA:1454:C:O2'	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:595:A:OP2	41:BV:78:LYS:NZ	2.40	0.54
25:BA:2603:C:H2'	25:BA:2604:G:C8	2.42	0.54
40:BU:58:ARG:HA	40:BU:61:TRP:CE3	2.41	0.54
49:B3:7:LYS:HG3	49:B3:34:GLU:HG3	1.89	0.54
3:CC:179:ARG:NH1	3:CC:206:GLU:OE1	2.40	0.54
13:CM:3:ARG:HA	50:D4:34:GLU:HG2	1.88	0.54
19:CS:63:THR:OG1	19:CS:65:ASN:ND2	2.40	0.54
25:DA:2357:U:OP1	46:D0:20:ARG:NH1	2.35	0.54
25:DA:2530:A:OP2	25:DA:2535:G:N2	2.40	0.54
2:AB:178:ARG:HH22	8:AH:68:ARG:HH12	1.53	0.54
25:BA:1114:G:H2'	25:BA:1115:A:O4'	2.06	0.54
27:BD:17:THR:O	27:BD:211:ARG:NH2	2.40	0.54
1:CA:35:G:O2'	12:CL:118:SER:O	2.25	0.54
1:CA:45:U:H2'	1:CA:46:G:C8	2.42	0.54
25:DA:997:G:OP1	40:DU:92:ARG:HG2	2.08	0.54
19:AS:65:ASN:HD22	19:AS:65:ASN:N	2.05	0.54
25:BA:1452:U:H2'	25:BA:1453:C:C6	2.42	0.54
44:BY:6:HIS:H	44:BY:6:HIS:CD2	2.24	0.54
1:CA:1288:A:N1	1:CA:1371:G:H1'	2.21	0.54
25:DA:885:C:H2'	25:DA:886:C:H4'	1.89	0.54
25:DA:1116:C:H2'	25:DA:1117:G:C8	2.42	0.54
35:DP:59:LEU:HD21	54:D8:10:ALA:HA	1.89	0.54
37:DR:72:ASP:O	37:DR:76:VAL:HG23	2.07	0.54
1:AA:625:G:H4'	16:AP:16:HIS:CD2	2.42	0.54
1:AA:1292:U:P	7:AG:41:ARG:HH22	2.30	0.54
23:AY:5:G:H1'	23:AY:69:G:C2	2.42	0.54
32:BI:133:HIS:ND1	32:BI:134:PRO:O	2.40	0.54
1:CA:54:C:N4	1:CA:353:A:OP2	2.38	0.54
1:CA:447:G:O6	1:CA:485:G:O2'	2.23	0.54
2:CB:178:ARG:HH22	8:CH:68:ARG:HH12	1.56	0.54
20:CT:53:LEU:HA	20:CT:56:MET:HG2	1.90	0.54
25:DA:861:A:N3	26:DB:79:C:O2'	2.36	0.54
25:DA:864:G:OP2	36:DQ:22:LYS:HE3	2.08	0.54
25:DA:1220:A:OP2	40:DU:19:LYS:NZ	2.33	0.54
25:DA:2167:U:H2'	25:DA:2168:G:H21	1.71	0.54
39:DT:17:THR:O	39:DT:17:THR:OG1	2.21	0.54
50:D4:64:GLY:C	50:D4:66:SER:H	2.15	0.54
1:CA:157:G:H1	1:CA:164:U:H3	1.54	0.54
9:CI:81:ILE:O	9:CI:85:LEU:HG	2.08	0.54
35:DP:121:LYS:O	35:DP:123:LEU:N	2.40	0.54
1:AA:1032:G:H2'	1:AA:1033:G:C8	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1149:C:H2'	1:AA:1150:U:C6	2.42	0.54
1:AA:1239:A:H4'	1:AA:1240:U:H5"	1.90	0.54
1:AA:1305:G:H22	1:AA:1331:G:H1'	1.72	0.54
4:AD:53:ASP:O	4:AD:57:ARG:HG3	2.07	0.54
25:BA:354:A:H2	25:BA:1255:A:O2'	1.90	0.54
25:BA:1717:C:OP1	61:BA:4143:HOH:O	2.18	0.54
25:BA:2339:A:H2'	25:BA:2340:A:C8	2.43	0.54
25:BA:2807:C:N3	25:BA:2813:G:N2	2.47	0.54
27:BD:164:GLN:NE2	27:BD:176:ARG:HH12	2.06	0.54
3:CC:138:VAL:HG23	3:CC:151:VAL:HG23	1.90	0.54
25:DA:287:C:H2'	25:DA:288:C:H6	1.73	0.54
25:DA:2134:A:H2'	25:DA:2134:A:N3	2.23	0.54
38:DS:15:ARG:HE	38:DS:88:ASP:CG	2.15	0.54
1:AA:202:U:O2'	1:AA:203:U:O5'	2.23	0.54
25:BA:1002:A:H5'	36:BQ:76:LYS:HG3	1.90	0.54
25:BA:2132:G:O2'	25:BA:2142:G:OP2	2.25	0.54
26:BB:7:G:H8	26:BB:7:G:H5"	1.73	0.54
1:CA:1028:C:N3	1:CA:1033:G:C5	2.74	0.54
4:CD:6:GLY:H	4:CD:115:ARG:HH12	1.56	0.54
4:CD:58:LEU:HD22	4:CD:62:GLN:HG2	1.90	0.54
13:CM:90:LEU:HD23	13:CM:93:ARG:HE	1.73	0.54
25:DA:116:C:H2'	25:DA:117:G:O4'	2.08	0.54
25:DA:2118:U:N3	25:DA:2149:G:H1'	2.22	0.54
25:DA:2650:U:H2'	25:DA:2651:C:C6	2.43	0.54
30:DG:19:LEU:HD13	30:DG:32:PRO:HG2	1.90	0.54
32:DI:104:GLN:O	32:DI:105:HIS:ND1	2.38	0.54
35:DP:63:PRO:HG2	54:D8:25:MET:HB2	1.88	0.54
1:AA:346:G:N3	1:AA:347:G:H1'	2.22	0.54
18:AR:32:ARG:HA	18:AR:69:THR:HG21	1.89	0.54
25:BA:215:G:H21	25:BA:217:A:H62	1.54	0.54
25:BA:794:U:O2	25:BA:2036:A:H1'	2.08	0.54
38:BS:61:ASN:HB3	38:BS:64:GLU:HB2	1.90	0.54
49:B3:26:LEU:O	49:B3:35:ARG:NE	2.39	0.54
1:CA:93:G:O2'	1:CA:96:U:H5'	2.07	0.54
1:CA:396:G:O2'	1:CA:398:C:OP1	2.16	0.54
24:CX:50:U:H3	24:CX:64:G:H1	1.53	0.54
23:CY:50:U:N3	23:CY:64:A:N6	2.55	0.54
25:DA:236:C:H2'	25:DA:237:C:H6	1.72	0.54
25:DA:687:C:OP2	61:DA:4768:HOH:O	2.18	0.54
25:DA:878:A:N6	25:DA:899:A:O2'	2.41	0.54
25:DA:1971:A:OP1	61:DA:4259:HOH:O	2.18	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:DI:71:ILE:O	32:DI:75:LEU:HD13	2.08	0.54
52:D6:14:THR:OG1	52:D6:48:VAL:O	2.26	0.54
1:AA:309:G:O2'	1:AA:607:A:N1	2.40	0.54
2:AB:59:GLU:HB2	2:AB:221:LEU:HD12	1.90	0.54
13:AM:17:VAL:O	13:AM:20:THR:OG1	2.20	0.54
35:BP:50:ARG:HD3	54:B8:7:HIS:CD2	2.43	0.54
1:CA:964:A:N3	1:CA:969:A:O2'	2.36	0.54
25:DA:296:C:O3'	44:DY:95:LYS:NZ	2.41	0.54
25:DA:1495:A:H2'	25:DA:1496:A:C8	2.43	0.54
25:DA:2630:G:H2'	25:DA:2631:G:C8	2.43	0.54
1:AA:974:A:H8	1:AA:974:A:OP1	1.91	0.54
1:AA:1025:U:H3	1:AA:1036:G:H1	1.55	0.54
32:BI:65:ALA:O	32:BI:69:LYS:N	2.38	0.54
1:CA:684:A:N6	61:CA:4138:HOH:O	2.40	0.54
1:CA:1456:G:O3'	20:CT:39:LYS:NZ	2.41	0.54
16:CP:58:TYR:O	16:CP:61:SER:OG	2.19	0.54
55:D9:10:ILE:HD12	55:D9:32:HIS:HA	1.90	0.54
20:AT:86:ARG:C	20:AT:90:GLN:HE22	2.17	0.53
25:BA:2830:A:OP2	37:BR:2:ARG:NH2	2.41	0.53
26:BB:13:A:N1	26:BB:69:G:O2'	2.37	0.53
32:BI:77:LEU:HB3	32:BI:142:VAL:HG12	1.88	0.53
1:CA:375:U:OP1	16:CP:69:THR:HG21	2.08	0.53
7:CG:90:GLU:CD	7:CG:90:GLU:H	2.15	0.53
9:CI:9:ARG:H	9:CI:79:LEU:HD23	1.73	0.53
13:CM:106:ASN:C	13:CM:108:ARG:H	2.16	0.53
23:CW:21:A:N6	23:CW:46:7MG:C4	2.77	0.53
25:DA:882:G:H2'	25:DA:883:G:C8	2.43	0.53
25:DA:1300:U:H4'	25:DA:1301:A:C5'	2.39	0.53
26:DB:9:G:H1	26:DB:112:U:H3	1.54	0.53
39:DT:59:THR:HG23	39:DT:78:LEU:HB3	1.90	0.53
45:DZ:159:PRO:HA	45:DZ:161:VAL:N	2.23	0.53
1:AA:447:G:H2'	1:AA:485:G:N2	2.23	0.53
1:AA:527:G:O2'	1:AA:535:A:N1	2.31	0.53
1:AA:1008:C:N3	1:AA:1021:G:C2	2.76	0.53
4:AD:164:ALA:O	4:AD:168:ARG:HD3	2.07	0.53
25:BA:484:G:O2'	25:BA:495:G:O6	2.25	0.53
25:BA:924:U:H2'	25:BA:925:A:H2	1.73	0.53
25:BA:1044:C:P	40:BU:92:ARG:HH22	2.31	0.53
1:CA:93:G:C2'	1:CA:96:U:H5'	2.38	0.53
1:CA:328:C:H4'	1:CA:329:A:H5'	1.91	0.53
6:CF:23:LYS:HG2	6:CF:61:LEU:HD21	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:CJ:12:ASP:OD2	10:CJ:15:THR:HG23	2.08	0.53
20:CT:18:GLN:O	20:CT:22:ARG:HG3	2.08	0.53
25:DA:952:G:OP1	36:DQ:16:ARG:NH2	2.42	0.53
27:DD:164:GLN:NE2	27:DD:176:ARG:HH22	2.05	0.53
1:AA:117:G:OP2	61:AA:4254:HOH:O	2.19	0.53
1:AA:1030(A):G:O2'	1:AA:1031:G:N1	2.41	0.53
1:AA:1136:U:H5"	1:AA:1137:C:C4	2.43	0.53
1:AA:1399:C:C2	1:AA:1502:A:N6	2.77	0.53
23:AY:9:A:H4'	23:AY:46:7MG:OP2	2.07	0.53
25:BA:236:G:H4'	25:BA:413:G:C5	2.43	0.53
25:BA:843:C:H2'	25:BA:844:C:C6	2.44	0.53
25:BA:2152:U:O2'	25:BA:2180:A:N1	2.34	0.53
30:BG:5:VAL:HG22	30:BG:8:LYS:H	1.74	0.53
38:BS:15:ARG:NE	38:BS:88:ASP:OD2	2.34	0.53
1:CA:1118:C:OP1	9:CI:104:ARG:NH1	2.42	0.53
1:CA:1148:U:H2'	1:CA:1149:C:O4'	2.08	0.53
1:CA:1149:C:H2'	1:CA:1150:U:C6	2.43	0.53
1:CA:1249:C:O4'	9:CI:70:LYS:NZ	2.42	0.53
2:CB:15:VAL:HG13	2:CB:209:ARG:HB3	1.90	0.53
2:CB:120:ALA:C	2:CB:122:PHE:H	2.14	0.53
24:CX:66:C:H2'	24:CX:67:C:O4'	2.08	0.53
23:CY:52:G:O6	23:CY:62:C:N3	2.41	0.53
23:CY:58:A:H1'	23:CY:60:U:H3	1.72	0.53
31:DH:69:ARG:HG3	31:DH:70:THR:N	2.23	0.53
43:DX:43:VAL:HG21	43:DX:81:VAL:HG11	1.91	0.53
1:AA:1275:A:C2'	1:AA:1276:G:H5'	2.38	0.53
11:AK:34:ASP:OD2	11:AK:38:ASN:HB2	2.09	0.53
25:BA:265:U:H2'	25:BA:266:C:C6	2.43	0.53
25:BA:1014:U:H2'	25:BA:1015:C:C6	2.43	0.53
25:BA:2158:C:N3	25:BA:2177:G:C2	2.76	0.53
27:BD:164:GLN:HE21	27:BD:176:ARG:HH12	1.56	0.53
1:CA:1152:A:OP1	10:CJ:70:ARG:NH2	2.42	0.53
2:CB:77:ALA:HA	2:CB:80:ILE:HG22	1.90	0.53
9:CI:8:GLY:O	9:CI:14:VAL:HA	2.08	0.53
23:CW:28:G:H2'	23:CW:29:G:O4'	2.08	0.53
24:CX:2:G:OP1	46:D0:5:LYS:NZ	2.38	0.53
25:DA:315:G:H2'	25:DA:316:C:C6	2.44	0.53
25:DA:922:U:H2'	25:DA:923:C:C6	2.43	0.53
25:DA:1713:U:H2'	25:DA:1714:G:H8	1.74	0.53
25:DA:1957:C:OP1	61:DA:4713:HOH:O	2.19	0.53
1:AA:841:U:C5	1:AA:848:C:H1'	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:848:C:H2'	1:AA:849:C:H6	1.74	0.53
2:AB:95:GLN:OE1	2:AB:147:LYS:NZ	2.28	0.53
18:AR:58:LEU:HD12	18:AR:62:GLU:HB2	1.89	0.53
25:BA:390:G:H2'	25:BA:391:G:C8	2.44	0.53
1:CA:1192:C:OP1	3:CC:4:LYS:NZ	2.41	0.53
19:CS:52:TYR:HB2	19:CS:57:HIS:CE1	2.43	0.53
24:CX:15:G:H2'	24:CX:59:A:N1	2.24	0.53
25:DA:888:C:H5"	25:DA:889:C:OP2	2.07	0.53
26:DB:22:U:H3	26:DB:61:G:H1	1.56	0.53
30:DG:151:ALA:O	30:DG:153:ARG:NH1	2.41	0.53
1:AA:1239:A:H62	1:AA:1299:A:N6	2.06	0.53
25:BA:764:G:H2'	25:BA:765:A:O4'	2.08	0.53
25:BA:1001:G:H5"	36:BQ:77:LYS:HD2	1.90	0.53
25:BA:1077:G:H21	55:B9:36:GLN:HE22	1.57	0.53
53:B7:34:ARG:NH2	61:B7:201:HOH:O	2.41	0.53
4:CD:176:LEU:HD12	4:CD:182:LYS:O	2.08	0.53
12:CL:83:VAL:HG23	12:CL:107:ALA:HB2	1.90	0.53
25:DA:1817:G:OP1	27:DD:88:ARG:NH2	2.42	0.53
25:DA:2022:U:O2'	25:DA:2617:C:H5'	2.09	0.53
26:DB:1:U:O2'	26:DB:2:C:O5'	2.20	0.53
27:DD:132:PRO:HG2	27:DD:135:PHE:HD2	1.72	0.53
7:AG:48:LYS:O	7:AG:52:GLU:HG2	2.08	0.53
1:CA:56:U:H2'	1:CA:57:G:C8	2.43	0.53
1:CA:757:U:H2'	1:CA:758:G:O4'	2.09	0.53
10:CJ:42:THR:HG23	10:CJ:68:HIS:HA	1.91	0.53
13:CM:23:TYR:HB3	13:CM:67:GLU:HA	1.91	0.53
15:CO:6:GLU:N	15:CO:6:GLU:OE2	2.39	0.53
23:CY:18:G:N1	23:CY:55:PSU:C4	2.76	0.53
30:DG:46:ALA:HB2	30:DG:53:LEU:HG	1.91	0.53
32:DI:38:LEU:HD12	32:DI:38:LEU:H	1.73	0.53
44:DY:88:LYS:HZ3	44:DY:90:LEU:HA	1.73	0.53
1:AA:1027:C:C4	1:AA:1034:G:C6	2.89	0.53
3:AC:121:ALA:O	3:AC:125:GLU:HG3	2.09	0.53
25:BA:125:A:H5"	25:BA:126:C:C6	2.43	0.53
25:BA:2073:A:H5'	25:BA:2590:G:O4'	2.09	0.53
27:BD:20:ASP:OD2	27:BD:22:SER:OG	2.22	0.53
30:BG:106:LEU:HA	30:BG:110:ALA:HB3	1.91	0.53
1:CA:1121:U:C4	1:CA:1122:U:C4	2.97	0.53
6:CF:76:ALA:O	6:CF:80:ARG:HG3	2.08	0.53
12:CL:124:LYS:HD3	12:CL:125:PRO:HD2	1.91	0.53
23:CW:18:G:O2'	23:CW:57:G:N2	2.33	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:CW:50:U:H2'	23:CW:51:U:C6	2.44	0.53
25:DA:1250:G:OP2	35:DP:21:ARG:NH1	2.42	0.53
25:DA:1579:A:H2'	25:DA:1580:A:C8	2.43	0.53
25:DA:2121:G:N2	25:DA:2177:C:N3	2.46	0.53
37:DR:21:TYR:OH	37:DR:43:GLU:HG2	2.09	0.53
16:AP:19:ILE:HG22	16:AP:37:GLY:C	2.33	0.53
25:BA:387:G:H2'	25:BA:388:A:H8	1.74	0.53
25:BA:2178:G:H8	25:BA:2178:G:OP2	1.92	0.53
25:BA:2486:C:OP2	25:BA:2487:C:N4	2.39	0.53
41:BV:76:LYS:HB2	41:BV:81:TYR:HB3	1.90	0.53
1:CA:838:G:H1	1:CA:848:C:N4	2.07	0.53
1:CA:1002:G:C4	1:CA:1003:G:C8	2.97	0.53
1:CA:1435:G:H2'	1:CA:1436:U:C6	2.44	0.53
8:CH:46:LYS:HA	8:CH:64:LYS:HE3	1.90	0.53
15:CO:28:GLN:NE2	15:CO:66:LEU:HD21	2.24	0.53
23:CW:44:G:H2'	23:CW:45:U:H5'	1.90	0.53
24:CX:31:G:H3'	24:CX:32:5MC:HM53	1.90	0.53
25:DA:2135:A:H61	25:DA:2157:G:H21	1.56	0.53
25:DA:2137:C:H2'	25:DA:2138:C:H6	1.73	0.53
25:DA:2144:U:O2	25:DA:2148:G:N1	2.42	0.53
30:DG:64:THR:HB	30:DG:94:LEU:HD21	1.91	0.53
31:DH:106:THR:HG22	31:DH:112:PRO:HB3	1.91	0.53
1:AA:1179:A:H4'	9:AI:103:THR:HA	1.91	0.53
23:AW:26:A:N1	23:AW:44:G:N2	2.52	0.53
25:BA:1716:A:H5"	25:BA:2562:G:OP1	2.09	0.53
25:BA:1744:G:OP2	25:BA:1745:A:O2'	2.23	0.53
1:CA:1060:C:H5"	10:CJ:51:ARG:HB3	1.91	0.53
1:CA:1179:A:H4'	9:CI:103:THR:HA	1.91	0.53
9:CI:26:VAL:HG13	9:CI:61:ALA:HB3	1.91	0.53
10:CJ:32:ALA:HB1	10:CJ:33:GLN:HG2	1.91	0.53
25:DA:2144:U:O2'	25:DA:2148:G:N2	2.42	0.53
28:DE:9:VAL:HG22	28:DE:25:VAL:HB	1.92	0.53
29:DF:150:GLY:HA2	29:DF:172:TRP:CE3	2.43	0.53
45:DZ:121:HIS:N	45:DZ:171:ILE:O	2.41	0.53
9:AI:23:ASN:HB2	9:AI:25:LYS:HE2	1.91	0.52
24:AX:66:C:H2'	24:AX:67:C:O4'	2.09	0.52
25:BA:278:G:OP1	47:B1:76:ARG:NH1	2.42	0.52
34:BO:59:LYS:NZ	34:BO:89:ASN:OD1	2.42	0.52
1:CA:141:A:H1'	1:CA:182:U:O2	2.09	0.52
2:CB:21:ARG:HA	2:CB:39:ILE:HD13	1.91	0.52
15:CO:28:GLN:HE21	15:CO:66:LEU:HD21	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2303:G:O2'	30:DG:132:ASN:ND2	2.39	0.52
1:AA:630:G:O2'	1:AA:631:G:H5'	2.09	0.52
25:BA:1845:G:H4'	27:BD:51:VAL:HG21	1.91	0.52
25:BA:2784:C:H2'	25:BA:2785:C:C6	2.44	0.52
1:CA:200:G:H2'	1:CA:201:C:O4'	2.09	0.52
1:CA:976:G:OP1	14:CN:32:SER:N	2.38	0.52
1:CA:1151:A:H5"	10:CJ:41:PRO:HA	1.92	0.52
45:DZ:77:ASP:N	45:DZ:82:ARG:O	2.36	0.52
48:D2:1:MET:N	48:D2:52:ASP:OD1	2.31	0.52
3:AC:116:VAL:HG21	3:AC:202:ILE:HD11	1.91	0.52
5:AE:12:LEU:HB3	5:AE:31:LEU:HB2	1.91	0.52
13:AM:84:ILE:HG13	13:AM:85:GLY:CA	2.39	0.52
25:BA:671:A:H2'	25:BA:672:G:O4'	2.08	0.52
1:CA:825:G:H21	8:CH:11:THR:HG21	1.73	0.52
1:CA:1246:C:H2'	1:CA:1247:U:H6	1.74	0.52
18:CR:22:VAL:HB	18:CR:56:THR:HA	1.92	0.52
19:CS:13:ASP:HA	19:CS:16:LEU:HB3	1.91	0.52
25:DA:1607:C:N4	25:DA:1622:G:OP2	2.28	0.52
34:DO:115:VAL:HG13	34:DO:121:VAL:HG21	1.90	0.52
35:DP:38:GLN:O	35:DP:40:SER:N	2.38	0.52
35:DP:97:PRO:HD3	35:DP:126:VAL:O	2.10	0.52
23:AW:7:A:H61	23:AW:66:U:H3	1.57	0.52
25:BA:661:G:OP1	35:BP:132:LYS:HE2	2.09	0.52
25:BA:1067:A:H3'	25:BA:1067:A:C8	2.44	0.52
25:BA:1356:G:OP2	53:B7:9:ARG:HD2	2.09	0.52
25:BA:1735:U:O2	25:BA:1747:A:H5'	2.09	0.52
25:BA:2130:C:H2'	25:BA:2131:U:H6	1.75	0.52
31:BH:97:ARG:NE	31:BH:104:GLU:OE1	2.29	0.52
32:BI:100:ALA:HA	32:BI:103:ARG:HD2	1.91	0.52
1:CA:353:A:H5'	1:CA:353:A:H8	1.74	0.52
4:CD:72:GLU:OE1	4:CD:207:TYR:OH	2.25	0.52
25:DA:1358:G:O2'	25:DA:1359:A:H5"	2.10	0.52
25:DA:2114:A:H62	25:DA:2115:G:H21	1.58	0.52
25:DA:2123:G:H1	25:DA:2175:C:H42	1.57	0.52
4:AD:107:ARG:NH2	4:AD:194:LEU:HD11	2.24	0.52
10:AJ:11:PHE:HE1	10:AJ:67:THR:HG22	1.75	0.52
23:AY:8:4SU:N3	23:AY:15:G:O6	2.43	0.52
25:BA:968:U:H2'	25:BA:969:C:C6	2.45	0.52
25:BA:2186:C:H2'	25:BA:2187:G:H5'	1.91	0.52
1:CA:986:A:H1'	19:CS:55:LYS:HA	1.90	0.52
13:CM:40:ASN:ND2	13:CM:41:PRO:HD2	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:CT:43:LEU:HD13	20:CT:51:GLU:HB3	1.92	0.52
25:DA:855:G:H2'	25:DA:856:C:C6	2.44	0.52
25:DA:890:A:H2'	25:DA:892:G:C8	2.44	0.52
25:DA:2037:G:H2'	25:DA:2038:G:C8	2.45	0.52
25:DA:2133:G:N2	25:DA:2157:G:H1'	2.23	0.52
25:DA:2142:C:N3	25:DA:2149:G:O6	2.42	0.52
25:DA:2239:G:OP2	61:DA:4263:HOH:O	2.19	0.52
6:AF:99:ALA:HB3	18:AR:29:PHE:CE1	2.40	0.52
7:AG:14:PRO:HG3	7:AG:21:VAL:HG13	1.91	0.52
12:AL:71:PRO:O	12:AL:102:ARG:NH1	2.41	0.52
25:BA:510:C:H2'	25:BA:511:C:C6	2.45	0.52
25:BA:1466:U:HO2'	25:BA:1467:G:P	2.32	0.52
39:BT:53:ARG:HB3	39:BT:53:ARG:HH11	1.75	0.52
1:CA:441:A:H5'	1:CA:442:C:OP2	2.10	0.52
3:CC:150:LYS:HB3	3:CC:201:TYR:HB2	1.92	0.52
11:CK:45:GLY:O	11:CK:50:TYR:HB2	2.10	0.52
25:DA:93:G:H2'	25:DA:94:C:C6	2.44	0.52
25:DA:784:A:C6	27:DD:229:VAL:HG11	2.45	0.52
35:DP:44:GLY:CA	35:DP:45:LEU:HB2	2.39	0.52
1:AA:62:U:OP1	1:AA:385:C:O2'	2.23	0.52
1:AA:411:A:OP2	4:AD:25:ARG:NH2	2.43	0.52
1:AA:642:A:N3	8:AH:113:SER:OG	2.32	0.52
1:AA:1159:U:OP1	2:AB:133:LYS:NZ	2.39	0.52
2:AB:24:TRP:CD1	2:AB:24:TRP:H	2.27	0.52
7:AG:79:ARG:HB3	7:AG:80:VAL:HA	1.92	0.52
23:AY:19:G:C2	23:AY:56:C:N3	2.78	0.52
25:BA:615:G:O6	61:BA:5060:HOH:O	2.17	0.52
1:CA:784:C:H4'	25:DA:1837:C:OP1	2.10	0.52
1:CA:1048:G:OP1	14:CN:3:ARG:NH2	2.40	0.52
1:CA:1087:G:N2	1:CA:1099:G:H1'	2.25	0.52
1:CA:1360:A:H8	1:CA:1360:A:OP1	1.92	0.52
25:DA:1771:C:OP1	61:DA:4536:HOH:O	2.19	0.52
25:DA:2469:A:H5'	25:DA:2470:G:OP2	2.10	0.52
7:AG:46:ALA:O	7:AG:50:ILE:HG22	2.09	0.52
14:AN:24:CYS:HB2	14:AN:40:CYS:HB3	1.90	0.52
25:BA:1102:G:H5"	25:BA:1103:A:O4'	2.10	0.52
25:BA:2736:C:H4'	37:BR:1:MET:HG3	1.92	0.52
35:BP:116:GLY:O	35:BP:137:LYS:NZ	2.34	0.52
43:BX:31:HIS:CD2	43:BX:33:LYS:H	2.14	0.52
1:CA:473:G:H2'	1:CA:474:G:H8	1.75	0.52
1:CA:828:A:H5"	1:CA:859:A:C2	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1202:G:O4'	14:CN:29:ARG:NH1	2.42	0.52
1:CA:1352:C:H2'	1:CA:1353:G:C8	2.45	0.52
3:CC:113:ALA:N	3:CC:183:ASP:OD2	2.39	0.52
23:CY:15:G:N2	23:CY:48:C:H42	2.07	0.52
25:DA:883:G:C6	25:DA:884:C:C4	2.98	0.52
25:DA:2144:U:H1'	25:DA:2148:G:H22	1.75	0.52
25:DA:2787:C:H1'	28:DE:62:PRO:HG3	1.92	0.52
29:DF:129:PHE:CD2	29:DF:163:VAL:HG21	2.45	0.52
31:DH:24:VAL:HG22	31:DH:35:VAL:HB	1.91	0.52
35:DP:96:THR:H	35:DP:99:LEU:CD2	2.23	0.52
43:DX:53:LYS:HB3	43:DX:82:GLN:HB3	1.91	0.52
1:AA:442:C:H42	1:AA:492:G:H1	1.56	0.52
25:BA:1159:U:H2'	25:BA:1160:G:H8	1.73	0.52
25:BA:1451:U:H2'	25:BA:1452:U:C6	2.45	0.52
1:CA:1042:G:H2'	1:CA:1043:C:O4'	2.10	0.52
1:CA:1152:A:C5'	10:CJ:13:HIS:HB2	2.39	0.52
2:CB:16:HIS:HB2	2:CB:204:ASN:CB	2.35	0.52
2:CB:167:PRO:HG2	2:CB:192:SER:HB2	1.91	0.52
8:CH:10:LEU:HD22	8:CH:83:ILE:HD11	1.91	0.52
25:DA:71:A:N7	43:DX:31:HIS:HE1	2.07	0.52
25:DA:184:C:H2'	25:DA:185:U:C6	2.45	0.52
30:DG:106:LEU:O	30:DG:111:LEU:HD12	2.10	0.52
1:AA:78:G:O2'	1:AA:79:G:H8	1.84	0.52
9:AI:7:THR:O	9:AI:83:ARG:NH1	2.43	0.52
12:AL:53:ARG:NH1	12:AL:92:ASP:OD2	2.42	0.52
24:AX:19:G:H4'	24:AX:20:U:OP2	2.10	0.52
25:BA:551:A:O2'	25:BA:2065:C:O2	2.28	0.52
25:BA:2169:G:H3'	25:BA:2169:G:N3	2.25	0.52
48:B2:1:MET:HE3	48:B2:5:GLU:HB3	1.92	0.52
1:CA:1134:G:H2'	1:CA:1135:U:H5'	1.92	0.52
2:CB:91:PRO:HG3	2:CB:154:LEU:HB2	1.92	0.52
4:CD:18:LYS:NZ	4:CD:31:CYS:SG	2.83	0.52
8:CH:24:THR:HG22	8:CH:63:LEU:HD21	1.92	0.52
25:DA:668:G:H5'	25:DA:669:G:OP2	2.10	0.52
25:DA:2815:C:H2'	25:DA:2816:C:H6	1.74	0.52
27:DD:142:VAL:HG13	27:DD:191:ALA:HB1	1.92	0.52
30:DG:115:ARG:HB3	30:DG:115:ARG:CZ	2.40	0.52
13:AM:15:VAL:HG22	13:AM:43:THR:O	2.10	0.51
25:BA:1091:A:OP1	25:BA:1092:A:H3'	2.10	0.51
3:CC:6:HIS:HD2	3:CC:8:ILE:H	1.58	0.51
4:CD:157:LEU:HD22	4:CD:161:ASN:HD21	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:882:G:H2'	25:DA:883:G:H8	1.75	0.51
25:DA:887:A:H4'	25:DA:888:C:H5	1.74	0.51
25:DA:1231:G:H2'	25:DA:1232:G:C8	2.44	0.51
25:DA:2507:C:H2'	25:DA:2508:G:O4'	2.10	0.51
27:DD:134:ARG:NH1	27:DD:188:GLU:OE2	2.43	0.51
28:DE:36:ARG:NH1	28:DE:85:ASN:OD1	2.44	0.51
28:DE:143:ASN:HD22	28:DE:147:PRO:HD3	1.75	0.51
1:AA:659:U:C2'	1:AA:660:G:H5'	2.40	0.51
25:BA:553:A:OP1	61:BA:4814:HOH:O	2.19	0.51
25:BA:599:U:H2'	25:BA:600:G:C8	2.45	0.51
25:BA:718:C:N4	61:BA:5028:HOH:O	2.43	0.51
25:BA:1140:U:N3	25:BA:1142:A:H3'	2.24	0.51
25:BA:1552:C:H2'	25:BA:1553:A:H8	1.75	0.51
1:CA:1423:G:P	34:DO:49:ARG:HH12	2.33	0.51
16:CP:18:ARG:HD3	16:CP:35:LYS:HD2	1.91	0.51
27:DD:69:ARG:NH2	27:DD:128:GLY:O	2.43	0.51
50:D4:46:GLN:C	50:D4:48:ARG:H	2.17	0.51
1:AA:154:C:H2'	1:AA:155:C:H5'	1.92	0.51
1:AA:250:A:H4'	1:AA:251:G:O5'	2.09	0.51
1:AA:1002:G:C5	1:AA:1003:G:H1'	2.45	0.51
13:AM:80:ARG:NH2	19:AS:69:HIS:HE1	2.08	0.51
23:AY:18:G:O2'	23:AY:19:G:H5'	2.09	0.51
25:BA:1898:A:H2'	25:BA:1899:A:C8	2.44	0.51
52:B6:10:LEU:HG	52:B6:54:ILE:HG13	1.91	0.51
1:CA:222:U:H2'	1:CA:223:U:C6	2.45	0.51
1:CA:344:A:H5"	1:CA:345:C:C5	2.44	0.51
15:CO:26:GLU:OE2	15:CO:77:ARG:NE	2.37	0.51
23:CW:51:U:H2'	23:CW:52:G:H8	1.75	0.51
23:CY:66:U:H2'	23:CY:67:C:O4'	2.10	0.51
25:DA:11:G:H2'	25:DA:12:U:H5'	1.93	0.51
25:DA:947:G:H2'	25:DA:948:G:C8	2.45	0.51
25:DA:2183:C:H2'	25:DA:2184:G:H8	1.75	0.51
29:DF:114:VAL:HG21	29:DF:202:PHE:CE1	2.46	0.51
30:DG:173:LEU:HD23	30:DG:176:LEU:HD12	1.92	0.51
32:DI:26:ALA:O	32:DI:31:LEU:HB2	2.11	0.51
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.92	0.51
25:BA:2167:C:O2'	25:BA:2169:G:N7	2.38	0.51
35:BP:63:PRO:HG2	54:B8:25:MET:HB2	1.92	0.51
1:CA:922:G:N3	1:CA:1398:A:H2	2.08	0.51
1:CA:1095:U:H5"	1:CA:1109:C:O2	2.10	0.51
1:CA:1227:A:OP2	13:CM:111:LYS:NZ	2.33	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:178:ARG:NH1	2:CB:196:LEU:O	2.43	0.51
20:CT:50:GLU:HB2	20:CT:99:LEU:HD23	1.92	0.51
25:DA:602:G:O2'	25:DA:655:A:N6	2.44	0.51
25:DA:1025:G:C4	25:DA:1135:C:H1'	2.45	0.51
25:DA:1029:A:N1	25:DA:2465:C:O2'	2.39	0.51
25:DA:2646:C:H2'	25:DA:2647:U:O4'	2.10	0.51
26:DB:92:C:H5"	45:DZ:79:ARG:NH1	2.25	0.51
37:DR:33:ARG:NH1	37:DR:115:GLU:OE2	2.35	0.51
1:AA:1036:G:N2	1:AA:1037:C:O2	2.44	0.51
9:AI:49:PRO:HG3	9:AI:101:PHE:CD2	2.46	0.51
19:AS:63:THR:OG1	19:AS:65:ASN:ND2	2.43	0.51
23:AY:3:C:H42	23:AY:70:G:H1	1.58	0.51
1:CA:356:A:N3	1:CA:368:U:O2'	2.37	0.51
1:CA:1095:U:P	1:CA:1108:G:H1	2.34	0.51
1:CA:1218:C:H2'	1:CA:1219:U:C6	2.46	0.51
8:CH:82:HIS:NE2	8:CH:84:ARG:HG2	2.25	0.51
37:DR:87:TYR:OH	37:DR:116:LEU:HB3	2.10	0.51
1:AA:1021:G:O2'	1:AA:1022:G:O5'	2.27	0.51
19:AS:64:GLU:HB3	50:B4:59:PHE:CE1	2.45	0.51
25:BA:1133:G:H2'	25:BA:1135:G:C8	2.46	0.51
25:BA:1150:C:H2'	25:BA:1151:U:C6	2.46	0.51
25:BA:2156:A:N6	25:BA:2179:G:O2'	2.44	0.51
25:BA:2885:C:O2'	39:BT:2:ASN:OD1	2.25	0.51
27:BD:68:LYS:HD3	27:BD:70:TRP:CZ2	2.46	0.51
1:CA:1013:G:N2	1:CA:1016:A:OP2	2.43	0.51
11:CK:20:TYR:CZ	11:CK:83:ILE:HD12	2.46	0.51
25:DA:2110:G:H4'	25:DA:2111:C:OP2	2.10	0.51
29:DF:13:SER:OG	29:DF:16:GLY:O	2.22	0.51
37:DR:118:GLU:H	37:DR:118:GLU:CD	2.18	0.51
44:DY:88:LYS:HZ2	44:DY:90:LEU:HD12	1.74	0.51
1:AA:1030(C):G:H2'	1:AA:1030(D):A:C8	2.46	0.51
18:AR:31:LEU:HD12	18:AR:65:ILE:HB	1.92	0.51
20:AT:60:GLU:HG3	20:AT:81:LYS:HD2	1.92	0.51
25:BA:1634:C:H2'	25:BA:1635:C:H6	1.76	0.51
25:BA:2623:U:H5'	25:BA:2623:U:H6	1.76	0.51
32:BI:130:TYR:HB3	32:BI:138:ILE:HB	1.93	0.51
38:BS:25:ARG:HB3	38:BS:25:ARG:HH11	1.75	0.51
1:CA:1041:A:H2'	1:CA:1042:G:C8	2.45	0.51
5:CE:74:GLY:HA3	5:CE:116:THR:HG22	1.92	0.51
7:CG:113:GLU:HG3	7:CG:119:ARG:HG2	1.93	0.51
25:DA:2031:A:N3	25:DA:2455:G:O2'	2.34	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2141:G:O6	25:DA:2150:U:C2	2.62	0.51
27:DD:108:PRO:HG2	27:DD:111:LEU:HB2	1.92	0.51
1:AA:976:G:N2	1:AA:1363:C:OP2	2.40	0.51
1:AA:1218:C:H2'	1:AA:1219:U:C6	2.46	0.51
16:AP:56:ALA:O	16:AP:60:LEU:HB2	2.10	0.51
25:BA:1118:C:C2	25:BA:1138:C:N4	2.79	0.51
25:BA:1137:G:C6	25:BA:1138:C:C4	2.99	0.51
33:BN:4:TYR:CD2	40:BU:100:VAL:HG11	2.46	0.51
37:BR:67:LEU:HD13	37:BR:76:VAL:HG21	1.91	0.51
40:BU:86:ALA:O	41:BV:49:THR:HG23	2.11	0.51
46:B0:32:ARG:H	46:B0:35:ASN:ND2	2.09	0.51
1:CA:192:U:H2'	1:CA:193:C:C6	2.46	0.51
25:DA:2139:C:H2'	25:DA:2140:C:O4'	2.11	0.51
25:DA:2208:A:O2'	25:DA:2218:U:OP2	2.28	0.51
30:DG:56:ALA:O	30:DG:60:LEU:HB2	2.11	0.51
36:DQ:52:VAL:HA	36:DQ:55:VAL:HG12	1.93	0.51
38:DS:35:ILE:HD12	38:DS:101:LEU:HD12	1.92	0.51
50:D4:61:ARG:NH1	50:D4:62:ARG:O	2.44	0.51
10:AJ:37:PRO:HA	10:AJ:72:VAL:HG12	1.92	0.51
25:BA:1465:A:O2'	25:BA:1467:G:N7	2.43	0.51
25:BA:1700:G:H3'	37:BR:2:ARG:HD3	1.91	0.51
25:BA:2371:C:H2'	25:BA:2372:A:O4'	2.10	0.51
2:CB:16:HIS:CB	2:CB:204:ASN:HB3	2.37	0.51
25:DA:247:G:H4'	25:DA:386:G:C5	2.46	0.51
25:DA:528:A:C2	25:DA:2042:A:H2'	2.45	0.51
25:DA:796:C:H2'	25:DA:797:C:C6	2.46	0.51
25:DA:1355:G:O6	61:DA:4423:HOH:O	2.18	0.51
25:DA:2149:G:C5	25:DA:2150:U:C2	2.99	0.51
38:DS:10:ARG:NE	38:DS:91:PRO:O	2.37	0.51
49:D3:7:LYS:HE3	49:D3:32:GLN:HG3	1.93	0.51
11:AK:99:GLN:HG2	11:AK:105:VAL:HG21	1.92	0.51
39:BT:95:ARG:HG2	39:BT:95:ARG:NH1	2.25	0.51
3:CC:77:ILE:O	3:CC:84:ILE:N	2.41	0.51
8:CH:113:SER:HB2	8:CH:134:ILE:HD11	1.92	0.51
25:DA:125:G:H1'	53:D7:48:LYS:HE2	1.92	0.51
25:DA:868:U:H2'	25:DA:869:G:O4'	2.11	0.51
27:DD:147:LEU:HD13	27:DD:155:LEU:HD21	1.93	0.51
34:DO:120:GLU:HB2	39:DT:68:TYR:HE2	1.76	0.51
36:DQ:75:THR:HG21	36:DQ:87:LYS:HZ3	1.76	0.51
1:AA:222:U:H2'	1:AA:223:U:C6	2.46	0.50
1:AA:1392:G:N2	1:AA:1502:A:H8	2.09	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:47:THR:HA	2:AB:202:PRO:HG2	1.93	0.50
23:AY:28:G:H1	23:AY:42:C:N4	2.08	0.50
25:BA:715:G:H5'	25:BA:716:G:OP2	2.11	0.50
25:BA:1827:U:H2'	25:BA:1828:C:C6	2.45	0.50
30:BG:9:ARG:O	30:BG:13:GLU:HG2	2.10	0.50
30:BG:41:GLN:NE2	30:BG:154:GLY:O	2.44	0.50
30:BG:48:GLU:HA	30:BG:51:ARG:NE	2.26	0.50
39:BT:56:GLY:O	39:BT:59:THR:HG22	2.11	0.50
44:BY:98:VAL:HG12	44:BY:105:ALA:HA	1.92	0.50
8:CH:20:TYR:HA	8:CH:65:TYR:CZ	2.46	0.50
23:CY:13:C:H2'	23:CY:14:A:H5"	1.93	0.50
25:DA:866:A:H2	25:DA:867:C:C5	2.29	0.50
25:DA:1007:C:OP1	33:DN:35:ARG:NH1	2.37	0.50
25:DA:1580:A:H3'	25:DA:1581:G:H8	1.76	0.50
1:AA:352:C:O2	1:AA:355:C:N4	2.45	0.50
1:AA:1124:G:OP1	10:AJ:36:GLY:N	2.40	0.50
2:AB:93:VAL:HG21	2:AB:97:TRP:CD1	2.46	0.50
31:BH:56:SER:HB3	31:BH:61:HIS:ND1	2.26	0.50
40:BU:17:ILE:HG13	40:BU:32:PHE:HE1	1.75	0.50
50:B4:15:ILE:HD12	50:B4:21:VAL:HG22	1.93	0.50
1:CA:170:U:O2'	1:CA:171:A:H5'	2.11	0.50
1:CA:392:G:H2'	1:CA:393:A:H8	1.75	0.50
1:CA:1006:C:H2'	1:CA:1007:C:C6	2.47	0.50
2:CB:16:HIS:HB3	2:CB:210:SER:CB	2.40	0.50
3:CC:37:GLN:NE2	14:CN:52:GLN:OE1	2.44	0.50
9:CI:16:ARG:HB2	9:CI:64:THR:HB	1.92	0.50
23:CY:15:G:H22	23:CY:48:C:N4	2.09	0.50
25:DA:536:A:H2'	25:DA:537:C:C6	2.46	0.50
25:DA:994:C:O2'	25:DA:996:A:OP1	2.17	0.50
44:DY:38:ILE:HD13	44:DY:66:PRO:HA	1.93	0.50
45:DZ:28:MET:HA	45:DZ:88:PHE:O	2.11	0.50
1:AA:784:C:H4'	25:BA:1868:C:OP1	2.11	0.50
10:AJ:11:PHE:HB3	14:AN:55:GLY:HA3	1.91	0.50
23:AY:33:U:H2'	23:AY:33:U:O2	2.10	0.50
25:BA:1417:G:H2'	25:BA:1418:U:H5	1.76	0.50
25:BA:2152:U:H2'	25:BA:2153:G:H21	1.77	0.50
38:BS:48:LEU:HD23	38:BS:82:ILE:HD11	1.93	0.50
1:CA:297:G:N2	1:CA:300:A:OP2	2.43	0.50
1:CA:1163:C:N4	1:CA:1173:G:H1	2.07	0.50
1:CA:1376:U:H2'	1:CA:1377:A:C8	2.46	0.50
10:CJ:37:PRO:HA	10:CJ:72:VAL:HG12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:321:G:OP2	29:DF:135:LYS:HG3	2.11	0.50
1:AA:501:C:H2'	1:AA:502:G:C8	2.46	0.50
1:AA:509:A:O2'	1:AA:510:A:OP1	2.25	0.50
2:AB:19:HIS:CD2	2:AB:20:GLU:HG3	2.47	0.50
3:AC:112:SER:HB3	3:AC:115:LEU:HB2	1.94	0.50
6:AF:91:VAL:HG11	18:AR:72:ARG:NH1	2.25	0.50
8:AH:17:THR:HG22	8:AH:63:LEU:HG	1.92	0.50
9:AI:55:ALA:HB1	9:AI:59:PHE:HD2	1.76	0.50
25:BA:1105:G:H2'	25:BA:1106:U:C5	2.46	0.50
1:CA:1412:C:H2'	1:CA:1413:A:C8	2.46	0.50
2:CB:9:GLU:O	2:CB:11:LEU:N	2.45	0.50
4:CD:25:ARG:NH1	4:CD:30:LYS:O	2.44	0.50
7:CG:132:GLY:O	7:CG:136:LYS:HG2	2.12	0.50
25:DA:141:A:C8	25:DA:1408:C:O2'	2.65	0.50
25:DA:566:U:H5"	35:DP:29:LYS:HE3	1.92	0.50
25:DA:2119:A:H62	25:DA:2170:A:H62	1.59	0.50
33:DN:15:LEU:HB2	33:DN:135:PRO:HB2	1.92	0.50
50:D4:42:PHE:HA	50:D4:48:ARG:HH22	1.75	0.50
15:AO:55:GLY:HA2	15:AO:58:MET:HE2	1.93	0.50
17:AQ:18:THR:OG1	17:AQ:69:LYS:NZ	2.26	0.50
25:BA:173:C:H2'	25:BA:174:U:C6	2.47	0.50
25:BA:821:A:N3	25:BA:821:A:H2'	2.27	0.50
25:BA:1223:C:H2'	25:BA:1224:C:H6	1.77	0.50
26:BB:106:G:C5'	45:BZ:31:ARG:HG2	2.40	0.50
27:BD:2:ALA:N	61:BD:415:HOH:O	2.44	0.50
28:BE:105:THR:OG1	28:BE:199:ARG:NH2	2.45	0.50
30:BG:150:ASP:OD1	30:BG:150:ASP:N	2.39	0.50
30:BG:151:ALA:O	30:BG:153:ARG:NH1	2.44	0.50
31:BH:40:GLU:O	31:BH:55:PRO:HG3	2.11	0.50
1:CA:352:C:O2'	1:CA:354:G:OP1	2.27	0.50
1:CA:537:G:H2'	1:CA:538:G:C8	2.47	0.50
1:CA:1226:C:H4'	19:CS:80:TYR:CZ	2.47	0.50
23:CY:62:C:H2'	23:CY:63:G:C8	2.47	0.50
25:DA:422:A:H2'	25:DA:423:A:C8	2.46	0.50
25:DA:636:G:O2'	25:DA:638:G:O2'	2.27	0.50
25:DA:646:A:H2'	25:DA:647:G:O4'	2.11	0.50
25:DA:2723:C:OP2	28:DE:109:LYS:NZ	2.45	0.50
38:DS:50:SER:O	38:DS:76:LYS:NZ	2.30	0.50
1:AA:946:A:H2'	1:AA:947:G:C8	2.46	0.50
1:AA:1318:A:H5"	19:AS:3:ARG:HH12	1.76	0.50
2:AB:48:MET:HA	2:AB:51:LEU:HD12	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:942:A:H4'	25:BA:943:C:OP1	2.10	0.50
25:BA:1634:C:H2'	25:BA:1635:C:C6	2.47	0.50
50:B4:15:ILE:HB	50:B4:32:TYR:CD1	2.44	0.50
1:CA:1039:C:N4	1:CA:1040:U:C4	2.80	0.50
25:DA:493:G:H2'	25:DA:494:G:O4'	2.12	0.50
25:DA:1270:C:H5"	25:DA:1271:G:O5'	2.11	0.50
46:D0:70:GLN:OE1	46:D0:80:HIS:NE2	2.44	0.50
23:AW:18:G:O2'	23:AW:57:G:N2	2.30	0.50
23:AY:20:U:H4'	23:AY:21:A:OP1	2.10	0.50
25:BA:1170:C:OP1	61:BA:5067:HOH:O	2.20	0.50
25:BA:1806:U:OP1	25:BA:2001:C:O2'	2.24	0.50
25:BA:2359:C:H2'	25:BA:2360:U:C6	2.47	0.50
27:BD:148:GLU:HB2	27:BD:151:LYS:HD2	1.93	0.50
32:BI:106:GLY:HA2	32:BI:107:VAL:O	2.12	0.50
37:BR:53:HIS:O	37:BR:56:LYS:HB2	2.12	0.50
1:CA:250:A:H4'	1:CA:251:G:O5'	2.11	0.50
4:CD:15:GLU:OE2	4:CD:66:ARG:NH1	2.44	0.50
31:DH:98:LEU:HD13	31:DH:102:ALA:O	2.12	0.50
35:DP:82:GLY:HA2	35:DP:113:LYS:O	2.11	0.50
44:DY:44:ILE:HA	44:DY:63:LYS:O	2.11	0.50
1:AA:161:A:H8	1:AA:161:A:O5'	1.95	0.50
1:AA:973:G:H3'	1:AA:974:A:H5"	1.93	0.50
2:AB:212:GLN:NE2	2:AB:234:PRO:O	2.45	0.50
23:AY:32:PSU:C2	23:AY:33:U:H5	2.30	0.50
25:BA:815:G:O2'	25:BA:1425:A:N1	2.35	0.50
25:BA:1566:U:H2'	25:BA:1567:G:O4'	2.12	0.50
25:BA:2576:A:C2	25:BA:2659:U:H4'	2.47	0.50
32:BI:38:LEU:H	32:BI:38:LEU:HD12	1.77	0.50
45:BZ:92:SER:OG	45:BZ:93:ASP:N	2.45	0.50
47:B1:89:GLU:O	47:B1:93:GLU:HG2	2.12	0.50
25:DA:1335:U:OP1	43:DX:65:ARG:NH2	2.45	0.50
35:DP:86:LYS:HB3	35:DP:118:GLY:HA3	1.93	0.50
45:DZ:6:LYS:HD2	45:DZ:8:TYR:CE1	2.47	0.50
51:D5:16:ARG:HG3	51:D5:17:ASP:N	2.26	0.50
1:AA:346:G:C2	1:AA:347:G:H1'	2.47	0.50
1:AA:1510:U:H2'	1:AA:1511:G:C8	2.46	0.50
25:BA:1085:G:H1	25:BA:1162:C:H42	1.60	0.50
1:CA:1034:G:H3'	1:CA:1035:A:C8	2.47	0.50
19:CS:77:THR:HG22	19:CS:78:ARG:HG2	1.94	0.50
25:DA:212:G:H2'	25:DA:213:A:O4'	2.12	0.50
25:DA:829:A:N7	25:DA:2248:C:H5'	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1341:U:OP2	25:DA:1394:U:O2'	2.25	0.50
25:DA:1354:A:H2'	25:DA:1355:G:O4'	2.12	0.50
25:DA:2352:A:N6	25:DA:2365:G:O2'	2.44	0.50
35:DP:3:LEU:HD13	35:DP:6:LEU:HD12	1.93	0.50
41:DV:98:GLU:CD	41:DV:100:ARG:HH12	2.20	0.50
1:AA:130:A:H5'	17:AQ:63:ARG:HE	1.77	0.49
3:AC:36:ASP:O	3:AC:40:ARG:HG3	2.11	0.49
16:AP:18:ARG:HD3	16:AP:35:LYS:HD2	1.94	0.49
25:BA:83:A:H5"	44:BY:8:LYS:HE3	1.94	0.49
25:BA:1108:G:H5"	25:BA:1116:A:H5"	1.93	0.49
48:B2:18:PRO:O	48:B2:22:GLU:HG3	2.12	0.49
53:B7:1:MET:HE3	53:B7:3:ARG:NH2	2.27	0.49
1:CA:1051:C:H2'	1:CA:1052:U:C6	2.47	0.49
1:CA:1053:G:N7	1:CA:1200:C:H5"	2.26	0.49
3:CC:43:LEU:HD11	3:CC:91:LEU:HD11	1.94	0.49
3:CC:131:ARG:NH1	5:CE:50:GLU:HG3	2.25	0.49
24:CX:55:PSU:O2'	24:CX:57:A:N7	2.41	0.49
25:DA:855:G:O2'	46:D0:27:GLU:OE2	2.30	0.49
25:DA:1683:C:H2'	25:DA:1684:C:C6	2.47	0.49
25:DA:1717:G:H2'	25:DA:1718:G:C8	2.47	0.49
25:DA:2117:A:O2'	25:DA:2118:U:H5"	2.11	0.49
25:DA:2149:G:H3'	25:DA:2150:U:O4'	2.11	0.49
25:DA:2206:G:H3'	25:DA:2207:G:N7	2.27	0.49
25:DA:2849:U:H4'	25:DA:2868:A:C2	2.46	0.49
36:DQ:56:ARG:O	36:DQ:56:ARG:HD3	2.12	0.49
37:DR:56:LYS:NZ	37:DR:90:ARG:O	2.44	0.49
47:D1:5:CYS:SG	47:D1:62:VAL:HG23	2.51	0.49
1:AA:749:C:H2'	1:AA:750:G:H8	1.77	0.49
5:AE:152:ARG:NH2	8:AH:107:LEU:O	2.46	0.49
14:AN:23:ARG:NH1	14:AN:30:ALA:HB2	2.26	0.49
20:AT:99:LEU:HA	20:AT:100:ILE:O	2.12	0.49
25:BA:1425:A:H4'	25:BA:1426:G:OP2	2.12	0.49
25:BA:2320:G:O2'	25:BA:2322:A:N7	2.45	0.49
1:CA:918:A:H2'	1:CA:919:A:O4'	2.13	0.49
1:CA:1103:C:P	2:CB:96:ARG:HH22	2.34	0.49
1:CA:1251:A:N1	1:CA:1354:C:O2'	2.42	0.49
3:CC:115:LEU:O	3:CC:118:GLN:HG2	2.12	0.49
25:DA:729:G:H5'	25:DA:730:C:H5"	1.94	0.49
27:DD:108:PRO:HB3	27:DD:143:HIS:CE1	2.47	0.49
30:DG:11:TYR:CZ	30:DG:16:ARG:HD3	2.47	0.49
1:AA:767:A:H2'	1:AA:768:A:O4'	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1030(C):G:N7	1:AA:1031:G:N2	2.59	0.49
3:AC:87:LEU:O	3:AC:91:LEU:N	2.44	0.49
5:AE:91:LEU:HD12	5:AE:120:THR:HG22	1.93	0.49
13:AM:32:GLU:HG3	13:AM:33:ALA:N	2.27	0.49
23:AY:19:G:C4'	23:AY:57:G:H22	2.25	0.49
25:BA:1140:U:H2'	25:BA:1142:A:N7	2.28	0.49
33:BN:96:GLU:CD	33:BN:96:GLU:H	2.20	0.49
1:CA:1285:A:H4'	1:CA:1286:A:O5'	2.12	0.49
2:CB:91:PRO:HA	2:CB:151:GLY:O	2.12	0.49
3:CC:122:GLU:HA	3:CC:125:GLU:OE2	2.11	0.49
14:CN:26:ARG:NH2	14:CN:47:LEU:HD21	2.27	0.49
25:DA:1996:C:H4'	25:DA:1997:G:OP1	2.12	0.49
28:DE:27:LEU:HD22	39:DT:1:MET:HE1	1.95	0.49
30:DG:126:ASP:OD1	30:DG:130:ASN:ND2	2.39	0.49
32:DI:110:ASP:H	32:DI:130:TYR:HH	1.58	0.49
32:DI:133:HIS:HD2	32:DI:134:PRO:HD2	1.77	0.49
40:DU:86:ALA:O	41:DV:49:THR:HG23	2.12	0.49
1:AA:1251:A:H2'	1:AA:1252:A:C8	2.46	0.49
6:AF:86:ARG:O	6:AF:87:ARG:HG2	2.11	0.49
25:BA:757:G:H2'	25:BA:758:G:H8	1.77	0.49
25:BA:2331:G:N2	38:BS:3:ARG:HA	2.27	0.49
1:CA:1136:U:OP2	1:CA:1137:C:N4	2.46	0.49
1:CA:1176:A:H2'	1:CA:1177:G:O4'	2.12	0.49
28:DE:14:ILE:HG13	28:DE:21:VAL:HG13	1.94	0.49
1:AA:436:C:H2'	1:AA:437:U:H6	1.78	0.49
1:AA:943:U:H2'	1:AA:944:G:H5'	1.95	0.49
1:AA:1064:G:H1'	1:AA:1190:G:N2	2.28	0.49
6:AF:19:LEU:HD21	6:AF:59:TYR:CE1	2.48	0.49
19:AS:42:PRO:HD3	50:B4:61:ARG:HH21	1.77	0.49
19:AS:50:ALA:HB1	19:AS:57:HIS:HB3	1.94	0.49
23:AW:19:G:N2	23:AW:56:C:N3	2.61	0.49
25:BA:957:A:H2'	36:BQ:9:TYR:OH	2.12	0.49
25:BA:1405:A:H2'	25:BA:1406:A:H5'	1.93	0.49
25:BA:1958:A:OP1	25:BA:1959:A:H5'	2.12	0.49
27:BD:68:LYS:HD3	27:BD:70:TRP:CH2	2.47	0.49
1:CA:152:A:N6	1:CA:169:C:N3	2.58	0.49
2:CB:48:MET:HA	2:CB:51:LEU:HD12	1.94	0.49
8:CH:119:LEU:HD13	8:CH:127:LEU:HD23	1.94	0.49
25:DA:811:U:H2'	35:DP:21:ARG:HA	1.94	0.49
25:DA:1359:A:N6	25:DA:1372:U:H3	2.10	0.49
31:DH:97:ARG:O	31:DH:103:LEU:HD12	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:DP:42:SER:O	61:DP:303:HOH:O	2.20	0.49
1:AA:49:U:O4	1:AA:365:U:H5	1.95	0.49
1:AA:625:G:H2'	1:AA:626:U:C6	2.48	0.49
1:AA:1027:C:H3'	1:AA:1028:C:C6	2.47	0.49
25:BA:2209:G:H2'	25:BA:2210:C:O4'	2.11	0.49
25:BA:2227:G:H8	25:BA:2228:G:N7	2.11	0.49
1:CA:1009:G:N2	1:CA:1010:G:H1'	2.27	0.49
1:CA:1347:G:N2	1:CA:1373:G:H2'	2.27	0.49
8:CH:73:ASP:OD1	8:CH:75:ARG:HD3	2.11	0.49
14:CN:24:CYS:HB2	14:CN:40:CYS:HB3	1.95	0.49
23:CY:23:A:H2'	23:CY:24:G:H5"	1.94	0.49
23:CY:58:A:N3	23:CY:60:U:N3	2.60	0.49
25:DA:236:C:H2'	25:DA:237:C:C6	2.48	0.49
25:DA:1231:G:H2'	25:DA:1232:G:H8	1.78	0.49
25:DA:1263:U:C4	25:DA:1264:G:C6	3.01	0.49
27:DD:108:PRO:HB3	27:DD:143:HIS:HE1	1.78	0.49
29:DF:7:TYR:O	29:DF:22:ALA:N	2.44	0.49
35:DP:63:PRO:HD3	54:D8:27:THR:HG22	1.94	0.49
43:DX:84:ALA:HB3	43:DX:87:GLN:NE2	2.28	0.49
25:BA:559:U:H2'	25:BA:560:C:C6	2.47	0.49
25:BA:930:G:N2	25:BA:939:C:O2	2.45	0.49
25:BA:1525:G:O2'	25:BA:1605:A:N1	2.46	0.49
25:BA:2418:U:OP1	25:BA:2423:A:N6	2.46	0.49
25:BA:2827:G:OP1	37:BR:99:LYS:HE2	2.13	0.49
1:CA:1024:G:H2'	1:CA:1024:G:N3	2.27	0.49
25:DA:441:U:H2'	25:DA:442:G:C8	2.47	0.49
32:DI:130:TYR:HB3	32:DI:138:ILE:HB	1.95	0.49
39:DT:51:ARG:HG3	39:DT:98:LYS:HD2	1.94	0.49
42:DW:71:VAL:HA	42:DW:107:LEU:HD12	1.94	0.49
1:AA:1077:G:N2	1:AA:1080:A:OP2	2.44	0.49
2:AB:211:ILE:O	2:AB:215:LEU:HB2	2.12	0.49
25:BA:1221:G:H1'	25:BA:1222:A:C5'	2.42	0.49
25:BA:1480:A:H2'	25:BA:1481:G:C8	2.48	0.49
25:BA:1552:C:H2'	25:BA:1553:A:C8	2.48	0.49
25:BA:2584:A:N7	28:BE:145:LYS:HB2	2.28	0.49
25:BA:2874:G:OP1	39:BT:119:LYS:HE3	2.13	0.49
41:BV:1:MET:HB2	41:BV:43:GLU:OE2	2.12	0.49
1:CA:646:U:H2'	1:CA:647:C:H6	1.76	0.49
6:CF:69:GLU:O	6:CF:72:VAL:HG12	2.13	0.49
9:CI:28:VAL:HG22	9:CI:63:ILE:HB	1.93	0.49
9:CI:89:ASN:O	9:CI:92:TYR:HB2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:CY:2:C:N3	23:CY:71:G:O6	2.46	0.49
25:DA:857:C:OP2	46:D0:77:ARG:NH2	2.46	0.49
26:DB:58:A:H2'	26:DB:59:A:O4'	2.13	0.49
54:D8:6:THR:HG22	54:D8:63:PRO:HD2	1.95	0.49
1:AA:454:C:H3'	1:AA:455:C:C6	2.47	0.49
1:AA:711:G:OP1	6:AF:54:LYS:NZ	2.42	0.49
13:AM:3:ARG:HG2	13:AM:8:GLU:HA	1.94	0.49
25:BA:137:G:O2'	25:BA:138:G:H5'	2.13	0.49
25:BA:670:C:H5'	25:BA:671:A:OP2	2.12	0.49
25:BA:2348:A:H61	46:B0:43:THR:HG22	1.78	0.49
32:BI:61:ARG:HH12	32:BI:64:GLU:HG3	1.78	0.49
33:BN:62:VAL:HG22	33:BN:66:LYS:HD2	1.94	0.49
34:BO:2:ILE:HD12	34:BO:6:THR:HG21	1.95	0.49
1:CA:1168:A:C6	1:CA:1169:A:C6	3.00	0.49
1:CA:1262:C:H2'	1:CA:1263:C:H6	1.78	0.49
1:CA:1359:C:H1'	1:CA:1362:C:H41	1.78	0.49
2:CB:162:ILE:HD11	2:CB:184:VAL:HG22	1.94	0.49
4:CD:153:ARG:HD3	4:CD:181:MET:HE1	1.95	0.49
12:CL:60:LEU:HD21	12:CL:66:VAL:HG22	1.93	0.49
1:AA:1312:G:H5'	19:AS:5:LEU:HD21	1.94	0.49
7:AG:44:TYR:HE2	9:AI:41:VAL:HG11	1.78	0.49
7:AG:79:ARG:HB3	7:AG:80:VAL:CA	2.42	0.49
10:AJ:7:LYS:HE2	10:AJ:9:ARG:HH12	1.78	0.49
14:AN:26:ARG:NH1	14:AN:46:GLU:OE2	2.44	0.49
25:BA:1477:U:H2'	25:BA:1478:C:C6	2.48	0.49
29:BF:89:VAL:HG12	29:BF:90:PHE:CD2	2.48	0.49
38:BS:5:THR:OG1	38:BS:8:GLU:HG3	2.13	0.49
43:BX:94:GLY:CA	43:BX:95:LEU:HB2	2.42	0.49
1:CA:49:U:O4	1:CA:365:U:H5	1.96	0.49
19:CS:30:LEU:HA	19:CS:48:THR:O	2.13	0.49
19:CS:51:VAL:O	19:CS:58:VAL:N	2.35	0.49
25:DA:874:G:H5'	25:DA:875:G:OP2	2.12	0.49
25:DA:2099:U:H3	25:DA:2190:G:H1	1.61	0.49
25:DA:2124:G:N2	25:DA:2174:C:N3	2.51	0.49
26:DB:40:U:H1'	26:DB:45:A:H61	1.78	0.49
29:DF:113:ALA:HB1	29:DF:186:ILE:HG21	1.94	0.49
36:DQ:77:LYS:NZ	36:DQ:86:GLY:O	2.46	0.49
36:DQ:81:VAL:HG12	46:D0:5:LYS:HD3	1.94	0.49
1:AA:376:G:C5'	16:AP:5:ARG:HG2	2.42	0.48
1:AA:953:G:H5'	1:AA:965:A:N6	2.24	0.48
1:AA:955:U:O2'	19:AS:83:HIS:HD2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1030(C):G:H2'	1:AA:1030(D):A:H8	1.78	0.48
1:AA:1202:G:H1'	14:AN:29:ARG:HD2	1.95	0.48
2:AB:97:TRP:CZ2	2:AB:102:LEU:HD13	2.48	0.48
6:AF:69:GLU:O	6:AF:72:VAL:HG12	2.13	0.48
19:AS:80:TYR:CZ	19:AS:82:GLY:HA2	2.47	0.48
25:BA:30:G:H2'	25:BA:31:C:C6	2.48	0.48
25:BA:1289:G:O2'	35:BP:7:ARG:NH2	2.45	0.48
25:BA:2169:G:H2'	25:BA:2170:G:O4'	2.13	0.48
25:BA:2389:A:H2'	25:BA:2390:A:C8	2.48	0.48
25:BA:2658:C:H2'	25:BA:2659:U:O4'	2.13	0.48
25:BA:2860:A:OP2	25:BA:2876:U:H5	1.94	0.48
1:CA:750:G:H1'	15:CO:22:THR:OG1	2.12	0.48
1:CA:1360:A:H2'	1:CA:1361:G:O4'	2.13	0.48
2:CB:71:VAL:HB	2:CB:164:VAL:HG13	1.94	0.48
25:DA:2137:C:H2'	25:DA:2138:C:C6	2.48	0.48
26:DB:55:U:H1'	30:DG:29:TRP:HE1	1.77	0.48
30:DG:115:ARG:HD2	30:DG:136:ARG:NH2	2.24	0.48
50:D4:15:ILE:HB	50:D4:32:TYR:HD1	1.77	0.48
5:AE:144:THR:O	5:AE:148:VAL:HG23	2.12	0.48
9:AI:55:ALA:HB1	9:AI:59:PHE:CD2	2.47	0.48
25:BA:469:A:H1'	25:BA:1246:C:O4'	2.12	0.48
25:BA:1993:A:OP2	27:BD:242:ARG:NH2	2.40	0.48
25:BA:2856:G:H2'	25:BA:2857:U:O4'	2.13	0.48
1:CA:1012:U:H2'	1:CA:1013:G:C8	2.48	0.48
23:CY:44:G:C2'	23:CY:45:U:H5'	2.44	0.48
25:DA:801:G:O6	29:DF:53:THR:OG1	2.30	0.48
28:DE:24:THR:HG22	28:DE:186:GLY:O	2.13	0.48
31:DH:40:GLU:O	31:DH:55:PRO:HG3	2.13	0.48
1:AA:45:U:H2'	1:AA:46:G:C8	2.48	0.48
1:AA:1258:G:O2'	1:AA:1259:C:H5'	2.14	0.48
4:AD:88:VAL:HG22	5:AE:97:GLY:HA2	1.95	0.48
9:AI:128:ARG:NH2	24:AX:33:U:OP2	2.45	0.48
23:AY:53:G:N2	23:AY:61:C:N3	2.58	0.48
25:BA:1829:U:H5'	27:BD:259:THR:CG2	2.36	0.48
29:BF:150:GLY:HA2	29:BF:172:TRP:CE3	2.48	0.48
53:B7:12:ARG:NH2	53:B7:44:PRO:HB3	2.27	0.48
1:CA:692:U:O2'	1:CA:694:A:N7	2.25	0.48
1:CA:1002:G:N3	1:CA:1003:G:C8	2.81	0.48
1:CA:1352:C:OP1	21:CU:3:LYS:NZ	2.36	0.48
2:CB:144:ARG:O	2:CB:147:LYS:HB3	2.13	0.48
2:CB:230:VAL:HG22	2:CB:231:GLU:H	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CF:9:VAL:HB	6:CF:87:ARG:HB2	1.94	0.48
6:CF:68:PRO:HG2	6:CF:71:ARG:NH1	2.29	0.48
35:DP:2:LYS:HG2	35:DP:5:ASP:OD2	2.12	0.48
45:DZ:130:PRO:HA	45:DZ:133:ILE:HG13	1.96	0.48
1:AA:1226:C:H4'	19:AS:80:TYR:CZ	2.49	0.48
9:AI:48:GLU:H	9:AI:49:PRO:CD	2.26	0.48
25:BA:904:C:N4	25:BA:905:U:O4	2.46	0.48
25:BA:1218:G:N2	25:BA:1222:A:OP2	2.47	0.48
25:BA:2296:C:OP1	52:B6:3:SER:OG	2.29	0.48
25:BA:2303:U:H2'	25:BA:2304:C:C6	2.49	0.48
25:BA:2584:A:N7	28:BE:144:ARG:HD2	2.29	0.48
1:CA:1273:G:H3'	1:CA:1274:G:H8	1.78	0.48
2:CB:80:ILE:HD11	2:CB:212:GLN:HA	1.96	0.48
2:CB:211:ILE:O	2:CB:215:LEU:HB2	2.13	0.48
2:CB:213:LEU:HD22	2:CB:214:ILE:HD13	1.94	0.48
25:DA:468:G:N7	53:D7:39:ARG:NH2	2.56	0.48
25:DA:597:U:H2'	25:DA:598:G:C8	2.48	0.48
25:DA:839:U:H2'	25:DA:840:C:C6	2.48	0.48
25:DA:1155:A:H5"	40:DU:55:ARG:HD3	1.94	0.48
25:DA:1833:U:O2'	25:DA:1969:A:N1	2.38	0.48
25:DA:2110:G:H5"	25:DA:2111:C:H5	1.78	0.48
25:DA:2116:G:O6	25:DA:2165:G:N2	2.47	0.48
25:DA:2149:G:C6	25:DA:2150:U:C2	3.01	0.48
25:DA:2151:G:H2'	25:DA:2152:G:C8	2.46	0.48
25:DA:2273:A:H2'	25:DA:2274:A:C8	2.48	0.48
1:AA:236:G:H5"	17:AQ:42:TYR:OH	2.13	0.48
1:AA:346:G:O6	1:AA:347:G:N2	2.47	0.48
1:AA:815:A:N7	1:AA:1509:C:O2'	2.43	0.48
1:AA:1060:C:C5	3:AC:2:GLY:HA3	2.48	0.48
1:AA:1129:C:O2'	1:AA:1139:G:N7	2.35	0.48
1:AA:1516:G:H2'	1:AA:1518:A:OP2	2.13	0.48
2:AB:77:ALA:HB2	2:AB:211:ILE:HD13	1.95	0.48
2:AB:84:GLU:HB3	2:AB:219:VAL:HG21	1.95	0.48
6:AF:19:LEU:HD11	6:AF:59:TYR:CE2	2.49	0.48
25:BA:757:G:H2'	25:BA:758:G:C8	2.48	0.48
25:BA:2149:G:H1	25:BA:2183:C:H42	1.61	0.48
35:BP:100:LEU:HD12	35:BP:112:LEU:HD11	1.94	0.48
36:BQ:75:THR:HG21	36:BQ:87:LYS:NZ	2.28	0.48
1:CA:22:G:H4'	1:CA:885:G:C8	2.48	0.48
1:CA:397:A:H3'	1:CA:397:A:N3	2.28	0.48
1:CA:946:A:H2'	1:CA:947:G:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1258:G:O2'	1:CA:1259:C:H5'	2.13	0.48
3:CC:85:ARG:O	3:CC:89:GLU:N	2.44	0.48
8:CH:69:ARG:HD3	8:CH:75:ARG:O	2.14	0.48
23:CY:7:A:N6	23:CY:66:U:H3	2.08	0.48
25:DA:2320:A:H2'	25:DA:2320:A:N3	2.28	0.48
26:DB:66:A:N6	26:DB:109:C:H5'	2.28	0.48
27:DD:242:ARG:N	27:DD:242:ARG:HD3	2.28	0.48
32:DI:12:LEU:HD22	32:DI:19:VAL:HG21	1.94	0.48
33:DN:73:THR:HA	33:DN:83:LYS:O	2.14	0.48
38:DS:105:ALA:HB1	38:DS:110:LEU:HD23	1.95	0.48
48:D2:18:PRO:O	48:D2:22:GLU:HG3	2.13	0.48
1:AA:975:A:H5'	1:AA:975:A:C8	2.46	0.48
23:AY:19:G:C6	23:AY:56:C:N4	2.81	0.48
23:AY:20:U:H3'	23:AY:20:U:OP2	2.13	0.48
25:BA:308:U:H2'	25:BA:309:C:C6	2.49	0.48
25:BA:692:C:H2'	25:BA:693:G:O4'	2.14	0.48
25:BA:2152:U:H2'	25:BA:2153:G:N2	2.28	0.48
25:BA:2187:G:H2'	25:BA:2188:G:C8	2.48	0.48
25:BA:2658:C:OP2	25:BA:2745:G:O2'	2.30	0.48
33:BN:15:LEU:HB2	33:BN:135:PRO:HB2	1.95	0.48
1:CA:1005:A:C8	1:CA:1024:G:N2	2.82	0.48
1:CA:1221:G:C2'	1:CA:1222:G:H5'	2.44	0.48
1:CA:1308:U:OP1	13:CM:98:VAL:HG23	2.13	0.48
3:CC:23:TYR:CD1	10:CJ:10:GLY:HA2	2.49	0.48
25:DA:740:U:H2'	25:DA:741:G:C8	2.49	0.48
26:DB:31:C:H4'	30:DG:29:TRP:CH2	2.48	0.48
32:DI:66:GLU:OE1	32:DI:69:LYS:HD3	2.13	0.48
39:DT:51:ARG:HB3	39:DT:62:THR:HB	1.96	0.48
4:AD:98:GLU:HG2	4:AD:189:PRO:HG2	1.95	0.48
9:AI:58:HIS:H	9:AI:58:HIS:CD2	2.30	0.48
17:AQ:58:GLU:O	17:AQ:74:LEU:N	2.42	0.48
25:BA:1335:C:H2'	25:BA:1336:C:H6	1.78	0.48
31:BH:125:VAL:HG12	31:BH:127:GLU:O	2.13	0.48
32:BI:93:THR:HG22	32:BI:119:PRO:HB3	1.96	0.48
1:CA:429:U:O3'	4:CD:22:LYS:NZ	2.45	0.48
1:CA:811:C:N4	61:CA:4019:HOH:O	2.45	0.48
1:CA:1240:U:OP2	7:CG:116:ALA:N	2.46	0.48
1:CA:1275:A:C2'	1:CA:1276:G:H5'	2.43	0.48
1:CA:1513:A:H2'	1:CA:1514:C:C6	2.48	0.48
10:CJ:7:LYS:HB2	10:CJ:97:GLU:HB2	1.95	0.48
18:CR:41:LYS:HE3	18:CR:41:LYS:HB3	1.73	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:CY:29:G:N2	23:CY:41:C:N3	2.55	0.48
23:CY:65:G:H2'	23:CY:66:U:C6	2.48	0.48
25:DA:99:U:H4'	25:DA:100:G:H5"	1.94	0.48
25:DA:303:U:H2'	25:DA:304:G:C8	2.48	0.48
25:DA:775:G:N3	61:DA:4553:HOH:O	2.35	0.48
25:DA:848:G:H2'	25:DA:849:A:C8	2.48	0.48
25:DA:1399:C:OP1	43:DX:25:LYS:NZ	2.47	0.48
25:DA:2507:C:H5"	25:DA:2573:C:C4	2.49	0.48
28:DE:4:ILE:HD11	28:DE:29:GLY:HA2	1.94	0.48
40:DU:61:TRP:CH2	40:DU:93:LYS:HB2	2.48	0.48
45:DZ:45:ASP:OD1	45:DZ:49:ARG:HD2	2.12	0.48
1:AA:339:C:H2'	1:AA:340:U:H6	1.78	0.48
1:AA:461:A:O2'	1:AA:471:G:N7	2.44	0.48
12:AL:24:VAL:HB	12:AL:27:LEU:HD22	1.95	0.48
13:AM:87:TYR:O	13:AM:91:ARG:HG2	2.14	0.48
27:BD:79:VAL:HG21	27:BD:111:LEU:HD11	1.95	0.48
1:CA:1073:U:O2	2:CB:104:ASN:ND2	2.38	0.48
12:CL:28:LYS:N	12:CL:29:GLY:HA2	2.29	0.48
25:DA:24:G:O2'	42:DW:78:GLU:O	2.27	0.48
25:DA:1400:G:H2'	25:DA:1401:G:C8	2.48	0.48
25:DA:1548:C:H2'	25:DA:1549:C:H6	1.77	0.48
25:DA:2849:U:O4	39:DT:23:ARG:NH2	2.32	0.48
30:DG:67:LYS:HD3	50:D4:5:ILE:HD12	1.96	0.48
1:AA:1060:C:OP1	14:AN:45:ARG:NH2	2.42	0.48
1:AA:1530:G:OP1	1:AA:1530:G:H4'	2.13	0.48
20:AT:100:ILE:HB	20:AT:101:GLY:H	1.47	0.48
25:BA:323:A:N1	25:BA:346:A:O2'	2.43	0.48
25:BA:1093:G:O2'	25:BA:1094:A:O5'	2.31	0.48
25:BA:1733:C:H2'	25:BA:1734:G:O4'	2.14	0.48
25:BA:2158:C:N4	25:BA:2159:C:C4	2.82	0.48
25:BA:2250:G:H2'	25:BA:2250:G:N3	2.28	0.48
25:BA:2642:G:H21	25:BA:2901:A:H1'	1.78	0.48
31:BH:41:MET:HE1	31:BH:54:ARG:HB3	1.96	0.48
1:CA:1033:G:H2'	1:CA:1034:G:H8	1.78	0.48
1:CA:1292:U:P	7:CG:41:ARG:HH22	2.37	0.48
1:CA:1397:C:OP2	5:CE:24:ARG:NH2	2.46	0.48
5:CE:93:PRO:HG2	8:CH:105:ARG:NE	2.29	0.48
25:DA:1779:U:H2'	61:DA:4825:HOH:O	2.13	0.48
25:DA:2102:U:H2'	25:DA:2103:C:C6	2.48	0.48
25:DA:2103:C:N4	25:DA:2186:G:H1	2.11	0.48
25:DA:2495:G:H5"	36:DQ:82:ARG:HG2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2893:G:OP2	25:DA:2893:G:H8	1.97	0.48
36:DQ:57:HIS:HD2	36:DQ:117:ALA:HB2	1.79	0.48
43:DX:4:ALA:HB1	43:DX:42:ALA:HA	1.95	0.48
52:D6:13:CYS:SG	52:D6:47:THR:HG21	2.54	0.48
1:AA:56:U:H2'	1:AA:57:G:C8	2.49	0.48
25:BA:231:G:C8	54:B8:5:LYS:HG2	2.49	0.48
27:BD:179:SER:O	27:BD:275:LYS:HB2	2.14	0.48
31:BH:69:ARG:HG3	31:BH:70:THR:N	2.28	0.48
35:BP:95:VAL:HG13	35:BP:125:VAL:HB	1.94	0.48
38:BS:3:ARG:HD3	38:BS:4:LEU:N	2.28	0.48
45:BZ:151:HIS:C	45:BZ:153:SER:H	2.19	0.48
50:B4:49:PHE:HB3	50:B4:50:VAL:H	1.36	0.48
2:CB:63:MET:HG3	2:CB:225:ALA:HB1	1.95	0.48
25:DA:500:G:N1	25:DA:503:A:OP2	2.46	0.48
25:DA:910:A:N1	25:DA:2277:G:H1'	2.29	0.48
41:DV:37:VAL:HG11	41:DV:40:LEU:HG	1.96	0.48
1:AA:353:A:H5'	1:AA:353:A:C8	2.47	0.47
1:AA:1009:G:O6	1:AA:1020:U:O2	2.31	0.47
1:AA:1062:U:H2'	1:AA:1063:C:C6	2.49	0.47
2:AB:24:TRP:H	2:AB:24:TRP:HD1	1.61	0.47
3:AC:19:GLU:HG2	3:AC:54:ARG:NH1	2.28	0.47
3:AC:148:GLY:HA3	3:AC:172:ARG:O	2.14	0.47
25:BA:185:A:O2'	25:BA:852:G:O6	2.23	0.47
25:BA:701:A:OP2	61:BA:4864:HOH:O	2.19	0.47
25:BA:1313:U:OP2	25:BA:2034:G:N1	2.33	0.47
25:BA:2255:U:H2'	25:BA:2256:U:C6	2.49	0.47
26:BB:6:C:H2'	26:BB:7:G:H5"	1.95	0.47
30:BG:15:VAL:HG21	30:BG:176:LEU:HD23	1.95	0.47
43:BX:94:GLY:N	43:BX:95:LEU:HB2	2.29	0.47
45:BZ:137:ILE:HA	45:BZ:156:LYS:HE2	1.96	0.47
1:CA:345:C:H3'	39:DT:41:ARG:NH2	2.29	0.47
1:CA:659:U:C2'	1:CA:660:G:H5'	2.44	0.47
1:CA:1272:G:H2'	1:CA:1273:G:O4'	2.14	0.47
3:CC:149:ALA:HA	3:CC:201:TYR:O	2.14	0.47
13:CM:65:LYS:N	50:D4:50:VAL:HG21	2.29	0.47
25:DA:597:U:H2'	25:DA:598:G:H8	1.79	0.47
25:DA:1218:C:H42	25:DA:1231:G:H1	1.62	0.47
25:DA:2127:G:H22	25:DA:2161:C:H2'	1.78	0.47
1:AA:339:C:OP2	34:BO:97:ARG:NH1	2.45	0.47
12:AL:56:ALA:HB2	12:AL:70:ILE:HD11	1.96	0.47
12:AL:88:GLY:O	12:AL:99:HIS:HD2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:1093:G:H2'	25:BA:1156:G:N1	2.28	0.47
39:BT:65:LYS:HG2	39:BT:66:VAL:N	2.30	0.47
50:B4:63:TYR:N	50:B4:63:TYR:CD1	2.80	0.47
1:CA:1016:A:H2'	1:CA:1017:G:O4'	2.14	0.47
1:CA:1069:C:O2'	1:CA:1192:C:H1'	2.14	0.47
2:CB:48:MET:O	2:CB:52:GLU:N	2.44	0.47
3:CC:174:PRO:HD2	3:CC:182:ILE:HD11	1.96	0.47
23:CY:61:C:H2'	23:CY:62:C:C6	2.48	0.47
25:DA:589:C:H2'	25:DA:590:A:C8	2.49	0.47
25:DA:2136:C:O2'	25:DA:2137:C:H6	1.97	0.47
45:DZ:144:LEU:HD22	45:DZ:174:VAL:HG23	1.96	0.47
50:D4:59:PHE:N	50:D4:60:GLN:HB2	2.29	0.47
1:AA:269:C:H2'	1:AA:270:A:C8	2.49	0.47
1:AA:568:G:O2'	1:AA:574:A:N1	2.45	0.47
1:AA:1003:G:N2	1:AA:1038:C:H42	2.13	0.47
1:AA:1004:A:N1	1:AA:1035:A:N6	2.63	0.47
2:AB:15:VAL:HG22	2:AB:15:VAL:O	2.13	0.47
5:AE:72:GLN:O	5:AE:75:THR:HG22	2.14	0.47
10:AJ:4:ILE:HA	10:AJ:100:THR:HA	1.96	0.47
23:AY:76:A:N6	25:BA:2434:A:O4'	2.48	0.47
28:BE:47:VAL:HG22	28:BE:84:PHE:O	2.15	0.47
34:BO:110:GLY:HA2	34:BO:112:MET:HE2	1.96	0.47
39:BT:108:ARG:NH1	39:BT:109:GLU:HG3	2.30	0.47
42:BW:19:LEU:HB3	51:B5:25:LEU:HD11	1.97	0.47
1:CA:1142:G:H2'	1:CA:1143:G:O4'	2.15	0.47
1:CA:1162:C:N3	1:CA:1174:G:N2	2.61	0.47
7:CG:79:ARG:HG2	7:CG:79:ARG:HH21	1.79	0.47
9:CI:85:LEU:HD12	9:CI:96:LEU:HD11	1.95	0.47
23:CY:55:PSU:HN1	23:CY:57:G:H5'	1.78	0.47
25:DA:373:U:H2'	25:DA:374:A:H8	1.78	0.47
25:DA:1040:C:H2'	25:DA:1041:C:O4'	2.15	0.47
25:DA:1784:A:O2'	61:DA:4872:HOH:O	2.15	0.47
25:DA:1857:G:C6	25:DA:1858:G:C6	3.01	0.47
25:DA:2029:G:H2'	25:DA:2031:A:OP1	2.13	0.47
31:DH:20:ALA:HB1	31:DH:21:PRO:HD2	1.96	0.47
32:DI:61:ARG:HD3	32:DI:61:ARG:HA	1.70	0.47
45:DZ:30:ASN:HA	45:DZ:89:PHE:HE1	1.79	0.47
1:AA:656:C:O2'	15:AO:28:GLN:NE2	2.48	0.47
1:AA:715:A:H2'	1:AA:716:A:C8	2.49	0.47
1:AA:1345:U:OP1	9:AI:120:ARG:NH1	2.48	0.47
9:AI:16:ARG:HB2	9:AI:64:THR:HB	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:551:A:H5”	25:BA:552:C:OP1	2.14	0.47
25:BA:1140:U:C4	25:BA:1142:A:H5”	2.49	0.47
25:BA:1315:A:N7	61:BA:4537:HOH:O	2.36	0.47
25:BA:1431:G:O2’	25:BA:1442:U:O2	2.24	0.47
25:BA:2018:C:H4’	25:BA:2019:G:OP1	2.13	0.47
27:BD:39:LYS:NZ	27:BD:57:GLY:O	2.45	0.47
33:BN:67:LEU:HD13	33:BN:87:LEU:HD13	1.95	0.47
34:BO:87:ILE:HD12	34:BO:91:LEU:HA	1.95	0.47
2:CB:163:PHE:HA	2:CB:185:ILE:HG12	1.96	0.47
20:CT:14:LYS:O	20:CT:18:GLN:HG3	2.14	0.47
25:DA:956:G:H5”	36:DQ:77:LYS:HD2	1.97	0.47
25:DA:1453:U:O2’	25:DA:1455:G:N7	2.44	0.47
25:DA:1548:C:H2’	25:DA:1549:C:C6	2.49	0.47
25:DA:2010:G:H5”	42:DW:42:ARG:HB2	1.96	0.47
43:DX:35:THR:HG22	43:DX:38:GLU:H	1.79	0.47
50:D4:53:GLU:O	50:D4:55:ARG:N	2.43	0.47
3:AC:19:GLU:HG2	3:AC:54:ARG:HH11	1.79	0.47
5:AE:92:LYS:HB3	5:AE:119:LEU:HB2	1.95	0.47
6:AF:100:ASN:C	18:AR:28:GLU:HG2	2.40	0.47
13:AM:92:HIS:CE1	13:AM:98:VAL:HG21	2.49	0.47
25:BA:878:G:O2’	35:BP:38:GLN:NE2	2.47	0.47
32:BI:29:TYR:O	32:BI:32:PRO:HD2	2.14	0.47
40:BU:89:GLU:HG3	41:BV:50:PRO:HB3	1.97	0.47
41:BV:49:THR:O	41:BV:49:THR:HG22	2.15	0.47
44:BY:86:ARG:HH11	44:BY:100:ALA:HB1	1.79	0.47
1:CA:1273:G:H3’	1:CA:1274:G:C8	2.49	0.47
1:CA:1330:U:H4’	13:CM:23:TYR:CE1	2.49	0.47
1:CA:1519:A:H5”	1:CA:1520:G:OP2	2.15	0.47
9:CI:23:ASN:HD22	9:CI:24:GLY:N	2.13	0.47
25:DA:927:G:H2’	25:DA:928:G:O4’	2.13	0.47
25:DA:987:G:O2’	25:DA:1000:A:N3	2.43	0.47
25:DA:1506:C:H2’	25:DA:1507:A:H5’	1.95	0.47
25:DA:1518:U:H2’	25:DA:1519:G:O4’	2.14	0.47
25:DA:1721:G:N1	25:DA:1739:U:OP2	2.47	0.47
25:DA:2115:G:H4’	25:DA:2167:U:O4	2.15	0.47
45:DZ:52:SER:OG	45:DZ:53:ILE:N	2.26	0.47
1:AA:1001:A:H2’	1:AA:1001(A):G:O4’	2.14	0.47
1:AA:1006:C:H2’	1:AA:1007:C:C6	2.49	0.47
1:AA:1008:C:C2	1:AA:1021:G:N2	2.79	0.47
1:AA:1239:A:H62	1:AA:1299:A:H62	1.61	0.47
5:AE:82:VAL:HG21	5:AE:138:ALA:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:37:ASN:O	7:AG:41:ARG:HD2	2.14	0.47
10:AJ:27:ALA:HB2	10:AJ:81:THR:HG21	1.96	0.47
11:AK:45:GLY:O	11:AK:50:TYR:HB2	2.15	0.47
25:BA:572:A:H61	41:BV:19:LYS:H	1.63	0.47
25:BA:1314:A:C2	25:BA:2035:A:C4	3.03	0.47
25:BA:2149:G:C2'	25:BA:2150:C:H5'	2.45	0.47
25:BA:2303:U:OP1	25:BA:2392:C:O2'	2.23	0.47
25:BA:2762:A:OP1	31:BH:3:ARG:NH2	2.39	0.47
26:BB:48:A:H2'	26:BB:49:C:C6	2.49	0.47
7:CG:97:GLN:O	7:CG:101:LEU:HG	2.15	0.47
16:CP:8:ARG:HB3	16:CP:28:ARG:NH1	2.30	0.47
23:CW:3:C:N3	23:CW:70:G:O6	2.47	0.47
23:CW:7:A:H5'	23:CW:8:4SU:H5	1.95	0.47
25:DA:747:U:O2	25:DA:2014:A:H1'	2.14	0.47
25:DA:1022:G:H22	25:DA:1142(A):A:H2	1.61	0.47
25:DA:1446:C:H42	25:DA:1465:G:H1	1.62	0.47
32:DI:4:ILE:HG12	32:DI:18:VAL:HG22	1.97	0.47
32:DI:40:THR:O	32:DI:44:LEU:HB2	2.15	0.47
34:DO:120:GLU:OE2	34:DO:122:LEU:HD21	2.13	0.47
50:D4:64:GLY:O	50:D4:66:SER:N	2.37	0.47
1:AA:975:A:H4'	1:AA:976:G:C5'	2.40	0.47
1:AA:1038:C:C2'	1:AA:1039:C:H5'	2.45	0.47
1:AA:1124:G:H5"	10:AJ:35:SER:OG	2.15	0.47
1:AA:1493:A:H5"	1:AA:1494:G:OP2	2.14	0.47
3:AC:71:ALA:HA	3:AC:106:VAL:HB	1.97	0.47
3:AC:134:ILE:HG23	3:AC:151:VAL:HB	1.97	0.47
5:AE:40:ARG:HH21	5:AE:68:GLU:HA	1.79	0.47
15:AO:18:PHE:CZ	15:AO:21:ASP:HB3	2.49	0.47
25:BA:271:U:H1'	32:BI:50:ARG:CZ	2.44	0.47
25:BA:847:A:H8	25:BA:847:A:OP1	1.97	0.47
25:BA:909:G:H2'	25:BA:910:A:O4'	2.15	0.47
25:BA:1067:A:H3'	25:BA:1067:A:H8	1.80	0.47
25:BA:2418:U:H2'	25:BA:2418:U:OP2	2.14	0.47
25:BA:2744:G:O3'	28:BE:203:LYS:NZ	2.48	0.47
27:BD:146:GLU:HG2	27:BD:152:GLY:C	2.40	0.47
29:BF:184:TYR:CE2	29:BF:188:ARG:HD2	2.50	0.47
53:B7:11:LYS:HE3	53:B7:15:THR:OG1	2.14	0.47
1:CA:1120:G:C6	1:CA:1121:U:C4	3.03	0.47
1:CA:1194:U:H4'	5:CE:22:GLY:HA3	1.96	0.47
2:CB:71:VAL:HG21	2:CB:164:VAL:HG22	1.97	0.47
3:CC:152:ILE:HD12	3:CC:199:LYS:HD2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CH:51:VAL:HG12	8:CH:52:ASP:H	1.79	0.47
25:DA:265:A:C8	25:DA:266:G:H1'	2.49	0.47
25:DA:322:A:OP1	29:DF:168:ARG:HD2	2.15	0.47
25:DA:631:A:H2'	25:DA:632:A:O4'	2.15	0.47
25:DA:1539:G:H2'	25:DA:1540:U:O4'	2.15	0.47
25:DA:2243:U:H2'	25:DA:2244:U:C6	2.49	0.47
25:DA:2751:G:C8	31:DH:2:SER:HA	2.47	0.47
31:DH:86:GLU:OE2	31:DH:132:ARG:NH2	2.47	0.47
37:DR:44:LEU:HD23	37:DR:44:LEU:HA	1.73	0.47
40:DU:85:LYS:HB3	40:DU:116:ALA:HB1	1.97	0.47
50:D4:59:PHE:N	50:D4:59:PHE:CD1	2.83	0.47
1:AA:1302:U:OP2	13:AM:21:TYR:OH	2.29	0.47
7:AG:89:MET:SD	7:AG:155:ARG:HB2	2.54	0.47
10:AJ:57:LYS:HE2	10:AJ:60:ARG:NH2	2.30	0.47
19:AS:45:VAL:HG13	19:AS:63:THR:HA	1.97	0.47
20:AT:56:MET:HE2	20:AT:85:MET:HA	1.96	0.47
23:AW:51:U:H2'	23:AW:52:G:H8	1.78	0.47
24:AX:8:4SU:O2	24:AX:21:A:H2	1.96	0.47
25:BA:572:A:N6	41:BV:19:LYS:H	2.11	0.47
25:BA:2044:U:O2'	25:BA:2629:C:H5'	2.15	0.47
25:BA:2830:A:C5	37:BR:4:LEU:HD11	2.50	0.47
32:BI:116:LEU:HD11	32:BI:120:ILE:HG13	1.96	0.47
37:BR:56:LYS:NZ	37:BR:90:ARG:O	2.46	0.47
54:B8:61:LEU:C	54:B8:63:PRO:HD3	2.40	0.47
4:CD:20:TYR:CD2	4:CD:26:CYS:HB3	2.50	0.47
4:CD:111:ALA:HB2	4:CD:120:LEU:HD12	1.95	0.47
4:CD:173:TRP:CZ3	4:CD:193:ASP:HB3	2.50	0.47
7:CG:108:ALA:HA	7:CG:111:ARG:HD2	1.97	0.47
9:CI:128:ARG:HH21	24:CX:32:5MC:P	2.38	0.47
17:CQ:54:GLY:O	17:CQ:81:ARG:N	2.41	0.47
19:CS:27:GLU:HB3	19:CS:28:LYS:HD3	1.97	0.47
25:DA:38:A:H2'	25:DA:39:C:C6	2.50	0.47
25:DA:323:G:O2'	25:DA:1205:U:N3	2.37	0.47
25:DA:866:A:H2	25:DA:867:C:C4	2.32	0.47
25:DA:985:C:H2'	25:DA:986:C:H6	1.79	0.47
25:DA:1219:G:H1	25:DA:1230:C:H42	1.62	0.47
25:DA:2125:G:H21	25:DA:2173:A:H62	1.62	0.47
25:DA:2125:G:N2	25:DA:2173:A:H62	2.13	0.47
25:DA:2756:U:H1'	25:DA:2757:A:H5"	1.97	0.47
25:DA:2815:C:H2'	25:DA:2816:C:C6	2.50	0.47
26:DB:80:U:H2'	26:DB:81:G:N7	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:DE:28:ALA:HB3	28:DE:93:VAL:HG12	1.96	0.47
37:DR:33:ARG:NH2	51:D5:57:VAL:O	2.35	0.47
1:AA:581:G:OP1	15:AO:65:ARG:NH2	2.48	0.47
1:AA:1095:U:H5"	1:AA:1109:C:O2	2.15	0.47
2:AB:163:PHE:HA	2:AB:185:ILE:HG13	1.97	0.47
10:AJ:45:ARG:HG2	10:AJ:47:PHE:CZ	2.50	0.47
17:AQ:45:HIS:CD2	17:AQ:47:PRO:HG3	2.49	0.47
25:BA:1093:G:H2'	25:BA:1156:G:N2	2.30	0.47
25:BA:1335:C:H2'	25:BA:1336:C:C6	2.50	0.47
25:BA:2129:C:H42	25:BA:2204:G:H1	1.62	0.47
25:BA:2724:U:H2'	25:BA:2727:G:H5"	1.97	0.47
27:BD:71:ASP:HB3	27:BD:103:ARG:NH2	2.29	0.47
1:CA:7:G:H5'	1:CA:298:A:O4'	2.14	0.47
5:CE:24:ARG:NH1	22:CV:24:A:OP2	2.48	0.47
13:CM:84:ILE:HG13	13:CM:85:GLY:N	2.29	0.47
25:DA:27:G:N2	25:DA:512:G:H1'	2.29	0.47
25:DA:117:G:OP2	25:DA:119:A:O2'	2.22	0.47
25:DA:250:G:P	54:D8:13:ARG:HH22	2.38	0.47
25:DA:896:A:H5"	45:DZ:147:GLY:HA3	1.96	0.47
25:DA:1183:G:H2'	25:DA:1184:G:C8	2.49	0.47
25:DA:2469:A:H3'	25:DA:2470:G:H8	1.79	0.47
26:DB:91:C:OP2	36:DQ:16:ARG:NH1	2.47	0.47
27:DD:92:ILE:HD12	27:DD:104:TYR:CE1	2.49	0.47
29:DF:150:GLY:HA2	29:DF:172:TRP:CD2	2.50	0.47
30:DG:109:VAL:HG21	50:D4:14:ILE:HG21	1.97	0.47
31:DH:84:SER:HB3	31:DH:132:ARG:NH1	2.27	0.47
44:DY:89:PHE:CZ	44:DY:95:LYS:HE2	2.50	0.47
1:AA:337:C:H2'	1:AA:338:A:C8	2.50	0.47
1:AA:690:G:C6	1:AA:691:G:C6	3.03	0.47
1:AA:1025:U:C2	1:AA:1036:G:O6	2.66	0.47
1:AA:1125:U:H4'	10:AJ:5:ARG:NH2	2.30	0.47
24:AX:8:4SU:O5'	24:AX:8:4SU:H6	2.15	0.47
25:BA:1346:U:H4'	25:BA:1347:A:H5'	1.95	0.47
52:B6:14:THR:HB	52:B6:48:VAL:O	2.15	0.47
1:CA:520:A:N1	1:CA:536:C:H1'	2.30	0.47
1:CA:750:G:O2'	15:CO:21:ASP:OD1	2.33	0.47
1:CA:1034:G:H3'	1:CA:1035:A:H8	1.78	0.47
1:CA:1178:G:N2	1:CA:1180:A:H3'	2.30	0.47
1:CA:1318:A:H5"	19:CS:3:ARG:NH2	2.30	0.47
2:CB:188:ALA:HB1	2:CB:192:SER:OG	2.15	0.47
3:CC:34:LEU:O	3:CC:38:ARG:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CE:43:LEU:O	5:CE:65:ASN:ND2	2.38	0.47
25:DA:851:U:H5'	49:D3:49:LYS:HD2	1.97	0.47
27:DD:218:ARG:HB3	27:DD:219:PRO:HD2	1.96	0.47
29:DF:116:ASP:OD1	29:DF:119:ARG:NH2	2.49	0.47
33:DN:67:LEU:C	33:DN:88:GLU:HG3	2.40	0.47
45:DZ:6:LYS:HD2	45:DZ:8:TYR:HE1	1.78	0.47
1:AA:175:C:H2'	1:AA:176:C:C6	2.49	0.46
1:AA:1118:C:H1'	1:AA:1179:A:C4	2.51	0.46
1:AA:1531:A:H2'	1:AA:1532:U:C4	2.50	0.46
6:AF:94:GLN:HG2	18:AR:32:ARG:HH21	1.80	0.46
9:AI:15:ALA:HB2	9:AI:65:VAL:HG23	1.97	0.46
13:AM:3:ARG:HG3	13:AM:4:ILE:H	1.80	0.46
25:BA:482:C:O2'	25:BA:483:A:OP2	2.32	0.46
25:BA:1410:G:OP2	47:B1:3:LYS:HG3	2.15	0.46
25:BA:1921:G:H2'	25:BA:1921:G:N3	2.30	0.46
25:BA:2204:G:H2'	25:BA:2205:C:C6	2.50	0.46
39:BT:117:ASP:OD2	39:BT:120:ARG:NE	2.36	0.46
50:B4:54:GLY:N	50:B4:55:ARG:HA	2.30	0.46
1:CA:19:C:H5"	5:CE:86:ALA:HB3	1.97	0.46
1:CA:664:G:N2	1:CA:741:G:H1	2.11	0.46
1:CA:1207:G:C6	1:CA:1208:C:C4	3.03	0.46
1:CA:1239:A:H62	1:CA:1299:A:N6	2.12	0.46
22:CV:23:A:H4'	22:CV:24:A:C5'	2.42	0.46
25:DA:908:C:OP2	36:DQ:22:LYS:NZ	2.33	0.46
25:DA:1021:A:H3'	25:DA:1021:A:H8	1.80	0.46
25:DA:1991:U:H2'	25:DA:1992:G:H5"	1.96	0.46
25:DA:2182:G:H2'	25:DA:2183:C:C6	2.50	0.46
26:DB:4:C:N4	26:DB:117:G:H1	2.06	0.46
27:DD:164:GLN:HE21	27:DD:176:ARG:HH22	1.63	0.46
27:DD:276:LYS:HD3	27:DD:276:LYS:H	1.79	0.46
35:DP:50:ARG:HH21	54:D8:7:HIS:CD2	2.29	0.46
36:DQ:75:THR:HG21	36:DQ:87:LYS:NZ	2.30	0.46
39:DT:56:GLY:O	39:DT:59:THR:HG22	2.15	0.46
1:AA:130:A:H5'	17:AQ:63:ARG:NE	2.29	0.46
1:AA:1063:C:OP2	1:AA:1064:G:O2'	2.29	0.46
1:AA:1152:A:H5'	10:AJ:13:HIS:HB2	1.96	0.46
1:AA:1221:G:C2'	1:AA:1222:G:H5'	2.45	0.46
25:BA:11:G:H2'	25:BA:12:U:H5"	1.98	0.46
25:BA:2181:G:H2'	25:BA:2182:G:C8	2.51	0.46
1:CA:707:C:OP1	11:CK:85:ARG:NH1	2.48	0.46
3:CC:134:ILE:HG22	3:CC:168:ALA:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:CY:58:A:O2'	23:CY:60:U:OP2	2.31	0.46
25:DA:229:A:H5'	25:DA:230:U:H5'	1.97	0.46
25:DA:582:G:H2'	25:DA:583:G:C8	2.49	0.46
25:DA:1899:G:N3	25:DA:1899:G:H2'	2.30	0.46
25:DA:2663:G:H2'	25:DA:2664:G:O4'	2.15	0.46
25:DA:2820:A:C5	37:DR:4:LEU:HD11	2.50	0.46
48:D2:1:MET:HE3	48:D2:5:GLU:HB3	1.97	0.46
1:AA:262:A:C6	1:AA:263:A:C6	3.02	0.46
1:AA:848:C:H2'	1:AA:849:C:C6	2.51	0.46
1:AA:1009:G:C5	1:AA:1021:G:C6	3.03	0.46
7:AG:28:ASN:HD21	7:AG:36:LYS:NZ	2.12	0.46
15:AO:6:GLU:N	15:AO:6:GLU:OE2	2.49	0.46
19:AS:20:LEU:HD23	19:AS:23:ASN:ND2	2.30	0.46
25:BA:1834:A:H4'	27:BD:259:THR:HG23	1.97	0.46
28:BE:170:LEU:HB3	28:BE:184:VAL:HG22	1.98	0.46
35:BP:81:GLN:NE2	35:BP:105:LEU:O	2.46	0.46
44:BY:35:TYR:CE2	44:BY:69:ALA:HB3	2.50	0.46
52:B6:11:LEU:HB2	52:B6:21:TYR:HB2	1.97	0.46
1:CA:8:A:N6	4:CD:209:ARG:HB2	2.31	0.46
1:CA:807:A:H2'	1:CA:808:C:C6	2.51	0.46
1:CA:1410:G:H2'	1:CA:1411:C:H6	1.80	0.46
2:CB:16:HIS:CG	2:CB:17:PHE:H	2.33	0.46
2:CB:118:LEU:HD13	2:CB:142:LEU:HB2	1.96	0.46
10:CJ:50:ILE:HB	14:CN:41:ARG:NH2	2.30	0.46
13:CM:93:ARG:NH1	25:DA:888:C:OP1	2.41	0.46
25:DA:868:U:C4	25:DA:869:G:N7	2.83	0.46
25:DA:2131:G:OP1	25:DA:2132:U:O2'	2.18	0.46
25:DA:2336:A:H61	46:D0:43:THR:HG22	1.81	0.46
25:DA:2756:U:H5"	55:D9:19:ARG:HB3	1.96	0.46
26:DB:105:A:OP1	45:DZ:72:ARG:NH1	2.49	0.46
28:DE:1:MET:HE1	28:DE:199:ARG:HB3	1.97	0.46
28:DE:111:ARG:HA	37:DR:1:MET:SD	2.56	0.46
29:DF:11:VAL:HB	29:DF:18:ARG:HB3	1.97	0.46
30:DG:33:ARG:NH2	30:DG:162:THR:HG21	2.30	0.46
33:DN:130:HIS:HB3	33:DN:133:GLN:HG2	1.97	0.46
34:DO:16:ALA:HB2	34:DO:52:VAL:HG21	1.96	0.46
4:AD:3:ARG:O	4:AD:5:ILE:HG22	2.15	0.46
4:AD:18:LYS:HE3	4:AD:20:TYR:CZ	2.51	0.46
7:AG:50:ILE:HD11	7:AG:61:VAL:HG21	1.96	0.46
15:AO:6:GLU:O	15:AO:10:LYS:HG3	2.14	0.46
25:BA:1081:U:H2'	25:BA:1082:G:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2150:C:H2'	25:BA:2151:C:O4'	2.15	0.46
30:BG:43:LEU:HB3	30:BG:44:GLY:H	1.55	0.46
54:B8:23:VAL:CG1	54:B8:47:LYS:HD3	2.45	0.46
1:CA:972:C:O2'	10:CJ:55:LYS:O	2.27	0.46
1:CA:975:A:H8	1:CA:975:A:H5'	1.81	0.46
1:CA:1001(A):G:H3'	1:CA:1002:G:O4'	2.16	0.46
1:CA:1002:G:H2'	1:CA:1003:G:H8	1.81	0.46
3:CC:102:ASN:HD22	3:CC:102:ASN:N	2.13	0.46
3:CC:125:GLU:O	3:CC:127:ARG:NH1	2.45	0.46
25:DA:1339:G:H5"	43:DX:16:LYS:HD3	1.98	0.46
25:DA:2119:A:N6	25:DA:2170:A:H62	2.13	0.46
25:DA:2552:U:H2'	25:DA:2554:U:OP2	2.15	0.46
37:DR:24:GLN:HB3	37:DR:44:LEU:HD11	1.98	0.46
1:AA:691:G:H2'	1:AA:692:U:C6	2.50	0.46
1:AA:719:C:O2'	18:AR:49:LYS:HB3	2.15	0.46
1:AA:1376:U:H2'	1:AA:1377:A:C8	2.51	0.46
2:AB:112:VAL:HG12	2:AB:149:LEU:HD13	1.98	0.46
4:AD:162:LEU:CD1	4:AD:181:MET:HG2	2.44	0.46
10:AJ:64:GLU:OE2	10:AJ:66:ARG:NE	2.43	0.46
25:BA:225:C:H2'	25:BA:226:C:C6	2.50	0.46
25:BA:1756:U:H2'	25:BA:1757:C:C6	2.50	0.46
25:BA:2762:A:P	31:BH:3:ARG:HH21	2.38	0.46
29:BF:172:TRP:H	29:BF:172:TRP:CD1	2.33	0.46
32:BI:31:LEU:HD21	32:BI:38:LEU:HD11	1.98	0.46
37:BR:83:ILE:O	37:BR:86:ARG:HG2	2.16	0.46
1:CA:444:C:H2'	1:CA:445:G:H8	1.80	0.46
1:CA:922:G:O2'	1:CA:1398:A:N1	2.46	0.46
1:CA:975:A:H4'	1:CA:976:G:C5'	2.43	0.46
8:CH:49:GLU:HG2	8:CH:62:TYR:HE1	1.81	0.46
13:CM:92:HIS:CE1	13:CM:98:VAL:HG21	2.51	0.46
25:DA:1665:A:H2'	25:DA:1666:G:O4'	2.15	0.46
25:DA:2748:A:H5'	31:DH:4:ILE:HD13	1.97	0.46
26:DB:14:U:H1'	26:DB:108:U:O2'	2.16	0.46
39:DT:91:ARG:HB2	39:DT:121:ILE:HG13	1.97	0.46
1:AA:411:A:OP2	4:AD:30:LYS:HE3	2.16	0.46
1:AA:454:C:N4	1:AA:479:C:N3	2.62	0.46
2:AB:133:LYS:O	2:AB:137:ARG:HG3	2.15	0.46
4:AD:98:GLU:OE1	4:AD:103:ASN:ND2	2.43	0.46
5:AE:91:LEU:HG	5:AE:118:ILE:HD11	1.98	0.46
23:AW:63:G:H2'	23:AW:64:A:O4'	2.15	0.46
25:BA:714:U:O2	54:B8:2:PRO:HD2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2033:U:OP1	42:BW:42:ARG:NH1	2.46	0.46
25:BA:2189:U:H3	25:BA:2190:G:H21	1.64	0.46
25:BA:2602:A:H2'	25:BA:2603:C:C6	2.50	0.46
25:BA:2800:C:H1'	28:BE:62:PRO:HG3	1.96	0.46
1:CA:165:C:H2'	1:CA:166:G:H8	1.80	0.46
1:CA:392:G:H2'	1:CA:393:A:C8	2.51	0.46
1:CA:560:U:O2'	1:CA:561:U:OP2	2.27	0.46
1:CA:735:C:H2'	1:CA:736:C:H6	1.80	0.46
1:CA:828:A:H2'	1:CA:829:G:O4'	2.16	0.46
7:CG:32:ARG:HH12	7:CG:109:ASN:ND2	2.12	0.46
10:CJ:8:LEU:HD12	10:CJ:20:ALA:HB2	1.97	0.46
20:CT:60:GLU:HG3	20:CT:81:LYS:HD2	1.98	0.46
23:CW:51:U:O5'	23:CW:51:U:H6	1.97	0.46
23:CY:8:4SU:O2	23:CY:21:A:H2	1.97	0.46
25:DA:1830:C:OP2	61:DA:4650:HOH:O	2.19	0.46
26:DB:40:U:H2'	50:D4:2:LYS:HE3	1.98	0.46
26:DB:55:U:O2'	30:DG:27:ASN:ND2	2.46	0.46
27:DD:134:ARG:HD3	27:DD:135:PHE:CE1	2.51	0.46
27:DD:164:GLN:HE21	27:DD:176:ARG:HH12	1.63	0.46
30:DG:11:TYR:OH	30:DG:33:ARG:HG2	2.16	0.46
31:DH:25:LYS:HE2	31:DH:27:LYS:HZ3	1.80	0.46
31:DH:154:PRO:HB3	31:DH:163:TYR:CE2	2.50	0.46
1:AA:192:U:H2'	1:AA:193:C:C6	2.50	0.46
1:AA:1004:A:N7	1:AA:1036:G:N2	2.64	0.46
1:AA:1148:U:H2'	1:AA:1149:C:O4'	2.16	0.46
8:AH:6:ILE:HB	8:AH:85:ARG:NH1	2.30	0.46
9:AI:96:LEU:HA	9:AI:96:LEU:HD23	1.84	0.46
15:AO:82:ILE:O	15:AO:86:GLY:N	2.48	0.46
25:BA:785:G:C6	25:BA:786:G:C2	3.04	0.46
25:BA:2156:A:N6	25:BA:2179:G:H1'	2.29	0.46
28:BE:178:GLU:OE2	28:BE:178:GLU:N	2.30	0.46
29:BF:135:LYS:HB2	29:BF:138:GLU:HG3	1.97	0.46
52:B6:13:CYS:SG	52:B6:47:THR:HG21	2.56	0.46
1:CA:1122:U:C4	1:CA:1123:A:N7	2.84	0.46
4:CD:8:VAL:HG13	4:CD:21:LEU:HD12	1.97	0.46
6:CF:36:ARG:HH11	6:CF:38:GLU:HG2	1.81	0.46
12:CL:37:CYS:SG	12:CL:81:SER:HB2	2.56	0.46
13:CM:122:LYS:HD3	13:CM:123:ALA:N	2.17	0.46
16:CP:69:THR:HB	16:CP:72:ARG:HH12	1.81	0.46
25:DA:889:C:O2'	25:DA:890:A:OP2	2.30	0.46
25:DA:1257:C:H4'	29:DF:83:PHE:CD2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1507:A:O2'	25:DA:1508:A:O4'	2.32	0.46
28:DE:101:ARG:CZ	28:DE:171:GLU:HB2	2.45	0.46
29:DF:192:LEU:HD13	29:DF:194:MET:HE2	1.97	0.46
31:DH:95:ARG:HG2	31:DH:96:ALA:N	2.30	0.46
31:DH:125:VAL:HG13	31:DH:131:VAL:HG22	1.98	0.46
31:DH:149:ARG:HA	31:DH:162:ILE:HB	1.98	0.46
33:DN:73:THR:OG1	33:DN:82:LEU:HD11	2.15	0.46
38:DS:65:VAL:O	38:DS:69:VAL:HG12	2.16	0.46
51:D5:16:ARG:HD2	51:D5:17:ASP:OD1	2.15	0.46
1:AA:1392:G:N2	1:AA:1502:A:C8	2.84	0.46
2:AB:230:VAL:HG22	2:AB:231:GLU:H	1.80	0.46
3:AC:119:ARG:O	3:AC:123:GLN:HG3	2.15	0.46
14:AN:50:LYS:HZ3	14:AN:50:LYS:HB2	1.81	0.46
21:AU:18:TYR:CD2	21:AU:24:ARG:HD3	2.51	0.46
25:BA:302:A:H2'	25:BA:303:C:C6	2.51	0.46
25:BA:553:A:C2	25:BA:2065:C:H4'	2.51	0.46
25:BA:2096:U:H2'	25:BA:2097:U:C6	2.50	0.46
25:BA:2163:G:C5	25:BA:2173:G:C2	3.04	0.46
25:BA:2661:U:H2'	25:BA:2662:U:C6	2.50	0.46
25:BA:2820:A:N6	25:BA:2900:G:O2'	2.42	0.46
26:BB:2:C:H2'	26:BB:3:C:C6	2.51	0.46
31:BH:59:ARG:HH11	31:BH:59:ARG:CG	2.29	0.46
34:BO:80:ASP:OD1	39:BT:64:ARG:NH2	2.48	0.46
1:CA:976:G:OP2	1:CA:1358:U:O2'	2.30	0.46
1:CA:1032:G:H2'	1:CA:1033:G:C8	2.51	0.46
1:CA:1380:U:C4	7:CG:3:ARG:HG2	2.50	0.46
3:CC:137:ALA:HA	3:CC:140:ARG:CZ	2.45	0.46
13:CM:3:ARG:N	50:D4:34:GLU:OE1	2.49	0.46
13:CM:19:LEU:HD11	13:CM:56:LEU:HD21	1.97	0.46
23:CW:34:G:H2'	23:CW:35:A:C8	2.51	0.46
25:DA:795:C:H2'	25:DA:796:C:C6	2.51	0.46
25:DA:1114:G:C2'	25:DA:1115:G:H5'	2.45	0.46
25:DA:2270:G:H2'	25:DA:2271:G:O4'	2.15	0.46
25:DA:2708:G:H1'	37:DR:71:GLN:HE22	1.79	0.46
35:DP:111:ARG:HG2	35:DP:128:HIS:CD2	2.51	0.46
1:AA:339:C:H2'	1:AA:340:U:C6	2.50	0.46
1:AA:436:C:H2'	1:AA:437:U:C6	2.51	0.46
1:AA:731:G:H5'	1:AA:766:A:H4'	1.98	0.46
1:AA:1343:G:H1'	9:AI:121:ARG:NH1	2.31	0.46
1:AA:1392:G:H21	1:AA:1502:A:H8	1.64	0.46
8:AH:112:LEU:HD11	8:AH:124:ALA:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:153:C:OP2	47:B1:92:LYS:NZ	2.49	0.46
25:BA:1517:G:H5"	25:BA:1518:A:OP1	2.16	0.46
25:BA:2023:A:H2'	25:BA:2024:G:C8	2.51	0.46
25:BA:2156:A:OP1	25:BA:2178:G:N2	2.49	0.46
25:BA:2897:U:H2'	25:BA:2898:C:C6	2.50	0.46
27:BD:77:ALA:O	27:BD:116:GLN:HG3	2.16	0.46
1:CA:841:U:C5	1:CA:848:C:H1'	2.51	0.46
1:CA:1001(A):G:C4	1:CA:1002:G:H1'	2.50	0.46
1:CA:1105:A:H2'	1:CA:1106:G:H8	1.81	0.46
2:CB:189:ASP:OD1	2:CB:189:ASP:N	2.49	0.46
3:CC:157:ILE:HD13	3:CC:166:GLU:HG3	1.97	0.46
14:CN:21:TYR:HE1	14:CN:23:ARG:NE	2.14	0.46
16:CP:22:THR:HA	16:CP:33:ILE:HG13	1.98	0.46
16:CP:53:VAL:O	16:CP:57:ARG:HB2	2.16	0.46
23:CY:63:G:H2'	23:CY:64:A:O4'	2.16	0.46
25:DA:287:C:H2'	25:DA:288:C:C6	2.49	0.46
25:DA:676:A:N1	25:DA:2069:G:O2'	2.45	0.46
25:DA:882:G:N2	25:DA:894:C:N3	2.49	0.46
25:DA:2173:A:H2'	25:DA:2174:C:O4'	2.16	0.46
27:DD:148:GLU:HB2	27:DD:151:LYS:HD2	1.98	0.46
28:DE:115:GLY:O	28:DE:119:ARG:HB2	2.16	0.46
33:DN:96:GLU:H	33:DN:96:GLU:CD	2.23	0.46
1:AA:954:G:H21	1:AA:1227:A:H62	1.63	0.46
1:AA:1070:U:H2'	1:AA:1071:C:C6	2.51	0.46
1:AA:1106:G:H5"	3:AC:172:ARG:HG2	1.98	0.46
1:AA:1149:C:P	9:AI:9:ARG:HH21	2.39	0.46
2:AB:22:LYS:HA	2:AB:40:HIS:HE1	1.81	0.46
3:AC:28:GLN:O	3:AC:32:LEU:HD23	2.16	0.46
11:AK:48:ILE:O	11:AK:50:TYR:N	2.48	0.46
25:BA:139:A:C8	25:BA:1454:C:O2'	2.65	0.46
1:CA:142:G:H2'	1:CA:143:A:C8	2.51	0.46
1:CA:1004:A:C2	1:CA:1038:C:C4	3.04	0.46
1:CA:1063:C:OP2	1:CA:1064:G:O2'	2.29	0.46
1:CA:1236:A:O2'	1:CA:1304:G:H4'	2.16	0.46
5:CE:42:GLY:HA2	5:CE:65:ASN:O	2.16	0.46
5:CE:53:LEU:HD12	5:CE:53:LEU:H	1.80	0.46
7:CG:10:ARG:HA	7:CG:10:ARG:HD2	1.56	0.46
24:CX:13:C:O2'	25:DA:1924:C:H4'	2.16	0.46
25:DA:2136:C:N4	25:DA:2155:G:H1	2.14	0.46
25:DA:2882:A:H5'	37:DR:96:ARG:HG3	1.96	0.46
26:DB:78:A:C2	26:DB:100:A:C4	3.04	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:DD:2:ALA:O	27:DD:3:VAL:HB	2.16	0.46
28:DE:9:VAL:HG13	28:DE:25:VAL:O	2.16	0.46
33:DN:39:ARG:HA	33:DN:40:PRO:HD3	1.79	0.46
38:DS:83:LYS:HE3	38:DS:84:GLN:HG3	1.98	0.46
44:DY:13:VAL:HG12	44:DY:74:PRO:HA	1.98	0.46
1:AA:920:U:H2'	1:AA:921:U:C6	2.50	0.45
25:BA:1324:A:OP1	37:BR:36:THR:HG23	2.17	0.45
25:BA:1513:G:HO2'	25:BA:1593:C:HO2'	1.53	0.45
25:BA:2346:G:H5'	38:BS:9:ARG:HG2	1.98	0.45
28:BE:24:THR:HG22	28:BE:186:GLY:O	2.15	0.45
30:BG:115:ARG:HB3	30:BG:136:ARG:HH12	1.82	0.45
38:BS:52:SER:O	38:BS:56:LEU:HD12	2.16	0.45
1:CA:1302:U:OP2	13:CM:21:TYR:OH	2.13	0.45
23:CY:62:C:H2'	23:CY:63:G:H8	1.80	0.45
25:DA:1278:A:OP1	37:DR:36:THR:HG23	2.16	0.45
25:DA:2657:A:O2'	31:DH:160:LYS:NZ	2.35	0.45
45:DZ:128:VAL:HG22	45:DZ:129:SER:O	2.15	0.45
1:AA:375:U:OP1	16:AP:69:THR:HG21	2.16	0.45
1:AA:1226:C:O2'	13:AM:111:LYS:NZ	2.48	0.45
2:AB:223:ILE:HD12	2:AB:230:VAL:HG12	1.97	0.45
7:AG:79:ARG:CB	7:AG:80:VAL:HA	2.46	0.45
25:BA:704:U:H2'	25:BA:705:C:C6	2.51	0.45
25:BA:1232:G:H5"	41:BV:81:TYR:CE1	2.52	0.45
25:BA:1495:G:H4'	25:BA:1589:A:OP1	2.16	0.45
25:BA:1875:C:H2'	25:BA:1876:G:H8	1.81	0.45
25:BA:2652:G:OP1	33:BN:97:ARG:NH2	2.44	0.45
28:BE:144:ARG:HB3	28:BE:145:LYS:H	1.48	0.45
33:BN:68:GLU:H	33:BN:68:GLU:HG2	1.50	0.45
34:BO:8:LEU:HD13	34:BO:82:ASN:HB3	1.98	0.45
49:B3:5:LYS:NZ	49:B3:55:ARG:HH12	2.14	0.45
1:CA:91:C:H2'	1:CA:92:C:C6	2.51	0.45
1:CA:232:G:H1'	1:CA:262:A:N1	2.31	0.45
1:CA:833:U:H2'	1:CA:834:C:C6	2.51	0.45
1:CA:992:U:H4'	1:CA:993:G:O5'	2.16	0.45
1:CA:1039:C:C4	1:CA:1040:U:C4	3.05	0.45
2:CB:88:ALA:HB1	2:CB:90:MET:HG3	1.98	0.45
2:CB:97:TRP:NE1	2:CB:173:ALA:HB2	2.31	0.45
14:CN:23:ARG:NH1	14:CN:30:ALA:HB2	2.31	0.45
25:DA:918:A:C5	25:DA:919:G:H1'	2.51	0.45
25:DA:2127:G:N1	25:DA:2161:C:C2	2.84	0.45
25:DA:2674:G:H2'	25:DA:2675:A:C8	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2888:C:H2'	25:DA:2889:C:C6	2.51	0.45
26:DB:83:G:N2	26:DB:94:C:O2	2.43	0.45
28:DE:44:TYR:HB2	28:DE:82:ARG:HH12	1.81	0.45
36:DQ:85:LYS:HG2	46:D0:7:LEU:HB3	1.97	0.45
47:D1:67:ILE:N	47:D1:68:PRO:HD2	2.32	0.45
1:AA:520:A:N1	1:AA:536:C:H1'	2.32	0.45
1:AA:731:G:OP1	1:AA:766:A:H1'	2.17	0.45
1:AA:1036:G:H3'	1:AA:1037:C:H6	1.82	0.45
1:AA:1181:G:H1'	1:AA:1182:G:C4	2.51	0.45
2:AB:109:SER:O	2:AB:112:VAL:HG22	2.16	0.45
2:AB:221:LEU:HA	2:AB:221:LEU:HD22	1.69	0.45
10:AJ:62:HIS:HB3	14:AN:59:ALA:HB3	1.97	0.45
13:AM:50:GLU:O	13:AM:54:VAL:HG22	2.15	0.45
25:BA:1717:C:O2	28:BE:129:HIS:NE2	2.42	0.45
25:BA:2013:U:H2'	25:BA:2014:G:H5"	1.99	0.45
30:BG:109:VAL:C	30:BG:112:PRO:HD2	2.41	0.45
1:CA:659:U:H2'	1:CA:660:G:H5'	1.99	0.45
1:CA:1392:G:N2	1:CA:1502:A:H8	2.14	0.45
2:CB:98:LEU:HD23	2:CB:101:MET:HE3	1.99	0.45
8:CH:19:VAL:HG23	8:CH:21:LYS:HG3	1.98	0.45
9:CI:58:HIS:H	9:CI:58:HIS:CD2	2.33	0.45
23:CW:50:U:O2	23:CW:64:A:N1	2.50	0.45
25:DA:265:A:H1'	25:DA:266:G:O4'	2.16	0.45
25:DA:484:C:H2'	25:DA:485:C:C6	2.52	0.45
25:DA:817:C:O2'	25:DA:839:U:H5"	2.16	0.45
25:DA:844:C:C5	25:DA:845:G:C6	3.05	0.45
25:DA:2203:U:O2'	25:DA:2205:C:H5'	2.16	0.45
26:DB:79:C:H2'	26:DB:80:U:O4'	2.17	0.45
29:DF:108:LYS:HB2	29:DF:108:LYS:NZ	2.31	0.45
30:DG:75:LYS:HE3	30:DG:77:ILE:HD11	1.98	0.45
35:DP:65:ARG:HG3	54:D8:25:MET:HG2	1.99	0.45
39:DT:11:GLU:O	39:DT:15:VAL:HG23	2.17	0.45
40:DU:79:PHE:CZ	40:DU:83:LEU:HD21	2.51	0.45
1:AA:152:A:N6	1:AA:169:C:N3	2.65	0.45
1:AA:881:G:P	12:AL:12:ARG:HH22	2.38	0.45
1:AA:1074:G:O2'	1:AA:1101:A:N1	2.44	0.45
4:AD:194:LEU:HA	4:AD:194:LEU:HD13	1.70	0.45
24:AX:13:C:O2'	25:BA:1946:C:H4'	2.17	0.45
24:AX:17:C:H5'	24:AX:61:C:OP1	2.16	0.45
25:BA:180:A:H2'	25:BA:181:C:C6	2.51	0.45
25:BA:2116:G:P	32:BI:22:LYS:HD2	2.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2163:G:C6	25:BA:2164:C:C2	3.04	0.45
25:BA:2832:G:N7	61:BA:5454:HOH:O	2.36	0.45
31:BH:6:ARG:HE	31:BH:6:ARG:HB3	1.25	0.45
35:BP:135:LEU:HD23	35:BP:135:LEU:HA	1.79	0.45
39:BT:6:LEU:O	39:BT:10:VAL:HG23	2.16	0.45
47:B1:89:GLU:H	47:B1:89:GLU:HG2	1.58	0.45
1:CA:187:C:H2'	1:CA:188:C:H6	1.82	0.45
1:CA:728:A:OP1	1:CA:742:G:O2'	2.34	0.45
2:CB:78:GLN:O	2:CB:94:ASN:ND2	2.49	0.45
7:CG:77:SER:HA	7:CG:85:TYR:O	2.16	0.45
12:CL:60:LEU:HD11	12:CL:85:ILE:HD13	1.98	0.45
20:CT:50:GLU:O	20:CT:100:ILE:HD11	2.15	0.45
25:DA:1187:G:H5'	41:DV:81:TYR:CE1	2.51	0.45
25:DA:1721:G:H2'	25:DA:1740:G:O6	2.17	0.45
25:DA:1932:A:H2'	25:DA:1933:G:O4'	2.17	0.45
25:DA:2119:A:N6	25:DA:2170:A:N7	2.64	0.45
25:DA:2139:C:N4	25:DA:2152:G:C6	2.82	0.45
30:DG:72:ARG:NH1	30:DG:87:PRO:HG3	2.31	0.45
30:DG:111:LEU:HD23	30:DG:117:PHE:HE2	1.81	0.45
37:DR:97:VAL:HG22	37:DR:114:VAL:HG22	1.98	0.45
1:AA:110:C:H2'	1:AA:111:G:O4'	2.16	0.45
1:AA:984:C:N4	1:AA:1221:G:H1	2.15	0.45
1:AA:1025:U:O2	1:AA:1036:G:C6	2.69	0.45
1:AA:1275:A:H2'	1:AA:1276:G:H5'	1.99	0.45
1:AA:1352:C:H2'	1:AA:1353:G:C8	2.51	0.45
2:AB:7:VAL:HG21	2:AB:221:LEU:HD21	1.98	0.45
25:BA:1093:G:H2'	25:BA:1156:G:H1	1.82	0.45
25:BA:2102:G:OP1	47:B1:35:THR:HG21	2.17	0.45
44:BY:86:ARG:NH1	44:BY:100:ALA:HB1	2.32	0.45
1:CA:109:A:C6	1:CA:326:G:C6	3.05	0.45
1:CA:154:C:C2'	1:CA:155:C:H5'	2.47	0.45
1:CA:955:U:O2'	19:CS:83:HIS:HD2	2.00	0.45
1:CA:1055:A:C5	1:CA:1206:G:C2	3.05	0.45
57:CA:3202:UAM:OAE	57:CA:3202:UAM:NAD	2.49	0.45
5:CE:13:ILE:O	5:CE:13:ILE:HG13	2.16	0.45
25:DA:111:A:H4'	48:D2:69:ARG:NH1	2.31	0.45
25:DA:774:A:N3	25:DA:774:A:H2'	2.31	0.45
25:DA:800:A:H8	25:DA:800:A:OP1	1.98	0.45
25:DA:1149:G:H2'	25:DA:1150:C:C6	2.51	0.45
25:DA:1561:G:H2'	25:DA:1562:A:C8	2.50	0.45
25:DA:2331:G:O2'	46:D0:43:THR:HG22	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:DE:11:MET:HG2	28:DE:24:THR:HB	1.98	0.45
29:DF:53:THR:HG23	29:DF:55:GLY:N	2.28	0.45
42:DW:86:LEU:HD22	42:DW:96:ILE:HD11	1.99	0.45
1:AA:953:G:H2'	1:AA:954:G:O4'	2.17	0.45
1:AA:1279:A:O2'	1:AA:1281:U:OP2	2.25	0.45
2:AB:178:ARG:NH2	8:AH:74:PRO:HB3	2.32	0.45
8:AH:14:ARG:O	8:AH:18:ARG:HD2	2.16	0.45
14:AN:39:LEU:HD11	14:AN:47:LEU:HD12	1.99	0.45
23:AW:1:G:H2'	23:AW:2:C:C6	2.51	0.45
23:AY:5:G:H1'	23:AY:69:G:N2	2.32	0.45
25:BA:2331:G:N2	38:BS:3:ARG:HE	2.03	0.45
25:BA:2473:C:H2'	25:BA:2474:U:C6	2.52	0.45
54:B8:23:VAL:HG11	54:B8:47:LYS:HD3	1.99	0.45
1:CA:509:A:H5"	4:CD:55:ALA:HB2	1.98	0.45
1:CA:1133:G:H1	1:CA:1141:C:H42	1.65	0.45
1:CA:1162:C:N4	1:CA:1174:G:N1	2.63	0.45
7:CG:15:ASP:OD2	7:CG:44:TYR:OH	2.31	0.45
15:CO:18:PHE:CE2	15:CO:21:ASP:HB2	2.51	0.45
18:CR:33:ASP:CG	18:CR:36:ASN:HB2	2.42	0.45
23:CY:69:G:H2'	23:CY:70:G:O4'	2.16	0.45
25:DA:224:G:H2'	25:DA:225:A:O4'	2.16	0.45
25:DA:887:A:H4'	25:DA:888:C:C5	2.50	0.45
25:DA:1803:A:H4'	27:DD:259:THR:HG23	1.98	0.45
25:DA:2147:G:C2	25:DA:2148:G:H1'	2.52	0.45
41:DV:25:LEU:HA	41:DV:25:LEU:HD23	1.77	0.45
43:DX:50:LYS:O	43:DX:84:ALA:N	2.49	0.45
52:D6:14:THR:OG1	52:D6:48:VAL:HG13	2.17	0.45
1:AA:542:G:H5'	4:AD:41:GLY:HA3	1.98	0.45
4:AD:152:SER:O	4:AD:155:LEU:HB2	2.16	0.45
4:AD:173:TRP:CD2	4:AD:189:PRO:HG3	2.51	0.45
14:AN:29:ARG:HD3	14:AN:40:CYS:SG	2.56	0.45
25:BA:275:C:H2'	25:BA:276:C:C6	2.52	0.45
25:BA:485:U:H5"	53:B7:40:TRP:CD2	2.51	0.45
25:BA:1212:C:H2'	25:BA:1213:U:C6	2.51	0.45
27:BD:92:ILE:HD12	27:BD:104:TYR:CD1	2.52	0.45
35:BP:47:ASP:OD2	35:BP:49:ARG:NH2	2.49	0.45
37:BR:21:TYR:OH	37:BR:43:GLU:HG2	2.16	0.45
38:BS:11:LYS:O	38:BS:15:ARG:HG3	2.16	0.45
38:BS:39:ILE:HB	38:BS:49:VAL:HG13	1.99	0.45
47:B1:21:ARG:HD2	47:B1:35:THR:HB	1.99	0.45
1:CA:836:G:C6	1:CA:851:G:C6	3.04	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1134:G:C2'	1:CA:1135:U:H5'	2.46	0.45
1:CA:1291:G:C6	1:CA:1292:U:C4	3.04	0.45
6:CF:50:TYR:CE2	18:CR:77:GLY:HA2	2.52	0.45
10:CJ:70:ARG:HA	10:CJ:70:ARG:HD3	1.84	0.45
19:CS:27:GLU:HG2	19:CS:47:HIS:NE2	2.32	0.45
19:CS:80:TYR:CZ	19:CS:82:GLY:HA2	2.51	0.45
23:CY:18:G:C2	23:CY:55:PSU:C4	3.05	0.45
25:DA:1810:A:H2'	25:DA:1811:G:O4'	2.17	0.45
25:DA:1999:C:H2'	25:DA:2000:G:O4'	2.17	0.45
29:DF:20:LEU:HD13	29:DF:21:ALA:N	2.32	0.45
25:BA:552:C:C5	25:BA:2792:U:H2'	2.52	0.45
25:BA:2343:G:O2'	46:B0:43:THR:HG22	2.17	0.45
25:BA:2859:U:H4'	25:BA:2878:A:C2	2.52	0.45
27:BD:69:ARG:C	27:BD:71:ASP:H	2.24	0.45
33:BN:10:GLU:OE1	33:BN:11:PRO:HD2	2.16	0.45
39:BT:84:GLN:HG2	39:BT:85:LYS:HG2	1.98	0.45
54:B8:62:LEU:HB3	54:B8:65:GLU:HG2	1.99	0.45
1:CA:408:A:H4'	4:CD:112:VAL:HG21	1.99	0.45
1:CA:1036:G:H2'	1:CA:1037:C:O4'	2.17	0.45
1:CA:1305:G:H5'	21:CU:4:GLY:HA3	1.98	0.45
5:CE:100:VAL:HG22	5:CE:118:ILE:HG22	1.99	0.45
10:CJ:27:ALA:HB1	10:CJ:74:ILE:HD13	1.98	0.45
13:CM:82:MET:HE3	13:CM:92:HIS:HB3	1.98	0.45
23:CW:76:A:H4'	25:DA:2506:U:O2'	2.17	0.45
25:DA:304:G:O6	61:DA:4492:HOH:O	2.19	0.45
25:DA:492:A:H2'	25:DA:493:G:O4'	2.17	0.45
25:DA:2133:G:O2'	25:DA:2157:G:N2	2.50	0.45
27:DD:69:ARG:C	27:DD:71:ASP:H	2.23	0.45
30:DG:11:TYR:OH	30:DG:16:ARG:HD3	2.17	0.45
36:DQ:21:THR:HG21	36:DQ:101:ARG:HD3	1.99	0.45
47:D1:2:SER:HB3	47:D1:46:LEU:HD12	1.99	0.45
1:AA:452:A:H4'	16:AP:72:ARG:NH1	2.32	0.45
1:AA:620:C:C2	4:AD:135:LEU:HG	2.52	0.45
1:AA:735:C:H2'	1:AA:736:C:H6	1.82	0.45
1:AA:946:A:O2'	1:AA:1333:A:N3	2.44	0.45
18:AR:31:LEU:HD23	18:AR:31:LEU:H	1.81	0.45
19:AS:37:ARG:H	19:AS:37:ARG:HG3	1.42	0.45
25:BA:1102:G:H4'	25:BA:1132:A:C8	2.52	0.45
25:BA:2602:A:H2'	25:BA:2603:C:H6	1.82	0.45
1:CA:188:C:O4'	20:CT:89:ARG:NH2	2.50	0.45
1:CA:1151:A:O4'	10:CJ:39:PRO:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:8:ILE:HD13	3:CC:184:TYR:HB3	1.99	0.45
12:CL:32:PHE:HB3	12:CL:84:LEU:HD11	1.99	0.45
17:CQ:43:LEU:HG	17:CQ:68:ARG:HH11	1.80	0.45
20:CT:57:ARG:NH1	20:CT:101:GLY:O	2.50	0.45
25:DA:448:U:H5"	61:DA:4950:HOH:O	2.17	0.45
25:DA:918:A:H5"	26:DB:98:G:O2'	2.17	0.45
25:DA:1140:C:O3'	33:DN:25:ARG:NH1	2.50	0.45
25:DA:2096:U:H2'	25:DA:2097:C:C6	2.52	0.45
25:DA:2483:C:H2'	25:DA:2484:G:O4'	2.17	0.45
25:DA:2543:G:H2'	25:DA:2544:G:C8	2.52	0.45
33:DN:67:LEU:HB3	33:DN:88:GLU:HG3	1.99	0.45
47:D1:89:GLU:O	47:D1:93:GLU:HG2	2.17	0.45
50:D4:15:ILE:HB	50:D4:32:TYR:CD1	2.52	0.45
1:AA:141:A:H1'	1:AA:182:U:O2	2.17	0.45
1:AA:441:A:H5'	1:AA:442:C:OP2	2.17	0.45
1:AA:445:G:H2'	1:AA:446:G:O4'	2.17	0.45
1:AA:741:G:H2'	1:AA:742:G:O4'	2.17	0.45
1:AA:1027:C:O2	1:AA:1027:C:H2'	2.17	0.45
9:AI:23:ASN:ND2	9:AI:23:ASN:H	2.13	0.45
31:BH:149:ARG:NH1	31:BH:167:GLU:OE2	2.48	0.45
1:CA:1004:A:H5"	1:CA:1025:U:C5	2.52	0.45
1:CA:1004:A:H3'	1:CA:1005:A:C5'	2.47	0.45
1:CA:1298:C:H2'	7:CG:114:ARG:HH12	1.82	0.45
1:CA:1469:G:H2'	1:CA:1470:G:C8	2.52	0.45
2:CB:53:ARG:O	2:CB:56:ARG:HB3	2.17	0.45
3:CC:7:PRO:O	3:CC:11:ARG:NH1	2.46	0.45
3:CC:148:GLY:HA3	3:CC:172:ARG:O	2.17	0.45
5:CE:33:VAL:HG13	5:CE:112:LEU:HD12	1.98	0.45
6:CF:82:ARG:HD2	6:CF:82:ARG:HA	1.66	0.45
7:CG:38:LEU:O	7:CG:42:ILE:HG13	2.17	0.45
20:CT:43:LEU:HD12	20:CT:55:ILE:HG13	1.98	0.45
23:CY:59:U:H3'	23:CY:60:U:O2	2.17	0.45
25:DA:90:U:H1'	25:DA:92:A:C8	2.51	0.45
25:DA:443:A:H1'	25:DA:1201:C:O4'	2.17	0.45
25:DA:1226:A:OP1	41:DV:84:LYS:HE2	2.17	0.45
25:DA:1247:A:OP1	29:DF:95:ARG:NH2	2.45	0.45
25:DA:1653:G:H3'	37:DR:2:ARG:HD3	1.98	0.45
25:DA:2035:G:OP1	61:DA:4502:HOH:O	2.20	0.45
25:DA:2064:C:H1'	25:DA:2450:A:C2	2.52	0.45
45:DZ:105:VAL:O	45:DZ:140:ASP:HA	2.17	0.45
49:D3:18:ASP:OD1	49:D3:18:ASP:N	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:10:LEU:HA	2:AB:48:MET:HE1	1.99	0.44
2:AB:15:VAL:HG23	2:AB:209:ARG:HB3	1.99	0.44
4:AD:129:ASN:OD1	4:AD:145:GLU:N	2.38	0.44
13:AM:50:GLU:HA	13:AM:53:VAL:HB	1.99	0.44
25:BA:196:A:H2'	25:BA:197:C:O4'	2.16	0.44
47:B1:3:LYS:HB2	47:B1:61:ARG:NH1	2.31	0.44
1:CA:142:G:H2'	1:CA:143:A:H8	1.82	0.44
1:CA:162:A:H8	1:CA:162:A:O5'	2.00	0.44
1:CA:1080:A:H5"	1:CA:1081:G:OP2	2.17	0.44
2:CB:97:TRP:CZ2	2:CB:173:ALA:HA	2.52	0.44
18:CR:53:ARG:HH21	18:CR:59:SER:HA	1.82	0.44
24:CX:21:A:N6	24:CX:46:G:H2'	2.32	0.44
25:DA:466:A:N1	25:DA:795:C:O2'	2.51	0.44
25:DA:1786:A:H1'	25:DA:1938:A:N6	2.32	0.44
25:DA:1915:U:H2'	25:DA:1916:A:O4'	2.17	0.44
25:DA:1999:C:H4'	25:DA:2723:C:O2	2.17	0.44
27:DD:71:ASP:HB3	27:DD:103:ARG:NH2	2.30	0.44
43:DX:12:VAL:HG22	43:DX:29:TRP:CE2	2.52	0.44
53:D7:9:ARG:CG	53:D7:46:VAL:HG23	2.47	0.44
1:AA:78:G:C2	1:AA:91:C:N4	2.85	0.44
1:AA:255:G:H1'	17:AQ:16:GLN:NE2	2.32	0.44
1:AA:453:A:C5	1:AA:454:C:C4	3.05	0.44
5:AE:31:LEU:HD23	5:AE:31:LEU:HA	1.90	0.44
5:AE:105:VAL:HB	5:AE:106:PRO:HD3	1.99	0.44
23:AW:18:G:H4'	23:AW:60:U:C6	2.52	0.44
25:BA:2186:C:C3'	25:BA:2187:G:H5'	2.47	0.44
25:BA:2699:U:H2'	25:BA:2700:U:O4'	2.15	0.44
32:BI:131:LYS:H	32:BI:138:ILE:H	1.64	0.44
35:BP:82:GLY:HA2	35:BP:113:LYS:O	2.16	0.44
40:BU:86:ALA:HB2	40:BU:116:ALA:HB2	1.99	0.44
1:CA:580:U:H2'	1:CA:581:G:O4'	2.16	0.44
1:CA:651:C:N4	1:CA:753:A:OP2	2.50	0.44
1:CA:987:G:H1	1:CA:1218:C:H42	1.65	0.44
1:CA:1246:C:H2'	1:CA:1247:U:C6	2.53	0.44
20:CT:16:HIS:O	20:CT:19:SER:OG	2.26	0.44
23:CY:19:G:N1	23:CY:56:C:C4	2.85	0.44
25:DA:848:G:C2	25:DA:933:A:H1'	2.51	0.44
25:DA:2167:U:H2'	25:DA:2168:G:N3	2.32	0.44
25:DA:2184:G:C2'	25:DA:2185:C:H5'	2.47	0.44
25:DA:2238:G:H2'	25:DA:2238:G:N3	2.33	0.44
32:DI:29:TYR:O	32:DI:32:PRO:HD2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:DO:4:PRO:O	34:DO:5:GLN:HB2	2.18	0.44
54:D8:58:ILE:HA	54:D8:61:LEU:HD12	1.99	0.44
55:D9:17:ILE:HD12	55:D9:17:ILE:HA	1.78	0.44
1:AA:1112:C:H1'	3:AC:179:ARG:HG2	1.99	0.44
1:AA:1356:G:H2'	1:AA:1357:A:C8	2.53	0.44
3:AC:150:LYS:HG3	3:AC:169:ALA:HB2	1.99	0.44
5:AE:52:PRO:HG2	5:AE:53:LEU:HD12	1.97	0.44
6:AF:100:ASN:HB2	18:AR:28:GLU:HA	1.99	0.44
9:AI:26:VAL:HB	9:AI:33:PHE:HB2	1.98	0.44
20:AT:18:GLN:O	20:AT:22:ARG:HG3	2.16	0.44
25:BA:861:C:O2'	25:BA:862:C:H5'	2.17	0.44
25:BA:2745:G:H3'	25:BA:2746:A:O4'	2.16	0.44
32:BI:12:LEU:HA	32:BI:12:LEU:HD23	1.74	0.44
37:BR:72:ASP:O	37:BR:76:VAL:HG23	2.18	0.44
43:BX:53:LYS:HB3	43:BX:82:GLN:HB3	1.99	0.44
1:CA:371:G:H1'	1:CA:482:A:H1'	2.00	0.44
1:CA:1001(A):G:C5	1:CA:1002:G:H1'	2.52	0.44
1:CA:1262:C:H2'	1:CA:1263:C:C6	2.53	0.44
9:CI:23:ASN:HD22	9:CI:24:GLY:H	1.64	0.44
9:CI:37:PHE:HD1	9:CI:40:LEU:HD12	1.82	0.44
23:CW:61:C:O2'	23:CW:62:C:O4'	2.36	0.44
25:DA:143:G:H2'	25:DA:143(A):C:C6	2.51	0.44
25:DA:271(D):G:H2'	25:DA:271(E):U:C6	2.52	0.44
25:DA:601:C:O2	25:DA:605:C:H4'	2.17	0.44
25:DA:614(B):G:O2'	29:DF:44:ARG:HD2	2.17	0.44
25:DA:652(A):A:C3'	25:DA:652(B):A:H5'	2.47	0.44
25:DA:1006:C:C2	25:DA:1138:G:N2	2.85	0.44
25:DA:1204:A:N6	25:DA:1240:U:H2'	2.32	0.44
25:DA:1336:A:H2'	25:DA:1337:G:C8	2.53	0.44
25:DA:1557:C:OP2	25:DA:1558:A:O2'	2.22	0.44
25:DA:2114:A:O2'	25:DA:2167:U:H1'	2.17	0.44
28:DE:72:VAL:HA	28:DE:73:GLU:CB	2.48	0.44
30:DG:43:LEU:HD12	30:DG:43:LEU:HA	1.80	0.44
33:DN:30:ILE:O	33:DN:34:LEU:HD22	2.17	0.44
36:DQ:16:ARG:HG2	36:DQ:18:LYS:HE2	1.98	0.44
38:DS:94:TYR:CE1	38:DS:99:LYS:HG3	2.53	0.44
45:DZ:54:HIS:ND1	45:DZ:101:PRO:HG3	2.32	0.44
49:D3:3:ARG:HD3	49:D3:60:GLU:CB	2.47	0.44
52:D6:15:GLU:HG3	52:D6:47:THR:CG2	2.48	0.44
52:D6:40:CYS:O	52:D6:44:ARG:N	2.51	0.44
1:AA:93:G:C2'	1:AA:96:U:H5'	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:426:G:OP1	4:AD:38:TYR:OH	2.29	0.44
1:AA:434:U:H2'	1:AA:435:C:C6	2.52	0.44
1:AA:1169:A:H2'	1:AA:1170:A:C8	2.52	0.44
2:AB:184:VAL:HG12	2:AB:197:VAL:HG13	1.99	0.44
11:AK:82:VAL:HB	11:AK:108:ILE:HG12	1.99	0.44
15:AO:56:LEU:O	15:AO:60:VAL:HG23	2.17	0.44
16:AP:14:ASN:OD1	16:AP:42:ARG:NH2	2.50	0.44
19:AS:41:VAL:HG22	50:B4:61:ARG:HH22	1.81	0.44
23:AY:22:G:H5'	23:AY:23:A:OP2	2.17	0.44
25:BA:602:G:H2'	25:BA:603:C:C6	2.52	0.44
25:BA:2408:G:OP1	47:B1:25:LYS:NZ	2.42	0.44
25:BA:2812:A:H1'	25:BA:2904:U:H1'	2.00	0.44
1:CA:1261:A:H3'	1:CA:1262:C:C6	2.52	0.44
2:CB:111:ARG:HD3	2:CB:111:ARG:HA	1.71	0.44
2:CB:185:ILE:HG22	2:CB:199:TYR:HB2	1.99	0.44
5:CE:79:GLU:OE1	5:CE:79:GLU:N	2.38	0.44
5:CE:144:THR:O	5:CE:148:VAL:HG23	2.18	0.44
23:CW:4:C:N3	23:CW:69:G:C2	2.85	0.44
24:CX:19:G:H4'	24:CX:20:U:OP2	2.16	0.44
23:CY:2:C:H2'	23:CY:3:C:C6	2.52	0.44
25:DA:667:U:O2	54:D8:2:PRO:HD2	2.18	0.44
25:DA:743:G:OP1	28:DE:130:GLY:HA2	2.16	0.44
25:DA:1359:A:H2'	25:DA:1360:A:H5'	2.00	0.44
25:DA:1363:C:H2'	25:DA:1364:G:H8	1.81	0.44
25:DA:2024:G:H2'	25:DA:2025:C:H6	1.81	0.44
26:DB:55:U:O3'	30:DG:27:ASN:ND2	2.51	0.44
40:DU:58:ARG:HA	40:DU:61:TRP:CE3	2.53	0.44
42:DW:9:TYR:HA	42:DW:100:THR:CG2	2.47	0.44
1:AA:922:G:C6	1:AA:923:A:C6	3.06	0.44
2:AB:208:ILE:O	2:AB:212:GLN:HB2	2.18	0.44
3:AC:65:ALA:HA	3:AC:100:ALA:HB3	1.99	0.44
4:AD:61:LYS:HE2	4:AD:206:PHE:CE2	2.52	0.44
12:AL:113:ARG:NE	12:AL:115:LYS:O	2.47	0.44
23:AW:23:A:H3'	23:AW:24:G:H8	1.83	0.44
23:AY:19:G:H1	25:BA:2191:A:N6	2.16	0.44
25:BA:696:C:H2'	25:BA:697:C:C6	2.53	0.44
25:BA:1201:A:OP1	40:BU:55:ARG:HD3	2.18	0.44
25:BA:2051:G:H2'	25:BA:2053:A:OP1	2.17	0.44
25:BA:2486:C:H5"	25:BA:2487:C:OP2	2.17	0.44
50:B4:48:ARG:HA	50:B4:48:ARG:HD3	1.73	0.44
52:B6:35:GLU:OE2	52:B6:50:ARG:NH1	2.44	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:B8:54:GLU:O	54:B8:58:ILE:HG13	2.17	0.44
55:B9:17:ILE:HG12	55:B9:26:ILE:HG12	1.99	0.44
1:CA:1022:G:H2'	1:CA:1023:G:C8	2.53	0.44
1:CA:1095:U:OP1	1:CA:1108:G:N2	2.44	0.44
5:CE:76:ILE:O	5:CE:93:PRO:HB3	2.17	0.44
20:CT:77:ALA:O	20:CT:81:LYS:HG3	2.18	0.44
25:DA:2193:G:H2'	25:DA:2194:G:H8	1.83	0.44
27:DD:26:LYS:NZ	27:DD:30:GLU:OE1	2.49	0.44
29:DF:187:VAL:HG12	35:DP:3:LEU:HD22	1.98	0.44
30:DG:38:VAL:HG22	30:DG:93:THR:HG23	2.00	0.44
40:DU:61:TRP:CZ3	40:DU:93:LYS:HB2	2.53	0.44
45:DZ:126:VAL:CG1	45:DZ:161:VAL:HG23	2.47	0.44
1:AA:334:C:O2'	1:AA:1434:A:O2'	2.28	0.44
1:AA:971:G:N1	1:AA:1363(A):A:OP2	2.42	0.44
1:AA:1030(A):G:H2'	1:AA:1030(C):G:OP2	2.17	0.44
1:AA:1145:C:H4'	1:AA:1146:A:H5'	1.99	0.44
3:AC:18:TRP:HE3	3:AC:18:TRP:H	1.64	0.44
13:AM:108:ARG:HA	13:AM:108:ARG:HD3	1.80	0.44
25:BA:273:G:O2'	25:BA:274:U:H5"	2.18	0.44
25:BA:1085:G:H1	25:BA:1162:C:N4	2.16	0.44
25:BA:2136:A:O2'	25:BA:2189:U:H1'	2.18	0.44
25:BA:2285:A:H2'	25:BA:2286:A:C8	2.52	0.44
1:CA:920:U:H2'	1:CA:921:U:H6	1.82	0.44
1:CA:952:U:O4	13:CM:104:ARG:HD3	2.17	0.44
1:CA:1245:A:H61	1:CA:1292:U:H3	1.66	0.44
2:CB:98:LEU:CD2	2:CB:101:MET:HE3	2.48	0.44
2:CB:197:VAL:HB	2:CB:200:ILE:HG23	2.00	0.44
2:CB:213:LEU:O	2:CB:217:ARG:HB2	2.17	0.44
17:CQ:66:SER:O	17:CQ:70:ARG:NH1	2.50	0.44
23:CY:21:A:N6	23:CY:46:7MG:H1'	2.32	0.44
25:DA:214:G:O2'	25:DA:216:A:O2'	2.22	0.44
25:DA:613:G:H2'	25:DA:614:U:O4'	2.16	0.44
25:DA:1022:G:N7	33:DN:66:LYS:HE2	2.32	0.44
25:DA:2150:U:H2'	25:DA:2151:G:C8	2.53	0.44
27:DD:134:ARG:HD3	27:DD:135:PHE:CZ	2.52	0.44
27:DD:182:LEU:HB2	27:DD:272:ALA:HB3	1.99	0.44
29:DF:130:ALA:H	29:DF:142:TRP:CD1	2.36	0.44
44:DY:11:ASP:OD2	44:DY:11:ASP:N	2.50	0.44
45:DZ:126:VAL:HG13	45:DZ:161:VAL:HG23	1.99	0.44
1:AA:308:C:H2'	1:AA:309:G:C8	2.52	0.44
1:AA:418:C:H1'	1:AA:540:G:O2'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:1151:A:O4'	10:AJ:39:PRO:HB2	2.18	0.44
5:AE:51:VAL:O	5:AE:55:VAL:HG23	2.18	0.44
6:AF:6:VAL:HG22	6:AF:90:VAL:HG22	1.98	0.44
14:AN:35:ARG:HE	14:AN:35:ARG:HB3	1.54	0.44
25:BA:213:G:H2'	25:BA:214:A:O4'	2.17	0.44
25:BA:1199:C:H2'	25:BA:1200:G:O4'	2.18	0.44
25:BA:1874:C:H5'	27:BD:253:GLN:NE2	2.32	0.44
25:BA:1898:A:H2'	25:BA:1899:A:H8	1.82	0.44
25:BA:2186:C:C2'	25:BA:2187:G:H5'	2.47	0.44
30:BG:82:LEU:HD21	30:BG:88:ILE:HG21	1.99	0.44
30:BG:108:ASN:HB3	50:B4:22:ILE:HD13	1.99	0.44
34:BO:104:ARG:NH1	39:BT:34:VAL:HG21	2.33	0.44
36:BQ:26:TYR:O	36:BQ:67:ARG:NH1	2.49	0.44
37:BR:2:ARG:O	37:BR:2:ARG:HG2	2.17	0.44
39:BT:23:ARG:HG3	39:BT:120:ARG:NH1	2.33	0.44
45:BZ:156:LYS:HE3	45:BZ:158:PRO:HD3	1.99	0.44
1:CA:583:A:H2'	1:CA:584:G:O4'	2.17	0.44
1:CA:977:A:O2'	1:CA:981:U:N3	2.45	0.44
1:CA:983:A:H2	1:CA:984:C:C6	2.36	0.44
1:CA:986:A:H2'	1:CA:987:G:O4'	2.16	0.44
10:CJ:48:THR:OG1	10:CJ:62:HIS:ND1	2.46	0.44
11:CK:80:VAL:HG13	11:CK:103:LEU:HD12	1.98	0.44
18:CR:45:SER:OG	18:CR:47:THR:HG22	2.18	0.44
18:CR:76:LEU:HD12	18:CR:76:LEU:HA	1.77	0.44
18:CR:84:LYS:H	18:CR:84:LYS:HG2	1.53	0.44
24:CX:23:C:H2'	24:CX:24:U:C6	2.53	0.44
25:DA:348:G:H2'	25:DA:349:G:C8	2.53	0.44
25:DA:686:G:C2	53:D7:11:LYS:HE2	2.52	0.44
25:DA:792:G:N3	25:DA:2072:G:O2'	2.42	0.44
25:DA:820:A:N3	25:DA:943:U:H4'	2.33	0.44
25:DA:975(A):G:C2	25:DA:990:A:C8	3.05	0.44
25:DA:2650:U:H2'	25:DA:2651:C:H6	1.82	0.44
25:DA:2748:A:H2'	25:DA:2749:A:O4'	2.17	0.44
27:DD:274:ARG:O	27:DD:275:LYS:HD3	2.17	0.44
29:DF:53:THR:HG22	29:DF:56:GLU:HG3	2.00	0.44
33:DN:4:TYR:HB2	40:DU:101:ARG:NH1	2.32	0.44
34:DO:26:LYS:O	34:DO:30:ALA:HB2	2.18	0.44
44:DY:43:ASN:CG	44:DY:65:ALA:HB3	2.43	0.44
45:DZ:148:ASP:OD1	45:DZ:148:ASP:N	2.50	0.44
55:D9:12:ASP:OD1	55:D9:12:ASP:N	2.51	0.44
1:AA:620:C:H2'	1:AA:621:A:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:AI:81:ILE:O	9:AI:85:LEU:HG	2.18	0.44
23:AY:55:PSU:N3	23:AY:57:G:H5'	2.33	0.44
25:BA:858:U:H2'	35:BP:21:ARG:HA	2.00	0.44
25:BA:1058:U:C5	33:BN:28:THR:HG21	2.52	0.44
25:BA:1084:C:H42	25:BA:1163:G:H1	1.63	0.44
25:BA:2083:G:H5"	25:BA:2515:A:C2	2.52	0.44
25:BA:2158:C:C4	25:BA:2177:G:N1	2.86	0.44
25:BA:2329:C:H2'	25:BA:2330:G:O4'	2.18	0.44
25:BA:2543:A:H5"	31:BH:157:TYR:CZ	2.53	0.44
25:BA:2721:G:H2'	25:BA:2722:C:C6	2.52	0.44
28:BE:3:GLY:HA3	28:BE:81:ILE:HD12	1.99	0.44
32:BI:126:TYR:HB2	32:BI:142:VAL:HG23	1.99	0.44
33:BN:15:LEU:HD12	33:BN:137:LYS:HG3	1.98	0.44
3:CC:22:TRP:CZ2	14:CN:54:PRO:HG3	2.53	0.44
3:CC:36:ASP:O	3:CC:40:ARG:HG3	2.17	0.44
4:CD:47:ARG:O	4:CD:47:ARG:HD3	2.18	0.44
9:CI:46:ALA:HB2	9:CI:74:ILE:HG23	1.99	0.44
10:CJ:49:VAL:HG21	14:CN:41:ARG:O	2.18	0.44
25:DA:570:G:H2'	25:DA:2030:A:C5	2.53	0.44
25:DA:866:A:N6	25:DA:914:C:C4	2.86	0.44
25:DA:1406:U:H2'	25:DA:1407:C:C6	2.53	0.44
25:DA:2156:G:H8	25:DA:2156:G:O5'	2.01	0.44
25:DA:2357:U:OP1	46:D0:20:ARG:HD3	2.18	0.44
25:DA:2567:G:H2'	25:DA:2568:C:C6	2.52	0.44
25:DA:2745:C:H4'	31:DH:142:GLY:C	2.42	0.44
26:DB:46:A:H2'	26:DB:47:C:C6	2.53	0.44
29:DF:178:PRO:HB3	29:DF:198:ALA:HA	1.99	0.44
30:DG:136:ARG:HD2	30:DG:137:GLU:N	2.33	0.44
35:DP:59:LEU:HD23	54:D8:58:ILE:HD13	1.98	0.44
1:AA:713:G:H2'	1:AA:714:G:C8	2.53	0.44
1:AA:769:G:N7	61:AA:4049:HOH:O	2.37	0.44
1:AA:1066:C:C2'	1:AA:1067:A:H5'	2.47	0.44
1:AA:1070:U:H2'	1:AA:1071:C:H6	1.82	0.44
2:AB:8:LYS:HG2	2:AB:9:GLU:H	1.83	0.44
2:AB:16:HIS:CD2	2:AB:17:PHE:N	2.80	0.44
2:AB:187:LEU:HD13	2:AB:205:ASP:HA	1.99	0.44
8:AH:64:LYS:HG2	8:AH:79:VAL:HG21	1.99	0.44
25:BA:354:A:H2	25:BA:1255:A:C2'	2.31	0.44
25:BA:518:G:H2'	25:BA:519:G:O4'	2.18	0.44
25:BA:672:G:H2'	25:BA:673:G:O4'	2.17	0.44
25:BA:2627:U:H2'	25:BA:2628:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:BF:53:THR:CG2	29:BF:55:GLY:H	2.31	0.44
30:BG:41:GLN:HG3	30:BG:60:LEU:HD22	1.98	0.44
39:BT:128:GLU:O	39:BT:128:GLU:HG2	2.18	0.44
44:BY:14:LEU:HB2	44:BY:75:ILE:HD11	2.00	0.44
1:CA:109:A:H5'	1:CA:110:C:C5	2.53	0.44
1:CA:748:C:H4'	1:CA:749:C:O5'	2.18	0.44
1:CA:1157:A:H4'	1:CA:1158:C:O5'	2.18	0.44
5:CE:78:HIS:HA	8:CH:105:ARG:HG3	2.00	0.44
8:CH:82:HIS:HE2	8:CH:84:ARG:HG2	1.83	0.44
17:CQ:27:PHE:CE2	17:CQ:36:ILE:HD11	2.53	0.44
23:CY:9:A:O2'	23:CY:11:C:N4	2.45	0.44
25:DA:11:G:C2'	25:DA:12:U:H5'	2.47	0.44
25:DA:191:A:H2'	25:DA:192:C:C6	2.52	0.44
25:DA:1420:U:HO2'	25:DA:1421:G:P	2.40	0.44
25:DA:1510:G:H2'	25:DA:1511:C:O4'	2.18	0.44
25:DA:1593:G:H2'	25:DA:1594:G:C8	2.53	0.44
25:DA:1803:A:HO2'	27:DD:259:THR:HG21	1.83	0.44
25:DA:1835:G:H5'	25:DA:1836:C:OP2	2.17	0.44
25:DA:2263:C:H2'	25:DA:2264:C:O4'	2.18	0.44
25:DA:2750:A:H8	25:DA:2750:A:OP1	2.01	0.44
27:DD:77:ALA:O	27:DD:116:GLN:HG3	2.17	0.44
29:DF:9:ILE:HD13	29:DF:123:LEU:HD23	1.98	0.44
35:DP:65:ARG:HG3	54:D8:25:MET:CG	2.48	0.44
45:DZ:133:ILE:HG22	45:DZ:134:PRO:O	2.18	0.44
52:D6:11:LEU:HB2	52:D6:21:TYR:HB2	1.99	0.44
1:AA:129(A):G:C6	1:AA:189(E):U:H4'	2.52	0.43
1:AA:501:C:H2'	1:AA:502:G:H8	1.81	0.43
1:AA:524:G:H2'	1:AA:525:C:C6	2.52	0.43
6:AF:99:ALA:HB1	18:AR:23:LYS:HZ3	1.83	0.43
7:AG:29:LYS:HA	7:AG:29:LYS:HD2	1.72	0.43
7:AG:97:GLN:HE21	7:AG:97:GLN:HB2	1.62	0.43
9:AI:4:TYR:CE2	9:AI:88:TYR:HA	2.53	0.43
20:AT:48:LYS:HA	20:AT:48:LYS:HD3	1.71	0.43
21:AU:5:ASP:O	21:AU:11:GLY:HA3	2.18	0.43
25:BA:831:A:H5'	25:BA:832:G:OP1	2.18	0.43
25:BA:2310:A:H2'	25:BA:2311:G:O4'	2.18	0.43
30:BG:129:GLY:O	30:BG:161:THR:OG1	2.36	0.43
35:BP:3:LEU:HD12	35:BP:3:LEU:HA	1.90	0.43
48:B2:65:ASN:OD1	48:B2:69:ARG:NH1	2.44	0.43
1:CA:833:U:H2'	1:CA:834:C:H6	1.82	0.43
1:CA:1117:G:N2	1:CA:1180:A:H1'	2.31	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:1236:A:H2'	1:CA:1237:C:C6	2.53	0.43
2:CB:55:PHE:CE1	2:CB:218:ALA:HA	2.53	0.43
3:CC:175:LEU:HD21	3:CC:201:TYR:CE1	2.53	0.43
4:CD:155:LEU:O	4:CD:159:ARG:HG3	2.17	0.43
9:CI:11:LYS:HA	9:CI:108:VAL:HG13	1.99	0.43
16:CP:40:ASP:O	16:CP:48:TRP:HB2	2.18	0.43
25:DA:303:U:H2'	25:DA:304:G:H8	1.83	0.43
25:DA:1313:U:OP1	61:DA:4345:HOH:O	2.21	0.43
25:DA:1651:G:H5'	37:DR:39:PRO:HG2	2.00	0.43
25:DA:2119:A:N6	25:DA:2171:A:C6	2.86	0.43
30:DG:129:GLY:O	30:DG:161:THR:HB	2.18	0.43
32:DI:54:GLN:HA	32:DI:57:ARG:HE	1.82	0.43
32:DI:57:ARG:O	32:DI:61:ARG:HB2	2.17	0.43
32:DI:131:LYS:HA	32:DI:137:PRO:HA	1.99	0.43
44:DY:1:MET:HB3	44:DY:1:MET:HE2	1.61	0.43
1:AA:6:G:H4'	1:AA:298:A:H4'	1.99	0.43
1:AA:165:C:H2'	1:AA:166:G:H8	1.81	0.43
1:AA:736:C:H2'	1:AA:737:A:C8	2.53	0.43
1:AA:1190:G:O2'	1:AA:1191:A:OP2	2.34	0.43
8:AH:25:ASP:OD1	8:AH:60:ARG:HG3	2.18	0.43
9:AI:21:PRO:HA	9:AI:59:PHE:HA	1.99	0.43
13:AM:67:GLU:OE2	13:AM:71:ARG:NH2	2.51	0.43
25:BA:492:A:N3	25:BA:730:C:H1'	2.33	0.43
25:BA:790:G:OP1	28:BE:130:GLY:HA2	2.18	0.43
26:BB:66:A:H61	26:BB:108:U:H2'	1.82	0.43
27:BD:142:VAL:CG1	27:BD:191:ALA:HB1	2.48	0.43
34:BO:104:ARG:HE	39:BT:36:GLU:HG3	1.82	0.43
1:CA:1424:C:H2'	1:CA:1425:U:O4'	2.18	0.43
3:CC:131:ARG:HH11	5:CE:50:GLU:HG3	1.83	0.43
8:CH:25:ASP:OD1	8:CH:25:ASP:N	2.50	0.43
9:CI:102:LEU:HD13	9:CI:103:THR:N	2.28	0.43
10:CJ:16:LEU:HD12	10:CJ:70:ARG:HG2	1.99	0.43
13:CM:96:LEU:O	13:CM:110:ARG:NH1	2.50	0.43
18:CR:58:LEU:HD12	18:CR:62:GLU:HB2	2.00	0.43
25:DA:307:G:H21	25:DA:330:A:H62	1.65	0.43
25:DA:359:A:H2'	25:DA:360:G:O4'	2.18	0.43
25:DA:376:C:H2'	25:DA:377:C:C6	2.53	0.43
25:DA:1291:C:H2'	25:DA:1292:U:C6	2.53	0.43
25:DA:1477:A:H2'	25:DA:1478:G:O4'	2.18	0.43
25:DA:1958:C:OP2	61:DA:4710:HOH:O	2.20	0.43
25:DA:2129:C:C2	25:DA:2160:G:N1	2.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2354:G:H21	46:D0:36:ILE:HD11	1.82	0.43
31:DH:9:ILE:HG12	31:DH:69:ARG:HD2	2.00	0.43
31:DH:121:ILE:HD11	31:DH:140:LYS:HG2	2.01	0.43
35:DP:83:VAL:HG12	35:DP:112:LEU:HD21	1.99	0.43
52:D6:19:ARG:N	52:D6:19:ARG:HD2	2.33	0.43
1:AA:189(F):U:C4	17:AQ:72:ARG:NH1	2.87	0.43
1:AA:659:U:H2'	1:AA:660:G:H5'	2.01	0.43
1:AA:1236:A:H2'	1:AA:1237:C:C6	2.53	0.43
1:AA:1327:C:O2'	1:AA:1328:C:H5'	2.18	0.43
6:AF:68:PRO:HG2	6:AF:71:ARG:NH1	2.34	0.43
13:AM:84:ILE:HD12	19:AS:74:PHE:CZ	2.53	0.43
14:AN:6:LEU:HD12	14:AN:6:LEU:HA	1.84	0.43
25:BA:1068:G:N7	33:BN:66:LYS:HE2	2.34	0.43
26:BB:8:U:O3'	38:BS:25:ARG:NH2	2.51	0.43
40:BU:74:LEU:H	40:BU:74:LEU:HD12	1.83	0.43
41:BV:50:PRO:HG2	41:BV:51:VAL:HG12	2.00	0.43
54:B8:6:THR:HG22	54:B8:64:TYR:HD1	1.84	0.43
1:CA:340:U:H2'	1:CA:341:C:C6	2.53	0.43
1:CA:689:C:P	11:CK:46:GLY:HA3	2.59	0.43
1:CA:1134:G:H2'	1:CA:1134:G:N3	2.34	0.43
1:CA:1441:G:H8	1:CA:1441:G:O5'	2.02	0.43
4:CD:11:LEU:O	4:CD:15:GLU:HG2	2.18	0.43
5:CE:10:MET:HE2	5:CE:55:VAL:HG11	2.00	0.43
9:CI:50:LEU:H	9:CI:50:LEU:HG	1.46	0.43
20:CT:50:GLU:HB2	20:CT:99:LEU:CD2	2.47	0.43
25:DA:866:A:C2	25:DA:867:C:C5	3.06	0.43
25:DA:1268:A:C2	25:DA:2013:A:C4	3.06	0.43
25:DA:2207:G:H3'	25:DA:2208:A:H5"	2.00	0.43
25:DA:2802:G:H2'	25:DA:2803:C:O4'	2.19	0.43
34:DO:64:ARG:HB2	34:DO:83:ALA:HB3	1.99	0.43
37:DR:103:ARG:HD3	37:DR:108:GLY:O	2.17	0.43
45:DZ:163:LEU:HD12	45:DZ:163:LEU:HA	1.86	0.43
1:AA:1442:G:O2'	1:AA:1442(A):G:OP1	2.28	0.43
4:AD:178:VAL:O	4:AD:179:GLU:HB2	2.17	0.43
8:AH:10:LEU:HD12	8:AH:85:ARG:HG2	1.99	0.43
9:AI:118:LYS:HB2	9:AI:121:ARG:HB3	2.01	0.43
25:BA:60:G:H5'	48:B2:50:ILE:HG21	2.01	0.43
25:BA:906:G:O2'	25:BA:962:G:O6	2.31	0.43
25:BA:1091:A:O2'	25:BA:1093:G:C4	2.71	0.43
25:BA:1255:A:H5"	25:BA:1257:G:O4'	2.18	0.43
25:BA:2504:U:H2'	25:BA:2505:U:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2588:G:H1'	61:BA:4594:HOH:O	2.16	0.43
36:BQ:39:PRO:HA	36:BQ:97:VAL:O	2.18	0.43
40:BU:76:TYR:OH	40:BU:92:ARG:HD3	2.18	0.43
1:CA:179:A:H2'	1:CA:180:U:C6	2.54	0.43
1:CA:1159:U:H5"	1:CA:1182:G:H21	1.83	0.43
1:CA:1316:G:N1	1:CA:1319:A:OP2	2.49	0.43
2:CB:101:MET:HA	2:CB:108:ILE:HG12	2.00	0.43
8:CH:33:GLU:HG2	8:CH:48:TYR:CE2	2.53	0.43
10:CJ:10:GLY:HA3	10:CJ:16:LEU:HD21	2.01	0.43
19:CS:36:ARG:HD2	19:CS:52:TYR:O	2.19	0.43
25:DA:348:G:H2'	25:DA:349:G:H8	1.82	0.43
25:DA:1599:C:OP1	61:DA:5027:HOH:O	2.20	0.43
25:DA:2018:G:H2'	25:DA:2019:A:O4'	2.19	0.43
25:DA:2136:C:O2'	25:DA:2137:C:O5'	2.36	0.43
25:DA:2831:G:OP1	25:DA:2834:G:H4'	2.19	0.43
30:DG:124:SER:O	30:DG:124:SER:OG	2.32	0.43
31:DH:148:ILE:O	31:DH:162:ILE:HD13	2.18	0.43
44:DY:5:MET:HE2	44:DY:5:MET:HB2	1.73	0.43
44:DY:21:LYS:HB3	44:DY:21:LYS:NZ	2.33	0.43
45:DZ:8:TYR:HB2	45:DZ:38:TYR:CE2	2.54	0.43
52:D6:15:GLU:HG3	52:D6:47:THR:HG23	1.99	0.43
1:AA:118:U:O4	61:AA:4255:HOH:O	2.21	0.43
1:AA:429:U:H4'	1:AA:430:A:O5'	2.18	0.43
1:AA:811:C:O2'	1:AA:901:A:N1	2.49	0.43
1:AA:1239:A:C4	1:AA:1298:C:N4	2.87	0.43
3:AC:152:ILE:HG23	3:AC:167:TRP:HB3	2.00	0.43
4:AD:162:LEU:HD13	4:AD:181:MET:HG2	2.00	0.43
8:AH:86:ILE:HG21	8:AH:133:LEU:HD13	2.00	0.43
9:AI:32:ASP:OD1	9:AI:33:PHE:N	2.51	0.43
10:AJ:40:LEU:HB2	10:AJ:69:ASN:HB3	2.01	0.43
13:AM:88:ARG:HG3	13:AM:98:VAL:CG1	2.49	0.43
61:BA:4094:HOH:O	29:BF:74:ARG:HG2	2.18	0.43
41:BV:52:VAL:HG22	41:BV:55:ALA:HB3	2.01	0.43
44:BY:8:LYS:HD3	44:BY:97:ARG:NH1	2.34	0.43
1:CA:187:C:H2'	1:CA:188:C:C6	2.53	0.43
1:CA:523:A:H61	12:CL:92:ASP:HB2	1.83	0.43
1:CA:769:G:H4'	1:CA:1513:A:H4'	2.01	0.43
1:CA:1133:G:C4	1:CA:1134:G:C8	3.07	0.43
1:CA:1368:G:OP1	9:CI:111:ARG:NH2	2.35	0.43
2:CB:12:GLU:HA	2:CB:15:VAL:HG23	2.01	0.43
2:CB:19:HIS:CG	2:CB:20:GLU:H	2.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:105:PHE:CE1	2:CB:155:LEU:HD12	2.53	0.43
12:CL:24:VAL:HB	12:CL:27:LEU:HD22	1.98	0.43
16:CP:57:ARG:HH21	16:CP:79:VAL:HA	1.83	0.43
19:CS:12:ASP:OD1	19:CS:37:ARG:NH1	2.51	0.43
23:CW:39:PSU:H2'	23:CW:40:C:C6	2.53	0.43
23:CW:40:C:H2'	23:CW:41:C:H6	1.82	0.43
25:DA:263:C:H2'	25:DA:264:C:O4'	2.19	0.43
25:DA:530:G:O4'	25:DA:530:G:N3	2.50	0.43
25:DA:2061:G:H5"	25:DA:2503:A:C2	2.53	0.43
25:DA:2612:C:OP2	51:D5:2:ALA:N	2.51	0.43
25:DA:2735:G:H2'	25:DA:2736:G:H8	1.83	0.43
25:DA:2896:C:H2'	25:DA:2897:U:C6	2.53	0.43
26:DB:80:U:H2'	26:DB:81:G:C8	2.53	0.43
30:DG:47:LYS:HD2	30:DG:81:LYS:O	2.19	0.43
31:DH:27:LYS:HE3	31:DH:27:LYS:HB3	1.62	0.43
1:AA:523:A:H61	12:AL:92:ASP:HB2	1.84	0.43
1:AA:839:U:H4'	1:AA:840:C:OP2	2.19	0.43
1:AA:1226:C:H4'	19:AS:80:TYR:OH	2.19	0.43
2:AB:45:GLN:O	2:AB:49:GLU:HB2	2.19	0.43
25:BA:927:G:H2'	25:BA:928:G:H8	1.84	0.43
25:BA:2005:C:H4'	25:BA:2618:C:O3'	2.18	0.43
25:BA:2205:C:H2'	25:BA:2206:G:C8	2.50	0.43
27:BD:180:GLY:HA3	27:BD:275:LYS:HG3	2.01	0.43
36:BQ:17:LEU:HD23	36:BQ:17:LEU:HA	1.85	0.43
45:BZ:149:SER:OG	45:BZ:150:LEU:N	2.52	0.43
1:CA:299:G:H2'	1:CA:300:A:C8	2.53	0.43
1:CA:643:C:H2'	1:CA:644:G:H8	1.84	0.43
1:CA:742:G:H5'	15:CO:58:MET:HE1	1.99	0.43
1:CA:1119:C:N4	1:CA:1154:G:H1	2.13	0.43
1:CA:1144:G:N2	1:CA:1146:A:H62	2.16	0.43
2:CB:13:ALA:C	2:CB:15:VAL:H	2.25	0.43
4:CD:180:GLY:O	4:CD:182:LYS:HD3	2.18	0.43
4:CD:196:LEU:H	4:CD:196:LEU:HD12	1.83	0.43
8:CH:6:ILE:O	8:CH:10:LEU:HG	2.18	0.43
23:CY:19:G:N2	23:CY:56:C:C2	2.83	0.43
25:DA:446:G:OP1	40:DU:3:ARG:NH1	2.52	0.43
25:DA:902:C:H2'	25:DA:903:C:C6	2.51	0.43
25:DA:1021:A:H3'	25:DA:1021:A:C8	2.53	0.43
25:DA:2792:G:H2'	25:DA:2792:G:N3	2.34	0.43
34:DO:98:VAL:HG22	34:DO:118:ALA:HA	2.00	0.43
45:DZ:73:GLN:O	45:DZ:87:ASP:N	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:410:G:O6	61:AA:4018:HOH:O	2.21	0.43
3:AC:52:LEU:HD21	3:AC:55:VAL:HG23	2.00	0.43
3:AC:181:ASN:HD21	3:AC:204:LEU:HD12	1.83	0.43
14:AN:26:ARG:HD3	14:AN:43:CYS:SG	2.58	0.43
17:AQ:62:SER:OG	17:AQ:72:ARG:HD2	2.18	0.43
23:AY:55:PSU:C2	23:AY:57:G:H5'	2.53	0.43
25:BA:2142:G:O2'	25:BA:2143:G:H5'	2.19	0.43
25:BA:2376:C:H2'	25:BA:2377:G:O4'	2.19	0.43
25:BA:2840:G:O2'	25:BA:2893:A:N1	2.47	0.43
32:BI:26:ALA:HA	32:BI:30:LEU:HB2	2.01	0.43
32:BI:127:VAL:HA	32:BI:140:LEU:O	2.17	0.43
34:BO:122:LEU:HD13	39:BT:72:VAL:HG11	1.99	0.43
42:BW:68:ARG:NH1	42:BW:112:GLY:H	2.17	0.43
45:BZ:152:ALA:O	45:BZ:155:LEU:HB2	2.17	0.43
50:B4:59:PHE:CD1	50:B4:59:PHE:N	2.86	0.43
1:CA:1020:U:C2	1:CA:1021:G:C8	3.07	0.43
1:CA:1066:C:C2'	1:CA:1067:A:H5'	2.49	0.43
2:CB:17:PHE:HA	2:CB:44:LEU:HD11	1.99	0.43
4:CD:3:ARG:O	4:CD:5:ILE:HG22	2.18	0.43
5:CE:33:VAL:HG21	5:CE:109:ILE:HA	2.00	0.43
7:CG:20:ASP:OD1	7:CG:22:LEU:HB3	2.19	0.43
15:CO:62:GLN:O	15:CO:66:LEU:HD13	2.19	0.43
16:CP:74:LEU:O	16:CP:79:VAL:HG23	2.19	0.43
25:DA:828:U:H4'	25:DA:831:G:N1	2.33	0.43
25:DA:880:G:N2	25:DA:898:C:O2	2.52	0.43
25:DA:2128:C:N4	25:DA:2161:C:N3	2.67	0.43
25:DA:2376:A:H2'	25:DA:2377:A:O4'	2.18	0.43
25:DA:2526:G:H5'	25:DA:2742:C:O2'	2.19	0.43
25:DA:2659:G:N2	25:DA:2662:A:OP2	2.51	0.43
25:DA:2671:A:H2'	25:DA:2672:G:O4'	2.19	0.43
25:DA:2773:C:H2'	25:DA:2774:C:H6	1.83	0.43
28:DE:144:ARG:HB3	28:DE:145:LYS:H	1.45	0.43
29:DF:126:VAL:HG21	29:DF:129:PHE:CZ	2.53	0.43
38:DS:62:LYS:O	38:DS:66:ALA:N	2.44	0.43
40:DU:49:HIS:O	40:DU:53:ARG:N	2.51	0.43
1:AA:91:C:H4'	1:AA:91:C:OP1	2.18	0.43
1:AA:438:G:H4'	4:AD:123:HIS:CE1	2.54	0.43
1:AA:551:U:H2'	1:AA:552:U:C6	2.53	0.43
1:AA:743:U:H2'	1:AA:744:C:C6	2.53	0.43
2:AB:189:ASP:OD1	2:AB:189:ASP:N	2.47	0.43
3:AC:53:ALA:HB2	3:AC:115:LEU:HD13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:66:VAL:HG12	7:AG:70:LYS:HE3	2.01	0.43
14:AN:14:PRO:HG3	14:AN:20:ALA:HB2	2.01	0.43
15:AO:61:GLY:O	15:AO:65:ARG:HG3	2.19	0.43
17:AQ:50:LYS:HG3	17:AQ:51:TYR:N	2.33	0.43
19:AS:15:LEU:O	19:AS:19:VAL:HG23	2.19	0.43
25:BA:504:A:N1	25:BA:525:G:H4'	2.34	0.43
25:BA:605:G:H2'	25:BA:606:G:C8	2.54	0.43
25:BA:1809:U:H2'	25:BA:1815:A:N6	2.34	0.43
28:BE:108:SER:O	28:BE:162:ALA:HA	2.19	0.43
31:BH:154:PRO:HB3	31:BH:163:TYR:CE2	2.53	0.43
37:BR:97:VAL:HG22	37:BR:114:VAL:HG13	2.01	0.43
47:B1:86:SER:OG	47:B1:89:GLU:HG2	2.19	0.43
1:CA:376:G:H4'	16:CP:5:ARG:HD3	2.01	0.43
1:CA:539:A:H2'	1:CA:540:G:C8	2.53	0.43
1:CA:1064:G:H4'	1:CA:1065:U:O5'	2.19	0.43
1:CA:1095:U:H2'	1:CA:1096:C:C6	2.54	0.43
1:CA:1162:C:C2	1:CA:1174:G:N2	2.86	0.43
1:CA:1375:A:H4'	7:CG:29:LYS:HD3	1.99	0.43
2:CB:80:ILE:HD11	2:CB:212:GLN:CA	2.48	0.43
25:DA:322:A:H5'	25:DA:340:A:H1'	2.00	0.43
25:DA:484:C:H2'	25:DA:485:C:H6	1.84	0.43
25:DA:2141:G:C6	25:DA:2150:U:O2	2.71	0.43
25:DA:2793:G:N2	25:DA:2804:C:H1'	2.34	0.43
26:DB:39:A:O2'	26:DB:40:U:H5'	2.19	0.43
28:DE:178:GLU:OE2	28:DE:178:GLU:N	2.29	0.43
32:DI:12:LEU:HD23	32:DI:12:LEU:HA	1.82	0.43
33:DN:71:ILE:HG21	33:DN:84:LYS:HB3	2.01	0.43
43:DX:8:ILE:O	48:D2:36:ARG:NH2	2.52	0.43
45:DZ:33:LEU:HD21	45:DZ:90:VAL:HG21	2.01	0.43
1:AA:7:G:H5'	1:AA:298:A:O4'	2.19	0.43
1:AA:300:A:H2'	1:AA:301:G:O4'	2.19	0.43
1:AA:936:C:H2'	1:AA:937:A:O4'	2.19	0.43
1:AA:1104:G:H4'	2:AB:111:ARG:NH1	2.34	0.43
1:AA:1183:A:H3'	1:AA:1184:G:C5'	2.45	0.43
1:AA:1458:G:OP1	20:AT:35:THR:OG1	2.30	0.43
25:BA:640:A:C4	29:BF:180:GLY:HA2	2.54	0.43
25:BA:1793:A:H2'	61:BA:5307:HOH:O	2.18	0.43
25:BA:1825:U:H2'	25:BA:1826:C:C6	2.53	0.43
25:BA:2524:C:H2'	25:BA:2525:G:O4'	2.19	0.43
25:BA:2901:A:C6	25:BA:2902:G:C6	3.07	0.43
36:BQ:75:THR:HG22	61:BQ:3105:HOH:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BR:104:ARG:HG3	37:BR:111:LEU:HD21	2.00	0.43
1:CA:7:G:O2'	5:CE:120:THR:O	2.36	0.43
1:CA:619:U:N3	4:CD:134:ASP:OD1	2.46	0.43
1:CA:620:C:H2'	1:CA:621:A:O4'	2.19	0.43
1:CA:1132:C:N3	1:CA:1142:G:N2	2.61	0.43
2:CB:185:ILE:HG22	2:CB:199:TYR:CD2	2.51	0.43
22:CV:14:A:C6	23:CY:34:G:C5	3.06	0.43
23:CW:67:C:H2'	23:CW:68:C:C6	2.54	0.43
25:DA:118:A:N3	25:DA:178:G:H1'	2.34	0.43
25:DA:244:A:C2	25:DA:255:A:C4	3.07	0.43
25:DA:1805:U:O2	27:DD:50:THR:HB	2.19	0.43
25:DA:2741:A:H2'	25:DA:2742:C:O4'	2.19	0.43
25:DA:2811:G:N2	25:DA:2891:G:H1'	2.34	0.43
28:DE:7:VAL:HG12	28:DE:27:LEU:HB3	2.00	0.43
1:AA:69:G:H2'	1:AA:70:G:C8	2.54	0.43
1:AA:146:G:C2	1:AA:147:G:C4	3.06	0.43
1:AA:392:G:H2'	1:AA:393:A:H8	1.83	0.43
1:AA:735:C:H2'	1:AA:736:C:C6	2.54	0.43
1:AA:1004:A:C5	1:AA:1037:C:N3	2.87	0.43
4:AD:50:ARG:HA	4:AD:51:PRO:HD3	1.82	0.43
24:AX:23:C:H2'	24:AX:24:U:C6	2.54	0.43
25:BA:1537:G:O2'	27:BD:101:GLU:HB2	2.19	0.43
25:BA:1781:G:N3	25:BA:2870:A:H2	2.17	0.43
25:BA:2053:A:C6	25:BA:2510:C:H1'	2.54	0.43
25:BA:2156:A:H8	25:BA:2156:A:OP2	2.02	0.43
42:BW:13:SER:HA	42:BW:14:PRO:HD3	1.88	0.43
1:CA:545:C:OP2	4:CD:65:ARG:NH2	2.52	0.43
1:CA:701:C:OP1	1:CA:702:A:O2'	2.21	0.43
1:CA:1084:G:H5'	1:CA:1102:A:OP2	2.19	0.43
1:CA:1516:G:H2'	1:CA:1518:A:OP2	2.19	0.43
5:CE:13:ILE:HA	5:CE:29:GLY:O	2.19	0.43
5:CE:113:ALA:HB3	5:CE:115:VAL:HG23	2.01	0.43
7:CG:100:ALA:O	7:CG:104:LEU:HB2	2.18	0.43
8:CH:64:LYS:HB3	8:CH:79:VAL:HG21	2.01	0.43
17:CQ:45:HIS:CD2	17:CQ:47:PRO:HD3	2.54	0.43
25:DA:286:C:H2'	25:DA:287:C:C6	2.54	0.43
25:DA:686:G:N2	25:DA:788:A:H61	2.17	0.43
25:DA:1374:G:H2'	25:DA:1375:C:C6	2.54	0.43
25:DA:2051:A:H5'	25:DA:2578:G:O4'	2.19	0.43
34:DO:87:ILE:HD12	34:DO:91:LEU:HA	2.01	0.43
42:DW:88:ARG:NH1	42:DW:94:ASP:OD2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:271:C:H2'	1:AA:272:C:C6	2.54	0.42
1:AA:948:C:OP1	13:AM:109:THR:OG1	2.34	0.42
1:AA:1030(A):G:O2'	1:AA:1031:G:C2	2.72	0.42
2:AB:103:THR:HA	2:AB:180:LEU:HD11	2.01	0.42
6:AF:39:LYS:HE2	6:AF:39:LYS:HB3	1.83	0.42
15:AO:5:LYS:O	15:AO:9:GLN:HG2	2.20	0.42
25:BA:705:C:H2'	25:BA:706:C:C6	2.54	0.42
25:BA:1000:C:OP1	36:BQ:87:LYS:HE2	2.19	0.42
25:BA:1022:C:H5'	25:BA:1202:A:N6	2.34	0.42
25:BA:1070:G:C6	25:BA:1071:G:C6	3.07	0.42
25:BA:1631:C:O2'	25:BA:1632:A:H5'	2.19	0.42
25:BA:2122:G:O2'	25:BA:2123:G:H5'	2.19	0.42
25:BA:2138:G:H2'	25:BA:2139:A:C5	2.54	0.42
1:CA:78:G:C2'	1:CA:79:G:H5'	2.49	0.42
1:CA:194:C:H2'	1:CA:195:A:H5"	2.00	0.42
1:CA:524:G:H2'	1:CA:525:C:C6	2.53	0.42
1:CA:1220:G:N2	19:CS:54:GLY:O	2.50	0.42
9:CI:4:TYR:CE2	9:CI:88:TYR:HA	2.54	0.42
13:CM:108:ARG:HD3	13:CM:108:ARG:HA	1.74	0.42
18:CR:53:ARG:HA	18:CR:56:THR:OG1	2.19	0.42
23:CW:6:G:O6	23:CW:67:C:N3	2.52	0.42
25:DA:27:G:C2	25:DA:512:G:N3	2.87	0.42
25:DA:81:G:HO2'	25:DA:295:G:HO2'	1.63	0.42
25:DA:271(E):U:H2'	25:DA:271(F):C:C6	2.54	0.42
25:DA:478:A:N1	25:DA:500:G:H4'	2.34	0.42
25:DA:858:U:O2	25:DA:2268:A:H2'	2.19	0.42
25:DA:1668:A:C8	25:DA:1674:G:C6	3.07	0.42
25:DA:1777:U:O2'	25:DA:1778:U:H5'	2.19	0.42
25:DA:2142:C:H2'	25:DA:2143:C:C6	2.54	0.42
25:DA:2277:G:OP2	46:D0:10:THR:HG21	2.19	0.42
25:DA:2474:C:H5"	25:DA:2475:C:OP2	2.19	0.42
25:DA:2611:U:H5'	25:DA:2611:U:H6	1.84	0.42
35:DP:63:PRO:O	54:D8:13:ARG:HG2	2.19	0.42
37:DR:97:VAL:HG22	37:DR:114:VAL:HG13	2.00	0.42
1:AA:437:U:O2'	4:AD:123:HIS:CD2	2.72	0.42
1:AA:935:A:C2	1:AA:936:C:C2	3.07	0.42
1:AA:1064:G:H1'	1:AA:1190:G:H21	1.83	0.42
1:AA:1346:A:OP1	9:AI:120:ARG:NH1	2.40	0.42
10:AJ:38:ILE:H	10:AJ:38:ILE:HG13	1.74	0.42
25:BA:593:G:C6	25:BA:2052:A:C2	3.07	0.42
25:BA:1945:U:H2'	25:BA:1946:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2150:C:H42	25:BA:2182:G:H1	1.66	0.42
25:BA:2707:C:H2'	25:BA:2708:U:C6	2.54	0.42
27:BD:147:LEU:HD22	27:BD:155:LEU:HD11	1.99	0.42
32:BI:47:LEU:O	32:BI:50:ARG:HG2	2.18	0.42
35:BP:79:ARG:NH2	35:BP:109:GLY:O	2.52	0.42
41:BV:89:GLN:HA	41:BV:90:PRO:HD3	1.93	0.42
1:CA:255:G:C6	1:CA:256:U:C4	3.08	0.42
1:CA:662:G:O2'	1:CA:836:G:OP1	2.33	0.42
1:CA:1023:G:H3'	1:CA:1024:G:H8	1.84	0.42
1:CA:1228:C:H2'	1:CA:1229:A:H8	1.83	0.42
2:CB:16:HIS:HB3	2:CB:210:SER:HB2	2.01	0.42
8:CH:13:ILE:O	8:CH:17:THR:HG23	2.19	0.42
9:CI:7:THR:HB	9:CI:83:ARG:NH1	2.34	0.42
14:CN:6:LEU:HB3	14:CN:23:ARG:NH2	2.35	0.42
16:CP:3:LYS:O	16:CP:21:VAL:HA	2.19	0.42
23:CW:8:4SU:H1'	23:CW:48:C:H1'	2.01	0.42
23:CY:8:4SU:S4	23:CY:14:A:N7	2.92	0.42
23:CY:46:7MG:H82	23:CY:46:7MG:H2'	1.74	0.42
23:CY:68:C:H2'	23:CY:69:G:H5'	2.01	0.42
25:DA:361:G:O2'	25:DA:362:U:H5'	2.18	0.42
25:DA:652(A):A:O2'	25:DA:652(B):A:H5'	2.19	0.42
25:DA:1379:A:H4'	25:DA:1380:G:OP2	2.19	0.42
25:DA:1639:U:C2'	25:DA:1640:C:H5"	2.46	0.42
34:DO:68:GLU:HB3	34:DO:78:ARG:HB2	2.00	0.42
41:DV:21:ARG:HG2	41:DV:91:TYR:CD2	2.54	0.42
47:D1:64:ALA:HA	47:D1:67:ILE:HG13	2.01	0.42
1:AA:562:C:H1'	12:AL:15:ARG:HB3	2.01	0.42
1:AA:977:A:H1'	1:AA:982:U:O4	2.19	0.42
1:AA:1009:G:C6	1:AA:1010:G:C5	3.07	0.42
1:AA:1213:A:O2'	1:AA:1215:G:N7	2.47	0.42
1:AA:1355:G:H2'	1:AA:1356:G:C8	2.55	0.42
4:AD:173:TRP:CE2	4:AD:189:PRO:HG3	2.53	0.42
9:AI:50:LEU:HD21	9:AI:81:ILE:HD11	2.01	0.42
9:AI:117:HIS:HB2	9:AI:121:ARG:HG3	2.00	0.42
13:AM:80:ARG:NH2	19:AS:69:HIS:CE1	2.86	0.42
14:AN:33:VAL:HA	14:AN:40:CYS:HA	2.01	0.42
15:AO:15:PHE:CZ	15:AO:84:LYS:HD2	2.53	0.42
23:AY:2:C:N4	23:AY:71:G:H1	2.17	0.42
25:BA:973:G:N7	61:BA:4553:HOH:O	2.37	0.42
25:BA:1843:A:O2'	27:BD:45:ASN:N	2.47	0.42
25:BA:1935:A:H4'	25:BA:1936:C:H5"	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2190:G:O6	25:BA:2193:A:H8	2.02	0.42
25:BA:2545:A:H2'	25:BA:2546:A:O4'	2.18	0.42
25:BA:2707:C:H2'	25:BA:2708:U:H6	1.85	0.42
32:BI:72:LEU:C	32:BI:74:ASN:N	2.76	0.42
43:BX:88:LYS:NZ	43:BX:90:GLU:OE1	2.30	0.42
45:BZ:40:ASP:OD2	45:BZ:43:GLU:HG3	2.19	0.42
50:B4:44:THR:O	50:B4:45:GLY:C	2.62	0.42
1:CA:69:G:H2'	1:CA:70:G:H8	1.84	0.42
1:CA:457:C:H2'	1:CA:458:C:C6	2.53	0.42
1:CA:1012:U:O2	1:CA:1017:G:O6	2.37	0.42
1:CA:1135:U:H4'	1:CA:1136:U:H5	1.84	0.42
1:CA:1222:G:OP1	19:CS:77:THR:HG21	2.19	0.42
2:CB:210:SER:OG	2:CB:211:ILE:N	2.51	0.42
9:CI:48:GLU:O	9:CI:51:ARG:HB2	2.19	0.42
12:CL:39:VAL:HG11	12:CL:41:ARG:HH11	1.84	0.42
23:CY:51:U:O2	23:CY:63:G:N2	2.40	0.42
25:DA:247:G:OP2	25:DA:249:C:N4	2.46	0.42
25:DA:652(C):G:H2'	25:DA:652(D):C:H6	1.85	0.42
25:DA:952:G:P	36:DQ:16:ARG:HH21	2.43	0.42
25:DA:1171:G:H1	25:DA:1178:C:N4	2.05	0.42
25:DA:1300:U:H4'	25:DA:1301:A:H5'	2.01	0.42
25:DA:1790:C:H5"	25:DA:1791:A:OP1	2.19	0.42
25:DA:1815:A:H8	25:DA:1815:A:OP1	2.02	0.42
25:DA:2564:A:C2	25:DA:2647:U:H4'	2.54	0.42
25:DA:2690:C:OP2	37:DR:14:SER:HB3	2.19	0.42
31:DH:98:LEU:HB2	31:DH:125:VAL:CG2	2.49	0.42
36:DQ:21:THR:HG21	36:DQ:101:ARG:HB2	2.02	0.42
38:DS:14:VAL:O	38:DS:18:ILE:HG12	2.20	0.42
45:DZ:69:THR:HG22	45:DZ:90:VAL:HA	2.00	0.42
49:D3:6:VAL:HG13	49:D3:56:VAL:HG22	2.01	0.42
1:AA:584:G:H5'	17:AQ:91:ARG:NH2	2.34	0.42
2:AB:197:VAL:HB	2:AB:200:ILE:HG22	2.00	0.42
4:AD:119:GLN:HG2	4:AD:123:HIS:CD2	2.54	0.42
5:AE:53:LEU:HD12	5:AE:53:LEU:H	1.84	0.42
25:BA:505:A:N3	25:BA:507:G:H5"	2.34	0.42
25:BA:613:A:H2'	25:BA:614:C:O4'	2.19	0.42
25:BA:1475:G:H2'	25:BA:1476:C:H6	1.85	0.42
25:BA:1525:G:O2'	25:BA:1605:A:C2	2.71	0.42
25:BA:2896:G:H2'	25:BA:2897:U:C6	2.55	0.42
31:BH:3:ARG:HG2	31:BH:6:ARG:HD2	2.01	0.42
37:BR:2:ARG:HG2	37:BR:5:LYS:HB2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:153:C:H2'	1:CA:154:C:C6	2.55	0.42
1:CA:1009:G:C2	1:CA:1021:G:N3	2.87	0.42
1:CA:1009:G:H22	1:CA:1021:G:H1'	1.85	0.42
2:CB:47:THR:HA	2:CB:202:PRO:CG	2.46	0.42
4:CD:153:ARG:HD3	4:CD:181:MET:CE	2.50	0.42
4:CD:173:TRP:CD1	4:CD:174:LEU:HG	2.55	0.42
13:CM:4:ILE:HG23	13:CM:5:ALA:N	2.30	0.42
17:CQ:26:GLN:HG2	17:CQ:37:LYS:HG2	2.01	0.42
25:DA:18:C:O2'	25:DA:554:U:OP1	2.32	0.42
25:DA:662:G:OP1	61:DA:4487:HOH:O	2.21	0.42
25:DA:2461:C:H2'	25:DA:2462:U:C6	2.54	0.42
26:DB:11:C:OP2	26:DB:12:C:H5	2.02	0.42
27:DD:146:GLU:HG2	27:DD:152:GLY:C	2.45	0.42
29:DF:197:ASP:O	29:DF:200:GLU:HB2	2.20	0.42
35:DP:45:LEU:HD22	35:DP:45:LEU:HA	1.61	0.42
1:AA:262:A:H2'	1:AA:263:A:C8	2.55	0.42
1:AA:271:C:H2'	1:AA:272:C:H6	1.84	0.42
3:AC:130:VAL:O	3:AC:134:ILE:HG13	2.19	0.42
11:AK:20:TYR:CE1	11:AK:83:ILE:HD12	2.54	0.42
16:AP:52:ASP:HB3	16:AP:55:ARG:HB2	2.01	0.42
20:AT:59:ALA:O	20:AT:63:ILE:HG13	2.20	0.42
23:AW:42:C:O2'	23:AW:43:C:H5'	2.20	0.42
25:BA:32:C:O2'	25:BA:33:U:H5'	2.20	0.42
25:BA:174:U:H4'	25:BA:207:A:H4'	2.02	0.42
25:BA:439:A:H8	25:BA:439:A:O5'	2.02	0.42
25:BA:561:A:H2'	25:BA:562:C:C6	2.54	0.42
25:BA:1090:G:H5'	25:BA:1091:A:OP2	2.19	0.42
25:BA:1639:G:H2'	25:BA:1640:G:C8	2.54	0.42
25:BA:2107:C:OP1	27:BD:261:LYS:NZ	2.53	0.42
27:BD:164:GLN:HE21	27:BD:176:ARG:NH1	2.18	0.42
28:BE:35:GLN:OE1	28:BE:66:HIS:HE1	2.02	0.42
44:BY:20:TYR:CE1	44:BY:43:ASN:HA	2.54	0.42
50:B4:55:ARG:H	50:B4:56:VAL:HA	1.84	0.42
1:CA:300:A:H1'	1:CA:565:U:O2	2.19	0.42
1:CA:664:G:P	18:CR:64:ARG:HH21	2.41	0.42
2:CB:120:ALA:C	2:CB:122:PHE:N	2.77	0.42
4:CD:22:LYS:HB2	4:CD:26:CYS:SG	2.59	0.42
5:CE:105:VAL:HB	5:CE:106:PRO:HD3	2.01	0.42
15:CO:29:VAL:HG13	15:CO:63:ARG:HG3	2.01	0.42
19:CS:48:THR:HA	19:CS:60:VAL:O	2.19	0.42
25:DA:58:G:O2'	25:DA:73:A:N1	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:71:A:H5"	25:DA:73:A:C8	2.55	0.42
25:DA:218:A:C2	25:DA:235:U:H4'	2.53	0.42
25:DA:1412:A:H2'	25:DA:1413:G:C8	2.54	0.42
25:DA:1641:A:H2'	25:DA:1642:G:O4'	2.20	0.42
25:DA:2110:G:H5"	25:DA:2111:C:C5	2.53	0.42
25:DA:2335:A:C8	25:DA:2337:G:C5	3.07	0.42
25:DA:2516:G:H1	25:DA:2568:C:H42	1.67	0.42
30:DG:106:LEU:HA	30:DG:110:ALA:HB3	2.01	0.42
31:DH:2:SER:O	31:DH:3:ARG:HG2	2.19	0.42
1:AA:69:G:H2'	1:AA:70:G:H8	1.85	0.42
3:AC:65:ALA:O	3:AC:66:VAL:HB	2.19	0.42
8:AH:138:TRP:CD1	8:AH:138:TRP:C	2.97	0.42
11:AK:48:ILE:O	11:AK:48:ILE:HG12	2.17	0.42
16:AP:19:ILE:HG23	16:AP:36:ILE:HG13	2.02	0.42
23:AY:50:U:C4	23:AY:64:A:C2	3.08	0.42
25:BA:552:C:H5	61:BA:4993:HOH:O	2.02	0.42
25:BA:722:A:C8	25:BA:851:A:C6	3.08	0.42
25:BA:895:G:O6	25:BA:974:G:H2'	2.19	0.42
25:BA:1223:C:H2'	25:BA:1224:C:C6	2.55	0.42
25:BA:1506:G:H5"	25:BA:1507:A:OP2	2.19	0.42
25:BA:2430:A:H2'	25:BA:2431:U:C6	2.54	0.42
26:BB:14:U:OP2	26:BB:70:C:O2'	2.31	0.42
32:BI:106:GLY:HA2	32:BI:107:VAL:HB	2.02	0.42
38:BS:110:LEU:HD12	38:BS:110:LEU:HA	1.82	0.42
39:BT:65:LYS:HD3	39:BT:67:SER:HB2	2.00	0.42
1:CA:391:G:C6	1:CA:392:G:C5	3.07	0.42
1:CA:683:G:O6	61:CA:4140:HOH:O	2.19	0.42
1:CA:1286:A:H8	1:CA:1287:A:H4'	1.83	0.42
20:CT:87:LYS:O	20:CT:91:LEU:HG	2.19	0.42
24:CX:20:U:H5"	24:CX:21:A:OP2	2.19	0.42
25:DA:117:G:C6	25:DA:119:A:C6	3.08	0.42
25:DA:184:C:H2'	25:DA:185:U:H6	1.85	0.42
25:DA:1877:A:H5'	25:DA:1878:G:OP2	2.18	0.42
25:DA:2224:G:H4'	25:DA:2226:C:C2	2.55	0.42
25:DA:2298:A:H2'	25:DA:2299:G:O4'	2.19	0.42
40:DU:27:LEU:HB3	40:DU:31:SER:HB3	2.01	0.42
1:AA:1124:G:N7	1:AA:1145:C:O2'	2.50	0.42
57:AA:3232:UAM:OAH	57:AA:3232:UAM:OAG	2.34	0.42
2:AB:134:GLU:HA	2:AB:137:ARG:HE	1.84	0.42
4:AD:157:LEU:HD22	4:AD:161:ASN:ND2	2.32	0.42
7:AG:124:LEU:HD23	7:AG:124:LEU:HA	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AJ:38:ILE:HG13	10:AJ:71:LEU:O	2.20	0.42
15:AO:4:THR:N	15:AO:7:GLU:OE1	2.43	0.42
23:AY:58:A:N6	23:AY:61:C:C2	2.87	0.42
25:BA:313:A:N6	25:BA:375:G:O2'	2.53	0.42
25:BA:1830:G:O2'	27:BD:181:GLU:OE2	2.20	0.42
25:BA:2627:U:H2'	25:BA:2628:C:H6	1.85	0.42
29:BF:150:GLY:HA2	29:BF:172:TRP:CD2	2.55	0.42
34:BO:108:GLU:H	34:BO:108:GLU:HG3	1.46	0.42
36:BQ:4:PRO:HB2	36:BQ:7:MET:HE2	2.02	0.42
43:BX:12:VAL:HG22	43:BX:29:TRP:CE2	2.54	0.42
47:B1:64:ALA:HA	47:B1:67:ILE:HG13	2.02	0.42
1:CA:26:A:N6	1:CA:558:G:O2'	2.48	0.42
1:CA:337:C:H2'	1:CA:338:A:C8	2.55	0.42
1:CA:942:G:C2	1:CA:1342:C:C2	3.08	0.42
1:CA:978:A:H1'	1:CA:1322:C:O2	2.20	0.42
1:CA:1410:G:H2'	1:CA:1411:C:C6	2.55	0.42
13:CM:60:VAL:HG22	13:CM:66:LEU:HD11	2.01	0.42
23:CY:55:PSU:HN1	23:CY:57:G:C5'	2.32	0.42
25:DA:277:C:O2	25:DA:277:C:H2'	2.19	0.42
25:DA:833:U:OP1	35:DP:45:LEU:HD11	2.20	0.42
25:DA:1184:G:C6	25:DA:1185:C:C4	3.08	0.42
25:DA:2396:G:OP1	47:D1:25:LYS:NZ	2.44	0.42
25:DA:2469:A:C6	25:DA:2470:G:C4	3.07	0.42
28:DE:78:LEU:HD12	28:DE:78:LEU:HA	1.93	0.42
28:DE:143:ASN:HD22	28:DE:147:PRO:CD	2.32	0.42
30:DG:7:LEU:HD22	30:DG:100:TRP:HE3	1.85	0.42
31:DH:144:VAL:O	31:DH:148:ILE:HG12	2.19	0.42
33:DN:38:HIS:H	33:DN:38:HIS:CD2	2.37	0.42
36:DQ:99:PRO:HG2	45:DZ:79:ARG:HH22	1.84	0.42
1:AA:1358:U:OP1	14:AN:35:ARG:HG2	2.20	0.42
1:AA:1509:C:H2'	1:AA:1510:U:O4'	2.19	0.42
2:AB:16:HIS:HB3	2:AB:210:SER:HB2	2.02	0.42
5:AE:85:GLY:C	5:AE:87:SER:H	2.28	0.42
6:AF:33:TYR:CD2	6:AF:75:LEU:HD23	2.55	0.42
14:AN:53:LEU:HA	14:AN:54:PRO:HD2	1.88	0.42
19:AS:64:GLU:O	19:AS:67:VAL:HG23	2.19	0.42
25:BA:1222:A:N3	25:BA:1222:A:H2'	2.34	0.42
25:BA:1312:G:O2'	25:BA:2034:G:O6	2.31	0.42
25:BA:1992:A:H4'	25:BA:1993:A:OP1	2.20	0.42
25:BA:2052:A:H4'	25:BA:2053:A:C8	2.55	0.42
25:BA:2193:A:O2'	25:BA:2194:U:H5"	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:BH:4:ILE:O	31:BH:69:ARG:HG2	2.19	0.42
35:BP:120:ALA:HB1	35:BP:138:LEU:HA	2.00	0.42
44:BY:5:MET:HE2	44:BY:5:MET:HB2	1.89	0.42
44:BY:102:CYS:SG	44:BY:103:GLY:N	2.92	0.42
48:B2:30:ARG:NH2	61:B2:4001:HOH:O	2.52	0.42
1:CA:881:G:OP2	12:CL:12:ARG:NH2	2.52	0.42
1:CA:1027:C:O2'	1:CA:1034:G:N2	2.53	0.42
1:CA:1510:U:H2'	1:CA:1511:G:C8	2.55	0.42
2:CB:15:VAL:HB	2:CB:16:HIS:CD2	2.54	0.42
9:CI:55:ALA:HA	9:CI:58:HIS:CD2	2.54	0.42
20:CT:90:GLN:HE21	20:CT:90:GLN:HB2	1.58	0.42
25:DA:479:A:N3	25:DA:481:G:H5"	2.34	0.42
25:DA:652(C):G:H2'	25:DA:652(D):C:C6	2.54	0.42
25:DA:1478:G:O2'	25:DA:1558:A:N1	2.52	0.42
25:DA:1636:C:H2'	25:DA:1637:A:C8	2.55	0.42
25:DA:1676:A:H2'	25:DA:1677:A:O4'	2.20	0.42
25:DA:2140:C:O2	25:DA:2140:C:H2'	2.19	0.42
25:DA:2366:A:H2'	25:DA:2367:G:O4'	2.19	0.42
25:DA:2783:G:H2'	25:DA:2784:C:C6	2.55	0.42
25:DA:2865:U:C4	25:DA:2866:U:C4	3.08	0.42
28:DE:21:VAL:HA	28:DE:22:PRO:HD3	1.88	0.42
31:DH:3:ARG:NH2	31:DH:5:GLY:H	2.18	0.42
42:DW:23:LEU:O	42:DW:27:LYS:NZ	2.53	0.42
45:DZ:18:LEU:HD12	45:DZ:18:LEU:HA	1.84	0.42
5:AE:131:ILE:HD13	5:AE:131:ILE:HA	1.94	0.42
16:AP:74:LEU:HG	16:AP:79:VAL:HG21	2.00	0.42
25:BA:606:G:OP2	40:BU:10:ARG:NH1	2.47	0.42
25:BA:1938:A:H2'	25:BA:1939:U:O4'	2.20	0.42
25:BA:2697:G:H5'	34:BO:68:GLU:OE1	2.19	0.42
27:BD:2:ALA:HB3	27:BD:20:ASP:OD2	2.19	0.42
29:BF:110:LEU:HD12	29:BF:205:ARG:HG2	2.01	0.42
30:BG:16:ARG:HH21	30:BG:31:VAL:CG1	2.32	0.42
34:BO:120:GLU:OE2	34:BO:122:LEU:HD21	2.19	0.42
1:CA:110:C:H2'	1:CA:111:G:O4'	2.20	0.42
1:CA:636:U:H5'	17:CQ:2:PRO:HD3	2.02	0.42
1:CA:857:C:H2'	1:CA:858:G:O4'	2.20	0.42
2:CB:69:LEU:HD13	2:CB:91:PRO:HB2	2.02	0.42
7:CG:137:LYS:O	7:CG:141:VAL:HG23	2.20	0.42
12:CL:51:ALA:O	12:CL:52:LEU:HD13	2.19	0.42
17:CQ:74:LEU:HD13	17:CQ:75:ARG:HG2	2.01	0.42
25:DA:79:G:H2'	25:DA:80:G:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:373:U:H2'	25:DA:374:A:C8	2.54	0.42
25:DA:441:U:O2	29:DF:46:ARG:NH2	2.44	0.42
32:DI:29:TYR:C	32:DI:32:PRO:HD2	2.45	0.42
32:DI:70:GLU:O	32:DI:74:ASN:HB2	2.19	0.42
32:DI:124:GLY:N	32:DI:144:VAL:HG23	2.35	0.42
33:DN:15:LEU:HB3	33:DN:137:LYS:HA	2.02	0.42
36:DQ:18:LYS:HE3	36:DQ:18:LYS:HB2	1.77	0.42
37:DR:2:ARG:HG2	37:DR:5:LYS:HB2	2.01	0.42
50:D4:62:ARG:HE	50:D4:62:ARG:N	2.18	0.42
1:AA:346:G:H2'	1:AA:347:G:O3'	2.20	0.42
1:AA:1262:C:H2'	1:AA:1263:C:C6	2.55	0.42
1:AA:1316:G:H22	1:AA:1319:A:H5"	1.85	0.42
1:AA:1329:A:H5"	13:AM:26:GLY:H	1.84	0.42
3:AC:136:GLN:HE21	3:AC:136:GLN:HB2	1.63	0.42
25:BA:250:G:O2'	25:BA:633:G:O2'	2.25	0.42
25:BA:1119:A:H2'	25:BA:1120:G:O4'	2.20	0.42
25:BA:2579:G:H2'	25:BA:2580:C:C6	2.55	0.42
29:BF:28:ILE:O	29:BF:30:PRO:HD3	2.20	0.42
30:BG:132:ASN:HA	30:BG:157:ILE:O	2.20	0.42
35:BP:63:PRO:HD3	54:B8:27:THR:HG22	2.01	0.42
40:BU:8:VAL:HG13	40:BU:12:ARG:HD2	2.02	0.42
47:B1:50:ARG:HD2	47:B1:57:GLU:OE1	2.19	0.42
1:CA:779:C:H2'	1:CA:780:A:O4'	2.19	0.42
1:CA:1112:C:H1'	3:CC:179:ARG:HG2	2.02	0.42
1:CA:1287:A:H2	1:CA:1353:G:H1'	1.85	0.42
1:CA:1323:G:H2'	1:CA:1324:A:C8	2.55	0.42
1:CA:1366:C:H2'	1:CA:1367:C:C6	2.54	0.42
1:CA:1517:G:N3	25:DA:1919:A:O2'	2.49	0.42
2:CB:16:HIS:HB3	2:CB:210:SER:HB3	2.02	0.42
4:CD:121:VAL:O	4:CD:134:ASP:HA	2.20	0.42
8:CH:14:ARG:CG	8:CH:18:ARG:HH22	2.32	0.42
8:CH:82:HIS:HB3	8:CH:138:TRP:CE2	2.55	0.42
23:CW:49:C:O5'	23:CW:49:C:H6	2.03	0.42
25:DA:217:G:H2'	25:DA:218:A:O4'	2.20	0.42
25:DA:228:A:O2'	25:DA:229:A:P	2.77	0.42
25:DA:328:U:H4'	44:DY:68:HIS:CE1	2.55	0.42
25:DA:1359:A:N1	25:DA:1372:U:O4	2.53	0.42
25:DA:1400:G:H2'	25:DA:1401:G:H8	1.84	0.42
25:DA:2114:A:N6	25:DA:2119:A:H62	2.16	0.42
25:DA:2122:U:C4	25:DA:2176:A:N1	2.88	0.42
25:DA:2781:A:H5"	25:DA:2782:G:H5'	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2896:C:H2'	25:DA:2897:U:H6	1.85	0.42
29:DF:33:LEU:HD12	29:DF:33:LEU:HA	1.91	0.42
32:DI:90:GLY:O	32:DI:121:LYS:HE3	2.20	0.42
35:DP:100:LEU:HD22	35:DP:105:LEU:HD12	2.02	0.42
46:D0:37:LEU:HG	46:D0:60:PHE:HA	2.02	0.42
47:D1:83:GLU:HA	47:D1:84:GLY:HA2	1.72	0.42
1:AA:486:U:H2'	1:AA:487:A:H8	1.85	0.41
1:AA:714:G:H2'	1:AA:715:A:C8	2.55	0.41
1:AA:828:A:H2'	1:AA:829:G:O4'	2.20	0.41
6:AF:14:LEU:HD11	6:AF:84:ASN:ND2	2.35	0.41
20:AT:77:ALA:O	20:AT:81:LYS:HG3	2.20	0.41
23:AW:55:PSU:O3'	25:BA:943:C:H4'	2.20	0.41
25:BA:402:C:OP1	61:BA:5278:HOH:O	2.20	0.41
25:BA:930:G:N2	25:BA:939:C:N3	2.64	0.41
25:BA:1214:G:H2'	25:BA:1215:G:O4'	2.19	0.41
25:BA:1825:U:H2'	25:BA:1826:C:H6	1.85	0.41
25:BA:2144:U:H3	25:BA:2198:A:H2	1.64	0.41
40:BU:17:ILE:HG23	40:BU:39:LEU:HD12	2.02	0.41
53:B7:30:VAL:O	53:B7:34:ARG:HG3	2.20	0.41
1:CA:735:C:H2'	1:CA:736:C:C6	2.55	0.41
1:CA:825:G:H1	1:CA:875:C:H42	1.67	0.41
1:CA:1035:A:H8	1:CA:1035:A:O5'	2.02	0.41
1:CA:1146:A:H5'	1:CA:1146:A:H8	1.85	0.41
1:CA:1476:G:H2'	1:CA:1477:C:C6	2.55	0.41
11:CK:120:ARG:HA	11:CK:121:PRO:HD3	1.89	0.41
17:CQ:81:ARG:NH2	17:CQ:84:LEU:HD21	2.35	0.41
25:DA:398:G:OP1	25:DA:2090:G:O2'	2.34	0.41
25:DA:436:C:H2'	25:DA:437:G:C8	2.55	0.41
25:DA:566:U:O2'	25:DA:809:G:OP2	2.28	0.41
25:DA:1580:A:OP2	25:DA:1580:A:H8	2.03	0.41
25:DA:2391:G:O6	25:DA:2425:A:H8	2.03	0.41
25:DA:2648:C:H2'	25:DA:2649:U:C6	2.54	0.41
25:DA:2821:A:O2'	25:DA:2826:A:N1	2.52	0.41
26:DB:1:U:H2'	26:DB:2:C:C6	2.55	0.41
28:DE:50:GLY:HA3	28:DE:75:VAL:HG11	2.02	0.41
28:DE:76:ARG:NH1	61:DE:405:HOH:O	2.53	0.41
30:DG:76:SER:N	30:DG:84:LYS:HB2	2.35	0.41
33:DN:4:TYR:CD2	40:DU:100:VAL:HG11	2.55	0.41
41:DV:50:PRO:HG2	41:DV:51:VAL:HG12	2.01	0.41
42:DW:45:TYR:CZ	42:DW:49:LYS:HE3	2.55	0.41
45:DZ:138:GLU:H	45:DZ:156:LYS:HE2	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:162:A:H8	1:AA:162:A:O5'	2.03	0.41
1:AA:193:C:H2'	1:AA:194:C:C6	2.55	0.41
1:AA:1022:G:H5'	1:AA:1023:G:OP2	2.20	0.41
4:AD:112:VAL:HG23	4:AD:116:GLN:OE1	2.20	0.41
5:AE:113:ALA:HB3	5:AE:115:VAL:HG23	2.02	0.41
16:AP:17:TYR:HE2	16:AP:41:PRO:HG3	1.84	0.41
25:BA:287:G:N7	25:BA:448:U:H2'	2.35	0.41
25:BA:992:G:O2'	25:BA:1030:A:N1	2.46	0.41
25:BA:1289:G:H2'	25:BA:1290:G:O4'	2.19	0.41
25:BA:1501:U:O2'	25:BA:1502:G:N7	2.49	0.41
25:BA:2760:G:O6	25:BA:2768:C:H5"	2.20	0.41
27:BD:242:ARG:HD3	27:BD:242:ARG:N	2.35	0.41
28:BE:47:VAL:O	28:BE:80:GLU:HA	2.20	0.41
32:BI:66:GLU:HA	32:BI:69:LYS:HB3	2.01	0.41
32:BI:103:ARG:HE	32:BI:103:ARG:HB3	1.58	0.41
33:BN:14:VAL:HG11	33:BN:138:LEU:HD12	2.02	0.41
33:BN:75:TYR:CE2	33:BN:77:GLY:HA2	2.54	0.41
1:CA:266:G:H5"	1:CA:268:C:H41	1.85	0.41
1:CA:671:G:H5'	6:CF:77:ARG:HH22	1.85	0.41
1:CA:1038:C:C2'	1:CA:1039:C:H5'	2.50	0.41
1:CA:1086:U:H3	1:CA:1099:G:N2	2.17	0.41
1:CA:1391:U:H2'	1:CA:1392:G:C8	2.55	0.41
1:CA:1394:A:N1	1:CA:1500:A:O2'	2.46	0.41
3:CC:33:LEU:HA	3:CC:36:ASP:HB2	2.03	0.41
5:CE:37:ARG:C	5:CE:38:GLN:HE21	2.28	0.41
5:CE:79:GLU:OE1	8:CH:104:ARG:HA	2.20	0.41
13:CM:13:LYS:NZ	13:CM:21:TYR:OH	2.54	0.41
25:DA:146:G:H2'	25:DA:147:U:C6	2.56	0.41
25:DA:676:A:H2	25:DA:2069:G:N3	2.18	0.41
25:DA:705:A:H2'	25:DA:706:A:O4'	2.20	0.41
25:DA:729:G:C6	27:DD:208:LYS:HB2	2.55	0.41
25:DA:1885:A:H2'	25:DA:1886:C:O4'	2.20	0.41
31:DH:73:ALA:O	31:DH:76:VAL:HG22	2.19	0.41
31:DH:98:LEU:HD23	31:DH:125:VAL:HG22	2.02	0.41
45:DZ:121:HIS:HB3	45:DZ:123:ASP:O	2.19	0.41
1:AA:396:G:O2'	1:AA:398:C:OP1	2.24	0.41
1:AA:1298:C:H4'	1:AA:1299:A:O4'	2.19	0.41
1:AA:1424:C:H2'	1:AA:1425:U:O4'	2.20	0.41
3:AC:87:LEU:O	3:AC:91:LEU:HB2	2.19	0.41
7:AG:27:ILE:HD12	7:AG:40:ALA:HA	2.02	0.41
8:AH:39:LEU:HD12	8:AH:39:LEU:HA	1.91	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AH:86:ILE:HG13	8:AH:133:LEU:HD22	2.01	0.41
19:AS:42:PRO:HD3	50:B4:61:ARG:NH2	2.35	0.41
25:BA:310:C:H2'	25:BA:311:C:H6	1.85	0.41
25:BA:1104:G:OP1	25:BA:1104:G:H4'	2.21	0.41
25:BA:1570:G:H2'	25:BA:1571:G:O4'	2.20	0.41
25:BA:2108:U:H2'	25:BA:2109:G:C8	2.55	0.41
25:BA:2388:A:H2'	25:BA:2389:A:O4'	2.20	0.41
25:BA:2787:C:H2'	25:BA:2788:A:O4'	2.19	0.41
35:BP:121:LYS:HE2	35:BP:121:LYS:HB3	1.87	0.41
1:CA:316:G:OP2	1:CA:351:G:O2'	2.31	0.41
1:CA:900:A:H2'	1:CA:901:A:C8	2.56	0.41
22:CV:12:A:H8	22:CV:12:A:OP2	2.03	0.41
25:DA:514:A:N3	25:DA:581:C:O2'	2.44	0.41
25:DA:657:U:H2'	25:DA:658:C:C6	2.55	0.41
25:DA:1027:A:O2'	25:DA:1028:A:H5'	2.20	0.41
25:DA:1198:U:H2'	25:DA:1199:U:C6	2.55	0.41
25:DA:1782:C:O2	25:DA:2608:G:O2'	2.37	0.41
25:DA:1857:G:C6	25:DA:1858:G:N1	2.88	0.41
25:DA:2315:G:H2'	25:DA:2316:C:C6	2.55	0.41
25:DA:2330:G:O2'	46:D0:41:ARG:O	2.36	0.41
25:DA:2365:G:H4'	46:D0:60:PHE:CZ	2.55	0.41
25:DA:2749:A:H1'	31:DH:63:SER:HA	2.02	0.41
30:DG:43:LEU:HB3	30:DG:44:GLY:H	1.51	0.41
34:DO:36:GLY:HA2	34:DO:106:LEU:HD23	2.02	0.41
38:DS:5:THR:OG1	38:DS:8:GLU:HG3	2.20	0.41
40:DU:108:GLU:O	40:DU:112:ARG:HG2	2.20	0.41
1:AA:406:G:H21	4:AD:119:GLN:CD	2.28	0.41
1:AA:445:G:H2'	1:AA:446:G:C8	2.55	0.41
1:AA:711:G:O2'	1:AA:712:A:H5'	2.21	0.41
1:AA:922:G:H2'	1:AA:923:A:C8	2.55	0.41
4:AD:194:LEU:HG	4:AD:196:LEU:HD11	2.01	0.41
10:AJ:6:ILE:HA	10:AJ:97:GLU:O	2.20	0.41
11:AK:70:LYS:HB2	11:AK:70:LYS:HE2	1.86	0.41
13:AM:3:ARG:CG	13:AM:8:GLU:HA	2.50	0.41
18:AR:26:LEU:HD12	18:AR:26:LEU:HA	1.93	0.41
18:AR:45:SER:OG	18:AR:47:THR:HG22	2.20	0.41
20:AT:16:HIS:O	20:AT:19:SER:OG	2.38	0.41
23:AY:19:G:N2	23:AY:56:C:C2	2.88	0.41
25:BA:9:U:N3	25:BA:2641:A:C2	2.87	0.41
25:BA:207:A:C2	25:BA:224:U:H4'	2.56	0.41
25:BA:630:U:OP1	29:BF:102:PRO:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:668:A:N1	25:BA:2381:A:O2'	2.52	0.41
25:BA:768:C:H2'	25:BA:769:A:C8	2.55	0.41
25:BA:1417:G:H2'	25:BA:1418:U:C5	2.55	0.41
25:BA:2054:G:O2'	28:BE:145:LYS:HE3	2.19	0.41
27:BD:182:LEU:HA	27:BD:182:LEU:HD23	1.79	0.41
50:B4:18:CYS:SG	50:B4:20:ASN:HB2	2.60	0.41
1:CA:96:U:HO2'	1:CA:97:G:H8	1.65	0.41
1:CA:589:C:H5"	8:CH:29:SER:OG	2.20	0.41
2:CB:158:LEU:HA	2:CB:159:PRO:HD3	1.88	0.41
3:CC:152:ILE:CD1	3:CC:199:LYS:HD2	2.50	0.41
7:CG:51:GLN:HE21	7:CG:51:GLN:HB3	1.62	0.41
13:CM:88:ARG:HG3	13:CM:98:VAL:CG1	2.48	0.41
20:CT:56:MET:HE2	20:CT:56:MET:HB2	1.88	0.41
21:CU:5:ASP:O	21:CU:11:GLY:HA3	2.20	0.41
25:DA:1357:U:H2'	25:DA:1358:G:O4'	2.20	0.41
25:DA:1589:C:H2'	25:DA:1590:U:C6	2.52	0.41
26:DB:24:G:H4'	26:DB:25:A:C8	2.55	0.41
27:DD:29:PRO:HA	27:DD:83:GLU:OE1	2.21	0.41
28:DE:111:ARG:HB3	37:DR:1:MET:CE	2.50	0.41
37:DR:67:LEU:CD1	37:DR:76:VAL:HG21	2.48	0.41
39:DT:59:THR:HG23	39:DT:78:LEU:CB	2.50	0.41
42:DW:13:SER:HA	42:DW:14:PRO:HD3	1.91	0.41
44:DY:6:HIS:H	44:DY:6:HIS:CD2	2.38	0.41
49:D3:4:LEU:O	49:D3:36:VAL:HA	2.20	0.41
51:D5:20:ARG:HG2	51:D5:23:HIS:CE1	2.55	0.41
1:AA:447:G:O6	1:AA:485:G:O2'	2.32	0.41
1:AA:674:G:H2'	1:AA:675:A:H8	1.85	0.41
1:AA:1016:A:H2'	1:AA:1017:G:O4'	2.21	0.41
2:AB:192:SER:O	2:AB:194:PRO:HD3	2.20	0.41
10:AJ:23:ILE:HD13	10:AJ:23:ILE:HA	1.85	0.41
15:AO:84:LYS:O	15:AO:84:LYS:HD3	2.19	0.41
18:AR:53:ARG:HG2	18:AR:58:LEU:O	2.21	0.41
23:AW:44:G:H8	23:AW:44:G:O5'	2.04	0.41
23:AY:7:A:C6	23:AY:49:C:C4	3.08	0.41
23:AY:67:C:H2'	23:AY:68:C:C6	2.55	0.41
25:BA:302:A:HO2'	25:BA:303:C:P	2.36	0.41
25:BA:923:C:H2'	25:BA:924:U:O4'	2.20	0.41
25:BA:1139:G:H3'	25:BA:1140:U:C5'	2.49	0.41
25:BA:1140:U:OP1	25:BA:1140:U:H4'	2.20	0.41
25:BA:2143:G:N2	25:BA:2199:C:N3	2.55	0.41
25:BA:2504:U:H2'	25:BA:2505:U:H6	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2784:C:H2'	25:BA:2785:C:H6	1.84	0.41
27:BD:36:PRO:HA	27:BD:61:LEU:HD12	2.02	0.41
27:BD:102:LYS:C	27:BD:103:ARG:HG2	2.45	0.41
30:BG:114:ILE:HA	30:BG:140:ILE:HD11	2.03	0.41
45:BZ:124:ILE:HG23	45:BZ:126:VAL:HG23	2.02	0.41
46:B0:43:THR:HG23	46:B0:43:THR:O	2.21	0.41
1:CA:353:A:H5'	1:CA:353:A:C8	2.55	0.41
1:CA:411:A:OP2	4:CD:30:LYS:HE3	2.20	0.41
1:CA:695:A:C6	1:CA:696:A:C6	3.09	0.41
1:CA:1243:C:H42	1:CA:1294:G:H1	1.68	0.41
4:CD:119:GLN:HG2	4:CD:123:HIS:CD2	2.55	0.41
5:CE:127:ASN:HA	5:CE:128:PRO:HD3	1.89	0.41
7:CG:22:LEU:HG	7:CG:62:PHE:CE2	2.56	0.41
23:CW:34:G:H2'	23:CW:35:A:H8	1.85	0.41
25:DA:26:G:C6	25:DA:27:G:N1	2.88	0.41
25:DA:320:A:H4'	25:DA:322:A:N7	2.35	0.41
25:DA:702:G:C2	25:DA:731:C:C2	3.08	0.41
25:DA:1670:C:C5	25:DA:1671:U:C4	3.09	0.41
25:DA:2167:U:H2'	25:DA:2168:G:N2	2.33	0.41
25:DA:2273:A:O2'	25:DA:2274:A:H5'	2.20	0.41
25:DA:2506:U:OP1	28:DE:144:ARG:NH2	2.54	0.41
25:DA:2857:G:N2	25:DA:2860:A:OP2	2.50	0.41
26:DB:30:C:OP2	38:DS:32:LEU:HD11	2.20	0.41
32:DI:117:GLU:HG3	32:DI:118:LYS:H	1.86	0.41
35:DP:84:ASN:CG	35:DP:117:GLU:HB2	2.46	0.41
35:DP:95:VAL:HG13	35:DP:125:VAL:HB	2.02	0.41
43:DX:92:LEU:C	43:DX:94:GLY:H	2.28	0.41
1:AA:254:G:OP1	17:AQ:68:ARG:HB3	2.21	0.41
1:AA:431:A:H2'	1:AA:432:A:O4'	2.21	0.41
1:AA:837:G:H1	1:AA:849:C:H42	1.67	0.41
1:AA:1005:A:H62	1:AA:1023:G:N2	2.18	0.41
1:AA:1131:G:H8	1:AA:1131:G:O5'	2.03	0.41
23:AW:19:G:H4'	23:AW:20:U:OP1	2.20	0.41
25:BA:329:U:H2'	25:BA:330:U:C6	2.56	0.41
25:BA:653:G:H5"	54:B8:18:ALA:HB2	2.01	0.41
25:BA:1093:G:H2'	25:BA:1156:G:C2	2.55	0.41
25:BA:1140:U:O2	25:BA:1143:U:H6	2.03	0.41
25:BA:2141:A:O2'	25:BA:2142:G:H5"	2.21	0.41
25:BA:2346:G:O6	46:B0:74:ARG:NH2	2.50	0.41
25:BA:2455:C:H2'	25:BA:2456:G:H8	1.85	0.41
28:BE:7:VAL:CG1	28:BE:27:LEU:HB3	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:BH:20:ALA:HB1	31:BH:21:PRO:HD2	2.03	0.41
1:CA:714:G:H2'	1:CA:715:A:C8	2.55	0.41
1:CA:1245:A:H2'	1:CA:1246:C:O4'	2.21	0.41
2:CB:214:ILE:H	2:CB:214:ILE:HG12	1.70	0.41
2:CB:215:LEU:HD22	2:CB:215:LEU:HA	1.94	0.41
7:CG:50:ILE:HG22	7:CG:125:MET:HG3	2.01	0.41
8:CH:114:THR:C	8:CH:116:LYS:H	2.27	0.41
17:CQ:62:SER:OG	17:CQ:72:ARG:HD3	2.21	0.41
17:CQ:66:SER:OG	17:CQ:69:LYS:HB2	2.21	0.41
25:DA:2386:C:H2'	25:DA:2387:U:C6	2.55	0.41
25:DA:2393:A:H2'	25:DA:2394:C:O4'	2.21	0.41
26:DB:66:A:H61	26:DB:108:U:H3'	1.84	0.41
31:DH:116:GLU:HA	31:DH:117:PRO:HD3	1.89	0.41
35:DP:36:LYS:O	61:DP:304:HOH:O	2.22	0.41
54:D8:50:LEU:HD23	54:D8:50:LEU:HA	1.93	0.41
54:D8:61:LEU:C	54:D8:63:PRO:HD3	2.44	0.41
1:AA:90:U:C2'	1:AA:91:C:H5"	2.45	0.41
1:AA:113:G:H2'	1:AA:114:U:C6	2.56	0.41
1:AA:454:C:H3'	1:AA:455:C:H6	1.84	0.41
2:AB:91:PRO:HG3	2:AB:154:LEU:HB2	2.03	0.41
12:AL:60:LEU:HD21	12:AL:66:VAL:HG22	2.02	0.41
14:AN:3:ARG:HD3	14:AN:3:ARG:HA	1.68	0.41
20:AT:90:GLN:O	20:AT:93:GLU:HB3	2.19	0.41
23:AW:21:A:C6	23:AW:46:7MG:C6	3.08	0.41
25:BA:616:G:H4'	54:B8:4:MET:HE2	2.02	0.41
25:BA:956:A:N1	25:BA:2289:G:H1'	2.35	0.41
25:BA:2331:G:H22	38:BS:3:ARG:HA	1.86	0.41
25:BA:2589:A:OP2	51:B5:3:LYS:NZ	2.50	0.41
26:BB:55:U:H2'	26:BB:56:G:O4'	2.20	0.41
50:B4:55:ARG:N	50:B4:56:VAL:CA	2.83	0.41
1:CA:9:G:H2'	1:CA:10:A:H8	1.85	0.41
1:CA:407:G:H2'	1:CA:408:A:C8	2.55	0.41
1:CA:1060:C:C4	3:CC:2:GLY:HA2	2.56	0.41
1:CA:1392:G:N2	1:CA:1502:A:C8	2.89	0.41
7:CG:47:CYS:HA	7:CG:50:ILE:HD11	2.03	0.41
7:CG:52:GLU:H	7:CG:52:GLU:HG2	1.45	0.41
15:CO:17:ARG:HG3	15:CO:17:ARG:NH1	2.35	0.41
20:CT:51:GLU:O	20:CT:55:ILE:HG12	2.20	0.41
25:DA:811:U:C2	25:DA:1251:C:C5	3.09	0.41
25:DA:1219:G:H1	25:DA:1230:C:N4	2.19	0.41
25:DA:1272:A:H3'	25:DA:1273:U:H5"	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:1364:G:C5	47:D1:3:LYS:HE2	2.55	0.41
25:DA:2347:C:H2'	25:DA:2348:U:C6	2.55	0.41
25:DA:2794:C:N4	25:DA:2802:G:O6	2.53	0.41
35:DP:55:ARG:HG2	35:DP:56:SER:N	2.33	0.41
36:DQ:141:GLN:NE2	45:DZ:74:VAL:O	2.54	0.41
44:DY:9:LYS:HA	44:DY:10:GLY:HA2	1.58	0.41
45:DZ:97:GLU:HA	45:DZ:126:VAL:O	2.20	0.41
45:DZ:163:LEU:HG	45:DZ:165:VAL:HG22	2.01	0.41
1:AA:154:C:N3	1:AA:168:G:C2	2.89	0.41
1:AA:676:A:H1'	11:AK:115:PRO:HB3	2.03	0.41
1:AA:792:A:O2'	1:AA:794:A:N7	2.44	0.41
1:AA:1347:G:H5"	9:AI:107:ARG:HB3	2.02	0.41
2:AB:178:ARG:NH1	2:AB:196:LEU:O	2.54	0.41
3:AC:63:ASN:HA	3:AC:97:LYS:HB3	2.01	0.41
13:AM:15:VAL:O	13:AM:19:LEU:HD22	2.20	0.41
13:AM:40:ASN:HB3	13:AM:43:THR:HG23	2.02	0.41
15:AO:17:ARG:HD2	15:AO:17:ARG:HA	1.85	0.41
24:AX:64:G:H2'	24:AX:65:C:C6	2.56	0.41
25:BA:449:A:H2'	25:BA:450:A:C8	2.55	0.41
25:BA:696:C:P	25:BA:696:C:H6	2.43	0.41
25:BA:787:U:H2'	25:BA:788:G:C8	2.55	0.41
25:BA:1067:A:C8	25:BA:1067:A:C3'	3.04	0.41
25:BA:2282:G:H2'	25:BA:2283:G:O4'	2.19	0.41
25:BA:2851:C:H2'	25:BA:2852:G:H8	1.85	0.41
27:BD:275:LYS:HB3	27:BD:276:LYS:H	1.22	0.41
1:CA:719:C:O2'	18:CR:49:LYS:HB3	2.20	0.41
1:CA:854:G:C2	1:CA:855:G:C8	3.09	0.41
1:CA:865:A:H5'	1:CA:1078:U:C5	2.56	0.41
1:CA:1060:C:C5'	10:CJ:51:ARG:HB3	2.51	0.41
1:CA:1423:G:C6	1:CA:1424:C:C4	3.09	0.41
4:CD:173:TRP:CD1	4:CD:189:PRO:HG3	2.55	0.41
6:CF:95:GLU:HA	6:CF:96:PRO:HD3	1.87	0.41
7:CG:65:ALA:HB1	7:CG:127:ALA:HB3	2.02	0.41
10:CJ:16:LEU:HD22	10:CJ:16:LEU:HA	1.84	0.41
18:CR:40:LEU:HB3	18:CR:79:LEU:HD11	2.02	0.41
25:DA:699:A:H2'	25:DA:700:G:O4'	2.20	0.41
25:DA:856:C:HO2'	25:DA:857:C:P	2.43	0.41
25:DA:1594:G:H2'	25:DA:1595:G:O4'	2.21	0.41
25:DA:1794:U:H2'	25:DA:1795:C:C6	2.56	0.41
25:DA:1916:A:H2'	25:DA:1917:U:O4'	2.21	0.41
25:DA:2000:G:N7	61:DA:4385:HOH:O	2.37	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:DA:2086:U:H2'	25:DA:2087:G:C8	2.55	0.41
25:DA:2522:U:O2'	25:DA:2647:U:OP1	2.33	0.41
26:DB:73:A:N1	45:DZ:34:ASN:ND2	2.68	0.41
30:DG:16:ARG:HG3	30:DG:16:ARG:HH11	1.85	0.41
30:DG:166:ASP:O	30:DG:170:ARG:HB2	2.21	0.41
32:DI:123:LEU:HA	32:DI:144:VAL:HG23	2.03	0.41
41:DV:31:ALA:O	41:DV:61:VAL:HG12	2.20	0.41
50:D4:61:ARG:NH1	50:D4:61:ARG:O	2.49	0.41
1:AA:28:G:O2'	1:AA:296:U:OP1	2.29	0.41
1:AA:138:G:H1	1:AA:225:C:H42	1.69	0.41
1:AA:148:G:H2'	1:AA:149:A:C8	2.51	0.41
1:AA:235:C:H2'	1:AA:236:G:H8	1.86	0.41
1:AA:390:C:H2'	1:AA:391:G:C8	2.56	0.41
1:AA:1014:A:H2'	1:AA:1015:A:C8	2.56	0.41
1:AA:1034:G:C6	1:AA:1035:A:C5	3.09	0.41
1:AA:1049:U:OP1	14:AN:3:ARG:HB2	2.21	0.41
1:AA:1095:U:P	1:AA:1108:G:H1	2.44	0.41
1:AA:1181:G:H1'	1:AA:1182:G:C5	2.56	0.41
1:AA:1216:G:OP1	14:AN:2:ALA:HA	2.21	0.41
1:AA:1412:C:H2'	1:AA:1413:A:C8	2.56	0.41
1:AA:1442(A):G:C8	39:BT:118:ARG:HG2	2.56	0.41
3:AC:131:ARG:NH1	5:AE:50:GLU:HG3	2.35	0.41
11:AK:84:VAL:HG11	11:AK:91:ARG:HD2	2.02	0.41
23:AW:58:A:C6	23:AW:61:C:C2	3.09	0.41
23:AY:53:G:H1	23:AY:61:C:H42	1.69	0.41
25:BA:63:A:O3'	43:BX:71:GLY:HA3	2.21	0.41
25:BA:116:A:C8	25:BA:117:A:C8	3.09	0.41
25:BA:939:C:H2'	25:BA:940:C:C6	2.56	0.41
25:BA:1065:U:H3	25:BA:1188:A:H62	1.68	0.41
25:BA:1091:A:H1'	25:BA:1093:G:N3	2.35	0.41
25:BA:1222:A:H3'	25:BA:1223:C:C6	2.56	0.41
25:BA:1405:A:N1	25:BA:1418:U:C4	2.89	0.41
25:BA:1773:C:H2'	25:BA:1774:C:H6	1.86	0.41
25:BA:2118:U:H3	25:BA:2215:G:H1	1.69	0.41
25:BA:2156:A:H2	25:BA:2181:G:H4'	1.85	0.41
25:BA:2201:C:H2'	25:BA:2202:U:C6	2.56	0.41
25:BA:2372:A:H2'	25:BA:2373:A:O4'	2.21	0.41
25:BA:2412:G:H4'	52:B6:18:ARG:HD2	2.02	0.41
27:BD:5:LYS:HG2	27:BD:17:THR:HG22	2.03	0.41
30:BG:16:ARG:NH2	30:BG:28:VAL:O	2.53	0.41
31:BH:13:LYS:HA	31:BH:14:GLY:HA2	1.58	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:BI:129:THR:HG22	32:BI:139:GLN:NE2	2.36	0.41
42:BW:75:TYR:CZ	42:BW:104:THR:HG21	2.56	0.41
43:BX:11:PRO:HB3	43:BX:92:LEU:HD11	2.02	0.41
44:BY:9:LYS:HA	44:BY:10:GLY:HA2	1.62	0.41
44:BY:83:THR:HG21	44:BY:99:CYS:HB2	2.02	0.41
49:B3:5:LYS:HZ1	49:B3:55:ARG:HH12	1.68	0.41
52:B6:16:CYS:SG	52:B6:18:ARG:HG2	2.61	0.41
1:CA:991:U:O2'	1:CA:1212:U:C4	2.71	0.41
1:CA:1191:A:H5"	3:CC:4:LYS:HD3	2.02	0.41
1:CA:1327:C:OP1	21:CU:12:LYS:NZ	2.53	0.41
2:CB:28:PHE:O	2:CB:32:ILE:HG13	2.20	0.41
3:CC:63:ASN:HB3	3:CC:98:ASN:HD22	1.86	0.41
3:CC:126:ARG:HB3	3:CC:128:PHE:CE1	2.56	0.41
8:CH:97:VAL:HG23	8:CH:129:VAL:O	2.21	0.41
8:CH:121:ASP:OD1	8:CH:121:ASP:N	2.53	0.41
9:CI:7:THR:HB	9:CI:83:ARG:HH12	1.85	0.41
20:CT:56:MET:HE3	20:CT:88:VAL:HG11	2.03	0.41
25:DA:271(O):C:H2'	25:DA:271(P):C:C6	2.56	0.41
25:DA:637:A:H8	35:DP:117:GLU:HG3	1.86	0.41
25:DA:686:G:N3	53:D7:11:LYS:HE2	2.36	0.41
25:DA:752:A:H3'	53:D7:1:MET:SD	2.60	0.41
25:DA:784:A:N6	27:DD:229:VAL:HG11	2.36	0.41
25:DA:1223:G:N2	25:DA:1226:A:OP2	2.46	0.41
25:DA:1306:C:H1'	25:DA:1623:G:N2	2.36	0.41
25:DA:1752:C:H2'	25:DA:1753:G:C8	2.55	0.41
25:DA:1878:G:C2	25:DA:1879:C:C2	3.08	0.41
25:DA:2114:A:N3	25:DA:2114:A:H2'	2.36	0.41
25:DA:2168:G:C8	25:DA:2170:A:N7	2.89	0.41
25:DA:2846:G:H2'	25:DA:2847:U:O4'	2.20	0.41
26:DB:17:C:H2'	26:DB:18:G:O4'	2.21	0.41
26:DB:33:G:C2	26:DB:50:G:C2	3.09	0.41
26:DB:33:G:H5'	30:DG:2:PRO:HD3	2.01	0.41
26:DB:55:U:H2'	26:DB:56:G:O4'	2.21	0.41
26:DB:105:A:H2'	26:DB:106:G:O4'	2.21	0.41
26:DB:115:G:O4'	38:DS:47:THR:HB	2.21	0.41
27:DD:9:TYR:CZ	27:DD:13:ARG:HG2	2.56	0.41
27:DD:61:LEU:HD12	27:DD:61:LEU:HA	1.99	0.41
29:DF:176:LEU:HD23	29:DF:176:LEU:HA	1.91	0.41
31:DH:13:LYS:HA	31:DH:14:GLY:HA2	1.57	0.41
35:DP:107:LYS:O	35:DP:110:TYR:HB2	2.20	0.41
42:DW:54:ALA:HB1	42:DW:107:LEU:HD22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:D4:20:ASN:OD1	50:D4:21:VAL:N	2.54	0.41
53:D7:9:ARG:HG3	53:D7:46:VAL:HG23	2.02	0.41
54:D8:62:LEU:HB3	54:D8:65:GLU:HG2	2.03	0.41
1:AA:942:G:C2	1:AA:1342:C:C2	3.09	0.41
1:AA:943:U:C2'	1:AA:944:G:H5'	2.51	0.41
1:AA:1072:G:H2'	1:AA:1073:U:C6	2.55	0.41
1:AA:1236:A:H4'	1:AA:1304:G:H4'	2.02	0.41
3:AC:115:LEU:HA	3:AC:115:LEU:HD12	1.87	0.41
9:AI:65:VAL:HG21	9:AI:73:GLN:HB3	2.03	0.41
13:AM:80:ARG:HH21	19:AS:69:HIS:HE1	1.68	0.41
15:AO:17:ARG:HG3	15:AO:17:ARG:NH1	2.35	0.41
25:BA:26:G:H1'	25:BA:540:A:H61	1.86	0.41
25:BA:1093:G:H2'	25:BA:1156:G:H22	1.86	0.41
25:BA:1688:A:H2'	25:BA:1689:G:O4'	2.20	0.41
25:BA:2705:A:H2'	25:BA:2706:G:C8	2.56	0.41
28:BE:96:PHE:O	28:BE:175:VAL:HG11	2.20	0.41
31:BH:116:GLU:HA	31:BH:117:PRO:HD3	1.88	0.41
33:BN:82:LEU:HD12	33:BN:82:LEU:HA	1.90	0.41
48:B2:69:ARG:HB3	48:B2:70:GLN:H	1.45	0.41
50:B4:62:ARG:HB2	50:B4:63:TYR:CD1	2.56	0.41
1:CA:565:U:OP2	1:CA:566:G:O2'	2.34	0.41
1:CA:685:G:C2	1:CA:686:U:C4	3.09	0.41
1:CA:765:G:H5"	1:CA:766:A:OP1	2.21	0.41
1:CA:839:U:O3'	1:CA:840:C:H6	2.04	0.41
1:CA:926:G:O2'	22:CV:13:A:N3	2.47	0.41
1:CA:1027:C:H5'	1:CA:1028:C:OP2	2.21	0.41
1:CA:1032:G:C2	1:CA:1033:G:C5	3.09	0.41
1:CA:1228:C:P	13:CM:108:ARG:HH22	2.39	0.41
3:CC:32:LEU:HD13	3:CC:32:LEU:HA	1.90	0.41
5:CE:51:VAL:O	5:CE:55:VAL:HG23	2.20	0.41
5:CE:84:PHE:N	5:CE:87:SER:O	2.53	0.41
9:CI:3:GLN:HG3	9:CI:20:ARG:HE	1.86	0.41
10:CJ:23:ILE:HD13	10:CJ:23:ILE:HA	1.87	0.41
25:DA:867:C:N4	25:DA:868:U:O4	2.54	0.41
25:DA:2557:G:H2'	25:DA:2558:C:H6	1.86	0.41
25:DA:2888:C:H2'	25:DA:2889:C:H6	1.86	0.41
29:DF:137:LYS:HA	29:DF:140:LEU:HB2	2.03	0.41
41:DV:40:LEU:HB2	41:DV:46:VAL:CG1	2.51	0.41
45:DZ:171:ILE:H	45:DZ:171:ILE:HD13	1.86	0.41
47:D1:85:LEU:HD13	47:D1:85:LEU:HA	1.91	0.41
51:D5:41:PRO:O	51:D5:44:THR:OG1	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:921:U:O4	61:AA:4075:HOH:O	2.21	0.40
1:AA:1068:G:OP2	1:AA:1068:G:H8	2.04	0.40
1:AA:1517:G:H1'	25:BA:1941:A:O3'	2.21	0.40
8:AH:20:TYR:CE2	8:AH:76:PRO:HG2	2.56	0.40
24:AX:21:A:N6	24:AX:46:G:H2'	2.36	0.40
23:AY:5:G:C6	23:AY:6:G:C5	3.09	0.40
25:BA:217:A:H8	25:BA:218:A:H5'	1.86	0.40
25:BA:427:G:N7	61:BA:5129:HOH:O	2.37	0.40
25:BA:510:C:H2'	25:BA:511:C:H6	1.86	0.40
25:BA:1257:G:N3	25:BA:1282:G:C2	2.89	0.40
25:BA:1445:C:OP1	43:BX:25:LYS:NZ	2.54	0.40
25:BA:2332:A:N3	25:BA:2332:A:H2'	2.36	0.40
28:BE:174:ASP:OD1	28:BE:175:VAL:N	2.54	0.40
30:BG:60:LEU:HD12	30:BG:60:LEU:HA	1.89	0.40
43:BX:41:ASN:O	43:BX:45:THR:HG23	2.21	0.40
50:B4:28:LYS:HA	50:B4:29:PRO:HD3	1.84	0.40
1:CA:219:C:H2'	1:CA:220:G:O4'	2.22	0.40
1:CA:360:A:C6	1:CA:361:G:C6	3.08	0.40
1:CA:540:G:H2'	1:CA:541:G:O4'	2.21	0.40
1:CA:682:G:N7	61:CA:4142:HOH:O	2.37	0.40
1:CA:985:C:H2'	1:CA:986:A:C8	2.56	0.40
1:CA:1179:A:H5"	9:CI:102:LEU:HD22	2.03	0.40
1:CA:1326:C:H2'	1:CA:1327:C:C6	2.56	0.40
3:CC:119:ARG:O	3:CC:123:GLN:HG3	2.21	0.40
15:CO:69:TYR:CZ	15:CO:73:GLU:HG3	2.56	0.40
23:CY:9:A:C2'	23:CY:11:C:H41	2.34	0.40
25:DA:118:A:C8	25:DA:119:A:C8	3.09	0.40
25:DA:222:A:H5"	25:DA:421:U:OP1	2.21	0.40
25:DA:839:U:H2'	25:DA:840:C:H6	1.85	0.40
25:DA:1453:U:O4	37:DR:67:LEU:HD21	2.21	0.40
25:DA:1557:C:H5"	25:DA:1558:A:OP2	2.21	0.40
30:DG:111:LEU:CD2	30:DG:120:LEU:HD21	2.51	0.40
31:DH:41:MET:HE1	31:DH:54:ARG:CB	2.51	0.40
37:DR:28:LEU:HD23	37:DR:28:LEU:HA	1.91	0.40
40:DU:106:PHE:HA	40:DU:109:LEU:HD12	2.02	0.40
44:DY:20:TYR:CE1	44:DY:43:ASN:HA	2.56	0.40
50:D4:59:PHE:HD1	50:D4:59:PHE:N	2.14	0.40
1:AA:895:G:H2'	1:AA:896:C:C6	2.56	0.40
1:AA:990:C:N4	1:AA:991:U:O4	2.55	0.40
1:AA:1022:G:H4'	1:AA:1022:G:OP1	2.21	0.40
2:AB:21:ARG:H	2:AB:21:ARG:HH21	1.68	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AC:50:ALA:HB1	3:AC:70:VAL:HG11	2.03	0.40
5:AE:90:VAL:O	5:AE:120:THR:HA	2.21	0.40
25:BA:215:G:N2	25:BA:217:A:H62	2.16	0.40
25:BA:354:A:H2	25:BA:1255:A:H2'	1.86	0.40
25:BA:1074:A:N6	25:BA:1171:G:H2'	2.36	0.40
25:BA:1094:A:N1	25:BA:1158:G:O2'	2.36	0.40
25:BA:1110:C:H2'	25:BA:1111:U:O4'	2.20	0.40
25:BA:2549:U:H2'	25:BA:2550:C:C6	2.56	0.40
27:BD:38:LYS:HA	27:BD:38:LYS:HD2	1.92	0.40
29:BF:123:LEU:HD13	29:BF:192:LEU:HB3	2.03	0.40
34:BO:8:LEU:HB2	34:BO:19:ILE:HG13	2.03	0.40
37:BR:54:LEU:HD12	37:BR:54:LEU:HA	1.97	0.40
44:BY:65:ALA:HA	44:BY:66:PRO:HD3	1.93	0.40
50:B4:26:SER:OG	50:B4:27:THR:N	2.53	0.40
1:CA:93:G:C6	1:CA:96:U:C4	3.10	0.40
1:CA:390:C:H2'	1:CA:391:G:C8	2.56	0.40
1:CA:593:G:H2'	1:CA:594:G:O4'	2.22	0.40
1:CA:731:G:OP1	1:CA:766:A:H1'	2.21	0.40
2:CB:97:TRP:HE1	2:CB:173:ALA:HB2	1.86	0.40
3:CC:131:ARG:NE	3:CC:166:GLU:OE2	2.54	0.40
12:CL:54:LYS:HG2	12:CL:75:HIS:CD2	2.56	0.40
12:CL:88:GLY:O	12:CL:99:HIS:HD2	2.04	0.40
15:CO:18:PHE:CZ	15:CO:21:ASP:HB2	2.56	0.40
18:CR:33:ASP:OD2	18:CR:36:ASN:HB2	2.22	0.40
18:CR:44:LEU:HD23	18:CR:50:ILE:HA	2.03	0.40
24:CX:17:C:H2'	24:CX:17(A):U:C5	2.56	0.40
23:CY:9:A:H8	23:CY:11:C:N4	2.19	0.40
25:DA:242:G:C8	54:D8:5:LYS:HG2	2.56	0.40
25:DA:526:A:N3	25:DA:2044:C:H1'	2.36	0.40
25:DA:1610:A:OP1	61:DA:4119:HOH:O	2.21	0.40
25:DA:1759:A:H1'	25:DA:2711:A:C2	2.56	0.40
25:DA:2404:C:O3'	35:DP:77:ARG:NH2	2.53	0.40
25:DA:2514:U:H2'	25:DA:2515:C:C6	2.56	0.40
30:DG:3:LEU:HD22	50:D4:25:TYR:CE2	2.56	0.40
30:DG:101:ILE:HG22	30:DG:105:LYS:HE2	2.03	0.40
31:DH:3:ARG:NH1	31:DH:5:GLY:H	2.20	0.40
1:AA:77:G:C6	1:AA:78:G:C6	3.10	0.40
1:AA:857:C:H2'	1:AA:858:G:O4'	2.20	0.40
2:AB:44:LEU:HA	2:AB:47:THR:OG1	2.21	0.40
5:AE:24:ARG:H	5:AE:24:ARG:HG2	1.67	0.40
5:AE:71:LEU:HD21	5:AE:115:VAL:HG22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AG:65:ALA:O	7:AG:69:VAL:HG23	2.21	0.40
12:AL:83:VAL:HG23	12:AL:107:ALA:HB2	2.03	0.40
23:AY:36:A:C6	23:AY:37:MIA:C5	3.05	0.40
25:BA:388:A:H2'	25:BA:389:G:H8	1.81	0.40
25:BA:601:A:OP1	25:BA:1301:U:O2'	2.32	0.40
25:BA:841:G:H2'	25:BA:842:C:C6	2.56	0.40
25:BA:943:C:C2	25:BA:944:C:C4	3.09	0.40
25:BA:1086:C:H2'	25:BA:1087:C:O4'	2.20	0.40
25:BA:2203:G:HO2'	25:BA:2204:G:P	2.45	0.40
25:BA:2230:U:O2	47:B1:52:ARG:NH2	2.53	0.40
25:BA:2357:G:N3	25:BA:2393:C:H2'	2.36	0.40
29:BF:129:PHE:CD1	29:BF:163:VAL:HG21	2.56	0.40
34:BO:21:CYS:HB2	34:BO:39:ILE:HD12	2.02	0.40
38:BS:3:ARG:HH11	38:BS:3:ARG:HD2	1.75	0.40
40:BU:76:TYR:CE1	40:BU:80:ILE:HG13	2.56	0.40
1:CA:126:G:H4'	1:CA:634:C:O2	2.21	0.40
1:CA:811:C:H4'	1:CA:900:A:N6	2.35	0.40
1:CA:952:U:H2'	1:CA:953:G:H8	1.86	0.40
1:CA:1305:G:O2'	1:CA:1331:G:N2	2.53	0.40
1:CA:1325:C:O2'	1:CA:1326:C:H5'	2.21	0.40
2:CB:77:ALA:HA	2:CB:80:ILE:CG2	2.51	0.40
19:CS:12:ASP:OD2	19:CS:14:HIS:NE2	2.55	0.40
25:DA:330:A:H2	25:DA:1210:A:H2'	1.85	0.40
25:DA:1031:G:H21	55:D9:36:GLN:HE22	1.69	0.40
25:DA:1856:G:H2'	25:DA:1857:G:O4'	2.21	0.40
25:DA:2305:A:H5"	30:DG:134:GLY:HA3	2.02	0.40
27:DD:92:ILE:HD12	27:DD:104:TYR:CD1	2.56	0.40
29:DF:64:ILE:HD11	29:DF:75:HIS:HB2	2.03	0.40
30:DG:179:PRO:HB2	50:D4:42:PHE:HE1	1.85	0.40
30:DG:179:PRO:HG3	50:D4:43:TYR:CZ	2.56	0.40
32:DI:116:LEU:HD12	32:DI:128:LEU:HD13	2.04	0.40
35:DP:62:LEU:O	54:D8:13:ARG:HD3	2.22	0.40
39:DT:28:VAL:HG13	39:DT:86:ILE:HG23	2.02	0.40
1:AA:118:U:O5'	1:AA:118:U:H6	2.04	0.40
1:AA:163:C:H2'	1:AA:164:U:O4'	2.21	0.40
1:AA:848:C:O2'	1:AA:849:C:H5'	2.22	0.40
1:AA:877:C:H5"	8:AH:88:LYS:HD3	2.03	0.40
1:AA:918:A:H2'	1:AA:919:A:O4'	2.21	0.40
1:AA:1057:G:H2'	1:AA:1058:G:O4'	2.21	0.40
1:AA:1241:G:H2'	1:AA:1242:C:C6	2.56	0.40
1:AA:1442:G:H3'	1:AA:1442:G:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:84:GLU:OE1	2:AB:216:SER:HA	2.21	0.40
2:AB:160:ASP:O	2:AB:183:PRO:HD2	2.21	0.40
4:AD:170:VAL:HG13	4:AD:174:LEU:HB2	2.04	0.40
4:AD:187:ARG:NH1	4:AD:193:ASP:OD2	2.40	0.40
15:AO:26:GLU:OE2	15:AO:77:ARG:NE	2.54	0.40
15:AO:68:ARG:O	15:AO:71:GLN:HB3	2.21	0.40
25:BA:266:C:H2'	25:BA:267:C:O4'	2.22	0.40
25:BA:589:U:H5"	35:BP:29:LYS:HE3	2.04	0.40
25:BA:637:U:H5'	25:BA:640:A:N6	2.35	0.40
25:BA:718:C:H2'	25:BA:719:C:C6	2.57	0.40
25:BA:1073:A:C6	25:BA:1172:A:C4	3.09	0.40
25:BA:1405:A:C2	25:BA:1418:U:O4	2.74	0.40
25:BA:1440:U:H2'	25:BA:1441:A:O4'	2.22	0.40
25:BA:2665:U:H2'	25:BA:2666:A:C8	2.56	0.40
1:CA:266:G:H8	1:CA:266:G:H2'	1.71	0.40
1:CA:943:U:H2'	1:CA:944:G:H5'	2.02	0.40
1:CA:1004:A:H2'	1:CA:1038:C:H1'	2.03	0.40
1:CA:1327:C:O2'	1:CA:1328:C:H5'	2.21	0.40
1:CA:1442(A):G:C8	39:DT:118:ARG:HG2	2.57	0.40
2:CB:179:LYS:HA	8:CH:72:PRO:HG3	2.04	0.40
3:CC:164:ARG:HG2	3:CC:165:THR:H	1.86	0.40
7:CG:50:ILE:HD11	7:CG:58:PRO:HB3	2.03	0.40
13:CM:84:ILE:HG22	19:CS:65:ASN:HB2	2.04	0.40
25:DA:57:C:H2'	25:DA:58:G:O4'	2.21	0.40
25:DA:288:C:H2'	25:DA:289:A:C8	2.57	0.40
25:DA:1843:C:H5'	27:DD:253:GLN:NE2	2.36	0.40
25:DA:2070:G:H2'	25:DA:2071:A:O4'	2.21	0.40
25:DA:2184:G:O2'	25:DA:2185:C:H5'	2.21	0.40
25:DA:2821:A:H2'	25:DA:2822:G:C8	2.57	0.40
35:DP:126:VAL:HG12	35:DP:148:LEU:HD23	2.03	0.40
39:DT:127:ALA:C	39:DT:129:ARG:H	2.30	0.40
41:DV:89:GLN:HA	41:DV:90:PRO:HD3	1.91	0.40
45:DZ:100:VAL:HA	45:DZ:101:PRO:HD3	1.91	0.40
50:D4:48:ARG:HA	50:D4:48:ARG:HD3	1.69	0.40
1:AA:580:U:H2'	1:AA:581:G:O4'	2.21	0.40
1:AA:1182:G:C4'	1:AA:1183:A:H5'	2.44	0.40
1:AA:1504:G:OP1	1:AA:1507:A:H4'	2.22	0.40
2:AB:200:ILE:H	2:AB:200:ILE:HD13	1.86	0.40
17:AQ:50:LYS:HD2	17:AQ:51:TYR:CE1	2.57	0.40
25:BA:1071:G:H3'	25:BA:1072:U:H5'	2.04	0.40
25:BA:1587:U:H2'	25:BA:1588:G:O4'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BA:2045:G:H4'	25:BA:2629:C:O3'	2.21	0.40
25:BA:2134:G:C6	25:BA:2135:U:C2	3.09	0.40
27:BD:142:VAL:HG13	27:BD:191:ALA:HB1	2.02	0.40
27:BD:166:GLN:HB2	27:BD:174:ILE:HG22	2.03	0.40
30:BG:45:GLU:H	30:BG:45:GLU:HG2	1.49	0.40
39:BT:16:ARG:HD2	39:BT:18:ASP:OD1	2.21	0.40
43:BX:44:GLU:HG2	43:BX:49:VAL:O	2.21	0.40
45:BZ:146:ILE:HA	45:BZ:147:GLY:HA2	1.65	0.40
48:B2:53:LEU:HD23	48:B2:53:LEU:HA	1.77	0.40
50:B4:40:HIS:HB3	50:B4:43:TYR:CD1	2.56	0.40
1:CA:1032:G:H8	1:CA:1032:G:OP2	2.04	0.40
1:CA:1051:C:H2'	1:CA:1052:U:H6	1.86	0.40
1:CA:1119:C:OP1	9:CI:83:ARG:NH2	2.54	0.40
2:CB:49:GLU:O	2:CB:52:GLU:HB3	2.21	0.40
24:CX:5:G:H1	24:CX:68:C:N4	2.18	0.40
25:DA:207:A:H2'	25:DA:208:C:O4'	2.22	0.40
25:DA:271(H):G:O2'	25:DA:271(I):G:C8	2.70	0.40
25:DA:580:C:H2'	25:DA:581:C:H6	1.87	0.40
25:DA:812:C:H2'	25:DA:813:U:H6	1.86	0.40
25:DA:836:G:C5	25:DA:837:C:C4	3.09	0.40
25:DA:848:G:C4	25:DA:933:A:H8	2.40	0.40
25:DA:1789:A:H2'	25:DA:1790:C:O4'	2.21	0.40
25:DA:2094:G:P	32:DI:22:LYS:HD2	2.61	0.40
25:DA:2107:C:H42	25:DA:2182:G:H1	1.69	0.40
25:DA:2136:C:N4	25:DA:2155:G:N1	2.69	0.40
25:DA:2143:C:C2	25:DA:2144:U:H1'	2.57	0.40
25:DA:2149:G:C6	25:DA:2150:U:O2	2.74	0.40
25:DA:2494:G:C4	25:DA:2495:G:C8	3.10	0.40
28:DE:119:ARG:HB3	28:DE:120:TRP:CD1	2.56	0.40
38:DS:38:GLN:HE21	38:DS:47:THR:HG1	1.57	0.40
50:D4:62:ARG:HB3	50:D4:63:TYR:CD2	2.56	0.40
52:D6:18:ARG:HD2	52:D6:42:TRP:CD1	2.57	0.40
54:D8:23:VAL:CG1	54:D8:47:LYS:HD3	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	AB	229/256 (90%)	204 (89%)	19 (8%)	6 (3%)	4 4
2	CB	229/256 (90%)	201 (88%)	16 (7%)	12 (5%)	1 1
3	AC	204/239 (85%)	189 (93%)	14 (7%)	1 (0%)	24 37
3	CC	204/239 (85%)	188 (92%)	13 (6%)	3 (2%)	8 12
4	AD	206/209 (99%)	199 (97%)	6 (3%)	1 (0%)	24 37
4	CD	206/209 (99%)	201 (98%)	5 (2%)	0	100 100
5	AE	146/162 (90%)	140 (96%)	3 (2%)	3 (2%)	5 7
5	CE	146/162 (90%)	140 (96%)	5 (3%)	1 (1%)	18 28
6	AF	98/101 (97%)	96 (98%)	2 (2%)	0	100 100
6	CF	98/101 (97%)	95 (97%)	3 (3%)	0	100 100
7	AG	153/156 (98%)	146 (95%)	7 (5%)	0	100 100
7	CG	153/156 (98%)	144 (94%)	7 (5%)	2 (1%)	9 14
8	AH	135/138 (98%)	131 (97%)	4 (3%)	0	100 100
8	CH	135/138 (98%)	129 (96%)	6 (4%)	0	100 100
9	AI	125/128 (98%)	114 (91%)	8 (6%)	3 (2%)	4 5
9	CI	125/128 (98%)	114 (91%)	10 (8%)	1 (1%)	16 25
10	AJ	95/105 (90%)	85 (90%)	7 (7%)	3 (3%)	3 3
10	CJ	94/105 (90%)	84 (89%)	8 (8%)	2 (2%)	5 7
11	AK	112/129 (87%)	108 (96%)	2 (2%)	2 (2%)	6 9
11	CK	112/129 (87%)	108 (96%)	2 (2%)	2 (2%)	6 9
12	AL	120/132 (91%)	117 (98%)	3 (2%)	0	100 100
12	CL	120/132 (91%)	116 (97%)	4 (3%)	0	100 100
13	AM	121/126 (96%)	116 (96%)	5 (4%)	0	100 100
13	CM	120/126 (95%)	114 (95%)	4 (3%)	2 (2%)	7 10
14	AN	58/61 (95%)	56 (97%)	2 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	CN	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
15	AO	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
15	CO	86/89 (97%)	83 (96%)	2 (2%)	1 (1%)	10	16
16	AP	80/88 (91%)	77 (96%)	2 (2%)	1 (1%)	9	14
16	CP	80/88 (91%)	78 (98%)	1 (1%)	1 (1%)	9	14
17	AQ	97/105 (92%)	94 (97%)	3 (3%)	0	100	100
17	CQ	97/105 (92%)	96 (99%)	1 (1%)	0	100	100
18	AR	66/88 (75%)	65 (98%)	1 (2%)	0	100	100
18	CR	66/88 (75%)	65 (98%)	1 (2%)	0	100	100
19	AS	81/93 (87%)	74 (91%)	7 (9%)	0	100	100
19	CS	81/93 (87%)	74 (91%)	6 (7%)	1 (1%)	10	16
20	AT	94/106 (89%)	87 (93%)	4 (4%)	3 (3%)	3	3
20	CT	94/106 (89%)	87 (93%)	2 (2%)	5 (5%)	1	1
21	AU	21/27 (78%)	20 (95%)	1 (5%)	0	100	100
21	CU	21/27 (78%)	19 (90%)	2 (10%)	0	100	100
27	BD	273/276 (99%)	264 (97%)	8 (3%)	1 (0%)	30	43
27	DD	273/276 (99%)	265 (97%)	7 (3%)	1 (0%)	30	43
28	BE	202/206 (98%)	198 (98%)	3 (2%)	1 (0%)	24	37
28	DE	202/206 (98%)	196 (97%)	4 (2%)	2 (1%)	12	20
29	BF	201/210 (96%)	199 (99%)	1 (0%)	1 (0%)	24	37
29	DF	201/210 (96%)	198 (98%)	1 (0%)	2 (1%)	12	20
30	BG	179/182 (98%)	168 (94%)	11 (6%)	0	100	100
30	DG	179/182 (98%)	167 (93%)	10 (6%)	2 (1%)	11	18
31	BH	172/180 (96%)	166 (96%)	6 (4%)	0	100	100
31	DH	172/180 (96%)	165 (96%)	7 (4%)	0	100	100
32	BI	144/148 (97%)	128 (89%)	12 (8%)	4 (3%)	4	3
32	DI	144/148 (97%)	133 (92%)	10 (7%)	1 (1%)	18	28
33	BN	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
33	DN	138/140 (99%)	136 (99%)	1 (1%)	1 (1%)	18	28
34	BO	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
34	DO	120/122 (98%)	115 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
35	BP	147/150 (98%)	140 (95%)	6 (4%)	1 (1%)	18 28
35	DP	147/150 (98%)	138 (94%)	6 (4%)	3 (2%)	6 7
36	BQ	139/141 (99%)	135 (97%)	4 (3%)	0	100 100
36	DQ	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	18 28
37	BR	116/118 (98%)	113 (97%)	3 (3%)	0	100 100
37	DR	116/118 (98%)	112 (97%)	4 (3%)	0	100 100
38	BS	108/112 (96%)	106 (98%)	2 (2%)	0	100 100
38	DS	108/112 (96%)	106 (98%)	1 (1%)	1 (1%)	14 22
39	BT	129/146 (88%)	121 (94%)	7 (5%)	1 (1%)	16 25
39	DT	129/146 (88%)	125 (97%)	4 (3%)	0	100 100
40	BU	114/118 (97%)	114 (100%)	0	0	100 100
40	DU	114/118 (97%)	114 (100%)	0	0	100 100
41	BV	99/101 (98%)	96 (97%)	2 (2%)	1 (1%)	12 20
41	DV	99/101 (98%)	97 (98%)	1 (1%)	1 (1%)	12 20
42	BW	110/113 (97%)	110 (100%)	0	0	100 100
42	DW	110/113 (97%)	110 (100%)	0	0	100 100
43	BX	93/96 (97%)	92 (99%)	1 (1%)	0	100 100
43	DX	93/96 (97%)	91 (98%)	1 (1%)	1 (1%)	11 18
44	BY	105/110 (96%)	96 (91%)	9 (9%)	0	100 100
44	DY	105/110 (96%)	100 (95%)	5 (5%)	0	100 100
45	BZ	148/206 (72%)	140 (95%)	6 (4%)	2 (1%)	9 13
45	DZ	156/206 (76%)	149 (96%)	6 (4%)	1 (1%)	21 32
46	B0	81/85 (95%)	80 (99%)	0	1 (1%)	10 16
46	D0	81/85 (95%)	79 (98%)	2 (2%)	0	100 100
47	B1	95/98 (97%)	94 (99%)	0	1 (1%)	11 18
47	D1	95/98 (97%)	93 (98%)	1 (1%)	1 (1%)	11 18
48	B2	68/72 (94%)	67 (98%)	0	1 (2%)	8 12
48	D2	68/72 (94%)	67 (98%)	1 (2%)	0	100 100
49	B3	57/60 (95%)	56 (98%)	1 (2%)	0	100 100
49	D3	57/60 (95%)	55 (96%)	2 (4%)	0	100 100
50	B4	67/71 (94%)	57 (85%)	4 (6%)	6 (9%)	0 0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
50	D4	67/71 (94%)	55 (82%)	6 (9%)	6 (9%)	0 0
51	B5	57/60 (95%)	57 (100%)	0	0	100 100
51	D5	57/60 (95%)	57 (100%)	0	0	100 100
52	B6	51/54 (94%)	49 (96%)	2 (4%)	0	100 100
52	D6	51/54 (94%)	50 (98%)	1 (2%)	0	100 100
53	B7	46/49 (94%)	46 (100%)	0	0	100 100
53	D7	46/49 (94%)	44 (96%)	1 (2%)	1 (2%)	5 6
54	B8	62/65 (95%)	62 (100%)	0	0	100 100
54	D8	62/65 (95%)	62 (100%)	0	0	100 100
55	B9	35/37 (95%)	35 (100%)	0	0	100 100
55	D9	35/37 (95%)	35 (100%)	0	0	100 100
All	All	11372/12128 (94%)	10883 (96%)	387 (3%)	102 (1%)	14 22

All (102) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	15	VAL
2	AB	16	HIS
2	AB	17	PHE
9	AI	54	ASP
27	BD	275	LYS
45	BZ	159	PRO
47	B1	3	LYS
50	B4	47	GLN
2	CB	10	LEU
2	CB	16	HIS
2	CB	20	GLU
2	CB	21	ARG
2	CB	121	LEU
2	CB	126	GLU
7	CG	80	VAL
9	CI	54	ASP
13	CM	5	ALA
20	CT	10	LEU
20	CT	95	ALA
28	DE	52	LEU
28	DE	73	GLU
29	DF	21	ALA

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Mol	Chain	Res	Type
29	DF	130	ALA
30	DG	81	LYS
36	DQ	28	ALA
50	D4	45	GLY
50	D4	49	PHE
50	D4	60	GLN
53	D7	46	VAL
4	AD	5	ILE
5	AE	85	GLY
9	AI	51	ARG
11	AK	105	VAL
16	AP	53	VAL
20	AT	100	ILE
29	BF	130	ALA
32	BI	106	GLY
45	BZ	152	ALA
46	B0	13	GLY
48	B2	69	ARG
50	B4	54	GLY
50	B4	56	VAL
2	CB	8	LYS
2	CB	17	PHE
2	CB	234	PRO
7	CG	7	ALA
30	DG	47	LYS
32	DI	10	GLU
35	DP	45	LEU
50	D4	54	GLY
2	AB	20	GLU
2	AB	231	GLU
10	AJ	78	ASN
10	AJ	79	ARG
11	AK	49	GLY
28	BE	52	LEU
39	BT	37	GLY
50	B4	45	GLY
3	CC	181	ASN
10	CJ	78	ASN
11	CK	49	GLY
16	CP	53	VAL
20	CT	99	LEU
20	CT	102	GLY

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Mol	Chain	Res	Type
33	DN	2	LYS
43	DX	2	LYS
50	D4	62	ARG
2	AB	126	GLU
10	AJ	77	PRO
20	AT	102	GLY
32	BI	11	ASN
32	BI	73	GLU
50	B4	48	ARG
2	CB	123	ALA
3	CC	91	LEU
10	CJ	77	PRO
11	CK	105	VAL
15	CO	88	ARG
35	DP	38	GLN
41	DV	79	VAL
50	D4	46	GLN
3	AC	66	VAL
5	AE	86	ALA
9	AI	48	GLU
20	AT	9	ASN
32	BI	107	VAL
35	BP	122	PRO
41	BV	79	VAL
50	B4	57	GLU
20	CT	100	ILE
27	DD	3	VAL
38	DS	84	GLN
47	D1	3	LYS
5	AE	69	VAL
2	CB	128	GLU
2	CB	231	GLU
19	CS	29	ARG
35	DP	122	PRO
5	CE	69	VAL
3	CC	108	ASN
45	DZ	165	VAL
13	CM	4	ILE

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	AB	192/220 (87%)	165 (86%)	27 (14%)	3 4
2	CB	187/220 (85%)	156 (83%)	31 (17%)	2 3
3	AC	142/188 (76%)	124 (87%)	18 (13%)	4 6
3	CC	140/188 (74%)	122 (87%)	18 (13%)	4 6
4	AD	169/181 (93%)	154 (91%)	15 (9%)	9 15
4	CD	173/181 (96%)	156 (90%)	17 (10%)	7 12
5	AE	113/123 (92%)	103 (91%)	10 (9%)	9 15
5	CE	114/123 (93%)	100 (88%)	14 (12%)	4 6
6	AF	84/90 (93%)	76 (90%)	8 (10%)	8 13
6	CF	85/90 (94%)	78 (92%)	7 (8%)	10 18
7	AG	119/127 (94%)	105 (88%)	14 (12%)	5 7
7	CG	120/127 (94%)	102 (85%)	18 (15%)	3 3
8	AH	114/119 (96%)	102 (90%)	12 (10%)	6 10
8	CH	114/119 (96%)	101 (89%)	13 (11%)	5 8
9	AI	90/99 (91%)	78 (87%)	12 (13%)	4 5
9	CI	89/99 (90%)	74 (83%)	15 (17%)	2 3
10	AJ	66/92 (72%)	60 (91%)	6 (9%)	9 14
10	CJ	69/92 (75%)	66 (96%)	3 (4%)	26 44
11	AK	82/99 (83%)	78 (95%)	4 (5%)	22 39
11	CK	83/99 (84%)	78 (94%)	5 (6%)	17 31
12	AL	97/109 (89%)	89 (92%)	8 (8%)	10 18
12	CL	97/109 (89%)	87 (90%)	10 (10%)	7 11
13	AM	93/101 (92%)	78 (84%)	15 (16%)	2 3
13	CM	92/101 (91%)	77 (84%)	15 (16%)	2 3
14	AN	49/50 (98%)	37 (76%)	12 (24%)	1 1
14	CN	49/50 (98%)	40 (82%)	9 (18%)	1 2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
15	AO	78/80 (98%)	71 (91%)	7 (9%)	9 15
15	CO	78/80 (98%)	69 (88%)	9 (12%)	5 8
16	AP	69/74 (93%)	57 (83%)	12 (17%)	2 2
16	CP	68/74 (92%)	61 (90%)	7 (10%)	7 11
17	AQ	94/97 (97%)	83 (88%)	11 (12%)	5 7
17	CQ	94/97 (97%)	87 (93%)	7 (7%)	13 22
18	AR	59/77 (77%)	51 (86%)	8 (14%)	3 5
18	CR	59/77 (77%)	53 (90%)	6 (10%)	7 11
19	AS	69/80 (86%)	63 (91%)	6 (9%)	9 16
19	CS	67/80 (84%)	61 (91%)	6 (9%)	9 15
20	AT	70/82 (85%)	61 (87%)	9 (13%)	4 6
20	CT	70/82 (85%)	63 (90%)	7 (10%)	7 11
21	AU	18/22 (82%)	15 (83%)	3 (17%)	2 3
21	CU	18/22 (82%)	15 (83%)	3 (17%)	2 3
27	BD	215/218 (99%)	202 (94%)	13 (6%)	17 31
27	DD	215/218 (99%)	200 (93%)	15 (7%)	14 24
28	BE	164/166 (99%)	144 (88%)	20 (12%)	5 7
28	DE	164/166 (99%)	139 (85%)	25 (15%)	3 3
29	BF	160/166 (96%)	139 (87%)	21 (13%)	4 5
29	DF	159/166 (96%)	138 (87%)	21 (13%)	4 5
30	BG	144/156 (92%)	127 (88%)	17 (12%)	5 7
30	DG	143/156 (92%)	121 (85%)	22 (15%)	2 3
31	BH	144/148 (97%)	133 (92%)	11 (8%)	12 21
31	DH	144/148 (97%)	127 (88%)	17 (12%)	5 7
32	BI	113/124 (91%)	91 (80%)	22 (20%)	1 2
32	DI	105/124 (85%)	85 (81%)	20 (19%)	1 2
33	BN	118/119 (99%)	104 (88%)	14 (12%)	5 7
33	DN	118/119 (99%)	103 (87%)	15 (13%)	4 6
34	BO	100/100 (100%)	92 (92%)	8 (8%)	11 19
34	DO	100/100 (100%)	95 (95%)	5 (5%)	22 38
35	BP	115/116 (99%)	100 (87%)	15 (13%)	4 5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
35	DP	115/116 (99%)	102 (89%)	13 (11%)	5 8
36	BQ	111/111 (100%)	99 (89%)	12 (11%)	6 9
36	DQ	111/111 (100%)	96 (86%)	15 (14%)	4 5
37	BR	101/101 (100%)	80 (79%)	21 (21%)	1 1
37	DR	101/101 (100%)	83 (82%)	18 (18%)	2 2
38	BS	86/88 (98%)	77 (90%)	9 (10%)	6 10
38	DS	85/88 (97%)	71 (84%)	14 (16%)	2 3
39	BT	115/127 (91%)	105 (91%)	10 (9%)	9 16
39	DT	113/127 (89%)	102 (90%)	11 (10%)	8 12
40	BU	93/94 (99%)	85 (91%)	8 (9%)	10 16
40	DU	93/94 (99%)	88 (95%)	5 (5%)	20 35
41	BV	80/82 (98%)	69 (86%)	11 (14%)	3 4
41	DV	80/82 (98%)	69 (86%)	11 (14%)	3 4
42	BW	90/92 (98%)	85 (94%)	5 (6%)	19 33
42	DW	90/92 (98%)	83 (92%)	7 (8%)	11 20
43	BX	77/78 (99%)	73 (95%)	4 (5%)	21 36
43	DX	77/78 (99%)	71 (92%)	6 (8%)	11 20
44	BY	85/91 (93%)	76 (89%)	9 (11%)	6 10
44	DY	85/91 (93%)	76 (89%)	9 (11%)	6 10
45	BZ	135/179 (75%)	117 (87%)	18 (13%)	4 5
45	DZ	137/179 (76%)	121 (88%)	16 (12%)	5 7
46	B0	65/67 (97%)	62 (95%)	3 (5%)	24 41
46	D0	65/67 (97%)	62 (95%)	3 (5%)	24 41
47	B1	80/83 (96%)	72 (90%)	8 (10%)	7 11
47	D1	80/83 (96%)	71 (89%)	9 (11%)	5 8
48	B2	65/67 (97%)	58 (89%)	7 (11%)	6 9
48	D2	65/67 (97%)	60 (92%)	5 (8%)	12 20
49	B3	51/52 (98%)	45 (88%)	6 (12%)	5 7
49	D3	50/52 (96%)	42 (84%)	8 (16%)	2 3
50	B4	59/63 (94%)	48 (81%)	11 (19%)	1 2
50	D4	53/63 (84%)	39 (74%)	14 (26%)	0 0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
51	B5	50/52 (96%)	46 (92%)	4 (8%)	11 19
51	D5	50/52 (96%)	45 (90%)	5 (10%)	7 11
52	B6	51/52 (98%)	46 (90%)	5 (10%)	7 12
52	D6	50/52 (96%)	47 (94%)	3 (6%)	17 31
53	B7	41/42 (98%)	36 (88%)	5 (12%)	5 7
53	D7	41/42 (98%)	35 (85%)	6 (15%)	3 4
54	B8	54/55 (98%)	47 (87%)	7 (13%)	4 5
54	D8	54/55 (98%)	48 (89%)	6 (11%)	6 9
55	B9	34/34 (100%)	33 (97%)	1 (3%)	37 60
55	D9	34/34 (100%)	33 (97%)	1 (3%)	37 60
All	All	9306/10066 (92%)	8239 (88%)	1067 (12%)	5 8

All (1067) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	8	LYS
2	AB	11	LEU
2	AB	21	ARG
2	AB	39	ILE
2	AB	48	MET
2	AB	80	ILE
2	AB	96	ARG
2	AB	114	ARG
2	AB	127	ILE
2	AB	128	GLU
2	AB	139	LYS
2	AB	153	ARG
2	AB	155	LEU
2	AB	156	LYS
2	AB	158	LEU
2	AB	169	LYS
2	AB	170	GLU
2	AB	179	LYS
2	AB	185	ILE
2	AB	187	LEU
2	AB	197	VAL
2	AB	200	ILE
2	AB	208	ILE

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Mol	Chain	Res	Type
2	AB	215	LEU
2	AB	217	ARG
2	AB	221	LEU
2	AB	231	GLU
3	AC	3	ASN
3	AC	15	THR
3	AC	26	LYS
3	AC	37	GLN
3	AC	45	LYS
3	AC	54	ARG
3	AC	70	VAL
3	AC	85	ARG
3	AC	104	GLN
3	AC	105	GLU
3	AC	115	LEU
3	AC	119	ARG
3	AC	131	ARG
3	AC	138	VAL
3	AC	178	LEU
3	AC	182	ILE
3	AC	195	VAL
3	AC	207	VAL
4	AD	5	ILE
4	AD	15	GLU
4	AD	31	CYS
4	AD	45	GLN
4	AD	50	ARG
4	AD	58	LEU
4	AD	65	ARG
4	AD	74	GLN
4	AD	135	LEU
4	AD	157	LEU
4	AD	158	ILE
4	AD	170	VAL
4	AD	178	VAL
4	AD	182	LYS
4	AD	194	LEU
5	AE	10	MET
5	AE	13	ILE
5	AE	24	ARG
5	AE	31	LEU
5	AE	38	GLN

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Mol	Chain	Res	Type
5	AE	41	VAL
5	AE	47	LYS
5	AE	51	VAL
5	AE	57	LYS
5	AE	91	LEU
6	AF	10	LEU
6	AF	24	GLU
6	AF	69	GLU
6	AF	70	ASP
6	AF	74	ASP
6	AF	75	LEU
6	AF	82	ARG
6	AF	92	LYS
7	AG	12	LEU
7	AG	13	GLN
7	AG	21	VAL
7	AG	30	ILE
7	AG	50	ILE
7	AG	51	GLN
7	AG	52	GLU
7	AG	63	LYS
7	AG	72	ARG
7	AG	73	MET
7	AG	76	ARG
7	AG	104	LEU
7	AG	113	GLU
7	AG	114	ARG
8	AH	21	LYS
8	AH	26	VAL
8	AH	39	LEU
8	AH	51	VAL
8	AH	52	ASP
8	AH	63	LEU
8	AH	77	GLU
8	AH	78	GLN
8	AH	91	ARG
8	AH	97	VAL
8	AH	98	LYS
8	AH	112	LEU
9	AI	3	GLN
9	AI	23	ASN
9	AI	26	VAL

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Mol	Chain	Res	Type
9	AI	27	THR
9	AI	42	ARG
9	AI	50	LEU
9	AI	56	LEU
9	AI	65	VAL
9	AI	66	ARG
9	AI	83	ARG
9	AI	127	LYS
9	AI	128	ARG
10	AJ	5	ARG
10	AJ	7	LYS
10	AJ	38	ILE
10	AJ	89	ASP
10	AJ	92	THR
10	AJ	96	ILE
11	AK	16	SER
11	AK	31	THR
11	AK	48	ILE
11	AK	114	VAL
12	AL	27	LEU
12	AL	33	ARG
12	AL	34	ARG
12	AL	53	ARG
12	AL	60	LEU
12	AL	83	VAL
12	AL	84	LEU
12	AL	114	LYS
13	AM	3	ARG
13	AM	4	ILE
13	AM	11	ARG
13	AM	15	VAL
13	AM	19	LEU
13	AM	32	GLU
13	AM	48	LEU
13	AM	52	GLU
13	AM	70	LEU
13	AM	73	GLU
13	AM	109	THR
13	AM	110	ARG
13	AM	117	VAL
13	AM	121	LYS
13	AM	122	LYS

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Mol	Chain	Res	Type
14	AN	3	ARG
14	AN	6	LEU
14	AN	7	ILE
14	AN	13	THR
14	AN	15	LYS
14	AN	18	VAL
14	AN	22	THR
14	AN	23	ARG
14	AN	33	VAL
14	AN	35	ARG
14	AN	44	LEU
14	AN	50	LYS
15	AO	3	ILE
15	AO	5	LYS
15	AO	26	GLU
15	AO	39	LEU
15	AO	48	LYS
15	AO	76	GLU
15	AO	83	GLU
16	AP	2	VAL
16	AP	4	ILE
16	AP	19	ILE
16	AP	20	VAL
16	AP	21	VAL
16	AP	27	LYS
16	AP	45	THR
16	AP	50	LYS
16	AP	60	LEU
16	AP	62	VAL
16	AP	67	THR
16	AP	74	LEU
17	AQ	9	VAL
17	AQ	50	LYS
17	AQ	52	LYS
17	AQ	63	ARG
17	AQ	68	ARG
17	AQ	72	ARG
17	AQ	74	LEU
17	AQ	91	ARG
17	AQ	92	ARG
17	AQ	98	LEU
17	AQ	100	LYS

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Mol	Chain	Res	Type
18	AR	26	LEU
18	AR	29	PHE
18	AR	31	LEU
18	AR	32	ARG
18	AR	37	VAL
18	AR	41	LYS
18	AR	76	LEU
18	AR	84	LYS
19	AS	5	LEU
19	AS	28	LYS
19	AS	37	ARG
19	AS	41	VAL
19	AS	63	THR
19	AS	65	ASN
20	AT	8	ARG
20	AT	10	LEU
20	AT	13	LEU
20	AT	24	LEU
20	AT	45	GLN
20	AT	56	MET
20	AT	80	ARG
20	AT	84	LEU
20	AT	90	GLN
21	AU	7	ARG
21	AU	12	LYS
21	AU	15	ARG
27	BD	3	VAL
27	BD	61	LEU
27	BD	94	LEU
27	BD	142	VAL
27	BD	155	LEU
27	BD	193	VAL
27	BD	211	ARG
27	BD	217	ARG
27	BD	221	VAL
27	BD	229	VAL
27	BD	257	LEU
27	BD	259	THR
27	BD	260	ARG
28	BE	9	VAL
28	BE	14	ILE
28	BE	21	VAL

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Mol	Chain	Res	Type
28	BE	24	THR
28	BE	33	VAL
28	BE	34	VAL
28	BE	47	VAL
28	BE	73	GLU
28	BE	75	VAL
28	BE	77	ILE
28	BE	78	LEU
28	BE	82	ARG
28	BE	97	LYS
28	BE	116	VAL
28	BE	119	ARG
28	BE	144	ARG
28	BE	152	LYS
28	BE	175	VAL
28	BE	181	LEU
28	BE	195	LEU
29	BF	19	GLU
29	BF	20	LEU
29	BF	24	LEU
29	BF	28	ILE
29	BF	33	LEU
29	BF	53	THR
29	BF	57	VAL
29	BF	70	THR
29	BF	88	VAL
29	BF	106	ARG
29	BF	110	LEU
29	BF	125	LEU
29	BF	132	VAL
29	BF	140	LEU
29	BF	162	LEU
29	BF	170	LEU
29	BF	175	THR
29	BF	183	VAL
29	BF	192	LEU
29	BF	200	GLU
29	BF	201	VAL
30	BG	5	VAL
30	BG	7	LEU
30	BG	31	VAL
30	BG	43	LEU

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Mol	Chain	Res	Type
30	BG	45	GLU
30	BG	49	ASP
30	BG	51	ARG
30	BG	81	LYS
30	BG	82	LEU
30	BG	137	GLU
30	BG	140	ILE
30	BG	143	GLU
30	BG	148	MET
30	BG	150	ASP
30	BG	159	VAL
30	BG	175	LEU
30	BG	181	ARG
31	BH	6	ARG
31	BH	15	VAL
31	BH	23	ARG
31	BH	27	LYS
31	BH	43	VAL
31	BH	59	ARG
31	BH	69	ARG
31	BH	71	LEU
31	BH	124	GLU
31	BH	125	VAL
31	BH	129	THR
32	BI	5	LEU
32	BI	9	LEU
32	BI	10	GLU
32	BI	15	VAL
32	BI	43	ASN
32	BI	44	LEU
32	BI	47	LEU
32	BI	50	ARG
32	BI	61	ARG
32	BI	64	GLU
32	BI	66	GLU
32	BI	68	LEU
32	BI	76	THR
32	BI	77	LEU
32	BI	78	THR
32	BI	85	GLU
32	BI	87	LYS
32	BI	92	VAL

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Mol	Chain	Res	Type
32	BI	103	ARG
32	BI	109	ILE
32	BI	114	LEU
32	BI	140	LEU
33	BN	28	THR
33	BN	33	LEU
33	BN	34	LEU
33	BN	46	VAL
33	BN	48	MET
33	BN	61	ARG
33	BN	62	VAL
33	BN	67	LEU
33	BN	68	GLU
33	BN	87	LEU
33	BN	97	ARG
33	BN	99	LEU
33	BN	120	LEU
33	BN	134	ARG
34	BO	8	LEU
34	BO	10	VAL
34	BO	23	ARG
34	BO	24	VAL
34	BO	69	ILE
34	BO	98	VAL
34	BO	108	GLU
34	BO	113	LYS
35	BP	3	LEU
35	BP	7	ARG
35	BP	15	ARG
35	BP	21	ARG
35	BP	55	ARG
35	BP	59	LEU
35	BP	75	ILE
35	BP	95	VAL
35	BP	98	GLU
35	BP	101	VAL
35	BP	106	LEU
35	BP	112	LEU
35	BP	125	VAL
35	BP	147	LEU
35	BP	149	GLU
36	BQ	1	MET

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Mol	Chain	Res	Type
36	BQ	7	MET
36	BQ	8	LYS
36	BQ	35	VAL
36	BQ	38	GLU
36	BQ	45	GLN
36	BQ	54	MET
36	BQ	60	ARG
36	BQ	75	THR
36	BQ	109	VAL
36	BQ	110	THR
36	BQ	112	GLU
37	BR	1	MET
37	BR	18	LEU
37	BR	24	GLN
37	BR	28	LEU
37	BR	29	LEU
37	BR	33	ARG
37	BR	36	THR
37	BR	44	LEU
37	BR	54	LEU
37	BR	57	ARG
37	BR	65	LEU
37	BR	67	LEU
37	BR	75	LEU
37	BR	79	LEU
37	BR	91	GLN
37	BR	99	LYS
37	BR	100	LEU
37	BR	102	GLU
37	BR	111	LEU
37	BR	114	VAL
37	BR	118	GLU
38	BS	14	VAL
38	BS	25	ARG
38	BS	46	VAL
38	BS	49	VAL
38	BS	57	LYS
38	BS	75	GLU
38	BS	83	LYS
38	BS	103	GLU
38	BS	110	LEU
39	BT	6	LEU

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Mol	Chain	Res	Type
39	BT	13	ARG
39	BT	16	ARG
39	BT	28	VAL
39	BT	49	VAL
39	BT	53	ARG
39	BT	89	VAL
39	BT	96	ARG
39	BT	108	ARG
39	BT	118	ARG
40	BU	8	VAL
40	BU	36	ARG
40	BU	59	ARG
40	BU	74	LEU
40	BU	83	LEU
40	BU	95	LEU
40	BU	104	GLN
40	BU	108	GLU
41	BV	18	LEU
41	BV	21	ARG
41	BV	43	GLU
41	BV	46	VAL
41	BV	51	VAL
41	BV	52	VAL
41	BV	61	VAL
41	BV	62	LEU
41	BV	72	VAL
41	BV	79	VAL
41	BV	95	LEU
42	BW	11	ARG
42	BW	17	VAL
42	BW	19	LEU
42	BW	51	LEU
42	BW	107	LEU
43	BX	1	MET
43	BX	35	THR
43	BX	57	LEU
43	BX	76	ARG
44	BY	1	MET
44	BY	7	VAL
44	BY	23	ARG
44	BY	43	ASN
44	BY	55	TYR

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Mol	Chain	Res	Type
44	BY	72	VAL
44	BY	90	LEU
44	BY	91	GLU
44	BY	99	CYS
45	BZ	1	MET
45	BZ	5	LEU
45	BZ	18	LEU
45	BZ	42	VAL
45	BZ	46	LYS
45	BZ	76	LEU
45	BZ	86	VAL
45	BZ	91	LEU
45	BZ	92	SER
45	BZ	119	GLU
45	BZ	122	ARG
45	BZ	135	GLU
45	BZ	136	PHE
45	BZ	148	ASP
45	BZ	154	ASP
45	BZ	155	LEU
45	BZ	170	THR
45	BZ	171	ILE
46	B0	11	ARG
46	B0	20	ARG
46	B0	55	ARG
47	B1	3	LYS
47	B1	30	VAL
47	B1	52	ARG
47	B1	59	THR
47	B1	75	GLU
47	B1	81	LYS
47	B1	89	GLU
47	B1	95	LEU
48	B2	19	VAL
48	B2	28	LYS
48	B2	32	LEU
48	B2	40	SER
48	B2	52	ASP
48	B2	54	LYS
48	B2	70	GLN
49	B3	8	LEU
49	B3	23	LEU

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Mol	Chain	Res	Type
49	B3	31	LEU
49	B3	54	VAL
49	B3	56	VAL
49	B3	60	GLU
50	B4	1	MET
50	B4	8	LYS
50	B4	27	THR
50	B4	34	GLU
50	B4	50	VAL
50	B4	56	VAL
50	B4	58	ARG
50	B4	63	TYR
50	B4	66	SER
50	B4	68	ARG
50	B4	69	LYS
51	B5	6	VAL
51	B5	16	ARG
51	B5	29	THR
51	B5	40	LYS
52	B6	4	GLU
52	B6	14	THR
52	B6	38	LYS
52	B6	48	VAL
52	B6	52	VAL
53	B7	9	ARG
53	B7	24	THR
53	B7	43	THR
53	B7	46	VAL
53	B7	48	LYS
54	B8	6	THR
54	B8	13	ARG
54	B8	14	VAL
54	B8	23	VAL
54	B8	30	ARG
54	B8	32	LEU
54	B8	46	ARG
55	B9	17	ILE
2	CB	7	VAL
2	CB	8	LYS
2	CB	10	LEU
2	CB	11	LEU
2	CB	15	VAL

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Mol	Chain	Res	Type
2	CB	23	ARG
2	CB	48	MET
2	CB	71	VAL
2	CB	76	GLN
2	CB	80	ILE
2	CB	81	VAL
2	CB	87	ARG
2	CB	94	ASN
2	CB	96	ARG
2	CB	97	TRP
2	CB	115	LEU
2	CB	124	SER
2	CB	126	GLU
2	CB	127	ILE
2	CB	155	LEU
2	CB	175	ARG
2	CB	179	LYS
2	CB	185	ILE
2	CB	187	LEU
2	CB	197	VAL
2	CB	200	ILE
2	CB	208	ILE
2	CB	215	LEU
2	CB	217	ARG
2	CB	222	ILE
2	CB	223	ILE
3	CC	3	ASN
3	CC	8	ILE
3	CC	15	THR
3	CC	36	ASP
3	CC	45	LYS
3	CC	54	ARG
3	CC	70	VAL
3	CC	85	ARG
3	CC	102	ASN
3	CC	104	GLN
3	CC	115	LEU
3	CC	125	GLU
3	CC	131	ARG
3	CC	138	VAL
3	CC	152	ILE
3	CC	178	LEU

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Mol	Chain	Res	Type
3	CC	196	LEU
3	CC	198	VAL
4	CD	8	VAL
4	CD	19	LEU
4	CD	31	CYS
4	CD	34	GLU
4	CD	47	ARG
4	CD	58	LEU
4	CD	61	LYS
4	CD	65	ARG
4	CD	74	GLN
4	CD	108	LEU
4	CD	135	LEU
4	CD	141	ARG
4	CD	150	GLU
4	CD	157	LEU
4	CD	170	VAL
4	CD	182	LYS
4	CD	194	LEU
5	CE	13	ILE
5	CE	24	ARG
5	CE	31	LEU
5	CE	38	GLN
5	CE	41	VAL
5	CE	47	LYS
5	CE	51	VAL
5	CE	57	LYS
5	CE	64	ARG
5	CE	71	LEU
5	CE	75	THR
5	CE	79	GLU
5	CE	137	GLU
5	CE	150	ARG
6	CF	21	LEU
6	CF	28	ARG
6	CF	41	GLU
6	CF	70	ASP
6	CF	74	ASP
6	CF	75	LEU
6	CF	82	ARG
7	CG	9	VAL
7	CG	13	GLN

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Mol	Chain	Res	Type
7	CG	32	ARG
7	CG	41	ARG
7	CG	50	ILE
7	CG	51	GLN
7	CG	52	GLU
7	CG	73	MET
7	CG	76	ARG
7	CG	78	ARG
7	CG	79	ARG
7	CG	90	GLU
7	CG	98	SER
7	CG	104	LEU
7	CG	113	GLU
7	CG	114	ARG
7	CG	136	LYS
7	CG	155	ARG
8	CH	25	ASP
8	CH	26	VAL
8	CH	29	SER
8	CH	51	VAL
8	CH	52	ASP
8	CH	63	LEU
8	CH	68	ARG
8	CH	78	GLN
8	CH	84	ARG
8	CH	91	ARG
8	CH	97	VAL
8	CH	112	LEU
8	CH	127	LEU
9	CI	3	GLN
9	CI	17	VAL
9	CI	23	ASN
9	CI	27	THR
9	CI	42	ARG
9	CI	50	LEU
9	CI	56	LEU
9	CI	65	VAL
9	CI	81	ILE
9	CI	83	ARG
9	CI	89	ASN
9	CI	102	LEU
9	CI	108	VAL

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Mol	Chain	Res	Type
9	CI	112	LYS
9	CI	128	ARG
10	CJ	9	ARG
10	CJ	16	LEU
10	CJ	33	GLN
11	CK	28	THR
11	CK	54	ARG
11	CK	103	LEU
11	CK	104	GLN
11	CK	114	VAL
12	CL	18	VAL
12	CL	27	LEU
12	CL	28	LYS
12	CL	33	ARG
12	CL	37	CYS
12	CL	52	LEU
12	CL	60	LEU
12	CL	83	VAL
12	CL	114	LYS
12	CL	124	LYS
13	CM	11	ARG
13	CM	15	VAL
13	CM	17	VAL
13	CM	19	LEU
13	CM	32	GLU
13	CM	34	LEU
13	CM	48	LEU
13	CM	50	GLU
13	CM	52	GLU
13	CM	98	VAL
13	CM	103	THR
13	CM	110	ARG
13	CM	117	VAL
13	CM	121	LYS
13	CM	122	LYS
14	CN	3	ARG
14	CN	6	LEU
14	CN	7	ILE
14	CN	12	ARG
14	CN	22	THR
14	CN	23	ARG
14	CN	29	ARG

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Mol	Chain	Res	Type
14	CN	33	VAL
14	CN	44	LEU
15	CO	3	ILE
15	CO	5	LYS
15	CO	10	LYS
15	CO	26	GLU
15	CO	39	LEU
15	CO	41	GLU
15	CO	54	ARG
15	CO	71	GLN
15	CO	83	GLU
16	CP	2	VAL
16	CP	4	ILE
16	CP	20	VAL
16	CP	21	VAL
16	CP	45	THR
16	CP	60	LEU
16	CP	62	VAL
17	CQ	9	VAL
17	CQ	36	ILE
17	CQ	49	GLU
17	CQ	53	LEU
17	CQ	63	ARG
17	CQ	74	LEU
17	CQ	86	GLU
18	CR	26	LEU
18	CR	32	ARG
18	CR	37	VAL
18	CR	46	GLU
18	CR	76	LEU
18	CR	84	LYS
19	CS	5	LEU
19	CS	27	GLU
19	CS	37	ARG
19	CS	41	VAL
19	CS	65	ASN
19	CS	77	THR
20	CT	24	LEU
20	CT	36	LEU
20	CT	43	LEU
20	CT	45	GLN
20	CT	56	MET

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Mol	Chain	Res	Type
20	CT	80	ARG
20	CT	90	GLN
21	CU	7	ARG
21	CU	12	LYS
21	CU	24	ARG
27	DD	3	VAL
27	DD	5	LYS
27	DD	61	LEU
27	DD	94	LEU
27	DD	122	ASP
27	DD	134	ARG
27	DD	138	VAL
27	DD	142	VAL
27	DD	155	LEU
27	DD	193	VAL
27	DD	211	ARG
27	DD	217	ARG
27	DD	260	ARG
27	DD	275	LYS
27	DD	276	LYS
28	DE	9	VAL
28	DE	12	THR
28	DE	14	ILE
28	DE	21	VAL
28	DE	24	THR
28	DE	33	VAL
28	DE	34	VAL
28	DE	40	GLU
28	DE	52	LEU
28	DE	72	VAL
28	DE	73	GLU
28	DE	75	VAL
28	DE	77	ILE
28	DE	78	LEU
28	DE	82	ARG
28	DE	111	ARG
28	DE	116	VAL
28	DE	119	ARG
28	DE	134	ILE
28	DE	144	ARG
28	DE	152	LYS
28	DE	154	LYS

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Mol	Chain	Res	Type
28	DE	163	GLU
28	DE	175	VAL
28	DE	181	LEU
29	DF	19	GLU
29	DF	20	LEU
29	DF	24	LEU
29	DF	33	LEU
29	DF	38	ARG
29	DF	53	THR
29	DF	57	VAL
29	DF	70	THR
29	DF	88	VAL
29	DF	106	ARG
29	DF	108	LYS
29	DF	110	LEU
29	DF	120	GLU
29	DF	127	GLU
29	DF	132	VAL
29	DF	135	LYS
29	DF	140	LEU
29	DF	170	LEU
29	DF	183	VAL
29	DF	192	LEU
29	DF	201	VAL
30	DG	5	VAL
30	DG	21	ARG
30	DG	31	VAL
30	DG	43	LEU
30	DG	45	GLU
30	DG	47	LYS
30	DG	49	ASP
30	DG	51	ARG
30	DG	60	LEU
30	DG	115	ARG
30	DG	124	SER
30	DG	128	ARG
30	DG	135	LEU
30	DG	136	ARG
30	DG	140	ILE
30	DG	143	GLU
30	DG	148	MET
30	DG	150	ASP

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Mol	Chain	Res	Type
30	DG	159	VAL
30	DG	162	THR
30	DG	170	ARG
30	DG	175	LEU
31	DH	2	SER
31	DH	3	ARG
31	DH	15	VAL
31	DH	27	LYS
31	DH	51	ARG
31	DH	59	ARG
31	DH	69	ARG
31	DH	71	LEU
31	DH	72	ILE
31	DH	76	VAL
31	DH	88	LEU
31	DH	98	LEU
31	DH	116	GLU
31	DH	124	GLU
31	DH	125	VAL
31	DH	136	ILE
31	DH	139	GLN
32	DI	15	VAL
32	DI	37	VAL
32	DI	41	GLU
32	DI	43	ASN
32	DI	44	LEU
32	DI	47	LEU
32	DI	50	ARG
32	DI	57	ARG
32	DI	61	ARG
32	DI	68	LEU
32	DI	73	GLU
32	DI	75	LEU
32	DI	76	THR
32	DI	77	LEU
32	DI	92	VAL
32	DI	104	GLN
32	DI	108	THR
32	DI	114	LEU
32	DI	123	LEU
32	DI	140	LEU
33	DN	15	LEU

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Mol	Chain	Res	Type
33	DN	28	THR
33	DN	33	LEU
33	DN	34	LEU
33	DN	46	VAL
33	DN	48	MET
33	DN	62	VAL
33	DN	85	ILE
33	DN	87	LEU
33	DN	97	ARG
33	DN	99	LEU
33	DN	104	LYS
33	DN	120	LEU
33	DN	137	LYS
33	DN	139	GLU
34	DO	8	LEU
34	DO	10	VAL
34	DO	69	ILE
34	DO	98	VAL
34	DO	108	GLU
35	DP	3	LEU
35	DP	21	ARG
35	DP	45	LEU
35	DP	55	ARG
35	DP	59	LEU
35	DP	65	ARG
35	DP	95	VAL
35	DP	99	LEU
35	DP	112	LEU
35	DP	119	GLU
35	DP	125	VAL
35	DP	147	LEU
35	DP	149	GLU
36	DQ	1	MET
36	DQ	2	LEU
36	DQ	7	MET
36	DQ	8	LYS
36	DQ	11	LYS
36	DQ	21	THR
36	DQ	22	LYS
36	DQ	45	GLN
36	DQ	48	GLU
36	DQ	54	MET

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Mol	Chain	Res	Type
36	DQ	56	ARG
36	DQ	60	ARG
36	DQ	75	THR
36	DQ	110	THR
36	DQ	112	GLU
37	DR	1	MET
37	DR	18	LEU
37	DR	28	LEU
37	DR	29	LEU
37	DR	33	ARG
37	DR	36	THR
37	DR	44	LEU
37	DR	54	LEU
37	DR	60	LEU
37	DR	63	ARG
37	DR	65	LEU
37	DR	75	LEU
37	DR	79	LEU
37	DR	99	LYS
37	DR	100	LEU
37	DR	102	GLU
37	DR	111	LEU
37	DR	118	GLU
38	DS	14	VAL
38	DS	25	ARG
38	DS	35	ILE
38	DS	49	VAL
38	DS	57	LYS
38	DS	58	LEU
38	DS	68	GLN
38	DS	69	VAL
38	DS	71	ARG
38	DS	75	GLU
38	DS	76	LYS
38	DS	80	LEU
38	DS	103	GLU
38	DS	110	LEU
39	DT	6	LEU
39	DT	13	ARG
39	DT	16	ARG
39	DT	17	THR
39	DT	23	ARG

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Mol	Chain	Res	Type
39	DT	28	VAL
39	DT	49	VAL
39	DT	89	VAL
39	DT	96	ARG
39	DT	113	LYS
39	DT	118	ARG
40	DU	36	ARG
40	DU	74	LEU
40	DU	83	LEU
40	DU	92	ARG
40	DU	104	GLN
41	DV	15	GLU
41	DV	21	ARG
41	DV	46	VAL
41	DV	51	VAL
41	DV	52	VAL
41	DV	61	VAL
41	DV	62	LEU
41	DV	72	VAL
41	DV	79	VAL
41	DV	95	LEU
41	DV	100	ARG
42	DW	11	ARG
42	DW	17	VAL
42	DW	19	LEU
42	DW	23	LEU
42	DW	51	LEU
42	DW	60	ASN
42	DW	107	LEU
43	DX	23	GLU
43	DX	35	THR
43	DX	57	LEU
43	DX	76	ARG
43	DX	88	LYS
43	DX	90	GLU
44	DY	1	MET
44	DY	7	VAL
44	DY	11	ASP
44	DY	21	LYS
44	DY	72	VAL
44	DY	90	LEU
44	DY	91	GLU

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Mol	Chain	Res	Type
44	DY	99	CYS
44	DY	107	ASP
45	DZ	5	LEU
45	DZ	11	GLU
45	DZ	18	LEU
45	DZ	33	LEU
45	DZ	42	VAL
45	DZ	50	GLN
45	DZ	97	GLU
45	DZ	126	VAL
45	DZ	132	ASN
45	DZ	136	PHE
45	DZ	141	VAL
45	DZ	145	GLU
45	DZ	148	ASP
45	DZ	154	ASP
45	DZ	170	THR
45	DZ	171	ILE
46	D0	11	ARG
46	D0	20	ARG
46	D0	77	ARG
47	D1	3	LYS
47	D1	4	VAL
47	D1	40	ARG
47	D1	76	ARG
47	D1	78	LYS
47	D1	80	LEU
47	D1	85	LEU
47	D1	89	GLU
47	D1	95	LEU
48	D2	19	VAL
48	D2	28	LYS
48	D2	32	LEU
48	D2	44	LEU
48	D2	70	GLN
49	D3	7	LYS
49	D3	23	LEU
49	D3	24	LYS
49	D3	30	ARG
49	D3	31	LEU
49	D3	32	GLN
49	D3	54	VAL

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Mol	Chain	Res	Type
49	D3	56	VAL
50	D4	1	MET
50	D4	8	LYS
50	D4	13	ARG
50	D4	27	THR
50	D4	34	GLU
50	D4	37	SER
50	D4	48	ARG
50	D4	50	VAL
50	D4	56	VAL
50	D4	58	ARG
50	D4	59	PHE
50	D4	62	ARG
50	D4	68	ARG
50	D4	69	LYS
51	D5	6	VAL
51	D5	16	ARG
51	D5	29	THR
51	D5	40	LYS
51	D5	48	GLU
52	D6	14	THR
52	D6	48	VAL
52	D6	52	VAL
53	D7	1	MET
53	D7	9	ARG
53	D7	14	LYS
53	D7	41	ARG
53	D7	43	THR
53	D7	46	VAL
54	D8	13	ARG
54	D8	14	VAL
54	D8	23	VAL
54	D8	26	LYS
54	D8	30	ARG
54	D8	32	LEU
55	D9	17	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (140) such sidechains are listed below:

Mol	Chain	Res	Type
2	AB	16	HIS
2	AB	40	HIS

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Mol	Chain	Res	Type
2	AB	76	GLN
3	AC	6	HIS
3	AC	28	GLN
3	AC	69	HIS
3	AC	136	GLN
3	AC	162	GLN
3	AC	181	ASN
4	AD	77	ASN
4	AD	123	HIS
4	AD	125	HIS
4	AD	160	GLN
4	AD	161	ASN
5	AE	38	GLN
5	AE	73	ASN
5	AE	78	HIS
5	AE	141	GLN
6	AF	100	ASN
7	AG	28	ASN
7	AG	51	GLN
7	AG	97	GLN
9	AI	23	ASN
9	AI	58	HIS
9	AI	124	GLN
12	AL	78	GLN
12	AL	99	HIS
13	AM	92	HIS
15	AO	28	GLN
15	AO	50	HIS
17	AQ	16	GLN
19	AS	23	ASN
19	AS	65	ASN
19	AS	69	HIS
19	AS	83	HIS
20	AT	45	GLN
20	AT	75	ASN
20	AT	90	GLN
27	BD	164	GLN
27	BD	253	GLN
28	BE	121	ASN
28	BE	143	ASN
29	BF	69	HIS
29	BF	169	ASN

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Mol	Chain	Res	Type
29	BF	203	GLN
30	BG	40	ASN
30	BG	132	ASN
32	BI	43	ASN
35	BP	38	GLN
36	BQ	12	GLN
36	BQ	57	HIS
37	BR	71	GLN
38	BS	84	GLN
39	BT	123	GLN
40	BU	94	ASN
43	BX	31	HIS
43	BX	82	GLN
44	BY	6	HIS
44	BY	43	ASN
45	BZ	32	HIS
45	BZ	121	HIS
48	B2	38	GLN
48	B2	70	GLN
49	B3	32	GLN
50	B4	46	GLN
54	B8	35	GLN
55	B9	36	GLN
2	CB	78	GLN
2	CB	95	GLN
2	CB	146	GLN
3	CC	6	HIS
3	CC	28	GLN
3	CC	98	ASN
3	CC	102	ASN
3	CC	136	GLN
4	CD	77	ASN
4	CD	123	HIS
4	CD	125	HIS
4	CD	160	GLN
4	CD	161	ASN
5	CE	38	GLN
5	CE	73	ASN
6	CF	100	ASN
7	CG	13	GLN
7	CG	28	ASN
7	CG	51	GLN

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Mol	Chain	Res	Type
7	CG	97	GLN
7	CG	109	ASN
7	CG	148	ASN
9	CI	23	ASN
9	CI	58	HIS
9	CI	124	GLN
10	CJ	13	HIS
10	CJ	33	GLN
12	CL	78	GLN
12	CL	99	HIS
13	CM	40	ASN
13	CM	92	HIS
15	CO	28	GLN
17	CQ	16	GLN
19	CS	23	ASN
19	CS	47	HIS
19	CS	65	ASN
19	CS	69	HIS
20	CT	16	HIS
20	CT	75	ASN
20	CT	90	GLN
27	DD	87	ASN
27	DD	164	GLN
27	DD	253	GLN
28	DE	143	ASN
28	DE	180	ASN
29	DF	69	HIS
29	DF	169	ASN
29	DF	203	GLN
30	DG	41	GLN
32	DI	43	ASN
32	DI	104	GLN
32	DI	133	HIS
33	DN	38	HIS
36	DQ	13	GLN
36	DQ	57	HIS
36	DQ	123	HIS
37	DR	31	HIS
37	DR	71	GLN
38	DS	38	GLN
39	DT	43	GLN
39	DT	123	GLN

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Mol	Chain	Res	Type
40	DU	72	HIS
41	DV	64	HIS
43	DX	31	HIS
43	DX	82	GLN
44	DY	43	ASN
45	DZ	34	ASN
45	DZ	50	GLN
45	DZ	132	ASN
45	DZ	151	HIS
48	D2	38	GLN
54	D8	35	GLN
55	D9	36	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1494/1521 (98%)	298 (19%)	24 (1%)
1	CA	1501/1521 (98%)	308 (20%)	23 (1%)
22	AV	12/24 (50%)	2 (16%)	0
22	CV	12/24 (50%)	1 (8%)	0
23	AW	72/76 (94%)	30 (41%)	2 (2%)
23	AY	72/76 (94%)	29 (40%)	1 (1%)
23	CW	69/76 (90%)	27 (39%)	1 (1%)
23	CY	70/76 (92%)	29 (41%)	3 (4%)
24	AX	75/77 (97%)	15 (20%)	1 (1%)
24	CX	75/77 (97%)	16 (21%)	1 (1%)
25	BA	2864/2915 (98%)	451 (15%)	39 (1%)
25	DA	2791/2915 (95%)	486 (17%)	29 (1%)
26	BB	120/121 (99%)	19 (15%)	1 (0%)
26	DB	119/121 (98%)	20 (16%)	1 (0%)
All	All	9346/9620 (97%)	1731 (18%)	126 (1%)

All (1731) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	6	G
1	AA	9	G
1	AA	22	G
1	AA	32	A
1	AA	39	G
1	AA	47	C

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Mol	Chain	Res	Type
1	AA	48	C
1	AA	51	A
1	AA	61	G
1	AA	79	G
1	AA	91	C
1	AA	92	C
1	AA	96	U
1	AA	97	G
1	AA	101	A
1	AA	111	G
1	AA	115	G
1	AA	116	A
1	AA	121	C
1	AA	131	C
1	AA	144	G
1	AA	155	C
1	AA	156	G
1	AA	157	G
1	AA	158	G
1	AA	163	C
1	AA	172	A
1	AA	174	C
1	AA	179	A
1	AA	180	U
1	AA	182	U
1	AA	186	C
1	AA	189	G
1	AA	189(D)	C
1	AA	195	A
1	AA	197	A
1	AA	201	C
1	AA	202	U
1	AA	203	U
1	AA	204	U
1	AA	216	G
1	AA	217	C
1	AA	226	G
1	AA	247	G
1	AA	251	G
1	AA	258	G
1	AA	266	G
1	AA	267	C

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Mol	Chain	Res	Type
1	AA	289	G
1	AA	301	G
1	AA	321	A
1	AA	328	C
1	AA	332	G
1	AA	347	G
1	AA	348	G
1	AA	352	C
1	AA	353	A
1	AA	354	G
1	AA	355	C
1	AA	367	U
1	AA	372	C
1	AA	373	A
1	AA	381	C
1	AA	384	G
1	AA	397	A
1	AA	398	C
1	AA	406	G
1	AA	412	A
1	AA	414	A
1	AA	424	G
1	AA	426	G
1	AA	429	U
1	AA	430	A
1	AA	441	A
1	AA	442	C
1	AA	443	C
1	AA	452	A
1	AA	461	A
1	AA	470	C
1	AA	471	G
1	AA	477	A
1	AA	484	G
1	AA	485	G
1	AA	496	A
1	AA	498	U
1	AA	505	G
1	AA	509	A
1	AA	510	A
1	AA	511	C
1	AA	518	C

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Mol	Chain	Res	Type
1	AA	521	G
1	AA	524	G
1	AA	527	G
1	AA	528	C
1	AA	531	U
1	AA	532	A
1	AA	533	A
1	AA	547	A
1	AA	559	A
1	AA	561	U
1	AA	572	A
1	AA	573	A
1	AA	576	G
1	AA	577	G
1	AA	590	C
1	AA	592	G
1	AA	596	C
1	AA	599	C
1	AA	619	U
1	AA	627	G
1	AA	630	G
1	AA	631	G
1	AA	637	G
1	AA	639	G
1	AA	653	A
1	AA	660	G
1	AA	665	A
1	AA	673	G
1	AA	687	A
1	AA	688	G
1	AA	695	A
1	AA	723	U
1	AA	724	G
1	AA	731	G
1	AA	749	C
1	AA	752	G
1	AA	755	G
1	AA	759	A
1	AA	773	G
1	AA	774	G
1	AA	777	A
1	AA	793	U

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Mol	Chain	Res	Type
1	AA	794	A
1	AA	815	A
1	AA	817	C
1	AA	821	G
1	AA	828	A
1	AA	840	C
1	AA	841	U
1	AA	851	G
1	AA	859	A
1	AA	874	G
1	AA	902	G
1	AA	913	A
1	AA	914	A
1	AA	926	G
1	AA	927	G
1	AA	931	C
1	AA	934	C
1	AA	936	C
1	AA	960	U
1	AA	961	U
1	AA	968	A
1	AA	969	A
1	AA	971	G
1	AA	972	C
1	AA	974	A
1	AA	975	A
1	AA	976	G
1	AA	977	A
1	AA	982	U
1	AA	989	C
1	AA	992	U
1	AA	993	G
1	AA	996	A
1	AA	998	G
1	AA	1000	U
1	AA	1001(A)	G
1	AA	1003	G
1	AA	1004	A
1	AA	1005	A
1	AA	1006	C
1	AA	1008	C
1	AA	1009	G

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Mol	Chain	Res	Type
1	AA	1011	G
1	AA	1020	U
1	AA	1021	G
1	AA	1022	G
1	AA	1023	G
1	AA	1024	G
1	AA	1025	U
1	AA	1026	G
1	AA	1027	C
1	AA	1028	C
1	AA	1029	C
1	AA	1030	C
1	AA	1030(A)	G
1	AA	1030(B)	C
1	AA	1030(D)	A
1	AA	1032	G
1	AA	1033	G
1	AA	1035	A
1	AA	1036	G
1	AA	1037	C
1	AA	1039	C
1	AA	1044	A
1	AA	1046	A
1	AA	1052	U
1	AA	1054	C
1	AA	1064	G
1	AA	1065	U
1	AA	1066	C
1	AA	1067	A
1	AA	1068	G
1	AA	1081	G
1	AA	1085	U
1	AA	1089	G
1	AA	1094	G
1	AA	1095	U
1	AA	1097	C
1	AA	1101	A
1	AA	1104	G
1	AA	1108	G
1	AA	1110	A
1	AA	1111	A
1	AA	1123	A

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Mol	Chain	Res	Type
1	AA	1130	A
1	AA	1132	C
1	AA	1134	G
1	AA	1135	U
1	AA	1136	U
1	AA	1137	C
1	AA	1138	G
1	AA	1139	G
1	AA	1140	C
1	AA	1141	C
1	AA	1146	A
1	AA	1151	A
1	AA	1152	A
1	AA	1154	G
1	AA	1157	A
1	AA	1158	C
1	AA	1159	U
1	AA	1161	C
1	AA	1165	C
1	AA	1166	G
1	AA	1183	A
1	AA	1184	G
1	AA	1196	U
1	AA	1197	G
1	AA	1201	A
1	AA	1202	G
1	AA	1212	U
1	AA	1213	A
1	AA	1222	G
1	AA	1224	G
1	AA	1227	A
1	AA	1228	C
1	AA	1238	A
1	AA	1240	U
1	AA	1250	A
1	AA	1256	A
1	AA	1257	U
1	AA	1258	G
1	AA	1269	A
1	AA	1270	C
1	AA	1273	G
1	AA	1276	G

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Mol	Chain	Res	Type
1	AA	1278	U
1	AA	1279	A
1	AA	1280	A
1	AA	1281	U
1	AA	1282	C
1	AA	1286	A
1	AA	1287	A
1	AA	1299	A
1	AA	1300	G
1	AA	1302	U
1	AA	1305	G
1	AA	1317	C
1	AA	1320	C
1	AA	1338	G
1	AA	1340	A
1	AA	1347	G
1	AA	1353	G
1	AA	1358	U
1	AA	1363	C
1	AA	1394	A
1	AA	1397	C
1	AA	1419	G
1	AA	1442	G
1	AA	1442(A)	G
1	AA	1446	U
1	AA	1447	A
1	AA	1452	C
1	AA	1456	G
1	AA	1475	G
1	AA	1492	A
1	AA	1493	A
1	AA	1502	A
1	AA	1503	A
1	AA	1504	G
1	AA	1506	U
1	AA	1517	G
1	AA	1529	G
1	AA	1530	G
1	AA	1531	A
1	AA	1532	U
22	AV	13	A
22	AV	24	A

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Mol	Chain	Res	Type
23	AW	2	C
23	AW	3	C
23	AW	4	C
23	AW	6	G
23	AW	8	4SU
23	AW	9	A
23	AW	12	U
23	AW	19	G
23	AW	20	U
23	AW	21	A
23	AW	22	G
23	AW	24	G
23	AW	25	C
23	AW	27	G
23	AW	29	G
23	AW	34	G
23	AW	45	U
23	AW	46	7MG
23	AW	47	U
23	AW	48	C
23	AW	49	C
23	AW	50	U
23	AW	61	C
23	AW	62	C
23	AW	63	G
23	AW	64	A
23	AW	68	C
23	AW	70	G
23	AW	73	A
23	AW	74	C
24	AX	9	G
24	AX	16	C
24	AX	18	G
24	AX	19	G
24	AX	20	U
24	AX	21	A
24	AX	31	G
24	AX	46	G
24	AX	48	C
24	AX	50	U
24	AX	56	C
24	AX	64	G

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Mol	Chain	Res	Type
24	AX	67	C
24	AX	68	C
24	AX	76	A
23	AY	3	C
23	AY	5	G
23	AY	9	A
23	AY	11	C
23	AY	13	C
23	AY	15	G
23	AY	19	G
23	AY	20	U
23	AY	21	A
23	AY	23	A
23	AY	25	C
23	AY	34	G
23	AY	44	G
23	AY	45	U
23	AY	46	7MG
23	AY	47	U
23	AY	48	C
23	AY	49	C
23	AY	54	5MU
23	AY	56	C
23	AY	57	G
23	AY	59	U
23	AY	61	C
23	AY	62	C
23	AY	65	G
23	AY	68	C
23	AY	69	G
23	AY	70	G
23	AY	73	A
25	BA	12	U
25	BA	13	A
25	BA	34	C
25	BA	45	C
25	BA	54	G
25	BA	57	G
25	BA	60	G
25	BA	70	A
25	BA	73	A
25	BA	74	G

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Mol	Chain	Res	Type
25	BA	83	A
25	BA	91	G
25	BA	94	G
25	BA	116	A
25	BA	117	A
25	BA	118	U
25	BA	138	G
25	BA	162	G
25	BA	170	A
25	BA	185	A
25	BA	186	A
25	BA	194	G
25	BA	203	G
25	BA	204	G
25	BA	205	A
25	BA	211	A
25	BA	218	A
25	BA	222	A
25	BA	237	G
25	BA	265	U
25	BA	267	C
25	BA	271	U
25	BA	272	U
25	BA	273	G
25	BA	274	U
25	BA	275	C
25	BA	279	G
25	BA	289	G
25	BA	294	C
25	BA	299	G
25	BA	303	C
25	BA	306	A
25	BA	335	A
25	BA	351	G
25	BA	353	G
25	BA	354	A
25	BA	376	G
25	BA	387	G
25	BA	389	G
25	BA	397	G
25	BA	399	G
25	BA	407	U

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Mol	Chain	Res	Type
25	BA	413	G
25	BA	423	G
25	BA	432	U
25	BA	438	G
25	BA	455	A
25	BA	470	C
25	BA	474	U
25	BA	477	C
25	BA	482	C
25	BA	483	A
25	BA	496	A
25	BA	507	G
25	BA	530	A
25	BA	534	C
25	BA	555	G
25	BA	556	C
25	BA	557	A
25	BA	558	G
25	BA	569	G
25	BA	573	G
25	BA	586	G
25	BA	596	G
25	BA	598	A
25	BA	609	A
25	BA	615	G
25	BA	626	A
25	BA	627	G
25	BA	630	U
25	BA	639	G
25	BA	641	G
25	BA	642	G
25	BA	652	A
25	BA	662	A
25	BA	670	C
25	BA	671	A
25	BA	692	C
25	BA	693	G
25	BA	697	C
25	BA	716	G
25	BA	733	G
25	BA	764	G
25	BA	777	C

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Mol	Chain	Res	Type
25	BA	793	A
25	BA	794	U
25	BA	811	A
25	BA	812	G
25	BA	821	A
25	BA	822	G
25	BA	823	G
25	BA	829	A
25	BA	830	A
25	BA	831	A
25	BA	832	G
25	BA	837	C
25	BA	839	G
25	BA	852	G
25	BA	859	C
25	BA	866	A
25	BA	874	U
25	BA	875	U
25	BA	877	G
25	BA	906	G
25	BA	913	A
25	BA	924	U
25	BA	925	A
25	BA	926	G
25	BA	927	G
25	BA	930	G
25	BA	931	C
25	BA	932	C
25	BA	933	C
25	BA	934	A
25	BA	935	C
25	BA	936	C
25	BA	937	A
25	BA	939	C
25	BA	941	U
25	BA	942	A
25	BA	943	C
25	BA	944	C
25	BA	945	A
25	BA	953	U
25	BA	956	A
25	BA	977	G

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Mol	Chain	Res	Type
25	BA	986	A
25	BA	990	A
25	BA	991	G
25	BA	1004	A
25	BA	1006	C
25	BA	1008	U
25	BA	1019	G
25	BA	1020	C
25	BA	1029	A
25	BA	1042	A
25	BA	1058	U
25	BA	1059	C
25	BA	1068	G
25	BA	1072	U
25	BA	1079	U
25	BA	1087	C
25	BA	1092	A
25	BA	1093	G
25	BA	1094	A
25	BA	1097	G
25	BA	1099	C
25	BA	1100	A
25	BA	1104	G
25	BA	1109	G
25	BA	1114	G
25	BA	1116	A
25	BA	1117	G
25	BA	1118	C
25	BA	1119	A
25	BA	1121	C
25	BA	1122	C
25	BA	1124	U
25	BA	1125	C
25	BA	1129	U
25	BA	1134	A
25	BA	1136	U
25	BA	1138	C
25	BA	1139	G
25	BA	1140	U
25	BA	1141	A
25	BA	1142	A
25	BA	1143	U

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Mol	Chain	Res	Type
25	BA	1144	A
25	BA	1145	G
25	BA	1146	C
25	BA	1147	U
25	BA	1155	C
25	BA	1156	G
25	BA	1158	G
25	BA	1161	G
25	BA	1162	C
25	BA	1174	A
25	BA	1180	C
25	BA	1181	G
25	BA	1196	C
25	BA	1216	G
25	BA	1217	G
25	BA	1218	G
25	BA	1219	A
25	BA	1220	U
25	BA	1221	G
25	BA	1222	A
25	BA	1223	C
25	BA	1255	A
25	BA	1256	U
25	BA	1265	A
25	BA	1287	A
25	BA	1290	G
25	BA	1299	A
25	BA	1302	G
25	BA	1317	G
25	BA	1318	A
25	BA	1319	U
25	BA	1327	G
25	BA	1346	U
25	BA	1347	A
25	BA	1349	G
25	BA	1391	C
25	BA	1398	U
25	BA	1405	A
25	BA	1406	A
25	BA	1411	A
25	BA	1416	C
25	BA	1430	A

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Mol	Chain	Res	Type
25	BA	1431	G
25	BA	1432	C
25	BA	1441	A
25	BA	1462	G
25	BA	1463	C
25	BA	1466	U
25	BA	1467	G
25	BA	1474	C
25	BA	1491	A
25	BA	1497	G
25	BA	1502	G
25	BA	1506	G
25	BA	1508	G
25	BA	1514	C
25	BA	1518	A
25	BA	1529	G
25	BA	1540	A
25	BA	1554	A
25	BA	1555	C
25	BA	1556	A
25	BA	1557	A
25	BA	1561	C
25	BA	1571	G
25	BA	1578	C
25	BA	1601	A
25	BA	1605	A
25	BA	1616	A
25	BA	1625	U
25	BA	1627	A
25	BA	1628	G
25	BA	1631	C
25	BA	1632	A
25	BA	1654	A
25	BA	1656	A
25	BA	1659	G
25	BA	1695	C
25	BA	1701	A
25	BA	1721	G
25	BA	1743	G
25	BA	1747	A
25	BA	1748	A
25	BA	1750	G

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Mol	Chain	Res	Type
25	BA	1767	A
25	BA	1768	U
25	BA	1776	G
25	BA	1777	G
25	BA	1781	G
25	BA	1787	G
25	BA	1793	A
25	BA	1794	G
25	BA	1795	G
25	BA	1804	A
25	BA	1811	A
25	BA	1813	C
25	BA	1817	A
25	BA	1822	A
25	BA	1831	C
25	BA	1847	G
25	BA	1848	G
25	BA	1859	G
25	BA	1860	A
25	BA	1870	G
25	BA	1878	A
25	BA	1879	A
25	BA	1889	G
25	BA	1899	A
25	BA	1900	G
25	BA	1911	A
25	BA	1922	A
25	BA	1928	G
25	BA	1951	G
25	BA	1952	G
25	BA	1959	A
25	BA	1960	A
25	BA	1977	U
25	BA	1985	U
25	BA	1989	C
25	BA	1992	A
25	BA	1993	A
25	BA	1994	A
25	BA	2014	G
25	BA	2015	U
25	BA	2019	G
25	BA	2042	A

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Mol	Chain	Res	Type
25	BA	2045	G
25	BA	2053	A
25	BA	2054	G
25	BA	2055	A
25	BA	2065	C
25	BA	2077	C
25	BA	2078	G
25	BA	2082	A
25	BA	2083	G
25	BA	2084	A
25	BA	2091	G
25	BA	2124	U
25	BA	2132	G
25	BA	2134	G
25	BA	2135	U
25	BA	2136	A
25	BA	2138	G
25	BA	2141	A
25	BA	2143	G
25	BA	2144	U
25	BA	2149	G
25	BA	2150	C
25	BA	2153	G
25	BA	2154	U
25	BA	2155	G
25	BA	2156	A
25	BA	2157	A
25	BA	2160	C
25	BA	2162	C
25	BA	2164	C
25	BA	2166	U
25	BA	2168	C
25	BA	2177	G
25	BA	2178	G
25	BA	2179	G
25	BA	2180	A
25	BA	2181	G
25	BA	2182	G
25	BA	2187	G
25	BA	2188	G
25	BA	2189	U
25	BA	2193	A

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Mol	Chain	Res	Type
25	BA	2194	U
25	BA	2195	A
25	BA	2196	C
25	BA	2200	C
25	BA	2202	U
25	BA	2203	G
25	BA	2204	G
25	BA	2206	G
25	BA	2210	C
25	BA	2212	G
25	BA	2214	G
25	BA	2220	A
25	BA	2227	G
25	BA	2228	G
25	BA	2229	A
25	BA	2237	A
25	BA	2247	G
25	BA	2250	G
25	BA	2251	G
25	BA	2280	A
25	BA	2281	A
25	BA	2287	C
25	BA	2295	C
25	BA	2299	A
25	BA	2301	G
25	BA	2317	A
25	BA	2320	G
25	BA	2324	U
25	BA	2332	A
25	BA	2337	G
25	BA	2346	G
25	BA	2348	A
25	BA	2359	C
25	BA	2362	C
25	BA	2373	A
25	BA	2395	G
25	BA	2397	C
25	BA	2418	U
25	BA	2419	G
25	BA	2422	G
25	BA	2436	C
25	BA	2437	A

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Mol	Chain	Res	Type
25	BA	2441	G
25	BA	2442	A
25	BA	2447	A
25	BA	2451	A
25	BA	2453	C
25	BA	2460	A
25	BA	2480	G
25	BA	2486	C
25	BA	2488	A
25	BA	2503	U
25	BA	2510	C
25	BA	2514	G
25	BA	2517	G
25	BA	2518	U
25	BA	2530	A
25	BA	2541	G
25	BA	2566	U
25	BA	2578	A
25	BA	2579	G
25	BA	2585	C
25	BA	2594	G
25	BA	2614	A
25	BA	2621	U
25	BA	2623	U
25	BA	2624	C
25	BA	2641	A
25	BA	2642	G
25	BA	2653	G
25	BA	2681	G
25	BA	2682	A
25	BA	2701	U
25	BA	2702	C
25	BA	2703	C
25	BA	2715	C
25	BA	2725	A
25	BA	2726	A
25	BA	2739	U
25	BA	2746	A
25	BA	2770	A
25	BA	2771	A
25	BA	2774	G
25	BA	2777	A

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Mol	Chain	Res	Type
25	BA	2778	A
25	BA	2782	C
25	BA	2791	A
25	BA	2803	A
25	BA	2804	C
25	BA	2806	G
25	BA	2807	C
25	BA	2813	G
25	BA	2814	C
25	BA	2816	G
25	BA	2817	G
25	BA	2828	G
25	BA	2830	A
25	BA	2831	A
25	BA	2845	A
25	BA	2882	G
25	BA	2886	G
25	BA	2890	C
25	BA	2901	A
25	BA	2903	G
25	BA	2904	U
26	BB	2	C
26	BB	7	G
26	BB	13	A
26	BB	15	A
26	BB	17	C
26	BB	20	C
26	BB	25	A
26	BB	32	C
26	BB	40	U
26	BB	42	C
26	BB	56	G
26	BB	57	A
26	BB	65	C
26	BB	67	G
26	BB	73	A
26	BB	84	C
26	BB	106	G
26	BB	110	G
26	BB	120	A
1	CA	6	G
1	CA	9	G

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Mol	Chain	Res	Type
1	CA	22	G
1	CA	31	G
1	CA	32	A
1	CA	39	G
1	CA	47	C
1	CA	48	C
1	CA	51	A
1	CA	66	G
1	CA	73	G
1	CA	78	G
1	CA	79	G
1	CA	80	G
1	CA	88	A
1	CA	89	C
1	CA	91	C
1	CA	92	C
1	CA	96	U
1	CA	101	A
1	CA	111	G
1	CA	115	G
1	CA	116	A
1	CA	121	C
1	CA	131	C
1	CA	138	G
1	CA	142	G
1	CA	144	G
1	CA	155	C
1	CA	156	G
1	CA	163	C
1	CA	166	G
1	CA	172	A
1	CA	174	C
1	CA	179	A
1	CA	180	U
1	CA	182	U
1	CA	186	C
1	CA	189	G
1	CA	189(D)	C
1	CA	195	A
1	CA	197	A
1	CA	201	C
1	CA	202	U

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Mol	Chain	Res	Type
1	CA	203	U
1	CA	204	U
1	CA	216	G
1	CA	226	G
1	CA	247	G
1	CA	251	G
1	CA	258	G
1	CA	266	G
1	CA	267	C
1	CA	289	G
1	CA	321	A
1	CA	328	C
1	CA	332	G
1	CA	344	A
1	CA	345	C
1	CA	352	C
1	CA	353	A
1	CA	354	G
1	CA	355	C
1	CA	367	U
1	CA	372	C
1	CA	373	A
1	CA	381	C
1	CA	384	G
1	CA	397	A
1	CA	398	C
1	CA	406	G
1	CA	412	A
1	CA	414	A
1	CA	424	G
1	CA	426	G
1	CA	429	U
1	CA	430	A
1	CA	439	A
1	CA	441	A
1	CA	442	C
1	CA	443	C
1	CA	452	A
1	CA	461	A
1	CA	470	C
1	CA	471	G
1	CA	477	A

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Mol	Chain	Res	Type
1	CA	484	G
1	CA	485	G
1	CA	496	A
1	CA	498	U
1	CA	505	G
1	CA	509	A
1	CA	510	A
1	CA	511	C
1	CA	518	C
1	CA	521	G
1	CA	524	G
1	CA	528	C
1	CA	531	U
1	CA	532	A
1	CA	533	A
1	CA	547	A
1	CA	559	A
1	CA	561	U
1	CA	572	A
1	CA	573	A
1	CA	576	G
1	CA	577	G
1	CA	590	C
1	CA	592	G
1	CA	596	C
1	CA	599	C
1	CA	619	U
1	CA	627	G
1	CA	630	G
1	CA	631	G
1	CA	637	G
1	CA	639	G
1	CA	650	G
1	CA	653	A
1	CA	660	G
1	CA	665	A
1	CA	673	G
1	CA	687	A
1	CA	688	G
1	CA	695	A
1	CA	723	U
1	CA	724	G

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Mol	Chain	Res	Type
1	CA	731	G
1	CA	749	C
1	CA	752	G
1	CA	755	G
1	CA	759	A
1	CA	773	G
1	CA	774	G
1	CA	777	A
1	CA	792	A
1	CA	793	U
1	CA	794	A
1	CA	815	A
1	CA	816	A
1	CA	817	C
1	CA	821	G
1	CA	828	A
1	CA	840	C
1	CA	841	U
1	CA	848	C
1	CA	851	G
1	CA	859	A
1	CA	873	A
1	CA	874	G
1	CA	902	G
1	CA	913	A
1	CA	914	A
1	CA	926	G
1	CA	927	G
1	CA	931	C
1	CA	932	C
1	CA	934	C
1	CA	936	C
1	CA	960	U
1	CA	961	U
1	CA	968	A
1	CA	969	A
1	CA	971	G
1	CA	972	C
1	CA	974	A
1	CA	975	A
1	CA	976	G
1	CA	977	A

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Mol	Chain	Res	Type
1	CA	982	U
1	CA	989	C
1	CA	992	U
1	CA	993	G
1	CA	996	A
1	CA	1000	U
1	CA	1001(A)	G
1	CA	1002	G
1	CA	1003	G
1	CA	1004	A
1	CA	1005	A
1	CA	1006	C
1	CA	1008	C
1	CA	1011	G
1	CA	1021	G
1	CA	1022	G
1	CA	1024	G
1	CA	1025	U
1	CA	1026	G
1	CA	1027	C
1	CA	1028	C
1	CA	1030	C
1	CA	1030(A)	G
1	CA	1032	G
1	CA	1033	G
1	CA	1035	A
1	CA	1037	C
1	CA	1039	C
1	CA	1046	A
1	CA	1052	U
1	CA	1054	C
1	CA	1055	A
1	CA	1065	U
1	CA	1066	C
1	CA	1067	A
1	CA	1068	G
1	CA	1077	G
1	CA	1081	G
1	CA	1085	U
1	CA	1088	G
1	CA	1089	G
1	CA	1094	G

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Mol	Chain	Res	Type
1	CA	1095	U
1	CA	1097	C
1	CA	1101	A
1	CA	1104	G
1	CA	1108	G
1	CA	1110	A
1	CA	1111	A
1	CA	1117	G
1	CA	1118	C
1	CA	1129	C
1	CA	1130	A
1	CA	1132	C
1	CA	1134	G
1	CA	1135	U
1	CA	1136	U
1	CA	1137	C
1	CA	1138	G
1	CA	1139	G
1	CA	1140	C
1	CA	1141	C
1	CA	1146	A
1	CA	1147	C
1	CA	1151	A
1	CA	1152	A
1	CA	1154	G
1	CA	1157	A
1	CA	1158	C
1	CA	1159	U
1	CA	1161	C
1	CA	1165	C
1	CA	1182	G
1	CA	1183	A
1	CA	1184	G
1	CA	1190	G
1	CA	1191	A
1	CA	1196	U
1	CA	1197	G
1	CA	1201	A
1	CA	1202	G
1	CA	1211	U
1	CA	1212	U
1	CA	1213	A

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Mol	Chain	Res	Type
1	CA	1222	G
1	CA	1224	G
1	CA	1227	A
1	CA	1228	C
1	CA	1238	A
1	CA	1240	U
1	CA	1250	A
1	CA	1256	A
1	CA	1257	U
1	CA	1258	G
1	CA	1269	A
1	CA	1270	C
1	CA	1273	G
1	CA	1276	G
1	CA	1278	U
1	CA	1279	A
1	CA	1280	A
1	CA	1281	U
1	CA	1282	C
1	CA	1287	A
1	CA	1300	G
1	CA	1305	G
1	CA	1317	C
1	CA	1320	C
1	CA	1338	G
1	CA	1340	A
1	CA	1347	G
1	CA	1353	G
1	CA	1357	A
1	CA	1358	U
1	CA	1363	C
1	CA	1370	G
1	CA	1379	G
1	CA	1394	A
1	CA	1397	C
1	CA	1419	G
1	CA	1442	G
1	CA	1442(A)	G
1	CA	1446	U
1	CA	1447	A
1	CA	1456	G
1	CA	1475	G

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Mol	Chain	Res	Type
1	CA	1492	A
1	CA	1493	A
1	CA	1502	A
1	CA	1503	A
1	CA	1504	G
1	CA	1506	U
1	CA	1517	G
1	CA	1520	G
1	CA	1529	G
1	CA	1530	G
1	CA	1531	A
1	CA	1532	U
22	CV	13	A
23	CW	3	C
23	CW	4	C
23	CW	6	G
23	CW	8	4SU
23	CW	9	A
23	CW	12	U
23	CW	14	A
23	CW	19	G
23	CW	22	G
23	CW	25	C
23	CW	26	A
23	CW	27	G
23	CW	29	G
23	CW	34	G
23	CW	46	7MG
23	CW	48	C
23	CW	49	C
23	CW	50	U
23	CW	61	C
23	CW	62	C
23	CW	63	G
23	CW	64	A
23	CW	66	U
23	CW	68	C
23	CW	70	G
23	CW	73	A
23	CW	74	C
24	CX	9	G
24	CX	16	C

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Mol	Chain	Res	Type
24	CX	18	G
24	CX	19	G
24	CX	20	U
24	CX	21	A
24	CX	31	G
24	CX	46	G
24	CX	47	U
24	CX	48	C
24	CX	50	U
24	CX	54	5MU
24	CX	56	C
24	CX	64	G
24	CX	68	C
24	CX	76	A
23	CY	3	C
23	CY	11	C
23	CY	13	C
23	CY	14	A
23	CY	15	G
23	CY	19	G
23	CY	23	A
23	CY	24	G
23	CY	25	C
23	CY	34	G
23	CY	37	MIA
23	CY	44	G
23	CY	45	U
23	CY	47	U
23	CY	48	C
23	CY	49	C
23	CY	52	G
23	CY	54	5MU
23	CY	55	PSU
23	CY	56	C
23	CY	57	G
23	CY	58	A
23	CY	59	U
23	CY	61	C
23	CY	62	C
23	CY	65	G
23	CY	68	C
23	CY	70	G

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Mol	Chain	Res	Type
23	CY	73	A
25	DA	9	U
25	DA	10	G
25	DA	11	G
25	DA	12	U
25	DA	15	G
25	DA	34	C
25	DA	36	G
25	DA	45	C
25	DA	61	G
25	DA	71	A
25	DA	74	A
25	DA	75	G
25	DA	84	A
25	DA	90	U
25	DA	95	G
25	DA	100	G
25	DA	102	G
25	DA	118	A
25	DA	119	A
25	DA	120	U
25	DA	125	G
25	DA	154(A)	C
25	DA	157	U
25	DA	173	G
25	DA	181	A
25	DA	196	A
25	DA	199	A
25	DA	205	G
25	DA	215	G
25	DA	216	A
25	DA	221	A
25	DA	222	A
25	DA	228	A
25	DA	229	A
25	DA	230	U
25	DA	232	G
25	DA	233	A
25	DA	248	G
25	DA	250	G
25	DA	271(A)	A
25	DA	271(I)	G

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Mol	Chain	Res	Type
25	DA	271(K)	U
25	DA	271(L)	U
25	DA	271(M)	G
25	DA	271(N)	U
25	DA	272	G
25	DA	272(A)	U
25	DA	272(B)	G
25	DA	277	C
25	DA	278	A
25	DA	294	A
25	DA	311	A
25	DA	312	G
25	DA	324	A
25	DA	327	G
25	DA	329	G
25	DA	330	A
25	DA	338	G
25	DA	352	G
25	DA	362	U
25	DA	363	G
25	DA	363(B)	G
25	DA	386	G
25	DA	389	G
25	DA	396	G
25	DA	405	U
25	DA	411	G
25	DA	412	A
25	DA	421	U
25	DA	422	A
25	DA	435	C
25	DA	443	A
25	DA	444	C
25	DA	454	A
25	DA	455	C
25	DA	457	A
25	DA	470	A
25	DA	480	A
25	DA	481	G
25	DA	505	A
25	DA	508	G
25	DA	509	C
25	DA	522	G

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Mol	Chain	Res	Type
25	DA	528	A
25	DA	529	A
25	DA	530	G
25	DA	531	C
25	DA	532	A
25	DA	533	G
25	DA	545	G
25	DA	563	G
25	DA	568	U
25	DA	573	G
25	DA	575	A
25	DA	587	C
25	DA	588	U
25	DA	603	A
25	DA	604	G
25	DA	607	U
25	DA	614(B)	G
25	DA	615	G
25	DA	616	G
25	DA	627	A
25	DA	637	A
25	DA	639	U
25	DA	640	C
25	DA	645	C
25	DA	646	A
25	DA	652(B)	A
25	DA	652(C)	G
25	DA	652(U)	G
25	DA	668	G
25	DA	669	G
25	DA	686	G
25	DA	701	G
25	DA	717	G
25	DA	730	C
25	DA	752	A
25	DA	753	C
25	DA	765	G
25	DA	774	A
25	DA	775	G
25	DA	776	G
25	DA	782	A
25	DA	783	A

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Mol	Chain	Res	Type
25	DA	784	A
25	DA	785	G
25	DA	790	C
25	DA	792	G
25	DA	805	G
25	DA	812	C
25	DA	819	A
25	DA	827	U
25	DA	828	U
25	DA	847	U
25	DA	848	G
25	DA	857	C
25	DA	859	G
25	DA	866	A
25	DA	867	C
25	DA	873	G
25	DA	874	G
25	DA	875	G
25	DA	879	G
25	DA	884	C
25	DA	885	C
25	DA	886	C
25	DA	887	A
25	DA	888	C
25	DA	889	C
25	DA	890	A
25	DA	893	C
25	DA	894	C
25	DA	896	A
25	DA	897	C
25	DA	899	A
25	DA	900	A
25	DA	901	A
25	DA	902	C
25	DA	910	A
25	DA	917	A
25	DA	932	G
25	DA	941	A
25	DA	945	A
25	DA	946	G
25	DA	950	G
25	DA	953	A

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Mol	Chain	Res	Type
25	DA	958	U
25	DA	959	A
25	DA	961	C
25	DA	974	G
25	DA	975	C
25	DA	983	A
25	DA	996	A
25	DA	1005	C
25	DA	1012	U
25	DA	1013	C
25	DA	1017	G
25	DA	1020	A
25	DA	1022	G
25	DA	1025	G
25	DA	1026	U
25	DA	1027	A
25	DA	1033	U
25	DA	1034	G
25	DA	1038	C
25	DA	1039	G
25	DA	1040	C
25	DA	1041	C
25	DA	1043	C
25	DA	1114	G
25	DA	1115	G
25	DA	1130	U
25	DA	1135	C
25	DA	1136	G
25	DA	1139	G
25	DA	1143	A
25	DA	1153	C
25	DA	1170	G
25	DA	1171	G
25	DA	1205	U
25	DA	1206	G
25	DA	1210	A
25	DA	1211	U
25	DA	1212	G
25	DA	1219	G
25	DA	1220	A
25	DA	1229	G
25	DA	1237	A

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Mol	Chain	Res	Type
25	DA	1244	G
25	DA	1253	A
25	DA	1256	G
25	DA	1271	G
25	DA	1272	A
25	DA	1273	U
25	DA	1300	U
25	DA	1301	A
25	DA	1309	G
25	DA	1314	C
25	DA	1352	U
25	DA	1359	A
25	DA	1360	A
25	DA	1365	A
25	DA	1370	C
25	DA	1384	A
25	DA	1385	G
25	DA	1395	A
25	DA	1416	G
25	DA	1417	C
25	DA	1420	U
25	DA	1421	G
25	DA	1427	A
25	DA	1428	C
25	DA	1435	G
25	DA	1437	C
25	DA	1445	A
25	DA	1449	A
25	DA	1450	G
25	DA	1455	G
25	DA	1460	A
25	DA	1461	G
25	DA	1467	C
25	DA	1471	A
25	DA	1482	G
25	DA	1490	A
25	DA	1493	C
25	DA	1494	A
25	DA	1495	A
25	DA	1496	A
25	DA	1497	U
25	DA	1508	A

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Mol	Chain	Res	Type
25	DA	1509	C
25	DA	1509(A)	A
25	DA	1528(A)	A
25	DA	1531	C
25	DA	1532	C
25	DA	1533	G
25	DA	1541	G
25	DA	1543	C
25	DA	1554	A
25	DA	1558	A
25	DA	1559	G
25	DA	1566	A
25	DA	1569	A
25	DA	1578	U
25	DA	1582	C
25	DA	1583	A
25	DA	1584	C
25	DA	1586	A
25	DA	1591	G
25	DA	1608	A
25	DA	1610	A
25	DA	1616	A
25	DA	1631(A)	A
25	DA	1640	C
25	DA	1648	C
25	DA	1654	A
25	DA	1674	G
25	DA	1696	G
25	DA	1700	A
25	DA	1721	G
25	DA	1722	A
25	DA	1746	G
25	DA	1756	G
25	DA	1762	A
25	DA	1763	G
25	DA	1764	G
25	DA	1773	A
25	DA	1780	A
25	DA	1782	C
25	DA	1791	A
25	DA	1800	C
25	DA	1801	G

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Mol	Chain	Res	Type
25	DA	1812	A
25	DA	1816	G
25	DA	1829	A
25	DA	1847	A
25	DA	1848	A
25	DA	1877	A
25	DA	1878	G
25	DA	1900	A
25	DA	1906	G
25	DA	1913	A
25	DA	1914	C
25	DA	1929	G
25	DA	1930	G
25	DA	1936	A
25	DA	1938	A
25	DA	1955	U
25	DA	1963	U
25	DA	1967	C
25	DA	1970	A
25	DA	1971	A
25	DA	1972	A
25	DA	1993	U
25	DA	1997	G
25	DA	2023	G
25	DA	2031	A
25	DA	2032	G
25	DA	2033	A
25	DA	2043	C
25	DA	2055	C
25	DA	2056	G
25	DA	2060	A
25	DA	2061	G
25	DA	2062	A
25	DA	2069	G
25	DA	2099	U
25	DA	2101	G
25	DA	2104	G
25	DA	2105	C
25	DA	2107	C
25	DA	2108	C
25	DA	2110	G
25	DA	2111	C

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Mol	Chain	Res	Type
25	DA	2116	G
25	DA	2117	A
25	DA	2119	A
25	DA	2122	U
25	DA	2126	A
25	DA	2127	G
25	DA	2130	U
25	DA	2131	G
25	DA	2132	U
25	DA	2133	G
25	DA	2134	A
25	DA	2135	A
25	DA	2137	C
25	DA	2138	C
25	DA	2139	C
25	DA	2144	U
25	DA	2145	C
25	DA	2146	C
25	DA	2148	G
25	DA	2149	G
25	DA	2150	U
25	DA	2151	G
25	DA	2153	G
25	DA	2154	G
25	DA	2155	G
25	DA	2156	G
25	DA	2157	G
25	DA	2158	A
25	DA	2159	G
25	DA	2160	G
25	DA	2163	C
25	DA	2166	G
25	DA	2167	U
25	DA	2168	G
25	DA	2169	A
25	DA	2172	U
25	DA	2173	A
25	DA	2175	C
25	DA	2178	C
25	DA	2184	G
25	DA	2185	C
25	DA	2186	G

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Mol	Chain	Res	Type
25	DA	2189	U
25	DA	2192	G
25	DA	2198	A
25	DA	2206	G
25	DA	2207	G
25	DA	2208	A
25	DA	2218	U
25	DA	2225	A
25	DA	2238	G
25	DA	2239	G
25	DA	2268	A
25	DA	2275	C
25	DA	2279	G
25	DA	2283	C
25	DA	2287	A
25	DA	2305	A
25	DA	2308	G
25	DA	2311	A
25	DA	2312	U
25	DA	2319	G
25	DA	2320	A
25	DA	2325	G
25	DA	2334	G
25	DA	2336	A
25	DA	2347	C
25	DA	2350	C
25	DA	2376	A
25	DA	2383	G
25	DA	2385	C
25	DA	2396	G
25	DA	2406	U
25	DA	2425	A
25	DA	2428	G
25	DA	2429	G
25	DA	2430	A
25	DA	2434	A
25	DA	2435	A
25	DA	2439	A
25	DA	2441	C
25	DA	2445	G
25	DA	2448	A
25	DA	2474	C

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Mol	Chain	Res	Type
25	DA	2476	A
25	DA	2480	C
25	DA	2487	G
25	DA	2494	G
25	DA	2502	G
25	DA	2505	G
25	DA	2506	U
25	DA	2507	C
25	DA	2518	A
25	DA	2520	C
25	DA	2529	G
25	DA	2554	U
25	DA	2566	A
25	DA	2567	G
25	DA	2573	C
25	DA	2578	G
25	DA	2582	G
25	DA	2602	A
25	DA	2611	U
25	DA	2612	C
25	DA	2629	A
25	DA	2630	G
25	DA	2652	C
25	DA	2654	A
25	DA	2656	U
25	DA	2663	G
25	DA	2673	G
25	DA	2689	U
25	DA	2690	C
25	DA	2694	G
25	DA	2702	U
25	DA	2703	C
25	DA	2712(A)	A
25	DA	2713	A
25	DA	2714	G
25	DA	2718	G
25	DA	2726	U
25	DA	2733	A
25	DA	2748	A
25	DA	2751	G
25	DA	2752	C
25	DA	2757	A

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Mol	Chain	Res	Type
25	DA	2761	G
25	DA	2764	A
25	DA	2765	A
25	DA	2766	G
25	DA	2778	A
25	DA	2789	C
25	DA	2793	G
25	DA	2794	C
25	DA	2802	G
25	DA	2807	G
25	DA	2818	G
25	DA	2820	A
25	DA	2821	A
25	DA	2833	G
25	DA	2835	A
25	DA	2839	G
25	DA	2872	G
25	DA	2875	C
25	DA	2880	C
25	DA	2892	A
25	DA	2893	G
25	DA	2894	G
25	DA	2895	U
25	DA	2896	C
25	DA	2897	U
26	DB	2	C
26	DB	7	G
26	DB	13	A
26	DB	15	A
26	DB	17	C
26	DB	25	A
26	DB	32	C
26	DB	40	U
26	DB	42	C
26	DB	56	G
26	DB	64	C
26	DB	65	C
26	DB	73	A
26	DB	75	G
26	DB	84	C
26	DB	88	C
26	DB	108	U

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Mol	Chain	Res	Type
26	DB	110	G
26	DB	116	G
26	DB	120	A

All (126) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	96	U
1	AA	115	G
1	AA	250	A
1	AA	266	G
1	AA	347	G
1	AA	429	U
1	AA	509	A
1	AA	560	U
1	AA	687	A
1	AA	748	C
1	AA	839	U
1	AA	913	A
1	AA	991	U
1	AA	1026	G
1	AA	1036	G
1	AA	1064	G
1	AA	1065	U
1	AA	1067	A
1	AA	1181	G
1	AA	1201	A
1	AA	1281	U
1	AA	1285	A
1	AA	1442	G
1	AA	1492	A
23	AW	45	U
23	AW	47	U
24	AX	16	C
23	AY	58	A
25	BA	184	A
25	BA	185	A
25	BA	271	U
25	BA	302	A
25	BA	572	A
25	BA	596	G
25	BA	793	A

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Mol	Chain	Res	Type
25	BA	811	A
25	BA	821	A
25	BA	941	U
25	BA	1005	A
25	BA	1019	G
25	BA	1093	G
25	BA	1099	C
25	BA	1135	G
25	BA	1219	A
25	BA	1220	U
25	BA	1221	G
25	BA	1255	A
25	BA	1346	U
25	BA	1347	A
25	BA	1466	U
25	BA	1554	A
25	BA	1577	C
25	BA	1700	G
25	BA	2014	G
25	BA	2153	G
25	BA	2156	A
25	BA	2166	U
25	BA	2167	C
25	BA	2192	A
25	BA	2203	G
25	BA	2205	C
25	BA	2209	G
25	BA	2418	U
25	BA	2623	U
25	BA	2701	U
25	BA	2769	U
25	BA	2902	G
26	BB	1	U
1	CA	65	U
1	CA	115	G
1	CA	250	A
1	CA	266	G
1	CA	429	U
1	CA	509	A
1	CA	560	U
1	CA	687	A
1	CA	748	C

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Mol	Chain	Res	Type
1	CA	839	U
1	CA	913	A
1	CA	1027	C
1	CA	1064	G
1	CA	1065	U
1	CA	1067	A
1	CA	1128	C
1	CA	1181	G
1	CA	1183	A
1	CA	1190	G
1	CA	1201	A
1	CA	1212	U
1	CA	1442	G
1	CA	1492	A
23	CW	13	C
24	CX	16	C
23	CY	14	A
23	CY	46	7MG
23	CY	58	A
25	DA	195	A
25	DA	196	A
25	DA	228	A
25	DA	271(K)	U
25	DA	271(M)	G
25	DA	277	C
25	DA	528	A
25	DA	529	A
25	DA	587	C
25	DA	752	A
25	DA	764	A
25	DA	774	A
25	DA	827	U
25	DA	856	C
25	DA	900	A
25	DA	1210	A
25	DA	1300	U
25	DA	1420	U
25	DA	1493	C
25	DA	1530	C
25	DA	1653	G
25	DA	1913	A
25	DA	1992	G

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Mol	Chain	Res	Type
25	DA	2110	G
25	DA	2119	A
25	DA	2126	A
25	DA	2406	U
25	DA	2689	U
25	DA	2756	U
26	DB	1	U

5.4 Non-standard residues in protein, DNA, RNA chains (i)

36 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
23	4SU	CW	8	23	18,21,22	1.81	5 (27%)	25,30,33	1.98	5 (20%)
23	5MU	CY	54	23	19,22,23	1.47	5 (26%)	27,32,35	2.16	5 (18%)
23	PSU	CW	32	23	18,21,22	1.37	2 (11%)	21,30,33	1.92	3 (14%)
23	7MG	AW	46	23	23,26,27	1.42	3 (13%)	27,39,42	2.59	7 (25%)
23	5MU	CW	54	23	19,22,23	1.36	5 (26%)	27,32,35	1.92	7 (25%)
23	PSU	CY	39	23	18,21,22	1.37	2 (11%)	21,30,33	1.94	4 (19%)
24	4SU	CX	8	24	18,21,22	2.08	4 (22%)	25,30,33	1.45	5 (20%)
23	PSU	CY	32	23	18,21,22	1.31	2 (11%)	21,30,33	1.95	3 (14%)
23	MIA	CY	37	23	21,24,32	1.57	4 (19%)	30,35,47	2.04	9 (30%)
23	PSU	AW	55	23	18,21,22	1.42	2 (11%)	21,30,33	2.11	4 (19%)
23	MIA	CW	37	23	24,27,32	1.99	5 (20%)	32,39,47	2.43	11 (34%)
23	4SU	AY	8	23	18,21,22	1.75	4 (22%)	25,30,33	2.09	5 (20%)
23	PSU	CW	39	23	18,21,22	1.44	2 (11%)	21,30,33	1.79	3 (14%)
23	PSU	CY	55	23	18,21,22	1.52	4 (22%)	21,30,33	2.06	4 (19%)
24	5MU	AX	54	24,56	19,22,23	1.45	6 (31%)	27,32,35	1.89	6 (22%)
23	7MG	CY	46	23	23,26,27	1.39	3 (13%)	27,39,42	2.92	8 (29%)
23	PSU	AY	55	23	18,21,22	1.35	2 (11%)	21,30,33	2.10	4 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
24	4SU	AX	8	24	18,21,22	2.23	6 (33%)	25,30,33	1.73	6 (24%)
23	4SU	AW	8	23	18,21,22	1.92	5 (27%)	25,30,33	1.80	5 (20%)
24	5MC	AX	32	24	19,22,23	1.70	3 (15%)	26,32,35	1.19	3 (11%)
23	PSU	AW	32	23	18,21,22	1.38	2 (11%)	21,30,33	2.03	3 (14%)
23	MIA	AY	37	23	21,24,32	1.63	4 (19%)	30,35,47	2.03	7 (23%)
23	7MG	CW	46	23	23,26,27	1.30	4 (17%)	27,39,42	2.67	6 (22%)
23	PSU	AY	39	23	18,21,22	1.39	2 (11%)	21,30,33	1.83	4 (19%)
23	PSU	CW	55	23	18,21,22	1.40	2 (11%)	21,30,33	2.04	3 (14%)
24	5MU	CX	54	24	19,22,23	1.45	6 (31%)	27,32,35	2.16	7 (25%)
24	PSU	CX	55	24	18,21,22	1.37	2 (11%)	21,30,33	1.99	5 (23%)
24	5MC	CX	32	24	19,22,23	1.75	3 (15%)	26,32,35	1.29	5 (19%)
23	MIA	AW	37	23	28,31,32	2.38	7 (25%)	38,44,47	2.60	13 (34%)
23	5MU	AY	54	23	19,22,23	1.54	5 (26%)	27,32,35	2.27	6 (22%)
23	PSU	AW	39	23	18,21,22	1.38	2 (11%)	21,30,33	1.96	3 (14%)
23	PSU	AY	32	23	18,21,22	1.31	2 (11%)	21,30,33	1.93	3 (14%)
24	PSU	AX	55	24	18,21,22	1.35	2 (11%)	21,30,33	2.00	4 (19%)
23	4SU	CY	8	23	18,21,22	1.78	4 (22%)	25,30,33	2.50	7 (28%)
23	7MG	AY	46	23	23,26,27	1.35	5 (21%)	27,39,42	2.63	6 (22%)
23	5MU	AW	54	23	19,22,23	1.36	5 (26%)	27,32,35	2.02	6 (22%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	4SU	CW	8	23	-	0/7/25/26	0/2/2/2
23	5MU	CY	54	23	-	2/7/25/26	0/2/2/2
23	PSU	CW	32	23	-	0/7/25/26	0/2/2/2
23	7MG	AW	46	23	-	1/7/37/38	0/3/3/3
23	5MU	CW	54	23	-	0/7/25/26	0/2/2/2
23	PSU	CY	39	23	-	0/7/25/26	0/2/2/2
24	4SU	CX	8	24	-	0/7/25/26	0/2/2/2
23	PSU	CY	32	23	-	0/7/25/26	0/2/2/2
23	MIA	CY	37	23	-	2/7/25/34	0/3/3/3
23	PSU	AW	55	23	-	0/7/25/26	0/2/2/2
23	MIA	CW	37	23	-	4/11/29/34	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	4SU	AY	8	23	-	0/7/25/26	0/2/2/2
23	PSU	CW	39	23	-	0/7/25/26	0/2/2/2
23	PSU	CY	55	23	-	2/7/25/26	0/2/2/2
24	5MU	AX	54	24,56	-	0/7/25/26	0/2/2/2
23	7MG	CY	46	23	-	3/7/37/38	0/3/3/3
23	PSU	AY	55	23	-	2/7/25/26	0/2/2/2
24	4SU	AX	8	24	-	0/7/25/26	0/2/2/2
23	4SU	AW	8	23	-	0/7/25/26	0/2/2/2
24	5MC	AX	32	24	-	0/7/25/26	0/2/2/2
23	PSU	AW	32	23	-	0/7/25/26	0/2/2/2
23	MIA	AY	37	23	-	2/7/25/34	0/3/3/3
23	7MG	CW	46	23	-	2/7/37/38	0/3/3/3
23	PSU	AY	39	23	-	0/7/25/26	0/2/2/2
23	PSU	CW	55	23	-	0/7/25/26	0/2/2/2
24	5MU	CX	54	24	-	2/7/25/26	0/2/2/2
24	PSU	CX	55	24	-	0/7/25/26	0/2/2/2
24	5MC	CX	32	24	-	0/7/25/26	0/2/2/2
23	MIA	AW	37	23	-	3/15/33/34	0/3/3/3
23	5MU	AY	54	23	-	3/7/25/26	0/2/2/2
23	PSU	AW	39	23	-	0/7/25/26	0/2/2/2
23	PSU	AY	32	23	-	0/7/25/26	0/2/2/2
24	PSU	AX	55	24	-	0/7/25/26	0/2/2/2
23	4SU	CY	8	23	-	0/7/25/26	0/2/2/2
23	7MG	AY	46	23	-	3/7/37/38	0/3/3/3
23	5MU	AW	54	23	-	0/7/25/26	0/2/2/2

All (131) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AW	37	MIA	C2-S10	-7.26	1.69	1.75
23	AW	37	MIA	C13-C14	6.97	1.53	1.32
24	CX	32	5MC	C5-C4	6.42	1.49	1.44
23	CW	37	MIA	C2-S10	-6.15	1.70	1.75
24	AX	32	5MC	C5-C4	6.15	1.48	1.44
24	AX	8	4SU	C4-N3	-5.46	1.32	1.37
23	AY	37	MIA	C5-C4	5.11	1.48	1.39
23	CY	37	MIA	C5-C4	4.99	1.48	1.39
23	AW	8	4SU	C4-S4	-4.92	1.60	1.68
23	CY	8	4SU	C4-S4	-4.88	1.60	1.68
24	CX	8	4SU	C4-N3	-4.81	1.32	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	CW	37	MIA	C5-C4	4.78	1.47	1.39
23	AW	37	MIA	C5-C4	4.72	1.47	1.39
23	CW	8	4SU	C4-S4	-4.66	1.60	1.68
23	AY	8	4SU	C4-S4	-4.61	1.60	1.68
24	CX	8	4SU	C4-S4	-4.53	1.60	1.68
24	AX	8	4SU	C4-S4	-4.45	1.60	1.68
23	CW	39	PSU	C6-C5	4.13	1.39	1.35
23	CW	55	PSU	C6-C5	3.99	1.39	1.35
23	AW	55	PSU	C6-C5	3.98	1.39	1.35
24	AX	8	4SU	C2-N3	-3.93	1.31	1.38
23	AY	39	PSU	C6-C5	3.86	1.39	1.35
23	AW	46	7MG	C4-N9	-3.76	1.33	1.37
24	CX	55	PSU	C6-C5	3.69	1.39	1.35
23	CW	32	PSU	C6-C5	3.62	1.39	1.35
23	AY	46	7MG	C5-C4	3.62	1.48	1.37
23	CY	39	PSU	C6-C5	3.58	1.39	1.35
23	AY	55	PSU	C6-C5	3.57	1.39	1.35
23	AY	32	PSU	C6-C5	3.52	1.39	1.35
23	CY	32	PSU	C6-C5	3.46	1.39	1.35
23	CY	46	7MG	C5-C4	3.44	1.48	1.37
23	AW	32	PSU	C6-C5	3.43	1.39	1.35
23	AW	39	PSU	C6-C5	3.42	1.39	1.35
24	CX	8	4SU	C2-N3	-3.41	1.32	1.38
23	CY	55	PSU	C6-C5	3.38	1.39	1.35
23	AW	8	4SU	C4-N3	-3.35	1.34	1.37
23	AW	46	7MG	C5-C4	3.29	1.47	1.37
23	CW	46	7MG	C5-C4	3.19	1.47	1.37
24	CX	8	4SU	C5-C4	-3.17	1.38	1.42
23	CW	8	4SU	C4-N3	-3.16	1.34	1.37
23	AW	8	4SU	C5-C4	-3.13	1.38	1.42
24	AX	55	PSU	C6-C5	3.10	1.38	1.35
24	AX	8	4SU	C5-C4	-3.07	1.38	1.42
23	CY	8	4SU	C4-N3	-3.02	1.34	1.37
23	AY	54	5MU	C2-N1	3.01	1.43	1.38
24	CX	54	5MU	C6-C5	2.94	1.39	1.34
23	AY	37	MIA	C5-C6	2.94	1.49	1.41
23	AY	54	5MU	C6-C5	2.92	1.39	1.34
23	CY	54	5MU	C6-C5	2.92	1.39	1.34
23	CW	37	MIA	C5-C6	2.90	1.48	1.41
23	CY	54	5MU	C2-N1	2.86	1.42	1.38
23	CY	55	PSU	C4-N3	-2.86	1.33	1.38
23	CW	46	7MG	C4-N9	-2.84	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AY	8	4SU	C4-N3	-2.81	1.34	1.37
23	AW	54	5MU	C6-C5	2.81	1.39	1.34
24	AX	54	5MU	C6-C5	2.78	1.39	1.34
24	AX	32	5MC	C6-C5	2.78	1.39	1.34
24	AX	54	5MU	C4-N3	-2.76	1.33	1.38
23	AY	54	5MU	C4-C5	2.76	1.49	1.44
24	CX	32	5MC	C6-C5	2.71	1.39	1.34
24	CX	54	5MU	C4-C5	2.70	1.49	1.44
23	AY	8	4SU	C5-C4	-2.70	1.39	1.42
23	CY	8	4SU	C2-N1	2.70	1.42	1.38
24	AX	55	PSU	C4-N3	-2.69	1.33	1.38
23	CY	46	7MG	C8-N9	2.67	1.47	1.45
23	CW	54	5MU	C6-C5	2.66	1.38	1.34
23	CY	37	MIA	C5-C6	2.66	1.48	1.41
23	AY	54	5MU	C4-N3	-2.66	1.33	1.38
23	CW	8	4SU	C5-C4	-2.65	1.39	1.42
23	AW	37	MIA	C5-C6	2.64	1.48	1.41
23	CW	39	PSU	C4-N3	-2.64	1.33	1.38
23	AW	32	PSU	C4-N3	-2.62	1.34	1.38
24	CX	54	5MU	C4-N3	-2.61	1.34	1.38
23	AY	39	PSU	C4-N3	-2.61	1.34	1.38
23	CY	46	7MG	C6-N1	-2.59	1.34	1.38
24	CX	55	PSU	C4-N3	-2.58	1.34	1.38
23	AW	39	PSU	C4-N3	-2.57	1.34	1.38
23	CY	39	PSU	C4-N3	-2.55	1.34	1.38
23	AW	8	4SU	C2-N1	2.55	1.42	1.38
23	AY	55	PSU	C4-N3	-2.55	1.34	1.38
23	CY	54	5MU	C4-N3	-2.54	1.34	1.38
23	CW	8	4SU	C2-N1	2.54	1.42	1.38
23	CW	55	PSU	C4-N3	-2.54	1.34	1.38
23	AW	54	5MU	C4-N3	-2.52	1.34	1.38
23	CY	54	5MU	C4-C5	2.50	1.48	1.44
23	AW	37	MIA	C5-N7	-2.49	1.34	1.39
23	AW	37	MIA	C8-N7	2.46	1.36	1.31
23	AY	37	MIA	C8-N7	2.45	1.36	1.31
24	AX	54	5MU	C4-C5	2.44	1.48	1.44
24	AX	8	4SU	O2-C2	2.43	1.27	1.23
24	AX	32	5MC	C6-N1	-2.43	1.33	1.38
23	CW	54	5MU	C4-C5	2.39	1.48	1.44
23	AW	8	4SU	O2-C2	2.39	1.27	1.23
23	AY	46	7MG	C4-N9	-2.37	1.34	1.37
24	CX	32	5MC	C6-N1	-2.37	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	AW	46	7MG	C6-N1	-2.35	1.34	1.38
24	CX	54	5MU	C2-N1	2.34	1.42	1.38
23	CW	37	MIA	C5-N7	-2.34	1.34	1.39
23	CY	8	4SU	C5-C4	-2.33	1.39	1.42
23	CY	55	PSU	C2-N3	-2.33	1.33	1.37
23	CW	54	5MU	C4-N3	-2.31	1.34	1.38
23	AY	8	4SU	C2-N1	2.31	1.42	1.38
23	CW	37	MIA	C8-N7	2.31	1.36	1.31
23	AY	32	PSU	C4-N3	-2.30	1.34	1.38
23	CY	32	PSU	C4-N3	-2.29	1.34	1.38
23	AW	55	PSU	C4-N3	-2.26	1.34	1.38
23	AY	46	7MG	C8-N9	2.24	1.47	1.45
23	AW	54	5MU	C4-C5	2.24	1.48	1.44
23	CY	37	MIA	C8-N7	2.22	1.36	1.31
23	AY	54	5MU	C6-N1	-2.22	1.34	1.38
23	CW	46	7MG	C6-N1	-2.22	1.34	1.38
23	CW	32	PSU	C4-N3	-2.21	1.34	1.38
23	CY	55	PSU	C2-N1	-2.21	1.33	1.36
23	AW	37	MIA	C4-N9	-2.18	1.33	1.37
24	AX	54	5MU	C2-N1	2.17	1.41	1.38
23	CW	54	5MU	C2-N1	2.17	1.41	1.38
24	AX	54	5MU	C6-N1	-2.16	1.34	1.38
23	AW	54	5MU	C2-N1	2.15	1.41	1.38
23	CW	8	4SU	C2-N3	-2.13	1.34	1.38
23	AY	46	7MG	C6-N1	-2.12	1.34	1.38
23	CW	46	7MG	C5-C6	2.11	1.48	1.43
23	CY	37	MIA	C5-N7	-2.09	1.35	1.39
24	AX	54	5MU	C2-N3	-2.09	1.34	1.38
24	CX	54	5MU	C6-N1	-2.04	1.34	1.38
23	AY	37	MIA	C5-N7	-2.03	1.35	1.39
23	AW	54	5MU	C6-N1	-2.03	1.34	1.38
23	AY	46	7MG	C5-C6	2.02	1.48	1.43
23	CY	54	5MU	C6-N1	-2.02	1.34	1.38
23	CW	54	5MU	C6-N1	-2.02	1.34	1.38
24	AX	8	4SU	C6-C5	2.01	1.39	1.35
24	CX	54	5MU	C2-N3	-2.00	1.34	1.38

All (195) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	CY	46	7MG	N9-C4-N3	10.40	140.70	125.46
23	AY	46	7MG	N9-C4-N3	9.26	139.04	125.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	AW	46	7MG	N9-C4-N3	8.85	138.42	125.46
23	CW	46	7MG	N9-C4-N3	8.62	138.09	125.46
23	AW	37	MIA	C12-C13-C14	-8.07	112.52	127.01
23	CW	37	MIA	C5-C4-N3	-8.05	118.70	127.18
23	CY	8	4SU	C4-N3-C2	-7.44	120.18	127.31
23	AW	37	MIA	C5-C4-N3	-7.39	119.40	127.18
23	CY	55	PSU	N1-C2-N3	6.61	122.14	115.17
23	AY	55	PSU	N1-C2-N3	6.48	122.01	115.17
23	AW	32	PSU	N1-C2-N3	6.35	121.87	115.17
23	AW	55	PSU	N1-C2-N3	6.28	121.80	115.17
24	AX	55	PSU	N1-C2-N3	6.22	121.73	115.17
23	CY	46	7MG	C5-C4-N3	-6.14	116.60	128.13
23	CW	37	MIA	N3-C4-N9	6.13	134.76	126.99
23	AW	39	PSU	N1-C2-N3	6.10	121.61	115.17
24	CX	55	PSU	N1-C2-N3	6.07	121.57	115.17
23	CW	55	PSU	N1-C2-N3	6.03	121.53	115.17
23	CY	39	PSU	N1-C2-N3	5.97	121.47	115.17
23	AY	37	MIA	C5-C4-N3	-5.97	118.50	126.72
23	AY	8	4SU	C4-N3-C2	-5.95	121.61	127.31
23	AY	32	PSU	N1-C2-N3	5.90	121.40	115.17
23	CY	32	PSU	N1-C2-N3	5.88	121.37	115.17
23	CW	32	PSU	N1-C2-N3	5.88	121.37	115.17
23	AY	54	5MU	C4-N3-C2	-5.81	119.72	127.34
23	CY	8	4SU	C5-C4-N3	5.78	120.13	114.75
23	AW	46	7MG	N9-C8-N7	-5.72	95.27	103.37
23	CW	39	PSU	N1-C2-N3	5.66	121.14	115.17
23	AY	39	PSU	N1-C2-N3	5.61	121.08	115.17
23	AY	54	5MU	N3-C2-N1	5.59	122.17	114.89
23	CW	46	7MG	N9-C8-N7	-5.59	95.46	103.37
23	CY	37	MIA	C5-C4-N3	-5.58	119.03	126.72
23	CW	46	7MG	C5-C4-N3	-5.52	117.77	128.13
23	AW	37	MIA	N3-C4-N9	5.52	134.00	126.99
23	CW	8	4SU	C4-N3-C2	-5.51	122.04	127.31
24	CX	54	5MU	C4-N3-C2	-5.35	120.33	127.34
24	CX	54	5MU	N3-C2-N1	5.26	121.74	114.89
23	CY	54	5MU	C4-N3-C2	-5.24	120.47	127.34
23	AW	8	4SU	C5-C4-N3	5.23	119.61	114.75
23	AY	46	7MG	C5-C4-N3	-5.19	118.39	128.13
23	AY	46	7MG	N9-C8-N7	-5.13	96.11	103.37
23	AW	54	5MU	N3-C2-N1	5.13	121.56	114.89
23	AY	8	4SU	C5-C4-N3	5.12	119.51	114.75
23	CY	37	MIA	N3-C4-N9	4.95	135.59	127.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	CW	8	4SU	C5-C4-N3	4.94	119.34	114.75
23	AY	54	5MU	C5-C4-N3	4.89	119.58	115.32
23	CY	8	4SU	N3-C2-N1	4.89	121.25	114.89
23	CY	54	5MU	C5-C4-N3	4.88	119.57	115.32
23	CY	54	5MU	N3-C2-N1	4.84	121.19	114.89
23	CW	46	7MG	C2-N3-C4	4.82	120.60	112.30
23	AW	54	5MU	C4-N3-C2	-4.79	121.06	127.34
23	CY	46	7MG	C2-N3-C4	4.79	120.55	112.30
23	AW	46	7MG	C5-C4-N3	-4.76	119.19	128.13
23	AY	37	MIA	N3-C4-N9	4.66	135.10	127.17
23	CY	46	7MG	N9-C8-N7	-4.65	96.79	103.37
24	AX	54	5MU	N3-C2-N1	4.61	120.89	114.89
24	CX	54	5MU	C5-C4-N3	4.57	119.30	115.32
24	AX	54	5MU	C4-N3-C2	-4.44	121.52	127.34
23	CW	54	5MU	C4-N3-C2	-4.40	121.57	127.34
23	AY	46	7MG	C2-N3-C4	4.32	119.73	112.30
23	AY	55	PSU	C4-N3-C2	-4.30	120.45	126.37
24	CX	55	PSU	C4-N3-C2	-4.27	120.49	126.37
23	AW	55	PSU	O2-C2-N1	-4.27	118.39	122.79
23	CW	54	5MU	N3-C2-N1	4.25	120.42	114.89
23	CY	8	4SU	C5-C4-S4	-4.20	119.51	124.31
23	AW	54	5MU	O4-C4-C5	-4.14	120.18	124.92
23	AY	8	4SU	C5-C4-S4	-4.14	119.58	124.31
23	CW	54	5MU	C5-C4-N3	4.14	118.92	115.32
23	CY	54	5MU	O4-C4-C5	-4.13	120.19	124.92
23	CW	55	PSU	C4-N3-C2	-4.04	120.80	126.37
23	AW	8	4SU	C4-N3-C2	-4.03	123.45	127.31
24	AX	55	PSU	C4-N3-C2	-4.03	120.82	126.37
23	AW	32	PSU	C4-N3-C2	-4.02	120.83	126.37
23	CW	54	5MU	O4-C4-C5	-4.00	120.34	124.92
24	AX	8	4SU	O2-C2-N1	3.97	127.96	122.80
24	AX	8	4SU	C6-C5-C4	-3.97	116.52	119.95
23	AY	54	5MU	C5-C6-N1	-3.95	119.02	123.31
23	CW	32	PSU	C4-N3-C2	-3.94	120.94	126.37
23	AW	54	5MU	C5-C4-N3	3.94	118.75	115.32
23	CY	32	PSU	C4-N3-C2	-3.93	120.95	126.37
23	AW	46	7MG	C2-N3-C4	3.91	119.03	112.30
23	AY	32	PSU	C4-N3-C2	-3.88	121.03	126.37
23	AW	55	PSU	C4-N3-C2	-3.87	121.04	126.37
23	AW	39	PSU	C4-N3-C2	-3.86	121.05	126.37
24	AX	54	5MU	C5-C4-N3	3.85	118.67	115.32
23	CY	55	PSU	C4-N3-C2	-3.83	121.09	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	CY	39	PSU	C4-N3-C2	-3.83	121.10	126.37
23	CW	37	MIA	C4-C5-N7	-3.80	106.23	110.58
24	CX	54	5MU	C5-C6-N1	-3.80	119.18	123.31
23	AW	32	PSU	O2-C2-N1	-3.78	118.89	122.79
23	AY	37	MIA	C2-N3-C4	3.72	120.92	111.83
23	AW	37	MIA	C15-C14-C13	-3.69	111.58	122.66
23	CW	8	4SU	N3-C2-N1	3.69	119.69	114.89
23	CY	32	PSU	O2-C2-N1	-3.66	119.01	122.79
23	CY	54	5MU	C5-C6-N1	-3.64	119.36	123.31
23	AW	37	MIA	C4-C5-N7	-3.63	106.43	110.58
23	AW	8	4SU	C5-C4-S4	-3.63	120.16	124.31
23	AY	8	4SU	N3-C2-N1	3.62	119.60	114.89
23	AY	37	MIA	C4-C5-N7	-3.61	106.46	110.58
23	CY	55	PSU	O2-C2-N1	-3.60	119.07	122.79
23	AW	39	PSU	O2-C2-N1	-3.59	119.08	122.79
23	AY	39	PSU	C4-N3-C2	-3.58	121.44	126.37
23	AW	37	MIA	C16-C14-C13	-3.56	111.97	122.66
23	CY	37	MIA	N3-C2-N1	-3.54	123.22	128.58
23	AW	37	MIA	C6-C5-N7	3.53	136.28	132.43
23	AY	54	5MU	O4-C4-C5	-3.53	120.88	124.92
23	CW	37	MIA	C2-N3-C4	3.53	121.53	112.29
23	CY	37	MIA	C2-N3-C4	3.52	120.44	111.83
23	CW	55	PSU	O2-C2-N1	-3.52	119.16	122.79
23	AY	55	PSU	O2-C2-N1	-3.51	119.17	122.79
23	AY	32	PSU	O2-C2-N1	-3.46	119.22	122.79
23	CW	39	PSU	C4-N3-C2	-3.41	121.67	126.37
24	AX	54	5MU	O4-C4-C5	-3.39	121.04	124.92
23	CW	8	4SU	C5-C4-S4	-3.37	120.45	124.31
23	AY	37	MIA	N3-C2-N1	-3.35	123.51	128.58
23	CW	37	MIA	C6-C5-N7	3.35	136.08	132.43
24	AX	32	5MC	C5-C4-N3	-3.33	118.34	121.75
24	AX	55	PSU	O2-C2-N1	-3.31	119.37	122.79
24	AX	54	5MU	C5-C6-N1	-3.30	119.73	123.31
24	CX	32	5MC	C5-C6-N1	-3.26	119.77	123.31
24	CX	54	5MU	O4-C4-C5	-3.26	121.19	124.92
24	AX	8	4SU	S4-C4-N3	-3.25	116.80	120.20
23	AW	37	MIA	C2-N3-C4	3.24	120.79	112.29
24	AX	32	5MC	C5-C6-N1	-3.21	119.83	123.31
23	CY	39	PSU	O2-C2-N1	-3.19	119.50	122.79
23	CY	37	MIA	C4-N9-C8	3.17	109.06	105.74
24	AX	8	4SU	C5-C4-N3	3.13	117.66	114.75
23	CW	32	PSU	O2-C2-N1	-3.11	119.58	122.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	CW	46	7MG	C5-C6-N1	3.11	116.41	110.94
24	CX	8	4SU	C1'-N1-C2	3.10	123.17	117.59
23	AW	46	7MG	C5-C4-N9	-3.08	102.39	106.33
24	CX	32	5MC	C5-C4-N3	-3.04	118.64	121.75
24	CX	8	4SU	C6-C5-C4	-3.03	117.33	119.95
23	AW	8	4SU	C1'-N1-C2	3.01	122.99	117.59
24	CX	8	4SU	C5-C4-N3	3.00	117.54	114.75
23	AY	46	7MG	C5-C4-N9	-2.94	102.57	106.33
23	CY	37	MIA	C4-C5-N7	-2.94	107.23	110.58
23	AW	54	5MU	O2-C2-N1	-2.90	119.02	122.80
23	AW	54	5MU	C5-C6-N1	-2.90	120.17	123.31
23	CW	54	5MU	C5-C6-N1	-2.87	120.20	123.31
23	CY	46	7MG	C5-C4-N9	-2.87	102.66	106.33
23	CW	37	MIA	C12-N6-C6	-2.80	120.25	122.85
23	CW	37	MIA	C5-N7-C8	2.78	107.82	103.45
23	AY	8	4SU	C1'-N1-C2	2.78	122.58	117.59
24	CX	8	4SU	O2-C2-N1	2.71	126.32	122.80
23	CY	46	7MG	C5-C6-N1	2.69	115.68	110.94
23	CW	8	4SU	C1'-N1-C2	2.67	122.39	117.59
23	AW	37	MIA	C4-N9-C8	2.60	108.47	105.74
23	AW	37	MIA	C5-N7-C8	2.58	107.50	103.45
24	CX	32	5MC	O2-C2-N3	-2.53	118.34	122.33
23	CW	37	MIA	N3-C2-N1	-2.52	122.39	127.00
24	AX	8	4SU	C1'-N1-C2	2.52	122.12	117.59
23	AY	37	MIA	C5-N7-C8	2.52	107.40	103.45
23	CW	37	MIA	C4-N9-C8	2.49	108.35	105.74
23	CW	37	MIA	C2-N1-C6	2.49	122.26	117.54
23	CY	46	7MG	O6-C6-C5	-2.48	121.54	127.62
23	AW	37	MIA	C2-N1-C6	2.47	122.23	117.54
23	CW	54	5MU	C5M-C5-C4	2.47	121.42	118.78
24	CX	55	PSU	O2-C2-N1	-2.46	120.25	122.79
24	AX	54	5MU	O2-C2-N1	-2.44	119.61	122.80
24	AX	8	4SU	O2-C2-N3	-2.43	117.00	121.49
23	CY	37	MIA	C5-N7-C8	2.42	107.25	103.45
23	AY	46	7MG	C5-C6-N1	2.41	115.19	110.94
23	AY	37	MIA	C4-N9-C8	2.38	108.24	105.74
24	CX	54	5MU	O2-C2-N1	-2.37	119.71	122.80
24	AX	55	PSU	C5-C6-N1	-2.33	118.91	122.14
23	AW	37	MIA	N3-C2-N1	-2.30	122.80	127.00
23	CW	39	PSU	O2-C2-N1	-2.29	120.43	122.79
23	AW	46	7MG	C5-C6-N1	2.27	114.93	110.94
24	CX	55	PSU	C5-C6-N1	-2.27	119.00	122.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
24	CX	8	4SU	O2-C2-N3	-2.26	117.32	121.49
23	CY	46	7MG	C4-C5-N7	2.24	108.03	105.38
23	AY	54	5MU	O2-C2-N3	-2.22	117.39	121.49
23	AW	46	7MG	O6-C6-C5	-2.21	122.20	127.62
23	AY	55	PSU	C5-C6-N1	-2.19	119.10	122.14
23	CY	8	4SU	C1'-N1-C2	2.18	121.50	117.59
24	CX	32	5MC	CM5-C5-C6	-2.17	119.91	122.85
24	AX	32	5MC	O2-C2-N3	-2.15	118.94	122.33
23	AW	8	4SU	N3-C2-N1	2.12	117.65	114.89
23	CY	8	4SU	C6-N1-C2	-2.12	118.42	121.00
23	AW	55	PSU	C6-C5-C4	-2.12	116.75	118.17
23	CY	55	PSU	O4'-C1'-C2'	2.10	108.05	105.15
24	CX	54	5MU	C5M-C5-C4	2.09	121.01	118.78
23	AW	37	MIA	N9-C8-N7	-2.08	110.99	113.94
24	CX	55	PSU	O2-C2-N3	-2.07	118.18	121.86
23	AY	39	PSU	O2-C2-N3	-2.07	118.18	121.86
23	CW	54	5MU	O2-C2-N1	-2.06	120.11	122.80
23	CY	8	4SU	O2-C2-N1	-2.06	120.12	122.80
23	CY	37	MIA	C2-N1-C6	2.05	122.09	118.73
23	CW	46	7MG	O6-C6-C5	-2.04	122.60	127.62
23	CW	37	MIA	N9-C8-N7	-2.03	111.06	113.94
23	AY	39	PSU	C6-C5-C4	-2.02	116.81	118.17
23	CY	37	MIA	N9-C8-N7	-2.01	111.08	113.94
24	CX	32	5MC	C1'-N1-C6	-2.01	117.84	121.15
23	CY	39	PSU	C5-C6-N1	-2.00	119.36	122.14

There are no chirality outliers.

All (31) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	AW	37	MIA	C12-C13-C14-C15
23	AW	37	MIA	C12-C13-C14-C16
23	AY	46	7MG	C4'-C5'-O5'-P
23	AY	54	5MU	O4'-C4'-C5'-O5'
23	CW	37	MIA	C5-C6-N6-C12
23	CW	37	MIA	N1-C6-N6-C12
23	CW	37	MIA	N1-C2-S10-C11
23	CW	37	MIA	N3-C2-S10-C11
24	CX	54	5MU	O4'-C4'-C5'-O5'
23	CY	54	5MU	O4'-C4'-C5'-O5'
23	CY	55	PSU	C2'-C1'-C5-C4
23	CY	55	PSU	C2'-C1'-C5-C6

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Mol	Chain	Res	Type	Atoms
23	CY	37	MIA	C3'-C4'-C5'-O5'
23	CY	54	5MU	C3'-C4'-C5'-O5'
23	CY	37	MIA	O4'-C4'-C5'-O5'
23	AY	54	5MU	C3'-C4'-C5'-O5'
24	CX	54	5MU	C3'-C4'-C5'-O5'
23	CY	46	7MG	O4'-C1'-N9-C4
23	CY	46	7MG	C2'-C1'-N9-C8
23	AW	46	7MG	C4'-C5'-O5'-P
23	AY	55	PSU	O4'-C1'-C5-C4
23	AW	37	MIA	C5-C6-N6-C12
23	CW	46	7MG	O4'-C4'-C5'-O5'
23	AY	54	5MU	C4'-C5'-O5'-P
23	AY	55	PSU	O4'-C1'-C5-C6
23	AY	37	MIA	C3'-C4'-C5'-O5'
23	CY	46	7MG	O4'-C1'-N9-C8
23	AY	46	7MG	C2'-C1'-N9-C8
23	CW	46	7MG	C3'-C4'-C5'-O5'
23	AY	37	MIA	C4'-C5'-O5'-P
23	AY	46	7MG	C3'-C4'-C5'-O5'

There are no ring outliers.

17 monomers are involved in 32 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	CW	8	4SU	2	0
23	AW	46	7MG	1	0
23	CY	37	MIA	1	0
23	AW	55	PSU	1	0
23	AY	8	4SU	3	0
23	CW	39	PSU	1	0
23	CY	55	PSU	6	0
23	CY	46	7MG	3	0
23	AY	55	PSU	2	0
24	AX	8	4SU	2	0
23	AY	37	MIA	2	0
23	CW	46	7MG	1	0
24	CX	55	PSU	1	0
24	CX	32	5MC	2	0
23	AY	32	PSU	1	0
23	CY	8	4SU	2	0
23	AY	46	7MG	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2325 ligands modelled in this entry, 2321 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
58	SF4	AD	501	4	0,12,12	-	-	-		
57	UAM	CA	3202	-	31,31,31	1.45	3 (9%)	38,44,44	1.29	6 (15%)
57	UAM	AA	3232	56	31,31,31	1.42	3 (9%)	38,44,44	1.22	3 (7%)
58	SF4	CD	501	4	0,12,12	-	-	-		

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	SF4	AD	501	4	-	-	0/6/5/5
57	UAM	CA	3202	-	-	5/28/40/40	0/2/2/2
57	UAM	AA	3232	56	-	5/28/40/40	0/2/2/2
58	SF4	CD	501	4	-	-	0/6/5/5

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	AA	3232	UAM	CAO-CAW	-6.47	1.39	1.51
57	CA	3202	UAM	CAO-CAW	-6.23	1.39	1.51
57	CA	3202	UAM	CAX-CAU	-3.65	1.38	1.46
57	AA	3232	UAM	CAX-CAU	-3.03	1.39	1.46
57	CA	3202	UAM	OAR-CAU	2.07	1.38	1.34
57	AA	3232	UAM	OAR-CAU	2.05	1.38	1.34

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
57	AA	3232	UAM	CAY-CAP-CBC	-3.55	108.39	115.54
57	CA	3202	UAM	OAR-CAU-OAG	3.46	121.32	117.53
57	AA	3232	UAM	OAR-CAU-OAG	3.13	120.96	117.53
57	AA	3232	UAM	CBD-OAR-CAU	-3.12	113.28	118.93
57	CA	3202	UAM	CBD-OAR-CAU	-2.88	113.71	118.93
57	CA	3202	UAM	CAY-CAP-CBC	-2.75	109.99	115.54
57	CA	3202	UAM	CAP-CBC-CBD	-2.72	108.58	112.49
57	CA	3202	UAM	OAH-CAV-CAX	-2.46	116.59	121.14
57	CA	3202	UAM	OAG-CAU-CAX	-2.06	119.23	124.45

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	CA	3202	UAM	CAY-CAP-CBC-CBD
57	CA	3202	UAM	CBD-CBC-NAQ-CAT
57	AA	3232	UAM	CAZ-CAN-CAS-OAE
57	AA	3232	UAM	CAZ-CAN-CAS-NAC
57	CA	3202	UAM	CAP-CBC-NAQ-CAT
57	CA	3202	UAM	CAY-CAP-CBC-NAQ
57	AA	3232	UAM	CBC-CAP-CAY-CAB
57	AA	3232	UAM	CAS-CAN-CAZ-NAD
57	AA	3232	UAM	CBC-CAP-CAY-CAA
57	CA	3202	UAM	CAT-CBA-CBB-OAJ

There are no ring outliers.

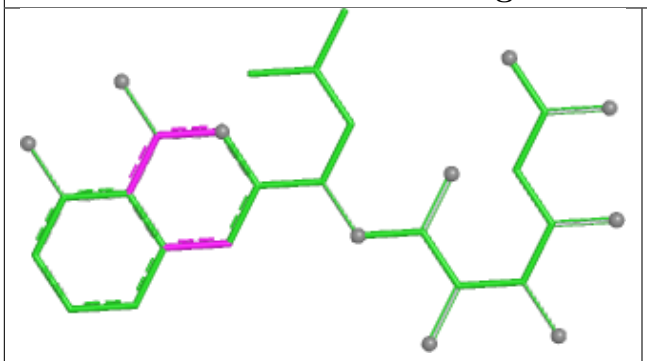
2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	CA	3202	UAM	1	0
57	AA	3232	UAM	1	0

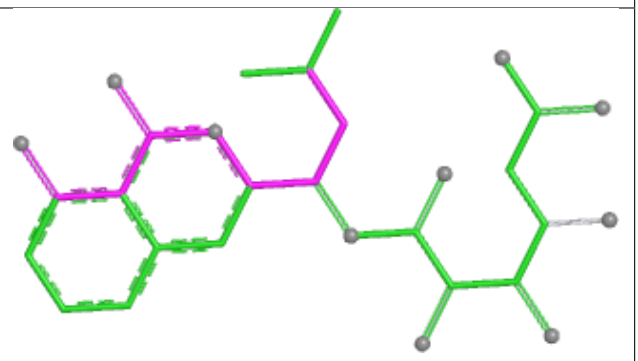
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

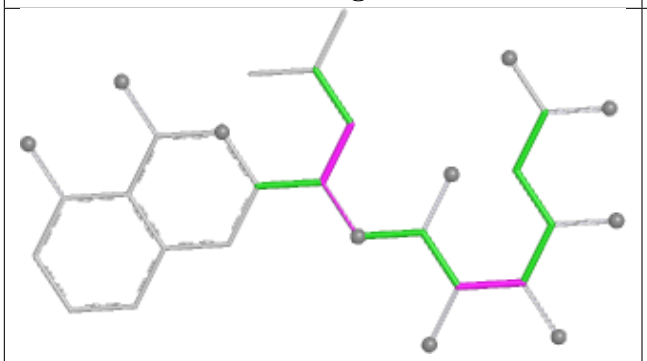
Ligand UAM CA 3202



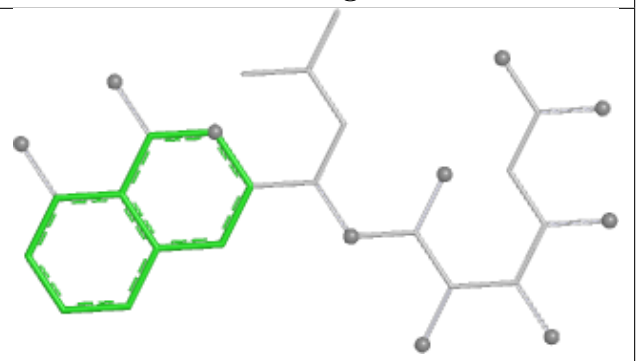
Bond lengths



Bond angles

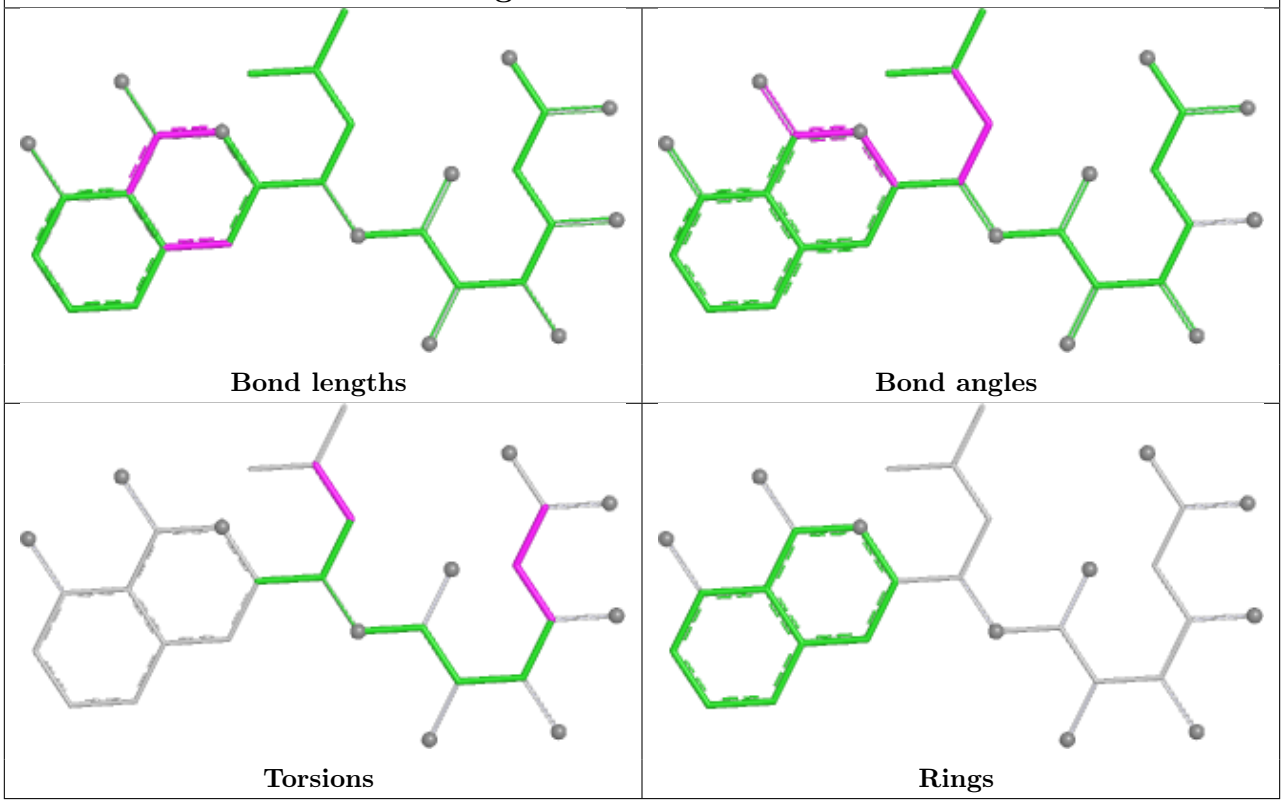


Torsions



Rings

Ligand UAM AA 3232



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	AA	1497/1521 (98%)	0.56	60 (4%) 42 38	36, 63, 86, 100	0
1	CA	1503/1521 (98%)	0.73	94 (6%) 26 22	38, 65, 87, 100	0
2	AB	231/256 (90%)	1.59	60 (25%) 1 1	62, 75, 84, 89	0
2	CB	231/256 (90%)	2.02	104 (45%) 0 0	64, 77, 84, 90	0
3	AC	206/239 (86%)	1.34	30 (14%) 6 4	59, 70, 80, 85	0
3	CC	206/239 (86%)	1.93	96 (46%) 0 0	61, 72, 81, 86	0
4	AD	208/209 (99%)	1.30	39 (18%) 3 3	48, 63, 72, 77	0
4	CD	208/209 (99%)	1.16	17 (8%) 17 14	49, 63, 72, 76	0
5	AE	148/162 (91%)	1.24	17 (11%) 9 7	49, 63, 73, 80	0
5	CE	148/162 (91%)	1.40	28 (18%) 3 2	49, 65, 74, 80	0
6	AF	100/101 (99%)	0.74	0 100 100	50, 60, 69, 74	0
6	CF	100/101 (99%)	0.79	2 (2%) 65 60	49, 61, 70, 75	0
7	AG	155/156 (99%)	1.21	19 (12%) 8 6	54, 66, 76, 83	0
7	CG	155/156 (99%)	1.33	26 (16%) 4 3	55, 68, 77, 85	0
8	AH	137/138 (99%)	1.17	11 (8%) 18 15	53, 64, 71, 78	0
8	CH	137/138 (99%)	1.43	25 (18%) 3 3	54, 66, 72, 78	0
9	AI	127/128 (99%)	1.73	39 (30%) 1 1	49, 72, 79, 83	0
9	CI	127/128 (99%)	2.16	69 (54%) 0 0	55, 74, 81, 84	0
10	AJ	97/105 (92%)	1.64	31 (31%) 1 1	46, 69, 84, 88	0
10	CJ	96/105 (91%)	2.50	61 (63%) 0 0	58, 78, 87, 91	0
11	AK	114/129 (88%)	0.95	11 (9%) 13 10	42, 61, 72, 76	0
11	CK	114/129 (88%)	1.07	13 (11%) 10 7	43, 63, 73, 77	0
12	AL	122/132 (92%)	0.82	9 (7%) 20 17	43, 54, 65, 72	0
12	CL	122/132 (92%)	0.98	10 (8%) 17 14	46, 56, 66, 74	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
13	AM	123/126 (97%)	1.27	16 (13%) 7 5	51, 66, 73, 77	0
13	CM	122/126 (96%)	1.74	43 (35%) 1 1	53, 69, 74, 79	0
14	AN	60/61 (98%)	1.58	12 (20%) 3 2	60, 67, 74, 76	0
14	CN	60/61 (98%)	2.51	40 (66%) 0 0	61, 70, 76, 79	0
15	AO	88/89 (98%)	1.02	6 (6%) 23 20	41, 61, 70, 75	0
15	CO	88/89 (98%)	0.98	8 (9%) 15 12	45, 61, 71, 77	0
16	AP	82/88 (93%)	1.43	15 (18%) 3 3	53, 62, 72, 74	0
16	CP	82/88 (93%)	1.40	14 (17%) 4 3	52, 62, 71, 74	0
17	AQ	99/105 (94%)	1.16	7 (7%) 22 18	50, 62, 72, 74	0
17	CQ	99/105 (94%)	1.15	10 (10%) 12 9	50, 63, 73, 75	0
18	AR	68/88 (77%)	0.77	3 (4%) 39 34	44, 57, 70, 73	0
18	CR	68/88 (77%)	0.90	7 (10%) 12 9	51, 64, 72, 77	0
19	AS	83/93 (89%)	1.38	15 (18%) 3 3	60, 70, 78, 85	0
19	CS	83/93 (89%)	1.91	37 (44%) 0 0	64, 72, 80, 87	0
20	AT	96/106 (90%)	1.36	13 (13%) 7 5	53, 64, 75, 76	0
20	CT	96/106 (90%)	1.37	18 (18%) 3 3	53, 63, 76, 78	0
21	AU	23/27 (85%)	1.61	8 (34%) 1 1	58, 64, 67, 70	0
21	CU	23/27 (85%)	1.92	8 (34%) 1 1	60, 66, 70, 74	0
22	AV	13/24 (54%)	0.81	1 (7%) 19 16	50, 59, 78, 86	0
22	CV	13/24 (54%)	1.37	3 (23%) 2 1	54, 62, 81, 88	0
23	AW	67/76 (88%)	1.36	12 (17%) 3 3	42, 83, 94, 98	0
23	AY	67/76 (88%)	1.45	20 (29%) 1 1	36, 88, 94, 99	0
23	CW	65/76 (85%)	1.56	14 (21%) 2 2	45, 84, 94, 99	0
23	CY	66/76 (86%)	1.49	17 (25%) 1 1	39, 88, 94, 96	0
24	AX	72/77 (93%)	0.71	4 (5%) 30 26	35, 66, 80, 89	0
24	CX	72/77 (93%)	0.62	0 100 100	38, 69, 81, 90	0
25	BA	2871/2915 (98%)	-0.15	161 (5%) 30 26	19, 38, 88, 103	0
25	DA	2800/2915 (96%)	-0.11	107 (3%) 44 40	24, 42, 84, 100	0
26	BB	120/121 (99%)	0.31	1 (0%) 82 80	36, 56, 68, 86	0
26	DB	120/121 (99%)	0.73	2 (1%) 69 65	42, 60, 71, 88	0
27	BD	275/276 (99%)	0.04	3 (1%) 78 74	21, 36, 51, 75	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
27	DD	275/276 (99%)	0.11	4 (1%) 72 68	22, 38, 53, 75	0
28	BE	204/206 (99%)	0.23	2 (0%) 79 76	21, 42, 59, 72	0
28	DE	204/206 (99%)	0.40	7 (3%) 48 44	23, 45, 62, 74	0
29	BF	203/210 (96%)	0.49	7 (3%) 48 44	20, 46, 68, 82	0
29	DF	203/210 (96%)	0.56	5 (2%) 58 54	23, 52, 69, 83	0
30	BG	181/182 (99%)	1.08	19 (10%) 11 8	45, 61, 73, 84	0
30	DG	181/182 (99%)	1.33	30 (16%) 4 3	50, 63, 75, 84	0
31	BH	174/180 (96%)	1.18	17 (9%) 13 10	47, 60, 69, 77	0
31	DH	174/180 (96%)	1.62	50 (28%) 1 1	51, 65, 73, 78	0
32	BI	146/148 (98%)	1.08	10 (6%) 23 20	43, 66, 77, 81	0
32	DI	146/148 (98%)	1.12	14 (9%) 13 10	43, 67, 77, 81	0
33	BN	140/140 (100%)	0.56	4 (2%) 53 50	29, 42, 62, 72	0
33	DN	140/140 (100%)	0.70	5 (3%) 46 42	34, 47, 66, 74	0
34	BO	122/122 (100%)	0.33	1 (0%) 82 80	31, 42, 59, 65	0
34	DO	122/122 (100%)	0.38	0 100 100	35, 45, 60, 67	0
35	BP	149/150 (99%)	0.52	9 (6%) 27 24	22, 51, 68, 76	0
35	DP	149/150 (99%)	0.76	5 (3%) 48 44	25, 54, 70, 77	0
36	BQ	141/141 (100%)	0.57	4 (2%) 55 51	29, 45, 62, 70	0
36	DQ	141/141 (100%)	0.83	8 (5%) 29 25	34, 50, 66, 71	0
37	BR	118/118 (100%)	0.16	0 100 100	24, 35, 46, 56	0
37	DR	118/118 (100%)	0.10	0 100 100	26, 38, 49, 58	0
38	BS	110/112 (98%)	0.90	5 (4%) 38 34	41, 54, 66, 71	0
38	DS	110/112 (98%)	1.24	13 (11%) 9 6	45, 58, 68, 73	0
39	BT	131/146 (89%)	0.64	5 (3%) 44 40	34, 46, 66, 75	0
39	DT	131/146 (89%)	0.67	3 (2%) 61 57	38, 50, 70, 76	0
40	BU	116/118 (98%)	0.13	2 (1%) 69 65	23, 33, 52, 64	0
40	DU	116/118 (98%)	0.47	2 (1%) 69 65	29, 39, 56, 66	0
41	BV	101/101 (100%)	-0.30	2 (1%) 65 60	15, 31, 49, 71	0
41	DV	101/101 (100%)	1.06	6 (5%) 28 24	40, 66, 74, 84	0
42	BW	112/113 (99%)	-0.06	2 (1%) 67 63	23, 31, 50, 75	0
42	DW	112/113 (99%)	0.01	2 (1%) 67 63	27, 35, 54, 76	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
43	BX	95/96 (98%)	0.46	3 (3%) 50 46	28, 40, 61, 75	0
43	DX	95/96 (98%)	0.53	4 (4%) 40 36	30, 44, 62, 75	0
44	BY	107/110 (97%)	0.92	6 (5%) 30 26	36, 52, 68, 76	0
44	DY	107/110 (97%)	1.24	14 (13%) 7 5	38, 56, 70, 76	0
45	BZ	154/206 (74%)	0.95	23 (14%) 5 4	34, 59, 80, 89	0
45	DZ	160/206 (77%)	1.87	57 (35%) 1 1	62, 77, 87, 97	0
46	B0	83/85 (97%)	0.02	3 (3%) 46 42	25, 33, 50, 61	0
46	D0	83/85 (97%)	1.23	10 (12%) 9 6	42, 61, 69, 73	0
47	B1	97/98 (98%)	0.50	2 (2%) 63 59	27, 43, 66, 70	0
47	D1	97/98 (98%)	0.47	4 (4%) 41 37	30, 44, 66, 73	0
48	B2	70/72 (97%)	0.25	2 (2%) 53 50	25, 42, 57, 67	0
48	D2	70/72 (97%)	0.96	3 (4%) 40 36	51, 64, 70, 72	0
49	B3	59/60 (98%)	-0.23	1 (1%) 69 65	16, 29, 52, 70	0
49	D3	59/60 (98%)	1.12	7 (11%) 9 6	49, 63, 74, 78	0
50	B4	69/71 (97%)	1.46	16 (23%) 2 1	55, 71, 83, 88	0
50	D4	69/71 (97%)	1.82	23 (33%) 1 1	61, 74, 85, 89	0
51	B5	59/60 (98%)	-0.11	1 (1%) 69 65	19, 32, 48, 58	0
51	D5	59/60 (98%)	0.01	0 100 100	25, 35, 52, 59	0
52	B6	53/54 (98%)	-0.10	0 100 100	22, 38, 55, 57	0
52	D6	53/54 (98%)	0.79	2 (3%) 44 40	42, 56, 67, 73	0
53	B7	48/49 (97%)	-0.11	3 (6%) 26 22	15, 26, 50, 64	0
53	D7	48/49 (97%)	0.11	2 (4%) 40 36	25, 37, 63, 68	0
54	B8	64/65 (98%)	-0.31	0 100 100	21, 28, 35, 52	0
54	D8	64/65 (98%)	0.79	2 (3%) 51 47	39, 51, 58, 64	0
55	B9	37/37 (100%)	0.54	0 100 100	26, 44, 62, 69	0
55	D9	37/37 (100%)	1.01	4 (10%) 11 8	39, 49, 64, 73	0
All	All	20920/21748 (96%)	0.61	1931 (9%) 14 12	15, 56, 82, 103	0

All (1931) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
45	DZ	174	VAL	6.3
25	BA	2167	C	6.3

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Mol	Chain	Res	Type	RSRZ
25	DA	2802	G	6.3
47	B1	2	SER	6.1
1	CA	1030(B)	C	5.9
39	BT	131	ALA	5.8
1	CA	1030	C	5.8
44	BY	1	MET	5.8
10	CJ	32	ALA	5.6
25	BA	934	A	5.6
2	CB	165	VAL	5.6
7	CG	81	GLY	5.6
45	DZ	144	LEU	5.5
14	AN	2	ALA	5.5
50	B4	54	GLY	5.4
14	CN	38	GLY	5.3
25	BA	935	C	5.3
25	BA	932	C	5.3
25	BA	2806	G	5.2
25	BA	942	A	5.1
1	CA	1033	G	5.1
19	CS	80	TYR	5.1
7	AG	82	GLY	5.0
25	BA	2168	C	5.0
31	BH	2	SER	5.0
1	CA	1030(A)	G	4.9
25	BA	1137	G	4.9
7	AG	83	ALA	4.8
25	BA	1126	C	4.8
14	CN	34	TYR	4.8
50	D4	49	PHE	4.8
25	BA	931	C	4.8
25	BA	936	C	4.8
9	AI	15	ALA	4.7
1	AA	1030(B)	C	4.7
2	CB	31	TYR	4.7
14	CN	7	ILE	4.7
25	BA	1112	U	4.7
10	CJ	10	GLY	4.7
45	BZ	146	ILE	4.6
2	CB	123	ALA	4.6
45	DZ	172	ALA	4.6
27	BD	276	LYS	4.6
25	DA	2896	C	4.5

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Mol	Chain	Res	Type	RSRZ
25	BA	1124	U	4.5
25	BA	2166	U	4.5
9	CI	126	SER	4.5
1	AA	1257	U	4.5
25	BA	1142	A	4.5
45	DZ	146	ILE	4.4
1	CA	1032	G	4.4
27	DD	275	LYS	4.4
10	CJ	34	VAL	4.4
25	BA	1118	C	4.4
25	BA	1122	C	4.4
11	CK	14	VAL	4.4
7	AG	84	ASN	4.4
45	DZ	166	SER	4.4
1	AA	1532	U	4.4
30	BG	49	ASP	4.4
1	CA	1029	C	4.4
10	CJ	90	LEU	4.4
25	BA	943	C	4.3
25	BA	1105	G	4.3
10	CJ	65	LEU	4.3
45	DZ	170	THR	4.3
23	AW	72	C	4.3
1	AA	1447	A	4.3
25	BA	1123	A	4.3
25	BA	1134	A	4.3
1	AA	1030(A)	G	4.3
17	CQ	100	LYS	4.3
2	CB	188	ALA	4.3
25	BA	1120	G	4.3
2	CB	32	ILE	4.3
45	DZ	171	ILE	4.3
1	AA	1030	C	4.3
2	CB	236	TYR	4.3
40	BU	117	GLN	4.2
12	AL	18	VAL	4.2
9	CI	115	GLY	4.2
29	BF	208	GLY	4.2
25	BA	930	G	4.2
1	CA	1001	A	4.2
19	AS	84	GLY	4.2
45	DZ	147	GLY	4.2

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Mol	Chain	Res	Type	RSRZ
9	AI	2	GLU	4.2
25	BA	2816	G	4.2
25	BA	1136	U	4.2
9	CI	102	LEU	4.2
10	CJ	85	LEU	4.2
14	CN	2	ALA	4.2
10	CJ	87	THR	4.1
25	BA	1138	C	4.1
43	DX	92	LEU	4.1
10	AJ	4	ILE	4.1
25	BA	1141	A	4.1
25	BA	2163	G	4.1
7	CG	82	GLY	4.1
14	CN	18	VAL	4.1
33	BN	9	VAL	4.1
1	CA	1286	A	4.1
10	CJ	63	PHE	4.1
1	AA	1030(C)	G	4.1
23	AY	20	U	4.0
25	DA	2144	U	4.0
13	CM	122	LYS	4.0
30	BG	146	TYR	4.0
1	CA	1034	G	4.0
7	AG	80	VAL	4.0
1	AA	1030(D)	A	4.0
3	CC	124	ILE	4.0
43	BX	95	LEU	4.0
50	B4	56	VAL	4.0
25	BA	1110	C	4.0
3	CC	155	GLY	4.0
5	AE	85	GLY	4.0
1	AA	204	U	4.0
25	BA	1140	U	4.0
10	CJ	72	VAL	4.0
45	DZ	141	VAL	4.0
1	AA	1031	G	4.0
5	CE	22	GLY	4.0
25	DA	896	A	4.0
25	BA	933	C	4.0
25	DA	2794	C	4.0
13	AM	122	LYS	3.9
2	AB	237	ALA	3.9

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Mol	Chain	Res	Type	RSRZ
25	BA	1133	G	3.9
1	AA	841	U	3.9
17	AQ	98	LEU	3.9
2	AB	29	ALA	3.9
45	DZ	173	ALA	3.9
12	CL	95	GLY	3.9
31	BH	174	GLY	3.9
1	AA	1531	A	3.9
1	CA	1035	A	3.9
23	CW	2	C	3.9
25	BA	2807	C	3.9
25	BA	2814	C	3.9
11	AK	75	TYR	3.9
1	CA	1002	G	3.9
50	D4	56	VAL	3.9
25	BA	944	C	3.9
25	BA	2165	C	3.9
12	CL	64	TYR	3.9
19	CS	10	PHE	3.9
21	CU	2	GLY	3.9
9	CI	64	THR	3.9
19	CS	9	VAL	3.9
25	BA	1127	U	3.8
1	CA	1001(A)	G	3.8
25	BA	1114	G	3.8
25	BA	1135	G	3.8
20	AT	103	GLY	3.8
25	BA	1144	A	3.8
25	DA	2801(A)	A	3.8
13	CM	123	ALA	3.8
14	CN	25	VAL	3.8
10	CJ	47	PHE	3.8
28	DE	204	ALA	3.8
14	CN	55	GLY	3.8
21	AU	2	GLY	3.8
14	CN	39	LEU	3.8
23	AW	71	G	3.8
25	DA	883	G	3.8
50	D4	57	GLU	3.8
50	B4	50	VAL	3.8
2	CB	29	ALA	3.8
7	CG	7	ALA	3.8

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Mol	Chain	Res	Type	RSRZ
16	CP	48	TRP	3.8
23	AW	73	A	3.8
10	CJ	78	ASN	3.8
2	AB	127	ILE	3.7
14	CN	6	LEU	3.7
30	DG	146	TYR	3.7
45	BZ	148	ASP	3.7
10	CJ	41	PRO	3.7
10	CJ	86	MET	3.7
25	DA	2146	C	3.7
25	DA	2803	C	3.7
3	CC	2	GLY	3.7
50	B4	45	GLY	3.7
25	BA	2135	U	3.7
20	CT	98	PRO	3.7
10	CJ	42	THR	3.7
2	CB	136	VAL	3.7
25	BA	929	G	3.7
25	BA	1221	G	3.7
45	BZ	147	GLY	3.7
7	CG	84	ASN	3.7
16	CP	82	GLN	3.7
44	DY	57	GLN	3.7
25	BA	2164	C	3.7
1	CA	1030(C)	G	3.7
25	BA	1109	G	3.7
25	BA	2805	G	3.7
15	AO	87	ILE	3.7
14	CN	14	PRO	3.7
14	CN	3	ARG	3.7
25	BA	1113	A	3.6
31	DH	52	VAL	3.6
32	BI	107	VAL	3.6
2	AB	207	ALA	3.6
9	CI	82	ALA	3.6
39	BT	130	ALA	3.6
3	CC	51	GLY	3.6
12	CL	63	GLY	3.6
10	CJ	74	ILE	3.6
2	AB	36	ARG	3.6
25	DA	2793	G	3.6
25	BA	1106	U	3.6

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Mol	Chain	Res	Type	RSRZ
25	BA	937	A	3.6
27	DD	2	ALA	3.6
2	AB	125	PRO	3.6
20	CT	9	ASN	3.6
1	CA	1532	U	3.6
25	BA	1111	U	3.6
1	AA	1034	G	3.6
1	CA	1031	G	3.6
3	AC	193	TYR	3.6
9	CI	28	VAL	3.6
11	AK	14	VAL	3.6
1	CA	1030(D)	A	3.6
25	BA	2803	A	3.6
39	DT	131	ALA	3.6
2	CB	187	LEU	3.6
1	CA	1112	C	3.6
23	CW	3	C	3.6
20	AT	9	ASN	3.6
1	AA	1025	U	3.6
21	CU	14	TRP	3.6
13	CM	102	ARG	3.6
2	CB	211	ILE	3.6
29	BF	14	PRO	3.6
23	CW	72	C	3.5
25	BA	1143	U	3.5
13	CM	7	VAL	3.5
50	B4	55	ARG	3.5
3	CC	87	LEU	3.5
25	BA	2181	G	3.5
25	DA	2155	G	3.5
46	B0	6	GLY	3.5
2	CB	127	ILE	3.5
10	CJ	77	PRO	3.5
30	BG	80	PHE	3.5
25	BA	2815	C	3.5
30	BG	35	GLU	3.5
2	CB	93	VAL	3.5
50	B4	63	TYR	3.5
45	DZ	149	SER	3.5
9	CI	67	GLY	3.5
10	AJ	36	GLY	3.5
13	CM	64	TRP	3.5

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Mol	Chain	Res	Type	RSRZ
10	CJ	38	ILE	3.5
25	DA	229	A	3.5
25	DA	882	G	3.5
25	DA	2159	G	3.5
1	CA	1027	C	3.5
12	AL	64	TYR	3.5
4	AD	194	LEU	3.5
9	AI	47	LEU	3.5
10	AJ	77	PRO	3.5
50	D4	45	GLY	3.5
3	CC	182	ILE	3.5
1	CA	1036	G	3.5
2	CB	189	ASP	3.5
1	AA	1027	C	3.5
3	AC	87	LEU	3.5
7	AG	16	LEU	3.5
45	BZ	120	ILE	3.5
27	BD	275	LYS	3.5
44	BY	92	ASN	3.4
1	AA	1503	A	3.4
23	CW	71	G	3.4
25	BA	1139	G	3.4
3	CC	95	THR	3.4
7	CG	16	LEU	3.4
10	CJ	40	LEU	3.4
13	CM	124	PRO	3.4
25	DA	2139	C	3.4
8	AH	80	ILE	3.4
50	D4	63	TYR	3.4
14	CN	61	TRP	3.4
3	CC	207	VAL	3.4
25	BA	926	G	3.4
30	BG	53	LEU	3.4
10	CJ	31	GLY	3.4
2	CB	200	ILE	3.4
25	BA	271	U	3.4
8	CH	4	ASP	3.4
10	CJ	14	LYS	3.4
10	CJ	88	LEU	3.4
14	CN	44	LEU	3.4
4	CD	23	GLY	3.4
2	CB	237	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
25	BA	1117	G	3.4
30	BG	50	ALA	3.4
39	DT	130	ALA	3.4
10	CJ	35	SER	3.4
25	BA	2906	U	3.4
25	DA	2897	U	3.4
25	BA	2162	C	3.4
1	AA	1005	A	3.4
1	CA	1531	A	3.4
3	CC	188	LEU	3.4
10	CJ	92	THR	3.4
14	CN	22	THR	3.4
23	CW	73	A	3.4
7	AG	2	ALA	3.4
44	DY	55	TYR	3.3
9	CI	91	ASP	3.3
48	B2	70	GLN	3.3
2	CB	154	LEU	3.3
2	CB	232	PRO	3.3
3	CC	151	VAL	3.3
9	CI	14	VAL	3.3
10	CJ	91	PRO	3.3
2	CB	203	GLY	3.3
25	BA	1104	G	3.3
29	BF	23	ASP	3.3
9	CI	19	LEU	3.3
16	AP	2	VAL	3.3
2	CB	218	ALA	3.3
4	AD	5	ILE	3.3
2	AB	132	LYS	3.3
13	CM	90	LEU	3.3
18	CR	85	LEU	3.3
43	DX	95	LEU	3.3
20	CT	103	GLY	3.3
31	DH	2	SER	3.3
50	B4	59	PHE	3.3
4	CD	47	ARG	3.3
9	CI	9	ARG	3.3
9	CI	99	LEU	3.3
1	AA	1036	G	3.3
2	CB	112	VAL	3.3
25	BA	2134	G	3.3

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Mol	Chain	Res	Type	RSRZ
10	CJ	36	GLY	3.3
12	AL	63	GLY	3.3
25	BA	696	C	3.3
32	BI	106	GLY	3.3
15	CO	3	ILE	3.3
45	DZ	52	SER	3.2
50	B4	49	PHE	3.2
50	D4	59	PHE	3.2
45	DZ	148	ASP	3.2
50	D4	65	ASP	3.2
4	AD	118	ARG	3.2
1	CA	1257	U	3.2
9	AI	19	LEU	3.2
2	CB	164	VAL	3.2
3	CC	195	VAL	3.2
45	DZ	128	VAL	3.2
14	CN	51	GLY	3.2
2	CB	201	ILE	3.2
25	DA	10	G	3.2
7	CG	4	ARG	3.2
25	BA	302	A	3.2
8	AH	2	LEU	3.2
19	CS	2	PRO	3.2
3	CC	198	VAL	3.2
10	CJ	49	VAL	3.2
19	AS	9	VAL	3.2
3	CC	15	THR	3.2
9	CI	84	ALA	3.2
30	DG	50	ALA	3.2
1	AA	1032	G	3.2
23	CY	19	G	3.2
25	BA	945	A	3.2
30	BG	82	LEU	3.2
9	CI	11	LYS	3.2
3	AC	2	GLY	3.2
4	AD	2	GLY	3.2
12	CL	39	VAL	3.2
25	BA	1072	U	3.2
9	CI	27	THR	3.2
38	BS	22	GLY	3.2
50	D4	44	THR	3.2
10	CJ	75	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
3	CC	187	ALA	3.2
2	CB	21	ARG	3.2
10	AJ	29	ARG	3.2
14	CN	35	ARG	3.2
1	AA	163	C	3.2
9	AI	59	PHE	3.2
23	AW	2	C	3.2
29	BF	15	SER	3.2
1	AA	1024	G	3.2
2	CB	10	LEU	3.2
28	DE	74	PRO	3.2
10	CJ	76	ASN	3.2
25	DA	2173	A	3.2
4	CD	20	TYR	3.2
9	CI	125	TYR	3.2
2	AB	229	VAL	3.2
10	CJ	44	VAL	3.2
31	DH	45	VAL	3.2
31	DH	169	VAL	3.2
10	CJ	79	ARG	3.1
2	CB	17	PHE	3.1
9	AI	126	SER	3.1
8	CH	67	PRO	3.1
25	BA	2158	C	3.1
26	BB	88	C	3.1
18	CR	66	LEU	3.1
25	DA	2116	G	3.1
9	CI	36	TYR	3.1
25	BA	1091	A	3.1
45	BZ	141	VAL	3.1
2	CB	161	ALA	3.1
16	AP	82	GLN	3.1
2	CB	86	GLU	3.1
5	CE	84	PHE	3.1
2	CB	16	HIS	3.1
10	CJ	13	HIS	3.1
20	AT	10	LEU	3.1
46	D0	84	LEU	3.1
1	AA	1029	C	3.1
1	CA	1038	C	3.1
2	AB	93	VAL	3.1
13	CM	15	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
19	CS	11	VAL	3.1
3	CC	77	ILE	3.1
25	DA	1171	G	3.1
9	CI	10	ARG	3.1
14	CN	20	ALA	3.1
25	DA	9	U	3.1
46	D0	3	HIS	3.1
19	CS	13	ASP	3.1
30	DG	147	ASP	3.1
31	DH	171	LEU	3.1
7	CG	156	TRP	3.1
10	AJ	78	ASN	3.1
3	CC	145	GLY	3.1
5	CE	85	GLY	3.1
7	CG	34	GLY	3.1
25	BA	1121	C	3.1
25	DA	888	C	3.1
44	DY	58	GLY	3.1
2	AB	188	ALA	3.1
2	CB	77	ALA	3.1
7	CG	83	ALA	3.1
13	AM	123	ALA	3.1
14	CN	11	LYS	3.1
25	BA	2153	G	3.1
25	BA	2169	G	3.1
25	BA	2813	G	3.1
31	BH	13	LYS	3.1
1	AA	202	U	3.1
3	CC	176	HIS	3.1
28	BE	1	MET	3.1
2	CB	121	LEU	3.1
3	CC	196	LEU	3.1
50	D4	66	SER	3.1
3	AC	205	GLY	3.1
4	AD	167	GLY	3.1
7	AG	81	GLY	3.1
19	CS	68	GLY	3.1
2	AB	15	VAL	3.1
1	CA	1039	C	3.1
2	CB	162	ILE	3.1
2	CB	172	ILE	3.1
10	AJ	100	THR	3.0

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Mol	Chain	Res	Type	RSRZ
10	CJ	67	THR	3.0
25	DA	1536	C	3.1
8	CH	124	ALA	3.0
10	AJ	32	ALA	3.0
13	CM	23	TYR	3.0
1	CA	1447	A	3.0
25	BA	2152	U	3.0
10	CJ	37	PRO	3.0
25	DA	2149	G	3.0
25	DA	2893	G	3.0
45	DZ	125	LEU	3.0
2	CB	210	SER	3.0
2	AB	30	ARG	3.0
7	AG	79	ARG	3.0
5	CE	114	GLY	3.0
14	CN	33	VAL	3.0
49	D3	47	VAL	3.0
3	CC	65	ALA	3.0
25	BA	1125	C	3.0
25	BA	2130	C	3.0
2	AB	126	GLU	3.0
9	AI	21	PRO	3.0
45	DZ	150	LEU	3.0
1	AA	1003	G	3.0
1	AA	1033	G	3.0
1	CA	993	G	3.0
9	CI	66	ARG	3.0
25	BA	2132	G	3.0
25	BA	2173	G	3.0
25	DA	2153	G	3.0
47	D1	2	SER	3.0
3	CC	27	LYS	3.0
36	DQ	22	LYS	3.0
53	B7	48	LYS	3.0
30	BG	42	GLY	3.0
45	DZ	143	GLY	3.0
20	AT	55	ILE	3.0
45	BZ	170	THR	3.0
3	CC	24	ALA	3.0
3	CC	206	GLU	3.0
9	CI	61	ALA	3.0
13	AM	2	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
20	CT	97	ALA	3.0
1	AA	1028	C	3.0
9	CI	114	TYR	3.0
25	BA	1555	C	3.0
2	CB	155	LEU	3.0
13	AM	90	LEU	3.0
22	CV	12	A	3.0
25	BA	2901	A	3.0
2	AB	17	PHE	3.0
30	BG	182	LYS	3.0
23	AW	1	G	3.0
23	AY	15	G	3.0
23	CW	70	G	3.0
25	BA	2188	G	3.0
25	DA	2131	G	3.0
5	CE	74	GLY	3.0
20	CT	47	GLY	3.0
2	CB	185	ILE	3.0
9	CI	109	VAL	3.0
14	AN	7	ILE	3.0
45	DZ	152	ALA	3.0
46	B0	3	HIS	3.0
2	CB	159	PRO	3.0
25	BA	1146	C	3.0
25	DA	897	C	3.0
32	DI	38	LEU	3.0
35	BP	147	LEU	3.0
45	BZ	155	LEU	3.0
10	CJ	55	LYS	3.0
2	CB	55	PHE	3.0
25	BA	9	U	3.0
23	CW	31	A	3.0
25	BA	2139	A	3.0
4	CD	154	ASN	3.0
3	CC	205	GLY	3.0
5	CE	23	GLY	3.0
10	AJ	33	GLN	3.0
43	DX	94	GLY	3.0
3	CC	75	VAL	2.9
30	BG	88	ILE	2.9
7	AG	8	GLU	2.9
53	D7	46	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
3	CC	129	ALA	2.9
14	CN	5	ALA	2.9
9	CI	49	PRO	2.9
9	AI	127	LYS	2.9
25	BA	2159	C	2.9
1	CA	204	U	2.9
1	AA	532	A	2.9
19	CS	8	GLY	2.9
31	BH	14	GLY	2.9
3	AC	39	ILE	2.9
3	AC	206	GLU	2.9
9	CI	35	GLU	2.9
30	DG	15	VAL	2.9
45	BZ	165	VAL	2.9
50	B4	52	THR	2.9
31	BH	3	ARG	2.9
18	AR	31	LEU	2.9
3	CC	193	TYR	2.9
5	CE	60	TYR	2.9
1	AA	162	A	2.9
1	AA	1286	A	2.9
25	BA	925	A	2.9
25	BA	1219	A	2.9
30	BG	48	GLU	2.9
2	CB	223	ILE	2.9
14	CN	42	ILE	2.9
7	CG	5	ARG	2.9
3	CC	109	PRO	2.9
2	CB	51	LEU	2.9
45	BZ	150	LEU	2.9
4	AD	173	TRP	2.9
7	CG	154	TYR	2.9
2	CB	105	PHE	2.9
9	CI	101	PHE	2.9
45	DZ	104	PHE	2.9
9	CI	2	GLU	2.9
13	AM	26	GLY	2.9
9	CI	81	ILE	2.9
25	DA	2136	C	2.9
25	DA	2804	C	2.9
26	DB	88	C	2.9
44	DY	44	ILE	2.9

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Mol	Chain	Res	Type	RSRZ
7	CG	80	VAL	2.9
9	AI	117	HIS	2.9
14	AN	18	VAL	2.9
14	CN	31	ARG	2.9
16	CP	2	VAL	2.9
25	BA	2812	A	2.9
25	DA	2126	A	2.9
31	DH	79	VAL	2.9
39	BT	125	ARG	2.9
3	CC	189	ALA	2.9
11	AK	74	ALA	2.9
1	CA	998	G	2.9
23	CW	15	G	2.9
25	DA	2166	G	2.9
45	DZ	89	PHE	2.9
2	AB	38	GLY	2.9
20	AT	100	ILE	2.8
29	BF	17	ARG	2.8
53	D7	48	LYS	2.8
2	AB	165	VAL	2.8
2	CB	81	VAL	2.8
3	AC	207	VAL	2.8
18	AR	86	VAL	2.8
31	BH	169	VAL	2.8
25	BA	2180	A	2.8
3	CC	115	LEU	2.8
17	CQ	84	LEU	2.8
19	AS	71	LEU	2.8
30	DG	53	LEU	2.8
2	CB	48	MET	2.8
31	DH	123	PHE	2.8
2	CB	33	TYR	2.8
13	CM	59	TYR	2.8
1	AA	630	G	2.8
2	AB	19	HIS	2.8
2	CB	41	ILE	2.8
5	CE	13	ILE	2.8
25	DA	2147	G	2.8
25	DA	2168	G	2.8
1	CA	1196	U	2.8
2	AB	136	VAL	2.8
4	AD	121	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
31	DH	49	VAL	2.8
30	DG	2	PRO	2.8
9	CI	103	THR	2.8
25	DA	2140	C	2.8
25	DA	1847	A	2.8
48	D2	60	LEU	2.8
44	DY	107	ASP	2.8
2	AB	97	TRP	2.8
8	CH	122	ARG	2.8
2	AB	236	TYR	2.8
3	CC	48	TYR	2.8
9	AI	81	ILE	2.8
10	AJ	76	ASN	2.8
51	B5	60	VAL	2.8
1	AA	1026	G	2.8
1	CA	1154	G	2.8
23	AY	19	G	2.8
25	BA	1108	G	2.8
11	CK	74	ALA	2.8
45	BZ	152	ALA	2.8
1	CA	980	C	2.8
25	BA	670	C	2.8
25	DA	885	C	2.8
32	DI	135	GLU	2.8
14	AN	3	ARG	2.8
16	AP	47	ASP	2.8
2	CB	97	TRP	2.8
3	CC	184	TYR	2.8
10	AJ	98	ILE	2.8
13	AM	4	ILE	2.8
15	AO	3	ILE	2.8
16	AP	19	ILE	2.8
38	DS	35	ILE	2.8
45	BZ	171	ILE	2.8
2	AB	131	PRO	2.8
9	CI	17	VAL	2.8
3	CC	180	ALA	2.8
16	AP	69	THR	2.8
25	DA	2172	U	2.8
1	AA	1023	G	2.8
1	CA	1021	G	2.8
25	BA	927	G	2.8

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Mol	Chain	Res	Type	RSRZ
25	DA	892	G	2.8
2	CB	133	LYS	2.8
38	DS	3	ARG	2.8
44	DY	46	LYS	2.8
46	D0	5	LYS	2.8
1	AA	161	A	2.8
1	CA	1004	A	2.8
25	BA	2160	C	2.8
25	BA	2905	C	2.8
25	DA	34	C	2.8
9	CI	105	ASP	2.8
10	AJ	75	ILE	2.7
10	CJ	96	ILE	2.7
13	CM	4	ILE	2.7
19	AS	40	ILE	2.7
20	CT	55	ILE	2.7
19	AS	80	TYR	2.7
3	CC	154	SER	2.7
10	CJ	48	THR	2.7
43	BX	92	LEU	2.7
13	CM	28	ALA	2.7
14	CN	10	ALA	2.7
18	AR	20	ALA	2.7
25	BA	941	U	2.7
21	AU	24	ARG	2.7
35	BP	15	ARG	2.7
50	B4	62	ARG	2.7
1	AA	347	G	2.7
1	CA	1115	C	2.7
23	AY	35	A	2.7
20	CT	101	GLY	2.7
28	DE	71	GLY	2.7
46	D0	45	PHE	2.7
2	CB	131	PRO	2.7
7	CG	37	ASN	2.7
9	CI	65	VAL	2.7
30	DG	12	TYR	2.7
33	DN	140	VAL	2.7
3	CC	52	LEU	2.7
19	CS	22	LEU	2.7
2	CB	34	ALA	2.7
3	AC	189	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
3	CC	168	ALA	2.7
21	CU	24	ARG	2.7
31	BH	6	ARG	2.7
38	DS	20	ARG	2.7
32	DI	64	GLU	2.7
10	CJ	17	ASP	2.7
1	CA	630	G	2.7
23	CY	57	G	2.7
24	AX	46	G	2.7
25	BA	2138	G	2.7
25	DA	2156	G	2.7
25	DA	2319	G	2.7
1	CA	1005	A	2.7
14	CN	16	PHE	2.7
14	CN	37	PHE	2.7
22	CV	14	A	2.7
25	BA	1119	A	2.7
2	AB	172	ILE	2.7
2	CB	132	LYS	2.7
40	DU	90	VAL	2.7
45	DZ	86	VAL	2.7
3	CC	12	LEU	2.7
11	CK	25	TYR	2.7
19	CS	16	LEU	2.7
32	DI	68	LEU	2.7
44	DY	1	MET	2.7
54	D8	64	TYR	2.7
11	CK	126	ARG	2.7
19	CS	79	THR	2.7
20	CT	12	ALA	2.7
21	AU	10	ARG	2.7
1	CA	1040	U	2.7
10	CJ	68	HIS	2.7
9	CI	18	PHE	2.7
1	AA	1035	A	2.7
2	CB	158	LEU	2.7
9	AI	56	LEU	2.7
13	CM	54	VAL	2.7
20	AT	13	LEU	2.7
31	DH	17	VAL	2.7
2	AB	12	GLU	2.7
9	AI	125	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
11	CK	75	TYR	2.7
19	CS	61	TYR	2.7
9	CI	45	ALA	2.7
45	DZ	7	ALA	2.7
25	BA	12	U	2.7
25	DA	2167	U	2.7
10	CJ	93	GLY	2.6
13	CM	68	GLY	2.6
35	BP	93	GLY	2.6
2	AB	200	ILE	2.6
3	CC	5	ILE	2.6
14	CN	40	CYS	2.6
19	CS	18	LYS	2.6
2	AB	37	ASN	2.6
2	CB	137	ARG	2.6
8	CH	104	ARG	2.6
38	BS	3	ARG	2.6
14	AN	56	VAL	2.6
19	AS	30	LEU	2.6
23	CY	23	A	2.6
25	BA	218	A	2.6
25	DA	2158	A	2.6
23	CY	15	G	2.6
25	DA	884	C	2.6
30	DG	35	GLU	2.6
45	DZ	11	GLU	2.6
2	CB	199	TYR	2.6
3	CC	100	ALA	2.6
9	CI	52	ALA	2.6
16	CP	69	THR	2.6
50	D4	25	TYR	2.6
16	CP	59	TRP	2.6
54	D8	34	TRP	2.6
2	CB	140	HIS	2.6
2	AB	228	GLY	2.6
9	CI	69	GLY	2.6
41	DV	26	ASP	2.6
50	D4	54	GLY	2.6
13	AM	124	PRO	2.6
30	DG	52	ILE	2.6
31	DH	128	PRO	2.6
45	BZ	104	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
45	DZ	95	PRO	2.6
2	AB	11	LEU	2.6
3	CC	42	LEU	2.6
4	AD	188	LEU	2.6
5	AE	119	LEU	2.6
2	CB	71	VAL	2.6
3	CC	130	VAL	2.6
4	CD	112	VAL	2.6
45	DZ	139	VAL	2.6
19	AS	4	SER	2.6
1	CA	1006	C	2.6
2	CB	120	ALA	2.6
3	AC	60	ALA	2.6
3	CC	60	ALA	2.6
5	AE	138	ALA	2.6
19	CS	48	THR	2.6
25	DA	898	C	2.6
3	AC	184	TYR	2.6
9	CI	62	TYR	2.6
23	AW	65	G	2.6
25	DA	2792	G	2.6
27	DD	276	LYS	2.6
10	CJ	73	ASP	2.6
2	AB	21	ARG	2.6
5	AE	96	PRO	2.6
13	CM	104	ARG	2.6
45	DZ	167	PRO	2.6
2	AB	61	LEU	2.6
2	CB	12	GLU	2.6
2	CB	126	GLU	2.6
2	CB	145	LEU	2.6
3	AC	204	LEU	2.6
16	AP	74	LEU	2.6
34	BO	91	LEU	2.6
9	CI	53	VAL	2.6
17	CQ	9	VAL	2.6
36	DQ	109	VAL	2.6
10	CJ	62	HIS	2.6
25	BA	1116	A	2.6
25	DA	878	A	2.6
1	AA	848	C	2.6
25	BA	34	C	2.6

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Mol	Chain	Res	Type	RSRZ
25	BA	2210	C	2.6
12	CL	28	LYS	2.6
50	B4	69	LYS	2.6
23	AW	70	G	2.6
23	CY	18	G	2.6
25	BA	1145	G	2.6
25	BA	2228	G	2.6
25	DA	2112	G	2.6
25	DA	2141	G	2.6
25	DA	2157	G	2.6
9	CI	8	GLY	2.6
9	CI	80	GLY	2.6
11	CK	49	GLY	2.6
30	DG	118	ARG	2.6
31	DH	174	GLY	2.6
33	BN	61	ARG	2.6
2	AB	39	ILE	2.6
45	DZ	124	ILE	2.6
7	CG	26	PHE	2.6
9	AI	33	PHE	2.6
23	CY	45	U	2.6
2	CB	221	LEU	2.6
7	CG	12	LEU	2.6
9	AI	12	GLU	2.6
3	AC	76	VAL	2.6
3	CC	173	VAL	2.6
9	CI	106	ALA	2.6
17	AQ	37	LYS	2.6
25	BA	2157	A	2.6
17	CQ	95	TYR	2.6
1	CA	1018	C	2.5
1	CA	1116	C	2.5
21	CU	10	ARG	2.5
23	AW	67	C	2.5
23	AY	48	C	2.5
25	BA	2133	C	2.5
25	BA	2183	C	2.5
27	BD	262	ARG	2.5
42	BW	92	ARG	2.5
2	CB	205	ASP	2.5
9	AI	8	GLY	2.5
9	CI	68	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
10	CJ	58	ASP	2.5
13	CM	6	GLY	2.5
20	AT	69	GLY	2.5
30	DG	17	PRO	2.5
1	CA	1026	G	2.5
23	AW	44	G	2.5
23	AY	18	G	2.5
25	BA	2174	G	2.5
25	DA	7	G	2.5
25	DA	2115	G	2.5
25	DA	2154	G	2.5
9	CI	37	PHE	2.5
13	CM	70	LEU	2.5
25	DA	1026	U	2.5
10	CJ	94	VAL	2.5
13	CM	60	VAL	2.5
46	D0	79	VAL	2.5
2	AB	13	ALA	2.5
2	AB	120	ALA	2.5
8	CH	29	SER	2.5
9	CI	119	ALA	2.5
10	CJ	59	SER	2.5
14	CN	43	CYS	2.5
20	CT	74	LYS	2.5
3	CC	192	THR	2.5
31	DH	106	THR	2.5
10	CJ	43	ARG	2.5
14	CN	12	ARG	2.5
53	B7	47	ARG	2.5
25	BA	1103	A	2.5
48	D2	1	MET	2.5
1	CA	1066	C	2.5
3	AC	171	GLY	2.5
9	CI	39	GLY	2.5
20	AT	102	GLY	2.5
31	BH	21	PRO	2.5
25	DA	2175	C	2.5
45	DZ	63	ASP	2.5
2	CB	222	ILE	2.5
45	BZ	168	GLU	2.5
45	DZ	169	GLU	2.5
3	CC	34	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
3	CC	128	PHE	2.5
30	DG	139	LEU	2.5
31	DH	64	LEU	2.5
45	DZ	136	PHE	2.5
25	DA	1533	G	2.5
1	AA	203	U	2.5
1	AA	1446	U	2.5
3	CC	86	VAL	2.5
4	AD	170	VAL	2.5
28	DE	59	VAL	2.5
30	BG	149	VAL	2.5
31	BH	15	VAL	2.5
31	DH	50	VAL	2.5
45	BZ	161	VAL	2.5
47	D1	62	VAL	2.5
9	CI	15	ALA	2.5
31	DH	145	ALA	2.5
32	DI	146	ALA	2.5
10	AJ	87	THR	2.5
45	BZ	149	SER	2.5
10	AJ	79	ARG	2.5
5	AE	10	MET	2.5
2	AB	232	PRO	2.5
11	AK	25	TYR	2.5
31	DH	39	PRO	2.5
1	CA	1092	A	2.5
4	AD	180	GLY	2.5
25	DA	899	A	2.5
25	DA	2629	A	2.5
29	BF	207	GLY	2.5
42	DW	112	GLY	2.5
4	CD	179	GLU	2.5
31	BH	58	GLU	2.5
45	DZ	137	ILE	2.5
3	AC	18	TRP	2.5
23	AY	13	C	2.5
35	BP	99	LEU	2.5
46	B0	7	LEU	2.5
2	CB	110	GLN	2.5
14	CN	9	LYS	2.5
45	DZ	50	GLN	2.5
1	CA	4	U	2.5

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Mol	Chain	Res	Type	RSRZ
2	AB	7	VAL	2.5
3	AC	86	VAL	2.5
3	CC	70	VAL	2.5
23	AY	59	U	2.5
25	BA	1220	U	2.5
36	DQ	27	VAL	2.5
1	AA	216	G	2.5
23	CW	19	G	2.5
23	CY	22	G	2.5
25	DA	2124	G	2.5
25	DA	2894	G	2.5
3	CC	149	ALA	2.5
9	AI	106	ALA	2.5
13	AM	102	ARG	2.5
15	AO	88	ARG	2.5
16	CP	77	ALA	2.5
19	CS	36	ARG	2.5
53	B7	45	ALA	2.5
9	AI	64	THR	2.5
32	DI	108	THR	2.5
31	DH	10	PRO	2.5
2	CB	18	GLY	2.5
2	CB	66	GLY	2.5
3	CC	25	GLY	2.5
2	AB	92	TYR	2.5
1	CA	1183	A	2.5
25	BA	1115	A	2.5
2	AB	44	LEU	2.5
2	CB	138	LEU	2.5
3	CC	32	LEU	2.5
3	CC	43	LEU	2.5
2	CB	57	PHE	2.5
50	B4	60	GLN	2.5
1	CA	1019	C	2.5
1	CA	1028	C	2.5
1	CA	1277	C	2.5
1	CA	1322	C	2.5
25	DA	886	C	2.5
25	DA	2137	C	2.5
25	DA	2145	C	2.5
2	CB	7	VAL	2.5
4	AD	140	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
14	CN	56	VAL	2.5
2	CB	130	ARG	2.5
25	DA	272(A)	U	2.5
25	DA	2150	U	2.5
27	DD	262	ARG	2.5
14	CN	30	ALA	2.5
1	AA	78	G	2.5
1	CA	1003	G	2.5
1	CA	1024	G	2.5
1	CA	1356	G	2.5
25	BA	2137	G	2.5
25	BA	2170	G	2.5
25	BA	2817	G	2.5
16	AP	41	PRO	2.4
32	DI	132	PRO	2.4
11	CK	90	GLY	2.4
38	DS	45	GLY	2.4
4	CD	18	LYS	2.4
9	CI	5	TYR	2.4
15	AO	69	TYR	2.4
16	AP	4	ILE	2.4
31	DH	13	LYS	2.4
50	B4	46	GLN	2.4
4	AD	110	PHE	2.4
10	CJ	11	PHE	2.4
45	DZ	48	PHE	2.4
2	AB	24	TRP	2.4
7	CG	10	ARG	2.4
8	CH	18	ARG	2.4
30	DG	136	ARG	2.4
31	DH	6	ARG	2.4
1	CA	1037	C	2.4
1	CA	1149	C	2.4
5	CE	51	VAL	2.4
13	CM	53	VAL	2.4
25	DA	893	C	2.4
25	DA	2789	C	2.4
33	DN	9	VAL	2.4
2	CB	101	MET	2.4
3	AC	100	ALA	2.4
4	CD	164	ALA	2.4
5	AE	94	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
10	AJ	86	MET	2.4
23	AY	12	U	2.4
25	BA	924	U	2.4
25	BA	1128	U	2.4
9	CI	90	PRO	2.4
9	CI	123	PRO	2.4
35	BP	122	PRO	2.4
13	CM	69	GLU	2.4
1	CA	1042	G	2.4
1	CA	1117	G	2.4
5	CE	99	GLY	2.4
9	AI	30	GLY	2.4
9	AI	113	LYS	2.4
12	AL	95	GLY	2.4
12	AL	126	LYS	2.4
19	AS	68	GLY	2.4
25	BA	2182	G	2.4
25	BA	2902	G	2.4
25	DA	879	G	2.4
10	CJ	6	ILE	2.4
16	AP	68	ASP	2.4
30	DG	20	ILE	2.4
30	DG	49	ASP	2.4
3	CC	170	GLN	2.4
8	CH	94	TYR	2.4
10	CJ	71	LEU	2.4
16	CP	76	GLN	2.4
19	CS	30	LEU	2.4
45	DZ	70	LEU	2.4
50	B4	67	TYR	2.4
19	CS	14	HIS	2.4
4	AD	139	ARG	2.4
5	AE	40	ARG	2.4
45	BZ	136	PHE	2.4
1	CA	1041	A	2.4
25	BA	572	A	2.4
25	DA	2117	A	2.4
4	AD	154	ASN	2.4
7	AG	9	VAL	2.4
31	BH	44	VAL	2.4
3	CC	92	ALA	2.4
9	AI	52	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
25	BA	2129	C	2.4
1	CA	1281	U	2.4
15	CO	4	THR	2.4
25	BA	2154	U	2.4
2	CB	216	SER	2.4
9	CI	97	LYS	2.4
10	AJ	97	GLU	2.4
31	DH	36	PRO	2.4
42	BW	112	GLY	2.4
2	CB	214	ILE	2.4
4	AD	158	ILE	2.4
5	AE	11	ILE	2.4
8	AH	100	ILE	2.4
19	CS	49	ILE	2.4
1	AA	346	G	2.4
1	AA	1002	G	2.4
2	CB	11	LEU	2.4
4	AD	201	GLN	2.4
9	CI	56	LEU	2.4
17	CQ	98	LEU	2.4
20	AT	24	LEU	2.4
23	CY	44	G	2.4
25	BA	938	G	2.4
25	DA	2133	G	2.4
32	BI	75	LEU	2.4
45	DZ	33	LEU	2.4
2	CB	19	HIS	2.4
13	AM	94	ARG	2.4
15	AO	68	ARG	2.4
2	AB	33	TYR	2.4
5	CE	133	TYR	2.4
43	BX	69	TYR	2.4
50	D4	32	TYR	2.4
3	AC	10	PHE	2.4
4	AD	198	VAL	2.4
5	CE	10	MET	2.4
5	CE	148	VAL	2.4
8	CH	51	VAL	2.4
25	BA	2136	A	2.4
25	BA	2141	A	2.4
3	AC	65	ALA	2.4
4	AD	195	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
9	CI	13	ALA	2.4
11	AK	15	ALA	2.4
2	CB	73	THR	2.4
8	CH	17	THR	2.4
10	CJ	15	THR	2.4
13	CM	103	THR	2.4
19	CS	6	LYS	2.4
23	CW	13	C	2.4
25	BA	2131	U	2.4
25	DA	2142	C	2.4
31	DH	173	PRO	2.4
26	DB	1	U	2.4
2	AB	18	GLY	2.4
4	CD	124	GLY	2.4
8	CH	128	GLY	2.4
8	CH	100	ILE	2.4
9	CI	63	ILE	2.4
30	BG	77	ILE	2.4
2	AB	51	LEU	2.4
13	CM	88	ARG	2.4
14	AN	35	ARG	2.4
19	CS	78	ARG	2.4
31	DH	132	ARG	2.4
40	DU	117	GLN	2.4
46	D0	7	LEU	2.4
1	AA	77	G	2.4
1	CA	1182	G	2.4
1	CA	1202	G	2.4
2	CB	152	PHE	2.4
3	CC	201	TYR	2.4
4	CD	4	TYR	2.4
23	AW	69	G	2.4
25	BA	694	G	2.4
25	BA	2155	G	2.4
25	DA	271(M)	G	2.4
2	CB	219	VAL	2.4
17	CQ	23	VAL	2.4
33	BN	140	VAL	2.4
1	CA	1248	A	2.4
14	AN	59	ALA	2.4
15	CO	16	ALA	2.4
19	CS	24	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
22	AV	13	A	2.4
25	BA	554	A	2.4
25	DA	2119	A	2.4
29	BF	27	GLU	2.4
29	DF	127	GLU	2.4
13	CM	105	THR	2.3
30	DG	122	PRO	2.3
10	CJ	30	SER	2.3
17	CQ	99	SER	2.3
23	AY	47	U	2.3
25	BA	1129	U	2.3
25	BA	2172	U	2.3
25	DA	2895	U	2.3
2	AB	227	GLY	2.3
3	CC	185	GLY	2.3
10	AJ	10	GLY	2.3
25	BA	2186	C	2.3
25	DA	894	C	2.3
45	BZ	12	GLY	2.3
2	CB	39	ILE	2.3
2	CB	149	LEU	2.3
2	CB	215	LEU	2.3
3	CC	62	ASP	2.3
3	CC	178	LEU	2.3
5	AE	109	ILE	2.3
8	AH	112	LEU	2.3
17	AQ	36	ILE	2.3
17	CQ	65	ILE	2.3
20	CT	100	ILE	2.3
4	AD	38	TYR	2.3
4	CD	185	PHE	2.3
16	CP	9	PHE	2.3
5	AE	34	VAL	2.3
5	CE	41	VAL	2.3
19	CS	19	VAL	2.3
32	DI	19	VAL	2.3
33	DN	118	LYS	2.3
25	BA	2175	G	2.3
29	DF	160	ASN	2.3
45	DZ	168	GLU	2.3
31	DH	117	PRO	2.3
8	AH	3	THR	2.3

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Mol	Chain	Res	Type	RSRZ
9	AI	7	THR	2.3
1	CA	1044	A	2.3
3	CC	18	TRP	2.3
2	AB	72	GLY	2.3
2	CB	175	ARG	2.3
3	AC	81	GLY	2.3
16	CP	10	GLY	2.3
30	DG	85	GLY	2.3
30	DG	115	ARG	2.3
41	BV	101	GLY	2.3
45	DZ	106	GLY	2.3
23	CY	33	U	2.3
25	BA	1985	U	2.3
25	DA	1113	U	2.3
2	CB	108	ILE	2.3
4	AD	155	LEU	2.3
13	CM	19	LEU	2.3
19	CS	15	LEU	2.3
55	D9	17	ILE	2.3
5	AE	5	ASP	2.3
23	CY	4	C	2.3
36	BQ	135	ASP	2.3
45	DZ	28	MET	2.3
7	CG	35	LYS	2.3
30	DG	141	PHE	2.3
2	CB	92	TYR	2.3
7	AG	154	TYR	2.3
9	CI	44	VAL	2.3
10	AJ	44	VAL	2.3
19	CS	58	VAL	2.3
28	DE	72	VAL	2.3
32	DI	15	VAL	2.3
41	DV	12	TYR	2.3
45	DZ	9	TYR	2.3
2	CB	94	ASN	2.3
30	DG	123	ASN	2.3
4	AD	37	PRO	2.3
5	AE	95	ALA	2.3
7	AG	39	ALA	2.3
13	CM	18	ALA	2.3
13	CM	33	ALA	2.3
32	DI	63	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	CA	1023	G	2.3
1	CA	1190	G	2.3
16	CP	67	THR	2.3
25	BA	299	G	2.3
25	BA	2190	G	2.3
25	DA	2165	G	2.3
25	DA	2805	G	2.3
30	BG	83	ARG	2.3
1	CA	1503	A	2.3
22	CV	24	A	2.3
23	CY	21	A	2.3
25	DA	2134	A	2.3
25	DA	2135	A	2.3
2	AB	40	HIS	2.3
3	CC	162	GLN	2.3
10	CJ	33	GLN	2.3
31	DH	38	SER	2.3
3	AC	182	ILE	2.3
3	CC	84	ILE	2.3
3	CC	202	ILE	2.3
19	CS	20	LEU	2.3
30	BG	52	ILE	2.3
30	DG	173	LEU	2.3
1	CA	1358	U	2.3
23	AY	33	U	2.3
9	CI	32	ASP	2.3
1	CA	990	C	2.3
2	AB	22	LYS	2.3
3	AC	72	LYS	2.3
13	CM	120	LYS	2.3
25	BA	940	C	2.3
3	CC	186	PHE	2.3
8	CH	79	VAL	2.3
9	AI	88	TYR	2.3
9	AI	114	TYR	2.3
12	CL	18	VAL	2.3
14	AN	33	VAL	2.3
15	CO	60	VAL	2.3
35	BP	98	GLU	2.3
31	DH	83	TYR	2.3
2	AB	85	ALA	2.3
9	CI	43	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
10	CJ	5	ARG	2.3
16	CP	55	ARG	2.3
21	AU	15	ARG	2.3
31	DH	51	ARG	2.3
3	CC	31	HIS	2.3
1	AA	266	G	2.3
4	AD	137	SER	2.3
10	CJ	56	HIS	2.3
17	AQ	54	GLY	2.3
20	CT	69	GLY	2.3
31	DH	111	HIS	2.3
3	CC	14	ILE	2.3
3	CC	157	ILE	2.3
3	CC	167	TRP	2.3
8	CH	133	LEU	2.3
11	AK	48	ILE	2.3
23	AY	24	G	2.3
23	CY	34	G	2.3
25	BA	273	G	2.3
25	BA	569	G	2.3
25	DA	2148	G	2.3
38	BS	48	LEU	2.3
38	BS	82	ILE	2.3
13	CM	65	LYS	2.3
1	AA	999	C	2.3
1	CA	999	C	2.3
1	CA	1452	C	2.3
2	AB	9	GLU	2.3
2	AB	163	PHE	2.3
24	AX	69	C	2.3
25	BA	2197	C	2.3
25	DA	2111	C	2.3
25	DA	2138	C	2.3
45	BZ	169	GLU	2.3
9	AI	28	VAL	2.3
32	DI	107	VAL	2.3
2	AB	91	PRO	2.3
3	CC	179	ARG	2.3
7	AG	6	ARG	2.3
9	CI	21	PRO	2.3
21	CU	15	ARG	2.3
29	DF	14	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
32	DI	50	ARG	2.3
2	CB	207	ALA	2.2
3	CC	137	ALA	2.2
10	CJ	18	ALA	2.2
13	CM	30	ALA	2.2
50	B4	43	TYR	2.3
9	CI	72	GLY	2.2
17	CQ	33	GLY	2.2
19	CS	82	GLY	2.2
33	DN	130	HIS	2.2
2	AB	27	LYS	2.2
3	CC	39	ILE	2.2
4	AD	86	LYS	2.2
4	CD	5	ILE	2.2
5	CE	53	LEU	2.2
6	CF	93	SER	2.2
8	AH	111	ILE	2.2
9	CI	95	LYS	2.2
10	AJ	85	LEU	2.2
10	CJ	82	ILE	2.2
14	CN	15	LYS	2.2
20	CT	10	LEU	2.2
45	DZ	57	ILE	2.2
45	DZ	155	LEU	2.2
1	CA	1250	A	2.2
1	CA	1256	A	2.2
3	AC	62	ASP	2.2
3	AC	167	TRP	2.2
9	AI	91	ASP	2.2
23	CY	36	A	2.2
25	DA	2176	A	2.2
25	BA	2178	G	2.2
25	DA	2160	G	2.2
1	CA	1126	U	2.2
23	AW	20	U	2.2
25	BA	274	U	2.2
25	DA	2130	U	2.2
3	CC	90	GLU	2.2
35	BP	149	GLU	2.2
2	AB	23	ARG	2.2
3	CC	66	VAL	2.2
3	CC	88	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	AA	840	C	2.2
1	CA	1007	C	2.2
8	AH	61	VAL	2.2
9	AI	109	VAL	2.2
31	DH	60	ARG	2.2
23	AY	56	C	2.2
25	DA	1043	C	2.2
25	DA	2163	C	2.2
32	DI	136	VAL	2.2
44	BY	7	VAL	2.2
3	CC	53	ALA	2.2
7	CG	2	ALA	2.2
13	CM	12	ASN	2.2
18	CR	20	ALA	2.2
31	DH	20	ALA	2.2
9	AI	4	TYR	2.2
11	CK	50	TYR	2.2
2	CB	40	HIS	2.2
3	CC	107	GLN	2.2
5	CE	120	THR	2.2
13	CM	101	GLN	2.2
19	AS	48	THR	2.2
20	AT	18	GLN	2.2
45	DZ	121	HIS	2.2
12	CL	126	LYS	2.2
13	AM	121	LYS	2.2
20	CT	96	GLY	2.2
21	CU	3	LYS	2.2
31	BH	41	MET	2.2
31	DH	14	GLY	2.2
31	DH	175	LYS	2.2
36	DQ	19	GLY	2.2
3	AC	47	LEU	2.2
20	AT	62	LEU	2.2
32	BI	72	LEU	2.2
52	D6	11	LEU	2.2
31	DH	72	ILE	2.2
45	DZ	129	SER	2.2
19	AS	13	ASP	2.2
39	BT	107	ASP	2.2
2	CB	24	TRP	2.2
2	CB	9	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
4	AD	150	GLU	2.2
23	CY	35	A	2.2
25	BA	702	A	2.2
1	CA	1131	G	2.2
3	CC	59	ARG	2.2
25	BA	698	G	2.2
25	BA	2184	G	2.2
25	DA	2151	G	2.2
25	DA	2162	G	2.2
8	CH	31	PHE	2.2
3	CC	68	VAL	2.2
5	CE	100	VAL	2.2
7	AG	91	VAL	2.2
10	AJ	24	VAL	2.2
19	CS	76	PRO	2.2
32	BI	19	VAL	2.2
49	D3	2	PRO	2.2
49	D3	58	VAL	2.2
52	D6	48	VAL	2.2
1	AA	76	C	2.2
1	CA	1043	C	2.2
1	CA	1254	C	2.2
3	CC	61	ALA	2.2
4	AD	164	ALA	2.2
13	CM	72	ALA	2.2
20	CT	94	ALA	2.2
23	CW	4	C	2.2
25	DA	2174	C	2.2
31	DH	96	ALA	2.2
32	BI	146	ALA	2.2
9	AI	95	LYS	2.2
9	CI	92	TYR	2.2
10	AJ	68	HIS	2.2
13	CM	92	HIS	2.2
31	DH	25	LYS	2.2
38	DS	95	HIS	2.2
42	DW	111	HIS	2.2
44	DY	47	LYS	2.2
12	CL	61	THR	2.2
45	DZ	99	TYR	2.2
3	AC	178	LEU	2.2
5	AE	151	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
5	CE	71	LEU	2.2
9	CI	85	LEU	2.2
10	AJ	88	LEU	2.2
12	CL	60	LEU	2.2
13	CM	100	GLY	2.2
31	DH	103	LEU	2.2
44	BY	80	GLY	2.2
3	CC	8	ILE	2.2
8	CH	111	ILE	2.2
10	CJ	23	ILE	2.2
18	CR	65	ILE	2.2
2	AB	128	GLU	2.2
14	CN	8	GLU	2.2
17	AQ	78	GLU	2.2
36	BQ	112	GLU	2.2
19	AS	81	ARG	2.2
19	CS	34	TRP	2.2
21	CU	9	ARG	2.2
50	D4	68	ARG	2.2
1	CA	1025	U	2.2
23	CW	45	U	2.2
25	BA	1092	A	2.2
25	DA	887	A	2.2
25	DA	2118	U	2.2
7	AG	43	PHE	2.2
50	D4	29	PRO	2.2
7	CG	21	VAL	2.2
8	CH	53	VAL	2.2
31	DH	15	VAL	2.2
1	AA	1001(A)	G	2.2
25	BA	2187	G	2.2
25	DA	11	G	2.2
5	CE	86	ALA	2.2
13	AM	5	ALA	2.2
14	CN	49	HIS	2.2
39	BT	38	ASN	2.2
44	DY	48	ALA	2.2
45	DZ	164	ALA	2.2
4	AD	160	GLN	2.2
5	AE	20	GLN	2.2
8	CH	70	GLN	2.2
11	AK	73	MET	2.2

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Mol	Chain	Res	Type	RSRZ
41	DV	11	GLN	2.2
1	AA	150	C	2.2
1	CA	1045	C	2.2
2	CB	168	THR	2.2
2	AB	154	LEU	2.2
2	AB	221	LEU	2.2
2	CB	72	GLY	2.2
3	AC	185	GLY	2.2
4	CD	186	LEU	2.2
7	CG	85	TYR	2.2
9	CI	4	TYR	2.2
9	CI	100	GLY	2.2
10	CJ	16	LEU	2.2
14	CN	21	TYR	2.2
16	CP	38	TYR	2.2
18	CR	47	THR	2.2
19	AS	5	LEU	2.2
19	CS	26	GLY	2.2
28	DE	63	LEU	2.2
30	BG	43	LEU	2.2
36	DQ	61	GLY	2.2
38	DS	36	TYR	2.2
41	DV	8	GLY	2.2
50	D4	67	TYR	2.2
4	AD	204	ILE	2.2
10	CJ	98	ILE	2.2
10	AJ	35	SER	2.2
20	CT	70	SER	2.2
30	BG	76	SER	2.2
9	AI	105	ASP	2.2
4	AD	153	ARG	2.2
4	CD	3	ARG	2.2
7	CG	6	ARG	2.2
7	CG	32	ARG	2.2
9	AI	42	ARG	2.2
9	CI	16	ARG	2.2
30	BG	51	ARG	2.2
31	BH	95	ARG	2.2
1	AA	4	U	2.2
1	CA	1086	U	2.2
18	CR	39	VAL	2.1
25	BA	2641	A	2.1

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Mol	Chain	Res	Type	RSRZ
25	DA	6	A	2.1
25	DA	900	A	2.1
25	DA	2171	A	2.1
30	BG	75	LYS	2.2
3	CC	76	VAL	2.1
5	AE	69	VAL	2.1
5	CE	67	VAL	2.1
8	AH	26	VAL	2.1
29	DF	6	VAL	2.1
31	BH	76	VAL	2.1
45	DZ	71	VAL	2.1
3	CC	181	ASN	2.1
3	CC	200	ALA	2.1
4	AD	161	ASN	2.1
14	CN	59	ALA	2.1
19	AS	24	ALA	2.1
31	DH	156	ALA	2.1
33	BN	131	GLN	2.1
40	BU	116	ALA	2.1
49	D3	25	ALA	2.1
1	AA	1353	G	2.1
1	CA	181	G	2.1
2	AB	10	LEU	2.1
4	AD	135	LEU	2.1
8	CH	3	THR	2.1
9	AI	103	THR	2.1
10	CJ	100	THR	2.1
11	CK	103	LEU	2.1
15	AO	4	THR	2.1
16	CP	73	LEU	2.1
20	AT	43	LEU	2.1
20	CT	62	LEU	2.1
23	AY	63	G	2.1
25	DA	881	G	2.1
13	AM	78	ILE	2.1
19	CS	52	TYR	2.1
31	DH	162	ILE	2.1
1	AA	92	C	2.1
23	CY	68	C	2.1
25	BA	2161	C	2.1
3	CC	19	GLU	2.1
5	CE	24	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
31	DH	42	ARG	2.1
32	BI	70	GLU	2.1
45	DZ	4	ARG	2.1
47	D1	83	GLU	2.1
45	DZ	66	SER	2.1
48	D2	51	ARG	2.1
14	CN	17	LYS	2.1
17	AQ	100	LYS	2.1
33	DN	11	PRO	2.1
2	AB	28	PHE	2.1
2	CB	122	PHE	2.1
16	AP	21	VAL	2.1
19	CS	45	VAL	2.1
21	AU	14	TRP	2.1
30	DG	117	PHE	2.1
30	DG	180	PHE	2.1
44	DY	89	PHE	2.1
1	CA	997	U	2.1
2	AB	16	HIS	2.1
7	AG	17	VAL	2.1
35	DP	101	VAL	2.1
38	DS	85	VAL	2.1
49	D3	59	VAL	2.1
25	DA	895	U	2.1
3	CC	71	ALA	2.1
11	CK	23	ALA	2.1
25	BA	1130	A	2.1
25	BA	1222	A	2.1
36	BQ	136	ALA	2.1
11	AK	117	ASN	2.1
13	AM	12	ASN	2.1
2	CB	67	THR	2.1
3	CC	41	GLY	2.1
9	AI	50	LEU	2.1
9	CI	96	LEU	2.1
10	AJ	93	GLY	2.1
11	CK	86	GLY	2.1
13	CM	48	LEU	2.1
13	CM	81	LEU	2.1
41	DV	49	THR	2.1
44	DY	80	GLY	2.1
44	DY	90	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
46	D0	59	LEU	2.1
47	B1	82	LEU	2.1
45	DZ	53	ILE	2.1
8	CH	58	TYR	2.1
9	AI	16	ARG	2.1
13	CM	29	ARG	2.1
14	CN	29	ARG	2.1
16	AP	75	ARG	2.1
19	CS	3	ARG	2.1
21	CU	6	ARG	2.1
31	DH	94	TYR	2.1
35	DP	15	ARG	2.1
1	AA	1021	G	2.1
23	CW	6	G	2.1
48	B2	11	GLU	2.1
50	D4	30	GLU	2.1
1	CA	1129	C	2.1
2	CB	166	ASP	2.1
2	CB	192	SER	2.1
4	AD	53	ASP	2.1
4	AD	134	ASP	2.1
23	AY	67	C	2.1
23	AY	68	C	2.1
25	DA	1509	C	2.1
2	CB	163	PHE	2.1
44	DY	5	MET	2.1
2	CB	184	VAL	2.1
5	CE	34	VAL	2.1
11	AK	78	GLN	2.1
14	AN	25	VAL	2.1
19	CS	60	VAL	2.1
31	DH	37	VAL	2.1
55	D9	16	VAL	2.1
29	DF	172	TRP	2.1
1	CA	1000	U	2.1
1	CA	1150	U	2.1
20	AT	75	ASN	2.1
25	BA	2818	U	2.1
32	DI	59	ALA	2.1
2	AB	14	GLY	2.1
2	CB	196	LEU	2.1
4	AD	162	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
4	CD	135	LEU	2.1
5	AE	142	LEU	2.1
8	CH	2	LEU	2.1
20	CT	24	LEU	2.1
25	DA	2169	A	2.1
30	DG	24	GLY	2.1
46	D0	37	LEU	2.1
2	AB	190	THR	2.1
8	AH	24	THR	2.1
10	AJ	42	THR	2.1
2	CB	36	ARG	2.1
5	CE	18	ARG	2.1
7	CG	79	ARG	2.1
8	CH	30	ARG	2.1
19	CS	81	ARG	2.1
31	BH	23	ARG	2.1
43	DX	68	ARG	2.1
5	CE	109	ILE	2.1
30	DG	137	GLU	2.1
14	AN	21	TYR	2.1
16	AP	17	TYR	2.1
17	AQ	95	TYR	2.1
46	D0	78	TYR	2.1
50	D4	43	TYR	2.1
16	AP	31	LYS	2.1
50	D4	69	LYS	2.1
5	CE	125	SER	2.1
8	AH	23	SER	2.1
8	CH	135	CYS	2.1
9	CI	71	SER	2.1
31	DH	56	SER	2.1
1	CA	485	G	2.1
24	AX	4	G	2.1
25	BA	1218	G	2.1
25	BA	2122	G	2.1
2	CB	183	PRO	2.1
4	AD	29	PRO	2.1
13	CM	41	PRO	2.1
25	BA	270	C	2.1
25	DA	2128	C	2.1
25	DA	2143	C	2.1
35	DP	122	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
35	DP	1	MET	2.1
2	CB	229	VAL	2.1
7	CG	43	PHE	2.1
9	AI	18	PHE	2.1
9	CI	86	VAL	2.1
11	AK	105	VAL	2.1
12	AL	11	VAL	2.1
12	CL	40	VAL	2.1
31	BH	45	VAL	2.1
31	DH	43	VAL	2.1
38	DS	49	VAL	2.1
39	DT	28	VAL	2.1
44	DY	3	VAL	2.1
45	BZ	96	VAL	2.1
45	DZ	90	VAL	2.1
50	D4	42	PHE	2.1
50	D4	50	VAL	2.1
2	CB	173	ALA	2.1
36	DQ	107	ALA	2.1
1	CA	1020	U	2.1
1	CA	1148	U	2.1
1	CA	1446	U	2.1
3	CC	63	ASN	2.1
4	AD	19	LEU	2.1
3	CC	171	GLY	2.1
4	AD	49	ARG	2.1
5	CE	12	LEU	2.1
19	CS	53	ASN	2.1
9	CI	111	ARG	2.1
12	AL	41	ARG	2.1
16	AP	18	ARG	2.1
25	DA	271(N)	U	2.1
30	DG	34	LEU	2.1
31	DH	120	GLY	2.1
31	DH	170	ARG	2.1
44	BY	106	LEU	2.1
45	DZ	76	LEU	2.1
21	AU	11	GLY	2.1
36	BQ	23	GLY	2.1
36	DQ	86	GLY	2.1
38	DS	60	GLY	2.1
38	DS	109	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
41	DV	67	GLY	2.1
49	D3	29	ARG	2.1
50	B4	64	GLY	2.1
2	CB	134	GLU	2.1
13	CM	20	THR	2.1
13	CM	43	THR	2.1
41	BV	43	GLU	2.1
50	D4	52	THR	2.1
1	AA	152	A	2.1
1	AA	160	A	2.1
1	CA	1357	A	2.1
3	CC	152	ILE	2.1
23	AY	21	A	2.1
25	BA	1878	A	2.1
31	BH	4	ILE	2.1
16	AP	38	TYR	2.1
17	CQ	51	TYR	2.1
30	DG	25	TYR	2.1
45	BZ	99	TYR	2.1
55	D9	12	ASP	2.1
2	CB	91	PRO	2.1
14	CN	24	CYS	2.1
31	DH	21	PRO	2.1
31	DH	126	PRO	2.1
46	D0	83	PRO	2.1
49	B3	2	PRO	2.1
31	DH	41	MET	2.1
1	AA	79	G	2.0
1	AA	93	G	2.0
1	CA	1060	C	2.1
1	CA	1249	C	2.1
23	AY	4	C	2.1
25	BA	1584	G	2.0
3	AC	75	VAL	2.0
3	CC	99	VAL	2.0
3	CC	138	VAL	2.0
38	DS	69	VAL	2.0
45	BZ	139	VAL	2.0
45	DZ	88	PHE	2.0
49	D3	36	VAL	2.0
50	D4	10	VAL	2.0
3	AC	61	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
4	AD	73	ARG	2.0
5	CE	25	ARG	2.0
7	AG	5	ARG	2.0
7	CG	78	ARG	2.0
9	AI	13	ALA	2.0
9	AI	119	ALA	2.0
11	CK	89	ALA	2.0
13	AM	93	ARG	2.0
14	CN	23	ARG	2.0
15	CO	88	ARG	2.0
16	CP	7	ALA	2.0
36	DQ	136	ALA	2.0
45	DZ	51	ALA	2.0
2	CB	142	LEU	2.0
6	CF	98	LEU	2.0
8	CH	59	LEU	2.0
9	AI	102	LEU	2.0
10	AJ	8	LEU	2.0
30	DG	60	LEU	2.0
31	DH	7	LEU	2.0
32	BI	43	ASN	2.0
32	BI	68	LEU	2.0
35	BP	105	LEU	2.0
35	BP	148	LEU	2.0
45	BZ	102	LEU	2.0
45	DZ	5	LEU	2.0
3	CC	44	GLU	2.0
7	AG	132	GLY	2.0
9	CI	110	GLU	2.0
10	AJ	83	GLU	2.0
13	CM	89	GLY	2.0
19	AS	82	GLY	2.0
19	CS	17	GLU	2.0
28	DE	115	GLY	2.0
31	DH	135	GLY	2.0
3	AC	14	ILE	2.0
3	CC	26	LYS	2.0
5	AE	80	ILE	2.0
9	CI	7	THR	2.0
10	AJ	74	ILE	2.0
10	AJ	82	ILE	2.0
10	CJ	80	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
13	AM	39	ILE	2.0
13	AM	84	ILE	2.0
14	AN	11	LYS	2.0
30	DG	145	THR	2.0
23	AW	64	A	2.0
23	AY	14	A	2.0
11	AK	81	ASP	2.0
12	AL	92	ASP	2.0
8	CH	5	PRO	2.0
45	DZ	54	HIS	2.0
3	CC	106	VAL	2.0
3	CC	116	VAL	2.0
3	CC	172	ARG	2.0
4	AD	115	ARG	2.0
4	CD	115	ARG	2.0
5	CE	27	ARG	2.0
7	CG	76	ARG	2.0
9	AI	66	ARG	2.0
10	CJ	54	PHE	2.0
11	CK	105	VAL	2.0
12	AL	43	VAL	2.0
15	CO	18	PHE	2.0
18	CR	37	VAL	2.0
35	DP	102	ARG	2.0
44	BY	73	ARG	2.0
50	D4	48	ARG	2.0
1	AA	73	G	2.0
1	AA	1356	G	2.0
2	AB	62	ALA	2.0
10	AJ	26	ALA	2.0
20	CT	95	ALA	2.0
23	CY	5	G	2.0
25	BA	10	G	2.0
25	BA	2204	G	2.0
25	DA	545	G	2.0
25	DA	1042	G	2.0
28	BE	73	GLU	2.0
30	DG	48	GLU	2.0
38	BS	4	LEU	2.0
3	CC	159	GLY	2.0
4	CD	87	GLY	2.0
10	AJ	69	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
10	AJ	80	LYS	2.0
15	CO	89	GLY	2.0
19	AS	8	GLY	2.0
21	AU	16	GLY	2.0
38	DS	59	LYS	2.0
38	DS	61	ASN	2.0
45	DZ	160	GLY	2.0
47	D1	84	GLY	2.0
55	D9	21	GLY	2.0
3	AC	177	THR	2.0
9	AI	27	THR	2.0
13	CM	39	ILE	2.0
32	BI	78	THR	2.0
1	AA	343	U	2.0
1	CA	84	U	2.0
14	AN	61	TRP	2.0
23	AY	45	U	2.0
23	CY	12	U	2.0
24	AX	47	U	2.0
25	BA	2140	U	2.0
1	CA	965	A	2.0
1	CA	969	A	2.0
1	CA	1252	A	2.0
2	AB	234	PRO	2.0
2	CB	202	PRO	2.0
3	CC	142	MET	2.0
4	AD	189	PRO	2.0
23	CW	14	A	2.0
25	BA	217	A	2.0
25	BA	1100	A	2.0
25	BA	2191	A	2.0
45	BZ	167	PRO	2.0
45	DZ	159	PRO	2.0
7	AG	77	SER	2.0
8	AH	62	TYR	2.0
13	CM	87	TYR	2.0
15	CO	69	TYR	2.0
19	CS	47	HIS	2.0
21	AU	18	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
23	7MG	AY	46	24/25	0.58	0.17	76,92,102,121	0
23	7MG	AW	46	24/25	0.64	0.17	66,84,103,129	0
23	4SU	CY	8	20/21	0.64	0.18	76,90,105,117	0
23	4SU	AY	8	20/21	0.65	0.16	77,91,110,118	0
23	5MU	CY	54	21/22	0.67	0.17	78,87,97,118	0
23	PSU	CY	55	20/21	0.67	0.15	80,91,104,111	0
23	4SU	CW	8	20/21	0.68	0.15	78,89,106,119	0
23	7MG	CW	46	24/25	0.72	0.16	81,92,99,121	0
23	7MG	CY	46	24/25	0.72	0.16	84,93,103,111	0
23	PSU	AY	55	20/21	0.74	0.15	82,92,102,111	0
23	MIA	CY	37	22/30	0.75	0.14	65,78,95,107	0
23	5MU	AY	54	21/22	0.76	0.15	70,85,94,111	0
23	PSU	CY	32	20/21	0.78	0.14	71,78,92,94	0
23	PSU	CW	55	20/21	0.80	0.13	64,74,85,87	0
23	4SU	AW	8	20/21	0.84	0.13	56,80,91,93	0
23	MIA	AY	37	22/30	0.84	0.14	69,78,88,91	0
23	5MU	CW	54	21/22	0.85	0.14	65,75,84,86	0
24	4SU	CX	8	20/21	0.85	0.13	65,74,85,85	0
23	PSU	AY	32	20/21	0.86	0.13	71,79,89,91	0
23	PSU	AW	55	20/21	0.87	0.12	62,70,81,83	0
24	PSU	CX	55	20/21	0.87	0.12	48,69,86,88	0
23	PSU	CW	32	20/21	0.88	0.15	66,72,78,78	0
23	PSU	CY	39	20/21	0.89	0.11	64,74,81,84	0
24	5MU	CX	54	21/22	0.89	0.13	70,78,82,89	0
23	PSU	AY	39	20/21	0.90	0.12	67,73,79,81	0
24	5MU	AX	54	21/22	0.91	0.12	54,66,74,75	0
23	PSU	AW	32	20/21	0.91	0.12	61,69,75,77	0
24	5MC	CX	32	21/22	0.91	0.13	51,66,72,75	0
24	PSU	AX	55	20/21	0.92	0.10	45,66,84,85	0
23	PSU	CW	39	20/21	0.92	0.11	57,65,69,71	0
24	4SU	AX	8	20/21	0.94	0.10	53,60,66,68	0
24	5MC	AX	32	21/22	0.95	0.13	43,51,61,70	0
23	5MU	AW	54	21/22	0.95	0.09	38,59,67,72	0
23	PSU	AW	39	20/21	0.95	0.10	55,62,65,67	0
23	MIA	AW	37	29/30	0.95	0.12	37,49,63,66	0
23	MIA	CW	37	25/30	0.95	0.10	36,64,70,71	0

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BE	310	1/1	0.57	0.30	80,80,80,80	0
56	MG	BA	3361	1/1	0.58	0.21	41,41,41,41	0
56	MG	BA	3469	1/1	0.59	0.28	61,61,61,61	0
56	MG	BE	302	1/1	0.62	0.13	27,27,27,27	0
56	MG	BB	3021	1/1	0.64	0.26	73,73,73,73	0
56	MG	CA	3056	1/1	0.65	0.32	84,84,84,84	0
56	MG	DA	3621	1/1	0.66	0.21	48,48,48,48	0
56	MG	DA	3582	1/1	0.68	0.23	52,52,52,52	0
56	MG	DA	3404	1/1	0.68	0.19	49,49,49,49	0
56	MG	DA	3424	1/1	0.69	0.22	47,47,47,47	0
56	MG	DE	305	1/1	0.69	0.20	49,49,49,49	0
56	MG	AA	3122	1/1	0.70	0.21	61,61,61,61	0
56	MG	DA	3596	1/1	0.70	0.20	62,62,62,62	0
56	MG	CA	3144	1/1	0.71	0.30	69,69,69,69	0
56	MG	BA	3694	1/1	0.72	0.28	62,62,62,62	0
56	MG	CA	3188	1/1	0.72	0.25	72,72,72,72	0
56	MG	DA	3276	1/1	0.72	0.19	60,60,60,60	0
56	MG	CA	3193	1/1	0.73	0.20	66,66,66,66	0
56	MG	DA	3593	1/1	0.73	0.15	60,60,60,60	0
56	MG	BA	3505	1/1	0.73	0.19	44,44,44,44	0
56	MG	AA	3166	1/1	0.73	0.19	81,81,81,81	0
56	MG	BA	3793	1/1	0.73	0.20	64,64,64,64	0
56	MG	DA	3325	1/1	0.74	0.25	53,53,53,53	0
56	MG	BZ	3001	1/1	0.74	0.28	69,69,69,69	0
56	MG	BA	3643	1/1	0.74	0.18	60,60,60,60	0
56	MG	BA	3743	1/1	0.74	0.20	50,50,50,50	0
56	MG	BA	3704	1/1	0.75	0.20	57,57,57,57	0
56	MG	BA	3720	1/1	0.75	0.23	73,73,73,73	0
56	MG	BA	3638	1/1	0.75	0.14	58,58,58,58	0
56	MG	CA	3129	1/1	0.75	0.26	69,69,69,69	0
56	MG	BA	3759	1/1	0.76	0.12	44,44,44,44	0
56	MG	CA	3192	1/1	0.76	0.25	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3640	1/1	0.76	0.15	60,60,60,60	0
56	MG	AA	3117	1/1	0.76	0.21	68,68,68,68	0
56	MG	BA	3508	1/1	0.76	0.16	48,48,48,48	0
56	MG	DA	3393	1/1	0.76	0.17	55,55,55,55	0
56	MG	BA	3527	1/1	0.76	0.22	57,57,57,57	0
56	MG	BA	3707	1/1	0.76	0.22	53,53,53,53	0
56	MG	DA	3524	1/1	0.76	0.15	53,53,53,53	0
56	MG	BA	3718	1/1	0.76	0.17	47,47,47,47	0
56	MG	CA	3120	1/1	0.76	0.19	62,62,62,62	0
56	MG	CA	3126	1/1	0.76	0.22	68,68,68,68	0
56	MG	BA	3580	1/1	0.76	0.17	35,35,35,35	0
56	MG	AA	3182	1/1	0.76	0.32	65,65,65,65	0
56	MG	BA	3659	1/1	0.77	0.21	55,55,55,55	0
56	MG	BA	3671	1/1	0.77	0.16	50,50,50,50	0
56	MG	CA	3127	1/1	0.77	0.17	57,57,57,57	0
56	MG	AH	201	1/1	0.77	0.18	67,67,67,67	0
56	MG	BA	3635	1/1	0.77	0.19	65,65,65,65	0
56	MG	BA	3086	1/1	0.77	0.16	57,57,57,57	0
56	MG	AA	3201	1/1	0.77	0.14	60,60,60,60	0
56	MG	BA	3409	1/1	0.77	0.16	65,65,65,65	0
56	MG	CJ	5001	1/1	0.77	0.12	70,70,70,70	0
56	MG	BA	3729	1/1	0.77	0.22	56,56,56,56	0
56	MG	BA	3631	1/1	0.78	0.18	38,38,38,38	0
56	MG	BA	3757	1/1	0.78	0.17	49,49,49,49	0
56	MG	DA	3426	1/1	0.78	0.14	41,41,41,41	0
56	MG	DA	3449	1/1	0.78	0.12	45,45,45,45	0
56	MG	CA	3007	1/1	0.78	0.35	66,66,66,66	0
56	MG	BA	3673	1/1	0.78	0.24	62,62,62,62	0
56	MG	BA	3619	1/1	0.78	0.23	68,68,68,68	0
56	MG	BA	3873	1/1	0.78	0.17	26,26,26,26	0
56	MG	DA	3610	1/1	0.78	0.25	61,61,61,61	0
56	MG	BA	3630	1/1	0.78	0.14	29,29,29,29	0
56	MG	BA	3731	1/1	0.78	0.14	64,64,64,64	0
56	MG	DR	5001	1/1	0.78	0.14	51,51,51,51	0
56	MG	BA	3819	1/1	0.79	0.21	61,61,61,61	0
56	MG	BA	3021	1/1	0.79	0.18	53,53,53,53	0
56	MG	DA	3472	1/1	0.79	0.12	57,57,57,57	0
56	MG	DA	3241	1/1	0.79	0.18	60,60,60,60	0
56	MG	DA	3526	1/1	0.79	0.18	42,42,42,42	0
56	MG	AW	102	1/1	0.79	0.21	69,69,69,69	0
56	MG	CA	3108	1/1	0.80	0.27	57,57,57,57	0
56	MG	CW	3004	1/1	0.80	0.22	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BB	3011	1/1	0.80	0.20	66,66,66,66	0
56	MG	DA	3541	1/1	0.80	0.24	59,59,59,59	0
56	MG	DA	3560	1/1	0.80	0.21	50,50,50,50	0
56	MG	DA	3575	1/1	0.80	0.15	51,51,51,51	0
56	MG	BA	3719	1/1	0.80	0.15	61,61,61,61	0
56	MG	BA	3581	1/1	0.80	0.13	33,33,33,33	0
56	MG	BA	3611	1/1	0.80	0.15	61,61,61,61	0
56	MG	AA	3055	1/1	0.80	0.23	61,61,61,61	0
56	MG	DA	3619	1/1	0.80	0.17	65,65,65,65	0
56	MG	BA	3844	1/1	0.80	0.18	49,49,49,49	0
56	MG	DA	3641	1/1	0.80	0.14	62,62,62,62	0
56	MG	DE	301	1/1	0.80	0.15	47,47,47,47	0
56	MG	CA	3050	1/1	0.80	0.25	72,72,72,72	0
56	MG	BA	3501	1/1	0.80	0.20	50,50,50,50	0
56	MG	AA	3139	1/1	0.81	0.23	82,82,82,82	0
56	MG	CA	3182	1/1	0.81	0.25	58,58,58,58	0
56	MG	DA	3328	1/1	0.81	0.18	64,64,64,64	0
56	MG	DA	3574	1/1	0.81	0.16	48,48,48,48	0
56	MG	DA	3349	1/1	0.81	0.11	50,50,50,50	0
56	MG	BA	3446	1/1	0.81	0.22	63,63,63,63	0
56	MG	BA	3575	1/1	0.81	0.17	27,27,27,27	0
56	MG	DA	3414	1/1	0.81	0.20	56,56,56,56	0
56	MG	BA	3108	1/1	0.81	0.12	45,45,45,45	0
56	MG	BA	3208	1/1	0.81	0.32	62,62,62,62	0
56	MG	DA	3447	1/1	0.81	0.22	50,50,50,50	0
56	MG	AA	3141	1/1	0.81	0.26	70,70,70,70	0
56	MG	DB	3001	1/1	0.81	0.31	71,71,71,71	0
56	MG	BA	3871	1/1	0.81	0.16	55,55,55,55	0
56	MG	DA	3511	1/1	0.81	0.10	31,31,31,31	0
56	MG	DA	3244	1/1	0.81	0.11	47,47,47,47	0
56	MG	BA	3750	1/1	0.82	0.18	54,54,54,54	0
56	MG	DA	3432	1/1	0.82	0.22	57,57,57,57	0
56	MG	BA	3493	1/1	0.82	0.12	41,41,41,41	0
56	MG	AA	3111	1/1	0.82	0.17	57,57,57,57	0
56	MG	DA	3454	1/1	0.82	0.17	44,44,44,44	0
56	MG	BA	3348	1/1	0.82	0.16	65,65,65,65	0
56	MG	DA	3505	1/1	0.82	0.18	61,61,61,61	0
56	MG	DA	3506	1/1	0.82	0.18	55,55,55,55	0
56	MG	BA	3798	1/1	0.82	0.22	55,55,55,55	0
56	MG	DA	3519	1/1	0.82	0.13	46,46,46,46	0
56	MG	DA	3521	1/1	0.82	0.22	56,56,56,56	0
56	MG	CA	3174	1/1	0.82	0.23	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3359	1/1	0.82	0.23	58,58,58,58	0
56	MG	DA	3529	1/1	0.82	0.13	48,48,48,48	0
56	MG	BA	3838	1/1	0.82	0.14	47,47,47,47	0
56	MG	DA	3542	1/1	0.82	0.12	45,45,45,45	0
56	MG	AA	3158	1/1	0.82	0.27	54,54,54,54	0
56	MG	BA	3849	1/1	0.82	0.13	29,29,29,29	0
56	MG	BA	3556	1/1	0.82	0.18	48,48,48,48	0
56	MG	AA	3223	1/1	0.82	0.12	72,72,72,72	0
56	MG	BA	3417	1/1	0.82	0.16	46,46,46,46	0
56	MG	BA	3432	1/1	0.82	0.14	55,55,55,55	0
56	MG	BA	3596	1/1	0.82	0.19	44,44,44,44	0
56	MG	DA	3612	1/1	0.82	0.16	52,52,52,52	0
56	MG	AA	3063	1/1	0.82	0.18	55,55,55,55	0
56	MG	BA	3447	1/1	0.82	0.16	46,46,46,46	0
56	MG	DA	3628	1/1	0.82	0.15	47,47,47,47	0
56	MG	BA	3111	1/1	0.82	0.19	60,60,60,60	0
56	MG	BA	3479	1/1	0.82	0.15	41,41,41,41	0
56	MG	BA	3739	1/1	0.82	0.17	49,49,49,49	0
56	MG	CA	3088	1/1	0.82	0.31	62,62,62,62	0
56	MG	DF	302	1/1	0.82	0.15	55,55,55,55	0
56	MG	BA	3485	1/1	0.82	0.13	29,29,29,29	0
56	MG	AA	3147	1/1	0.83	0.21	65,65,65,65	0
56	MG	AA	3218	1/1	0.83	0.13	75,75,75,75	0
56	MG	BA	3459	1/1	0.83	0.16	38,38,38,38	0
56	MG	DA	3040	1/1	0.83	0.12	51,51,51,51	0
56	MG	DA	3117	1/1	0.83	0.24	62,62,62,62	0
56	MG	DA	3134	1/1	0.83	0.27	56,56,56,56	0
56	MG	CA	3049	1/1	0.83	0.15	67,67,67,67	0
56	MG	BA	3764	1/1	0.83	0.17	32,32,32,32	0
56	MG	DA	3247	1/1	0.83	0.17	63,63,63,63	0
56	MG	BA	3271	1/1	0.83	0.20	54,54,54,54	0
56	MG	DA	3301	1/1	0.83	0.13	52,52,52,52	0
56	MG	DA	3303	1/1	0.83	0.09	30,30,30,30	0
56	MG	BA	3699	1/1	0.83	0.11	45,45,45,45	0
56	MG	BA	3809	1/1	0.83	0.17	58,58,58,58	0
56	MG	AA	3099	1/1	0.83	0.20	64,64,64,64	0
56	MG	AA	3162	1/1	0.83	0.18	67,67,67,67	0
56	MG	AA	3060	1/1	0.83	0.30	62,62,62,62	0
56	MG	BA	3372	1/1	0.83	0.14	55,55,55,55	0
56	MG	AA	3174	1/1	0.83	0.17	58,58,58,58	0
56	MG	CA	3160	1/1	0.83	0.19	55,55,55,55	0
56	MG	CA	3173	1/1	0.83	0.21	81,81,81,81	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	AA	3008	1/1	0.83	0.29	71,71,71,71	0
56	MG	DB	3003	1/1	0.83	0.16	62,62,62,62	0
56	MG	DB	3018	1/1	0.83	0.20	62,62,62,62	0
56	MG	CA	3180	1/1	0.83	0.28	55,55,55,55	0
56	MG	AA	3198	1/1	0.83	0.14	58,58,58,58	0
56	MG	BA	3541	1/1	0.83	0.18	59,59,59,59	0
56	MG	BA	3549	1/1	0.83	0.15	38,38,38,38	0
56	MG	AA	3062	1/1	0.84	0.25	61,61,61,61	0
56	MG	CA	3162	1/1	0.84	0.16	68,68,68,68	0
56	MG	BA	3116	1/1	0.84	0.14	56,56,56,56	0
56	MG	BA	3515	1/1	0.84	0.16	64,64,64,64	0
56	MG	BA	3445	1/1	0.84	0.14	48,48,48,48	0
56	MG	BA	3741	1/1	0.84	0.24	63,63,63,63	0
56	MG	BB	3025	1/1	0.84	0.14	71,71,71,71	0
56	MG	AN	502	1/1	0.84	0.10	45,45,45,45	0
56	MG	AA	3179	1/1	0.84	0.23	66,66,66,66	0
56	MG	BP	205	1/1	0.84	0.11	44,44,44,44	0
56	MG	CJ	5002	1/1	0.84	0.12	65,65,65,65	0
56	MG	BA	3318	1/1	0.84	0.19	53,53,53,53	0
56	MG	B4	502	1/1	0.84	0.15	65,65,65,65	0
56	MG	AX	3013	1/1	0.84	0.18	61,61,61,61	0
56	MG	DA	3555	1/1	0.84	0.10	30,30,30,30	0
56	MG	BA	3763	1/1	0.84	0.15	58,58,58,58	0
56	MG	AY	3001	1/1	0.84	0.31	76,76,76,76	0
56	MG	BA	3784	1/1	0.84	0.12	49,49,49,49	0
56	MG	CA	3074	1/1	0.84	0.14	73,73,73,73	0
56	MG	AA	3114	1/1	0.84	0.17	65,65,65,65	0
56	MG	CA	3089	1/1	0.84	0.23	65,65,65,65	0
56	MG	CA	3090	1/1	0.84	0.26	74,74,74,74	0
56	MG	DA	3611	1/1	0.84	0.14	65,65,65,65	0
56	MG	BA	3492	1/1	0.84	0.10	43,43,43,43	0
56	MG	CA	3114	1/1	0.84	0.24	60,60,60,60	0
56	MG	BA	3603	1/1	0.84	0.12	42,42,42,42	0
56	MG	DA	3353	1/1	0.84	0.11	34,34,34,34	0
56	MG	DA	3631	1/1	0.84	0.13	52,52,52,52	0
56	MG	DA	3383	1/1	0.84	0.13	41,41,41,41	0
56	MG	BA	3818	1/1	0.84	0.18	58,58,58,58	0
56	MG	AA	3222	1/1	0.84	0.15	55,55,55,55	0
56	MG	DB	3017	1/1	0.84	0.17	58,58,58,58	0
56	MG	BA	3617	1/1	0.84	0.10	44,44,44,44	0
56	MG	CA	3131	1/1	0.84	0.20	76,76,76,76	0
56	MG	AA	3194	1/1	0.84	0.15	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3428	1/1	0.84	0.13	42,42,42,42	0
56	MG	CA	3155	1/1	0.84	0.18	72,72,72,72	0
57	UAM	CA	3202	30/30	0.84	0.19	45,72,83,85	0
56	MG	BA	3751	1/1	0.85	0.12	51,51,51,51	0
56	MG	DA	3503	1/1	0.85	0.12	57,57,57,57	0
56	MG	BA	3754	1/1	0.85	0.15	54,54,54,54	0
56	MG	BA	3665	1/1	0.85	0.14	49,49,49,49	0
56	MG	DA	3507	1/1	0.85	0.18	63,63,63,63	0
56	MG	CA	3195	1/1	0.85	0.30	69,69,69,69	0
56	MG	B0	106	1/1	0.85	0.16	66,66,66,66	0
56	MG	BA	3590	1/1	0.85	0.09	23,23,23,23	0
56	MG	CW	3002	1/1	0.85	0.15	60,60,60,60	0
56	MG	CA	3004	1/1	0.85	0.21	66,66,66,66	0
56	MG	AA	3219	1/1	0.85	0.19	63,63,63,63	0
56	MG	AX	3007	1/1	0.85	0.19	58,58,58,58	0
56	MG	BA	3778	1/1	0.85	0.19	40,40,40,40	0
56	MG	BA	3468	1/1	0.85	0.14	36,36,36,36	0
56	MG	BA	3787	1/1	0.85	0.08	24,24,24,24	0
56	MG	DA	3572	1/1	0.85	0.11	45,45,45,45	0
56	MG	AA	3149	1/1	0.85	0.12	51,51,51,51	0
56	MG	BA	3795	1/1	0.85	0.13	22,22,22,22	0
56	MG	DA	3279	1/1	0.85	0.19	56,56,56,56	0
56	MG	DA	3588	1/1	0.85	0.18	64,64,64,64	0
56	MG	DA	3289	1/1	0.85	0.16	53,53,53,53	0
56	MG	AA	3188	1/1	0.85	0.19	67,67,67,67	0
56	MG	DA	3597	1/1	0.85	0.15	54,54,54,54	0
56	MG	BA	3716	1/1	0.85	0.13	47,47,47,47	0
56	MG	BA	3717	1/1	0.85	0.12	57,57,57,57	0
56	MG	BA	3620	1/1	0.85	0.14	39,39,39,39	0
56	MG	BA	3622	1/1	0.85	0.18	56,56,56,56	0
56	MG	BA	3480	1/1	0.85	0.13	54,54,54,54	0
56	MG	BA	3727	1/1	0.85	0.24	64,64,64,64	0
56	MG	BA	3550	1/1	0.85	0.15	29,29,29,29	0
56	MG	DA	3632	1/1	0.85	0.14	57,57,57,57	0
56	MG	DA	3395	1/1	0.85	0.13	45,45,45,45	0
56	MG	BA	3426	1/1	0.85	0.16	42,42,42,42	0
56	MG	BA	3881	1/1	0.85	0.11	47,47,47,47	0
56	MG	BB	3004	1/1	0.85	0.25	59,59,59,59	0
56	MG	BA	3571	1/1	0.85	0.13	23,23,23,23	0
56	MG	AD	502	1/1	0.85	0.30	55,55,55,55	0
56	MG	AA	3210	1/1	0.85	0.12	76,76,76,76	0
56	MG	CA	3175	1/1	0.85	0.15	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BB	3026	1/1	0.85	0.19	66,66,66,66	0
56	MG	D0	3001	1/1	0.85	0.12	51,51,51,51	0
56	MG	AA	3089	1/1	0.85	0.31	66,66,66,66	0
56	MG	DA	3482	1/1	0.86	0.11	53,53,53,53	0
56	MG	BA	3627	1/1	0.86	0.14	34,34,34,34	0
56	MG	CX	3004	1/1	0.86	0.15	61,61,61,61	0
56	MG	CX	3006	1/1	0.86	0.14	50,50,50,50	0
56	MG	DA	3002	1/1	0.86	0.17	60,60,60,60	0
56	MG	DA	3510	1/1	0.86	0.13	46,46,46,46	0
56	MG	AA	3012	1/1	0.86	0.25	63,63,63,63	0
56	MG	DA	3116	1/1	0.86	0.29	66,66,66,66	0
56	MG	AX	3012	1/1	0.86	0.14	60,60,60,60	0
56	MG	AA	3090	1/1	0.86	0.12	51,51,51,51	0
56	MG	DA	3157	1/1	0.86	0.13	54,54,54,54	0
56	MG	DA	3167	1/1	0.86	0.09	48,48,48,48	0
56	MG	BA	3734	1/1	0.86	0.14	32,32,32,32	0
56	MG	AA	3056	1/1	0.86	0.23	60,60,60,60	0
56	MG	DA	3549	1/1	0.86	0.08	49,49,49,49	0
56	MG	AA	3108	1/1	0.86	0.30	65,65,65,65	0
56	MG	DA	3559	1/1	0.86	0.17	64,64,64,64	0
56	MG	DA	3249	1/1	0.86	0.16	37,37,37,37	0
56	MG	BA	3876	1/1	0.86	0.18	62,62,62,62	0
56	MG	BA	3470	1/1	0.86	0.15	46,46,46,46	0
56	MG	DA	3285	1/1	0.86	0.18	42,42,42,42	0
56	MG	BA	3657	1/1	0.86	0.19	65,65,65,65	0
56	MG	BA	3474	1/1	0.86	0.11	53,53,53,53	0
56	MG	AA	3109	1/1	0.86	0.25	60,60,60,60	0
56	MG	DA	3311	1/1	0.86	0.14	55,55,55,55	0
56	MG	BA	3104	1/1	0.86	0.21	58,58,58,58	0
56	MG	BA	3374	1/1	0.86	0.19	54,54,54,54	0
56	MG	DA	3329	1/1	0.86	0.15	51,51,51,51	0
56	MG	CA	3158	1/1	0.86	0.11	76,76,76,76	0
56	MG	BA	3486	1/1	0.86	0.14	29,29,29,29	0
56	MG	BE	304	1/1	0.86	0.25	56,56,56,56	0
56	MG	BA	3698	1/1	0.86	0.16	55,55,55,55	0
56	MG	BA	3383	1/1	0.86	0.11	42,42,42,42	0
56	MG	BR	202	1/1	0.86	0.14	38,38,38,38	0
56	MG	DA	3633	1/1	0.86	0.15	50,50,50,50	0
56	MG	BA	3107	1/1	0.86	0.18	50,50,50,50	0
56	MG	DA	3668	1/1	0.86	0.17	61,61,61,61	0
56	MG	DA	3417	1/1	0.86	0.13	53,53,53,53	0
56	MG	DB	3002	1/1	0.86	0.14	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3616	1/1	0.86	0.15	43,43,43,43	0
56	MG	DB	3014	1/1	0.86	0.23	61,61,61,61	0
56	MG	AA	3018	1/1	0.86	0.17	73,73,73,73	0
56	MG	AA	3050	1/1	0.86	0.27	67,67,67,67	0
56	MG	BA	3113	1/1	0.86	0.15	66,66,66,66	0
56	MG	CA	3011	1/1	0.86	0.19	56,56,56,56	0
56	MG	CA	3021	1/1	0.86	0.26	79,79,79,79	0
56	MG	BA	3808	1/1	0.86	0.13	40,40,40,40	0
56	MG	DA	3463	1/1	0.86	0.13	52,52,52,52	0
56	MG	AA	3054	1/1	0.86	0.24	68,68,68,68	0
56	MG	BA	3367	1/1	0.87	0.14	49,49,49,49	0
56	MG	CA	3183	1/1	0.87	0.23	69,69,69,69	0
56	MG	CA	3186	1/1	0.87	0.13	62,62,62,62	0
56	MG	AA	3096	1/1	0.87	0.14	60,60,60,60	0
56	MG	CA	3003	1/1	0.87	0.26	63,63,63,63	0
56	MG	BA	3803	1/1	0.87	0.20	67,67,67,67	0
56	MG	BA	3073	1/1	0.87	0.14	49,49,49,49	0
56	MG	BA	3722	1/1	0.87	0.12	52,52,52,52	0
56	MG	BA	3813	1/1	0.87	0.19	59,59,59,59	0
56	MG	CW	3001	1/1	0.87	0.13	57,57,57,57	0
56	MG	BA	3381	1/1	0.87	0.15	56,56,56,56	0
56	MG	AA	3005	1/1	0.87	0.14	66,66,66,66	0
56	MG	CX	3002	1/1	0.87	0.17	63,63,63,63	0
56	MG	BA	3639	1/1	0.87	0.14	59,59,59,59	0
56	MG	CA	3071	1/1	0.87	0.12	68,68,68,68	0
56	MG	BA	3209	1/1	0.87	0.23	58,58,58,58	0
56	MG	DA	3514	1/1	0.87	0.12	45,45,45,45	0
56	MG	DA	3034	1/1	0.87	0.12	51,51,51,51	0
56	MG	CA	3085	1/1	0.87	0.15	53,53,53,53	0
56	MG	BA	3237	1/1	0.87	0.20	57,57,57,57	0
56	MG	BA	3262	1/1	0.87	0.19	48,48,48,48	0
56	MG	BA	3589	1/1	0.87	0.20	42,42,42,42	0
56	MG	DA	3143	1/1	0.87	0.20	56,56,56,56	0
56	MG	DA	3151	1/1	0.87	0.24	59,59,59,59	0
56	MG	DA	3546	1/1	0.87	0.13	53,53,53,53	0
56	MG	DA	3154	1/1	0.87	0.29	57,57,57,57	0
56	MG	BA	3748	1/1	0.87	0.28	58,58,58,58	0
56	MG	BA	3487	1/1	0.87	0.15	50,50,50,50	0
56	MG	DA	3220	1/1	0.87	0.25	69,69,69,69	0
56	MG	DA	3566	1/1	0.87	0.12	67,67,67,67	0
56	MG	DA	3229	1/1	0.87	0.18	43,43,43,43	0
56	MG	BA	3594	1/1	0.87	0.11	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	CA	3125	1/1	0.87	0.11	61,61,61,61	0
56	MG	BA	3428	1/1	0.87	0.10	40,40,40,40	0
56	MG	BB	3016	1/1	0.87	0.13	49,49,49,49	0
56	MG	BB	3020	1/1	0.87	0.14	64,64,64,64	0
56	MG	DA	3278	1/1	0.87	0.17	49,49,49,49	0
56	MG	CA	3130	1/1	0.87	0.13	62,62,62,62	0
56	MG	BA	3675	1/1	0.87	0.12	38,38,38,38	0
56	MG	CA	3132	1/1	0.87	0.17	64,64,64,64	0
56	MG	CA	3137	1/1	0.87	0.33	66,66,66,66	0
56	MG	CA	3142	1/1	0.87	0.16	61,61,61,61	0
56	MG	DA	3306	1/1	0.87	0.08	33,33,33,33	0
56	MG	BA	3103	1/1	0.87	0.24	58,58,58,58	0
56	MG	DA	3322	1/1	0.87	0.09	41,41,41,41	0
56	MG	CA	3150	1/1	0.87	0.28	58,58,58,58	0
56	MG	DA	3327	1/1	0.87	0.16	48,48,48,48	0
56	MG	BA	3499	1/1	0.87	0.12	35,35,35,35	0
56	MG	BA	3439	1/1	0.87	0.18	53,53,53,53	0
56	MG	DA	3673	1/1	0.87	0.13	61,61,61,61	0
56	MG	AA	3019	1/1	0.87	0.14	54,54,54,54	0
56	MG	BA	3782	1/1	0.87	0.14	46,46,46,46	0
56	MG	DA	3369	1/1	0.87	0.18	58,58,58,58	0
56	MG	DA	3372	1/1	0.87	0.10	51,51,51,51	0
56	MG	DA	3380	1/1	0.87	0.13	49,49,49,49	0
56	MG	CA	3167	1/1	0.87	0.21	65,65,65,65	0
56	MG	CA	3171	1/1	0.87	0.14	52,52,52,52	0
56	MG	AA	3040	1/1	0.87	0.27	68,68,68,68	0
56	MG	AA	3137	1/1	0.87	0.11	64,64,64,64	0
56	MG	DA	3408	1/1	0.87	0.12	53,53,53,53	0
56	MG	DZ	5001	1/1	0.87	0.20	73,73,73,73	0
56	MG	AA	3216	1/1	0.87	0.19	68,68,68,68	0
56	MG	BZ	3003	1/1	0.87	0.19	51,51,51,51	0
56	MG	AA	3170	1/1	0.88	0.20	67,67,67,67	0
56	MG	DA	3504	1/1	0.88	0.12	58,58,58,58	0
56	MG	CA	3161	1/1	0.88	0.15	61,61,61,61	0
56	MG	BA	3865	1/1	0.88	0.10	36,36,36,36	0
56	MG	BA	3465	1/1	0.88	0.18	43,43,43,43	0
56	MG	BA	3488	1/1	0.88	0.14	31,31,31,31	0
56	MG	CA	3172	1/1	0.88	0.14	54,54,54,54	0
56	MG	DA	3267	1/1	0.88	0.13	53,53,53,53	0
56	MG	BA	3557	1/1	0.88	0.11	41,41,41,41	0
56	MG	BA	3558	1/1	0.88	0.21	46,46,46,46	0
56	MG	BA	3906	1/1	0.88	0.20	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	CA	3077	1/1	0.88	0.20	54,54,54,54	0
56	MG	BA	3623	1/1	0.88	0.09	48,48,48,48	0
56	MG	DA	3294	1/1	0.88	0.11	39,39,39,39	0
56	MG	BA	3568	1/1	0.88	0.15	56,56,56,56	0
56	MG	BA	3629	1/1	0.88	0.08	25,25,25,25	0
56	MG	BA	3016	1/1	0.88	0.23	51,51,51,51	0
56	MG	DA	3309	1/1	0.88	0.14	43,43,43,43	0
56	MG	CA	3091	1/1	0.88	0.19	67,67,67,67	0
56	MG	CA	3094	1/1	0.88	0.10	47,47,47,47	0
56	MG	CA	3099	1/1	0.88	0.24	72,72,72,72	0
56	MG	DA	3569	1/1	0.88	0.23	47,47,47,47	0
56	MG	DA	3326	1/1	0.88	0.13	34,34,34,34	0
56	MG	CF	3002	1/1	0.88	0.18	59,59,59,59	0
56	MG	CA	3102	1/1	0.88	0.17	52,52,52,52	0
56	MG	AA	3047	1/1	0.88	0.12	56,56,56,56	0
56	MG	DA	3340	1/1	0.88	0.14	45,45,45,45	0
56	MG	BA	3065	1/1	0.88	0.24	51,51,51,51	0
56	MG	CA	3115	1/1	0.88	0.16	60,60,60,60	0
56	MG	DA	3355	1/1	0.88	0.10	48,48,48,48	0
56	MG	DA	3604	1/1	0.88	0.11	50,50,50,50	0
56	MG	DA	3605	1/1	0.88	0.15	51,51,51,51	0
56	MG	AA	3231	1/1	0.88	0.28	61,61,61,61	0
56	MG	BA	3585	1/1	0.88	0.10	36,36,36,36	0
56	MG	BA	3801	1/1	0.88	0.09	27,27,27,27	0
56	MG	BA	3476	1/1	0.88	0.11	54,54,54,54	0
56	MG	DA	3390	1/1	0.88	0.10	42,42,42,42	0
56	MG	BG	205	1/1	0.88	0.08	40,40,40,40	0
56	MG	DA	3005	1/1	0.88	0.23	52,52,52,52	0
56	MG	AA	3165	1/1	0.88	0.08	57,57,57,57	0
56	MG	BA	3406	1/1	0.88	0.11	28,28,28,28	0
56	MG	DA	3050	1/1	0.88	0.12	45,45,45,45	0
56	MG	DA	3644	1/1	0.88	0.12	60,60,60,60	0
56	MG	BA	3810	1/1	0.88	0.14	46,46,46,46	0
56	MG	BA	3658	1/1	0.88	0.15	44,44,44,44	0
56	MG	BA	3484	1/1	0.88	0.15	42,42,42,42	0
56	MG	BA	3533	1/1	0.88	0.14	47,47,47,47	0
56	MG	DA	3149	1/1	0.88	0.26	59,59,59,59	0
56	MG	DB	3011	1/1	0.88	0.24	60,60,60,60	0
56	MG	DA	3446	1/1	0.88	0.17	68,68,68,68	0
56	MG	DA	3150	1/1	0.88	0.18	42,42,42,42	0
56	MG	CA	3149	1/1	0.88	0.28	71,71,71,71	0
56	MG	BA	3610	1/1	0.88	0.12	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3458	1/1	0.88	0.15	55,55,55,55	0
56	MG	BA	3840	1/1	0.88	0.13	50,50,50,50	0
56	MG	AA	3010	1/1	0.88	0.18	52,52,52,52	0
56	MG	DA	3217	1/1	0.88	0.27	63,63,63,63	0
56	MG	DA	3486	1/1	0.88	0.15	38,38,38,38	0
56	MG	DA	3490	1/1	0.88	0.09	51,51,51,51	0
56	MG	DA	3421	1/1	0.89	0.18	44,44,44,44	0
56	MG	AA	3002	1/1	0.89	0.16	55,55,55,55	0
56	MG	BA	3882	1/1	0.89	0.20	53,53,53,53	0
56	MG	AA	3150	1/1	0.89	0.16	66,66,66,66	0
56	MG	DA	3067	1/1	0.89	0.23	54,54,54,54	0
56	MG	DA	3445	1/1	0.89	0.11	45,45,45,45	0
56	MG	DA	3075	1/1	0.89	0.13	57,57,57,57	0
56	MG	DA	3076	1/1	0.89	0.15	44,44,44,44	0
56	MG	DA	3081	1/1	0.89	0.10	33,33,33,33	0
56	MG	DA	3453	1/1	0.89	0.12	51,51,51,51	0
56	MG	DA	3105	1/1	0.89	0.12	56,56,56,56	0
56	MG	DA	3457	1/1	0.89	0.10	30,30,30,30	0
56	MG	BA	3130	1/1	0.89	0.17	43,43,43,43	0
56	MG	CA	3118	1/1	0.89	0.16	63,63,63,63	0
56	MG	DA	3470	1/1	0.89	0.12	46,46,46,46	0
56	MG	BA	3161	1/1	0.89	0.10	46,46,46,46	0
56	MG	DA	3473	1/1	0.89	0.13	43,43,43,43	0
56	MG	DA	3477	1/1	0.89	0.11	51,51,51,51	0
56	MG	BB	3013	1/1	0.89	0.14	52,52,52,52	0
56	MG	DA	3147	1/1	0.89	0.09	53,53,53,53	0
56	MG	BA	3206	1/1	0.89	0.21	59,59,59,59	0
56	MG	DA	3500	1/1	0.89	0.19	67,67,67,67	0
56	MG	AA	3045	1/1	0.89	0.18	47,47,47,47	0
56	MG	AA	3026	1/1	0.89	0.28	50,50,50,50	0
56	MG	BA	3448	1/1	0.89	0.10	48,48,48,48	0
56	MG	BA	3450	1/1	0.89	0.16	35,35,35,35	0
56	MG	DA	3162	1/1	0.89	0.09	48,48,48,48	0
56	MG	DA	3509	1/1	0.89	0.11	55,55,55,55	0
56	MG	AA	3203	1/1	0.89	0.18	59,59,59,59	0
56	MG	DA	3199	1/1	0.89	0.10	51,51,51,51	0
56	MG	DA	3513	1/1	0.89	0.10	54,54,54,54	0
56	MG	DA	3212	1/1	0.89	0.20	52,52,52,52	0
56	MG	DA	3216	1/1	0.89	0.10	48,48,48,48	0
56	MG	BA	3567	1/1	0.89	0.11	46,46,46,46	0
56	MG	AA	3163	1/1	0.89	0.23	53,53,53,53	0
56	MG	DA	3222	1/1	0.89	0.15	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	AA	3027	1/1	0.89	0.35	60,60,60,60	0
56	MG	BA	3295	1/1	0.89	0.12	37,37,37,37	0
56	MG	BA	3666	1/1	0.89	0.17	74,74,74,74	0
56	MG	BW	202	1/1	0.89	0.20	49,49,49,49	0
56	MG	BA	3300	1/1	0.89	0.18	58,58,58,58	0
56	MG	DA	3252	1/1	0.89	0.14	57,57,57,57	0
56	MG	DA	3253	1/1	0.89	0.13	41,41,41,41	0
56	MG	BZ	3002	1/1	0.89	0.08	50,50,50,50	0
56	MG	DA	3562	1/1	0.89	0.14	49,49,49,49	0
56	MG	AA	3136	1/1	0.89	0.17	52,52,52,52	0
56	MG	BA	3583	1/1	0.89	0.18	35,35,35,35	0
56	MG	AA	3167	1/1	0.89	0.20	53,53,53,53	0
56	MG	CA	3169	1/1	0.89	0.16	60,60,60,60	0
56	MG	B5	105	1/1	0.89	0.10	52,52,52,52	0
56	MG	DA	3290	1/1	0.89	0.13	52,52,52,52	0
56	MG	BA	3351	1/1	0.89	0.11	33,33,33,33	0
56	MG	DA	3591	1/1	0.89	0.13	55,55,55,55	0
56	MG	DA	3295	1/1	0.89	0.10	38,38,38,38	0
56	MG	DA	3595	1/1	0.89	0.11	45,45,45,45	0
56	MG	BA	3067	1/1	0.89	0.28	62,62,62,62	0
56	MG	AA	3104	1/1	0.89	0.26	64,64,64,64	0
56	MG	AA	3107	1/1	0.89	0.13	53,53,53,53	0
56	MG	CA	3176	1/1	0.89	0.21	62,62,62,62	0
56	MG	DA	3607	1/1	0.89	0.11	35,35,35,35	0
56	MG	DA	3608	1/1	0.89	0.09	55,55,55,55	0
56	MG	CA	3017	1/1	0.89	0.21	56,56,56,56	0
56	MG	DA	3318	1/1	0.89	0.12	59,59,59,59	0
56	MG	DA	3321	1/1	0.89	0.15	39,39,39,39	0
56	MG	BA	3713	1/1	0.89	0.12	59,59,59,59	0
56	MG	CA	3025	1/1	0.89	0.19	51,51,51,51	0
56	MG	DA	3622	1/1	0.89	0.09	51,51,51,51	0
56	MG	DA	3626	1/1	0.89	0.22	41,41,41,41	0
56	MG	BA	3095	1/1	0.89	0.12	43,43,43,43	0
56	MG	BA	3097	1/1	0.89	0.12	48,48,48,48	0
56	MG	AA	3177	1/1	0.89	0.18	57,57,57,57	0
56	MG	CA	3058	1/1	0.89	0.21	63,63,63,63	0
56	MG	CA	3194	1/1	0.89	0.20	66,66,66,66	0
56	MG	DA	3341	1/1	0.89	0.14	43,43,43,43	0
56	MG	DA	3655	1/1	0.89	0.21	57,57,57,57	0
56	MG	DA	3664	1/1	0.89	0.20	71,71,71,71	0
56	MG	CA	3059	1/1	0.89	0.17	58,58,58,58	0
56	MG	BA	3824	1/1	0.89	0.15	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	CG	5001	1/1	0.89	0.13	64,64,64,64	0
56	MG	DA	3362	1/1	0.89	0.20	61,61,61,61	0
56	MG	BA	3614	1/1	0.89	0.09	53,53,53,53	0
56	MG	AB	3002	1/1	0.89	0.16	70,70,70,70	0
56	MG	BA	3721	1/1	0.89	0.21	52,52,52,52	0
56	MG	AA	3037	1/1	0.89	0.27	63,63,63,63	0
56	MG	DA	3386	1/1	0.89	0.15	46,46,46,46	0
56	MG	AE	3001	1/1	0.89	0.09	65,65,65,65	0
56	MG	BA	3866	1/1	0.89	0.10	54,54,54,54	0
56	MG	AA	3074	1/1	0.89	0.22	57,57,57,57	0
56	MG	BA	3420	1/1	0.89	0.08	47,47,47,47	0
56	MG	DV	201	1/1	0.89	0.27	51,51,51,51	0
56	MG	CA	3096	1/1	0.89	0.10	39,39,39,39	0
56	MG	BA	3732	1/1	0.89	0.09	24,24,24,24	0
56	MG	D5	101	1/1	0.89	0.10	45,45,45,45	0
56	MG	DA	3016	1/1	0.89	0.12	59,59,59,59	0
56	MG	DA	3053	1/1	0.90	0.14	43,43,43,43	0
56	MG	BA	3826	1/1	0.90	0.09	42,42,42,42	0
56	MG	DA	3071	1/1	0.90	0.11	41,41,41,41	0
56	MG	BA	3830	1/1	0.90	0.14	56,56,56,56	0
56	MG	BA	3466	1/1	0.90	0.19	46,46,46,46	0
56	MG	BA	3352	1/1	0.90	0.12	42,42,42,42	0
56	MG	BA	3578	1/1	0.90	0.07	23,23,23,23	0
56	MG	BA	3356	1/1	0.90	0.11	52,52,52,52	0
56	MG	AA	3059	1/1	0.90	0.22	60,60,60,60	0
56	MG	DA	3459	1/1	0.90	0.21	50,50,50,50	0
56	MG	DA	3462	1/1	0.90	0.10	42,42,42,42	0
56	MG	DA	3125	1/1	0.90	0.12	44,44,44,44	0
56	MG	DA	3128	1/1	0.90	0.09	45,45,45,45	0
56	MG	CA	3103	1/1	0.90	0.15	63,63,63,63	0
56	MG	BA	3472	1/1	0.90	0.10	31,31,31,31	0
56	MG	AY	3002	1/1	0.90	0.10	66,66,66,66	0
56	MG	BA	3001	1/1	0.90	0.18	45,45,45,45	0
56	MG	AA	3189	1/1	0.90	0.13	53,53,53,53	0
56	MG	DA	3488	1/1	0.90	0.10	55,55,55,55	0
56	MG	BA	3132	1/1	0.90	0.13	57,57,57,57	0
56	MG	DA	3491	1/1	0.90	0.24	53,53,53,53	0
56	MG	AA	3077	1/1	0.90	0.34	60,60,60,60	0
56	MG	BA	3192	1/1	0.90	0.13	41,41,41,41	0
56	MG	BA	3405	1/1	0.90	0.15	42,42,42,42	0
56	MG	CA	3128	1/1	0.90	0.17	49,49,49,49	0
56	MG	BA	3194	1/1	0.90	0.08	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3200	1/1	0.90	0.09	46,46,46,46	0
56	MG	BA	3031	1/1	0.90	0.12	40,40,40,40	0
56	MG	AA	3015	1/1	0.90	0.12	71,71,71,71	0
56	MG	AA	3200	1/1	0.90	0.18	61,61,61,61	0
56	MG	CA	3135	1/1	0.90	0.27	57,57,57,57	0
56	MG	BA	3495	1/1	0.90	0.12	40,40,40,40	0
56	MG	BB	3023	1/1	0.90	0.17	71,71,71,71	0
56	MG	CA	3143	1/1	0.90	0.21	65,65,65,65	0
56	MG	AA	3049	1/1	0.90	0.33	62,62,62,62	0
56	MG	BA	3242	1/1	0.90	0.12	60,60,60,60	0
56	MG	BB	3027	1/1	0.90	0.14	58,58,58,58	0
56	MG	DA	3532	1/1	0.90	0.21	61,61,61,61	0
56	MG	DA	3535	1/1	0.90	0.11	41,41,41,41	0
56	MG	CA	3153	1/1	0.90	0.14	60,60,60,60	0
56	MG	BA	3747	1/1	0.90	0.13	57,57,57,57	0
56	MG	AA	3058	1/1	0.90	0.14	54,54,54,54	0
56	MG	DA	3272	1/1	0.90	0.09	52,52,52,52	0
56	MG	AA	3067	1/1	0.90	0.19	56,56,56,56	0
56	MG	BF	312	1/1	0.90	0.14	49,49,49,49	0
56	MG	BA	3628	1/1	0.90	0.11	51,51,51,51	0
56	MG	DA	3280	1/1	0.90	0.12	57,57,57,57	0
56	MG	BA	3441	1/1	0.90	0.09	26,26,26,26	0
56	MG	DA	3568	1/1	0.90	0.12	30,30,30,30	0
56	MG	BQ	3006	1/1	0.90	0.12	53,53,53,53	0
56	MG	BA	3522	1/1	0.90	0.12	50,50,50,50	0
56	MG	DA	3292	1/1	0.90	0.10	53,53,53,53	0
56	MG	BA	3525	1/1	0.90	0.12	59,59,59,59	0
56	MG	DA	3579	1/1	0.90	0.11	48,48,48,48	0
56	MG	BA	3762	1/1	0.90	0.11	60,60,60,60	0
56	MG	DA	3583	1/1	0.90	0.11	54,54,54,54	0
56	MG	BA	3633	1/1	0.90	0.09	42,42,42,42	0
56	MG	BA	3442	1/1	0.90	0.11	37,37,37,37	0
56	MG	DA	3304	1/1	0.90	0.08	40,40,40,40	0
56	MG	DA	3594	1/1	0.90	0.16	56,56,56,56	0
56	MG	AR	101	1/1	0.90	0.22	56,56,56,56	0
56	MG	BA	3535	1/1	0.90	0.10	46,46,46,46	0
56	MG	BA	3783	1/1	0.90	0.08	33,33,33,33	0
56	MG	B8	102	1/1	0.90	0.14	42,42,42,42	0
56	MG	CA	3184	1/1	0.90	0.32	68,68,68,68	0
56	MG	BA	3540	1/1	0.90	0.09	50,50,50,50	0
56	MG	CA	3187	1/1	0.90	0.09	51,51,51,51	0
56	MG	AA	3214	1/1	0.90	0.17	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	CA	3190	1/1	0.90	0.14	67,67,67,67	0
56	MG	BA	3314	1/1	0.90	0.28	60,60,60,60	0
56	MG	AA	3120	1/1	0.90	0.10	67,67,67,67	0
56	MG	AA	3073	1/1	0.90	0.13	53,53,53,53	0
56	MG	BA	3663	1/1	0.90	0.08	39,39,39,39	0
56	MG	CA	3200	1/1	0.90	0.25	62,62,62,62	0
56	MG	CA	3023	1/1	0.90	0.26	60,60,60,60	0
56	MG	BA	3802	1/1	0.90	0.10	27,27,27,27	0
56	MG	BA	3455	1/1	0.90	0.11	31,31,31,31	0
56	MG	DA	3363	1/1	0.90	0.08	42,42,42,42	0
56	MG	DA	3639	1/1	0.90	0.15	57,57,57,57	0
56	MG	DA	3368	1/1	0.90	0.11	47,47,47,47	0
56	MG	BA	3805	1/1	0.90	0.09	32,32,32,32	0
56	MG	DA	3648	1/1	0.90	0.12	39,39,39,39	0
56	MG	DA	3371	1/1	0.90	0.09	42,42,42,42	0
56	MG	CR	3001	1/1	0.90	0.17	64,64,64,64	0
56	MG	BA	3349	1/1	0.90	0.13	42,42,42,42	0
56	MG	CA	3057	1/1	0.90	0.15	59,59,59,59	0
56	MG	BA	3669	1/1	0.90	0.15	44,44,44,44	0
56	MG	BA	3464	1/1	0.90	0.07	25,25,25,25	0
56	MG	CA	3062	1/1	0.90	0.25	64,64,64,64	0
56	MG	DB	3007	1/1	0.90	0.21	64,64,64,64	0
56	MG	CX	3005	1/1	0.90	0.25	60,60,60,60	0
56	MG	DA	3400	1/1	0.90	0.10	36,36,36,36	0
56	MG	DB	3016	1/1	0.90	0.19	61,61,61,61	0
56	MG	CA	3069	1/1	0.90	0.23	57,57,57,57	0
56	MG	DA	3407	1/1	0.90	0.18	67,67,67,67	0
56	MG	AA	3124	1/1	0.90	0.12	58,58,58,58	0
56	MG	DA	3410	1/1	0.90	0.26	55,55,55,55	0
56	MG	BA	3569	1/1	0.90	0.14	48,48,48,48	0
56	MG	DQ	3003	1/1	0.90	0.13	57,57,57,57	0
56	MG	DA	3415	1/1	0.90	0.14	39,39,39,39	0
56	MG	DU	3004	1/1	0.90	0.08	48,48,48,48	0
56	MG	DA	3007	1/1	0.90	0.12	54,54,54,54	0
56	MG	BA	3683	1/1	0.90	0.09	37,37,37,37	0
56	MG	CA	3084	1/1	0.90	0.16	57,57,57,57	0
56	MG	BA	3570	1/1	0.90	0.17	51,51,51,51	0
57	UAM	AA	3232	30/30	0.90	0.16	44,65,77,80	0
56	MG	BA	3825	1/1	0.90	0.10	39,39,39,39	0
56	MG	AA	3113	1/1	0.91	0.27	55,55,55,55	0
56	MG	AA	3233	1/1	0.91	0.19	52,52,52,52	0
56	MG	DA	3397	1/1	0.91	0.08	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	AA	3042	1/1	0.91	0.25	47,47,47,47	0
56	MG	DA	3401	1/1	0.91	0.11	37,37,37,37	0
56	MG	CL	202	1/1	0.91	0.12	50,50,50,50	0
56	MG	CP	101	1/1	0.91	0.21	57,57,57,57	0
56	MG	BA	3800	1/1	0.91	0.09	29,29,29,29	0
56	MG	CA	3026	1/1	0.91	0.24	56,56,56,56	0
56	MG	CA	3029	1/1	0.91	0.17	60,60,60,60	0
56	MG	CA	3030	1/1	0.91	0.15	61,61,61,61	0
56	MG	CA	3035	1/1	0.91	0.20	49,49,49,49	0
56	MG	DA	3420	1/1	0.91	0.12	45,45,45,45	0
56	MG	CA	3036	1/1	0.91	0.25	64,64,64,64	0
56	MG	AA	3187	1/1	0.91	0.26	65,65,65,65	0
56	MG	AA	3043	1/1	0.91	0.19	56,56,56,56	0
56	MG	CA	3053	1/1	0.91	0.21	61,61,61,61	0
56	MG	AA	3044	1/1	0.91	0.24	54,54,54,54	0
56	MG	DA	3433	1/1	0.91	0.10	40,40,40,40	0
56	MG	DA	3442	1/1	0.91	0.08	46,46,46,46	0
56	MG	BA	3378	1/1	0.91	0.13	43,43,43,43	0
56	MG	AA	3153	1/1	0.91	0.08	58,58,58,58	0
56	MG	AA	3197	1/1	0.91	0.23	65,65,65,65	0
56	MG	DA	3039	1/1	0.91	0.08	29,29,29,29	0
56	MG	BA	3386	1/1	0.91	0.09	47,47,47,47	0
56	MG	CA	3064	1/1	0.91	0.24	53,53,53,53	0
56	MG	BA	3398	1/1	0.91	0.10	58,58,58,58	0
56	MG	DA	3060	1/1	0.91	0.11	53,53,53,53	0
56	MG	DA	3066	1/1	0.91	0.10	49,49,49,49	0
56	MG	BA	3817	1/1	0.91	0.11	50,50,50,50	0
56	MG	DA	3068	1/1	0.91	0.27	58,58,58,58	0
56	MG	AA	3154	1/1	0.91	0.09	44,44,44,44	0
56	MG	DA	3471	1/1	0.91	0.09	49,49,49,49	0
56	MG	AW	104	1/1	0.91	0.13	64,64,64,64	0
56	MG	CA	3079	1/1	0.91	0.15	58,58,58,58	0
56	MG	CA	3081	1/1	0.91	0.23	56,56,56,56	0
56	MG	BA	3821	1/1	0.91	0.14	42,42,42,42	0
56	MG	DA	3106	1/1	0.91	0.21	63,63,63,63	0
56	MG	DA	3487	1/1	0.91	0.12	48,48,48,48	0
56	MG	DA	3110	1/1	0.91	0.13	38,38,38,38	0
56	MG	AA	3156	1/1	0.91	0.20	62,62,62,62	0
56	MG	BA	3414	1/1	0.91	0.10	32,32,32,32	0
56	MG	BA	3545	1/1	0.91	0.07	43,43,43,43	0
56	MG	DA	3502	1/1	0.91	0.10	63,63,63,63	0
56	MG	BA	3133	1/1	0.91	0.13	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3132	1/1	0.91	0.22	50,50,50,50	0
56	MG	BA	3678	1/1	0.91	0.07	25,25,25,25	0
56	MG	DA	3137	1/1	0.91	0.09	45,45,45,45	0
56	MG	CA	3092	1/1	0.91	0.30	63,63,63,63	0
56	MG	CA	3093	1/1	0.91	0.10	65,65,65,65	0
56	MG	BA	3140	1/1	0.91	0.17	49,49,49,49	0
56	MG	BA	3689	1/1	0.91	0.15	44,44,44,44	0
56	MG	CA	3098	1/1	0.91	0.11	57,57,57,57	0
56	MG	BA	3553	1/1	0.91	0.07	19,19,19,19	0
56	MG	DA	3515	1/1	0.91	0.17	59,59,59,59	0
56	MG	DA	3516	1/1	0.91	0.09	56,56,56,56	0
56	MG	CA	3101	1/1	0.91	0.23	60,60,60,60	0
56	MG	BA	3851	1/1	0.91	0.12	33,33,33,33	0
56	MG	BA	3861	1/1	0.91	0.14	34,34,34,34	0
56	MG	DA	3176	1/1	0.91	0.15	36,36,36,36	0
56	MG	DA	3188	1/1	0.91	0.09	44,44,44,44	0
56	MG	DA	3191	1/1	0.91	0.09	52,52,52,52	0
56	MG	BA	3423	1/1	0.91	0.09	34,34,34,34	0
56	MG	CA	3112	1/1	0.91	0.22	65,65,65,65	0
56	MG	DA	3210	1/1	0.91	0.09	30,30,30,30	0
56	MG	BA	3159	1/1	0.91	0.12	50,50,50,50	0
56	MG	BA	3700	1/1	0.91	0.12	51,51,51,51	0
56	MG	DA	3551	1/1	0.91	0.10	53,53,53,53	0
56	MG	CA	3116	1/1	0.91	0.14	54,54,54,54	0
56	MG	AA	3025	1/1	0.91	0.11	50,50,50,50	0
56	MG	BA	3705	1/1	0.91	0.12	56,56,56,56	0
56	MG	DA	3228	1/1	0.91	0.08	38,38,38,38	0
56	MG	BA	3171	1/1	0.91	0.17	42,42,42,42	0
56	MG	DA	3237	1/1	0.91	0.11	47,47,47,47	0
56	MG	BA	3436	1/1	0.91	0.20	54,54,54,54	0
56	MG	BA	3885	1/1	0.91	0.20	55,55,55,55	0
56	MG	DA	3246	1/1	0.91	0.10	59,59,59,59	0
56	MG	BA	3901	1/1	0.91	0.10	39,39,39,39	0
56	MG	BA	3903	1/1	0.91	0.11	42,42,42,42	0
56	MG	AA	3078	1/1	0.91	0.22	47,47,47,47	0
56	MG	AA	3207	1/1	0.91	0.10	53,53,53,53	0
56	MG	DA	3585	1/1	0.91	0.10	51,51,51,51	0
56	MG	DA	3263	1/1	0.91	0.08	40,40,40,40	0
56	MG	BA	3203	1/1	0.91	0.21	41,41,41,41	0
56	MG	BA	3443	1/1	0.91	0.07	22,22,22,22	0
56	MG	CA	3136	1/1	0.91	0.10	59,59,59,59	0
56	MG	AA	3125	1/1	0.91	0.08	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	AA	3126	1/1	0.91	0.28	54,54,54,54	0
56	MG	BA	3011	1/1	0.91	0.09	37,37,37,37	0
56	MG	BA	3210	1/1	0.91	0.16	53,53,53,53	0
56	MG	CA	3147	1/1	0.91	0.15	64,64,64,64	0
56	MG	BB	3024	1/1	0.91	0.11	60,60,60,60	0
56	MG	BA	3217	1/1	0.91	0.13	49,49,49,49	0
56	MG	CA	3151	1/1	0.91	0.13	60,60,60,60	0
56	MG	AA	3130	1/1	0.91	0.19	62,62,62,62	0
56	MG	DA	3297	1/1	0.91	0.10	42,42,42,42	0
56	MG	AA	3131	1/1	0.91	0.11	56,56,56,56	0
56	MG	BD	303	1/1	0.91	0.12	40,40,40,40	0
56	MG	BD	304	1/1	0.91	0.24	49,49,49,49	0
56	MG	AA	3079	1/1	0.91	0.24	60,60,60,60	0
56	MG	BA	3268	1/1	0.91	0.11	46,46,46,46	0
56	MG	BA	3600	1/1	0.91	0.12	43,43,43,43	0
56	MG	BA	3042	1/1	0.91	0.17	43,43,43,43	0
56	MG	DA	3320	1/1	0.91	0.17	48,48,48,48	0
56	MG	DA	3635	1/1	0.91	0.12	44,44,44,44	0
56	MG	BF	313	1/1	0.91	0.14	49,49,49,49	0
56	MG	DA	3640	1/1	0.91	0.10	56,56,56,56	0
56	MG	BA	3744	1/1	0.91	0.12	41,41,41,41	0
56	MG	BA	3285	1/1	0.91	0.17	48,48,48,48	0
56	MG	BA	3288	1/1	0.91	0.25	51,51,51,51	0
56	MG	DA	3649	1/1	0.91	0.11	55,55,55,55	0
56	MG	DA	3650	1/1	0.91	0.14	53,53,53,53	0
56	MG	BA	3058	1/1	0.91	0.12	48,48,48,48	0
56	MG	DA	3659	1/1	0.91	0.24	53,53,53,53	0
56	MG	BA	3062	1/1	0.91	0.10	41,41,41,41	0
56	MG	AA	3220	1/1	0.91	0.19	57,57,57,57	0
56	MG	DA	3334	1/1	0.91	0.07	44,44,44,44	0
56	MG	BA	3066	1/1	0.91	0.17	54,54,54,54	0
56	MG	BA	3347	1/1	0.91	0.10	41,41,41,41	0
56	MG	DA	3344	1/1	0.91	0.10	54,54,54,54	0
56	MG	DB	3004	1/1	0.91	0.22	57,57,57,57	0
56	MG	DA	3348	1/1	0.91	0.10	32,32,32,32	0
56	MG	B0	103	1/1	0.91	0.11	49,49,49,49	0
56	MG	CA	3185	1/1	0.91	0.24	59,59,59,59	0
56	MG	BA	3621	1/1	0.91	0.14	50,50,50,50	0
56	MG	DA	3358	1/1	0.91	0.10	45,45,45,45	0
56	MG	B1	102	1/1	0.91	0.11	59,59,59,59	0
56	MG	DB	3019	1/1	0.91	0.30	60,60,60,60	0
56	MG	AA	3084	1/1	0.91	0.17	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DE	302	1/1	0.91	0.13	52,52,52,52	0
56	MG	DA	3367	1/1	0.91	0.18	57,57,57,57	0
56	MG	AA	3041	1/1	0.91	0.10	53,53,53,53	0
56	MG	DF	306	1/1	0.91	0.25	46,46,46,46	0
56	MG	BA	3625	1/1	0.91	0.09	20,20,20,20	0
56	MG	BA	3080	1/1	0.91	0.09	41,41,41,41	0
56	MG	AA	3228	1/1	0.91	0.29	58,58,58,58	0
56	MG	BA	3354	1/1	0.91	0.18	53,53,53,53	0
56	MG	DW	3003	1/1	0.91	0.12	47,47,47,47	0
56	MG	CA	3199	1/1	0.91	0.19	51,51,51,51	0
56	MG	DA	3385	1/1	0.91	0.12	47,47,47,47	0
56	MG	CA	3009	1/1	0.91	0.18	46,46,46,46	0
56	MG	BA	3355	1/1	0.91	0.12	35,35,35,35	0
56	MG	DA	3391	1/1	0.91	0.10	50,50,50,50	0
56	MG	DA	3405	1/1	0.92	0.11	44,44,44,44	0
56	MG	BA	3267	1/1	0.92	0.20	51,51,51,51	0
56	MG	BA	3390	1/1	0.92	0.06	33,33,33,33	0
56	MG	DA	3409	1/1	0.92	0.06	36,36,36,36	0
56	MG	CA	3100	1/1	0.92	0.16	65,65,65,65	0
56	MG	DA	3087	1/1	0.92	0.10	48,48,48,48	0
56	MG	DA	3100	1/1	0.92	0.10	46,46,46,46	0
56	MG	DA	3101	1/1	0.92	0.07	46,46,46,46	0
56	MG	DA	3418	1/1	0.92	0.14	44,44,44,44	0
56	MG	DA	3419	1/1	0.92	0.11	42,42,42,42	0
56	MG	BA	3769	1/1	0.92	0.10	46,46,46,46	0
56	MG	BA	3770	1/1	0.92	0.17	54,54,54,54	0
56	MG	BA	3129	1/1	0.92	0.08	37,37,37,37	0
56	MG	CA	3106	1/1	0.92	0.20	67,67,67,67	0
56	MG	BA	3400	1/1	0.92	0.10	32,32,32,32	0
56	MG	DA	3120	1/1	0.92	0.10	47,47,47,47	0
56	MG	DA	3122	1/1	0.92	0.11	51,51,51,51	0
56	MG	DA	3437	1/1	0.92	0.08	53,53,53,53	0
56	MG	DA	3438	1/1	0.92	0.14	42,42,42,42	0
56	MG	BA	3473	1/1	0.92	0.20	59,59,59,59	0
56	MG	BE	309	1/1	0.92	0.10	31,31,31,31	0
56	MG	DA	3129	1/1	0.92	0.12	37,37,37,37	0
56	MG	DA	3131	1/1	0.92	0.13	48,48,48,48	0
56	MG	BA	3668	1/1	0.92	0.10	48,48,48,48	0
56	MG	BF	301	1/1	0.92	0.12	41,41,41,41	0
56	MG	AA	3038	1/1	0.92	0.27	55,55,55,55	0
56	MG	DA	3142	1/1	0.92	0.11	50,50,50,50	0
56	MG	BA	3789	1/1	0.92	0.12	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3145	1/1	0.92	0.13	47,47,47,47	0
56	MG	CA	3122	1/1	0.92	0.19	66,66,66,66	0
56	MG	BG	204	1/1	0.92	0.09	58,58,58,58	0
56	MG	BA	3670	1/1	0.92	0.18	57,57,57,57	0
56	MG	BI	3001	1/1	0.92	0.09	60,60,60,60	0
56	MG	DA	3153	1/1	0.92	0.10	43,43,43,43	0
56	MG	BO	3001	1/1	0.92	0.13	62,62,62,62	0
56	MG	DA	3155	1/1	0.92	0.09	41,41,41,41	0
56	MG	BO	3002	1/1	0.92	0.22	50,50,50,50	0
56	MG	DA	3160	1/1	0.92	0.21	38,38,38,38	0
56	MG	BO	3005	1/1	0.92	0.11	61,61,61,61	0
56	MG	DA	3163	1/1	0.92	0.24	52,52,52,52	0
56	MG	DA	3165	1/1	0.92	0.12	27,27,27,27	0
56	MG	AA	3192	1/1	0.92	0.13	50,50,50,50	0
56	MG	BA	3672	1/1	0.92	0.07	24,24,24,24	0
56	MG	DA	3179	1/1	0.92	0.12	42,42,42,42	0
56	MG	DA	3180	1/1	0.92	0.23	57,57,57,57	0
56	MG	DA	3183	1/1	0.92	0.16	44,44,44,44	0
56	MG	BQ	3007	1/1	0.92	0.11	44,44,44,44	0
56	MG	AX	3003	1/1	0.92	0.17	50,50,50,50	0
56	MG	AX	3005	1/1	0.92	0.19	60,60,60,60	0
56	MG	BX	3004	1/1	0.92	0.28	48,48,48,48	0
56	MG	DA	3209	1/1	0.92	0.19	45,45,45,45	0
56	MG	BY	502	1/1	0.92	0.13	45,45,45,45	0
56	MG	DA	3512	1/1	0.92	0.24	54,54,54,54	0
56	MG	BA	3415	1/1	0.92	0.08	33,33,33,33	0
56	MG	DA	3215	1/1	0.92	0.12	60,60,60,60	0
56	MG	BA	3680	1/1	0.92	0.08	32,32,32,32	0
56	MG	BA	3148	1/1	0.92	0.09	36,36,36,36	0
56	MG	B0	101	1/1	0.92	0.23	44,44,44,44	0
56	MG	DA	3221	1/1	0.92	0.13	46,46,46,46	0
56	MG	BA	3686	1/1	0.92	0.10	52,52,52,52	0
56	MG	DA	3226	1/1	0.92	0.21	54,54,54,54	0
56	MG	B0	105	1/1	0.92	0.13	52,52,52,52	0
56	MG	AA	3030	1/1	0.92	0.27	49,49,49,49	0
56	MG	AA	3033	1/1	0.92	0.15	55,55,55,55	0
56	MG	CA	3159	1/1	0.92	0.15	61,61,61,61	0
56	MG	BA	3425	1/1	0.92	0.08	60,60,60,60	0
56	MG	BA	3592	1/1	0.92	0.13	27,27,27,27	0
56	MG	DA	3548	1/1	0.92	0.13	55,55,55,55	0
56	MG	B6	101	1/1	0.92	0.15	47,47,47,47	0
56	MG	DA	3550	1/1	0.92	0.10	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	CA	3166	1/1	0.92	0.13	53,53,53,53	0
56	MG	AA	3157	1/1	0.92	0.21	39,39,39,39	0
56	MG	CA	3001	1/1	0.92	0.15	67,67,67,67	0
56	MG	BA	3703	1/1	0.92	0.10	55,55,55,55	0
56	MG	BA	3182	1/1	0.92	0.20	59,59,59,59	0
56	MG	CA	3006	1/1	0.92	0.10	62,62,62,62	0
56	MG	AA	3175	1/1	0.92	0.11	62,62,62,62	0
56	MG	BA	3435	1/1	0.92	0.19	60,60,60,60	0
56	MG	CA	3010	1/1	0.92	0.28	52,52,52,52	0
56	MG	CA	3177	1/1	0.92	0.13	64,64,64,64	0
56	MG	BA	3350	1/1	0.92	0.08	29,29,29,29	0
56	MG	CA	3181	1/1	0.92	0.15	55,55,55,55	0
56	MG	CA	3014	1/1	0.92	0.13	51,51,51,51	0
56	MG	BA	3438	1/1	0.92	0.08	27,27,27,27	0
56	MG	BA	3612	1/1	0.92	0.17	53,53,53,53	0
56	MG	AA	3116	1/1	0.92	0.14	58,58,58,58	0
56	MG	DA	3589	1/1	0.92	0.09	50,50,50,50	0
56	MG	BA	3842	1/1	0.92	0.14	43,43,43,43	0
56	MG	DA	3298	1/1	0.92	0.10	50,50,50,50	0
56	MG	BA	3843	1/1	0.92	0.11	34,34,34,34	0
56	MG	CA	3028	1/1	0.92	0.17	58,58,58,58	0
56	MG	BA	3512	1/1	0.92	0.10	57,57,57,57	0
56	MG	BA	3440	1/1	0.92	0.09	32,32,32,32	0
56	MG	DA	3600	1/1	0.92	0.07	48,48,48,48	0
56	MG	DA	3602	1/1	0.92	0.12	44,44,44,44	0
56	MG	DA	3307	1/1	0.92	0.08	41,41,41,41	0
56	MG	CA	3033	1/1	0.92	0.10	65,65,65,65	0
56	MG	BA	3518	1/1	0.92	0.10	57,57,57,57	0
56	MG	DA	3314	1/1	0.92	0.09	38,38,38,38	0
56	MG	DA	3317	1/1	0.92	0.15	56,56,56,56	0
56	MG	BA	3857	1/1	0.92	0.13	46,46,46,46	0
56	MG	CA	3196	1/1	0.92	0.11	53,53,53,53	0
56	MG	DA	3613	1/1	0.92	0.13	44,44,44,44	0
56	MG	DA	3618	1/1	0.92	0.10	49,49,49,49	0
56	MG	CA	3039	1/1	0.92	0.14	55,55,55,55	0
56	MG	AA	3007	1/1	0.92	0.19	50,50,50,50	0
56	MG	DA	3324	1/1	0.92	0.15	47,47,47,47	0
56	MG	DA	3625	1/1	0.92	0.10	50,50,50,50	0
56	MG	BA	3101	1/1	0.92	0.12	42,42,42,42	0
56	MG	AA	3181	1/1	0.92	0.17	70,70,70,70	0
56	MG	DA	3630	1/1	0.92	0.12	45,45,45,45	0
56	MG	BA	3730	1/1	0.92	0.13	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3872	1/1	0.92	0.11	42,42,42,42	0
56	MG	BA	3529	1/1	0.92	0.11	53,53,53,53	0
56	MG	DA	3634	1/1	0.92	0.16	62,62,62,62	0
56	MG	DA	3331	1/1	0.92	0.08	30,30,30,30	0
56	MG	DA	3636	1/1	0.92	0.12	55,55,55,55	0
56	MG	DA	3332	1/1	0.92	0.15	53,53,53,53	0
56	MG	BA	3875	1/1	0.92	0.17	51,51,51,51	0
56	MG	AA	3098	1/1	0.92	0.11	60,60,60,60	0
56	MG	DA	3642	1/1	0.92	0.09	40,40,40,40	0
56	MG	CT	3001	1/1	0.92	0.16	46,46,46,46	0
56	MG	AA	3184	1/1	0.92	0.14	60,60,60,60	0
56	MG	DA	3347	1/1	0.92	0.09	38,38,38,38	0
56	MG	CA	3065	1/1	0.92	0.26	58,58,58,58	0
56	MG	DA	3653	1/1	0.92	0.10	46,46,46,46	0
56	MG	BA	3736	1/1	0.92	0.17	45,45,45,45	0
56	MG	DA	3352	1/1	0.92	0.13	35,35,35,35	0
56	MG	DA	3662	1/1	0.92	0.19	52,52,52,52	0
56	MG	BA	3211	1/1	0.92	0.34	63,63,63,63	0
56	MG	DA	3354	1/1	0.92	0.08	34,34,34,34	0
56	MG	BA	3894	1/1	0.92	0.20	44,44,44,44	0
56	MG	CA	3075	1/1	0.92	0.09	52,52,52,52	0
56	MG	DA	3360	1/1	0.92	0.11	47,47,47,47	0
56	MG	BA	3897	1/1	0.92	0.11	49,49,49,49	0
56	MG	BA	3028	1/1	0.92	0.09	45,45,45,45	0
56	MG	DB	3005	1/1	0.92	0.20	61,61,61,61	0
56	MG	DA	3366	1/1	0.92	0.21	53,53,53,53	0
56	MG	DB	3008	1/1	0.92	0.18	55,55,55,55	0
56	MG	BA	3543	1/1	0.92	0.09	48,48,48,48	0
56	MG	AA	3164	1/1	0.92	0.21	62,62,62,62	0
56	MG	BB	3002	1/1	0.92	0.15	43,43,43,43	0
56	MG	DA	3018	1/1	0.92	0.09	45,45,45,45	0
56	MG	BA	3632	1/1	0.92	0.10	41,41,41,41	0
56	MG	DA	3379	1/1	0.92	0.11	46,46,46,46	0
56	MG	DB	3021	1/1	0.92	0.15	67,67,67,67	0
56	MG	BA	3546	1/1	0.92	0.09	47,47,47,47	0
56	MG	DA	3381	1/1	0.92	0.10	47,47,47,47	0
56	MG	AA	3135	1/1	0.92	0.13	54,54,54,54	0
56	MG	DA	3043	1/1	0.92	0.08	39,39,39,39	0
56	MG	DF	304	1/1	0.92	0.07	38,38,38,38	0
56	MG	DA	3048	1/1	0.92	0.07	46,46,46,46	0
56	MG	DP	201	1/1	0.92	0.11	57,57,57,57	0
56	MG	DA	3387	1/1	0.92	0.09	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3248	1/1	0.92	0.09	47,47,47,47	0
56	MG	DU	3003	1/1	0.92	0.12	45,45,45,45	0
56	MG	BA	3051	1/1	0.92	0.16	51,51,51,51	0
56	MG	BA	3554	1/1	0.92	0.14	48,48,48,48	0
56	MG	BA	3263	1/1	0.92	0.15	42,42,42,42	0
56	MG	CA	3095	1/1	0.92	0.17	46,46,46,46	0
56	MG	BA	3385	1/1	0.92	0.05	32,32,32,32	0
56	MG	D3	3001	1/1	0.92	0.12	62,62,62,62	0
56	MG	CA	3097	1/1	0.92	0.08	43,43,43,43	0
56	MG	DA	3403	1/1	0.92	0.09	46,46,46,46	0
56	MG	DA	3073	1/1	0.92	0.10	45,45,45,45	0
56	MG	AA	3144	1/1	0.93	0.09	47,47,47,47	0
56	MG	BA	3645	1/1	0.93	0.13	57,57,57,57	0
56	MG	BA	3652	1/1	0.93	0.14	46,46,46,46	0
56	MG	BA	3654	1/1	0.93	0.15	54,54,54,54	0
56	MG	BU	201	1/1	0.93	0.14	39,39,39,39	0
56	MG	BA	3655	1/1	0.93	0.11	44,44,44,44	0
56	MG	CA	3138	1/1	0.93	0.09	59,59,59,59	0
56	MG	DA	3456	1/1	0.93	0.11	55,55,55,55	0
56	MG	CA	3139	1/1	0.93	0.10	61,61,61,61	0
56	MG	BA	3534	1/1	0.93	0.16	54,54,54,54	0
56	MG	BX	3005	1/1	0.93	0.08	42,42,42,42	0
56	MG	DA	3460	1/1	0.93	0.11	51,51,51,51	0
56	MG	DA	3461	1/1	0.93	0.07	48,48,48,48	0
56	MG	DA	3181	1/1	0.93	0.16	52,52,52,52	0
56	MG	BA	3427	1/1	0.93	0.10	57,57,57,57	0
56	MG	DA	3184	1/1	0.93	0.20	37,37,37,37	0
56	MG	CA	3145	1/1	0.93	0.21	46,46,46,46	0
56	MG	BY	503	1/1	0.93	0.07	47,47,47,47	0
56	MG	DA	3193	1/1	0.93	0.13	59,59,59,59	0
56	MG	CA	3148	1/1	0.93	0.08	50,50,50,50	0
56	MG	BA	3114	1/1	0.93	0.28	55,55,55,55	0
56	MG	BA	3661	1/1	0.93	0.08	47,47,47,47	0
56	MG	BA	3293	1/1	0.93	0.08	42,42,42,42	0
56	MG	BA	3434	1/1	0.93	0.12	41,41,41,41	0
56	MG	DA	3214	1/1	0.93	0.17	53,53,53,53	0
56	MG	AA	3076	1/1	0.93	0.31	58,58,58,58	0
56	MG	CA	3157	1/1	0.93	0.13	72,72,72,72	0
56	MG	AA	3039	1/1	0.93	0.22	51,51,51,51	0
56	MG	DA	3218	1/1	0.93	0.30	62,62,62,62	0
56	MG	BA	3301	1/1	0.93	0.12	47,47,47,47	0
56	MG	BA	3815	1/1	0.93	0.09	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	B2	3002	1/1	0.93	0.10	43,43,43,43	0
56	MG	DA	3223	1/1	0.93	0.14	51,51,51,51	0
56	MG	BA	3017	1/1	0.93	0.14	52,52,52,52	0
56	MG	BA	3316	1/1	0.93	0.07	43,43,43,43	0
56	MG	BA	3020	1/1	0.93	0.08	46,46,46,46	0
56	MG	BA	3555	1/1	0.93	0.15	64,64,64,64	0
56	MG	BA	3322	1/1	0.93	0.26	57,57,57,57	0
56	MG	DA	3242	1/1	0.93	0.09	40,40,40,40	0
56	MG	CA	3002	1/1	0.93	0.10	55,55,55,55	0
56	MG	BA	3330	1/1	0.93	0.13	41,41,41,41	0
56	MG	AA	3020	1/1	0.93	0.08	45,45,45,45	0
56	MG	BA	3566	1/1	0.93	0.07	25,25,25,25	0
56	MG	DA	3251	1/1	0.93	0.09	43,43,43,43	0
56	MG	BA	3022	1/1	0.93	0.08	40,40,40,40	0
56	MG	BA	3839	1/1	0.93	0.08	47,47,47,47	0
56	MG	CA	3179	1/1	0.93	0.11	49,49,49,49	0
56	MG	DA	3265	1/1	0.93	0.09	39,39,39,39	0
56	MG	AA	3230	1/1	0.93	0.15	56,56,56,56	0
56	MG	DA	3269	1/1	0.93	0.11	54,54,54,54	0
56	MG	DA	3545	1/1	0.93	0.11	52,52,52,52	0
56	MG	BA	3841	1/1	0.93	0.17	56,56,56,56	0
56	MG	DA	3275	1/1	0.93	0.09	33,33,33,33	0
56	MG	BA	3152	1/1	0.93	0.09	48,48,48,48	0
56	MG	CA	3015	1/1	0.93	0.22	57,57,57,57	0
56	MG	BA	3695	1/1	0.93	0.16	56,56,56,56	0
56	MG	DA	3552	1/1	0.93	0.10	55,55,55,55	0
56	MG	CA	3019	1/1	0.93	0.07	44,44,44,44	0
56	MG	DA	3556	1/1	0.93	0.11	57,57,57,57	0
56	MG	BA	3029	1/1	0.93	0.14	48,48,48,48	0
56	MG	DA	3286	1/1	0.93	0.08	29,29,29,29	0
56	MG	BA	3847	1/1	0.93	0.13	52,52,52,52	0
56	MG	AA	3169	1/1	0.93	0.09	62,62,62,62	0
56	MG	BA	3572	1/1	0.93	0.14	48,48,48,48	0
56	MG	CA	3191	1/1	0.93	0.11	71,71,71,71	0
56	MG	DA	3570	1/1	0.93	0.06	28,28,28,28	0
56	MG	CA	3027	1/1	0.93	0.12	49,49,49,49	0
56	MG	DA	3573	1/1	0.93	0.10	46,46,46,46	0
56	MG	DA	3296	1/1	0.93	0.12	56,56,56,56	0
56	MG	BA	3854	1/1	0.93	0.09	51,51,51,51	0
56	MG	DA	3577	1/1	0.93	0.08	54,54,54,54	0
56	MG	BA	3168	1/1	0.93	0.13	35,35,35,35	0
56	MG	DA	3580	1/1	0.93	0.10	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3581	1/1	0.93	0.08	55,55,55,55	0
56	MG	BA	3859	1/1	0.93	0.06	34,34,34,34	0
56	MG	BA	3576	1/1	0.93	0.19	39,39,39,39	0
56	MG	CA	3034	1/1	0.93	0.12	52,52,52,52	0
56	MG	BA	3862	1/1	0.93	0.12	29,29,29,29	0
56	MG	BA	3864	1/1	0.93	0.10	26,26,26,26	0
56	MG	CA	3038	1/1	0.93	0.08	51,51,51,51	0
56	MG	BA	3037	1/1	0.93	0.07	35,35,35,35	0
56	MG	CA	3044	1/1	0.93	0.19	52,52,52,52	0
56	MG	CA	3045	1/1	0.93	0.09	47,47,47,47	0
56	MG	CA	3048	1/1	0.93	0.21	53,53,53,53	0
56	MG	DA	3319	1/1	0.93	0.08	43,43,43,43	0
56	MG	DA	3598	1/1	0.93	0.13	63,63,63,63	0
56	MG	CQ	3002	1/1	0.93	0.12	65,65,65,65	0
56	MG	BA	3706	1/1	0.93	0.11	54,54,54,54	0
56	MG	BA	3868	1/1	0.93	0.07	8,8,8,8	0
56	MG	DA	3323	1/1	0.93	0.07	34,34,34,34	0
56	MG	AA	3195	1/1	0.93	0.09	38,38,38,38	0
56	MG	AA	3196	1/1	0.93	0.09	42,42,42,42	0
56	MG	AA	3152	1/1	0.93	0.15	54,54,54,54	0
56	MG	BA	3362	1/1	0.93	0.08	37,37,37,37	0
56	MG	BA	3363	1/1	0.93	0.10	45,45,45,45	0
56	MG	CA	3061	1/1	0.93	0.17	58,58,58,58	0
56	MG	BA	3471	1/1	0.93	0.13	57,57,57,57	0
56	MG	BA	3365	1/1	0.93	0.11	44,44,44,44	0
56	MG	AA	3172	1/1	0.93	0.08	43,43,43,43	0
56	MG	DA	3338	1/1	0.93	0.08	43,43,43,43	0
56	MG	DA	3623	1/1	0.93	0.10	54,54,54,54	0
56	MG	CA	3068	1/1	0.93	0.31	53,53,53,53	0
56	MG	BA	3890	1/1	0.93	0.13	34,34,34,34	0
56	MG	BA	3368	1/1	0.93	0.09	37,37,37,37	0
56	MG	BA	3896	1/1	0.93	0.07	41,41,41,41	0
56	MG	DA	3035	1/1	0.93	0.07	36,36,36,36	0
56	MG	BA	3723	1/1	0.93	0.13	27,27,27,27	0
56	MG	AA	3065	1/1	0.93	0.18	45,45,45,45	0
56	MG	BA	3902	1/1	0.93	0.30	55,55,55,55	0
56	MG	BA	3207	1/1	0.93	0.21	52,52,52,52	0
56	MG	BA	3606	1/1	0.93	0.13	29,29,29,29	0
56	MG	DA	3637	1/1	0.93	0.09	48,48,48,48	0
56	MG	AA	3080	1/1	0.93	0.25	61,61,61,61	0
56	MG	DA	3058	1/1	0.93	0.19	56,56,56,56	0
56	MG	CA	3086	1/1	0.93	0.11	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3061	1/1	0.93	0.10	43,43,43,43	0
56	MG	CA	3087	1/1	0.93	0.22	60,60,60,60	0
56	MG	BA	3482	1/1	0.93	0.09	39,39,39,39	0
56	MG	AA	3176	1/1	0.93	0.15	47,47,47,47	0
56	MG	BA	3613	1/1	0.93	0.13	54,54,54,54	0
56	MG	BB	3015	1/1	0.93	0.13	51,51,51,51	0
56	MG	AW	101	1/1	0.93	0.10	58,58,58,58	0
56	MG	DA	3657	1/1	0.93	0.11	44,44,44,44	0
56	MG	AA	3204	1/1	0.93	0.14	53,53,53,53	0
56	MG	DA	3661	1/1	0.93	0.07	39,39,39,39	0
56	MG	DA	3078	1/1	0.93	0.07	39,39,39,39	0
56	MG	AA	3205	1/1	0.93	0.20	56,56,56,56	0
56	MG	DA	3085	1/1	0.93	0.08	39,39,39,39	0
56	MG	DA	3671	1/1	0.93	0.13	36,36,36,36	0
56	MG	BA	3226	1/1	0.93	0.12	52,52,52,52	0
56	MG	DA	3088	1/1	0.93	0.09	47,47,47,47	0
56	MG	DA	3092	1/1	0.93	0.08	50,50,50,50	0
56	MG	BA	3746	1/1	0.93	0.20	57,57,57,57	0
56	MG	BA	3396	1/1	0.93	0.10	42,42,42,42	0
56	MG	DA	3392	1/1	0.93	0.10	39,39,39,39	0
56	MG	AA	3206	1/1	0.93	0.11	53,53,53,53	0
56	MG	AA	3103	1/1	0.93	0.14	50,50,50,50	0
56	MG	DB	3010	1/1	0.93	0.16	45,45,45,45	0
56	MG	DA	3109	1/1	0.93	0.16	34,34,34,34	0
56	MG	BA	3403	1/1	0.93	0.19	52,52,52,52	0
56	MG	AA	3075	1/1	0.93	0.15	44,44,44,44	0
56	MG	DA	3402	1/1	0.93	0.14	56,56,56,56	0
56	MG	BA	3502	1/1	0.93	0.15	56,56,56,56	0
56	MG	BA	3251	1/1	0.93	0.09	45,45,45,45	0
56	MG	BA	3507	1/1	0.93	0.11	33,33,33,33	0
56	MG	AX	3008	1/1	0.93	0.15	54,54,54,54	0
56	MG	DA	3127	1/1	0.93	0.09	47,47,47,47	0
56	MG	CA	3110	1/1	0.93	0.08	51,51,51,51	0
56	MG	AA	3119	1/1	0.93	0.10	60,60,60,60	0
56	MG	BA	3766	1/1	0.93	0.07	48,48,48,48	0
56	MG	AA	3106	1/1	0.93	0.21	54,54,54,54	0
56	MG	DF	307	1/1	0.93	0.11	48,48,48,48	0
56	MG	DG	3001	1/1	0.93	0.09	53,53,53,53	0
56	MG	DA	3133	1/1	0.93	0.21	50,50,50,50	0
56	MG	BF	314	1/1	0.93	0.09	46,46,46,46	0
56	MG	AA	3088	1/1	0.93	0.16	46,46,46,46	0
56	MG	BA	3418	1/1	0.93	0.09	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3779	1/1	0.93	0.12	30,30,30,30	0
56	MG	CA	3123	1/1	0.93	0.15	51,51,51,51	0
56	MG	DW	3001	1/1	0.93	0.25	44,44,44,44	0
56	MG	DW	3002	1/1	0.93	0.07	44,44,44,44	0
56	MG	CA	3124	1/1	0.93	0.10	57,57,57,57	0
56	MG	BN	3002	1/1	0.93	0.09	38,38,38,38	0
56	MG	DA	3430	1/1	0.93	0.10	35,35,35,35	0
56	MG	BA	3269	1/1	0.93	0.09	45,45,45,45	0
56	MG	AA	3185	1/1	0.93	0.26	52,52,52,52	0
56	MG	D8	102	1/1	0.93	0.20	52,52,52,52	0
56	MG	BO	3004	1/1	0.93	0.11	53,53,53,53	0
56	MG	BA	3275	1/1	0.93	0.14	62,62,62,62	0
56	MG	AA	3160	1/1	0.94	0.06	38,38,38,38	0
56	MG	DA	3396	1/1	0.94	0.07	41,41,41,41	0
56	MG	BA	3388	1/1	0.94	0.11	44,44,44,44	0
56	MG	BA	3212	1/1	0.94	0.09	49,49,49,49	0
56	MG	DA	3062	1/1	0.94	0.11	49,49,49,49	0
56	MG	BA	3848	1/1	0.94	0.13	45,45,45,45	0
56	MG	CA	3054	1/1	0.94	0.15	53,53,53,53	0
56	MG	BA	3667	1/1	0.94	0.09	43,43,43,43	0
56	MG	DA	3069	1/1	0.94	0.18	58,58,58,58	0
56	MG	DA	3070	1/1	0.94	0.09	39,39,39,39	0
56	MG	BA	3391	1/1	0.94	0.07	24,24,24,24	0
56	MG	DA	3072	1/1	0.94	0.11	45,45,45,45	0
56	MG	BA	3852	1/1	0.94	0.07	33,33,33,33	0
56	MG	DA	3413	1/1	0.94	0.14	42,42,42,42	0
56	MG	DA	3074	1/1	0.94	0.07	45,45,45,45	0
56	MG	BA	3523	1/1	0.94	0.11	49,49,49,49	0
56	MG	DA	3416	1/1	0.94	0.17	47,47,47,47	0
56	MG	BA	3214	1/1	0.94	0.09	44,44,44,44	0
56	MG	AA	3161	1/1	0.94	0.07	35,35,35,35	0
56	MG	CA	3063	1/1	0.94	0.16	53,53,53,53	0
56	MG	BA	3399	1/1	0.94	0.13	57,57,57,57	0
56	MG	DA	3086	1/1	0.94	0.18	59,59,59,59	0
56	MG	DA	3422	1/1	0.94	0.09	52,52,52,52	0
56	MG	AA	3021	1/1	0.94	0.10	41,41,41,41	0
56	MG	AA	3035	1/1	0.94	0.09	41,41,41,41	0
56	MG	DA	3090	1/1	0.94	0.33	53,53,53,53	0
56	MG	BA	3677	1/1	0.94	0.08	29,29,29,29	0
56	MG	DA	3098	1/1	0.94	0.08	36,36,36,36	0
56	MG	CA	3070	1/1	0.94	0.20	59,59,59,59	0
56	MG	AA	3036	1/1	0.94	0.15	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3243	1/1	0.94	0.09	39,39,39,39	0
56	MG	DA	3441	1/1	0.94	0.07	44,44,44,44	0
56	MG	AA	3101	1/1	0.94	0.07	45,45,45,45	0
56	MG	BA	3685	1/1	0.94	0.07	29,29,29,29	0
56	MG	BA	3412	1/1	0.94	0.07	42,42,42,42	0
56	MG	DA	3112	1/1	0.94	0.08	42,42,42,42	0
56	MG	BA	3249	1/1	0.94	0.10	41,41,41,41	0
56	MG	DA	3450	1/1	0.94	0.07	35,35,35,35	0
56	MG	DA	3452	1/1	0.94	0.12	49,49,49,49	0
56	MG	BA	3690	1/1	0.94	0.14	53,53,53,53	0
56	MG	BA	3692	1/1	0.94	0.14	47,47,47,47	0
56	MG	BA	3083	1/1	0.94	0.15	54,54,54,54	0
56	MG	BA	3883	1/1	0.94	0.20	45,45,45,45	0
56	MG	BA	3259	1/1	0.94	0.08	33,33,33,33	0
56	MG	AT	3001	1/1	0.94	0.19	54,54,54,54	0
56	MG	BA	3552	1/1	0.94	0.10	38,38,38,38	0
56	MG	BA	3094	1/1	0.94	0.12	33,33,33,33	0
56	MG	AA	3102	1/1	0.94	0.07	44,44,44,44	0
56	MG	BA	3898	1/1	0.94	0.09	44,44,44,44	0
56	MG	DA	3464	1/1	0.94	0.12	31,31,31,31	0
56	MG	DA	3469	1/1	0.94	0.07	45,45,45,45	0
56	MG	AA	3134	1/1	0.94	0.14	47,47,47,47	0
56	MG	AW	103	1/1	0.94	0.18	45,45,45,45	0
56	MG	DA	3138	1/1	0.94	0.12	55,55,55,55	0
56	MG	DA	3140	1/1	0.94	0.13	43,43,43,43	0
56	MG	DA	3476	1/1	0.94	0.09	42,42,42,42	0
56	MG	AA	3202	1/1	0.94	0.07	46,46,46,46	0
56	MG	BA	3904	1/1	0.94	0.12	46,46,46,46	0
56	MG	AA	3023	1/1	0.94	0.21	56,56,56,56	0
56	MG	BA	3708	1/1	0.94	0.08	40,40,40,40	0
56	MG	BA	3561	1/1	0.94	0.18	54,54,54,54	0
56	MG	BA	3715	1/1	0.94	0.11	53,53,53,53	0
56	MG	BB	3012	1/1	0.94	0.09	61,61,61,61	0
56	MG	DA	3495	1/1	0.94	0.11	48,48,48,48	0
56	MG	BA	3430	1/1	0.94	0.10	44,44,44,44	0
56	MG	CA	3104	1/1	0.94	0.06	53,53,53,53	0
56	MG	BA	3431	1/1	0.94	0.08	54,54,54,54	0
56	MG	AX	3004	1/1	0.94	0.17	53,53,53,53	0
56	MG	CA	3109	1/1	0.94	0.17	45,45,45,45	0
56	MG	BA	3286	1/1	0.94	0.11	52,52,52,52	0
56	MG	BA	3287	1/1	0.94	0.15	48,48,48,48	0
56	MG	AA	3017	1/1	0.94	0.19	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3437	1/1	0.94	0.08	31,31,31,31	0
56	MG	DA	3171	1/1	0.94	0.10	45,45,45,45	0
56	MG	DA	3174	1/1	0.94	0.24	49,49,49,49	0
56	MG	BA	3290	1/1	0.94	0.24	54,54,54,54	0
56	MG	CA	3117	1/1	0.94	0.11	58,58,58,58	0
56	MG	BA	3725	1/1	0.94	0.08	42,42,42,42	0
56	MG	AX	3006	1/1	0.94	0.10	46,46,46,46	0
56	MG	DA	3517	1/1	0.94	0.11	48,48,48,48	0
56	MG	BB	3030	1/1	0.94	0.11	39,39,39,39	0
56	MG	AA	3061	1/1	0.94	0.16	51,51,51,51	0
56	MG	DA	3187	1/1	0.94	0.19	44,44,44,44	0
56	MG	BA	3579	1/1	0.94	0.09	42,42,42,42	0
56	MG	DA	3527	1/1	0.94	0.06	22,22,22,22	0
56	MG	BD	305	1/1	0.94	0.12	35,35,35,35	0
56	MG	BA	3296	1/1	0.94	0.12	40,40,40,40	0
56	MG	DA	3534	1/1	0.94	0.09	39,39,39,39	0
56	MG	BA	3297	1/1	0.94	0.08	45,45,45,45	0
56	MG	DA	3536	1/1	0.94	0.10	51,51,51,51	0
56	MG	BE	306	1/1	0.94	0.23	34,34,34,34	0
56	MG	DA	3201	1/1	0.94	0.10	52,52,52,52	0
56	MG	DA	3543	1/1	0.94	0.07	47,47,47,47	0
56	MG	DA	3544	1/1	0.94	0.10	44,44,44,44	0
56	MG	DA	3207	1/1	0.94	0.17	52,52,52,52	0
56	MG	BE	307	1/1	0.94	0.09	37,37,37,37	0
56	MG	AA	3048	1/1	0.94	0.21	46,46,46,46	0
56	MG	BA	3444	1/1	0.94	0.10	39,39,39,39	0
56	MG	DA	3213	1/1	0.94	0.14	44,44,44,44	0
56	MG	BE	312	1/1	0.94	0.15	56,56,56,56	0
56	MG	CA	3134	1/1	0.94	0.25	53,53,53,53	0
56	MG	DA	3554	1/1	0.94	0.12	48,48,48,48	0
56	MG	BA	3587	1/1	0.94	0.14	32,32,32,32	0
56	MG	BA	3588	1/1	0.94	0.07	30,30,30,30	0
56	MG	DA	3558	1/1	0.94	0.14	47,47,47,47	0
56	MG	AA	3011	1/1	0.94	0.16	46,46,46,46	0
56	MG	DA	3219	1/1	0.94	0.21	55,55,55,55	0
56	MG	BA	3302	1/1	0.94	0.07	43,43,43,43	0
56	MG	DA	3563	1/1	0.94	0.14	60,60,60,60	0
56	MG	BG	201	1/1	0.94	0.07	58,58,58,58	0
56	MG	CA	3141	1/1	0.94	0.15	65,65,65,65	0
56	MG	BG	203	1/1	0.94	0.12	51,51,51,51	0
56	MG	BA	3745	1/1	0.94	0.10	45,45,45,45	0
56	MG	BA	3305	1/1	0.94	0.11	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BG	206	1/1	0.94	0.07	59,59,59,59	0
56	MG	DA	3231	1/1	0.94	0.24	49,49,49,49	0
56	MG	BH	3001	1/1	0.94	0.16	40,40,40,40	0
56	MG	DA	3238	1/1	0.94	0.13	48,48,48,48	0
56	MG	DA	3240	1/1	0.94	0.09	45,45,45,45	0
56	MG	BA	3308	1/1	0.94	0.09	40,40,40,40	0
56	MG	BA	3595	1/1	0.94	0.10	36,36,36,36	0
56	MG	AA	3209	1/1	0.94	0.12	61,61,61,61	0
56	MG	AX	3014	1/1	0.94	0.08	51,51,51,51	0
56	MG	BA	3602	1/1	0.94	0.06	20,20,20,20	0
56	MG	DA	3587	1/1	0.94	0.12	64,64,64,64	0
56	MG	DA	3248	1/1	0.94	0.13	50,50,50,50	0
56	MG	AA	3086	1/1	0.94	0.07	45,45,45,45	0
56	MG	BA	3604	1/1	0.94	0.12	52,52,52,52	0
56	MG	DA	3592	1/1	0.94	0.13	54,54,54,54	0
56	MG	BA	3460	1/1	0.94	0.04	20,20,20,20	0
56	MG	BA	3607	1/1	0.94	0.07	57,57,57,57	0
56	MG	DA	3254	1/1	0.94	0.08	37,37,37,37	0
56	MG	DA	3261	1/1	0.94	0.11	47,47,47,47	0
56	MG	DA	3262	1/1	0.94	0.08	36,36,36,36	0
56	MG	AA	3087	1/1	0.94	0.07	38,38,38,38	0
56	MG	AA	3178	1/1	0.94	0.09	49,49,49,49	0
56	MG	BU	202	1/1	0.94	0.13	31,31,31,31	0
56	MG	DA	3603	1/1	0.94	0.08	52,52,52,52	0
56	MG	CA	3163	1/1	0.94	0.17	47,47,47,47	0
56	MG	DA	3270	1/1	0.94	0.09	33,33,33,33	0
56	MG	BA	3768	1/1	0.94	0.10	29,29,29,29	0
56	MG	DA	3274	1/1	0.94	0.06	47,47,47,47	0
56	MG	DA	3609	1/1	0.94	0.09	53,53,53,53	0
56	MG	BX	3003	1/1	0.94	0.12	36,36,36,36	0
56	MG	CA	3168	1/1	0.94	0.16	65,65,65,65	0
56	MG	BA	3332	1/1	0.94	0.11	43,43,43,43	0
56	MG	CA	3170	1/1	0.94	0.17	61,61,61,61	0
56	MG	DA	3614	1/1	0.94	0.08	47,47,47,47	0
56	MG	BA	3333	1/1	0.94	0.28	55,55,55,55	0
56	MG	DA	3281	1/1	0.94	0.14	42,42,42,42	0
56	MG	DA	3620	1/1	0.94	0.09	49,49,49,49	0
56	MG	BA	3774	1/1	0.94	0.15	47,47,47,47	0
56	MG	BA	3142	1/1	0.94	0.21	46,46,46,46	0
56	MG	BA	3002	1/1	0.94	0.09	53,53,53,53	0
56	MG	BA	3781	1/1	0.94	0.18	47,47,47,47	0
56	MG	BA	3005	1/1	0.94	0.10	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3156	1/1	0.94	0.12	46,46,46,46	0
56	MG	DA	3629	1/1	0.94	0.07	36,36,36,36	0
56	MG	BA	3157	1/1	0.94	0.18	41,41,41,41	0
56	MG	BA	3785	1/1	0.94	0.08	39,39,39,39	0
56	MG	AA	3217	1/1	0.94	0.09	48,48,48,48	0
56	MG	AA	3009	1/1	0.94	0.10	49,49,49,49	0
56	MG	BA	3791	1/1	0.94	0.09	47,47,47,47	0
56	MG	BA	3163	1/1	0.94	0.09	46,46,46,46	0
56	MG	BA	3166	1/1	0.94	0.17	31,31,31,31	0
56	MG	BA	3796	1/1	0.94	0.08	29,29,29,29	0
56	MG	DA	3638	1/1	0.94	0.09	50,50,50,50	0
56	MG	BA	3797	1/1	0.94	0.13	52,52,52,52	0
56	MG	B9	502	1/1	0.94	0.20	47,47,47,47	0
56	MG	AA	3052	1/1	0.94	0.30	58,58,58,58	0
56	MG	AA	3004	1/1	0.94	0.20	68,68,68,68	0
56	MG	DA	3643	1/1	0.94	0.12	51,51,51,51	0
56	MG	AA	3092	1/1	0.94	0.16	52,52,52,52	0
56	MG	DA	3647	1/1	0.94	0.12	39,39,39,39	0
56	MG	BA	3184	1/1	0.94	0.13	41,41,41,41	0
56	MG	CA	3005	1/1	0.94	0.09	55,55,55,55	0
56	MG	BA	3188	1/1	0.94	0.20	55,55,55,55	0
56	MG	DA	3651	1/1	0.94	0.12	50,50,50,50	0
56	MG	AA	3093	1/1	0.94	0.18	53,53,53,53	0
56	MG	BA	3490	1/1	0.94	0.12	31,31,31,31	0
56	MG	BA	3491	1/1	0.94	0.12	44,44,44,44	0
56	MG	DA	3658	1/1	0.94	0.17	60,60,60,60	0
56	MG	CD	503	1/1	0.94	0.28	53,53,53,53	0
56	MG	CE	3001	1/1	0.94	0.13	67,67,67,67	0
56	MG	BA	3636	1/1	0.94	0.07	28,28,28,28	0
56	MG	CA	3012	1/1	0.94	0.08	57,57,57,57	0
56	MG	DA	3665	1/1	0.94	0.07	34,34,34,34	0
56	MG	DA	3667	1/1	0.94	0.14	36,36,36,36	0
56	MG	CA	3013	1/1	0.94	0.27	62,62,62,62	0
56	MG	AA	3224	1/1	0.94	0.23	51,51,51,51	0
56	MG	BA	3369	1/1	0.94	0.11	12,12,12,12	0
56	MG	CA	3016	1/1	0.94	0.09	45,45,45,45	0
56	MG	AA	3094	1/1	0.94	0.21	49,49,49,49	0
56	MG	DA	3337	1/1	0.94	0.07	44,44,44,44	0
56	MG	BA	3498	1/1	0.94	0.09	26,26,26,26	0
56	MG	AA	3095	1/1	0.94	0.30	58,58,58,58	0
56	MG	CV	101	1/1	0.94	0.18	51,51,51,51	0
56	MG	BA	3647	1/1	0.94	0.10	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DB	3009	1/1	0.94	0.22	59,59,59,59	0
56	MG	BA	3648	1/1	0.94	0.16	56,56,56,56	0
56	MG	CW	3003	1/1	0.94	0.08	58,58,58,58	0
56	MG	DB	3013	1/1	0.94	0.07	53,53,53,53	0
56	MG	BA	3375	1/1	0.94	0.06	30,30,30,30	0
56	MG	AA	3123	1/1	0.94	0.15	46,46,46,46	0
56	MG	BA	3828	1/1	0.94	0.12	46,46,46,46	0
56	MG	BA	3503	1/1	0.94	0.09	44,44,44,44	0
56	MG	BA	3831	1/1	0.94	0.09	53,53,53,53	0
56	MG	DB	3020	1/1	0.94	0.10	52,52,52,52	0
56	MG	DA	3356	1/1	0.94	0.11	44,44,44,44	0
56	MG	DD	306	1/1	0.94	0.15	46,46,46,46	0
56	MG	CX	3007	1/1	0.94	0.16	57,57,57,57	0
56	MG	DA	3001	1/1	0.94	0.07	55,55,55,55	0
56	MG	CA	3032	1/1	0.94	0.19	56,56,56,56	0
56	MG	DE	306	1/1	0.94	0.08	43,43,43,43	0
56	MG	BA	3833	1/1	0.94	0.18	57,57,57,57	0
56	MG	BA	3836	1/1	0.94	0.17	59,59,59,59	0
56	MG	BA	3837	1/1	0.94	0.09	52,52,52,52	0
56	MG	AA	3190	1/1	0.94	0.12	54,54,54,54	0
56	MG	DA	3020	1/1	0.94	0.09	48,48,48,48	0
56	MG	DA	3023	1/1	0.94	0.08	48,48,48,48	0
56	MG	DA	3026	1/1	0.94	0.13	41,41,41,41	0
56	MG	DA	3031	1/1	0.94	0.09	44,44,44,44	0
56	MG	DU	3001	1/1	0.94	0.16	43,43,43,43	0
56	MG	DA	3033	1/1	0.94	0.07	40,40,40,40	0
56	MG	AA	3234	1/1	0.94	0.09	40,40,40,40	0
56	MG	DA	3382	1/1	0.94	0.10	40,40,40,40	0
56	MG	DV	202	1/1	0.94	0.13	49,49,49,49	0
56	MG	AB	3001	1/1	0.94	0.07	73,73,73,73	0
56	MG	DA	3384	1/1	0.94	0.10	55,55,55,55	0
56	MG	CA	3040	1/1	0.94	0.12	57,57,57,57	0
56	MG	DX	3001	1/1	0.94	0.15	44,44,44,44	0
56	MG	CA	3041	1/1	0.94	0.17	49,49,49,49	0
56	MG	CA	3043	1/1	0.94	0.29	57,57,57,57	0
56	MG	DA	3389	1/1	0.94	0.10	54,54,54,54	0
56	MG	BA	3660	1/1	0.94	0.21	46,46,46,46	0
56	MG	D5	102	1/1	0.94	0.20	38,38,38,38	0
56	MG	BA	3510	1/1	0.94	0.12	49,49,49,49	0
56	MG	DA	3052	1/1	0.94	0.06	38,38,38,38	0
56	MG	CA	3046	1/1	0.94	0.09	42,42,42,42	0
56	MG	DA	3411	1/1	0.95	0.06	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3412	1/1	0.95	0.14	50,50,50,50	0
56	MG	AA	3211	1/1	0.95	0.12	56,56,56,56	0
56	MG	CA	3080	1/1	0.95	0.27	55,55,55,55	0
56	MG	BA	3115	1/1	0.95	0.09	44,44,44,44	0
56	MG	CA	3082	1/1	0.95	0.12	58,58,58,58	0
56	MG	CA	3083	1/1	0.95	0.28	52,52,52,52	0
56	MG	BA	3542	1/1	0.95	0.09	43,43,43,43	0
56	MG	DA	3095	1/1	0.95	0.13	46,46,46,46	0
56	MG	DA	3097	1/1	0.95	0.19	44,44,44,44	0
56	MG	AA	3212	1/1	0.95	0.12	59,59,59,59	0
56	MG	BA	3402	1/1	0.95	0.06	39,39,39,39	0
56	MG	DA	3423	1/1	0.95	0.11	56,56,56,56	0
56	MG	BA	3258	1/1	0.95	0.12	38,38,38,38	0
56	MG	DA	3425	1/1	0.95	0.10	53,53,53,53	0
56	MG	BA	3900	1/1	0.95	0.35	40,40,40,40	0
56	MG	BA	3117	1/1	0.95	0.05	29,29,29,29	0
56	MG	DA	3429	1/1	0.95	0.08	35,35,35,35	0
56	MG	BA	3119	1/1	0.95	0.18	40,40,40,40	0
56	MG	BA	3407	1/1	0.95	0.05	13,13,13,13	0
56	MG	DA	3111	1/1	0.95	0.09	40,40,40,40	0
56	MG	DA	3435	1/1	0.95	0.09	39,39,39,39	0
56	MG	BA	3408	1/1	0.95	0.10	41,41,41,41	0
56	MG	DA	3114	1/1	0.95	0.17	55,55,55,55	0
56	MG	BA	3124	1/1	0.95	0.20	26,26,26,26	0
56	MG	BA	3709	1/1	0.95	0.07	34,34,34,34	0
56	MG	DA	3443	1/1	0.95	0.07	50,50,50,50	0
56	MG	DA	3444	1/1	0.95	0.08	40,40,40,40	0
56	MG	BA	3710	1/1	0.95	0.16	49,49,49,49	0
56	MG	BB	3005	1/1	0.95	0.07	52,52,52,52	0
56	MG	BA	3711	1/1	0.95	0.11	53,53,53,53	0
56	MG	BA	3411	1/1	0.95	0.15	44,44,44,44	0
56	MG	BA	3264	1/1	0.95	0.10	38,38,38,38	0
56	MG	DA	3451	1/1	0.95	0.06	34,34,34,34	0
56	MG	BB	3014	1/1	0.95	0.10	43,43,43,43	0
56	MG	BA	3126	1/1	0.95	0.06	38,38,38,38	0
56	MG	BA	3128	1/1	0.95	0.20	35,35,35,35	0
56	MG	DA	3455	1/1	0.95	0.07	35,35,35,35	0
56	MG	BB	3019	1/1	0.95	0.10	49,49,49,49	0
56	MG	AA	3028	1/1	0.95	0.23	50,50,50,50	0
56	MG	DA	3135	1/1	0.95	0.13	47,47,47,47	0
56	MG	CA	3105	1/1	0.95	0.14	53,53,53,53	0
56	MG	BA	3562	1/1	0.95	0.12	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	CA	3107	1/1	0.95	0.12	54,54,54,54	0
56	MG	DA	3141	1/1	0.95	0.06	42,42,42,42	0
56	MG	BB	3022	1/1	0.95	0.12	46,46,46,46	0
56	MG	BA	3563	1/1	0.95	0.06	43,43,43,43	0
56	MG	DA	3467	1/1	0.95	0.09	40,40,40,40	0
56	MG	DA	3468	1/1	0.95	0.09	49,49,49,49	0
56	MG	BA	3564	1/1	0.95	0.07	39,39,39,39	0
56	MG	DA	3146	1/1	0.95	0.05	40,40,40,40	0
56	MG	CA	3111	1/1	0.95	0.15	53,53,53,53	0
56	MG	AA	3024	1/1	0.95	0.07	39,39,39,39	0
56	MG	BA	3419	1/1	0.95	0.06	38,38,38,38	0
56	MG	BA	3724	1/1	0.95	0.07	37,37,37,37	0
56	MG	BA	3131	1/1	0.95	0.07	37,37,37,37	0
56	MG	DA	3478	1/1	0.95	0.10	50,50,50,50	0
56	MG	BA	3278	1/1	0.95	0.07	42,42,42,42	0
56	MG	DA	3483	1/1	0.95	0.07	45,45,45,45	0
56	MG	AA	3148	1/1	0.95	0.10	43,43,43,43	0
56	MG	BA	3032	1/1	0.95	0.11	29,29,29,29	0
56	MG	DA	3158	1/1	0.95	0.07	49,49,49,49	0
56	MG	CA	3121	1/1	0.95	0.21	52,52,52,52	0
56	MG	BA	3139	1/1	0.95	0.19	45,45,45,45	0
56	MG	DA	3492	1/1	0.95	0.16	51,51,51,51	0
56	MG	BA	3574	1/1	0.95	0.20	42,42,42,42	0
56	MG	DA	3498	1/1	0.95	0.07	42,42,42,42	0
56	MG	BA	3033	1/1	0.95	0.08	37,37,37,37	0
56	MG	AA	3053	1/1	0.95	0.07	42,42,42,42	0
56	MG	DA	3170	1/1	0.95	0.13	36,36,36,36	0
56	MG	BA	3737	1/1	0.95	0.16	29,29,29,29	0
56	MG	BA	3577	1/1	0.95	0.11	40,40,40,40	0
56	MG	DA	3175	1/1	0.95	0.12	50,50,50,50	0
56	MG	BA	3291	1/1	0.95	0.22	49,49,49,49	0
56	MG	DA	3177	1/1	0.95	0.17	44,44,44,44	0
56	MG	BA	3292	1/1	0.95	0.14	42,42,42,42	0
56	MG	BF	302	1/1	0.95	0.08	37,37,37,37	0
56	MG	BF	311	1/1	0.95	0.07	40,40,40,40	0
56	MG	BA	3145	1/1	0.95	0.09	41,41,41,41	0
56	MG	CA	3133	1/1	0.95	0.14	53,53,53,53	0
56	MG	BA	3147	1/1	0.95	0.13	39,39,39,39	0
56	MG	BA	3038	1/1	0.95	0.09	42,42,42,42	0
56	MG	AA	3193	1/1	0.95	0.18	51,51,51,51	0
56	MG	DA	3518	1/1	0.95	0.06	34,34,34,34	0
56	MG	DA	3192	1/1	0.95	0.17	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3298	1/1	0.95	0.14	51,51,51,51	0
56	MG	DA	3523	1/1	0.95	0.06	46,46,46,46	0
56	MG	DA	3197	1/1	0.95	0.08	32,32,32,32	0
56	MG	BA	3299	1/1	0.95	0.14	51,51,51,51	0
56	MG	BA	3154	1/1	0.95	0.20	31,31,31,31	0
56	MG	DA	3528	1/1	0.95	0.07	67,67,67,67	0
56	MG	CA	3140	1/1	0.95	0.09	56,56,56,56	0
56	MG	DA	3203	1/1	0.95	0.10	46,46,46,46	0
56	MG	DA	3205	1/1	0.95	0.08	37,37,37,37	0
56	MG	BA	3043	1/1	0.95	0.12	43,43,43,43	0
56	MG	BA	3755	1/1	0.95	0.07	45,45,45,45	0
56	MG	DA	3537	1/1	0.95	0.09	38,38,38,38	0
56	MG	BA	3591	1/1	0.95	0.12	31,31,31,31	0
56	MG	BA	3758	1/1	0.95	0.11	48,48,48,48	0
56	MG	AA	3091	1/1	0.95	0.09	50,50,50,50	0
56	MG	CA	3146	1/1	0.95	0.18	43,43,43,43	0
56	MG	AA	3151	1/1	0.95	0.07	48,48,48,48	0
56	MG	BA	3306	1/1	0.95	0.07	28,28,28,28	0
56	MG	BA	3160	1/1	0.95	0.07	44,44,44,44	0
56	MG	BA	3310	1/1	0.95	0.19	44,44,44,44	0
56	MG	BQ	3001	1/1	0.95	0.30	41,41,41,41	0
56	MG	CA	3152	1/1	0.95	0.13	67,67,67,67	0
56	MG	BA	3767	1/1	0.95	0.14	34,34,34,34	0
56	MG	BA	3601	1/1	0.95	0.08	33,33,33,33	0
56	MG	CA	3156	1/1	0.95	0.15	59,59,59,59	0
56	MG	DA	3225	1/1	0.95	0.13	38,38,38,38	0
56	MG	BR	201	1/1	0.95	0.11	35,35,35,35	0
56	MG	BA	3311	1/1	0.95	0.12	43,43,43,43	0
56	MG	BA	3312	1/1	0.95	0.23	54,54,54,54	0
56	MG	DA	3230	1/1	0.95	0.24	54,54,54,54	0
56	MG	BA	3773	1/1	0.95	0.11	29,29,29,29	0
56	MG	DA	3234	1/1	0.95	0.17	47,47,47,47	0
56	MG	BU	203	1/1	0.95	0.15	44,44,44,44	0
56	MG	BV	204	1/1	0.95	0.12	44,44,44,44	0
56	MG	AA	3006	1/1	0.95	0.08	50,50,50,50	0
56	MG	CA	3164	1/1	0.95	0.08	63,63,63,63	0
56	MG	CA	3165	1/1	0.95	0.05	36,36,36,36	0
56	MG	BW	203	1/1	0.95	0.15	47,47,47,47	0
56	MG	DA	3245	1/1	0.95	0.10	48,48,48,48	0
56	MG	BA	3776	1/1	0.95	0.13	27,27,27,27	0
56	MG	DA	3578	1/1	0.95	0.08	46,46,46,46	0
56	MG	BA	3777	1/1	0.95	0.11	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3451	1/1	0.95	0.09	38,38,38,38	0
56	MG	BA	3454	1/1	0.95	0.12	39,39,39,39	0
56	MG	DA	3250	1/1	0.95	0.13	50,50,50,50	0
56	MG	AA	3064	1/1	0.95	0.31	54,54,54,54	0
56	MG	BA	3456	1/1	0.95	0.11	41,41,41,41	0
56	MG	BA	3317	1/1	0.95	0.10	47,47,47,47	0
56	MG	BA	3165	1/1	0.95	0.07	32,32,32,32	0
56	MG	DA	3258	1/1	0.95	0.15	39,39,39,39	0
56	MG	BA	3461	1/1	0.95	0.13	23,23,23,23	0
56	MG	BA	3462	1/1	0.95	0.07	30,30,30,30	0
56	MG	BA	3320	1/1	0.95	0.15	50,50,50,50	0
56	MG	DA	3264	1/1	0.95	0.07	48,48,48,48	0
56	MG	BA	3618	1/1	0.95	0.06	19,19,19,19	0
56	MG	AA	3225	1/1	0.95	0.23	48,48,48,48	0
56	MG	BA	3794	1/1	0.95	0.06	48,48,48,48	0
56	MG	BA	3326	1/1	0.95	0.11	38,38,38,38	0
56	MG	B5	102	1/1	0.95	0.21	36,36,36,36	0
56	MG	DA	3601	1/1	0.95	0.08	38,38,38,38	0
56	MG	AX	3009	1/1	0.95	0.10	32,32,32,32	0
56	MG	BA	3331	1/1	0.95	0.08	32,32,32,32	0
56	MG	B6	103	1/1	0.95	0.06	44,44,44,44	0
56	MG	B7	103	1/1	0.95	0.06	44,44,44,44	0
56	MG	BA	3070	1/1	0.95	0.13	47,47,47,47	0
56	MG	CA	3189	1/1	0.95	0.12	57,57,57,57	0
56	MG	B8	103	1/1	0.95	0.07	31,31,31,31	0
56	MG	DA	3282	1/1	0.95	0.07	32,32,32,32	0
56	MG	BA	3624	1/1	0.95	0.07	40,40,40,40	0
56	MG	BA	3179	1/1	0.95	0.08	37,37,37,37	0
56	MG	DA	3288	1/1	0.95	0.09	44,44,44,44	0
56	MG	BA	3342	1/1	0.95	0.13	41,41,41,41	0
56	MG	DA	3616	1/1	0.95	0.12	54,54,54,54	0
56	MG	DA	3617	1/1	0.95	0.09	49,49,49,49	0
56	MG	BA	3181	1/1	0.95	0.11	38,38,38,38	0
56	MG	AX	3010	1/1	0.95	0.07	53,53,53,53	0
56	MG	BA	3807	1/1	0.95	0.20	46,46,46,46	0
56	MG	BA	3074	1/1	0.95	0.16	33,33,33,33	0
56	MG	BA	3079	1/1	0.95	0.20	40,40,40,40	0
56	MG	CD	502	1/1	0.95	0.07	51,51,51,51	0
56	MG	DA	3624	1/1	0.95	0.06	32,32,32,32	0
56	MG	BA	3189	1/1	0.95	0.09	30,30,30,30	0
56	MG	DA	3299	1/1	0.95	0.05	37,37,37,37	0
56	MG	DA	3627	1/1	0.95	0.07	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3481	1/1	0.95	0.06	31,31,31,31	0
56	MG	BA	3814	1/1	0.95	0.07	43,43,43,43	0
56	MG	BA	3634	1/1	0.95	0.14	23,23,23,23	0
56	MG	DA	3305	1/1	0.95	0.05	42,42,42,42	0
56	MG	AX	3011	1/1	0.95	0.12	53,53,53,53	0
56	MG	BA	3353	1/1	0.95	0.17	49,49,49,49	0
56	MG	CK	3001	1/1	0.95	0.07	46,46,46,46	0
56	MG	DA	3310	1/1	0.95	0.12	54,54,54,54	0
56	MG	BA	3637	1/1	0.95	0.17	32,32,32,32	0
56	MG	DA	3313	1/1	0.95	0.09	42,42,42,42	0
56	MG	BA	3193	1/1	0.95	0.08	50,50,50,50	0
56	MG	DA	3315	1/1	0.95	0.11	27,27,27,27	0
56	MG	AA	3046	1/1	0.95	0.09	43,43,43,43	0
56	MG	BA	3200	1/1	0.95	0.11	35,35,35,35	0
56	MG	BA	3358	1/1	0.95	0.12	28,28,28,28	0
56	MG	BA	3827	1/1	0.95	0.06	41,41,41,41	0
56	MG	AA	3081	1/1	0.95	0.08	48,48,48,48	0
56	MG	DA	3645	1/1	0.95	0.10	49,49,49,49	0
56	MG	BA	3829	1/1	0.95	0.09	51,51,51,51	0
56	MG	BA	3204	1/1	0.95	0.07	34,34,34,34	0
56	MG	BA	3205	1/1	0.95	0.10	50,50,50,50	0
56	MG	BA	3650	1/1	0.95	0.17	33,33,33,33	0
56	MG	CX	3003	1/1	0.95	0.22	59,59,59,59	0
56	MG	DA	3652	1/1	0.95	0.10	53,53,53,53	0
56	MG	BA	3651	1/1	0.95	0.07	52,52,52,52	0
56	MG	DA	3654	1/1	0.95	0.08	53,53,53,53	0
56	MG	AA	3034	1/1	0.95	0.12	52,52,52,52	0
56	MG	DA	3656	1/1	0.95	0.12	56,56,56,56	0
56	MG	BA	3494	1/1	0.95	0.09	32,32,32,32	0
56	MG	DA	3330	1/1	0.95	0.09	47,47,47,47	0
56	MG	AA	3097	1/1	0.95	0.13	54,54,54,54	0
56	MG	DA	3660	1/1	0.95	0.06	34,34,34,34	0
56	MG	BA	3096	1/1	0.95	0.15	42,42,42,42	0
56	MG	AA	3180	1/1	0.95	0.10	57,57,57,57	0
56	MG	DA	3336	1/1	0.95	0.09	27,27,27,27	0
56	MG	CA	3037	1/1	0.95	0.14	50,50,50,50	0
56	MG	BA	3098	1/1	0.95	0.14	43,43,43,43	0
56	MG	DA	3012	1/1	0.95	0.10	42,42,42,42	0
56	MG	AA	3085	1/1	0.95	0.10	47,47,47,47	0
56	MG	DA	3017	1/1	0.95	0.14	42,42,42,42	0
56	MG	AA	3003	1/1	0.95	0.17	62,62,62,62	0
56	MG	AA	3183	1/1	0.95	0.10	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3021	1/1	0.95	0.10	29,29,29,29	0
56	MG	DA	3022	1/1	0.95	0.14	34,34,34,34	0
56	MG	BA	3376	1/1	0.95	0.11	32,32,32,32	0
56	MG	DA	3024	1/1	0.95	0.08	46,46,46,46	0
56	MG	BA	3105	1/1	0.95	0.14	44,44,44,44	0
56	MG	BA	3850	1/1	0.95	0.10	47,47,47,47	0
56	MG	BA	3379	1/1	0.95	0.10	52,52,52,52	0
56	MG	DA	3359	1/1	0.95	0.18	47,47,47,47	0
56	MG	DB	3012	1/1	0.95	0.07	50,50,50,50	0
56	MG	CA	3047	1/1	0.95	0.27	53,53,53,53	0
56	MG	BA	3380	1/1	0.95	0.08	45,45,45,45	0
56	MG	DA	3038	1/1	0.95	0.06	34,34,34,34	0
56	MG	BA	3513	1/1	0.95	0.17	51,51,51,51	0
56	MG	BA	3219	1/1	0.95	0.10	28,28,28,28	0
56	MG	CA	3052	1/1	0.95	0.27	53,53,53,53	0
56	MG	DA	3046	1/1	0.95	0.12	40,40,40,40	0
56	MG	BA	3858	1/1	0.95	0.09	61,61,61,61	0
56	MG	DD	303	1/1	0.95	0.20	46,46,46,46	0
56	MG	DA	3049	1/1	0.95	0.10	43,43,43,43	0
56	MG	DA	3374	1/1	0.95	0.05	36,36,36,36	0
56	MG	DA	3378	1/1	0.95	0.11	43,43,43,43	0
56	MG	DE	304	1/1	0.95	0.08	43,43,43,43	0
56	MG	BA	3221	1/1	0.95	0.19	49,49,49,49	0
56	MG	CA	3055	1/1	0.95	0.16	57,57,57,57	0
56	MG	DF	301	1/1	0.95	0.13	36,36,36,36	0
56	MG	BA	3520	1/1	0.95	0.08	42,42,42,42	0
56	MG	DF	303	1/1	0.95	0.08	42,42,42,42	0
56	MG	DA	3054	1/1	0.95	0.24	52,52,52,52	0
56	MG	DA	3056	1/1	0.95	0.11	41,41,41,41	0
56	MG	AA	3118	1/1	0.95	0.10	45,45,45,45	0
56	MG	DA	3059	1/1	0.95	0.06	39,39,39,39	0
56	MG	BA	3863	1/1	0.95	0.15	44,44,44,44	0
56	MG	BA	3228	1/1	0.95	0.09	35,35,35,35	0
56	MG	CA	3060	1/1	0.95	0.24	55,55,55,55	0
56	MG	DA	3065	1/1	0.95	0.08	50,50,50,50	0
56	MG	DU	3002	1/1	0.95	0.19	52,52,52,52	0
56	MG	BA	3676	1/1	0.95	0.08	50,50,50,50	0
56	MG	AF	3001	1/1	0.95	0.12	31,31,31,31	0
56	MG	BA	3526	1/1	0.95	0.08	43,43,43,43	0
56	MG	BA	3870	1/1	0.95	0.07	24,24,24,24	0
56	MG	BA	3389	1/1	0.95	0.09	21,21,21,21	0
56	MG	BA	3528	1/1	0.95	0.09	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3238	1/1	0.95	0.07	42,42,42,42	0
56	MG	AA	3016	1/1	0.95	0.18	57,57,57,57	0
56	MG	DY	502	1/1	0.95	0.10	44,44,44,44	0
56	MG	AA	3142	1/1	0.95	0.06	44,44,44,44	0
56	MG	CA	3073	1/1	0.95	0.10	64,64,64,64	0
56	MG	D1	101	1/1	0.95	0.14	44,44,44,44	0
56	MG	BA	3397	1/1	0.95	0.09	46,46,46,46	0
56	MG	DA	3077	1/1	0.95	0.07	44,44,44,44	0
56	MG	BA	3691	1/1	0.95	0.13	55,55,55,55	0
56	MG	DA	3079	1/1	0.95	0.15	49,49,49,49	0
56	MG	BA	3537	1/1	0.95	0.07	31,31,31,31	0
56	MG	DA	3082	1/1	0.95	0.09	48,48,48,48	0
59	ZN	D4	501	1/1	0.95	0.09	95,95,95,95	0
56	MG	BA	3887	1/1	0.96	0.11	35,35,35,35	0
56	MG	BA	3027	1/1	0.96	0.07	37,37,37,37	0
56	MG	AA	3229	1/1	0.96	0.17	50,50,50,50	0
56	MG	BA	3382	1/1	0.96	0.10	26,26,26,26	0
56	MG	DA	3474	1/1	0.96	0.09	35,35,35,35	0
56	MG	DA	3475	1/1	0.96	0.10	42,42,42,42	0
56	MG	BA	3279	1/1	0.96	0.16	32,32,32,32	0
56	MG	BA	3384	1/1	0.96	0.05	48,48,48,48	0
56	MG	BA	3280	1/1	0.96	0.05	23,23,23,23	0
56	MG	DA	3480	1/1	0.96	0.06	43,43,43,43	0
56	MG	BA	3740	1/1	0.96	0.11	41,41,41,41	0
56	MG	BA	3099	1/1	0.96	0.12	49,49,49,49	0
56	MG	DA	3484	1/1	0.96	0.08	39,39,39,39	0
56	MG	DA	3235	1/1	0.96	0.15	52,52,52,52	0
56	MG	DA	3236	1/1	0.96	0.06	36,36,36,36	0
56	MG	BA	3742	1/1	0.96	0.05	43,43,43,43	0
56	MG	BA	3387	1/1	0.96	0.08	60,60,60,60	0
56	MG	BA	3905	1/1	0.96	0.06	47,47,47,47	0
56	MG	AA	3070	1/1	0.96	0.23	51,51,51,51	0
56	MG	DA	3493	1/1	0.96	0.07	38,38,38,38	0
56	MG	BB	3001	1/1	0.96	0.12	41,41,41,41	0
56	MG	DA	3496	1/1	0.96	0.08	53,53,53,53	0
56	MG	DA	3243	1/1	0.96	0.06	39,39,39,39	0
56	MG	DA	3499	1/1	0.96	0.10	44,44,44,44	0
56	MG	BA	3102	1/1	0.96	0.11	44,44,44,44	0
56	MG	DA	3501	1/1	0.96	0.20	33,33,33,33	0
56	MG	BA	3173	1/1	0.96	0.05	35,35,35,35	0
56	MG	BA	3497	1/1	0.96	0.16	49,49,49,49	0
56	MG	BB	3006	1/1	0.96	0.09	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BB	3009	1/1	0.96	0.08	52,52,52,52	0
56	MG	AA	3071	1/1	0.96	0.08	61,61,61,61	0
56	MG	BA	3749	1/1	0.96	0.06	24,24,24,24	0
56	MG	DA	3508	1/1	0.96	0.14	39,39,39,39	0
56	MG	BA	3392	1/1	0.96	0.10	48,48,48,48	0
56	MG	BA	3393	1/1	0.96	0.08	23,23,23,23	0
56	MG	DA	3006	1/1	0.96	0.09	41,41,41,41	0
56	MG	AA	3110	1/1	0.96	0.08	51,51,51,51	0
56	MG	DA	3255	1/1	0.96	0.16	23,23,23,23	0
56	MG	DA	3257	1/1	0.96	0.11	53,53,53,53	0
56	MG	AA	3031	1/1	0.96	0.09	43,43,43,43	0
56	MG	DA	3259	1/1	0.96	0.09	41,41,41,41	0
56	MG	CA	3067	1/1	0.96	0.15	55,55,55,55	0
56	MG	BB	3017	1/1	0.96	0.12	37,37,37,37	0
56	MG	BA	3504	1/1	0.96	0.06	31,31,31,31	0
56	MG	BA	3626	1/1	0.96	0.09	22,22,22,22	0
56	MG	DA	3522	1/1	0.96	0.06	35,35,35,35	0
56	MG	BA	3036	1/1	0.96	0.21	34,34,34,34	0
56	MG	DA	3266	1/1	0.96	0.10	44,44,44,44	0
56	MG	DA	3525	1/1	0.96	0.12	46,46,46,46	0
56	MG	CA	3072	1/1	0.96	0.07	55,55,55,55	0
56	MG	BA	3761	1/1	0.96	0.11	52,52,52,52	0
56	MG	BA	3506	1/1	0.96	0.08	34,34,34,34	0
56	MG	DA	3025	1/1	0.96	0.24	48,48,48,48	0
56	MG	DA	3530	1/1	0.96	0.05	30,30,30,30	0
56	MG	DA	3273	1/1	0.96	0.06	30,30,30,30	0
56	MG	AA	3138	1/1	0.96	0.20	57,57,57,57	0
56	MG	BA	3110	1/1	0.96	0.11	17,17,17,17	0
56	MG	CA	3078	1/1	0.96	0.12	48,48,48,48	0
56	MG	DA	3277	1/1	0.96	0.15	41,41,41,41	0
56	MG	DA	3538	1/1	0.96	0.17	57,57,57,57	0
56	MG	BA	3765	1/1	0.96	0.14	33,33,33,33	0
56	MG	BA	3509	1/1	0.96	0.07	48,48,48,48	0
56	MG	AA	3112	1/1	0.96	0.08	40,40,40,40	0
56	MG	AA	3066	1/1	0.96	0.07	30,30,30,30	0
56	MG	AA	3032	1/1	0.96	0.09	60,60,60,60	0
56	MG	DA	3284	1/1	0.96	0.05	36,36,36,36	0
56	MG	DA	3547	1/1	0.96	0.10	52,52,52,52	0
56	MG	BA	3514	1/1	0.96	0.04	9,9,9,9	0
56	MG	DA	3045	1/1	0.96	0.14	52,52,52,52	0
56	MG	BE	301	1/1	0.96	0.06	36,36,36,36	0
56	MG	BA	3195	1/1	0.96	0.08	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BE	303	1/1	0.96	0.10	35,35,35,35	0
56	MG	DA	3291	1/1	0.96	0.15	52,52,52,52	0
56	MG	BA	3517	1/1	0.96	0.07	31,31,31,31	0
56	MG	DA	3051	1/1	0.96	0.12	45,45,45,45	0
56	MG	DA	3557	1/1	0.96	0.07	54,54,54,54	0
56	MG	BA	3044	1/1	0.96	0.10	32,32,32,32	0
56	MG	BA	3047	1/1	0.96	0.12	31,31,31,31	0
56	MG	BA	3521	1/1	0.96	0.06	38,38,38,38	0
56	MG	DA	3561	1/1	0.96	0.07	51,51,51,51	0
56	MG	BA	3641	1/1	0.96	0.05	22,22,22,22	0
56	MG	BE	311	1/1	0.96	0.10	37,37,37,37	0
56	MG	DA	3564	1/1	0.96	0.10	43,43,43,43	0
56	MG	BA	3048	1/1	0.96	0.11	36,36,36,36	0
56	MG	DA	3567	1/1	0.96	0.12	44,44,44,44	0
56	MG	DA	3302	1/1	0.96	0.11	57,57,57,57	0
56	MG	BA	3118	1/1	0.96	0.12	38,38,38,38	0
56	MG	BA	3524	1/1	0.96	0.07	24,24,24,24	0
56	MG	BF	306	1/1	0.96	0.07	34,34,34,34	0
56	MG	BF	307	1/1	0.96	0.05	31,31,31,31	0
56	MG	BA	3307	1/1	0.96	0.07	36,36,36,36	0
56	MG	DA	3308	1/1	0.96	0.06	45,45,45,45	0
56	MG	BA	3050	1/1	0.96	0.04	15,15,15,15	0
56	MG	BA	3786	1/1	0.96	0.08	20,20,20,20	0
56	MG	BA	3309	1/1	0.96	0.20	50,50,50,50	0
56	MG	AE	3002	1/1	0.96	0.10	57,57,57,57	0
56	MG	BA	3653	1/1	0.96	0.15	45,45,45,45	0
56	MG	AA	3115	1/1	0.96	0.14	54,54,54,54	0
56	MG	BA	3530	1/1	0.96	0.08	43,43,43,43	0
56	MG	BA	3656	1/1	0.96	0.08	32,32,32,32	0
56	MG	BA	3531	1/1	0.96	0.15	46,46,46,46	0
56	MG	BA	3532	1/1	0.96	0.13	50,50,50,50	0
56	MG	AA	3127	1/1	0.96	0.05	33,33,33,33	0
56	MG	BA	3799	1/1	0.96	0.11	22,22,22,22	0
56	MG	BA	3313	1/1	0.96	0.18	60,60,60,60	0
56	MG	DA	3080	1/1	0.96	0.09	33,33,33,33	0
56	MG	CA	3113	1/1	0.96	0.08	37,37,37,37	0
56	MG	BO	3003	1/1	0.96	0.06	42,42,42,42	0
56	MG	DA	3083	1/1	0.96	0.07	31,31,31,31	0
56	MG	DA	3084	1/1	0.96	0.09	35,35,35,35	0
56	MG	BA	3064	1/1	0.96	0.08	40,40,40,40	0
56	MG	BA	3662	1/1	0.96	0.12	23,23,23,23	0
56	MG	BP	203	1/1	0.96	0.15	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3424	1/1	0.96	0.05	50,50,50,50	0
56	MG	BA	3664	1/1	0.96	0.13	46,46,46,46	0
56	MG	DA	3335	1/1	0.96	0.07	28,28,28,28	0
56	MG	BQ	3004	1/1	0.96	0.23	46,46,46,46	0
56	MG	DA	3093	1/1	0.96	0.07	26,26,26,26	0
56	MG	AL	5001	1/1	0.96	0.11	52,52,52,52	0
56	MG	DA	3096	1/1	0.96	0.11	44,44,44,44	0
56	MG	AA	3129	1/1	0.96	0.05	46,46,46,46	0
56	MG	DA	3342	1/1	0.96	0.12	44,44,44,44	0
56	MG	DA	3343	1/1	0.96	0.05	39,39,39,39	0
56	MG	BA	3213	1/1	0.96	0.25	48,48,48,48	0
56	MG	DA	3345	1/1	0.96	0.06	36,36,36,36	0
56	MG	DA	3615	1/1	0.96	0.13	50,50,50,50	0
56	MG	DA	3346	1/1	0.96	0.05	31,31,31,31	0
56	MG	DA	3099	1/1	0.96	0.09	44,44,44,44	0
56	MG	AA	3221	1/1	0.96	0.08	55,55,55,55	0
56	MG	BS	3003	1/1	0.96	0.07	48,48,48,48	0
56	MG	DA	3351	1/1	0.96	0.08	36,36,36,36	0
56	MG	DA	3102	1/1	0.96	0.07	51,51,51,51	0
56	MG	DA	3104	1/1	0.96	0.09	45,45,45,45	0
56	MG	BA	3811	1/1	0.96	0.08	40,40,40,40	0
56	MG	BA	3429	1/1	0.96	0.10	51,51,51,51	0
56	MG	DA	3107	1/1	0.96	0.11	48,48,48,48	0
56	MG	BA	3068	1/1	0.96	0.16	44,44,44,44	0
56	MG	BU	204	1/1	0.96	0.07	48,48,48,48	0
56	MG	BA	3323	1/1	0.96	0.20	48,48,48,48	0
56	MG	BV	205	1/1	0.96	0.07	46,46,46,46	0
56	MG	BW	201	1/1	0.96	0.08	45,45,45,45	0
56	MG	DA	3364	1/1	0.96	0.14	58,58,58,58	0
56	MG	BA	3324	1/1	0.96	0.08	36,36,36,36	0
56	MG	BA	3218	1/1	0.96	0.14	33,33,33,33	0
56	MG	DA	3119	1/1	0.96	0.12	36,36,36,36	0
56	MG	BX	3002	1/1	0.96	0.06	37,37,37,37	0
56	MG	DA	3121	1/1	0.96	0.08	41,41,41,41	0
56	MG	BA	3137	1/1	0.96	0.06	35,35,35,35	0
56	MG	DA	3123	1/1	0.96	0.09	38,38,38,38	0
56	MG	BA	3004	1/1	0.96	0.10	33,33,33,33	0
56	MG	BA	3822	1/1	0.96	0.17	18,18,18,18	0
56	MG	BA	3823	1/1	0.96	0.10	57,57,57,57	0
56	MG	BA	3222	1/1	0.96	0.15	42,42,42,42	0
56	MG	DA	3130	1/1	0.96	0.10	49,49,49,49	0
56	MG	BA	3071	1/1	0.96	0.08	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3334	1/1	0.96	0.10	35,35,35,35	0
56	MG	DA	3646	1/1	0.96	0.09	27,27,27,27	0
56	MG	BA	3681	1/1	0.96	0.08	39,39,39,39	0
56	MG	BA	3338	1/1	0.96	0.13	44,44,44,44	0
56	MG	BA	3339	1/1	0.96	0.11	30,30,30,30	0
56	MG	AA	3082	1/1	0.96	0.17	34,34,34,34	0
56	MG	BA	3343	1/1	0.96	0.07	45,45,45,45	0
56	MG	B0	107	1/1	0.96	0.07	46,46,46,46	0
56	MG	BA	3143	1/1	0.96	0.18	37,37,37,37	0
56	MG	BA	3144	1/1	0.96	0.18	53,53,53,53	0
56	MG	B3	3002	1/1	0.96	0.12	39,39,39,39	0
56	MG	DA	3144	1/1	0.96	0.19	49,49,49,49	0
56	MG	BA	3239	1/1	0.96	0.10	38,38,38,38	0
56	MG	DA	3398	1/1	0.96	0.06	42,42,42,42	0
56	MG	DA	3399	1/1	0.96	0.07	47,47,47,47	0
56	MG	CA	3154	1/1	0.96	0.13	56,56,56,56	0
56	MG	BA	3693	1/1	0.96	0.11	39,39,39,39	0
56	MG	BA	3240	1/1	0.96	0.06	39,39,39,39	0
56	MG	BA	3006	1/1	0.96	0.07	43,43,43,43	0
56	MG	BA	3696	1/1	0.96	0.10	46,46,46,46	0
56	MG	DA	3666	1/1	0.96	0.06	55,55,55,55	0
56	MG	B7	101	1/1	0.96	0.08	41,41,41,41	0
56	MG	DA	3406	1/1	0.96	0.05	39,39,39,39	0
56	MG	DA	3669	1/1	0.96	0.11	46,46,46,46	0
56	MG	B7	102	1/1	0.96	0.09	27,27,27,27	0
56	MG	BA	3146	1/1	0.96	0.13	62,62,62,62	0
56	MG	B8	101	1/1	0.96	0.10	47,47,47,47	0
56	MG	BA	3245	1/1	0.96	0.13	26,26,26,26	0
56	MG	AA	3068	1/1	0.96	0.23	55,55,55,55	0
56	MG	DA	3161	1/1	0.96	0.08	41,41,41,41	0
56	MG	BA	3845	1/1	0.96	0.07	28,28,28,28	0
56	MG	BA	3702	1/1	0.96	0.06	39,39,39,39	0
56	MG	DA	3164	1/1	0.96	0.12	61,61,61,61	0
56	MG	AA	3186	1/1	0.96	0.10	43,43,43,43	0
56	MG	BA	3149	1/1	0.96	0.06	35,35,35,35	0
56	MG	DA	3169	1/1	0.96	0.15	44,44,44,44	0
56	MG	BA	3253	1/1	0.96	0.07	29,29,29,29	0
56	MG	BA	3257	1/1	0.96	0.10	45,45,45,45	0
56	MG	BA	3360	1/1	0.96	0.06	49,49,49,49	0
56	MG	DB	3015	1/1	0.96	0.06	44,44,44,44	0
56	MG	BA	3853	1/1	0.96	0.05	41,41,41,41	0
56	MG	CA	3008	1/1	0.96	0.10	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3151	1/1	0.96	0.15	41,41,41,41	0
56	MG	BA	3855	1/1	0.96	0.08	53,53,53,53	0
56	MG	BA	3856	1/1	0.96	0.05	40,40,40,40	0
56	MG	DA	3427	1/1	0.96	0.06	35,35,35,35	0
56	MG	BA	3463	1/1	0.96	0.08	23,23,23,23	0
56	MG	CA	3178	1/1	0.96	0.08	52,52,52,52	0
56	MG	AA	3132	1/1	0.96	0.04	42,42,42,42	0
56	MG	DA	3186	1/1	0.96	0.17	54,54,54,54	0
56	MG	BA	3260	1/1	0.96	0.06	40,40,40,40	0
56	MG	DA	3434	1/1	0.96	0.08	47,47,47,47	0
56	MG	BA	3364	1/1	0.96	0.20	57,57,57,57	0
56	MG	DE	307	1/1	0.96	0.09	53,53,53,53	0
56	MG	DA	3189	1/1	0.96	0.16	39,39,39,39	0
56	MG	BA	3714	1/1	0.96	0.05	58,58,58,58	0
56	MG	BA	3586	1/1	0.96	0.21	40,40,40,40	0
56	MG	BA	3085	1/1	0.96	0.10	27,27,27,27	0
56	MG	DA	3195	1/1	0.96	0.07	39,39,39,39	0
56	MG	DA	3196	1/1	0.96	0.08	46,46,46,46	0
56	MG	CA	3020	1/1	0.96	0.21	57,57,57,57	0
56	MG	DA	3198	1/1	0.96	0.14	45,45,45,45	0
56	MG	DQ	3002	1/1	0.96	0.05	35,35,35,35	0
56	MG	BA	3366	1/1	0.96	0.10	25,25,25,25	0
56	MG	DA	3448	1/1	0.96	0.13	36,36,36,36	0
56	MG	DT	3001	1/1	0.96	0.22	54,54,54,54	0
56	MG	BA	3155	1/1	0.96	0.06	39,39,39,39	0
56	MG	CA	3024	1/1	0.96	0.14	55,55,55,55	0
56	MG	DA	3202	1/1	0.96	0.16	42,42,42,42	0
56	MG	BA	3019	1/1	0.96	0.12	34,34,34,34	0
56	MG	BA	3088	1/1	0.96	0.16	28,28,28,28	0
56	MG	BA	3371	1/1	0.96	0.18	34,34,34,34	0
56	MG	DA	3208	1/1	0.96	0.19	46,46,46,46	0
56	MG	AA	3227	1/1	0.96	0.05	25,25,25,25	0
56	MG	AX	3002	1/1	0.96	0.14	49,49,49,49	0
56	MG	BA	3477	1/1	0.96	0.19	41,41,41,41	0
56	MG	CA	3031	1/1	0.96	0.11	51,51,51,51	0
56	MG	AA	3133	1/1	0.96	0.10	32,32,32,32	0
56	MG	CA	3197	1/1	0.96	0.07	43,43,43,43	0
56	MG	BA	3877	1/1	0.96	0.08	44,44,44,44	0
56	MG	BA	3726	1/1	0.96	0.14	39,39,39,39	0
56	MG	BA	3272	1/1	0.96	0.15	40,40,40,40	0
56	MG	DA	3465	1/1	0.96	0.10	38,38,38,38	0
56	MG	DA	3466	1/1	0.96	0.13	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3273	1/1	0.96	0.10	50,50,50,50	0
56	MG	BA	3884	1/1	0.96	0.14	27,27,27,27	0
59	ZN	CN	501	1/1	0.96	0.08	83,83,83,83	0
56	MG	BA	3274	1/1	0.96	0.21	45,45,45,45	0
60	K	AX	3001	1/1	0.96	0.06	45,45,45,45	0
60	K	CX	3001	1/1	0.96	0.09	62,62,62,62	0
56	MG	BA	3246	1/1	0.97	0.05	30,30,30,30	0
56	MG	DA	3063	1/1	0.97	0.07	34,34,34,34	0
56	MG	BQ	3003	1/1	0.97	0.09	54,54,54,54	0
56	MG	BA	3679	1/1	0.97	0.06	33,33,33,33	0
56	MG	BQ	3005	1/1	0.97	0.06	37,37,37,37	0
56	MG	AA	3215	1/1	0.97	0.07	47,47,47,47	0
56	MG	BA	3164	1/1	0.97	0.07	33,33,33,33	0
56	MG	DA	3283	1/1	0.97	0.09	44,44,44,44	0
56	MG	BA	3682	1/1	0.97	0.09	39,39,39,39	0
56	MG	BA	3559	1/1	0.97	0.05	37,37,37,37	0
56	MG	BS	3002	1/1	0.97	0.12	39,39,39,39	0
56	MG	DA	3287	1/1	0.97	0.06	33,33,33,33	0
56	MG	BA	3684	1/1	0.97	0.10	55,55,55,55	0
56	MG	BT	5002	1/1	0.97	0.04	49,49,49,49	0
56	MG	BA	3560	1/1	0.97	0.08	28,28,28,28	0
56	MG	DA	3520	1/1	0.97	0.07	38,38,38,38	0
56	MG	BA	3112	1/1	0.97	0.20	49,49,49,49	0
56	MG	BA	3687	1/1	0.97	0.13	49,49,49,49	0
56	MG	BA	3688	1/1	0.97	0.09	41,41,41,41	0
56	MG	CA	3119	1/1	0.97	0.17	48,48,48,48	0
56	MG	BU	206	1/1	0.97	0.12	38,38,38,38	0
56	MG	BU	207	1/1	0.97	0.15	37,37,37,37	0
56	MG	BU	208	1/1	0.97	0.15	34,34,34,34	0
56	MG	BA	3252	1/1	0.97	0.10	38,38,38,38	0
56	MG	BA	3835	1/1	0.97	0.05	34,34,34,34	0
56	MG	BA	3024	1/1	0.97	0.04	40,40,40,40	0
56	MG	DA	3531	1/1	0.97	0.08	56,56,56,56	0
56	MG	BA	3255	1/1	0.97	0.06	42,42,42,42	0
56	MG	DA	3533	1/1	0.97	0.06	59,59,59,59	0
56	MG	BA	3565	1/1	0.97	0.07	45,45,45,45	0
56	MG	BW	204	1/1	0.97	0.11	23,23,23,23	0
56	MG	DA	3089	1/1	0.97	0.08	46,46,46,46	0
56	MG	BX	3001	1/1	0.97	0.20	37,37,37,37	0
56	MG	DA	3091	1/1	0.97	0.12	32,32,32,32	0
56	MG	DA	3539	1/1	0.97	0.06	56,56,56,56	0
56	MG	BA	3452	1/1	0.97	0.08	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3167	1/1	0.97	0.14	33,33,33,33	0
56	MG	AA	3100	1/1	0.97	0.05	41,41,41,41	0
56	MG	DA	3312	1/1	0.97	0.07	36,36,36,36	0
56	MG	BA	3357	1/1	0.97	0.07	40,40,40,40	0
56	MG	BX	3006	1/1	0.97	0.09	35,35,35,35	0
56	MG	BA	3457	1/1	0.97	0.09	25,25,25,25	0
56	MG	DA	3316	1/1	0.97	0.05	29,29,29,29	0
56	MG	BA	3458	1/1	0.97	0.06	25,25,25,25	0
56	MG	BA	3169	1/1	0.97	0.12	40,40,40,40	0
56	MG	BA	3170	1/1	0.97	0.08	40,40,40,40	0
56	MG	BA	3261	1/1	0.97	0.06	38,38,38,38	0
56	MG	DA	3103	1/1	0.97	0.06	45,45,45,45	0
56	MG	BA	3069	1/1	0.97	0.10	32,32,32,32	0
56	MG	B0	102	1/1	0.97	0.07	47,47,47,47	0
56	MG	BA	3172	1/1	0.97	0.13	32,32,32,32	0
56	MG	AA	3155	1/1	0.97	0.04	42,42,42,42	0
56	MG	DA	3108	1/1	0.97	0.10	38,38,38,38	0
56	MG	BA	3266	1/1	0.97	0.17	28,28,28,28	0
56	MG	BA	3176	1/1	0.97	0.07	53,53,53,53	0
56	MG	BA	3177	1/1	0.97	0.15	40,40,40,40	0
56	MG	B2	3001	1/1	0.97	0.07	44,44,44,44	0
56	MG	DA	3113	1/1	0.97	0.06	39,39,39,39	0
56	MG	BA	3582	1/1	0.97	0.09	34,34,34,34	0
56	MG	DA	3333	1/1	0.97	0.09	31,31,31,31	0
56	MG	AA	3105	1/1	0.97	0.07	48,48,48,48	0
56	MG	BA	3584	1/1	0.97	0.13	40,40,40,40	0
56	MG	DA	3118	1/1	0.97	0.19	47,47,47,47	0
56	MG	DA	3571	1/1	0.97	0.12	43,43,43,43	0
56	MG	BA	3180	1/1	0.97	0.19	31,31,31,31	0
56	MG	AA	3014	1/1	0.97	0.05	47,47,47,47	0
56	MG	BA	3860	1/1	0.97	0.08	37,37,37,37	0
56	MG	BA	3370	1/1	0.97	0.09	34,34,34,34	0
56	MG	DA	3576	1/1	0.97	0.05	49,49,49,49	0
56	MG	AA	3128	1/1	0.97	0.10	27,27,27,27	0
56	MG	BA	3120	1/1	0.97	0.13	50,50,50,50	0
56	MG	DA	3126	1/1	0.97	0.05	33,33,33,33	0
56	MG	BA	3373	1/1	0.97	0.09	28,28,28,28	0
56	MG	BA	3187	1/1	0.97	0.07	41,41,41,41	0
56	MG	BA	3276	1/1	0.97	0.15	42,42,42,42	0
56	MG	BA	3867	1/1	0.97	0.08	58,58,58,58	0
56	MG	AA	3208	1/1	0.97	0.05	48,48,48,48	0
56	MG	BA	3125	1/1	0.97	0.12	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3190	1/1	0.97	0.20	38,38,38,38	0
56	MG	BA	3599	1/1	0.97	0.07	60,60,60,60	0
56	MG	DA	3590	1/1	0.97	0.05	37,37,37,37	0
56	MG	BA	3483	1/1	0.97	0.06	30,30,30,30	0
56	MG	BA	3284	1/1	0.97	0.07	39,39,39,39	0
56	MG	BA	3035	1/1	0.97	0.10	27,27,27,27	0
56	MG	BA	3082	1/1	0.97	0.04	23,23,23,23	0
56	MG	BA	3880	1/1	0.97	0.05	35,35,35,35	0
56	MG	BA	3003	1/1	0.97	0.05	24,24,24,24	0
56	MG	BA	3605	1/1	0.97	0.07	49,49,49,49	0
56	MG	BA	3733	1/1	0.97	0.10	42,42,42,42	0
56	MG	DA	3599	1/1	0.97	0.09	51,51,51,51	0
56	MG	BA	3084	1/1	0.97	0.10	42,42,42,42	0
56	MG	BA	3735	1/1	0.97	0.09	30,30,30,30	0
56	MG	BA	3489	1/1	0.97	0.06	60,60,60,60	0
56	MG	DA	3148	1/1	0.97	0.13	50,50,50,50	0
56	MG	BA	3888	1/1	0.97	0.08	26,26,26,26	0
56	MG	DA	3370	1/1	0.97	0.06	49,49,49,49	0
56	MG	BA	3608	1/1	0.97	0.12	58,58,58,58	0
56	MG	BA	3609	1/1	0.97	0.04	30,30,30,30	0
56	MG	DA	3373	1/1	0.97	0.14	60,60,60,60	0
56	MG	BA	3895	1/1	0.97	0.04	30,30,30,30	0
56	MG	DA	3377	1/1	0.97	0.09	43,43,43,43	0
56	MG	BA	3199	1/1	0.97	0.10	31,31,31,31	0
56	MG	AA	3168	1/1	0.97	0.17	53,53,53,53	0
56	MG	DA	3156	1/1	0.97	0.10	33,33,33,33	0
56	MG	BA	3202	1/1	0.97	0.09	30,30,30,30	0
56	MG	AA	3199	1/1	0.97	0.10	54,54,54,54	0
56	MG	DA	3159	1/1	0.97	0.06	45,45,45,45	0
56	MG	BA	3294	1/1	0.97	0.09	38,38,38,38	0
56	MG	BA	3615	1/1	0.97	0.06	28,28,28,28	0
56	MG	BA	3087	1/1	0.97	0.08	45,45,45,45	0
56	MG	BA	3136	1/1	0.97	0.15	49,49,49,49	0
56	MG	BA	3041	1/1	0.97	0.11	31,31,31,31	0
56	MG	BA	3138	1/1	0.97	0.15	40,40,40,40	0
56	MG	BA	3395	1/1	0.97	0.09	44,44,44,44	0
56	MG	BA	3089	1/1	0.97	0.07	47,47,47,47	0
56	MG	BA	3092	1/1	0.97	0.15	31,31,31,31	0
56	MG	DA	3394	1/1	0.97	0.08	55,55,55,55	0
56	MG	BA	3093	1/1	0.97	0.25	41,41,41,41	0
56	MG	DA	3172	1/1	0.97	0.14	38,38,38,38	0
56	MG	DA	3173	1/1	0.97	0.15	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	AA	3069	1/1	0.97	0.10	44,44,44,44	0
56	MG	BB	3008	1/1	0.97	0.17	50,50,50,50	0
56	MG	BA	3303	1/1	0.97	0.06	27,27,27,27	0
56	MG	BB	3010	1/1	0.97	0.12	38,38,38,38	0
56	MG	DA	3178	1/1	0.97	0.08	31,31,31,31	0
56	MG	CA	3198	1/1	0.97	0.07	39,39,39,39	0
56	MG	BA	3304	1/1	0.97	0.08	43,43,43,43	0
56	MG	BA	3760	1/1	0.97	0.09	36,36,36,36	0
56	MG	CA	3201	1/1	0.97	0.10	51,51,51,51	0
56	MG	BA	3007	1/1	0.97	0.11	43,43,43,43	0
56	MG	DA	3185	1/1	0.97	0.09	39,39,39,39	0
56	MG	CA	3042	1/1	0.97	0.17	48,48,48,48	0
56	MG	BA	3404	1/1	0.97	0.13	38,38,38,38	0
56	MG	BA	3009	1/1	0.97	0.05	23,23,23,23	0
56	MG	BA	3511	1/1	0.97	0.06	38,38,38,38	0
56	MG	AA	3029	1/1	0.97	0.30	56,56,56,56	0
56	MG	BB	3018	1/1	0.97	0.07	32,32,32,32	0
56	MG	BA	3216	1/1	0.97	0.12	35,35,35,35	0
56	MG	CL	201	1/1	0.97	0.07	55,55,55,55	0
56	MG	BA	3015	1/1	0.97	0.07	33,33,33,33	0
56	MG	BA	3049	1/1	0.97	0.12	32,32,32,32	0
56	MG	BA	3516	1/1	0.97	0.06	49,49,49,49	0
56	MG	BA	3410	1/1	0.97	0.09	19,19,19,19	0
56	MG	BA	3100	1/1	0.97	0.13	33,33,33,33	0
56	MG	BA	3519	1/1	0.97	0.15	46,46,46,46	0
56	MG	AA	3226	1/1	0.97	0.08	34,34,34,34	0
56	MG	AK	3001	1/1	0.97	0.13	41,41,41,41	0
56	MG	DA	3204	1/1	0.97	0.05	42,42,42,42	0
56	MG	BB	3029	1/1	0.97	0.05	21,21,21,21	0
56	MG	DA	3206	1/1	0.97	0.05	33,33,33,33	0
56	MG	BA	3223	1/1	0.97	0.21	36,36,36,36	0
56	MG	BA	3224	1/1	0.97	0.20	30,30,30,30	0
56	MG	DA	3663	1/1	0.97	0.10	46,46,46,46	0
56	MG	BA	3225	1/1	0.97	0.18	32,32,32,32	0
56	MG	DA	3431	1/1	0.97	0.06	34,34,34,34	0
56	MG	BA	3153	1/1	0.97	0.17	31,31,31,31	0
56	MG	DA	3211	1/1	0.97	0.05	37,37,37,37	0
56	MG	BD	313	1/1	0.97	0.13	39,39,39,39	0
56	MG	BA	3319	1/1	0.97	0.07	36,36,36,36	0
56	MG	DA	3436	1/1	0.97	0.07	38,38,38,38	0
56	MG	BA	3649	1/1	0.97	0.08	24,24,24,24	0
56	MG	CA	3066	1/1	0.97	0.17	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3440	1/1	0.97	0.05	34,34,34,34	0
56	MG	BA	3422	1/1	0.97	0.05	24,24,24,24	0
56	MG	BA	3227	1/1	0.97	0.07	33,33,33,33	0
56	MG	BA	3321	1/1	0.97	0.06	43,43,43,43	0
56	MG	DB	3006	1/1	0.97	0.04	40,40,40,40	0
56	MG	BA	3056	1/1	0.97	0.09	47,47,47,47	0
56	MG	DA	3010	1/1	0.97	0.08	36,36,36,36	0
56	MG	DA	3011	1/1	0.97	0.05	34,34,34,34	0
56	MG	BA	3790	1/1	0.97	0.04	21,21,21,21	0
56	MG	DA	3013	1/1	0.97	0.15	39,39,39,39	0
56	MG	DA	3224	1/1	0.97	0.06	32,32,32,32	0
56	MG	DA	3014	1/1	0.97	0.10	33,33,33,33	0
56	MG	BA	3229	1/1	0.97	0.17	33,33,33,33	0
56	MG	DA	3227	1/1	0.97	0.12	39,39,39,39	0
56	MG	BA	3230	1/1	0.97	0.10	35,35,35,35	0
56	MG	BA	3232	1/1	0.97	0.05	33,33,33,33	0
56	MG	DA	3019	1/1	0.97	0.05	30,30,30,30	0
56	MG	BA	3328	1/1	0.97	0.05	36,36,36,36	0
56	MG	DA	3232	1/1	0.97	0.07	44,44,44,44	0
56	MG	DA	3233	1/1	0.97	0.07	36,36,36,36	0
56	MG	DD	301	1/1	0.97	0.07	38,38,38,38	0
56	MG	DD	302	1/1	0.97	0.05	42,42,42,42	0
56	MG	CA	3076	1/1	0.97	0.12	42,42,42,42	0
56	MG	DD	304	1/1	0.97	0.09	26,26,26,26	0
56	MG	BA	3234	1/1	0.97	0.07	43,43,43,43	0
56	MG	BF	304	1/1	0.97	0.08	34,34,34,34	0
56	MG	BA	3536	1/1	0.97	0.12	34,34,34,34	0
56	MG	BA	3018	1/1	0.97	0.11	32,32,32,32	0
56	MG	DA	3239	1/1	0.97	0.10	44,44,44,44	0
56	MG	BA	3539	1/1	0.97	0.12	38,38,38,38	0
56	MG	DA	3027	1/1	0.97	0.10	42,42,42,42	0
56	MG	DA	3029	1/1	0.97	0.10	36,36,36,36	0
56	MG	DA	3030	1/1	0.97	0.23	43,43,43,43	0
56	MG	BA	3061	1/1	0.97	0.10	19,19,19,19	0
56	MG	DA	3032	1/1	0.97	0.16	44,44,44,44	0
56	MG	DF	305	1/1	0.97	0.11	39,39,39,39	0
56	MG	BA	3433	1/1	0.97	0.05	34,34,34,34	0
56	MG	BA	3106	1/1	0.97	0.04	27,27,27,27	0
56	MG	BF	315	1/1	0.97	0.08	47,47,47,47	0
56	MG	DO	5001	1/1	0.97	0.08	51,51,51,51	0
56	MG	DA	3037	1/1	0.97	0.08	32,32,32,32	0
56	MG	DQ	3001	1/1	0.97	0.07	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3158	1/1	0.97	0.06	12,12,12,12	0
56	MG	BG	202	1/1	0.97	0.09	36,36,36,36	0
56	MG	BA	3804	1/1	0.97	0.06	37,37,37,37	0
56	MG	DA	3042	1/1	0.97	0.07	27,27,27,27	0
56	MG	DA	3479	1/1	0.97	0.07	43,43,43,43	0
56	MG	BA	3544	1/1	0.97	0.05	40,40,40,40	0
56	MG	DA	3481	1/1	0.97	0.06	41,41,41,41	0
56	MG	DA	3044	1/1	0.97	0.10	48,48,48,48	0
56	MG	DA	3256	1/1	0.97	0.05	47,47,47,47	0
56	MG	BA	3806	1/1	0.97	0.06	44,44,44,44	0
56	MG	BA	3337	1/1	0.97	0.16	24,24,24,24	0
56	MG	DA	3047	1/1	0.97	0.17	38,38,38,38	0
56	MG	BA	3241	1/1	0.97	0.17	48,48,48,48	0
56	MG	DA	3489	1/1	0.97	0.09	40,40,40,40	0
56	MG	BA	3547	1/1	0.97	0.07	48,48,48,48	0
56	MG	BN	3001	1/1	0.97	0.20	41,41,41,41	0
56	MG	AA	3213	1/1	0.97	0.06	64,64,64,64	0
56	MG	AM	201	1/1	0.97	0.05	53,53,53,53	0
56	MG	BA	3551	1/1	0.97	0.07	37,37,37,37	0
56	MG	BA	3244	1/1	0.97	0.05	39,39,39,39	0
56	MG	DA	3497	1/1	0.97	0.11	50,50,50,50	0
56	MG	D8	101	1/1	0.97	0.12	50,50,50,50	0
56	MG	BA	3674	1/1	0.97	0.17	31,31,31,31	0
56	MG	DA	3057	1/1	0.97	0.04	20,20,20,20	0
56	MG	DA	3271	1/1	0.97	0.08	48,48,48,48	0
56	MG	BA	3344	1/1	0.97	0.18	33,33,33,33	0
56	MG	BA	3345	1/1	0.97	0.09	47,47,47,47	0
56	MG	BP	204	1/1	0.97	0.10	19,19,19,19	0
56	MG	AA	3146	1/1	0.97	0.07	42,42,42,42	0
56	MG	BD	309	1/1	0.98	0.05	32,32,32,32	0
56	MG	BD	310	1/1	0.98	0.06	46,46,46,46	0
56	MG	BD	311	1/1	0.98	0.05	40,40,40,40	0
56	MG	BA	3277	1/1	0.98	0.10	21,21,21,21	0
56	MG	BA	3416	1/1	0.98	0.05	29,29,29,29	0
56	MG	BA	3346	1/1	0.98	0.12	38,38,38,38	0
56	MG	BA	3832	1/1	0.98	0.06	38,38,38,38	0
56	MG	BA	3030	1/1	0.98	0.06	28,28,28,28	0
56	MG	BE	305	1/1	0.98	0.15	21,21,21,21	0
56	MG	BA	3834	1/1	0.98	0.10	35,35,35,35	0
56	MG	BA	3175	1/1	0.98	0.05	39,39,39,39	0
56	MG	DA	3094	1/1	0.98	0.05	41,41,41,41	0
56	MG	BE	308	1/1	0.98	0.05	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	AA	3057	1/1	0.98	0.06	32,32,32,32	0
56	MG	BA	3738	1/1	0.98	0.05	46,46,46,46	0
56	MG	BA	3496	1/1	0.98	0.11	22,22,22,22	0
56	MG	BA	3573	1/1	0.98	0.07	34,34,34,34	0
56	MG	BA	3421	1/1	0.98	0.03	24,24,24,24	0
56	MG	BA	3281	1/1	0.98	0.09	38,38,38,38	0
56	MG	DA	3260	1/1	0.98	0.08	39,39,39,39	0
56	MG	BF	303	1/1	0.98	0.05	31,31,31,31	0
56	MG	BA	3282	1/1	0.98	0.11	32,32,32,32	0
56	MG	BA	3500	1/1	0.98	0.06	15,15,15,15	0
56	MG	BA	3283	1/1	0.98	0.05	43,43,43,43	0
56	MG	BF	308	1/1	0.98	0.05	33,33,33,33	0
56	MG	BF	309	1/1	0.98	0.08	30,30,30,30	0
56	MG	BF	310	1/1	0.98	0.17	37,37,37,37	0
56	MG	DA	3268	1/1	0.98	0.07	36,36,36,36	0
56	MG	DA	3606	1/1	0.98	0.04	61,61,61,61	0
56	MG	BA	3072	1/1	0.98	0.07	27,27,27,27	0
56	MG	BA	3846	1/1	0.98	0.07	30,30,30,30	0
56	MG	BA	3178	1/1	0.98	0.10	29,29,29,29	0
56	MG	DA	3439	1/1	0.98	0.15	50,50,50,50	0
56	MG	BA	3008	1/1	0.98	0.13	24,24,24,24	0
56	MG	AA	3121	1/1	0.98	0.08	49,49,49,49	0
56	MG	BA	3141	1/1	0.98	0.09	32,32,32,32	0
56	MG	DA	3115	1/1	0.98	0.12	44,44,44,44	0
56	MG	BA	3289	1/1	0.98	0.12	30,30,30,30	0
56	MG	BA	3752	1/1	0.98	0.09	54,54,54,54	0
56	MG	BA	3753	1/1	0.98	0.09	39,39,39,39	0
56	MG	BA	3076	1/1	0.98	0.10	17,17,17,17	0
56	MG	BA	3231	1/1	0.98	0.10	21,21,21,21	0
56	MG	BA	3756	1/1	0.98	0.05	53,53,53,53	0
56	MG	BA	3183	1/1	0.98	0.12	35,35,35,35	0
56	MG	BA	3233	1/1	0.98	0.04	26,26,26,26	0
56	MG	DA	3124	1/1	0.98	0.13	35,35,35,35	0
56	MG	BA	3077	1/1	0.98	0.13	27,27,27,27	0
56	MG	BN	3003	1/1	0.98	0.09	41,41,41,41	0
56	MG	BN	3004	1/1	0.98	0.15	37,37,37,37	0
56	MG	BA	3235	1/1	0.98	0.08	17,17,17,17	0
56	MG	BA	3236	1/1	0.98	0.05	30,30,30,30	0
56	MG	BA	3186	1/1	0.98	0.13	37,37,37,37	0
56	MG	CF	3001	1/1	0.98	0.09	31,31,31,31	0
56	MG	BA	3593	1/1	0.98	0.04	44,44,44,44	0
56	MG	BA	3078	1/1	0.98	0.04	11,11,11,11	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BP	201	1/1	0.98	0.16	29,29,29,29	0
56	MG	AA	3072	1/1	0.98	0.06	40,40,40,40	0
56	MG	BA	3109	1/1	0.98	0.13	20,20,20,20	0
56	MG	BA	3597	1/1	0.98	0.03	18,18,18,18	0
56	MG	DA	3139	1/1	0.98	0.04	35,35,35,35	0
56	MG	DA	3300	1/1	0.98	0.05	29,29,29,29	0
56	MG	BP	206	1/1	0.98	0.04	31,31,31,31	0
56	MG	BA	3052	1/1	0.98	0.10	15,15,15,15	0
56	MG	CQ	3001	1/1	0.98	0.05	56,56,56,56	0
56	MG	BQ	3002	1/1	0.98	0.08	24,24,24,24	0
56	MG	BA	3869	1/1	0.98	0.08	20,20,20,20	0
56	MG	BA	3081	1/1	0.98	0.04	21,21,21,21	0
56	MG	BA	3054	1/1	0.98	0.04	20,20,20,20	0
56	MG	BA	3771	1/1	0.98	0.13	29,29,29,29	0
56	MG	BA	3772	1/1	0.98	0.15	26,26,26,26	0
56	MG	BA	3150	1/1	0.98	0.06	42,42,42,42	0
56	MG	BA	3055	1/1	0.98	0.08	25,25,25,25	0
56	MG	BS	3001	1/1	0.98	0.08	39,39,39,39	0
56	MG	DA	3152	1/1	0.98	0.15	39,39,39,39	0
56	MG	BA	3775	1/1	0.98	0.12	35,35,35,35	0
56	MG	BA	3878	1/1	0.98	0.05	15,15,15,15	0
56	MG	BT	5001	1/1	0.98	0.10	56,56,56,56	0
56	MG	BA	3879	1/1	0.98	0.13	28,28,28,28	0
56	MG	DA	3485	1/1	0.98	0.05	31,31,31,31	0
56	MG	BA	3196	1/1	0.98	0.07	26,26,26,26	0
56	MG	BA	3247	1/1	0.98	0.07	35,35,35,35	0
56	MG	BA	3197	1/1	0.98	0.18	27,27,27,27	0
56	MG	DA	3003	1/1	0.98	0.13	24,24,24,24	0
56	MG	DA	3004	1/1	0.98	0.12	36,36,36,36	0
56	MG	BA	3198	1/1	0.98	0.14	34,34,34,34	0
56	MG	BU	205	1/1	0.98	0.05	42,42,42,42	0
56	MG	BA	3780	1/1	0.98	0.07	45,45,45,45	0
56	MG	DA	3009	1/1	0.98	0.07	39,39,39,39	0
56	MG	BA	3250	1/1	0.98	0.12	38,38,38,38	0
56	MG	DA	3168	1/1	0.98	0.04	28,28,28,28	0
56	MG	BA	3453	1/1	0.98	0.05	17,17,17,17	0
56	MG	BU	210	1/1	0.98	0.07	28,28,28,28	0
56	MG	DA	3670	1/1	0.98	0.07	51,51,51,51	0
56	MG	BV	201	1/1	0.98	0.09	32,32,32,32	0
56	MG	BV	202	1/1	0.98	0.03	23,23,23,23	0
56	MG	DA	3015	1/1	0.98	0.11	37,37,37,37	0
56	MG	BV	203	1/1	0.98	0.11	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3023	1/1	0.98	0.04	20,20,20,20	0
56	MG	BA	3057	1/1	0.98	0.04	39,39,39,39	0
56	MG	BA	3891	1/1	0.98	0.16	33,33,33,33	0
56	MG	BA	3892	1/1	0.98	0.07	28,28,28,28	0
56	MG	DA	3339	1/1	0.98	0.07	57,57,57,57	0
56	MG	BA	3893	1/1	0.98	0.10	26,26,26,26	0
56	MG	BA	3201	1/1	0.98	0.07	17,17,17,17	0
56	MG	BW	205	1/1	0.98	0.07	34,34,34,34	0
56	MG	DA	3182	1/1	0.98	0.11	33,33,33,33	0
56	MG	BA	3254	1/1	0.98	0.06	41,41,41,41	0
56	MG	BA	3315	1/1	0.98	0.04	39,39,39,39	0
56	MG	AA	3191	1/1	0.98	0.06	40,40,40,40	0
56	MG	BA	3697	1/1	0.98	0.10	35,35,35,35	0
56	MG	BA	3899	1/1	0.98	0.09	40,40,40,40	0
56	MG	BA	3256	1/1	0.98	0.05	39,39,39,39	0
56	MG	DA	3350	1/1	0.98	0.07	29,29,29,29	0
56	MG	BA	3059	1/1	0.98	0.05	36,36,36,36	0
56	MG	DA	3190	1/1	0.98	0.17	47,47,47,47	0
56	MG	BA	3060	1/1	0.98	0.10	39,39,39,39	0
56	MG	BA	3701	1/1	0.98	0.17	44,44,44,44	0
56	MG	BA	3025	1/1	0.98	0.08	23,23,23,23	0
56	MG	BA	3090	1/1	0.98	0.04	28,28,28,28	0
56	MG	DA	3036	1/1	0.98	0.04	34,34,34,34	0
56	MG	BA	3121	1/1	0.98	0.05	33,33,33,33	0
56	MG	BA	3123	1/1	0.98	0.20	28,28,28,28	0
56	MG	DA	3361	1/1	0.98	0.06	44,44,44,44	0
56	MG	BA	3467	1/1	0.98	0.07	27,27,27,27	0
56	MG	BB	3003	1/1	0.98	0.09	31,31,31,31	0
56	MG	BA	3394	1/1	0.98	0.08	20,20,20,20	0
56	MG	DA	3365	1/1	0.98	0.06	38,38,38,38	0
56	MG	BA	3091	1/1	0.98	0.04	30,30,30,30	0
56	MG	B1	101	1/1	0.98	0.21	40,40,40,40	0
56	MG	BA	3325	1/1	0.98	0.12	33,33,33,33	0
56	MG	BB	3007	1/1	0.98	0.12	56,56,56,56	0
56	MG	BA	3548	1/1	0.98	0.04	49,49,49,49	0
56	MG	BA	3040	1/1	0.98	0.09	25,25,25,25	0
56	MG	DA	3540	1/1	0.98	0.05	51,51,51,51	0
56	MG	BA	3712	1/1	0.98	0.14	32,32,32,32	0
56	MG	B5	101	1/1	0.98	0.16	32,32,32,32	0
56	MG	BA	3265	1/1	0.98	0.10	23,23,23,23	0
56	MG	B5	104	1/1	0.98	0.19	27,27,27,27	0
56	MG	BA	3329	1/1	0.98	0.07	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3063	1/1	0.98	0.14	41,41,41,41	0
56	MG	BA	3401	1/1	0.98	0.06	10,10,10,10	0
56	MG	BA	3026	1/1	0.98	0.05	42,42,42,42	0
56	MG	BA	3812	1/1	0.98	0.04	22,22,22,22	0
56	MG	AA	3173	1/1	0.98	0.04	43,43,43,43	0
56	MG	AA	3051	1/1	0.98	0.10	22,22,22,22	0
56	MG	BA	3270	1/1	0.98	0.04	28,28,28,28	0
56	MG	BA	3816	1/1	0.98	0.04	35,35,35,35	0
56	MG	BA	3335	1/1	0.98	0.09	33,33,33,33	0
56	MG	DA	3064	1/1	0.98	0.09	44,44,44,44	0
56	MG	BA	3336	1/1	0.98	0.13	43,43,43,43	0
56	MG	AA	3140	1/1	0.98	0.04	45,45,45,45	0
56	MG	BA	3820	1/1	0.98	0.07	30,30,30,30	0
56	MG	BA	3045	1/1	0.98	0.12	35,35,35,35	0
56	MG	BA	3046	1/1	0.98	0.06	30,30,30,30	0
56	MG	BA	3642	1/1	0.98	0.05	27,27,27,27	0
56	MG	BB	3028	1/1	0.98	0.04	42,42,42,42	0
56	MG	BA	3134	1/1	0.98	0.15	29,29,29,29	0
56	MG	BA	3728	1/1	0.98	0.06	36,36,36,36	0
56	MG	BD	301	1/1	0.98	0.06	31,31,31,31	0
56	MG	BD	302	1/1	0.98	0.18	39,39,39,39	0
56	MG	BA	3220	1/1	0.98	0.08	34,34,34,34	0
56	MG	BA	3646	1/1	0.98	0.06	46,46,46,46	0
56	MG	BA	3135	1/1	0.98	0.10	37,37,37,37	0
58	SF4	AD	501	8/8	0.98	0.04	50,60,65,68	0
58	SF4	CD	501	8/8	0.98	0.04	50,59,70,75	0
56	MG	BD	306	1/1	0.98	0.12	25,25,25,25	0
59	ZN	DY	501	1/1	0.98	0.04	81,81,81,81	0
56	MG	BD	307	1/1	0.98	0.09	30,30,30,30	0
59	ZN	D9	501	1/1	0.98	0.05	63,63,63,63	0
56	MG	BD	308	1/1	0.98	0.05	41,41,41,41	0
56	MG	CA	3018	1/1	0.98	0.13	46,46,46,46	0
56	MG	BP	202	1/1	0.99	0.08	27,27,27,27	0
56	MG	BA	3039	1/1	0.99	0.11	17,17,17,17	0
56	MG	BA	3598	1/1	0.99	0.06	40,40,40,40	0
56	MG	DA	3553	1/1	0.99	0.04	58,58,58,58	0
56	MG	BA	3014	1/1	0.99	0.03	21,21,21,21	0
56	MG	BY	504	1/1	0.99	0.14	39,39,39,39	0
56	MG	BA	3174	1/1	0.99	0.13	34,34,34,34	0
56	MG	DA	3494	1/1	0.99	0.03	39,39,39,39	0
56	MG	AA	3145	1/1	0.99	0.03	35,35,35,35	0
56	MG	BA	3475	1/1	0.99	0.12	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	BA	3538	1/1	0.99	0.10	25,25,25,25	0
56	MG	DA	3375	1/1	0.99	0.05	37,37,37,37	0
56	MG	DA	3376	1/1	0.99	0.03	27,27,27,27	0
56	MG	DA	3041	1/1	0.99	0.03	30,30,30,30	0
56	MG	CA	3022	1/1	0.99	0.02	33,33,33,33	0
56	MG	DA	3565	1/1	0.99	0.02	27,27,27,27	0
56	MG	DD	305	1/1	0.99	0.26	38,38,38,38	0
56	MG	AA	3001	1/1	0.99	0.10	35,35,35,35	0
56	MG	AA	3159	1/1	0.99	0.07	32,32,32,32	0
56	MG	B0	104	1/1	0.99	0.07	35,35,35,35	0
56	MG	DE	303	1/1	0.99	0.05	38,38,38,38	0
56	MG	BA	3478	1/1	0.99	0.04	27,27,27,27	0
56	MG	BA	3122	1/1	0.99	0.05	22,22,22,22	0
56	MG	BA	3886	1/1	0.99	0.10	37,37,37,37	0
56	MG	BF	305	1/1	0.99	0.12	28,28,28,28	0
56	MG	BR	203	1/1	0.99	0.10	29,29,29,29	0
56	MG	BA	3449	1/1	0.99	0.10	39,39,39,39	0
56	MG	DA	3388	1/1	0.99	0.03	32,32,32,32	0
56	MG	BA	3340	1/1	0.99	0.12	34,34,34,34	0
56	MG	B3	3001	1/1	0.99	0.03	23,23,23,23	0
56	MG	BA	3889	1/1	0.99	0.07	29,29,29,29	0
56	MG	DA	3055	1/1	0.99	0.05	33,33,33,33	0
56	MG	BA	3341	1/1	0.99	0.18	28,28,28,28	0
56	MG	BA	3644	1/1	0.99	0.05	18,18,18,18	0
56	MG	AA	3013	1/1	0.99	0.06	21,21,21,21	0
56	MG	DA	3166	1/1	0.99	0.06	39,39,39,39	0
56	MG	DA	3584	1/1	0.99	0.03	57,57,57,57	0
56	MG	BA	3075	1/1	0.99	0.07	22,22,22,22	0
56	MG	DA	3586	1/1	0.99	0.04	31,31,31,31	0
56	MG	AA	3022	1/1	0.99	0.03	35,35,35,35	0
56	MG	DA	3008	1/1	0.99	0.04	33,33,33,33	0
56	MG	BA	3162	1/1	0.99	0.09	26,26,26,26	0
56	MG	AA	3143	1/1	0.99	0.04	38,38,38,38	0
56	MG	BA	3127	1/1	0.99	0.16	33,33,33,33	0
56	MG	BA	3185	1/1	0.99	0.03	23,23,23,23	0
56	MG	BA	3788	1/1	0.99	0.05	25,25,25,25	0
56	MG	BU	209	1/1	0.99	0.09	24,24,24,24	0
56	MG	AA	3083	1/1	0.99	0.05	34,34,34,34	0
56	MG	BA	3034	1/1	0.99	0.04	20,20,20,20	0
56	MG	BA	3377	1/1	0.99	0.07	35,35,35,35	0
56	MG	BA	3792	1/1	0.99	0.05	47,47,47,47	0
56	MG	BA	3010	1/1	0.99	0.08	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
56	MG	DA	3293	1/1	0.99	0.05	34,34,34,34	0
56	MG	CA	3051	1/1	0.99	0.10	32,32,32,32	0
56	MG	AA	3171	1/1	0.99	0.07	46,46,46,46	0
56	MG	BA	3327	1/1	0.99	0.12	20,20,20,20	0
56	MG	BA	3012	1/1	0.99	0.04	31,31,31,31	0
56	MG	BA	3191	1/1	0.99	0.03	31,31,31,31	0
56	MG	DA	3672	1/1	0.99	0.03	43,43,43,43	0
56	MG	BD	312	1/1	0.99	0.11	27,27,27,27	0
56	MG	DA	3357	1/1	0.99	0.04	24,24,24,24	0
56	MG	BA	3013	1/1	0.99	0.11	25,25,25,25	0
56	MG	BA	3215	1/1	0.99	0.06	38,38,38,38	0
59	ZN	AN	501	1/1	0.99	0.05	62,62,62,62	0
59	ZN	BY	501	1/1	0.99	0.03	63,63,63,63	0
59	ZN	B4	501	1/1	0.99	0.04	75,75,75,75	0
56	MG	DA	3028	1/1	0.99	0.04	40,40,40,40	0
56	MG	BA	3053	1/1	0.99	0.10	28,28,28,28	0
56	MG	DA	3136	1/1	0.99	0.06	41,41,41,41	0
59	ZN	D5	103	1/1	0.99	0.04	51,51,51,51	0
59	ZN	D6	501	1/1	0.99	0.03	58,58,58,58	0
56	MG	BA	3413	1/1	0.99	0.06	30,30,30,30	0
56	MG	BA	3874	1/1	0.99	0.10	31,31,31,31	0
56	MG	DA	3194	1/1	0.99	0.03	40,40,40,40	0
59	ZN	B9	501	1/1	1.00	0.04	38,38,38,38	0
59	ZN	B5	103	1/1	1.00	0.03	40,40,40,40	0
59	ZN	B6	102	1/1	1.00	0.06	39,39,39,39	0

6.5 Other polymers (i)

There are no such residues in this entry.