



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2026 – 09:39 AM EDT

PDB ID : 8FC6 / pdb_00008fc6
Title : Crystal structure of the A2058-N6-dimethylated *Thermus thermophilus* 70S ribosome in complex with protein Y, hygromycin A, and telithromycin at 2.35Å resolution
Authors : Chen, C.-W.; Syroegin, E.A.; Svetlov, M.S.; Polikanov, Y.S.
Deposited on : 2022-12-01
Resolution : 2.35 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)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

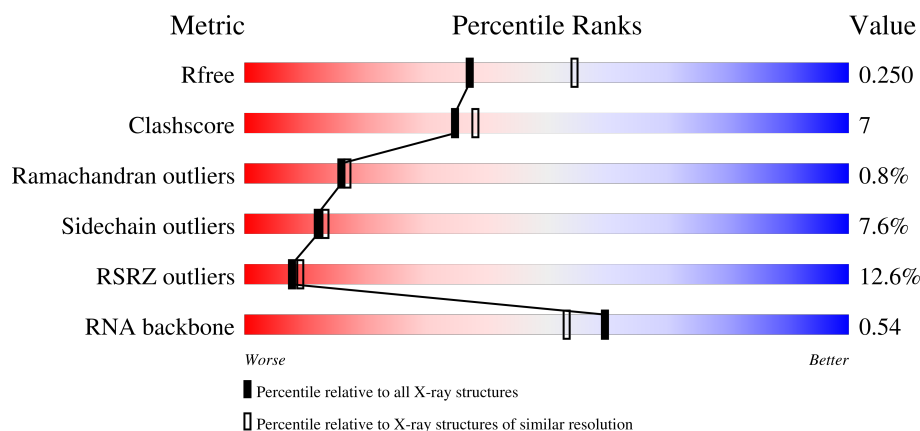
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)
RNA backbone	3983	1027 (2.66-2.06)

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 $\leq 5\%$. 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	1A	2915	6% 69% 24% 5%
1	2A	2915	7% 64% 28% 7%
2	1B	121	2% 78% 17% 5%

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Mol	Chain	Length	Quality of chain
2	2B	121	
3	1D	276	
3	2D	276	
4	1E	206	
4	2E	206	
5	1F	210	
5	2F	210	
6	1G	182	
6	2G	182	
7	1H	180	
7	2H	180	
8	1I	148	
8	2I	148	
9	1N	140	
9	2N	140	
10	1O	122	
10	2O	122	
11	1P	150	
11	2P	150	
12	1Q	141	
12	2Q	141	
13	1R	118	
13	2R	118	
14	1S	112	
14	2S	112	

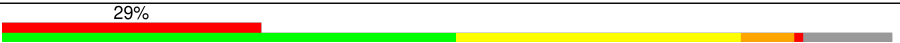
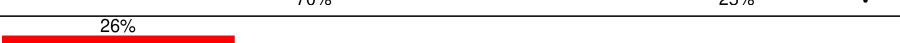
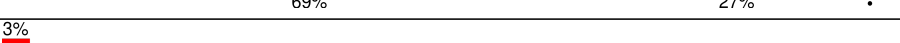
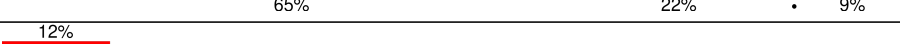
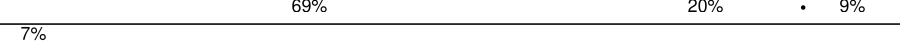
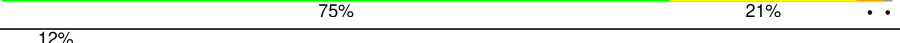
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Mol	Chain	Length	Quality of chain
15	1T	146	
15	2T	146	
16	1U	118	
16	2U	118	
17	1V	101	
17	2V	101	
18	1W	113	
18	2W	113	
19	1X	96	
19	2X	96	
20	1Y	110	
20	2Y	110	
21	1Z	206	
21	2Z	206	
22	10	85	
22	20	85	
23	11	98	
23	21	98	
24	12	72	
24	22	72	
25	13	60	
25	23	60	
26	14	71	
26	24	71	
27	15	60	

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Mol	Chain	Length	Quality of chain
27	25	60	
28	16	54	
28	26	54	
29	17	49	
29	27	49	
30	18	65	
30	28	65	
31	19	37	
31	29	37	
32	1a	1521	
32	2a	1521	
33	1b	256	
33	2b	256	
34	1c	239	
34	2c	239	
35	1d	209	
35	2d	209	
36	1e	162	
36	2e	162	
37	1f	101	
37	2f	101	
38	1g	156	
38	2g	156	
39	1h	138	
39	2h	138	

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Mol	Chain	Length	Quality of chain
40	1i	128	
40	2i	128	
41	1j	105	
41	2j	105	
42	1k	129	
42	2k	129	
43	1l	132	
43	2l	132	
44	1m	126	
44	2m	126	
45	1n	61	
45	2n	61	
46	1o	89	
46	2o	89	
47	1p	88	
47	2p	88	
48	1q	105	
48	2q	105	
49	1r	88	
49	2r	88	
50	1s	93	
50	2s	93	
51	1t	106	
51	2t	106	
52	1u	27	

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Mol	Chain	Length	Quality of chain
52	2u	27	
53	1y	113	
53	2y	113	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
54	MG	1A	4012	-	-	-	X
54	MG	1a	3039	-	-	-	X
54	MG	1a	3081	-	-	-	X
54	MG	1a	3099	-	-	-	X
54	MG	2A	3286	-	-	-	X
54	MG	2A	3715	-	-	-	X
54	MG	2a	3020	-	-	-	X
54	MG	2a	3047	-	-	-	X

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 298008 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 23S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1A	2872	Total	C	N	O	P	0	0	0
			61871	27542	11574	19884	2871			
1	2A	2867	Total	C	N	O	P	0	0	0
			61760	27493	11552	19850	2865			

- Molecule 2 is a RNA chain called 5S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	1B	120	Total	C	N	O	P	0	0	0
			2572	1145	476	832	119			
2	2B	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	1D	275	Total	C	N	O	S	0	0	0
			2131	1346	422	360	3			
3	2D	275	Total	C	N	O	S	0	0	0
			2136	1349	423	361	3			

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	1E	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			
4	2E	204	Total	C	N	O	S	0	0	0
			1559	985	298	270	6			

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	1F	203	Total	C	N	O	S	0	0	1
			1584	1009	298	275	2			
5	2F	203	Total	C	N	O	S	0	0	1
			1580	1007	297	274	2			

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	1G	181	Total	C	N	O	S	0	0	0
			1426	916	253	253	4			
6	2G	181	Total	C	N	O	S	0	0	0
			1424	912	259	249	4			

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	1H	174	Total	C	N	O	S	0	0	0
			1330	845	248	236	1			
7	2H	173	Total	C	N	O	S	0	0	0
			1324	842	247	234	1			

- Molecule 8 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	1I	147	Total	C	N	O	S	0	0	0
			1094	699	191	203	1			
8	2I	146	Total	C	N	O	S	0	0	0
			1076	687	186	202	1			

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	1N	140	Total	C	N	O	S	0	0	0
			1121	722	208	187	4			
9	2N	140	Total	C	N	O	S	0	0	0
			1117	719	207	187	4			

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	1O	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	2O	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	1P	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			
11	2P	149	Total	C	N	O	S	0	0	0
			1135	706	230	196	3			

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	1Q	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			
12	2Q	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	1R	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			
13	2R	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	1S	110	Total	C	N	O	0	0	0
			877	553	175	149			
14	2S	110	Total	C	N	O	0	0	0
			870	549	173	148			

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	1T	131	Total	C	N	O	S	0	0	0
			1091	680	225	185	1			
15	2T	131	Total	C	N	O	S	0	0	0
			1083	675	224	183	1			

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	1U	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			
16	2U	116	Total	C	N	O	S	0	0	0
			959	608	201	149	1			

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	1V	101	Total	C	N	O	S	0	0	0
			775	498	141	135	1			
17	2V	101	Total	C	N	O	S	0	0	0
			771	495	140	135	1			

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	1W	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			
18	2W	112	Total	C	N	O	S	0	0	0
			886	557	174	153	2			

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	1X	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			
19	2X	95	Total	C	N	O	S	0	0	0
			750	488	135	126	1			

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	1Y	107	Total	C	N	O	S	0	0	0
			810	520	153	131	6			
20	2Y	107	Total	C	N	O	S	0	0	0
			810	519	153	132	6			

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	1Z	203	Total	C	N	O	S	0	0	0
			1587	1011	282	292	2			
21	2Z	201	Total	C	N	O	S	0	0	0
			1557	995	274	286	2			

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	10	77	Total	C	N	O	S	0	0	0
			608	375	129	103	1			
22	20	77	Total	C	N	O	S	0	0	0
			608	375	129	103	1			

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	11	97	Total	C	N	O	S	0	0	0
			754	475	148	130	1			
23	21	97	Total	C	N	O	S	0	0	0
			759	478	149	131	1			

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	12	70	Total	C	N	O	S	0	0	0
			588	365	118	103	2			
24	22	70	Total	C	N	O	S	0	0	0
			592	368	119	103	2			

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
25	13	59	Total	C	N	O	0	0	0
			469	298	90	81			
25	23	59	Total	C	N	O	0	0	0
			464	296	90	78			

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	14	69	Total	C	N	O	S	0	0	0
			546	346	96	99	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	24	69	Total	C	N	O	S	0	0	0
			536	342	98	91	5			

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	15	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			
27	25	59	Total	C	N	O	S	0	0	0
			455	285	89	76	5			

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	16	53	Total	C	N	O	S	0	0	0
			453	281	91	77	4			
28	26	53	Total	C	N	O	S	0	0	0
			449	279	91	75	4			

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	17	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			
29	27	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	18	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			
30	28	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	19	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			
31	29	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 32 is a RNA chain called 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	1a	1500	Total	C	N	O	P	0	0	0
			32246	14358	5975	10413	1500			
32	2a	1504	Total	C	N	O	P	0	0	0
			32331	14396	5990	10441	1504			

- Molecule 33 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	1b	231	Total	C	N	O	S	0	0	0
			1842	1175	330	332	5			
33	2b	231	Total	C	N	O	S	0	0	0
			1825	1167	326	327	5			

- Molecule 34 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	1c	206	Total	C	N	O	S	0	0	0
			1558	979	305	273	1			
34	2c	206	Total	C	N	O	S	0	0	0
			1542	968	300	273	1			

- Molecule 35 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	1d	208	Total	C	N	O	S	0	0	0
			1665	1043	329	286	7			
35	2d	208	Total	C	N	O	S	0	0	0
			1668	1047	330	284	7			

- Molecule 36 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	1e	148	Total	C	N	O	S	0	0	0
			1133	716	214	199	4			
36	2e	148	Total	C	N	O	S	0	0	0
			1133	716	214	199	4			

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	1f	100	Total	C	N	O	S	0	0	0
			814	516	144	151	3			
37	2f	100	Total	C	N	O	S	0	0	0
			816	516	146	151	3			

- Molecule 38 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	1g	155	Total	C	N	O	S	0	0	0
			1235	769	244	216	6			
38	2g	155	Total	C	N	O	S	0	0	0
			1229	766	241	216	6			

- Molecule 39 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	1h	137	Total	C	N	O	S	0	0	0
			1098	694	210	192	2			
39	2h	137	Total	C	N	O	S	0	0	0
			1088	689	206	191	2			

- Molecule 40 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
40	1i	127	Total	C	N	O	0	0	0
			986	625	193	168			
40	2i	126	Total	C	N	O	0	0	0
			966	613	186	167			

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
41	1j	97	Total	C	N	O	0	0	0
			719	446	142	131			
41	2j	96	Total	C	N	O	0	0	0
			710	442	137	131			

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	1k	114	Total	C	N	O	S	0	0	0
			834	520	156	155	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	2k	114	Total	C	N	O	S	0	0	0
			833	519	156	155	3			

- Molecule 43 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	1l	122	Total	C	N	O	S	0	0	0
			932	586	185	159	2			
43	2l	122	Total	C	N	O	S	0	0	0
			932	586	185	159	2			

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	1m	116	Total	C	N	O	S	0	0	0
			914	564	189	159	2			
44	2m	114	Total	C	N	O	S	0	0	0
			895	550	186	157	2			

- Molecule 45 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	1n	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			
45	2n	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			

- Molecule 46 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	1o	88	Total	C	N	O	S	0	0	0
			728	456	144	126	2			
46	2o	88	Total	C	N	O	S	0	0	0
			728	456	144	126	2			

- Molecule 47 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	1p	82	Total	C	N	O	S	0	0	0
			681	433	134	113	1			
47	2p	82	Total	C	N	O	S	0	0	0
			677	430	133	113	1			

- Molecule 48 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	1q	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			
48	2q	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	1r	68	Total	C	N	O		0	0	0
			555	355	108	92				
49	2r	68	Total	C	N	O		0	0	0
			555	355	108	92				

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	1s	83	Total	C	N	O	S	0	0	0
			648	415	120	111	2			
50	2s	83	Total	C	N	O	S	0	0	0
			645	410	118	115	2			

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	1t	96	Total	C	N	O	S	0	0	0
			732	449	157	124	2			
51	2t	98	Total	C	N	O	S	0	0	0
			733	451	154	126	2			

- Molecule 52 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	1u	23	Total	C	N	O		0	0	0
			199	122	48	29				
52	2u	23	Total	C	N	O		0	0	0
			199	122	48	29				

- Molecule 53 is a protein called Ribosome-associated inhibitor A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	1y	97	Total	C	N	O	S	0	0	0
			764	478	144	139	3			
53	2y	96	Total	C	N	O	S	0	0	0
			749	468	141	137	3			

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
54	1A	1019	Total	Mg	0	0
			1019	1019		
54	1B	30	Total	Mg	0	0
			30	30		
54	1D	15	Total	Mg	0	0
			15	15		
54	1E	9	Total	Mg	0	0
			9	9		
54	1F	19	Total	Mg	0	0
			19	19		
54	1G	4	Total	Mg	0	0
			4	4		
54	1H	2	Total	Mg	0	0
			2	2		
54	1N	4	Total	Mg	0	0
			4	4		
54	1O	1	Total	Mg	0	0
			1	1		
54	1P	7	Total	Mg	0	0
			7	7		
54	1Q	5	Total	Mg	0	0
			5	5		
54	1R	4	Total	Mg	0	0
			4	4		
54	1T	5	Total	Mg	0	0
			5	5		
54	1U	8	Total	Mg	0	0
			8	8		
54	1V	7	Total	Mg	0	0
			7	7		
54	1W	3	Total	Mg	0	0
			3	3		
54	1X	1	Total	Mg	0	0
			1	1		
54	1Z	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
54	10	7	Total 7	Mg 7	0	0
54	11	4	Total 4	Mg 4	0	0
54	13	4	Total 4	Mg 4	0	0
54	14	1	Total 1	Mg 1	0	0
54	15	9	Total 9	Mg 9	0	0
54	17	7	Total 7	Mg 7	0	0
54	18	4	Total 4	Mg 4	0	0
54	19	2	Total 2	Mg 2	0	0
54	1a	278	Total 278	Mg 278	0	0
54	1b	1	Total 1	Mg 1	0	0
54	1d	4	Total 4	Mg 4	0	0
54	1e	3	Total 3	Mg 3	0	0
54	1f	1	Total 1	Mg 1	0	0
54	1g	2	Total 2	Mg 2	0	0
54	1h	2	Total 2	Mg 2	0	0
54	1i	1	Total 1	Mg 1	0	0
54	1k	1	Total 1	Mg 1	0	0
54	1l	2	Total 2	Mg 2	0	0
54	1m	1	Total 1	Mg 1	0	0
54	1n	2	Total 2	Mg 2	0	0
54	1o	2	Total 2	Mg 2	0	0

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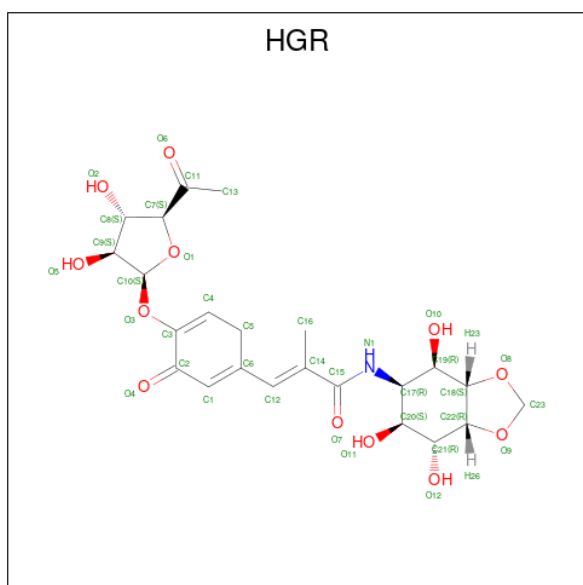
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
54	1r	1	Total 1	Mg 1	0	0
54	1t	1	Total 1	Mg 1	0	0
54	1y	3	Total 3	Mg 3	0	0
54	2A	742	Total 742	Mg 742	0	0
54	2B	17	Total 17	Mg 17	0	0
54	2D	10	Total 10	Mg 10	0	0
54	2E	6	Total 6	Mg 6	0	0
54	2F	4	Total 4	Mg 4	0	0
54	2G	2	Total 2	Mg 2	0	0
54	2I	1	Total 1	Mg 1	0	0
54	2N	1	Total 1	Mg 1	0	0
54	2O	1	Total 1	Mg 1	0	0
54	2P	4	Total 4	Mg 4	0	0
54	2Q	2	Total 2	Mg 2	0	0
54	2R	2	Total 2	Mg 2	0	0
54	2T	4	Total 4	Mg 4	0	0
54	2V	3	Total 3	Mg 3	0	0
54	2W	4	Total 4	Mg 4	0	0
54	20	1	Total 1	Mg 1	0	0
54	21	1	Total 1	Mg 1	0	0
54	23	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
54	25	2	Total Mg 2 2	0	0
54	27	1	Total Mg 1 1	0	0
54	28	2	Total Mg 2 2	0	0
54	2a	192	Total Mg 192 192	0	0
54	2e	1	Total Mg 1 1	0	0
54	2f	1	Total Mg 1 1	0	0
54	2j	1	Total Mg 1 1	0	0
54	2k	1	Total Mg 1 1	0	0
54	2p	1	Total Mg 1 1	0	0
54	2t	1	Total Mg 1 1	0	0

- Molecule 55 is Hygromycin A (CCD ID: HGR) (formula: $C_{23}H_{29}NO_{12}$) (labeled as "Ligand of Interest" by depositor).



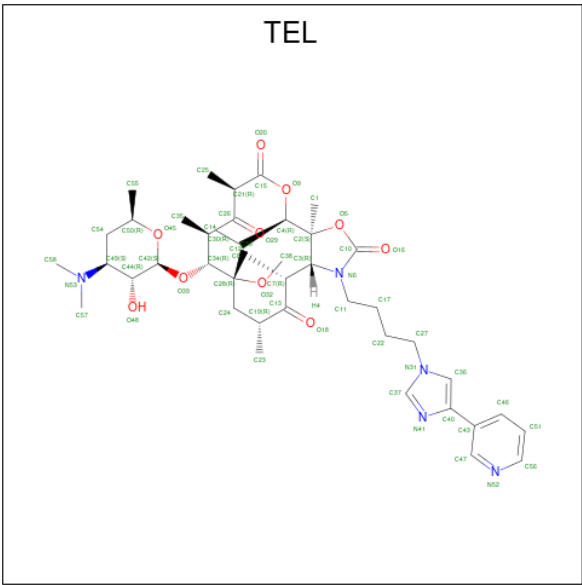
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
55	1A	1	Total	C	N	O	0	0
			36	23	1	12		

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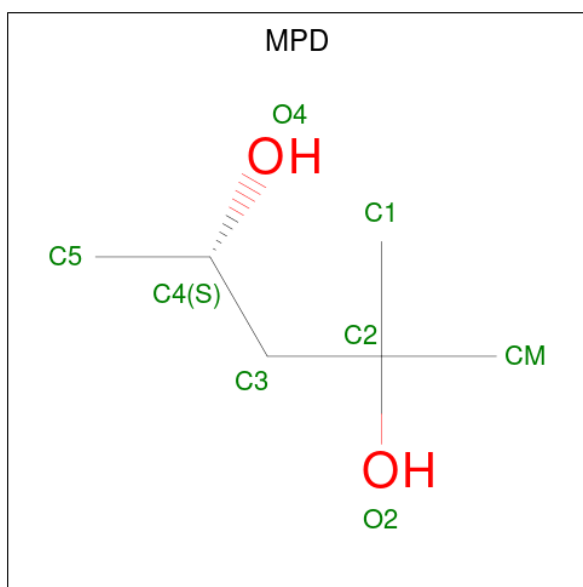
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
55	2A	1	Total	C	N	O	0	0
			36	23	1	12		

- Molecule 56 is TELITHROMYCIN (CCD ID: TEL) (formula: C₄₃H₆₅N₅O₁₀) (labeled as "Ligand of Interest" by depositor).



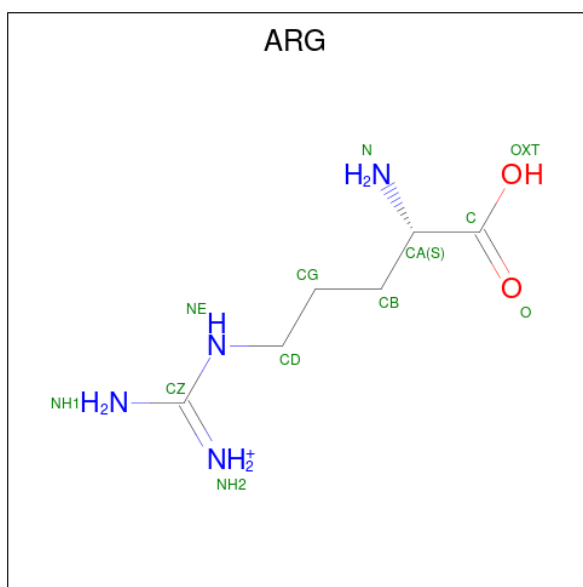
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
56	1A	1	Total	C	N	O	0	0
			58	43	5	10		
56	2A	1	Total	C	N	O	0	0
			58	43	5	10		

- Molecule 57 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
57	1A	1	Total	C	O	0	0
			8	6	2		
57	1T	1	Total	C	O	0	0
			8	6	2		
57	18	1	Total	C	O	0	0
			8	6	2		
57	1a	1	Total	C	O	0	0
			8	6	2		
57	2A	1	Total	C	O	0	0
			8	6	2		
57	2A	1	Total	C	O	0	0
			8	6	2		
57	2A	1	Total	C	O	0	0
			8	6	2		

- Molecule 58 is ARGinine (CCD ID: ARG) (formula: $C_6H_{15}N_4O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
58	1B	1	Total	C	N	O	0	0
			12	6	4	2		
58	1F	1	Total	C	N	O	0	0
			12	6	4	2		

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

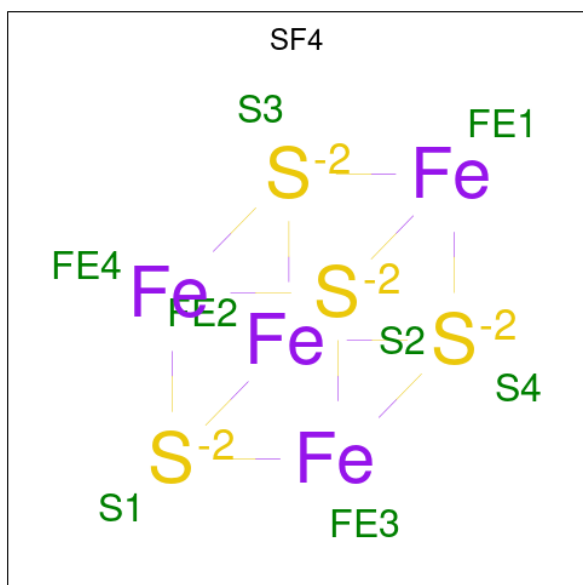
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	1Y	1	Total	Zn	0	0
			1	1		
59	14	1	Total	Zn	0	0
			1	1		
59	15	1	Total	Zn	0	0
			1	1		
59	16	1	Total	Zn	0	0
			1	1		
59	19	1	Total	Zn	0	0
			1	1		
59	1n	1	Total	Zn	0	0
			1	1		
59	2Y	1	Total	Zn	0	0
			1	1		
59	24	1	Total	Zn	0	0
			1	1		
59	25	1	Total	Zn	0	0
			1	1		
59	26	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	29	1	Total	Zn	0	0
			1	1		
59	2n	1	Total	Zn	0	0
			1	1		

- Molecule 60 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
60	1d	1	Total	Fe	S	0	0
			8	4	4		
60	2d	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 61 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	1A	4030	Total	O	0	0
			4030	4030		
61	1B	101	Total	O	0	0
			101	101		
61	1D	118	Total	O	0	0
			118	118		
61	1E	76	Total	O	0	0
			76	76		
61	1F	67	Total	O	0	0
			67	67		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	1G	17	Total	O	0	0
			17	17		
61	1H	16	Total	O	0	0
			16	16		
61	1I	7	Total	O	0	0
			7	7		
61	1N	56	Total	O	0	0
			56	56		
61	1O	22	Total	O	0	0
			22	22		
61	1P	59	Total	O	0	0
			59	59		
61	1Q	39	Total	O	0	0
			39	39		
61	1R	36	Total	O	0	0
			36	36		
61	1S	13	Total	O	0	0
			13	13		
61	1T	36	Total	O	0	0
			36	36		
61	1U	50	Total	O	0	0
			50	50		
61	1V	34	Total	O	0	0
			34	34		
61	1W	26	Total	O	0	0
			26	26		
61	1X	26	Total	O	0	0
			26	26		
61	1Y	15	Total	O	0	0
			15	15		
61	1Z	13	Total	O	0	0
			13	13		
61	10	23	Total	O	0	0
			23	23		
61	11	24	Total	O	0	0
			24	24		
61	12	13	Total	O	0	0
			13	13		
61	13	27	Total	O	0	0
			27	27		
61	14	2	Total	O	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	15	23	Total 23	O 23	0	0
61	16	15	Total 15	O 15	0	0
61	17	16	Total 16	O 16	0	0
61	18	27	Total 27	O 27	0	0
61	19	7	Total 7	O 7	0	0
61	1a	483	Total 483	O 483	0	0
61	1b	1	Total 1	O 1	0	0
61	1d	9	Total 9	O 9	0	0
61	1e	6	Total 6	O 6	0	0
61	1f	2	Total 2	O 2	0	0
61	1h	1	Total 1	O 1	0	0
61	1j	1	Total 1	O 1	0	0
61	1l	3	Total 3	O 3	0	0
61	1m	1	Total 1	O 1	0	0
61	1o	2	Total 2	O 2	0	0
61	1p	1	Total 1	O 1	0	0
61	1u	1	Total 1	O 1	0	0
61	1y	3	Total 3	O 3	0	0
61	2A	2427	Total 2427	O 2427	0	0
61	2B	56	Total 56	O 56	0	0
61	2D	60	Total 60	O 60	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	2E	30	Total 30	O 30	0	0
61	2F	26	Total 26	O 26	0	0
61	2G	3	Total 3	O 3	0	0
61	2H	2	Total 2	O 2	0	0
61	2I	4	Total 4	O 4	0	0
61	2N	5	Total 5	O 5	0	0
61	2O	24	Total 24	O 24	0	0
61	2P	30	Total 30	O 30	0	0
61	2Q	18	Total 18	O 18	0	0
61	2R	18	Total 18	O 18	0	0
61	2S	4	Total 4	O 4	0	0
61	2T	9	Total 9	O 9	0	0
61	2U	14	Total 14	O 14	0	0
61	2V	4	Total 4	O 4	0	0
61	2W	18	Total 18	O 18	0	0
61	2X	5	Total 5	O 5	0	0
61	2Y	3	Total 3	O 3	0	0
61	2Z	9	Total 9	O 9	0	0
61	20	13	Total 13	O 13	0	0
61	21	21	Total 21	O 21	0	0
61	22	2	Total 2	O 2	0	0

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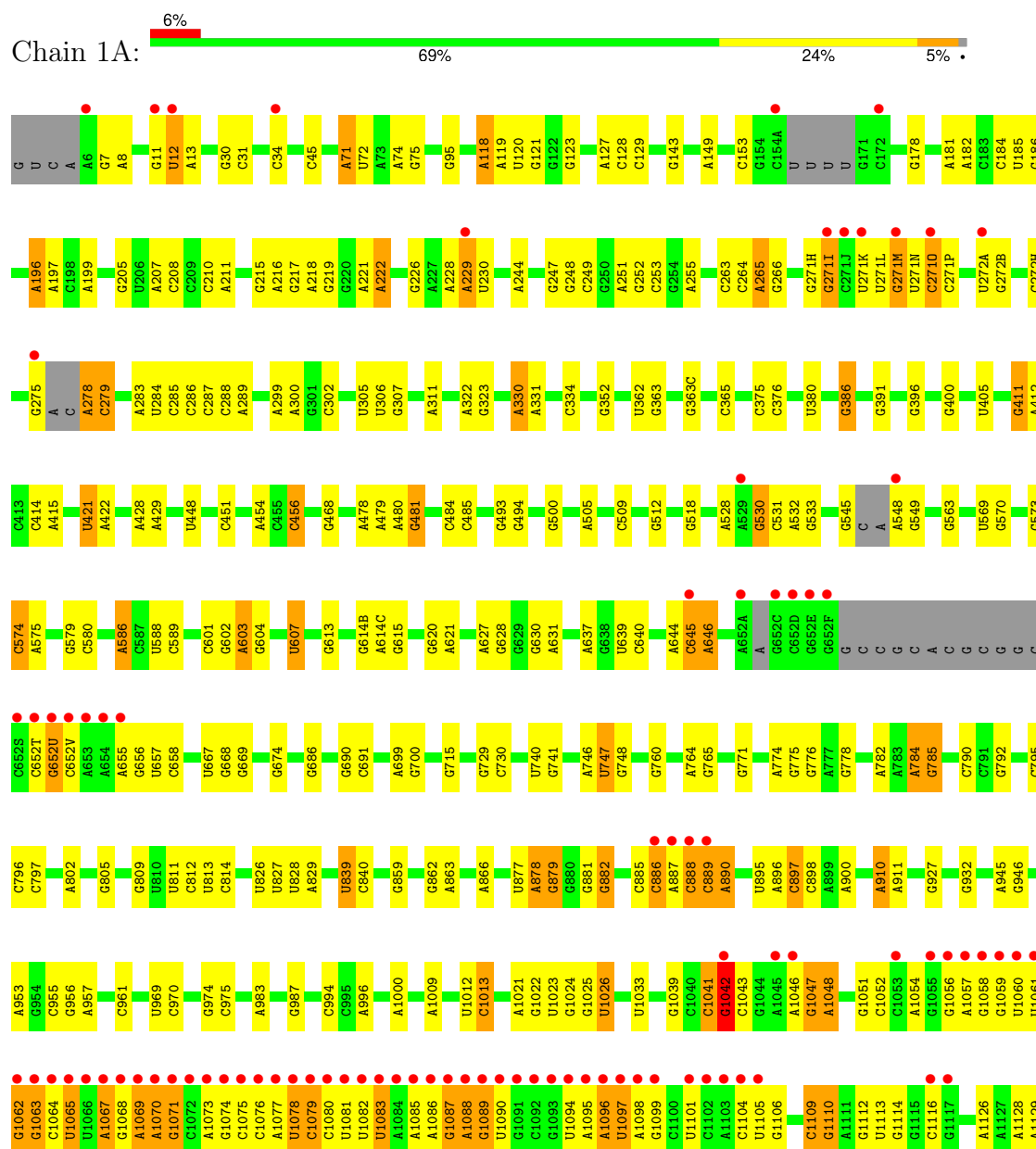
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	23	2	Total	O	0	0
			2	2		
61	25	9	Total	O	0	0
			9	9		
61	26	6	Total	O	0	0
			6	6		
61	27	9	Total	O	0	0
			9	9		
61	28	13	Total	O	0	0
			13	13		
61	29	1	Total	O	0	0
			1	1		
61	2a	428	Total	O	0	0
			428	428		
61	2d	6	Total	O	0	0
			6	6		
61	2e	1	Total	O	0	0
			1	1		
61	2f	2	Total	O	0	0
			2	2		
61	2j	2	Total	O	0	0
			2	2		
61	2l	3	Total	O	0	0
			3	3		
61	2m	1	Total	O	0	0
			1	1		
61	2n	1	Total	O	0	0
			1	1		
61	2o	2	Total	O	0	0
			2	2		
61	2p	2	Total	O	0	0
			2	2		
61	2q	1	Total	O	0	0
			1	1		
61	2r	4	Total	O	0	0
			4	4		
61	2t	2	Total	O	0	0
			2	2		
61	2y	3	Total	O	0	0
			3	3		

3 Residue-property plots

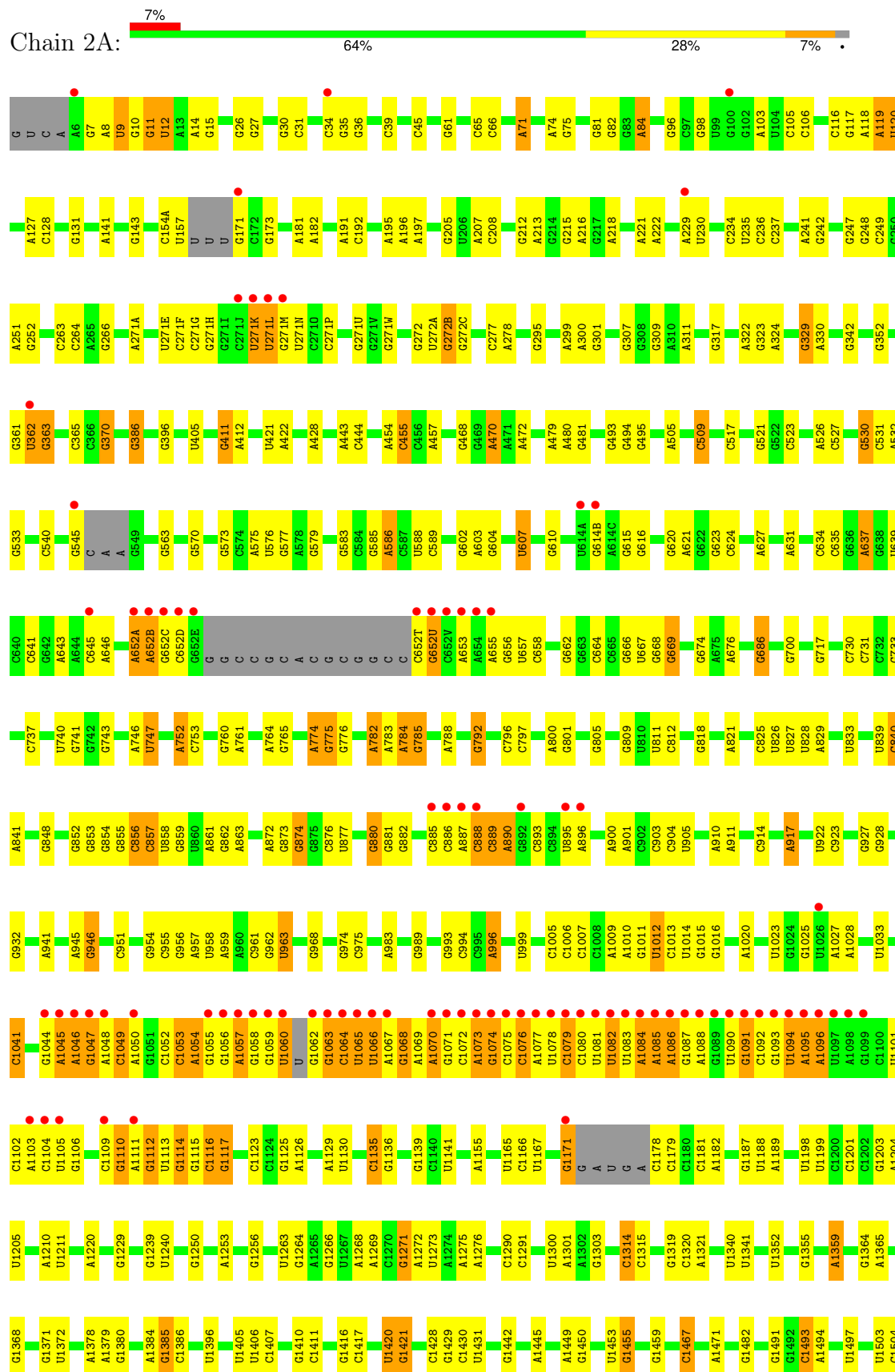
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

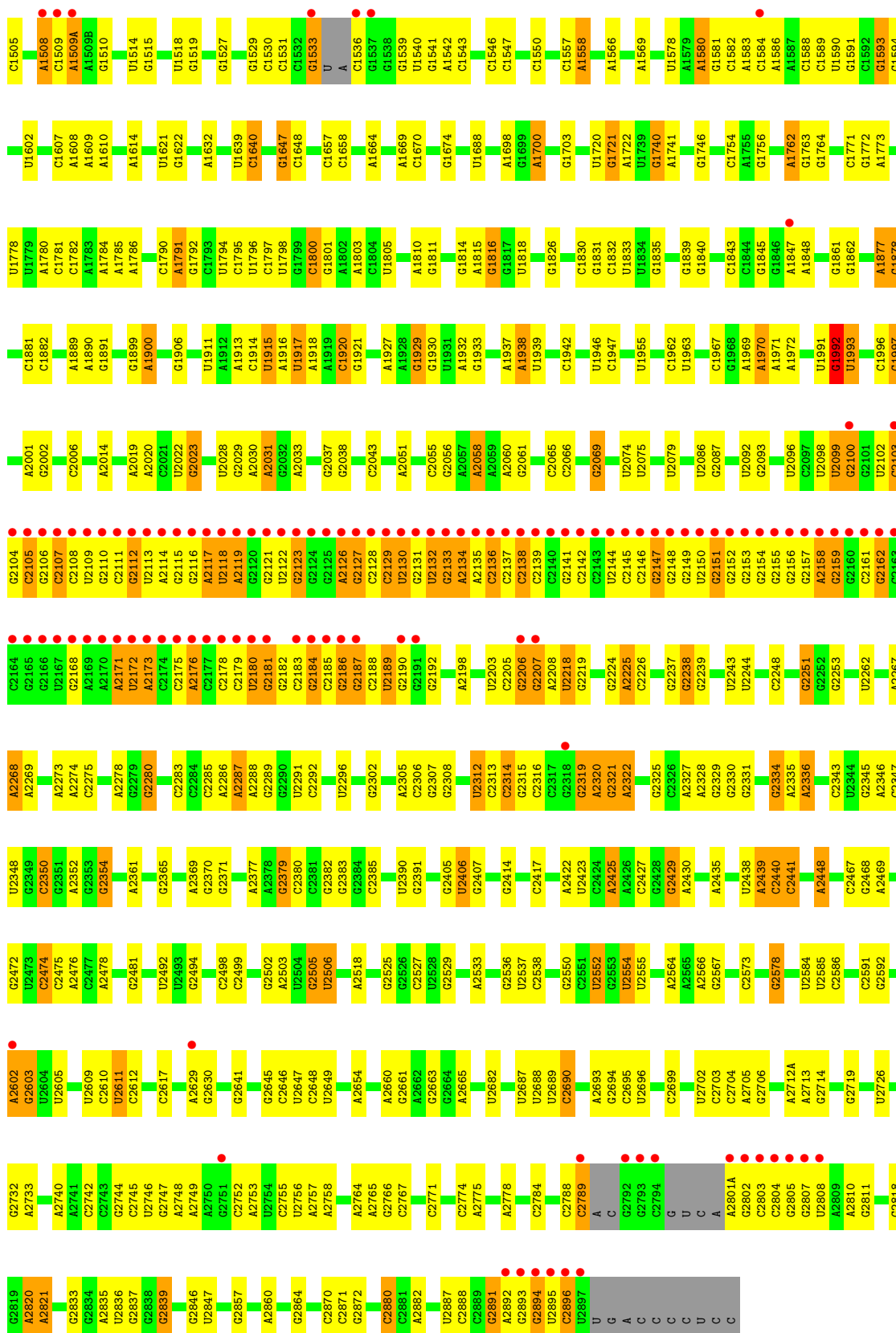
• Molecule 1: 23S Ribosomal RNA

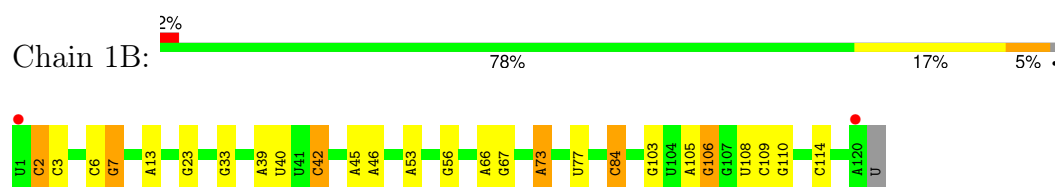




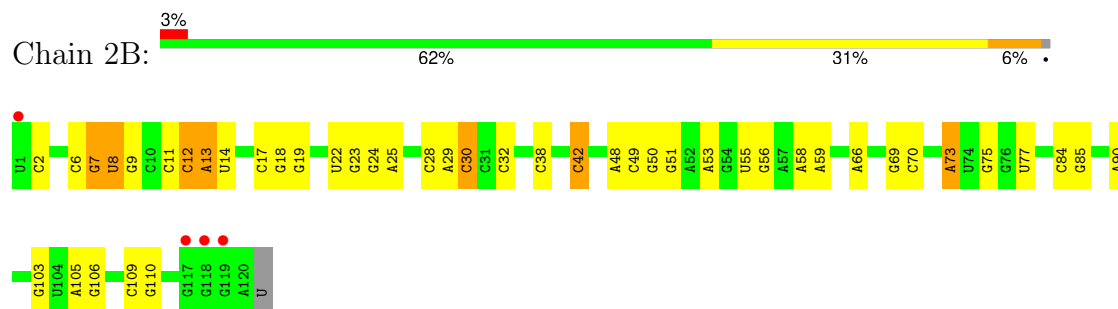
- Molecule 1: 23S Ribosomal RNA



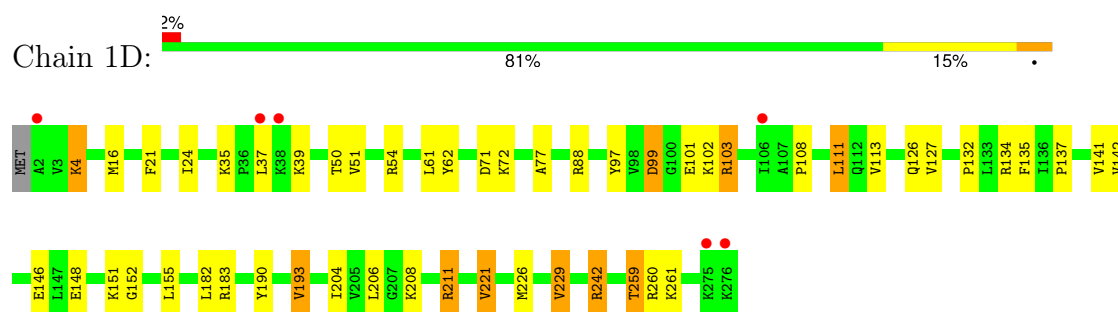




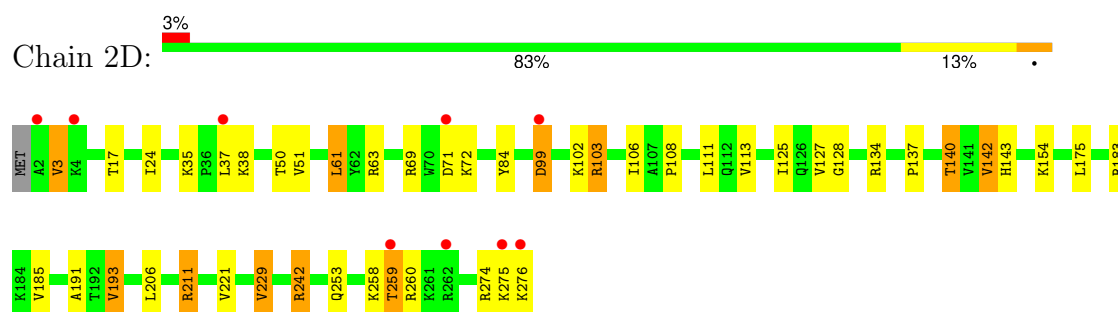
- Molecule 2: 5S Ribosomal RNA



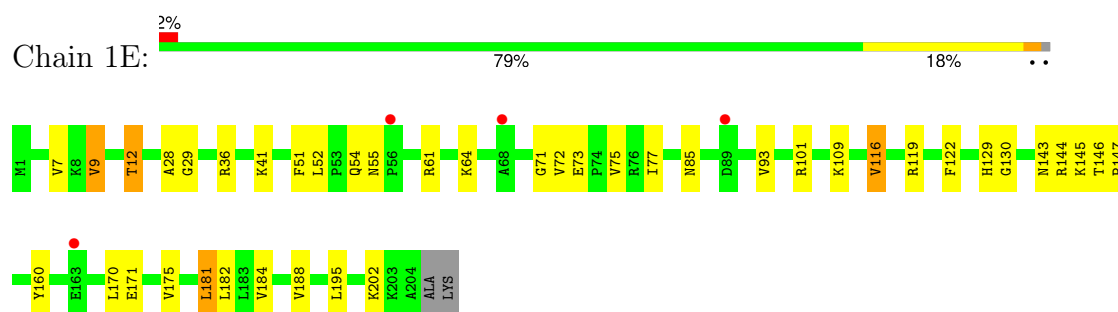
- Molecule 3: 50S ribosomal protein L2



- Molecule 3: 50S ribosomal protein L2

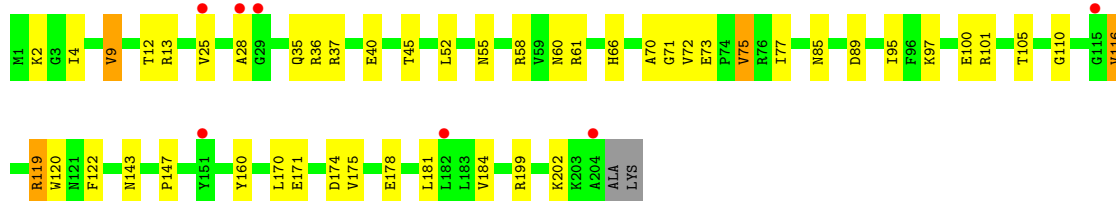


- Molecule 4: 50S ribosomal protein L3



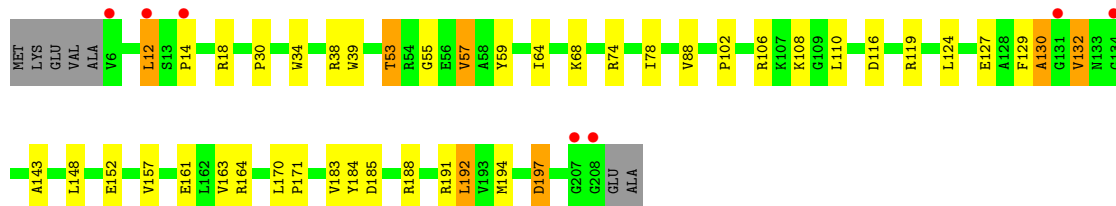
- Molecule 4: 50S ribosomal protein L3

Chain 2E: 



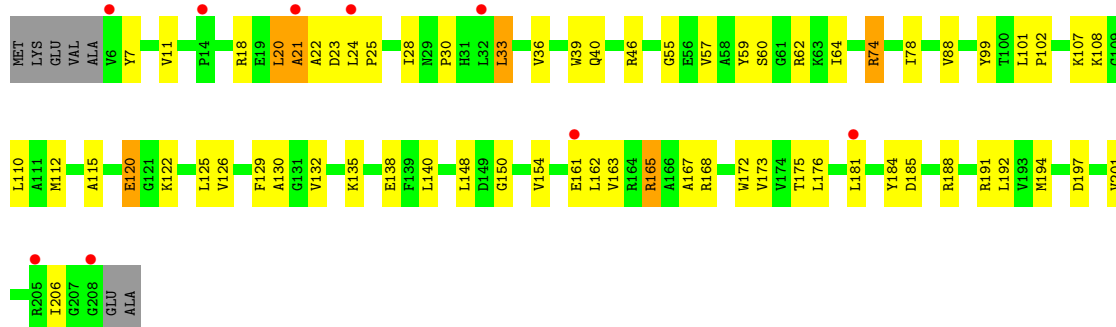
- Molecule 5: 50S ribosomal protein L4

Chain 1F: 



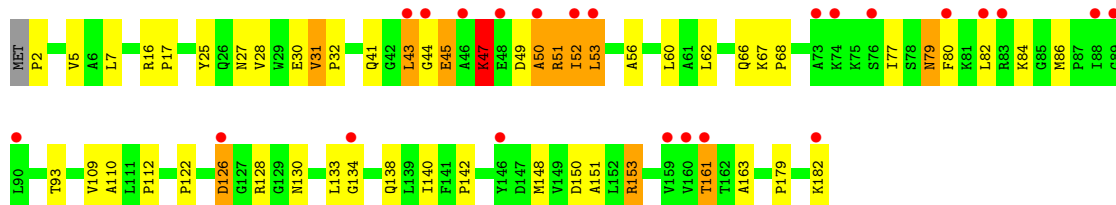
- Molecule 5: 50S ribosomal protein L4

Chain 2F: 



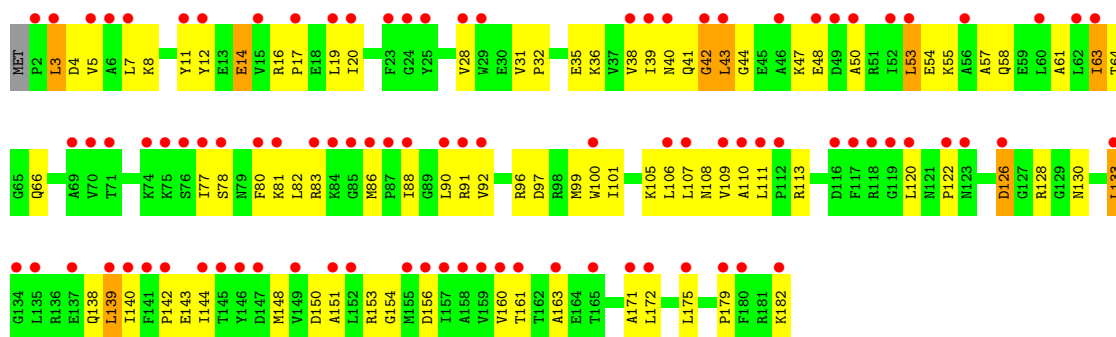
- Molecule 6: 50S ribosomal protein L5

Chain 1G: 

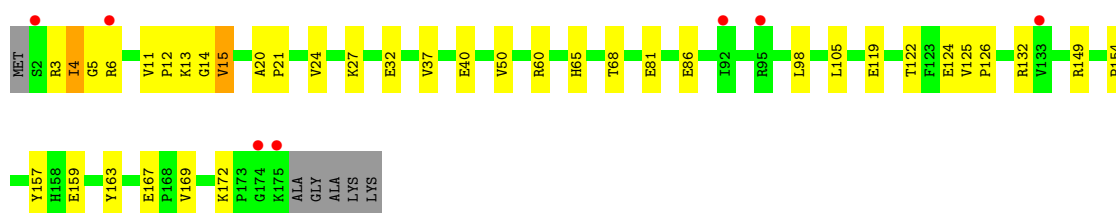
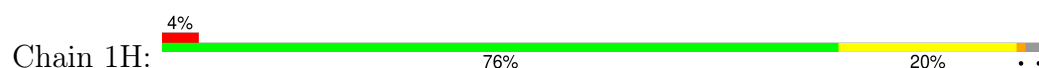


- Molecule 6: 50S ribosomal protein L5

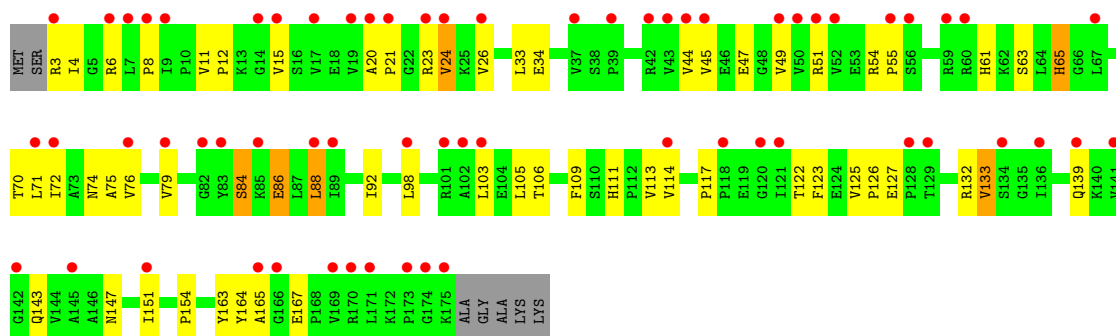
Chain 2G: 



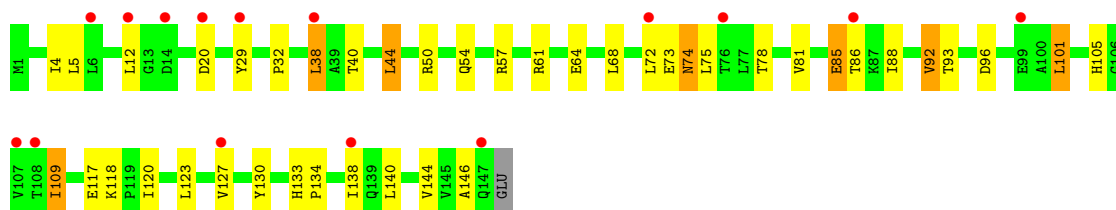
• Molecule 7: 50S ribosomal protein L6



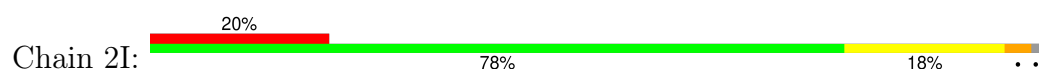
• Molecule 7: 50S ribosomal protein L6

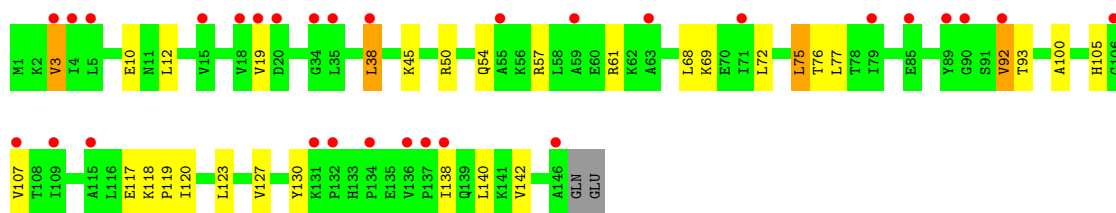


• Molecule 8: 50S ribosomal protein L9

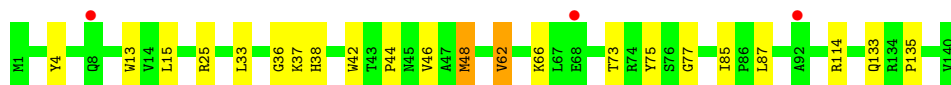
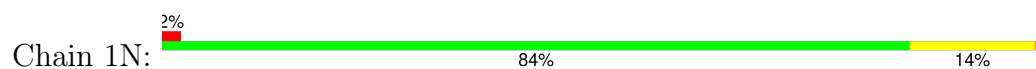


• Molecule 8: 50S ribosomal protein L9

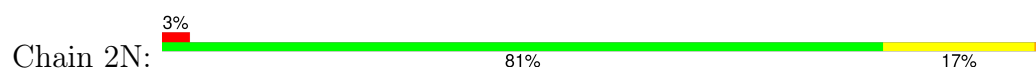




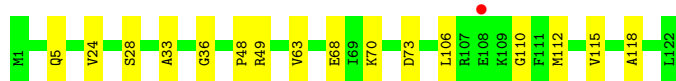
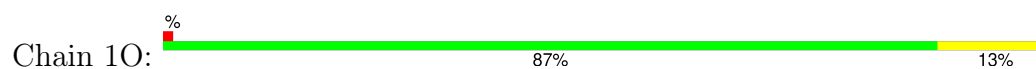
• Molecule 9: 50S ribosomal protein L13



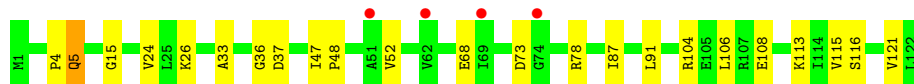
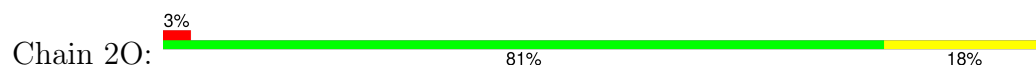
• Molecule 9: 50S ribosomal protein L13



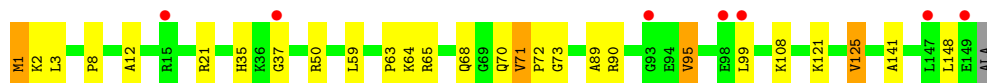
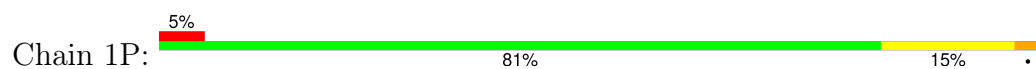
• Molecule 10: 50S ribosomal protein L14



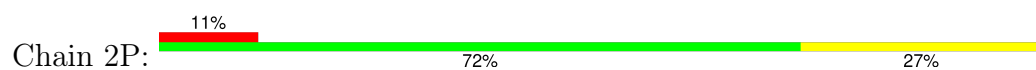
• Molecule 10: 50S ribosomal protein L14

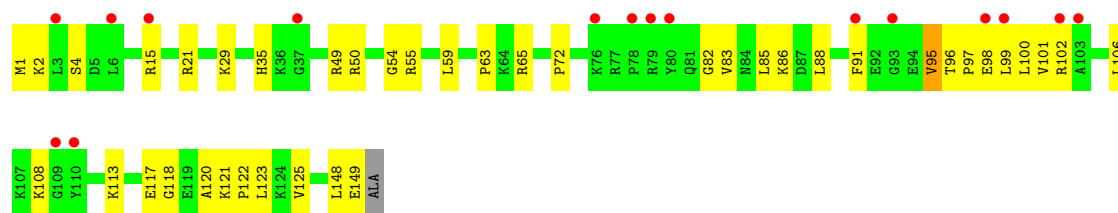


• Molecule 11: 50S ribosomal protein L15



• Molecule 11: 50S ribosomal protein L15

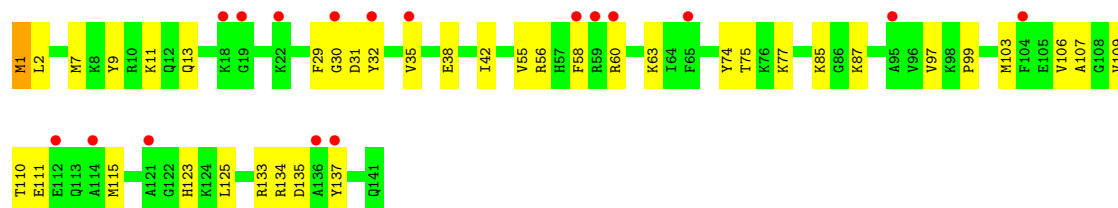
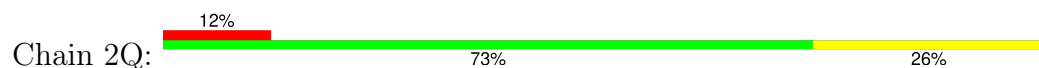




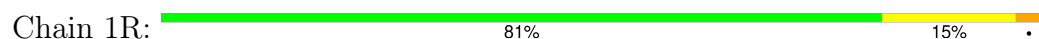
- Molecule 12: 50S ribosomal protein L16



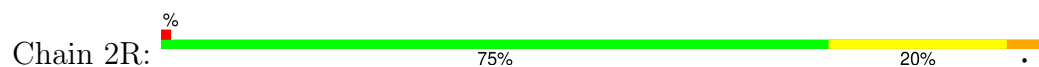
- Molecule 12: 50S ribosomal protein L16



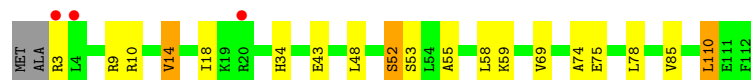
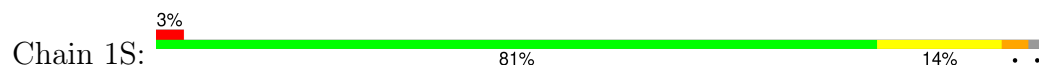
- Molecule 13: 50S ribosomal protein L17



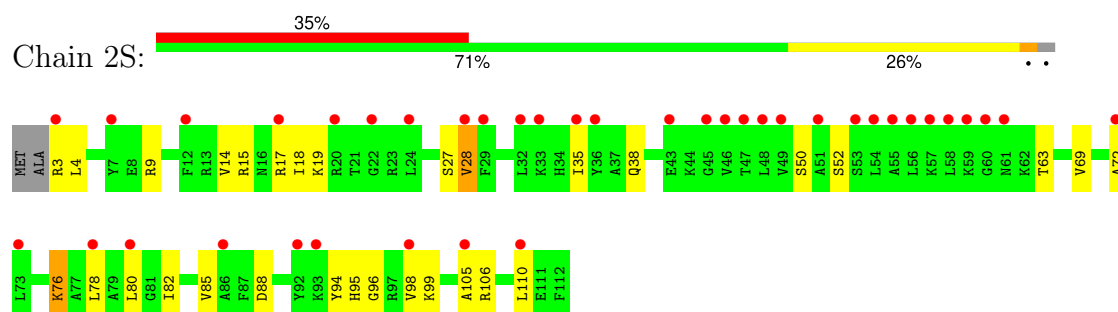
- Molecule 13: 50S ribosomal protein L17



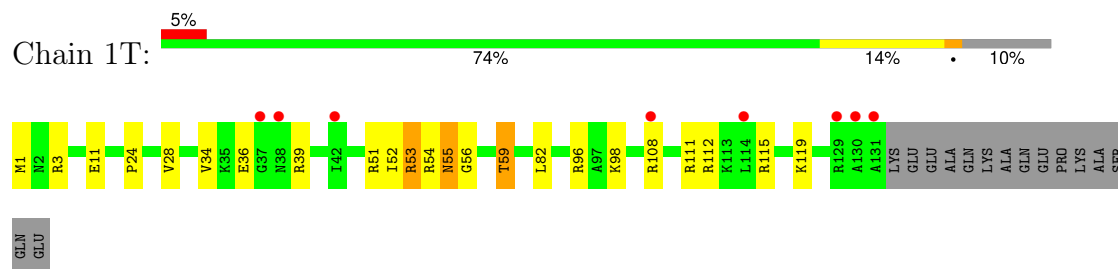
- Molecule 14: 50S ribosomal protein L18



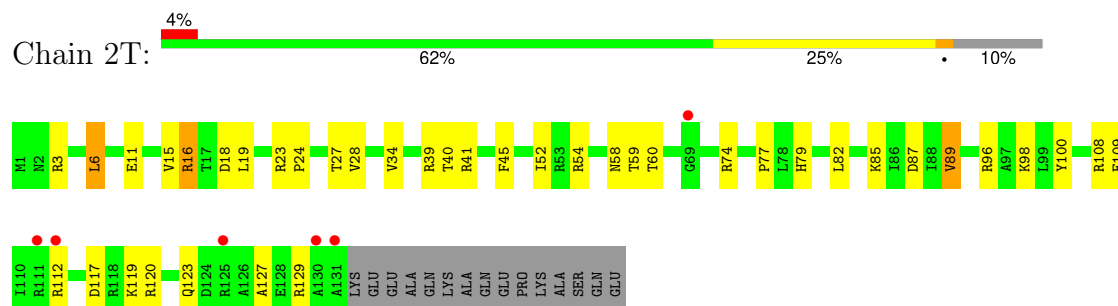
- Molecule 14: 50S ribosomal protein L18



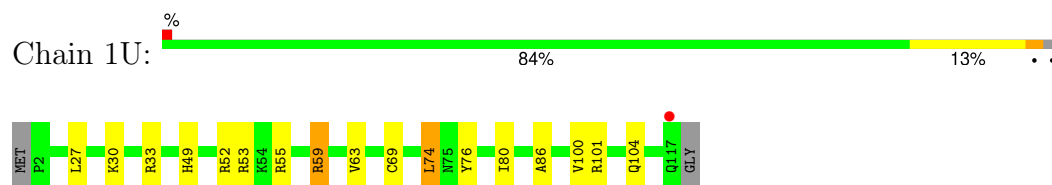
- Molecule 15: 50S ribosomal protein L19



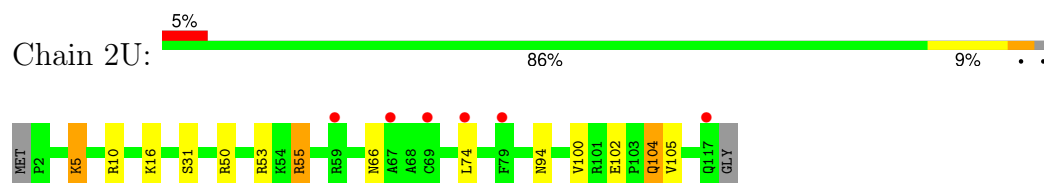
- Molecule 15: 50S ribosomal protein L19



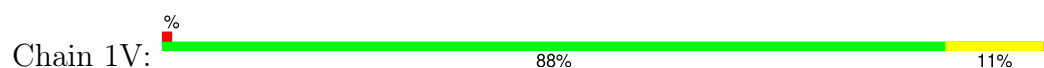
- Molecule 16: 50S ribosomal protein L20



- Molecule 16: 50S ribosomal protein L20

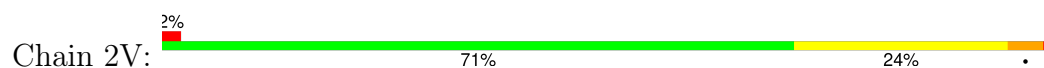


- Molecule 17: 50S ribosomal protein L21

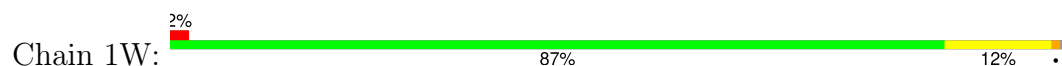




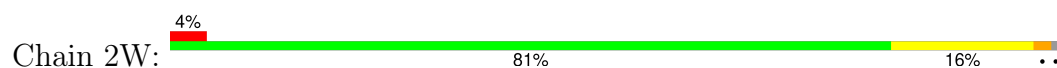
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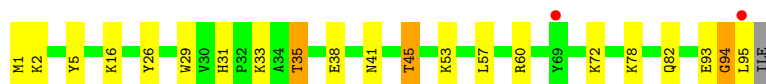
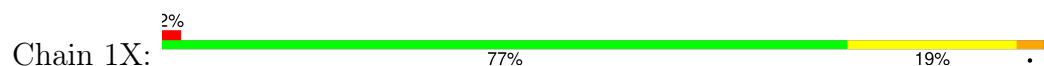
- Molecule 18: 50S ribosomal protein L22



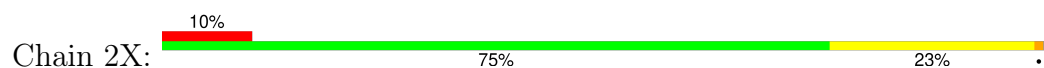
- Molecule 18: 50S ribosomal protein L22



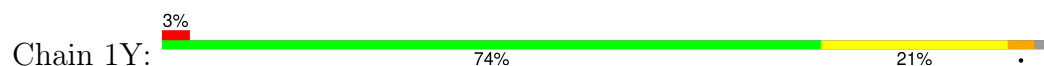
- Molecule 19: 50S ribosomal protein L23



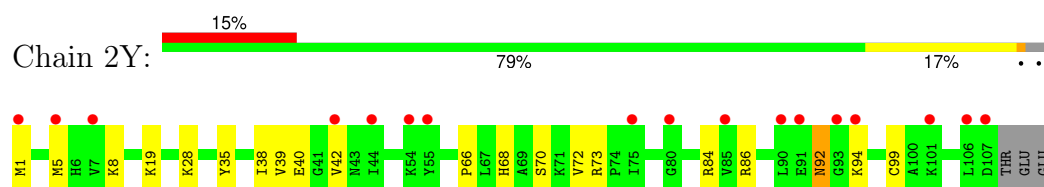
- Molecule 19: 50S ribosomal protein L23



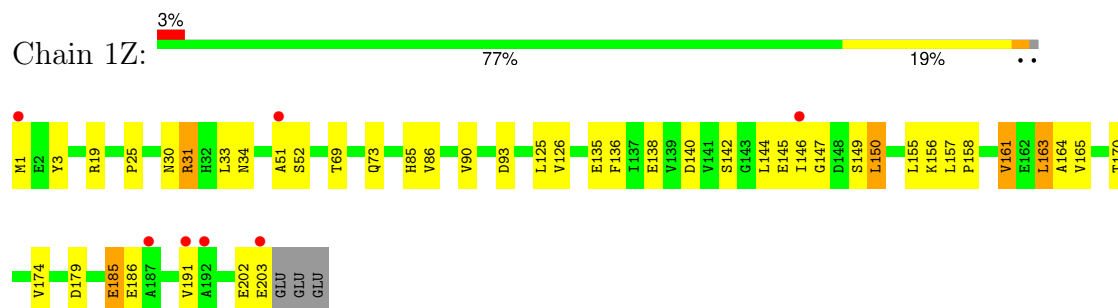
- Molecule 20: 50S ribosomal protein L24



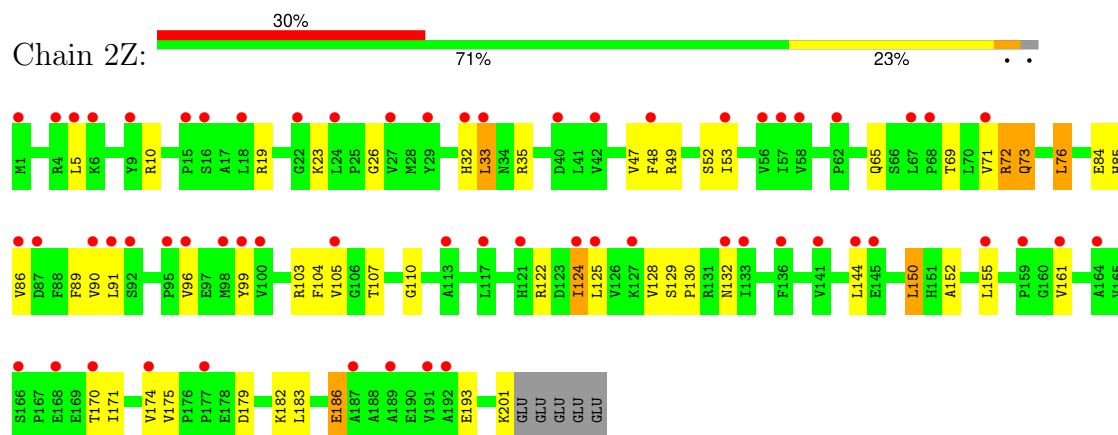
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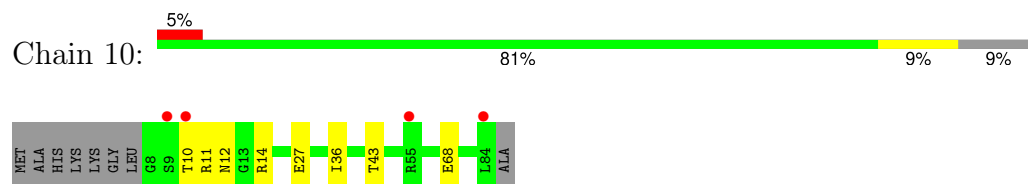
- Molecule 21: 50S ribosomal protein L25



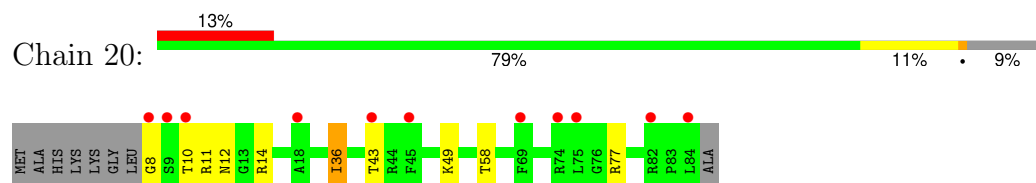
- Molecule 21: 50S ribosomal protein L25



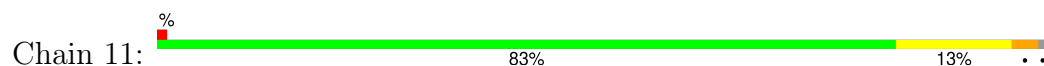
- Molecule 22: 50S ribosomal protein L27



- Molecule 22: 50S ribosomal protein L27

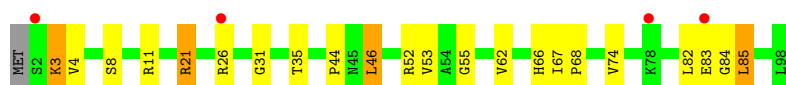
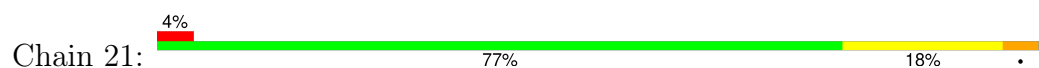


- Molecule 23: 50S ribosomal protein L28





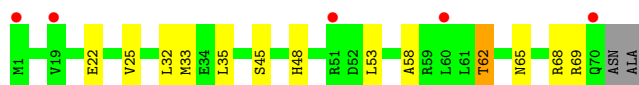
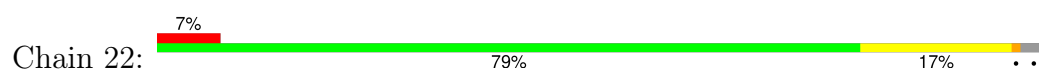
- Molecule 23: 50S ribosomal protein L28



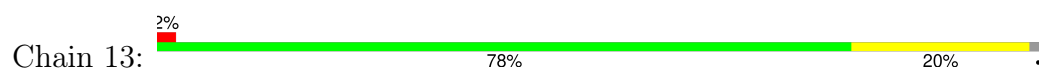
- Molecule 24: 50S ribosomal protein L29



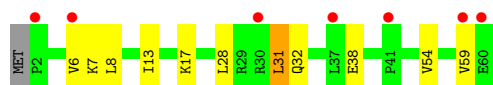
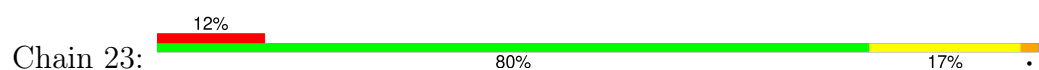
- Molecule 24: 50S ribosomal protein L29



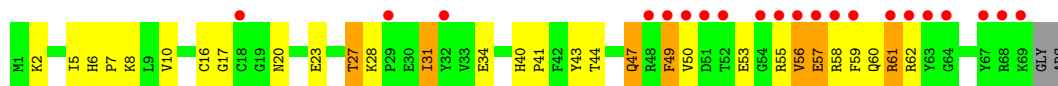
- Molecule 25: 50S ribosomal protein L30



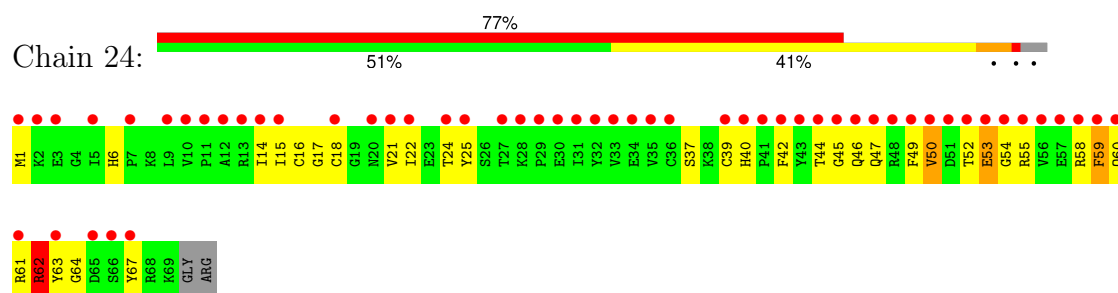
- Molecule 25: 50S ribosomal protein L30



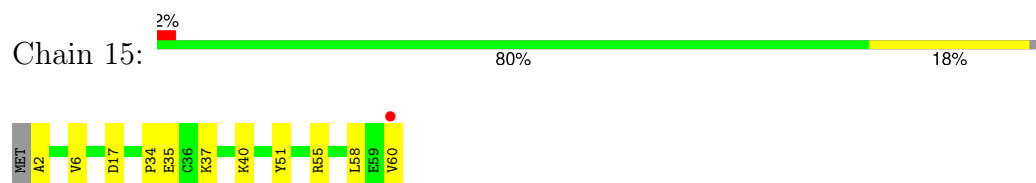
- Molecule 26: 50S ribosomal protein L31



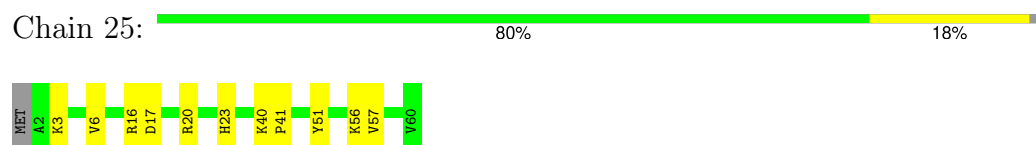
- Molecule 26: 50S ribosomal protein L31



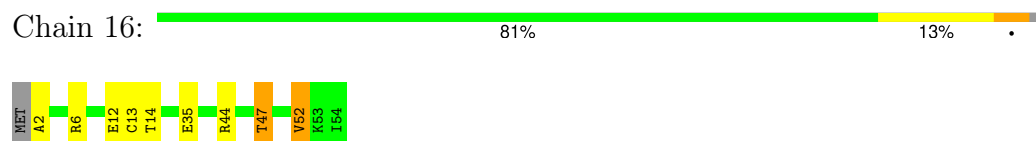
- Molecule 27: 50S ribosomal protein L32



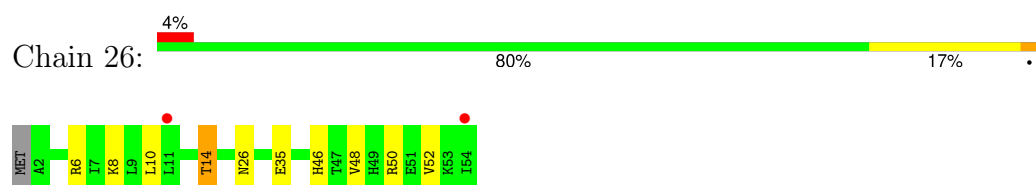
- Molecule 27: 50S ribosomal protein L32



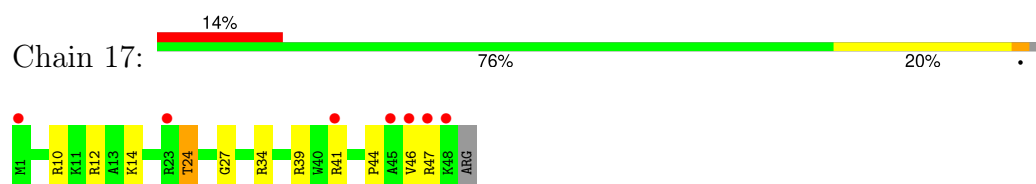
- Molecule 28: 50S ribosomal protein L33



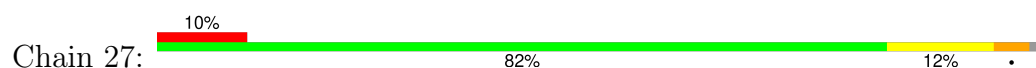
- Molecule 28: 50S ribosomal protein L33



- Molecule 29: 50S ribosomal protein L34



- Molecule 29: 50S ribosomal protein L34

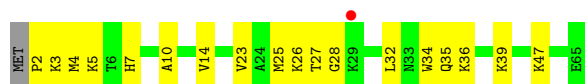




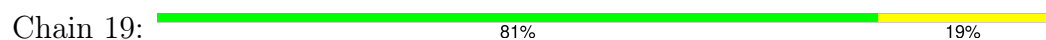
- Molecule 30: 50S ribosomal protein L35



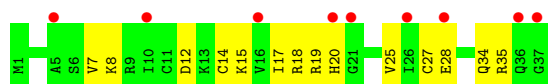
- Molecule 30: 50S ribosomal protein L35



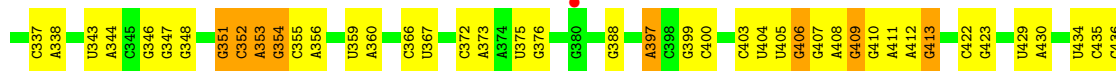
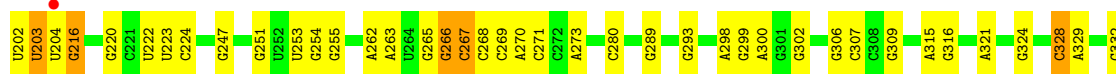
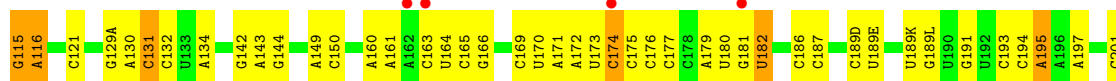
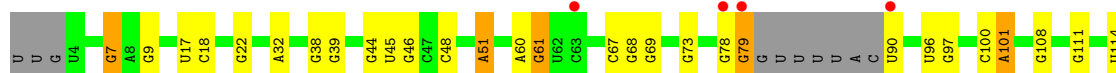
- Molecule 31: 50S ribosomal protein L36

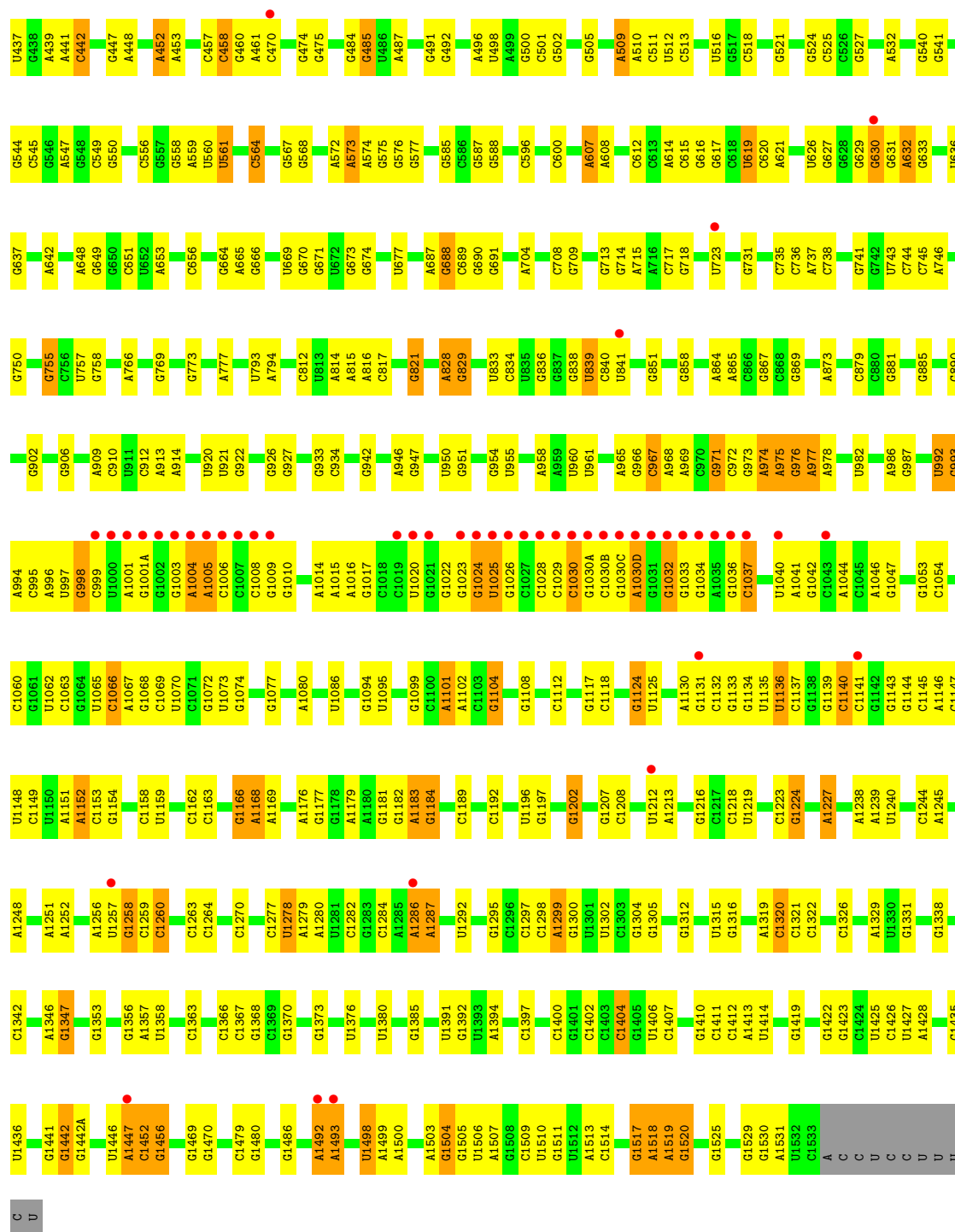


- Molecule 31: 50S ribosomal protein L36



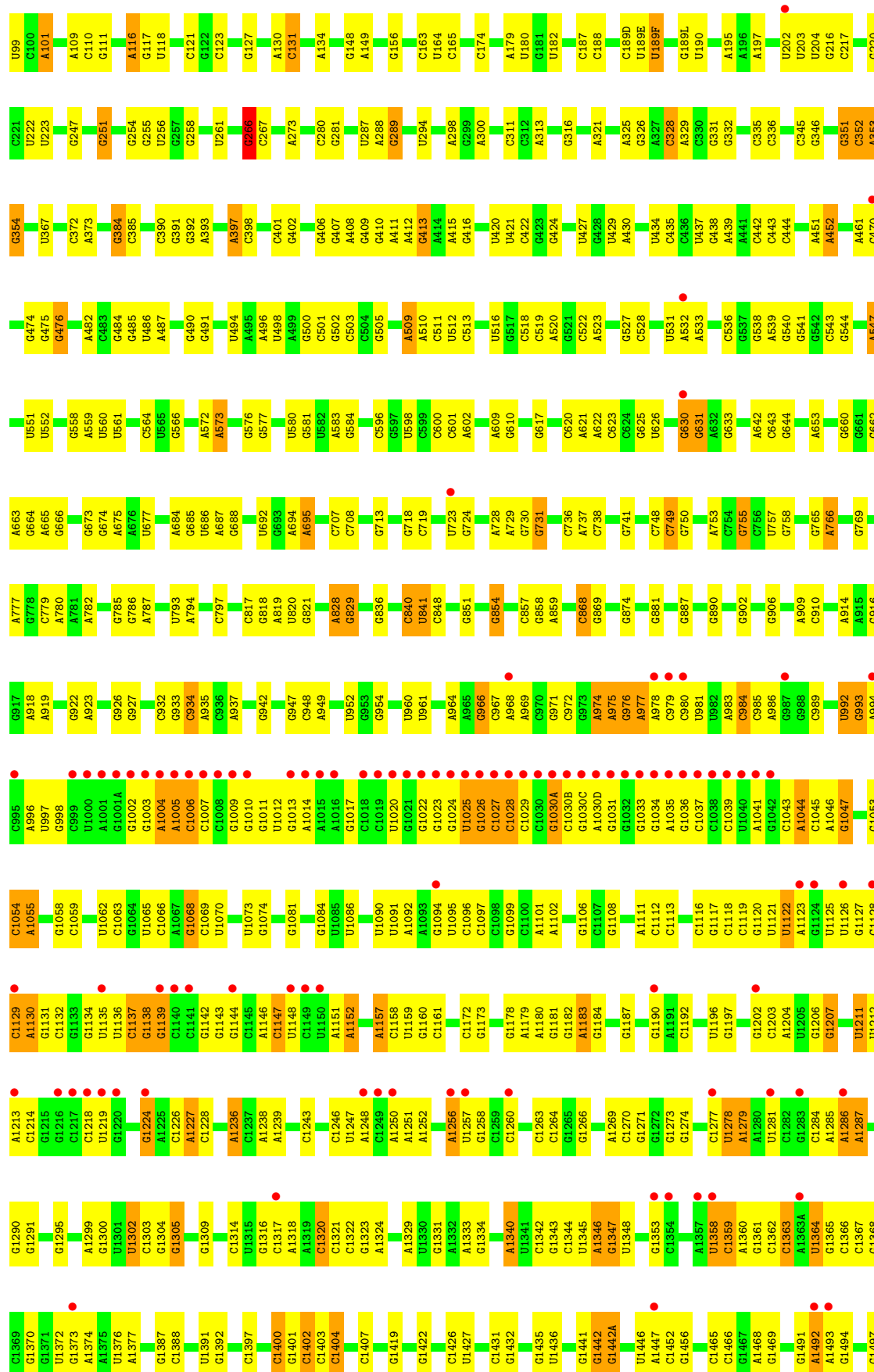
- Molecule 32: 16S Ribosomal RNA





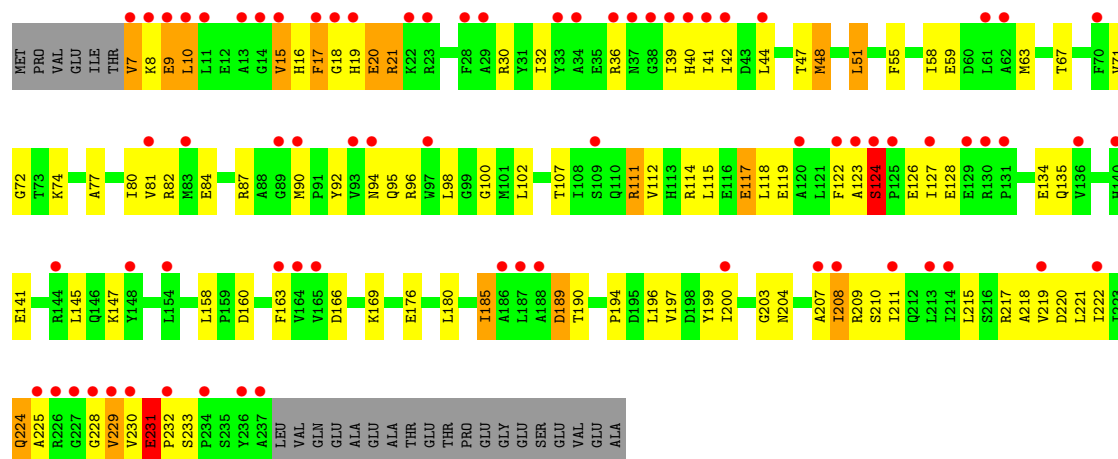
- Molecule 32: 16S Ribosomal RNA



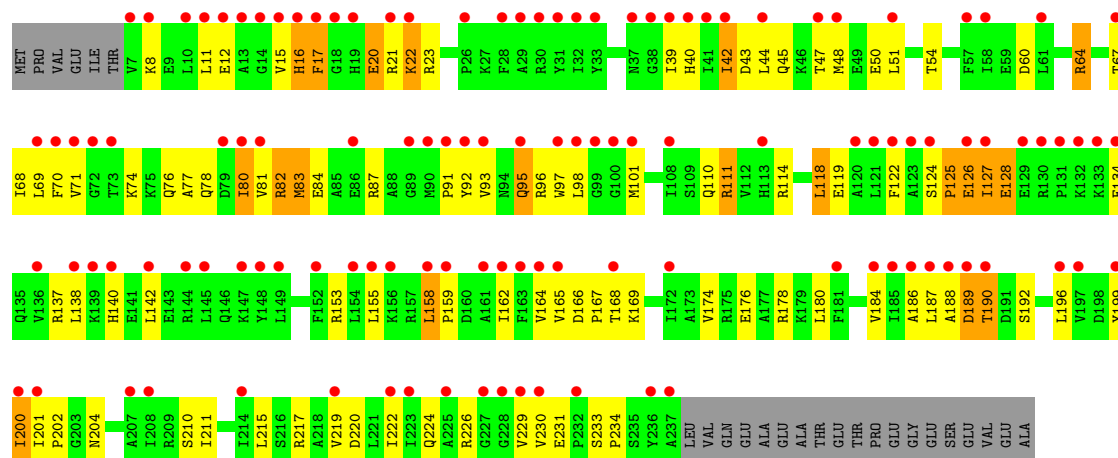




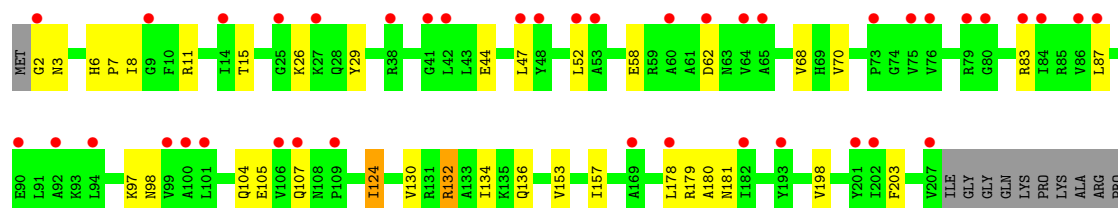
• Molecule 33: 30S ribosomal protein S2



• Molecule 33: 30S ribosomal protein S2

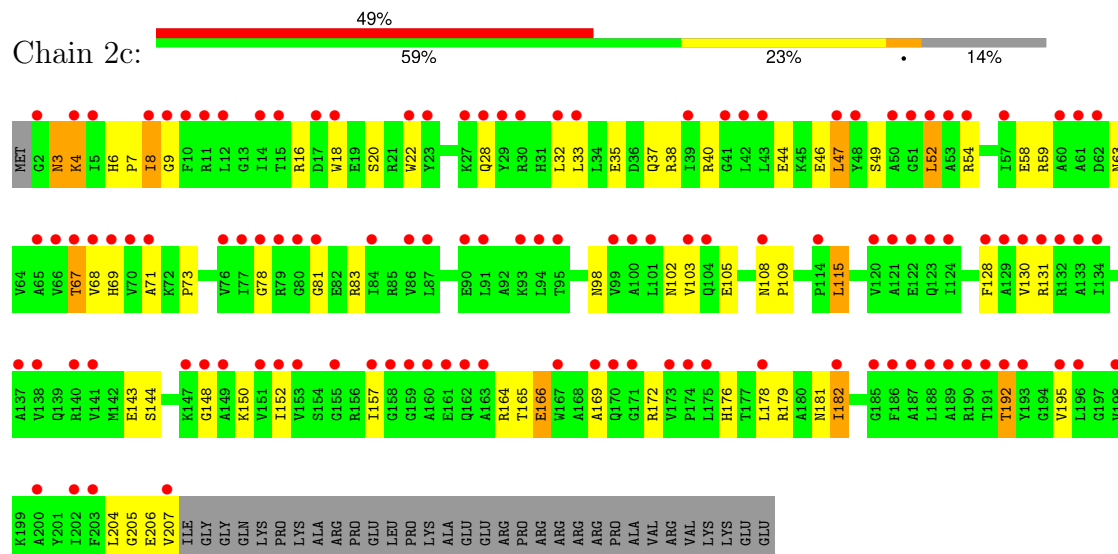


• Molecule 34: 30S ribosomal protein S3

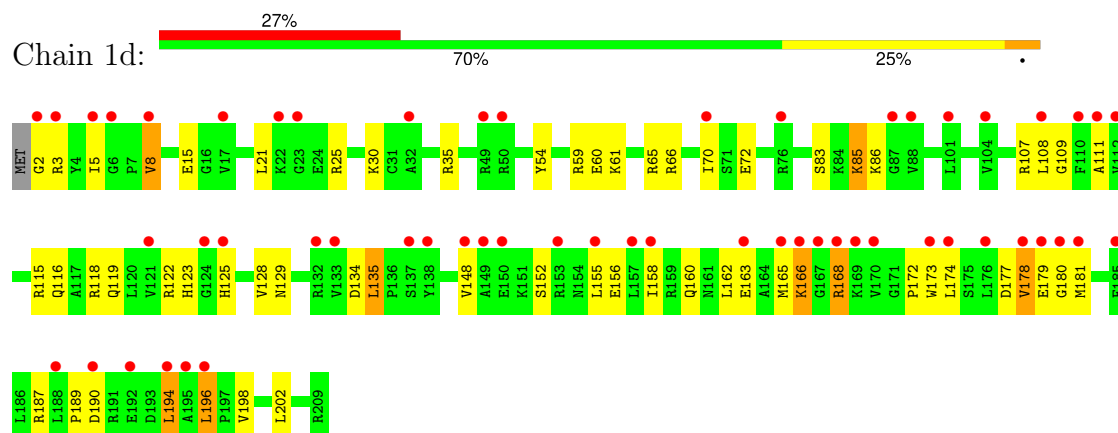


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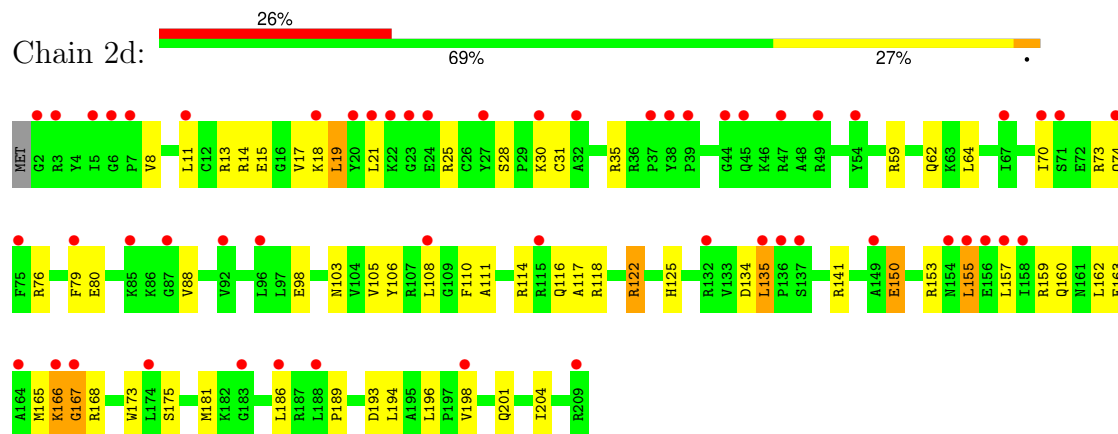
• Molecule 34: 30S ribosomal protein S3



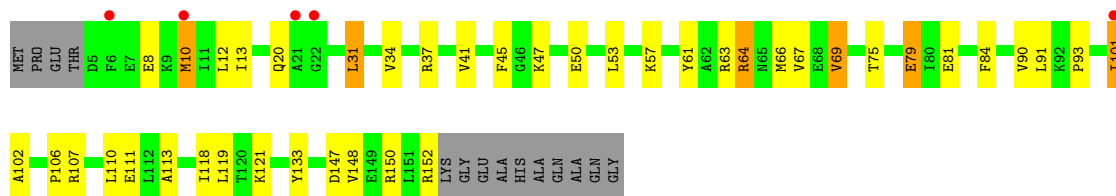
• Molecule 35: 30S ribosomal protein S4



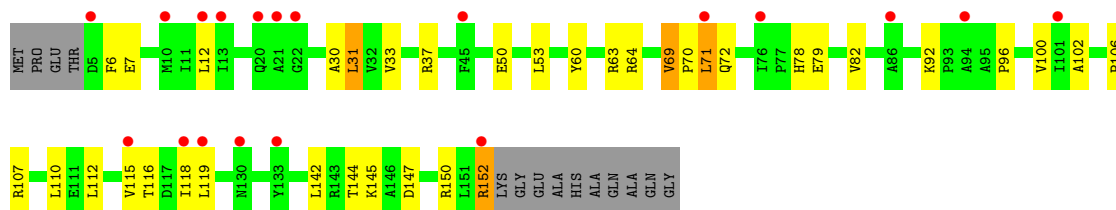
• Molecule 35: 30S ribosomal protein S4



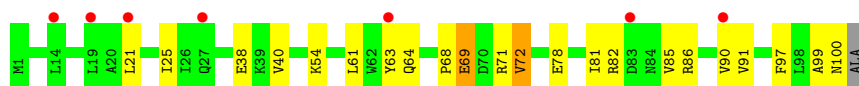
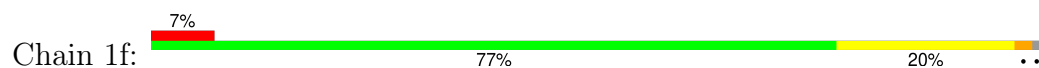
• Molecule 36: 30S ribosomal protein S5



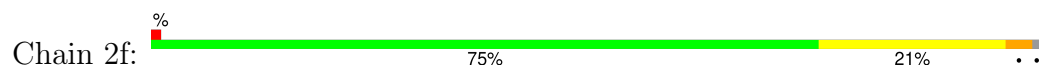
• Molecule 36: 30S ribosomal protein S5



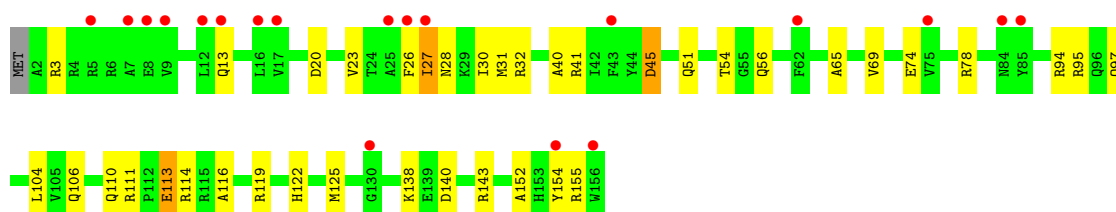
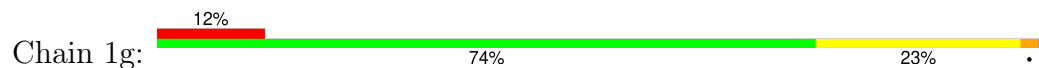
• Molecule 37: 30S ribosomal protein S6



• Molecule 37: 30S ribosomal protein S6

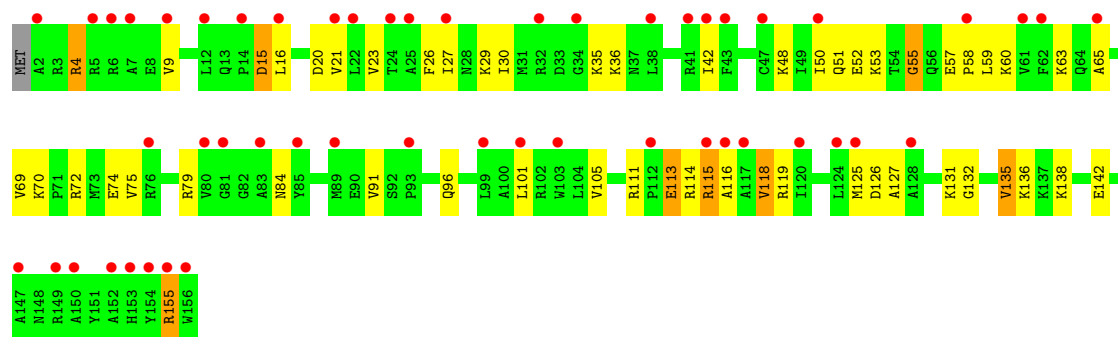


• Molecule 38: 30S ribosomal protein S7

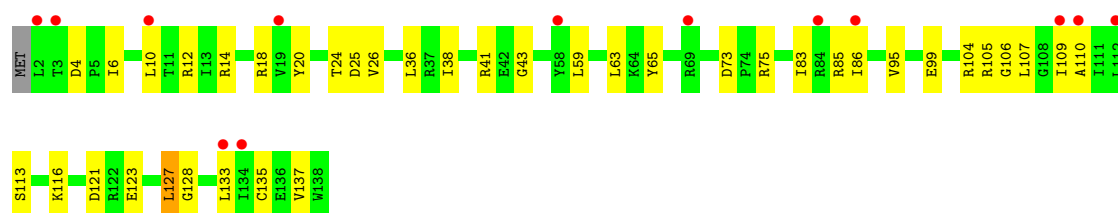


• Molecule 38: 30S ribosomal protein S7

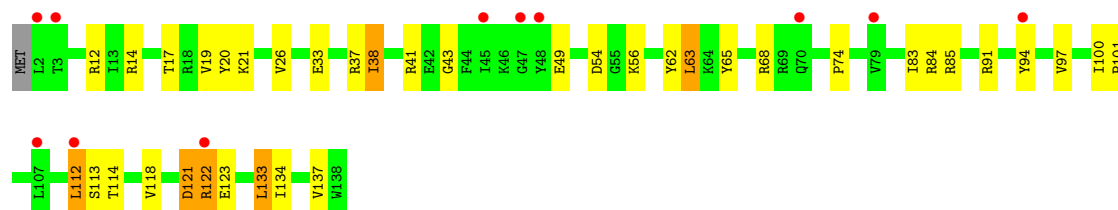




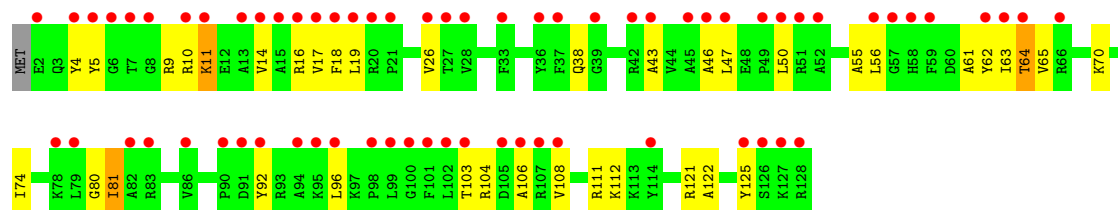
• Molecule 39: 30S ribosomal protein S8



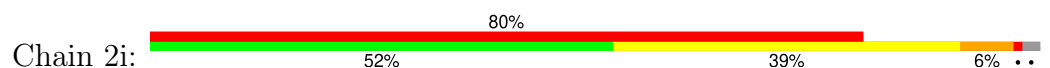
• Molecule 39: 30S ribosomal protein S8

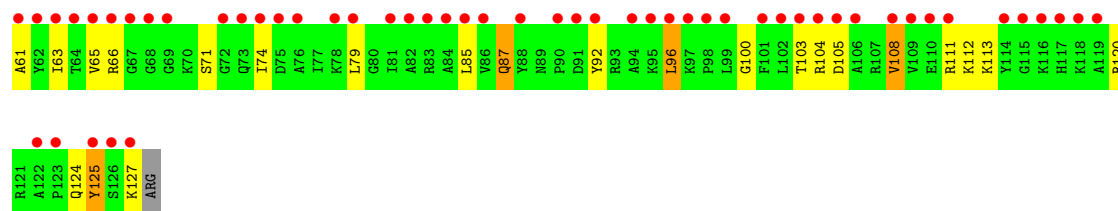


• Molecule 40: 30S ribosomal protein S9

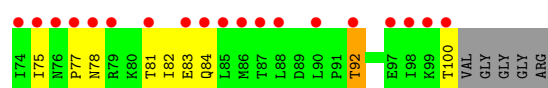
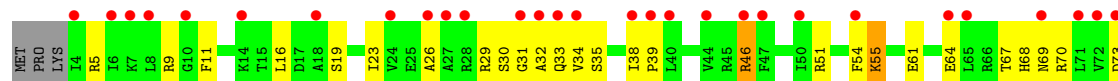


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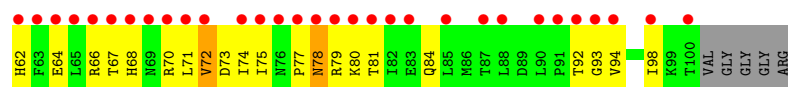
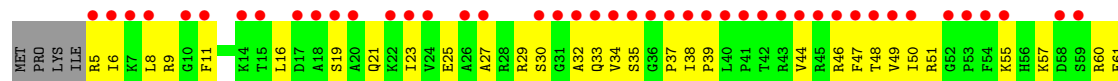




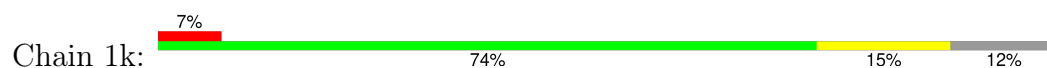
- Molecule 41: 30S ribosomal protein S10



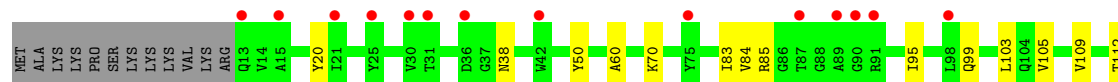
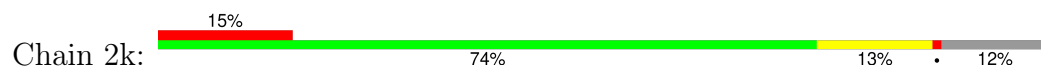
- Molecule 41: 30S ribosomal protein S10



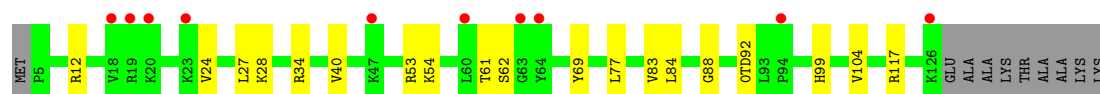
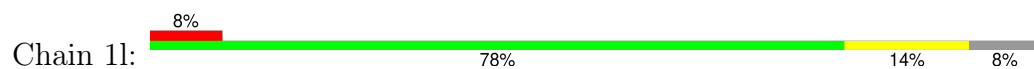
- Molecule 42: 30S ribosomal protein S11



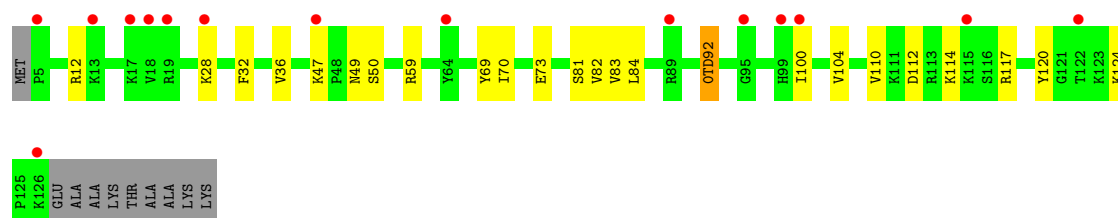
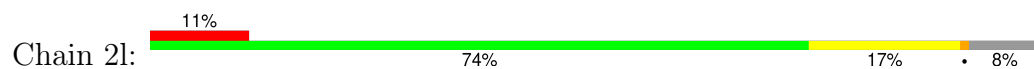
- Molecule 42: 30S ribosomal protein S11



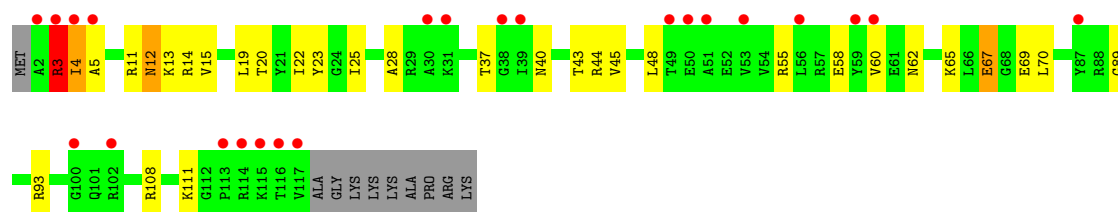
- Molecule 43: 30S ribosomal protein S12



- Molecule 43: 30S ribosomal protein S12



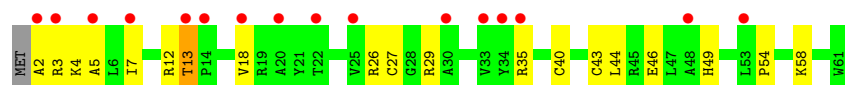
- Molecule 44: 30S ribosomal protein S13



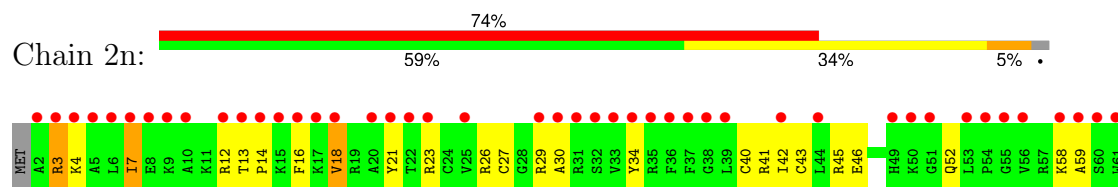
- Molecule 44: 30S ribosomal protein S13



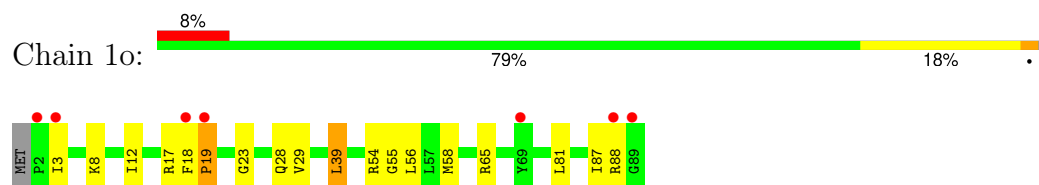
- Molecule 45: 30S ribosomal protein S14 type Z



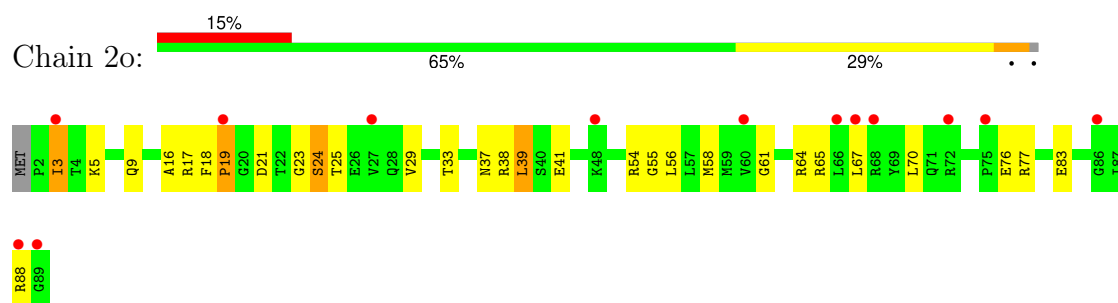
- Molecule 45: 30S ribosomal protein S14 type Z



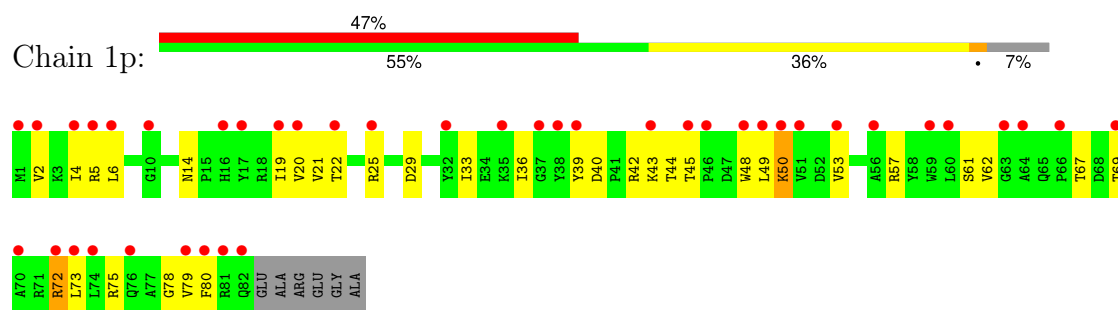
- Molecule 46: 30S ribosomal protein S15



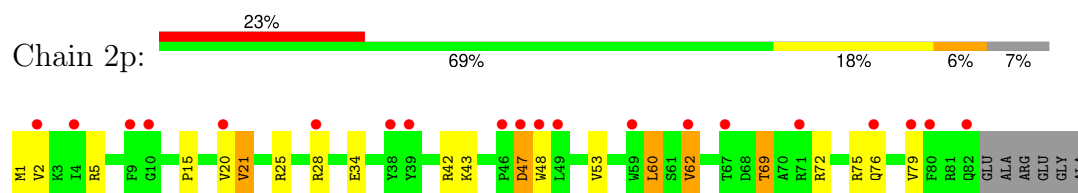
- Molecule 46: 30S ribosomal protein S15



- Molecule 47: 30S ribosomal protein S16

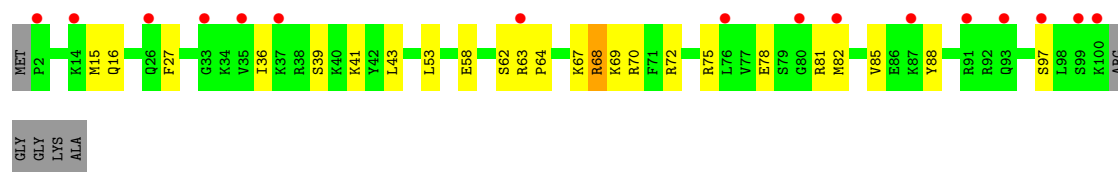


- Molecule 47: 30S ribosomal protein S16

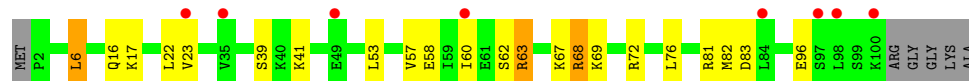
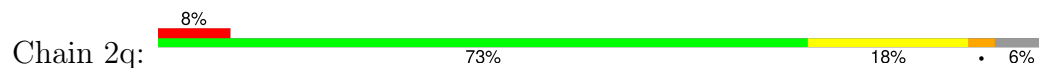


- Molecule 48: 30S ribosomal protein S17





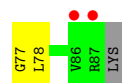
- Molecule 48: 30S ribosomal protein S17



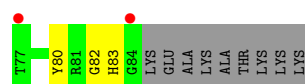
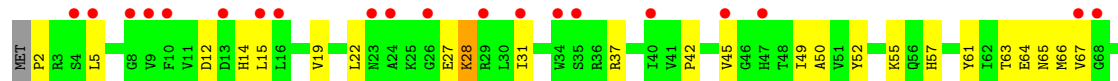
- Molecule 49: 30S ribosomal protein S18



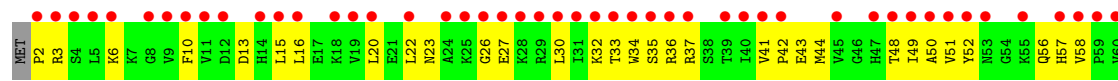
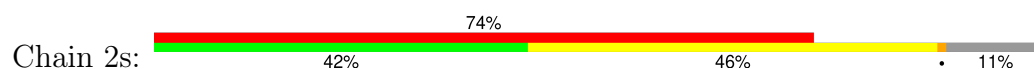
- Molecule 49: 30S ribosomal protein S18

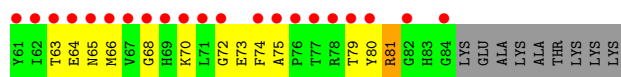


- Molecule 50: 30S ribosomal protein S19

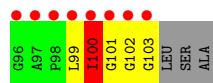


- Molecule 50: 30S ribosomal protein S19

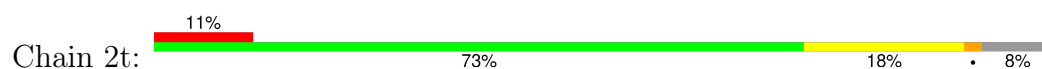




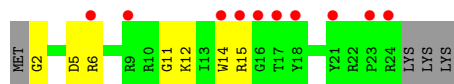
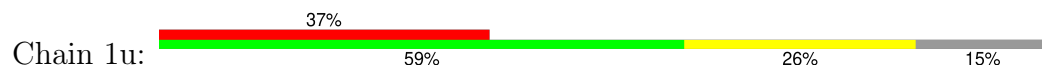
- Molecule 51: 30S ribosomal protein S20



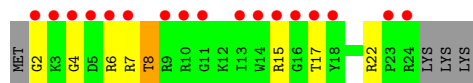
- Molecule 51: 30S ribosomal protein S20



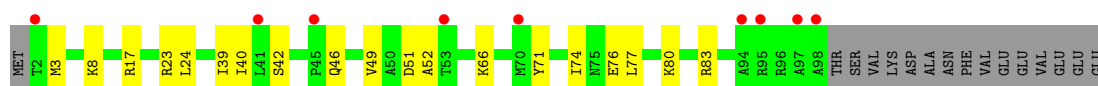
- Molecule 52: 30S ribosomal protein Thx



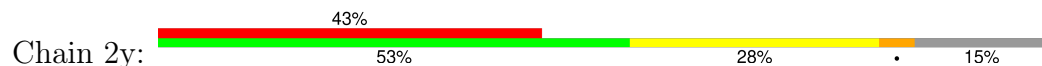
- Molecule 52: 30S ribosomal protein Thx

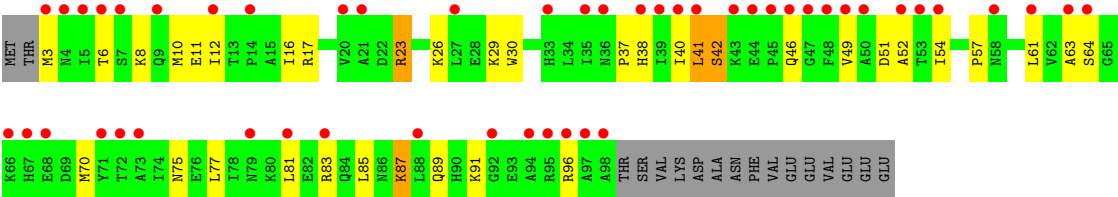


- Molecule 53: Ribosome-associated inhibitor A



- Molecule 53: Ribosome-associated inhibitor A





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	209.60Å 449.65Å 619.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	181.99 – 2.35 181.99 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.8 (181.99-2.35) 99.8 (181.99-2.35)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.16 (at 2.34Å)	Xtriage
Refinement program	PHENIX 1.8.2	Depositor
R, R_{free}	0.211 , 0.248 0.213 , 0.250	Depositor DCC
R_{free} test set	119489 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	50.5	Xtriage
Anisotropy	0.216	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 55.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	298008	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.62% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 0TD, OMU, MG, 5MU, ZN, 4OC, MA6, PSU, OMG, MPD, 2MG, 5MC, 2MA, G7M, OMC, HGR, TEL, SF4, M2G, UR3

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	1A	0.31	0/69005	0.51	8/107711 (0.0%)
1	2A	0.24	1/68877 (0.0%)	0.44	1/107509 (0.0%)
2	1B	0.25	0/2876	0.45	0/4486
2	2B	0.19	0/2878	0.37	0/4490
3	1D	0.30	0/2181	0.58	0/2940
3	2D	0.24	0/2186	0.50	0/2944
4	1E	0.28	0/1592	0.53	0/2149
4	2E	0.22	0/1592	0.45	0/2149
5	1F	0.27	0/1619	0.52	0/2193
5	2F	0.22	0/1615	0.48	2/2188 (0.1%)
6	1G	0.20	0/1451	0.44	0/1961
6	2G	0.20	0/1449	0.40	0/1957
7	1H	0.22	0/1356	0.41	0/1834
7	2H	0.19	0/1350	0.42	0/1826
8	1I	0.18	0/1109	0.41	0/1512
8	2I	0.18	0/1091	0.40	0/1490
9	1N	0.26	0/1148	0.47	0/1547
9	2N	0.19	0/1144	0.39	0/1543
10	1O	0.25	0/943	0.48	0/1269
10	2O	0.22	0/943	0.46	0/1269
11	1P	0.27	0/1152	0.53	0/1533
11	2P	0.21	0/1152	0.48	0/1533
12	1Q	0.27	0/1143	0.49	0/1527
12	2Q	0.20	0/1143	0.44	0/1527
13	1R	0.30	0/982	0.53	0/1312
13	2R	0.22	0/982	0.44	0/1312
14	1S	0.22	0/887	0.46	0/1180
14	2S	0.20	0/880	0.44	0/1172
15	1T	0.27	0/1105	0.50	0/1477
15	2T	0.21	0/1097	0.42	0/1468
16	1U	0.30	0/977	0.51	0/1301

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	2U	0.20	0/977	0.41	0/1301
17	1V	0.27	0/786	0.48	0/1053
17	2V	0.19	0/782	0.41	0/1049
18	1W	0.31	0/897	0.48	0/1205
18	2W	0.23	0/897	0.41	0/1205
19	1X	0.26	0/764	0.50	0/1025
19	2X	0.21	0/764	0.41	0/1025
20	1Y	0.24	0/823	0.52	0/1099
20	2Y	0.18	0/823	0.46	0/1100
21	1Z	0.21	0/1620	0.43	0/2200
21	2Z	0.20	0/1590	0.43	0/2162
22	10	0.26	0/616	0.48	0/821
22	20	0.20	0/616	0.43	0/821
23	11	0.24	0/761	0.46	0/1013
23	21	0.24	0/766	0.43	0/1018
24	12	0.24	0/590	0.46	0/781
24	22	0.20	0/594	0.39	0/785
25	13	0.28	0/474	0.51	0/635
25	23	0.18	0/469	0.39	0/630
26	14	0.25	0/559	0.62	0/754
26	24	0.29	0/549	0.66	2/741 (0.3%)
27	15	0.29	0/473	0.53	0/639
27	25	0.23	0/469	0.46	0/635
28	16	0.26	0/460	0.47	0/613
28	26	0.20	0/456	0.41	0/608
29	17	0.34	0/426	0.58	0/561
29	27	0.26	0/426	0.52	0/561
30	18	0.30	0/525	0.51	0/691
30	28	0.21	0/525	0.40	0/691
31	19	0.27	0/310	0.49	0/407
31	29	0.20	0/310	0.41	0/407
32	1a	0.21	0/35795	0.40	0/55864
32	2a	0.20	0/35890	0.39	2/56012 (0.0%)
33	1b	0.22	0/1876	0.47	0/2533
33	2b	0.26	0/1860	0.48	0/2518
34	1c	0.19	0/1582	0.40	0/2137
34	2c	0.22	0/1566	0.41	0/2119
35	1d	0.20	0/1695	0.43	0/2274
35	2d	0.19	0/1698	0.44	0/2277
36	1e	0.21	0/1149	0.45	0/1548
36	2e	0.19	0/1149	0.42	0/1548
37	1f	0.20	0/827	0.40	0/1120
37	2f	0.19	0/829	0.42	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	1g	0.18	0/1254	0.36	0/1683
38	2g	0.19	0/1248	0.40	0/1676
39	1h	0.18	0/1118	0.42	0/1506
39	2h	0.18	0/1108	0.39	0/1494
40	1i	0.20	0/1005	0.45	0/1351
40	2i	0.21	0/985	0.44	0/1329
41	1j	0.20	0/732	0.38	0/993
41	2j	0.23	0/723	0.44	0/984
42	1k	0.20	0/849	0.43	0/1150
42	2k	0.23	0/848	0.46	0/1149
43	1l	0.21	0/937	0.45	0/1260
43	2l	0.18	0/937	0.40	0/1260
44	1m	0.20	0/924	0.45	0/1242
44	2m	0.22	0/905	0.48	0/1217
45	1n	0.20	0/501	0.47	0/664
45	2n	0.20	0/501	0.42	0/664
46	1o	0.22	0/739	0.42	0/985
46	2o	0.19	0/739	0.38	0/985
47	1p	0.20	0/697	0.49	0/939
47	2p	0.19	0/693	0.44	0/935
48	1q	0.20	0/836	0.41	0/1117
48	2q	0.20	0/836	0.41	0/1117
49	1r	0.18	0/560	0.39	0/746
49	2r	0.19	0/560	0.41	0/746
50	1s	0.18	0/663	0.45	0/895
50	2s	0.22	0/660	0.41	0/893
51	1t	0.20	0/734	0.47	0/969
51	2t	0.18	0/736	0.41	0/976
52	1u	0.18	0/203	0.43	0/266
52	2u	0.21	0/203	0.45	0/266
53	1y	0.18	0/776	0.38	0/1048
53	2y	0.20	0/761	0.37	0/1030
All	All	0.24	1/309889 (0.0%)	0.45	15/463153 (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
11	1P	0	1
11	2P	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
33	1b	0	1
42	2k	0	1
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2A	2552	OMU	O3'-P	5.17	1.61	1.56

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	1042	G	OP1-P-O3'	-9.17	80.50	108.00
1	1A	1042	G	OP2-P-O3'	-6.83	87.53	108.00
1	2A	1992	G	C2'-C3'-O3'	6.21	118.81	109.50
32	2a	266	G	C2'-C3'-O3'	6.20	118.80	109.50
1	1A	1653	G	C2'-C3'-O3'	5.67	118.00	109.50
1	1A	1210	A	C4'-C3'-O3'	5.62	117.83	109.40
1	1A	512	G	O4'-C1'-N9	5.61	116.61	108.20
1	1A	2689	U	C4'-C3'-O3'	5.61	117.81	109.40
1	1A	1791	A	C5'-C4'-C3'	-5.46	107.81	116.00
32	2a	266	G	P-O3'-C3'	5.34	128.21	120.20
1	1A	1139	G	O5'-P-OP2	-5.25	92.24	108.00
5	2F	21	ALA	CA-C-N	5.07	130.82	121.70
5	2F	21	ALA	C-N-CA	5.07	130.82	121.70
26	24	59	PHE	CA-C-N	5.01	130.72	121.70
26	24	59	PHE	C-N-CA	5.01	130.72	121.70

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	1P	35	HIS	Peptide
33	1b	231	GLU	Peptide
11	2P	35	HIS	Peptide
42	2k	117	ASN	Peptide

5.2 Too-close contacts

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	1A	61871	0	31210	493	0
1	2A	61760	0	31157	631	1
2	1B	2572	0	1305	22	0
2	2B	2573	0	1306	37	0
3	1D	2131	0	2207	38	0
3	2D	2136	0	2218	35	0
4	1E	1559	0	1618	24	0
4	2E	1559	0	1618	31	0
5	1F	1584	0	1625	33	0
5	2F	1580	0	1619	43	0
6	1G	1426	0	1445	36	0
6	2G	1424	0	1441	62	0
7	1H	1330	0	1407	22	0
7	2H	1324	0	1402	35	0
8	1I	1094	0	1127	23	0
8	2I	1076	0	1094	17	0
9	1N	1121	0	1195	14	0
9	2N	1117	0	1184	13	0
10	1O	933	0	996	13	0
10	2O	933	0	996	11	0
11	1P	1135	0	1212	23	0
11	2P	1135	0	1212	29	0
12	1Q	1122	0	1179	6	0
12	2Q	1122	0	1179	24	0
13	1R	968	0	1033	15	0
13	2R	968	0	1033	19	0
14	1S	877	0	938	12	0
14	2S	870	0	923	20	0
15	1T	1091	0	1151	15	0
15	2T	1083	0	1136	27	0
16	1U	959	0	1019	15	0
16	2U	959	0	1019	12	0
17	1V	775	0	841	11	0
17	2V	771	0	830	17	0
18	1W	886	0	940	6	0
18	2W	886	0	940	11	0
19	1X	750	0	814	20	0
19	2X	750	0	814	20	0
20	1Y	810	0	892	14	0
20	2Y	810	0	887	12	0
21	1Z	1587	0	1598	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	2Z	1557	0	1564	44	0
22	10	608	0	622	9	0
22	20	608	0	622	7	0
23	11	754	0	823	11	0
23	21	759	0	837	16	0
24	12	588	0	643	11	0
24	22	592	0	654	6	0
25	13	469	0	518	6	0
25	23	464	0	514	8	0
26	14	546	0	522	23	0
26	24	536	0	514	24	0
27	15	459	0	476	6	0
27	25	455	0	465	7	0
28	16	453	0	473	4	0
28	26	449	0	469	7	0
29	17	418	0	467	10	0
29	27	418	0	467	10	0
30	18	517	0	582	16	0
30	28	517	0	582	15	0
31	19	307	0	335	6	0
31	29	307	0	335	9	0
32	1a	32246	0	16294	381	1
32	2a	32331	0	16337	405	0
33	1b	1842	0	1862	59	0
33	2b	1825	0	1828	71	0
34	1c	1558	0	1557	21	0
34	2c	1542	0	1517	42	0
35	1d	1665	0	1687	55	0
35	2d	1668	0	1703	42	0
36	1e	1133	0	1191	29	0
36	2e	1133	0	1191	21	0
37	1f	814	0	808	15	0
37	2f	816	0	808	15	0
38	1g	1235	0	1249	25	0
38	2g	1229	0	1238	30	0
39	1h	1098	0	1143	22	0
39	2h	1088	0	1126	20	0
40	1i	986	0	990	32	0
40	2i	966	0	953	45	0
41	1j	719	0	672	24	0
41	2j	710	0	661	33	0
42	1k	834	0	838	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	2k	833	0	836	12	0
43	1l	932	0	981	10	0
43	2l	932	0	981	15	0
44	1m	914	0	954	21	0
44	2m	895	0	920	43	0
45	1n	492	0	529	14	0
45	2n	492	0	529	22	0
46	1o	728	0	760	14	0
46	2o	728	0	760	17	0
47	1p	681	0	697	23	0
47	2p	677	0	686	13	0
48	1q	823	0	891	15	0
48	2q	823	0	891	17	0
49	1r	555	0	618	13	0
49	2r	555	0	618	16	0
50	1s	648	0	658	17	0
50	2s	645	0	635	29	0
51	1t	732	0	809	20	0
51	2t	733	0	795	12	0
52	1u	199	0	208	5	0
52	2u	199	0	208	3	0
53	1y	764	0	786	11	0
53	2y	749	0	757	24	0
54	10	7	0	0	0	0
54	11	4	0	0	0	0
54	13	4	0	0	0	0
54	14	1	0	0	0	0
54	15	9	0	0	0	0
54	17	7	0	0	0	0
54	18	4	0	0	0	0
54	19	2	0	0	0	0
54	1A	1019	0	0	0	0
54	1B	30	0	0	0	0
54	1D	15	0	0	0	0
54	1E	9	0	0	0	0
54	1F	19	0	0	0	0
54	1G	4	0	0	0	0
54	1H	2	0	0	0	0
54	1N	4	0	0	0	0
54	1O	1	0	0	0	0
54	1P	7	0	0	0	0
54	1Q	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	1R	4	0	0	0	0
54	1T	5	0	0	0	0
54	1U	8	0	0	0	0
54	1V	7	0	0	0	0
54	1W	3	0	0	0	0
54	1X	1	0	0	0	0
54	1Z	1	0	0	0	0
54	1a	278	0	0	0	0
54	1b	1	0	0	0	0
54	1d	4	0	0	0	0
54	1e	3	0	0	0	0
54	1f	1	0	0	0	0
54	1g	2	0	0	0	0
54	1h	2	0	0	0	0
54	1i	1	0	0	0	0
54	1k	1	0	0	0	0
54	1l	2	0	0	0	0
54	1m	1	0	0	0	0
54	1n	2	0	0	0	0
54	1o	2	0	0	0	0
54	1r	1	0	0	0	0
54	1t	1	0	0	0	0
54	1y	3	0	0	0	0
54	20	1	0	0	0	0
54	21	1	0	0	0	0
54	23	1	0	0	0	0
54	25	2	0	0	0	0
54	27	1	0	0	0	0
54	28	2	0	0	0	0
54	2A	742	0	0	0	0
54	2B	17	0	0	0	0
54	2D	10	0	0	0	0
54	2E	6	0	0	0	0
54	2F	4	0	0	0	0
54	2G	2	0	0	0	0
54	2I	1	0	0	0	0
54	2N	1	0	0	0	0
54	2O	1	0	0	0	0
54	2P	4	0	0	0	0
54	2Q	2	0	0	0	0
54	2R	2	0	0	0	0
54	2T	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	2V	3	0	0	0	0
54	2W	4	0	0	0	0
54	2a	192	0	0	0	0
54	2e	1	0	0	0	0
54	2f	1	0	0	0	0
54	2j	1	0	0	0	0
54	2k	1	0	0	0	0
54	2p	1	0	0	0	0
54	2t	1	0	0	0	0
55	1A	36	0	29	1	0
55	2A	36	0	29	1	0
56	1A	58	0	65	5	0
56	2A	58	0	65	3	0
57	18	8	0	14	1	0
57	1A	8	0	14	1	0
57	1T	8	0	14	0	0
57	1a	8	0	11	4	0
57	2A	24	0	42	3	0
58	1B	12	0	12	1	0
58	1F	12	0	12	1	0
59	14	1	0	0	0	0
59	15	1	0	0	0	0
59	16	1	0	0	0	0
59	19	1	0	0	0	0
59	1Y	1	0	0	0	0
59	1n	1	0	0	0	0
59	24	1	0	0	0	0
59	25	1	0	0	0	0
59	26	1	0	0	0	0
59	29	1	0	0	0	0
59	2Y	1	0	0	0	0
59	2n	1	0	0	0	0
60	1d	8	0	0	0	0
60	2d	8	0	0	0	0
61	10	23	0	0	0	0
61	11	24	0	0	0	0
61	12	13	0	0	2	0
61	13	27	0	0	1	0
61	14	2	0	0	0	0
61	15	23	0	0	1	0
61	16	15	0	0	1	0
61	17	16	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	18	27	0	0	2	0
61	19	7	0	0	1	0
61	1A	4030	0	0	69	0
61	1B	101	0	0	5	0
61	1D	118	0	0	2	0
61	1E	76	0	0	3	0
61	1F	67	0	0	2	0
61	1G	17	0	0	0	0
61	1H	16	0	0	1	0
61	1I	7	0	0	0	0
61	1N	56	0	0	1	0
61	1O	22	0	0	0	0
61	1P	59	0	0	3	0
61	1Q	39	0	0	0	0
61	1R	36	0	0	0	0
61	1S	13	0	0	0	0
61	1T	36	0	0	1	0
61	1U	50	0	0	6	0
61	1V	34	0	0	2	0
61	1W	26	0	0	0	0
61	1X	26	0	0	0	0
61	1Y	15	0	0	2	0
61	1Z	13	0	0	1	0
61	1a	483	0	0	24	0
61	1b	1	0	0	0	0
61	1d	9	0	0	0	0
61	1e	6	0	0	1	0
61	1f	2	0	0	0	0
61	1h	1	0	0	0	0
61	1j	1	0	0	0	0
61	1l	3	0	0	1	0
61	1m	1	0	0	0	0
61	1o	2	0	0	0	0
61	1p	1	0	0	0	0
61	1u	1	0	0	0	0
61	1y	3	0	0	0	0
61	20	13	0	0	0	0
61	21	21	0	0	1	0
61	22	2	0	0	0	0
61	23	2	0	0	1	0
61	25	9	0	0	0	0
61	26	6	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	27	9	0	0	0	0
61	28	13	0	0	0	0
61	29	1	0	0	0	0
61	2A	2427	0	0	87	0
61	2B	56	0	0	11	0
61	2D	60	0	0	0	0
61	2E	30	0	0	1	0
61	2F	26	0	0	0	0
61	2G	3	0	0	0	0
61	2H	2	0	0	0	0
61	2I	4	0	0	0	0
61	2N	5	0	0	0	0
61	2O	24	0	0	1	0
61	2P	30	0	0	2	0
61	2Q	18	0	0	0	0
61	2R	18	0	0	2	0
61	2S	4	0	0	0	0
61	2T	9	0	0	0	0
61	2U	14	0	0	0	0
61	2V	4	0	0	0	0
61	2W	18	0	0	0	0
61	2X	5	0	0	0	0
61	2Y	3	0	0	0	0
61	2Z	9	0	0	2	0
61	2a	428	0	0	29	0
61	2d	6	0	0	0	0
61	2e	1	0	0	0	0
61	2f	2	0	0	0	0
61	2j	2	0	0	1	0
61	2l	3	0	0	0	0
61	2m	1	0	0	0	0
61	2n	1	0	0	0	0
61	2o	2	0	0	0	0
61	2p	2	0	0	0	0
61	2q	1	0	0	0	0
61	2r	4	0	0	0	0
61	2t	2	0	0	0	0
61	2y	3	0	0	1	0
All	All	298008	0	194711	3519	1

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 7.

All (3519) 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)
1:1A:1082:U:H3	1:1A:1086:A:N6	1.47	1.10
1:1A:2319:G:H22	14:1S:3:ARG:HD3	1.15	1.05
1:2A:2139:C:N4	1:2A:2152:G:H1	1.55	1.03
1:2A:2099:U:H3	1:2A:2190:G:H1	1.10	0.98
1:1A:2137:C:N4	1:1A:2154:G:H1	1.63	0.97
1:2A:2107:C:H42	1:2A:2182:G:H1	1.14	0.96
1:2A:1041:C:H42	1:2A:1114:G:H1	1.14	0.95
29:17:24:THR:HG22	29:17:27:GLY:H	1.31	0.94
15:1T:55:ASN:H	15:1T:59:THR:HG22	1.33	0.94
1:2A:2499:C:OP1	61:2A:3802:HOH:O	1.86	0.93
1:2A:2100:G:H1	1:2A:2189:U:H3	0.95	0.92
32:2a:1003:G:H2'	32:2a:1004:A:H4'	1.52	0.92
1:2A:1669:A:OP2	61:2A:3803:HOH:O	1.88	0.91
32:1a:201:C:H42	32:1a:216:G:H1	1.11	0.90
1:1A:2137:C:N3	1:1A:2154:G:N2	2.19	0.90
10:2O:48:PRO:HB3	32:2a:1422:G:H5''	1.54	0.90
2:1B:106:G:H5'	21:1Z:31:ARG:HG2	1.53	0.90
1:2A:1670:C:OP2	61:2A:3803:HOH:O	1.88	0.89
1:2A:1798:U:H5'	3:2D:259:THR:HG22	1.55	0.89
32:2a:1129:C:N4	32:2a:1143:G:H1	1.71	0.89
32:1a:1441:G:H5''	32:1a:1442:G:H5'	1.53	0.88
33:1b:185:ILE:HG22	33:1b:199:TYR:HB2	1.55	0.88
1:2A:2427:C:OP1	61:2A:3804:HOH:O	1.91	0.87
1:2A:585:G:OP2	61:2A:3805:HOH:O	1.92	0.87
1:2A:2104:G:N2	1:2A:2105:C:N3	2.22	0.87
20:1Y:92:ASN:HB2	20:1Y:94:LYS:H	1.39	0.87
3:1D:71:ASP:HB3	3:1D:103:ARG:HH22	1.41	0.86
32:1a:664:G:H22	32:1a:741:G:H1	1.24	0.86
4:2E:110:GLY:O	61:2R:301:HOH:O	1.94	0.85
32:1a:406:G:H21	35:1d:119:GLN:HE22	1.25	0.85
32:1a:1158:C:H5	32:1a:1181:G:H1	1.24	0.85
29:27:24:THR:HG22	29:27:27:GLY:H	1.39	0.84
19:1X:31:HIS:HD2	19:1X:33:LYS:H	1.22	0.84
1:1A:1701:A:OP2	61:1A:4103:HOH:O	1.94	0.84
1:1A:1798:U:H5'	3:1D:259:THR:HG22	1.60	0.84
32:1a:1086:U:H3	32:1a:1099:G:H22	1.23	0.84
1:1A:2464:C:O2'	61:1A:4104:HOH:O	1.94	0.83
1:1A:1359:A:H61	1:1A:1372:U:H3	1.23	0.83
22:10:11:ARG:O	22:10:14:ARG:NH2	2.11	0.83
1:1A:1082:U:H3	1:1A:1086:A:H61	0.86	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1648:C:OP1	61:1A:4105:HOH:O	1.96	0.83
1:1A:2447:G:OP2	61:1A:4106:HOH:O	1.96	0.83
26:14:7:PRO:HB2	26:14:27:THR:HG21	1.61	0.82
8:2I:92:VAL:HG23	8:2I:120:ILE:HB	1.60	0.82
33:2b:166:ASP:HB3	33:2b:169:LYS:HB3	1.61	0.82
39:1h:95:VAL:HB	39:1h:99:GLU:HG3	1.61	0.81
1:2A:2141:G:O6	1:2A:2150:U:O2	1.97	0.81
34:2c:108:ASN:HD21	34:2c:144:SER:HB3	1.45	0.81
1:2A:2104:G:N7	1:2A:2186:G:N2	2.28	0.81
1:2A:2139:C:N3	1:2A:2152:G:N2	2.29	0.81
32:2a:1402:4OC:HM22	32:2a:1403:C:H5'	1.61	0.81
1:1A:1082:U:O4	1:1A:1086:A:N1	2.12	0.81
1:2A:1271:G:OP2	61:2A:3806:HOH:O	1.99	0.80
1:2A:2296:U:OP2	14:2S:9:ARG:NH2	2.14	0.80
1:2A:2748:A:H5'	7:2H:4:ILE:HD12	1.63	0.80
32:2a:1182:G:H4'	32:2a:1183:A:H3'	1.63	0.80
40:2i:29:ASN:HD21	40:2i:65:VAL:H	1.25	0.80
1:1A:2137:C:N4	1:1A:2154:G:N1	2.29	0.80
46:2o:54:ARG:HG2	46:2o:58:MET:HE2	1.62	0.80
1:1A:1816:G:O6	3:1D:35:LYS:NZ	2.14	0.80
33:2b:77:ALA:HB2	33:2b:211:ILE:HD13	1.62	0.80
1:1A:217:G:OP2	61:1A:4107:HOH:O	1.99	0.79
1:2A:2536:G:O6	61:2A:3807:HOH:O	2.00	0.79
32:2a:1500:A:OP1	61:2a:3205:HOH:O	1.99	0.79
32:1a:1025:U:C2	32:1a:1036:G:O6	2.35	0.79
1:1A:2822:G:OP2	61:1A:4108:HOH:O	2.01	0.79
1:2A:1602:U:O4	61:2A:3808:HOH:O	2.01	0.79
1:2A:2354:G:N7	61:2A:3827:HOH:O	2.14	0.79
32:2a:1054:C:H41	53:2y:46:GLN:HG3	1.48	0.78
1:2A:2365:G:N7	30:28:39:LYS:NZ	2.32	0.78
4:1E:119:ARG:HD3	4:1E:160:TYR:HB2	1.66	0.78
1:1A:1865:G:OP1	61:1A:4109:HOH:O	2.01	0.78
1:2A:2102:U:O2	1:2A:2187:G:O6	2.02	0.78
1:2A:2732:G:O6	61:2A:3809:HOH:O	2.02	0.78
15:1T:54:ARG:HA	15:1T:59:THR:HB	1.66	0.77
32:2a:427:U:OP1	35:2d:13:ARG:NH2	2.17	0.77
2:1B:114:C:N3	61:1B:301:HOH:O	2.17	0.77
1:1A:2102:U:O2	1:1A:2187:G:O6	2.03	0.77
1:2A:1314:C:OP1	61:2A:3810:HOH:O	2.02	0.77
1:2A:2115:G:H22	1:2A:2119:A:H5'	1.48	0.77
1:2A:1607:C:N4	1:2A:1622:G:OP2	2.17	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:6:HIS:HD2	34:2c:8:ILE:H	1.31	0.76
36:1e:107:ARG:NH1	61:1e:301:HOH:O	2.18	0.76
1:2A:2527:C:N4	61:2A:3807:HOH:O	2.16	0.76
38:2g:113:GLU:HG3	38:2g:119:ARG:HG2	1.67	0.76
61:1A:4545:HOH:O	11:1P:37:GLY:HA3	1.85	0.76
32:2a:1129:C:H2'	32:2a:1139:G:N7	2.00	0.76
35:2d:122:ARG:NH1	35:2d:134:ASP:O	2.19	0.76
1:2A:2131:G:H5''	1:2A:2132:U:H5'	1.68	0.76
22:20:11:ARG:O	22:20:14:ARG:NH2	2.19	0.76
44:2m:54:VAL:HG12	44:2m:57:ARG:HH12	1.50	0.76
32:2a:1046:A:N6	32:2a:1211:U:O2	2.19	0.75
42:1k:99:GLN:HG2	42:1k:105:VAL:HG21	1.67	0.75
1:1A:11:G:H2'	1:1A:12:U:H5''	1.68	0.75
1:1A:1271:G:OP2	61:1A:4105:HOH:O	2.03	0.75
1:1A:1971:A:OP1	61:1A:4110:HOH:O	2.04	0.75
32:1a:975:A:H4'	32:1a:976:G:H5''	1.68	0.75
1:1A:1378:A:OP1	29:17:10:ARG:NH2	2.19	0.75
41:2j:49:VAL:HG23	45:2n:41:ARG:HB2	1.69	0.75
1:2A:1647:G:OP1	61:2A:3806:HOH:O	2.03	0.75
3:1D:148:GLU:HB2	3:1D:151:LYS:HD2	1.69	0.75
26:14:16:CYS:SG	26:14:17:GLY:N	2.60	0.75
1:2A:2139:C:H42	1:2A:2152:G:H1	0.80	0.75
41:1j:35:SER:HB3	41:1j:73:ASP:HB2	1.68	0.75
32:2a:975:A:H4'	32:2a:976:G:H5''	1.68	0.75
1:2A:826:U:OP1	61:2A:3804:HOH:O	2.03	0.74
1:2A:989:G:O2'	61:2A:3811:HOH:O	2.05	0.74
33:2b:93:VAL:HG21	33:2b:97:TRP:HD1	1.50	0.74
1:1A:1059:G:O6	1:1A:1079:C:N3	2.20	0.74
46:1o:54:ARG:HG2	46:1o:58:MET:HE2	1.69	0.74
1:2A:2602:A:H1'	1:2A:2603:G:H5''	1.68	0.74
32:2a:664:G:H22	32:2a:741:G:H1	1.32	0.74
1:1A:219:G:OP2	61:1A:4111:HOH:O	2.04	0.74
10:1O:48:PRO:HB3	32:1a:1422:G:H5''	1.70	0.74
7:2H:3:ARG:HG2	7:2H:6:ARG:HE	1.52	0.74
35:2d:18:LYS:NZ	35:2d:31:CYS:SG	2.60	0.74
32:1a:73:G:H1	32:1a:96:U:H3	1.34	0.74
32:1a:1385:G:N7	61:1a:3311:HOH:O	2.19	0.74
32:2a:1003:G:H22	32:2a:1035:A:H61	1.34	0.74
1:1A:802:A:OP1	61:1A:4112:HOH:O	2.06	0.74
32:2a:21:G:OP1	61:2a:3206:HOH:O	2.06	0.74
32:2a:1285:A:H4'	32:2a:1286:A:H5'	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:2i:46:ALA:HB2	40:2i:74:ILE:HG23	1.68	0.74
1:1A:2470:G:OP2	61:1A:4113:HOH:O	2.06	0.74
1:2A:2107:C:N4	1:2A:2182:G:H1	1.84	0.74
32:1a:587:G:N7	61:1a:3315:HOH:O	2.20	0.73
32:1a:574:A:OP2	61:1a:3301:HOH:O	2.05	0.73
32:1a:544:G:OP1	35:1d:59:ARG:NH2	2.22	0.73
32:2a:1401:G:N7	53:2y:83:ARG:NH1	2.31	0.73
28:16:13:CYS:SG	28:16:47:THR:HG21	2.29	0.73
1:1A:1013:C:OP2	61:1A:4114:HOH:O	2.07	0.73
1:1A:2821:A:OP2	61:1A:4108:HOH:O	2.07	0.73
1:2A:1315:C:OP2	61:2A:3810:HOH:O	2.06	0.73
1:1A:1058:G:O6	1:1A:1080:C:N3	2.22	0.72
61:1A:4108:HOH:O	13:1R:3:HIS:NE2	2.20	0.72
26:24:16:CYS:SG	26:24:17:GLY:N	2.62	0.72
1:2A:1062:G:H2'	1:2A:1063:G:H8	1.53	0.72
32:2a:1128:C:H1'	32:2a:1147:C:H42	1.54	0.72
8:1I:92:VAL:HG13	8:1I:120:ILE:HB	1.71	0.72
40:1i:50:LEU:HB2	40:1i:55:ALA:HB3	1.72	0.72
1:1A:2058:MA6:H103	56:1A:4021:TEL:H583	1.71	0.72
6:1G:49:ASP:O	6:1G:51:ARG:N	2.21	0.72
1:2A:1007:C:OP1	9:2N:35:ARG:NH1	2.23	0.72
32:2a:401:C:OP2	35:2d:73:ARG:NH2	2.23	0.72
44:2m:65:LYS:HD2	44:2m:69:GLU:HB2	1.70	0.72
1:2A:955:C:OP1	12:2Q:87:LYS:NZ	2.23	0.72
4:2E:119:ARG:HD3	4:2E:160:TYR:HB2	1.71	0.72
5:2F:21:ALA:HB3	5:2F:22:ALA:HA	1.72	0.72
27:25:16:ARG:NH1	27:25:17:ASP:OD1	2.23	0.72
16:1U:59:ARG:NH1	61:1U:302:HOH:O	2.23	0.72
32:1a:1108:G:O6	61:1a:3302:HOH:O	2.08	0.72
1:1A:2427:C:OP1	61:1A:4115:HOH:O	2.08	0.72
1:2A:2377:A:N6	61:2A:3869:HOH:O	2.23	0.72
2:2B:85:G:OP1	61:2B:301:HOH:O	2.08	0.72
34:2c:35:GLU:OE2	34:2c:59:ARG:NH2	2.23	0.71
11:1P:59:LEU:HD21	30:18:10:ALA:HB2	1.72	0.71
1:2A:2126:A:H4'	1:2A:2127:G:O5'	1.89	0.71
24:22:65:ASN:OD1	24:22:69:ARG:NH1	2.24	0.71
1:2A:1970:A:N1	61:2A:3861:HOH:O	2.22	0.71
40:2i:51:ARG:HG2	40:2i:56:LEU:HD21	1.71	0.71
1:1A:1047:G:H2'	1:1A:1110:G:H22	1.55	0.71
1:2A:143:G:H4'	19:2X:35:THR:HG21	1.72	0.71
32:2a:1028:C:H2'	32:2a:1033:G:H22	1.56	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:1h:14:ARG:NH1	39:1h:83:ILE:O	2.23	0.71
3:1D:204:ILE:O	61:1D:402:HOH:O	2.08	0.71
1:2A:218:A:OP2	61:2A:3812:HOH:O	2.08	0.71
38:2g:70:LYS:HB3	38:2g:96:GLN:HB3	1.71	0.70
2:1B:77:U:OP1	21:1Z:19:ARG:NH2	2.23	0.70
1:2A:2448:A:OP1	61:2A:3802:HOH:O	2.08	0.70
1:2A:2839:G:H5'	13:2R:46:GLY:HA2	1.74	0.70
2:2B:49:C:OP1	61:2B:302:HOH:O	2.08	0.70
15:2T:60:THR:HG22	15:2T:77:PRO:HA	1.73	0.70
21:2Z:19:ARG:NH1	21:2Z:84:GLU:O	2.24	0.70
32:1a:44:G:N7	61:1a:3325:HOH:O	2.25	0.70
32:1a:405:U:O4	35:1d:2:GLY:N	2.24	0.70
1:2A:652(T):C:H2'	1:2A:652(U):G:C8	2.26	0.70
1:2A:994:C:OP1	16:2U:53:ARG:NH2	2.24	0.70
34:1c:6:HIS:HD2	34:1c:8:ILE:H	1.39	0.70
7:2H:143:GLN:NE2	7:2H:147:ASN:OD1	2.25	0.70
50:2s:50:ALA:HB1	50:2s:57:HIS:HB3	1.73	0.70
1:2A:1053:C:H2'	1:2A:1054:A:H8	1.57	0.70
5:1F:192:LEU:HD13	5:1F:194:MET:HE2	1.73	0.70
32:1a:1189:C:OP1	41:1j:51:ARG:NH2	2.25	0.70
32:1a:1518:MA6:H93	32:1a:1519:MA6:H92	1.72	0.70
1:2A:2115:G:N2	1:2A:2119:A:H5'	2.06	0.70
1:2A:2206:G:H3'	1:2A:2207:G:H8	1.56	0.70
32:2a:390:C:O3'	47:2p:28:ARG:NH2	2.25	0.70
1:1A:760:G:OP1	61:1A:4116:HOH:O	2.08	0.70
33:1b:21:ARG:HA	33:1b:39:ILE:HA	1.74	0.70
1:2A:2306:C:N4	6:2G:42:GLY:O	2.25	0.70
1:2A:2805:G:H2'	1:2A:2807:G:C8	2.27	0.70
32:2a:980:C:OP2	61:2a:3207:HOH:O	2.10	0.70
1:2A:1993:U:OP2	61:2A:3813:HOH:O	2.09	0.69
32:1a:1101:A:OP2	33:1b:96:ARG:NH1	2.26	0.69
1:1A:1647:G:OP1	61:1A:4105:HOH:O	2.08	0.69
36:1e:50:GLU:HB2	36:1e:53:LEU:HD13	1.73	0.69
1:2A:785:G:OP2	61:2A:3814:HOH:O	2.09	0.69
36:1e:37:ARG:HH12	36:1e:111:GLU:HG2	1.56	0.69
1:2A:641:C:O2'	1:2A:2350:C:OP1	2.11	0.69
19:2X:57:LEU:HD11	19:2X:78:LYS:HE3	1.73	0.69
1:1A:1069:A:H4'	1:1A:1070:A:H5''	1.74	0.69
44:1m:37:THR:O	44:1m:55:ARG:NH1	2.24	0.69
10:2O:115:VAL:HG13	10:2O:121:VAL:HG21	1.75	0.69
21:2Z:129:SER:HB3	21:2Z:132:ASN:HD22	1.56	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:271(U):G:N7	61:2A:3876:HOH:O	2.25	0.69
1:1A:1062:G:H2'	1:1A:1063:G:H8	1.56	0.69
44:2m:91:ARG:NE	44:2m:97:PRO:O	2.26	0.69
1:1A:271(M):G:H21	8:1I:50:ARG:HD3	1.56	0.69
3:1D:108:PRO:HD2	3:1D:111:LEU:HG	1.74	0.69
20:1Y:23:ARG:NH1	61:1Y:601:HOH:O	2.19	0.69
47:1p:43:LYS:HG2	47:1p:48:TRP:CE2	2.28	0.69
38:2g:50:ILE:HD11	38:2g:58:PRO:HA	1.75	0.69
1:2A:1754:C:OP1	15:2T:96:ARG:NH1	2.26	0.69
19:2X:35:THR:HG22	19:2X:37:THR:H	1.58	0.69
32:2a:1348:U:H4'	40:2i:120:ARG:HD2	1.75	0.69
34:2c:7:PRO:HB2	34:2c:182:ILE:HG21	1.75	0.69
1:1A:2153:G:H2'	1:1A:2154:G:C8	2.27	0.69
32:1a:1158:C:H5	32:1a:1181:G:N1	1.92	0.69
1:2A:527:C:N3	61:2A:3882:HOH:O	2.26	0.69
1:2A:848:G:OP1	61:2A:3815:HOH:O	2.11	0.69
32:2a:558:G:OP1	61:2a:3208:HOH:O	2.11	0.69
32:2a:1129:C:N3	32:2a:1143:G:N2	2.39	0.69
44:2m:13:LYS:HA	44:2m:44:ARG:HH11	1.57	0.69
1:1A:253:C:OP1	61:1A:4118:HOH:O	2.11	0.68
1:1A:2116:G:OP2	1:1A:2166:G:N2	2.17	0.68
1:1A:2126:A:H4'	1:1A:2127:G:O5'	1.93	0.68
1:1A:2789:C:O2	1:1A:2894:G:N1	2.26	0.68
1:2A:2023:G:H5'	1:2A:2617:C:H4'	1.75	0.68
40:2i:9:ARG:HB2	40:2i:104:ARG:HE	1.59	0.68
50:2s:22:LEU:O	50:2s:26:GLY:N	2.25	0.68
1:2A:2505:G:OP1	61:2A:3819:HOH:O	2.12	0.68
5:2F:30:PRO:HB3	11:2P:1:MET:HE1	1.74	0.68
32:2a:1508:G:OP1	61:2a:3205:HOH:O	2.12	0.68
47:2p:5:ARG:HH21	47:2p:28:ARG:HA	1.56	0.68
1:1A:1669:A:OP2	61:1A:4117:HOH:O	2.11	0.68
1:2A:7:G:H1	1:2A:2896:C:H42	1.41	0.68
16:1U:101:ARG:NH2	61:1U:303:HOH:O	2.25	0.68
40:1i:121:ARG:NH1	40:1i:122:ALA:O	2.27	0.68
5:2F:24:LEU:HD23	5:2F:115:ALA:HA	1.75	0.68
21:2Z:152:ALA:HA	21:2Z:155:LEU:HD13	1.74	0.68
26:14:56:VAL:HB	26:14:60:GLN:HG2	1.75	0.68
32:2a:986:A:N3	50:2s:52:TYR:OH	2.25	0.68
39:2h:19:VAL:HG23	39:2h:21:LYS:HD3	1.75	0.68
8:1I:109:ILE:HG13	8:1I:130:TYR:CZ	2.28	0.68
29:17:34:ARG:NH1	29:17:41:ARG:O	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:493:G:OP2	61:2A:3818:HOH:O	2.12	0.68
1:2A:1101:U:H2'	1:2A:1102:C:H6	1.58	0.68
1:2A:2550:G:OP1	61:2A:3803:HOH:O	2.11	0.68
1:1A:1319:G:OP2	61:1A:4122:HOH:O	2.12	0.68
1:2A:1047:G:H21	1:2A:1111:A:H62	1.42	0.68
32:2a:528:C:N4	43:2l:49:ASN:OD1	2.26	0.68
32:2a:887:G:N7	61:2a:3232:HOH:O	2.27	0.68
1:1A:826:U:OP1	61:1A:4115:HOH:O	2.11	0.68
1:1A:2222:G:OP2	61:1A:4120:HOH:O	2.12	0.68
36:1e:148:VAL:HG21	39:1h:107:LEU:HB3	1.76	0.68
1:2A:962:G:OP1	61:2A:3820:HOH:O	2.12	0.68
3:2D:71:ASP:HB3	3:2D:103:ARG:HH22	1.59	0.68
33:2b:50:GLU:O	33:2b:54:THR:N	2.25	0.68
1:1A:602:G:O2'	1:1A:655:A:N6	2.26	0.68
34:1c:15:THR:HG21	34:1c:181:ASN:HA	1.76	0.68
1:2A:526:A:OP1	61:2A:3821:HOH:O	2.12	0.68
19:2X:60:ARG:HH22	29:27:47:ARG:HH12	1.42	0.68
1:1A:1634:A:OP2	61:1A:4123:HOH:O	2.12	0.67
32:1a:612:C:O2	32:1a:629:G:N2	2.28	0.67
2:2B:58:A:OP2	61:2B:304:HOH:O	2.12	0.67
1:1A:1509(A):A:H2'	1:1A:1509(B):A:O4'	1.93	0.67
32:1a:79:G:N1	32:1a:90:U:N3	2.40	0.67
47:1p:53:VAL:HG12	47:1p:79:VAL:HG12	1.75	0.67
1:2A:2319:G:H22	14:2S:3:ARG:HD3	1.58	0.67
50:1s:50:ALA:HB1	50:1s:57:HIS:HB3	1.76	0.67
5:2F:185:ASP:HA	5:2F:188:ARG:HD3	1.75	0.67
40:2i:9:ARG:HG2	40:2i:14:VAL:HG12	1.77	0.67
50:1s:63:THR:OG1	50:1s:65:ASN:OD1	2.13	0.67
1:1A:330:A:H2	1:1A:1210:A:HO2'	1.41	0.67
1:1A:1024:G:OP2	61:1A:4119:HOH:O	2.11	0.67
1:1A:1364:G:N7	23:11:3:LYS:HE2	2.09	0.67
1:2A:2058:MA6:H93	56:2A:3744:TEL:H583	1.75	0.67
1:2A:2278:A:OP2	61:2A:3824:HOH:O	2.13	0.67
1:2A:2749:A:OP1	7:2H:3:ARG:NH1	2.28	0.67
33:1b:82:ARG:NH1	33:1b:92:TYR:OH	2.27	0.67
1:2A:1006:C:OP2	61:2A:3816:HOH:O	2.12	0.67
1:2A:1023:U:OP2	61:2A:3817:HOH:O	2.12	0.67
38:2g:57:GLU:HG3	38:2g:60:LYS:H	1.59	0.67
1:1A:1970:A:OP1	61:1A:4110:HOH:O	2.11	0.67
40:2i:42:ARG:NH2	40:2i:71:SER:OG	2.28	0.67
32:1a:38:G:H22	32:1a:397:A:H5'	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:2S:94:TYR:OH	14:2S:106:ARG:NH1	2.28	0.67
32:2a:573:A:OP2	61:2a:3209:HOH:O	2.12	0.67
32:2a:617:G:OP2	61:2a:3211:HOH:O	2.13	0.67
1:1A:365:C:OP1	61:1A:4121:HOH:O	2.12	0.67
1:1A:1382:G:N7	61:1A:4163:HOH:O	2.28	0.67
33:1b:231:GLU:HB3	33:1b:232:PRO:HD3	1.77	0.67
1:2A:752:A:H3'	29:27:1:MET:HE2	1.77	0.67
1:2A:2134:A:O2'	1:2A:2159:G:N3	2.28	0.67
1:2A:2821:A:OP2	61:2R:301:HOH:O	2.11	0.67
32:1a:992:U:H4'	32:1a:993:G:H5'	1.76	0.67
38:1g:111:ARG:NH1	38:1g:113:GLU:OE2	2.28	0.67
22:20:10:THR:HG22	22:20:12:ASN:H	1.60	0.67
5:1F:197:ASP:N	5:1F:197:ASP:OD1	2.28	0.66
44:2m:94:ARG:HB3	44:2m:96:LEU:HD12	1.76	0.66
36:1e:110:LEU:HD13	36:1e:118:ILE:HG21	1.78	0.66
1:2A:2115:G:H21	1:2A:2171:A:H61	1.43	0.66
1:1A:631:A:OP1	11:1P:65:ARG:NH1	2.26	0.66
1:2A:743:G:N7	61:2A:3898:HOH:O	2.28	0.66
7:2H:86:GLU:OE2	7:2H:132:ARG:NH2	2.28	0.66
18:2W:12:ILE:HD13	18:2W:17:VAL:HG13	1.77	0.66
1:1A:2611:U:H5'	1:1A:2611:U:H6	1.61	0.66
3:1D:206:LEU:HD22	3:1D:211:ARG:HG2	1.77	0.66
14:1S:52:SER:HB2	14:1S:55:ALA:H	1.59	0.66
35:1d:60:GLU:HG3	35:1d:202:LEU:HD12	1.76	0.66
2:2B:66:A:H61	2:2B:109:C:H5'	1.59	0.66
26:24:59:PHE:HA	26:24:61:ARG:N	2.11	0.66
26:24:62:ARG:O	26:24:64:GLY:N	2.28	0.66
32:2a:977:A:N6	32:2a:1224:G:OP1	2.26	0.66
1:2A:775:G:O3'	61:2A:3823:HOH:O	2.13	0.66
1:2A:1527:G:OP1	61:2A:3826:HOH:O	2.13	0.66
23:21:52:ARG:NH1	23:21:55:GLY:O	2.28	0.66
33:2b:74:LYS:O	33:2b:78:GLN:N	2.28	0.66
21:2Z:144:LEU:HD21	21:2Z:150:LEU:HD13	1.76	0.66
26:24:44:THR:O	26:24:46:GLN:N	2.27	0.66
32:2a:13:U:OP1	61:2a:3210:HOH:O	2.13	0.66
20:1Y:28:LYS:HD2	20:1Y:40:GLU:HG3	1.78	0.66
2:2B:58:A:OP2	61:2B:303:HOH:O	2.12	0.66
1:1A:365:C:OP2	61:1A:4124:HOH:O	2.13	0.66
32:2a:1271:G:O2'	61:2a:3212:HOH:O	2.14	0.66
1:1A:2319:G:N2	14:1S:3:ARG:HD3	2.00	0.66
1:2A:301:G:OP2	20:2Y:84:ARG:NH2	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2162:G:H4'	1:2A:2172:U:O2'	1.95	0.66
6:2G:150:ASP:OD1	6:2G:151:ALA:N	2.29	0.65
21:2Z:10:ARG:NH1	21:2Z:26:GLY:O	2.29	0.65
32:1a:1414:U:H3	32:1a:1486:G:H1	1.43	0.65
33:1b:40:HIS:HB3	33:1b:190:THR:HG21	1.76	0.65
17:2V:62:LEU:HD11	17:2V:95:LEU:HB2	1.78	0.65
36:2e:50:GLU:HB2	36:2e:53:LEU:HD13	1.79	0.65
11:1P:89:ALA:HA	11:1P:121:LYS:HD3	1.77	0.65
1:2A:1508:A:H4'	1:2A:1509(A):A:C6	2.31	0.65
1:1A:1315:C:OP2	61:1A:4125:HOH:O	2.14	0.65
2:2B:42:C:O2'	61:2B:305:HOH:O	2.14	0.65
25:23:13:ILE:O	61:23:5801:HOH:O	2.15	0.65
1:1A:1173:G:O2'	1:1A:1174:A:O5'	2.14	0.65
32:1a:812:C:N3	61:1a:3338:HOH:O	2.30	0.65
32:2a:300:A:N1	61:2a:3235:HOH:O	2.28	0.65
44:1m:11:ARG:HA	44:1m:45:VAL:HB	1.79	0.65
1:2A:1913:A:N1	32:2a:1491:G:N2	2.44	0.65
46:2o:16:ALA:HB1	46:2o:21:ASP:HB3	1.79	0.65
1:1A:1340:U:OP1	19:1X:16:LYS:NZ	2.26	0.65
1:2A:1762:A:N1	61:2A:3900:HOH:O	2.28	0.65
6:2G:40:ASN:HB3	6:2G:156:ASP:HB2	1.79	0.65
3:2D:206:LEU:HD22	3:2D:211:ARG:HG2	1.78	0.65
32:2a:1086:U:H3	32:2a:1099:G:H22	1.42	0.65
1:1A:2023:G:H5'	1:1A:2617:C:H4'	1.78	0.65
1:2A:1920:OMC:HM22	1:2A:1921:G:H5'	1.78	0.65
28:26:35:GLU:OE2	28:26:50:ARG:NH1	2.30	0.65
1:1A:226:G:H21	1:1A:228:A:H62	1.43	0.64
23:11:21:ARG:HD3	23:11:35:THR:HG21	1.79	0.64
5:2F:101:LEU:HD12	5:2F:102:PRO:HD2	1.79	0.64
35:1d:172:PRO:HB2	35:1d:187:ARG:HH21	1.62	0.64
21:2Z:72:ARG:HG2	21:2Z:89:PHE:HB2	1.78	0.64
26:24:59:PHE:HA	26:24:60:GLN:C	2.22	0.64
34:2c:109:PRO:HB3	34:2c:115:LEU:HD23	1.79	0.64
1:1A:1143:A:OP1	9:1N:25:ARG:NH2	2.29	0.64
9:1N:46:VAL:HG23	9:1N:48:MET:HG2	1.78	0.64
34:1c:180:ALA:HB1	34:1c:203:PHE:HE1	1.63	0.64
1:2A:664:C:OP1	61:2A:3825:HOH:O	2.13	0.64
6:2G:3:LEU:HD23	6:2G:3:LEU:H	1.62	0.64
39:2h:121:ASP:N	39:2h:121:ASP:OD1	2.30	0.64
1:2A:2123:G:O6	1:2A:2175:C:N3	2.30	0.64
1:1A:602:G:N7	61:1A:4169:HOH:O	2.29	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2142:C:N3	1:1A:2149:G:O6	2.31	0.64
32:2a:273:A:H1'	48:2q:16:GLN:HE21	1.62	0.64
40:2i:4:TYR:HB2	40:2i:19:LEU:HB2	1.78	0.64
1:1A:1175:U:O2'	1:1A:1176:G:O5'	2.15	0.64
1:1A:2115:G:H2'	1:1A:2117:A:N6	2.12	0.64
32:1a:1278:U:H5'	32:1a:1279:A:O4'	1.97	0.64
47:2p:47:ASP:OD1	47:2p:47:ASP:N	2.31	0.64
1:2A:1171:G:N2	1:2A:1179:C:N3	2.46	0.64
32:2a:117:G:OP2	61:2a:3213:HOH:O	2.14	0.64
6:1G:79:ASN:OD1	6:1G:79:ASN:N	2.30	0.64
1:2A:731:C:OP1	61:2A:3828:HOH:O	2.15	0.64
1:2A:1891:G:N7	61:2A:3906:HOH:O	2.29	0.64
6:2G:97:ASP:HA	6:2G:100:TRP:HD1	1.62	0.64
1:1A:2142:C:C2	1:1A:2149:G:N1	2.65	0.64
6:1G:126:ASP:HB2	6:1G:130:ASN:H	1.62	0.64
1:2A:607:U:OP1	5:2F:102:PRO:HA	1.97	0.64
32:2a:1028:C:H2'	32:2a:1033:G:N2	2.13	0.64
32:1a:201:C:N4	32:1a:216:G:H1	1.91	0.63
32:1a:366:C:N3	61:1a:3339:HOH:O	2.30	0.63
38:1g:140:ASP:OD1	38:1g:143:ARG:NH2	2.31	0.63
1:2A:1010:A:OP2	61:2A:3829:HOH:O	2.15	0.63
32:2a:437:U:H5''	35:2d:155:LEU:HD11	1.80	0.63
1:2A:2156:G:N7	1:2A:2157:G:N2	2.46	0.63
41:2j:16:LEU:HD12	41:2j:94:VAL:HG22	1.80	0.63
5:1F:164:ARG:HE	58:1F:320:ARG:HH12	1.45	0.63
1:2A:2206:G:H5''	1:2A:2207:G:C8	2.32	0.63
4:2E:116:VAL:HG13	4:2E:122:PHE:HB2	1.79	0.63
24:22:22:GLU:OE2	24:22:68:ARG:NH2	2.32	0.63
1:1A:1359:A:N6	1:1A:1372:U:H3	1.93	0.63
21:1Z:69:THR:HG22	21:1Z:90:VAL:HG12	1.80	0.63
26:14:61:ARG:HG3	26:14:62:ARG:H	1.64	0.63
32:1a:588:G:OP2	61:1a:3304:HOH:O	2.15	0.63
1:2A:2810:A:N6	1:2A:2891:G:O2'	2.32	0.63
6:2G:43:LEU:HD11	6:2G:153:ARG:HD2	1.79	0.63
1:1A:994:C:OP1	16:1U:53:ARG:NH2	2.30	0.63
7:1H:98:LEU:HD13	7:1H:125:VAL:HG23	1.79	0.63
32:2a:1002:G:H2'	32:2a:1003:G:C8	2.34	0.63
32:2a:1286:A:H8	32:2a:1287:A:H4'	1.62	0.63
51:1t:47:GLY:HA2	51:1t:48:LYS:HB2	1.79	0.63
1:2A:307:G:N7	61:2A:3914:HOH:O	2.30	0.63
34:2c:22:TRP:HA	41:2j:93:GLY:HA2	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2079:U:OP1	23:11:21:ARG:NH2	2.32	0.63
21:1Z:144:LEU:HD21	21:1Z:150:LEU:HD13	1.79	0.63
32:1a:189(K):U:H2'	32:1a:189(L):G:H8	1.63	0.63
1:2A:2206:G:H3'	1:2A:2207:G:C8	2.34	0.63
32:2a:1010:G:H2'	32:2a:1011:G:H8	1.63	0.63
33:2b:93:VAL:HG21	33:2b:97:TRP:CD1	2.33	0.63
19:1X:2:LYS:NZ	19:1X:38:GLU:OE2	2.20	0.63
19:1X:41:ASN:O	19:1X:45:THR:HG23	1.98	0.63
38:2g:111:ARG:NH2	38:2g:126:ASP:OD2	2.32	0.63
1:1A:123:G:OP2	61:1A:4126:HOH:O	2.15	0.63
1:2A:2538:C:N4	61:2A:3832:HOH:O	2.30	0.63
5:2F:11:VAL:HG22	5:2F:125:LEU:HB2	1.81	0.62
6:2G:106:LEU:HA	6:2G:110:ALA:HB3	1.81	0.62
32:2a:954:G:H21	32:2a:1227:A:H62	1.47	0.62
41:2j:38:ILE:HD11	41:2j:71:LEU:HD23	1.81	0.62
1:1A:607:U:OP1	5:1F:102:PRO:HA	1.99	0.62
35:1d:166:LYS:HD3	35:1d:168:ARG:HH12	1.64	0.62
1:2A:825:C:O2	11:2P:55:ARG:NH1	2.32	0.62
10:2O:104:ARG:NH1	61:2O:303:HOH:O	2.32	0.62
1:1A:2133:G:H3'	1:1A:2157:G:H21	1.64	0.62
32:1a:299:G:O6	61:1a:3303:HOH:O	2.14	0.62
1:2A:2429:G:OP1	61:2A:3804:HOH:O	2.16	0.62
33:2b:174:VAL:O	33:2b:178:ARG:HG2	1.99	0.62
40:2i:47:LEU:HB3	40:2i:50:LEU:HD12	1.82	0.62
32:1a:1182:G:H4'	32:1a:1183:A:H5'	1.80	0.62
2:2B:53:A:OP2	61:2B:306:HOH:O	2.16	0.62
13:2R:72:ASP:HB3	13:2R:75:LEU:HB3	1.82	0.62
1:1A:2805:G:H2'	1:1A:2807:G:C8	2.34	0.62
21:2Z:110:GLY:HA3	21:2Z:174:VAL:HG11	1.80	0.62
32:2a:316:G:OP2	32:2a:351:G:O2'	2.16	0.62
50:2s:36:ARG:HH12	50:2s:75:ALA:HB3	1.65	0.62
1:1A:2602:A:H4'	1:1A:2603:G:OP1	2.00	0.62
35:1d:122:ARG:NH1	35:1d:134:ASP:O	2.32	0.62
4:2E:2:LYS:NZ	4:2E:95:ILE:O	2.28	0.62
13:2R:87:TYR:OH	13:2R:117:VAL:O	2.16	0.62
32:2a:1030(C):G:H2'	32:2a:1030(D):A:C8	2.34	0.62
32:2a:1129:C:N4	32:2a:1143:G:N1	2.44	0.62
1:1A:1059:G:N1	1:1A:1079:C:O2	2.31	0.62
1:1A:1155:A:OP1	16:1U:55:ARG:HD3	1.99	0.62
7:1H:124:GLU:HB2	7:1H:132:ARG:HB3	1.82	0.62
24:12:65:ASN:OD1	24:12:69:ARG:NH1	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1014:U:H2'	1:2A:1015:G:H8	1.65	0.62
1:2A:1796:U:H2'	1:2A:1797:C:C6	2.34	0.62
9:2N:46:VAL:HG23	9:2N:48:MET:HG2	1.81	0.62
35:2d:79:PHE:HE1	35:2d:204:ILE:HD13	1.62	0.62
41:2j:8:LEU:HB2	41:2j:70:ARG:HB2	1.82	0.62
2:1B:6:C:H2'	2:1B:7:G:H5''	1.82	0.62
1:2A:733:G:N1	61:2A:3854:HOH:O	2.20	0.62
1:2A:1057:A:N6	1:2A:1087:G:OP1	2.32	0.62
32:2a:1295:G:O2'	44:2m:14:ARG:NH1	2.33	0.62
32:2a:1518:MA6:H93	32:2a:1519:MA6:H102	1.79	0.62
36:1e:91:LEU:HB3	36:1e:118:ILE:HD11	1.82	0.62
1:2A:300:A:OP1	20:2Y:86:ARG:NH2	2.33	0.62
1:2A:1123:C:H1'	31:29:18:ARG:HH12	1.63	0.62
41:2j:62:HIS:HB3	45:2n:59:ALA:HB3	1.81	0.62
44:2m:23:TYR:HB3	44:2m:67:GLU:HA	1.82	0.62
1:1A:1671:U:O4	61:1A:4117:HOH:O	2.15	0.61
5:2F:110:LEU:HD11	5:2F:181:LEU:HG	1.81	0.61
32:2a:1347:G:N2	32:2a:1373:G:H2'	2.14	0.61
34:2c:54:ARG:HB2	34:2c:69:HIS:HB2	1.81	0.61
47:2p:43:LYS:HG2	47:2p:48:TRP:CD2	2.35	0.61
51:2t:51:GLU:HA	51:2t:54:LYS:HE2	1.82	0.61
1:1A:2099:U:H3	1:1A:2190:G:H1	1.46	0.61
21:1Z:158:PRO:HG2	21:1Z:161:VAL:HG11	1.83	0.61
32:1a:60:A:H4'	32:1a:61:G:H5'	1.82	0.61
32:1a:266:G:H5'	32:1a:268:C:H41	1.66	0.61
32:1a:1151:A:HO2'	32:1a:1152:A:H8	1.48	0.61
44:1m:23:TYR:HB3	44:1m:67:GLU:HA	1.82	0.61
47:1p:75:ARG:HG3	47:1p:80:PHE:HD2	1.65	0.61
37:2f:35:ALA:HA	37:2f:67:MET:HB3	1.82	0.61
48:2q:53:LEU:HD23	48:2q:82:MET:HE1	1.82	0.61
11:1P:64:LYS:NZ	61:1P:302:HOH:O	2.30	0.61
20:1Y:92:ASN:HB2	20:1Y:94:LYS:N	2.15	0.61
32:1a:1183:A:O2'	32:1a:1184:G:OP1	2.17	0.61
1:2A:1803:A:O2'	61:2A:3833:HOH:O	2.16	0.61
3:2D:106:ILE:HD11	3:2D:143:HIS:HD2	1.65	0.61
32:2a:134:A:N6	47:2p:25:ARG:HH22	1.97	0.61
37:2f:68:PRO:HG2	37:2f:71:ARG:HH11	1.64	0.61
51:2t:57:ARG:HH22	51:2t:100:ILE:HD12	1.65	0.61
21:1Z:3:TYR:CD2	21:1Z:51:ALA:HB2	2.36	0.61
38:2g:72:ARG:NH2	38:2g:142:GLU:OE1	2.33	0.61
50:2s:63:THR:HG23	50:2s:65:ASN:H	1.64	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1094:U:H1'	1:1A:1097:U:H5	1.65	0.61
1:1A:1803:A:O2'	3:1D:259:THR:HG21	1.99	0.61
1:1A:2142:C:O2	1:1A:2149:G:N1	2.33	0.61
2:1B:7:G:N2	61:1B:308:HOH:O	2.32	0.61
32:2a:17:U:H2'	32:2a:18:C:C6	2.35	0.61
1:1A:548:A:N6	17:1V:19:LYS:H	1.99	0.61
1:1A:2820:A:OP2	13:1R:2:ARG:NH2	2.33	0.61
2:1B:7:G:H5''	2:1B:7:G:H8	1.65	0.61
2:2B:75:G:H22	21:2Z:73:GLN:NE2	1.99	0.61
10:1O:63:VAL:HG12	10:1O:106:LEU:HD11	1.82	0.61
33:1b:59:GLU:HB3	33:1b:221:LEU:HD11	1.80	0.61
44:1m:58:GLU:O	44:1m:62:ASN:ND2	2.32	0.61
56:2A:3744:TEL:H381	56:2A:3744:TEL:H171	1.83	0.61
32:2a:1278:U:H5''	32:2a:1279:A:H5'	1.81	0.61
44:2m:3:ARG:HB2	44:2m:8:GLU:HA	1.81	0.61
1:1A:1113:U:H2'	1:1A:1114:G:C8	2.36	0.61
32:1a:946:A:H2'	32:1a:947:G:C8	2.35	0.61
1:2A:1639:U:H2'	1:2A:1640:C:H5''	1.83	0.61
1:2A:1890:A:OP2	61:2A:3834:HOH:O	2.16	0.61
36:2e:144:THR:H	36:2e:147:ASP:HB2	1.65	0.61
1:2A:2153:G:H2'	1:2A:2154:G:C8	2.35	0.61
1:2A:2469:A:H4'	12:2Q:56:ARG:HG2	1.82	0.61
2:2B:14:U:OP2	2:2B:70:C:O2'	2.19	0.61
32:2a:179:A:H2'	32:2a:180:U:H6	1.65	0.61
1:1A:1078:U:C5	1:1A:1088:A:H5''	2.36	0.61
1:1A:2791:C:H5'	1:1A:2893:G:N2	2.16	0.61
5:1F:53:THR:CG2	5:1F:55:GLY:H	2.13	0.61
31:19:8:LYS:NZ	61:19:201:HOH:O	2.33	0.61
32:1a:315:A:OP1	61:1a:3305:HOH:O	2.15	0.61
32:1a:965:A:OP2	53:1y:8:LYS:NZ	2.34	0.61
1:2A:666:G:OP2	61:2A:3835:HOH:O	2.16	0.61
1:2A:2584:U:H2'	1:2A:2585:U:H2'	1.83	0.61
6:2G:138:GLN:HE22	6:2G:153:ARG:NH2	1.99	0.61
32:2a:402:G:O2'	32:2a:620:C:N3	2.34	0.61
33:2b:119:GLU:OE2	33:2b:153:ARG:NH1	2.34	0.61
1:1A:1062:G:N3	1:1A:1088:A:N6	2.49	0.60
4:1E:12:THR:HG21	15:1T:11:GLU:OE2	2.00	0.60
35:1d:59:ARG:HH12	35:1d:66:ARG:HH12	1.47	0.60
41:1j:81:THR:HA	41:1j:84:GLN:HE21	1.64	0.60
1:2A:889:C:O2'	1:2A:890:A:O5'	2.19	0.60
1:2A:957:A:OP2	61:2A:3831:HOH:O	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1004:A:H5''	32:2a:1025:U:C5	2.36	0.60
32:2a:1047:G:H5''	45:2n:4:LYS:HE2	1.83	0.60
32:2a:1435:G:H2'	32:2a:1436:U:C6	2.37	0.60
1:1A:1300:U:H4'	1:1A:1301:A:H5''	1.83	0.60
7:1H:20:ALA:HB1	7:1H:21:PRO:HD2	1.83	0.60
32:1a:269:C:H2'	32:1a:270:A:C8	2.35	0.60
33:1b:163:PHE:HA	33:1b:185:ILE:HG12	1.83	0.60
46:1o:39:LEU:HD13	46:1o:56:LEU:HB2	1.83	0.60
3:1D:88:ARG:NH1	61:1D:405:HOH:O	2.33	0.60
20:1Y:92:ASN:H	20:1Y:92:ASN:HD22	1.47	0.60
39:1h:10:LEU:HD22	39:1h:83:ILE:HD11	1.84	0.60
6:2G:47:LYS:HG3	6:2G:48:GLU:H	1.66	0.60
32:2a:1003:G:H3'	32:2a:1003:G:N3	2.16	0.60
41:2j:11:PHE:HE1	41:2j:67:THR:HG22	1.65	0.60
1:1A:1187:G:H5''	17:1V:81:TYR:CE1	2.36	0.60
15:1T:56:GLY:O	15:1T:59:THR:HG23	2.02	0.60
15:1T:59:THR:HG21	61:1T:324:HOH:O	2.01	0.60
35:1d:85:LYS:HE3	35:1d:86:LYS:HG3	1.84	0.60
1:2A:271(G):C:H2'	1:2A:271(H):G:H8	1.64	0.60
1:2A:737:C:OP1	61:2A:3836:HOH:O	2.16	0.60
1:2A:1187:G:H5'	17:2V:81:TYR:CE1	2.36	0.60
32:2a:1172:C:H2'	32:2a:1173:G:H8	1.66	0.60
1:1A:548:A:H61	17:1V:19:LYS:H	1.48	0.60
1:1A:2805:G:H2'	1:1A:2807:G:H8	1.67	0.60
33:2b:84:GLU:HB3	33:2b:219:VAL:HG21	1.82	0.60
51:2t:65:LYS:HA	51:2t:68:LYS:HD3	1.84	0.60
1:1A:1796:U:H2'	1:1A:1797:C:C6	2.36	0.60
1:1A:2753:A:N3	31:19:15:LYS:NZ	2.50	0.60
4:1E:36:ARG:NH1	4:1E:85:ASN:OD1	2.34	0.60
7:1H:40:GLU:OE1	7:1H:60:ARG:NH1	2.35	0.60
32:1a:1316:G:N1	32:1a:1319:A:OP2	2.35	0.60
32:2a:662:G:H2'	32:2a:663:A:C8	2.36	0.60
40:2i:25:LYS:H	40:2i:60:ASP:HB3	1.67	0.60
1:1A:889:C:O2'	1:1A:890:A:O5'	2.18	0.60
1:1A:2683:C:OP1	15:1T:53:ARG:NH2	2.34	0.60
26:24:59:PHE:HB2	26:24:62:ARG:HH12	1.67	0.60
42:2k:117:ASN:N	42:2k:117:ASN:OD1	2.34	0.60
32:1a:636:U:H2'	32:1a:637:G:C8	2.37	0.60
1:2A:1056:G:H5''	1:2A:1057:A:H5'	1.82	0.60
5:2F:154:VAL:HG22	5:2F:191:ARG:HB2	1.84	0.60
10:2O:73:ASP:HB2	15:2T:82:LEU:HD13	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2d:14:ARG:HG3	35:2d:59:ARG:NH1	2.17	0.60
1:1A:1240:U:OP1	61:1A:4128:HOH:O	2.16	0.60
6:1G:67:LYS:HD3	26:14:5:ILE:HB	1.84	0.60
32:1a:1456:G:N1	51:1t:51:GLU:OE2	2.34	0.60
36:1e:8:GLU:HG2	36:1e:34:VAL:HG12	1.84	0.60
1:2A:362:U:O2'	1:2A:363:G:H5'	2.02	0.60
1:1A:1508:A:H4'	1:1A:1509(A):A:C6	2.36	0.60
32:1a:316:G:OP2	32:1a:351:G:O2'	2.18	0.60
32:1a:673:G:H2'	32:1a:674:G:C8	2.37	0.60
33:1b:67:THR:HA	33:1b:90:MET:HE2	1.83	0.60
1:2A:271(L):U:H5'	8:2I:50:ARG:HH22	1.66	0.60
1:2A:509:C:OP1	61:2A:3830:HOH:O	2.16	0.60
1:1A:674:G:H1'	5:1F:74:ARG:HD3	1.83	0.59
31:19:8:LYS:H	31:19:34:GLN:HE22	1.49	0.59
41:1j:33:GLN:O	41:1j:75:ILE:N	2.35	0.59
1:2A:1025:G:C4	1:2A:1135:C:H1'	2.37	0.59
1:2A:1533:G:N2	1:2A:1536:C:N3	2.49	0.59
1:2A:2525:G:O6	61:2A:3832:HOH:O	2.16	0.59
1:2A:1493:C:N4	1:2A:2206:G:O2'	2.33	0.59
30:28:23:VAL:HG11	30:28:47:LYS:HD3	1.83	0.59
35:2d:201:GLN:NE2	36:2e:116:THR:O	2.34	0.59
13:1R:2:ARG:HG2	13:1R:5:LYS:HB2	1.84	0.59
32:1a:558:G:OP1	61:1a:3303:HOH:O	2.17	0.59
32:1a:1442:G:H2'	32:1a:1442:G:N3	2.17	0.59
5:2F:20:LEU:HD23	5:2F:21:ALA:H	1.67	0.59
32:2a:750:G:N3	46:2o:23:GLY:HA3	2.17	0.59
33:2b:118:LEU:HD22	33:2b:142:LEU:HB2	1.84	0.59
1:1A:71:A:N7	19:1X:31:HIS:HE1	2.00	0.59
1:1A:1056:G:O3'	1:1A:1057:A:H8	1.84	0.59
4:1E:116:VAL:HG13	4:1E:122:PHE:HB2	1.84	0.59
33:1b:224:GLN:HB2	33:1b:229:VAL:HG13	1.83	0.59
41:1j:9:ARG:HG2	41:1j:69:ASN:HD22	1.67	0.59
1:2A:857:C:OP2	22:20:77:ARG:NH2	2.34	0.59
1:2A:1064:C:H3'	1:2A:1065:U:H5'	1.83	0.59
8:2I:57:ARG:HH11	8:2I:61:ARG:HH22	1.50	0.59
12:2Q:75:THR:HG21	12:2Q:87:LYS:HE3	1.83	0.59
33:2b:47:THR:HG22	33:2b:202:PRO:HG2	1.85	0.59
1:1A:1508:A:H4'	1:1A:1509(A):A:C5	2.37	0.59
1:1A:2228:G:OP1	3:1D:261:LYS:NZ	2.27	0.59
19:1X:53:LYS:HB3	19:1X:82:GLN:HB3	1.85	0.59
21:1Z:144:LEU:HD11	21:1Z:150:LEU:HD22	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:222:U:H2'	32:1a:223:U:C6	2.38	0.59
32:1a:1077:G:N2	32:1a:1080:A:OP2	2.36	0.59
1:2A:963:U:OP2	61:2A:3820:HOH:O	2.16	0.59
18:2W:18:ARG:NH1	18:2W:76:VAL:O	2.35	0.59
5:1F:188:ARG:NH2	61:1F:401:HOH:O	2.28	0.59
32:1a:1003:G:N2	32:1a:1004:A:N3	2.50	0.59
1:2A:2150:U:H2'	1:2A:2151:G:C8	2.38	0.59
1:2A:2218:U:O4'	23:21:52:ARG:NH2	2.36	0.59
49:2r:52:PRO:HB2	49:2r:54:ARG:HG2	1.83	0.59
32:1a:1025:U:O2	32:1a:1036:G:O6	2.20	0.59
33:1b:123:ALA:O	33:1b:124:SER:HB2	2.03	0.59
26:24:58:ARG:HH21	50:2s:68:GLY:H	1.49	0.59
32:2a:978:A:O2'	32:2a:1322:C:N3	2.34	0.59
1:1A:2882:A:OP1	13:1R:96:ARG:HD3	2.03	0.59
33:1b:102:LEU:HB3	33:1b:180:LEU:HD12	1.84	0.59
35:1d:109:GLY:HA3	35:1d:165:MET:HG3	1.85	0.59
32:2a:164:U:H2'	32:2a:165:C:C6	2.38	0.59
33:2b:48:MET:HA	33:2b:51:LEU:HD12	1.84	0.59
1:1A:456:C:H4'	61:1A:4807:HOH:O	2.03	0.59
10:2O:87:ILE:HD12	10:2O:91:LEU:HA	1.83	0.59
15:2T:109:GLU:HG2	15:2T:112:ARG:HH22	1.67	0.59
15:2T:127:ALA:C	15:2T:129:ARG:H	2.10	0.59
32:2a:673:G:H2'	32:2a:674:G:C8	2.37	0.59
32:2a:1025:U:O2'	32:2a:1026:G:N7	2.35	0.59
33:2b:114:ARG:O	33:2b:118:LEU:HB2	2.03	0.59
38:2g:132:GLY:O	38:2g:136:LYS:HG2	2.03	0.59
1:1A:13:A:H4'	61:1A:4189:HOH:O	2.02	0.59
1:1A:1266:G:O5'	18:1W:15:ARG:NH2	2.35	0.59
2:1B:103:G:H21	21:1Z:73:GLN:HE22	1.51	0.59
32:1a:1010:G:N2	32:1a:1020:U:H1'	2.18	0.59
1:2A:2237:G:OP1	61:2A:3839:HOH:O	2.17	0.59
6:1G:66:GLN:NE2	6:1G:93:THR:O	2.33	0.58
32:1a:67:C:H2'	32:1a:68:G:C8	2.38	0.58
32:1a:413:G:N7	35:1d:35:ARG:NH1	2.51	0.58
32:1a:976:G:H5'	32:1a:1358:U:O2'	2.03	0.58
1:2A:1530:C:H42	1:2A:1539:G:H1	1.51	0.58
48:2q:22:LEU:HD11	48:2q:39:SER:HB2	1.85	0.58
1:1A:249:C:O2'	11:1P:64:LYS:NZ	2.17	0.58
8:1I:123:LEU:HD23	8:1I:144:VAL:HG12	1.86	0.58
23:11:80:LEU:HB3	23:11:82:LEU:HG	1.85	0.58
32:1a:614:A:OP1	35:1d:85:LYS:NZ	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:731:G:H5'	32:1a:766:A:H4'	1.84	0.58
32:1a:1435:G:H2'	32:1a:1436:U:C6	2.39	0.58
53:1y:49:VAL:HG22	53:1y:66:LYS:HG2	1.85	0.58
32:2a:1521:G:N3	61:2a:3245:HOH:O	2.32	0.58
41:1j:5:ARG:NE	41:1j:73:ASP:OD1	2.27	0.58
47:1p:14:ASN:OD1	47:1p:42:ARG:NH2	2.35	0.58
1:2A:570:G:O6	61:2A:3802:HOH:O	2.14	0.58
32:2a:437:U:H5'	35:2d:155:LEU:HD21	1.84	0.58
32:2a:942:G:N2	40:2i:124:GLN:OE1	2.35	0.58
8:1I:68:LEU:HD21	8:1I:109:ILE:HD11	1.84	0.58
32:1a:973:G:H3'	32:1a:974:A:H5''	1.86	0.58
1:2A:1250:G:H5''	61:2A:5569:HOH:O	2.02	0.58
21:2Z:53:ILE:HG22	21:2Z:71:VAL:HG23	1.84	0.58
28:26:8:LYS:NZ	61:26:601:HOH:O	2.36	0.58
33:2b:164:VAL:HB	33:2b:186:ALA:HB2	1.84	0.58
34:2c:67:THR:HG23	34:2c:102:ASN:HB2	1.85	0.58
6:1G:50:ALA:O	6:1G:52:ILE:N	2.34	0.58
16:1U:33:ARG:NH2	61:1U:304:HOH:O	2.34	0.58
32:1a:7:G:H5'	32:1a:298:A:O4'	2.02	0.58
32:1a:1312:G:N7	50:1s:2:PRO:HD2	2.19	0.58
36:1e:152:ARG:HB2	39:1h:43:GLY:HA3	1.85	0.58
44:1m:12:ASN:O	44:1m:44:ARG:NH1	2.36	0.58
24:22:35:LEU:HD12	24:22:53:LEU:HD12	1.84	0.58
32:2a:266:G:N3	32:2a:266:G:H5''	2.18	0.58
32:2a:1014:A:C2	32:2a:1219:U:H1'	2.38	0.58
34:2c:8:ILE:HD12	34:2c:16:ARG:HD2	1.83	0.58
46:2o:39:LEU:HD13	46:2o:56:LEU:HB2	1.84	0.58
30:18:56:GLU:HG2	61:18:220:HOH:O	2.03	0.58
38:1g:152:ALA:O	38:1g:155:ARG:NH1	2.29	0.58
32:2a:1151:A:O2'	32:2a:1152:A:H8	1.87	0.58
11:1P:95:VAL:HG22	11:1P:125:VAL:HB	1.86	0.58
33:1b:166:ASP:HB3	33:1b:169:LYS:HB3	1.86	0.58
41:1j:61:GLU:OE2	45:1n:58:LYS:NZ	2.31	0.58
1:2A:2079:U:O3'	23:21:35:THR:OG1	2.20	0.58
2:2B:13:A:N1	2:2B:69:G:O2'	2.32	0.58
1:1A:1176:G:H1'	1:1A:1177:A:H5''	1.86	0.58
32:1a:407:G:H5''	35:1d:115:ARG:HB3	1.86	0.58
37:1f:69:GLU:H	37:1f:69:GLU:CD	2.11	0.58
2:2B:38:C:OP2	61:2B:307:HOH:O	2.17	0.58
40:2i:53:VAL:O	40:2i:55:ALA:N	2.37	0.58
41:1j:46:ARG:NH2	41:1j:64:GLU:OE1	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:2X:60:ARG:NH1	29:27:47:ARG:HH22	2.01	0.58
32:2a:1010:G:H2'	32:2a:1011:G:C8	2.39	0.58
36:2e:102:ALA:HB1	36:2e:106:PRO:HG2	1.86	0.58
32:1a:1510:U:H2'	32:1a:1511:G:C8	2.39	0.58
1:2A:621:A:OP2	11:2P:108:LYS:NZ	2.34	0.58
1:2A:2127:G:N1	1:2A:2161:C:O2	2.36	0.58
2:2B:77:U:OP1	21:2Z:19:ARG:NH2	2.37	0.58
34:2c:28:GLN:HB3	34:2c:32:LEU:HD11	1.85	0.58
39:2h:49:GLU:OE2	39:2h:62:TYR:OH	2.20	0.58
1:1A:588:U:H2'	1:1A:589:C:C6	2.39	0.57
1:1A:911:A:H2'	12:1Q:9:TYR:OH	2.03	0.57
1:2A:951:C:OP1	61:2A:3840:HOH:O	2.17	0.57
1:2A:2379:G:O2'	14:2S:17:ARG:NH1	2.34	0.57
6:2G:12:TYR:HA	6:2G:16:ARG:HG3	1.86	0.57
31:29:25:VAL:HB	31:29:34:GLN:HB2	1.86	0.57
32:2a:1129:C:H42	32:2a:1143:G:H1	1.50	0.57
1:1A:330:A:H2	1:1A:1210:A:O2'	1.87	0.57
12:2Q:135:ASP:OD2	21:2Z:49:ARG:NH1	2.36	0.57
21:2Z:128:VAL:HG12	21:2Z:161:VAL:HA	1.85	0.57
32:2a:890:G:O2'	32:2a:906:G:O6	2.16	0.57
32:2a:992:U:H4'	32:2a:993:G:O5'	2.04	0.57
35:2d:175:SER:HB3	35:2d:186:LEU:HD21	1.85	0.57
34:1c:124:ILE:HG22	34:1c:130:VAL:HG22	1.86	0.57
1:2A:1371:G:HO2'	1:2A:1372:U:H5	1.52	0.57
32:2a:769:G:H4'	32:2a:1513:A:H4'	1.86	0.57
41:2j:5:ARG:N	61:2j:302:HOH:O	2.38	0.57
1:1A:72:U:OP1	61:1A:4130:HOH:O	2.17	0.57
1:1A:1405:U:H2'	1:1A:1406:U:C6	2.39	0.57
37:1f:68:PRO:HG2	37:1f:71:ARG:HD2	1.85	0.57
1:2A:668:G:H5'	1:2A:669:G:OP2	2.03	0.57
1:2A:1378:A:OP1	29:27:10:ARG:NH2	2.37	0.57
1:2A:1803:A:O2'	3:2D:259:THR:HG21	2.03	0.57
32:2a:544:G:OP1	35:2d:59:ARG:NH2	2.37	0.57
32:2a:1513:A:H2'	32:2a:1514:C:C6	2.39	0.57
43:2l:32:PHE:HB3	43:2l:84:LEU:HD11	1.87	0.57
1:1A:1178:C:H2'	1:1A:1179:C:H6	1.68	0.57
40:1i:26:VAL:HA	40:1i:61:ALA:HB3	1.87	0.57
32:2a:38:G:H22	32:2a:397:A:H5''	1.69	0.57
1:1A:2243:U:H2'	1:1A:2244:U:C6	2.39	0.57
24:12:14:ARG:O	24:12:67:LYS:NZ	2.37	0.57
1:2A:2302:G:O2'	6:2G:126:ASP:O	2.21	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1305:G:N2	32:2a:1331:G:H1'	2.20	0.57
33:2b:91:PRO:HG3	33:2b:155:LEU:HD13	1.87	0.57
1:1A:1178:C:H2'	1:1A:1179:C:C6	2.40	0.57
1:1A:2390:U:OP2	61:1A:4129:HOH:O	2.17	0.57
6:1G:161:THR:HG22	6:1G:163:ALA:H	1.70	0.57
32:1a:1356:G:H2'	32:1a:1357:A:C8	2.40	0.57
36:2e:100:VAL:O	36:2e:107:ARG:NH2	2.37	0.57
1:1A:602:G:N1	1:1A:655:A:OP2	2.27	0.57
2:1B:23:G:O6	61:1B:302:HOH:O	2.17	0.57
1:2A:271(A):A:N7	1:2A:271(W):G:N2	2.49	0.57
1:2A:2788:C:OP1	4:2E:61:ARG:NH2	2.38	0.57
2:2B:75:G:H22	21:2Z:73:GLN:HE21	1.52	0.57
32:2a:609:A:N7	61:2a:3247:HOH:O	2.33	0.57
35:2d:25:ARG:NH1	35:2d:30:LYS:O	2.37	0.57
35:2d:76:ARG:NH2	35:2d:80:GLU:OE1	2.33	0.57
25:13:39:ASP:OD2	25:13:44:ARG:NH2	2.37	0.57
36:1e:10:MET:HE2	36:1e:13:ILE:HD11	1.87	0.57
38:1g:78:ARG:NH1	38:1g:154:TYR:O	2.37	0.57
1:2A:2880:C:O3'	13:2R:90:ARG:NH1	2.38	0.57
44:2m:17:VAL:O	44:2m:20:THR:HG22	2.05	0.57
44:2m:88:ARG:HG2	44:2m:98:VAL:HG13	1.87	0.57
1:1A:601:C:OP1	5:1F:108:LYS:NZ	2.37	0.57
1:1A:2469:A:H5'	1:1A:2470:G:OP2	2.04	0.57
7:1H:159:GLU:HG2	7:1H:169:VAL:HG11	1.86	0.57
16:1U:69:CYS:HB3	16:1U:74:LEU:HD13	1.86	0.57
29:17:34:ARG:NH2	61:17:201:HOH:O	2.30	0.57
32:1a:1240:U:OP2	38:1g:116:ALA:N	2.38	0.57
38:1g:20:ASP:HB3	38:1g:23:VAL:HB	1.87	0.57
32:2a:1318:A:H1'	50:2s:37:ARG:HH11	1.69	0.57
53:2y:52:ALA:HB2	53:2y:77:LEU:HD21	1.85	0.57
1:1A:1068:G:O2'	1:1A:1096:A:O2'	2.17	0.56
1:1A:1126:A:OP2	61:1A:4104:HOH:O	2.17	0.56
49:1r:58:LEU:HB3	49:1r:62:GLU:HG3	1.87	0.56
6:2G:80:PHE:O	6:2G:82:LEU:N	2.38	0.56
32:2a:1291:G:O2'	40:2i:38:GLN:OE1	2.22	0.56
41:2j:21:GLN:NE2	41:2j:25:GLU:OE2	2.38	0.56
46:2o:55:GLY:HA2	46:2o:58:MET:HE3	1.86	0.56
53:2y:51:ASP:OD1	53:2y:64:SER:OG	2.19	0.56
32:1a:79:G:N2	32:1a:90:U:O2	2.37	0.56
32:1a:1118:C:H1'	32:1a:1179:A:C4	2.40	0.56
35:1d:173:TRP:CD1	35:1d:173:TRP:H	2.23	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1405:U:H2'	1:2A:1406:U:C6	2.39	0.56
1:2A:1639:U:C2'	1:2A:1640:C:H5''	2.34	0.56
1:2A:2112:G:H2'	1:2A:2113:U:H6	1.71	0.56
6:2G:54:GLU:O	6:2G:58:GLN:N	2.37	0.56
1:1A:1721:G:H5'	1:1A:1722:A:OP2	2.05	0.56
6:1G:27:ASN:HB3	6:1G:30:GLU:HG3	1.85	0.56
32:1a:1030(C):G:H2'	32:1a:1030(D):A:H8	1.69	0.56
32:1a:1104:G:OP1	33:1b:111:ARG:NH1	2.37	0.56
39:1h:4:ASP:OD1	39:1h:85:ARG:NH1	2.38	0.56
1:2A:81:G:HO2'	1:2A:295:G:HO2'	1.51	0.56
1:2A:1102:C:H2'	1:2A:1103:A:H8	1.70	0.56
1:2A:1104:C:H2'	1:2A:1105:U:C6	2.40	0.56
1:2A:1721:G:H8	1:2A:1741:A:H62	1.53	0.56
1:2A:2602:A:H4'	1:2A:2603:G:OP1	2.06	0.56
5:2F:33:LEU:HD13	5:2F:112:MET:HE2	1.88	0.56
6:2G:11:TYR:CZ	6:2G:16:ARG:HD3	2.41	0.56
32:2a:1062:U:H2'	32:2a:1063:C:C6	2.41	0.56
32:2a:1376:U:H2'	32:2a:1377:A:H8	1.70	0.56
43:2l:110:VAL:HG23	43:2l:120:TYR:HB3	1.87	0.56
44:2m:19:LEU:HD21	44:2m:56:LEU:HD21	1.86	0.56
5:1F:184:TYR:CE2	5:1F:188:ARG:HD2	2.41	0.56
38:1g:41:ARG:O	38:1g:45:ASP:HB2	2.05	0.56
40:1i:17:VAL:HG23	40:1i:63:ILE:HG12	1.87	0.56
1:2A:1786:A:H1'	1:2A:1938:A:N6	2.21	0.56
1:2A:2127:G:O6	1:2A:2161:C:N3	2.38	0.56
1:2A:2134:A:N6	1:2A:2156:G:O2'	2.37	0.56
40:2i:26:VAL:HG13	40:2i:33:PHE:HB2	1.87	0.56
40:2i:34:ASN:N	40:2i:34:ASN:OD1	2.38	0.56
6:1G:16:ARG:HE	6:1G:31:VAL:HG21	1.71	0.56
6:1G:150:ASP:OD1	6:1G:151:ALA:N	2.32	0.56
1:2A:154(A):C:H42	1:2A:171:G:H1	1.53	0.56
1:2A:1771:C:OP1	61:2A:3837:HOH:O	2.17	0.56
1:2A:2105:C:N4	1:2A:2106:G:O6	2.38	0.56
4:2E:40:GLU:H	4:2E:40:GLU:CD	2.14	0.56
6:2G:55:LYS:HA	6:2G:58:GLN:HB3	1.87	0.56
32:2a:662:G:H2'	32:2a:663:A:H8	1.70	0.56
1:1A:1507:A:C2	1:1A:1508:A:H1'	2.41	0.56
1:2A:2611:U:H6	1:2A:2611:U:H5'	1.70	0.56
32:2a:547:A:OP1	61:2a:3216:HOH:O	2.18	0.56
32:2a:1286:A:C8	32:2a:1287:A:H4'	2.40	0.56
20:1Y:92:ASN:N	20:1Y:93:GLY:HA2	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1359:A:N3	1:2A:1359:A:H5'	2.20	0.56
1:2A:2291:U:H2'	1:2A:2292:C:C6	2.41	0.56
7:2H:20:ALA:HB3	7:2H:23:ARG:HB2	1.87	0.56
1:1A:2345:G:N3	1:1A:2381:C:H2'	2.21	0.56
33:1b:77:ALA:HB2	33:1b:211:ILE:HD13	1.88	0.56
33:1b:189:ASP:OD1	33:1b:189:ASP:N	2.34	0.56
35:1d:65:ARG:NH1	35:1d:70:ILE:O	2.38	0.56
46:1o:87:ILE:HG22	46:1o:88:ARG:H	1.71	0.56
1:2A:2138:C:H2'	1:2A:2139:C:C6	2.41	0.56
32:2a:434:U:H2'	32:2a:435:C:C6	2.41	0.56
32:2a:580:U:OP2	61:2a:3215:HOH:O	2.18	0.56
6:1G:126:ASP:HB3	6:1G:128:ARG:H	1.71	0.56
32:1a:100:C:H2'	32:1a:101:A:C8	2.41	0.56
36:1e:8:GLU:OE2	36:1e:63:ARG:NH2	2.38	0.56
6:2G:161:THR:HG22	6:2G:163:ALA:H	1.70	0.56
34:2c:35:GLU:HA	34:2c:38:ARG:HD2	1.87	0.56
40:2i:3:GLN:NE2	40:2i:20:ARG:HH21	2.04	0.56
1:1A:2612:C:OP2	27:15:2:ALA:N	2.39	0.56
32:1a:346:G:H5''	57:1a:3279:MPD:H4	1.87	0.56
32:1a:1304:G:OP1	52:1u:2:GLY:N	2.40	0.56
5:2F:192:LEU:HD21	5:2F:194:MET:HE2	1.88	0.56
17:2V:60:GLU:OE1	17:2V:97:LYS:NZ	2.39	0.56
26:24:1:MET:HE2	26:24:6:HIS:CE1	2.41	0.56
44:2m:3:ARG:HB2	44:2m:9:ILE:H	1.71	0.56
1:1A:2867:G:OP2	15:1T:119:LYS:NZ	2.33	0.55
13:1R:97:VAL:HG22	13:1R:114:VAL:HG13	1.88	0.55
26:14:57:GLU:HB2	26:14:58:ARG:HA	1.88	0.55
32:1a:1060:C:C5	34:1c:2:GLY:HA3	2.40	0.55
37:1f:38:GLU:OE1	37:1f:64:GLN:NE2	2.35	0.55
44:1m:40:ASN:HB3	44:1m:43:THR:HG23	1.87	0.55
32:2a:287:U:O4	61:2a:3214:HOH:O	2.14	0.55
1:1A:247:G:H4'	1:1A:386:G:C5	2.41	0.55
32:1a:1069:C:OP2	61:1a:3306:HOH:O	2.18	0.55
1:2A:1064:C:H3'	1:2A:1065:U:C5'	2.35	0.55
1:2A:2122:U:H3	1:2A:2176:A:H61	1.53	0.55
32:2a:560:U:H5'	32:2a:566:G:N2	2.22	0.55
32:2a:1030(D):A:H3'	32:2a:1031:G:C8	2.41	0.55
1:2A:1009:A:OP2	61:2A:3829:HOH:O	2.17	0.55
1:2A:1593:G:H2'	1:2A:1594:G:C8	2.41	0.55
32:2a:1266:G:N2	32:2a:1269:A:OP2	2.30	0.55
39:2h:17:THR:HG22	39:2h:63:LEU:HG	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1165:U:H2'	1:1A:1166:C:C6	2.41	0.55
30:18:23:VAL:HG11	30:18:47:LYS:HD3	1.87	0.55
32:1a:347:G:C8	57:1a:3279:MPD:H53	2.42	0.55
35:1d:148:VAL:HG11	35:1d:158:ILE:HD12	1.89	0.55
41:1j:11:PHE:HE1	41:1j:67:THR:HG22	1.72	0.55
4:2E:119:ARG:HG2	4:2E:120:TRP:CD1	2.42	0.55
18:2W:1:MET:HE2	18:2W:62:HIS:HB3	1.89	0.55
20:2Y:73:ARG:HG2	20:2Y:73:ARG:HH11	1.69	0.55
24:12:59:ARG:NH2	61:12:101:HOH:O	2.29	0.55
32:1a:224:C:OP1	51:1t:74:LYS:NZ	2.37	0.55
32:1a:636:U:H2'	32:1a:637:G:H8	1.72	0.55
26:24:14:ILE:HB	26:24:22:ILE:HD13	1.87	0.55
32:2a:1027:C:H5''	32:2a:1028:C:C5	2.41	0.55
38:2g:111:ARG:HB2	38:2g:119:ARG:HD2	1.89	0.55
1:1A:987:G:O2'	1:1A:1000:A:N3	2.36	0.55
30:18:62:LEU:HB3	30:18:65:GLU:HG2	1.88	0.55
32:1a:1183:A:H3'	32:1a:1184:G:H5''	1.88	0.55
35:1d:15:GLU:OE2	35:1d:59:ARG:NH1	2.39	0.55
1:2A:2648:C:H2'	1:2A:2649:U:C6	2.42	0.55
8:2I:72:LEU:HA	8:2I:75:LEU:HD22	1.88	0.55
32:1a:632:A:H5'	32:1a:633:G:OP2	2.06	0.55
44:1m:11:ARG:O	44:1m:13:LYS:N	2.33	0.55
1:2A:657:U:H2'	1:2A:658:C:C6	2.41	0.55
1:2A:2104:G:O6	1:2A:2185:C:N3	2.40	0.55
2:2B:75:G:O3'	21:2Z:10:ARG:NH2	2.39	0.55
5:2F:148:LEU:HD22	5:2F:154:VAL:HG21	1.89	0.55
6:2G:63:ILE:HG22	6:2G:64:THR:HG23	1.87	0.55
32:2a:1374:A:OP1	38:2g:36:LYS:NZ	2.34	0.55
1:1A:1022:G:N7	9:1N:66:LYS:HE2	2.22	0.55
2:1B:66:A:H61	2:1B:108:U:H2'	1.70	0.55
7:1H:3:ARG:NH2	7:1H:65:HIS:HB3	2.22	0.55
8:1I:133:HIS:ND1	8:1I:134:PRO:O	2.39	0.55
32:1a:1068:G:OP1	61:1a:3307:HOH:O	2.18	0.55
32:1a:1304:G:OP2	61:1a:3308:HOH:O	2.18	0.55
37:1f:78:GLU:O	37:1f:81:ILE:HG22	2.07	0.55
1:2A:521:G:O6	61:2A:3842:HOH:O	2.18	0.55
1:2A:1062:G:N7	1:2A:1070:A:H1'	2.22	0.55
3:2D:137:PRO:O	3:2D:140:THR:HG23	2.07	0.55
10:2O:68:GLU:HB3	10:2O:78:ARG:HD3	1.89	0.55
40:2i:21:PRO:HA	40:2i:59:PHE:HA	1.89	0.55
24:12:22:GLU:HG2	24:12:64:LEU:HD11	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:222:A:H3'	1:1A:421:U:H5'	1.89	0.55
2:1B:7:G:H5''	2:1B:7:G:C8	2.41	0.55
7:1H:163:TYR:OH	61:1H:301:HOH:O	2.16	0.55
26:14:16:CYS:HB3	26:14:20:ASN:HB3	1.89	0.55
32:1a:411:A:OP2	35:1d:25:ARG:NH2	2.40	0.55
35:1d:173:TRP:CE3	35:1d:174:LEU:HG	2.42	0.55
51:1t:57:ARG:HH22	51:1t:100:ILE:HD12	1.72	0.55
1:2A:2180:U:H2'	1:2A:2181:G:C8	2.42	0.55
32:2a:222:U:H2'	32:2a:223:U:C6	2.42	0.55
32:2a:1096:C:H2'	32:2a:1097:C:H6	1.71	0.55
34:2c:164:ARG:NH1	34:2c:166:GLU:OE1	2.40	0.55
50:2s:20:LEU:HD21	50:2s:43:GLU:HG2	1.88	0.55
52:2u:17:THR:O	52:2u:22:ARG:NH1	2.40	0.55
32:1a:130:A:H5'	48:1q:63:ARG:HE	1.71	0.54
32:1a:642:A:N3	39:1h:113:SER:OG	2.39	0.54
33:1b:16:HIS:HB2	33:1b:204:ASN:HB3	1.88	0.54
33:1b:16:HIS:HB3	33:1b:210:SER:HB2	1.87	0.54
34:1c:134:ILE:HD11	34:1c:153:VAL:HB	1.89	0.54
35:1d:8:VAL:HG22	35:1d:21:LEU:HD13	1.88	0.54
1:2A:1833:U:O2'	1:2A:1969:A:N1	2.32	0.54
21:2Z:91:LEU:HG	21:2Z:130:PRO:HG3	1.87	0.54
1:1A:1762:A:H2'	61:1A:7327:HOH:O	2.08	0.54
1:1A:1840:G:N7	61:1A:4201:HOH:O	2.34	0.54
32:1a:737:A:H2'	32:1a:738:C:C6	2.42	0.54
35:1d:111:ALA:HB1	35:1d:116:GLN:HB3	1.90	0.54
1:2A:2112:G:H2'	1:2A:2113:U:C6	2.42	0.54
1:2A:2753:A:N3	31:29:15:LYS:NZ	2.54	0.54
33:2b:83:MET:SD	33:2b:234:PRO:HB2	2.47	0.54
33:2b:162:ILE:HD11	33:2b:184:VAL:HG22	1.89	0.54
40:2i:92:TYR:O	40:2i:96:LEU:HB2	2.07	0.54
53:2y:23:ARG:NH1	53:2y:75:ASN:OD1	2.40	0.54
1:1A:1095:A:H2'	1:1A:1096:A:O4'	2.07	0.54
4:1E:7:VAL:HG23	4:1E:51:PHE:HE2	1.73	0.54
4:1E:29:GLY:HA3	61:1E:410:HOH:O	2.06	0.54
14:1S:14:VAL:O	14:1S:18:ILE:HG12	2.07	0.54
14:2S:14:VAL:O	14:2S:18:ILE:HG12	2.07	0.54
32:2a:1314:C:N4	50:2s:2:PRO:O	2.41	0.54
43:2l:84:LEU:HB3	43:2l:104:VAL:HG21	1.89	0.54
48:2q:6:LEU:HB3	48:2q:23:VAL:HG11	1.89	0.54
32:1a:717:C:H4'	42:1k:117:ASN:HD22	1.73	0.54
44:1m:15:VAL:HG11	44:1m:48:LEU:HD21	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:2b:22:LYS:HA	33:2b:40:HIS:HE1	1.72	0.54
40:2i:54:ASP:O	40:2i:56:LEU:N	2.39	0.54
1:1A:1359:A:N1	1:1A:1372:U:O4	2.40	0.54
1:2A:84:A:N1	1:2A:98:G:O2'	2.38	0.54
1:2A:2128:C:H1'	1:2A:2173:A:H2	1.73	0.54
1:2A:2152:G:H2'	1:2A:2153:G:C8	2.43	0.54
5:2F:129:PHE:CD2	5:2F:163:VAL:HG21	2.43	0.54
11:1P:70:GLN:NE2	61:1P:304:HOH:O	2.40	0.54
32:1a:179:A:H2'	32:1a:180:U:H6	1.72	0.54
1:2A:370:G:OP2	1:2A:370:G:H8	1.90	0.54
4:2E:105:THR:OG1	4:2E:199:ARG:NH2	2.41	0.54
6:2G:41:GLN:NE2	6:2G:154:GLY:O	2.39	0.54
7:2H:98:LEU:HG	7:2H:125:VAL:HG12	1.89	0.54
11:2P:82:GLY:HA2	11:2P:113:LYS:O	2.07	0.54
14:2S:15:ARG:HB3	14:2S:19:LYS:HE3	1.89	0.54
18:2W:86:LEU:HD22	18:2W:96:ILE:HD11	1.90	0.54
32:2a:411:A:OP1	35:2d:30:LYS:NZ	2.37	0.54
32:2a:664:G:N2	32:2a:741:G:H1	2.05	0.54
33:2b:178:ARG:HH12	39:2h:68:ARG:HH22	1.56	0.54
47:2p:53:VAL:HG13	47:2p:79:VAL:HG22	1.90	0.54
1:2A:8:A:H2'	1:2A:9:U:C6	2.43	0.54
1:2A:818:G:OP2	61:2A:3844:HOH:O	2.18	0.54
1:2A:1550:C:OP1	1:2A:1720:U:O2'	2.21	0.54
3:2D:108:PRO:HB3	3:2D:143:HIS:CE1	2.43	0.54
32:2a:1518:MA6:H8	32:2a:1518:MA6:O5'	2.07	0.54
39:2h:12:ARG:HD2	39:2h:26:VAL:HG12	1.90	0.54
1:1A:774:A:N3	1:1A:774:A:H2'	2.23	0.54
1:1A:969:U:H2'	1:1A:970:C:C6	2.42	0.54
26:14:59:PHE:CZ	50:1s:64:GLU:HG3	2.42	0.54
32:1a:328:C:OP1	61:1a:3310:HOH:O	2.19	0.54
44:1m:3:ARG:HG3	44:1m:4:ILE:H	1.73	0.54
53:1y:24:LEU:HD11	53:1y:39:ILE:HD11	1.90	0.54
1:2A:2836:U:H2'	1:2A:2837:G:C8	2.43	0.54
6:2G:57:ALA:HB2	6:2G:90:LEU:HD13	1.90	0.54
6:2G:101:ILE:HD13	26:24:25:TYR:HB2	1.89	0.54
32:2a:1142:G:H3'	32:2a:1143:G:H8	1.71	0.54
33:2b:54:THR:HG23	33:2b:199:TYR:HB3	1.90	0.54
1:1A:1610:A:N7	61:1A:4202:HOH:O	2.34	0.54
32:1a:735:C:H2'	32:1a:736:C:H6	1.73	0.54
32:1a:1030:C:N4	32:1a:1032:G:O6	2.40	0.54
32:1a:1062:U:H2'	32:1a:1063:C:C6	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1305:G:N2	32:1a:1331:G:H1'	2.23	0.54
1:2A:2537:U:O4	61:2A:3838:HOH:O	2.17	0.54
19:2X:65:ARG:HB2	19:2X:70:LEU:HD23	1.90	0.54
34:2c:63:ASN:HB2	34:2c:98:ASN:HB2	1.89	0.54
1:1A:620:G:N3	1:1A:620:G:H5'	2.23	0.54
1:1A:1250:G:H5''	61:1U:331:HOH:O	2.07	0.54
1:1A:2126:A:C6	1:1A:2163:C:H4'	2.43	0.54
32:1a:745:C:H2'	32:1a:746:A:C8	2.42	0.54
36:1e:12:LEU:HB3	36:1e:31:LEU:HB2	1.90	0.54
51:1t:46:GLU:HG3	51:1t:48:LYS:HG3	1.90	0.54
21:2Z:128:VAL:HG11	21:2Z:161:VAL:HG22	1.90	0.54
32:2a:1368:G:OP1	40:2i:111:ARG:NH2	2.39	0.54
32:2a:1441:G:H5''	32:2a:1442:G:H5'	1.90	0.54
1:2A:784:A:N6	3:2D:229:VAL:HG11	2.23	0.53
1:2A:874:G:OP1	12:2Q:63:LYS:NZ	2.42	0.53
25:23:6:VAL:HG13	25:23:54:VAL:HG11	1.90	0.53
32:2a:1218:C:H2'	32:2a:1219:U:C6	2.43	0.53
1:1A:1026:U:OP1	61:1A:4119:HOH:O	2.19	0.53
1:1A:2749:A:OP1	7:1H:3:ARG:NH1	2.40	0.53
7:1H:27:LYS:HG2	7:1H:32:GLU:HG2	1.90	0.53
32:1a:273:A:H1'	48:1q:16:GLN:NE2	2.24	0.53
11:2P:50:ARG:HD3	30:28:7:HIS:CD2	2.43	0.53
1:1A:1899:G:N3	1:1A:1899:G:H2'	2.22	0.53
5:1F:64:ILE:HG21	5:1F:78:ILE:HG23	1.91	0.53
6:1G:67:LYS:NZ	6:1G:68:PRO:O	2.41	0.53
32:1a:189(K):U:H2'	32:1a:189(L):G:C8	2.41	0.53
32:1a:1015:A:H2'	32:1a:1016:A:C8	2.42	0.53
32:1a:1054:C:N4	53:1y:46:GLN:OE1	2.41	0.53
1:2A:517:C:OP1	27:25:16:ARG:NH2	2.41	0.53
1:2A:1379:A:H4'	1:2A:1380:G:OP2	2.07	0.53
32:2a:1510:U:H2'	32:2a:1511:G:C8	2.43	0.53
49:2r:26:LEU:HD21	49:2r:42:ARG:HH21	1.74	0.53
1:1A:2155:G:H2'	1:1A:2156:G:O4'	2.07	0.53
32:1a:656:C:O2'	46:1o:28:GLN:NE2	2.41	0.53
43:1l:53:ARG:HB3	43:1l:69:TYR:HE1	1.73	0.53
1:2A:2128:C:H3'	1:2A:2129:C:H5''	1.91	0.53
11:2P:85:LEU:HA	11:2P:88:LEU:HD12	1.90	0.53
32:2a:54:C:N4	32:2a:353:A:OP2	2.39	0.53
32:2a:1035:A:O2'	32:2a:1036:G:H8	1.92	0.53
33:2b:111:ARG:HH11	33:2b:111:ARG:HA	1.72	0.53
32:1a:266:G:H5''	32:1a:267:C:C5	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2327:A:H2'	1:2A:2328:A:C8	2.43	0.53
17:2V:98:GLU:OE2	17:2V:100:ARG:NH1	2.41	0.53
40:2i:26:VAL:HA	40:2i:61:ALA:O	2.09	0.53
41:2j:38:ILE:O	41:2j:38:ILE:HG13	2.09	0.53
1:1A:1025:G:C4	1:1A:1135:C:H1'	2.44	0.53
1:1A:1800:C:OP1	3:1D:260:ARG:NH2	2.42	0.53
32:1a:955:U:O2'	50:1s:83:HIS:HD2	1.91	0.53
1:2A:2104:G:N2	1:2A:2184:G:H1	2.06	0.53
1:2A:2149:G:C2	1:2A:2150:U:H1'	2.43	0.53
4:2E:199:ARG:NH1	61:2E:402:HOH:O	2.36	0.53
6:2G:32:PRO:HB3	6:2G:163:ALA:HB2	1.91	0.53
32:2a:1030(A):G:N2	32:2a:1030(D):A:OP2	2.41	0.53
34:2c:58:GLU:HB3	41:2j:92:THR:HG21	1.90	0.53
1:1A:603:A:O4'	1:1A:655:A:N6	2.41	0.53
6:1G:67:LYS:H	26:14:6:HIS:CE1	2.26	0.53
9:1N:4:TYR:CD2	16:1U:100:VAL:HG11	2.44	0.53
32:1a:186:C:H2'	32:1a:187:C:C6	2.44	0.53
32:1a:769:G:H4'	32:1a:1513:A:H4'	1.91	0.53
32:1a:1003:G:C2'	32:1a:1004:A:H4'	2.39	0.53
32:1a:1074:G:OP1	36:1e:64:ARG:NH1	2.42	0.53
32:1a:1124:G:N7	32:1a:1145:C:O2'	2.42	0.53
38:1g:113:GLU:HG2	38:1g:119:ARG:HG2	1.90	0.53
40:1i:10:ARG:HG3	40:1i:11:LYS:H	1.73	0.53
4:2E:143:ASN:HD22	4:2E:147:PRO:HD3	1.73	0.53
15:2T:85:LYS:NZ	15:2T:87:ASP:OD2	2.42	0.53
19:2X:60:ARG:NH2	29:27:47:ARG:HH12	2.07	0.53
32:2a:677:U:H3	32:2a:713:G:H22	1.57	0.53
32:2a:1260:C:O5'	32:2a:1284:C:H4'	2.08	0.53
1:1A:2129:C:N3	1:1A:2159:G:O6	2.42	0.53
13:1R:38:VAL:HB	13:1R:39:PRO:HD3	1.91	0.53
32:1a:828:A:H2'	32:1a:829:G:O4'	2.07	0.53
32:1a:1010:G:H22	32:1a:1020:U:H1'	1.74	0.53
33:1b:87:ARG:HD2	33:1b:233:SER:HB2	1.91	0.53
4:2E:36:ARG:NH1	4:2E:85:ASN:OD1	2.39	0.53
6:2G:19:LEU:HD13	6:2G:32:PRO:HD2	1.91	0.53
32:2a:1203:C:H2'	32:2a:1204:A:C8	2.44	0.53
36:2e:69:VAL:HG22	36:2e:71:LEU:HD23	1.90	0.53
53:2y:3:MET:HG3	53:2y:37:PRO:HG2	1.90	0.53
1:1A:1877:A:H5'	1:1A:1878:G:OP2	2.09	0.53
15:1T:51:ARG:HG3	15:1T:98:LYS:HE3	1.91	0.53
21:1Z:33:LEU:HD21	21:1Z:90:VAL:HG21	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:885:C:H2'	1:2A:886:C:O4'	2.09	0.53
12:2Q:31:ASP:OD1	12:2Q:134:ARG:NH1	2.30	0.53
32:2a:101:A:H5'	51:2t:10:LEU:HD21	1.90	0.53
34:2c:179:ARG:NH1	34:2c:206:GLU:HB3	2.23	0.53
38:2g:115:ARG:HG2	38:2g:118:VAL:HB	1.90	0.53
51:2t:57:ARG:HH12	51:2t:100:ILE:HB	1.74	0.53
1:1A:1085:A:O2'	1:1A:1104:C:O2'	2.25	0.53
1:1A:2183:C:H2'	1:1A:2184:G:H8	1.74	0.53
1:1A:2183:C:H2'	1:1A:2184:G:C8	2.44	0.53
3:1D:77:ALA:HB2	3:1D:97:TYR:CD1	2.44	0.53
35:1d:162:LEU:HD13	35:1d:181:MET:HG2	1.91	0.53
47:1p:69:THR:O	47:1p:73:LEU:HG	2.09	0.53
1:2A:212:G:H2'	1:2A:213:A:O4'	2.08	0.53
1:2A:527:C:OP1	61:2A:3821:HOH:O	2.19	0.53
1:1A:185:U:H4'	1:1A:218:A:H4'	1.91	0.52
25:13:7:LYS:HE3	25:13:32:GLN:HE21	1.73	0.52
32:1a:171:A:H2'	32:1a:172:A:C8	2.44	0.52
32:1a:757:U:H2'	32:1a:758:G:O4'	2.09	0.52
32:1a:1366:C:H2'	32:1a:1367:C:H6	1.74	0.52
32:1a:1410:G:H2'	32:1a:1411:C:C6	2.42	0.52
1:2A:1064:C:H1'	1:2A:1076:C:C5	2.44	0.52
1:2A:2115:G:N2	1:2A:2171:A:H61	2.06	0.52
32:2a:975:A:N1	41:2j:48:THR:HB	2.24	0.52
32:2a:1135:U:H2'	32:2a:1137:C:N3	2.24	0.52
32:2a:1187:G:H5'	40:2i:113:LYS:HE2	1.92	0.52
32:2a:1305:G:H22	32:2a:1331:G:H1'	1.73	0.52
32:2a:1442:G:H2'	32:2a:1442:G:N3	2.22	0.52
32:1a:96:U:H2'	32:1a:97:G:C8	2.44	0.52
1:2A:2243:U:H2'	1:2A:2244:U:C6	2.44	0.52
32:2a:620:C:C2	35:2d:135:LEU:HG	2.44	0.52
32:2a:1251:A:H2'	32:2a:1252:A:C8	2.45	0.52
32:2a:1318:A:H4'	50:2s:10:PHE:CE2	2.43	0.52
1:1A:2681:C:OP2	4:1E:109:LYS:NZ	2.29	0.52
6:1G:53:LEU:O	6:1G:56:ALA:N	2.43	0.52
10:1O:110:GLY:HA2	10:1O:112:MET:HE1	1.90	0.52
22:10:27:GLU:HG3	22:10:68:GLU:HA	1.92	0.52
32:1a:160:A:H2'	32:1a:161:A:O4'	2.09	0.52
32:1a:1140:C:H2'	32:1a:1141:C:H6	1.74	0.52
37:1f:61:LEU:HD23	37:1f:63:TYR:OH	2.09	0.52
39:1h:6:ILE:O	39:1h:10:LEU:HG	2.09	0.52
1:2A:876:C:H2'	1:2A:877:U:O4'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2808:U:H5''	1:2A:2891:G:O6	2.09	0.52
5:2F:120:GLU:HB2	5:2F:122:LYS:HG2	1.92	0.52
30:28:28:GLY:O	30:28:36:LYS:NZ	2.42	0.52
30:28:32:LEU:O	30:28:36:LYS:HE3	2.10	0.52
32:2a:118:U:H3'	32:2a:288:A:H61	1.74	0.52
32:2a:1465:C:H2'	32:2a:1466:C:O4'	2.10	0.52
45:2n:23:ARG:NH1	45:2n:30:ALA:HB2	2.25	0.52
5:1F:53:THR:HG22	5:1F:55:GLY:H	1.74	0.52
49:1r:37:VAL:HG22	49:1r:78:LEU:HB3	1.92	0.52
32:2a:1503:A:H5'	32:2a:1531:A:H1'	1.91	0.52
1:1A:910:A:N1	1:1A:2277:G:H1'	2.25	0.52
1:1A:1509:C:H3'	1:1A:1509:C:OP1	2.08	0.52
30:18:23:VAL:CG1	30:18:47:LYS:HD3	2.39	0.52
40:1i:16:ARG:HH11	40:1i:64:THR:HG21	1.74	0.52
1:2A:2203:U:H2'	1:2A:2205:C:C6	2.44	0.52
26:24:53:GLU:OE1	26:24:54:GLY:N	2.40	0.52
34:2c:6:HIS:CD2	34:2c:8:ILE:H	2.20	0.52
39:2h:37:ARG:NH1	39:2h:41:ARG:HH21	2.07	0.52
1:1A:323:G:C8	5:1F:171:PRO:HG3	2.45	0.52
1:1A:380:U:OP1	61:1A:4133:HOH:O	2.19	0.52
6:1G:50:ALA:C	6:1G:52:ILE:H	2.18	0.52
32:1a:573:A:OP2	61:1a:3301:HOH:O	2.19	0.52
32:1a:1239:A:H62	32:1a:1299:A:N6	2.07	0.52
32:1a:1412:C:H2'	32:1a:1413:A:C8	2.45	0.52
33:1b:63:MET:HG3	33:1b:225:ALA:HB1	1.91	0.52
1:2A:9:U:O4	1:2A:2629:A:H2	1.93	0.52
8:2I:117:GLU:HG3	8:2I:118:LYS:H	1.73	0.52
8:1I:4:ILE:HD11	8:1I:44:LEU:HD13	1.92	0.52
14:1S:10:ARG:O	14:1S:14:VAL:HG13	2.10	0.52
32:1a:201:C:N3	32:1a:216:G:N2	2.48	0.52
32:1a:620:C:OP1	61:1a:3309:HOH:O	2.19	0.52
32:1a:1074:G:O2'	32:1a:1101:A:N1	2.40	0.52
33:1b:197:VAL:HG23	33:1b:200:ILE:HG13	1.92	0.52
1:2A:1064:C:H5	1:2A:1065:U:C6	2.28	0.52
1:2A:2156:G:OP2	1:2A:2157:G:N1	2.43	0.52
3:2D:71:ASP:HB3	3:2D:103:ARG:NH2	2.24	0.52
31:29:7:VAL:HG12	31:29:34:GLN:HE21	1.73	0.52
32:2a:1226:C:OP2	44:2m:91:ARG:NH1	2.39	0.52
1:1A:1087:G:H2'	1:1A:1089:G:O4'	2.09	0.52
16:1U:33:ARG:NH1	61:1U:308:HOH:O	2.43	0.52
32:1a:194:C:H2'	32:1a:195:A:H5''	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:410:G:H5''	35:1d:30:LYS:HZ2	1.75	0.52
44:1m:65:LYS:HE2	44:1m:69:GLU:HG2	1.92	0.52
50:1s:52:TYR:HB2	50:1s:57:HIS:CE1	2.45	0.52
1:2A:1011:G:OP2	16:2U:66:ASN:ND2	2.38	0.52
1:2A:1266:G:O5'	18:2W:15:ARG:NH2	2.42	0.52
1:2A:2687:U:H2'	1:2A:2688:U:O4'	2.10	0.52
28:26:6:ARG:NH1	28:26:26:ASN:HB2	2.25	0.52
32:2a:1263:C:H2'	32:2a:1264:C:C6	2.45	0.52
1:1A:1486:A:H2'	1:1A:1487:G:H8	1.75	0.52
13:1R:44:LEU:HD22	13:1R:48:VAL:HG23	1.91	0.52
32:1a:203:U:H5'	32:1a:216:G:N2	2.25	0.52
32:1a:1140:C:H2'	32:1a:1141:C:C6	2.44	0.52
41:1j:39:PRO:HA	41:1j:70:ARG:HD3	1.92	0.52
1:2A:2315:G:H2'	1:2A:2316:C:C6	2.45	0.52
2:2B:42:C:N3	6:2G:91:ARG:NH1	2.47	0.52
8:2I:72:LEU:HD21	8:2I:107:VAL:HG11	1.90	0.52
8:2I:77:LEU:HD21	8:2I:100:ALA:HB3	1.91	0.52
32:2a:289:G:OP2	61:2a:3213:HOH:O	2.18	0.52
35:2d:173:TRP:CD1	35:2d:189:PRO:HG3	2.44	0.52
37:2f:50:TYR:CE2	49:2r:77:GLY:HA2	2.45	0.52
44:2m:81:LEU:HA	44:2m:84:ILE:HG12	1.91	0.52
1:1A:771:G:OP1	29:17:14:LYS:HE2	2.10	0.52
1:1A:2328:A:H2'	1:1A:2329:G:C8	2.45	0.52
3:1D:134:ARG:HG3	3:1D:135:PHE:CE1	2.45	0.52
6:1G:43:LEU:O	6:1G:45:GLU:N	2.41	0.52
32:1a:626:U:H2'	32:1a:627:G:C8	2.46	0.52
32:1a:1024:G:H2'	32:1a:1024:G:N3	2.24	0.52
40:1i:50:LEU:HD13	40:1i:56:LEU:HA	1.91	0.52
1:2A:1189:A:OP2	61:2A:3846:HOH:O	2.19	0.52
1:2A:1778:U:H2'	1:2A:1784:A:N6	2.25	0.52
32:2a:452:A:N3	47:2p:72:ARG:NH1	2.58	0.52
32:2a:1401:G:O6	53:2y:83:ARG:NH2	2.41	0.52
42:2k:115:PRO:C	42:2k:117:ASN:HA	2.35	0.52
1:1A:1429:G:H2'	1:1A:1430:C:C6	2.45	0.51
32:1a:262:A:H2'	32:1a:263:A:C8	2.46	0.51
37:1f:69:GLU:OE1	37:1f:69:GLU:N	2.43	0.51
1:2A:2693:A:H2'	1:2A:2694:G:H8	1.74	0.51
6:2G:16:ARG:O	6:2G:20:ILE:HG13	2.09	0.51
32:2a:738:C:OP1	37:2f:2:ARG:NH1	2.43	0.51
32:2a:881:G:P	43:2l:12:ARG:HH22	2.33	0.51
36:2e:92:LYS:HB3	36:2e:119:LEU:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:2f:100:ASN:ND2	49:2r:23:LYS:HE2	2.25	0.51
48:2q:22:LEU:HD13	48:2q:41:LYS:HG2	1.90	0.51
1:1A:2086:U:H2'	1:1A:2087:G:C8	2.46	0.51
32:1a:280:C:N3	48:1q:39:SER:OG	2.42	0.51
1:2A:1087:G:H22	1:2A:1102:C:H42	1.58	0.51
6:2G:35:GLU:HB3	6:2G:160:VAL:HG12	1.92	0.51
6:2G:36:LYS:HE3	6:2G:160:VAL:HG21	1.92	0.51
13:2R:44:LEU:HD22	13:2R:48:VAL:HG23	1.93	0.51
32:2a:1492:A:H5''	43:2l:47:LYS:HD3	1.92	0.51
34:2c:37:GLN:HE22	45:2n:52:GLN:HB3	1.75	0.51
39:2h:122:ARG:HG3	39:2h:123:GLU:N	2.24	0.51
44:2m:15:VAL:HG12	44:2m:45:VAL:HG22	1.93	0.51
1:1A:2291:U:H2'	1:1A:2292:C:C6	2.45	0.51
4:1E:54:GLN:OE1	4:1E:55:ASN:N	2.44	0.51
34:1c:7:PRO:O	34:1c:11:ARG:NH1	2.42	0.51
1:2A:1028:A:N6	1:2A:1125:G:H2'	2.25	0.51
1:2A:2105:C:H2'	1:2A:2106:G:C8	2.44	0.51
1:2A:2171:A:H4'	1:2A:2172:U:OP1	2.11	0.51
1:2A:2291:U:OP1	1:2A:2380:C:O2'	2.26	0.51
2:2B:11:C:OP2	2:2B:12:C:N4	2.33	0.51
13:2R:8:ARG:NE	13:2R:43:GLU:OE2	2.41	0.51
32:2a:1090:U:H2'	32:2a:1091:U:C6	2.45	0.51
32:2a:1179:A:H2'	32:2a:1180:A:O4'	2.10	0.51
1:1A:1518:U:H2'	1:1A:1519:G:O4'	2.10	0.51
35:1d:168:ARG:N	35:1d:168:ARG:HH11	2.08	0.51
43:1l:117:ARG:HD3	61:1l:302:HOH:O	2.10	0.51
1:2A:881:G:H1	1:2A:895:U:H3	1.57	0.51
1:2A:1514:U:H2'	1:2A:1515:G:H8	1.75	0.51
1:2A:2273:A:H2'	1:2A:2274:A:C8	2.45	0.51
12:2Q:42:ILE:HD13	12:2Q:97:VAL:HB	1.91	0.51
32:2a:392:G:H2'	32:2a:393:A:H8	1.75	0.51
32:2a:443:C:H2'	32:2a:444:C:C6	2.45	0.51
32:2a:952:U:H4'	32:2a:964:A:N1	2.25	0.51
32:2a:974:A:OP2	45:2n:29:ARG:NH2	2.42	0.51
32:2a:1329:A:H5'	44:2m:29:ARG:HD2	1.92	0.51
32:2a:1376:U:H2'	32:2a:1377:A:C8	2.46	0.51
44:2m:92:HIS:CE1	44:2m:98:VAL:HG21	2.45	0.51
46:2o:25:THR:HG21	46:2o:70:LEU:HB2	1.91	0.51
50:2s:30:LEU:HD11	50:2s:50:ALA:HB2	1.90	0.51
32:1a:435:C:H2'	32:1a:436:C:H6	1.76	0.51
32:1a:1277:C:O2'	32:1a:1279:A:H1'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:1d:173:TRP:CD2	35:1d:189:PRO:HG3	2.45	0.51
43:1l:88:GLY:O	43:1l:99:HIS:HD2	1.93	0.51
1:2A:271(G):C:H2'	1:2A:271(H):G:C8	2.45	0.51
1:2A:2206:G:H5''	1:2A:2207:G:N7	2.26	0.51
1:2A:2552:OMU:H6	1:2A:2552:OMU:O5'	2.10	0.51
1:2A:2706:G:N7	61:2A:3940:HOH:O	2.34	0.51
5:2F:132:VAL:HA	5:2F:138:GLU:HB3	1.92	0.51
19:2X:31:HIS:CD2	19:2X:33:LYS:HB2	2.46	0.51
32:2a:1084:G:H5'	32:2a:1102:A:OP2	2.10	0.51
32:2a:1202:G:N2	45:2n:46:GLU:OE2	2.41	0.51
34:2c:181:ASN:HB3	34:2c:205:GLY:H	1.76	0.51
1:1A:1721:G:H8	1:1A:1741:A:H62	1.58	0.51
1:1A:2207:G:O2'	1:1A:2208:A:OP1	2.28	0.51
32:1a:352:C:O2'	32:1a:354:G:OP1	2.26	0.51
32:1a:447:G:O6	32:1a:485:G:O2'	2.26	0.51
35:1d:108:LEU:HD12	35:1d:174:LEU:HD13	1.92	0.51
1:2A:784:A:C6	3:2D:229:VAL:HG11	2.46	0.51
1:2A:1020:A:N1	1:2A:1141:U:O2'	2.43	0.51
6:2G:122:PRO:HG3	6:2G:182:LYS:C	2.35	0.51
42:2k:99:GLN:HG3	42:2k:105:VAL:HG21	1.92	0.51
50:2s:70:LYS:HB2	50:2s:73:GLU:HG3	1.90	0.51
1:1A:271(O):C:H2'	1:1A:271(P):C:C6	2.46	0.51
1:1A:288:C:H2'	1:1A:289:A:H8	1.74	0.51
1:1A:1175:U:H1'	1:1A:1176:G:OP1	2.11	0.51
32:1a:179:A:H2'	32:1a:180:U:C6	2.46	0.51
34:1c:58:GLU:HG2	41:1j:92:THR:HG21	1.93	0.51
40:1i:92:TYR:O	40:1i:96:LEU:HB2	2.11	0.51
1:2A:652(T):C:H2'	1:2A:652(U):G:H8	1.71	0.51
1:2A:1059:G:OP2	1:2A:1060:U:H2'	2.11	0.51
1:2A:1796:U:H2'	1:2A:1797:C:H6	1.74	0.51
1:2A:1845:G:OP1	3:2D:258:LYS:NZ	2.39	0.51
1:2A:2074:U:H2'	1:2A:2075:U:C6	2.45	0.51
7:2H:8:PRO:HB3	7:2H:51:ARG:HG2	1.92	0.51
8:2I:75:LEU:HD12	8:2I:105:HIS:CD2	2.46	0.51
21:2Z:33:LEU:HD21	21:2Z:90:VAL:HG21	1.93	0.51
31:29:19:ARG:HG2	31:29:20:HIS:ND1	2.26	0.51
33:2b:83:MET:HE1	33:2b:234:PRO:O	2.10	0.51
50:2s:41:VAL:HG22	50:2s:42:PRO:HD2	1.92	0.51
1:1A:1287:A:H8	13:1R:104:ARG:HD3	1.76	0.51
1:2A:2104:G:H22	1:2A:2184:G:H1	1.58	0.51
32:2a:1190:G:H5'	34:2c:176:HIS:CE1	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:2c:40:ARG:O	34:2c:44:GLU:HB2	2.11	0.51
38:2g:79:ARG:HA	38:2g:84:ASN:HA	1.93	0.51
1:1A:1688:U:O2	1:1A:1700:A:H5'	2.10	0.51
11:1P:59:LEU:HD11	30:18:10:ALA:HA	1.93	0.51
13:1R:33:ARG:NH1	13:1R:115:GLU:OE1	2.35	0.51
32:1a:17:U:H2'	32:1a:18:C:C6	2.46	0.51
32:1a:376:G:H5''	47:1p:5:ARG:HD2	1.93	0.51
34:1c:130:VAL:HG21	34:1c:157:ILE:HG23	1.93	0.51
36:1e:81:GLU:HG2	36:1e:90:VAL:HG22	1.92	0.51
41:1j:26:ALA:HA	41:1j:29:ARG:HH21	1.76	0.51
1:2A:2130:U:H2'	1:2A:2158:A:H61	1.76	0.51
7:2H:70:THR:HG22	7:2H:74:ASN:HD21	1.76	0.51
21:2Z:73:GLN:NE2	61:2Z:304:HOH:O	2.43	0.51
32:2a:251:G:N7	61:2a:3246:HOH:O	2.32	0.51
32:2a:384:G:H2'	32:2a:385:C:C6	2.46	0.51
44:2m:34:LEU:HD13	44:2m:41:PRO:HB3	1.92	0.51
53:2y:54:ILE:HB	53:2y:61:LEU:HD12	1.93	0.51
1:1A:1166:C:H2'	1:1A:1167:U:C6	2.46	0.51
1:1A:1416:G:O2'	1:1A:1417:C:OP2	2.20	0.51
1:1A:2443:C:OP1	5:1F:68:LYS:HD3	2.11	0.51
3:1D:221:VAL:HG22	3:1D:226:MET:HE3	1.93	0.51
32:1a:1149:C:OP1	40:1i:9:ARG:NE	2.34	0.51
40:1i:43:ALA:HA	40:1i:74:ILE:HD13	1.93	0.51
1:2A:954:G:H5''	12:2Q:13:GLN:HB3	1.93	0.51
1:2A:956:G:H5''	12:2Q:77:LYS:HD2	1.92	0.51
14:2S:15:ARG:O	14:2S:19:LYS:HG2	2.10	0.51
32:2a:1320:C:C2	50:2s:72:GLY:HA3	2.45	0.51
38:2g:74:GLU:HG2	38:2g:91:VAL:HG22	1.93	0.51
51:2t:18:GLN:O	51:2t:22:ARG:HG3	2.11	0.51
1:1A:630:G:OP2	30:18:15:LYS:NZ	2.40	0.50
1:1A:1448:G:N7	61:1A:4197:HOH:O	2.33	0.50
32:1a:452:A:H4'	47:1p:72:ARG:NH1	2.26	0.50
32:1a:1391:U:H2'	32:1a:1392:G:C8	2.46	0.50
39:1h:14:ARG:O	39:1h:18:ARG:HG2	2.10	0.50
51:1t:50:GLU:HG3	51:1t:100:ILE:HD11	1.93	0.50
1:2A:14:A:OP2	61:2A:3847:HOH:O	2.19	0.50
1:2A:2439:A:H5'	1:2A:2439:A:C8	2.47	0.50
61:2A:3972:HOH:O	16:2U:5:LYS:NZ	2.44	0.50
61:2A:4829:HOH:O	5:2F:74:ARG:HD2	2.10	0.50
15:2T:117:ASP:OD2	15:2T:120:ARG:NE	2.35	0.50
16:2U:104:GLN:OE1	16:2U:105:VAL:HG23	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:2X:46:ALA:HB1	24:22:33:MET:HE1	1.93	0.50
26:24:18:CYS:SG	26:24:39:CYS:HB3	2.50	0.50
27:25:51:TYR:CE2	27:25:56:LYS:HD3	2.46	0.50
32:2a:1143:G:H2'	32:2a:1144:G:C8	2.45	0.50
32:2a:1263:C:H2'	32:2a:1264:C:H6	1.76	0.50
37:2f:38:GLU:HB2	37:2f:64:GLN:HG2	1.93	0.50
1:1A:1489:U:HO2'	1:1A:1490:A:H8	1.57	0.50
1:1A:2602:A:H1'	1:1A:2603:G:H5''	1.93	0.50
22:10:10:THR:HG22	22:10:12:ASN:H	1.75	0.50
32:1a:1202:G:N2	45:1n:46:GLU:OE2	2.40	0.50
32:1a:1216:G:OP1	45:1n:2:ALA:HA	2.12	0.50
37:1f:97:PHE:HD2	49:1r:31:LEU:HD12	1.75	0.50
21:2Z:179:ASP:O	21:2Z:182:LYS:HG2	2.10	0.50
32:2a:56:U:H2'	32:2a:57:G:C8	2.46	0.50
32:2a:187:C:O2'	51:2t:89:ARG:HD3	2.12	0.50
37:2f:68:PRO:HB2	37:2f:71:ARG:HD2	1.94	0.50
40:2i:29:ASN:HD21	40:2i:65:VAL:N	2.04	0.50
1:1A:1069:A:H5'	1:1A:1070:A:C2	2.47	0.50
1:1A:2889:C:H2'	1:1A:2891:G:O4'	2.10	0.50
6:1G:142:PRO:HB2	26:14:31:ILE:HG21	1.92	0.50
32:1a:986:A:N3	50:1s:52:TYR:OH	2.43	0.50
32:1a:1125:U:H4'	41:1j:5:ARG:NH2	2.26	0.50
53:1y:76:GLU:HG2	53:1y:80:LYS:HE2	1.93	0.50
1:2A:1101:U:H2'	1:2A:1102:C:C6	2.43	0.50
8:2I:3:VAL:HG12	8:2I:38:LEU:HA	1.94	0.50
38:2g:65:ALA:HB1	38:2g:127:ALA:HB3	1.94	0.50
1:1A:796:C:H2'	1:1A:797:C:C6	2.46	0.50
1:1A:881:G:H2'	1:1A:882:G:O4'	2.11	0.50
1:1A:886:C:H3'	1:1A:887:A:H5''	1.94	0.50
16:1U:33:ARG:NH2	61:1U:307:HOH:O	2.43	0.50
17:1V:49:THR:HG22	17:1V:49:THR:O	2.12	0.50
32:1a:1504:G:OP1	32:1a:1507:A:H4'	2.11	0.50
1:2A:922:U:H2'	1:2A:923:C:C6	2.46	0.50
1:2A:1045:A:H5'	1:2A:1047:G:O4'	2.11	0.50
32:2a:353:A:H5'	32:2a:353:A:H8	1.77	0.50
32:2a:934:C:OP1	61:2a:3217:HOH:O	2.19	0.50
32:2a:1286:A:H2'	32:2a:1287:A:H4'	1.92	0.50
32:2a:1318:A:H5''	50:2s:3:ARG:NH2	2.26	0.50
44:2m:51:ALA:O	44:2m:55:ARG:HB2	2.12	0.50
49:2r:55:ARG:HB3	49:2r:55:ARG:CZ	2.42	0.50
1:1A:1810:A:H2'	1:1A:1811:G:O4'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2137:C:C2	1:1A:2154:G:N2	2.76	0.50
4:1E:9:VAL:HB	15:1T:3:ARG:HG2	1.94	0.50
11:1P:63:PRO:HD3	30:18:27:THR:HG22	1.93	0.50
32:1a:458:C:H2'	32:1a:460:G:O4'	2.12	0.50
39:1h:12:ARG:NH1	39:1h:25:ASP:O	2.45	0.50
44:1m:11:ARG:C	44:1m:13:LYS:H	2.18	0.50
1:2A:247:G:H4'	1:2A:386:G:C5	2.47	0.50
1:2A:443:A:H1'	1:2A:1201:C:O4'	2.11	0.50
1:2A:1047:G:H2'	1:2A:1110:G:H22	1.76	0.50
1:2A:2537:U:H2'	1:2A:2538:C:C6	2.47	0.50
32:2a:523:A:H61	43:2l:92:OTD:CG	2.25	0.50
36:2e:71:LEU:HD21	36:2e:115:VAL:HG22	1.93	0.50
1:1A:878:A:H2'	1:1A:879:G:H5'	1.94	0.50
7:1H:11:VAL:HG21	7:1H:50:VAL:HG23	1.93	0.50
32:1a:922:G:H4'	36:1e:20:GLN:HA	1.92	0.50
33:1b:114:ARG:NH1	33:1b:117:GLU:OE2	2.38	0.50
40:1i:16:ARG:HB2	40:1i:64:THR:HG22	1.94	0.50
46:1o:55:GLY:HA2	46:1o:58:MET:HE3	1.92	0.50
1:2A:271(E):U:H2'	1:2A:271(F):C:C6	2.46	0.50
1:2A:2141:G:C6	1:2A:2150:U:O2	2.63	0.50
2:2B:66:A:N6	2:2B:109:C:H5'	2.24	0.50
3:2D:71:ASP:CB	3:2D:103:ARG:HH22	2.24	0.50
34:2c:73:PRO:HB3	34:2c:103:VAL:HG11	1.93	0.50
41:2j:27:ALA:HB1	41:2j:74:ILE:HD13	1.94	0.50
45:2n:26:ARG:HD3	45:2n:43:CYS:HB3	1.92	0.50
1:1A:579:G:H2'	1:1A:580:C:C6	2.47	0.50
1:1A:1430:C:H2'	1:1A:1431:U:C6	2.46	0.50
1:1A:1929:G:H4'	1:1A:1930:G:OP1	2.11	0.50
1:1A:2273:A:H2'	1:1A:2274:A:C8	2.46	0.50
19:1X:57:LEU:HD11	19:1X:78:LYS:HE3	1.94	0.50
20:1Y:102:CYS:SG	20:1Y:103:GLY:N	2.85	0.50
32:1a:255:G:OP1	48:1q:69:LYS:NZ	2.44	0.50
34:1c:29:TYR:OH	45:1n:54:PRO:O	2.28	0.50
1:2A:2168:G:N2	1:2A:2171:A:OP2	2.44	0.50
32:2a:1146:A:H3'	32:2a:1147:C:H5''	1.93	0.50
40:2i:28:VAL:HG13	40:2i:63:ILE:HG22	1.94	0.50
41:2j:51:ARG:O	45:2n:45:ARG:NH1	2.45	0.50
1:1A:153:C:OP2	23:11:92:LYS:NZ	2.45	0.50
32:1a:45:U:H2'	32:1a:46:G:C8	2.47	0.50
32:1a:1166:G:H5'	32:1a:1168:A:OP2	2.12	0.50
33:1b:7:VAL:HG12	33:1b:217:ARG:HD2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1087:G:H22	1:2A:1102:C:N4	2.09	0.50
1:2A:1503:U:H2'	1:2A:1504:C:C6	2.47	0.50
1:2A:2321:G:O2'	1:2A:2322:A:OP1	2.26	0.50
11:2P:95:VAL:HG22	11:2P:125:VAL:HA	1.94	0.50
32:2a:134:A:N1	47:2p:25:ARG:NH2	2.60	0.50
33:2b:69:LEU:HB3	33:2b:162:ILE:HG22	1.93	0.50
33:2b:178:ARG:NH2	39:2h:74:PRO:HB3	2.27	0.50
38:2g:59:LEU:O	38:2g:63:LYS:HG3	2.12	0.50
43:2l:70:ILE:HG12	43:2l:100:ILE:HD12	1.94	0.50
44:2m:81:LEU:HD22	44:2m:88:ARG:HB2	1.94	0.50
1:1A:1697:G:OP2	1:1A:1698:A:O2'	2.29	0.50
1:1A:2206:G:OP2	1:1A:2206:G:H4'	2.11	0.50
22:10:43:THR:O	22:10:43:THR:HG23	2.12	0.50
32:1a:309:G:O2'	32:1a:607:A:N1	2.44	0.50
32:1a:890:G:O2'	32:1a:906:G:O6	2.16	0.50
1:2A:271(K):U:O2	8:2I:50:ARG:HD2	2.11	0.50
1:2A:1781:C:H5	29:27:1:MET:HE1	1.77	0.50
1:2A:2051:A:H5'	1:2A:2578:G:O4'	2.12	0.50
3:2D:125:ILE:HB	37:2f:81:ILE:HD13	1.94	0.50
4:2E:119:ARG:HG2	4:2E:120:TRP:NE1	2.27	0.50
11:2P:63:PRO:HD3	30:28:27:THR:HG22	1.94	0.50
1:1A:652(U):G:H3'	1:1A:652(V):C:C6	2.46	0.49
6:1G:77:ILE:HG22	6:1G:80:PHE:H	1.76	0.49
17:1V:21:ARG:HD3	17:1V:91:TYR:CD1	2.47	0.49
23:11:11:ARG:HG3	23:11:12:PRO:HD2	1.93	0.49
32:1a:38:G:N2	32:1a:397:A:H5'	2.26	0.49
32:1a:1218:C:H2'	32:1a:1219:U:C6	2.47	0.49
51:1t:14:LYS:HG2	51:1t:18:GLN:NE2	2.27	0.49
1:2A:1341:U:O4'	19:2X:57:LEU:HD23	2.12	0.49
1:2A:2122:U:H3	1:2A:2176:A:N6	2.09	0.49
33:2b:134:GLU:O	33:2b:138:LEU:HG	2.12	0.49
35:2d:166:LYS:HE2	35:2d:167:GLY:N	2.27	0.49
44:2m:60:VAL:HG12	44:2m:66:LEU:HD11	1.94	0.49
1:1A:330:A:H2	1:1A:1210:A:C2'	2.24	0.49
1:1A:748:G:C8	18:1W:89:ALA:HB1	2.46	0.49
1:1A:1439:A:OP1	61:1A:4135:HOH:O	2.19	0.49
1:1A:2133:G:C2	1:1A:2157:G:H2'	2.46	0.49
1:1A:2347:C:H2'	1:1A:2348:U:C6	2.46	0.49
30:18:23:VAL:HG13	30:18:47:LYS:HB3	1.93	0.49
32:1a:324:G:N7	61:1a:3349:HOH:O	2.35	0.49
32:1a:967:5MC:H4'	40:1i:125:TYR:HE1	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1394:A:N1	32:1a:1500:A:O2'	2.44	0.49
41:1j:35:SER:N	41:1j:73:ASP:O	2.33	0.49
2:2B:55:U:OP2	61:2B:309:HOH:O	2.20	0.49
15:2T:16:ARG:HG3	15:2T:18:ASP:OD1	2.11	0.49
19:2X:12:VAL:HG22	19:2X:29:TRP:CE2	2.47	0.49
19:2X:53:LYS:HB3	19:2X:82:GLN:HB3	1.93	0.49
21:2Z:103:ARG:O	21:2Z:105:VAL:N	2.44	0.49
23:21:31:GLY:O	61:21:3901:HOH:O	2.20	0.49
39:2h:20:TYR:HA	39:2h:65:TYR:CZ	2.47	0.49
20:1Y:23:ARG:NH2	61:1Y:604:HOH:O	2.45	0.49
25:13:8:LEU:HG	25:13:31:LEU:HD23	1.95	0.49
45:1n:3:ARG:O	45:1n:7:ILE:HG13	2.12	0.49
1:2A:530:G:N1	1:2A:2023:G:OP1	2.40	0.49
1:2A:1068:G:H3'	1:2A:1096:A:OP2	2.11	0.49
1:2A:1840:G:OP2	61:2A:3843:HOH:O	2.18	0.49
1:2A:2312:U:H5'	6:2G:88:ILE:HD11	1.94	0.49
1:2A:2321:G:OP2	61:2A:3845:HOH:O	2.19	0.49
5:2F:64:ILE:HG21	5:2F:78:ILE:HG23	1.94	0.49
7:2H:70:THR:O	7:2H:74:ASN:ND2	2.45	0.49
8:2I:130:TYR:HB3	8:2I:138:ILE:HB	1.94	0.49
26:24:59:PHE:HB2	26:24:62:ARG:NH1	2.28	0.49
32:2a:1116:C:O2'	40:2i:108:VAL:HG21	2.12	0.49
32:2a:1402:4OC:HM43	53:2y:83:ARG:CZ	2.42	0.49
34:2c:164:ARG:HG2	34:2c:165:THR:H	1.77	0.49
1:1A:493:G:H2'	1:1A:494:G:O4'	2.12	0.49
1:1A:1379:A:H4'	1:1A:1380:G:OP2	2.13	0.49
1:1A:2439:A:H5'	1:1A:2439:A:C8	2.47	0.49
7:1H:37:VAL:HG22	7:1H:68:THR:HG23	1.94	0.49
21:1Z:3:TYR:CE2	21:1Z:51:ALA:HB2	2.47	0.49
32:1a:176:C:H2'	32:1a:177:C:C6	2.46	0.49
32:1a:437:U:H5'	35:1d:155:LEU:HD21	1.94	0.49
33:1b:30:ARG:NH2	33:1b:194:PRO:HB2	2.27	0.49
1:2A:271(P):C:OP1	8:2I:45:LYS:HD3	2.13	0.49
1:2A:1063:G:H1	1:2A:1075:C:H42	1.59	0.49
1:2A:1991:U:H2'	1:2A:1992:G:H5''	1.94	0.49
1:2A:2100:G:O6	1:2A:2189:U:O4	2.31	0.49
2:2B:75:G:OP1	61:2B:310:HOH:O	2.20	0.49
14:2S:28:VAL:HG11	14:2S:98:VAL:HG13	1.93	0.49
32:2a:255:G:OP1	48:2q:69:LYS:NZ	2.38	0.49
32:2a:731:G:H5'	32:2a:766:A:H4'	1.93	0.49
32:2a:1004:A:N7	32:2a:1037:C:H2'	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:2n:42:ILE:O	45:2n:46:GLU:HG3	2.11	0.49
1:1A:1067:A:H2'	1:1A:1067:A:N3	2.27	0.49
10:1O:118:ALA:O	57:1a:3279:MPD:H12	2.12	0.49
19:1X:60:ARG:HH12	29:17:47:ARG:HH12	1.59	0.49
33:1b:219:VAL:HA	33:1b:222:ILE:HD12	1.94	0.49
1:2A:1814:G:H4'	3:2D:51:VAL:HG21	1.95	0.49
1:2A:2887:U:H2'	1:2A:2888:C:C6	2.47	0.49
19:2X:31:HIS:CD2	19:2X:33:LYS:H	2.31	0.49
26:24:59:PHE:CZ	50:2s:64:GLU:HB2	2.47	0.49
32:2a:536:C:OP2	61:2a:3218:HOH:O	2.19	0.49
1:1A:284:U:H2'	1:1A:285:C:C6	2.47	0.49
1:1A:2801(A):A:H1'	1:1A:2895:U:H1'	1.94	0.49
32:1a:79:G:O6	32:1a:90:U:O4	2.29	0.49
32:1a:169:C:H2'	32:1a:170:U:C6	2.47	0.49
32:1a:626:U:H2'	32:1a:627:G:H8	1.76	0.49
32:1a:1469:G:H2'	32:1a:1470:G:C8	2.48	0.49
35:1d:15:GLU:OE2	35:1d:66:ARG:NH1	2.46	0.49
1:2A:1084:A:H3'	1:2A:1085:A:H4'	1.94	0.49
1:2A:1877:A:H5'	1:2A:1878:G:OP2	2.11	0.49
1:2A:2086:U:H2'	1:2A:2087:G:C8	2.47	0.49
1:2A:2887:U:H2'	1:2A:2888:C:H6	1.77	0.49
7:2H:3:ARG:NH2	7:2H:65:HIS:HB3	2.28	0.49
7:2H:88:LEU:HD21	7:2H:165:ALA:HA	1.94	0.49
7:2H:98:LEU:HD21	7:2H:123:PHE:HB2	1.93	0.49
17:2V:31:ALA:O	17:2V:61:VAL:HG22	2.12	0.49
34:2c:47:LEU:HD13	34:2c:68:VAL:HG11	1.93	0.49
41:2j:11:PHE:CE1	41:2j:67:THR:HG22	2.46	0.49
53:2y:87:LYS:O	53:2y:91:LYS:HB2	2.12	0.49
1:1A:639:U:H2'	1:1A:640:C:C6	2.48	0.49
1:1A:927:G:N7	61:1A:4205:HOH:O	2.34	0.49
1:1A:1506:C:H2'	1:1A:1507:A:O4'	2.13	0.49
1:1A:2400:G:O6	61:1A:4132:HOH:O	2.18	0.49
1:1A:2791:C:OP2	1:1A:2791:C:H6	1.96	0.49
5:1F:116:ASP:OD1	5:1F:119:ARG:NH2	2.46	0.49
32:1a:512:U:H2'	32:1a:513:C:C6	2.48	0.49
32:1a:986:A:H2'	32:1a:987:G:O4'	2.12	0.49
40:1i:9:ARG:HG2	40:1i:14:VAL:HG13	1.95	0.49
1:2A:127:A:H5''	1:2A:128:C:C6	2.47	0.49
32:2a:1323:G:O2'	32:2a:1362:C:O2'	2.30	0.49
33:2b:222:ILE:O	33:2b:226:ARG:HB2	2.12	0.49
50:2s:50:ALA:HA	50:2s:58:VAL:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:1G:62:LEU:HD12	6:1G:148:MET:HE1	1.94	0.49
33:1b:9:GLU:HB2	33:1b:217:ARG:HH22	1.78	0.49
47:1p:4:ILE:HG22	47:1p:19:ILE:HD11	1.93	0.49
1:2A:854:G:H2'	1:2A:855:G:H8	1.78	0.49
11:2P:86:LYS:HB3	11:2P:118:GLY:HA3	1.95	0.49
20:2Y:92:ASN:HD21	20:2Y:94:LYS:HE2	1.78	0.49
25:23:6:VAL:HG12	25:23:28:LEU:HD11	1.94	0.49
32:2a:130:A:O2'	32:2a:131:C:O5'	2.31	0.49
32:2a:1426:C:H2'	32:2a:1427:U:C6	2.48	0.49
35:2d:159:ARG:O	35:2d:163:GLU:N	2.42	0.49
47:2p:15:PRO:HD2	47:2p:42:ARG:HD3	1.95	0.49
11:1P:50:ARG:HD3	30:18:7:HIS:CD2	2.48	0.49
11:1P:59:LEU:HD13	30:18:58:ILE:HD13	1.94	0.49
11:1P:141:ALA:HA	25:23:38:GLU:HG2	1.94	0.49
32:1a:585:G:N3	32:1a:879:C:H4'	2.27	0.49
32:1a:995:C:O2	45:1n:4:LYS:NZ	2.46	0.49
32:1a:1248:A:N3	40:1i:70:LYS:HE3	2.27	0.49
45:1n:26:ARG:HD3	45:1n:43:CYS:HB3	1.95	0.49
47:1p:57:ARG:NH2	47:1p:78:GLY:O	2.46	0.49
52:1u:6:ARG:NH2	52:1u:15:ARG:HH21	2.10	0.49
1:2A:323:G:O2'	1:2A:1205:U:N3	2.39	0.49
1:2A:588:U:H2'	1:2A:589:C:C6	2.47	0.49
1:2A:800:A:H8	1:2A:800:A:OP1	1.96	0.49
1:2A:2186:G:C2	1:2A:2187:G:C5	3.01	0.49
1:2A:2336:A:H61	22:20:43:THR:HG22	1.77	0.49
2:2B:17:C:H2'	2:2B:18:G:O4'	2.13	0.49
7:2H:113:VAL:HG11	7:2H:151:ILE:HD13	1.94	0.49
21:2Z:152:ALA:O	21:2Z:155:LEU:HB2	2.12	0.49
32:2a:737:A:H2'	32:2a:738:C:C6	2.48	0.49
32:2a:1374:A:P	38:2g:36:LYS:HZ1	2.36	0.49
37:2f:68:PRO:HG2	37:2f:71:ARG:NH1	2.28	0.49
49:2r:53:ARG:NH1	49:2r:60:ALA:HB2	2.28	0.49
53:2y:38:HIS:HD2	53:2y:40:ILE:HD11	1.78	0.49
10:1O:73:ASP:HB2	15:1T:82:LEU:HD13	1.95	0.49
14:1S:34:HIS:ND1	14:1S:53:SER:OG	2.41	0.49
32:1a:399:G:H2'	32:1a:400:C:C6	2.47	0.49
32:1a:1136:U:H5''	32:1a:1137:C:C2	2.48	0.49
32:1a:1286:A:H2'	32:1a:1287:A:H4'	1.94	0.49
33:1b:10:LEU:HD13	33:1b:48:MET:SD	2.53	0.49
33:1b:84:GLU:HB3	33:1b:219:VAL:HG21	1.95	0.49
39:1h:86:ILE:HG12	39:1h:135:CYS:HA	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:1p:40:ASP:HB3	47:1p:48:TRP:HB2	1.94	0.49
1:2A:2206:G:H8	1:2A:2207:G:N7	2.11	0.49
1:2A:2224:G:H4'	1:2A:2226:C:C2	2.47	0.49
4:2E:9:VAL:HG13	4:2E:25:VAL:O	2.13	0.49
15:2T:41:ARG:NH2	32:2a:346:G:OP1	2.45	0.49
18:2W:71:VAL:HA	18:2W:107:LEU:HD23	1.94	0.49
32:2a:519:C:OP2	43:2l:50:SER:OG	2.29	0.49
36:2e:60:TYR:CZ	36:2e:64:ARG:HD3	2.48	0.49
26:14:44:THR:O	26:14:47:GLN:HB2	2.12	0.48
39:1h:116:LYS:HD3	39:1h:127:LEU:HD22	1.95	0.48
51:1t:63:ILE:HG21	51:1t:81:LYS:HG3	1.95	0.48
1:2A:667:U:O2	30:28:2:PRO:HD2	2.13	0.48
1:2A:1803:A:H4'	3:2D:259:THR:HG23	1.95	0.48
1:2A:2870:C:H2'	1:2A:2871:C:O4'	2.13	0.48
1:2A:2882:A:OP1	13:2R:96:ARG:HD3	2.13	0.48
6:2G:50:ALA:HB1	6:2G:53:LEU:HD23	1.94	0.48
26:24:67:TYR:HB2	50:2s:16:LEU:HD21	1.95	0.48
32:2a:110:C:H2'	32:2a:111:G:O4'	2.13	0.48
32:2a:123:C:OP1	32:2a:311:C:O2'	2.24	0.48
1:1A:1210:A:H5''	1:1A:1212:G:O4'	2.13	0.48
1:1A:2022:U:O2'	1:1A:2617:C:H5'	2.13	0.48
1:1A:2134:A:N6	1:1A:2157:G:H4'	2.28	0.48
1:1A:2251:OMG:HM23	1:1A:2251:OMG:H1'	1.71	0.48
10:1O:49:ARG:NH2	32:1a:1423:G:OP1	2.41	0.48
32:1a:1380:U:C4	38:1g:3:ARG:HG2	2.48	0.48
33:1b:115:LEU:O	33:1b:119:GLU:HG2	2.13	0.48
48:1q:58:GLU:OE2	48:1q:75:ARG:NH2	2.46	0.48
1:2A:84:A:H5''	20:2Y:8:LYS:HE3	1.95	0.48
1:2A:2641:G:P	9:2N:74:ARG:HH21	2.36	0.48
4:2E:9:VAL:HB	15:2T:3:ARG:HG2	1.95	0.48
6:2G:16:ARG:HB2	6:2G:17:PRO:HD3	1.95	0.48
21:2Z:96:VAL:N	21:2Z:128:VAL:O	2.29	0.48
32:2a:539:A:H2'	32:2a:540:G:C8	2.48	0.48
32:2a:1108:G:H5'	34:2c:176:HIS:CD2	2.48	0.48
32:2a:1391:U:H2'	32:2a:1392:G:C8	2.48	0.48
37:2f:61:LEU:HB3	37:2f:63:TYR:HE2	1.77	0.48
1:1A:644:A:H4'	1:1A:645:C:H5	1.78	0.48
7:1H:157:TYR:CE1	7:1H:172:LYS:HG3	2.47	0.48
9:1N:42:TRP:CH2	9:1N:44:PRO:HB3	2.49	0.48
1:2A:968:G:OP1	25:23:17:LYS:NZ	2.45	0.48
6:2G:113:ARG:NH2	6:2G:139:LEU:O	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:21:44:PRO:HB2	23:21:46:LEU:HD23	1.95	0.48
32:2a:1202:G:H1'	45:2n:29:ARG:HD2	1.94	0.48
32:2a:1273:G:H3'	32:2a:1274:G:H8	1.77	0.48
36:2e:78:HIS:CE1	36:2e:142:LEU:HD23	2.47	0.48
39:2h:14:ARG:NH1	39:2h:83:ILE:O	2.47	0.48
46:2o:18:PHE:HB2	46:2o:19:PRO:HD2	1.95	0.48
53:2y:42:SER:O	53:2y:49:VAL:N	2.45	0.48
32:1a:1315:U:H2'	32:1a:1316:G:O4'	2.12	0.48
51:1t:65:LYS:O	51:1t:68:LYS:HB2	2.14	0.48
1:2A:839:U:H2'	1:2A:840:C:C6	2.47	0.48
1:2A:927:G:H2'	1:2A:928:G:O4'	2.13	0.48
1:2A:993:G:OP1	16:2U:50:ARG:NH2	2.45	0.48
1:2A:1178:C:H2'	1:2A:1179:C:C6	2.49	0.48
5:2F:184:TYR:CE2	5:2F:188:ARG:HD2	2.48	0.48
6:2G:108:ASN:HA	26:24:37:SER:HB3	1.94	0.48
6:2G:126:ASP:HB3	6:2G:128:ARG:H	1.78	0.48
8:2I:50:ARG:O	8:2I:54:GLN:HG2	2.13	0.48
33:2b:189:ASP:OD1	33:2b:189:ASP:N	2.35	0.48
38:2g:69:VAL:HG22	38:2g:135:VAL:HG12	1.95	0.48
49:2r:37:VAL:HG22	49:2r:78:LEU:HB3	1.95	0.48
6:1G:122:PRO:HG3	6:1G:182:LYS:H	1.77	0.48
25:13:7:LYS:HE3	25:13:32:GLN:NE2	2.28	0.48
32:1a:1117:G:H4'	40:1i:104:ARG:NH1	2.28	0.48
33:1b:15:VAL:HG22	33:1b:209:ARG:HB3	1.95	0.48
40:1i:17:VAL:HG11	40:1i:80:GLY:C	2.38	0.48
1:2A:1081:U:H2'	1:2A:1082:U:O2	2.13	0.48
1:2A:2784:C:H1'	4:2E:37:ARG:HH12	1.79	0.48
2:2B:6:C:H2'	2:2B:7:G:H5''	1.96	0.48
4:2E:170:LEU:HD23	4:2E:184:VAL:HG11	1.94	0.48
7:2H:154:PRO:HB3	7:2H:163:TYR:CZ	2.48	0.48
11:2P:91:PHE:O	11:2P:121:LYS:NZ	2.46	0.48
32:2a:977:A:O2'	32:2a:981:U:N3	2.46	0.48
32:2a:1004:A:OP1	32:2a:1024:G:N2	2.47	0.48
51:2t:60:GLU:HG3	51:2t:81:LYS:HD2	1.96	0.48
53:2y:61:LEU:HB3	53:2y:81:LEU:HD22	1.94	0.48
1:1A:305:U:H2'	1:1A:306:U:C6	2.48	0.48
1:1A:813:U:H2'	1:1A:814:C:C6	2.49	0.48
1:1A:1058:G:N1	1:1A:1080:C:O2	2.32	0.48
24:12:1:MET:HG2	24:12:6:VAL:HG23	1.94	0.48
27:15:17:ASP:OD2	61:15:9501:HOH:O	2.20	0.48
32:1a:300:A:O2'	32:1a:564:C:N3	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:920:U:H2'	32:1a:921:U:C6	2.49	0.48
32:1a:1347:G:N2	32:1a:1373:G:H2'	2.28	0.48
33:1b:42:ILE:HD12	33:1b:203:GLY:HA2	1.95	0.48
1:2A:655:A:H8	1:2A:656:G:O4'	1.96	0.48
1:2A:821:A:H2'	1:2A:946:G:H5''	1.95	0.48
1:2A:1047:G:N2	1:2A:1111:A:H62	2.09	0.48
1:2A:1057:A:H62	1:2A:1086:A:H3'	1.78	0.48
1:2A:1688:U:O2	1:2A:1700:A:H5'	2.12	0.48
1:2A:2118:U:O2'	1:2A:2119:A:H5''	2.14	0.48
5:2F:108:LYS:O	5:2F:112:MET:HG3	2.13	0.48
21:2Z:48:PHE:HE1	21:2Z:71:VAL:HG21	1.79	0.48
32:2a:9:G:H2'	32:2a:10:A:C8	2.49	0.48
32:2a:1005:A:C5	32:2a:1006:C:H1'	2.49	0.48
44:2m:22:ILE:HB	44:2m:25:ILE:HD12	1.95	0.48
49:2r:59:SER:OG	49:2r:62:GLU:HG2	2.13	0.48
1:1A:207:A:H2'	1:1A:208:C:O4'	2.12	0.48
1:1A:1652:A:O2'	1:1A:1653:G:H5'	2.14	0.48
1:1A:2059:A:N1	56:1A:4021:TEL:H44	2.29	0.48
7:1H:13:LYS:HA	7:1H:14:GLY:HA2	1.60	0.48
12:1Q:109:VAL:HG22	12:1Q:113:GLN:CD	2.39	0.48
17:1V:84:LYS:NZ	61:1V:303:HOH:O	2.45	0.48
26:14:55:ARG:H	26:14:56:VAL:HA	1.79	0.48
32:1a:1003:G:C2	32:1a:1004:A:N3	2.82	0.48
33:1b:72:GLY:O	33:1b:94:ASN:HA	2.13	0.48
33:1b:87:ARG:NH1	33:1b:233:SER:OG	2.47	0.48
35:1d:172:PRO:HB2	35:1d:187:ARG:NH2	2.29	0.48
1:2A:774:A:H2'	1:2A:774:A:N3	2.29	0.48
1:2A:1165:U:H2'	1:2A:1166:C:C6	2.49	0.48
1:2A:1420:U:O2'	1:2A:1421:G:OP1	2.29	0.48
1:2A:2106:G:C4	1:2A:2107:C:H1'	2.48	0.48
1:2A:2788:C:N3	1:2A:2789:C:N4	2.60	0.48
7:2H:26:VAL:HG12	7:2H:79:VAL:HG21	1.96	0.48
32:2a:1290:G:OP1	38:2g:35:LYS:NZ	2.40	0.48
33:2b:134:GLU:HA	33:2b:137:ARG:NH2	2.28	0.48
38:2g:113:GLU:H	38:2g:113:GLU:HG2	1.35	0.48
44:2m:95:GLY:O	44:2m:110:ARG:HG3	2.13	0.48
1:1A:888:C:O5'	44:1m:93:ARG:HD2	2.14	0.48
1:1A:1570:A:H2'	1:1A:1571:A:C8	2.49	0.48
1:1A:2763:G:OP2	61:1A:4137:HOH:O	2.20	0.48
2:1B:66:A:N6	2:1B:108:U:H2'	2.29	0.48
19:1X:31:HIS:CD2	19:1X:33:LYS:H	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:1f:100:ASN:HD21	49:1r:23:LYS:HE2	1.79	0.48
42:1k:48:ILE:HD13	42:1k:63:LEU:HD12	1.94	0.48
1:2A:39:C:O2	5:2F:46:ARG:NH2	2.46	0.48
1:2A:309:G:N3	1:2A:329:G:O2'	2.42	0.48
1:2A:1085:A:H2'	1:2A:1086:A:C2	2.48	0.48
1:2A:2133:G:C2	1:2A:2157:G:H2'	2.49	0.48
10:2O:24:VAL:HG13	10:2O:33:ALA:HB2	1.94	0.48
32:2a:56:U:H2'	32:2a:57:G:H8	1.79	0.48
32:2a:280:C:N3	48:2q:39:SER:OG	2.45	0.48
32:2a:1119:C:H2'	32:2a:1120:G:C8	2.49	0.48
32:2a:1347:G:H22	32:2a:1373:G:H2'	1.77	0.48
46:2o:21:ASP:OD2	46:2o:24:SER:HB3	2.14	0.48
1:1A:652(U):G:H3'	1:1A:652(V):C:H6	1.79	0.48
21:1Z:157:LEU:HD11	21:1Z:163:LEU:HD13	1.96	0.48
23:11:53:VAL:HG22	23:11:74:VAL:HG13	1.95	0.48
26:14:8:LYS:HE2	26:14:10:VAL:HG12	1.96	0.48
1:2A:1929:G:H5'	61:2A:5113:HOH:O	2.14	0.48
1:2A:2141:G:O6	1:2A:2150:U:C2	2.66	0.48
1:2A:2142:C:N3	1:2A:2149:G:O6	2.47	0.48
1:1A:2336:A:H61	22:10:43:THR:CG2	2.26	0.48
5:1F:132:VAL:HG22	5:1F:163:VAL:HG22	1.96	0.48
21:1Z:1:MET:N	21:1Z:135:GLU:OE2	2.47	0.48
32:1a:1040:U:H2'	32:1a:1041:A:H8	1.78	0.48
32:1a:1295:G:O2'	44:1m:14:ARG:NH1	2.47	0.48
33:1b:96:ARG:HG2	33:1b:98:LEU:HD23	1.95	0.48
35:1d:59:ARG:NH1	35:1d:66:ARG:HH12	2.12	0.48
36:1e:79:GLU:HG3	36:1e:93:PRO:HD2	1.95	0.48
1:2A:747:U:O2	1:2A:2014:A:H1'	2.13	0.48
1:2A:1062:G:H2'	1:2A:1063:G:C8	2.42	0.48
1:2A:2186:G:H2'	1:2A:2187:G:H5''	1.95	0.48
32:2a:937:A:OP2	61:2a:3219:HOH:O	2.20	0.48
40:2i:92:TYR:HB3	40:2i:96:LEU:HD12	1.95	0.48
32:1a:1036:G:H5''	32:1a:1037:C:C5	2.49	0.47
35:1d:155:LEU:HB3	35:1d:158:ILE:HG12	1.96	0.47
52:1u:14:TRP:HZ3	52:1u:15:ARG:NH1	2.11	0.47
1:2A:1899:G:H2'	1:2A:1899:G:N3	2.29	0.47
17:2V:43:GLU:OE1	17:2V:43:GLU:N	2.47	0.47
32:2a:1320:C:H2'	32:2a:1321:C:O4'	2.13	0.47
33:2b:217:ARG:HA	33:2b:220:ASP:HB2	1.96	0.47
1:1A:1048:A:OP2	1:1A:1109:C:N4	2.47	0.47
5:1F:185:ASP:HA	5:1F:188:ARG:HD3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:14:40:HIS:HB3	26:14:43:TYR:HD2	1.79	0.47
32:1a:1066:C:OP2	61:1a:3313:HOH:O	2.20	0.47
47:1p:39:TYR:CD1	47:1p:49:LEU:HD23	2.49	0.47
32:2a:41:G:H2'	32:2a:42:G:C8	2.48	0.47
32:2a:189(D):C:H2'	32:2a:189(E):U:O4'	2.13	0.47
32:2a:643:C:H2'	32:2a:644:G:H8	1.79	0.47
32:2a:1400:5MC:C2	53:2y:63:ALA:HA	2.50	0.47
33:2b:70:PHE:HB3	33:2b:81:VAL:HG22	1.95	0.47
34:2c:28:GLN:HE21	34:2c:32:LEU:HD21	1.78	0.47
42:2k:85:ARG:HG2	42:2k:112:THR:HA	1.97	0.47
1:1A:956:G:O6	61:1A:4134:HOH:O	2.19	0.47
1:1A:1786:A:H1'	1:1A:1938:A:N6	2.30	0.47
1:1A:2564:A:C2	1:1A:2647:U:H4'	2.49	0.47
6:1G:43:LEU:O	6:1G:45:GLU:HG2	2.15	0.47
32:1a:111:G:OP2	61:1a:3314:HOH:O	2.20	0.47
32:1a:474:G:H2'	32:1a:475:G:C8	2.48	0.47
32:1a:1260:C:H5'	32:1a:1284:C:H4'	1.96	0.47
32:1a:1513:A:H2'	32:1a:1514:C:C6	2.49	0.47
1:2A:299:A:N1	1:2A:322:A:O2'	2.39	0.47
1:2A:2390:U:P	30:28:35:GLN:HE22	2.37	0.47
30:28:34:TRP:CE2	30:28:35:GLN:HB3	2.50	0.47
32:2a:1036:G:H3'	32:2a:1037:C:C6	2.49	0.47
33:2b:87:ARG:NH2	33:2b:220:ASP:OD1	2.41	0.47
35:2d:163:GLU:O	35:2d:166:LYS:HG3	2.13	0.47
40:2i:3:GLN:HE21	40:2i:20:ARG:HE	1.60	0.47
48:2q:67:LYS:O	48:2q:68:ARG:HB2	2.14	0.47
1:1A:1486:A:H2'	1:1A:1487:G:C8	2.48	0.47
1:1A:1939:5MU:OP1	1:1A:2604:U:O2'	2.31	0.47
4:1E:143:ASN:HD22	4:1E:147:PRO:HD3	1.79	0.47
13:1R:104:ARG:HD2	13:1R:107:ASP:OD1	2.13	0.47
20:1Y:38:ILE:HD11	20:1Y:66:PRO:HG3	1.96	0.47
1:2A:1946:U:H2'	1:2A:1947:C:C6	2.50	0.47
5:2F:167:ALA:HB1	5:2F:173:VAL:HG11	1.95	0.47
9:2N:104:LYS:HA	9:2N:107:LEU:HD12	1.95	0.47
13:2R:97:VAL:HG22	13:2R:114:VAL:HG13	1.96	0.47
32:2a:415:A:H2'	32:2a:416:G:O4'	2.15	0.47
32:2a:512:U:H2'	32:2a:513:C:C6	2.50	0.47
32:2a:581:G:OP1	46:2o:61:GLY:HA3	2.14	0.47
32:2a:1090:U:H2'	32:2a:1091:U:H6	1.79	0.47
32:2a:1239:A:H62	32:2a:1299:A:H62	1.62	0.47
33:2b:71:VAL:HG12	33:2b:93:VAL:HG22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2l:28:LYS:HA	43:2l:28:LYS:HD3	1.55	0.47
53:2y:8:LYS:O	53:2y:10:MET:HG3	2.15	0.47
1:1A:1069:A:H5'	1:1A:1070:A:H2	1.79	0.47
1:1A:2119:A:H2	1:1A:2171:A:H5'	1.80	0.47
1:1A:2849:U:H4'	1:1A:2868:A:C2	2.49	0.47
5:1F:53:THR:HG23	5:1F:55:GLY:H	1.79	0.47
6:1G:41:GLN:HG3	6:1G:60:LEU:HD11	1.96	0.47
32:1a:735:C:H2'	32:1a:736:C:C6	2.50	0.47
40:1i:16:ARG:HD3	40:1i:64:THR:HG21	1.97	0.47
1:2A:583:G:OP2	16:2U:10:ARG:HD2	2.14	0.47
1:2A:888:C:H2'	1:2A:889:C:N3	2.29	0.47
1:2A:1826:G:H4'	3:2D:242:ARG:CZ	2.45	0.47
1:2A:2022:U:O2'	1:2A:2617:C:H5'	2.15	0.47
3:2D:102:LYS:C	3:2D:103:ARG:HG2	2.38	0.47
4:2E:70:ALA:O	4:2E:72:VAL:N	2.48	0.47
11:2P:54:GLY:O	61:2P:301:HOH:O	2.20	0.47
12:2Q:32:TYR:CE1	12:2Q:133:ARG:HB3	2.49	0.47
21:2Z:32:HIS:NE2	61:2Z:302:HOH:O	2.27	0.47
32:2a:1054:C:N4	53:2y:46:GLN:HG3	2.24	0.47
32:2a:1323:G:H4'	32:2a:1363:C:C2	2.49	0.47
1:1A:2747:G:O6	1:1A:2755:C:H5''	2.13	0.47
2:1B:33:G:H5'	6:1G:2:PRO:HD3	1.97	0.47
5:1F:39:TRP:CH2	5:1F:106:ARG:HD3	2.50	0.47
19:1X:60:ARG:NH1	29:17:47:ARG:HH22	2.11	0.47
23:11:3:LYS:O	23:11:12:PRO:HD3	2.15	0.47
39:1h:36:LEU:HD12	39:1h:59:LEU:HD13	1.97	0.47
1:2A:300:A:P	20:2Y:86:ARG:HH21	2.38	0.47
1:2A:322:A:OP1	5:2F:168:ARG:NH1	2.48	0.47
1:2A:1647:G:H3'	1:2A:1647:G:OP2	2.14	0.47
3:2D:69:ARG:NH2	3:2D:128:GLY:O	2.45	0.47
6:2G:16:ARG:HH22	6:2G:28:VAL:HB	1.79	0.47
11:2P:97:PRO:O	11:2P:101:VAL:HG23	2.14	0.47
33:2b:178:ARG:HH22	39:2h:74:PRO:HB3	1.79	0.47
34:2c:20:SER:HB2	34:2c:40:ARG:HH21	1.80	0.47
34:2c:150:LYS:HG3	34:2c:169:ALA:HB2	1.95	0.47
41:2j:78:ASN:O	41:2j:80:LYS:N	2.48	0.47
1:1A:244:A:C2	1:1A:255:A:C4	3.03	0.47
1:1A:955:C:OP1	12:1Q:87:LYS:NZ	2.45	0.47
1:1A:1503:U:H2'	1:1A:1504:C:C6	2.50	0.47
1:1A:2010:G:H5''	18:1W:42:ARG:HB2	1.97	0.47
1:1A:2327:A:H2'	1:1A:2328:A:C8	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2584:U:H2'	1:1A:2585:U:H2'	1.97	0.47
61:1A:5493:HOH:O	3:1D:261:LYS:HE3	2.13	0.47
16:1U:86:ALA:O	17:1V:49:THR:HG23	2.15	0.47
23:11:64:ALA:HA	23:11:67:ILE:HG13	1.97	0.47
29:17:12:ARG:NH2	29:17:44:PRO:HB3	2.30	0.47
32:1a:108:G:C6	51:1t:15:ARG:HG2	2.50	0.47
32:1a:293:G:O6	61:1a:3312:HOH:O	2.19	0.47
32:1a:376:G:H4'	47:1p:5:ARG:HH11	1.80	0.47
33:1b:81:VAL:HG12	33:1b:215:LEU:HD11	1.97	0.47
33:1b:207:ALA:O	33:1b:211:ILE:HG13	2.15	0.47
34:1c:3:ASN:OD1	34:1c:3:ASN:N	2.48	0.47
34:1c:153:VAL:HG22	34:1c:198:VAL:HG22	1.96	0.47
36:1e:37:ARG:NH1	36:1e:111:GLU:HG2	2.27	0.47
52:1u:5:ASP:O	52:1u:11:GLY:HA3	2.14	0.47
53:1y:3:MET:HE2	53:1y:3:MET:HB3	1.77	0.47
1:2A:7:G:H2'	1:2A:8:A:C8	2.50	0.47
1:2A:861:A:C2	1:2A:917:A:C4	3.02	0.47
1:2A:1086:A:H4'	1:2A:1103:A:H2	1.80	0.47
1:2A:1102:C:H2'	1:2A:1103:A:C8	2.49	0.47
1:2A:1181:C:H2'	1:2A:1182:A:H8	1.79	0.47
1:2A:2179:C:C4	1:2A:2180:U:C4	3.03	0.47
1:2A:2646:C:OP2	1:2A:2732:G:O2'	2.25	0.47
5:2F:11:VAL:HB	5:2F:18:ARG:HG2	1.97	0.47
5:2F:172:TRP:H	5:2F:172:TRP:CD1	2.32	0.47
6:2G:83:ARG:H	6:2G:86:MET:CE	2.26	0.47
6:2G:101:ILE:HG22	6:2G:105:LYS:HE2	1.97	0.47
14:2S:3:ARG:HD2	14:2S:4:LEU:H	1.80	0.47
32:2a:41:G:H2'	32:2a:42:G:H8	1.79	0.47
32:2a:273:A:H1'	48:2q:16:GLN:NE2	2.29	0.47
32:2a:475:G:O2'	32:2a:476:G:H5'	2.14	0.47
32:2a:674:G:H2'	32:2a:675:A:H8	1.79	0.47
32:2a:719:C:O2'	49:2r:49:LYS:HB3	2.14	0.47
32:2a:1012:U:H2'	32:2a:1013:G:O4'	2.14	0.47
32:2a:1014:A:H2	32:2a:1219:U:H1'	1.80	0.47
32:2a:1359:C:H1'	32:2a:1362:C:H41	1.80	0.47
44:2m:15:VAL:HG11	44:2m:48:LEU:HD21	1.97	0.47
1:1A:271(H):G:O2'	1:1A:271(I):G:OP2	2.26	0.47
1:1A:811:U:H2'	11:1P:21:ARG:HA	1.97	0.47
1:1A:829:A:N7	1:1A:2248:C:H5'	2.30	0.47
1:1A:1188:U:H4'	17:1V:79:VAL:HG22	1.97	0.47
1:1A:1796:U:H2'	1:1A:1797:C:H6	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2206:G:H2'	1:1A:2207:G:C2	2.49	0.47
1:1A:2384:G:N7	61:1A:4227:HOH:O	2.36	0.47
8:1I:130:TYR:HB3	8:1I:138:ILE:HB	1.95	0.47
32:1a:1182:G:C4'	32:1a:1183:A:H5'	2.44	0.47
39:1h:73:ASP:OD1	39:1h:75:ARG:NH1	2.48	0.47
44:1m:4:ILE:HA	44:1m:5:ALA:HA	1.59	0.47
1:2A:234:C:H2'	1:2A:235:U:C6	2.50	0.47
1:2A:686:G:N2	1:2A:788:A:H61	2.13	0.47
1:2A:852:G:H2'	1:2A:853:G:H8	1.80	0.47
1:2A:2328:A:H2'	1:2A:2329:G:C8	2.50	0.47
1:2A:2645:G:N2	1:2A:2767:C:OP2	2.48	0.47
32:2a:1069:C:O2'	32:2a:1192:C:O2	2.30	0.47
33:2b:87:ARG:CZ	33:2b:233:SER:HB3	2.45	0.47
36:2e:6:PHE:HB2	36:2e:63:ARG:HH12	1.79	0.47
44:2m:60:VAL:HG13	44:2m:64:TRP:HE3	1.79	0.47
49:2r:58:LEU:HD23	49:2r:62:GLU:HG3	1.96	0.47
1:1A:330:A:H2	1:1A:1210:A:H2'	1.79	0.47
1:1A:715:G:C2	46:1o:56:LEU:HD21	2.50	0.47
1:1A:1641:A:H2'	1:1A:1642:G:O4'	2.15	0.47
8:1I:54:GLN:HE21	8:1I:57:ARG:NH2	2.13	0.47
32:1a:1298:C:P	38:1g:114:ARG:HH22	2.38	0.47
1:2A:1055:G:H2'	1:2A:1056:G:O4'	2.14	0.47
7:2H:164:TYR:HB2	7:2H:167:GLU:HB2	1.96	0.47
12:2Q:111:GLU:O	12:2Q:115:MET:HG2	2.15	0.47
32:2a:1343:G:H2'	32:2a:1344:C:C6	2.50	0.47
34:2c:78:GLY:HA3	34:2c:83:ARG:H	1.80	0.47
1:1A:569:U:C4	1:1A:570:G:C6	3.03	0.47
1:1A:747:U:O2	1:1A:2014:A:H1'	2.15	0.47
10:1O:49:ARG:NH1	32:1a:1422:G:O3'	2.42	0.47
32:1a:134:A:H61	47:1p:25:ARG:NH1	2.13	0.47
32:1a:651:C:OP1	61:1a:3316:HOH:O	2.21	0.47
32:1a:1368:G:OP2	40:1i:112:LYS:HG3	2.14	0.47
32:1a:1525:G:OP1	42:1k:120:ARG:NH2	2.47	0.47
49:1r:45:SER:OG	49:1r:47:THR:HG22	2.15	0.47
50:1s:12:ASP:HB3	50:1s:14:HIS:CD2	2.50	0.47
1:2A:241:A:H5''	61:2A:5729:HOH:O	2.15	0.47
1:2A:251:A:C5	1:2A:252:G:H1'	2.49	0.47
1:2A:470:A:OP1	5:2F:59:TYR:HE1	1.98	0.47
1:2A:1049:C:O2	1:2A:1113:U:H4'	2.15	0.47
1:2A:1467:C:C5	1:2A:1546:C:H2'	2.50	0.47
3:2D:24:ILE:HD13	3:2D:84:TYR:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:2Z:69:THR:HG22	21:2Z:90:VAL:HA	1.95	0.47
37:2f:6:VAL:HG22	37:2f:90:VAL:HG22	1.97	0.47
40:2i:5:TYR:H	40:2i:87:GLN:HE22	1.63	0.47
1:1A:586:A:N1	1:1A:809:G:O2'	2.40	0.46
1:1A:1174:A:H4'	1:1A:1175:U:OP1	2.14	0.46
1:1A:2038:G:H2'	1:1A:2039:C:O4'	2.15	0.46
10:1O:115:VAL:O	57:1a:3279:MPD:H13	2.15	0.46
19:1X:94:GLY:HA3	19:1X:95:LEU:C	2.40	0.46
36:1e:101:ILE:HG13	36:1e:119:LEU:HD23	1.97	0.46
40:1i:4:TYR:HB2	40:1i:19:LEU:HB2	1.98	0.46
40:1i:17:VAL:HG21	40:1i:81:ILE:HG22	1.97	0.46
1:2A:272:G:N7	1:2A:421:U:H2'	2.30	0.46
1:2A:674:G:O2'	5:2F:74:ARG:HD3	2.15	0.46
1:2A:1110:G:H1'	1:2A:1111:A:C8	2.50	0.46
1:2A:1581:G:H2'	1:2A:1582:C:O4'	2.15	0.46
1:2A:2098:U:H2'	1:2A:2099:U:O4'	2.15	0.46
1:2A:2104:G:N7	1:2A:2186:G:C2	2.83	0.46
41:2j:35:SER:HB3	41:2j:73:ASP:O	2.14	0.46
1:1A:2167:U:H2'	1:1A:2168:G:C8	2.51	0.46
1:1A:2563:U:H4'	10:1O:28:SER:HA	1.96	0.46
15:1T:112:ARG:HG2	15:1T:115:ARG:HH21	1.81	0.46
32:1a:452:A:H4'	47:1p:72:ARG:CZ	2.45	0.46
32:1a:998:G:H2'	32:1a:999:C:C6	2.50	0.46
32:1a:1131:G:H1	32:1a:1143:G:H21	1.62	0.46
32:1a:1425:U:H2'	32:1a:1426:C:C6	2.49	0.46
40:1i:5:TYR:HE1	40:1i:16:ARG:HB3	1.80	0.46
50:1s:22:LEU:HD22	50:1s:28:LYS:HA	1.97	0.46
1:2A:71:A:N7	19:2X:31:HIS:HE1	2.13	0.46
1:2A:468:G:O2'	5:2F:62:ARG:NH2	2.33	0.46
1:2A:637:A:H2'	11:2P:117:GLU:OE1	2.15	0.46
1:2A:1364:G:N7	23:21:3:LYS:HD2	2.29	0.46
1:2A:2253:G:O6	61:2A:3851:HOH:O	2.20	0.46
1:2A:2262:U:H4'	1:2A:2328:A:C2	2.51	0.46
12:2Q:11:LYS:HD3	12:2Q:87:LYS:HD3	1.97	0.46
32:2a:630:G:O2'	32:2a:631:G:H5'	2.15	0.46
32:2a:1129:C:H1'	32:2a:1130:A:N7	2.31	0.46
38:2g:51:GLN:O	38:2g:55:GLY:HA2	2.15	0.46
45:2n:27:CYS:SG	45:2n:29:ARG:HB2	2.56	0.46
1:1A:2142:C:N3	1:1A:2149:G:C6	2.83	0.46
1:1A:2319:G:N1	14:1S:3:ARG:HA	2.30	0.46
1:1A:2774:C:H2'	1:1A:2775:A:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:266:G:H5''	32:1a:267:C:H5	1.80	0.46
32:1a:1427:U:H2'	32:1a:1428:A:C8	2.50	0.46
32:1a:1492:A:H4'	32:1a:1493:A:N1	2.31	0.46
34:1c:180:ALA:HB1	34:1c:203:PHE:CE1	2.46	0.46
35:1d:156:GLU:O	35:1d:160:GLN:HG2	2.16	0.46
43:1l:28:LYS:HG3	43:1l:62:SER:HB2	1.97	0.46
1:2A:1014:U:H2'	1:2A:1015:G:C8	2.48	0.46
1:2A:2771:C:H5''	4:2E:202:LYS:HD3	1.97	0.46
1:2A:2839:G:H5'	13:2R:46:GLY:CA	2.44	0.46
32:2a:1151:A:O4'	41:2j:39:PRO:HB2	2.15	0.46
49:2r:39:VAL:O	49:2r:42:ARG:HG3	2.15	0.46
1:1A:286:C:H2'	1:1A:287:C:C6	2.51	0.46
1:1A:2114:A:H3'	1:1A:2115:G:C8	2.50	0.46
1:1A:2135:A:C2	1:1A:2136:C:H1'	2.50	0.46
6:1G:112:PRO:HG3	26:14:43:TYR:CE2	2.49	0.46
7:1H:3:ARG:NH1	7:1H:5:GLY:H	2.12	0.46
14:1S:58:LEU:HD23	14:1S:58:LEU:HA	1.79	0.46
32:1a:164:U:H2'	32:1a:165:C:C6	2.50	0.46
32:1a:375:U:OP1	47:1p:69:THR:HG21	2.15	0.46
32:1a:1404:5MC:O2	32:1a:1519:MA6:O2'	2.30	0.46
35:1d:128:VAL:HG12	35:1d:129:ASN:HD22	1.81	0.46
38:1g:26:PHE:CE2	38:1g:30:ILE:HD11	2.50	0.46
40:1i:18:PHE:N	40:1i:62:TYR:O	2.44	0.46
5:2F:150:GLY:HA2	5:2F:172:TRP:CD2	2.51	0.46
6:2G:44:GLY:O	6:2G:47:LYS:HG2	2.15	0.46
28:26:14:THR:OG1	28:26:48:VAL:O	2.34	0.46
32:2a:70:G:H1	32:2a:99:U:H3	1.61	0.46
32:2a:335:C:H2'	32:2a:336:C:C6	2.51	0.46
32:2a:1121:U:H2'	32:2a:1122:U:C6	2.51	0.46
32:2a:1323:G:H2'	32:2a:1324:A:C8	2.51	0.46
50:2s:33:THR:HG22	50:2s:35:SER:H	1.80	0.46
1:1A:121:G:H4'	1:1A:149:A:H5'	1.97	0.46
1:1A:1759:A:H1'	1:1A:2711:A:C2	2.51	0.46
1:1A:2142:C:H2'	1:1A:2143:C:C6	2.51	0.46
1:1A:2430:A:N3	1:1A:2430:A:H2'	2.29	0.46
21:1Z:125:LEU:HG	21:1Z:164:ALA:HB3	1.98	0.46
26:14:28:LYS:HB2	26:14:31:ILE:HD11	1.96	0.46
32:1a:942:G:C2	32:1a:1342:C:C2	3.03	0.46
35:1d:194:LEU:HD13	35:1d:194:LEU:HA	1.78	0.46
47:1p:22:THR:HA	47:1p:33:ILE:HG13	1.98	0.46
51:1t:72:LEU:HD11	51:1t:80:ARG:HD2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:96:G:H4'	24:22:48:HIS:CD2	2.51	0.46
1:2A:1041:C:N4	1:2A:1114:G:H1	1.98	0.46
1:2A:1063:G:H1	1:2A:1075:C:N4	2.13	0.46
23:21:83:GLU:HA	23:21:84:GLY:HA2	1.66	0.46
32:2a:1092:A:H5''	38:2g:4:ARG:NH2	2.30	0.46
41:2j:6:ILE:HB	41:2j:72:VAL:HG22	1.98	0.46
1:1A:1051:G:H2'	1:1A:1052:C:O4'	2.16	0.46
1:1A:1171:G:H3'	1:1A:1173:G:H5'	1.97	0.46
1:1A:1512:U:H2'	1:1A:1513:C:C6	2.51	0.46
1:1A:2377:A:H2'	1:1A:2378:A:C8	2.50	0.46
3:1D:72:LYS:NZ	3:1D:99:ASP:OD2	2.42	0.46
8:1I:38:LEU:HB3	8:1I:40:THR:HG23	1.98	0.46
9:1N:62:VAL:CG1	9:1N:66:LYS:HB2	2.46	0.46
32:1a:131:C:H2'	32:1a:132:C:C6	2.51	0.46
32:1a:474:G:H2'	32:1a:475:G:H8	1.80	0.46
32:1a:743:U:H2'	32:1a:744:C:C6	2.50	0.46
32:1a:1135:U:H4'	32:1a:1136:U:C4	2.50	0.46
49:1r:26:LEU:HD11	49:1r:42:ARG:HD3	1.97	0.46
50:1s:42:PRO:HA	50:1s:45:VAL:HG23	1.97	0.46
1:2A:11:G:H2'	1:2A:12:U:H5'	1.97	0.46
1:2A:272(B):G:H2'	1:2A:272(C):G:H8	1.81	0.46
1:2A:856:C:H2'	1:2A:857:C:C6	2.51	0.46
1:2A:1181:C:H2'	1:2A:1182:A:C8	2.50	0.46
1:2A:1669:A:H5''	1:2A:2550:G:OP1	2.15	0.46
4:2E:55:ASN:HB3	4:2E:58:ARG:HG3	1.96	0.46
11:2P:59:LEU:HD11	30:28:10:ALA:HA	1.96	0.46
32:2a:1491:G:O2'	32:2a:1492:A:OP1	2.27	0.46
39:2h:101:PRO:HG3	39:2h:133:LEU:HD11	1.98	0.46
50:2s:20:LEU:HA	50:2s:23:ASN:HB2	1.98	0.46
1:1A:129:C:H5''	61:1A:5467:HOH:O	2.14	0.46
1:1A:391:G:H1'	1:1A:411:G:O4'	2.15	0.46
1:1A:1056:G:H5''	1:1A:1057:A:O4'	2.16	0.46
1:1A:1062:G:H1'	1:1A:1088:A:H62	1.80	0.46
1:1A:1101:U:O5'	1:1A:1101:U:H6	1.99	0.46
1:1A:2336:A:H61	22:10:43:THR:HG22	1.81	0.46
5:1F:143:ALA:HB1	5:1F:148:LEU:HB2	1.97	0.46
32:1a:1101:A:H4'	32:1a:1102:A:O5'	2.15	0.46
49:1r:52:PRO:HB2	49:1r:54:ARG:HG2	1.96	0.46
1:2A:760:G:H2'	1:2A:761:A:O4'	2.15	0.46
1:2A:1514:U:H2'	1:2A:1515:G:C8	2.51	0.46
1:2A:1657:C:H2'	1:2A:1658:C:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:2747:G:O6	1:2A:2755:C:H5''	2.16	0.46
9:2N:120:LEU:HG	9:2N:122:VAL:HG23	1.97	0.46
33:2b:16:HIS:HB2	33:2b:210:SER:HB3	1.98	0.46
34:2c:8:ILE:HD13	34:2c:8:ILE:HA	1.80	0.46
41:2j:29:ARG:HD3	41:2j:29:ARG:HA	1.77	0.46
32:1a:191:G:H1'	51:1t:103:GLY:HA3	1.98	0.46
32:1a:971:G:OP1	32:1a:972:C:H5''	2.16	0.46
32:1a:1014:A:H4'	50:1s:14:HIS:CE1	2.51	0.46
38:1g:74:GLU:CD	38:1g:95:ARG:HH21	2.23	0.46
41:1j:54:PHE:CD2	41:1j:55:LYS:HG2	2.50	0.46
51:1t:18:GLN:O	51:1t:22:ARG:HG3	2.16	0.46
1:2A:1529:G:C6	1:2A:1530:C:N4	2.84	0.46
1:2A:2107:C:N3	1:2A:2182:G:N2	2.56	0.46
1:2A:2319:G:N1	14:2S:3:ARG:HA	2.30	0.46
1:2A:2352:A:N6	1:2A:2365:G:O2'	2.49	0.46
5:2F:132:VAL:HG21	5:2F:163:VAL:HG22	1.97	0.46
16:2U:102:GLU:OE2	17:2V:13:ARG:NH2	2.36	0.46
32:2a:474:G:H2'	32:2a:475:G:H8	1.81	0.46
53:2y:12:ILE:HG22	53:2y:17:ARG:HG3	1.97	0.46
53:2y:29:LYS:HE3	53:2y:30:TRP:CZ3	2.50	0.46
1:1A:1105:U:H2'	1:1A:1106:G:C8	2.51	0.46
1:1A:1790:C:H2'	1:1A:1791:A:C5	2.51	0.46
1:1A:2141:G:H2'	1:1A:2142:C:H5'	1.97	0.46
2:1B:114:C:C4	61:1B:301:HOH:O	2.65	0.46
4:1E:119:ARG:HD2	61:1E:454:HOH:O	2.14	0.46
21:1Z:34:ASN:HB2	61:1Z:410:HOH:O	2.15	0.46
21:1Z:146:ILE:HA	21:1Z:147:GLY:HA2	1.65	0.46
21:1Z:185:GLU:HG2	21:1Z:186:GLU:N	2.30	0.46
32:1a:165:C:H2'	32:1a:166:G:C8	2.51	0.46
32:1a:343:U:O2'	32:1a:344:A:H2'	2.16	0.46
32:1a:1406:U:O2	32:1a:1517:G:N2	2.48	0.46
34:1c:62:ASP:O	34:1c:97:LYS:HB2	2.16	0.46
35:1d:168:ARG:HH11	35:1d:168:ARG:H	1.64	0.46
45:1n:3:ARG:NH1	45:1n:27:CYS:O	2.48	0.46
1:2A:811:U:H2'	11:2P:21:ARG:HA	1.98	0.46
1:2A:852:G:H2'	1:2A:853:G:C8	2.50	0.46
1:2A:1116:C:H2'	1:2A:1117:G:C8	2.51	0.46
1:2A:1794:U:H2'	1:2A:1795:C:C6	2.51	0.46
1:2A:2161:C:O2'	1:2A:2173:A:O2'	2.29	0.46
1:2A:2286:A:H4'	1:2A:2287:A:O4'	2.16	0.46
6:2G:77:ILE:HG21	6:2G:80:PHE:HD2	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:2H:11:VAL:HG22	7:2H:15:VAL:HG23	1.98	0.46
7:2H:24:VAL:HG11	7:2H:72:ILE:HD11	1.97	0.46
7:2H:55:PRO:HG2	7:2H:61:HIS:CE1	2.51	0.46
12:2Q:30:GLY:HA2	12:2Q:107:ALA:HB2	1.97	0.46
21:2Z:52:SER:OG	21:2Z:53:ILE:N	2.49	0.46
21:2Z:129:SER:HB3	21:2Z:132:ASN:ND2	2.26	0.46
31:29:14:CYS:HA	31:29:27:CYS:HB2	1.97	0.46
32:2a:976:G:H5'	32:2a:1358:U:O2'	2.16	0.46
32:2a:1111:A:OP2	61:2a:3221:HOH:O	2.21	0.46
37:2f:95:GLU:O	49:2r:32:ARG:NH1	2.43	0.46
46:2o:29:VAL:O	46:2o:33:THR:OG1	2.30	0.46
32:1a:1102:A:O3'	33:1b:96:ARG:NH2	2.48	0.46
33:1b:208:ILE:HA	33:1b:211:ILE:HD12	1.98	0.46
36:1e:57:LYS:HG2	36:1e:61:TYR:CE2	2.51	0.46
48:1q:67:LYS:O	48:1q:68:ARG:HB2	2.16	0.46
1:2A:116:C:H2'	1:2A:117:G:O4'	2.16	0.46
1:2A:1504:C:H2'	1:2A:1505:C:C6	2.51	0.46
1:2A:1621:U:OP1	61:2A:3852:HOH:O	2.20	0.46
19:2X:40:LYS:HG3	19:2X:51:VAL:HB	1.97	0.46
32:2a:1247:U:H1'	32:2a:1291:G:N2	2.31	0.46
33:2b:122:PHE:HA	33:2b:127:ILE:HG12	1.97	0.46
35:2d:64:LEU:HB2	35:2d:198:VAL:HG11	1.98	0.46
44:2m:82:MET:HE3	44:2m:93:ARG:HD3	1.98	0.46
47:2p:69:THR:O	47:2p:69:THR:OG1	2.31	0.46
1:1A:2031:A:C6	1:1A:2498:C:H1'	2.51	0.45
7:1H:12:PRO:O	7:1H:15:VAL:HG13	2.15	0.45
9:1N:15:LEU:HB2	9:1N:135:PRO:HB2	1.97	0.45
32:1a:67:C:H2'	32:1a:68:G:H8	1.79	0.45
32:1a:269:C:H2'	32:1a:270:A:H8	1.81	0.45
32:1a:996:A:H2'	32:1a:997:U:C6	2.50	0.45
36:1e:69:VAL:HG11	36:1e:113:ALA:HB1	1.98	0.45
53:1y:40:ILE:HB	53:1y:51:ASP:HB2	1.98	0.45
1:2A:2405:G:O2'	1:2A:2406:U:OP1	2.27	0.45
1:2A:2846:G:H2'	1:2A:2847:U:O4'	2.17	0.45
5:2F:25:PRO:HD2	5:2F:115:ALA:HB2	1.98	0.45
17:2V:95:LEU:HG	17:2V:97:LYS:HD3	1.97	0.45
21:2Z:125:LEU:HD12	21:2Z:125:LEU:HA	1.81	0.45
32:2a:1126:U:C4	41:2j:71:LEU:HD22	2.51	0.45
32:2a:1226:C:H4'	50:2s:80:TYR:OH	2.16	0.45
32:2a:1345:U:OP1	61:2a:3220:HOH:O	2.21	0.45
34:2c:130:VAL:HG21	34:2c:157:ILE:HG23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:2e:152:ARG:HB3	39:2h:43:GLY:O	2.16	0.45
42:2k:116:HIS:N	42:2k:117:ASN:HA	2.31	0.45
1:1A:1113:U:H2'	1:1A:1114:G:H8	1.78	0.45
1:1A:1289:C:H2'	1:1A:1290:C:C6	2.51	0.45
24:12:3:LEU:HD23	24:12:3:LEU:HA	1.75	0.45
32:1a:545:C:OP1	35:1d:61:LYS:NZ	2.49	0.45
32:1a:1447:A:H5''	32:1a:1452:C:OP2	2.16	0.45
33:1b:128:GLU:O	33:1b:135:GLN:NE2	2.49	0.45
1:2A:154(A):C:N4	1:2A:171:G:H1	2.14	0.45
1:2A:634:C:H2'	1:2A:635:C:C6	2.51	0.45
1:2A:1188:U:H4'	17:2V:79:VAL:HG22	1.98	0.45
1:2A:2136:C:C6	1:2A:2137:C:H5	2.33	0.45
1:2A:2188:C:H2'	1:2A:2189:U:O4'	2.15	0.45
1:2A:2611:U:C4	27:25:3:LYS:HG2	2.52	0.45
1:2A:2646:C:H2'	1:2A:2647:U:O4'	2.16	0.45
32:2a:179:A:H2'	32:2a:180:U:C6	2.47	0.45
32:2a:373:A:O2'	32:2a:451:A:N7	2.49	0.45
32:2a:779:C:H2'	32:2a:780:A:O4'	2.17	0.45
33:2b:158:LEU:HD21	33:2b:180:LEU:HD13	1.98	0.45
45:2n:4:LYS:HA	45:2n:7:ILE:HG13	1.98	0.45
1:1A:286:C:H2'	1:1A:287:C:H6	1.80	0.45
1:1A:1239:G:OP2	61:1A:4139:HOH:O	2.21	0.45
1:1A:1814:G:O6	61:1A:4136:HOH:O	2.20	0.45
6:1G:179:PRO:HG3	26:14:43:TYR:OH	2.17	0.45
17:1V:71:LEU:HA	17:1V:71:LEU:HD23	1.80	0.45
32:1a:266:G:C5'	32:1a:268:C:H41	2.28	0.45
32:1a:540:G:H2'	32:1a:541:G:O4'	2.16	0.45
43:1l:84:LEU:HB3	43:1l:104:VAL:HG21	1.98	0.45
46:1o:87:ILE:HG22	46:1o:88:ARG:N	2.31	0.45
1:2A:11:G:H2'	1:2A:11:G:N3	2.31	0.45
1:2A:154(A):C:N3	1:2A:171:G:N2	2.56	0.45
1:2A:999:U:OP2	61:2A:3856:HOH:O	2.21	0.45
1:2A:2320:A:N3	1:2A:2320:A:H2'	2.32	0.45
1:2A:2382:G:OP2	61:2A:3848:HOH:O	2.20	0.45
1:2A:2391:G:O6	1:2A:2425:A:H8	2.00	0.45
16:2U:55:ARG:H	16:2U:55:ARG:HG3	1.49	0.45
32:2a:409:G:H2'	32:2a:410:G:O4'	2.17	0.45
32:2a:420:U:H2'	32:2a:422:C:C5	2.51	0.45
32:2a:1340:A:OP1	53:2y:57:PRO:HB3	2.17	0.45
33:2b:44:LEU:H	33:2b:44:LEU:HD12	1.82	0.45
1:1A:184:C:H2'	1:1A:185:U:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1166:C:H2'	1:1A:1167:U:H6	1.81	0.45
1:1A:2119:A:N6	1:1A:2171:A:N7	2.65	0.45
6:1G:110:ALA:HB1	6:1G:140:ILE:HG22	1.97	0.45
15:1T:24:PRO:HD3	15:1T:52:ILE:HD12	1.97	0.45
16:1U:76:TYR:CE2	16:1U:80:ILE:HG13	2.52	0.45
17:1V:23:GLU:OE2	61:1V:301:HOH:O	2.21	0.45
19:1X:26:TYR:OH	19:1X:93:GLU:OE2	2.23	0.45
35:1d:65:ARG:HD2	35:1d:72:GLU:HA	1.97	0.45
36:1e:45:PHE:CD2	36:1e:47:LYS:HE2	2.51	0.45
38:1g:65:ALA:O	38:1g:69:VAL:HG23	2.16	0.45
47:1p:44:THR:OG1	47:1p:45:THR:N	2.49	0.45
1:2A:1557:C:H5''	1:2A:1558:A:OP2	2.17	0.45
1:2A:2110:G:H4'	1:2A:2111:C:OP2	2.16	0.45
5:2F:36:VAL:O	5:2F:40:GLN:HG3	2.17	0.45
9:2N:96:GLU:CD	9:2N:96:GLU:H	2.23	0.45
32:2a:390:C:H2'	32:2a:391:G:C8	2.51	0.45
32:2a:718:G:C8	42:2k:116:HIS:HB3	2.52	0.45
1:1A:897:C:H2'	1:1A:898:C:C6	2.52	0.45
1:1A:2331:G:O2'	22:10:43:THR:HG22	2.16	0.45
1:1A:2552:OMU:O5'	1:1A:2552:OMU:H6	2.17	0.45
1:1A:2811:G:N2	1:1A:2891:G:H1'	2.32	0.45
4:1E:28:ALA:HB3	4:1E:93:VAL:CG1	2.46	0.45
8:1I:93:THR:OG1	8:1I:96:ASP:OD1	2.25	0.45
9:1N:75:TYR:CE2	9:1N:77:GLY:HA2	2.51	0.45
13:1R:87:TYR:OH	13:1R:117:VAL:O	2.34	0.45
33:1b:114:ARG:O	33:1b:118:LEU:HG	2.17	0.45
34:1c:44:GLU:HA	34:1c:52:LEU:HD23	1.99	0.45
48:1q:53:LEU:HD23	48:1q:82:MET:HE1	1.98	0.45
1:2A:1588:C:H2'	1:2A:1589:C:C6	2.51	0.45
1:2A:2330:G:H2'	1:2A:2331:G:O4'	2.17	0.45
1:2A:2591:C:H2'	1:2A:2592:G:C8	2.51	0.45
4:2E:101:ARG:CZ	4:2E:171:GLU:HB2	2.46	0.45
12:2Q:1:MET:HE2	12:2Q:1:MET:HB3	1.84	0.45
14:2S:95:HIS:HA	14:2S:99:LYS:HE2	1.98	0.45
14:2S:105:ALA:O	14:2S:110:LEU:HB2	2.17	0.45
17:2V:6:LYS:HB2	17:2V:38:LEU:HD11	1.99	0.45
19:2X:43:VAL:HG21	19:2X:81:VAL:HG11	1.99	0.45
26:24:24:THR:OG1	26:24:25:TYR:N	2.47	0.45
32:2a:437:U:O2'	35:2d:125:HIS:HE1	1.98	0.45
32:2a:1302:U:P	44:2m:13:LYS:HZ1	2.40	0.45
40:2i:43:ALA:O	40:2i:45:ALA:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2693:A:H2'	1:1A:2694:G:H8	1.82	0.45
61:1A:6320:HOH:O	19:1X:16:LYS:HE3	2.17	0.45
3:1D:102:LYS:C	3:1D:103:ARG:HG2	2.42	0.45
21:1Z:140:ASP:OD1	21:1Z:142:SER:OG	2.34	0.45
26:14:61:ARG:HH21	50:1s:42:PRO:HD3	1.81	0.45
32:1a:858:G:O6	32:1a:869:G:H3'	2.17	0.45
32:1a:1258:G:H1	32:1a:1277:C:H42	1.65	0.45
33:1b:128:GLU:HG2	33:1b:135:GLN:NE2	2.31	0.45
1:2A:35:G:H2'	1:2A:36:G:O4'	2.16	0.45
1:2A:1012:U:C5	9:2N:28:THR:HG21	2.52	0.45
1:2A:1639:U:H4'	1:2A:2699:C:H4'	1.99	0.45
1:2A:2441:C:OP2	1:2A:2586:C:O2'	2.31	0.45
2:2B:8:U:H6	2:2B:8:U:H5''	1.82	0.45
5:2F:28:ILE:O	5:2F:30:PRO:HD3	2.15	0.45
15:2T:119:LYS:O	15:2T:123:GLN:HG3	2.17	0.45
17:2V:1:MET:HG3	17:2V:41:GLY:O	2.16	0.45
32:2a:490:G:H2'	32:2a:491:G:C8	2.51	0.45
32:2a:520:A:N1	32:2a:536:C:H1'	2.31	0.45
32:2a:1441:G:H8	32:2a:1441:G:O5'	1.99	0.45
33:2b:82:ARG:HB2	33:2b:92:TYR:CE1	2.51	0.45
35:2d:59:ARG:NH2	35:2d:62:GLN:HG3	2.31	0.45
45:2n:21:TYR:HE1	45:2n:23:ARG:NE	2.15	0.45
1:1A:628:G:H5''	30:18:18:ALA:HB2	1.98	0.45
16:1U:30:LYS:N	16:1U:30:LYS:HD2	2.32	0.45
16:1U:76:TYR:CZ	16:1U:80:ILE:HG13	2.52	0.45
32:1a:1008:C:H2'	32:1a:1009:G:O4'	2.17	0.45
35:1d:30:LYS:HA	35:1d:35:ARG:HE	1.80	0.45
1:2A:82:G:N1	1:2A:103:A:OP2	2.38	0.45
1:2A:2118:U:OP2	1:2A:2147:G:O2'	2.26	0.45
8:2I:12:LEU:HD22	8:2I:19:VAL:HG21	1.98	0.45
15:2T:39:ARG:NH2	32:2a:345:C:OP2	2.33	0.45
24:22:58:ALA:O	24:22:62:THR:OG1	2.35	0.45
32:2a:979:C:H42	45:2n:18:VAL:HB	1.81	0.45
33:2b:60:ASP:OD2	33:2b:64:ARG:NE	2.49	0.45
38:2g:53:LYS:HD3	38:2g:125:MET:HE1	1.98	0.45
1:1A:1094:U:C2	1:1A:1096:A:H5'	2.51	0.45
1:1A:1110:G:OP2	1:1A:1110:G:H8	2.00	0.45
1:1A:2286:A:H4'	1:1A:2287:A:O4'	2.16	0.45
4:1E:64:LYS:HB2	4:1E:64:LYS:HE3	1.66	0.45
7:1H:86:GLU:OE2	7:1H:132:ARG:NH2	2.50	0.45
20:1Y:86:ARG:HD2	20:1Y:100:ALA:HA	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:353:A:H5'	32:1a:353:A:H8	1.82	0.45
32:1a:664:G:N2	32:1a:741:G:H1	2.04	0.45
32:1a:708:C:H2'	32:1a:709:G:H8	1.81	0.45
32:1a:714:G:H2'	32:1a:715:A:C8	2.52	0.45
51:1t:36:LEU:HD12	51:1t:62:LEU:HD12	1.98	0.45
53:1y:71:TYR:HA	53:1y:74:ILE:HD12	1.98	0.45
1:2A:623:G:H2'	1:2A:624:C:C6	2.52	0.45
1:2A:662:G:OP1	61:2A:3849:HOH:O	2.20	0.45
1:2A:1772:G:O6	57:2A:3745:MPD:H32	2.17	0.45
2:2B:22:U:H2'	2:2B:23:G:C8	2.52	0.45
2:2B:23:G:O6	61:2B:308:HOH:O	2.20	0.45
3:2D:72:LYS:NZ	3:2D:99:ASP:OD2	2.35	0.45
6:2G:63:ILE:HG13	6:2G:144:ILE:HD11	1.99	0.45
15:2T:98:LYS:HB3	15:2T:100:TYR:CE2	2.52	0.45
18:2W:18:ARG:HG3	18:2W:76:VAL:HB	1.97	0.45
32:2a:413:G:O6	35:2d:35:ARG:HD2	2.17	0.45
32:2a:692:U:H1'	32:2a:695:A:N7	2.32	0.45
32:2a:786:G:C2	32:2a:797:C:C2	3.05	0.45
32:2a:1112:C:C4	34:2c:178:LEU:HD12	2.52	0.45
42:2k:50:TYR:HD2	42:2k:60:ALA:HB2	1.80	0.45
1:1A:888:C:O2'	1:1A:889:C:OP1	2.25	0.45
1:1A:2790:A:H2'	1:1A:2790:A:N3	2.31	0.45
10:1O:36:GLY:HA2	10:1O:106:LEU:HD23	1.98	0.45
32:1a:328:C:H4'	32:1a:329:A:H5'	1.99	0.45
41:1j:31:GLY:HA2	41:1j:32:ALA:HA	1.45	0.45
45:1n:12:ARG:HG2	45:1n:13:THR:O	2.17	0.45
1:2A:272(B):G:H2'	1:2A:272(C):G:C8	2.51	0.45
57:2A:3745:MPD:HM2	61:2A:4801:HOH:O	2.16	0.45
2:2B:7:G:N3	14:2S:38:GLN:NE2	2.49	0.45
4:2E:75:VAL:HG13	4:2E:77:ILE:H	1.82	0.45
13:2R:9:LYS:O	13:2R:17:ARG:HD3	2.17	0.45
20:2Y:5:MET:HE1	20:2Y:35:TYR:HA	1.99	0.45
32:2a:67:C:H2'	32:2a:68:G:C8	2.52	0.45
32:2a:992:U:H5''	32:2a:993:G:C8	2.52	0.45
32:2a:1068:G:H8	32:2a:1068:G:OP2	1.99	0.45
33:2b:12:GLU:OE2	33:2b:48:MET:HG3	2.17	0.45
1:1A:7:G:H2'	1:1A:8:A:O4'	2.17	0.45
1:1A:478:A:C6	1:1A:480:A:C6	3.05	0.45
1:1A:2114:A:H3'	1:1A:2115:G:H8	1.81	0.45
1:1A:2334:G:H5'	14:1S:9:ARG:HG2	1.99	0.45
4:1E:130:GLY:O	61:1E:402:HOH:O	2.20	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:1P:68:GLN:HG3	61:1P:302:HOH:O	2.15	0.45
32:1a:266:G:H2'	32:1a:266:G:N3	2.32	0.45
32:1a:1258:G:H2'	32:1a:1259:C:C6	2.52	0.45
33:1b:55:PHE:CD1	33:1b:58:ILE:HD12	2.52	0.45
37:1f:99:ALA:HB1	49:1r:23:LYS:HE3	1.99	0.45
53:1y:52:ALA:HB2	53:1y:77:LEU:HD21	1.99	0.45
1:2A:829:A:N7	1:2A:2248:C:H5'	2.32	0.45
1:2A:1115:G:H2'	1:2A:1116:C:C6	2.52	0.45
1:2A:2370:G:C6	1:2A:2371:G:C6	3.05	0.45
32:2a:189(F):U:C4	48:2q:72:ARG:NH1	2.85	0.45
32:2a:728:A:H2'	32:2a:729:A:C8	2.52	0.45
32:2a:1036:G:H3'	32:2a:1037:C:H6	1.82	0.45
40:2i:125:TYR:HE1	40:2i:127:LYS:HB3	1.81	0.45
41:2j:32:ALA:HB1	41:2j:33:GLN:CD	2.42	0.45
44:2m:50:GLU:HA	44:2m:53:VAL:HG22	1.98	0.45
51:2t:10:LEU:HD12	51:2t:10:LEU:HA	1.86	0.45
1:1A:1803:A:H4'	3:1D:259:THR:HG23	1.98	0.44
1:1A:2687:U:H2'	1:1A:2688:U:O4'	2.16	0.44
20:1Y:9:LYS:HA	20:1Y:10:GLY:HA2	1.61	0.44
28:16:2:ALA:N	61:16:602:HOH:O	2.50	0.44
32:1a:501:C:H1'	32:1a:549:C:H1'	1.99	0.44
32:1a:1298:C:OP2	38:1g:114:ARG:NH2	2.38	0.44
41:1j:81:THR:C	41:1j:83:GLU:H	2.25	0.44
1:2A:65:C:H2'	1:2A:66:C:C6	2.52	0.44
1:2A:862:G:H2'	1:2A:863:A:O4'	2.17	0.44
1:2A:1045:A:H5''	1:2A:1046:A:OP1	2.18	0.44
1:2A:1079:C:N4	1:2A:1080:C:O2	2.50	0.44
1:2A:1319:G:C6	1:2A:1320:C:N4	2.85	0.44
1:2A:2740:A:C6	1:2A:2764:A:C8	3.05	0.44
1:2A:2801(A):A:N3	1:2A:2895:U:H1'	2.32	0.44
7:2H:154:PRO:HB3	7:2H:163:TYR:CE1	2.51	0.44
15:2T:11:GLU:O	15:2T:15:VAL:HG23	2.17	0.44
15:2T:54:ARG:HA	15:2T:59:THR:HG23	1.98	0.44
23:21:53:VAL:HG22	23:21:74:VAL:HG13	1.97	0.44
32:2a:551:U:H2'	32:2a:552:U:C6	2.52	0.44
32:2a:1002:G:N3	32:2a:1003:G:C8	2.85	0.44
35:2d:165:MET:SD	35:2d:168:ARG:NH1	2.73	0.44
1:1A:1289:C:H2'	1:1A:1290:C:H6	1.81	0.44
1:1A:1523:U:H6	1:1A:1523:U:O5'	2.00	0.44
1:1A:1583:A:H5'	1:1A:1584:C:OP1	2.17	0.44
1:1A:2591:C:H2'	1:1A:2592:G:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2685:G:H5'	10:1O:68:GLU:OE2	2.17	0.44
2:1B:66:A:H61	2:1B:109:C:H5'	1.83	0.44
9:1N:13:TRP:CE2	9:1N:133:GLN:HG2	2.53	0.44
39:1h:109:ILE:O	39:1h:109:ILE:HG13	2.17	0.44
1:2A:643:A:N1	1:2A:2369:A:O2'	2.50	0.44
1:2A:1814:G:C4'	3:2D:51:VAL:HG21	2.47	0.44
2:2B:103:G:H21	21:2Z:73:GLN:NE2	2.14	0.44
6:2G:19:LEU:HD23	6:2G:19:LEU:HA	1.86	0.44
6:2G:126:ASP:HB2	6:2G:130:ASN:H	1.82	0.44
11:2P:86:LYS:HD2	11:2P:117:GLU:HG2	1.99	0.44
12:2Q:103:MET:HE1	12:2Q:125:LEU:HD13	1.99	0.44
32:2a:947:G:H2'	32:2a:948:C:O4'	2.17	0.44
1:1A:1814:G:H4'	3:1D:51:VAL:HG21	1.99	0.44
1:1A:1815:A:P	3:1D:54:ARG:HH22	2.40	0.44
1:1A:1826:G:H4'	3:1D:242:ARG:CZ	2.48	0.44
1:1A:2839:G:H5'	13:1R:46:GLY:HA2	1.98	0.44
1:1A:2869:G:H2'	1:1A:2870:C:O4'	2.17	0.44
6:1G:47:LYS:H	6:1G:47:LYS:HG2	1.55	0.44
12:1Q:135:ASP:O	12:1Q:139:GLU:HG3	2.17	0.44
18:1W:10:VAL:HG12	18:1W:12:ILE:HG22	1.99	0.44
32:1a:833:U:H2'	32:1a:834:C:H6	1.82	0.44
33:1b:7:VAL:O	33:1b:9:GLU:N	2.51	0.44
33:1b:141:GLU:HG2	33:1b:145:LEU:HD12	2.00	0.44
40:1i:18:PHE:HB2	40:1i:62:TYR:HB3	2.00	0.44
42:1k:18:ARG:HB2	42:1k:33:THR:OG1	2.18	0.44
1:2A:652(A):A:O2'	1:2A:652(B):A:H5'	2.17	0.44
1:2A:2864:G:OP1	15:2T:119:LYS:HE3	2.16	0.44
7:2H:109:PHE:C	7:2H:111:HIS:H	2.25	0.44
20:2Y:68:HIS:ND1	20:2Y:70:SER:HB3	2.32	0.44
32:2a:977:A:H1'	32:2a:981:U:H3	1.82	0.44
32:2a:1206:G:H4'	34:2c:192:THR:O	2.18	0.44
32:2a:1316:G:N2	32:2a:1318:A:H3'	2.32	0.44
32:2a:1426:C:H2'	32:2a:1427:U:H6	1.82	0.44
35:2d:114:ARG:O	35:2d:118:ARG:N	2.50	0.44
1:1A:278:A:H2'	1:1A:279:C:C6	2.51	0.44
1:1A:2583:G:OP2	61:1A:4138:HOH:O	2.21	0.44
32:1a:1166:G:N2	32:1a:1169:A:H3'	2.32	0.44
32:1a:1202:G:O4'	45:1n:29:ARG:NH1	2.51	0.44
34:1c:132:ARG:O	34:1c:136:GLN:HG3	2.17	0.44
37:1f:100:ASN:ND2	49:1r:23:LYS:HE2	2.33	0.44
42:1k:124:LYS:HE3	42:1k:125:PHE:CZ	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:479:A:H4'	1:2A:480:A:OP1	2.17	0.44
1:2A:1110:G:H8	1:2A:1110:G:OP2	2.00	0.44
1:2A:1430:C:H2'	1:2A:1431:U:C6	2.52	0.44
61:2A:5419:HOH:O	23:21:3:LYS:HE2	2.17	0.44
9:2N:58:ASP:OD1	9:2N:58:ASP:N	2.50	0.44
12:2Q:85:LYS:HE2	22:20:8:GLY:HA3	1.99	0.44
17:2V:52:VAL:HG23	17:2V:55:ALA:HB3	2.00	0.44
32:2a:1006:C:H2'	32:2a:1007:C:C6	2.52	0.44
32:2a:1106:G:H5''	34:2c:172:ARG:HG2	1.98	0.44
33:2b:95:GLN:HG3	33:2b:96:ARG:H	1.82	0.44
40:2i:4:TYR:O	40:2i:19:LEU:N	2.39	0.44
1:1A:2058:MA6:H103	56:1A:4021:TEL:O48	2.18	0.44
1:1A:2646:C:H2'	1:1A:2647:U:O4'	2.17	0.44
5:1F:38:ARG:NH2	61:1F:405:HOH:O	2.50	0.44
5:1F:129:PHE:CD2	5:1F:163:VAL:HG21	2.53	0.44
5:1F:184:TYR:O	5:1F:188:ARG:HG3	2.18	0.44
8:1I:81:VAL:O	8:1I:146:ALA:HA	2.17	0.44
32:1a:149:A:H2'	32:1a:150:C:C6	2.53	0.44
32:1a:458:C:H2'	32:1a:460:G:H8	1.82	0.44
32:1a:1136:U:H2'	32:1a:1136:U:O2	2.16	0.44
36:1e:148:VAL:O	36:1e:152:ARG:HG2	2.18	0.44
43:1l:40:VAL:HG11	43:1l:77:LEU:O	2.17	0.44
1:2A:1065:U:H3	1:2A:1073:A:H61	1.66	0.44
1:2A:1155:A:OP1	16:2U:55:ARG:HD3	2.17	0.44
1:2A:1355:G:P	3:2D:38:LYS:HE2	2.58	0.44
1:2A:1364:G:OP2	23:21:3:LYS:HG3	2.17	0.44
1:2A:2113:U:H2'	1:2A:2114:A:O4'	2.18	0.44
1:2A:2610:C:O2'	61:2A:3822:HOH:O	2.12	0.44
4:2E:13:ARG:HG2	15:2T:58:ASN:HD21	1.83	0.44
6:2G:77:ILE:HG21	6:2G:80:PHE:CD2	2.52	0.44
32:2a:755:G:OP2	46:2o:65:ARG:HD2	2.17	0.44
32:2a:1190:G:H5'	34:2c:176:HIS:HE1	1.82	0.44
32:2a:1291:G:H4'	40:2i:39:GLY:HA3	1.99	0.44
32:2a:1359:C:O2'	32:2a:1361:G:N7	2.51	0.44
33:2b:110:GLN:HG2	33:2b:111:ARG:HH12	1.82	0.44
41:2j:37:PRO:HA	41:2j:72:VAL:HG12	2.00	0.44
43:2l:117:ARG:NH2	43:2l:124:LYS:HB2	2.32	0.44
1:1A:1593:G:H2'	1:1A:1594:G:C8	2.53	0.44
8:1I:109:ILE:HD12	8:1I:109:ILE:HA	1.80	0.44
22:10:10:THR:CG2	22:10:12:ASN:H	2.31	0.44
32:1a:677:U:H3	32:1a:713:G:H22	1.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:933:G:O6	38:1g:3:ARG:NH2	2.49	0.44
32:1a:978:A:O2'	32:1a:1322:C:N3	2.47	0.44
33:1b:19:HIS:CG	33:1b:20:GLU:N	2.86	0.44
37:1f:21:LEU:O	37:1f:25:ILE:HG12	2.18	0.44
46:1o:3:ILE:H	46:1o:3:ILE:HD12	1.83	0.44
46:1o:17:ARG:HH11	46:1o:17:ARG:HG3	1.82	0.44
51:1t:57:ARG:HH12	51:1t:100:ILE:HD12	1.83	0.44
1:2A:242:G:C8	30:28:5:LYS:HG2	2.53	0.44
1:2A:365:C:OP2	61:2A:3855:HOH:O	2.21	0.44
1:2A:579:G:O2'	1:2A:2019:A:OP1	2.33	0.44
1:2A:796:C:H2'	1:2A:797:C:C6	2.52	0.44
1:2A:1068:G:C6	1:2A:1095:A:H8	2.35	0.44
1:2A:1091:G:H2'	1:2A:1091:G:N3	2.33	0.44
4:2E:97:LYS:N	4:2E:100:GLU:OE2	2.45	0.44
6:2G:61:ALA:HA	6:2G:66:GLN:O	2.18	0.44
32:2a:580:U:H5''	46:2o:58:MET:HG2	2.00	0.44
32:2a:765:G:H5''	32:2a:766:A:OP1	2.17	0.44
32:2a:881:G:OP2	43:2l:12:ARG:NH2	2.51	0.44
32:2a:1148:U:O2'	40:2i:66:ARG:NH2	2.49	0.44
35:2d:98:GLU:HG3	35:2d:194:LEU:HD21	1.99	0.44
35:2d:114:ARG:HA	35:2d:117:ALA:HB3	1.99	0.44
41:2j:78:ASN:O	41:2j:81:THR:N	2.47	0.44
53:2y:26:LYS:NZ	61:2y:201:HOH:O	2.50	0.44
1:1A:375:C:H2'	1:1A:376:C:C6	2.53	0.44
1:1A:1083:U:H1'	1:1A:1086:A:N6	2.33	0.44
61:1A:4546:HOH:O	5:1F:74:ARG:HD2	2.16	0.44
26:14:34:GLU:H	26:14:34:GLU:CD	2.26	0.44
32:1a:174:C:H2'	32:1a:175:C:H6	1.82	0.44
32:1a:434:U:H2'	32:1a:435:C:C6	2.53	0.44
32:1a:1244:C:H2'	32:1a:1245:A:C8	2.52	0.44
41:1j:19:SER:O	41:1j:23:ILE:HG12	2.17	0.44
46:1o:8:LYS:O	46:1o:12:ILE:HG13	2.18	0.44
46:1o:29:VAL:HB	46:1o:81:LEU:HD21	2.00	0.44
1:2A:523:C:H4'	1:2A:540:C:O2	2.18	0.44
1:2A:2280:G:H5'	21:2Z:201:LYS:HD2	2.00	0.44
7:2H:103:LEU:O	7:2H:114:VAL:HA	2.17	0.44
9:2N:4:TYR:CD2	16:2U:100:VAL:HG11	2.52	0.44
12:2Q:58:PHE:C	12:2Q:60:ARG:H	2.24	0.44
15:2T:6:LEU:HD12	15:2T:6:LEU:HA	1.77	0.44
20:2Y:39:VAL:HB	20:2Y:42:VAL:HB	2.00	0.44
27:25:20:ARG:HG2	27:25:23:HIS:CE1	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1044:A:C5	32:2a:1045:C:H1'	2.52	0.44
32:2a:1118:C:OP1	40:2i:9:ARG:NH1	2.51	0.44
32:2a:1206:G:C6	32:2a:1207:2MG:C6	3.06	0.44
32:2a:1277:C:O2'	32:2a:1279:A:C8	2.69	0.44
41:2j:21:GLN:O	41:2j:25:GLU:HG2	2.17	0.44
1:1A:30:G:H2'	1:1A:31:C:C6	2.52	0.44
1:1A:2331:G:O2'	1:1A:2336:A:N1	2.47	0.44
1:1A:2870:C:H2'	1:1A:2871:C:O4'	2.17	0.44
32:1a:958:A:C2	50:1s:55:LYS:HB2	2.52	0.44
32:1a:1227:A:P	44:1m:111:LYS:HZ1	2.38	0.44
32:1a:1492:A:H4'	32:1a:1493:A:C6	2.53	0.44
32:1a:1499:A:H1'	32:1a:1520:G:H5'	1.99	0.44
35:1d:3:ARG:NH1	35:1d:5:ILE:HG22	2.32	0.44
41:1j:9:ARG:HG2	41:1j:69:ASN:ND2	2.30	0.44
42:1k:92:GLU:HG3	42:1k:96:ARG:NH1	2.32	0.44
1:2A:635:C:O2'	1:2A:639:U:OP1	2.34	0.44
1:2A:840:C:H2'	1:2A:841:A:C8	2.52	0.44
1:2A:1074:G:N1	1:2A:1075:C:H1'	2.33	0.44
1:2A:1518:U:H2'	1:2A:1519:G:O4'	2.18	0.44
1:2A:1792:G:O2'	1:2A:1830:C:OP1	2.27	0.44
1:2A:1861:G:C2	1:2A:1862:G:C8	3.06	0.44
1:2A:1996:C:H4'	1:2A:1997:G:OP1	2.18	0.44
11:2P:49:ARG:NH1	30:28:4:MET:HE1	2.32	0.44
13:2R:33:ARG:NH2	27:25:57:VAL:O	2.36	0.44
32:2a:109:A:C6	32:2a:326:G:C6	3.06	0.44
32:2a:261:U:OP2	51:2t:79:ARG:NH2	2.50	0.44
32:2a:352:C:H4'	32:2a:354:G:OP1	2.17	0.44
32:2a:490:G:H2'	32:2a:491:G:H8	1.82	0.44
32:2a:501:C:H2'	32:2a:502:G:C8	2.52	0.44
32:2a:1157:A:C5	32:2a:1181:G:C6	3.06	0.44
33:2b:187:LEU:HA	33:2b:201:ILE:HB	2.00	0.44
45:2n:29:ARG:HD3	45:2n:40:CYS:SG	2.58	0.44
46:2o:67:LEU:HD23	46:2o:67:LEU:HA	1.85	0.44
52:2u:2:GLY:C	52:2u:4:GLY:H	2.25	0.44
1:1A:2887:U:H2'	1:1A:2888:C:C6	2.52	0.44
4:1E:101:ARG:CZ	4:1E:171:GLU:HB2	2.47	0.44
27:15:35:GLU:OE1	27:15:35:GLU:N	2.51	0.44
32:1a:254:G:H21	48:1q:16:GLN:NE2	2.16	0.44
32:1a:620:C:C2	35:1d:135:LEU:HG	2.53	0.44
32:1a:629:G:H2'	32:1a:630:G:O4'	2.18	0.44
32:1a:1162:C:H2'	32:1a:1163:C:H6	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:1b:211:ILE:HG13	33:1b:211:ILE:H	1.67	0.44
47:1p:39:TYR:HD1	47:1p:49:LEU:HD23	1.83	0.44
1:2A:422:A:OP1	61:2A:3850:HOH:O	2.20	0.44
1:2A:493:G:H2'	1:2A:494:G:O4'	2.17	0.44
1:2A:1784:A:H4'	1:2A:1785:A:O5'	2.17	0.44
1:2A:2784:C:H1'	4:2E:37:ARG:NH1	2.33	0.44
2:2B:73:A:C4	2:2B:105:A:C2	3.06	0.44
23:21:8:SER:HB3	23:21:66:HIS:CD2	2.53	0.44
32:2a:1027:C:H5''	32:2a:1028:C:C6	2.53	0.44
32:2a:1073:U:H2'	32:2a:1074:G:H8	1.82	0.44
35:2d:111:ALA:HB1	35:2d:116:GLN:HE21	1.82	0.44
44:2m:60:VAL:HG13	44:2m:64:TRP:CE3	2.52	0.44
1:1A:886:C:C3'	1:1A:887:A:H5''	2.48	0.43
1:1A:1778:U:H2'	1:1A:1784:A:N6	2.32	0.43
1:1A:1783:A:H5'	1:1A:2608:G:H4'	2.00	0.43
1:1A:2115:G:N3	1:1A:2117:A:N6	2.66	0.43
1:1A:2207:G:H2'	1:1A:2208:A:C2	2.53	0.43
2:1B:2:C:H2'	2:1B:3:C:C6	2.53	0.43
3:1D:132:PRO:HG3	3:1D:190:TYR:CE2	2.54	0.43
8:1I:72:LEU:HD12	8:1I:138:ILE:HG21	1.99	0.43
25:13:55:ARG:NH1	61:13:205:HOH:O	2.51	0.43
26:14:58:ARG:O	26:14:61:ARG:HG2	2.18	0.43
32:1a:222:U:H2'	32:1a:223:U:H6	1.83	0.43
32:1a:265:G:H5'	48:1q:64:PRO:O	2.18	0.43
32:1a:750:G:N3	46:1o:23:GLY:HA3	2.33	0.43
33:1b:16:HIS:CG	33:1b:17:PHE:N	2.85	0.43
35:1d:178:VAL:C	35:1d:180:GLY:H	2.25	0.43
39:1h:110:ALA:HB3	39:1h:121:ASP:HB3	2.00	0.43
41:1j:30:SER:CB	41:1j:81:THR:HG22	2.48	0.43
51:1t:53:LEU:O	51:1t:57:ARG:HG3	2.18	0.43
1:2A:2105:C:H2'	1:2A:2106:G:H8	1.83	0.43
1:2A:2238:G:H2'	1:2A:2238:G:N3	2.33	0.43
4:2E:170:LEU:HB3	4:2E:184:VAL:HG13	2.00	0.43
6:2G:96:ARG:H	6:2G:99:MET:HE2	1.83	0.43
12:2Q:29:PHE:O	21:2Z:122:ARG:NH2	2.51	0.43
32:2a:538:G:H5''	43:2L:114:LYS:HB2	2.00	0.43
32:2a:1026:G:N3	32:2a:1026:G:H2'	2.33	0.43
38:2g:26:PHE:O	38:2g:30:ILE:HG13	2.18	0.43
1:1A:479:A:N3	1:1A:481:G:H5''	2.33	0.43
4:1E:175:VAL:HG22	4:1E:182:LEU:HD12	2.00	0.43
32:1a:181:G:H4'	32:1a:182:U:H5'	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:458:C:H2'	32:1a:460:G:C8	2.53	0.43
32:1a:524:G:H2'	32:1a:525:C:C6	2.52	0.43
32:1a:815:A:N7	32:1a:1509:C:O2'	2.47	0.43
32:1a:1004:A:H8	32:1a:1005:A:O4'	2.01	0.43
32:1a:1320:C:H2'	32:1a:1321:C:O4'	2.17	0.43
32:1a:1525:G:P	42:1k:120:ARG:HH22	2.40	0.43
40:1i:46:ALA:HB2	40:1i:74:ILE:HG23	2.00	0.43
50:1s:31:ILE:HB	50:1s:49:ILE:HG13	1.99	0.43
1:2A:1073:A:C8	1:2A:1073:A:H3'	2.53	0.43
1:2A:1087:G:H1	1:2A:1102:C:H42	1.66	0.43
1:2A:1754:C:P	15:2T:96:ARG:HH12	2.42	0.43
1:2A:2322:A:OP2	61:2A:3857:HOH:O	2.21	0.43
1:2A:2371:G:N3	28:26:46:HIS:HE1	2.16	0.43
3:2D:142:VAL:HG13	3:2D:191:ALA:HB1	2.00	0.43
4:2E:4:ILE:HG21	4:2E:28:ALA:HB1	2.00	0.43
6:2G:109:VAL:HG11	6:2G:142:PRO:HB3	2.00	0.43
7:2H:20:ALA:HB1	7:2H:21:PRO:HD2	2.00	0.43
11:2P:85:LEU:HD13	11:2P:120:ALA:HB2	1.99	0.43
14:2S:72:ALA:O	14:2S:76:LYS:HG3	2.17	0.43
15:2T:16:ARG:HH11	15:2T:19:LEU:HD21	1.83	0.43
17:2V:24:LYS:HG3	17:2V:64:HIS:HD2	1.82	0.43
32:2a:522:C:OP2	43:2l:69:TYR:OH	2.29	0.43
32:2a:1525:G:OP1	42:2k:120:ARG:NH2	2.51	0.43
33:2b:21:ARG:O	33:2b:23:ARG:N	2.44	0.43
36:2e:69:VAL:HA	36:2e:70:PRO:HD3	1.83	0.43
36:2e:72:GLN:HE21	36:2e:144:THR:HG22	1.82	0.43
38:2g:42:ILE:HD13	38:2g:116:ALA:HB3	2.00	0.43
1:1A:530:G:N1	1:1A:2023:G:OP1	2.40	0.43
1:1A:1082:U:C4	1:1A:1086:A:N1	2.84	0.43
1:1A:2141:G:C2'	1:1A:2142:C:H5'	2.49	0.43
1:1A:2165:G:H2'	1:1A:2166:G:C8	2.54	0.43
56:1A:4021:TEL:H112	56:1A:4021:TEL:O18	2.18	0.43
58:1B:231:ARG:N	61:1B:317:HOH:O	2.51	0.43
4:1E:77:ILE:HD13	4:1E:195:LEU:HD13	1.99	0.43
6:1G:32:PRO:HB3	6:1G:163:ALA:HB2	2.00	0.43
32:1a:299:G:H2'	32:1a:300:A:C8	2.53	0.43
32:1a:448:A:C4	32:1a:487:A:C2	3.06	0.43
32:1a:620:C:H2'	32:1a:621:A:O4'	2.18	0.43
32:1a:773:G:OP1	61:1a:3319:HOH:O	2.21	0.43
32:1a:833:U:H2'	32:1a:834:C:C6	2.53	0.43
47:1p:75:ARG:HG3	47:1p:80:PHE:CD2	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:740:U:H2'	1:2A:741:G:C8	2.54	0.43
1:2A:1203:G:C6	1:2A:1204:A:N6	2.87	0.43
1:2A:2704:C:H2'	1:2A:2705:A:O4'	2.18	0.43
2:2B:48:A:H4'	14:2S:95:HIS:HD2	1.83	0.43
6:2G:5:VAL:HG23	6:2G:8:LYS:H	1.83	0.43
6:2G:171:ALA:O	6:2G:175:LEU:HG	2.16	0.43
17:2V:5:VAL:HG11	17:2V:57:VAL:HG21	2.00	0.43
32:2a:748:C:H4'	32:2a:749:C:O5'	2.18	0.43
34:2c:6:HIS:CD2	34:2c:9:GLY:H	2.37	0.43
36:2e:110:LEU:HD13	36:2e:118:ILE:HG21	2.00	0.43
37:2f:4:TYR:CE1	37:2f:92:LYS:HG2	2.53	0.43
44:2m:86:CYS:HB3	50:2s:74:PHE:CE1	2.54	0.43
50:2s:15:LEU:HD11	50:2s:49:ILE:HD13	2.00	0.43
1:1A:862:G:H2'	1:1A:863:A:O4'	2.19	0.43
1:1A:877:U:H2'	1:1A:878:A:H5''	2.00	0.43
1:1A:1098:A:H2'	1:1A:1099:G:O4'	2.17	0.43
1:1A:2140:C:H2'	1:1A:2141:G:C8	2.53	0.43
1:1A:2615:U:H2'	1:1A:2616:C:H6	1.84	0.43
1:1A:2789:C:O3'	1:1A:2790:A:H4'	2.18	0.43
2:1B:42:C:O2'	6:1G:66:GLN:HG2	2.19	0.43
18:1W:18:ARG:HG2	18:1W:76:VAL:HB	2.00	0.43
23:11:3:LYS:HG2	23:11:4:VAL:HG23	2.00	0.43
32:1a:616:G:O2'	32:1a:617:G:H5'	2.19	0.43
44:1m:13:LYS:C	44:1m:44:ARG:HD2	2.44	0.43
44:1m:89:GLY:O	44:1m:93:ARG:HG3	2.18	0.43
1:2A:1084:A:H3'	1:2A:1085:A:C4'	2.48	0.43
1:2A:1340:U:OP1	19:2X:16:LYS:NZ	2.46	0.43
1:2A:2251:OMG:HM23	1:2A:2251:OMG:H1'	1.72	0.43
1:2A:2468:G:C2	1:2A:2481:G:N3	2.87	0.43
4:2E:174:ASP:OD1	4:2E:175:VAL:N	2.51	0.43
5:2F:161:GLU:O	5:2F:165:ARG:HG3	2.18	0.43
15:2T:96:ARG:NH1	15:2T:96:ARG:HB2	2.33	0.43
26:24:47:GLN:O	26:24:49:PHE:N	2.50	0.43
32:2a:9:G:H2'	32:2a:10:A:H8	1.81	0.43
32:2a:438:G:O2'	32:2a:494:U:O4	2.28	0.43
32:2a:857:C:H2'	32:2a:858:G:O4'	2.17	0.43
32:2a:918:A:H2'	32:2a:919:A:O4'	2.18	0.43
32:2a:1157:A:H4'	32:2a:1158:C:O5'	2.19	0.43
39:2h:122:ARG:NH1	39:2h:122:ARG:HB2	2.34	0.43
46:2o:3:ILE:H	46:2o:3:ILE:HD12	1.82	0.43
47:2p:60:LEU:C	47:2p:62:VAL:H	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:2y:41:LEU:HD12	53:2y:41:LEU:HA	1.80	0.43
1:1A:229:A:H3'	1:1A:230:U:H5'	2.00	0.43
1:1A:1791:A:H5'	1:1A:1792:G:OP2	2.18	0.43
1:1A:2693:A:H2'	1:1A:2694:G:C8	2.54	0.43
10:1O:70:LYS:HB3	10:1O:70:LYS:HE2	1.88	0.43
32:1a:669:U:H2'	32:1a:670:G:C8	2.52	0.43
32:1a:1277:C:H1'	32:1a:1282:C:O2	2.19	0.43
32:1a:1366:C:H2'	32:1a:1367:C:C6	2.52	0.43
32:1a:1469:G:H2'	32:1a:1470:G:H8	1.83	0.43
36:1e:41:VAL:HB	36:1e:113:ALA:HB2	2.00	0.43
38:1g:28:ASN:HA	38:1g:31:MET:HE2	2.00	0.43
40:1i:10:ARG:O	40:1i:11:LYS:C	2.61	0.43
43:1l:24:VAL:HB	43:1l:27:LEU:HD12	1.99	0.43
1:2A:218:A:C2	1:2A:235:U:H4'	2.54	0.43
1:2A:602:G:N2	1:2A:655:A:OP2	2.46	0.43
1:2A:1112:G:H2'	1:2A:1113:U:O4'	2.18	0.43
1:2A:2031:A:C6	1:2A:2498:C:H1'	2.53	0.43
1:2A:2079:U:OP1	23:21:21:ARG:NH2	2.51	0.43
1:2A:2306:C:H3'	1:2A:2307:G:H2'	2.00	0.43
1:2A:2417:C:OP1	11:2P:65:ARG:NH2	2.51	0.43
5:2F:184:TYR:O	5:2F:188:ARG:HG3	2.18	0.43
6:2G:179:PRO:HB2	26:24:42:PHE:HE2	1.83	0.43
26:24:50:VAL:HG11	44:2m:64:TRP:C	2.44	0.43
32:2a:294:U:OP1	32:2a:610:G:O2'	2.31	0.43
32:2a:1256:A:H61	32:2a:1278:U:H1'	1.82	0.43
35:2d:14:ARG:HA	35:2d:14:ARG:HD3	1.91	0.43
39:2h:38:ILE:HD12	39:2h:118:VAL:HG12	2.00	0.43
40:2i:22:GLY:HA3	40:2i:60:ASP:OD2	2.18	0.43
44:2m:13:LYS:O	44:2m:45:VAL:HG23	2.19	0.43
46:2o:5:LYS:O	46:2o:9:GLN:HG2	2.17	0.43
46:2o:37:ASN:O	46:2o:41:GLU:HG2	2.17	0.43
48:2q:81:ARG:NE	48:2q:83:ASP:OD1	2.51	0.43
49:2r:45:SER:OG	49:2r:47:THR:HG22	2.18	0.43
53:2y:30:TRP:CD1	53:2y:89:GLN:HG3	2.54	0.43
1:1A:1628:G:H2'	1:1A:1629:U:C6	2.54	0.43
9:1N:36:GLY:HA2	9:1N:38:HIS:CE1	2.53	0.43
17:1V:21:ARG:HD3	17:1V:91:TYR:CE1	2.53	0.43
32:1a:355:C:O2'	32:1a:388:G:N3	2.43	0.43
32:1a:575:G:O2'	32:1a:821:G:H5'	2.18	0.43
32:1a:615:C:C2	32:1a:616:G:C8	3.07	0.43
32:1a:1014:A:C2	32:1a:1219:U:H1'	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1329:A:P	44:1m:28:ALA:HB3	2.58	0.43
32:1a:1410:G:H2'	32:1a:1411:C:H6	1.83	0.43
35:1d:152:SER:O	35:1d:155:LEU:HB2	2.19	0.43
41:1j:16:LEU:HD22	41:1j:68:HIS:HB2	2.00	0.43
48:1q:41:LYS:NZ	48:1q:88:TYR:OH	2.40	0.43
51:1t:34:LYS:HE3	51:1t:80:ARG:HH22	1.84	0.43
1:2A:1364:G:P	23:21:3:LYS:HG3	2.58	0.43
1:2A:1915:5MU:H2'	1:2A:1916:A:O4'	2.19	0.43
1:2A:2285:C:OP2	28:26:6:ARG:NH1	2.51	0.43
2:2B:24:G:H4'	2:2B:25:A:C8	2.53	0.43
2:2B:50:G:OP1	14:2S:63:THR:OG1	2.32	0.43
10:2O:4:PRO:O	10:2O:5:GLN:HB2	2.19	0.43
22:20:10:THR:HG22	22:20:12:ASN:N	2.29	0.43
26:24:62:ARG:HD2	26:24:62:ARG:N	2.32	0.43
32:2a:684:A:C2	32:2a:685:G:C4	3.07	0.43
32:2a:730:G:C5	32:2a:731:G:H1'	2.54	0.43
32:2a:984:C:H2'	32:2a:985:C:H6	1.83	0.43
32:2a:1005:A:OP2	32:2a:1024:G:N2	2.52	0.43
35:2d:79:PHE:CE1	35:2d:204:ILE:HD13	2.49	0.43
40:2i:8:GLY:HA2	40:2i:79:LEU:HD23	2.01	0.43
40:2i:53:VAL:HG11	40:2i:92:TYR:HE1	1.83	0.43
42:2k:70:LYS:HE3	42:2k:70:LYS:HB2	1.80	0.43
1:1A:570:G:H2'	1:1A:2030:A:C5	2.53	0.43
1:1A:2417:C:OP1	11:1P:65:ARG:NH2	2.52	0.43
1:1A:2691:C:O3'	1:1A:2871:C:H4'	2.19	0.43
3:1D:127:VAL:HA	3:1D:193:VAL:HG22	1.99	0.43
32:1a:410:G:H5''	35:1d:30:LYS:NZ	2.32	0.43
32:1a:1176:A:H2'	32:1a:1177:G:C8	2.53	0.43
32:1a:1498:UR3:H4'	32:1a:1519:MA6:H2	2.00	0.43
34:1c:47:LEU:HB2	34:1c:52:LEU:HD22	2.00	0.43
1:2A:495:G:N3	18:2W:61:ASN:ND2	2.60	0.43
1:2A:782:A:H5'	1:2A:783:A:N7	2.34	0.43
1:2A:904:C:H2'	1:2A:905:U:C6	2.54	0.43
1:2A:1810:A:H2'	1:2A:1811:G:O4'	2.18	0.43
1:2A:1818:U:O2'	3:2D:154:LYS:O	2.35	0.43
1:2A:2327:A:H5'	21:2Z:201:LYS:HG2	2.00	0.43
1:2A:2857:G:N2	1:2A:2860:A:OP2	2.45	0.43
2:2B:29:A:H2'	2:2B:30:C:O4'	2.18	0.43
11:2P:63:PRO:HG2	30:28:25:MET:HB2	2.01	0.43
32:2a:130:A:H5'	48:2q:63:ARG:HE	1.83	0.43
32:2a:502:G:H2'	32:2a:503:C:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1002:G:N2	32:2a:1039:C:C2	2.86	0.43
48:2q:62:SER:OG	48:2q:72:ARG:NH1	2.52	0.43
49:2r:58:LEU:HB3	49:2r:62:GLU:HG3	2.01	0.43
1:1A:226:G:N2	1:1A:228:A:H62	2.14	0.43
1:1A:613:G:N2	1:1A:614(C):A:O2'	2.51	0.43
1:1A:1063:G:H2'	1:1A:1063:G:N3	2.33	0.43
1:1A:1851:U:H2'	1:1A:1852:C:O4'	2.18	0.43
1:1A:2206:G:H8	1:1A:2207:G:N2	2.16	0.43
1:1A:2607:G:H2'	1:1A:2608:G:O4'	2.18	0.43
8:1I:88:ILE:HD11	8:1I:144:VAL:HG11	2.01	0.43
16:1U:49:HIS:HA	16:1U:52:ARG:HB3	2.01	0.43
19:1X:29:TRP:CZ3	19:1X:78:LYS:HG3	2.54	0.43
19:1X:57:LEU:HD12	19:1X:57:LEU:O	2.19	0.43
24:12:54:LYS:NZ	61:12:103:HOH:O	2.52	0.43
32:1a:560:U:O2'	32:1a:561:U:OP2	2.25	0.43
32:1a:1151:A:O2'	32:1a:1152:A:H8	1.99	0.43
32:1a:1425:U:H2'	32:1a:1426:C:H6	1.84	0.43
35:1d:166:LYS:HA	35:1d:178:VAL:HG21	2.01	0.43
36:1e:66:MET:HE3	36:1e:66:MET:HB3	1.94	0.43
44:1m:108:ARG:HA	44:1m:108:ARG:HD3	1.84	0.43
45:1n:27:CYS:SG	45:1n:29:ARG:HB2	2.58	0.43
50:1s:61:TYR:CE2	50:1s:63:THR:HG22	2.54	0.43
1:2A:26:G:C6	1:2A:27:G:N1	2.87	0.43
1:2A:234:C:H2'	1:2A:235:U:H6	1.84	0.43
1:2A:323:G:H1'	1:2A:1205:U:O2	2.18	0.43
1:2A:2361:A:OP2	30:28:26:LYS:NZ	2.50	0.43
4:2E:178:GLU:CD	4:2E:178:GLU:H	2.27	0.43
5:2F:107:LYS:HG3	5:2F:206:ILE:HA	2.01	0.43
6:2G:32:PRO:HB2	6:2G:172:LEU:HD22	2.00	0.43
14:2S:80:LEU:C	14:2S:82:ILE:H	2.27	0.43
25:23:6:VAL:HG13	25:23:54:VAL:CG1	2.49	0.43
25:23:7:LYS:HE3	25:23:32:GLN:HE21	1.83	0.43
32:2a:134:A:H61	47:2p:25:ARG:HH22	1.66	0.43
32:2a:600:C:H2'	32:2a:601:C:C6	2.54	0.43
32:2a:1387:G:H2'	32:2a:1388:C:C6	2.54	0.43
33:2b:74:LYS:HD3	33:2b:76:GLN:HB2	2.00	0.43
36:2e:31:LEU:HD23	36:2e:31:LEU:HA	1.86	0.43
45:2n:14:PRO:HG2	45:2n:16:PHE:O	2.18	0.43
1:1A:729:G:C6	3:1D:208:LYS:HB2	2.54	0.43
1:1A:2168:G:C2	1:1A:2171:A:C8	3.06	0.43
5:1F:18:ARG:NH1	5:1F:127:GLU:OE2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:19:13:LYS:HD3	31:19:13:LYS:HA	1.80	0.43
37:1f:69:GLU:O	37:1f:72:VAL:HG12	2.19	0.43
1:2A:784:A:C8	1:2A:792:G:C5	3.07	0.43
1:2A:1449:A:N3	1:2A:1529:G:H1'	2.34	0.43
1:2A:1580:A:H8	1:2A:1580:A:OP2	2.02	0.43
1:2A:2321:G:N3	1:2A:2321:G:H2'	2.32	0.43
7:2H:84:SER:HA	7:2H:133:VAL:O	2.19	0.43
11:2P:101:VAL:HA	11:2P:106:LEU:O	2.19	0.43
13:2R:103:ARG:NH1	13:2R:108:GLY:O	2.47	0.43
15:2T:45:PHE:CE1	15:2T:74:ARG:HG3	2.53	0.43
32:2a:66:G:H8	32:2a:66:G:OP1	2.02	0.43
32:2a:1236:A:O2'	32:2a:1304:G:H4'	2.19	0.43
32:2a:1360:A:H2'	32:2a:1361:G:O4'	2.19	0.43
33:2b:42:ILE:H	33:2b:42:ILE:HG12	1.62	0.43
33:2b:98:LEU:HB2	33:2b:101:MET:HG3	2.01	0.43
41:2j:46:ARG:HG2	41:2j:64:GLU:HB3	2.00	0.43
42:2k:38:ASN:OD1	42:2k:38:ASN:N	2.52	0.43
1:1A:251:A:C5	1:1A:252:G:H1'	2.54	0.43
1:1A:1009:A:OP2	9:1N:37:LYS:NZ	2.47	0.43
1:1A:2305:A:H5''	6:1G:134:GLY:HA3	2.01	0.43
32:1a:142:G:H2'	32:1a:143:A:C8	2.54	0.43
32:1a:376:G:H4'	47:1p:5:ARG:NH1	2.33	0.43
32:1a:864:A:H2'	32:1a:865:A:C8	2.54	0.43
48:1q:78:GLU:OE1	48:1q:81:ARG:HD3	2.19	0.43
1:2A:1530:C:N4	1:2A:1539:G:H1	2.14	0.43
1:2A:2695:C:H2'	1:2A:2696:U:C6	2.54	0.43
6:2G:144:ILE:HA	6:2G:148:MET:SD	2.58	0.43
12:2Q:58:PHE:O	12:2Q:60:ARG:N	2.43	0.43
19:2X:31:HIS:HD2	19:2X:33:LYS:HB2	1.84	0.43
32:2a:254:G:H21	48:2q:16:GLN:NE2	2.17	0.43
32:2a:407:G:H2'	32:2a:408:A:C8	2.54	0.43
32:2a:474:G:H2'	32:2a:475:G:C8	2.54	0.43
32:2a:685:G:C2	32:2a:686:U:C4	3.07	0.43
32:2a:909:A:H2'	32:2a:910:C:O4'	2.19	0.43
32:2a:1226:C:N4	44:2m:104:ARG:HE	2.17	0.43
33:2b:97:TRP:HH2	33:2b:176:GLU:CD	2.27	0.43
38:2g:48:LYS:O	38:2g:52:GLU:HG2	2.19	0.43
44:2m:50:GLU:O	44:2m:54:VAL:HG13	2.19	0.43
50:2s:52:TYR:HA	50:2s:56:GLN:O	2.19	0.43
1:1A:1041:C:H5'	1:1A:1042:G:OP2	2.19	0.42
1:1A:1344:G:O6	61:1A:4140:HOH:O	2.21	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1578:U:H2'	1:1A:1579:A:H5'	2.02	0.42
1:1A:1678:G:H5''	1:1A:1678:G:N3	2.33	0.42
1:1A:2193:G:H2'	1:1A:2194:G:O4'	2.19	0.42
8:1I:117:GLU:HG3	8:1I:118:LYS:H	1.84	0.42
11:1P:8:PRO:HB2	11:1P:12:ALA:HB3	2.01	0.42
24:12:10:LEU:HD23	24:12:10:LEU:HA	1.89	0.42
24:12:62:THR:O	24:12:66:GLU:HG3	2.18	0.42
32:1a:615:C:H2'	32:1a:616:G:O4'	2.19	0.42
32:1a:1112:C:H1'	34:1c:179:ARG:HE	1.84	0.42
33:1b:218:ALA:O	33:1b:222:ILE:HG13	2.19	0.42
36:1e:79:GLU:CD	36:1e:79:GLU:H	2.27	0.42
1:2A:586:A:N1	1:2A:809:G:O2'	2.47	0.42
1:2A:833:U:O2	11:2P:55:ARG:NH2	2.51	0.42
1:2A:1005:C:H2'	1:2A:1006:C:C6	2.54	0.42
1:2A:1429:G:H2'	1:2A:1430:C:C6	2.54	0.42
1:2A:2093:G:C6	1:2A:2225:A:C8	3.07	0.42
1:2A:2313:C:H4'	6:2G:91:ARG:HD3	2.01	0.42
1:2A:2533:A:OP1	1:2A:2665:A:O2'	2.34	0.42
1:2A:2564:A:C2	1:2A:2647:U:H4'	2.54	0.42
1:2A:2802:G:H2'	1:2A:2803:C:O4'	2.18	0.42
56:2A:3744:TEL:H112	56:2A:3744:TEL:O18	2.19	0.42
6:2G:126:ASP:CG	6:2G:130:ASN:HB2	2.44	0.42
14:2S:95:HIS:CG	14:2S:96:GLY:N	2.87	0.42
29:27:18:PHE:HA	29:27:43:THR:HG21	2.01	0.42
32:2a:625:G:H2'	32:2a:626:U:C6	2.54	0.42
32:2a:868:C:H2'	32:2a:869:G:O4'	2.19	0.42
32:2a:1346:A:N1	32:2a:1374:A:H5''	2.34	0.42
33:2b:80:ILE:HD13	33:2b:211:ILE:HG22	2.01	0.42
40:2i:42:ARG:HE	40:2i:42:ARG:HB3	1.58	0.42
1:1A:271(I):G:H1	1:1A:271(O):C:H42	1.67	0.42
1:1A:300:A:H2'	1:1A:334:C:H1'	2.00	0.42
1:1A:657:U:H2'	1:1A:658:C:C6	2.54	0.42
1:1A:1805:U:O2	3:1D:50:THR:HB	2.18	0.42
1:1A:2119:A:C2	1:1A:2171:A:H5'	2.54	0.42
3:1D:21:PHE:HB3	3:1D:24:ILE:HD12	2.01	0.42
3:1D:137:PRO:HG2	37:1f:81:ILE:HD11	2.00	0.42
5:1F:129:PHE:O	5:1F:130:ALA:C	2.62	0.42
31:19:7:VAL:HA	31:19:34:GLN:NE2	2.34	0.42
32:1a:737:A:H5'	37:1f:90:VAL:O	2.18	0.42
32:1a:1072:G:H2'	32:1a:1073:U:C6	2.53	0.42
32:1a:1148:U:O4'	40:1i:16:ARG:HD2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1179:A:O3'	40:1i:103:THR:OG1	2.32	0.42
32:1a:1347:G:O2'	32:1a:1373:G:O6	2.29	0.42
36:1e:102:ALA:HB1	36:1e:106:PRO:HG2	2.00	0.42
37:1f:82:ARG:HB2	37:1f:85:VAL:HG23	2.01	0.42
1:2A:30:G:H2'	1:2A:31:C:C6	2.53	0.42
1:2A:1015:G:O2'	1:2A:1016:G:H5'	2.19	0.42
1:2A:1410:G:H2'	1:2A:1411:C:C6	2.54	0.42
1:2A:1790:C:H5''	1:2A:1791:A:OP1	2.18	0.42
1:2A:2142:C:O2	1:2A:2149:G:N1	2.52	0.42
57:2A:3746:MPD:O4	57:2A:3746:MPD:O2	2.34	0.42
11:2P:15:ARG:NH1	61:2P:303:HOH:O	2.52	0.42
12:2Q:38:GLU:HA	12:2Q:99:PRO:HG3	2.00	0.42
16:2U:16:LYS:HB3	16:2U:16:LYS:HE2	1.81	0.42
21:2Z:91:LEU:HD11	21:2Z:96:VAL:HG11	1.99	0.42
25:23:8:LEU:HG	25:23:31:LEU:HD22	2.02	0.42
32:2a:932:C:H2'	32:2a:933:G:C8	2.54	0.42
1:1A:307:G:H21	1:1A:330:A:H62	1.67	0.42
1:1A:330:A:HO2'	1:1A:331:A:H8	1.67	0.42
4:1E:181:LEU:HA	4:1E:181:LEU:HD12	1.78	0.42
6:1G:43:LEU:C	6:1G:45:GLU:H	2.25	0.42
8:1I:101:LEU:HD23	8:1I:101:LEU:HA	1.90	0.42
14:1S:110:LEU:HD12	14:1S:110:LEU:HA	1.86	0.42
28:16:12:GLU:OE1	28:16:52:VAL:HG21	2.19	0.42
32:1a:177:C:OP1	51:1t:65:LYS:NZ	2.39	0.42
32:1a:453:A:H4'	47:1p:72:ARG:HB2	2.01	0.42
32:1a:867:G:O2'	32:1a:873:A:N1	2.51	0.42
32:1a:1183:A:H3'	32:1a:1184:G:C5'	2.49	0.42
33:1b:18:GLY:HA3	33:1b:42:ILE:HG13	2.00	0.42
40:1i:26:VAL:HG13	40:1i:61:ALA:HB3	2.02	0.42
40:1i:111:ARG:HG2	40:1i:112:LYS:O	2.19	0.42
1:2A:119:A:H4'	1:2A:120:U:OP1	2.19	0.42
1:2A:602:G:O2'	1:2A:655:A:N6	2.52	0.42
1:2A:620:G:N3	1:2A:620:G:H5'	2.35	0.42
1:2A:1057:A:N7	1:2A:1086:A:H2'	2.34	0.42
1:2A:2438:U:O2'	1:2A:2440:C:OP1	2.34	0.42
6:2G:143:GLU:OE1	6:2G:143:GLU:N	2.51	0.42
27:25:40:LYS:NZ	27:25:41:PRO:O	2.52	0.42
30:28:4:MET:HE2	30:28:4:MET:HB3	1.78	0.42
32:2a:93:G:H2'	32:2a:96:U:O4'	2.20	0.42
32:2a:384:G:H2'	32:2a:385:C:H6	1.84	0.42
32:2a:1005:A:H5''	32:2a:1006:C:C5	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:1431:C:H2'	32:2a:1432:G:O4'	2.19	0.42
33:2b:111:ARG:HA	33:2b:111:ARG:HD3	1.82	0.42
47:2p:21:VAL:HG13	47:2p:34:GLU:HB3	2.01	0.42
53:2y:8:LYS:HE2	53:2y:8:LYS:HB3	1.79	0.42
1:1A:1802:A:N1	1:1A:1822:G:H1'	2.34	0.42
1:1A:1932:A:H2'	1:1A:1933:G:O4'	2.20	0.42
1:1A:2615:U:H2'	1:1A:2616:C:C6	2.54	0.42
2:1B:40:U:H2'	26:14:2:LYS:HE3	2.01	0.42
20:1Y:53:PRO:O	20:1Y:56:PRO:HD3	2.19	0.42
32:1a:302:G:O2'	32:1a:556:C:H5''	2.19	0.42
32:1a:437:U:O3'	35:1d:125:HIS:CE1	2.72	0.42
32:1a:1305:G:H22	32:1a:1331:G:H1'	1.84	0.42
40:1i:5:TYR:HB2	40:1i:18:PHE:CE1	2.53	0.42
1:2A:455:C:N3	1:2A:472:A:H2'	2.35	0.42
1:2A:570:G:H2'	1:2A:2030:A:C5	2.53	0.42
1:2A:1268:A:H2'	1:2A:1269:A:O4'	2.20	0.42
1:2A:2187:G:N7	1:2A:2188:C:C4	2.87	0.42
1:2A:2467:C:H4'	12:2Q:123:HIS:CD2	2.54	0.42
1:2A:2805:G:C6	1:2A:2807:G:C6	3.07	0.42
1:2A:2811:G:OP1	4:2E:60:ASN:HB2	2.19	0.42
7:2H:12:PRO:O	7:2H:15:VAL:HG22	2.19	0.42
26:24:1:MET:HB3	26:24:6:HIS:NE2	2.34	0.42
32:2a:601:C:H2'	32:2a:602:A:C8	2.54	0.42
32:2a:674:G:H2'	32:2a:675:A:C8	2.55	0.42
32:2a:840:C:H4'	32:2a:841:U:OP2	2.16	0.42
32:2a:1138:G:H5'	32:2a:1139:G:OP1	2.19	0.42
35:2d:173:TRP:CZ3	35:2d:193:ASP:HB3	2.54	0.42
1:1A:1071:G:N2	1:1A:1089:G:HO2'	2.17	0.42
1:1A:1450:G:H2'	1:1A:1450(A):C:C6	2.54	0.42
1:1A:2074:U:H2'	1:1A:2075:U:C6	2.54	0.42
2:1B:66:A:N6	2:1B:109:C:H5'	2.35	0.42
3:1D:101:GLU:OE2	3:1D:103:ARG:HD3	2.19	0.42
5:1F:57:VAL:HG13	5:1F:59:TYR:CD2	2.54	0.42
6:1G:138:GLN:NE2	6:1G:153:ARG:HG3	2.34	0.42
8:1I:85:GLU:HG3	8:1I:86:THR:N	2.34	0.42
21:1Z:25:PRO:O	21:1Z:85:HIS:HA	2.19	0.42
21:1Z:30:ASN:ND2	21:1Z:90:VAL:HG23	2.34	0.42
27:15:37:LYS:HA	27:15:37:LYS:HD3	1.82	0.42
32:1a:129(A):G:C6	32:1a:189(E):U:H4'	2.54	0.42
32:1a:403:C:O3'	35:1d:122:ARG:HD3	2.19	0.42
32:1a:881:G:P	43:1l:12:ARG:HH22	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:950:U:H2'	32:1a:951:G:C8	2.55	0.42
32:1a:1144:G:N2	32:1a:1146:A:H62	2.18	0.42
32:1a:1251:A:H2'	32:1a:1252:A:C8	2.54	0.42
32:1a:1479:C:H2'	32:1a:1480:G:H8	1.85	0.42
39:1h:104:ARG:C	39:1h:106:GLY:H	2.27	0.42
1:2A:1074:G:C2	1:2A:1075:C:H1'	2.54	0.42
1:2A:1075:C:O2	1:2A:1075:C:H2'	2.19	0.42
1:2A:1406:U:H2'	1:2A:1407:C:C6	2.53	0.42
1:2A:1540:U:H2'	1:2A:1541:G:O4'	2.19	0.42
1:2A:2092:U:H4'	1:2A:2093:G:O5'	2.19	0.42
2:2B:48:A:H2'	2:2B:49:C:C6	2.55	0.42
5:2F:23:ASP:O	5:2F:24:LEU:HD12	2.20	0.42
5:2F:33:LEU:HD12	5:2F:33:LEU:HA	1.72	0.42
9:2N:73:THR:HA	9:2N:83:LYS:O	2.19	0.42
14:2S:27:SER:HA	14:2S:88:ASP:HB3	2.00	0.42
21:2Z:183:LEU:HD23	21:2Z:183:LEU:HA	1.90	0.42
23:21:82:LEU:O	23:21:85:LEU:HD22	2.19	0.42
32:2a:116:A:H61	32:2a:313:A:H1'	1.83	0.42
32:2a:540:G:C6	32:2a:541:G:C5	3.07	0.42
33:2b:155:LEU:HD21	33:2b:159:PRO:HG3	2.02	0.42
36:2e:12:LEU:O	36:2e:30:ALA:HA	2.19	0.42
38:2g:101:LEU:O	38:2g:105:VAL:HG23	2.19	0.42
40:2i:85:LEU:HB3	40:2i:92:TYR:CD2	2.54	0.42
52:2u:6:ARG:C	52:2u:8:THR:H	2.27	0.42
1:1A:957:A:N1	1:1A:2458:G:H4'	2.35	0.42
1:1A:1816:G:H8	3:1D:62:TYR:CZ	2.38	0.42
1:1A:2354:G:H21	22:10:36:ILE:HD11	1.85	0.42
1:1A:2506:U:O2	55:1A:4020:HGR:H23	2.19	0.42
3:1D:146:GLU:HG2	3:1D:152:GLY:C	2.44	0.42
11:1P:63:PRO:HG2	30:18:25:MET:HB2	2.01	0.42
26:14:41:PRO:HB3	26:14:47:GLN:O	2.19	0.42
32:1a:253:U:H2'	32:1a:254:G:H8	1.85	0.42
32:1a:1376:U:P	38:1g:94:ARG:HH12	2.43	0.42
32:1a:1492:A:H4'	32:1a:1493:A:C2	2.55	0.42
33:1b:9:GLU:HB2	33:1b:217:ARG:NH2	2.34	0.42
33:1b:194:PRO:O	33:1b:197:VAL:HG22	2.20	0.42
35:1d:85:LYS:HD2	35:1d:85:LYS:HA	1.65	0.42
35:1d:107:ARG:NH2	35:1d:194:LEU:HD21	2.35	0.42
8:2I:57:ARG:NH1	8:2I:61:ARG:HH22	2.16	0.42
9:2N:1:MET:HE1	16:2U:94:ASN:ND2	2.35	0.42
26:24:59:PHE:CE2	50:2s:64:GLU:HB2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2a:434:U:H2'	32:2a:435:C:H6	1.82	0.42
32:2a:1368:G:OP2	40:2i:112:LYS:HG3	2.20	0.42
35:2d:70:ILE:HD11	35:2d:74:GLN:HB3	2.01	0.42
35:2d:98:GLU:OE1	35:2d:103:ASN:ND2	2.52	0.42
44:2m:92:HIS:HA	44:2m:110:ARG:NH2	2.35	0.42
48:2q:57:VAL:HG12	48:2q:76:LEU:HA	2.02	0.42
1:1A:143:G:H4'	19:1X:35:THR:HG21	2.00	0.42
1:1A:302:C:P	20:1Y:73:ARG:HH22	2.40	0.42
1:1A:645:C:H5'	1:1A:646:A:OP2	2.20	0.42
1:1A:1354:A:H2'	1:1A:1355:G:O4'	2.20	0.42
15:1T:1:MET:HE2	15:1T:3:ARG:HG3	2.02	0.42
18:1W:1:MET:HE2	18:1W:62:HIS:HB3	2.00	0.42
19:1X:5:TYR:CE1	24:12:30:ARG:HB2	2.55	0.42
32:1a:838:G:H5'	32:1a:839:U:OP2	2.19	0.42
51:1t:101:GLY:HA2	51:1t:102:GLY:HA2	1.76	0.42
1:2A:263:C:H2'	1:2A:264:C:O4'	2.19	0.42
1:2A:1049:C:H2'	1:2A:1050:A:H8	1.83	0.42
1:2A:1263:U:C4	1:2A:1264:G:C6	3.07	0.42
1:2A:1290:C:H2'	1:2A:1291:C:H6	1.85	0.42
1:2A:2314:C:H5''	6:2G:38:VAL:HG21	2.02	0.42
1:2A:2693:A:H2'	1:2A:2694:G:C8	2.54	0.42
1:2A:2893:G:H5''	1:2A:2894:G:O4'	2.20	0.42
7:2H:71:LEU:O	7:2H:75:ALA:N	2.46	0.42
10:2O:15:GLY:O	10:2O:47:ILE:HG12	2.20	0.42
17:2V:20:LEU:HD12	17:2V:21:ARG:H	1.84	0.42
17:2V:35:LEU:HB2	17:2V:57:VAL:HG23	2.01	0.42
21:2Z:182:LYS:HG3	21:2Z:186:GLU:OE1	2.19	0.42
26:24:59:PHE:HB3	26:24:61:ARG:HB2	2.00	0.42
32:2a:1054:C:H4'	32:2a:1055:A:O5'	2.19	0.42
32:2a:1358:U:H5''	45:2n:34:TYR:HA	2.00	0.42
32:2a:1401:G:C2	32:2a:1402:4OC:H1'	2.55	0.42
33:2b:98:LEU:HB2	33:2b:101:MET:HE3	2.01	0.42
36:2e:7:GLU:CD	36:2e:37:ARG:HH21	2.28	0.42
40:2i:53:VAL:HG21	40:2i:92:TYR:CE1	2.55	0.42
41:2j:19:SER:O	41:2j:23:ILE:HG12	2.20	0.42
1:1A:699:A:H2'	1:1A:700:G:O4'	2.20	0.42
1:1A:910:A:H2'	1:1A:911:A:C8	2.54	0.42
1:1A:1568:G:N7	61:1A:4243:HOH:O	2.37	0.42
1:1A:1712:C:H2'	1:1A:1713:U:O4'	2.20	0.42
11:1P:71:VAL:HG22	11:1P:72:PRO:HA	2.02	0.42
13:1R:12:ARG:O	13:1R:17:ARG:NH1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:1R:53:HIS:ND1	13:1R:94:TYR:OH	2.40	0.42
32:1a:115:G:H4'	32:1a:116:A:O5'	2.18	0.42
32:1a:814:A:H2'	32:1a:816:A:H5''	2.00	0.42
32:1a:1152:A:H2'	32:1a:1153:C:C6	2.54	0.42
36:1e:84:PHE:CE2	36:1e:133:TYR:HD2	2.38	0.42
49:1r:59:SER:OG	49:1r:62:GLU:HG2	2.20	0.42
1:2A:411:G:C5	11:2P:72:PRO:HB3	2.55	0.42
1:2A:1073:A:C2	1:2A:1074:G:C5	3.08	0.42
1:2A:1508:A:H4'	1:2A:1509(A):A:C5	2.54	0.42
1:2A:2030:A:H4'	1:2A:2031:A:C8	2.55	0.42
1:2A:2611:U:H3'	1:2A:2611:U:OP2	2.20	0.42
1:2A:2745:C:H2'	1:2A:2746:U:O4'	2.19	0.42
21:2Z:72:ARG:HD3	21:2Z:72:ARG:HA	1.85	0.42
28:26:10:LEU:HB2	28:26:52:VAL:HG12	2.00	0.42
29:27:24:THR:CG2	29:27:27:GLY:H	2.21	0.42
32:2a:36:C:O2'	43:2l:117:ARG:NH2	2.52	0.42
32:2a:620:C:H2'	32:2a:621:A:O4'	2.18	0.42
32:2a:818:G:O2'	32:2a:819:A:H5'	2.19	0.42
32:2a:1002:G:C4	32:2a:1003:G:N7	2.88	0.42
32:2a:1127:G:OP1	32:2a:1281:U:H4'	2.20	0.42
32:2a:1131:G:H2'	32:2a:1132:C:C6	2.55	0.42
32:2a:1157:A:C5	32:2a:1180:A:C6	3.07	0.42
32:2a:1203:C:H5''	45:2n:3:ARG:NH1	2.34	0.42
33:2b:82:ARG:HB2	33:2b:92:TYR:CZ	2.54	0.42
33:2b:211:ILE:O	33:2b:215:LEU:HB2	2.19	0.42
38:2g:114:ARG:H	38:2g:115:ARG:NH2	2.18	0.42
1:1A:1177:A:H2'	1:1A:1177:A:N3	2.34	0.42
1:1A:1246:A:OP1	5:1F:38:ARG:NH1	2.53	0.42
1:1A:2130:U:O2'	1:1A:2133:G:O2'	2.30	0.42
12:1Q:60:ARG:HD2	21:1Z:179:ASP:CG	2.45	0.42
32:1a:79:G:C2	32:1a:90:U:O2	2.73	0.42
32:1a:1054:C:H41	53:1y:46:GLN:CD	2.28	0.42
33:1b:84:GLU:OE1	33:1b:87:ARG:NH1	2.50	0.42
39:1h:6:ILE:HB	39:1h:85:ARG:NH1	2.35	0.42
43:1l:54:LYS:HD2	43:1l:54:LYS:N	2.34	0.42
1:2A:271(K):U:H4'	1:2A:271(L):U:OP1	2.20	0.42
1:2A:801:G:OP2	5:2F:55:GLY:HA2	2.19	0.42
1:2A:1105:U:H2'	1:2A:1106:G:C8	2.54	0.42
1:2A:1364:G:C8	23:21:3:LYS:HD2	2.54	0.42
1:2A:1453:U:O2'	1:2A:1455:G:N7	2.45	0.42
1:2A:1800:C:OP1	3:2D:260:ARG:NH2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1816:G:O6	3:2D:35:LYS:NZ	2.28	0.42
1:2A:2028:U:H2'	1:2A:2029:G:O4'	2.20	0.42
5:2F:39:TRP:NE1	5:2F:99:TYR:O	2.52	0.42
19:2X:72:LYS:HG2	19:2X:73:ARG:O	2.20	0.42
32:2a:256:U:OP1	48:2q:17:LYS:NZ	2.43	0.42
32:2a:622:A:C8	32:2a:623:C:C6	3.08	0.42
32:2a:854:G:N7	61:2a:3257:HOH:O	2.36	0.42
32:2a:1323:G:HO2'	32:2a:1362:C:HO2'	1.62	0.42
33:2b:127:ILE:O	33:2b:128:GLU:HB2	2.19	0.42
38:2g:29:LYS:O	38:2g:105:VAL:HG11	2.20	0.42
50:2s:32:LYS:HD3	50:2s:34:TRP:CH2	2.55	0.42
1:1A:1064:C:N4	1:1A:1065:U:O2	2.53	0.42
1:1A:1587:A:H2'	1:1A:1588:C:C6	2.55	0.42
1:1A:1817:G:OP1	3:1D:88:ARG:NH2	2.41	0.42
1:1A:2621:A:H5''	61:1A:4395:HOH:O	2.19	0.42
1:1A:2730:C:O2'	1:1A:2731:G:H5'	2.20	0.42
19:1X:60:ARG:NH1	29:17:47:ARG:HH12	2.18	0.42
32:1a:1069:C:O2'	32:1a:1192:C:H1'	2.20	0.42
32:1a:1152:A:H2'	32:1a:1153:C:H6	1.84	0.42
32:1a:1479:C:H2'	32:1a:1480:G:C8	2.55	0.42
35:1d:166:LYS:HB2	35:1d:166:LYS:HE3	1.80	0.42
35:1d:196:LEU:O	35:1d:198:VAL:N	2.45	0.42
38:1g:122:HIS:CD2	38:1g:125:MET:HE2	2.55	0.42
42:1k:97:ALA:O	42:1k:101:SER:HB3	2.19	0.42
1:2A:911:A:H2'	12:2Q:9:TYR:OH	2.19	0.42
1:2A:1166:C:H2'	1:2A:1167:U:C6	2.55	0.42
1:2A:1815:A:OP2	61:2A:3858:HOH:O	2.21	0.42
1:2A:2102:U:H2'	1:2A:2103:C:C6	2.54	0.42
11:2P:98:GLU:HG3	11:2P:102:ARG:NH2	2.35	0.42
32:2a:187:C:H2'	32:2a:188:C:H6	1.84	0.42
36:2e:33:VAL:HG13	36:2e:112:LEU:HD12	2.02	0.42
1:1A:690:G:H2'	1:1A:691:C:C6	2.55	0.41
1:1A:778:G:OP2	61:1A:4142:HOH:O	2.22	0.41
1:1A:1794:U:H2'	1:1A:1795:C:C6	2.54	0.41
3:1D:16:MET:HG3	3:1D:211:ARG:HH21	1.85	0.41
5:1F:30:PRO:HB3	11:1P:1:MET:HE1	2.01	0.41
5:1F:152:GLU:OE1	5:1F:191:ARG:HD2	2.20	0.41
6:1G:25:TYR:CZ	6:1G:32:PRO:HD3	2.55	0.41
20:1Y:99:CYS:HB2	20:1Y:106:LEU:HD21	2.02	0.41
30:18:47:LYS:CE	57:18:105:MPD:H51	2.50	0.41
32:1a:448:A:P	32:1a:485:G:H22	2.42	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1326:C:OP1	52:1u:12:LYS:NZ	2.40	0.41
32:1a:1446:U:O2'	32:1a:1447:A:H3'	2.20	0.41
47:1p:19:ILE:HG23	47:1p:36:ILE:HG13	2.02	0.41
1:2A:361:G:C2'	1:2A:362:U:H5'	2.49	0.41
1:2A:1590:U:H2'	1:2A:1591:G:C8	2.55	0.41
1:2A:2494:G:OP2	61:2A:3853:HOH:O	2.20	0.41
15:2T:24:PRO:HD3	15:2T:52:ILE:HD12	2.01	0.41
21:2Z:5:LEU:HB2	21:2Z:47:VAL:HG21	2.02	0.41
21:2Z:23:LYS:HA	21:2Z:23:LYS:HD3	1.87	0.41
34:2c:37:GLN:NE2	45:2n:52:GLN:HB3	2.34	0.41
1:1A:468:G:N7	29:17:39:ARG:NH2	2.60	0.41
1:1A:1662:C:O2	1:1A:2687:U:H5''	2.20	0.41
1:1A:2359:C:H2'	1:1A:2360:A:O4'	2.21	0.41
5:1F:12:LEU:HD22	5:1F:124:LEU:HD21	2.00	0.41
23:11:80:LEU:HD12	23:11:80:LEU:HA	1.92	0.41
32:1a:1298:C:H4'	32:1a:1299:A:C4	2.55	0.41
41:1j:30:SER:HB3	41:1j:81:THR:HG22	2.01	0.41
1:2A:656:G:H2'	1:2A:657:U:O4'	2.20	0.41
1:2A:1056:G:H4'	1:2A:1057:A:H8	1.85	0.41
1:2A:1721:G:H2'	1:2A:1740:G:O6	2.20	0.41
1:2A:2115:G:H21	1:2A:2171:A:N6	2.13	0.41
1:2A:2155:G:C2	1:2A:2156:G:H1'	2.55	0.41
2:2B:18:G:H2'	2:2B:19:G:C8	2.55	0.41
2:2B:105:A:H2'	2:2B:106:G:O4'	2.20	0.41
6:2G:105:LYS:NZ	6:2G:143:GLU:OE2	2.43	0.41
6:2G:107:LEU:HA	6:2G:111:LEU:HD12	2.02	0.41
13:2R:28:LEU:HD23	13:2R:48:VAL:HG21	2.02	0.41
29:27:47:ARG:HE	29:27:47:ARG:HB3	1.72	0.41
32:2a:325:A:H2'	32:2a:326:G:O4'	2.19	0.41
32:2a:820:U:OP1	61:2a:3222:HOH:O	2.22	0.41
32:2a:1142:G:H2'	32:2a:1143:G:O4'	2.20	0.41
32:2a:1178:G:N2	32:2a:1180:A:H3'	2.35	0.41
34:2c:47:LEU:HB3	34:2c:52:LEU:HG	2.01	0.41
38:2g:155:ARG:O	38:2g:155:ARG:HG2	2.21	0.41
40:2i:100:GLY:O	40:2i:103:THR:HG22	2.20	0.41
50:2s:6:LYS:HE2	50:2s:6:LYS:HB3	1.82	0.41
1:1A:1171:G:H5'	61:1A:5598:HOH:O	2.20	0.41
1:1A:2023:G:H4'	1:1A:2617:C:O3'	2.20	0.41
1:1A:2165:G:H2'	1:1A:2166:G:H8	1.86	0.41
1:1A:2543:G:H21	1:1A:2646:C:H5''	1.86	0.41
26:14:55:ARG:N	26:14:56:VAL:HA	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:337:C:H2'	32:1a:338:A:C8	2.56	0.41
32:1a:457:C:H2'	32:1a:458:C:C6	2.54	0.41
32:1a:688:G:O2'	32:1a:704:A:N1	2.38	0.41
32:1a:977:A:H1'	32:1a:982:U:O4	2.20	0.41
32:1a:1304:G:C6	32:1a:1305:G:N1	2.89	0.41
36:1e:150:ARG:HE	36:1e:150:ARG:HB2	1.52	0.41
39:1h:41:ARG:NH2	39:1h:123:GLU:OE2	2.53	0.41
41:1j:16:LEU:HD21	41:1j:70:ARG:HG2	2.02	0.41
48:1q:27:PHE:CE1	48:1q:36:ILE:HD11	2.55	0.41
50:1s:80:TYR:CZ	50:1s:82:GLY:HA2	2.55	0.41
1:2A:207:A:H2'	1:2A:208:C:O4'	2.20	0.41
1:2A:236:C:H2'	1:2A:237:C:C6	2.55	0.41
1:2A:958:U:OP1	12:2Q:74:TYR:OH	2.25	0.41
1:2A:1027:A:C6	1:2A:1126:A:C4	3.09	0.41
2:2B:28:C:H2'	2:2B:29:A:O4'	2.21	0.41
3:2D:17:THR:O	3:2D:211:ARG:NH2	2.46	0.41
6:2G:14:GLU:C	6:2G:17:PRO:HD2	2.46	0.41
10:2O:26:LYS:NZ	10:2O:37:ASP:OD2	2.35	0.41
13:2R:12:ARG:O	13:2R:17:ARG:NH1	2.53	0.41
15:2T:27:THR:HB	15:2T:89:VAL:HG22	2.02	0.41
20:2Y:38:ILE:HD11	20:2Y:66:PRO:HG3	2.01	0.41
31:29:8:LYS:H	31:29:34:GLN:HE22	1.67	0.41
32:2a:694:A:N1	32:2a:787:A:O2'	2.52	0.41
32:2a:757:U:H2'	32:2a:758:G:O4'	2.19	0.41
32:2a:848:C:O5'	32:2a:848:C:H6	2.04	0.41
32:2a:1246:C:H2'	32:2a:1247:U:C6	2.56	0.41
35:2d:88:VAL:HG22	36:2e:96:PRO:HB2	2.01	0.41
39:2h:97:VAL:HA	39:2h:100:ILE:HG13	2.02	0.41
41:2j:57:LYS:O	41:2j:60:ARG:NE	2.44	0.41
44:2m:47:ASP:OD1	44:2m:47:ASP:N	2.52	0.41
1:1A:185:U:H2'	1:1A:186:G:C8	2.56	0.41
1:1A:271(H):G:O2'	1:1A:271(I):G:C8	2.73	0.41
1:1A:478:A:N1	1:1A:500:G:H4'	2.35	0.41
1:1A:1175:U:OP1	1:1A:1177:A:N6	2.54	0.41
1:1A:2315:G:H2'	1:1A:2316:C:C6	2.55	0.41
1:1A:2406:U:N3	11:1P:73:GLY:O	2.43	0.41
1:1A:2722:G:H2'	1:1A:2723:C:C6	2.56	0.41
6:1G:161:THR:CG2	6:1G:163:ALA:H	2.33	0.41
32:1a:441:A:H3'	32:1a:442:C:H6	1.85	0.41
32:1a:567:G:H2'	32:1a:568:G:O4'	2.19	0.41
32:1a:912:C:O2'	32:1a:913:A:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1003:G:O2'	32:1a:1004:A:H4'	2.21	0.41
33:1b:18:GLY:HA2	33:1b:204:ASN:HB2	2.02	0.41
34:1c:68:VAL:O	34:1c:104:GLN:N	2.52	0.41
34:1c:83:ARG:O	34:1c:87:LEU:HG	2.20	0.41
42:1k:92:GLU:HG3	42:1k:96:ARG:HH12	1.85	0.41
1:2A:1385:G:O2'	1:2A:1396:U:O2	2.31	0.41
1:2A:2001:A:H2'	1:2A:2002:G:C8	2.55	0.41
1:2A:2345:G:H4'	1:2A:2346:A:H5''	2.02	0.41
1:2A:2554:U:H2'	1:2A:2555:U:C6	2.55	0.41
7:2H:72:ILE:O	7:2H:76:VAL:HG23	2.21	0.41
9:2N:91:LEU:HA	9:2N:95:PRO:HA	2.02	0.41
13:2R:70:LEU:C	13:2R:72:ASP:H	2.28	0.41
32:2a:64:G:H4'	32:2a:65:U:H3'	2.01	0.41
32:2a:328:C:H4'	32:2a:329:A:H5'	2.03	0.41
32:2a:1342:C:H2'	32:2a:1343:G:C8	2.56	0.41
32:2a:1403:C:H2'	32:2a:1404:5MC:HM53	2.02	0.41
33:2b:230:VAL:HG22	33:2b:231:GLU:H	1.85	0.41
35:2d:19:LEU:HB3	35:2d:21:LEU:HG	2.02	0.41
36:2e:71:LEU:HA	36:2e:71:LEU:HD22	1.78	0.41
49:2r:33:ASP:OD2	49:2r:36:ASN:HB2	2.20	0.41
1:1A:299:A:N1	1:1A:322:A:O2'	2.47	0.41
1:1A:655:A:H8	1:1A:656:G:C1'	2.33	0.41
1:1A:1087:G:H8	1:1A:1087:G:O5'	2.03	0.41
1:1A:1153:C:H2'	1:1A:1154:G:O4'	2.21	0.41
1:1A:1301:A:C8	1:1A:1303:G:C8	3.08	0.41
6:1G:16:ARG:HB2	6:1G:17:PRO:HD3	2.02	0.41
7:1H:3:ARG:HB3	7:1H:6:ARG:HG2	2.02	0.41
7:1H:149:ARG:NH1	7:1H:167:GLU:OE2	2.52	0.41
12:1Q:7:MET:HE3	12:1Q:7:MET:HB3	1.85	0.41
21:1Z:147:GLY:HA2	21:1Z:174:VAL:O	2.20	0.41
27:15:34:PRO:HG2	27:15:35:GLU:OE1	2.19	0.41
32:1a:441:A:H3'	32:1a:442:C:C6	2.55	0.41
32:1a:909:A:H2'	32:1a:910:C:O4'	2.20	0.41
32:1a:954:G:H5'	53:1y:17:ARG:NH2	2.35	0.41
32:1a:1216:G:H5''	45:1n:5:ALA:HB2	2.01	0.41
32:1a:1297:C:O2'	38:1g:114:ARG:NH1	2.45	0.41
33:1b:47:THR:O	33:1b:51:LEU:HB2	2.21	0.41
39:1h:20:TYR:HA	39:1h:65:TYR:CZ	2.55	0.41
1:2A:631:A:OP1	11:2P:65:ARG:NH1	2.54	0.41
1:2A:652(D):C:N4	1:2A:652(U):G:H1	2.18	0.41
1:2A:2660:A:H2'	1:2A:2661:G:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2D:61:LEU:O	3:2D:63:ARG:NH1	2.53	0.41
6:2G:47:LYS:HG3	6:2G:48:GLU:N	2.34	0.41
21:2Z:124:ILE:HG13	21:2Z:125:LEU:N	2.34	0.41
31:29:27:CYS:SG	31:29:28:GLU:N	2.94	0.41
32:2a:598:U:H4'	39:2h:94:TYR:CD2	2.56	0.41
32:2a:642:A:N3	39:2h:113:SER:OG	2.47	0.41
32:2a:1364:U:O2'	32:2a:1365:G:H5'	2.20	0.41
1:1A:288:C:H2'	1:1A:289:A:C8	2.56	0.41
1:1A:784:A:C6	3:1D:229:VAL:HG11	2.55	0.41
1:1A:1023:U:OP2	61:1A:4119:HOH:O	2.22	0.41
1:1A:1176:G:H21	1:1A:1178:C:P	2.43	0.41
1:1A:1470:G:N2	1:1A:1520:G:OP2	2.45	0.41
1:1A:2119:A:C6	1:1A:2170:A:C5	3.09	0.41
1:1A:2572:A:C8	4:1E:144:ARG:HD3	2.55	0.41
1:1A:2751:G:H4'	7:1H:4:ILE:HD11	2.02	0.41
3:1D:134:ARG:HG3	3:1D:135:PHE:CD1	2.56	0.41
7:1H:86:GLU:CD	7:1H:132:ARG:HH21	2.29	0.41
9:1N:114:ARG:NH2	61:1N:310:HOH:O	2.53	0.41
32:1a:619:U:N3	35:1d:134:ASP:OD1	2.42	0.41
32:1a:1004:A:O4'	32:1a:1025:U:N3	2.54	0.41
33:1b:95:GLN:HG3	33:1b:147:LYS:O	2.19	0.41
35:1d:163:GLU:O	35:1d:166:LYS:HG3	2.20	0.41
48:1q:15:MET:HE1	48:1q:43:LEU:HD22	2.03	0.41
1:2A:872:A:H2'	1:2A:873:G:O4'	2.19	0.41
1:2A:903:C:H2'	1:2A:904:C:C6	2.56	0.41
1:2A:1698:A:C8	1:2A:1700:A:O4'	2.74	0.41
1:2A:1784:A:H4'	1:2A:1785:A:C5'	2.51	0.41
1:2A:1881:C:H2'	1:2A:1882:C:H6	1.85	0.41
1:2A:2313:C:H2'	1:2A:2314:C:C6	2.55	0.41
1:2A:2334:G:H5'	14:2S:9:ARG:HG2	2.02	0.41
4:2E:37:ARG:O	4:2E:45:THR:HA	2.20	0.41
7:2H:11:VAL:CG2	7:2H:15:VAL:HG23	2.50	0.41
11:2P:2:LYS:NZ	11:2P:4:SER:HB3	2.36	0.41
20:2Y:92:ASN:HD21	20:2Y:94:LYS:CE	2.33	0.41
32:2a:392:G:H2'	32:2a:393:A:C8	2.55	0.41
32:2a:500:G:H2'	32:2a:501:C:C6	2.56	0.41
32:2a:979:C:H2'	32:2a:980:C:H5'	2.02	0.41
33:2b:74:LYS:C	33:2b:76:GLN:N	2.78	0.41
40:2i:45:ALA:O	40:2i:48:GLU:HB2	2.21	0.41
44:2m:49:THR:O	44:2m:53:VAL:HG13	2.21	0.41
1:1A:210:C:H2'	1:1A:211:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:263:C:H2'	1:1A:264:C:O4'	2.20	0.41
1:1A:740:U:H2'	1:1A:741:G:C8	2.55	0.41
1:1A:795:C:H2'	1:1A:796:C:C6	2.55	0.41
1:1A:1058:G:C6	1:1A:1080:C:N3	2.88	0.41
1:1A:1670:C:OP2	61:1A:4117:HOH:O	2.21	0.41
1:1A:2611:U:C5	56:1A:4021:TEL:H352	2.56	0.41
61:1A:5160:HOH:O	4:1E:129:HIS:HE1	2.03	0.41
5:1F:14:PRO:HD2	5:1F:127:GLU:OE1	2.20	0.41
32:1a:359:U:H2'	32:1a:360:A:C8	2.55	0.41
32:1a:690:G:C6	32:1a:691:G:C6	3.09	0.41
35:1d:3:ARG:HD3	35:1d:118:ARG:NE	2.35	0.41
36:1e:45:PHE:CE2	36:1e:47:LYS:HE2	2.56	0.41
38:1g:26:PHE:O	38:1g:30:ILE:HG13	2.21	0.41
38:1g:122:HIS:HD2	38:1g:125:MET:HE2	1.85	0.41
44:1m:20:THR:HA	44:1m:25:ILE:O	2.21	0.41
48:1q:62:SER:OG	48:1q:72:ARG:HG3	2.21	0.41
1:2A:1198:U:H2'	1:2A:1199:U:C6	2.56	0.41
1:2A:1614:A:C2	18:2W:93:ALA:HB2	2.56	0.41
1:2A:2682:U:O2'	15:2T:58:ASN:ND2	2.54	0.41
1:2A:2719:G:O6	61:2A:3841:HOH:O	2.18	0.41
1:2A:2804:C:H2'	1:2A:2805:G:O4'	2.21	0.41
3:2D:175:LEU:HD12	3:2D:185:VAL:HG21	2.02	0.41
11:2P:83:VAL:HG21	11:2P:100:LEU:HD13	2.02	0.41
21:2Z:183:LEU:HD23	21:2Z:186:GLU:OE1	2.21	0.41
32:2a:486:U:H2'	32:2a:487:A:C8	2.56	0.41
32:2a:1309:G:N7	44:2m:99:ARG:NH2	2.69	0.41
32:2a:1333:A:H2'	32:2a:1334:G:O4'	2.20	0.41
33:2b:74:LYS:HB2	33:2b:76:GLN:HE21	1.86	0.41
34:2c:148:GLY:HA3	34:2c:172:ARG:O	2.19	0.41
35:2d:150:GLU:HA	35:2d:153:ARG:HE	1.84	0.41
1:1A:839:U:H2'	1:1A:840:C:C6	2.56	0.41
1:1A:1058:G:C2	1:1A:1081:U:H1'	2.56	0.41
1:1A:1607:C:H4'	1:1A:1608:A:O5'	2.21	0.41
1:1A:2168:G:N2	1:1A:2170:A:H3'	2.36	0.41
1:1A:2187:G:C6	1:1A:2188:C:C2	3.09	0.41
1:1A:2864:G:OP1	15:1T:119:LYS:HD2	2.20	0.41
3:1D:242:ARG:HG3	3:1D:242:ARG:HH11	1.85	0.41
8:1I:75:LEU:HD13	8:1I:105:HIS:ND1	2.35	0.41
15:1T:108:ARG:HA	15:1T:111:ARG:NH1	2.35	0.41
19:1X:1:MET:HE3	19:1X:1:MET:HB2	1.88	0.41
21:1Z:136:PHE:HE1	21:1Z:138:GLU:HG3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:7:G:H21	36:1e:121:LYS:HG2	1.85	0.41
32:1a:169:C:H2'	32:1a:170:U:H6	1.85	0.41
32:1a:491:G:H2'	32:1a:492:G:O4'	2.21	0.41
32:1a:509:A:H5'	35:1d:54:TYR:HD2	1.86	0.41
32:1a:972:C:OP1	61:1a:3318:HOH:O	2.21	0.41
32:1a:1047:G:H5''	45:1n:4:LYS:HE3	2.02	0.41
42:1k:70:LYS:HE2	42:1k:70:LYS:HB2	1.87	0.41
1:2A:858:U:O2	1:2A:2268:A:H2'	2.20	0.41
1:2A:880:G:C2	1:2A:881:G:C8	3.08	0.41
1:2A:1102:C:C2	1:2A:1103:A:C8	3.09	0.41
1:2A:2115:G:H2'	1:2A:2117:A:N6	2.36	0.41
2:2B:59:A:N6	61:2B:308:HOH:O	2.40	0.41
7:2H:71:LEU:HA	7:2H:74:ASN:HD22	1.85	0.41
32:2a:331:G:N7	61:2a:3260:HOH:O	2.37	0.41
32:2a:509:A:N3	32:2a:543:C:O2'	2.46	0.41
32:2a:922:G:C6	32:2a:923:A:C6	3.09	0.41
32:2a:983:A:H2	32:2a:984:C:C6	2.38	0.41
32:2a:1108:G:H5'	34:2c:176:HIS:HD2	1.86	0.41
32:2a:1372:U:OP1	40:2i:71:SER:HB3	2.20	0.41
32:2a:1493:A:H2'	32:2a:1494:G:H5'	2.02	0.41
33:2b:168:THR:CG2	33:2b:192:SER:HA	2.51	0.41
39:2h:112:LEU:HA	39:2h:134:ILE:HG12	2.03	0.41
44:2m:107:ALA:O	44:2m:111:LYS:N	2.41	0.41
1:1A:228:A:H8	1:1A:229:A:H5'	1.85	0.41
1:1A:574:C:N3	4:1E:145:LYS:NZ	2.53	0.41
1:1A:729:G:C5	3:1D:208:LYS:HB2	2.56	0.41
1:1A:1881:C:H2'	1:1A:1882:C:H6	1.86	0.41
1:1A:1991:U:H2'	1:1A:1992:G:H5''	2.03	0.41
1:1A:2111:C:H4'	1:1A:2112:G:OP1	2.21	0.41
1:1A:2182:G:H2'	1:1A:2183:C:C6	2.56	0.41
1:1A:2572:A:N7	4:1E:145:LYS:HB2	2.35	0.41
1:1A:2712:U:H2'	1:1A:2714:G:H5''	2.03	0.41
2:1B:73:A:C4	2:1B:105:A:C2	3.09	0.41
7:1H:154:PRO:HB3	7:1H:163:TYR:CZ	2.55	0.41
8:1I:72:LEU:C	8:1I:74:ASN:H	2.29	0.41
10:1O:24:VAL:HG13	10:1O:33:ALA:HB2	2.02	0.41
14:1S:74:ALA:HA	14:1S:110:LEU:HD22	2.03	0.41
27:15:35:GLU:HG2	27:15:51:TYR:CD1	2.56	0.41
32:1a:108:G:N1	51:1t:15:ARG:HG2	2.35	0.41
32:1a:114:U:H1'	32:1a:353:A:H1'	2.02	0.41
32:1a:270:A:H2'	32:1a:271:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:404:U:H2'	32:1a:405:U:C6	2.56	0.41
32:1a:755:G:OP2	46:1o:65:ARG:HD2	2.21	0.41
32:1a:1016:A:H2'	32:1a:1017:G:O4'	2.21	0.41
32:1a:1151:A:O4'	41:1j:39:PRO:HB2	2.20	0.41
32:1a:1292:U:H5'	40:1i:38:GLN:OE1	2.20	0.41
38:1g:27:ILE:HD12	38:1g:40:ALA:HA	2.03	0.41
45:1n:40:CYS:O	45:1n:44:LEU:HB2	2.21	0.41
46:1o:18:PHE:HB2	46:1o:19:PRO:HD2	2.01	0.41
1:2A:676:A:H2	1:2A:2069:G:N3	2.18	0.41
1:2A:994:C:O2'	1:2A:996:A:OP1	2.36	0.41
1:2A:1094:U:H4'	1:2A:1096:A:N6	2.36	0.41
1:2A:1116:C:H2'	1:2A:1117:G:H8	1.86	0.41
1:2A:1139:G:OP1	9:2N:101:HIS:ND1	2.50	0.41
1:2A:1805:U:O2	3:2D:50:THR:HB	2.21	0.41
1:2A:1831:G:H2'	1:2A:1832:C:C6	2.55	0.41
1:2A:1843:C:H5'	3:2D:253:GLN:NE2	2.36	0.41
1:2A:1932:A:H2'	1:2A:1933:G:O4'	2.20	0.41
1:2A:2114:A:H2'	1:2A:2115:G:O4'	2.21	0.41
1:2A:2564:A:OP1	1:2A:2648:C:H4'	2.21	0.41
1:2A:2742:C:OP1	31:29:35:ARG:HD3	2.20	0.41
1:2A:2749:A:H1'	7:2H:63:SER:OG	2.21	0.41
3:2D:3:VAL:HG13	3:2D:17:THR:HB	2.02	0.41
3:2D:127:VAL:HA	3:2D:193:VAL:HG22	2.03	0.41
6:2G:106:LEU:HD12	6:2G:110:ALA:HB3	2.02	0.41
7:2H:3:ARG:HE	7:2H:54:ARG:NH1	2.19	0.41
7:2H:117:PRO:HG3	7:2H:123:PHE:CE2	2.56	0.41
8:2I:69:LYS:HB2	8:2I:138:ILE:HG12	2.03	0.41
32:2a:601:C:H2'	32:2a:602:A:H8	1.85	0.41
32:2a:949:A:H1'	32:2a:1364:U:H3	1.85	0.41
32:2a:997:U:H2'	32:2a:998:G:C8	2.56	0.41
32:2a:1122:U:C4	32:2a:1123:A:N7	2.88	0.41
33:2b:20:GLU:HB2	33:2b:190:THR:OG1	2.21	0.41
33:2b:50:GLU:HB3	33:2b:200:ILE:O	2.21	0.41
33:2b:167:PRO:HG3	33:2b:188:ALA:HB2	2.01	0.41
35:2d:162:LEU:HD13	35:2d:181:MET:HG2	2.02	0.41
37:2f:22:GLU:OE1	37:2f:84:ASN:HB2	2.21	0.41
42:2k:20:TYR:CE1	42:2k:83:ILE:HD12	2.56	0.41
42:2k:84:VAL:HG21	42:2k:95:ILE:HD11	2.03	0.41
48:2q:6:LEU:O	48:2q:58:GLU:HA	2.21	0.41
1:1A:621:A:OP2	11:1P:108:LYS:NZ	2.52	0.41
1:1A:1059:G:N2	1:1A:1080:C:H1'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1231:G:H2'	1:1A:1232:G:C8	2.56	0.41
1:1A:1639:U:O2'	1:1A:1640:C:H5'	2.21	0.41
1:1A:2788:C:OP1	4:1E:61:ARG:NH2	2.54	0.41
2:1B:39:A:O2'	2:1B:46:A:N1	2.46	0.41
19:1X:35:THR:HG22	19:1X:38:GLU:H	1.86	0.41
32:1a:174:C:H2'	32:1a:175:C:C6	2.56	0.41
32:1a:408:A:H2'	32:1a:409:G:O4'	2.21	0.41
38:1g:54:THR:O	38:1g:56:GLN:NE2	2.54	0.41
49:1r:58:LEU:HD23	49:1r:62:GLU:HB2	2.03	0.41
1:2A:2037:G:H2'	1:2A:2038:G:C8	2.56	0.41
1:2A:2474:C:H5''	1:2A:2475:C:OP2	2.21	0.41
4:2E:35:GLN:OE1	4:2E:66:HIS:HE1	2.03	0.41
5:2F:7:TYR:O	5:2F:22:ALA:N	2.54	0.41
21:2Z:99:TYR:HA	21:2Z:124:ILE:O	2.22	0.41
32:2a:148:G:H2'	32:2a:149:A:H8	1.86	0.41
32:2a:189(L):G:H2'	32:2a:190:U:C6	2.55	0.41
32:2a:782:A:O3'	32:2a:1515:C:H4'	2.21	0.41
32:2a:828:A:H2'	32:2a:829:G:O4'	2.20	0.41
32:2a:1058:G:H2'	32:2a:1059:C:O4'	2.20	0.41
33:2b:16:HIS:O	33:2b:17:PHE:C	2.64	0.41
34:2c:115:LEU:HD12	34:2c:115:LEU:HA	1.87	0.41
35:2d:11:LEU:O	35:2d:15:GLU:HG2	2.21	0.41
35:2d:105:VAL:HG13	35:2d:110:PHE:HB2	2.03	0.41
37:2f:61:LEU:HB3	37:2f:63:TYR:CE2	2.55	0.41
44:2m:108:ARG:HD3	44:2m:108:ARG:HA	1.76	0.41
51:2t:54:LYS:HE2	51:2t:54:LYS:HB3	1.74	0.41
1:1A:1097:U:H2'	1:1A:1098:A:O4'	2.21	0.40
1:1A:1268:A:C2	1:1A:2013:A:C4	3.09	0.40
1:1A:1791:A:H5''	1:1A:1791:A:H8	1.86	0.40
1:1A:1794:U:H2'	1:1A:1795:C:H6	1.86	0.40
1:1A:1809:A:H2'	1:1A:1810:A:C8	2.56	0.40
1:1A:2110:G:C2	1:1A:2120:G:H1'	2.55	0.40
2:1B:84:C:OP1	25:13:15:TYR:OH	2.29	0.40
7:1H:154:PRO:HB3	7:1H:163:TYR:CE1	2.56	0.40
8:1I:29:TYR:C	8:1I:32:PRO:HD2	2.46	0.40
8:1I:72:LEU:HD23	8:1I:75:LEU:HD21	2.02	0.40
9:1N:42:TRP:CE3	16:1U:63:VAL:HG11	2.55	0.40
9:1N:62:VAL:HG13	9:1N:66:LYS:HB2	2.02	0.40
31:19:13:LYS:HG3	31:19:28:GLU:OE2	2.21	0.40
32:1a:51:A:N7	32:1a:114:U:O2'	2.48	0.40
33:1b:220:ASP:O	33:1b:224:GLN:HB3	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:1h:86:ILE:HG21	39:1h:133:LEU:HD22	2.02	0.40
1:2A:106:C:H1'	20:2Y:1:MET:HG3	2.02	0.40
1:2A:576:U:H2'	1:2A:577:G:C8	2.56	0.40
1:2A:2006:C:OP2	61:2A:3862:HOH:O	2.22	0.40
1:2A:2136:C:C2	1:2A:2155:G:N2	2.87	0.40
1:2A:2267:A:H5''	1:2A:2268:A:H5'	2.02	0.40
3:2D:275:LYS:HA	3:2D:276:LYS:C	2.46	0.40
5:2F:21:ALA:CB	5:2F:22:ALA:HA	2.48	0.40
6:2G:12:TYR:HA	6:2G:16:ARG:CG	2.50	0.40
12:2Q:137:TYR:HB3	21:2Z:76:LEU:HD11	2.03	0.40
13:2R:67:LEU:HD23	13:2R:76:VAL:HG21	2.03	0.40
15:2T:127:ALA:C	15:2T:129:ARG:N	2.76	0.40
21:2Z:99:TYR:CE2	21:2Z:125:LEU:HD13	2.56	0.40
32:2a:736:C:H2'	32:2a:737:A:C8	2.56	0.40
32:2a:1329:A:P	44:2m:28:ALA:HB3	2.61	0.40
32:2a:1442:G:O2'	32:2a:1442(A):G:O5'	2.36	0.40
32:2a:1468:A:H2'	32:2a:1469:G:O4'	2.20	0.40
33:2b:178:ARG:HE	33:2b:178:ARG:HB3	1.73	0.40
41:2j:50:ILE:HB	45:2n:41:ARG:NH1	2.35	0.40
41:2j:77:PRO:O	41:2j:81:THR:OG1	2.35	0.40
1:1A:264:C:O2'	1:1A:265:A:H2'	2.21	0.40
1:1A:414:C:H2'	1:1A:415:A:C8	2.56	0.40
1:1A:1418:G:O5'	1:1A:1418:G:H8	2.04	0.40
1:1A:2157:G:H5''	1:1A:2158:A:OP1	2.22	0.40
1:1A:2319:G:C2	14:1S:3:ARG:HA	2.56	0.40
3:1D:4:LYS:HB3	3:1D:4:LYS:HE2	1.77	0.40
3:1D:182:LEU:HD23	3:1D:182:LEU:HA	1.91	0.40
4:1E:146:THR:HA	4:1E:147:PRO:HA	1.87	0.40
5:1F:12:LEU:HD12	5:1F:12:LEU:HA	1.82	0.40
32:1a:306:G:H2'	32:1a:307:C:H6	1.86	0.40
32:1a:501:C:H2'	32:1a:502:G:C8	2.56	0.40
32:1a:600:C:H4'	39:1h:128:GLY:O	2.22	0.40
32:1a:648:A:H2'	32:1a:649:G:H8	1.86	0.40
32:1a:689:C:H2'	32:1a:690:G:O4'	2.21	0.40
32:1a:1263:C:H2'	32:1a:1264:C:C6	2.56	0.40
49:1r:40:LEU:HB3	49:1r:79:LEU:HD11	2.02	0.40
49:1r:47:THR:CG2	49:1r:49:LYS:HG3	2.51	0.40
50:1s:15:LEU:O	50:1s:19:VAL:HG23	2.21	0.40
1:2A:652(D):C:H42	1:2A:652(U):G:H1	1.69	0.40
1:2A:700:G:O2'	1:2A:1632:A:N3	2.46	0.40
1:2A:1066:U:O2'	1:2A:1068:G:OP2	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2A:1239:G:H2'	1:2A:1240:U:O4'	2.22	0.40
1:2A:2472:G:H2'	1:2A:2475:C:H42	1.84	0.40
1:2A:2506:U:O2	55:2A:3743:HGR:H23	2.22	0.40
1:2A:2820:A:P	13:2R:2:ARG:HH22	2.44	0.40
7:2H:125:VAL:HG13	7:2H:125:VAL:O	2.22	0.40
11:2P:121:LYS:O	11:2P:123:LEU:N	2.54	0.40
22:20:36:ILE:HD13	22:20:58:THR:HG21	2.03	0.40
32:2a:54:C:H2'	32:2a:352:C:H41	1.86	0.40
32:2a:401:C:P	35:2d:73:ARG:HH21	2.44	0.40
32:2a:583:A:H2'	32:2a:584:G:O4'	2.21	0.40
32:2a:707:C:H2'	32:2a:708:C:C6	2.55	0.40
32:2a:942:G:C2	32:2a:1342:C:C2	3.09	0.40
33:2b:125:PRO:O	33:2b:127:ILE:N	2.54	0.40
34:2c:3:ASN:HB2	34:2c:4:LYS:H	1.73	0.40
35:2d:103:ASN:OD1	35:2d:114:ARG:NE	2.40	0.40
38:2g:15:ASP:OD1	38:2g:20:ASP:N	2.45	0.40
41:2j:66:ARG:HH21	41:2j:68:HIS:CE1	2.39	0.40
50:2s:51:VAL:O	50:2s:57:HIS:HA	2.21	0.40
53:2y:85:LEU:O	53:2y:89:GLN:HG2	2.21	0.40
1:1A:400:G:O6	61:1A:4143:HOH:O	2.22	0.40
1:1A:667:U:O2	30:18:2:PRO:HD2	2.22	0.40
1:1A:1071:G:O2'	1:1A:1089:G:H2'	2.22	0.40
1:1A:2108:C:O2	1:1A:2182:G:N2	2.54	0.40
1:1A:2846:G:H2'	1:1A:2847:U:O4'	2.22	0.40
57:1A:4022:MPD:HM2	57:1A:4022:MPD:H4	1.64	0.40
8:1I:72:LEU:O	8:1I:73:GLU:HB2	2.21	0.40
24:12:31:GLU:HB3	24:12:53:LEU:HD11	2.02	0.40
32:1a:437:U:O2'	35:1d:123:HIS:HD2	2.04	0.40
32:1a:500:G:H2'	32:1a:501:C:C6	2.57	0.40
32:1a:607:A:H2'	32:1a:608:A:H8	1.86	0.40
32:1a:1223:C:H3'	32:1a:1224:G:H5''	2.02	0.40
34:1c:124:ILE:H	34:1c:124:ILE:HG12	1.74	0.40
38:1g:111:ARG:HB2	38:1g:119:ARG:HD2	2.04	0.40
40:1i:106:ALA:O	40:1i:108:VAL:HG23	2.21	0.40
1:2A:191:A:H2'	1:2A:192:C:C6	2.56	0.40
1:2A:361:G:O2'	1:2A:362:U:H5'	2.21	0.40
1:2A:2321:G:HO2'	1:2A:2322:A:P	2.42	0.40
1:2A:2690:C:OP1	13:2R:17:ARG:NH2	2.49	0.40
1:2A:2774:C:H2'	1:2A:2775:A:O4'	2.21	0.40
6:2G:120:LEU:HD22	6:2G:133:LEU:HD13	2.04	0.40
10:2O:36:GLY:HA2	10:2O:106:LEU:HD23	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:2R:56:LYS:NZ	13:2R:90:ARG:O	2.55	0.40
15:2T:16:ARG:HD2	15:2T:79:HIS:HA	2.02	0.40
23:21:67:ILE:N	23:21:68:PRO:HD2	2.37	0.40
32:2a:109:A:H2'	32:2a:326:G:N2	2.36	0.40
32:2a:188:C:O4'	51:2t:89:ARG:NH2	2.52	0.40
32:2a:547:A:H5'	61:2a:3216:HOH:O	2.21	0.40
32:2a:1128:C:H1'	32:2a:1147:C:N4	2.31	0.40
32:2a:1387:G:H2'	32:2a:1388:C:H6	1.86	0.40
41:2j:44:VAL:HG22	41:2j:66:ARG:HG2	2.04	0.40
46:2o:17:ARG:HD3	46:2o:77:ARG:NH2	2.36	0.40
1:1A:118:A:N3	1:1A:178:G:H1'	2.36	0.40
1:1A:196:A:N3	1:1A:196:A:H2'	2.37	0.40
1:1A:484:C:H2'	1:1A:485:C:C6	2.57	0.40
1:1A:1021:A:N3	1:1A:1021:A:H3'	2.37	0.40
6:1G:109:VAL:C	6:1G:112:PRO:HD2	2.47	0.40
13:1R:29:LEU:HD12	13:1R:29:LEU:HA	1.89	0.40
32:1a:22:G:H4'	32:1a:885:G:C8	2.56	0.40
32:1a:718:G:H5'	42:1k:117:ASN:HB2	2.02	0.40
47:1p:49:LEU:HD13	47:1p:50:LYS:N	2.35	0.40
48:1q:62:SER:HB3	48:1q:72:ARG:HH11	1.86	0.40
1:2A:1900:A:N1	1:2A:1970:A:C6	2.89	0.40
1:2A:2065:C:H2'	1:2A:2066:C:C6	2.55	0.40
1:2A:2136:C:C6	1:2A:2136:C:OP2	2.75	0.40
2:2B:75:G:O2'	21:2Z:85:HIS:NE2	2.47	0.40
3:2D:275:LYS:HA	3:2D:275:LYS:HD2	1.96	0.40
5:2F:176:LEU:HD23	5:2F:176:LEU:HA	1.93	0.40
8:2I:93:THR:HG22	8:2I:119:PRO:HB3	2.02	0.40
17:2V:49:THR:O	17:2V:49:THR:OG1	2.26	0.40
18:2W:88:ARG:NH1	18:2W:94:ASP:OD2	2.55	0.40
32:2a:1034:G:H3'	32:2a:1035:A:C8	2.57	0.40
32:2a:1130:A:H5'	40:2i:18:PHE:CE2	2.57	0.40
32:2a:1324:A:O4'	32:2a:1362:C:H4'	2.20	0.40
33:2b:43:ASP:O	33:2b:47:THR:HG23	2.21	0.40
33:2b:47:THR:HA	33:2b:202:PRO:HG2	2.03	0.40
33:2b:158:LEU:HD12	33:2b:158:LEU:HA	1.93	0.40
35:2d:196:LEU:HD12	35:2d:196:LEU:H	1.86	0.40
38:2g:23:VAL:O	38:2g:27:ILE:HG13	2.21	0.40
41:2j:61:GLU:OE2	45:2n:58:LYS:NZ	2.50	0.40
1:1A:127:A:H5''	1:1A:128:C:C6	2.56	0.40
1:1A:362:U:H6	1:1A:362:U:H2'	1.70	0.40
1:1A:784:A:H5'	1:1A:785:G:OP1	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1170:G:N2	1:1A:1180:C:C2	2.89	0.40
1:1A:1864:U:OP1	1:1A:2410:G:O2'	2.35	0.40
1:1A:2550:G:OP1	61:1A:4117:HOH:O	2.22	0.40
1:1A:2881:C:H2'	1:1A:2882:A:O4'	2.21	0.40
2:1B:114:C:O5'	2:1B:114:C:H6	2.04	0.40
5:1F:34:TRP:NE1	11:1P:8:PRO:HD3	2.37	0.40
28:16:44:ARG:HG2	28:16:44:ARG:HH11	1.85	0.40
30:18:42:ARG:HD2	61:18:201:HOH:O	2.21	0.40
32:1a:193:C:H2'	32:1a:194:C:H6	1.87	0.40
32:1a:954:G:C2	32:1a:955:U:C2	3.10	0.40
33:1b:48:MET:HA	33:1b:48:MET:HE2	2.03	0.40
33:1b:74:LYS:HE3	33:1b:166:ASP:HB2	2.03	0.40
33:1b:100:GLY:N	33:1b:176:GLU:OE2	2.32	0.40
38:1g:106:GLN:O	38:1g:110:GLN:HG2	2.21	0.40
43:1l:34:ARG:O	43:1l:61:THR:HG23	2.22	0.40
44:1m:20:THR:C	44:1m:22:ILE:H	2.30	0.40
1:2A:105:C:H2'	1:2A:106:C:C6	2.56	0.40
1:2A:856:C:HO2'	1:2A:857:C:P	2.43	0.40
1:2A:1916:A:H2'	1:2A:1917:PSU:O4'	2.22	0.40
1:2A:2752:C:OP2	7:2H:4:ILE:HD11	2.22	0.40
6:2G:7:LEU:HD23	6:2G:100:TRP:HE3	1.87	0.40
18:2W:80:PRO:O	18:2W:100:THR:HB	2.21	0.40
19:2X:44:GLU:HG3	19:2X:51:VAL:HG23	2.03	0.40
32:2a:625:G:H2'	32:2a:626:U:H6	1.86	0.40
32:2a:662:G:O2'	32:2a:836:G:OP1	2.40	0.40
32:2a:1118:C:H1'	32:2a:1179:A:C4	2.56	0.40
32:2a:1226:C:H3'	44:2m:96:LEU:HD21	2.03	0.40
32:2a:1243:C:N4	61:2a:3250:HOH:O	2.53	0.40
32:2a:1366:C:H2'	32:2a:1367:C:C6	2.56	0.40
33:2b:16:HIS:CB	33:2b:210:SER:HB3	2.52	0.40
33:2b:204:ASN:HB3	33:2b:210:SER:HB3	2.03	0.40
34:2c:71:ALA:O	34:2c:73:PRO:HD3	2.21	0.40
44:2m:65:LYS:HA	44:2m:65:LYS:HD3	1.94	0.40
49:2r:26:LEU:HD11	49:2r:42:ARG:HD3	2.04	0.40
50:2s:81:ARG:HB2	50:2s:81:ARG:NH1	2.36	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:1a:1042:G:O2'	1:2A:2138:C:OP1[2_655]	2.17	0.03

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	
3	1D	273/276 (99%)	262 (96%)	11 (4%)	0	100	100
3	2D	273/276 (99%)	259 (95%)	14 (5%)	0	100	100
4	1E	202/206 (98%)	191 (95%)	9 (4%)	2 (1%)	12	12
4	2E	202/206 (98%)	192 (95%)	8 (4%)	2 (1%)	12	12
5	1F	201/210 (96%)	195 (97%)	5 (2%)	1 (0%)	24	27
5	2F	201/210 (96%)	196 (98%)	4 (2%)	1 (0%)	24	27
6	1G	179/182 (98%)	163 (91%)	12 (7%)	4 (2%)	5	3
6	2G	179/182 (98%)	158 (88%)	18 (10%)	3 (2%)	7	6
7	1H	172/180 (96%)	163 (95%)	8 (5%)	1 (1%)	21	24
7	2H	171/180 (95%)	154 (90%)	15 (9%)	2 (1%)	10	9
8	1I	145/148 (98%)	133 (92%)	12 (8%)	0	100	100
8	2I	144/148 (97%)	129 (90%)	14 (10%)	1 (1%)	18	20
9	1N	138/140 (99%)	135 (98%)	3 (2%)	0	100	100
9	2N	138/140 (99%)	131 (95%)	6 (4%)	1 (1%)	18	20
10	1O	120/122 (98%)	115 (96%)	4 (3%)	1 (1%)	16	17
10	2O	120/122 (98%)	113 (94%)	6 (5%)	1 (1%)	16	17
11	1P	147/150 (98%)	139 (95%)	8 (5%)	0	100	100
11	2P	147/150 (98%)	139 (95%)	6 (4%)	2 (1%)	9	7
12	1Q	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	18	20
12	2Q	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
13	1R	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
13	2R	116/118 (98%)	112 (97%)	4 (3%)	0	100	100
14	1S	108/112 (96%)	101 (94%)	7 (6%)	0	100	100
14	2S	108/112 (96%)	100 (93%)	8 (7%)	0	100	100
15	1T	129/146 (88%)	124 (96%)	4 (3%)	1 (1%)	16	17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	2T	129/146 (88%)	122 (95%)	7 (5%)	0	100	100
16	1U	114/118 (97%)	114 (100%)	0	0	100	100
16	2U	114/118 (97%)	114 (100%)	0	0	100	100
17	1V	99/101 (98%)	96 (97%)	3 (3%)	0	100	100
17	2V	99/101 (98%)	92 (93%)	6 (6%)	1 (1%)	12	12
18	1W	110/113 (97%)	110 (100%)	0	0	100	100
18	2W	110/113 (97%)	109 (99%)	1 (1%)	0	100	100
19	1X	93/96 (97%)	92 (99%)	0	1 (1%)	11	11
19	2X	93/96 (97%)	90 (97%)	2 (2%)	1 (1%)	11	11
20	1Y	105/110 (96%)	99 (94%)	6 (6%)	0	100	100
20	2Y	105/110 (96%)	97 (92%)	8 (8%)	0	100	100
21	1Z	201/206 (98%)	189 (94%)	11 (6%)	1 (0%)	24	27
21	2Z	199/206 (97%)	181 (91%)	17 (8%)	1 (0%)	24	27
22	10	75/85 (88%)	72 (96%)	3 (4%)	0	100	100
22	20	75/85 (88%)	73 (97%)	2 (3%)	0	100	100
23	11	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	11	11
23	21	95/98 (97%)	92 (97%)	2 (2%)	1 (1%)	11	11
24	12	68/72 (94%)	67 (98%)	1 (2%)	0	100	100
24	22	68/72 (94%)	64 (94%)	4 (6%)	0	100	100
25	13	57/60 (95%)	56 (98%)	1 (2%)	0	100	100
25	23	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
26	14	67/71 (94%)	50 (75%)	14 (21%)	3 (4%)	2	1
26	24	67/71 (94%)	44 (66%)	19 (28%)	4 (6%)	1	0
27	15	57/60 (95%)	57 (100%)	0	0	100	100
27	25	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
28	16	51/54 (94%)	49 (96%)	2 (4%)	0	100	100
28	26	51/54 (94%)	48 (94%)	3 (6%)	0	100	100
29	17	46/49 (94%)	46 (100%)	0	0	100	100
29	27	46/49 (94%)	46 (100%)	0	0	100	100
30	18	62/65 (95%)	62 (100%)	0	0	100	100
30	28	62/65 (95%)	62 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	19	35/37 (95%)	35 (100%)	0	0	100	100
31	29	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
33	1b	229/256 (90%)	192 (84%)	27 (12%)	10 (4%)	2	1
33	2b	229/256 (90%)	199 (87%)	21 (9%)	9 (4%)	2	1
34	1c	204/239 (85%)	186 (91%)	17 (8%)	1 (0%)	24	27
34	2c	204/239 (85%)	173 (85%)	28 (14%)	3 (2%)	8	7
35	1d	206/209 (99%)	192 (93%)	14 (7%)	0	100	100
35	2d	206/209 (99%)	191 (93%)	14 (7%)	1 (0%)	24	27
36	1e	146/162 (90%)	138 (94%)	8 (6%)	0	100	100
36	2e	146/162 (90%)	142 (97%)	4 (3%)	0	100	100
37	1f	98/101 (97%)	95 (97%)	3 (3%)	0	100	100
37	2f	98/101 (97%)	95 (97%)	3 (3%)	0	100	100
38	1g	153/156 (98%)	149 (97%)	4 (3%)	0	100	100
38	2g	153/156 (98%)	144 (94%)	7 (5%)	2 (1%)	9	8
39	1h	135/138 (98%)	127 (94%)	8 (6%)	0	100	100
39	2h	135/138 (98%)	127 (94%)	8 (6%)	0	100	100
40	1i	125/128 (98%)	110 (88%)	14 (11%)	1 (1%)	16	17
40	2i	124/128 (97%)	105 (85%)	15 (12%)	4 (3%)	3	2
41	1j	95/105 (90%)	82 (86%)	9 (10%)	4 (4%)	2	1
41	2j	94/105 (90%)	79 (84%)	11 (12%)	4 (4%)	2	1
42	1k	112/129 (87%)	106 (95%)	5 (4%)	1 (1%)	14	14
42	2k	112/129 (87%)	104 (93%)	8 (7%)	0	100	100
43	1l	119/132 (90%)	115 (97%)	4 (3%)	0	100	100
43	2l	119/132 (90%)	114 (96%)	5 (4%)	0	100	100
44	1m	114/126 (90%)	103 (90%)	8 (7%)	3 (3%)	4	2
44	2m	112/126 (89%)	97 (87%)	13 (12%)	2 (2%)	6	5
45	1n	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
45	2n	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
46	1o	86/89 (97%)	83 (96%)	2 (2%)	1 (1%)	10	9
46	2o	86/89 (97%)	82 (95%)	2 (2%)	2 (2%)	5	3
47	1p	80/88 (91%)	71 (89%)	9 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	2p	80/88 (91%)	69 (86%)	11 (14%)	0	100	100
48	1q	97/105 (92%)	89 (92%)	7 (7%)	1 (1%)	12	12
48	2q	97/105 (92%)	90 (93%)	6 (6%)	1 (1%)	12	12
49	1r	66/88 (75%)	64 (97%)	2 (3%)	0	100	100
49	2r	66/88 (75%)	65 (98%)	1 (2%)	0	100	100
50	1s	81/93 (87%)	74 (91%)	6 (7%)	1 (1%)	10	9
50	2s	81/93 (87%)	70 (86%)	11 (14%)	0	100	100
51	1t	94/106 (89%)	87 (93%)	3 (3%)	4 (4%)	2	1
51	2t	96/106 (91%)	91 (95%)	1 (1%)	4 (4%)	2	1
52	1u	21/27 (78%)	20 (95%)	1 (5%)	0	100	100
52	2u	21/27 (78%)	18 (86%)	2 (10%)	1 (5%)	2	0
53	1y	95/113 (84%)	94 (99%)	1 (1%)	0	100	100
53	2y	94/113 (83%)	91 (97%)	3 (3%)	0	100	100
All	All	11629/12354 (94%)	10880 (94%)	651 (6%)	98 (1%)	16	17

All (98) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1F	130	ALA
6	1G	47	LYS
6	1G	50	ALA
26	14	57	GLU
33	1b	21	ARG
33	1b	124	SER
33	1b	127	ILE
33	1b	231	GLU
41	1j	55	LYS
44	1m	67	GLU
4	2E	71	GLY
6	2G	81	LYS
7	2H	126	PRO
8	2I	10	GLU
19	2X	94	GLY
26	24	63	TYR
40	2i	43	ALA
40	2i	55	ALA
46	2o	88	ARG

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Mol	Chain	Res	Type
4	1E	71	GLY
6	1G	51	ARG
33	1b	8	LYS
33	1b	17	PHE
34	1c	107	GLN
40	1i	11	LYS
41	1j	82	ILE
44	1m	3	ARG
46	1o	19	PRO
48	1q	68	ARG
51	1t	47	GLY
51	1t	99	LEU
51	1t	100	ILE
23	21	3	LYS
26	24	45	GLY
26	24	62	ARG
40	2i	54	ASP
48	2q	68	ARG
51	2t	47	GLY
51	2t	100	ILE
10	1O	5	GLN
12	1Q	59	ARG
19	1X	94	GLY
21	1Z	52	SER
23	11	3	LYS
26	14	49	PHE
33	1b	126	GLU
41	1j	77	PRO
50	1s	27	GLU
5	2F	130	ALA
7	2H	65	HIS
10	2O	5	GLN
17	2V	79	VAL
33	2b	17	PHE
33	2b	22	LYS
33	2b	190	THR
38	2g	4	ARG
38	2g	55	GLY
41	2j	78	ASN
41	2j	79	ARG
46	2o	19	PRO
4	1E	52	LEU

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Mol	Chain	Res	Type
15	1T	55	ASN
33	1b	20	GLU
33	1b	36	ARG
33	1b	228	GLY
41	1j	78	ASN
51	1t	95	ALA
4	2E	52	LEU
6	2G	78	SER
11	2P	29	LYS
26	24	55	ARG
33	2b	95	GLN
34	2c	4	LYS
34	2c	18	TRP
41	2j	55	LYS
41	2j	75	ILE
26	14	61	ARG
42	1k	100	ALA
11	2P	122	PRO
21	2Z	104	PHE
33	2b	20	GLU
33	2b	165	VAL
40	2i	96	LEU
44	2m	67	GLU
51	2t	95	ALA
7	1H	126	PRO
44	1m	12	ASN
33	2b	16	HIS
33	2b	126	GLU
44	2m	80	ARG
52	2u	7	ARG
51	2t	102	GLY
35	2d	167	GLY
6	1G	44	GLY
6	2G	42	GLY
9	2N	129	PRO
33	2b	125	PRO
34	2c	81	GLY

5.3.2 Protein sidechains

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	
3	1D	214/218 (98%)	195 (91%)	19 (9%)	9	10
3	2D	215/218 (99%)	197 (92%)	18 (8%)	10	11
4	1E	164/166 (99%)	152 (93%)	12 (7%)	13	14
4	2E	164/166 (99%)	156 (95%)	8 (5%)	22	28
5	1F	160/166 (96%)	148 (92%)	12 (8%)	12	13
5	2F	159/166 (96%)	144 (91%)	15 (9%)	8	8
6	1G	144/156 (92%)	127 (88%)	17 (12%)	5	5
6	2G	142/156 (91%)	129 (91%)	13 (9%)	8	9
7	1H	144/148 (97%)	137 (95%)	7 (5%)	22	28
7	2H	143/148 (97%)	126 (88%)	17 (12%)	5	4
8	1I	111/124 (90%)	96 (86%)	15 (14%)	4	3
8	2I	108/124 (87%)	98 (91%)	10 (9%)	8	8
9	1N	119/119 (100%)	113 (95%)	6 (5%)	22	27
9	2N	118/119 (99%)	109 (92%)	9 (8%)	12	13
10	1O	100/100 (100%)	100 (100%)	0	100	100
10	2O	100/100 (100%)	96 (96%)	4 (4%)	28	37
11	1P	115/116 (99%)	106 (92%)	9 (8%)	11	12
11	2P	115/116 (99%)	110 (96%)	5 (4%)	26	34
12	1Q	111/111 (100%)	106 (96%)	5 (4%)	24	32
12	2Q	111/111 (100%)	103 (93%)	8 (7%)	13	14
13	1R	101/101 (100%)	97 (96%)	4 (4%)	28	37
13	2R	101/101 (100%)	92 (91%)	9 (9%)	9	10
14	1S	87/88 (99%)	77 (88%)	10 (12%)	5	5
14	2S	85/88 (97%)	77 (91%)	8 (9%)	8	8
15	1T	115/127 (91%)	108 (94%)	7 (6%)	17	20
15	2T	113/127 (89%)	105 (93%)	8 (7%)	13	15
16	1U	93/94 (99%)	89 (96%)	4 (4%)	26	34
16	2U	93/94 (99%)	88 (95%)	5 (5%)	20	24
17	1V	81/82 (99%)	77 (95%)	4 (5%)	22	28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	2V	80/82 (98%)	72 (90%)	8 (10%)	7	7
18	1W	90/92 (98%)	84 (93%)	6 (7%)	15	17
18	2W	90/92 (98%)	85 (94%)	5 (6%)	19	23
19	1X	77/78 (99%)	74 (96%)	3 (4%)	28	39
19	2X	77/78 (99%)	76 (99%)	1 (1%)	61	76
20	1Y	86/91 (94%)	76 (88%)	10 (12%)	5	5
20	2Y	86/91 (94%)	80 (93%)	6 (7%)	14	15
21	1Z	169/179 (94%)	152 (90%)	17 (10%)	7	6
21	2Z	165/179 (92%)	150 (91%)	15 (9%)	9	9
22	10	61/67 (91%)	61 (100%)	0	100	100
22	20	61/67 (91%)	59 (97%)	2 (3%)	33	44
23	11	79/83 (95%)	74 (94%)	5 (6%)	16	19
23	21	81/83 (98%)	74 (91%)	7 (9%)	10	10
24	12	65/67 (97%)	59 (91%)	6 (9%)	8	9
24	22	66/67 (98%)	62 (94%)	4 (6%)	17	20
25	13	51/52 (98%)	47 (92%)	4 (8%)	11	12
25	23	50/52 (96%)	48 (96%)	2 (4%)	28	37
26	14	58/63 (92%)	50 (86%)	8 (14%)	3	3
26	24	54/63 (86%)	47 (87%)	7 (13%)	4	4
27	15	51/52 (98%)	46 (90%)	5 (10%)	7	7
27	25	50/52 (96%)	49 (98%)	1 (2%)	48	63
28	16	51/52 (98%)	46 (90%)	5 (10%)	7	7
28	26	50/52 (96%)	49 (98%)	1 (2%)	48	63
29	17	41/42 (98%)	39 (95%)	2 (5%)	22	28
29	27	41/42 (98%)	38 (93%)	3 (7%)	13	14
30	18	54/55 (98%)	50 (93%)	4 (7%)	13	14
30	28	54/55 (98%)	52 (96%)	2 (4%)	30	40
31	19	34/34 (100%)	33 (97%)	1 (3%)	37	49
31	29	34/34 (100%)	32 (94%)	2 (6%)	18	22
33	1b	191/220 (87%)	164 (86%)	27 (14%)	3	3
33	2b	187/220 (85%)	162 (87%)	25 (13%)	4	3

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	1c	144/188 (77%)	137 (95%)	7 (5%)	22	28
34	2c	140/188 (74%)	120 (86%)	20 (14%)	3	3
35	1d	171/181 (94%)	159 (93%)	12 (7%)	14	15
35	2d	172/181 (95%)	158 (92%)	14 (8%)	11	12
36	1e	114/123 (93%)	105 (92%)	9 (8%)	11	12
36	2e	114/123 (93%)	106 (93%)	8 (7%)	14	15
37	1f	85/90 (94%)	79 (93%)	6 (7%)	13	15
37	2f	85/90 (94%)	77 (91%)	8 (9%)	8	8
38	1g	120/127 (94%)	111 (92%)	9 (8%)	12	13
38	2g	119/127 (94%)	107 (90%)	12 (10%)	7	6
39	1h	116/119 (98%)	109 (94%)	7 (6%)	17	21
39	2h	114/119 (96%)	100 (88%)	14 (12%)	4	4
40	1i	91/99 (92%)	87 (96%)	4 (4%)	25	33
40	2i	88/99 (89%)	78 (89%)	10 (11%)	5	5
41	1j	68/92 (74%)	63 (93%)	5 (7%)	13	14
41	2j	68/92 (74%)	61 (90%)	7 (10%)	7	6
42	1k	83/99 (84%)	80 (96%)	3 (4%)	31	41
42	2k	83/99 (84%)	80 (96%)	3 (4%)	31	41
43	1l	96/108 (89%)	95 (99%)	1 (1%)	68	81
43	2l	96/108 (89%)	89 (93%)	7 (7%)	13	14
44	1m	90/101 (89%)	85 (94%)	5 (6%)	19	23
44	2m	87/101 (86%)	79 (91%)	8 (9%)	8	9
45	1n	49/50 (98%)	45 (92%)	4 (8%)	10	11
45	2n	49/50 (98%)	44 (90%)	5 (10%)	7	6
46	1o	78/80 (98%)	77 (99%)	1 (1%)	61	76
46	2o	78/80 (98%)	71 (91%)	7 (9%)	9	9
47	1p	69/74 (93%)	59 (86%)	10 (14%)	3	2
47	2p	68/74 (92%)	58 (85%)	10 (15%)	3	2
48	1q	94/97 (97%)	91 (97%)	3 (3%)	34	46
48	2q	94/97 (97%)	90 (96%)	4 (4%)	26	34
49	1r	59/77 (77%)	56 (95%)	3 (5%)	21	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	2r	59/77 (77%)	56 (95%)	3 (5%)	21	26
50	1s	68/80 (85%)	63 (93%)	5 (7%)	13	14
50	2s	67/80 (84%)	60 (90%)	7 (10%)	7	6
51	1t	71/82 (87%)	68 (96%)	3 (4%)	26	35
51	2t	70/82 (85%)	64 (91%)	6 (9%)	10	10
52	1u	18/22 (82%)	18 (100%)	0	100	100
52	2u	18/22 (82%)	16 (89%)	2 (11%)	6	5
53	1y	82/98 (84%)	79 (96%)	3 (4%)	30	40
53	2y	79/98 (81%)	70 (89%)	9 (11%)	5	5
All	All	9524/10260 (93%)	8798 (92%)	726 (8%)	12	13

All (726) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	1D	4	LYS
3	1D	37	LEU
3	1D	39	LYS
3	1D	61	LEU
3	1D	99	ASP
3	1D	103	ARG
3	1D	111	LEU
3	1D	113	VAL
3	1D	126	GLN
3	1D	141	VAL
3	1D	142	VAL
3	1D	155	LEU
3	1D	183	ARG
3	1D	193	VAL
3	1D	211	ARG
3	1D	221	VAL
3	1D	229	VAL
3	1D	242	ARG
3	1D	259	THR
4	1E	9	VAL
4	1E	12	THR
4	1E	41	LYS
4	1E	72	VAL
4	1E	73	GLU
4	1E	75	VAL

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Mol	Chain	Res	Type
4	1E	116	VAL
4	1E	170	LEU
4	1E	181	LEU
4	1E	184	VAL
4	1E	188	VAL
4	1E	202	LYS
5	1F	12	LEU
5	1F	53	THR
5	1F	57	VAL
5	1F	88	VAL
5	1F	110	LEU
5	1F	132	VAL
5	1F	157	VAL
5	1F	161	GLU
5	1F	170	LEU
5	1F	183	VAL
5	1F	192	LEU
5	1F	197	ASP
6	1G	5	VAL
6	1G	7	LEU
6	1G	28	VAL
6	1G	31	VAL
6	1G	43	LEU
6	1G	45	GLU
6	1G	47	LYS
6	1G	52	ILE
6	1G	53	LEU
6	1G	79	ASN
6	1G	82	LEU
6	1G	84	LYS
6	1G	86	MET
6	1G	126	ASP
6	1G	133	LEU
6	1G	153	ARG
6	1G	161	THR
7	1H	4	ILE
7	1H	15	VAL
7	1H	24	VAL
7	1H	81	GLU
7	1H	105	LEU
7	1H	119	GLU
7	1H	122	THR

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Mol	Chain	Res	Type
8	1I	5	LEU
8	1I	12	LEU
8	1I	20	ASP
8	1I	38	LEU
8	1I	44	LEU
8	1I	61	ARG
8	1I	64	GLU
8	1I	74	ASN
8	1I	78	THR
8	1I	85	GLU
8	1I	92	VAL
8	1I	101	LEU
8	1I	109	ILE
8	1I	127	VAL
8	1I	140	LEU
9	1N	33	LEU
9	1N	48	MET
9	1N	62	VAL
9	1N	73	THR
9	1N	85	ILE
9	1N	87	LEU
11	1P	1	MET
11	1P	2	LYS
11	1P	3	LEU
11	1P	71	VAL
11	1P	90	ARG
11	1P	95	VAL
11	1P	99	LEU
11	1P	125	VAL
11	1P	148	LEU
12	1Q	7	MET
12	1Q	42	ILE
12	1Q	55	VAL
12	1Q	75	THR
12	1Q	109	VAL
13	1R	29	LEU
13	1R	33	ARG
13	1R	44	LEU
13	1R	114	VAL
14	1S	14	VAL
14	1S	43	GLU
14	1S	48	LEU

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Mol	Chain	Res	Type
14	1S	52	SER
14	1S	59	LYS
14	1S	69	VAL
14	1S	75	GLU
14	1S	78	LEU
14	1S	85	VAL
14	1S	110	LEU
15	1T	28	VAL
15	1T	34	VAL
15	1T	36	GLU
15	1T	39	ARG
15	1T	53	ARG
15	1T	59	THR
15	1T	96	ARG
16	1U	27	LEU
16	1U	59	ARG
16	1U	74	LEU
16	1U	104	GLN
17	1V	51	VAL
17	1V	61	VAL
17	1V	62	LEU
17	1V	79	VAL
18	1W	11	ARG
18	1W	15	ARG
18	1W	17	VAL
18	1W	23	LEU
18	1W	49	LYS
18	1W	63	ASP
19	1X	35	THR
19	1X	45	THR
19	1X	72	LYS
20	1Y	7	VAL
20	1Y	23	ARG
20	1Y	38	ILE
20	1Y	43	ASN
20	1Y	64	GLU
20	1Y	72	VAL
20	1Y	85	VAL
20	1Y	92	ASN
20	1Y	101	LYS
20	1Y	107	ASP
21	1Z	31	ARG

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Mol	Chain	Res	Type
21	1Z	86	VAL
21	1Z	93	ASP
21	1Z	126	VAL
21	1Z	145	GLU
21	1Z	149	SER
21	1Z	150	LEU
21	1Z	155	LEU
21	1Z	156	LYS
21	1Z	161	VAL
21	1Z	163	LEU
21	1Z	165	VAL
21	1Z	170	THR
21	1Z	185	GLU
21	1Z	191	VAL
21	1Z	202	GLU
21	1Z	203	GLU
23	11	21	ARG
23	11	30	VAL
23	11	40	ARG
23	11	51	VAL
23	11	80	LEU
24	12	1	MET
24	12	19	VAL
24	12	27	GLU
24	12	30	ARG
24	12	53	LEU
24	12	70	GLN
25	13	23	LEU
25	13	54	VAL
25	13	56	VAL
25	13	58	VAL
26	14	23	GLU
26	14	27	THR
26	14	31	ILE
26	14	47	GLN
26	14	49	PHE
26	14	50	VAL
26	14	53	GLU
26	14	56	VAL
27	15	6	VAL
27	15	40	LYS
27	15	55	ARG

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Mol	Chain	Res	Type
27	15	58	LEU
27	15	60	VAL
28	16	6	ARG
28	16	14	THR
28	16	35	GLU
28	16	47	THR
28	16	52	VAL
29	17	24	THR
29	17	46	VAL
30	18	14	VAL
30	18	23	VAL
30	18	29	LYS
30	18	30	ARG
31	19	4	ARG
33	1b	7	VAL
33	1b	9	GLU
33	1b	10	LEU
33	1b	15	VAL
33	1b	32	ILE
33	1b	41	ILE
33	1b	44	LEU
33	1b	48	MET
33	1b	51	LEU
33	1b	71	VAL
33	1b	80	ILE
33	1b	107	THR
33	1b	111	ARG
33	1b	112	VAL
33	1b	117	GLU
33	1b	122	PHE
33	1b	124	SER
33	1b	134	GLU
33	1b	158	LEU
33	1b	160	ASP
33	1b	185	ILE
33	1b	189	ASP
33	1b	196	LEU
33	1b	208	ILE
33	1b	224	GLN
33	1b	229	VAL
33	1b	230	VAL
34	1c	26	LYS

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Mol	Chain	Res	Type
34	1c	70	VAL
34	1c	98	ASN
34	1c	105	GLU
34	1c	124	ILE
34	1c	132	ARG
34	1c	178	LEU
35	1d	8	VAL
35	1d	83	SER
35	1d	85	LYS
35	1d	135	LEU
35	1d	166	LYS
35	1d	168	ARG
35	1d	177	ASP
35	1d	178	VAL
35	1d	179	GLU
35	1d	190	ASP
35	1d	194	LEU
35	1d	196	LEU
36	1e	10	MET
36	1e	31	LEU
36	1e	64	ARG
36	1e	67	VAL
36	1e	69	VAL
36	1e	75	THR
36	1e	79	GLU
36	1e	101	ILE
36	1e	147	ASP
37	1f	40	VAL
37	1f	54	LYS
37	1f	69	GLU
37	1f	72	VAL
37	1f	86	ARG
37	1f	91	VAL
38	1g	13	GLN
38	1g	27	ILE
38	1g	32	ARG
38	1g	45	ASP
38	1g	51	GLN
38	1g	97	GLN
38	1g	104	LEU
38	1g	113	GLU
38	1g	138	LYS

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Mol	Chain	Res	Type
39	1h	24	THR
39	1h	26	VAL
39	1h	38	ILE
39	1h	63	LEU
39	1h	105	ARG
39	1h	127	LEU
39	1h	137	VAL
40	1i	47	LEU
40	1i	64	THR
40	1i	65	VAL
40	1i	81	ILE
41	1j	34	VAL
41	1j	38	ILE
41	1j	46	ARG
41	1j	92	THR
41	1j	100	THR
42	1k	16	SER
42	1k	109	VAL
42	1k	114	VAL
43	1l	83	VAL
44	1m	3	ARG
44	1m	4	ILE
44	1m	19	LEU
44	1m	60	VAL
44	1m	70	LEU
45	1n	13	THR
45	1n	18	VAL
45	1n	35	ARG
45	1n	49	HIS
46	1o	39	LEU
47	1p	2	VAL
47	1p	6	LEU
47	1p	20	VAL
47	1p	21	VAL
47	1p	29	ASP
47	1p	50	LYS
47	1p	61	SER
47	1p	62	VAL
47	1p	67	THR
47	1p	72	ARG
48	1q	70	ARG
48	1q	85	VAL

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Mol	Chain	Res	Type
48	1q	97	SER
49	1r	25	THR
49	1r	47	THR
49	1r	76	LEU
50	1s	5	LEU
50	1s	28	LYS
50	1s	37	ARG
50	1s	66	MET
50	1s	67	VAL
51	1t	24	LEU
51	1t	56	MET
51	1t	100	ILE
53	1y	23	ARG
53	1y	42	SER
53	1y	83	ARG
3	2D	3	VAL
3	2D	37	LEU
3	2D	61	LEU
3	2D	99	ASP
3	2D	103	ARG
3	2D	111	LEU
3	2D	113	VAL
3	2D	134	ARG
3	2D	140	THR
3	2D	142	VAL
3	2D	183	ARG
3	2D	193	VAL
3	2D	211	ARG
3	2D	221	VAL
3	2D	229	VAL
3	2D	242	ARG
3	2D	259	THR
3	2D	274	ARG
4	2E	9	VAL
4	2E	12	THR
4	2E	73	GLU
4	2E	75	VAL
4	2E	89	ASP
4	2E	116	VAL
4	2E	119	ARG
4	2E	181	LEU
5	2F	20	LEU

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Mol	Chain	Res	Type
5	2F	33	LEU
5	2F	57	VAL
5	2F	60	SER
5	2F	74	ARG
5	2F	88	VAL
5	2F	120	GLU
5	2F	126	VAL
5	2F	135	LYS
5	2F	140	LEU
5	2F	162	LEU
5	2F	165	ARG
5	2F	175	THR
5	2F	197	ASP
5	2F	201	VAL
6	2G	3	LEU
6	2G	4	ASP
6	2G	14	GLU
6	2G	31	VAL
6	2G	39	ILE
6	2G	43	LEU
6	2G	53	LEU
6	2G	63	ILE
6	2G	92	VAL
6	2G	126	ASP
6	2G	133	LEU
6	2G	139	LEU
6	2G	140	ILE
7	2H	24	VAL
7	2H	33	LEU
7	2H	34	GLU
7	2H	44	VAL
7	2H	45	VAL
7	2H	47	GLU
7	2H	49	VAL
7	2H	84	SER
7	2H	86	GLU
7	2H	88	LEU
7	2H	92	ILE
7	2H	105	LEU
7	2H	106	THR
7	2H	122	THR
7	2H	127	GLU

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Mol	Chain	Res	Type
7	2H	133	VAL
7	2H	139	GLN
8	2I	3	VAL
8	2I	38	LEU
8	2I	68	LEU
8	2I	75	LEU
8	2I	76	THR
8	2I	92	VAL
8	2I	123	LEU
8	2I	127	VAL
8	2I	140	LEU
8	2I	142	VAL
9	2N	12	ARG
9	2N	28	THR
9	2N	62	VAL
9	2N	65	LYS
9	2N	68	GLU
9	2N	74	ARG
9	2N	133	GLN
9	2N	138	LEU
9	2N	139	GLU
10	2O	52	VAL
10	2O	108	GLU
10	2O	113	LYS
10	2O	116	SER
11	2P	95	VAL
11	2P	96	THR
11	2P	99	LEU
11	2P	148	LEU
11	2P	149	GLU
12	2Q	1	MET
12	2Q	2	LEU
12	2Q	7	MET
12	2Q	35	VAL
12	2Q	55	VAL
12	2Q	106	VAL
12	2Q	109	VAL
12	2Q	110	THR
13	2R	29	LEU
13	2R	33	ARG
13	2R	44	LEU
13	2R	86	ARG

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Mol	Chain	Res	Type
13	2R	96	ARG
13	2R	104	ARG
13	2R	114	VAL
13	2R	117	VAL
13	2R	118	GLU
14	2S	28	VAL
14	2S	35	ILE
14	2S	50	SER
14	2S	52	SER
14	2S	69	VAL
14	2S	76	LYS
14	2S	78	LEU
14	2S	85	VAL
15	2T	6	LEU
15	2T	16	ARG
15	2T	23	ARG
15	2T	28	VAL
15	2T	34	VAL
15	2T	40	THR
15	2T	89	VAL
15	2T	108	ARG
16	2U	5	LYS
16	2U	31	SER
16	2U	55	ARG
16	2U	74	LEU
16	2U	104	GLN
17	2V	5	VAL
17	2V	13	ARG
17	2V	32	THR
17	2V	35	LEU
17	2V	46	VAL
17	2V	51	VAL
17	2V	79	VAL
17	2V	97	LYS
18	2W	11	ARG
18	2W	17	VAL
18	2W	23	LEU
18	2W	49	LYS
18	2W	100	THR
19	2X	65	ARG
20	2Y	19	LYS
20	2Y	28	LYS

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Mol	Chain	Res	Type
20	2Y	40	GLU
20	2Y	72	VAL
20	2Y	92	ASN
20	2Y	99	CYS
21	2Z	33	LEU
21	2Z	35	ARG
21	2Z	65	GLN
21	2Z	72	ARG
21	2Z	73	GLN
21	2Z	76	LEU
21	2Z	86	VAL
21	2Z	107	THR
21	2Z	124	ILE
21	2Z	150	LEU
21	2Z	170	THR
21	2Z	171	ILE
21	2Z	175	VAL
21	2Z	186	GLU
21	2Z	193	GLU
22	20	36	ILE
22	20	49	LYS
23	21	4	VAL
23	21	11	ARG
23	21	21	ARG
23	21	26	ARG
23	21	46	LEU
23	21	62	VAL
23	21	85	LEU
24	22	25	VAL
24	22	32	LEU
24	22	45	SER
24	22	62	THR
25	23	31	LEU
25	23	59	VAL
26	24	15	ILE
26	24	21	VAL
26	24	40	HIS
26	24	50	VAL
26	24	52	THR
26	24	53	GLU
26	24	62	ARG
27	25	6	VAL

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Mol	Chain	Res	Type
28	26	14	THR
29	27	1	MET
29	27	24	THR
29	27	46	VAL
30	28	3	LYS
30	28	14	VAL
31	29	12	ASP
31	29	17	ILE
33	2b	8	LYS
33	2b	11	LEU
33	2b	15	VAL
33	2b	39	ILE
33	2b	42	ILE
33	2b	45	GLN
33	2b	64	ARG
33	2b	67	THR
33	2b	68	ILE
33	2b	80	ILE
33	2b	82	ARG
33	2b	83	MET
33	2b	111	ARG
33	2b	118	LEU
33	2b	124	SER
33	2b	126	GLU
33	2b	127	ILE
33	2b	128	GLU
33	2b	140	HIS
33	2b	158	LEU
33	2b	189	ASP
33	2b	196	LEU
33	2b	200	ILE
33	2b	224	GLN
33	2b	229	VAL
34	2c	3	ASN
34	2c	8	ILE
34	2c	33	LEU
34	2c	46	GLU
34	2c	47	LEU
34	2c	49	SER
34	2c	52	LEU
34	2c	67	THR
34	2c	105	GLU

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Mol	Chain	Res	Type
34	2c	115	LEU
34	2c	128	PHE
34	2c	131	ARG
34	2c	143	GLU
34	2c	152	ILE
34	2c	166	GLU
34	2c	182	ILE
34	2c	192	THR
34	2c	195	VAL
34	2c	204	LEU
34	2c	207	VAL
35	2d	8	VAL
35	2d	17	VAL
35	2d	19	LEU
35	2d	28	SER
35	2d	106	TYR
35	2d	108	LEU
35	2d	122	ARG
35	2d	135	LEU
35	2d	141	ARG
35	2d	150	GLU
35	2d	155	LEU
35	2d	157	LEU
35	2d	160	GLN
35	2d	166	LYS
36	2e	31	LEU
36	2e	69	VAL
36	2e	71	LEU
36	2e	79	GLU
36	2e	82	VAL
36	2e	145	LYS
36	2e	150	ARG
36	2e	152	ARG
37	2f	37	VAL
37	2f	57	GLN
37	2f	61	LEU
37	2f	63	TYR
37	2f	69	GLU
37	2f	72	VAL
37	2f	93	SER
37	2f	95	GLU
38	2g	9	VAL

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Mol	Chain	Res	Type
38	2g	15	ASP
38	2g	16	LEU
38	2g	21	VAL
38	2g	75	VAL
38	2g	113	GLU
38	2g	115	ARG
38	2g	118	VAL
38	2g	131	LYS
38	2g	135	VAL
38	2g	138	LYS
38	2g	155	ARG
39	2h	33	GLU
39	2h	38	ILE
39	2h	54	ASP
39	2h	56	LYS
39	2h	63	LEU
39	2h	84	ARG
39	2h	85	ARG
39	2h	91	ARG
39	2h	112	LEU
39	2h	114	THR
39	2h	121	ASP
39	2h	122	ARG
39	2h	133	LEU
39	2h	137	VAL
40	2i	7	THR
40	2i	17	VAL
40	2i	31	GLN
40	2i	34	ASN
40	2i	54	ASP
40	2i	56	LEU
40	2i	87	GLN
40	2i	105	ASP
40	2i	108	VAL
40	2i	125	TYR
41	2j	9	ARG
41	2j	30	SER
41	2j	34	VAL
41	2j	47	PHE
41	2j	72	VAL
41	2j	84	GLN
41	2j	98	ILE

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Mol	Chain	Res	Type
42	2k	103	LEU
42	2k	109	VAL
42	2k	117	ASN
43	2l	36	VAL
43	2l	59	ARG
43	2l	73	GLU
43	2l	81	SER
43	2l	82	VAL
43	2l	83	VAL
43	2l	112	ASP
44	2m	19	LEU
44	2m	27	LYS
44	2m	54	VAL
44	2m	81	LEU
44	2m	94	ARG
44	2m	102	ARG
44	2m	106	ASN
44	2m	116	THR
45	2n	3	ARG
45	2n	7	ILE
45	2n	12	ARG
45	2n	13	THR
45	2n	18	VAL
46	2o	3	ILE
46	2o	24	SER
46	2o	38	ARG
46	2o	39	LEU
46	2o	64	ARG
46	2o	76	GLU
46	2o	83	GLU
47	2p	1	MET
47	2p	2	VAL
47	2p	20	VAL
47	2p	21	VAL
47	2p	47	ASP
47	2p	60	LEU
47	2p	62	VAL
47	2p	69	THR
47	2p	75	ARG
47	2p	76	GLN
48	2q	6	LEU
48	2q	60	ILE

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Mol	Chain	Res	Type
48	2q	63	ARG
48	2q	96	GLU
49	2r	41	LYS
49	2r	55	ARG
49	2r	66	LEU
50	2s	13	ASP
50	2s	27	GLU
50	2s	44	MET
50	2s	48	THR
50	2s	66	MET
50	2s	79	THR
50	2s	81	ARG
51	2t	10	LEU
51	2t	38	LYS
51	2t	62	LEU
51	2t	71	THR
51	2t	84	LEU
51	2t	90	GLN
52	2u	8	THR
52	2u	15	ARG
53	2y	6	THR
53	2y	11	GLU
53	2y	16	ILE
53	2y	23	ARG
53	2y	41	LEU
53	2y	42	SER
53	2y	70	MET
53	2y	87	LYS
53	2y	96	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (146) such sidechains are listed below:

Mol	Chain	Res	Type
3	1D	116	GLN
3	1D	253	GLN
4	1E	143	ASN
5	1F	8	GLN
5	1F	69	HIS
5	1F	203	GLN
6	1G	26	GLN
6	1G	40	ASN
8	1I	54	GLN

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Mol	Chain	Res	Type
9	1N	56	ASN
9	1N	94	HIS
12	1Q	12	GLN
13	1R	24	GLN
13	1R	50	HIS
15	1T	58	ASN
15	1T	84	GLN
15	1T	123	GLN
16	1U	72	HIS
16	1U	94	ASN
18	1W	60	ASN
19	1X	31	HIS
19	1X	82	GLN
20	1Y	6	HIS
20	1Y	92	ASN
21	1Z	55	HIS
21	1Z	73	GLN
21	1Z	151	HIS
25	13	32	GLN
26	14	47	GLN
28	16	20	ASN
31	19	34	GLN
33	1b	76	GLN
33	1b	212	GLN
34	1c	6	HIS
34	1c	63	ASN
34	1c	98	ASN
34	1c	104	GLN
35	1d	45	GLN
35	1d	77	ASN
35	1d	119	GLN
35	1d	123	HIS
35	1d	129	ASN
37	1f	32	ASN
37	1f	94	GLN
37	1f	100	ASN
38	1g	28	ASN
38	1g	64	GLN
38	1g	86	GLN
38	1g	110	GLN
38	1g	122	HIS
40	1i	3	GLN

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Mol	Chain	Res	Type
40	1i	73	GLN
40	1i	87	GLN
41	1j	56	HIS
41	1j	69	ASN
42	1k	116	HIS
42	1k	117	ASN
43	1l	99	HIS
45	1n	49	HIS
46	1o	13	GLN
46	1o	28	GLN
47	1p	13	HIS
47	1p	16	HIS
48	1q	16	GLN
50	1s	23	ASN
50	1s	57	HIS
50	1s	69	HIS
50	1s	83	HIS
51	1t	9	ASN
51	1t	16	HIS
51	1t	18	GLN
53	1y	38	HIS
3	2D	126	GLN
3	2D	143	HIS
3	2D	253	GLN
4	2E	48	GLN
4	2E	143	ASN
5	2F	69	HIS
5	2F	133	ASN
6	2G	108	ASN
6	2G	138	GLN
7	2H	74	ASN
8	2I	43	ASN
8	2I	104	GLN
8	2I	105	HIS
9	2N	133	GLN
12	2Q	89	ASN
12	2Q	123	HIS
13	2R	13	HIS
13	2R	71	GLN
15	2T	58	ASN
15	2T	123	GLN
16	2U	94	ASN

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Mol	Chain	Res	Type
17	2V	64	HIS
19	2X	31	HIS
19	2X	82	GLN
20	2Y	92	ASN
21	2Z	73	GLN
21	2Z	132	ASN
21	2Z	151	HIS
23	21	16	ASN
25	23	32	GLN
26	24	20	ASN
28	26	20	ASN
30	28	35	GLN
31	29	34	GLN
33	2b	40	HIS
33	2b	76	GLN
33	2b	78	GLN
33	2b	146	GLN
34	2c	6	HIS
34	2c	28	GLN
34	2c	37	GLN
34	2c	108	ASN
34	2c	170	GLN
34	2c	176	HIS
34	2c	181	ASN
35	2d	77	ASN
35	2d	116	GLN
35	2d	125	HIS
35	2d	160	GLN
35	2d	161	ASN
36	2e	20	GLN
37	2f	57	GLN
37	2f	73	ASN
38	2g	11	GLN
38	2g	13	GLN
38	2g	28	ASN
38	2g	106	GLN
38	2g	148	ASN
40	2i	3	GLN
40	2i	29	ASN
40	2i	31	GLN
41	2j	68	HIS
41	2j	84	GLN

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Mol	Chain	Res	Type
43	2l	99	HIS
44	2m	12	ASN
45	2n	49	HIS
46	2o	9	GLN
46	2o	13	GLN
47	2p	13	HIS
47	2p	16	HIS
48	2q	16	GLN
53	2y	36	ASN
53	2y	38	HIS
53	2y	79	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	2865/2915 (98%)	406 (14%)	33 (1%)
1	2A	2858/2915 (98%)	448 (15%)	39 (1%)
2	1B	119/121 (98%)	12 (10%)	0
2	2B	119/121 (98%)	15 (12%)	0
32	1a	1497/1521 (98%)	217 (14%)	0
32	2a	1501/1521 (98%)	247 (16%)	0
All	All	8959/9114 (98%)	1345 (15%)	72 (0%)

All (1345) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	12	U
1	1A	34	C
1	1A	45	C
1	1A	71	A
1	1A	74	A
1	1A	75	G
1	1A	95	G
1	1A	118	A
1	1A	119	A
1	1A	120	U
1	1A	181	A
1	1A	182	A
1	1A	196	A
1	1A	197	A
1	1A	205	G

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Mol	Chain	Res	Type
1	1A	215	G
1	1A	216	A
1	1A	221	A
1	1A	222	A
1	1A	229	A
1	1A	248	G
1	1A	265	A
1	1A	271(I)	G
1	1A	271(K)	U
1	1A	271(L)	U
1	1A	271(M)	G
1	1A	271(N)	U
1	1A	271(O)	C
1	1A	272(A)	U
1	1A	272(B)	G
1	1A	272(H)	C
1	1A	275	G
1	1A	279	C
1	1A	283	A
1	1A	311	A
1	1A	330	A
1	1A	352	G
1	1A	363	G
1	1A	363(C)	G
1	1A	386	G
1	1A	396	G
1	1A	405	U
1	1A	411	G
1	1A	412	A
1	1A	421	U
1	1A	422	A
1	1A	428	A
1	1A	429	A
1	1A	448	U
1	1A	451	C
1	1A	454	A
1	1A	456	C
1	1A	481	G
1	1A	505	A
1	1A	509	C
1	1A	518	G
1	1A	528	A

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Mol	Chain	Res	Type
1	1A	530	G
1	1A	531	C
1	1A	532	A
1	1A	533	G
1	1A	545	G
1	1A	549	G
1	1A	563	G
1	1A	573	G
1	1A	574	C
1	1A	575	A
1	1A	586	A
1	1A	603	A
1	1A	604	G
1	1A	607	U
1	1A	614(B)	G
1	1A	615	G
1	1A	627	A
1	1A	637	A
1	1A	645	C
1	1A	646	A
1	1A	652(T)	C
1	1A	652(U)	G
1	1A	668	G
1	1A	669	G
1	1A	686	G
1	1A	730	C
1	1A	746	A
1	1A	747	U
1	1A	764	A
1	1A	765	G
1	1A	775	G
1	1A	776	G
1	1A	782	A
1	1A	784	A
1	1A	785	G
1	1A	790	C
1	1A	792	G
1	1A	805	G
1	1A	812	C
1	1A	827	U
1	1A	828	U
1	1A	859	G

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Mol	Chain	Res	Type
1	1A	866	A
1	1A	878	A
1	1A	879	G
1	1A	882	G
1	1A	885	C
1	1A	886	C
1	1A	888	C
1	1A	889	C
1	1A	890	A
1	1A	896	A
1	1A	897	C
1	1A	900	A
1	1A	910	A
1	1A	932	G
1	1A	945	A
1	1A	946	G
1	1A	953	A
1	1A	961	C
1	1A	974	G
1	1A	975	C
1	1A	983	A
1	1A	996	A
1	1A	1012	U
1	1A	1013	C
1	1A	1026	U
1	1A	1033	U
1	1A	1039	G
1	1A	1041	C
1	1A	1042	G
1	1A	1043	C
1	1A	1046	A
1	1A	1047	G
1	1A	1048	A
1	1A	1054	A
1	1A	1060	U
1	1A	1061	U
1	1A	1062	G
1	1A	1063	G
1	1A	1065	U
1	1A	1067	A
1	1A	1069	A
1	1A	1070	A

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Mol	Chain	Res	Type
1	1A	1071	G
1	1A	1073	A
1	1A	1074	G
1	1A	1075	C
1	1A	1076	C
1	1A	1077	A
1	1A	1078	U
1	1A	1079	C
1	1A	1083	U
1	1A	1087	G
1	1A	1088	A
1	1A	1089	G
1	1A	1090	U
1	1A	1096	A
1	1A	1097	U
1	1A	1109	C
1	1A	1110	G
1	1A	1112	G
1	1A	1116	C
1	1A	1128	A
1	1A	1129	A
1	1A	1130	U
1	1A	1135	C
1	1A	1136	G
1	1A	1142(A)	A
1	1A	1143	A
1	1A	1170	G
1	1A	1171	G
1	1A	1173	G
1	1A	1174	A
1	1A	1175	U
1	1A	1176	G
1	1A	1177	A
1	1A	1178	C
1	1A	1180	C
1	1A	1210	A
1	1A	1211	U
1	1A	1220	A
1	1A	1229	G
1	1A	1253	A
1	1A	1256	G
1	1A	1271	G

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Mol	Chain	Res	Type
1	1A	1272	A
1	1A	1273	U
1	1A	1300	U
1	1A	1301	A
1	1A	1303	G
1	1A	1345	C
1	1A	1352	U
1	1A	1359	A
1	1A	1365	A
1	1A	1370	C
1	1A	1380	G
1	1A	1384	A
1	1A	1385	G
1	1A	1416	G
1	1A	1417	C
1	1A	1420	U
1	1A	1421	G
1	1A	1428	C
1	1A	1445	A
1	1A	1450	G
1	1A	1459	G
1	1A	1467	C
1	1A	1471	A
1	1A	1482	G
1	1A	1493	C
1	1A	1494	A
1	1A	1509(A)	A
1	1A	1525	G
1	1A	1542	A
1	1A	1543	C
1	1A	1554	A
1	1A	1558	A
1	1A	1566	A
1	1A	1569	A
1	1A	1578	U
1	1A	1579	A
1	1A	1581	G
1	1A	1582	C
1	1A	1584	C
1	1A	1586	A
1	1A	1608	A
1	1A	1609	A

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Mol	Chain	Res	Type
1	1A	1610	A
1	1A	1616	A
1	1A	1648	C
1	1A	1653	G
1	1A	1654	A
1	1A	1674	G
1	1A	1696	G
1	1A	1700	A
1	1A	1701	A
1	1A	1722	A
1	1A	1739	U
1	1A	1746	G
1	1A	1747	G
1	1A	1756	G
1	1A	1762	A
1	1A	1763	G
1	1A	1764	G
1	1A	1773	A
1	1A	1780	A
1	1A	1782	C
1	1A	1791	A
1	1A	1800	C
1	1A	1801	G
1	1A	1812	A
1	1A	1816	G
1	1A	1829	A
1	1A	1839	G
1	1A	1847	A
1	1A	1877	A
1	1A	1878	G
1	1A	1900	A
1	1A	1906	G
1	1A	1913	A
1	1A	1929	G
1	1A	1930	G
1	1A	1937	A
1	1A	1938	A
1	1A	1955	U
1	1A	1963	U
1	1A	1967	C
1	1A	1970	A
1	1A	1971	A

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Mol	Chain	Res	Type
1	1A	1972	A
1	1A	1992	G
1	1A	1993	U
1	1A	1997	G
1	1A	2020	A
1	1A	2023	G
1	1A	2031	A
1	1A	2033	A
1	1A	2043	C
1	1A	2055	C
1	1A	2056	G
1	1A	2060	A
1	1A	2061	G
1	1A	2069	G
1	1A	2099	U
1	1A	2103	C
1	1A	2104	G
1	1A	2105	C
1	1A	2107	C
1	1A	2108	C
1	1A	2112	G
1	1A	2116	G
1	1A	2117	A
1	1A	2119	A
1	1A	2123	G
1	1A	2126	A
1	1A	2127	G
1	1A	2130	U
1	1A	2131	G
1	1A	2132	U
1	1A	2133	G
1	1A	2134	A
1	1A	2135	A
1	1A	2136	C
1	1A	2138	C
1	1A	2139	C
1	1A	2142	C
1	1A	2145	C
1	1A	2146	C
1	1A	2147	G
1	1A	2148	G
1	1A	2158	A

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Mol	Chain	Res	Type
1	1A	2159	G
1	1A	2162	G
1	1A	2173	A
1	1A	2185	C
1	1A	2186	G
1	1A	2187	G
1	1A	2189	U
1	1A	2190	G
1	1A	2192	G
1	1A	2198	A
1	1A	2206	G
1	1A	2207	G
1	1A	2208	A
1	1A	2225	A
1	1A	2238	G
1	1A	2239	G
1	1A	2268	A
1	1A	2269	A
1	1A	2280	G
1	1A	2283	C
1	1A	2287	A
1	1A	2289	G
1	1A	2305	A
1	1A	2308	G
1	1A	2320	A
1	1A	2325	G
1	1A	2334	G
1	1A	2336	A
1	1A	2347	C
1	1A	2350	C
1	1A	2383	G
1	1A	2385	C
1	1A	2393	A
1	1A	2406	U
1	1A	2407	G
1	1A	2422	A
1	1A	2424	C
1	1A	2425	A
1	1A	2428	G
1	1A	2429	G
1	1A	2430	A
1	1A	2431	U

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Mol	Chain	Res	Type
1	1A	2435	A
1	1A	2439	A
1	1A	2441	C
1	1A	2447	G
1	1A	2448	A
1	1A	2468	G
1	1A	2474	C
1	1A	2476	A
1	1A	2478	A
1	1A	2491	U
1	1A	2502	G
1	1A	2505	G
1	1A	2506	U
1	1A	2518	A
1	1A	2529	G
1	1A	2535	G
1	1A	2554	U
1	1A	2566	A
1	1A	2567	G
1	1A	2573	C
1	1A	2574	G
1	1A	2602	A
1	1A	2603	G
1	1A	2609	U
1	1A	2611	U
1	1A	2612	C
1	1A	2629	A
1	1A	2630	G
1	1A	2654	A
1	1A	2662	A
1	1A	2689	U
1	1A	2690	C
1	1A	2702	U
1	1A	2712(A)	A
1	1A	2713	A
1	1A	2714	G
1	1A	2726	U
1	1A	2733	A
1	1A	2757	A
1	1A	2758	A
1	1A	2765	A
1	1A	2766	G

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Mol	Chain	Res	Type
1	1A	2778	A
1	1A	2790	A
1	1A	2791	C
1	1A	2802	G
1	1A	2818	G
1	1A	2820	A
1	1A	2821	A
1	1A	2833	G
1	1A	2835	A
1	1A	2872	G
1	1A	2892	A
1	1A	2893	G
1	1A	2894	G
2	1B	2	C
2	1B	7	G
2	1B	13	A
2	1B	42	C
2	1B	45	A
2	1B	53	A
2	1B	56	G
2	1B	67	G
2	1B	73	A
2	1B	84	C
2	1B	106	G
2	1B	110	G
32	1a	7	G
32	1a	9	G
32	1a	32	A
32	1a	39	G
32	1a	48	C
32	1a	51	A
32	1a	61	G
32	1a	69	G
32	1a	78	G
32	1a	79	G
32	1a	101	A
32	1a	115	G
32	1a	116	A
32	1a	121	C
32	1a	131	C
32	1a	144	G
32	1a	163	C

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Mol	Chain	Res	Type
32	1a	173	U
32	1a	174	C
32	1a	182	U
32	1a	189(D)	C
32	1a	195	A
32	1a	197	A
32	1a	202	U
32	1a	203	U
32	1a	204	U
32	1a	216	G
32	1a	220	G
32	1a	247	G
32	1a	251	G
32	1a	266	G
32	1a	267	C
32	1a	289	G
32	1a	321	A
32	1a	328	C
32	1a	332	G
32	1a	348	G
32	1a	351	G
32	1a	352	C
32	1a	353	A
32	1a	354	G
32	1a	356	A
32	1a	367	U
32	1a	372	C
32	1a	373	A
32	1a	397	A
32	1a	406	G
32	1a	409	G
32	1a	412	A
32	1a	413	G
32	1a	422	C
32	1a	423	G
32	1a	429	U
32	1a	430	A
32	1a	439	A
32	1a	442	C
32	1a	452	A
32	1a	458	C
32	1a	461	A

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Mol	Chain	Res	Type
32	1a	470	C
32	1a	484	G
32	1a	485	G
32	1a	496	A
32	1a	498	U
32	1a	505	G
32	1a	509	A
32	1a	510	A
32	1a	511	C
32	1a	518	C
32	1a	521	G
32	1a	532	A
32	1a	547	A
32	1a	550	G
32	1a	559	A
32	1a	561	U
32	1a	564	C
32	1a	572	A
32	1a	573	A
32	1a	576	G
32	1a	577	G
32	1a	596	C
32	1a	607	A
32	1a	619	U
32	1a	630	G
32	1a	631	G
32	1a	632	A
32	1a	653	A
32	1a	665	A
32	1a	666	G
32	1a	671	G
32	1a	687	A
32	1a	688	G
32	1a	723	U
32	1a	755	G
32	1a	777	A
32	1a	793	U
32	1a	794	A
32	1a	817	C
32	1a	821	G
32	1a	828	A
32	1a	829	G

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Mol	Chain	Res	Type
32	1a	836	G
32	1a	839	U
32	1a	840	C
32	1a	841	U
32	1a	851	G
32	1a	902	G
32	1a	914	A
32	1a	926	G
32	1a	927	G
32	1a	934	C
32	1a	960	U
32	1a	961	U
32	1a	968	A
32	1a	969	A
32	1a	971	G
32	1a	974	A
32	1a	975	A
32	1a	976	G
32	1a	977	A
32	1a	992	U
32	1a	993	G
32	1a	994	A
32	1a	998	G
32	1a	1001	A
32	1a	1001(A)	G
32	1a	1004	A
32	1a	1005	A
32	1a	1006	C
32	1a	1022	G
32	1a	1023	G
32	1a	1024	G
32	1a	1025	U
32	1a	1026	G
32	1a	1028	C
32	1a	1029	C
32	1a	1030	C
32	1a	1030(A)	G
32	1a	1030(B)	C
32	1a	1030(D)	A
32	1a	1032	G
32	1a	1033	G
32	1a	1034	G

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Mol	Chain	Res	Type
32	1a	1037	C
32	1a	1044	A
32	1a	1046	A
32	1a	1053	G
32	1a	1065	U
32	1a	1066	C
32	1a	1067	A
32	1a	1070	U
32	1a	1094	G
32	1a	1095	U
32	1a	1101	A
32	1a	1104	G
32	1a	1124	G
32	1a	1130	A
32	1a	1132	C
32	1a	1133	G
32	1a	1134	G
32	1a	1136	U
32	1a	1139	G
32	1a	1140	C
32	1a	1147	C
32	1a	1152	A
32	1a	1154	G
32	1a	1159	U
32	1a	1166	G
32	1a	1168	A
32	1a	1183	A
32	1a	1184	G
32	1a	1196	U
32	1a	1197	G
32	1a	1202	G
32	1a	1208	C
32	1a	1212	U
32	1a	1213	A
32	1a	1224	G
32	1a	1227	A
32	1a	1238	A
32	1a	1256	A
32	1a	1257	U
32	1a	1258	G
32	1a	1260	C
32	1a	1270	C

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Mol	Chain	Res	Type
32	1a	1278	U
32	1a	1280	A
32	1a	1286	A
32	1a	1287	A
32	1a	1299	A
32	1a	1300	G
32	1a	1302	U
32	1a	1320	C
32	1a	1338	G
32	1a	1346	A
32	1a	1347	G
32	1a	1353	G
32	1a	1363	C
32	1a	1370	G
32	1a	1397	C
32	1a	1419	G
32	1a	1442	G
32	1a	1442(A)	G
32	1a	1447	A
32	1a	1452	C
32	1a	1456	G
32	1a	1492	A
32	1a	1493	A
32	1a	1503	A
32	1a	1504	G
32	1a	1505	G
32	1a	1506	U
32	1a	1517	G
32	1a	1520	G
32	1a	1529	G
32	1a	1530	G
32	1a	1531	A
1	2A	10	G
1	2A	11	G
1	2A	12	U
1	2A	15	G
1	2A	34	C
1	2A	45	C
1	2A	61	G
1	2A	71	A
1	2A	74	A
1	2A	75	G

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Mol	Chain	Res	Type
1	2A	84	A
1	2A	118	A
1	2A	119	A
1	2A	120	U
1	2A	131	G
1	2A	141	A
1	2A	157	U
1	2A	173	G
1	2A	181	A
1	2A	182	A
1	2A	196	A
1	2A	197	A
1	2A	205	G
1	2A	215	G
1	2A	216	A
1	2A	221	A
1	2A	222	A
1	2A	229	A
1	2A	230	U
1	2A	248	G
1	2A	271(K)	U
1	2A	271(L)	U
1	2A	271(M)	G
1	2A	271(N)	U
1	2A	272(A)	U
1	2A	272(B)	G
1	2A	277	C
1	2A	278	A
1	2A	311	A
1	2A	317	G
1	2A	324	A
1	2A	329	G
1	2A	330	A
1	2A	342	G
1	2A	352	G
1	2A	362	U
1	2A	363	G
1	2A	370	G
1	2A	386	G
1	2A	396	G
1	2A	405	U
1	2A	411	G

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Mol	Chain	Res	Type
1	2A	412	A
1	2A	428	A
1	2A	444	C
1	2A	454	A
1	2A	455	C
1	2A	457	A
1	2A	470	A
1	2A	481	G
1	2A	505	A
1	2A	509	C
1	2A	530	G
1	2A	531	C
1	2A	532	A
1	2A	533	G
1	2A	545	G
1	2A	563	G
1	2A	573	G
1	2A	575	A
1	2A	586	A
1	2A	603	A
1	2A	604	G
1	2A	607	U
1	2A	610	G
1	2A	614(B)	G
1	2A	615	G
1	2A	616	G
1	2A	627	A
1	2A	637	A
1	2A	645	C
1	2A	646	A
1	2A	652(A)	A
1	2A	652(B)	A
1	2A	652(C)	G
1	2A	652(U)	G
1	2A	653	A
1	2A	669	G
1	2A	686	G
1	2A	717	G
1	2A	730	C
1	2A	746	A
1	2A	747	U
1	2A	752	A

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Mol	Chain	Res	Type
1	2A	753	C
1	2A	764	A
1	2A	765	G
1	2A	775	G
1	2A	776	G
1	2A	782	A
1	2A	784	A
1	2A	785	G
1	2A	792	G
1	2A	805	G
1	2A	812	C
1	2A	827	U
1	2A	828	U
1	2A	857	C
1	2A	859	G
1	2A	874	G
1	2A	880	G
1	2A	882	G
1	2A	887	A
1	2A	888	C
1	2A	889	C
1	2A	890	A
1	2A	893	C
1	2A	896	A
1	2A	900	A
1	2A	901	A
1	2A	910	A
1	2A	914	C
1	2A	917	A
1	2A	932	G
1	2A	941	A
1	2A	945	A
1	2A	946	G
1	2A	959	A
1	2A	961	C
1	2A	963	U
1	2A	974	G
1	2A	975	C
1	2A	983	A
1	2A	996	A
1	2A	1012	U
1	2A	1013	C

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Mol	Chain	Res	Type
1	2A	1033	U
1	2A	1041	C
1	2A	1044	G
1	2A	1045	A
1	2A	1046	A
1	2A	1047	G
1	2A	1048	A
1	2A	1049	C
1	2A	1052	C
1	2A	1053	C
1	2A	1054	A
1	2A	1058	G
1	2A	1060	U
1	2A	1063	G
1	2A	1064	C
1	2A	1065	U
1	2A	1066	U
1	2A	1067	A
1	2A	1068	G
1	2A	1069	A
1	2A	1070	A
1	2A	1071	G
1	2A	1072	C
1	2A	1073	A
1	2A	1074	G
1	2A	1076	C
1	2A	1077	A
1	2A	1078	U
1	2A	1079	C
1	2A	1082	U
1	2A	1083	U
1	2A	1084	A
1	2A	1085	A
1	2A	1086	A
1	2A	1088	A
1	2A	1090	U
1	2A	1091	G
1	2A	1092	C
1	2A	1093	G
1	2A	1094	U
1	2A	1095	A
1	2A	1096	A

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Mol	Chain	Res	Type
1	2A	1109	C
1	2A	1110	G
1	2A	1112	G
1	2A	1114	G
1	2A	1116	C
1	2A	1117	G
1	2A	1129	A
1	2A	1130	U
1	2A	1135	C
1	2A	1136	G
1	2A	1171	G
1	2A	1211	U
1	2A	1220	A
1	2A	1229	G
1	2A	1253	A
1	2A	1256	G
1	2A	1271	G
1	2A	1272	A
1	2A	1273	U
1	2A	1276	A
1	2A	1300	U
1	2A	1301	A
1	2A	1303	G
1	2A	1314	C
1	2A	1321	A
1	2A	1352	U
1	2A	1359	A
1	2A	1365	A
1	2A	1368	G
1	2A	1384	A
1	2A	1385	G
1	2A	1386	C
1	2A	1416	G
1	2A	1417	C
1	2A	1420	U
1	2A	1421	G
1	2A	1428	C
1	2A	1445	A
1	2A	1450	G
1	2A	1455	G
1	2A	1459	G
1	2A	1467	C

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Mol	Chain	Res	Type
1	2A	1471	A
1	2A	1482	G
1	2A	1493	C
1	2A	1494	A
1	2A	1497	U
1	2A	1508	A
1	2A	1509	C
1	2A	1509(A)	A
1	2A	1510	G
1	2A	1531	C
1	2A	1533	G
1	2A	1542	A
1	2A	1543	C
1	2A	1547	C
1	2A	1558	A
1	2A	1566	A
1	2A	1569	A
1	2A	1578	U
1	2A	1580	A
1	2A	1583	A
1	2A	1584	C
1	2A	1586	A
1	2A	1593	G
1	2A	1608	A
1	2A	1609	A
1	2A	1610	A
1	2A	1640	C
1	2A	1647	G
1	2A	1648	C
1	2A	1664	A
1	2A	1674	G
1	2A	1700	A
1	2A	1703	G
1	2A	1721	G
1	2A	1722	A
1	2A	1740	G
1	2A	1746	G
1	2A	1756	G
1	2A	1762	A
1	2A	1763	G
1	2A	1764	G
1	2A	1773	A

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Mol	Chain	Res	Type
1	2A	1780	A
1	2A	1782	C
1	2A	1791	A
1	2A	1800	C
1	2A	1801	G
1	2A	1816	G
1	2A	1835	G
1	2A	1839	G
1	2A	1847	A
1	2A	1848	A
1	2A	1877	A
1	2A	1878	G
1	2A	1889	A
1	2A	1900	A
1	2A	1906	G
1	2A	1914	C
1	2A	1918	A
1	2A	1927	A
1	2A	1929	G
1	2A	1930	G
1	2A	1937	A
1	2A	1938	A
1	2A	1955	U
1	2A	1963	U
1	2A	1967	C
1	2A	1970	A
1	2A	1971	A
1	2A	1972	A
1	2A	1992	G
1	2A	1993	U
1	2A	1997	G
1	2A	2020	A
1	2A	2023	G
1	2A	2031	A
1	2A	2033	A
1	2A	2043	C
1	2A	2055	C
1	2A	2056	G
1	2A	2060	A
1	2A	2061	G
1	2A	2069	G
1	2A	2096	U

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Mol	Chain	Res	Type
1	2A	2099	U
1	2A	2100	G
1	2A	2103	C
1	2A	2105	C
1	2A	2107	C
1	2A	2108	C
1	2A	2109	U
1	2A	2112	G
1	2A	2116	G
1	2A	2117	A
1	2A	2118	U
1	2A	2119	A
1	2A	2121	G
1	2A	2123	G
1	2A	2126	A
1	2A	2127	G
1	2A	2129	C
1	2A	2130	U
1	2A	2132	U
1	2A	2133	G
1	2A	2134	A
1	2A	2135	A
1	2A	2136	C
1	2A	2138	C
1	2A	2144	U
1	2A	2145	C
1	2A	2146	C
1	2A	2147	G
1	2A	2148	G
1	2A	2151	G
1	2A	2158	A
1	2A	2159	G
1	2A	2162	G
1	2A	2172	U
1	2A	2173	A
1	2A	2176	A
1	2A	2178	C
1	2A	2180	U
1	2A	2181	G
1	2A	2183	C
1	2A	2184	G
1	2A	2186	G

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Mol	Chain	Res	Type
1	2A	2187	G
1	2A	2189	U
1	2A	2192	G
1	2A	2198	A
1	2A	2206	G
1	2A	2207	G
1	2A	2208	A
1	2A	2218	U
1	2A	2219	G
1	2A	2225	A
1	2A	2238	G
1	2A	2239	G
1	2A	2268	A
1	2A	2269	A
1	2A	2275	C
1	2A	2280	G
1	2A	2283	C
1	2A	2287	A
1	2A	2289	G
1	2A	2305	A
1	2A	2308	G
1	2A	2312	U
1	2A	2314	C
1	2A	2319	G
1	2A	2320	A
1	2A	2321	G
1	2A	2322	A
1	2A	2325	G
1	2A	2334	G
1	2A	2335	A
1	2A	2336	A
1	2A	2343	C
1	2A	2347	C
1	2A	2348	U
1	2A	2350	C
1	2A	2354	G
1	2A	2379	G
1	2A	2383	G
1	2A	2385	C
1	2A	2406	U
1	2A	2407	G
1	2A	2414	G

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Mol	Chain	Res	Type
1	2A	2422	A
1	2A	2423	U
1	2A	2425	A
1	2A	2429	G
1	2A	2430	A
1	2A	2435	A
1	2A	2439	A
1	2A	2440	C
1	2A	2441	C
1	2A	2448	A
1	2A	2474	C
1	2A	2476	A
1	2A	2478	A
1	2A	2492	U
1	2A	2502	G
1	2A	2505	G
1	2A	2506	U
1	2A	2518	A
1	2A	2529	G
1	2A	2554	U
1	2A	2566	A
1	2A	2567	G
1	2A	2573	C
1	2A	2578	G
1	2A	2602	A
1	2A	2603	G
1	2A	2609	U
1	2A	2611	U
1	2A	2612	C
1	2A	2630	G
1	2A	2654	A
1	2A	2663	G
1	2A	2689	U
1	2A	2690	C
1	2A	2702	U
1	2A	2703	C
1	2A	2712(A)	A
1	2A	2713	A
1	2A	2714	G
1	2A	2726	U
1	2A	2733	A
1	2A	2744	G

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Mol	Chain	Res	Type
1	2A	2757	A
1	2A	2758	A
1	2A	2765	A
1	2A	2766	G
1	2A	2778	A
1	2A	2789	C
1	2A	2818	G
1	2A	2820	A
1	2A	2821	A
1	2A	2833	G
1	2A	2835	A
1	2A	2839	G
1	2A	2872	G
1	2A	2880	C
1	2A	2891	G
1	2A	2892	A
1	2A	2894	G
1	2A	2896	C
2	2B	2	C
2	2B	7	G
2	2B	8	U
2	2B	9	G
2	2B	12	C
2	2B	13	A
2	2B	30	C
2	2B	32	C
2	2B	42	C
2	2B	51	G
2	2B	56	G
2	2B	73	A
2	2B	84	C
2	2B	90	A
2	2B	110	G
32	2a	5	U
32	2a	9	G
32	2a	22	G
32	2a	32	A
32	2a	39	G
32	2a	47	C
32	2a	48	C
32	2a	50	A
32	2a	51	A

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Mol	Chain	Res	Type
32	2a	52	G
32	2a	61	G
32	2a	66	G
32	2a	88	A
32	2a	89	C
32	2a	101	A
32	2a	116	A
32	2a	121	C
32	2a	127	G
32	2a	131	C
32	2a	156	G
32	2a	163	C
32	2a	174	C
32	2a	182	U
32	2a	189(F)	U
32	2a	195	A
32	2a	197	A
32	2a	202	U
32	2a	203	U
32	2a	204	U
32	2a	216	G
32	2a	217	C
32	2a	220	G
32	2a	247	G
32	2a	251	G
32	2a	258	G
32	2a	266	G
32	2a	267	C
32	2a	281	G
32	2a	289	G
32	2a	298	A
32	2a	321	A
32	2a	328	C
32	2a	332	G
32	2a	351	G
32	2a	352	C
32	2a	353	A
32	2a	354	G
32	2a	367	U
32	2a	372	C
32	2a	384	G
32	2a	397	A

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Mol	Chain	Res	Type
32	2a	398	C
32	2a	406	G
32	2a	412	A
32	2a	413	G
32	2a	421	U
32	2a	424	G
32	2a	429	U
32	2a	430	A
32	2a	439	A
32	2a	442	C
32	2a	452	A
32	2a	461	A
32	2a	470	C
32	2a	476	G
32	2a	482	A
32	2a	484	G
32	2a	485	G
32	2a	496	A
32	2a	498	U
32	2a	505	G
32	2a	509	A
32	2a	510	A
32	2a	511	C
32	2a	518	C
32	2a	531	U
32	2a	532	A
32	2a	533	A
32	2a	547	A
32	2a	559	A
32	2a	561	U
32	2a	564	C
32	2a	572	A
32	2a	573	A
32	2a	576	G
32	2a	577	G
32	2a	596	C
32	2a	630	G
32	2a	631	G
32	2a	633	G
32	2a	653	A
32	2a	660	G
32	2a	665	A

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Mol	Chain	Res	Type
32	2a	666	G
32	2a	687	A
32	2a	688	G
32	2a	695	A
32	2a	723	U
32	2a	724	G
32	2a	731	G
32	2a	749	C
32	2a	753	A
32	2a	755	G
32	2a	766	A
32	2a	777	A
32	2a	785	G
32	2a	793	U
32	2a	794	A
32	2a	817	C
32	2a	821	G
32	2a	828	A
32	2a	829	G
32	2a	840	C
32	2a	841	U
32	2a	851	G
32	2a	854	G
32	2a	859	A
32	2a	868	C
32	2a	874	G
32	2a	902	G
32	2a	914	A
32	2a	916	G
32	2a	926	G
32	2a	927	G
32	2a	934	C
32	2a	935	A
32	2a	960	U
32	2a	961	U
32	2a	966	M2G
32	2a	968	A
32	2a	969	A
32	2a	971	G
32	2a	972	C
32	2a	974	A
32	2a	975	A

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Mol	Chain	Res	Type
32	2a	976	G
32	2a	977	A
32	2a	984	C
32	2a	989	C
32	2a	992	U
32	2a	993	G
32	2a	994	A
32	2a	996	A
32	2a	1004	A
32	2a	1005	A
32	2a	1006	C
32	2a	1009	G
32	2a	1017	G
32	2a	1020	U
32	2a	1022	G
32	2a	1023	G
32	2a	1025	U
32	2a	1026	G
32	2a	1027	C
32	2a	1028	C
32	2a	1029	C
32	2a	1030(A)	G
32	2a	1030(B)	C
32	2a	1041	A
32	2a	1043	C
32	2a	1044	A
32	2a	1047	G
32	2a	1053	G
32	2a	1054	C
32	2a	1055	A
32	2a	1065	U
32	2a	1066	C
32	2a	1068	G
32	2a	1070	U
32	2a	1081	G
32	2a	1094	G
32	2a	1095	U
32	2a	1101	A
32	2a	1113	C
32	2a	1117	G
32	2a	1122	U
32	2a	1125	U

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Mol	Chain	Res	Type
32	2a	1129	C
32	2a	1130	A
32	2a	1134	G
32	2a	1136	U
32	2a	1137	C
32	2a	1138	G
32	2a	1139	G
32	2a	1147	C
32	2a	1152	A
32	2a	1157	A
32	2a	1159	U
32	2a	1160	G
32	2a	1161	C
32	2a	1183	A
32	2a	1184	G
32	2a	1196	U
32	2a	1197	G
32	2a	1211	U
32	2a	1212	U
32	2a	1213	A
32	2a	1214	C
32	2a	1224	G
32	2a	1227	A
32	2a	1228	C
32	2a	1236	A
32	2a	1238	A
32	2a	1248	A
32	2a	1250	A
32	2a	1256	A
32	2a	1257	U
32	2a	1258	G
32	2a	1270	C
32	2a	1278	U
32	2a	1279	A
32	2a	1286	A
32	2a	1287	A
32	2a	1300	G
32	2a	1302	U
32	2a	1303	C
32	2a	1305	G
32	2a	1317	C
32	2a	1320	C

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Mol	Chain	Res	Type
32	2a	1340	A
32	2a	1346	A
32	2a	1347	G
32	2a	1353	G
32	2a	1358	U
32	2a	1359	C
32	2a	1363	C
32	2a	1364	U
32	2a	1370	G
32	2a	1397	C
32	2a	1419	G
32	2a	1442	G
32	2a	1442(A)	G
32	2a	1446	U
32	2a	1447	A
32	2a	1452	C
32	2a	1456	G
32	2a	1492	A
32	2a	1497	G
32	2a	1499	A
32	2a	1504	G
32	2a	1505	G
32	2a	1506	U
32	2a	1507	A
32	2a	1517	G
32	2a	1520	G
32	2a	1529	G
32	2a	1530	G

All (72) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	196	A
1	1A	199	A
1	1A	266	G
1	1A	271(K)	U
1	1A	278	A
1	1A	573	G
1	1A	746	A
1	1A	764	A
1	1A	839	U
1	1A	888	C

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Mol	Chain	Res	Type
1	1A	895	U
1	1A	974	G
1	1A	1047	G
1	1A	1065	U
1	1A	1142(A)	A
1	1A	1175	U
1	1A	1176	G
1	1A	1210	A
1	1A	1442	G
1	1A	1608	A
1	1A	1653	G
1	1A	1997	G
1	1A	2126	A
1	1A	2172	U
1	1A	2250	G
1	1A	2406	U
1	1A	2422	A
1	1A	2430	A
1	1A	2439	A
1	1A	2602	A
1	1A	2611	U
1	1A	2689	U
1	1A	2756	U
1	2A	9	U
1	2A	195	A
1	2A	196	A
1	2A	249	C
1	2A	266	G
1	2A	271(M)	G
1	2A	277	C
1	2A	746	A
1	2A	752	A
1	2A	764	A
1	2A	774	A
1	2A	827	U
1	2A	840	C
1	2A	856	C
1	2A	900	A
1	2A	974	G
1	2A	1047	G
1	2A	1053	C
1	2A	1057	A

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Mol	Chain	Res	Type
1	2A	1065	U
1	2A	1067	A
1	2A	1073	A
1	2A	1076	C
1	2A	1210	A
1	2A	1275	A
1	2A	1420	U
1	2A	1442	G
1	2A	1491	G
1	2A	1992	G
1	2A	2126	A
1	2A	2171	A
1	2A	2172	U
1	2A	2288	A
1	2A	2321	G
1	2A	2406	U
1	2A	2439	A
1	2A	2602	A
1	2A	2689	U
1	2A	2756	U

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

50 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	$\# Z > 2$
1	OMU	1A	2552	54,1	19,22,23	1.30	4 (21%)	25,31,34	1.94	6 (24%)
32	5MC	2a	1407	32	19,22,23	1.59	2 (10%)	26,32,35	1.10	3 (11%)
1	OMC	1A	1920	54,1	19,22,23	0.79	0	25,31,34	0.92	1 (4%)
1	5MU	2A	1915	1	19,22,23	1.47	4 (21%)	27,32,35	2.19	9 (33%)
1	2MA	2A	2503	54,1	22,25,26	1.43	4 (18%)	32,37,40	2.31	9 (28%)
32	PSU	2a	516	32,54	18,21,22	1.32	2 (11%)	21,30,33	2.02	5 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	5MC	1A	1942	54,1	19,22,23	1.47	3 (15%)	26,32,35	1.10	2 (7%)
1	PSU	2A	1911	1	18,21,22	1.39	2 (11%)	21,30,33	2.10	5 (23%)
1	PSU	1A	1917	1	18,21,22	1.36	2 (11%)	21,30,33	1.87	4 (19%)
1	5MC	1A	1962	54,1	19,22,23	1.60	3 (15%)	26,32,35	1.19	4 (15%)
1	PSU	1A	1911	1	18,21,22	1.34	2 (11%)	21,30,33	2.05	5 (23%)
1	OMG	1A	2251	54,1	23,26,27	1.23	3 (13%)	32,38,41	2.02	7 (21%)
32	PSU	1a	516	32,54	18,21,22	1.38	2 (11%)	21,30,33	1.89	5 (23%)
32	MA6	1a	1519	32	23,26,27	0.42	0	33,38,41	2.03	9 (27%)
1	5MC	2A	1962	54,1	19,22,23	1.59	3 (15%)	26,32,35	1.16	2 (7%)
1	MA6	1A	2058	54,1	23,26,27	0.39	0	33,38,41	2.05	9 (27%)
1	5MU	2A	1939	54,1	19,22,23	1.39	5 (26%)	27,32,35	2.32	6 (22%)
1	OMU	2A	2552	54,1	19,22,23	1.26	3 (15%)	25,31,34	1.81	6 (24%)
32	M2G	2a	966	32,54	24,27,28	1.26	3 (12%)	33,40,43	1.79	6 (18%)
43	0TD	2l	92	43	8,9,10	4.69	2 (25%)	6,11,13	2.78	2 (33%)
32	2MG	1a	1207	32	23,26,27	1.24	3 (13%)	33,38,41	2.42	10 (30%)
32	G7M	1a	527	32,54	23,26,27	2.36	5 (21%)	34,39,42	2.94	10 (29%)
32	M2G	1a	966	32	24,27,28	1.33	3 (12%)	33,40,43	1.89	6 (18%)
1	2MA	1A	2503	54,1	22,25,26	1.45	5 (22%)	32,37,40	2.28	7 (21%)
32	5MC	2a	967	32	19,22,23	1.85	3 (15%)	26,32,35	1.10	2 (7%)
32	4OC	2a	1402	32	20,23,24	0.74	1 (5%)	25,32,35	0.94	1 (4%)
32	MA6	2a	1519	32	23,26,27	0.44	0	33,38,41	2.12	9 (27%)
32	5MC	1a	967	32	19,22,23	1.60	3 (15%)	26,32,35	1.10	2 (7%)
32	4OC	1a	1402	32	20,23,24	0.71	1 (5%)	25,32,35	1.07	2 (8%)
1	5MU	1A	1915	1	19,22,23	1.44	5 (26%)	27,32,35	2.36	10 (37%)
1	OMC	2A	1920	1	19,22,23	0.78	0	25,31,34	1.00	1 (4%)
1	PSU	1A	2605	54,1	18,21,22	1.36	3 (16%)	21,30,33	2.02	4 (19%)
32	2MG	2a	1207	32	23,26,27	1.20	2 (8%)	33,38,41	2.22	8 (24%)
1	PSU	2A	2605	1	18,21,22	1.29	2 (11%)	21,30,33	2.28	4 (19%)
32	MA6	2a	1518	32	23,26,27	0.42	0	33,38,41	1.99	10 (30%)
1	OMG	2A	2251	54,1	23,26,27	1.16	2 (8%)	32,38,41	1.98	6 (18%)
1	5MU	1A	1939	54,1	19,22,23	1.38	4 (21%)	27,32,35	2.16	6 (22%)
32	5MC	2a	1400	32	19,22,23	1.66	3 (15%)	26,32,35	1.19	2 (7%)
32	5MC	1a	1407	32	19,22,23	1.72	3 (15%)	26,32,35	1.12	3 (11%)
1	5MC	2A	1942	54,1	19,22,23	1.69	3 (15%)	26,32,35	1.19	2 (7%)
1	MA6	2A	2058	1	23,26,27	0.35	0	33,38,41	1.96	8 (24%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
32	5MC	1a	1400	32	19,22,23	1.79	3 (15%)	26,32,35	1.16	2 (7%)
32	MA6	1a	1518	32	23,26,27	0.40	0	33,38,41	1.92	8 (24%)
32	UR3	2a	1498	32	19,22,23	1.02	2 (10%)	26,32,35	1.71	3 (11%)
1	PSU	2A	1917	1	18,21,22	1.32	2 (11%)	21,30,33	2.06	3 (14%)
32	G7M	2a	527	32,54	23,26,27	2.38	5 (21%)	34,39,42	3.04	11 (32%)
32	5MC	2a	1404	32	19,22,23	1.67	3 (15%)	26,32,35	1.19	3 (11%)
32	UR3	1a	1498	32	19,22,23	0.99	0	26,32,35	1.92	4 (15%)
43	0TD	1l	92	43	8,9,10	4.74	1 (12%)	6,11,13	1.79	2 (33%)
32	5MC	1a	1404	32	19,22,23	1.73	3 (15%)	26,32,35	1.10	2 (7%)

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
1	OMU	1A	2552	54,1	-	0/9/27/28	0/2/2/2
32	5MC	2a	1407	32	-	0/7/25/26	0/2/2/2
1	OMC	1A	1920	54,1	-	1/9/27/28	0/2/2/2
1	5MU	2A	1915	1	-	2/7/25/26	0/2/2/2
1	2MA	2A	2503	54,1	-	1/7/25/26	0/3/3/3
32	PSU	2a	516	32,54	-	0/7/25/26	0/2/2/2
1	5MC	1A	1942	54,1	-	0/7/25/26	0/2/2/2
1	PSU	2A	1911	1	-	0/7/25/26	0/2/2/2
1	PSU	1A	1917	1	-	0/7/25/26	0/2/2/2
1	5MC	1A	1962	54,1	-	0/7/25/26	0/2/2/2
1	PSU	1A	1911	1	-	0/7/25/26	0/2/2/2
1	OMG	1A	2251	54,1	-	1/9/27/28	0/3/3/3
32	PSU	1a	516	32,54	-	0/7/25/26	0/2/2/2
32	MA6	1a	1519	32	-	2/11/29/30	0/3/3/3
1	5MC	2A	1962	54,1	-	0/7/25/26	0/2/2/2
1	MA6	1A	2058	54,1	-	0/11/29/30	0/3/3/3
1	5MU	2A	1939	54,1	-	0/7/25/26	0/2/2/2
1	OMU	2A	2552	54,1	-	0/9/27/28	0/2/2/2
32	M2G	2a	966	32,54	-	0/11/29/30	0/3/3/3
43	0TD	2l	92	43	-	2/7/12/14	-
32	2MG	1a	1207	32	-	0/9/27/28	0/3/3/3
32	G7M	1a	527	32,54	-	2/7/25/26	0/3/3/3
32	M2G	1a	966	32	-	0/11/29/30	0/3/3/3
1	2MA	1A	2503	54,1	-	1/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	5MC	2a	967	32	-	0/7/25/26	0/2/2/2
32	4OC	2a	1402	32	-	1/9/29/30	0/2/2/2
32	MA6	2a	1519	32	-	2/11/29/30	0/3/3/3
32	5MC	1a	967	32	-	0/7/25/26	0/2/2/2
32	4OC	1a	1402	32	-	0/9/29/30	0/2/2/2
1	5MU	1A	1915	1	-	2/7/25/26	0/2/2/2
1	OMC	2A	1920	1	-	0/9/27/28	0/2/2/2
1	PSU	1A	2605	54,1	-	0/7/25/26	0/2/2/2
32	2MG	2a	1207	32	-	0/9/27/28	0/3/3/3
1	PSU	2A	2605	1	-	0/7/25/26	0/2/2/2
32	MA6	2a	1518	32	-	0/11/29/30	0/3/3/3
1	OMG	2A	2251	54,1	-	0/9/27/28	0/3/3/3
1	5MU	1A	1939	54,1	-	0/7/25/26	0/2/2/2
32	5MC	2a	1400	32	-	0/7/25/26	0/2/2/2
32	5MC	1a	1407	32	-	0/7/25/26	0/2/2/2
1	5MC	2A	1942	54,1	-	0/7/25/26	0/2/2/2
1	MA6	2A	2058	1	-	0/11/29/30	0/3/3/3
32	5MC	1a	1400	32	-	1/7/25/26	0/2/2/2
32	MA6	1a	1518	32	-	0/11/29/30	0/3/3/3
32	UR3	2a	1498	32	-	0/7/25/26	0/2/2/2
1	PSU	2A	1917	1	-	0/7/25/26	0/2/2/2
32	G7M	2a	527	32,54	-	0/7/25/26	0/3/3/3
32	5MC	2a	1404	32	-	0/7/25/26	0/2/2/2
32	UR3	1a	1498	32	-	0/7/25/26	0/2/2/2
43	0TD	1l	92	43	-	1/7/12/14	-
32	5MC	1a	1404	32	-	0/7/25/26	0/2/2/2

All (119) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	1l	92	0TD	CB-SB	-12.94	1.69	1.82
43	2l	92	0TD	CB-SB	-12.70	1.69	1.82
32	2a	527	G7M	C8-N7	7.89	1.46	1.33
32	1a	527	G7M	C8-N7	7.53	1.45	1.33
32	2a	967	5MC	C5-C4	6.89	1.49	1.44
32	1a	1400	5MC	C5-C4	6.48	1.49	1.44
32	1a	1407	5MC	C5-C4	6.43	1.49	1.44
32	1a	1404	5MC	C5-C4	6.41	1.49	1.44
1	2A	1942	5MC	C5-C4	6.19	1.48	1.44
32	2a	1404	5MC	C5-C4	6.04	1.48	1.44
32	2a	1400	5MC	C5-C4	5.94	1.48	1.44
1	2A	1962	5MC	C5-C4	5.71	1.48	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	1a	967	5MC	C5-C4	5.71	1.48	1.44
32	2a	1407	5MC	C5-C4	5.63	1.48	1.44
1	1A	1962	5MC	C5-C4	5.62	1.48	1.44
1	1A	1942	5MC	C5-C4	4.83	1.47	1.44
32	1a	527	G7M	C5-N7	-4.75	1.33	1.39
1	2A	2503	2MA	C5-C4	4.35	1.46	1.39
32	2a	527	G7M	C5-N7	-4.33	1.34	1.39
32	2a	527	G7M	C8-N9	4.23	1.47	1.35
32	1a	527	G7M	C8-N9	4.21	1.47	1.35
1	1A	2503	2MA	C5-C4	4.17	1.46	1.39
32	1a	516	PSU	C6-C5	3.72	1.39	1.35
32	2a	527	G7M	C5-C4	3.67	1.47	1.38
32	1a	527	G7M	C5-C4	3.64	1.47	1.38
1	2A	1911	PSU	C6-C5	3.63	1.39	1.35
1	1A	1917	PSU	C6-C5	3.48	1.39	1.35
1	1A	1911	PSU	C6-C5	3.39	1.39	1.35
32	2a	516	PSU	C6-C5	3.35	1.39	1.35
32	1a	966	M2G	C5-C4	3.25	1.47	1.38
1	2A	1917	PSU	C6-C5	3.19	1.38	1.35
32	2a	1207	2MG	C5-C4	3.19	1.47	1.38
1	1A	2605	PSU	C4-N3	-3.18	1.32	1.38
1	2A	1915	5MU	C2-N1	3.18	1.43	1.38
32	2a	966	M2G	C5-C4	3.16	1.47	1.38
1	2A	2251	OMG	C5-C4	3.12	1.47	1.38
32	2a	1407	5MC	C6-C5	3.11	1.39	1.34
32	1a	966	M2G	C2-N2	3.09	1.40	1.35
1	2A	1915	5MU	C6-C5	3.03	1.39	1.34
32	1a	1400	5MC	C6-C5	3.00	1.39	1.34
1	1A	1915	5MU	C2-N1	2.99	1.43	1.38
1	1A	2605	PSU	C6-C5	2.97	1.38	1.35
1	1A	2251	OMG	C5-C4	2.96	1.46	1.38
32	2a	967	5MC	C6-C5	2.95	1.39	1.34
1	1A	1942	5MC	C6-C5	2.95	1.39	1.34
32	1a	1404	5MC	C6-C5	2.91	1.39	1.34
32	1a	1207	2MG	C5-C4	2.89	1.46	1.38
1	2A	1939	5MU	C6-C5	2.84	1.39	1.34
1	2A	2605	PSU	C6-C5	2.84	1.38	1.35
32	2a	1404	5MC	C6-C5	2.83	1.39	1.34
1	1A	2503	2MA	C5-N7	-2.80	1.34	1.39
1	1A	1939	5MU	C6-C5	2.78	1.39	1.34
32	1a	1407	5MC	C6-C5	2.75	1.39	1.34
1	2A	2552	OMU	C4-N3	-2.75	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	2a	1400	5MC	C6-C5	2.74	1.39	1.34
1	1A	1962	5MC	C6-N1	-2.72	1.33	1.38
32	2a	966	M2G	C2-N2	2.71	1.40	1.35
1	2A	1942	5MC	C6-C5	2.70	1.39	1.34
32	1a	967	5MC	C6-C5	2.69	1.39	1.34
1	1A	2251	OMG	C6-N1	-2.67	1.33	1.38
1	2A	1939	5MU	C4-N3	-2.63	1.33	1.38
1	1A	2552	OMU	C4-N3	-2.62	1.34	1.38
32	1a	966	M2G	C6-N1	-2.60	1.34	1.38
1	1A	1917	PSU	C4-N3	-2.59	1.34	1.38
1	2A	1962	5MC	C6-C5	2.58	1.38	1.34
1	1A	1939	5MU	C4-N3	-2.57	1.34	1.38
1	2A	1939	5MU	C4-C5	2.55	1.49	1.44
1	1A	1915	5MU	C4-C5	2.53	1.49	1.44
1	2A	1911	PSU	C4-N3	-2.52	1.34	1.38
1	1A	1911	PSU	C4-N3	-2.51	1.34	1.38
1	1A	1915	5MU	C6-C5	2.51	1.38	1.34
32	1a	1207	2MG	C6-N1	-2.50	1.34	1.38
1	1A	1915	5MU	C4-N3	-2.46	1.34	1.38
43	2l	92	0TD	CB-CA	-2.46	1.54	1.54
1	1A	1939	5MU	C2-N3	-2.46	1.33	1.38
1	2A	2503	2MA	C5-C6	2.44	1.47	1.41
1	1A	2552	OMU	C5-C4	2.44	1.49	1.43
1	1A	1942	5MC	C6-N1	-2.42	1.33	1.38
32	1a	516	PSU	C4-N3	-2.42	1.34	1.38
1	2A	1915	5MU	C4-C5	2.42	1.48	1.44
1	2A	1915	5MU	C4-N3	-2.41	1.34	1.38
1	2A	2251	OMG	C6-N1	-2.40	1.34	1.38
1	1A	1962	5MC	C6-C5	2.39	1.38	1.34
32	2a	1400	5MC	C6-N1	-2.38	1.34	1.38
32	2a	516	PSU	C4-N3	-2.38	1.34	1.38
32	2a	527	G7M	C6-N1	-2.35	1.34	1.38
32	1a	1400	5MC	C6-N1	-2.35	1.34	1.38
1	1A	2503	2MA	C5-C6	2.35	1.47	1.41
1	2A	1917	PSU	C4-N3	-2.35	1.34	1.38
32	1a	527	G7M	C6-N1	-2.33	1.34	1.38
1	1A	2251	OMG	C5-N7	-2.33	1.34	1.39
1	2A	1942	5MC	C6-N1	-2.31	1.34	1.38
1	2A	2605	PSU	C4-N3	-2.29	1.34	1.38
32	2a	966	M2G	C6-N1	-2.28	1.34	1.38
1	2A	1962	5MC	C6-N1	-2.27	1.34	1.38
32	2a	1498	UR3	C2-N1	2.25	1.41	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2A	2552	OMU	C2-N3	-2.19	1.34	1.38
32	1a	967	5MC	C6-N1	-2.18	1.34	1.38
32	2a	1404	5MC	C6-N1	-2.18	1.34	1.38
1	1A	1939	5MU	C6-N1	-2.15	1.34	1.38
1	2A	2503	2MA	C8-N7	2.15	1.35	1.31
32	2a	1498	UR3	C6-C5	2.14	1.40	1.35
1	2A	2552	OMU	C5-C4	2.14	1.48	1.43
32	2a	1207	2MG	C6-N1	-2.13	1.34	1.38
1	1A	2503	2MA	C4-N9	-2.12	1.33	1.37
1	2A	1939	5MU	C2-N1	2.10	1.41	1.38
1	2A	1939	5MU	C6-N1	-2.10	1.34	1.38
32	1a	1404	5MC	C6-N1	-2.10	1.34	1.38
32	1a	1407	5MC	C6-N1	-2.09	1.34	1.38
32	2a	967	5MC	C6-N1	-2.08	1.34	1.38
1	1A	2605	PSU	C2-N3	-2.06	1.34	1.37
1	1A	2552	OMU	C2-N3	-2.05	1.34	1.38
1	1A	2503	2MA	C8-N7	2.04	1.35	1.31
32	2a	1402	4OC	C6-C5	2.03	1.39	1.35
1	1A	1915	5MU	C6-N1	-2.03	1.34	1.38
1	2A	2503	2MA	C5-N7	-2.02	1.35	1.39
32	1a	1207	2MG	C2-N3	2.02	1.35	1.32
1	1A	2552	OMU	C2-N1	2.01	1.41	1.38
32	1a	1402	4OC	C6-C5	2.01	1.39	1.35

All (256) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	527	G7M	CN7-N7-C8	-8.33	112.18	124.79
1	1A	2503	2MA	C5-C4-N3	-8.15	118.60	127.18
1	2A	2503	2MA	C5-C4-N3	-7.96	118.79	127.18
32	1a	527	G7M	CN7-N7-C8	-7.93	112.77	124.79
32	1a	1498	UR3	C4-N3-C2	-7.62	118.45	124.58
32	1a	1207	2MG	C2-N3-C4	7.37	121.22	112.00
32	2a	527	G7M	N9-C8-N7	-7.08	95.29	112.48
32	2a	1498	UR3	C4-N3-C2	-6.94	119.00	124.58
32	2a	527	G7M	C8-N7-C5	6.88	116.39	107.78
32	1a	527	G7M	N9-C8-N7	-6.83	95.90	112.48
1	2A	2605	PSU	N1-C2-N3	6.81	122.35	115.17
32	2a	1207	2MG	C2-N3-C4	6.68	120.36	112.00
1	2A	1911	PSU	N1-C2-N3	6.61	122.15	115.17
1	2A	2503	2MA	N3-C4-N9	6.52	135.27	126.99
32	1a	527	G7M	C8-N7-C5	6.37	115.74	107.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	1911	PSU	N1-C2-N3	6.30	121.82	115.17
32	1a	966	M2G	C5-C4-N3	-6.28	118.39	128.39
1	2A	1917	PSU	N1-C2-N3	6.25	121.76	115.17
1	1A	2503	2MA	N3-C4-N9	6.15	134.80	126.99
32	2a	516	PSU	N1-C2-N3	6.13	121.63	115.17
1	1A	2251	OMG	C5-C4-N3	-6.10	118.67	128.39
1	2A	2251	OMG	C5-C4-N3	-5.99	118.85	128.39
32	2a	527	G7M	N9-C4-N3	5.93	137.81	125.95
32	1a	527	G7M	N9-C4-N3	5.92	137.78	125.95
32	1a	1207	2MG	C5-C4-N3	-5.91	118.99	128.39
43	2l	92	0TD	CSB-SB-CB	-5.85	91.85	102.36
1	1A	2605	PSU	N1-C2-N3	5.84	121.32	115.17
1	2A	1939	5MU	C4-N3-C2	-5.82	119.70	127.34
1	1A	1917	PSU	N1-C2-N3	5.70	121.18	115.17
32	2a	966	M2G	C5-C4-N3	-5.68	119.34	128.39
32	1a	516	PSU	N1-C2-N3	5.60	121.07	115.17
32	2a	1207	2MG	C5-C4-N3	-5.58	119.52	128.39
1	2A	1939	5MU	N3-C2-N1	5.57	122.14	114.89
1	1A	2552	OMU	N3-C2-N1	5.33	121.82	114.89
1	1A	1939	5MU	N3-C2-N1	5.31	121.80	114.89
1	1A	2058	MA6	N1-C2-N3	-5.30	120.56	128.58
1	2A	2251	OMG	C2-N3-C4	5.18	121.23	112.30
1	1A	1939	5MU	C4-N3-C2	-5.16	120.57	127.34
1	1A	2251	OMG	C2-N3-C4	5.11	121.10	112.30
32	2a	527	G7M	C5-C4-N3	-5.09	118.52	128.15
1	2A	1915	5MU	N3-C2-N1	5.05	121.47	114.89
32	1a	527	G7M	C5-C4-N3	-5.05	118.61	128.15
1	2A	2058	MA6	N1-C2-N3	-5.01	121.00	128.58
1	2A	1939	5MU	C5-C4-N3	4.95	119.62	115.32
1	2A	2605	PSU	C4-N3-C2	-4.93	119.58	126.37
32	1a	966	M2G	N9-C4-N3	4.89	135.74	125.95
1	1A	2552	OMU	C4-N3-C2	-4.84	120.60	126.61
32	1a	1519	MA6	N1-C2-N3	-4.84	121.26	128.58
32	1a	1518	MA6	N1-C2-N3	-4.74	121.41	128.58
1	1A	1915	5MU	C1'-N1-C2	4.72	126.06	117.59
1	1A	1939	5MU	C5-C4-N3	4.71	119.42	115.32
1	2A	2552	OMU	N3-C2-N1	4.68	120.98	114.89
1	1A	1915	5MU	C4-N3-C2	-4.65	121.24	127.34
1	1A	1915	5MU	N3-C2-N1	4.65	120.95	114.89
32	2a	1519	MA6	N1-C2-N3	-4.65	121.55	128.58
1	1A	2605	PSU	C4-N3-C2	-4.63	120.00	126.37
1	1A	1939	5MU	O4-C4-C5	-4.61	119.64	124.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1519	MA6	C5-C4-N3	-4.56	120.44	126.72
1	2A	1915	5MU	C4-N3-C2	-4.54	121.38	127.34
1	1A	2251	OMG	N9-C4-N3	4.51	134.97	125.95
32	1a	966	M2G	C2-N3-C4	4.51	120.85	112.51
32	2a	1518	MA6	N1-C2-N3	-4.50	121.76	128.58
32	2a	527	G7M	C8-N9-C4	4.49	118.21	107.09
32	1a	1519	MA6	C5-C4-N3	-4.47	120.56	126.72
1	2A	2605	PSU	O2-C2-N1	-4.47	118.18	122.79
32	2a	1518	MA6	C5-C4-N3	-4.43	120.62	126.72
1	2A	1939	5MU	O4-C4-C5	-4.38	119.91	124.92
1	2A	2058	MA6	C5-C4-N3	-4.37	120.69	126.72
1	2A	2552	OMU	C4-N3-C2	-4.37	121.19	126.61
1	2A	2251	OMG	N9-C4-N3	4.35	134.65	125.95
1	2A	1917	PSU	O2-C2-N1	-4.34	118.31	122.79
32	1a	527	G7M	C8-N9-C4	4.34	117.84	107.09
1	1A	1915	5MU	C5-C4-N3	4.32	119.08	115.32
32	2a	527	G7M	C2-N3-C4	4.30	119.70	112.30
1	1A	1915	5MU	C1'-N1-C6	-4.26	114.13	121.15
1	2A	1911	PSU	C4-N3-C2	-4.26	120.51	126.37
32	2a	1519	MA6	C4-C5-N7	-4.24	105.74	110.58
32	1a	527	G7M	C2-N3-C4	4.23	119.59	112.30
32	2a	966	M2G	C2-N3-C4	4.23	120.33	112.51
32	2a	966	M2G	N9-C4-N3	4.20	134.35	125.95
32	2a	1519	MA6	C5-N7-C8	4.14	109.96	103.45
1	1A	2058	MA6	C5-C4-N3	-4.09	121.08	126.72
1	1A	1911	PSU	C4-N3-C2	-4.09	120.73	126.37
1	2A	1917	PSU	C4-N3-C2	-4.09	120.74	126.37
32	2a	516	PSU	C4-N3-C2	-4.07	120.76	126.37
32	1a	1518	MA6	C2-N1-C6	4.06	121.76	111.83
1	2A	1915	5MU	C1'-N1-C2	4.01	124.79	117.59
1	2A	1939	5MU	C5-C6-N1	-3.98	118.99	123.31
1	1A	1911	PSU	O2-C2-N1	-3.95	118.71	122.79
32	2a	1518	MA6	C2-N1-C6	3.95	121.48	111.83
32	1a	516	PSU	C4-N3-C2	-3.92	120.97	126.37
32	2a	1518	MA6	C4-C5-N7	-3.92	106.11	110.58
32	1a	1519	MA6	C2-N1-C6	3.91	121.39	111.83
1	1A	2503	2MA	N6-C6-N1	3.91	122.31	117.03
1	1A	1917	PSU	C4-N3-C2	-3.90	120.99	126.37
1	2A	2058	MA6	C2-N1-C6	3.89	121.32	111.83
32	1a	1207	2MG	C6-C5-N7	3.88	137.35	130.29
32	2a	1400	5MC	C5-C6-N1	-3.87	119.11	123.31
1	1A	1915	5MU	O4-C4-C5	-3.85	120.51	124.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	1400	5MC	C5-C6-N1	-3.85	119.13	123.31
32	1a	1207	2MG	N9-C4-N3	3.83	133.61	125.95
32	2a	1519	MA6	C2-N1-C6	3.83	121.18	111.83
32	1a	1518	MA6	C5-C4-N3	-3.80	121.48	126.72
1	2A	1915	5MU	O4-C4-C5	-3.80	120.57	124.92
1	2A	1942	5MC	C5-C6-N1	-3.78	119.20	123.31
32	1a	527	G7M	CN7-N7-C5	3.76	131.49	126.80
1	1A	2058	MA6	C2-N1-C6	3.75	120.99	111.83
1	1A	2058	MA6	N9-C8-N7	-3.75	108.62	113.94
1	2A	1915	5MU	C5-C4-N3	3.72	118.56	115.32
32	2a	527	G7M	CN7-N7-C5	3.72	131.43	126.80
32	2a	1518	MA6	C5-N7-C8	3.71	109.28	103.45
1	1A	2058	MA6	C5-N7-C8	3.70	109.27	103.45
32	2a	1207	2MG	N9-C4-N3	3.70	133.36	125.95
1	1A	2058	MA6	C2-N3-C4	3.70	120.87	111.83
32	1a	1519	MA6	C4-C5-N7	-3.68	106.38	110.58
32	2a	1207	2MG	C6-C5-N7	3.68	136.98	130.29
32	1a	1518	MA6	C5-N7-C8	3.65	109.19	103.45
32	1a	1519	MA6	C5-N7-C8	3.63	109.16	103.45
32	2a	1207	2MG	N1-C2-N2	3.63	120.26	116.56
32	2a	1519	MA6	N9-C8-N7	-3.60	108.83	113.94
1	1A	1942	5MC	C5-C6-N1	-3.58	119.43	123.31
1	2A	2058	MA6	C2-N3-C4	3.55	120.49	111.83
32	2a	516	PSU	O2-C2-N1	-3.49	119.19	122.79
32	1a	1519	MA6	C2-N3-C4	3.46	120.27	111.83
1	1A	2251	OMG	C6-C5-N7	3.45	136.56	130.29
1	2A	2251	OMG	C6-C5-N7	3.45	136.56	130.29
32	2a	967	5MC	C5-C6-N1	-3.44	119.58	123.31
1	2A	2503	2MA	C4-C5-N7	-3.42	106.67	110.58
32	1a	1404	5MC	C5-C6-N1	-3.42	119.60	123.31
32	2a	1519	MA6	C2-N3-C4	3.41	120.16	111.83
32	1a	1518	MA6	C4-C5-N7	-3.41	106.69	110.58
1	2A	1911	PSU	O2-C2-N1	-3.40	119.28	122.79
32	1a	1518	MA6	N9-C8-N7	-3.38	109.14	113.94
1	2A	2058	MA6	C5-N7-C8	3.37	108.75	103.45
32	1a	1498	UR3	C5-C4-N3	3.34	119.44	115.04
32	1a	967	5MC	C5-C6-N1	-3.33	119.69	123.31
32	1a	1207	2MG	N1-C2-N2	3.33	119.96	116.56
32	2a	1498	UR3	C5-C4-N3	3.33	119.42	115.04
32	2a	1404	5MC	C5-C4-N3	-3.31	118.36	121.75
43	1l	92	0TD	OD2-CG-CB	3.30	120.28	113.15
1	2A	2058	MA6	C4-C5-N7	-3.30	106.81	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	2a	1407	5MC	C5-C6-N1	-3.27	119.77	123.31
32	2a	966	M2G	C6-C5-N7	3.26	136.22	130.29
1	2A	2503	2MA	C4-N9-C8	3.26	109.16	105.74
1	1A	2503	2MA	C4-C5-N7	-3.26	106.86	110.58
32	2a	1207	2MG	N2-C2-N3	-3.25	116.37	120.51
32	2a	1518	MA6	C2-N3-C4	3.23	119.71	111.83
32	1a	527	G7M	C1'-N9-C8	-3.22	115.87	126.74
1	1A	2058	MA6	N3-C4-N9	3.21	132.63	127.17
1	2A	1939	5MU	O2-C2-N1	-3.20	118.63	122.80
1	2A	2552	OMU	O2-C2-N1	-3.15	118.70	122.80
1	2A	1915	5MU	C1'-N1-C6	-3.15	115.97	121.15
32	1a	1518	MA6	C2-N3-C4	3.12	119.44	111.83
1	1A	1915	5MU	C5M-C5-C4	3.11	122.10	118.78
32	1a	1519	MA6	N9-C8-N7	-3.11	109.53	113.94
1	2A	2552	OMU	C5-C4-N3	3.10	119.14	114.80
32	2a	527	G7M	C1'-N9-C8	-3.08	116.33	126.74
32	1a	1407	5MC	C5-C6-N1	-3.07	119.98	123.31
1	1A	2605	PSU	C5-C6-N1	-3.06	117.89	122.14
32	2a	1518	MA6	N9-C8-N7	-3.06	109.59	113.94
1	1A	2552	OMU	O2-C2-N1	-3.06	118.81	122.80
1	1A	1962	5MC	C5-C6-N1	-2.98	120.08	123.31
32	2a	1207	2MG	C4-C5-N7	-2.96	105.97	110.67
32	1a	516	PSU	O2-C2-N1	-2.96	119.74	122.79
1	1A	1939	5MU	C5-C6-N1	-2.95	120.11	123.31
32	1a	1207	2MG	C4-C5-N7	-2.95	105.99	110.67
1	2A	2058	MA6	N9-C8-N7	-2.89	109.83	113.94
1	2A	1962	5MC	C5-C6-N1	-2.89	120.17	123.31
1	1A	2058	MA6	C4-C5-N7	-2.89	107.28	110.58
32	1a	966	M2G	C6-C5-N7	2.88	135.53	130.29
32	1a	1402	4OC	C6-C5-C4	2.84	120.42	117.00
32	1a	1407	5MC	C5-C4-N3	-2.80	118.89	121.75
1	1A	2552	OMU	C5-C4-N3	2.78	118.69	114.80
1	1A	2251	OMG	C4-C5-N7	-2.77	106.28	110.67
1	2A	2503	2MA	C2-N1-C6	2.75	122.33	118.10
32	2a	1404	5MC	C5-C6-N1	-2.73	120.35	123.31
1	2A	2058	MA6	N3-C4-N9	2.72	131.80	127.17
32	2a	1518	MA6	C4-C5-C6	2.72	118.72	115.91
1	2A	2552	OMU	C2'-C1'-N1	-2.72	109.08	114.24
32	1a	1498	UR3	C3U-N3-C2	2.68	122.01	117.33
1	2A	1920	OMC	O2-C2-N3	-2.68	118.10	122.33
1	2A	2503	2MA	C5-N7-C8	2.68	107.66	103.45
32	1a	1400	5MC	C5-C4-N3	-2.67	119.01	121.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	1917	PSU	O2-C2-N1	-2.67	120.03	122.79
1	1A	2058	MA6	C4-N9-C8	2.66	108.53	105.74
1	2A	2552	OMU	O4-C4-C5	-2.66	120.58	125.16
32	1a	1519	MA6	N3-C4-N9	2.64	131.66	127.17
1	2A	1942	5MC	C5-C4-N3	-2.64	119.05	121.75
1	1A	1962	5MC	C1'-N1-C6	-2.61	116.85	121.15
32	1a	1404	5MC	C5-C4-N3	-2.61	119.08	121.75
1	1A	2552	OMU	O4-C4-C5	-2.60	120.67	125.16
32	1a	527	G7M	O6-C6-C5	-2.60	122.21	128.01
1	2A	2503	2MA	N6-C6-N1	2.60	120.53	117.03
32	2a	1407	5MC	C5-C4-N3	-2.59	119.10	121.75
43	2l	92	0TD	OD2-CG-CB	2.59	118.75	113.15
32	2a	1519	MA6	N3-C4-N9	2.59	131.57	127.17
32	2a	967	5MC	C5-C4-N3	-2.58	119.11	121.75
1	1A	2552	OMU	C2'-C1'-N1	-2.56	109.38	114.24
1	2A	1962	5MC	C5-C4-N3	-2.54	119.15	121.75
32	2a	966	M2G	C4-C5-N7	-2.51	106.69	110.67
1	2A	2251	OMG	C4-C5-N7	-2.51	106.69	110.67
1	1A	1920	OMC	O2-C2-N3	-2.49	118.41	122.33
32	2a	1400	5MC	C5-C4-N3	-2.48	119.21	121.75
32	1a	1207	2MG	N2-C2-N3	-2.48	117.36	120.51
32	2a	1402	4OC	C6-C5-C4	2.45	119.95	117.00
32	2a	1518	MA6	N3-C4-N9	2.44	131.32	127.17
1	1A	2503	2MA	C2-N1-C6	2.43	121.84	118.10
32	1a	1518	MA6	N3-C4-N9	2.42	131.29	127.17
1	2A	1915	5MU	C5-C6-N1	-2.42	120.68	123.31
32	1a	967	5MC	C5-C4-N3	-2.40	119.30	121.75
1	1A	1939	5MU	O2-C2-N1	-2.40	119.67	122.80
32	2a	527	G7M	O6-C6-C5	-2.39	122.67	128.01
1	2A	1915	5MU	O2-C2-N3	-2.39	117.08	121.49
32	2a	1519	MA6	C4-C5-C6	2.39	118.38	115.91
32	1a	1207	2MG	CM2-N2-C2	-2.39	118.52	123.65
32	2a	1404	5MC	O2-C2-N3	-2.37	118.59	122.33
1	1A	1962	5MC	C5-C4-N3	-2.37	119.32	121.75
1	2A	2503	2MA	N9-C8-N7	-2.37	110.57	113.94
1	1A	2503	2MA	C5-N7-C8	2.36	107.16	103.45
1	1A	2605	PSU	O2-C2-N1	-2.35	120.36	122.79
32	2a	516	PSU	O4'-C1'-C2'	2.35	108.40	105.15
32	1a	1207	2MG	O3'-C3'-C2'	2.31	119.21	111.82
32	1a	1498	UR3	C6-N1-C2	-2.28	119.93	121.80
32	1a	966	M2G	C4-C5-N7	-2.28	107.06	110.67
32	2a	1207	2MG	CM2-N2-C2	-2.24	118.85	123.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1a	966	M2G	O6-C6-C5	-2.23	120.63	126.53
32	1a	1519	MA6	C4-C5-C6	2.23	118.21	115.91
32	2a	1407	5MC	O2-C2-N3	-2.20	118.86	122.33
1	1A	1962	5MC	CM5-C5-C6	-2.20	119.87	122.85
1	1A	1915	5MU	C5M-C5-C6	-2.19	119.89	122.85
1	1A	1915	5MU	C5-C6-N1	-2.19	120.94	123.31
43	1l	92	0TD	OD1-CG-CB	-2.18	117.86	122.44
1	1A	2251	OMG	O6-C6-C5	-2.16	120.84	126.53
1	1A	1942	5MC	C5-C4-N3	-2.15	119.55	121.75
1	1A	1915	5MU	O2-C2-N3	-2.15	117.52	121.49
1	2A	2503	2MA	C6-C5-N7	2.15	136.23	132.09
1	2A	1911	PSU	C5-C6-N1	-2.15	119.16	122.14
1	1A	2251	OMG	C8-N7-C5	2.14	108.06	104.26
32	2a	1498	UR3	C3U-N3-C4	2.13	120.82	117.87
1	2A	1915	5MU	C6-N1-C2	-2.10	119.21	121.30
32	1a	1407	5MC	O2-C2-N3	-2.09	119.04	122.33
1	2A	1911	PSU	O4'-C1'-C2'	2.09	108.04	105.15
1	1A	1911	PSU	C5-C6-N1	-2.07	119.27	122.14
1	1A	2503	2MA	C4-N9-C8	2.06	107.90	105.74
32	2a	1518	MA6	C5-C4-N9	2.06	108.06	105.81
32	1a	1402	4OC	O2-C2-N3	-2.06	119.08	122.33
1	2A	2605	PSU	C5-C6-N1	-2.05	119.29	122.14
32	2a	516	PSU	C5-C6-N1	-2.04	119.31	122.14
1	2A	2251	OMG	O6-C6-C5	-2.03	121.18	126.53
1	1A	1917	PSU	C5-C6-N1	-2.03	119.33	122.14
32	2a	527	G7M	C5-C6-N1	2.02	116.02	111.84
32	1a	516	PSU	O4'-C1'-C2'	2.02	107.94	105.15
32	1a	1207	2MG	C2-N1-C6	-2.01	122.11	124.55
1	1A	1911	PSU	O4'-C1'-C2'	2.01	107.94	105.15
32	1a	516	PSU	C6-C5-C4	-2.01	116.82	118.17
32	2a	966	M2G	O6-C6-C5	-2.00	121.25	126.53

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1A	1915	5MU	O4'-C1'-N1-C2
1	1A	1915	5MU	O4'-C1'-N1-C6
1	1A	2251	OMG	C1'-C2'-O2'-CM2
1	2A	1915	5MU	O4'-C1'-N1-C2
1	2A	1915	5MU	O4'-C1'-N1-C6
43	2l	92	0TD	CG-CB-SB-CSB

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Mol	Chain	Res	Type	Atoms
32	1a	1519	MA6	O4'-C4'-C5'-O5'
32	2a	1519	MA6	O4'-C4'-C5'-O5'
43	1l	92	0TD	CG-CB-SB-CSB
32	1a	1519	MA6	C3'-C4'-C5'-O5'
32	1a	527	G7M	C3'-C4'-C5'-O5'
1	1A	2503	2MA	C4'-C5'-O5'-P
32	2a	1402	4OC	O4'-C4'-C5'-O5'
32	2a	1519	MA6	C3'-C4'-C5'-O5'
43	2l	92	0TD	CA-CB-SB-CSB
32	1a	1400	5MC	O4'-C4'-C5'-O5'
1	2A	2503	2MA	C4'-C5'-O5'-P
32	1a	527	G7M	C4'-C5'-O5'-P
1	1A	1920	OMC	C2'-C1'-N1-C2

There are no ring outliers.

22 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1A	2552	OMU	1	0
1	2A	1915	5MU	1	0
1	1A	2251	OMG	1	0
32	1a	1519	MA6	3	0
1	1A	2058	MA6	2	0
1	2A	2552	OMU	1	0
43	2l	92	0TD	1	0
32	2a	1402	4OC	3	0
32	2a	1519	MA6	1	0
32	1a	967	5MC	1	0
1	2A	1920	OMC	1	0
32	2a	1207	2MG	1	0
32	2a	1518	MA6	2	0
1	2A	2251	OMG	1	0
1	1A	1939	5MU	1	0
32	2a	1400	5MC	1	0
1	2A	2058	MA6	1	0
32	1a	1518	MA6	1	0
1	2A	1917	PSU	1	0
32	2a	1404	5MC	1	0
32	1a	1498	UR3	1	0
32	1a	1404	5MC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2523 ligands modelled in this entry, 2508 are monoatomic - leaving 15 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
60	SF4	2d	501	35	0,12,12	-	-	-		
58	ARG	1F	320	-	10,11,11	0.71	1 (10%)	9,13,13	0.90	1 (11%)
57	MPD	1T	206	-	7,7,7	0.35	0	9,10,10	0.25	0
60	SF4	1d	305	35	0,12,12	-	-	-		
55	HGR	1A	4020	-	39,39,39	2.39	7 (17%)	48,58,58	1.76	13 (27%)
56	TEL	1A	4021	-	60,62,62	1.30	5 (8%)	78,92,92	1.78	15 (19%)
57	MPD	18	105	-	7,7,7	0.26	0	9,10,10	0.35	0
56	TEL	2A	3744	-	60,62,62	1.32	5 (8%)	78,92,92	1.99	15 (19%)
57	MPD	2A	3747	-	7,7,7	0.34	0	9,10,10	0.27	0
57	MPD	1A	4022	-	7,7,7	0.34	0	9,10,10	0.22	0
57	MPD	2A	3745	-	7,7,7	0.31	0	9,10,10	0.20	0
57	MPD	2A	3746	-	7,7,7	0.33	0	9,10,10	0.15	0
55	HGR	2A	3743	-	39,39,39	2.42	10 (25%)	48,58,58	1.68	12 (25%)
58	ARG	1B	231	54	10,11,11	0.79	1 (10%)	9,13,13	1.16	1 (11%)
57	MPD	1a	3279	32	7,7,7	0.44	0	9,10,10	0.71	0

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
60	SF4	2d	501	35	-	-	0/6/5/5
58	ARG	1F	320	-	-	1/11/11/11	-
57	MPD	1T	206	-	-	2/5/5/5	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	SF4	1d	305	35	-	-	0/6/5/5
55	HGR	1A	4020	-	-	5/20/79/79	0/4/4/4
56	TEL	1A	4021	-	-	4/73/108/108	0/4/5/5
57	MPD	18	105	-	-	2/5/5/5	-
56	TEL	2A	3744	-	-	9/73/108/108	0/4/5/5
57	MPD	2A	3747	-	-	5/5/5/5	-
57	MPD	1A	4022	-	-	1/5/5/5	-
57	MPD	2A	3745	-	-	0/5/5/5	-
57	MPD	2A	3746	-	-	5/5/5/5	-
55	HGR	2A	3743	-	-	6/20/79/79	0/4/4/4
58	ARG	1B	231	54	-	5/11/11/11	-
57	MPD	1a	3279	32	-	2/5/5/5	-

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	1A	4020	HGR	C12-C14	9.05	1.55	1.33
55	2A	3743	HGR	C12-C14	9.00	1.55	1.33
55	2A	3743	HGR	C5-C4	-5.47	1.39	1.49
55	1A	4020	HGR	C5-C4	-5.43	1.39	1.49
56	2A	3744	TEL	O5-C10	5.39	1.44	1.35
56	1A	4021	TEL	O5-C10	5.35	1.44	1.35
55	1A	4020	HGR	C5-C6	-5.24	1.39	1.50
55	2A	3743	HGR	C5-C6	-5.22	1.39	1.50
56	2A	3744	TEL	O9-C15	5.04	1.45	1.34
55	2A	3743	HGR	C3-C2	-4.90	1.39	1.48
56	1A	4021	TEL	O9-C15	4.80	1.45	1.34
55	1A	4020	HGR	C3-C2	-4.70	1.39	1.48
55	2A	3743	HGR	O4-C2	4.35	1.36	1.24
55	1A	4020	HGR	O4-C2	4.27	1.35	1.24
56	2A	3744	TEL	C40-N41	-3.37	1.35	1.38
56	1A	4021	TEL	C40-N41	-3.35	1.35	1.38
55	1A	4020	HGR	O8-C23	2.92	1.46	1.41
55	2A	3743	HGR	O8-C23	2.90	1.46	1.41
56	2A	3744	TEL	O5-C2	-2.78	1.43	1.47
56	1A	4021	TEL	O9-C4	-2.75	1.41	1.46
56	1A	4021	TEL	O5-C2	-2.53	1.43	1.47
58	1B	231	ARG	OXT-C	-2.36	1.23	1.30
55	2A	3743	HGR	O9-C23	2.31	1.45	1.41
55	2A	3743	HGR	O1-C10	2.24	1.45	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	2A	3743	HGR	C17-N1	2.12	1.49	1.45
55	2A	3743	HGR	C1-C2	-2.07	1.39	1.44
58	1F	320	ARG	OXT-C	-2.04	1.24	1.30
55	1A	4020	HGR	C1-C2	-2.02	1.39	1.44
56	2A	3744	TEL	O9-C4	-2.01	1.43	1.46

All (57) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	2A	3744	TEL	O9-C15-C21	9.03	119.84	110.93
56	1A	4021	TEL	O9-C15-C21	6.50	117.35	110.93
56	2A	3744	TEL	C17-C11-N6	-6.40	103.56	113.25
56	1A	4021	TEL	C17-C11-N6	-6.24	103.80	113.25
55	1A	4020	HGR	C4-C5-C6	4.44	121.83	112.35
55	2A	3743	HGR	C4-C5-C6	4.34	121.61	112.35
56	2A	3744	TEL	C8-C4-C2	-4.25	109.38	115.23
56	2A	3744	TEL	C4-O9-C15	-4.09	111.05	118.20
56	1A	4021	TEL	N31-C37-N41	-3.92	109.23	112.35
56	1A	4021	TEL	C4-O9-C15	-3.91	111.37	118.20
56	2A	3744	TEL	N31-C37-N41	-3.70	109.40	112.35
55	1A	4020	HGR	C23-O9-C22	-3.64	100.77	106.31
55	2A	3743	HGR	C12-C6-C1	-3.59	115.35	119.35
55	2A	3743	HGR	O8-C18-C22	-3.58	98.46	106.03
55	1A	4020	HGR	C4-C3-C2	-3.37	118.90	121.81
55	1A	4020	HGR	C12-C6-C1	-3.33	115.64	119.35
58	1B	231	ARG	OXT-C-O	-3.31	116.58	124.08
56	1A	4021	TEL	C38-O32-C28	3.27	124.17	117.51
55	1A	4020	HGR	O9-C22-C18	-3.20	99.26	106.03
56	2A	3744	TEL	O20-C15-C21	-3.20	120.50	124.65
56	2A	3744	TEL	C54-C49-N53	-3.10	106.89	115.59
55	1A	4020	HGR	O1-C10-C9	-3.04	101.11	104.98
56	1A	4021	TEL	O39-C34-C28	3.03	113.49	106.44
55	2A	3743	HGR	C9-C8-C7	-3.03	98.12	101.69
55	2A	3743	HGR	O1-C10-C9	-3.02	101.13	104.98
55	2A	3743	HGR	O4-C2-C3	-3.01	116.76	121.28
56	2A	3744	TEL	C37-N41-C40	2.95	108.31	105.94
55	2A	3743	HGR	C10-C9-C8	-2.93	98.63	102.29
55	1A	4020	HGR	O8-C18-C22	-2.90	99.90	106.03
55	1A	4020	HGR	O4-C2-C3	-2.89	116.94	121.28
55	2A	3743	HGR	C4-C3-C2	-2.81	119.39	121.81
56	1A	4021	TEL	O5-C2-C1	2.76	111.67	106.80
56	2A	3744	TEL	C56-N52-C47	2.75	121.67	116.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	1A	4020	HGR	C10-C9-C8	-2.75	98.86	102.29
55	1A	4020	HGR	C1-C2-C3	2.73	121.19	116.06
56	1A	4021	TEL	C36-N31-C37	2.71	108.04	106.71
56	1A	4021	TEL	C37-N41-C40	2.63	108.05	105.94
56	2A	3744	TEL	O5-C2-C1	2.60	111.39	106.80
56	1A	4021	TEL	C54-C49-N53	-2.57	108.38	115.59
55	1A	4020	HGR	O3-C10-C9	2.55	110.83	106.69
58	1F	320	ARG	OXT-C-O	-2.53	118.34	124.08
55	2A	3743	HGR	C23-O9-C22	-2.53	102.46	106.31
56	2A	3744	TEL	C38-O32-C28	2.51	122.62	117.51
55	2A	3743	HGR	C1-C2-C3	2.51	120.77	116.06
55	2A	3743	HGR	O9-C22-C18	-2.49	100.76	106.03
56	1A	4021	TEL	O45-C50-C55	2.44	111.45	106.88
55	1A	4020	HGR	O3-C3-C2	2.39	116.86	112.51
56	2A	3744	TEL	O9-C15-O20	-2.38	119.65	123.95
56	2A	3744	TEL	O39-C34-C28	2.38	111.97	106.44
56	1A	4021	TEL	C56-N52-C47	2.33	120.94	116.85
56	2A	3744	TEL	O9-C4-C8	2.20	111.45	107.36
56	1A	4021	TEL	O9-C15-O20	-2.16	120.05	123.95
56	1A	4021	TEL	C25-C21-C15	-2.13	106.17	110.34
55	1A	4020	HGR	C19-C17-N1	2.10	114.49	110.62
56	2A	3744	TEL	O18-C13-C19	-2.08	117.54	121.30
56	1A	4021	TEL	C44-C49-N53	2.04	116.83	110.94
55	2A	3743	HGR	O3-C10-C9	2.03	109.98	106.69

There are no chirality outliers.

All (47) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
56	2A	3744	TEL	C1-C2-C4-C8
56	2A	3744	TEL	O5-C2-C4-C8
56	2A	3744	TEL	C24-C28-O32-C38
56	2A	3744	TEL	C33-C28-O32-C38
56	2A	3744	TEL	C34-C28-O32-C38
57	18	105	MPD	C2-C3-C4-O4
57	1a	3279	MPD	C2-C3-C4-O4
57	1a	3279	MPD	C2-C3-C4-C5
57	2A	3747	MPD	C2-C3-C4-O4
57	2A	3747	MPD	C2-C3-C4-C5
58	1F	320	ARG	NE-CD-CG-CB
58	1B	231	ARG	NE-CD-CG-CB
58	1B	231	ARG	CA-CB-CG-CD

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Mol	Chain	Res	Type	Atoms
55	2A	3743	HGR	C14-C12-C6-C1
55	1A	4020	HGR	C12-C14-C15-O7
55	2A	3743	HGR	C12-C14-C15-O7
55	2A	3743	HGR	C12-C14-C15-N1
58	1B	231	ARG	C-CA-CB-CG
55	1A	4020	HGR	C2-C3-O3-C10
55	2A	3743	HGR	C2-C3-O3-C10
57	2A	3747	MPD	C1-C2-C3-C4
57	2A	3747	MPD	CM-C2-C3-C4
56	2A	3744	TEL	N6-C11-C17-C22
57	18	105	MPD	C2-C3-C4-C5
57	2A	3746	MPD	C2-C3-C4-C5
56	2A	3744	TEL	C44-C49-N53-C58
55	1A	4020	HGR	C12-C14-C15-N1
55	1A	4020	HGR	C16-C14-C15-O7
55	2A	3743	HGR	C16-C14-C15-O7
56	1A	4021	TEL	C24-C28-O32-C38
56	1A	4021	TEL	C33-C28-O32-C38
58	1B	231	ARG	O-C-CA-N
55	2A	3743	HGR	C16-C14-C15-N1
56	1A	4021	TEL	C34-C28-O32-C38
58	1B	231	ARG	OXT-C-CA-N
57	1T	206	MPD	O2-C2-C3-C4
57	2A	3746	MPD	O2-C2-C3-C4
57	2A	3747	MPD	O2-C2-C3-C4
57	1A	4022	MPD	C2-C3-C4-O4
57	1T	206	MPD	C2-C3-C4-O4
57	2A	3746	MPD	C2-C3-C4-O4
57	2A	3746	MPD	C1-C2-C3-C4
57	2A	3746	MPD	CM-C2-C3-C4
56	1A	4021	TEL	C1-C2-C4-C8
56	2A	3744	TEL	C3-C2-C4-C8
56	2A	3744	TEL	C3-C2-C4-O9
55	1A	4020	HGR	C16-C14-C15-N1

There are no ring outliers.

11 monomers are involved in 21 short contacts:

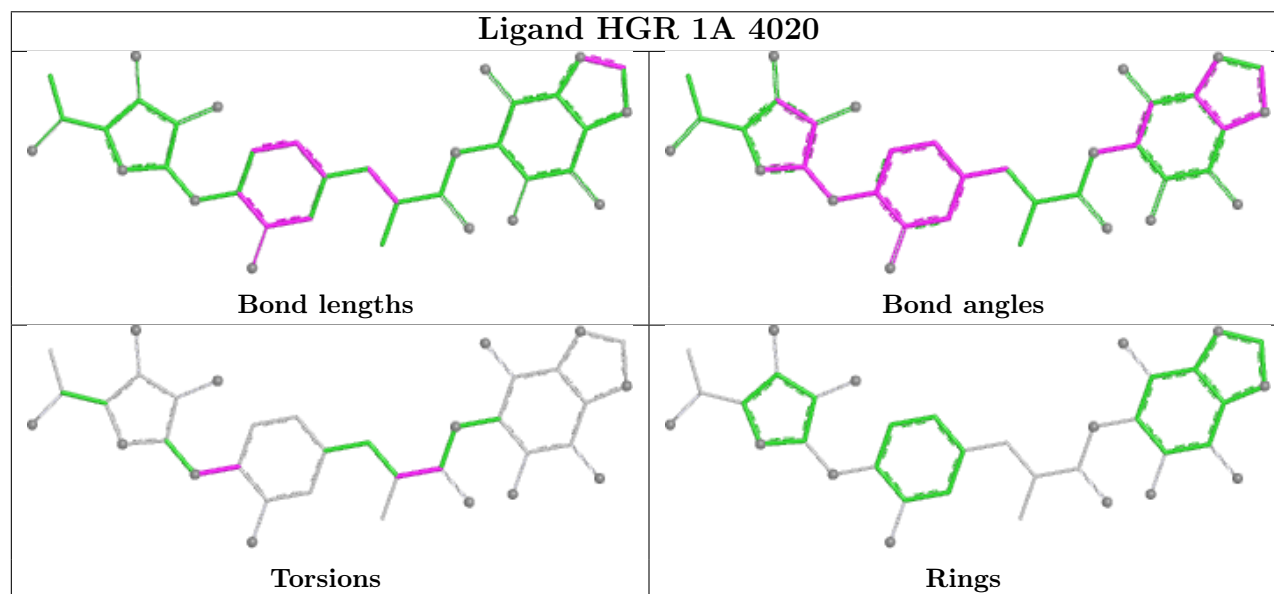
Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	1F	320	ARG	1	0
55	1A	4020	HGR	1	0
56	1A	4021	TEL	5	0

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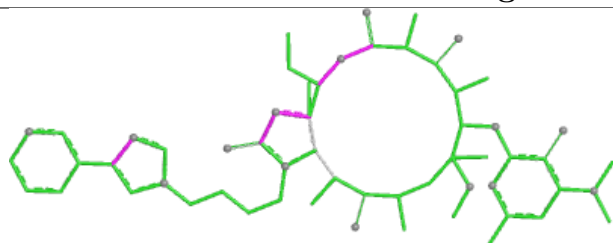
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	18	105	MPD	1	0
56	2A	3744	TEL	3	0
57	1A	4022	MPD	1	0
57	2A	3745	MPD	2	0
57	2A	3746	MPD	1	0
55	2A	3743	HGR	1	0
58	1B	231	ARG	1	0
57	1a	3279	MPD	4	0

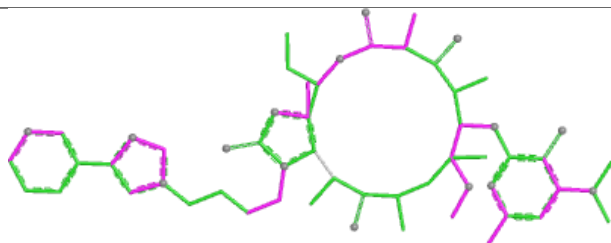
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 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.



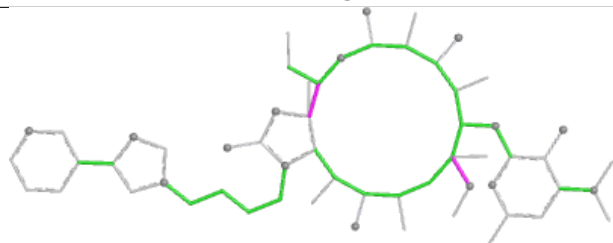
Ligand TEL 1A 4021



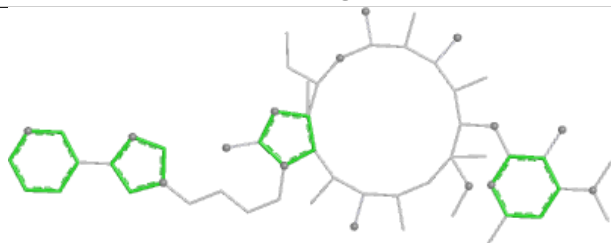
Bond lengths



Bond angles



Torsions

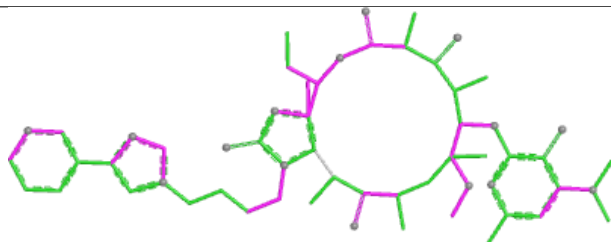


Rings

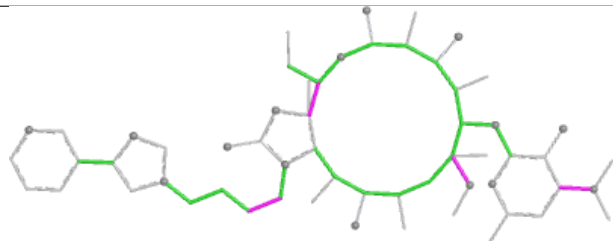
Ligand TEL 2A 3744



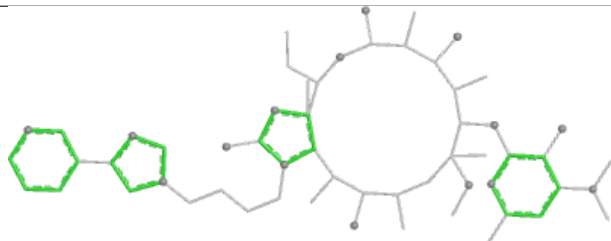
Bond lengths



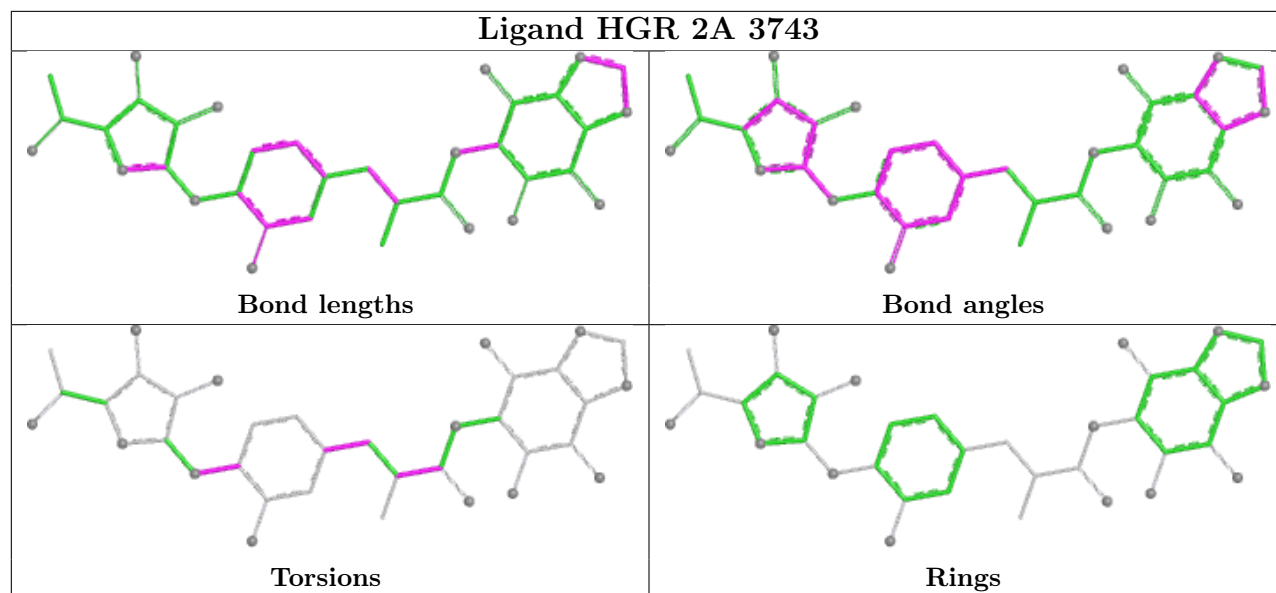
Bond angles



Torsions



Rings



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, 95th 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	1A	2860/2915 (98%)	-0.37	188 (6%) 24 27	22, 38, 89, 98	0
1	2A	2855/2915 (97%)	0.12	205 (7%) 21 24	33, 55, 90, 98	0
2	1B	120/121 (99%)	-0.11	2 (1%) 69 74	34, 53, 64, 82	0
2	2B	120/121 (99%)	0.80	4 (3%) 49 56	58, 73, 80, 85	0
3	1D	275/276 (99%)	0.06	6 (2%) 62 67	24, 36, 51, 73	0
3	2D	275/276 (99%)	0.42	9 (3%) 49 56	31, 49, 59, 73	0
4	1E	204/206 (99%)	0.11	4 (1%) 65 70	20, 41, 61, 70	0
4	2E	204/206 (99%)	0.61	7 (3%) 48 55	33, 55, 69, 77	0
5	1F	203/210 (96%)	0.28	7 (3%) 48 55	21, 45, 68, 79	0
5	2F	203/210 (96%)	0.79	9 (4%) 39 45	34, 62, 75, 80	0
6	1G	181/182 (99%)	1.15	23 (12%) 8 9	51, 65, 75, 82	0
6	2G	181/182 (99%)	2.17	95 (52%) 0 0	71, 79, 83, 86	0
7	1H	174/180 (96%)	0.50	7 (4%) 42 48	40, 53, 64, 67	0
7	2H	173/180 (96%)	1.82	63 (36%) 1 0	65, 76, 80, 86	0
8	1I	147/148 (99%)	1.26	15 (10%) 12 13	44, 68, 76, 81	0
8	2I	146/148 (98%)	1.49	30 (20%) 2 2	55, 70, 79, 82	0
9	1N	140/140 (100%)	0.11	3 (2%) 63 68	27, 39, 61, 74	0
9	2N	140/140 (100%)	0.84	4 (2%) 53 60	44, 61, 71, 74	0
10	1O	122/122 (100%)	0.05	1 (0%) 82 86	30, 40, 56, 65	0
10	2O	122/122 (100%)	0.60	4 (3%) 49 56	43, 52, 65, 71	0
11	1P	149/150 (99%)	0.36	7 (4%) 36 42	23, 47, 65, 73	0
11	2P	149/150 (99%)	0.99	16 (10%) 11 13	40, 65, 76, 82	0
12	1Q	141/141 (100%)	0.11	2 (1%) 73 78	30, 41, 54, 63	0
12	2Q	141/141 (100%)	1.21	17 (12%) 8 10	46, 61, 70, 77	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	1R	118/118 (100%)	-0.01	0 100 100	25, 37, 52, 62	0
13	2R	118/118 (100%)	0.50	1 (0%) 82 86	39, 51, 59, 67	0
14	1S	110/112 (98%)	0.78	3 (2%) 56 63	43, 54, 63, 67	0
14	2S	110/112 (98%)	1.76	39 (35%) 1 0	61, 69, 75, 79	0
15	1T	131/146 (89%)	0.44	8 (6%) 27 31	36, 45, 66, 79	0
15	2T	131/146 (89%)	0.73	6 (4%) 37 43	44, 57, 72, 77	0
16	1U	116/118 (98%)	-0.06	1 (0%) 81 84	24, 33, 49, 61	0
16	2U	116/118 (98%)	0.89	6 (5%) 33 38	40, 59, 70, 79	0
17	1V	101/101 (100%)	0.14	1 (0%) 79 83	25, 44, 58, 67	0
17	2V	101/101 (100%)	1.03	2 (1%) 65 70	41, 67, 73, 77	0
18	1W	112/113 (99%)	-0.01	2 (1%) 67 72	26, 33, 50, 81	0
18	2W	112/113 (99%)	0.48	4 (3%) 46 52	38, 49, 63, 83	0
19	1X	95/96 (98%)	0.29	2 (2%) 63 68	31, 42, 64, 72	0
19	2X	95/96 (98%)	0.93	10 (10%) 11 13	47, 58, 70, 77	0
20	1Y	107/110 (97%)	0.58	3 (2%) 55 61	38, 50, 65, 73	0
20	2Y	107/110 (97%)	1.33	17 (15%) 5 5	55, 66, 75, 82	0
21	1Z	203/206 (98%)	0.85	7 (3%) 48 55	44, 59, 71, 76	0
21	2Z	201/206 (97%)	1.74	61 (30%) 1 1	62, 73, 78, 82	0
22	10	77/85 (90%)	0.34	4 (5%) 33 38	32, 40, 57, 58	0
22	20	77/85 (90%)	1.35	11 (14%) 6 7	47, 61, 70, 74	0
23	11	97/98 (98%)	0.40	1 (1%) 79 83	30, 46, 68, 77	0
23	21	97/98 (98%)	0.66	4 (4%) 41 47	39, 54, 70, 73	0
24	12	70/72 (97%)	0.58	3 (4%) 40 45	38, 51, 61, 79	0
24	22	70/72 (97%)	1.07	5 (7%) 22 25	57, 66, 72, 75	0
25	13	59/60 (98%)	0.22	1 (1%) 69 74	28, 38, 62, 72	0
25	23	59/60 (98%)	1.14	7 (11%) 9 10	52, 60, 71, 76	0
26	14	69/71 (97%)	1.73	21 (30%) 1 1	60, 78, 85, 89	0
26	24	69/71 (97%)	2.82	55 (79%) 0 0	74, 82, 90, 92	0
27	15	59/60 (98%)	-0.06	1 (1%) 69 74	24, 37, 53, 65	0
27	25	59/60 (98%)	0.35	0 100 100	34, 51, 64, 72	0
28	16	53/54 (98%)	0.20	0 100 100	36, 45, 57, 61	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	26	53/54 (98%)	0.83	2 (3%) 44 50	52, 59, 66, 72	0
29	17	48/49 (97%)	0.15	7 (14%) 6 7	24, 29, 56, 62	0
29	27	48/49 (97%)	0.41	5 (10%) 11 13	34, 41, 62, 69	0
30	18	64/65 (98%)	0.04	0 100 100	31, 37, 43, 56	0
30	28	64/65 (98%)	0.66	1 (1%) 70 76	43, 53, 60, 62	0
31	19	37/37 (100%)	0.28	0 100 100	33, 42, 58, 59	0
31	29	37/37 (100%)	1.45	9 (24%) 2 1	57, 64, 71, 73	0
32	1a	1488/1521 (97%)	0.41	58 (3%) 43 49	38, 67, 87, 96	0
32	2a	1492/1521 (98%)	0.68	103 (6%) 23 26	45, 72, 88, 96	0
33	1b	231/256 (90%)	1.77	74 (32%) 1 0	62, 74, 81, 84	0
33	2b	231/256 (90%)	2.09	120 (51%) 0 0	70, 78, 83, 88	0
34	1c	206/239 (86%)	1.44	41 (19%) 3 3	63, 71, 80, 84	0
34	2c	206/239 (86%)	2.24	118 (57%) 0 0	67, 78, 82, 85	0
35	1d	208/209 (99%)	1.53	56 (26%) 1 1	56, 68, 75, 81	0
35	2d	208/209 (99%)	1.53	54 (25%) 1 1	58, 68, 75, 79	0
36	1e	148/162 (91%)	0.94	5 (3%) 48 55	46, 63, 70, 81	0
36	2e	148/162 (91%)	1.35	19 (12%) 7 9	56, 68, 76, 79	0
37	1f	100/101 (99%)	1.11	7 (7%) 22 25	52, 66, 72, 74	0
37	2f	100/101 (99%)	0.84	1 (1%) 79 83	53, 64, 72, 74	0
38	1g	155/156 (99%)	1.12	19 (12%) 8 10	63, 70, 77, 79	0
38	2g	155/156 (99%)	1.75	51 (32%) 1 0	69, 75, 80, 82	0
39	1h	137/138 (99%)	1.12	13 (9%) 14 16	51, 65, 72, 76	0
39	2h	137/138 (99%)	1.18	11 (8%) 18 21	61, 69, 74, 78	0
40	1i	127/128 (99%)	2.16	67 (52%) 0 0	61, 76, 81, 82	0
40	2i	126/128 (98%)	2.92	102 (80%) 0 0	70, 80, 84, 85	0
41	1j	97/105 (92%)	2.05	48 (49%) 0 0	63, 76, 82, 86	0
41	2j	96/105 (91%)	2.94	75 (78%) 0 0	70, 80, 83, 85	0
42	1k	114/129 (88%)	0.91	9 (7%) 18 21	48, 63, 71, 74	0
42	2k	114/129 (88%)	1.28	19 (16%) 4 4	55, 68, 75, 79	0
43	1l	121/132 (91%)	0.88	10 (8%) 17 19	47, 58, 67, 70	0
43	2l	121/132 (91%)	1.13	15 (12%) 8 9	53, 65, 69, 72	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	1m	116/126 (92%)	1.50	23 (19%) 3 3	62, 73, 78, 80	0
44	2m	114/126 (90%)	2.46	73 (64%) 0 0	75, 80, 83, 87	0
45	1n	60/61 (98%)	1.67	16 (26%) 1 1	63, 70, 75, 81	0
45	2n	60/61 (98%)	2.99	45 (75%) 0 0	71, 79, 83, 86	0
46	1o	88/89 (98%)	1.08	7 (7%) 18 21	45, 63, 72, 76	0
46	2o	88/89 (98%)	1.28	13 (14%) 5 6	55, 68, 74, 79	0
47	1p	82/88 (93%)	2.09	41 (50%) 0 0	60, 69, 76, 82	0
47	2p	82/88 (93%)	1.67	20 (24%) 2 1	61, 67, 75, 77	0
48	1q	99/105 (94%)	1.39	16 (16%) 4 5	54, 66, 74, 78	0
48	2q	99/105 (94%)	1.06	8 (8%) 18 20	53, 67, 74, 77	0
49	1r	68/88 (77%)	1.07	9 (13%) 7 8	55, 63, 74, 76	0
49	2r	68/88 (77%)	1.05	7 (10%) 12 13	59, 66, 74, 77	0
50	1s	83/93 (89%)	1.67	22 (26%) 1 1	66, 74, 79, 81	0
50	2s	83/93 (89%)	2.83	69 (83%) 0 0	75, 81, 85, 87	0
51	1t	96/106 (90%)	1.65	24 (25%) 2 1	61, 69, 77, 81	0
51	2t	98/106 (92%)	1.30	12 (12%) 8 10	56, 67, 78, 80	0
52	1u	23/27 (85%)	1.78	10 (43%) 0 0	66, 71, 74, 75	0
52	2u	23/27 (85%)	2.81	17 (73%) 0 0	74, 76, 79, 81	0
53	1y	97/113 (85%)	1.05	9 (9%) 14 17	51, 62, 72, 72	0
53	2y	96/113 (84%)	2.15	49 (51%) 0 0	65, 74, 80, 81	0
All	All	20764/21468 (96%)	0.67	2623 (12%) 8 9	20, 62, 82, 98	0

All (2623) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
45	2n	2	ALA	11.2
1	2A	652(U)	G	8.5
1	2A	653	A	8.4
1	2A	652(V)	C	8.3
1	2A	652(C)	G	7.9
15	1T	37	GLY	7.5
51	2t	6	PRO	7.1
41	2j	75	ILE	6.8
45	1n	2	ALA	6.8
26	24	56	VAL	6.6

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Mol	Chain	Res	Type	RSRZ
1	1A	654	A	6.6
1	2A	654	A	6.6
1	1A	1087	G	6.5
53	2y	98	ALA	6.5
1	2A	652(T)	C	6.4
26	24	49	PHE	6.3
26	14	56	VAL	6.2
41	2j	37	PRO	6.2
51	1t	103	GLY	6.1
40	2i	7	THR	6.1
1	2A	2139	C	6.1
40	2i	126	SER	6.1
1	1A	653	A	6.0
50	2s	2	PRO	5.9
40	1i	19	LEU	5.9
32	2a	1030(A)	G	5.8
1	1A	1076	C	5.8
41	2j	34	VAL	5.8
23	11	2	SER	5.8
1	1A	1088	A	5.6
7	2H	45	VAL	5.6
1	2A	2174	C	5.6
40	2i	18	PHE	5.6
1	1A	1078	U	5.6
35	1d	166	LYS	5.6
44	2m	102	ARG	5.5
53	1y	98	ALA	5.5
39	2h	2	LEU	5.5
15	1T	130	ALA	5.4
40	1i	106	ALA	5.4
40	2i	2	GLU	5.4
45	2n	5	ALA	5.4
1	2A	652(D)	C	5.4
7	1H	2	SER	5.3
1	2A	2127	G	5.3
45	2n	13	THR	5.3
40	1i	56	LEU	5.3
1	1A	1077	A	5.3
1	1A	1080	C	5.3
45	1n	22	THR	5.3
24	12	70	GLN	5.3
1	2A	2138	C	5.2

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Mol	Chain	Res	Type	RSRZ
33	2b	237	ALA	5.2
44	1m	2	ALA	5.2
1	2A	2125	G	5.2
41	2j	72	VAL	5.1
1	2A	1509	C	5.1
34	1c	2	GLY	5.1
41	1j	4	ILE	5.1
15	1T	131	ALA	5.1
45	2n	33	VAL	5.1
1	2A	2793	G	5.1
51	2t	103	GLY	5.1
52	2u	14	TRP	5.1
45	2n	18	VAL	5.1
40	2i	127	LYS	5.0
25	23	2	PRO	5.0
1	1A	1073	A	5.0
1	1A	652(V)	C	5.0
35	1d	194	LEU	5.0
23	21	2	SER	4.9
1	1A	2602	A	4.9
44	2m	116	THR	4.9
1	2A	2136	C	4.9
6	2G	3	LEU	4.9
21	1Z	192	ALA	4.9
40	2i	11	LYS	4.9
1	2A	2173	A	4.9
50	2s	34	TRP	4.9
1	2A	2172	U	4.9
1	2A	652(B)	A	4.9
7	2H	71	LEU	4.9
1	2A	1091	G	4.9
1	2A	2124	G	4.9
1	2A	2805	G	4.9
40	2i	125	TYR	4.9
45	2n	7	ILE	4.9
40	2i	102	LEU	4.8
29	27	48	LYS	4.8
1	1A	652(C)	G	4.8
1	1A	2805	G	4.8
40	2i	14	VAL	4.8
1	1A	1509	C	4.8
1	2A	2803	C	4.8

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Mol	Chain	Res	Type	RSRZ
44	2m	6	GLY	4.8
33	2b	236	TYR	4.8
15	2T	130	ALA	4.8
40	2i	10	ARG	4.8
41	2j	47	PHE	4.8
1	1A	1072	C	4.8
1	2A	2162	G	4.7
34	2c	207	VAL	4.7
1	1A	1090	U	4.7
33	2b	136	VAL	4.7
41	1j	34	VAL	4.7
41	2j	38	ILE	4.7
1	2A	1046	A	4.7
1	2A	2126	A	4.7
1	2A	2135	A	4.7
52	2u	16	GLY	4.7
50	2s	15	LEU	4.7
1	1A	2803	C	4.6
1	2A	652(E)	G	4.6
1	2A	2153	G	4.6
1	2A	2159	G	4.6
1	2A	2802	G	4.6
20	2Y	1	MET	4.6
6	2G	139	LEU	4.6
1	2A	2147	G	4.6
26	24	54	GLY	4.6
1	2A	2150	U	4.6
33	1b	230	VAL	4.6
1	1A	1089	G	4.6
50	2s	35	SER	4.6
1	1A	2804	C	4.6
34	2c	94	LEU	4.6
38	2g	80	VAL	4.6
1	2A	2152	G	4.5
26	14	59	PHE	4.5
1	1A	1066	U	4.5
1	2A	2140	C	4.5
40	2i	64	THR	4.5
1	1A	1086	A	4.5
32	2a	1031	G	4.5
33	2b	230	VAL	4.5
50	2s	9	VAL	4.5

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Mol	Chain	Res	Type	RSRZ
1	1A	1065	U	4.5
3	1D	275	LYS	4.5
12	2Q	104	PHE	4.5
12	2Q	59	ARG	4.5
41	2j	76	ASN	4.5
40	1i	125	TYR	4.4
47	1p	19	ILE	4.4
44	2m	100	GLY	4.4
32	1a	1257	U	4.4
1	1A	2107	C	4.4
52	2u	24	ARG	4.4
1	2A	1085	A	4.4
34	2c	87	LEU	4.4
44	2m	113	PRO	4.4
26	24	63	TYR	4.4
50	1s	9	VAL	4.4
1	1A	1062	G	4.4
1	2A	2168	G	4.4
33	2b	44	LEU	4.4
32	2a	1030(B)	C	4.4
34	2c	152	ILE	4.4
40	2i	17	VAL	4.4
40	2i	44	VAL	4.4
40	2i	5	TYR	4.3
6	2G	76	SER	4.3
40	2i	101	PHE	4.3
1	1A	1079	C	4.3
1	2A	1536	C	4.3
1	2A	2804	C	4.3
1	1A	2117	A	4.3
1	2A	1070	A	4.3
35	1d	169	LYS	4.3
45	2n	15	LYS	4.3
44	2m	90	LEU	4.3
26	24	45	GLY	4.3
14	2S	35	ILE	4.3
41	1j	74	ILE	4.3
26	14	63	TYR	4.3
47	1p	59	TRP	4.3
1	1A	1067	A	4.3
1	2A	2602	A	4.3
35	1d	168	ARG	4.3

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Mol	Chain	Res	Type	RSRZ
33	1b	17	PHE	4.3
1	1A	652(S)	C	4.3
1	1A	2794	C	4.3
1	2A	2128	C	4.3
1	2A	2137	C	4.3
1	2A	2145	C	4.3
32	2a	1027	C	4.3
44	1m	4	ILE	4.3
1	1A	1093	G	4.3
1	2A	2155	G	4.3
33	1b	237	ALA	4.2
39	1h	2	LEU	4.2
41	2j	55	LYS	4.2
1	1A	652(U)	G	4.2
26	24	50	VAL	4.2
53	2y	38	HIS	4.2
40	2i	45	ALA	4.2
41	2j	27	ALA	4.2
41	2j	40	LEU	4.2
51	1t	10	LEU	4.2
50	2s	68	GLY	4.2
51	2t	100	ILE	4.2
1	2A	2146	C	4.2
6	2G	109	VAL	4.2
1	1A	1091	G	4.2
1	2A	2148	G	4.2
51	1t	9	ASN	4.2
1	1A	2173	A	4.2
1	2A	2169	A	4.2
6	2G	146	TYR	4.2
44	2m	66	LEU	4.2
50	2s	71	LEU	4.2
33	2b	72	GLY	4.2
33	1b	7	VAL	4.2
1	2A	2154	G	4.2
32	2a	1001(A)	G	4.2
1	2A	2134	A	4.2
33	1b	236	TYR	4.2
40	2i	4	TYR	4.2
29	17	48	LYS	4.2
47	2p	48	TRP	4.2
50	2s	10	PHE	4.2

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Mol	Chain	Res	Type	RSRZ
40	1i	64	THR	4.2
44	2m	22	ILE	4.1
1	1A	2793	G	4.1
41	2j	91	PRO	4.1
20	1Y	1	MET	4.1
1	2A	2893	G	4.1
1	2A	2894	G	4.1
50	2s	16	LEU	4.1
33	2b	152	PHE	4.1
34	2c	192	THR	4.1
33	2b	97	TRP	4.1
41	2j	44	VAL	4.1
50	2s	3	ARG	4.1
1	1A	1075	C	4.1
50	2s	30	LEU	4.1
41	1j	87	THR	4.1
45	2n	3	ARG	4.1
50	2s	12	ASP	4.1
40	2i	41	VAL	4.1
6	2G	87	PRO	4.1
32	2a	1257	U	4.0
34	2c	33	LEU	4.0
50	2s	69	HIS	4.0
40	2i	62	TYR	4.0
34	1c	90	GLU	4.0
1	1A	1081	U	4.0
1	2A	1088	A	4.0
35	1d	157	LEU	4.0
40	1i	102	LEU	4.0
41	2j	32	ALA	4.0
34	2c	57	ILE	4.0
35	2d	5	ILE	4.0
53	2y	5	ILE	4.0
33	2b	165	VAL	4.0
1	2A	1076	C	4.0
3	1D	276	LYS	4.0
45	2n	16	PHE	4.0
35	1d	179	GLU	4.0
40	2i	88	TYR	4.0
6	1G	52	ILE	4.0
26	24	35	VAL	4.0
1	1A	652(T)	C	4.0

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Mol	Chain	Res	Type	RSRZ
1	1A	1104	C	4.0
41	1j	32	ALA	4.0
41	2j	65	LEU	4.0
1	2A	2133	G	4.0
41	2j	78	ASN	4.0
50	1s	13	ASP	4.0
46	1o	3	ILE	4.0
26	24	58	ARG	3.9
44	1m	102	ARG	3.9
40	2i	47	LEU	3.9
44	2m	24	GLY	3.9
51	1t	97	ALA	3.9
6	1G	48	GLU	3.9
45	2n	34	TYR	3.9
26	14	50	VAL	3.9
44	2m	7	VAL	3.9
50	2s	41	VAL	3.9
1	1A	652(D)	C	3.9
1	1A	888	C	3.9
1	2A	2129	C	3.9
40	2i	56	LEU	3.9
51	1t	99	LEU	3.9
53	2y	97	ALA	3.9
44	1m	116	THR	3.9
33	2b	122	PHE	3.9
1	1A	2155	G	3.9
32	2a	1036	G	3.9
35	2d	20	TYR	3.9
36	2e	13	ILE	3.9
38	2g	154	TYR	3.9
53	2y	9	GLN	3.9
40	1i	86	VAL	3.9
44	2m	98	VAL	3.9
40	2i	99	LEU	3.9
14	2S	61	ASN	3.9
38	2g	5	ARG	3.9
45	2n	14	PRO	3.9
1	1A	1063	G	3.9
1	1A	2159	G	3.9
32	2a	1032	G	3.9
14	2S	92	TYR	3.9
33	2b	93	VAL	3.9

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Mol	Chain	Res	Type	RSRZ
41	2j	36	GLY	3.9
1	1A	1064	C	3.9
1	1A	2174	C	3.9
32	2a	1030	C	3.9
34	2c	60	ALA	3.9
6	2G	20	ILE	3.8
1	1A	2112	G	3.8
34	2c	159	GLY	3.8
39	1h	112	LEU	3.8
41	2j	90	LEU	3.8
1	2A	2107	C	3.8
1	2A	2142	C	3.8
1	2A	2143	C	3.8
50	2s	29	ARG	3.8
26	24	51	ASP	3.8
32	1a	1447	A	3.8
32	1a	1492	A	3.8
26	14	49	PHE	3.8
52	2u	23	PRO	3.8
33	1b	200	ILE	3.8
32	2a	1003	G	3.8
8	2I	5	LEU	3.8
11	2P	15	ARG	3.8
22	20	84	LEU	3.8
26	14	55	ARG	3.8
33	2b	121	LEU	3.8
41	2j	93	GLY	3.8
1	1A	2129	C	3.8
1	2A	2896	C	3.8
32	1a	1030(B)	C	3.8
40	2i	46	ALA	3.8
1	1A	2119	A	3.8
1	2A	229	A	3.8
1	2A	1084	A	3.8
1	2A	1062	G	3.8
1	2A	2116	G	3.8
21	2Z	42	VAL	3.8
32	1a	1026	G	3.8
40	2i	108	VAL	3.8
5	2F	21	ALA	3.8
45	2n	59	ALA	3.8
1	1A	2143	C	3.8

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Mol	Chain	Res	Type	RSRZ
1	2A	2117	A	3.8
1	2A	2176	A	3.8
32	1a	1001	A	3.8
32	2a	1035	A	3.8
1	2A	2109	U	3.8
34	2c	77	ILE	3.8
33	2b	21	ARG	3.8
33	1b	10	LEU	3.8
1	1A	2115	G	3.7
33	1b	229	VAL	3.8
35	1d	174	LEU	3.8
38	2g	81	GLY	3.8
6	2G	145	THR	3.7
1	2A	1064	C	3.7
1	1A	2167	U	3.7
26	24	55	ARG	3.7
26	24	14	ILE	3.7
41	1j	72	VAL	3.7
1	2A	1087	G	3.7
1	2A	1089	G	3.7
32	1a	1036	G	3.7
29	17	45	ALA	3.7
1	2A	1079	C	3.7
1	2A	2119	A	3.7
1	1A	271(K)	U	3.7
35	2d	71	SER	3.7
35	1d	110	PHE	3.7
40	2i	59	PHE	3.7
7	2H	136	ILE	3.7
6	2G	175	LEU	3.7
19	1X	95	LEU	3.7
26	24	28	LYS	3.7
35	2d	23	GLY	3.7
44	1m	100	GLY	3.7
50	2s	26	GLY	3.7
7	2H	44	VAL	3.7
47	2p	82	GLN	3.7
18	2W	60	ASN	3.7
44	2m	23	TYR	3.7
44	2m	105	THR	3.7
1	1A	1068	G	3.7
1	2A	2110	G	3.7

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Mol	Chain	Res	Type	RSRZ
1	2A	2151	G	3.7
32	1a	1030(A)	G	3.7
40	1i	94	ALA	3.7
52	2u	6	ARG	3.7
1	2A	1067	A	3.7
26	24	29	PRO	3.7
50	2s	14	HIS	3.7
44	2m	9	ILE	3.7
8	1I	147	GLN	3.7
40	2i	6	GLY	3.7
40	2i	19	LEU	3.7
52	2u	2	GLY	3.7
34	1c	207	VAL	3.7
44	2m	82	MET	3.7
14	1S	3	ARG	3.7
10	2O	51	ALA	3.7
45	2n	30	ALA	3.7
1	1A	1058	G	3.7
1	1A	2166	G	3.7
1	2A	2160	G	3.7
1	1A	6	A	3.7
34	2c	128	PHE	3.6
41	2j	63	PHE	3.6
47	1p	82	GLN	3.6
21	2Z	170	THR	3.6
7	2H	165	ALA	3.6
40	1i	46	ALA	3.6
25	13	2	PRO	3.6
1	1A	2147	G	3.6
32	2a	1026	G	3.6
26	24	5	ILE	3.6
33	1b	127	ILE	3.6
33	2b	17	PHE	3.6
51	1t	18	GLN	3.6
53	2y	39	ILE	3.6
40	2i	69	GLY	3.6
6	2G	70	VAL	3.6
26	24	21	VAL	3.6
33	2b	7	VAL	3.6
35	1d	170	VAL	3.6
40	2i	53	VAL	3.6
45	2n	25	VAL	3.6

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Mol	Chain	Res	Type	RSRZ
47	1p	53	VAL	3.6
1	1A	2132	U	3.6
1	2A	2118	U	3.6
33	2b	123	ALA	3.6
49	1r	24	ALA	3.6
33	2b	148	TYR	3.6
45	2n	21	TYR	3.6
1	2A	2161	C	3.6
40	2i	67	GLY	3.6
5	2F	181	LEU	3.6
41	2j	8	LEU	3.6
44	1m	56	LEU	3.6
6	2G	147	ASP	3.6
44	2m	106	ASN	3.6
45	2n	22	THR	3.6
33	1b	97	TRP	3.6
50	2s	19	VAL	3.6
53	1y	97	ALA	3.6
43	1l	64	TYR	3.6
1	1A	2116	G	3.6
1	1A	2133	G	3.6
1	2A	2807	G	3.6
47	1p	1	MET	3.6
51	1t	100	ILE	3.6
5	1F	208	GLY	3.6
40	1i	33	PHE	3.6
41	2j	54	PHE	3.6
40	1i	127	LYS	3.6
41	2j	67	THR	3.6
50	2s	11	VAL	3.6
50	2s	59	PRO	3.6
1	1A	2108	C	3.5
1	1A	2153	G	3.5
6	2G	52	ILE	3.5
40	2i	37	PHE	3.5
34	2c	52	LEU	3.5
41	1j	76	ASN	3.5
3	2D	2	ALA	3.5
40	2i	61	ALA	3.5
41	1j	26	ALA	3.5
26	24	66	SER	3.5
41	2j	19	SER	3.5

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Mol	Chain	Res	Type	RSRZ
1	1A	34	C	3.5
32	1a	1023	G	3.5
44	2m	84	ILE	3.5
14	2S	58	LEU	3.5
33	1b	213	LEU	3.5
26	24	40	HIS	3.5
33	2b	16	HIS	3.5
22	20	43	THR	3.5
21	2Z	68	PRO	3.5
33	1b	131	PRO	3.5
40	1i	21	PRO	3.5
29	27	47	ARG	3.5
40	1i	128	ARG	3.5
40	1i	15	ALA	3.5
40	2i	15	ALA	3.5
21	2Z	1	MET	3.5
1	1A	2158	A	3.5
1	2A	2179	C	3.5
36	2e	22	GLY	3.5
41	2j	10	GLY	3.5
45	2n	55	GLY	3.5
1	2A	2149	G	3.5
33	1b	19	HIS	3.5
6	2G	80	PHE	3.5
1	2A	2144	U	3.5
14	2S	3	ARG	3.5
33	2b	67	THR	3.5
41	1j	100	THR	3.5
45	2n	12	ARG	3.5
44	2m	41	PRO	3.5
53	2y	14	PRO	3.5
7	2H	169	VAL	3.5
50	2s	51	VAL	3.5
34	2c	187	ALA	3.5
1	1A	1057	A	3.5
1	2A	2801(A)	A	3.5
32	1a	1030	C	3.5
46	1o	89	GLY	3.5
26	24	22	ILE	3.5
26	24	32	TYR	3.5
41	2j	23	ILE	3.5
53	2y	40	ILE	3.5

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Mol	Chain	Res	Type	RSRZ
1	1A	1176	G	3.5
1	2A	2141	G	3.5
1	2A	2157	G	3.5
26	24	59	PHE	3.5
32	2a	1033	G	3.5
40	2i	91	ASP	3.5
1	2A	2130	U	3.5
6	2G	5	VAL	3.4
8	2I	19	VAL	3.4
14	2S	33	LYS	3.4
44	1m	117	VAL	3.4
34	2c	65	ALA	3.4
53	2y	94	ALA	3.4
40	2i	117	HIS	3.4
40	2i	72	GLY	3.4
45	2n	38	GLY	3.4
1	2A	2111	C	3.4
1	2A	2175	C	3.4
26	14	32	TYR	3.4
26	24	9	LEU	3.4
41	2j	46	ARG	3.4
45	1n	3	ARG	3.4
34	1c	193	TYR	3.4
53	2y	4	ASN	3.4
1	1A	2154	G	3.4
6	2G	117	PHE	3.4
33	2b	70	PHE	3.4
33	1b	125	PRO	3.4
44	2m	43	THR	3.4
53	2y	45	PRO	3.4
33	1b	165	VAL	3.4
41	2j	64	GLU	3.4
50	2s	84	GLY	3.4
1	1A	2136	C	3.4
1	2A	2108	C	3.4
6	2G	53	LEU	3.4
32	1a	1029	C	3.4
38	1g	16	LEU	3.4
42	2k	117	ASN	3.4
47	2p	76	GLN	3.4
1	1A	1061	U	3.4
1	1A	1082	U	3.4

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Mol	Chain	Res	Type	RSRZ
1	2A	1090	U	3.4
42	1k	25	TYR	3.4
33	1b	122	PHE	3.4
38	2g	14	PRO	3.4
1	2A	1071	G	3.4
1	2A	2123	G	3.4
32	2a	1030(C)	G	3.4
34	2c	68	VAL	3.4
35	1d	88	VAL	3.4
38	2g	21	VAL	3.4
40	2i	109	VAL	3.4
6	1G	73	ALA	3.4
38	2g	128	ALA	3.4
40	2i	94	ALA	3.4
44	1m	51	ALA	3.4
7	2H	120	GLY	3.4
32	1a	1286	A	3.4
32	2a	1004	A	3.4
35	1d	167	GLY	3.4
8	1I	6	LEU	3.4
34	2c	5	ILE	3.4
1	2A	34	C	3.4
33	1b	232	PRO	3.4
40	2i	21	PRO	3.4
40	2i	36	TYR	3.4
41	2j	77	PRO	3.4
44	2m	59	TYR	3.4
41	2j	92	THR	3.4
1	2A	2207	G	3.4
32	2a	1002	G	3.4
26	24	10	VAL	3.4
40	2i	13	ALA	3.4
45	1n	5	ALA	3.4
50	2s	75	ALA	3.4
50	1s	68	GLY	3.4
1	1A	2130	U	3.3
6	2G	140	ILE	3.3
6	2G	152	LEU	3.3
38	2g	16	LEU	3.3
40	2i	40	LEU	3.3
40	2i	96	LEU	3.3
41	2j	98	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
1	2A	1075	C	3.3
1	2A	2164	C	3.3
38	1g	156	TRP	3.3
40	1i	37	PHE	3.3
44	2m	87	TYR	3.3
1	1A	652(E)	G	3.3
18	1W	111	HIS	3.3
6	2G	15	VAL	3.3
12	2Q	121	ALA	3.3
37	1f	90	VAL	3.3
40	2i	43	ALA	3.3
40	2i	86	VAL	3.3
41	1j	27	ALA	3.3
41	1j	33	GLN	3.3
22	20	8	GLY	3.3
35	1d	2	GLY	3.3
40	2i	105	ASP	3.3
41	1j	86	MET	3.3
1	1A	2109	U	3.3
45	2n	6	LEU	3.3
34	2c	14	ILE	3.3
41	1j	75	ILE	3.3
41	2j	74	ILE	3.3
1	1A	2145	C	3.3
32	2a	1028	C	3.3
33	2b	57	PHE	3.3
14	2S	36	TYR	3.3
26	24	30	GLU	3.3
35	1d	173	TRP	3.3
44	2m	58	GLU	3.3
1	1A	1071	G	3.3
1	2A	2106	G	3.3
32	2a	1034	G	3.3
33	2b	164	VAL	3.3
41	2j	35	SER	3.3
33	1b	62	ALA	3.3
51	1t	101	GLY	3.3
53	2y	3	MET	3.3
1	2A	2171	A	3.3
7	2H	7	LEU	3.3
11	2P	99	LEU	3.3
33	2b	11	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
34	1c	94	LEU	3.3
41	2j	88	LEU	3.3
34	2c	157	ILE	3.3
35	2d	70	ILE	3.3
38	2g	42	ILE	3.3
1	2A	1092	C	3.3
40	2i	9	ARG	3.3
40	2i	83	ARG	3.3
35	1d	138	TYR	3.3
38	2g	85	TYR	3.3
34	2c	86	VAL	3.3
38	2g	2	ALA	3.3
33	2b	37	ASN	3.3
41	2j	69	ASN	3.3
1	2A	614(A)	U	3.3
6	2G	62	LEU	3.3
32	2a	1286	A	3.3
40	1i	47	LEU	3.3
6	2G	88	ILE	3.3
51	1t	8	ARG	3.3
1	2A	2163	C	3.3
3	2D	275	LYS	3.3
32	2a	1029	C	3.3
50	2s	74	PHE	3.3
33	1b	33	TYR	3.3
40	1i	62	TYR	3.3
47	2p	38	TYR	3.3
34	2c	189	ALA	3.2
40	1i	14	VAL	3.3
41	2j	26	ALA	3.2
44	2m	5	ALA	3.2
44	2m	60	VAL	3.3
1	2A	2165	G	3.2
41	1j	78	ASN	3.2
1	1A	2113	U	3.2
1	2A	2132	U	3.2
21	2Z	117	LEU	3.2
50	2s	5	LEU	3.2
1	1A	1508	A	3.2
1	1A	2170	A	3.2
9	1N	68	GLU	3.2
32	2a	1030(D)	A	3.2

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Mol	Chain	Res	Type	RSRZ
33	1b	22	LYS	3.2
33	1b	214	ILE	3.2
26	14	18	CYS	3.2
8	2I	92	VAL	3.2
38	2g	156	TRP	3.2
41	2j	18	ALA	3.2
42	1k	14	VAL	3.2
44	2m	45	VAL	3.2
38	2g	32	ARG	3.2
41	2j	70	ARG	3.2
51	1t	102	GLY	3.2
1	1A	2125	G	3.2
32	1a	1024	G	3.2
44	2m	31	LYS	3.2
19	2X	95	LEU	3.2
33	1b	187	LEU	3.2
1	1A	655	A	3.2
1	2A	1073	A	3.2
41	2j	6	ILE	3.2
50	2s	33	THR	3.2
40	1i	126	SER	3.2
40	2i	42	ARG	3.2
4	2E	115	GLY	3.2
6	2G	160	VAL	3.2
26	24	33	VAL	3.2
34	2c	173	VAL	3.2
41	2j	31	GLY	3.2
50	2s	58	VAL	3.2
1	1A	1094	U	3.2
26	14	69	LYS	3.2
26	24	57	GLU	3.2
40	1i	95	LYS	3.2
1	2A	2131	G	3.2
41	2j	71	LEU	3.2
41	1j	77	PRO	3.2
1	1A	2126	A	3.2
1	1A	2134	A	3.2
1	1A	2176	A	3.2
32	1a	1035	A	3.2
44	2m	4	ILE	3.2
50	2s	31	ILE	3.2
35	1d	132	ARG	3.2

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Mol	Chain	Res	Type	RSRZ
40	1i	18	PHE	3.2
52	2u	15	ARG	3.2
33	2b	133	LYS	3.2
45	2n	4	LYS	3.2
50	2s	25	LYS	3.2
8	2I	146	ALA	3.2
33	2b	38	GLY	3.2
38	2g	116	ALA	3.2
40	2i	65	VAL	3.2
44	2m	72	ALA	3.2
44	2m	76	ALA	3.2
1	1A	1101	U	3.2
2	2B	1	U	3.2
33	2b	232	PRO	3.2
34	2c	178	LEU	3.2
1	1A	2123	G	3.2
32	1a	1493	A	3.2
3	2D	259	THR	3.2
7	2H	129	THR	3.2
40	2i	16	ARG	3.1
1	1A	1102	C	3.1
41	2j	14	LYS	3.1
44	2m	65	LYS	3.1
20	2Y	91	GLU	3.1
1	2A	2167	U	3.1
32	2a	723	U	3.1
34	2c	61	ALA	3.1
34	2c	80	GLY	3.1
40	1i	4	TYR	3.1
3	1D	37	LEU	3.1
6	2G	2	PRO	3.1
40	1i	99	LEU	3.1
45	2n	54	PRO	3.1
1	1A	2157	G	3.1
1	2A	1063	G	3.1
32	1a	1030(C)	G	3.1
1	1A	2169	A	3.1
1	2A	1096	A	3.1
1	1A	1092	C	3.1
34	2c	10	PHE	3.1
40	1i	59	PHE	3.1
1	2A	1060	U	3.1

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Mol	Chain	Res	Type	RSRZ
20	2Y	80	GLY	3.1
21	1Z	51	ALA	3.1
40	2i	29	ASN	3.1
6	2G	28	VAL	3.1
8	2I	3	VAL	3.1
34	1c	76	VAL	3.1
34	2c	66	VAL	3.1
7	2H	21	PRO	3.1
14	2S	7	TYR	3.1
34	1c	52	LEU	3.1
34	2c	23	TYR	3.1
47	1p	49	LEU	3.1
52	1u	6	ARG	3.1
34	2c	124	ILE	3.1
1	1A	271(M)	G	3.1
1	1A	652(F)	G	3.1
1	1A	1046	A	3.1
1	1A	2149	G	3.1
1	1A	2168	G	3.1
1	2A	1074	G	3.1
1	2A	2892	A	3.1
32	1a	1033	G	3.1
41	2j	48	THR	3.1
41	2j	83	GLU	3.1
1	1A	2161	C	3.1
47	2p	80	PHE	3.1
6	1G	44	GLY	3.1
18	2W	112	GLY	3.1
33	1b	228	GLY	3.1
34	1c	80	GLY	3.1
48	1q	80	GLY	3.1
40	2i	106	ALA	3.1
9	2N	140	VAL	3.1
47	1p	51	VAL	3.1
21	2Z	33	LEU	3.1
40	2i	98	PRO	3.1
41	2j	39	PRO	3.1
6	1G	146	TYR	3.1
40	2i	114	TYR	3.1
41	2j	66	ARG	3.1
1	1A	887	A	3.1
1	2A	6	A	3.1

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Mol	Chain	Res	Type	RSRZ
41	2j	100	THR	3.1
1	2A	1082	U	3.1
1	2A	2122	U	3.1
6	1G	80	PHE	3.1
32	1a	1027	C	3.1
50	2s	82	GLY	3.1
34	2c	160	ALA	3.1
40	2i	119	ALA	3.1
49	2r	20	ALA	3.1
6	2G	122	PRO	3.1
21	2Z	86	VAL	3.1
33	2b	15	VAL	3.1
41	2j	79	ARG	3.1
47	1p	81	ARG	3.1
45	2n	17	LYS	3.1
33	2b	31	TYR	3.0
53	2y	54	ILE	3.0
1	1A	1103	A	3.0
1	1A	1509(A)	A	3.0
1	2A	1095	A	3.0
1	2A	2158	A	3.0
32	2a	532	A	3.0
1	2A	2792	G	3.0
47	1p	48	TRP	3.0
6	1G	76	SER	3.0
38	1g	13	GLN	3.0
42	1k	117	ASN	3.0
46	2o	86	GLY	3.0
14	2S	59	LYS	3.0
45	2n	31	ARG	3.0
52	2u	9	ARG	3.0
44	2m	18	ALA	3.0
40	2i	123	PRO	3.0
41	2j	41	PRO	3.0
9	2N	9	VAL	3.0
45	2n	56	VAL	3.0
26	24	67	TYR	3.0
40	2i	92	TYR	3.0
42	2k	25	TYR	3.0
8	2I	71	ILE	3.0
45	1n	7	ILE	3.0
1	1A	2801(A)	A	3.0

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Mol	Chain	Res	Type	RSRZ
26	24	52	THR	3.0
1	1A	2156	G	3.0
1	2A	2100	G	3.0
45	2n	61	TRP	3.0
1	1A	2172	U	3.0
1	1A	2897	U	3.0
2	1B	1	U	3.0
32	1a	1000	U	3.0
53	2y	7	SER	3.0
14	2S	60	GLY	3.0
38	1g	84	ASN	3.0
40	1i	91	ASP	3.0
46	2o	89	GLY	3.0
6	1G	46	ALA	3.0
15	2T	131	ALA	3.0
40	2i	122	ALA	3.0
44	2m	75	ALA	3.0
34	2c	141	VAL	3.0
34	2c	153	VAL	3.0
35	1d	188	LEU	3.0
35	2d	21	LEU	3.0
36	2e	119	LEU	3.0
45	2n	39	LEU	3.0
47	1p	20	VAL	3.0
48	2q	98	LEU	3.0
8	2I	109	ILE	3.0
33	2b	172	ILE	3.0
33	2b	200	ILE	3.0
33	2b	201	ILE	3.0
45	2n	49	HIS	3.0
26	14	67	TYR	3.0
50	2s	80	TYR	3.0
1	1A	2135	A	3.0
1	2A	1103	A	3.0
45	1n	13	THR	3.0
53	1y	2	THR	3.0
45	2n	50	LYS	3.0
50	2s	55	LYS	3.0
51	2t	74	LYS	3.0
1	2A	2897	U	3.0
1	1A	2160	G	3.0
1	1A	889	C	3.0

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Mol	Chain	Res	Type	RSRZ
1	2A	645	C	3.0
1	2A	1104	C	3.0
14	2S	29	PHE	3.0
8	2I	134	PRO	3.0
32	2a	470	C	3.0
32	2a	1038	C	3.0
47	1p	80	PHE	3.0
6	2G	56	ALA	3.0
6	2G	171	ALA	3.0
25	23	60	GLU	3.0
40	2i	49	PRO	3.0
39	1h	110	ALA	3.0
6	2G	90	LEU	3.0
7	2H	24	VAL	3.0
7	2H	88	LEU	3.0
7	2H	103	LEU	3.0
8	2I	38	LEU	3.0
33	2b	98	LEU	3.0
34	2c	32	LEU	3.0
34	2c	91	LEU	3.0
41	1j	85	LEU	3.0
44	2m	19	LEU	3.0
44	2m	54	VAL	3.0
47	1p	6	LEU	3.0
53	2y	27	LEU	3.0
6	2G	157	ILE	3.0
33	1b	39	ILE	3.0
3	2D	276	LYS	3.0
12	2Q	18	LYS	3.0
40	1i	66	ARG	3.0
47	1p	22	THR	3.0
47	1p	38	TYR	3.0
1	1A	2892	A	3.0
1	2A	1086	A	3.0
32	2a	1005	A	3.0
1	2A	2113	U	3.0
51	1t	11	SER	3.0
33	1b	37	ASN	3.0
34	2c	158	GLY	3.0
1	2A	1047	G	3.0
32	1a	1032	G	3.0
26	24	41	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
50	2s	76	PRO	3.0
1	1A	2896	C	2.9
6	2G	151	ALA	2.9
21	2Z	125	LEU	2.9
34	2c	101	LEU	2.9
5	1F	6	VAL	2.9
7	2H	19	VAL	2.9
7	2H	50	VAL	2.9
41	2j	80	LYS	2.9
41	2j	33	GLN	2.9
50	2s	40	ILE	2.9
50	2s	49	ILE	2.9
41	2j	42	THR	2.9
1	1A	1095	A	2.9
1	2A	271(K)	U	2.9
1	2A	2170	A	2.9
22	20	9	SER	2.9
15	1T	38	ASN	2.9
31	29	37	GLY	2.9
1	1A	1059	G	2.9
1	1A	2894	G	2.9
1	2A	2121	G	2.9
6	2G	142	PRO	2.9
6	2G	43	LEU	2.9
6	2G	133	LEU	2.9
39	1h	133	LEU	2.9
40	2i	76	ALA	2.9
46	2o	60	VAL	2.9
53	2y	46	GLN	2.9
21	2Z	124	ILE	2.9
40	2i	63	ILE	2.9
52	1u	17	THR	2.9
32	1a	1005	A	2.9
32	2a	1357	A	2.9
12	1Q	32	TYR	2.9
34	2c	90	GLU	2.9
21	2Z	132	ASN	2.9
26	14	64	GLY	2.9
40	1i	8	GLY	2.9
52	2u	4	GLY	2.9
32	2a	1024	G	2.9
33	2b	154	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
34	2c	186	PHE	2.9
44	2m	115	LYS	2.9
1	1A	2138	C	2.9
3	2D	262	ARG	2.9
6	1G	50	ALA	2.9
32	2a	979	C	2.9
34	2c	79	ARG	2.9
40	1i	20	ARG	2.9
41	2j	43	ARG	2.9
52	1u	14	TRP	2.9
53	1y	41	LEU	2.9
7	2H	15	VAL	2.9
7	2H	17	VAL	2.9
6	1G	88	ILE	2.9
6	2G	39	ILE	2.9
22	20	10	THR	2.9
32	2a	1025	U	2.9
1	2A	2114	A	2.9
32	2a	1447	A	2.9
6	1G	126	ASP	2.9
41	2j	59	SER	2.9
6	2G	12	TYR	2.9
12	2Q	32	TYR	2.9
33	2b	92	TYR	2.9
34	2c	193	TYR	2.9
42	2k	90	GLY	2.9
6	2G	112	PRO	2.9
26	24	7	PRO	2.9
53	2y	83	ARG	2.9
6	2G	50	ALA	2.9
21	2Z	67	LEU	2.9
34	2c	47	LEU	2.9
34	2c	100	ALA	2.9
34	2c	188	LEU	2.9
35	2d	164	ALA	2.9
40	2i	82	ALA	2.9
44	2m	81	LEU	2.9
1	1A	154(A)	C	2.9
1	1A	2131	G	2.9
1	1A	2146	C	2.9
32	1a	1031	G	2.9
34	2c	195	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
40	1i	17	VAL	2.9
41	2j	24	VAL	2.9
43	2l	18	VAL	2.9
5	2F	161	GLU	2.9
1	1A	2144	U	2.9
1	2A	2808	U	2.9
32	2a	1219	U	2.9
33	2b	168	THR	2.9
34	2c	8	ILE	2.9
34	2c	15	THR	2.9
1	1A	548	A	2.8
1	2A	1057	A	2.8
32	2a	1001	A	2.8
40	2i	95	LYS	2.8
42	2k	124	LYS	2.8
43	2l	17	LYS	2.8
45	2n	60	SER	2.8
48	1q	97	SER	2.8
14	2S	17	ARG	2.8
21	2Z	29	TYR	2.8
26	24	43	TYR	2.8
35	2d	39	PRO	2.8
38	2g	76	ARG	2.8
41	2j	68	HIS	2.8
44	1m	113	PRO	2.8
53	1y	95	ARG	2.8
16	1U	117	GLN	2.8
45	2n	53	LEU	2.8
47	2p	49	LEU	2.8
53	2y	41	LEU	2.8
14	2S	51	ALA	2.8
34	1c	53	ALA	2.8
50	2s	24	ALA	2.8
1	2A	2789	C	2.8
32	2a	1006	C	2.8
21	2Z	58	VAL	2.8
34	2c	103	VAL	2.8
35	1d	178	VAL	2.8
50	2s	67	VAL	2.8
6	2G	100	TRP	2.8
23	21	83	GLU	2.8
6	2G	77	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
21	2Z	133	ILE	2.8
33	2b	127	ILE	2.8
40	2i	27	THR	2.8
40	2i	103	THR	2.8
41	1j	99	LYS	2.8
51	1t	74	LYS	2.8
1	1A	1070	A	2.8
17	1V	101	GLY	2.8
32	1a	1030(D)	A	2.8
38	1g	5	ARG	2.8
40	2i	66	ARG	2.8
41	1j	28	ARG	2.8
45	1n	35	ARG	2.8
50	2s	37	ARG	2.8
16	2U	117	GLN	2.8
33	1b	148	TYR	2.8
39	2h	48	TYR	2.8
40	1i	36	TYR	2.8
44	1m	59	TYR	2.8
47	1p	32	TYR	2.8
14	2S	80	LEU	2.8
6	2G	46	ALA	2.8
21	2Z	136	PHE	2.8
33	1b	186	ALA	2.8
36	2e	86	ALA	2.8
40	1i	101	PHE	2.8
1	1A	2137	C	2.8
1	2A	1072	C	2.8
1	2A	2103	C	2.8
1	2A	2105	C	2.8
1	2A	2183	C	2.8
32	2a	1007	C	2.8
32	2a	1140	C	2.8
1	1A	2792	G	2.8
6	2G	149	VAL	2.8
34	1c	86	VAL	2.8
35	2d	198	VAL	2.8
36	1e	10	MET	2.8
41	1j	44	VAL	2.8
45	1n	25	VAL	2.8
47	1p	2	VAL	2.8
50	2s	66	MET	2.8

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Mol	Chain	Res	Type	RSRZ
53	2y	20	VAL	2.8
1	1A	2150	U	2.8
1	2A	2180	U	2.8
32	2a	1020	U	2.8
35	2d	166	LYS	2.8
40	2i	97	LYS	2.8
45	2n	9	LYS	2.8
22	20	74	ARG	2.8
24	12	69	ARG	2.8
35	1d	70	ILE	2.8
41	1j	98	ILE	2.8
34	2c	62	ASP	2.8
18	1W	112	GLY	2.8
1	1A	2790	A	2.8
50	2s	42	PRO	2.8
33	1b	154	LEU	2.8
33	2b	69	LEU	2.8
34	1c	42	LEU	2.8
34	2c	196	LEU	2.8
37	1f	19	LEU	2.8
47	1p	73	LEU	2.8
38	2g	7	ALA	2.8
49	2r	24	ALA	2.8
6	2G	23	PHE	2.8
22	20	69	PHE	2.8
1	1A	2111	C	2.8
1	2A	271(J)	C	2.8
1	2A	888	C	2.8
32	1a	1037	C	2.8
1	1A	2118	U	2.8
6	2G	38	VAL	2.8
1	2A	171	G	2.8
1	2A	1058	G	2.8
1	2A	2166	G	2.8
6	1G	83	ARG	2.8
32	1a	1001(A)	G	2.8
32	2a	1022	G	2.8
39	2h	122	ARG	2.8
44	1m	114	ARG	2.8
46	1o	88	ARG	2.8
22	10	10	THR	2.8
41	2j	82	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
44	2m	20	THR	2.8
34	2c	167	TRP	2.8
44	2m	64	TRP	2.8
5	2F	208	GLY	2.8
26	14	54	GLY	2.8
34	1c	41	GLY	2.8
34	2c	155	GLY	2.8
35	2d	2	GLY	2.8
37	1f	27	GLN	2.8
1	1A	652(A)	A	2.8
40	2i	12	GLU	2.8
14	2S	32	LEU	2.8
34	1c	47	LEU	2.8
34	1c	101	LEU	2.8
34	2c	48	TYR	2.8
34	2c	175	LEU	2.8
44	2m	34	LEU	2.8
45	2n	58	LYS	2.8
4	2E	28	ALA	2.8
34	2c	163	ALA	2.8
38	2g	83	ALA	2.8
38	2g	152	ALA	2.8
42	2k	89	ALA	2.8
45	2n	10	ALA	2.8
50	1s	24	ALA	2.8
6	2G	141	PHE	2.8
14	2S	20	ARG	2.8
1	1A	2139	C	2.8
42	2k	30	VAL	2.8
45	1n	18	VAL	2.8
1	1A	2165	G	2.7
32	2a	630	G	2.7
32	2a	1021	G	2.7
21	1Z	146	ILE	2.7
34	2c	191	THR	2.7
50	2s	48	THR	2.7
40	2i	75	ASP	2.7
42	1k	36	ASP	2.7
53	2y	35	ILE	2.7
26	24	46	GLN	2.7
12	2Q	30	GLY	2.7
33	2b	227	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
41	2j	30	SER	2.7
21	2Z	95	PRO	2.7
1	1A	1098	A	2.7
1	1A	2114	A	2.7
38	1g	8	GLU	2.7
6	2G	120	LEU	2.7
50	2s	22	LEU	2.7
12	2Q	114	ALA	2.7
23	21	26	ARG	2.7
33	2b	199	TYR	2.7
51	1t	95	ALA	2.7
1	2A	1097	U	2.7
14	2S	12	PHE	2.7
26	24	42	PHE	2.7
1	2A	2794	C	2.7
7	2H	43	VAL	2.7
8	2I	15	VAL	2.7
14	2S	49	VAL	2.7
33	2b	40	HIS	2.7
34	2c	70	VAL	2.7
43	1l	18	VAL	2.7
33	2b	208	ILE	2.7
34	1c	62	ASP	2.7
41	2j	15	THR	2.7
44	2m	39	ILE	2.7
52	2u	5	ASP	2.7
1	1A	2124	G	2.7
6	2G	24	GLY	2.7
32	2a	1220	G	2.7
53	2y	47	GLY	2.7
1	1A	1084	A	2.7
1	1A	1085	A	2.7
1	2A	1508	A	2.7
14	2S	57	LYS	2.7
34	2c	22	TRP	2.7
48	1q	87	LYS	2.7
33	2b	138	LEU	2.7
38	2g	41	ARG	2.7
40	2i	104	ARG	2.7
33	1b	123	ALA	2.7
33	1b	188	ALA	2.7
40	1i	43	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
44	2m	51	ALA	2.7
51	1t	76	ALA	2.7
51	2t	97	ALA	2.7
12	2Q	65	PHE	2.7
21	1Z	191	VAL	2.7
21	2Z	71	VAL	2.7
29	17	46	VAL	2.7
41	1j	84	GLN	2.7
32	2a	1128	C	2.7
47	2p	79	VAL	2.7
6	2G	49	ASP	2.7
26	24	44	THR	2.7
50	2s	77	THR	2.7
52	2u	17	THR	2.7
33	1b	14	GLY	2.7
33	1b	38	GLY	2.7
33	2b	42	ILE	2.7
34	2c	9	GLY	2.7
46	2o	3	ILE	2.7
50	2s	62	ILE	2.7
1	1A	1074	G	2.7
1	1A	1099	G	2.7
1	2A	2186	G	2.7
1	2A	2206	G	2.7
7	2H	175	LYS	2.7
32	1a	1034	G	2.7
33	2b	22	LYS	2.7
34	2c	114	PRO	2.7
38	2g	93	PRO	2.7
43	1l	47	LYS	2.7
43	2l	28	LYS	2.7
43	2l	47	LYS	2.7
47	1p	46	PRO	2.7
48	1q	100	LYS	2.7
50	2s	18	LYS	2.7
51	1t	98	PRO	2.7
51	2t	98	PRO	2.7
1	1A	1045	A	2.7
35	1d	153	ARG	2.7
36	2e	10	MET	2.7
47	1p	5	ARG	2.7
50	1s	29	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
19	2X	92	LEU	2.7
34	1c	87	LEU	2.7
36	2e	71	LEU	2.7
14	2S	86	ALA	2.7
32	2a	1532	U	2.7
34	2c	200	ALA	2.7
6	2G	25	TYR	2.7
33	2b	95	GLN	2.7
34	1c	107	GLN	2.7
52	2u	18	TYR	2.7
38	1g	62	PHE	2.7
6	2G	71	THR	2.7
7	1H	175	LYS	2.7
20	1Y	92	ASN	2.7
21	2Z	105	VAL	2.7
26	24	65	ASP	2.7
32	2a	980	C	2.7
33	1b	94	ASN	2.7
33	1b	136	VAL	2.7
34	2c	99	VAL	2.7
34	2c	130	VAL	2.7
34	2c	138	VAL	2.7
17	2V	42	GLY	2.7
33	1b	41	ILE	2.7
33	2b	214	ILE	2.7
33	2b	131	PRO	2.7
47	1p	66	PRO	2.7
12	2Q	60	ARG	2.7
13	2R	68	ARG	2.7
15	2T	111	ARG	2.7
44	2m	3	ARG	2.7
45	2n	29	ARG	2.7
52	1u	24	ARG	2.7
1	1A	2127	G	2.7
1	1A	2151	G	2.7
1	1A	2893	G	2.7
1	2A	2112	G	2.7
1	2A	652(A)	A	2.7
1	2A	655	A	2.7
1	2A	1847	A	2.7
26	24	60	GLN	2.6
33	2b	13	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
33	2b	161	ALA	2.6
34	2c	104	GLN	2.6
35	1d	195	ALA	2.6
11	2P	76	LYS	2.6
11	2P	110	TYR	2.6
33	2b	132	LYS	2.6
21	2Z	168	GLU	2.6
41	1j	83	GLU	2.6
33	2b	219	VAL	2.6
41	2j	49	VAL	2.6
41	2j	58	ASP	2.6
1	1A	2142	C	2.6
1	1A	2164	C	2.6
6	2G	119	GLY	2.6
32	2a	1037	C	2.6
26	24	31	ILE	2.6
33	1b	89	GLY	2.6
33	2b	222	ILE	2.6
36	1e	22	GLY	2.6
40	2i	115	GLY	2.6
33	1b	36	ARG	2.6
33	1b	234	PRO	2.6
40	1i	90	PRO	2.6
41	2j	45	ARG	2.6
47	1p	25	ARG	2.6
50	1s	35	SER	2.6
1	1A	2141	G	2.6
1	1A	2152	G	2.6
1	2A	1171	G	2.6
1	2A	2104	G	2.6
32	2a	1373	G	2.6
1	1A	2171	A	2.6
1	2A	1509(A)	A	2.6
32	2a	1014	A	2.6
16	2U	74	LEU	2.6
28	26	11	LEU	2.6
33	2b	51	LEU	2.6
33	2b	196	LEU	2.6
38	2g	99	LEU	2.6
40	2i	50	LEU	2.6
41	1j	88	LEU	2.6
50	1s	5	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	2A	1066	U	2.6
34	1c	60	ALA	2.6
34	2c	133	ALA	2.6
36	2e	94	ALA	2.6
47	1p	56	ALA	2.6
10	1O	108	GLU	2.6
11	1P	98	GLU	2.6
33	1b	28	PHE	2.6
35	2d	54	TYR	2.6
40	1i	5	TYR	2.6
45	1n	34	TYR	2.6
46	1o	69	TYR	2.6
47	1p	17	TYR	2.6
49	2r	87	ARG	2.6
7	2H	76	VAL	2.6
7	2H	79	VAL	2.6
33	2b	71	VAL	2.6
50	2s	60	VAL	2.6
34	1c	25	GLY	2.6
35	1d	87	GLY	2.6
40	2i	39	GLY	2.6
1	1A	886	C	2.6
1	1A	2140	C	2.6
31	29	10	ILE	2.6
32	2a	1149	C	2.6
34	2c	39	ILE	2.6
40	2i	90	PRO	2.6
43	2l	5	PRO	2.6
1	1A	11	G	2.6
1	2A	1077	A	2.6
1	2A	2156	G	2.6
4	2E	182	LEU	2.6
22	10	84	LEU	2.6
33	2b	10	LEU	2.6
35	1d	101	LEU	2.6
35	1d	108	LEU	2.6
35	2d	155	LEU	2.6
35	2d	174	LEU	2.6
40	1i	96	LEU	2.6
44	2m	96	LEU	2.6
1	1A	1083	U	2.6
20	2Y	94	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
21	2Z	187	ALA	2.6
33	1b	13	ALA	2.6
33	2b	29	ALA	2.6
40	2i	23	ASN	2.6
4	2E	25	VAL	2.6
6	2G	42	GLY	2.6
7	1H	174	GLY	2.6
7	2H	52	VAL	2.6
21	2Z	99	TYR	2.6
21	2Z	161	VAL	2.6
26	24	25	TYR	2.6
34	2c	171	GLY	2.6
35	1d	133	VAL	2.6
35	2d	37	PRO	2.6
38	1g	85	TYR	2.6
40	1i	28	VAL	2.6
44	2m	21	TYR	2.6
50	2s	8	GLY	2.6
50	2s	63	THR	2.6
51	1t	96	GLY	2.6
32	1a	1028	C	2.6
32	2a	1039	C	2.6
38	2g	27	ILE	2.6
52	2u	13	ILE	2.6
23	2l	78	LYS	2.6
34	2c	147	LYS	2.6
1	2A	1045	A	2.6
32	2a	1492	A	2.6
33	2b	145	LEU	2.6
33	2b	155	LEU	2.6
48	2q	84	LEU	2.6
1	1A	1056	G	2.6
26	14	57	GLU	2.6
32	1a	1021	G	2.6
32	2a	1281	U	2.6
33	1b	129	GLU	2.6
35	2d	3	ARG	2.6
40	2i	20	ARG	2.6
3	1D	2	ALA	2.6
7	2H	20	ALA	2.6
14	2S	55	ALA	2.6
21	2Z	189	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
34	2c	121	ALA	2.6
53	1y	94	ALA	2.6
26	14	51	ASP	2.6
33	1b	83	MET	2.6
35	1d	165	MET	2.6
5	1F	14	PRO	2.6
7	2H	39	PRO	2.6
8	1I	76	THR	2.6
21	2Z	96	VAL	2.6
25	23	41	PRO	2.6
34	2c	95	THR	2.6
35	1d	6	GLY	2.6
36	2e	45	PHE	2.6
38	2g	112	PRO	2.6
41	1j	31	GLY	2.6
41	1j	54	PHE	2.6
42	2k	125	PHE	2.6
45	2n	36	PHE	2.6
47	1p	45	THR	2.6
49	1r	43	PHE	2.6
50	1s	77	THR	2.6
39	2h	79	VAL	2.6
44	2m	17	VAL	2.6
48	2q	35	VAL	2.6
10	2O	69	ILE	2.6
14	2S	53	SER	2.6
33	2b	185	ILE	2.6
34	1c	48	TYR	2.6
44	2m	78	ILE	2.6
50	2s	52	TYR	2.6
1	2A	2178	C	2.6
32	1a	1007	C	2.6
32	2a	1019	C	2.6
47	1p	16	HIS	2.6
43	1l	126	LYS	2.6
50	2s	28	LYS	2.6
6	1G	43	LEU	2.5
8	1I	38	LEU	2.5
1	2A	1111	A	2.5
32	2a	1000	U	2.5
37	1f	21	LEU	2.5
38	2g	12	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
29	27	41	ARG	2.5
34	1c	79	ARG	2.5
34	2c	131	ARG	2.5
34	2c	190	ARG	2.5
1	1A	2807	G	2.5
32	1a	630	G	2.5
32	2a	1042	G	2.5
26	24	12	ALA	2.5
26	24	39	CYS	2.5
33	1b	207	ALA	2.5
45	1n	30	ALA	2.5
47	1p	64	ALA	2.5
6	2G	123	ASN	2.5
21	2Z	98	MET	2.5
5	2F	14	PRO	2.5
6	2G	134	GLY	2.5
6	2G	180	PHE	2.5
7	2H	128	PRO	2.5
7	2H	173	PRO	2.5
8	1I	108	THR	2.5
42	2k	31	THR	2.5
47	1p	37	GLY	2.5
50	1s	26	GLY	2.5
51	2t	102	GLY	2.5
33	2b	181	PHE	2.5
5	2F	6	VAL	2.5
6	2G	159	VAL	2.5
21	2Z	90	VAL	2.5
27	15	60	VAL	2.5
41	2j	7	LYS	2.5
44	2m	27	LYS	2.5
47	1p	50	LYS	2.5
48	1q	37	LYS	2.5
53	2y	43	LYS	2.5
41	2j	50	ILE	2.5
6	2G	11	TYR	2.5
7	2H	83	TYR	2.5
20	2Y	55	TYR	2.5
34	2c	162	GLN	2.5
47	2p	39	TYR	2.5
33	2b	86	GLU	2.5
35	2d	24	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
40	2i	110	GLU	2.5
5	2F	205	ARG	2.5
6	2G	118	ARG	2.5
33	1b	130	ARG	2.5
34	2c	140	ARG	2.5
35	2d	49	ARG	2.5
48	1q	91	ARG	2.5
6	2G	107	LEU	2.5
34	2c	43	LEU	2.5
35	2d	108	LEU	2.5
35	2d	157	LEU	2.5
1	1A	1069	A	2.5
1	2A	887	A	2.5
1	1A	2148	G	2.5
6	2G	126	ASP	2.5
12	1Q	135	ASP	2.5
21	2Z	164	ALA	2.5
34	2c	129	ALA	2.5
36	1e	21	ALA	2.5
40	1i	52	ALA	2.5
41	1j	18	ALA	2.5
41	1j	73	ASP	2.5
42	1k	60	ALA	2.5
44	2m	28	ALA	2.5
51	1t	66	ALA	2.5
11	2P	109	GLY	2.5
20	2Y	54	LYS	2.5
33	1b	8	LYS	2.5
34	1c	73	PRO	2.5
34	2c	174	PRO	2.5
40	1i	39	GLY	2.5
40	2i	57	GLY	2.5
44	1m	115	LYS	2.5
50	2s	6	LYS	2.5
52	1u	23	PRO	2.5
53	1y	45	PRO	2.5
40	2i	58	HIS	2.5
24	12	37	PHE	2.5
42	1k	42	TRP	2.5
21	2Z	100	VAL	2.5
22	10	9	SER	2.5
48	2q	23	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
26	24	15	ILE	2.5
33	1b	211	ILE	2.5
1	2A	2185	C	2.5
11	1P	149	GLU	2.5
29	17	47	ARG	2.5
32	1a	1008	C	2.5
34	2c	29	TYR	2.5
50	2s	61	TYR	2.5
1	2A	1026	U	2.5
6	2G	7	LEU	2.5
11	2P	3	LEU	2.5
33	2b	61	LEU	2.5
41	1j	65	LEU	2.5
8	2I	131	LYS	2.5
21	2Z	87	ASP	2.5
34	1c	100	ALA	2.5
45	2n	20	ALA	2.5
50	1s	23	ASN	2.5
53	2y	58	ASN	2.5
7	2H	14	GLY	2.5
7	2H	82	GLY	2.5
11	2P	37	GLY	2.5
20	2Y	93	GLY	2.5
33	1b	18	GLY	2.5
33	1b	227	GLY	2.5
35	1d	124	GLY	2.5
44	2m	85	GLY	2.5
46	2o	75	PRO	2.5
47	1p	10	GLY	2.5
52	1u	16	GLY	2.5
41	2j	87	THR	2.5
44	2m	101	GLN	2.5
50	2s	39	THR	2.5
53	2y	53	THR	2.5
6	2G	144	ILE	2.5
21	2Z	191	VAL	2.5
33	1b	124	SER	2.5
33	2b	184	VAL	2.5
34	2c	122	GLU	2.5
34	2c	161	GLU	2.5
38	2g	43	PHE	2.5
34	1c	182	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
36	2e	118	ILE	2.5
38	2g	9	VAL	2.5
41	1j	24	VAL	2.5
46	2o	72	ARG	2.5
52	1u	9	ARG	2.5
53	2y	44	GLU	2.5
33	2b	39	ILE	2.5
1	1A	271(J)	C	2.5
32	1a	1006	C	2.5
32	2a	1260	C	2.5
6	2G	19	LEU	2.5
40	1i	79	LEU	2.5
46	2o	67	LEU	2.5
50	1s	15	LEU	2.5
6	2G	75	LYS	2.5
12	2Q	22	LYS	2.5
33	2b	79	ASP	2.5
33	2b	207	ALA	2.5
38	2g	25	ALA	2.5
42	2k	15	ALA	2.5
50	2s	50	ALA	2.5
1	2A	2120	G	2.5
21	2Z	177	PRO	2.5
34	2c	41	GLY	2.5
40	2i	73	GLN	2.5
41	1j	39	PRO	2.5
41	2j	53	PRO	2.5
42	2k	13	GLN	2.5
52	2u	11	GLY	2.5
8	2I	85	GLU	2.4
14	2S	47	THR	2.4
15	2T	112	ARG	2.4
15	2T	125	ARG	2.4
26	14	48	ARG	2.4
26	24	13	ARG	2.4
26	24	34	GLU	2.4
26	24	48	ARG	2.4
33	1b	23	ARG	2.4
40	1i	2	GLU	2.4
33	2b	124	SER	2.4
50	1s	4	SER	2.4
50	2s	45	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
53	2y	48	PHE	2.4
53	2y	64	SER	2.4
6	2G	63	ILE	2.4
6	2G	92	VAL	2.4
36	2e	76	ILE	2.4
36	2e	101	ILE	2.4
40	1i	63	ILE	2.4
47	1p	4	ILE	2.4
47	1p	79	VAL	2.4
50	1s	40	ILE	2.4
1	1A	1963	U	2.4
32	1a	1020	U	2.4
32	2a	1126	U	2.4
32	2a	1358	U	2.4
1	1A	2128	C	2.4
1	1A	2175	C	2.4
32	2a	1218	C	2.4
7	2H	98	LEU	2.4
14	2S	78	LEU	2.4
21	2Z	91	LEU	2.4
33	1b	44	LEU	2.4
33	2b	187	LEU	2.4
38	2g	38	LEU	2.4
38	2g	124	LEU	2.4
41	1j	8	LEU	2.4
41	1j	90	LEU	2.4
41	2j	85	LEU	2.4
35	2d	30	LYS	2.4
50	2s	32	LYS	2.4
53	2y	66	LYS	2.4
1	1A	1177	A	2.4
38	2g	153	HIS	2.4
43	2l	99	HIS	2.4
4	1E	56	PRO	2.4
7	2H	60	ARG	2.4
8	2I	55	ALA	2.4
35	1d	32	ALA	2.4
35	2d	149	ALA	2.4
41	1j	79	ARG	2.4
47	1p	70	ALA	2.4
6	2G	85	GLY	2.4
11	1P	37	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
34	2c	78	GLY	2.4
35	2d	87	GLY	2.4
40	1i	57	GLY	2.4
40	2i	30	GLY	2.4
41	1j	97	GLU	2.4
1	1A	275	G	2.4
1	2A	2190	G	2.4
33	2b	47	THR	2.4
7	2H	56	SER	2.4
26	24	18	CYS	2.4
7	2H	9	ILE	2.4
7	2H	26	VAL	2.4
31	29	16	VAL	2.4
33	1b	208	ILE	2.4
34	2c	202	ILE	2.4
35	1d	148	VAL	2.4
36	1e	6	PHE	2.4
40	2i	26	VAL	2.4
32	2a	1150	U	2.4
35	2d	18	LYS	2.4
1	2A	2177	C	2.4
24	22	1	MET	2.4
32	2a	1249	C	2.4
33	1b	11	LEU	2.4
38	1g	12	LEU	2.4
44	2m	48	LEU	2.4
33	2b	33	TYR	2.4
50	2s	47	HIS	2.4
7	2H	3	ARG	2.4
35	1d	49	ARG	2.4
35	2d	74	GLN	2.4
40	1i	42	ARG	2.4
46	2o	88	ARG	2.4
6	2G	158	ALA	2.4
7	2H	8	PRO	2.4
7	2H	145	ALA	2.4
8	2I	59	ALA	2.4
34	2c	71	ALA	2.4
36	2e	21	ALA	2.4
38	2g	58	PRO	2.4
38	2g	65	ALA	2.4
41	2j	20	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
42	2k	115	PRO	2.4
50	1s	8	GLY	2.4
53	2y	63	ALA	2.4
42	2k	87	THR	2.4
53	2y	6	THR	2.4
2	2B	118	G	2.4
32	2a	1224	G	2.4
1	2A	1083	U	2.4
7	2H	89	ILE	2.4
8	2I	79	ILE	2.4
33	2b	163	PHE	2.4
35	1d	185	PHE	2.4
38	2g	62	PHE	2.4
42	1k	21	ILE	2.4
47	2p	2	VAL	2.4
47	2p	9	PHE	2.4
53	2y	49	VAL	2.4
11	1P	147	LEU	2.4
32	1a	1019	C	2.4
32	1a	1043	C	2.4
33	2b	158	LEU	2.4
37	1f	14	LEU	2.4
39	2h	112	LEU	2.4
41	1j	40	LEU	2.4
45	1n	53	LEU	2.4
47	1p	74	LEU	2.4
49	1r	76	LEU	2.4
53	2y	88	LEU	2.4
33	2b	140	HIS	2.4
14	1S	20	ARG	2.4
16	2U	59	ARG	2.4
26	14	61	ARG	2.4
33	1b	144	ARG	2.4
35	2d	27	TYR	2.4
39	1h	84	ARG	2.4
53	2y	95	ARG	2.4
6	2G	137	GLU	2.4
32	2a	1015	A	2.4
6	2G	179	PRO	2.4
11	2P	103	ALA	2.4
33	2b	18	GLY	2.4
34	2c	2	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
34	2c	149	ALA	2.4
35	1d	180	GLY	2.4
35	2d	32	ALA	2.4
35	2d	44	GLY	2.4
38	1g	7	ALA	2.4
40	2i	24	GLY	2.4
43	2l	95	GLY	2.4
44	2m	33	ALA	2.4
45	2n	51	GLY	2.4
9	2N	73	THR	2.4
33	2b	190	THR	2.4
40	1i	11	LYS	2.4
43	1l	20	LYS	2.4
44	2m	109	THR	2.4
1	2A	1081	U	2.4
1	2A	2187	G	2.4
8	2I	136	VAL	2.4
14	2S	46	VAL	2.4
21	2Z	53	ILE	2.4
26	24	36	CYS	2.4
29	27	1	MET	2.4
32	2a	1040	U	2.4
34	1c	64	VAL	2.4
34	2c	203	PHE	2.4
46	2o	27	VAL	2.4
50	1s	31	ILE	2.4
50	1s	45	VAL	2.4
6	1G	53	LEU	2.4
14	2S	48	LEU	2.4
42	2k	98	LEU	2.4
46	2o	66	LEU	2.4
7	2H	101	ARG	2.4
29	17	41	ARG	2.4
43	2l	89	ARG	2.4
44	2m	110	ARG	2.4
45	2n	35	ARG	2.4
50	2s	78	ARG	2.4
1	1A	2178	C	2.4
24	22	70	GLN	2.4
32	2a	1008	C	2.4
35	1d	150	GLU	2.4
41	1j	64	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
21	2Z	40	ASP	2.3
35	2d	38	TYR	2.3
42	2k	75	TYR	2.3
1	1A	229	A	2.3
1	2A	896	A	2.3
32	2a	994	A	2.3
32	2a	1256	A	2.3
26	14	29	PRO	2.3
33	2b	91	PRO	2.3
35	2d	7	PRO	2.3
44	2m	10	PRO	2.3
7	2H	142	GLY	2.3
21	2Z	6	LYS	2.3
33	2b	228	GLY	2.3
35	1d	23	GLY	2.3
34	2c	169	ALA	2.3
49	1r	20	ALA	2.3
53	2y	73	ALA	2.3
40	1i	27	THR	2.3
6	2G	78	SER	2.3
32	1a	1212	U	2.3
1	1A	2120	G	2.3
1	1A	2802	G	2.3
1	2A	614(B)	G	2.3
20	2Y	7	VAL	2.3
20	2Y	42	VAL	2.3
31	29	26	ILE	2.3
33	1b	15	VAL	2.3
33	2b	28	PHE	2.3
36	2e	115	VAL	2.3
41	1j	6	ILE	2.3
41	1j	38	ILE	2.3
43	2l	100	ILE	2.3
9	2N	115	ARG	2.3
11	1P	15	ARG	2.3
29	17	23	ARG	2.3
34	1c	83	ARG	2.3
53	2y	67	HIS	2.3
11	2P	6	LEU	2.3
24	22	60	LEU	2.3
35	1d	155	LEU	2.3
35	2d	96	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
33	2b	134	GLU	2.3
36	2e	20	GLN	2.3
41	1j	71	LEU	2.3
43	1l	60	LEU	2.3
50	2s	20	LEU	2.3
26	24	3	GLU	2.3
44	2m	67	GLU	2.3
1	1A	1053	C	2.3
32	2a	999	C	2.3
1	2A	1098	A	2.3
3	1D	38	LYS	2.3
6	2G	84	LYS	2.3
7	2H	118	PRO	2.3
32	2a	1363(A)	A	2.3
39	2h	94	TYR	2.3
44	1m	87	TYR	2.3
31	29	21	GLY	2.3
50	1s	84	GLY	2.3
4	2E	204	ALA	2.3
8	2I	63	ALA	2.3
21	2Z	113	ALA	2.3
34	2c	50	ALA	2.3
40	2i	84	ALA	2.3
26	24	24	THR	2.3
33	2b	90	MET	2.3
40	1i	7	THR	2.3
1	1A	1097	U	2.3
6	2G	83	ARG	2.3
7	2H	6	ARG	2.3
7	2H	59	ARG	2.3
11	2P	102	ARG	2.3
25	23	30	ARG	2.3
26	24	61	ARG	2.3
33	2b	130	ARG	2.3
40	1i	16	ARG	2.3
7	2H	72	ILE	2.3
7	2H	121	ILE	2.3
21	2Z	57	ILE	2.3
8	1I	127	VAL	2.3
33	2b	81	VAL	2.3
33	2b	197	VAL	2.3
35	1d	121	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
41	2j	62	HIS	2.3
50	2s	57	HIS	2.3
33	1b	70	PHE	2.3
41	2j	11	PHE	2.3
1	2A	1093	G	2.3
1	2A	1533	G	2.3
1	2A	2184	G	2.3
20	2Y	106	LEU	2.3
32	1a	181	G	2.3
32	1a	1003	G	2.3
32	1a	1131	G	2.3
32	2a	1009	G	2.3
51	1t	72	LEU	2.3
1	2A	885	C	2.3
6	2G	81	LYS	2.3
42	2k	36	ASP	2.3
52	2u	3	LYS	2.3
43	1l	94	PRO	2.3
6	1G	134	GLY	2.3
8	2I	34	GLY	2.3
32	2a	1123	A	2.3
34	2c	185	GLY	2.3
39	2h	47	GLY	2.3
40	1i	6	GLY	2.3
40	2i	8	GLY	2.3
50	2s	72	GLY	2.3
31	29	5	ALA	2.3
33	1b	225	ALA	2.3
40	1i	82	ALA	2.3
49	1r	60	ALA	2.3
40	1i	103	THR	2.3
47	1p	69	THR	2.3
1	2A	1065	U	2.3
18	2W	92	ARG	2.3
32	1a	1040	U	2.3
34	2c	11	ARG	2.3
34	2c	132	ARG	2.3
40	1i	107	ARG	2.3
42	1k	16	SER	2.3
50	2s	36	ARG	2.3
4	1E	163	GLU	2.3
45	2n	8	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
33	2b	32	ILE	2.3
34	2c	84	ILE	2.3
38	1g	27	ILE	2.3
6	1G	160	VAL	2.3
12	2Q	58	PHE	2.3
21	2Z	48	PHE	2.3
21	2Z	174	VAL	2.3
34	2c	120	VAL	2.3
40	2i	28	VAL	2.3
45	1n	33	VAL	2.3
22	20	75	LEU	2.3
1	1A	1173	G	2.3
1	1A	2162	G	2.3
1	2A	100	G	2.3
1	2A	1044	G	2.3
6	1G	182	LYS	2.3
34	2c	12	LEU	2.3
44	2m	70	LEU	2.3
51	1t	62	LEU	2.3
32	2a	1353	G	2.3
3	2D	99	ASP	2.3
53	2y	79	ASN	2.3
1	1A	645	C	2.3
1	2A	1080	C	2.3
47	2p	46	PRO	2.3
14	2S	22	GLY	2.3
15	2T	69	GLY	2.3
33	2b	14	GLY	2.3
35	2d	167	GLY	2.3
44	2m	112	GLY	2.3
47	1p	63	GLY	2.3
19	1X	69	TYR	2.3
6	2G	29	TRP	2.3
6	2G	163	ALA	2.3
7	2H	51	ARG	2.3
19	2X	65	ARG	2.3
21	2Z	4	ARG	2.3
26	14	68	ARG	2.3
33	2b	144	ARG	2.3
33	2b	225	ALA	2.3
34	1c	65	ALA	2.3
34	2c	18	TRP	2.3

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Mol	Chain	Res	Type	RSRZ
34	2c	54	ARG	2.3
37	1f	63	TYR	2.3
40	1i	51	ARG	2.3
40	1i	114	TYR	2.3
33	1b	120	ALA	2.3
34	2c	137	ALA	2.3
38	2g	150	ALA	2.3
44	1m	3	ARG	2.3
51	2t	86	ARG	2.3
1	1A	12	U	2.3
1	1A	1175	U	2.3
1	2A	1078	U	2.3
1	2A	1105	U	2.3
26	24	27	THR	2.3
32	1a	1025	U	2.3
53	1y	53	THR	2.3
33	2b	129	GLU	2.3
35	2d	156	GLU	2.3
8	1I	138	ILE	2.3
33	2b	41	ILE	2.3
34	1c	84	ILE	2.3
3	2D	37	LEU	2.2
7	2H	49	VAL	2.3
21	2Z	5	LEU	2.2
25	23	6	VAL	2.3
33	1b	219	VAL	2.3
33	2b	229	VAL	2.3
36	2e	12	LEU	2.2
40	2i	79	LEU	2.2
44	2m	15	VAL	2.3
1	2A	1099	G	2.2
1	2A	2751	G	2.2
34	2c	108	ASN	2.2
40	2i	60	ASP	2.2
6	2G	17	PRO	2.2
26	24	11	PRO	2.2
46	2o	19	PRO	2.2
6	2G	86	MET	2.2
11	1P	93	GLY	2.2
17	2V	8	GLY	2.2
35	2d	115	ARG	2.2
35	2d	183	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
38	1g	130	GLY	2.2
40	1i	100	GLY	2.2
41	2j	52	GLY	2.2
46	2o	68	ARG	2.2
47	1p	72	ARG	2.2
51	2t	69	GLY	2.2
32	2a	1493	A	2.2
1	1A	272(A)	U	2.2
4	1E	68	ALA	2.2
8	1I	29	TYR	2.2
8	2I	115	ALA	2.2
32	2a	1148	U	2.2
33	2b	19	HIS	2.2
33	2b	126	GLU	2.2
34	2c	69	HIS	2.2
38	2g	24	THR	2.2
41	1j	92	THR	2.2
21	2Z	166	SER	2.2
49	1r	59	SER	2.2
40	2i	116	LYS	2.2
35	2d	67	ILE	2.2
36	1e	101	ILE	2.2
39	1h	86	ILE	2.2
39	1h	109	ILE	2.2
39	1h	134	ILE	2.2
42	2k	21	ILE	2.2
44	1m	39	ILE	2.2
49	2r	75	ILE	2.2
6	2G	111	LEU	2.2
7	2H	67	LEU	2.2
8	1I	107	VAL	2.2
8	2I	35	LEU	2.2
11	1P	99	LEU	2.2
14	2S	54	LEU	2.2
14	2S	56	LEU	2.2
21	2Z	18	LEU	2.2
34	1c	106	VAL	2.2
38	2g	22	LEU	2.2
20	1Y	60	PHE	2.2
40	2i	33	PHE	2.2
41	1j	47	PHE	2.2
47	2p	20	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
4	1E	89	ASP	2.2
8	2I	20	ASP	2.2
53	2y	36	ASN	2.2
1	1A	2100	G	2.2
1	2A	892	G	2.2
19	2X	60	ARG	2.2
22	10	55	ARG	2.2
32	1a	380	G	2.2
32	2a	1202	G	2.2
26	24	1	MET	2.2
44	2m	114	ARG	2.2
1	1A	2163	C	2.2
32	1a	163	C	2.2
32	2a	1129	C	2.2
32	2a	1277	C	2.2
34	2c	81	GLY	2.2
40	2i	68	GLY	2.2
41	1j	10	GLY	2.2
44	1m	38	GLY	2.2
1	1A	2629	A	2.2
32	2a	1213	A	2.2
35	1d	125	HIS	2.2
49	2r	46	GLU	2.2
1	1A	1105	U	2.2
21	1Z	187	ALA	2.2
26	24	2	LYS	2.2
35	2d	45	GLN	2.2
35	1d	111	ALA	2.2
40	2i	78	LYS	2.2
44	2m	30	ALA	2.2
44	2m	46	LYS	2.2
48	1q	93	GLN	2.2
26	14	52	THR	2.2
29	27	45	ALA	2.2
38	1g	154	TYR	2.2
48	2q	97	SER	2.2
38	2g	103	TRP	2.2
47	2p	59	TRP	2.2
7	1H	92	ILE	2.2
20	2Y	44	ILE	2.2
33	2b	108	ILE	2.2
34	1c	202	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
35	1d	5	ILE	2.2
53	2y	12	ILE	2.2
14	2S	73	LEU	2.2
20	2Y	90	LEU	2.2
33	1b	61	LEU	2.2
35	1d	176	LEU	2.2
12	2Q	35	VAL	2.2
14	2S	28	VAL	2.2
33	1b	93	VAL	2.2
35	1d	17	VAL	2.2
44	1m	60	VAL	2.2
11	2P	91	PHE	2.2
16	2U	79	PHE	2.2
3	2D	71	ASP	2.2
6	2G	156	ASP	2.2
7	1H	6	ARG	2.2
7	2H	42	ARG	2.2
11	2P	79	ARG	2.2
15	1T	129	ARG	2.2
26	24	20	ASN	2.2
35	2d	209	ARG	2.2
40	1i	83	ARG	2.2
42	2k	126	ARG	2.2
43	1l	19	ARG	2.2
44	2m	12	ASN	2.2
44	2m	99	ARG	2.2
52	2u	7	ARG	2.2
8	2I	137	PRO	2.2
21	1Z	1	MET	2.2
33	2b	159	PRO	2.2
40	1i	98	PRO	2.2
1	1A	1055	G	2.2
1	1A	2104	G	2.2
1	2A	1055	G	2.2
1	2A	1059	G	2.2
1	2A	2181	G	2.2
32	1a	78	G	2.2
32	2a	987	G	2.2
33	2b	89	GLY	2.2
33	2b	99	GLY	2.2
34	1c	9	GLY	2.2
34	2c	148	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
35	2d	6	GLY	2.2
43	1l	63	GLY	2.2
1	1A	271(O)	C	2.2
21	2Z	145	GLU	2.2
33	1b	140	HIS	2.2
33	2b	12	GLU	2.2
34	2c	123	GLN	2.2
43	2l	126	LYS	2.2
47	1p	76	GLN	2.2
1	2A	2895	U	2.2
2	1B	120	A	2.2
32	1a	162	A	2.2
32	2a	202	U	2.2
21	2Z	192	ALA	2.2
33	2b	73	THR	2.2
38	2g	117	ALA	2.2
40	1i	13	ALA	2.2
41	2j	81	THR	2.2
44	1m	49	THR	2.2
47	2p	67	THR	2.2
53	2y	50	ALA	2.2
53	2y	52	ALA	2.2
34	1c	201	TYR	2.2
47	1p	39	TYR	2.2
52	1u	18	TYR	2.2
42	2k	42	TRP	2.2
3	1D	106	ILE	2.2
6	2G	60	LEU	2.2
6	2G	172	LEU	2.2
7	2H	171	LEU	2.2
28	26	54	ILE	2.2
33	2b	80	ILE	2.2
37	2f	45	LEU	2.2
38	2g	50	ILE	2.2
41	1j	50	ILE	2.2
19	2X	68	ARG	2.2
35	1d	3	ARG	2.2
50	1s	16	LEU	2.2
51	1t	13	LEU	2.2
34	1c	75	VAL	2.2
34	2c	198	VAL	2.2
35	1d	8	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
40	1i	108	VAL	2.2
41	2j	17	ASP	2.2
48	1q	35	VAL	2.2
33	2b	101	MET	2.2
38	2g	89	MET	2.2
49	2r	29	PHE	2.2
53	1y	70	MET	2.2
48	1q	2	PRO	2.2
35	2d	85	LYS	2.2
43	2l	115	LYS	2.2
44	2m	13	LYS	2.2
47	1p	43	LYS	2.2
50	2s	27	GLU	2.2
5	1F	207	GLY	2.2
6	1G	89	GLY	2.2
7	2H	166	GLY	2.2
7	2H	174	GLY	2.2
8	2I	106	GLY	2.2
26	24	47	GLN	2.2
31	29	20	HIS	2.2
31	29	36	GLN	2.2
34	2c	51	GLY	2.2
40	1i	58	HIS	2.2
53	2y	92	GLY	2.2
1	1A	1042	G	2.2
1	1A	1060	U	2.2
1	1A	1117	G	2.2
1	2A	2191	G	2.2
32	1a	841	U	2.2
32	1a	1009	G	2.2
32	2a	1124	G	2.2
32	2a	1139	G	2.2
1	1A	1096	A	2.2
32	1a	1004	A	2.2
6	2G	161	THR	2.2
9	1N	92	ALA	2.2
12	2Q	95	ALA	2.2
34	1c	169	ALA	2.2
40	2i	52	ALA	2.2
43	2l	122	THR	2.2
45	1n	48	ALA	2.2
50	2s	4	SER	2.2

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Mol	Chain	Res	Type	RSRZ
15	1T	108	ARG	2.1
33	2b	30	ARG	2.1
38	2g	155	ARG	2.1
40	1i	92	TYR	2.1
48	1q	63	ARG	2.1
52	1u	21	TYR	2.1
53	2y	71	TYR	2.1
5	2F	24	LEU	2.1
8	1I	12	LEU	2.1
14	1S	4	LEU	2.1
15	1T	42	ILE	2.1
21	2Z	24	LEU	2.1
33	1b	42	ILE	2.1
33	2b	149	LEU	2.1
33	2b	162	ILE	2.1
45	2n	44	LEU	2.1
47	1p	60	LEU	2.1
6	2G	40	ASN	2.1
6	2G	116	ASP	2.1
35	1d	104	VAL	2.1
40	1i	26	VAL	2.1
12	2Q	112	GLU	2.1
19	2X	85	PRO	2.1
33	1b	9	GLU	2.1
44	1m	50	GLU	2.1
50	2s	70	LYS	2.1
46	1o	19	PRO	2.1
53	2y	33	HIS	2.1
8	2I	90	GLY	2.1
10	2O	74	GLY	2.1
1	1A	2122	U	2.1
32	1a	204	U	2.1
16	2U	69	CYS	2.1
1	1A	2110	G	2.1
32	1a	174	C	2.1
38	2g	47	CYS	2.1
32	2a	1013	G	2.1
32	2a	1144	G	2.1
32	2a	1216	G	2.1
1	1A	1847	A	2.1
32	2a	1016	A	2.1
32	2a	1531	A	2.1

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Mol	Chain	Res	Type	RSRZ
6	2G	6	ALA	2.1
6	2G	69	ALA	2.1
12	2Q	136	ALA	2.1
21	2Z	16	SER	2.1
33	2b	188	ALA	2.1
34	1c	92	ALA	2.1
35	1d	149	ALA	2.1
39	1h	3	THR	2.1
40	1i	45	ALA	2.1
44	1m	5	ALA	2.1
44	2m	107	ALA	2.1
33	1b	226	ARG	2.1
34	2c	30	ARG	2.1
41	1j	46	ARG	2.1
41	2j	5	ARG	2.1
44	2m	71	ARG	2.1
47	2p	28	ARG	2.1
12	2Q	137	TYR	2.1
21	2Z	9	TYR	2.1
6	1G	74	LYS	2.1
6	2G	74	LYS	2.1
6	2G	106	LEU	2.1
8	2I	4	ILE	2.1
19	2X	80	ILE	2.1
21	2Z	144	LEU	2.1
33	1b	90	MET	2.1
33	2b	48	MET	2.1
33	2b	58	ILE	2.1
34	2c	182	ILE	2.1
35	1d	181	MET	2.1
35	1d	196	LEU	2.1
35	2d	11	LEU	2.1
38	2g	125	MET	2.1
48	1q	82	MET	2.1
40	2i	118	LYS	2.1
44	1m	31	LYS	2.1
47	1p	35	LYS	2.1
51	2t	55	ILE	2.1
51	2t	72	LEU	2.1
6	2G	48	GLU	2.1
8	1I	20	ASP	2.1
33	2b	189	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
35	1d	163	GLU	2.1
36	2e	130	ASN	2.1
8	2I	107	VAL	2.1
14	2S	98	VAL	2.1
18	2W	111	HIS	2.1
21	2Z	56	VAL	2.1
33	1b	81	VAL	2.1
34	1c	109	PRO	2.1
35	2d	92	VAL	2.1
38	1g	9	VAL	2.1
38	1g	75	VAL	2.1
44	2m	74	VAL	2.1
45	1n	14	PRO	2.1
49	2r	86	VAL	2.1
50	1s	67	VAL	2.1
33	1b	163	PHE	2.1
14	2S	45	GLY	2.1
1	2A	895	U	2.1
32	1a	723	U	2.1
1	2A	1584	C	2.1
32	2a	995	C	2.1
1	2A	271(M)	G	2.1
1	2A	545	G	2.1
1	2A	2318	G	2.1
6	1G	161	THR	2.1
6	2G	110	ALA	2.1
21	2Z	92	SER	2.1
32	1a	1002	G	2.1
32	2a	1010	G	2.1
32	2a	1023	G	2.1
32	2a	1190	G	2.1
38	2g	115	ARG	2.1
40	2i	111	ARG	2.1
42	2k	91	ARG	2.1
49	1r	42	ARG	2.1
52	2u	10	ARG	2.1
35	2d	137	SER	2.1
45	2n	32	SER	2.1
51	1t	61	SER	2.1
53	2y	72	THR	2.1
20	2Y	101	LYS	2.1
21	2Z	127	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
6	1G	90	LEU	2.1
7	2H	151	ILE	2.1
14	2S	110	LEU	2.1
25	23	37	LEU	2.1
33	2b	142	LEU	2.1
34	1c	178	LEU	2.1
34	2c	42	LEU	2.1
35	1d	192	GLU	2.1
34	2c	134	ILE	2.1
35	2d	154	ASN	2.1
36	2e	133	TYR	2.1
37	1f	83	ASP	2.1
38	2g	120	ILE	2.1
40	2i	85	LEU	2.1
50	2s	64	GLU	2.1
53	2y	61	LEU	2.1
53	2y	68	GLU	2.1
8	2I	89	TYR	2.1
11	2P	80	TYR	2.1
19	2X	69	TYR	2.1
39	1h	58	TYR	2.1
33	1b	40	HIS	2.1
33	2b	113	HIS	2.1
40	2i	3	GLN	2.1
7	1H	133	VAL	2.1
7	2H	141	VAL	2.1
8	2I	18	VAL	2.1
8	2I	132	PRO	2.1
20	2Y	85	VAL	2.1
21	2Z	27	VAL	2.1
21	2Z	141	VAL	2.1
21	2Z	159	PRO	2.1
33	1b	164	VAL	2.1
34	1c	99	VAL	2.1
35	2d	136	PRO	2.1
38	1g	17	VAL	2.1
39	1h	19	VAL	2.1
40	1i	49	PRO	2.1
41	2j	94	VAL	2.1
46	1o	2	PRO	2.1
47	2p	62	VAL	2.1
22	20	45	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
35	2d	79	PHE	2.1
50	1s	34	TRP	2.1
12	2Q	19	GLY	2.1
1	2A	271(L)	U	2.1
26	14	58	ARG	2.1
35	1d	76	ARG	2.1
35	2d	47	ARG	2.1
35	2d	132	ARG	2.1
1	1A	172	C	2.1
1	2A	1048	A	2.1
1	2A	2629	A	2.1
1	1A	2106	G	2.1
1	2A	2115	G	2.1
6	2G	182	LYS	2.1
7	2H	102	ALA	2.1
14	2S	105	ALA	2.1
22	20	18	ALA	2.1
30	28	29	LYS	2.1
32	2a	1248	A	2.1
35	1d	137	SER	2.1
44	2m	49	THR	2.1
48	1q	99	SER	2.1
50	2s	79	THR	2.1
32	1a	79	G	2.1
32	2a	1283	G	2.1
33	2b	186	ALA	2.1
35	1d	22	LYS	2.1
35	2d	22	LYS	2.1
38	1g	25	ALA	2.1
40	1i	78	LYS	2.1
41	1j	14	LYS	2.1
45	1n	20	ALA	2.1
53	2y	21	ALA	2.1
14	2S	43	GLU	2.1
26	24	53	GLU	2.1
5	2F	32	LEU	2.1
6	1G	82	LEU	2.1
7	2H	139	GLN	2.1
8	1I	72	LEU	2.1
9	1N	8	GLN	2.1
14	2S	24	LEU	2.1
21	2Z	155	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
34	2c	170	GLN	2.1
35	2d	135	LEU	2.1
35	2d	186	LEU	2.1
35	2d	158	ILE	2.1
36	2e	5	ASP	2.1
39	2h	70	GLN	2.1
41	1j	69	ASN	2.1
42	1k	13	GLN	2.1
50	1s	47	HIS	2.1
53	2y	81	LEU	2.1
19	2X	8	ILE	2.1
20	2Y	107	ASP	2.1
40	2i	74	ILE	2.1
40	2i	81	ILE	2.1
45	2n	42	ILE	2.1
50	2s	53	ASN	2.1
51	1t	64	ASP	2.1
4	2E	151	TYR	2.1
7	2H	55	PRO	2.1
11	2P	78	PRO	2.1
33	2b	26	PRO	2.1
7	2H	37	VAL	2.1
10	2O	62	VAL	2.1
24	22	19	VAL	2.1
34	2c	76	VAL	2.1
35	1d	112	VAL	2.1
11	2P	93	GLY	2.1
21	2Z	22	GLY	2.1
33	2b	100	GLY	2.1
35	2d	75	PHE	2.1
48	1q	33	GLY	2.1
50	1s	10	PHE	2.1
1	2A	362	U	2.1
1	2A	1094	U	2.1
6	2G	91	ARG	2.1
7	2H	23	ARG	2.1
32	1a	90	U	2.1
32	2a	1135	U	2.1
35	1d	50	ARG	2.1
38	2g	6	ARG	2.1
38	2g	149	ARG	2.1
44	2m	104	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
3	2D	4	LYS	2.0
34	1c	27	LYS	2.0
34	2c	93	LYS	2.0
43	1l	23	LYS	2.0
43	2l	13	LYS	2.0
46	2o	48	LYS	2.0
48	2q	100	LYS	2.0
1	2A	1109	C	2.0
6	2G	165	THR	2.0
8	1I	86	THR	2.0
6	2G	155	MET	2.0
32	1a	63	C	2.0
32	1a	999	C	2.0
32	2a	968	A	2.0
32	2a	978	A	2.0
32	2a	1217	C	2.0
34	2c	67	THR	2.0
39	2h	3	THR	2.0
41	1j	81	THR	2.0
11	2P	98	GLU	2.0
21	1Z	203	GLU	2.0
33	1b	29	ALA	2.0
34	2c	53	ALA	2.0
38	2g	147	ALA	2.0
44	1m	30	ALA	2.0
48	2q	49	GLU	2.0
1	1A	271(I)	G	2.0
2	2B	117	G	2.0
32	2a	1094	G	2.0
21	2Z	121	HIS	2.0
6	2G	135	LEU	2.0
15	1T	114	LEU	2.0
35	2d	188	LEU	2.0
39	1h	10	LEU	2.0
39	2h	107	LEU	2.0
40	1i	50	LEU	2.0
40	1i	105	ASP	2.0
47	2p	47	ASP	2.0
50	2s	65	ASN	2.0
8	2I	138	ILE	2.0
35	1d	158	ILE	2.0
47	2p	4	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
43	2l	64	TYR	2.0
6	1G	159	VAL	2.0
7	1H	95	ARG	2.0
7	2H	114	VAL	2.0
19	2X	81	VAL	2.0
25	23	59	VAL	2.0
34	2c	151	VAL	2.0
36	2e	152	ARG	2.0
38	2g	61	VAL	2.0
39	1h	69	ARG	2.0
40	1i	10	ARG	2.0
44	1m	53	VAL	2.0
44	2m	53	VAL	2.0
44	2m	88	ARG	2.0
53	2y	96	ARG	2.0
4	2E	29	GLY	2.0
5	1F	131	GLY	2.0
5	1F	134	GLY	2.0
38	2g	34	GLY	2.0
47	2p	10	GLY	2.0
38	1g	26	PHE	2.0
38	1g	43	PHE	2.0
45	2n	37	PHE	2.0
46	1o	18	PHE	2.0
49	1r	29	PHE	2.0
33	2b	139	LYS	2.0
33	2b	147	LYS	2.0
34	2c	27	LYS	2.0
20	2Y	5	MET	2.0
29	17	1	MET	2.0
7	2H	134	SER	2.0
8	1I	99	GLU	2.0
31	29	28	GLU	2.0
33	1b	109	SER	2.0
1	1A	529	A	2.0
1	1A	1116	C	2.0
1	2A	886	C	2.0
1	2A	1050	A	2.0
14	2S	72	ALA	2.0
16	2U	67	ALA	2.0
32	1a	470	C	2.0
32	1a	1141	C	2.0

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Mol	Chain	Res	Type	RSRZ
32	2a	1018	C	2.0
32	2a	1041	A	2.0
32	2a	1141	C	2.0
32	2a	1250	A	2.0
32	2a	1317	C	2.0
32	2a	1354	C	2.0
33	1b	34	ALA	2.0
33	2b	120	ALA	2.0
51	1t	78	ALA	2.0
51	1t	94	ALA	2.0
21	2Z	32	HIS	2.0
34	2c	28	GLN	2.0
48	1q	26	GLN	2.0
1	2A	1056	G	2.0
1	2A	1537	G	2.0
2	2B	119	G	2.0
5	1F	12	LEU	2.0
8	1I	14	ASP	2.0
34	2c	17	ASP	2.0
35	1d	190	ASP	2.0
38	2g	101	LEU	2.0
48	1q	76	LEU	2.0
49	1r	79	LEU	2.0
7	2H	170	ARG	2.0
20	2Y	75	ILE	2.0
21	2Z	15	PRO	2.0
21	2Z	62	PRO	2.0
22	20	82	ARG	2.0
24	22	51	ARG	2.0
26	14	62	ARG	2.0
33	1b	222	ILE	2.0
33	2b	223	ILE	2.0
34	1c	14	ILE	2.0
34	1c	38	ARG	2.0
39	2h	45	ILE	2.0
43	2l	19	ARG	2.0
44	2m	11	ARG	2.0
45	2n	23	ARG	2.0
47	2p	71	ARG	2.0
48	2q	60	ILE	2.0
51	2t	41	ILE	2.0
52	1u	15	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
7	2H	85	LYS	2.0
14	2S	93	LYS	2.0
33	2b	8	LYS	2.0
33	2b	156	LYS	2.0
34	2c	4	LYS	2.0
40	2i	25	LYS	2.0
41	1j	7	LYS	2.0
41	2j	22	LYS	2.0
48	1q	14	LYS	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, 95th 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
1	5MU	2A	1915	21/22	0.84	0.13	76,83,86,97	0
1	5MU	1A	1915	21/22	0.85	0.13	70,77,82,89	0
32	2MG	2a	1207	24/25	0.85	0.15	78,84,89,90	0
43	0TD	2l	92	10/11	0.86	0.14	61,66,69,77	0
32	M2G	2a	966	25/26	0.87	0.16	57,69,80,91	0
32	5MC	2a	967	21/22	0.88	0.15	66,71,76,77	0
1	PSU	1A	1917	20/21	0.90	0.10	63,69,75,76	0
1	PSU	2A	1917	20/21	0.90	0.10	69,75,86,89	0
1	PSU	2A	1911	20/21	0.90	0.10	67,71,80,84	0
32	2MG	1a	1207	24/25	0.91	0.11	65,73,77,78	0
32	PSU	2a	516	20/21	0.91	0.10	72,76,82,82	0
43	0TD	1l	92	10/11	0.91	0.12	54,58,62,71	0
32	5MC	1a	967	21/22	0.92	0.12	62,67,74,76	0
32	G7M	2a	527	24/25	0.92	0.11	59,66,71,73	0
32	5MC	2a	1407	21/22	0.93	0.10	57,62,66,69	0
1	PSU	1A	1911	20/21	0.93	0.09	61,67,69,70	0
32	5MC	2a	1400	21/22	0.94	0.14	63,69,71,72	0
32	4OC	2a	1402	22/23	0.94	0.10	57,64,69,71	0
32	5MC	2a	1404	21/22	0.94	0.10	56,62,66,68	0
1	OMC	2A	1920	21/22	0.94	0.10	63,65,69,71	0
32	MA6	2a	1518	24/25	0.94	0.12	52,63,67,69	0
32	M2G	1a	966	25/26	0.94	0.11	58,63,68,72	0
32	5MC	1a	1400	21/22	0.95	0.11	48,55,60,62	0
32	UR3	2a	1498	21/22	0.95	0.10	56,61,67,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
32	MA6	1a	1519	24/25	0.95	0.10	41,50,53,55	0
32	MA6	2a	1519	24/25	0.95	0.12	53,63,66,68	0
32	PSU	1a	516	20/21	0.95	0.08	51,63,66,68	0
32	UR3	1a	1498	21/22	0.96	0.09	44,50,53,55	0
1	5MC	2A	1942	21/22	0.96	0.08	47,51,55,60	0
1	2MA	2A	2503	23/24	0.96	0.09	30,35,39,41	0
1	OMC	1A	1920	21/22	0.96	0.10	50,56,62,62	0
32	G7M	1a	527	24/25	0.96	0.10	48,55,58,61	0
1	5MC	1A	1942	21/22	0.96	0.08	32,37,41,44	0
32	5MC	1a	1404	21/22	0.96	0.09	40,47,51,53	0
32	5MC	1a	1407	21/22	0.96	0.09	43,52,58,62	0
1	5MC	2A	1962	21/22	0.97	0.08	40,46,51,60	0
1	OMG	2A	2251	24/25	0.97	0.08	37,42,47,49	0
32	MA6	1a	1518	24/25	0.97	0.09	44,49,53,55	0
1	OMU	2A	2552	21/22	0.97	0.07	35,40,43,49	0
1	PSU	2A	2605	20/21	0.97	0.07	34,40,49,51	0
1	5MC	1A	1962	21/22	0.97	0.07	32,37,41,46	0
1	OMU	1A	2552	21/22	0.97	0.08	27,32,35,40	0
1	5MU	2A	1939	21/22	0.97	0.07	33,38,42,48	0
32	4OC	1a	1402	22/23	0.97	0.08	46,53,54,59	0
1	MA6	2A	2058	24/25	0.98	0.08	34,39,45,48	0
1	MA6	1A	2058	24/25	0.98	0.06	17,27,34,42	0
1	OMG	1A	2251	24/25	0.98	0.06	21,27,30,31	0
1	2MA	1A	2503	23/24	0.98	0.06	20,25,29,30	0
1	5MU	1A	1939	21/22	0.98	0.07	26,30,36,38	0
1	PSU	1A	2605	20/21	0.98	0.08	26,29,34,37	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, 95th 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($\text{\AA}^2$)	Q<0.9
54	MG	1A	3976	1/1	0.42	0.27	43,43,43,43	0
54	MG	2a	3187	1/1	0.46	0.23	82,82,82,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3738	1/1	0.51	0.20	70,70,70,70	0
54	MG	2A	3286	1/1	0.53	0.41	90,90,90,90	0
54	MG	2A	3528	1/1	0.54	0.30	86,86,86,86	0
54	MG	2A	3503	1/1	0.54	0.23	80,80,80,80	0
54	MG	1a	3260	1/1	0.57	0.22	79,79,79,79	0
54	MG	2j	201	1/1	0.57	0.17	82,82,82,82	0
54	MG	1A	3828	1/1	0.59	0.22	72,72,72,72	0
54	MG	1a	3261	1/1	0.61	0.30	77,77,77,77	0
54	MG	2A	3473	1/1	0.62	0.27	60,60,60,60	0
54	MG	2A	3421	1/1	0.63	0.21	63,63,63,63	0
54	MG	1A	3355	1/1	0.63	0.26	62,62,62,62	0
54	MG	1A	3686	1/1	0.63	0.23	79,79,79,79	0
54	MG	1A	3749	1/1	0.64	0.24	75,75,75,75	0
54	MG	2A	3612	1/1	0.64	0.29	56,56,56,56	0
54	MG	1B	229	1/1	0.64	0.27	72,72,72,72	0
54	MG	1a	3178	1/1	0.64	0.40	76,76,76,76	0
54	MG	1A	3428	1/1	0.65	0.20	55,55,55,55	0
54	MG	1a	3275	1/1	0.65	0.21	76,76,76,76	0
54	MG	2A	3570	1/1	0.65	0.24	65,65,65,65	0
54	MG	1a	3218	1/1	0.65	0.28	83,83,83,83	0
54	MG	1a	3251	1/1	0.65	0.22	79,79,79,79	0
54	MG	1A	3681	1/1	0.65	0.21	79,79,79,79	0
54	MG	2A	3517	1/1	0.66	0.20	83,83,83,83	0
54	MG	2A	3696	1/1	0.66	0.17	73,73,73,73	0
54	MG	2a	3048	1/1	0.66	0.25	80,80,80,80	0
54	MG	14	101	1/1	0.66	0.17	78,78,78,78	0
54	MG	1a	3160	1/1	0.66	0.28	71,71,71,71	0
54	MG	1A	3577	1/1	0.67	0.24	63,63,63,63	0
54	MG	2A	3425	1/1	0.67	0.16	59,59,59,59	0
54	MG	2A	3622	1/1	0.67	0.20	74,74,74,74	0
54	MG	1A	4012	1/1	0.67	0.63	73,73,73,73	0
54	MG	1a	3211	1/1	0.67	0.23	77,77,77,77	0
54	MG	1a	3052	1/1	0.67	0.28	73,73,73,73	0
54	MG	1a	3250	1/1	0.67	0.20	69,69,69,69	0
54	MG	1B	228	1/1	0.68	0.27	71,71,71,71	0
54	MG	1A	3366	1/1	0.68	0.22	72,72,72,72	0
54	MG	2G	201	1/1	0.68	0.26	80,80,80,80	0
54	MG	1a	3081	1/1	0.69	0.45	78,78,78,78	0
54	MG	1a	3142	1/1	0.69	0.22	86,86,86,86	0
54	MG	1a	3039	1/1	0.69	0.62	80,80,80,80	0
54	MG	2A	3063	1/1	0.69	0.33	76,76,76,76	0
54	MG	10	107	1/1	0.69	0.20	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3300	1/1	0.69	0.21	64,64,64,64	0
54	MG	2A	3309	1/1	0.69	0.21	59,59,59,59	0
57	MPD	2A	3746	8/8	0.69	0.34	64,72,74,78	0
54	MG	1A	3588	1/1	0.70	0.24	74,74,74,74	0
54	MG	1A	3881	1/1	0.70	0.21	49,49,49,49	0
54	MG	1A	3966	1/1	0.70	0.24	64,64,64,64	0
54	MG	2A	3485	1/1	0.70	0.22	70,70,70,70	0
54	MG	2A	3241	1/1	0.70	0.22	78,78,78,78	0
54	MG	1a	3099	1/1	0.70	0.68	90,90,90,90	0
54	MG	1A	3711	1/1	0.70	0.16	47,47,47,47	0
54	MG	1A	3980	1/1	0.70	0.28	73,73,73,73	0
54	MG	2A	3364	1/1	0.71	0.22	76,76,76,76	0
54	MG	10	105	1/1	0.71	0.22	67,67,67,67	0
54	MG	1A	3673	1/1	0.71	0.14	74,74,74,74	0
54	MG	2a	3071	1/1	0.71	0.28	80,80,80,80	0
54	MG	2a	3175	1/1	0.71	0.23	74,74,74,74	0
54	MG	2A	3456	1/1	0.71	0.23	75,75,75,75	0
54	MG	1T	204	1/1	0.71	0.14	80,80,80,80	0
54	MG	2A	3169	1/1	0.71	0.19	65,65,65,65	0
54	MG	1a	3246	1/1	0.72	0.38	78,78,78,78	0
54	MG	2A	3142	1/1	0.72	0.25	73,73,73,73	0
54	MG	1A	3418	1/1	0.72	0.22	54,54,54,54	0
54	MG	2A	3217	1/1	0.72	0.27	75,75,75,75	0
54	MG	2A	3481	1/1	0.72	0.15	66,66,66,66	0
54	MG	1B	225	1/1	0.72	0.26	80,80,80,80	0
54	MG	2a	3100	1/1	0.72	0.26	83,83,83,83	0
54	MG	1a	3258	1/1	0.72	0.18	73,73,73,73	0
54	MG	1A	3552	1/1	0.72	0.25	64,64,64,64	0
54	MG	1A	3931	1/1	0.72	0.13	56,56,56,56	0
54	MG	1a	3109	1/1	0.72	0.24	76,76,76,76	0
54	MG	1A	3745	1/1	0.73	0.34	63,63,63,63	0
54	MG	2D	308	1/1	0.73	0.28	86,86,86,86	0
54	MG	1a	3193	1/1	0.73	0.33	86,86,86,86	0
54	MG	2I	201	1/1	0.73	0.14	70,70,70,70	0
54	MG	2a	3045	1/1	0.73	0.27	79,79,79,79	0
54	MG	2A	3436	1/1	0.73	0.21	64,64,64,64	0
54	MG	2a	3057	1/1	0.73	0.29	79,79,79,79	0
54	MG	2a	3069	1/1	0.73	0.26	80,80,80,80	0
54	MG	2A	3442	1/1	0.73	0.21	71,71,71,71	0
54	MG	1A	3350	1/1	0.73	0.12	40,40,40,40	0
54	MG	1a	3107	1/1	0.73	0.22	76,76,76,76	0
54	MG	2A	3616	1/1	0.73	0.12	78,78,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2a	3192	1/1	0.73	0.29	67,67,67,67	0
54	MG	2A	3371	1/1	0.73	0.24	79,79,79,79	0
54	MG	2A	3685	1/1	0.73	0.13	74,74,74,74	0
54	MG	2A	3703	1/1	0.74	0.12	57,57,57,57	0
54	MG	2A	3460	1/1	0.74	0.18	63,63,63,63	0
54	MG	1A	3996	1/1	0.74	0.20	64,64,64,64	0
54	MG	1A	3641	1/1	0.74	0.20	63,63,63,63	0
54	MG	2a	3020	1/1	0.74	0.45	79,79,79,79	0
54	MG	2a	3038	1/1	0.74	0.24	72,72,72,72	0
54	MG	1a	3244	1/1	0.74	0.23	67,67,67,67	0
54	MG	2A	3487	1/1	0.74	0.14	74,74,74,74	0
54	MG	2A	3051	1/1	0.74	0.32	71,71,71,71	0
54	MG	2A	3056	1/1	0.74	0.28	72,72,72,72	0
54	MG	1A	4014	1/1	0.74	0.24	74,74,74,74	0
54	MG	2A	3116	1/1	0.74	0.19	71,71,71,71	0
54	MG	2a	3110	1/1	0.74	0.19	74,74,74,74	0
54	MG	2A	3120	1/1	0.74	0.32	74,74,74,74	0
54	MG	1A	3671	1/1	0.74	0.28	75,75,75,75	0
54	MG	1A	3447	1/1	0.74	0.22	64,64,64,64	0
54	MG	1a	3203	1/1	0.74	0.25	77,77,77,77	0
57	MPD	1T	206	8/8	0.74	0.26	59,65,71,80	0
54	MG	2A	3459	1/1	0.74	0.22	60,60,60,60	0
54	MG	1a	3073	1/1	0.75	0.30	76,76,76,76	0
54	MG	1A	3283	1/1	0.75	0.18	82,82,82,82	0
54	MG	2a	3065	1/1	0.75	0.28	78,78,78,78	0
54	MG	1B	209	1/1	0.75	0.39	74,74,74,74	0
54	MG	1a	3270	1/1	0.75	0.13	87,87,87,87	0
54	MG	2A	3706	1/1	0.75	0.17	65,65,65,65	0
54	MG	1A	3531	1/1	0.75	0.28	78,78,78,78	0
54	MG	2A	3524	1/1	0.75	0.18	66,66,66,66	0
54	MG	1l	103	1/1	0.75	0.20	63,63,63,63	0
54	MG	20	101	1/1	0.75	0.25	75,75,75,75	0
54	MG	1A	3947	1/1	0.75	0.22	57,57,57,57	0
54	MG	1A	3432	1/1	0.75	0.26	75,75,75,75	0
54	MG	1R	204	1/1	0.75	0.26	53,53,53,53	0
58	ARG	1F	320	12/12	0.75	0.23	50,66,75,75	0
54	MG	1A	3777	1/1	0.76	0.25	66,66,66,66	0
54	MG	1A	3485	1/1	0.76	0.13	82,82,82,82	0
54	MG	2a	3002	1/1	0.76	0.20	74,74,74,74	0
54	MG	2A	3054	1/1	0.76	0.25	66,66,66,66	0
54	MG	2a	3037	1/1	0.76	0.12	87,87,87,87	0
54	MG	1A	3608	1/1	0.76	0.32	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3882	1/1	0.76	0.17	54,54,54,54	0
54	MG	2A	3406	1/1	0.76	0.24	77,77,77,77	0
54	MG	2A	3093	1/1	0.76	0.27	71,71,71,71	0
54	MG	2a	3059	1/1	0.76	0.28	74,74,74,74	0
54	MG	1A	3627	1/1	0.76	0.31	63,63,63,63	0
54	MG	1A	3375	1/1	0.76	0.18	59,59,59,59	0
54	MG	1a	3010	1/1	0.76	0.30	67,67,67,67	0
54	MG	2a	3086	1/1	0.76	0.23	70,70,70,70	0
54	MG	2A	3629	1/1	0.76	0.24	72,72,72,72	0
54	MG	2A	3682	1/1	0.76	0.15	60,60,60,60	0
54	MG	2a	3114	1/1	0.76	0.16	75,75,75,75	0
54	MG	2A	3451	1/1	0.76	0.21	68,68,68,68	0
54	MG	2A	3695	1/1	0.76	0.29	63,63,63,63	0
54	MG	1a	3032	1/1	0.76	0.13	66,66,66,66	0
54	MG	2A	3214	1/1	0.76	0.23	71,71,71,71	0
54	MG	1A	3378	1/1	0.76	0.25	61,61,61,61	0
54	MG	1A	3215	1/1	0.76	0.29	72,72,72,72	0
54	MG	2A	3256	1/1	0.76	0.22	61,61,61,61	0
54	MG	2A	3493	1/1	0.77	0.25	71,71,71,71	0
54	MG	1A	3689	1/1	0.77	0.22	57,57,57,57	0
54	MG	1A	3592	1/1	0.77	0.16	44,44,44,44	0
54	MG	2A	3521	1/1	0.77	0.32	69,69,69,69	0
54	MG	1a	3058	1/1	0.77	0.19	74,74,74,74	0
54	MG	2A	3097	1/1	0.77	0.31	76,76,76,76	0
54	MG	1T	201	1/1	0.77	0.24	66,66,66,66	0
54	MG	1a	3163	1/1	0.77	0.16	72,72,72,72	0
54	MG	2a	3004	1/1	0.77	0.20	69,69,69,69	0
54	MG	2A	3323	1/1	0.77	0.25	68,68,68,68	0
54	MG	2A	3463	1/1	0.77	0.16	66,66,66,66	0
54	MG	1o	101	1/1	0.77	0.23	68,68,68,68	0
54	MG	1A	3954	1/1	0.77	0.20	69,69,69,69	0
54	MG	2A	3180	1/1	0.77	0.18	74,74,74,74	0
54	MG	1A	3564	1/1	0.77	0.17	77,77,77,77	0
54	MG	2A	3237	1/1	0.78	0.34	67,67,67,67	0
54	MG	1A	3262	1/1	0.78	0.34	75,75,75,75	0
54	MG	1A	3556	1/1	0.78	0.19	60,60,60,60	0
54	MG	2A	3260	1/1	0.78	0.24	75,75,75,75	0
54	MG	2a	3062	1/1	0.78	0.36	79,79,79,79	0
54	MG	2A	3282	1/1	0.78	0.23	72,72,72,72	0
54	MG	1A	3636	1/1	0.78	0.30	40,40,40,40	0
54	MG	1A	3759	1/1	0.78	0.18	63,63,63,63	0
54	MG	1A	3431	1/1	0.78	0.12	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3801	1/1	0.78	0.21	77,77,77,77	0
54	MG	2a	3106	1/1	0.78	0.31	64,64,64,64	0
54	MG	1a	3091	1/1	0.78	0.32	74,74,74,74	0
54	MG	2a	3113	1/1	0.78	0.32	71,71,71,71	0
54	MG	2G	202	1/1	0.78	0.16	77,77,77,77	0
54	MG	2a	3121	1/1	0.78	0.25	80,80,80,80	0
54	MG	2a	3126	1/1	0.78	0.29	78,78,78,78	0
54	MG	1A	3652	1/1	0.78	0.11	22,22,22,22	0
54	MG	2a	3179	1/1	0.78	0.15	74,74,74,74	0
54	MG	1A	3663	1/1	0.78	0.15	48,48,48,48	0
54	MG	2a	3190	1/1	0.78	0.26	73,73,73,73	0
54	MG	1A	3725	1/1	0.78	0.14	66,66,66,66	0
54	MG	1a	3137	1/1	0.78	0.19	71,71,71,71	0
54	MG	1B	205	1/1	0.78	0.27	69,69,69,69	0
54	MG	1A	3920	1/1	0.78	0.16	61,61,61,61	0
54	MG	1a	3023	1/1	0.78	0.29	64,64,64,64	0
54	MG	2A	3508	1/1	0.79	0.17	37,37,37,37	0
54	MG	1a	3208	1/1	0.79	0.19	64,64,64,64	0
54	MG	2a	3023	1/1	0.79	0.28	75,75,75,75	0
54	MG	1A	3600	1/1	0.79	0.15	68,68,68,68	0
54	MG	1A	3371	1/1	0.79	0.18	71,71,71,71	0
54	MG	2a	3044	1/1	0.79	0.29	72,72,72,72	0
54	MG	1A	3462	1/1	0.79	0.16	57,57,57,57	0
54	MG	2A	3387	1/1	0.79	0.15	52,52,52,52	0
54	MG	2a	3052	1/1	0.79	0.21	70,70,70,70	0
54	MG	2a	3056	1/1	0.79	0.18	70,70,70,70	0
54	MG	2A	3599	1/1	0.79	0.14	47,47,47,47	0
54	MG	2A	3608	1/1	0.79	0.15	42,42,42,42	0
54	MG	2A	3108	1/1	0.79	0.20	73,73,73,73	0
54	MG	1A	3629	1/1	0.79	0.29	37,37,37,37	0
54	MG	1A	3992	1/1	0.79	0.25	63,63,63,63	0
54	MG	1A	3802	1/1	0.79	0.18	27,27,27,27	0
54	MG	2A	3630	1/1	0.79	0.24	75,75,75,75	0
54	MG	1A	3813	1/1	0.79	0.28	42,42,42,42	0
54	MG	1A	3634	1/1	0.79	0.22	56,56,56,56	0
54	MG	2A	3691	1/1	0.79	0.15	55,55,55,55	0
54	MG	2A	3194	1/1	0.79	0.22	77,77,77,77	0
54	MG	1A	3691	1/1	0.79	0.27	54,54,54,54	0
54	MG	1A	3575	1/1	0.79	0.28	44,44,44,44	0
54	MG	1a	3271	1/1	0.79	0.25	78,78,78,78	0
54	MG	2A	3710	1/1	0.79	0.15	65,65,65,65	0
54	MG	2A	3715	1/1	0.79	0.47	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2a	3181	1/1	0.79	0.18	68,68,68,68	0
54	MG	2B	203	1/1	0.79	0.17	81,81,81,81	0
54	MG	1A	3285	1/1	0.79	0.28	77,77,77,77	0
54	MG	1h	202	1/1	0.79	0.24	72,72,72,72	0
54	MG	1A	3146	1/1	0.79	0.15	57,57,57,57	0
54	MG	2A	3038	1/1	0.79	0.28	70,70,70,70	0
54	MG	1a	3197	1/1	0.79	0.20	70,70,70,70	0
54	MG	1A	3400	1/1	0.79	0.17	53,53,53,53	0
54	MG	2a	3047	1/1	0.80	0.41	76,76,76,76	0
54	MG	1A	3987	1/1	0.80	0.46	57,57,57,57	0
54	MG	1F	318	1/1	0.80	0.15	61,61,61,61	0
54	MG	1g	3101	1/1	0.80	0.22	78,78,78,78	0
54	MG	2A	3196	1/1	0.80	0.27	71,71,71,71	0
54	MG	2a	3058	1/1	0.80	0.26	74,74,74,74	0
54	MG	1A	3989	1/1	0.80	0.11	87,87,87,87	0
54	MG	1A	3991	1/1	0.80	0.21	69,69,69,69	0
54	MG	1A	3553	1/1	0.80	0.19	63,63,63,63	0
54	MG	2A	3469	1/1	0.80	0.22	75,75,75,75	0
54	MG	2A	3471	1/1	0.80	0.19	71,71,71,71	0
54	MG	2A	3045	1/1	0.80	0.15	51,51,51,51	0
54	MG	2A	3049	1/1	0.80	0.21	72,72,72,72	0
54	MG	1A	3581	1/1	0.80	0.16	38,38,38,38	0
54	MG	1a	3223	1/1	0.80	0.23	70,70,70,70	0
54	MG	1A	3525	1/1	0.80	0.15	47,47,47,47	0
54	MG	1A	3952	1/1	0.80	0.14	50,50,50,50	0
54	MG	1A	3557	1/1	0.80	0.12	67,67,67,67	0
54	MG	18	101	1/1	0.80	0.24	71,71,71,71	0
54	MG	2A	3358	1/1	0.80	0.19	51,51,51,51	0
54	MG	2A	3098	1/1	0.80	0.21	69,69,69,69	0
54	MG	2A	3525	1/1	0.80	0.13	75,75,75,75	0
54	MG	2a	3006	1/1	0.80	0.16	62,62,62,62	0
54	MG	2a	3188	1/1	0.80	0.14	90,90,90,90	0
54	MG	1a	3003	1/1	0.80	0.24	71,71,71,71	0
54	MG	1A	3682	1/1	0.80	0.23	61,61,61,61	0
54	MG	2e	201	1/1	0.80	0.30	75,75,75,75	0
54	MG	1A	3480	1/1	0.80	0.10	29,29,29,29	0
54	MG	2p	101	1/1	0.80	0.32	64,64,64,64	0
54	MG	2A	3124	1/1	0.80	0.25	73,73,73,73	0
54	MG	1A	3496	1/1	0.80	0.13	65,65,65,65	0
54	MG	2A	3430	1/1	0.80	0.20	58,58,58,58	0
54	MG	2A	3520	1/1	0.81	0.11	59,59,59,59	0
54	MG	2a	3008	1/1	0.81	0.18	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1a	3053	1/1	0.81	0.28	67,67,67,67	0
54	MG	2A	3522	1/1	0.81	0.23	68,68,68,68	0
54	MG	2A	3326	1/1	0.81	0.17	56,56,56,56	0
54	MG	1a	3055	1/1	0.81	0.28	63,63,63,63	0
54	MG	2A	3526	1/1	0.81	0.18	66,66,66,66	0
54	MG	1a	3212	1/1	0.81	0.26	76,76,76,76	0
54	MG	1A	3880	1/1	0.81	0.10	57,57,57,57	0
54	MG	2A	3578	1/1	0.81	0.22	53,53,53,53	0
54	MG	2A	3373	1/1	0.81	0.10	41,41,41,41	0
54	MG	2a	3054	1/1	0.81	0.26	64,64,64,64	0
54	MG	1A	3574	1/1	0.81	0.25	61,61,61,61	0
54	MG	2A	3388	1/1	0.81	0.21	53,53,53,53	0
54	MG	1a	3229	1/1	0.81	0.40	77,77,77,77	0
54	MG	2A	3621	1/1	0.81	0.17	71,71,71,71	0
54	MG	2a	3060	1/1	0.81	0.23	78,78,78,78	0
54	MG	1A	3635	1/1	0.81	0.17	63,63,63,63	0
54	MG	1A	3914	1/1	0.81	0.15	30,30,30,30	0
54	MG	1a	3247	1/1	0.81	0.19	80,80,80,80	0
54	MG	2A	3632	1/1	0.81	0.13	74,74,74,74	0
54	MG	2a	3082	1/1	0.81	0.33	65,65,65,65	0
54	MG	2a	3084	1/1	0.81	0.22	79,79,79,79	0
54	MG	2A	3671	1/1	0.81	0.18	81,81,81,81	0
54	MG	2a	3087	1/1	0.81	0.39	82,82,82,82	0
54	MG	2a	3094	1/1	0.81	0.37	73,73,73,73	0
54	MG	1a	3093	1/1	0.81	0.32	75,75,75,75	0
54	MG	1A	3426	1/1	0.81	0.15	33,33,33,33	0
54	MG	1A	3174	1/1	0.81	0.20	68,68,68,68	0
54	MG	1A	3569	1/1	0.81	0.15	70,70,70,70	0
54	MG	1A	3660	1/1	0.81	0.12	59,59,59,59	0
54	MG	2A	3702	1/1	0.81	0.29	66,66,66,66	0
54	MG	1B	202	1/1	0.81	0.22	70,70,70,70	0
54	MG	1A	3662	1/1	0.81	0.18	54,54,54,54	0
54	MG	1A	3958	1/1	0.81	0.13	79,79,79,79	0
54	MG	1A	3571	1/1	0.81	0.23	54,54,54,54	0
54	MG	2A	3737	1/1	0.81	0.32	75,75,75,75	0
54	MG	1a	3182	1/1	0.81	0.23	80,80,80,80	0
54	MG	2B	207	1/1	0.81	0.23	65,65,65,65	0
54	MG	2A	3242	1/1	0.81	0.17	73,73,73,73	0
54	MG	1A	3970	1/1	0.81	0.20	65,65,65,65	0
54	MG	2A	3036	1/1	0.81	0.25	69,69,69,69	0
54	MG	1a	3196	1/1	0.81	0.16	64,64,64,64	0
54	MG	1A	3666	1/1	0.81	0.14	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
57	MPD	1a	3279	8/8	0.81	0.14	52,63,67,73	0
54	MG	1a	3201	1/1	0.81	0.14	71,71,71,71	0
54	MG	1F	315	1/1	0.81	0.19	50,50,50,50	0
54	MG	2a	3046	1/1	0.82	0.50	77,77,77,77	0
54	MG	2A	3390	1/1	0.82	0.22	60,60,60,60	0
54	MG	2A	3392	1/1	0.82	0.16	58,58,58,58	0
54	MG	2A	3619	1/1	0.82	0.20	44,44,44,44	0
54	MG	1A	3522	1/1	0.82	0.22	57,57,57,57	0
54	MG	2A	3128	1/1	0.82	0.24	63,63,63,63	0
54	MG	1A	3298	1/1	0.82	0.17	88,88,88,88	0
54	MG	2A	3157	1/1	0.82	0.35	64,64,64,64	0
54	MG	2A	3166	1/1	0.82	0.40	59,59,59,59	0
54	MG	1A	3825	1/1	0.82	0.14	60,60,60,60	0
54	MG	1A	3594	1/1	0.82	0.12	46,46,46,46	0
54	MG	1B	227	1/1	0.82	0.13	69,69,69,69	0
54	MG	1A	3862	1/1	0.82	0.20	70,70,70,70	0
54	MG	2A	3198	1/1	0.82	0.26	66,66,66,66	0
54	MG	2a	3078	1/1	0.82	0.29	72,72,72,72	0
54	MG	2A	3462	1/1	0.82	0.16	66,66,66,66	0
54	MG	1a	3188	1/1	0.82	0.24	68,68,68,68	0
54	MG	1A	3972	1/1	0.82	0.13	63,63,63,63	0
54	MG	1a	3195	1/1	0.82	0.18	63,63,63,63	0
54	MG	1E	305	1/1	0.82	0.13	30,30,30,30	0
54	MG	1A	3876	1/1	0.82	0.10	29,29,29,29	0
54	MG	2A	3717	1/1	0.82	0.12	73,73,73,73	0
54	MG	2A	3718	1/1	0.82	0.13	74,74,74,74	0
54	MG	1A	3640	1/1	0.82	0.15	64,64,64,64	0
54	MG	2A	3044	1/1	0.82	0.37	77,77,77,77	0
54	MG	2A	3277	1/1	0.82	0.38	70,70,70,70	0
54	MG	2A	3279	1/1	0.82	0.17	79,79,79,79	0
54	MG	2a	3165	1/1	0.82	0.27	68,68,68,68	0
54	MG	2A	3506	1/1	0.82	0.22	61,61,61,61	0
54	MG	1a	3067	1/1	0.82	0.20	79,79,79,79	0
54	MG	1a	3070	1/1	0.82	0.25	61,61,61,61	0
54	MG	2a	3183	1/1	0.82	0.18	77,77,77,77	0
54	MG	1A	3680	1/1	0.82	0.29	75,75,75,75	0
54	MG	1a	3074	1/1	0.82	0.22	64,64,64,64	0
54	MG	2A	3311	1/1	0.82	0.22	62,62,62,62	0
54	MG	1A	3528	1/1	0.82	0.16	53,53,53,53	0
54	MG	1A	3460	1/1	0.82	0.12	67,67,67,67	0
54	MG	1a	3226	1/1	0.82	0.29	70,70,70,70	0
54	MG	1A	3918	1/1	0.82	0.15	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3774	1/1	0.82	0.19	49,49,49,49	0
54	MG	1A	3579	1/1	0.82	0.20	71,71,71,71	0
54	MG	1A	3323	1/1	0.82	0.11	55,55,55,55	0
54	MG	1a	3113	1/1	0.82	0.25	74,74,74,74	0
54	MG	1A	3583	1/1	0.83	0.12	54,54,54,54	0
54	MG	2a	3025	1/1	0.83	0.36	73,73,73,73	0
54	MG	1H	201	1/1	0.83	0.25	76,76,76,76	0
54	MG	2A	3362	1/1	0.83	0.18	71,71,71,71	0
54	MG	2a	3041	1/1	0.83	0.38	72,72,72,72	0
54	MG	2a	3043	1/1	0.83	0.23	79,79,79,79	0
54	MG	2A	3544	1/1	0.83	0.11	66,66,66,66	0
54	MG	2A	3545	1/1	0.83	0.12	77,77,77,77	0
54	MG	2A	3563	1/1	0.83	0.17	45,45,45,45	0
54	MG	2A	3121	1/1	0.83	0.30	73,73,73,73	0
54	MG	1A	3584	1/1	0.83	0.17	62,62,62,62	0
54	MG	1A	3282	1/1	0.83	0.15	72,72,72,72	0
54	MG	2a	3053	1/1	0.83	0.21	68,68,68,68	0
54	MG	1A	3830	1/1	0.83	0.12	54,54,54,54	0
54	MG	1A	3850	1/1	0.83	0.15	63,63,63,63	0
54	MG	2A	3163	1/1	0.83	0.27	62,62,62,62	0
54	MG	1A	3591	1/1	0.83	0.10	62,62,62,62	0
54	MG	2A	3402	1/1	0.83	0.10	65,65,65,65	0
54	MG	1i	201	1/1	0.83	0.24	77,77,77,77	0
54	MG	2A	3171	1/1	0.83	0.17	57,57,57,57	0
54	MG	2A	3176	1/1	0.83	0.32	62,62,62,62	0
54	MG	2A	3179	1/1	0.83	0.26	67,67,67,67	0
54	MG	1l	202	1/1	0.83	0.18	73,73,73,73	0
54	MG	1a	3087	1/1	0.83	0.30	73,73,73,73	0
54	MG	1r	101	1/1	0.83	0.21	73,73,73,73	0
54	MG	2A	3035	1/1	0.83	0.31	78,78,78,78	0
54	MG	2A	3211	1/1	0.83	0.41	79,79,79,79	0
54	MG	2A	3212	1/1	0.83	0.19	61,61,61,61	0
54	MG	2a	3093	1/1	0.83	0.56	79,79,79,79	0
54	MG	1A	3766	1/1	0.83	0.10	47,47,47,47	0
54	MG	1A	3704	1/1	0.83	0.14	31,31,31,31	0
54	MG	2A	3219	1/1	0.83	0.28	67,67,67,67	0
54	MG	1B	216	1/1	0.83	0.16	62,62,62,62	0
54	MG	1B	219	1/1	0.83	0.15	47,47,47,47	0
54	MG	1A	3971	1/1	0.83	0.16	61,61,61,61	0
54	MG	1A	3568	1/1	0.83	0.23	62,62,62,62	0
54	MG	1A	3799	1/1	0.83	0.22	71,71,71,71	0
54	MG	2a	3128	1/1	0.83	0.26	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2B	202	1/1	0.83	0.30	81,81,81,81	0
54	MG	1a	3138	1/1	0.83	0.28	58,58,58,58	0
54	MG	2A	3502	1/1	0.83	0.12	61,61,61,61	0
54	MG	2B	208	1/1	0.83	0.34	77,77,77,77	0
54	MG	2B	213	1/1	0.83	0.13	71,71,71,71	0
54	MG	2A	3057	1/1	0.83	0.37	73,73,73,73	0
54	MG	1a	3036	1/1	0.83	0.26	62,62,62,62	0
54	MG	2A	3083	1/1	0.83	0.23	81,81,81,81	0
54	MG	2A	3509	1/1	0.83	0.11	59,59,59,59	0
54	MG	2A	3510	1/1	0.83	0.20	68,68,68,68	0
54	MG	1a	3151	1/1	0.83	0.20	66,66,66,66	0
54	MG	1A	3883	1/1	0.83	0.17	58,58,58,58	0
54	MG	1A	3419	1/1	0.83	0.18	46,46,46,46	0
54	MG	2A	3318	1/1	0.83	0.18	72,72,72,72	0
54	MG	2a	3017	1/1	0.83	0.33	64,64,64,64	0
54	MG	1A	3727	1/1	0.83	0.11	59,59,59,59	0
54	MG	2A	3249	1/1	0.84	0.27	71,71,71,71	0
54	MG	1D	311	1/1	0.84	0.20	33,33,33,33	0
54	MG	1A	3450	1/1	0.84	0.18	55,55,55,55	0
54	MG	2A	3515	1/1	0.84	0.14	61,61,61,61	0
54	MG	1F	311	1/1	0.84	0.12	58,58,58,58	0
54	MG	1A	3756	1/1	0.84	0.20	70,70,70,70	0
54	MG	2a	3024	1/1	0.84	0.32	67,67,67,67	0
54	MG	1A	3458	1/1	0.84	0.15	51,51,51,51	0
54	MG	2a	3031	1/1	0.84	0.30	80,80,80,80	0
54	MG	1a	3198	1/1	0.84	0.16	67,67,67,67	0
54	MG	2A	3288	1/1	0.84	0.25	67,67,67,67	0
54	MG	2a	3039	1/1	0.84	0.26	73,73,73,73	0
54	MG	2A	3055	1/1	0.84	0.28	68,68,68,68	0
54	MG	1A	3413	1/1	0.84	0.23	70,70,70,70	0
54	MG	1A	3361	1/1	0.84	0.26	72,72,72,72	0
54	MG	2A	3538	1/1	0.84	0.11	64,64,64,64	0
54	MG	1A	3321	1/1	0.84	0.18	63,63,63,63	0
54	MG	2A	3076	1/1	0.84	0.24	70,70,70,70	0
54	MG	2A	3560	1/1	0.84	0.12	74,74,74,74	0
54	MG	1A	3779	1/1	0.84	0.18	53,53,53,53	0
54	MG	2A	3566	1/1	0.84	0.17	46,46,46,46	0
54	MG	2A	3355	1/1	0.84	0.17	55,55,55,55	0
54	MG	1A	3441	1/1	0.84	0.21	69,69,69,69	0
54	MG	2A	3587	1/1	0.84	0.12	52,52,52,52	0
54	MG	1A	4018	1/1	0.84	0.20	70,70,70,70	0
54	MG	2A	3603	1/1	0.84	0.13	62,62,62,62	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3606	1/1	0.84	0.17	52,52,52,52	0
54	MG	1A	3657	1/1	0.84	0.26	33,33,33,33	0
54	MG	1A	3032	1/1	0.84	0.34	63,63,63,63	0
54	MG	2A	3113	1/1	0.84	0.24	60,60,60,60	0
54	MG	1a	3102	1/1	0.84	0.43	72,72,72,72	0
54	MG	1a	3239	1/1	0.84	0.20	57,57,57,57	0
54	MG	1a	3105	1/1	0.84	0.18	67,67,67,67	0
54	MG	2A	3626	1/1	0.84	0.10	80,80,80,80	0
54	MG	1A	3626	1/1	0.84	0.23	57,57,57,57	0
54	MG	2A	3394	1/1	0.84	0.15	71,71,71,71	0
54	MG	1A	3719	1/1	0.84	0.15	70,70,70,70	0
54	MG	1A	3507	1/1	0.84	0.12	27,27,27,27	0
54	MG	1a	3128	1/1	0.84	0.19	66,66,66,66	0
54	MG	1a	3130	1/1	0.84	0.13	84,84,84,84	0
54	MG	1A	3664	1/1	0.84	0.22	68,68,68,68	0
54	MG	1a	3029	1/1	0.84	0.31	65,65,65,65	0
54	MG	2A	3170	1/1	0.84	0.23	94,94,94,94	0
54	MG	2A	3443	1/1	0.84	0.18	64,64,64,64	0
54	MG	2a	3124	1/1	0.84	0.26	70,70,70,70	0
54	MG	1a	3263	1/1	0.84	0.14	63,63,63,63	0
54	MG	1A	3737	1/1	0.84	0.23	71,71,71,71	0
54	MG	2a	3130	1/1	0.84	0.17	84,84,84,84	0
54	MG	2a	3163	1/1	0.84	0.13	63,63,63,63	0
54	MG	1a	3150	1/1	0.84	0.39	80,80,80,80	0
54	MG	1A	3509	1/1	0.84	0.14	60,60,60,60	0
54	MG	1b	301	1/1	0.84	0.18	79,79,79,79	0
54	MG	2A	3195	1/1	0.84	0.33	58,58,58,58	0
54	MG	1d	304	1/1	0.84	0.09	77,77,77,77	0
54	MG	1a	3153	1/1	0.84	0.26	77,77,77,77	0
54	MG	1a	3038	1/1	0.84	0.26	66,66,66,66	0
54	MG	2A	3479	1/1	0.84	0.26	64,64,64,64	0
54	MG	1a	3162	1/1	0.84	0.17	62,62,62,62	0
54	MG	1A	3632	1/1	0.84	0.16	45,45,45,45	0
54	MG	1a	3170	1/1	0.84	0.27	73,73,73,73	0
54	MG	1a	3045	1/1	0.84	0.26	67,67,67,67	0
54	MG	2A	3501	1/1	0.84	0.14	72,72,72,72	0
54	MG	2A	3032	1/1	0.84	0.15	73,73,73,73	0
57	MPD	2A	3745	8/8	0.84	0.27	46,53,59,59	0
54	MG	1a	3046	1/1	0.84	0.35	65,65,65,65	0
57	MPD	2A	3747	8/8	0.84	0.23	60,63,68,69	0
54	MG	1a	3184	1/1	0.84	0.14	67,67,67,67	0
54	MG	2N	201	1/1	0.85	0.09	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1a	3017	1/1	0.85	0.14	63,63,63,63	0
54	MG	1A	3782	1/1	0.85	0.19	70,70,70,70	0
54	MG	1A	3930	1/1	0.85	0.15	52,52,52,52	0
54	MG	1B	204	1/1	0.85	0.13	57,57,57,57	0
54	MG	1n	101	1/1	0.85	0.16	61,61,61,61	0
54	MG	2a	3011	1/1	0.85	0.27	67,67,67,67	0
54	MG	1a	3035	1/1	0.85	0.28	65,65,65,65	0
54	MG	1a	3166	1/1	0.85	0.12	64,64,64,64	0
54	MG	2A	3025	1/1	0.85	0.15	54,54,54,54	0
54	MG	1A	3272	1/1	0.85	0.15	53,53,53,53	0
54	MG	1A	3511	1/1	0.85	0.15	52,52,52,52	0
54	MG	1A	3950	1/1	0.85	0.12	70,70,70,70	0
54	MG	2a	3036	1/1	0.85	0.15	72,72,72,72	0
54	MG	2A	3523	1/1	0.85	0.16	62,62,62,62	0
54	MG	2A	3280	1/1	0.85	0.27	70,70,70,70	0
54	MG	1a	3183	1/1	0.85	0.20	77,77,77,77	0
54	MG	2A	3285	1/1	0.85	0.13	56,56,56,56	0
54	MG	1A	3320	1/1	0.85	0.12	50,50,50,50	0
54	MG	2A	3529	1/1	0.85	0.13	69,69,69,69	0
54	MG	2A	3287	1/1	0.85	0.17	42,42,42,42	0
54	MG	1A	3059	1/1	0.85	0.23	47,47,47,47	0
54	MG	1a	3189	1/1	0.85	0.32	72,72,72,72	0
54	MG	1a	3191	1/1	0.85	0.21	72,72,72,72	0
54	MG	2A	3310	1/1	0.85	0.16	68,68,68,68	0
54	MG	1a	3051	1/1	0.85	0.25	61,61,61,61	0
54	MG	1A	3955	1/1	0.85	0.13	52,52,52,52	0
54	MG	2A	3574	1/1	0.85	0.14	50,50,50,50	0
54	MG	1A	3814	1/1	0.85	0.16	42,42,42,42	0
54	MG	2A	3579	1/1	0.85	0.18	42,42,42,42	0
54	MG	1A	3965	1/1	0.85	0.20	57,57,57,57	0
54	MG	2A	3351	1/1	0.85	0.17	70,70,70,70	0
54	MG	2A	3058	1/1	0.85	0.43	72,72,72,72	0
54	MG	2a	3063	1/1	0.85	0.29	75,75,75,75	0
54	MG	2A	3062	1/1	0.85	0.17	62,62,62,62	0
54	MG	1a	3057	1/1	0.85	0.14	71,71,71,71	0
54	MG	2A	3070	1/1	0.85	0.17	53,53,53,53	0
54	MG	1a	3199	1/1	0.85	0.14	73,73,73,73	0
54	MG	1A	3822	1/1	0.85	0.14	54,54,54,54	0
54	MG	1a	3059	1/1	0.85	0.25	43,43,43,43	0
54	MG	1A	3967	1/1	0.85	0.30	55,55,55,55	0
54	MG	1A	3527	1/1	0.85	0.14	35,35,35,35	0
54	MG	2A	3627	1/1	0.85	0.26	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1F	313	1/1	0.85	0.13	33,33,33,33	0
54	MG	1A	3677	1/1	0.85	0.12	41,41,41,41	0
54	MG	1a	3221	1/1	0.85	0.18	65,65,65,65	0
54	MG	2A	3657	1/1	0.85	0.10	78,78,78,78	0
54	MG	1A	3743	1/1	0.85	0.21	44,44,44,44	0
54	MG	1A	3679	1/1	0.85	0.12	64,64,64,64	0
54	MG	1a	3227	1/1	0.85	0.16	73,73,73,73	0
54	MG	1A	3143	1/1	0.85	0.27	62,62,62,62	0
54	MG	1a	3233	1/1	0.85	0.12	76,76,76,76	0
54	MG	1A	3754	1/1	0.85	0.18	52,52,52,52	0
54	MG	1A	3443	1/1	0.85	0.12	44,44,44,44	0
54	MG	2a	3142	1/1	0.85	0.11	70,70,70,70	0
54	MG	1V	204	1/1	0.85	0.25	64,64,64,64	0
54	MG	1W	201	1/1	0.85	0.31	56,56,56,56	0
54	MG	1A	3642	1/1	0.85	0.09	29,29,29,29	0
54	MG	10	106	1/1	0.85	0.14	59,59,59,59	0
54	MG	1A	3267	1/1	0.85	0.39	70,70,70,70	0
54	MG	1a	3126	1/1	0.85	0.29	70,70,70,70	0
54	MG	1A	3610	1/1	0.85	0.17	64,64,64,64	0
54	MG	2B	201	1/1	0.85	0.22	72,72,72,72	0
54	MG	2A	3188	1/1	0.85	0.24	74,74,74,74	0
54	MG	2a	3191	1/1	0.85	0.23	73,73,73,73	0
54	MG	2A	3191	1/1	0.85	0.36	71,71,71,71	0
54	MG	1A	3998	1/1	0.85	0.15	46,46,46,46	0
54	MG	1a	3132	1/1	0.85	0.20	80,80,80,80	0
54	MG	2B	209	1/1	0.85	0.14	65,65,65,65	0
54	MG	2B	210	1/1	0.85	0.23	74,74,74,74	0
54	MG	15	109	1/1	0.85	0.19	72,72,72,72	0
54	MG	1A	3506	1/1	0.85	0.12	35,35,35,35	0
54	MG	2A	3492	1/1	0.85	0.13	59,59,59,59	0
54	MG	1A	3376	1/1	0.85	0.25	51,51,51,51	0
54	MG	1A	4017	1/1	0.85	0.22	70,70,70,70	0
54	MG	2A	3444	1/1	0.86	0.14	58,58,58,58	0
54	MG	2A	3449	1/1	0.86	0.26	67,67,67,67	0
54	MG	1a	3217	1/1	0.86	0.31	69,69,69,69	0
54	MG	2A	3453	1/1	0.86	0.13	70,70,70,70	0
54	MG	1A	3453	1/1	0.86	0.12	39,39,39,39	0
54	MG	1A	3674	1/1	0.86	0.11	73,73,73,73	0
54	MG	1a	3076	1/1	0.86	0.33	69,69,69,69	0
54	MG	2D	310	1/1	0.86	0.10	31,31,31,31	0
54	MG	1a	3225	1/1	0.86	0.14	73,73,73,73	0
54	MG	1A	3198	1/1	0.86	0.31	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3467	1/1	0.86	0.14	67,67,67,67	0
54	MG	2A	3164	1/1	0.86	0.20	68,68,68,68	0
54	MG	1A	3064	1/1	0.86	0.15	49,49,49,49	0
54	MG	2I	3801	1/1	0.86	0.09	74,74,74,74	0
54	MG	1G	202	1/1	0.86	0.12	55,55,55,55	0
54	MG	1A	3237	1/1	0.86	0.24	69,69,69,69	0
54	MG	1N	203	1/1	0.86	0.14	59,59,59,59	0
54	MG	1A	3467	1/1	0.86	0.16	49,49,49,49	0
54	MG	2a	3009	1/1	0.86	0.53	75,75,75,75	0
54	MG	1A	3811	1/1	0.86	0.14	67,67,67,67	0
54	MG	2A	3488	1/1	0.86	0.14	70,70,70,70	0
54	MG	2A	3490	1/1	0.86	0.16	65,65,65,65	0
54	MG	1A	3346	1/1	0.86	0.14	51,51,51,51	0
54	MG	1A	3415	1/1	0.86	0.12	70,70,70,70	0
54	MG	1a	3111	1/1	0.86	0.15	61,61,61,61	0
54	MG	1A	3974	1/1	0.86	0.19	64,64,64,64	0
54	MG	2a	3032	1/1	0.86	0.36	72,72,72,72	0
54	MG	1a	3120	1/1	0.86	0.17	54,54,54,54	0
54	MG	1A	3975	1/1	0.86	0.09	59,59,59,59	0
54	MG	1A	3347	1/1	0.86	0.17	60,60,60,60	0
54	MG	1A	3823	1/1	0.86	0.14	54,54,54,54	0
54	MG	1A	3148	1/1	0.86	0.10	78,78,78,78	0
54	MG	1a	3273	1/1	0.86	0.17	77,77,77,77	0
54	MG	1a	3134	1/1	0.86	0.21	73,73,73,73	0
54	MG	1A	3696	1/1	0.86	0.35	53,53,53,53	0
54	MG	2A	3222	1/1	0.86	0.25	63,63,63,63	0
54	MG	1A	3990	1/1	0.86	0.18	76,76,76,76	0
54	MG	1A	3425	1/1	0.86	0.21	63,63,63,63	0
54	MG	1a	3145	1/1	0.86	0.15	66,66,66,66	0
54	MG	1a	3149	1/1	0.86	0.26	66,66,66,66	0
54	MG	1a	3001	1/1	0.86	0.14	74,74,74,74	0
54	MG	2A	3257	1/1	0.86	0.24	66,66,66,66	0
54	MG	1A	3841	1/1	0.86	0.16	59,59,59,59	0
54	MG	2A	3275	1/1	0.86	0.37	67,67,67,67	0
54	MG	1a	3004	1/1	0.86	0.21	62,62,62,62	0
54	MG	1a	3156	1/1	0.86	0.17	68,68,68,68	0
54	MG	2A	3001	1/1	0.86	0.52	73,73,73,73	0
54	MG	2A	3562	1/1	0.86	0.14	40,40,40,40	0
54	MG	1A	3297	1/1	0.86	0.27	73,73,73,73	0
54	MG	2a	3068	1/1	0.86	0.23	69,69,69,69	0
54	MG	1a	3161	1/1	0.86	0.16	62,62,62,62	0
54	MG	1A	3858	1/1	0.86	0.10	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2a	3076	1/1	0.86	0.30	65,65,65,65	0
54	MG	1A	3063	1/1	0.86	0.14	59,59,59,59	0
54	MG	2a	3080	1/1	0.86	0.34	71,71,71,71	0
54	MG	2a	3081	1/1	0.86	0.48	66,66,66,66	0
54	MG	1A	3362	1/1	0.86	0.12	50,50,50,50	0
54	MG	1A	4015	1/1	0.86	0.17	63,63,63,63	0
54	MG	1A	3649	1/1	0.86	0.09	41,41,41,41	0
54	MG	1a	3181	1/1	0.86	0.11	79,79,79,79	0
54	MG	1A	3308	1/1	0.86	0.14	53,53,53,53	0
54	MG	1A	3656	1/1	0.86	0.13	54,54,54,54	0
54	MG	1A	3587	1/1	0.86	0.17	54,54,54,54	0
54	MG	1a	3042	1/1	0.86	0.18	59,59,59,59	0
54	MG	2A	3347	1/1	0.86	0.14	48,48,48,48	0
54	MG	2a	3112	1/1	0.86	0.14	65,65,65,65	0
54	MG	1A	3900	1/1	0.86	0.11	25,25,25,25	0
54	MG	2A	3354	1/1	0.86	0.16	45,45,45,45	0
54	MG	1A	3658	1/1	0.86	0.14	63,63,63,63	0
54	MG	1a	3047	1/1	0.86	0.28	73,73,73,73	0
54	MG	1B	215	1/1	0.86	0.20	72,72,72,72	0
54	MG	2a	3127	1/1	0.86	0.16	67,67,67,67	0
54	MG	2A	3628	1/1	0.86	0.18	61,61,61,61	0
54	MG	1A	3311	1/1	0.86	0.14	59,59,59,59	0
54	MG	2A	3071	1/1	0.86	0.23	61,61,61,61	0
54	MG	1A	3753	1/1	0.86	0.24	45,45,45,45	0
54	MG	2A	3655	1/1	0.86	0.13	56,56,56,56	0
54	MG	2A	3377	1/1	0.86	0.24	70,70,70,70	0
54	MG	1A	3589	1/1	0.86	0.10	47,47,47,47	0
54	MG	2A	3681	1/1	0.86	0.11	78,78,78,78	0
54	MG	2A	3086	1/1	0.86	0.18	68,68,68,68	0
54	MG	2A	3090	1/1	0.86	0.18	80,80,80,80	0
54	MG	2A	3092	1/1	0.86	0.18	71,71,71,71	0
54	MG	1A	3372	1/1	0.86	0.17	65,65,65,65	0
54	MG	2A	3096	1/1	0.86	0.17	68,68,68,68	0
54	MG	1A	3374	1/1	0.86	0.14	50,50,50,50	0
54	MG	2A	3411	1/1	0.86	0.15	70,70,70,70	0
54	MG	2A	3414	1/1	0.86	0.27	67,67,67,67	0
54	MG	2A	3419	1/1	0.86	0.14	45,45,45,45	0
54	MG	1A	3312	1/1	0.86	0.18	61,61,61,61	0
54	MG	2A	3105	1/1	0.86	0.24	59,59,59,59	0
54	MG	1a	3066	1/1	0.86	0.14	73,73,73,73	0
54	MG	1A	3951	1/1	0.86	0.14	71,71,71,71	0
54	MG	1A	3598	1/1	0.86	0.16	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1a	3215	1/1	0.86	0.17	70,70,70,70	0
54	MG	1A	3994	1/1	0.87	0.21	84,84,84,84	0
54	MG	2A	3317	1/1	0.87	0.18	52,52,52,52	0
54	MG	2A	3519	1/1	0.87	0.17	72,72,72,72	0
54	MG	1P	207	1/1	0.87	0.15	71,71,71,71	0
54	MG	2A	3320	1/1	0.87	0.17	66,66,66,66	0
54	MG	2A	3321	1/1	0.87	0.25	67,67,67,67	0
54	MG	1A	3290	1/1	0.87	0.12	47,47,47,47	0
54	MG	2A	3119	1/1	0.87	0.24	57,57,57,57	0
54	MG	2a	3018	1/1	0.87	0.10	75,75,75,75	0
54	MG	1A	3471	1/1	0.87	0.10	28,28,28,28	0
54	MG	2A	3350	1/1	0.87	0.11	41,41,41,41	0
54	MG	1a	3157	1/1	0.87	0.15	63,63,63,63	0
54	MG	1A	3831	1/1	0.87	0.16	52,52,52,52	0
54	MG	1A	3836	1/1	0.87	0.16	59,59,59,59	0
54	MG	2A	3543	1/1	0.87	0.09	55,55,55,55	0
54	MG	2A	3136	1/1	0.87	0.17	58,58,58,58	0
54	MG	1V	205	1/1	0.87	0.15	60,60,60,60	0
54	MG	2A	3150	1/1	0.87	0.19	65,65,65,65	0
54	MG	1a	3060	1/1	0.87	0.45	78,78,78,78	0
54	MG	2a	3040	1/1	0.87	0.40	72,72,72,72	0
54	MG	1a	3062	1/1	0.87	0.15	59,59,59,59	0
54	MG	2A	3565	1/1	0.87	0.13	48,48,48,48	0
54	MG	1a	3168	1/1	0.87	0.25	72,72,72,72	0
54	MG	2A	3383	1/1	0.87	0.12	40,40,40,40	0
54	MG	2A	3572	1/1	0.87	0.12	81,81,81,81	0
54	MG	1A	3700	1/1	0.87	0.13	71,71,71,71	0
54	MG	1a	3173	1/1	0.87	0.16	69,69,69,69	0
54	MG	1A	3847	1/1	0.87	0.09	58,58,58,58	0
54	MG	2A	3391	1/1	0.87	0.14	60,60,60,60	0
54	MG	1a	3068	1/1	0.87	0.32	76,76,76,76	0
54	MG	1A	3048	1/1	0.87	0.37	53,53,53,53	0
54	MG	1A	3963	1/1	0.87	0.11	47,47,47,47	0
54	MG	2A	3404	1/1	0.87	0.20	67,67,67,67	0
54	MG	1A	3637	1/1	0.87	0.14	61,61,61,61	0
54	MG	2A	3183	1/1	0.87	0.16	58,58,58,58	0
54	MG	2A	3618	1/1	0.87	0.12	86,86,86,86	0
54	MG	2A	3187	1/1	0.87	0.14	68,68,68,68	0
54	MG	2A	3416	1/1	0.87	0.14	60,60,60,60	0
54	MG	1A	3717	1/1	0.87	0.16	37,37,37,37	0
54	MG	1A	3271	1/1	0.87	0.10	61,61,61,61	0
54	MG	2a	3070	1/1	0.87	0.11	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1a	3082	1/1	0.87	0.24	83,83,83,83	0
54	MG	2a	3075	1/1	0.87	0.16	70,70,70,70	0
54	MG	2A	3034	1/1	0.87	0.37	62,62,62,62	0
54	MG	2A	3435	1/1	0.87	0.16	69,69,69,69	0
54	MG	1B	214	1/1	0.87	0.20	55,55,55,55	0
54	MG	1a	3090	1/1	0.87	0.17	51,51,51,51	0
54	MG	2A	3633	1/1	0.87	0.17	82,82,82,82	0
54	MG	2A	3653	1/1	0.87	0.15	90,90,90,90	0
54	MG	2A	3199	1/1	0.87	0.36	74,74,74,74	0
54	MG	18	104	1/1	0.87	0.09	61,61,61,61	0
54	MG	2a	3089	1/1	0.87	0.14	67,67,67,67	0
54	MG	2a	3092	1/1	0.87	0.18	65,65,65,65	0
54	MG	2A	3445	1/1	0.87	0.13	65,65,65,65	0
54	MG	2A	3676	1/1	0.87	0.11	61,61,61,61	0
54	MG	1A	3794	1/1	0.87	0.17	43,43,43,43	0
54	MG	2a	3101	1/1	0.87	0.14	69,69,69,69	0
54	MG	2a	3103	1/1	0.87	0.22	71,71,71,71	0
54	MG	1a	3002	1/1	0.87	0.17	66,66,66,66	0
54	MG	1a	3101	1/1	0.87	0.23	66,66,66,66	0
54	MG	2A	3689	1/1	0.87	0.10	71,71,71,71	0
54	MG	1A	3561	1/1	0.87	0.17	67,67,67,67	0
54	MG	2A	3694	1/1	0.87	0.14	68,68,68,68	0
54	MG	2a	3115	1/1	0.87	0.14	59,59,59,59	0
54	MG	2a	3116	1/1	0.87	0.16	63,63,63,63	0
54	MG	2A	3220	1/1	0.87	0.32	69,69,69,69	0
54	MG	2a	3123	1/1	0.87	0.17	68,68,68,68	0
54	MG	1A	3302	1/1	0.87	0.11	52,52,52,52	0
54	MG	1B	223	1/1	0.87	0.20	65,65,65,65	0
54	MG	1a	3011	1/1	0.87	0.21	72,72,72,72	0
54	MG	1a	3110	1/1	0.87	0.15	59,59,59,59	0
54	MG	2A	3248	1/1	0.87	0.34	72,72,72,72	0
54	MG	2a	3138	1/1	0.87	0.16	79,79,79,79	0
54	MG	1A	3643	1/1	0.87	0.15	57,57,57,57	0
54	MG	1a	3022	1/1	0.87	0.20	64,64,64,64	0
54	MG	1A	3899	1/1	0.87	0.09	13,13,13,13	0
54	MG	2A	3734	1/1	0.87	0.09	32,32,32,32	0
54	MG	1A	3061	1/1	0.87	0.15	48,48,48,48	0
54	MG	2A	3265	1/1	0.87	0.16	57,57,57,57	0
54	MG	1A	3309	1/1	0.87	0.27	62,62,62,62	0
54	MG	2a	3185	1/1	0.87	0.13	75,75,75,75	0
54	MG	1a	3129	1/1	0.87	0.11	57,57,57,57	0
54	MG	1A	3981	1/1	0.87	0.09	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3986	1/1	0.87	0.11	54,54,54,54	0
54	MG	1A	3543	1/1	0.87	0.16	46,46,46,46	0
54	MG	1A	3630	1/1	0.87	0.17	64,64,64,64	0
54	MG	1A	3925	1/1	0.87	0.17	67,67,67,67	0
54	MG	2A	3095	1/1	0.87	0.27	60,60,60,60	0
54	MG	2A	3504	1/1	0.87	0.19	71,71,71,71	0
54	MG	2E	303	1/1	0.87	0.17	62,62,62,62	0
54	MG	1A	3551	1/1	0.87	0.10	43,43,43,43	0
54	MG	1A	3633	1/1	0.87	0.20	39,39,39,39	0
54	MG	1a	3146	1/1	0.87	0.20	75,75,75,75	0
54	MG	1A	3993	1/1	0.87	0.14	51,51,51,51	0
54	MG	2A	3512	1/1	0.87	0.19	61,61,61,61	0
54	MG	1A	3449	1/1	0.88	0.12	50,50,50,50	0
54	MG	2a	3005	1/1	0.88	0.38	74,74,74,74	0
54	MG	1A	3860	1/1	0.88	0.09	37,37,37,37	0
54	MG	2A	3094	1/1	0.88	0.11	49,49,49,49	0
54	MG	2A	3316	1/1	0.88	0.30	69,69,69,69	0
54	MG	1A	3407	1/1	0.88	0.12	61,61,61,61	0
54	MG	1A	3977	1/1	0.88	0.14	49,49,49,49	0
54	MG	1A	3865	1/1	0.88	0.10	58,58,58,58	0
54	MG	1A	3252	1/1	0.88	0.16	54,54,54,54	0
54	MG	2a	3022	1/1	0.88	0.32	71,71,71,71	0
54	MG	1A	3454	1/1	0.88	0.11	26,26,26,26	0
54	MG	1A	3183	1/1	0.88	0.12	52,52,52,52	0
54	MG	2A	3340	1/1	0.88	0.14	61,61,61,61	0
54	MG	1A	3687	1/1	0.88	0.11	49,49,49,49	0
54	MG	1A	3781	1/1	0.88	0.13	26,26,26,26	0
54	MG	2a	3033	1/1	0.88	0.39	73,73,73,73	0
54	MG	1a	3056	1/1	0.88	0.17	59,59,59,59	0
54	MG	2A	3555	1/1	0.88	0.11	64,64,64,64	0
54	MG	2A	3557	1/1	0.88	0.10	74,74,74,74	0
54	MG	2A	3353	1/1	0.88	0.16	70,70,70,70	0
54	MG	1Q	203	1/1	0.88	0.18	56,56,56,56	0
54	MG	1a	3154	1/1	0.88	0.12	51,51,51,51	0
54	MG	1A	3890	1/1	0.88	0.13	57,57,57,57	0
54	MG	1A	3368	1/1	0.88	0.16	54,54,54,54	0
54	MG	2A	3129	1/1	0.88	0.23	69,69,69,69	0
54	MG	2A	3134	1/1	0.88	0.24	69,69,69,69	0
54	MG	1a	3264	1/1	0.88	0.22	65,65,65,65	0
54	MG	2A	3576	1/1	0.88	0.11	64,64,64,64	0
54	MG	2A	3375	1/1	0.88	0.12	62,62,62,62	0
54	MG	1a	3158	1/1	0.88	0.20	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3585	1/1	0.88	0.17	51,51,51,51	0
54	MG	2A	3378	1/1	0.88	0.10	75,75,75,75	0
54	MG	1A	3787	1/1	0.88	0.24	57,57,57,57	0
54	MG	2A	3384	1/1	0.88	0.13	50,50,50,50	0
54	MG	2A	3153	1/1	0.88	0.31	62,62,62,62	0
54	MG	1a	3272	1/1	0.88	0.20	69,69,69,69	0
54	MG	1A	3189	1/1	0.88	0.12	60,60,60,60	0
54	MG	1a	3065	1/1	0.88	0.22	77,77,77,77	0
54	MG	1A	3644	1/1	0.88	0.28	56,56,56,56	0
54	MG	1V	207	1/1	0.88	0.12	78,78,78,78	0
54	MG	2A	3620	1/1	0.88	0.18	47,47,47,47	0
54	MG	1A	3197	1/1	0.88	0.11	50,50,50,50	0
54	MG	1A	4011	1/1	0.88	0.15	64,64,64,64	0
54	MG	2a	3074	1/1	0.88	0.32	71,71,71,71	0
54	MG	1a	3171	1/1	0.88	0.13	76,76,76,76	0
54	MG	2A	3177	1/1	0.88	0.16	54,54,54,54	0
54	MG	1A	3469	1/1	0.88	0.10	25,25,25,25	0
54	MG	1a	3175	1/1	0.88	0.26	67,67,67,67	0
54	MG	1A	3707	1/1	0.88	0.18	46,46,46,46	0
54	MG	2A	3185	1/1	0.88	0.35	68,68,68,68	0
54	MG	1A	3106	1/1	0.88	0.14	69,69,69,69	0
54	MG	2A	3427	1/1	0.88	0.25	70,70,70,70	0
54	MG	1y	202	1/1	0.88	0.14	69,69,69,69	0
54	MG	1A	3560	1/1	0.88	0.18	61,61,61,61	0
54	MG	2A	3010	1/1	0.88	0.19	65,65,65,65	0
54	MG	2A	3016	1/1	0.88	0.36	71,71,71,71	0
54	MG	2A	3023	1/1	0.88	0.27	68,68,68,68	0
54	MG	2a	3099	1/1	0.88	0.14	49,49,49,49	0
54	MG	2A	3024	1/1	0.88	0.14	69,69,69,69	0
54	MG	1A	3817	1/1	0.88	0.11	74,74,74,74	0
54	MG	2a	3102	1/1	0.88	0.26	71,71,71,71	0
54	MG	2A	3029	1/1	0.88	0.17	58,58,58,58	0
54	MG	17	106	1/1	0.88	0.19	63,63,63,63	0
54	MG	2A	3213	1/1	0.88	0.20	61,61,61,61	0
54	MG	1a	3185	1/1	0.88	0.23	71,71,71,71	0
54	MG	2A	3457	1/1	0.88	0.23	67,67,67,67	0
54	MG	1A	3164	1/1	0.88	0.14	46,46,46,46	0
54	MG	1A	3429	1/1	0.88	0.19	62,62,62,62	0
54	MG	2A	3704	1/1	0.88	0.15	67,67,67,67	0
54	MG	1a	3190	1/1	0.88	0.18	64,64,64,64	0
54	MG	2A	3708	1/1	0.88	0.13	59,59,59,59	0
54	MG	1A	3624	1/1	0.88	0.16	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2a	3125	1/1	0.88	0.23	72,72,72,72	0
54	MG	2A	3226	1/1	0.88	0.20	69,69,69,69	0
54	MG	1a	3098	1/1	0.88	0.40	62,62,62,62	0
54	MG	2A	3239	1/1	0.88	0.17	61,61,61,61	0
54	MG	2a	3129	1/1	0.88	0.11	60,60,60,60	0
54	MG	2A	3732	1/1	0.88	0.10	67,67,67,67	0
54	MG	1A	3827	1/1	0.88	0.11	52,52,52,52	0
54	MG	2A	3050	1/1	0.88	0.12	58,58,58,58	0
54	MG	1B	213	1/1	0.88	0.13	63,63,63,63	0
54	MG	1A	3956	1/1	0.88	0.15	59,59,59,59	0
54	MG	2a	3166	1/1	0.88	0.14	74,74,74,74	0
54	MG	1A	3354	1/1	0.88	0.10	49,49,49,49	0
54	MG	1A	3499	1/1	0.88	0.09	49,49,49,49	0
54	MG	1B	217	1/1	0.88	0.12	53,53,53,53	0
54	MG	1A	3135	1/1	0.88	0.11	54,54,54,54	0
54	MG	1A	3381	1/1	0.88	0.10	29,29,29,29	0
54	MG	2B	211	1/1	0.88	0.12	84,84,84,84	0
54	MG	1a	3028	1/1	0.88	0.26	73,73,73,73	0
54	MG	2B	215	1/1	0.88	0.11	77,77,77,77	0
54	MG	2A	3278	1/1	0.88	0.38	69,69,69,69	0
54	MG	2A	3065	1/1	0.88	0.29	52,52,52,52	0
54	MG	1a	3116	1/1	0.88	0.35	72,72,72,72	0
54	MG	1A	3442	1/1	0.88	0.16	59,59,59,59	0
54	MG	1a	3124	1/1	0.88	0.10	56,56,56,56	0
57	MPD	1A	4022	8/8	0.88	0.23	50,57,61,65	0
54	MG	2A	3082	1/1	0.88	0.13	55,55,55,55	0
54	MG	1A	3399	1/1	0.88	0.26	62,62,62,62	0
54	MG	2T	204	1/1	0.88	0.22	61,61,61,61	0
54	MG	1A	3251	1/1	0.88	0.30	70,70,70,70	0
54	MG	1A	3853	1/1	0.88	0.09	52,52,52,52	0
54	MG	2A	3308	1/1	0.88	0.18	64,64,64,64	0
54	MG	1a	3167	1/1	0.89	0.10	63,63,63,63	0
54	MG	1a	3080	1/1	0.89	0.23	67,67,67,67	0
54	MG	1a	3278	1/1	0.89	0.18	74,74,74,74	0
54	MG	1A	3654	1/1	0.89	0.13	30,30,30,30	0
54	MG	2A	3352	1/1	0.89	0.12	42,42,42,42	0
54	MG	2A	3531	1/1	0.89	0.10	61,61,61,61	0
54	MG	2A	3533	1/1	0.89	0.10	33,33,33,33	0
54	MG	1A	3868	1/1	0.89	0.18	33,33,33,33	0
54	MG	2A	3145	1/1	0.89	0.11	44,44,44,44	0
54	MG	1a	3086	1/1	0.89	0.36	71,71,71,71	0
54	MG	1A	3701	1/1	0.89	0.12	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1a	3088	1/1	0.89	0.21	75,75,75,75	0
54	MG	2A	3162	1/1	0.89	0.12	64,64,64,64	0
54	MG	1A	3973	1/1	0.89	0.24	65,65,65,65	0
54	MG	1B	224	1/1	0.89	0.12	48,48,48,48	0
54	MG	1A	3184	1/1	0.89	0.19	71,71,71,71	0
54	MG	2a	3028	1/1	0.89	0.16	66,66,66,66	0
54	MG	1A	3456	1/1	0.89	0.14	70,70,70,70	0
54	MG	1A	3620	1/1	0.89	0.11	58,58,58,58	0
54	MG	2A	3379	1/1	0.89	0.14	64,64,64,64	0
54	MG	1y	203	1/1	0.89	0.15	83,83,83,83	0
54	MG	1A	3382	1/1	0.89	0.06	32,32,32,32	0
54	MG	2A	3002	1/1	0.89	0.15	52,52,52,52	0
54	MG	1A	3459	1/1	0.89	0.09	52,52,52,52	0
54	MG	2A	3012	1/1	0.89	0.15	64,64,64,64	0
54	MG	2A	3582	1/1	0.89	0.11	88,88,88,88	0
54	MG	1A	3325	1/1	0.89	0.15	32,32,32,32	0
54	MG	1A	3983	1/1	0.89	0.24	52,52,52,52	0
54	MG	2A	3597	1/1	0.89	0.11	73,73,73,73	0
54	MG	2A	3186	1/1	0.89	0.23	72,72,72,72	0
54	MG	2A	3400	1/1	0.89	0.13	67,67,67,67	0
54	MG	1A	3326	1/1	0.89	0.17	50,50,50,50	0
54	MG	1A	3906	1/1	0.89	0.14	52,52,52,52	0
54	MG	1A	3907	1/1	0.89	0.13	32,32,32,32	0
54	MG	2A	3410	1/1	0.89	0.15	56,56,56,56	0
54	MG	1A	3530	1/1	0.89	0.11	64,64,64,64	0
54	MG	2A	3033	1/1	0.89	0.31	62,62,62,62	0
54	MG	1a	3115	1/1	0.89	0.15	61,61,61,61	0
54	MG	1G	203	1/1	0.89	0.13	66,66,66,66	0
54	MG	1a	3200	1/1	0.89	0.13	67,67,67,67	0
54	MG	2A	3624	1/1	0.89	0.10	64,64,64,64	0
54	MG	2A	3424	1/1	0.89	0.11	61,61,61,61	0
54	MG	2A	3037	1/1	0.89	0.19	58,58,58,58	0
54	MG	1a	3041	1/1	0.89	0.18	73,73,73,73	0
54	MG	1A	3403	1/1	0.89	0.08	28,28,28,28	0
54	MG	1A	3286	1/1	0.89	0.10	64,64,64,64	0
54	MG	2A	3631	1/1	0.89	0.41	58,58,58,58	0
54	MG	2A	3216	1/1	0.89	0.19	65,65,65,65	0
54	MG	2A	3047	1/1	0.89	0.20	67,67,67,67	0
54	MG	2A	3651	1/1	0.89	0.11	49,49,49,49	0
54	MG	2A	3218	1/1	0.89	0.38	69,69,69,69	0
54	MG	1a	3209	1/1	0.89	0.20	73,73,73,73	0
54	MG	1a	3127	1/1	0.89	0.14	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3662	1/1	0.89	0.11	83,83,83,83	0
54	MG	2A	3665	1/1	0.89	0.11	41,41,41,41	0
54	MG	2A	3446	1/1	0.89	0.22	66,66,66,66	0
54	MG	1A	3084	1/1	0.89	0.15	54,54,54,54	0
54	MG	1A	3928	1/1	0.89	0.12	63,63,63,63	0
54	MG	2A	3235	1/1	0.89	0.19	65,65,65,65	0
54	MG	2A	3684	1/1	0.89	0.10	73,73,73,73	0
54	MG	1a	3048	1/1	0.89	0.31	65,65,65,65	0
54	MG	2a	3098	1/1	0.89	0.20	74,74,74,74	0
54	MG	1A	3008	1/1	0.89	0.11	44,44,44,44	0
54	MG	2A	3690	1/1	0.89	0.11	82,82,82,82	0
54	MG	1A	3444	1/1	0.89	0.10	52,52,52,52	0
54	MG	1a	3136	1/1	0.89	0.20	68,68,68,68	0
54	MG	1T	203	1/1	0.89	0.18	66,66,66,66	0
54	MG	2a	3105	1/1	0.89	0.08	65,65,65,65	0
54	MG	1A	3935	1/1	0.89	0.08	36,36,36,36	0
54	MG	2A	3464	1/1	0.89	0.12	58,58,58,58	0
54	MG	1A	3554	1/1	0.89	0.14	54,54,54,54	0
54	MG	1A	3590	1/1	0.89	0.12	41,41,41,41	0
54	MG	1A	3492	1/1	0.89	0.08	63,63,63,63	0
54	MG	1a	3236	1/1	0.89	0.11	75,75,75,75	0
54	MG	1a	3237	1/1	0.89	0.21	79,79,79,79	0
54	MG	2a	3117	1/1	0.89	0.11	66,66,66,66	0
54	MG	2A	3714	1/1	0.89	0.20	61,61,61,61	0
54	MG	1a	3148	1/1	0.89	0.11	58,58,58,58	0
54	MG	2A	3483	1/1	0.89	0.10	66,66,66,66	0
54	MG	1A	3839	1/1	0.89	0.10	53,53,53,53	0
54	MG	2A	3725	1/1	0.89	0.18	71,71,71,71	0
54	MG	1Z	301	1/1	0.89	0.15	62,62,62,62	0
54	MG	2A	3733	1/1	0.89	0.17	61,61,61,61	0
54	MG	1A	3763	1/1	0.89	0.09	44,44,44,44	0
54	MG	1a	3249	1/1	0.89	0.12	68,68,68,68	0
54	MG	2a	3131	1/1	0.89	0.10	64,64,64,64	0
54	MG	2A	3738	1/1	0.89	0.16	63,63,63,63	0
54	MG	2A	3739	1/1	0.89	0.15	67,67,67,67	0
54	MG	2A	3740	1/1	0.89	0.21	58,58,58,58	0
54	MG	1A	3314	1/1	0.89	0.12	63,63,63,63	0
54	MG	1A	3160	1/1	0.89	0.21	63,63,63,63	0
54	MG	2a	3169	1/1	0.89	0.15	69,69,69,69	0
54	MG	2a	3172	1/1	0.89	0.14	84,84,84,84	0
54	MG	1a	3252	1/1	0.89	0.09	72,72,72,72	0
54	MG	1a	3256	1/1	0.89	0.08	70,70,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3299	1/1	0.89	0.19	52,52,52,52	0
54	MG	1A	3595	1/1	0.89	0.10	38,38,38,38	0
54	MG	2A	3304	1/1	0.89	0.10	41,41,41,41	0
54	MG	2a	3186	1/1	0.89	0.22	71,71,71,71	0
54	MG	2A	3099	1/1	0.89	0.20	66,66,66,66	0
54	MG	2B	212	1/1	0.89	0.10	68,68,68,68	0
54	MG	1A	3857	1/1	0.89	0.19	46,46,46,46	0
54	MG	15	106	1/1	0.89	0.14	28,28,28,28	0
54	MG	2A	3112	1/1	0.89	0.15	53,53,53,53	0
54	MG	1a	3072	1/1	0.89	0.15	60,60,60,60	0
54	MG	1A	3424	1/1	0.89	0.16	43,43,43,43	0
54	MG	2E	304	1/1	0.89	0.12	37,37,37,37	0
54	MG	2E	306	1/1	0.89	0.23	66,66,66,66	0
54	MG	2A	3118	1/1	0.89	0.34	63,63,63,63	0
54	MG	1a	3267	1/1	0.89	0.12	65,65,65,65	0
54	MG	1A	3780	1/1	0.89	0.15	56,56,56,56	0
54	MG	1A	3200	1/1	0.89	0.24	52,52,52,52	0
54	MG	2T	202	1/1	0.89	0.18	71,71,71,71	0
54	MG	1a	3079	1/1	0.89	0.12	52,52,52,52	0
59	ZN	24	501	1/1	0.89	0.23	136,136,136,136	0
54	MG	1A	3697	1/1	0.90	0.17	60,60,60,60	0
54	MG	2A	3272	1/1	0.90	0.15	62,62,62,62	0
54	MG	1A	3370	1/1	0.90	0.09	36,36,36,36	0
54	MG	2A	3061	1/1	0.90	0.27	60,60,60,60	0
54	MG	1A	3188	1/1	0.90	0.17	64,64,64,64	0
54	MG	1A	3978	1/1	0.90	0.10	69,69,69,69	0
54	MG	1A	3558	1/1	0.90	0.10	55,55,55,55	0
54	MG	2A	3514	1/1	0.90	0.20	59,59,59,59	0
54	MG	2A	3068	1/1	0.90	0.11	50,50,50,50	0
54	MG	1A	3316	1/1	0.90	0.12	50,50,50,50	0
54	MG	1A	3708	1/1	0.90	0.11	63,63,63,63	0
54	MG	1A	3848	1/1	0.90	0.14	42,42,42,42	0
54	MG	1a	3104	1/1	0.90	0.24	63,63,63,63	0
54	MG	2A	3297	1/1	0.90	0.11	62,62,62,62	0
54	MG	1A	3474	1/1	0.90	0.09	27,27,27,27	0
54	MG	2a	3010	1/1	0.90	0.18	65,65,65,65	0
54	MG	1A	3475	1/1	0.90	0.15	35,35,35,35	0
54	MG	15	107	1/1	0.90	0.10	37,37,37,37	0
54	MG	1A	3854	1/1	0.90	0.09	49,49,49,49	0
54	MG	1A	3477	1/1	0.90	0.10	37,37,37,37	0
54	MG	1a	3231	1/1	0.90	0.29	73,73,73,73	0
54	MG	1A	3478	1/1	0.90	0.11	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3002	1/1	0.90	0.17	45,45,45,45	0
54	MG	1A	3728	1/1	0.90	0.18	54,54,54,54	0
54	MG	2a	3027	1/1	0.90	0.14	61,61,61,61	0
54	MG	1a	3118	1/1	0.90	0.16	58,58,58,58	0
54	MG	1a	3241	1/1	0.90	0.21	72,72,72,72	0
54	MG	2A	3100	1/1	0.90	0.11	67,67,67,67	0
54	MG	2A	3550	1/1	0.90	0.12	59,59,59,59	0
54	MG	1A	3735	1/1	0.90	0.24	54,54,54,54	0
54	MG	2A	3106	1/1	0.90	0.33	61,61,61,61	0
54	MG	2A	3330	1/1	0.90	0.12	49,49,49,49	0
54	MG	2A	3107	1/1	0.90	0.24	61,61,61,61	0
54	MG	1a	3245	1/1	0.90	0.12	72,72,72,72	0
54	MG	2A	3348	1/1	0.90	0.18	73,73,73,73	0
54	MG	2a	3042	1/1	0.90	0.17	72,72,72,72	0
54	MG	1a	3123	1/1	0.90	0.14	72,72,72,72	0
54	MG	1A	3430	1/1	0.90	0.16	54,54,54,54	0
54	MG	2A	3114	1/1	0.90	0.18	61,61,61,61	0
54	MG	1A	4003	1/1	0.90	0.20	51,51,51,51	0
54	MG	2A	3117	1/1	0.90	0.34	69,69,69,69	0
54	MG	1A	3191	1/1	0.90	0.10	67,67,67,67	0
54	MG	1A	3739	1/1	0.90	0.16	55,55,55,55	0
54	MG	1a	3015	1/1	0.90	0.14	72,72,72,72	0
54	MG	1a	3016	1/1	0.90	0.13	63,63,63,63	0
54	MG	2A	3369	1/1	0.90	0.26	61,61,61,61	0
54	MG	1A	3012	1/1	0.90	0.13	39,39,39,39	0
54	MG	1A	3744	1/1	0.90	0.12	54,54,54,54	0
54	MG	1A	3497	1/1	0.90	0.09	46,46,46,46	0
54	MG	1a	3025	1/1	0.90	0.12	64,64,64,64	0
54	MG	2A	3135	1/1	0.90	0.19	57,57,57,57	0
54	MG	1A	3079	1/1	0.90	0.11	49,49,49,49	0
54	MG	1a	3265	1/1	0.90	0.17	65,65,65,65	0
54	MG	1A	3897	1/1	0.90	0.13	55,55,55,55	0
54	MG	2A	3386	1/1	0.90	0.13	52,52,52,52	0
54	MG	1A	3502	1/1	0.90	0.11	53,53,53,53	0
54	MG	1A	3026	1/1	0.90	0.15	64,64,64,64	0
54	MG	2a	3072	1/1	0.90	0.43	71,71,71,71	0
54	MG	1A	3333	1/1	0.90	0.16	58,58,58,58	0
54	MG	2A	3623	1/1	0.90	0.10	63,63,63,63	0
54	MG	2A	3161	1/1	0.90	0.12	57,57,57,57	0
54	MG	2a	3077	1/1	0.90	0.13	71,71,71,71	0
54	MG	1A	3152	1/1	0.90	0.10	49,49,49,49	0
54	MG	1A	3216	1/1	0.90	0.09	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3399	1/1	0.90	0.21	69,69,69,69	0
54	MG	1A	3402	1/1	0.90	0.22	69,69,69,69	0
54	MG	1A	3770	1/1	0.90	0.12	31,31,31,31	0
54	MG	1A	3922	1/1	0.90	0.12	57,57,57,57	0
54	MG	1e	203	1/1	0.90	0.19	64,64,64,64	0
54	MG	1g	3100	1/1	0.90	0.36	74,74,74,74	0
54	MG	2A	3635	1/1	0.90	0.10	69,69,69,69	0
54	MG	1A	3771	1/1	0.90	0.14	47,47,47,47	0
54	MG	1B	220	1/1	0.90	0.14	57,57,57,57	0
54	MG	1A	3227	1/1	0.90	0.14	62,62,62,62	0
54	MG	2A	3418	1/1	0.90	0.15	83,83,83,83	0
54	MG	1A	3451	1/1	0.90	0.10	52,52,52,52	0
54	MG	2A	3664	1/1	0.90	0.15	40,40,40,40	0
54	MG	2A	3420	1/1	0.90	0.18	65,65,65,65	0
54	MG	1A	3665	1/1	0.90	0.21	38,38,38,38	0
54	MG	1A	3093	1/1	0.90	0.16	57,57,57,57	0
54	MG	1A	3937	1/1	0.90	0.10	40,40,40,40	0
54	MG	1A	3668	1/1	0.90	0.10	53,53,53,53	0
54	MG	1A	3948	1/1	0.90	0.14	41,41,41,41	0
54	MG	1A	3670	1/1	0.90	0.24	73,73,73,73	0
54	MG	1E	308	1/1	0.90	0.11	58,58,58,58	0
54	MG	2A	3438	1/1	0.90	0.09	50,50,50,50	0
54	MG	2A	3005	1/1	0.90	0.14	59,59,59,59	0
54	MG	1A	3529	1/1	0.90	0.10	51,51,51,51	0
54	MG	2a	3120	1/1	0.90	0.08	75,75,75,75	0
54	MG	1A	3305	1/1	0.90	0.21	51,51,51,51	0
54	MG	1A	3030	1/1	0.90	0.08	31,31,31,31	0
54	MG	2A	3701	1/1	0.90	0.16	46,46,46,46	0
54	MG	2A	3200	1/1	0.90	0.33	64,64,64,64	0
54	MG	2A	3448	1/1	0.90	0.10	50,50,50,50	0
54	MG	2A	3201	1/1	0.90	0.21	71,71,71,71	0
54	MG	2A	3207	1/1	0.90	0.15	58,58,58,58	0
54	MG	2A	3208	1/1	0.90	0.26	48,48,48,48	0
54	MG	1A	3417	1/1	0.90	0.17	39,39,39,39	0
54	MG	1a	3179	1/1	0.90	0.10	65,65,65,65	0
54	MG	2a	3135	1/1	0.90	0.08	76,76,76,76	0
54	MG	2A	3458	1/1	0.90	0.10	59,59,59,59	0
54	MG	1G	201	1/1	0.90	0.10	73,73,73,73	0
54	MG	2a	3149	1/1	0.90	0.15	77,77,77,77	0
54	MG	2a	3159	1/1	0.90	0.10	76,76,76,76	0
54	MG	1A	3546	1/1	0.90	0.17	29,29,29,29	0
54	MG	2A	3720	1/1	0.90	0.17	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3804	1/1	0.90	0.11	36,36,36,36	0
54	MG	1a	3071	1/1	0.90	0.32	72,72,72,72	0
54	MG	1A	3615	1/1	0.90	0.14	31,31,31,31	0
54	MG	1A	3616	1/1	0.90	0.14	58,58,58,58	0
54	MG	1P	204	1/1	0.90	0.13	41,41,41,41	0
54	MG	1A	3548	1/1	0.90	0.13	63,63,63,63	0
54	MG	2A	3472	1/1	0.90	0.12	61,61,61,61	0
54	MG	2A	3225	1/1	0.90	0.12	58,58,58,58	0
54	MG	1a	3077	1/1	0.90	0.21	68,68,68,68	0
54	MG	1a	3078	1/1	0.90	0.21	60,60,60,60	0
54	MG	2A	3482	1/1	0.90	0.10	68,68,68,68	0
54	MG	2B	205	1/1	0.90	0.13	73,73,73,73	0
54	MG	1a	3194	1/1	0.90	0.17	73,73,73,73	0
54	MG	1A	3684	1/1	0.90	0.08	53,53,53,53	0
54	MG	2A	3486	1/1	0.90	0.13	57,57,57,57	0
54	MG	2A	3048	1/1	0.90	0.10	63,63,63,63	0
54	MG	1A	3622	1/1	0.90	0.10	41,41,41,41	0
54	MG	1A	3123	1/1	0.90	0.20	53,53,53,53	0
54	MG	1A	3124	1/1	0.90	0.22	55,55,55,55	0
54	MG	1a	3083	1/1	0.90	0.14	61,61,61,61	0
54	MG	2D	303	1/1	0.90	0.32	48,48,48,48	0
54	MG	2A	3494	1/1	0.90	0.12	50,50,50,50	0
54	MG	2A	3498	1/1	0.90	0.14	71,71,71,71	0
54	MG	1A	3128	1/1	0.90	0.11	40,40,40,40	0
54	MG	1A	3466	1/1	0.90	0.15	59,59,59,59	0
54	MG	1A	3401	1/1	0.91	0.09	31,31,31,31	0
54	MG	2D	309	1/1	0.91	0.14	43,43,43,43	0
54	MG	1A	3088	1/1	0.91	0.10	49,49,49,49	0
54	MG	1A	3034	1/1	0.91	0.10	32,32,32,32	0
54	MG	1a	3009	1/1	0.91	0.34	59,59,59,59	0
54	MG	2A	3505	1/1	0.91	0.12	59,59,59,59	0
54	MG	2A	3080	1/1	0.91	0.09	53,53,53,53	0
54	MG	2A	3081	1/1	0.91	0.16	64,64,64,64	0
54	MG	1A	3915	1/1	0.91	0.10	45,45,45,45	0
54	MG	1a	3232	1/1	0.91	0.11	70,70,70,70	0
54	MG	2P	201	1/1	0.91	0.11	64,64,64,64	0
54	MG	2P	203	1/1	0.91	0.27	74,74,74,74	0
54	MG	2Q	202	1/1	0.91	0.10	71,71,71,71	0
54	MG	2R	201	1/1	0.91	0.11	50,50,50,50	0
54	MG	1B	201	1/1	0.91	0.19	56,56,56,56	0
54	MG	2T	203	1/1	0.91	0.13	64,64,64,64	0
54	MG	1a	3235	1/1	0.91	0.20	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2W	204	1/1	0.91	0.12	70,70,70,70	0
54	MG	1A	3599	1/1	0.91	0.23	31,31,31,31	0
54	MG	1A	3301	1/1	0.91	0.16	36,36,36,36	0
54	MG	28	102	1/1	0.91	0.26	67,67,67,67	0
54	MG	1A	3411	1/1	0.91	0.14	26,26,26,26	0
54	MG	1a	3020	1/1	0.91	0.24	62,62,62,62	0
54	MG	1A	3534	1/1	0.91	0.15	60,60,60,60	0
54	MG	1A	3788	1/1	0.91	0.17	63,63,63,63	0
54	MG	1A	3789	1/1	0.91	0.08	71,71,71,71	0
54	MG	1a	3027	1/1	0.91	0.34	68,68,68,68	0
54	MG	1A	3793	1/1	0.91	0.09	52,52,52,52	0
54	MG	1A	3933	1/1	0.91	0.15	69,69,69,69	0
54	MG	2a	3013	1/1	0.91	0.29	69,69,69,69	0
54	MG	2a	3014	1/1	0.91	0.28	64,64,64,64	0
54	MG	1A	3540	1/1	0.91	0.21	53,53,53,53	0
54	MG	1A	3241	1/1	0.91	0.20	53,53,53,53	0
54	MG	1A	3544	1/1	0.91	0.10	59,59,59,59	0
54	MG	2a	3021	1/1	0.91	0.09	53,53,53,53	0
54	MG	1A	3360	1/1	0.91	0.09	17,17,17,17	0
54	MG	2A	3536	1/1	0.91	0.16	37,37,37,37	0
54	MG	1a	3259	1/1	0.91	0.12	55,55,55,55	0
54	MG	1A	3623	1/1	0.91	0.09	26,26,26,26	0
54	MG	2a	3026	1/1	0.91	0.18	69,69,69,69	0
54	MG	2A	3342	1/1	0.91	0.12	37,37,37,37	0
54	MG	1A	3416	1/1	0.91	0.16	33,33,33,33	0
54	MG	2a	3030	1/1	0.91	0.23	67,67,67,67	0
54	MG	2A	3548	1/1	0.91	0.16	57,57,57,57	0
54	MG	1a	3147	1/1	0.91	0.13	53,53,53,53	0
54	MG	1B	226	1/1	0.91	0.23	64,64,64,64	0
54	MG	1a	3043	1/1	0.91	0.17	67,67,67,67	0
54	MG	2A	3558	1/1	0.91	0.10	62,62,62,62	0
54	MG	1a	3044	1/1	0.91	0.23	62,62,62,62	0
54	MG	1A	3072	1/1	0.91	0.08	38,38,38,38	0
54	MG	1A	3119	1/1	0.91	0.14	39,39,39,39	0
54	MG	1A	3254	1/1	0.91	0.11	50,50,50,50	0
54	MG	1D	301	1/1	0.91	0.15	51,51,51,51	0
54	MG	2A	3359	1/1	0.91	0.15	72,72,72,72	0
54	MG	2A	3132	1/1	0.91	0.22	67,67,67,67	0
54	MG	1D	310	1/1	0.91	0.25	42,42,42,42	0
54	MG	1A	3255	1/1	0.91	0.09	68,68,68,68	0
54	MG	1D	312	1/1	0.91	0.13	72,72,72,72	0
54	MG	1d	303	1/1	0.91	0.26	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2a	3049	1/1	0.91	0.45	76,76,76,76	0
54	MG	2a	3050	1/1	0.91	0.39	66,66,66,66	0
54	MG	2A	3581	1/1	0.91	0.17	63,63,63,63	0
54	MG	1A	3472	1/1	0.91	0.10	37,37,37,37	0
54	MG	2A	3146	1/1	0.91	0.17	57,57,57,57	0
54	MG	2A	3149	1/1	0.91	0.20	59,59,59,59	0
54	MG	1A	3961	1/1	0.91	0.12	66,66,66,66	0
54	MG	2A	3382	1/1	0.91	0.10	37,37,37,37	0
54	MG	1f	201	1/1	0.91	0.15	54,54,54,54	0
54	MG	2A	3605	1/1	0.91	0.10	42,42,42,42	0
54	MG	2A	3155	1/1	0.91	0.10	71,71,71,71	0
54	MG	2A	3156	1/1	0.91	0.22	60,60,60,60	0
54	MG	2A	3610	1/1	0.91	0.09	51,51,51,51	0
54	MG	2a	3066	1/1	0.91	0.22	69,69,69,69	0
54	MG	1A	3121	1/1	0.91	0.28	57,57,57,57	0
54	MG	2A	3614	1/1	0.91	0.14	46,46,46,46	0
54	MG	1a	3165	1/1	0.91	0.18	71,71,71,71	0
54	MG	1h	201	1/1	0.91	0.30	64,64,64,64	0
54	MG	1A	3151	1/1	0.91	0.11	42,42,42,42	0
54	MG	2a	3073	1/1	0.91	0.33	57,57,57,57	0
54	MG	1A	3192	1/1	0.91	0.38	70,70,70,70	0
54	MG	1A	3373	1/1	0.91	0.10	36,36,36,36	0
54	MG	2A	3168	1/1	0.91	0.18	65,65,65,65	0
54	MG	1m	201	1/1	0.91	0.08	73,73,73,73	0
54	MG	2A	3401	1/1	0.91	0.12	41,41,41,41	0
54	MG	1A	3036	1/1	0.91	0.09	40,40,40,40	0
54	MG	1a	3064	1/1	0.91	0.24	73,73,73,73	0
54	MG	2A	3172	1/1	0.91	0.16	66,66,66,66	0
54	MG	2a	3083	1/1	0.91	0.42	72,72,72,72	0
54	MG	2A	3409	1/1	0.91	0.13	48,48,48,48	0
54	MG	1o	102	1/1	0.91	0.27	58,58,58,58	0
54	MG	1A	3014	1/1	0.91	0.30	63,63,63,63	0
54	MG	2a	3088	1/1	0.91	0.40	65,65,65,65	0
54	MG	1t	201	1/1	0.91	0.10	59,59,59,59	0
54	MG	2A	3415	1/1	0.91	0.21	45,45,45,45	0
54	MG	1y	201	1/1	0.91	0.10	72,72,72,72	0
54	MG	2A	3638	1/1	0.91	0.09	57,57,57,57	0
54	MG	2a	3096	1/1	0.91	0.13	74,74,74,74	0
54	MG	2A	3640	1/1	0.91	0.11	85,85,85,85	0
54	MG	1A	3838	1/1	0.91	0.12	47,47,47,47	0
54	MG	2A	3652	1/1	0.91	0.09	62,62,62,62	0
54	MG	1A	3127	1/1	0.91	0.18	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3570	1/1	0.91	0.10	25,25,25,25	0
54	MG	1N	204	1/1	0.91	0.07	55,55,55,55	0
54	MG	2A	3661	1/1	0.91	0.11	62,62,62,62	0
54	MG	1O	201	1/1	0.91	0.14	67,67,67,67	0
54	MG	2a	3107	1/1	0.91	0.20	63,63,63,63	0
54	MG	1A	3729	1/1	0.91	0.11	36,36,36,36	0
54	MG	1A	3495	1/1	0.91	0.10	60,60,60,60	0
54	MG	1A	3434	1/1	0.91	0.19	62,62,62,62	0
54	MG	2A	3017	1/1	0.91	0.14	56,56,56,56	0
54	MG	2A	3197	1/1	0.91	0.16	53,53,53,53	0
54	MG	2A	3437	1/1	0.91	0.09	61,61,61,61	0
54	MG	1A	3437	1/1	0.91	0.12	50,50,50,50	0
54	MG	2a	3118	1/1	0.91	0.18	61,61,61,61	0
54	MG	2a	3119	1/1	0.91	0.18	67,67,67,67	0
54	MG	2A	3440	1/1	0.91	0.10	59,59,59,59	0
54	MG	2A	3686	1/1	0.91	0.08	53,53,53,53	0
54	MG	2a	3122	1/1	0.91	0.08	68,68,68,68	0
54	MG	1A	3576	1/1	0.91	0.25	59,59,59,59	0
54	MG	1A	3324	1/1	0.91	0.09	29,29,29,29	0
54	MG	2A	3026	1/1	0.91	0.14	52,52,52,52	0
54	MG	2A	3205	1/1	0.91	0.14	58,58,58,58	0
54	MG	1A	3500	1/1	0.91	0.11	27,27,27,27	0
54	MG	1U	201	1/1	0.91	0.14	40,40,40,40	0
54	MG	1A	3984	1/1	0.91	0.17	36,36,36,36	0
54	MG	1A	3501	1/1	0.91	0.14	78,78,78,78	0
54	MG	1A	3212	1/1	0.91	0.17	56,56,56,56	0
54	MG	2a	3133	1/1	0.91	0.12	71,71,71,71	0
54	MG	1A	3752	1/1	0.91	0.12	50,50,50,50	0
54	MG	1A	3167	1/1	0.91	0.24	58,58,58,58	0
54	MG	1A	3395	1/1	0.91	0.15	35,35,35,35	0
54	MG	2A	3039	1/1	0.91	0.19	52,52,52,52	0
54	MG	2a	3150	1/1	0.91	0.09	72,72,72,72	0
54	MG	2A	3040	1/1	0.91	0.36	68,68,68,68	0
54	MG	1A	3397	1/1	0.91	0.09	32,32,32,32	0
54	MG	1A	3758	1/1	0.91	0.07	33,33,33,33	0
54	MG	1a	3202	1/1	0.91	0.21	60,60,60,60	0
54	MG	1A	3448	1/1	0.91	0.10	66,66,66,66	0
54	MG	2A	3229	1/1	0.91	0.10	59,59,59,59	0
54	MG	2A	3727	1/1	0.91	0.08	76,76,76,76	0
54	MG	2a	3176	1/1	0.91	0.22	68,68,68,68	0
54	MG	2A	3730	1/1	0.91	0.17	62,62,62,62	0
54	MG	2a	3180	1/1	0.91	0.12	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3470	1/1	0.91	0.09	66,66,66,66	0
54	MG	2A	3234	1/1	0.91	0.28	51,51,51,51	0
54	MG	1a	3207	1/1	0.91	0.19	68,68,68,68	0
54	MG	1a	3095	1/1	0.91	0.27	71,71,71,71	0
54	MG	2A	3475	1/1	0.91	0.21	62,62,62,62	0
54	MG	2A	3476	1/1	0.91	0.12	77,77,77,77	0
54	MG	1A	3760	1/1	0.91	0.18	54,54,54,54	0
54	MG	1A	3513	1/1	0.91	0.11	54,54,54,54	0
54	MG	1A	4000	1/1	0.91	0.18	55,55,55,55	0
54	MG	1A	3172	1/1	0.91	0.33	62,62,62,62	0
54	MG	1A	4007	1/1	0.91	0.09	61,61,61,61	0
54	MG	1A	4009	1/1	0.91	0.08	20,20,20,20	0
54	MG	1A	3296	1/1	0.91	0.09	47,47,47,47	0
54	MG	1a	3222	1/1	0.91	0.15	68,68,68,68	0
54	MG	1A	3593	1/1	0.91	0.13	48,48,48,48	0
54	MG	1a	3224	1/1	0.91	0.10	83,83,83,83	0
54	MG	2A	3274	1/1	0.91	0.20	60,60,60,60	0
54	MG	2A	3067	1/1	0.91	0.09	48,48,48,48	0
54	MG	2A	3276	1/1	0.91	0.21	67,67,67,67	0
54	MG	2A	3499	1/1	0.91	0.10	70,70,70,70	0
54	MG	2A	3441	1/1	0.92	0.18	61,61,61,61	0
54	MG	1A	3609	1/1	0.92	0.15	34,34,34,34	0
54	MG	1A	3261	1/1	0.92	0.11	56,56,56,56	0
54	MG	1a	3155	1/1	0.92	0.17	66,66,66,66	0
54	MG	1A	3494	1/1	0.92	0.14	43,43,43,43	0
54	MG	2A	3258	1/1	0.92	0.24	63,63,63,63	0
54	MG	1A	3761	1/1	0.92	0.07	25,25,25,25	0
54	MG	2A	3263	1/1	0.92	0.35	44,44,44,44	0
54	MG	1A	3872	1/1	0.92	0.12	38,38,38,38	0
54	MG	1A	3874	1/1	0.92	0.13	64,64,64,64	0
54	MG	2A	3273	1/1	0.92	0.17	49,49,49,49	0
54	MG	1Q	202	1/1	0.92	0.07	34,34,34,34	0
54	MG	1a	3063	1/1	0.92	0.16	71,71,71,71	0
54	MG	1A	3122	1/1	0.92	0.30	56,56,56,56	0
54	MG	1A	3266	1/1	0.92	0.20	61,61,61,61	0
54	MG	1A	3356	1/1	0.92	0.10	39,39,39,39	0
54	MG	1A	3310	1/1	0.92	0.14	58,58,58,58	0
54	MG	1A	3204	1/1	0.92	0.15	56,56,56,56	0
54	MG	1A	3885	1/1	0.92	0.24	37,37,37,37	0
54	MG	2A	3468	1/1	0.92	0.09	62,62,62,62	0
54	MG	1A	3409	1/1	0.92	0.10	50,50,50,50	0
54	MG	2A	3659	1/1	0.92	0.11	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1a	3172	1/1	0.92	0.30	71,71,71,71	0
54	MG	1A	3995	1/1	0.92	0.10	16,16,16,16	0
54	MG	1A	3565	1/1	0.92	0.13	48,48,48,48	0
54	MG	2A	3290	1/1	0.92	0.07	51,51,51,51	0
54	MG	2A	3666	1/1	0.92	0.09	47,47,47,47	0
54	MG	2A	3667	1/1	0.92	0.07	42,42,42,42	0
54	MG	1A	3898	1/1	0.92	0.23	39,39,39,39	0
54	MG	2A	3673	1/1	0.92	0.10	74,74,74,74	0
54	MG	1W	203	1/1	0.92	0.10	65,65,65,65	0
54	MG	2A	3677	1/1	0.92	0.10	68,68,68,68	0
54	MG	2A	3478	1/1	0.92	0.13	42,42,42,42	0
54	MG	2a	3064	1/1	0.92	0.07	81,81,81,81	0
54	MG	2A	3126	1/1	0.92	0.16	37,37,37,37	0
54	MG	2A	3303	1/1	0.92	0.07	43,43,43,43	0
54	MG	1l	201	1/1	0.92	0.20	70,70,70,70	0
54	MG	2A	3305	1/1	0.92	0.09	46,46,46,46	0
54	MG	1A	3628	1/1	0.92	0.27	59,59,59,59	0
54	MG	1A	3688	1/1	0.92	0.32	40,40,40,40	0
54	MG	2A	3133	1/1	0.92	0.20	50,50,50,50	0
54	MG	1A	4005	1/1	0.92	0.08	70,70,70,70	0
54	MG	1A	3903	1/1	0.92	0.10	37,37,37,37	0
54	MG	1A	3904	1/1	0.92	0.07	37,37,37,37	0
54	MG	2A	3140	1/1	0.92	0.19	58,58,58,58	0
54	MG	1a	3186	1/1	0.92	0.14	70,70,70,70	0
54	MG	1A	3567	1/1	0.92	0.12	47,47,47,47	0
54	MG	2a	3079	1/1	0.92	0.18	53,53,53,53	0
54	MG	1A	3094	1/1	0.92	0.10	58,58,58,58	0
54	MG	1A	3908	1/1	0.92	0.12	46,46,46,46	0
54	MG	1A	3503	1/1	0.92	0.10	52,52,52,52	0
54	MG	2A	3709	1/1	0.92	0.10	57,57,57,57	0
54	MG	1a	3192	1/1	0.92	0.17	69,69,69,69	0
54	MG	2A	3712	1/1	0.92	0.14	54,54,54,54	0
54	MG	2A	3341	1/1	0.92	0.13	66,66,66,66	0
54	MG	1A	3412	1/1	0.92	0.15	33,33,33,33	0
54	MG	1A	3791	1/1	0.92	0.13	38,38,38,38	0
54	MG	1A	3095	1/1	0.92	0.10	38,38,38,38	0
54	MG	19	101	1/1	0.92	0.25	67,67,67,67	0
54	MG	19	102	1/1	0.92	0.13	64,64,64,64	0
54	MG	2A	3511	1/1	0.92	0.07	37,37,37,37	0
54	MG	1a	3097	1/1	0.92	0.22	70,70,70,70	0
54	MG	2A	3018	1/1	0.92	0.38	44,44,44,44	0
54	MG	1A	3099	1/1	0.92	0.11	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3795	1/1	0.92	0.34	41,41,41,41	0
54	MG	2A	3518	1/1	0.92	0.18	65,65,65,65	0
54	MG	1a	3100	1/1	0.92	0.33	70,70,70,70	0
54	MG	1A	3319	1/1	0.92	0.18	48,48,48,48	0
54	MG	1B	206	1/1	0.92	0.41	65,65,65,65	0
54	MG	1a	3205	1/1	0.92	0.13	75,75,75,75	0
54	MG	2a	3109	1/1	0.92	0.18	71,71,71,71	0
54	MG	1a	3007	1/1	0.92	0.11	65,65,65,65	0
54	MG	2a	3111	1/1	0.92	0.09	61,61,61,61	0
54	MG	2A	3370	1/1	0.92	0.11	57,57,57,57	0
54	MG	1A	3158	1/1	0.92	0.19	41,41,41,41	0
54	MG	2B	206	1/1	0.92	0.24	71,71,71,71	0
54	MG	1a	3106	1/1	0.92	0.47	67,67,67,67	0
54	MG	2A	3527	1/1	0.92	0.24	62,62,62,62	0
54	MG	1A	3514	1/1	0.92	0.06	21,21,21,21	0
54	MG	1a	3108	1/1	0.92	0.19	69,69,69,69	0
54	MG	1A	3932	1/1	0.92	0.09	43,43,43,43	0
54	MG	1A	3709	1/1	0.92	0.31	40,40,40,40	0
54	MG	1A	3515	1/1	0.92	0.21	43,43,43,43	0
54	MG	2B	214	1/1	0.92	0.11	65,65,65,65	0
54	MG	1a	3112	1/1	0.92	0.23	73,73,73,73	0
54	MG	2B	216	1/1	0.92	0.16	74,74,74,74	0
54	MG	1A	3713	1/1	0.92	0.15	61,61,61,61	0
54	MG	1A	3085	1/1	0.92	0.12	51,51,51,51	0
54	MG	1A	3238	1/1	0.92	0.34	72,72,72,72	0
54	MG	2A	3546	1/1	0.92	0.12	67,67,67,67	0
54	MG	1a	3117	1/1	0.92	0.20	64,64,64,64	0
54	MG	1A	3818	1/1	0.92	0.07	12,12,12,12	0
54	MG	1A	3821	1/1	0.92	0.07	24,24,24,24	0
54	MG	2F	302	1/1	0.92	0.08	44,44,44,44	0
54	MG	1A	3724	1/1	0.92	0.09	55,55,55,55	0
54	MG	1A	3526	1/1	0.92	0.10	54,54,54,54	0
54	MG	1A	3162	1/1	0.92	0.10	44,44,44,44	0
54	MG	2a	3146	1/1	0.92	0.10	47,47,47,47	0
54	MG	1a	3031	1/1	0.92	0.35	68,68,68,68	0
54	MG	1A	3248	1/1	0.92	0.14	35,35,35,35	0
54	MG	2a	3151	1/1	0.92	0.08	80,80,80,80	0
54	MG	2a	3154	1/1	0.92	0.15	69,69,69,69	0
54	MG	2a	3155	1/1	0.92	0.08	77,77,77,77	0
54	MG	2A	3564	1/1	0.92	0.09	66,66,66,66	0
54	MG	2a	3162	1/1	0.92	0.09	67,67,67,67	0
54	MG	2A	3060	1/1	0.92	0.16	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2a	3164	1/1	0.92	0.09	74,74,74,74	0
54	MG	1A	3653	1/1	0.92	0.22	56,56,56,56	0
54	MG	2R	202	1/1	0.92	0.20	57,57,57,57	0
54	MG	2A	3569	1/1	0.92	0.08	62,62,62,62	0
54	MG	1A	3468	1/1	0.92	0.17	63,63,63,63	0
54	MG	2A	3407	1/1	0.92	0.09	48,48,48,48	0
54	MG	2V	201	1/1	0.92	0.14	64,64,64,64	0
54	MG	1a	3131	1/1	0.92	0.11	68,68,68,68	0
54	MG	1A	3001	1/1	0.92	0.11	38,38,38,38	0
54	MG	2A	3215	1/1	0.92	0.30	50,50,50,50	0
54	MG	28	101	1/1	0.92	0.08	59,59,59,59	0
54	MG	2A	3413	1/1	0.92	0.07	58,58,58,58	0
54	MG	1A	3377	1/1	0.92	0.18	59,59,59,59	0
54	MG	1A	3195	1/1	0.92	0.26	49,49,49,49	0
54	MG	1A	3339	1/1	0.92	0.14	43,43,43,43	0
54	MG	1A	3341	1/1	0.92	0.12	55,55,55,55	0
54	MG	1A	3389	1/1	0.92	0.14	34,34,34,34	0
54	MG	2A	3221	1/1	0.92	0.10	51,51,51,51	0
54	MG	1A	3597	1/1	0.92	0.10	52,52,52,52	0
54	MG	1A	3391	1/1	0.92	0.08	45,45,45,45	0
54	MG	1A	3165	1/1	0.92	0.21	39,39,39,39	0
55	HGR	2A	3743	36/36	0.92	0.12	43,52,58,59	0
54	MG	1a	3253	1/1	0.92	0.10	54,54,54,54	0
54	MG	2A	3084	1/1	0.92	0.11	53,53,53,53	0
54	MG	1F	319	1/1	0.92	0.09	53,53,53,53	0
54	MG	2A	3613	1/1	0.92	0.13	60,60,60,60	0
54	MG	2A	3088	1/1	0.92	0.41	50,50,50,50	0
54	MG	1A	3039	1/1	0.92	0.20	60,60,60,60	0
54	MG	1A	3488	1/1	0.92	0.09	33,33,33,33	0
54	MG	1A	3757	1/1	0.92	0.09	42,42,42,42	0
54	MG	2T	201	1/1	0.93	0.21	65,65,65,65	0
54	MG	1A	3946	1/1	0.93	0.07	45,45,45,45	0
54	MG	2A	3345	1/1	0.93	0.23	71,71,71,71	0
54	MG	1A	3396	1/1	0.93	0.06	27,27,27,27	0
54	MG	2A	3539	1/1	0.93	0.07	77,77,77,77	0
54	MG	2V	203	1/1	0.93	0.16	75,75,75,75	0
54	MG	2A	3540	1/1	0.93	0.08	68,68,68,68	0
54	MG	2A	3138	1/1	0.93	0.14	67,67,67,67	0
54	MG	1e	202	1/1	0.93	0.12	76,76,76,76	0
54	MG	25	101	1/1	0.93	0.47	49,49,49,49	0
54	MG	25	102	1/1	0.93	0.12	64,64,64,64	0
54	MG	1A	3166	1/1	0.93	0.14	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3143	1/1	0.93	0.17	51,51,51,51	0
54	MG	2A	3547	1/1	0.93	0.09	83,83,83,83	0
54	MG	1A	3566	1/1	0.93	0.11	52,52,52,52	0
54	MG	2A	3549	1/1	0.93	0.08	63,63,63,63	0
54	MG	1A	3819	1/1	0.93	0.25	38,38,38,38	0
54	MG	2a	3007	1/1	0.93	0.26	58,58,58,58	0
54	MG	1a	3159	1/1	0.93	0.11	71,71,71,71	0
54	MG	1A	3031	1/1	0.93	0.09	21,21,21,21	0
54	MG	1A	3358	1/1	0.93	0.09	44,44,44,44	0
54	MG	2A	3360	1/1	0.93	0.20	60,60,60,60	0
54	MG	1A	3035	1/1	0.93	0.12	53,53,53,53	0
54	MG	1A	3053	1/1	0.93	0.07	41,41,41,41	0
54	MG	1a	3164	1/1	0.93	0.24	65,65,65,65	0
54	MG	2A	3160	1/1	0.93	0.24	63,63,63,63	0
54	MG	1A	3638	1/1	0.93	0.08	44,44,44,44	0
54	MG	2A	3372	1/1	0.93	0.14	70,70,70,70	0
54	MG	1A	3175	1/1	0.93	0.21	38,38,38,38	0
54	MG	1n	102	1/1	0.93	0.23	73,73,73,73	0
54	MG	1A	3829	1/1	0.93	0.09	29,29,29,29	0
54	MG	1A	3508	1/1	0.93	0.07	41,41,41,41	0
54	MG	1A	3405	1/1	0.93	0.24	51,51,51,51	0
54	MG	1A	3733	1/1	0.93	0.13	49,49,49,49	0
54	MG	1A	3364	1/1	0.93	0.08	29,29,29,29	0
54	MG	1A	3250	1/1	0.93	0.16	62,62,62,62	0
54	MG	1A	3578	1/1	0.93	0.09	44,44,44,44	0
54	MG	1A	3843	1/1	0.93	0.12	38,38,38,38	0
54	MG	2A	3592	1/1	0.93	0.08	72,72,72,72	0
54	MG	2a	3035	1/1	0.93	0.13	60,60,60,60	0
54	MG	1A	3846	1/1	0.93	0.09	53,53,53,53	0
54	MG	2A	3598	1/1	0.93	0.09	33,33,33,33	0
54	MG	1A	3651	1/1	0.93	0.12	63,63,63,63	0
54	MG	1a	3069	1/1	0.93	0.43	69,69,69,69	0
54	MG	1A	3295	1/1	0.93	0.24	42,42,42,42	0
54	MG	1A	3179	1/1	0.93	0.22	55,55,55,55	0
54	MG	1Q	204	1/1	0.93	0.10	42,42,42,42	0
54	MG	1R	203	1/1	0.93	0.12	51,51,51,51	0
54	MG	2A	3611	1/1	0.93	0.07	24,24,24,24	0
54	MG	1a	3187	1/1	0.93	0.08	75,75,75,75	0
54	MG	1A	3517	1/1	0.93	0.08	28,28,28,28	0
54	MG	1A	3979	1/1	0.93	0.09	43,43,43,43	0
54	MG	2A	3615	1/1	0.93	0.12	61,61,61,61	0
54	MG	1A	3201	1/1	0.93	0.33	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3617	1/1	0.93	0.34	69,69,69,69	0
54	MG	1A	3750	1/1	0.93	0.09	47,47,47,47	0
54	MG	1A	3523	1/1	0.93	0.20	57,57,57,57	0
54	MG	1A	3414	1/1	0.93	0.10	30,30,30,30	0
54	MG	1A	3985	1/1	0.93	0.21	43,43,43,43	0
54	MG	2A	3412	1/1	0.93	0.18	64,64,64,64	0
54	MG	1V	206	1/1	0.93	0.12	60,60,60,60	0
54	MG	1A	3055	1/1	0.93	0.20	54,54,54,54	0
54	MG	2A	3204	1/1	0.93	0.12	61,61,61,61	0
54	MG	1a	3084	1/1	0.93	0.08	60,60,60,60	0
54	MG	2A	3417	1/1	0.93	0.32	64,64,64,64	0
54	MG	1A	3755	1/1	0.93	0.08	36,36,36,36	0
54	MG	1A	3330	1/1	0.93	0.15	19,19,19,19	0
54	MG	2A	3210	1/1	0.93	0.29	61,61,61,61	0
54	MG	1A	3870	1/1	0.93	0.09	50,50,50,50	0
54	MG	2A	3042	1/1	0.93	0.12	52,52,52,52	0
54	MG	1A	3206	1/1	0.93	0.29	50,50,50,50	0
54	MG	2A	3636	1/1	0.93	0.10	73,73,73,73	0
54	MG	2A	3426	1/1	0.93	0.23	63,63,63,63	0
54	MG	1A	3337	1/1	0.93	0.08	33,33,33,33	0
54	MG	2A	3641	1/1	0.93	0.14	68,68,68,68	0
54	MG	1a	3092	1/1	0.93	0.11	52,52,52,52	0
54	MG	2A	3432	1/1	0.93	0.14	42,42,42,42	0
54	MG	1A	3210	1/1	0.93	0.30	68,68,68,68	0
54	MG	1A	3421	1/1	0.93	0.07	26,26,26,26	0
54	MG	1a	3096	1/1	0.93	0.30	60,60,60,60	0
54	MG	1A	3667	1/1	0.93	0.09	53,53,53,53	0
54	MG	2A	3439	1/1	0.93	0.11	63,63,63,63	0
54	MG	1A	3422	1/1	0.93	0.10	29,29,29,29	0
54	MG	1A	3764	1/1	0.93	0.06	27,27,27,27	0
54	MG	1a	3213	1/1	0.93	0.18	55,55,55,55	0
54	MG	15	108	1/1	0.93	0.09	59,59,59,59	0
54	MG	1a	3216	1/1	0.93	0.17	62,62,62,62	0
54	MG	2A	3669	1/1	0.93	0.08	76,76,76,76	0
54	MG	2A	3227	1/1	0.93	0.15	49,49,49,49	0
54	MG	2A	3228	1/1	0.93	0.10	64,64,64,64	0
54	MG	1A	3340	1/1	0.93	0.08	51,51,51,51	0
54	MG	2A	3230	1/1	0.93	0.23	58,58,58,58	0
54	MG	2A	3680	1/1	0.93	0.07	42,42,42,42	0
54	MG	2A	3450	1/1	0.93	0.10	66,66,66,66	0
54	MG	1A	3541	1/1	0.93	0.09	32,32,32,32	0
54	MG	1a	3103	1/1	0.93	0.30	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3236	1/1	0.93	0.24	63,63,63,63	0
54	MG	1A	3144	1/1	0.93	0.10	34,34,34,34	0
54	MG	1A	3057	1/1	0.93	0.08	50,50,50,50	0
54	MG	2A	3240	1/1	0.93	0.11	61,61,61,61	0
54	MG	1A	3601	1/1	0.93	0.21	35,35,35,35	0
54	MG	2A	3692	1/1	0.93	0.08	38,38,38,38	0
54	MG	2A	3461	1/1	0.93	0.19	67,67,67,67	0
54	MG	1A	3604	1/1	0.93	0.21	34,34,34,34	0
54	MG	2A	3243	1/1	0.93	0.24	65,65,65,65	0
54	MG	2A	3698	1/1	0.93	0.08	55,55,55,55	0
54	MG	2A	3699	1/1	0.93	0.08	54,54,54,54	0
54	MG	2A	3245	1/1	0.93	0.10	60,60,60,60	0
54	MG	1A	3606	1/1	0.93	0.17	32,32,32,32	0
54	MG	1A	3010	1/1	0.93	0.10	51,51,51,51	0
54	MG	2A	3251	1/1	0.93	0.16	63,63,63,63	0
54	MG	2A	3255	1/1	0.93	0.10	48,48,48,48	0
54	MG	1A	3547	1/1	0.93	0.11	43,43,43,43	0
54	MG	1A	3785	1/1	0.93	0.12	58,58,58,58	0
54	MG	1a	3006	1/1	0.93	0.11	66,66,66,66	0
54	MG	2A	3259	1/1	0.93	0.20	60,60,60,60	0
54	MG	1A	3383	1/1	0.93	0.10	38,38,38,38	0
54	MG	2A	3477	1/1	0.93	0.12	31,31,31,31	0
54	MG	1a	3114	1/1	0.93	0.23	67,67,67,67	0
54	MG	1A	3612	1/1	0.93	0.11	22,22,22,22	0
54	MG	1A	3549	1/1	0.93	0.12	51,51,51,51	0
54	MG	2A	3721	1/1	0.93	0.09	59,59,59,59	0
54	MG	2A	3723	1/1	0.93	0.10	65,65,65,65	0
54	MG	1A	3916	1/1	0.93	0.07	61,61,61,61	0
54	MG	1A	3481	1/1	0.93	0.09	59,59,59,59	0
54	MG	2A	3729	1/1	0.93	0.12	62,62,62,62	0
54	MG	1A	3385	1/1	0.93	0.08	34,34,34,34	0
54	MG	2a	3136	1/1	0.93	0.08	61,61,61,61	0
54	MG	1B	208	1/1	0.93	0.10	56,56,56,56	0
54	MG	2a	3141	1/1	0.93	0.07	75,75,75,75	0
54	MG	1a	3019	1/1	0.93	0.07	58,58,58,58	0
54	MG	1A	3348	1/1	0.93	0.08	36,36,36,36	0
54	MG	2A	3735	1/1	0.93	0.11	34,34,34,34	0
54	MG	1A	3923	1/1	0.93	0.11	34,34,34,34	0
54	MG	1A	3490	1/1	0.93	0.14	60,60,60,60	0
54	MG	1A	3390	1/1	0.93	0.08	36,36,36,36	0
54	MG	1A	3698	1/1	0.93	0.09	56,56,56,56	0
54	MG	2a	3156	1/1	0.93	0.11	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3741	1/1	0.93	0.33	63,63,63,63	0
54	MG	2A	3495	1/1	0.93	0.12	65,65,65,65	0
54	MG	1A	3270	1/1	0.93	0.07	57,57,57,57	0
54	MG	2A	3101	1/1	0.93	0.14	51,51,51,51	0
54	MG	2A	3500	1/1	0.93	0.12	58,58,58,58	0
54	MG	1B	218	1/1	0.93	0.11	44,44,44,44	0
54	MG	1a	3030	1/1	0.93	0.15	49,49,49,49	0
54	MG	1A	3435	1/1	0.93	0.10	41,41,41,41	0
54	MG	1A	3805	1/1	0.93	0.10	55,55,55,55	0
54	MG	1a	3033	1/1	0.93	0.08	43,43,43,43	0
54	MG	1a	3140	1/1	0.93	0.12	61,61,61,61	0
54	MG	1B	221	1/1	0.93	0.09	53,53,53,53	0
54	MG	2A	3115	1/1	0.93	0.11	57,57,57,57	0
54	MG	2A	3307	1/1	0.93	0.08	37,37,37,37	0
54	MG	1a	3144	1/1	0.93	0.10	60,60,60,60	0
54	MG	1a	3266	1/1	0.93	0.10	48,48,48,48	0
54	MG	1A	3392	1/1	0.93	0.10	25,25,25,25	0
54	MG	1a	3269	1/1	0.93	0.18	67,67,67,67	0
54	MG	2A	3315	1/1	0.93	0.18	68,68,68,68	0
54	MG	1a	3037	1/1	0.93	0.09	49,49,49,49	0
54	MG	1A	3218	1/1	0.93	0.10	46,46,46,46	0
54	MG	1A	3938	1/1	0.93	0.16	54,54,54,54	0
54	MG	2A	3125	1/1	0.93	0.08	47,47,47,47	0
54	MG	1a	3040	1/1	0.93	0.33	75,75,75,75	0
54	MG	1A	3941	1/1	0.93	0.10	75,75,75,75	0
56	TEL	2A	3744	58/58	0.93	0.12	38,53,59,65	0
54	MG	1a	3277	1/1	0.93	0.20	75,75,75,75	0
54	MG	2A	3328	1/1	0.93	0.10	42,42,42,42	0
54	MG	2A	3329	1/1	0.93	0.13	59,59,59,59	0
54	MG	1A	3944	1/1	0.93	0.14	33,33,33,33	0
54	MG	2A	3335	1/1	0.93	0.08	32,32,32,32	0
54	MG	1A	3945	1/1	0.93	0.07	26,26,26,26	0
54	MG	2A	3530	1/1	0.93	0.10	56,56,56,56	0
54	MG	1d	302	1/1	0.93	0.24	73,73,73,73	0
54	MG	1A	3182	1/1	0.94	0.09	61,61,61,61	0
54	MG	2a	3015	1/1	0.94	0.20	55,55,55,55	0
54	MG	1A	3607	1/1	0.94	0.17	42,42,42,42	0
54	MG	1A	3747	1/1	0.94	0.06	45,45,45,45	0
54	MG	1A	3154	1/1	0.94	0.39	45,45,45,45	0
54	MG	1A	3125	1/1	0.94	0.08	72,72,72,72	0
54	MG	2A	3252	1/1	0.94	0.21	57,57,57,57	0
54	MG	2A	3254	1/1	0.94	0.09	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3625	1/1	0.94	0.07	68,68,68,68	0
54	MG	1A	3953	1/1	0.94	0.09	66,66,66,66	0
54	MG	1A	3103	1/1	0.94	0.15	32,32,32,32	0
54	MG	1A	3842	1/1	0.94	0.16	35,35,35,35	0
54	MG	2A	3447	1/1	0.94	0.10	42,42,42,42	0
54	MG	1a	3034	1/1	0.94	0.11	45,45,45,45	0
54	MG	1A	3669	1/1	0.94	0.09	50,50,50,50	0
54	MG	1a	3143	1/1	0.94	0.10	39,39,39,39	0
54	MG	1A	3516	1/1	0.94	0.11	55,55,55,55	0
54	MG	2a	3034	1/1	0.94	0.15	43,43,43,43	0
54	MG	2A	3109	1/1	0.94	0.07	43,43,43,43	0
54	MG	2A	3267	1/1	0.94	0.21	40,40,40,40	0
54	MG	2A	3637	1/1	0.94	0.07	79,79,79,79	0
54	MG	1A	3263	1/1	0.94	0.22	45,45,45,45	0
54	MG	1A	3962	1/1	0.94	0.07	28,28,28,28	0
54	MG	1A	3037	1/1	0.94	0.10	55,55,55,55	0
54	MG	2A	3650	1/1	0.94	0.09	85,85,85,85	0
54	MG	1A	3619	1/1	0.94	0.09	55,55,55,55	0
54	MG	1E	309	1/1	0.94	0.10	63,63,63,63	0
54	MG	1F	308	1/1	0.94	0.14	39,39,39,39	0
54	MG	1A	3306	1/1	0.94	0.24	36,36,36,36	0
54	MG	1A	3190	1/1	0.94	0.28	59,59,59,59	0
54	MG	2A	3658	1/1	0.94	0.08	60,60,60,60	0
54	MG	2A	3466	1/1	0.94	0.10	34,34,34,34	0
54	MG	2A	3660	1/1	0.94	0.06	55,55,55,55	0
54	MG	1A	3856	1/1	0.94	0.12	47,47,47,47	0
54	MG	1F	316	1/1	0.94	0.11	55,55,55,55	0
54	MG	1F	317	1/1	0.94	0.19	42,42,42,42	0
54	MG	1A	3343	1/1	0.94	0.08	47,47,47,47	0
54	MG	1a	3049	1/1	0.94	0.14	47,47,47,47	0
54	MG	1A	3482	1/1	0.94	0.11	24,24,24,24	0
54	MG	1A	3625	1/1	0.94	0.07	43,43,43,43	0
54	MG	1A	3108	1/1	0.94	0.26	29,29,29,29	0
54	MG	1A	3863	1/1	0.94	0.10	45,45,45,45	0
54	MG	2a	3061	1/1	0.94	0.22	62,62,62,62	0
54	MG	1A	3765	1/1	0.94	0.13	50,50,50,50	0
54	MG	2A	3302	1/1	0.94	0.09	61,61,61,61	0
54	MG	1H	202	1/1	0.94	0.09	58,58,58,58	0
54	MG	1N	201	1/1	0.94	0.10	45,45,45,45	0
54	MG	1A	3866	1/1	0.94	0.05	22,22,22,22	0
54	MG	2A	3139	1/1	0.94	0.19	69,69,69,69	0
54	MG	1A	3486	1/1	0.94	0.06	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3767	1/1	0.94	0.10	26,26,26,26	0
54	MG	1P	202	1/1	0.94	0.21	46,46,46,46	0
54	MG	1A	3768	1/1	0.94	0.08	49,49,49,49	0
54	MG	2A	3312	1/1	0.94	0.10	40,40,40,40	0
54	MG	1A	3137	1/1	0.94	0.14	42,42,42,42	0
54	MG	2A	3693	1/1	0.94	0.11	65,65,65,65	0
54	MG	1A	3110	1/1	0.94	0.15	41,41,41,41	0
54	MG	1A	3879	1/1	0.94	0.13	52,52,52,52	0
54	MG	2A	3152	1/1	0.94	0.13	53,53,53,53	0
54	MG	1A	3533	1/1	0.94	0.20	28,28,28,28	0
54	MG	1R	202	1/1	0.94	0.13	40,40,40,40	0
54	MG	1a	3180	1/1	0.94	0.22	68,68,68,68	0
54	MG	1A	3690	1/1	0.94	0.21	51,51,51,51	0
54	MG	1A	3631	1/1	0.94	0.14	33,33,33,33	0
54	MG	1A	3692	1/1	0.94	0.18	46,46,46,46	0
54	MG	2a	3085	1/1	0.94	0.11	67,67,67,67	0
54	MG	1A	3693	1/1	0.94	0.11	55,55,55,55	0
54	MG	1A	3886	1/1	0.94	0.14	58,58,58,58	0
54	MG	2A	3336	1/1	0.94	0.10	43,43,43,43	0
54	MG	2A	3338	1/1	0.94	0.07	37,37,37,37	0
54	MG	2A	3711	1/1	0.94	0.09	72,72,72,72	0
54	MG	1A	3379	1/1	0.94	0.12	41,41,41,41	0
54	MG	1U	205	1/1	0.94	0.17	39,39,39,39	0
54	MG	1A	3894	1/1	0.94	0.10	62,62,62,62	0
54	MG	1A	3535	1/1	0.94	0.06	24,24,24,24	0
54	MG	1A	3536	1/1	0.94	0.07	30,30,30,30	0
54	MG	1A	3582	1/1	0.94	0.09	53,53,53,53	0
54	MG	2A	3516	1/1	0.94	0.13	67,67,67,67	0
54	MG	1A	3997	1/1	0.94	0.13	33,33,33,33	0
54	MG	2A	3724	1/1	0.94	0.12	43,43,43,43	0
54	MG	2A	3173	1/1	0.94	0.12	55,55,55,55	0
54	MG	2A	3726	1/1	0.94	0.07	47,47,47,47	0
54	MG	2A	3175	1/1	0.94	0.10	61,61,61,61	0
54	MG	2A	3019	1/1	0.94	0.30	50,50,50,50	0
54	MG	1A	3537	1/1	0.94	0.08	35,35,35,35	0
54	MG	1A	3380	1/1	0.94	0.07	32,32,32,32	0
54	MG	1a	3085	1/1	0.94	0.23	64,64,64,64	0
54	MG	2A	3182	1/1	0.94	0.22	56,56,56,56	0
54	MG	10	102	1/1	0.94	0.25	44,44,44,44	0
54	MG	2A	3736	1/1	0.94	0.17	65,65,65,65	0
54	MG	1A	3705	1/1	0.94	0.11	29,29,29,29	0
54	MG	1A	4004	1/1	0.94	0.13	56,56,56,56	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3368	1/1	0.94	0.24	61,61,61,61	0
54	MG	1A	3706	1/1	0.94	0.11	50,50,50,50	0
54	MG	1A	4006	1/1	0.94	0.16	40,40,40,40	0
54	MG	13	103	1/1	0.94	0.10	63,63,63,63	0
54	MG	2A	3532	1/1	0.94	0.12	58,58,58,58	0
54	MG	2A	3192	1/1	0.94	0.15	58,58,58,58	0
54	MG	13	104	1/1	0.94	0.09	44,44,44,44	0
54	MG	1A	3280	1/1	0.94	0.16	58,58,58,58	0
54	MG	1A	3542	1/1	0.94	0.07	48,48,48,48	0
54	MG	1a	3206	1/1	0.94	0.10	60,60,60,60	0
54	MG	1A	3054	1/1	0.94	0.18	40,40,40,40	0
54	MG	2A	3381	1/1	0.94	0.07	63,63,63,63	0
54	MG	1A	3243	1/1	0.94	0.09	47,47,47,47	0
54	MG	1A	3545	1/1	0.94	0.18	54,54,54,54	0
54	MG	1A	3455	1/1	0.94	0.10	47,47,47,47	0
54	MG	17	107	1/1	0.94	0.09	56,56,56,56	0
54	MG	1A	3810	1/1	0.94	0.08	52,52,52,52	0
54	MG	18	102	1/1	0.94	0.11	38,38,38,38	0
54	MG	2a	3139	1/1	0.94	0.08	58,58,58,58	0
54	MG	1A	3647	1/1	0.94	0.26	47,47,47,47	0
54	MG	2A	3209	1/1	0.94	0.26	63,63,63,63	0
54	MG	1A	4019	1/1	0.94	0.09	51,51,51,51	0
54	MG	2A	3559	1/1	0.94	0.07	63,63,63,63	0
54	MG	2A	3393	1/1	0.94	0.10	41,41,41,41	0
54	MG	1A	3812	1/1	0.94	0.09	27,27,27,27	0
54	MG	2a	3153	1/1	0.94	0.10	74,74,74,74	0
54	MG	2A	3396	1/1	0.94	0.08	37,37,37,37	0
54	MG	1a	3220	1/1	0.94	0.08	67,67,67,67	0
54	MG	1A	3721	1/1	0.94	0.10	55,55,55,55	0
54	MG	2a	3157	1/1	0.94	0.10	52,52,52,52	0
54	MG	1B	203	1/1	0.94	0.08	54,54,54,54	0
54	MG	2a	3161	1/1	0.94	0.11	68,68,68,68	0
54	MG	2A	3568	1/1	0.94	0.11	37,37,37,37	0
54	MG	1A	3022	1/1	0.94	0.06	43,43,43,43	0
54	MG	2O	201	1/1	0.94	0.14	62,62,62,62	0
54	MG	1A	3387	1/1	0.94	0.09	27,27,27,27	0
54	MG	2P	202	1/1	0.94	0.20	69,69,69,69	0
54	MG	2a	3168	1/1	0.94	0.08	75,75,75,75	0
54	MG	1a	3005	1/1	0.94	0.18	57,57,57,57	0
54	MG	1A	3028	1/1	0.94	0.19	35,35,35,35	0
54	MG	2A	3408	1/1	0.94	0.07	44,44,44,44	0
54	MG	2A	3577	1/1	0.94	0.06	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3596	1/1	0.94	0.12	55,55,55,55	0
54	MG	1A	3359	1/1	0.94	0.12	26,26,26,26	0
54	MG	1a	3230	1/1	0.94	0.12	64,64,64,64	0
54	MG	1B	210	1/1	0.94	0.06	61,61,61,61	0
54	MG	2A	3223	1/1	0.94	0.11	60,60,60,60	0
54	MG	1A	3289	1/1	0.94	0.21	62,62,62,62	0
54	MG	1A	3051	1/1	0.94	0.13	32,32,32,32	0
54	MG	2A	3596	1/1	0.94	0.06	42,42,42,42	0
54	MG	1A	3824	1/1	0.94	0.09	49,49,49,49	0
54	MG	23	101	1/1	0.94	0.12	53,53,53,53	0
54	MG	2A	3078	1/1	0.94	0.14	62,62,62,62	0
54	MG	1a	3119	1/1	0.94	0.14	76,76,76,76	0
54	MG	1A	3060	1/1	0.94	0.07	39,39,39,39	0
54	MG	2A	3233	1/1	0.94	0.21	54,54,54,54	0
55	HGR	1A	4020	36/36	0.94	0.10	31,39,47,55	0
54	MG	1a	3122	1/1	0.94	0.14	47,47,47,47	0
56	TEL	1A	4021	58/58	0.94	0.10	28,43,50,52	0
54	MG	1a	3240	1/1	0.94	0.22	67,67,67,67	0
54	MG	1A	3942	1/1	0.94	0.07	30,30,30,30	0
54	MG	1a	3243	1/1	0.94	0.11	65,65,65,65	0
57	MPD	18	105	8/8	0.94	0.13	30,42,48,52	0
54	MG	2A	3238	1/1	0.94	0.11	47,47,47,47	0
54	MG	1A	3555	1/1	0.94	0.11	46,46,46,46	0
54	MG	1A	3602	1/1	0.94	0.21	33,33,33,33	0
54	MG	2A	3434	1/1	0.94	0.07	49,49,49,49	0
54	MG	1A	3363	1/1	0.94	0.11	34,34,34,34	0
59	ZN	14	102	1/1	0.94	0.15	123,123,123,123	0
54	MG	1a	3024	1/1	0.94	0.15	54,54,54,54	0
54	MG	1A	3999	1/1	0.95	0.38	44,44,44,44	0
54	MG	1A	3659	1/1	0.95	0.08	53,53,53,53	0
54	MG	2A	3322	1/1	0.95	0.17	60,60,60,60	0
54	MG	1A	3020	1/1	0.95	0.32	42,42,42,42	0
54	MG	2A	3127	1/1	0.95	0.06	44,44,44,44	0
54	MG	1A	3156	1/1	0.95	0.26	37,37,37,37	0
54	MG	1A	3090	1/1	0.95	0.33	35,35,35,35	0
54	MG	1A	3049	1/1	0.95	0.17	44,44,44,44	0
54	MG	2A	3332	1/1	0.95	0.15	45,45,45,45	0
54	MG	2A	3333	1/1	0.95	0.11	39,39,39,39	0
54	MG	18	103	1/1	0.95	0.20	37,37,37,37	0
54	MG	1A	3299	1/1	0.95	0.24	41,41,41,41	0
54	MG	2A	3337	1/1	0.95	0.09	46,46,46,46	0
54	MG	1A	4008	1/1	0.95	0.10	69,69,69,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2W	203	1/1	0.95	0.17	47,47,47,47	0
54	MG	2A	3339	1/1	0.95	0.07	34,34,34,34	0
54	MG	1A	3408	1/1	0.95	0.09	40,40,40,40	0
54	MG	1A	3300	1/1	0.95	0.09	52,52,52,52	0
54	MG	1A	3021	1/1	0.95	0.13	36,36,36,36	0
54	MG	2A	3343	1/1	0.95	0.08	36,36,36,36	0
54	MG	1A	3249	1/1	0.95	0.12	49,49,49,49	0
54	MG	27	101	1/1	0.95	0.12	44,44,44,44	0
54	MG	1A	3011	1/1	0.95	0.16	58,58,58,58	0
54	MG	1A	4016	1/1	0.95	0.15	58,58,58,58	0
54	MG	2a	3001	1/1	0.95	0.08	49,49,49,49	0
54	MG	2A	3144	1/1	0.95	0.08	63,63,63,63	0
54	MG	2a	3003	1/1	0.95	0.32	66,66,66,66	0
54	MG	1A	3473	1/1	0.95	0.07	31,31,31,31	0
54	MG	1A	3134	1/1	0.95	0.23	33,33,33,33	0
54	MG	1a	3139	1/1	0.95	0.05	59,59,59,59	0
54	MG	1a	3008	1/1	0.95	0.09	63,63,63,63	0
54	MG	1a	3141	1/1	0.95	0.13	63,63,63,63	0
54	MG	2A	3356	1/1	0.95	0.06	42,42,42,42	0
54	MG	2A	3357	1/1	0.95	0.08	33,33,33,33	0
54	MG	1A	3603	1/1	0.95	0.23	41,41,41,41	0
54	MG	1A	3017	1/1	0.95	0.24	33,33,33,33	0
54	MG	1A	3605	1/1	0.95	0.12	46,46,46,46	0
54	MG	1A	3773	1/1	0.95	0.07	39,39,39,39	0
54	MG	1A	3199	1/1	0.95	0.32	44,44,44,44	0
54	MG	2A	3367	1/1	0.95	0.07	61,61,61,61	0
54	MG	1A	3775	1/1	0.95	0.06	45,45,45,45	0
54	MG	1A	3065	1/1	0.95	0.10	36,36,36,36	0
54	MG	1A	3257	1/1	0.95	0.09	52,52,52,52	0
54	MG	1A	3070	1/1	0.95	0.04	31,31,31,31	0
54	MG	1A	3685	1/1	0.95	0.27	57,57,57,57	0
54	MG	2A	3588	1/1	0.95	0.07	59,59,59,59	0
54	MG	2A	3590	1/1	0.95	0.09	59,59,59,59	0
54	MG	1k	201	1/1	0.95	0.11	44,44,44,44	0
54	MG	2A	3594	1/1	0.95	0.06	65,65,65,65	0
54	MG	2a	3029	1/1	0.95	0.13	63,63,63,63	0
54	MG	1A	3420	1/1	0.95	0.07	22,22,22,22	0
54	MG	1A	3783	1/1	0.95	0.07	35,35,35,35	0
54	MG	1A	3611	1/1	0.95	0.07	40,40,40,40	0
54	MG	1A	3173	1/1	0.95	0.13	38,38,38,38	0
54	MG	1A	3919	1/1	0.95	0.08	58,58,58,58	0
54	MG	1A	3613	1/1	0.95	0.07	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3550	1/1	0.95	0.09	49,49,49,49	0
54	MG	2A	3607	1/1	0.95	0.08	64,64,64,64	0
54	MG	1A	3790	1/1	0.95	0.07	48,48,48,48	0
54	MG	1A	3315	1/1	0.95	0.15	61,61,61,61	0
54	MG	1A	3926	1/1	0.95	0.12	45,45,45,45	0
54	MG	2A	3181	1/1	0.95	0.09	49,49,49,49	0
54	MG	1A	3792	1/1	0.95	0.20	54,54,54,54	0
54	MG	1A	3618	1/1	0.95	0.10	25,25,25,25	0
54	MG	2A	3184	1/1	0.95	0.12	66,66,66,66	0
54	MG	1A	3033	1/1	0.95	0.10	46,46,46,46	0
54	MG	1A	3694	1/1	0.95	0.18	41,41,41,41	0
54	MG	2A	3003	1/1	0.95	0.07	57,57,57,57	0
54	MG	2A	3397	1/1	0.95	0.19	54,54,54,54	0
54	MG	1A	3489	1/1	0.95	0.08	57,57,57,57	0
54	MG	2A	3189	1/1	0.95	0.10	48,48,48,48	0
54	MG	2a	3051	1/1	0.95	0.28	58,58,58,58	0
54	MG	2A	3190	1/1	0.95	0.25	69,69,69,69	0
54	MG	2A	3006	1/1	0.95	0.12	51,51,51,51	0
54	MG	2A	3403	1/1	0.95	0.08	52,52,52,52	0
54	MG	2A	3009	1/1	0.95	0.10	42,42,42,42	0
54	MG	2A	3405	1/1	0.95	0.10	41,41,41,41	0
54	MG	1A	3800	1/1	0.95	0.28	44,44,44,44	0
54	MG	1a	3169	1/1	0.95	0.14	65,65,65,65	0
54	MG	2A	3013	1/1	0.95	0.07	23,23,23,23	0
54	MG	1B	230	1/1	0.95	0.12	62,62,62,62	0
54	MG	1A	3936	1/1	0.95	0.05	28,28,28,28	0
54	MG	1D	302	1/1	0.95	0.10	52,52,52,52	0
54	MG	1A	3318	1/1	0.95	0.09	40,40,40,40	0
54	MG	2A	3022	1/1	0.95	0.26	50,50,50,50	0
54	MG	2A	3202	1/1	0.95	0.14	53,53,53,53	0
54	MG	2a	3067	1/1	0.95	0.07	70,70,70,70	0
54	MG	2A	3203	1/1	0.95	0.12	54,54,54,54	0
54	MG	1a	3174	1/1	0.95	0.15	51,51,51,51	0
54	MG	2A	3639	1/1	0.95	0.07	70,70,70,70	0
54	MG	1A	3491	1/1	0.95	0.06	22,22,22,22	0
54	MG	2A	3206	1/1	0.95	0.10	52,52,52,52	0
54	MG	1a	3176	1/1	0.95	0.08	70,70,70,70	0
54	MG	1A	3940	1/1	0.95	0.07	45,45,45,45	0
54	MG	1D	313	1/1	0.95	0.07	58,58,58,58	0
54	MG	2A	3422	1/1	0.95	0.06	32,32,32,32	0
54	MG	1D	315	1/1	0.95	0.13	44,44,44,44	0
54	MG	2A	3656	1/1	0.95	0.12	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3803	1/1	0.95	0.14	50,50,50,50	0
54	MG	1E	307	1/1	0.95	0.12	31,31,31,31	0
54	MG	1A	3699	1/1	0.95	0.06	37,37,37,37	0
54	MG	2A	3428	1/1	0.95	0.09	38,38,38,38	0
54	MG	1A	3943	1/1	0.95	0.07	36,36,36,36	0
54	MG	1F	305	1/1	0.95	0.10	37,37,37,37	0
54	MG	1A	3208	1/1	0.95	0.12	43,43,43,43	0
54	MG	1A	3806	1/1	0.95	0.07	32,32,32,32	0
54	MG	1A	3056	1/1	0.95	0.10	27,27,27,27	0
54	MG	2A	3041	1/1	0.95	0.11	44,44,44,44	0
54	MG	1A	3211	1/1	0.95	0.33	40,40,40,40	0
54	MG	1A	3081	1/1	0.95	0.23	43,43,43,43	0
54	MG	2A	3672	1/1	0.95	0.08	69,69,69,69	0
54	MG	1A	3949	1/1	0.95	0.07	60,60,60,60	0
54	MG	2A	3046	1/1	0.95	0.18	58,58,58,58	0
54	MG	1A	3149	1/1	0.95	0.08	51,51,51,51	0
54	MG	1A	3278	1/1	0.95	0.23	32,32,32,32	0
54	MG	1A	3815	1/1	0.95	0.30	39,39,39,39	0
54	MG	1A	3047	1/1	0.95	0.17	44,44,44,44	0
54	MG	1A	3328	1/1	0.95	0.08	26,26,26,26	0
54	MG	2A	3052	1/1	0.95	0.13	44,44,44,44	0
54	MG	2a	3104	1/1	0.95	0.10	54,54,54,54	0
54	MG	2A	3053	1/1	0.95	0.08	42,42,42,42	0
54	MG	2A	3688	1/1	0.95	0.10	69,69,69,69	0
54	MG	1A	3329	1/1	0.95	0.05	34,34,34,34	0
54	MG	1A	3439	1/1	0.95	0.15	37,37,37,37	0
54	MG	1A	3714	1/1	0.95	0.06	32,32,32,32	0
54	MG	1N	202	1/1	0.95	0.09	40,40,40,40	0
54	MG	2A	3455	1/1	0.95	0.19	57,57,57,57	0
54	MG	1A	3058	1/1	0.95	0.12	55,55,55,55	0
54	MG	1A	3718	1/1	0.95	0.11	51,51,51,51	0
54	MG	1A	3220	1/1	0.95	0.10	47,47,47,47	0
54	MG	1a	3075	1/1	0.95	0.19	65,65,65,65	0
54	MG	1A	3386	1/1	0.95	0.10	36,36,36,36	0
54	MG	2A	3064	1/1	0.95	0.08	43,43,43,43	0
54	MG	2A	3244	1/1	0.95	0.18	46,46,46,46	0
54	MG	1A	3722	1/1	0.95	0.09	30,30,30,30	0
54	MG	1A	3573	1/1	0.95	0.12	37,37,37,37	0
54	MG	2A	3465	1/1	0.95	0.11	64,64,64,64	0
54	MG	2A	3707	1/1	0.95	0.07	60,60,60,60	0
54	MG	1A	3335	1/1	0.95	0.10	51,51,51,51	0
54	MG	2A	3069	1/1	0.95	0.11	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3726	1/1	0.95	0.19	39,39,39,39	0
54	MG	1A	3833	1/1	0.95	0.10	49,49,49,49	0
54	MG	1Q	205	1/1	0.95	0.15	58,58,58,58	0
54	MG	1a	3214	1/1	0.95	0.07	74,74,74,74	0
54	MG	2A	3079	1/1	0.95	0.11	62,62,62,62	0
54	MG	1R	201	1/1	0.95	0.17	43,43,43,43	0
54	MG	2a	3132	1/1	0.95	0.15	60,60,60,60	0
54	MG	1A	3835	1/1	0.95	0.14	49,49,49,49	0
54	MG	2A	3719	1/1	0.95	0.10	71,71,71,71	0
54	MG	1A	3446	1/1	0.95	0.05	25,25,25,25	0
54	MG	1A	3222	1/1	0.95	0.12	36,36,36,36	0
54	MG	2A	3264	1/1	0.95	0.11	60,60,60,60	0
54	MG	1A	3338	1/1	0.95	0.15	54,54,54,54	0
54	MG	1T	202	1/1	0.95	0.07	57,57,57,57	0
54	MG	2A	3270	1/1	0.95	0.18	48,48,48,48	0
54	MG	2A	3271	1/1	0.95	0.32	50,50,50,50	0
54	MG	2A	3087	1/1	0.95	0.20	44,44,44,44	0
54	MG	1A	3731	1/1	0.95	0.07	22,22,22,22	0
54	MG	2a	3152	1/1	0.95	0.12	69,69,69,69	0
54	MG	2A	3089	1/1	0.95	0.14	40,40,40,40	0
54	MG	1A	3732	1/1	0.95	0.06	52,52,52,52	0
54	MG	2A	3489	1/1	0.95	0.07	34,34,34,34	0
54	MG	1A	3225	1/1	0.95	0.12	37,37,37,37	0
54	MG	1U	202	1/1	0.95	0.13	36,36,36,36	0
54	MG	1A	3186	1/1	0.95	0.21	35,35,35,35	0
54	MG	2a	3160	1/1	0.95	0.11	67,67,67,67	0
54	MG	1A	3646	1/1	0.95	0.10	58,58,58,58	0
54	MG	1A	3232	1/1	0.95	0.27	42,42,42,42	0
54	MG	1A	3849	1/1	0.95	0.11	31,31,31,31	0
54	MG	2A	3283	1/1	0.95	0.19	58,58,58,58	0
54	MG	2A	3742	1/1	0.95	0.07	52,52,52,52	0
54	MG	1A	3648	1/1	0.95	0.10	36,36,36,36	0
54	MG	1A	3742	1/1	0.95	0.09	28,28,28,28	0
54	MG	1A	3519	1/1	0.95	0.06	57,57,57,57	0
54	MG	2a	3171	1/1	0.95	0.07	78,78,78,78	0
54	MG	2B	204	1/1	0.95	0.34	64,64,64,64	0
54	MG	1A	3988	1/1	0.95	0.15	36,36,36,36	0
54	MG	2A	3289	1/1	0.95	0.06	37,37,37,37	0
54	MG	2A	3104	1/1	0.95	0.15	56,56,56,56	0
54	MG	2A	3291	1/1	0.95	0.12	23,23,23,23	0
54	MG	2A	3293	1/1	0.95	0.12	40,40,40,40	0
54	MG	2A	3296	1/1	0.95	0.07	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3521	1/1	0.95	0.30	28,28,28,28	0
54	MG	10	103	1/1	0.95	0.14	58,58,58,58	0
54	MG	10	104	1/1	0.95	0.10	51,51,51,51	0
54	MG	1A	3342	1/1	0.95	0.08	31,31,31,31	0
54	MG	1A	3585	1/1	0.95	0.18	60,60,60,60	0
54	MG	1A	3748	1/1	0.95	0.07	50,50,50,50	0
54	MG	2B	217	1/1	0.95	0.07	70,70,70,70	0
54	MG	11	101	1/1	0.95	0.14	48,48,48,48	0
54	MG	2f	201	1/1	0.95	0.15	55,55,55,55	0
54	MG	2D	304	1/1	0.95	0.32	45,45,45,45	0
54	MG	2D	306	1/1	0.95	0.23	52,52,52,52	0
54	MG	2t	201	1/1	0.95	0.21	49,49,49,49	0
54	MG	2D	307	1/1	0.95	0.14	65,65,65,65	0
54	MG	1A	3861	1/1	0.95	0.10	43,43,43,43	0
54	MG	11	104	1/1	0.95	0.07	32,32,32,32	0
54	MG	13	102	1/1	0.95	0.09	45,45,45,45	0
54	MG	2E	301	1/1	0.95	0.31	49,49,49,49	0
54	MG	1A	3292	1/1	0.95	0.07	48,48,48,48	0
54	MG	1A	3344	1/1	0.95	0.08	54,54,54,54	0
54	MG	1A	3864	1/1	0.95	0.07	44,44,44,44	0
54	MG	1A	3294	1/1	0.95	0.14	57,57,57,57	0
54	MG	2F	303	1/1	0.95	0.19	53,53,53,53	0
54	MG	2F	304	1/1	0.95	0.21	44,44,44,44	0
54	MG	1A	3457	1/1	0.95	0.13	56,56,56,56	0
54	MG	2A	3122	1/1	0.95	0.07	49,49,49,49	0
54	MG	2A	3123	1/1	0.95	0.24	49,49,49,49	0
54	MG	1A	3178	1/1	0.96	0.24	41,41,41,41	0
54	MG	1A	3939	1/1	0.96	0.07	54,54,54,54	0
54	MG	1A	3087	1/1	0.96	0.06	42,42,42,42	0
54	MG	1A	3113	1/1	0.96	0.31	41,41,41,41	0
54	MG	2A	3253	1/1	0.96	0.26	56,56,56,56	0
54	MG	2A	3429	1/1	0.96	0.11	62,62,62,62	0
54	MG	2a	3019	1/1	0.96	0.08	47,47,47,47	0
54	MG	1a	3255	1/1	0.96	0.05	64,64,64,64	0
54	MG	1A	3147	1/1	0.96	0.06	35,35,35,35	0
54	MG	1A	3226	1/1	0.96	0.24	37,37,37,37	0
54	MG	1A	3751	1/1	0.96	0.10	41,41,41,41	0
54	MG	1A	3357	1/1	0.96	0.10	20,20,20,20	0
54	MG	1A	3114	1/1	0.96	0.16	44,44,44,44	0
54	MG	1a	3262	1/1	0.96	0.07	50,50,50,50	0
54	MG	1A	3476	1/1	0.96	0.11	43,43,43,43	0
54	MG	1a	3133	1/1	0.96	0.09	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3185	1/1	0.96	0.13	40,40,40,40	0
54	MG	1a	3013	1/1	0.96	0.14	61,61,61,61	0
54	MG	2A	3268	1/1	0.96	0.14	51,51,51,51	0
54	MG	2A	3269	1/1	0.96	0.13	37,37,37,37	0
54	MG	1a	3014	1/1	0.96	0.11	61,61,61,61	0
54	MG	1A	3118	1/1	0.96	0.10	39,39,39,39	0
54	MG	1A	3479	1/1	0.96	0.09	34,34,34,34	0
54	MG	1D	304	1/1	0.96	0.07	42,42,42,42	0
54	MG	1A	3074	1/1	0.96	0.29	31,31,31,31	0
54	MG	1A	3089	1/1	0.96	0.17	39,39,39,39	0
54	MG	1A	3844	1/1	0.96	0.10	53,53,53,53	0
54	MG	2A	3452	1/1	0.96	0.07	35,35,35,35	0
54	MG	1A	3845	1/1	0.96	0.11	44,44,44,44	0
54	MG	1D	314	1/1	0.96	0.16	59,59,59,59	0
54	MG	1A	3304	1/1	0.96	0.17	41,41,41,41	0
54	MG	1d	301	1/1	0.96	0.24	70,70,70,70	0
54	MG	2A	3281	1/1	0.96	0.07	64,64,64,64	0
54	MG	1a	3026	1/1	0.96	0.07	48,48,48,48	0
54	MG	1E	304	1/1	0.96	0.13	35,35,35,35	0
54	MG	1A	3683	1/1	0.96	0.10	57,57,57,57	0
54	MG	1e	201	1/1	0.96	0.07	58,58,58,58	0
54	MG	1A	3483	1/1	0.96	0.06	26,26,26,26	0
54	MG	2A	3130	1/1	0.96	0.22	44,44,44,44	0
54	MG	1A	3959	1/1	0.96	0.13	43,43,43,43	0
54	MG	1A	3960	1/1	0.96	0.10	56,56,56,56	0
54	MG	1F	303	1/1	0.96	0.23	36,36,36,36	0
54	MG	2a	3055	1/1	0.96	0.11	49,49,49,49	0
54	MG	1A	3484	1/1	0.96	0.06	45,45,45,45	0
54	MG	2A	3295	1/1	0.96	0.13	47,47,47,47	0
54	MG	1A	3076	1/1	0.96	0.18	39,39,39,39	0
54	MG	1F	309	1/1	0.96	0.18	26,26,26,26	0
54	MG	1A	3851	1/1	0.96	0.06	45,45,45,45	0
54	MG	1F	312	1/1	0.96	0.08	38,38,38,38	0
54	MG	1A	3247	1/1	0.96	0.16	37,37,37,37	0
54	MG	1F	314	1/1	0.96	0.27	47,47,47,47	0
54	MG	2A	3683	1/1	0.96	0.05	49,49,49,49	0
54	MG	1A	3077	1/1	0.96	0.17	45,45,45,45	0
54	MG	1A	3617	1/1	0.96	0.19	57,57,57,57	0
54	MG	1A	3968	1/1	0.96	0.10	31,31,31,31	0
54	MG	1A	3769	1/1	0.96	0.06	40,40,40,40	0
54	MG	1A	3078	1/1	0.96	0.10	38,38,38,38	0
54	MG	2A	3151	1/1	0.96	0.15	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3484	1/1	0.96	0.08	42,42,42,42	0
54	MG	1A	3193	1/1	0.96	0.11	34,34,34,34	0
54	MG	1A	3772	1/1	0.96	0.07	39,39,39,39	0
54	MG	2A	3313	1/1	0.96	0.05	25,25,25,25	0
54	MG	2A	3314	1/1	0.96	0.21	67,67,67,67	0
54	MG	1A	3003	1/1	0.96	0.06	29,29,29,29	0
54	MG	1G	204	1/1	0.96	0.13	49,49,49,49	0
54	MG	1A	3196	1/1	0.96	0.14	63,63,63,63	0
54	MG	2A	3159	1/1	0.96	0.15	57,57,57,57	0
54	MG	2A	3319	1/1	0.96	0.09	51,51,51,51	0
54	MG	1A	3313	1/1	0.96	0.16	45,45,45,45	0
54	MG	2A	3496	1/1	0.96	0.08	63,63,63,63	0
54	MG	2A	3705	1/1	0.96	0.07	68,68,68,68	0
54	MG	2A	3497	1/1	0.96	0.12	41,41,41,41	0
54	MG	1A	3776	1/1	0.96	0.09	51,51,51,51	0
54	MG	1A	3559	1/1	0.96	0.09	60,60,60,60	0
54	MG	1a	3054	1/1	0.96	0.06	42,42,42,42	0
54	MG	1A	3161	1/1	0.96	0.10	37,37,37,37	0
54	MG	2A	3165	1/1	0.96	0.27	46,46,46,46	0
54	MG	1A	3096	1/1	0.96	0.12	46,46,46,46	0
54	MG	2A	3167	1/1	0.96	0.14	39,39,39,39	0
54	MG	2A	3331	1/1	0.96	0.10	53,53,53,53	0
54	MG	2a	3095	1/1	0.96	0.07	71,71,71,71	0
54	MG	1A	3562	1/1	0.96	0.19	40,40,40,40	0
54	MG	2a	3097	1/1	0.96	0.06	72,72,72,72	0
54	MG	1A	3256	1/1	0.96	0.14	45,45,45,45	0
54	MG	1A	3498	1/1	0.96	0.06	47,47,47,47	0
54	MG	1P	206	1/1	0.96	0.12	49,49,49,49	0
54	MG	1a	3061	1/1	0.96	0.11	69,69,69,69	0
54	MG	2A	3722	1/1	0.96	0.07	50,50,50,50	0
54	MG	1A	3877	1/1	0.96	0.12	64,64,64,64	0
54	MG	2A	3513	1/1	0.96	0.18	45,45,45,45	0
54	MG	2A	3174	1/1	0.96	0.15	44,44,44,44	0
54	MG	1A	3878	1/1	0.96	0.05	33,33,33,33	0
54	MG	1A	3163	1/1	0.96	0.08	34,34,34,34	0
54	MG	2a	3108	1/1	0.96	0.13	76,76,76,76	0
54	MG	1A	3259	1/1	0.96	0.24	35,35,35,35	0
54	MG	2A	3178	1/1	0.96	0.07	46,46,46,46	0
54	MG	1A	3066	1/1	0.96	0.31	42,42,42,42	0
54	MG	1A	3440	1/1	0.96	0.07	53,53,53,53	0
54	MG	1A	3129	1/1	0.96	0.32	43,43,43,43	0
54	MG	2A	3349	1/1	0.96	0.11	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3884	1/1	0.96	0.11	38,38,38,38	0
54	MG	2A	3031	1/1	0.96	0.11	30,30,30,30	0
54	MG	1A	3203	1/1	0.96	0.24	43,43,43,43	0
54	MG	1A	3572	1/1	0.96	0.09	28,28,28,28	0
54	MG	1A	3712	1/1	0.96	0.08	27,27,27,27	0
54	MG	1A	3130	1/1	0.96	0.17	38,38,38,38	0
54	MG	1A	3895	1/1	0.96	0.14	59,59,59,59	0
54	MG	1T	205	1/1	0.96	0.14	51,51,51,51	0
54	MG	1A	3205	1/1	0.96	0.22	40,40,40,40	0
54	MG	1A	3796	1/1	0.96	0.07	54,54,54,54	0
54	MG	1A	3797	1/1	0.96	0.08	58,58,58,58	0
54	MG	2A	3534	1/1	0.96	0.11	52,52,52,52	0
54	MG	2A	3193	1/1	0.96	0.23	67,67,67,67	0
54	MG	2A	3363	1/1	0.96	0.07	59,59,59,59	0
54	MG	1U	208	1/1	0.96	0.12	39,39,39,39	0
54	MG	1V	201	1/1	0.96	0.19	31,31,31,31	0
54	MG	2A	3541	1/1	0.96	0.09	77,77,77,77	0
54	MG	2A	3542	1/1	0.96	0.07	56,56,56,56	0
54	MG	1A	4001	1/1	0.96	0.05	39,39,39,39	0
54	MG	1A	3798	1/1	0.96	0.07	50,50,50,50	0
54	MG	1A	3901	1/1	0.96	0.07	31,31,31,31	0
54	MG	1A	3269	1/1	0.96	0.10	42,42,42,42	0
54	MG	1A	3510	1/1	0.96	0.10	26,26,26,26	0
54	MG	2a	3140	1/1	0.96	0.06	77,77,77,77	0
54	MG	1W	202	1/1	0.96	0.11	50,50,50,50	0
54	MG	1A	3905	1/1	0.96	0.11	24,24,24,24	0
54	MG	2a	3143	1/1	0.96	0.07	81,81,81,81	0
54	MG	1A	3102	1/1	0.96	0.14	38,38,38,38	0
54	MG	2A	3551	1/1	0.96	0.06	74,74,74,74	0
54	MG	1A	3207	1/1	0.96	0.17	37,37,37,37	0
54	MG	1A	4010	1/1	0.96	0.07	54,54,54,54	0
54	MG	1A	3168	1/1	0.96	0.06	34,34,34,34	0
54	MG	1A	3909	1/1	0.96	0.04	15,15,15,15	0
54	MG	1A	3911	1/1	0.96	0.16	42,42,42,42	0
54	MG	2A	3561	1/1	0.96	0.08	56,56,56,56	0
54	MG	1A	3913	1/1	0.96	0.09	53,53,53,53	0
54	MG	2A	3385	1/1	0.96	0.15	69,69,69,69	0
54	MG	2a	3158	1/1	0.96	0.14	55,55,55,55	0
54	MG	2F	301	1/1	0.96	0.16	48,48,48,48	0
54	MG	1A	3273	1/1	0.96	0.28	46,46,46,46	0
54	MG	1I	102	1/1	0.96	0.08	54,54,54,54	0
54	MG	1A	3275	1/1	0.96	0.13	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3389	1/1	0.96	0.12	48,48,48,48	0
54	MG	1A	3394	1/1	0.96	0.06	24,24,24,24	0
54	MG	1A	3807	1/1	0.96	0.04	35,35,35,35	0
54	MG	1A	3277	1/1	0.96	0.13	36,36,36,36	0
54	MG	1A	3209	1/1	0.96	0.39	39,39,39,39	0
54	MG	2A	3575	1/1	0.96	0.08	56,56,56,56	0
54	MG	2A	3066	1/1	0.96	0.10	50,50,50,50	0
54	MG	1A	3586	1/1	0.96	0.08	24,24,24,24	0
54	MG	2a	3173	1/1	0.96	0.06	62,62,62,62	0
54	MG	2Q	201	1/1	0.96	0.09	56,56,56,56	0
54	MG	1a	3228	1/1	0.96	0.08	65,65,65,65	0
54	MG	2a	3178	1/1	0.96	0.07	67,67,67,67	0
54	MG	15	102	1/1	0.96	0.08	38,38,38,38	0
54	MG	15	104	1/1	0.96	0.16	40,40,40,40	0
54	MG	1A	3169	1/1	0.96	0.13	33,33,33,33	0
54	MG	2A	3583	1/1	0.96	0.05	65,65,65,65	0
54	MG	2A	3075	1/1	0.96	0.09	48,48,48,48	0
54	MG	2A	3224	1/1	0.96	0.10	64,64,64,64	0
54	MG	1A	3924	1/1	0.96	0.06	55,55,55,55	0
54	MG	2V	202	1/1	0.96	0.19	49,49,49,49	0
54	MG	2a	3189	1/1	0.96	0.09	64,64,64,64	0
54	MG	2A	3077	1/1	0.96	0.19	56,56,56,56	0
54	MG	2W	202	1/1	0.96	0.10	54,54,54,54	0
54	MG	1A	3082	1/1	0.96	0.26	43,43,43,43	0
54	MG	2A	3593	1/1	0.96	0.07	62,62,62,62	0
54	MG	1A	3136	1/1	0.96	0.07	48,48,48,48	0
54	MG	17	103	1/1	0.96	0.13	38,38,38,38	0
54	MG	17	105	1/1	0.96	0.19	38,38,38,38	0
54	MG	1a	3238	1/1	0.96	0.12	50,50,50,50	0
54	MG	1A	3284	1/1	0.96	0.05	38,38,38,38	0
54	MG	1A	3214	1/1	0.96	0.17	35,35,35,35	0
54	MG	2A	3604	1/1	0.96	0.09	48,48,48,48	0
54	MG	2A	3085	1/1	0.96	0.13	55,55,55,55	0
54	MG	1A	3015	1/1	0.96	0.11	32,32,32,32	0
54	MG	1a	3242	1/1	0.96	0.07	72,72,72,72	0
54	MG	1A	3820	1/1	0.96	0.07	35,35,35,35	0
54	MG	1A	3465	1/1	0.96	0.05	44,44,44,44	0
54	MG	1A	3029	1/1	0.96	0.12	39,39,39,39	0
54	MG	2A	3091	1/1	0.96	0.08	45,45,45,45	0
54	MG	1A	3217	1/1	0.96	0.22	33,33,33,33	0
58	ARG	1B	231	12/12	0.96	0.08	34,50,53,58	0
54	MG	1A	3532	1/1	0.96	0.13	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1a	3121	1/1	0.96	0.08	40,40,40,40	0
54	MG	2A	3423	1/1	0.96	0.11	53,53,53,53	0
54	MG	1A	3145	1/1	0.97	0.26	40,40,40,40	0
54	MG	1a	3254	1/1	0.97	0.05	61,61,61,61	0
54	MG	1A	3067	1/1	0.97	0.27	35,35,35,35	0
54	MG	1A	3086	1/1	0.97	0.10	37,37,37,37	0
54	MG	2A	3687	1/1	0.97	0.06	36,36,36,36	0
54	MG	1a	3257	1/1	0.97	0.06	63,63,63,63	0
54	MG	1A	3832	1/1	0.97	0.06	38,38,38,38	0
54	MG	1P	205	1/1	0.97	0.09	64,64,64,64	0
54	MG	1A	3040	1/1	0.97	0.07	31,31,31,31	0
54	MG	1A	3834	1/1	0.97	0.07	51,51,51,51	0
54	MG	1A	3221	1/1	0.97	0.14	39,39,39,39	0
54	MG	1A	3279	1/1	0.97	0.31	39,39,39,39	0
54	MG	1A	3044	1/1	0.97	0.15	16,16,16,16	0
54	MG	1A	4013	1/1	0.97	0.10	48,48,48,48	0
54	MG	1A	3621	1/1	0.97	0.09	31,31,31,31	0
54	MG	1A	3563	1/1	0.97	0.11	24,24,24,24	0
54	MG	2A	3700	1/1	0.97	0.10	33,33,33,33	0
54	MG	1A	3281	1/1	0.97	0.11	50,50,50,50	0
54	MG	1A	3187	1/1	0.97	0.15	45,45,45,45	0
54	MG	1A	3388	1/1	0.97	0.09	26,26,26,26	0
54	MG	1A	3336	1/1	0.97	0.05	34,34,34,34	0
54	MG	1A	3073	1/1	0.97	0.21	46,46,46,46	0
54	MG	1A	3120	1/1	0.97	0.08	38,38,38,38	0
54	MG	2A	3231	1/1	0.97	0.13	47,47,47,47	0
54	MG	2A	3232	1/1	0.97	0.11	54,54,54,54	0
54	MG	1a	3276	1/1	0.97	0.19	61,61,61,61	0
54	MG	1a	3050	1/1	0.97	0.20	52,52,52,52	0
54	MG	1A	3228	1/1	0.97	0.19	31,31,31,31	0
54	MG	2A	3102	1/1	0.97	0.10	53,53,53,53	0
54	MG	1A	3512	1/1	0.97	0.04	53,53,53,53	0
54	MG	1A	3393	1/1	0.97	0.12	27,27,27,27	0
54	MG	1U	203	1/1	0.97	0.22	37,37,37,37	0
54	MG	1U	204	1/1	0.97	0.18	51,51,51,51	0
54	MG	1A	3153	1/1	0.97	0.20	39,39,39,39	0
54	MG	1U	206	1/1	0.97	0.18	30,30,30,30	0
54	MG	2A	3398	1/1	0.97	0.06	41,41,41,41	0
54	MG	2A	3111	1/1	0.97	0.09	66,66,66,66	0
54	MG	1U	207	1/1	0.97	0.18	39,39,39,39	0
54	MG	1B	207	1/1	0.97	0.11	50,50,50,50	0
54	MG	1A	3046	1/1	0.97	0.15	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1V	203	1/1	0.97	0.09	40,40,40,40	0
54	MG	1A	3703	1/1	0.97	0.05	39,39,39,39	0
54	MG	2A	3728	1/1	0.97	0.10	57,57,57,57	0
54	MG	1A	3855	1/1	0.97	0.10	53,53,53,53	0
54	MG	1B	211	1/1	0.97	0.12	56,56,56,56	0
54	MG	1B	212	1/1	0.97	0.07	47,47,47,47	0
54	MG	2A	3556	1/1	0.97	0.07	62,62,62,62	0
54	MG	1A	3155	1/1	0.97	0.09	34,34,34,34	0
54	MG	1A	3239	1/1	0.97	0.29	32,32,32,32	0
54	MG	1a	3177	1/1	0.97	0.10	69,69,69,69	0
54	MG	1A	3518	1/1	0.97	0.07	57,57,57,57	0
54	MG	2a	3090	1/1	0.97	0.10	61,61,61,61	0
54	MG	2a	3091	1/1	0.97	0.26	54,54,54,54	0
54	MG	1X	101	1/1	0.97	0.08	42,42,42,42	0
54	MG	1A	3398	1/1	0.97	0.05	23,23,23,23	0
54	MG	10	101	1/1	0.97	0.09	39,39,39,39	0
54	MG	1A	3075	1/1	0.97	0.15	42,42,42,42	0
54	MG	1A	3580	1/1	0.97	0.08	49,49,49,49	0
54	MG	1A	3710	1/1	0.97	0.17	40,40,40,40	0
54	MG	1A	3345	1/1	0.97	0.07	33,33,33,33	0
54	MG	2A	3131	1/1	0.97	0.19	45,45,45,45	0
54	MG	1A	3461	1/1	0.97	0.05	48,48,48,48	0
54	MG	1A	3027	1/1	0.97	0.17	30,30,30,30	0
54	MG	2A	3573	1/1	0.97	0.08	56,56,56,56	0
54	MG	1A	3244	1/1	0.97	0.39	42,42,42,42	0
54	MG	1A	3716	1/1	0.97	0.04	76,76,76,76	0
54	MG	1A	3871	1/1	0.97	0.07	49,49,49,49	0
54	MG	1A	3645	1/1	0.97	0.06	58,58,58,58	0
54	MG	13	101	1/1	0.97	0.11	35,35,35,35	0
54	MG	2A	3007	1/1	0.97	0.06	36,36,36,36	0
54	MG	2A	3141	1/1	0.97	0.08	47,47,47,47	0
54	MG	2A	3008	1/1	0.97	0.09	38,38,38,38	0
54	MG	1A	3873	1/1	0.97	0.09	23,23,23,23	0
54	MG	2A	3584	1/1	0.97	0.05	60,60,60,60	0
54	MG	1A	3245	1/1	0.97	0.14	36,36,36,36	0
54	MG	2D	301	1/1	0.97	0.11	44,44,44,44	0
54	MG	2D	302	1/1	0.97	0.11	51,51,51,51	0
54	MG	2A	3433	1/1	0.97	0.05	61,61,61,61	0
54	MG	1A	3349	1/1	0.97	0.05	25,25,25,25	0
54	MG	2D	305	1/1	0.97	0.11	40,40,40,40	0
54	MG	1A	3720	1/1	0.97	0.04	23,23,23,23	0
54	MG	2A	3591	1/1	0.97	0.08	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3284	1/1	0.97	0.08	44,44,44,44	0
54	MG	2A	3148	1/1	0.97	0.07	50,50,50,50	0
54	MG	2A	3014	1/1	0.97	0.07	53,53,53,53	0
54	MG	1A	3246	1/1	0.97	0.26	46,46,46,46	0
54	MG	2E	302	1/1	0.97	0.07	42,42,42,42	0
54	MG	15	103	1/1	0.97	0.21	32,32,32,32	0
54	MG	1a	3089	1/1	0.97	0.12	54,54,54,54	0
54	MG	1A	3352	1/1	0.97	0.13	33,33,33,33	0
54	MG	2A	3601	1/1	0.97	0.11	65,65,65,65	0
54	MG	2A	3154	1/1	0.97	0.07	44,44,44,44	0
54	MG	2A	3020	1/1	0.97	0.11	47,47,47,47	0
54	MG	2A	3021	1/1	0.97	0.05	39,39,39,39	0
54	MG	1D	305	1/1	0.97	0.21	44,44,44,44	0
54	MG	2A	3158	1/1	0.97	0.12	39,39,39,39	0
54	MG	1D	307	1/1	0.97	0.04	36,36,36,36	0
54	MG	1D	308	1/1	0.97	0.13	32,32,32,32	0
54	MG	2A	3301	1/1	0.97	0.09	50,50,50,50	0
54	MG	1a	3094	1/1	0.97	0.15	49,49,49,49	0
54	MG	1D	309	1/1	0.97	0.16	30,30,30,30	0
54	MG	2A	3027	1/1	0.97	0.10	52,52,52,52	0
54	MG	2A	3028	1/1	0.97	0.04	30,30,30,30	0
54	MG	2a	3144	1/1	0.97	0.05	65,65,65,65	0
54	MG	2a	3145	1/1	0.97	0.07	73,73,73,73	0
54	MG	17	101	1/1	0.97	0.10	33,33,33,33	0
54	MG	17	102	1/1	0.97	0.12	37,37,37,37	0
54	MG	1A	3723	1/1	0.97	0.06	37,37,37,37	0
54	MG	17	104	1/1	0.97	0.21	36,36,36,36	0
54	MG	1A	3004	1/1	0.97	0.07	43,43,43,43	0
54	MG	1A	3019	1/1	0.97	0.23	30,30,30,30	0
54	MG	1A	3097	1/1	0.97	0.18	49,49,49,49	0
54	MG	1A	3098	1/1	0.97	0.21	36,36,36,36	0
54	MG	1A	3023	1/1	0.97	0.05	18,18,18,18	0
54	MG	1E	301	1/1	0.97	0.10	31,31,31,31	0
54	MG	2W	201	1/1	0.97	0.31	44,44,44,44	0
54	MG	1E	302	1/1	0.97	0.18	39,39,39,39	0
54	MG	1A	3024	1/1	0.97	0.18	38,38,38,38	0
54	MG	1A	3730	1/1	0.97	0.08	48,48,48,48	0
54	MG	1A	3131	1/1	0.97	0.20	33,33,33,33	0
54	MG	1A	3538	1/1	0.97	0.06	35,35,35,35	0
54	MG	1A	3132	1/1	0.97	0.07	53,53,53,53	0
54	MG	1A	3982	1/1	0.97	0.05	22,22,22,22	0
54	MG	1F	304	1/1	0.97	0.19	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3634	1/1	0.97	0.07	64,64,64,64	0
54	MG	2A	3474	1/1	0.97	0.08	42,42,42,42	0
54	MG	2a	3170	1/1	0.97	0.14	51,51,51,51	0
54	MG	2A	3327	1/1	0.97	0.11	49,49,49,49	0
54	MG	1A	3038	1/1	0.97	0.08	37,37,37,37	0
54	MG	1F	307	1/1	0.97	0.13	36,36,36,36	0
54	MG	2a	3174	1/1	0.97	0.15	55,55,55,55	0
54	MG	1A	3736	1/1	0.97	0.07	61,61,61,61	0
54	MG	1A	3104	1/1	0.97	0.08	50,50,50,50	0
54	MG	1A	3170	1/1	0.97	0.11	50,50,50,50	0
54	MG	2A	3644	1/1	0.97	0.06	69,69,69,69	0
54	MG	2A	3648	1/1	0.97	0.06	66,66,66,66	0
54	MG	2A	3649	1/1	0.97	0.05	56,56,56,56	0
54	MG	1A	3260	1/1	0.97	0.07	29,29,29,29	0
54	MG	1A	3741	1/1	0.97	0.12	38,38,38,38	0
54	MG	1A	3816	1/1	0.97	0.27	30,30,30,30	0
54	MG	2a	3012	1/1	0.97	0.07	51,51,51,51	0
54	MG	1A	3083	1/1	0.97	0.34	39,39,39,39	0
54	MG	1A	3369	1/1	0.97	0.05	28,28,28,28	0
54	MG	2A	3059	1/1	0.97	0.10	50,50,50,50	0
54	MG	1A	3107	1/1	0.97	0.12	30,30,30,30	0
54	MG	1a	3125	1/1	0.97	0.12	49,49,49,49	0
54	MG	1a	3018	1/1	0.97	0.12	50,50,50,50	0
54	MG	1A	3138	1/1	0.97	0.10	36,36,36,36	0
54	MG	2A	3344	1/1	0.97	0.06	56,56,56,56	0
54	MG	2k	201	1/1	0.97	0.12	56,56,56,56	0
54	MG	1A	3427	1/1	0.97	0.06	38,38,38,38	0
54	MG	2A	3346	1/1	0.97	0.09	42,42,42,42	0
54	MG	1A	3912	1/1	0.97	0.04	48,48,48,48	0
54	MG	1A	3140	1/1	0.97	0.10	40,40,40,40	0
54	MG	1A	3016	1/1	0.97	0.22	36,36,36,36	0
54	MG	2A	3668	1/1	0.97	0.04	22,22,22,22	0
54	MG	1A	3213	1/1	0.97	0.16	30,30,30,30	0
54	MG	1A	3109	1/1	0.97	0.17	46,46,46,46	0
54	MG	1a	3248	1/1	0.97	0.06	50,50,50,50	0
54	MG	1A	3917	1/1	0.97	0.06	62,62,62,62	0
54	MG	2A	3674	1/1	0.97	0.06	62,62,62,62	0
54	MG	2A	3074	1/1	0.97	0.04	26,26,26,26	0
54	MG	1A	3180	1/1	0.97	0.15	36,36,36,36	0
54	MG	2A	3679	1/1	0.97	0.08	49,49,49,49	0
54	MG	1A	4002	1/1	0.97	0.05	63,63,63,63	0
54	MG	1A	3322	1/1	0.97	0.10	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
59	ZN	1n	103	1/1	0.97	0.05	77,77,77,77	0
59	ZN	2Y	501	1/1	0.97	0.06	88,88,88,88	0
54	MG	2A	3507	1/1	0.97	0.06	59,59,59,59	0
59	ZN	2n	501	1/1	0.97	0.07	92,92,92,92	0
60	SF4	2d	501	8/8	0.97	0.06	66,79,83,84	0
54	MG	1A	3964	1/1	0.98	0.09	58,58,58,58	0
54	MG	1A	3050	1/1	0.98	0.17	36,36,36,36	0
54	MG	1A	3520	1/1	0.98	0.04	31,31,31,31	0
54	MG	1A	3715	1/1	0.98	0.05	52,52,52,52	0
54	MG	1A	3159	1/1	0.98	0.12	33,33,33,33	0
54	MG	1A	3018	1/1	0.98	0.16	33,33,33,33	0
54	MG	2A	3731	1/1	0.98	0.04	41,41,41,41	0
54	MG	15	101	1/1	0.98	0.17	36,36,36,36	0
54	MG	2A	3580	1/1	0.98	0.07	59,59,59,59	0
54	MG	1A	3875	1/1	0.98	0.08	44,44,44,44	0
54	MG	1A	3068	1/1	0.98	0.17	33,33,33,33	0
54	MG	1A	3524	1/1	0.98	0.04	29,29,29,29	0
54	MG	1A	3141	1/1	0.98	0.05	31,31,31,31	0
54	MG	1A	3650	1/1	0.98	0.04	24,24,24,24	0
54	MG	2A	3586	1/1	0.98	0.13	49,49,49,49	0
54	MG	1A	3351	1/1	0.98	0.07	27,27,27,27	0
54	MG	1A	3142	1/1	0.98	0.06	38,38,38,38	0
54	MG	1A	3404	1/1	0.98	0.04	40,40,40,40	0
54	MG	1A	3069	1/1	0.98	0.05	41,41,41,41	0
54	MG	2A	3324	1/1	0.98	0.05	48,48,48,48	0
54	MG	2A	3454	1/1	0.98	0.04	57,57,57,57	0
54	MG	2A	3325	1/1	0.98	0.07	51,51,51,51	0
54	MG	2A	3595	1/1	0.98	0.04	50,50,50,50	0
54	MG	1A	3062	1/1	0.98	0.10	31,31,31,31	0
54	MG	1F	301	1/1	0.98	0.07	31,31,31,31	0
54	MG	1F	302	1/1	0.98	0.11	35,35,35,35	0
54	MG	1A	3126	1/1	0.98	0.06	35,35,35,35	0
54	MG	1A	3219	1/1	0.98	0.14	39,39,39,39	0
54	MG	2A	3602	1/1	0.98	0.05	64,64,64,64	0
54	MG	1A	3887	1/1	0.98	0.04	33,33,33,33	0
54	MG	1F	306	1/1	0.98	0.16	33,33,33,33	0
54	MG	1A	3410	1/1	0.98	0.05	29,29,29,29	0
54	MG	2A	3334	1/1	0.98	0.10	34,34,34,34	0
54	MG	1A	3893	1/1	0.98	0.07	39,39,39,39	0
54	MG	1A	3307	1/1	0.98	0.14	34,34,34,34	0
54	MG	2A	3103	1/1	0.98	0.06	44,44,44,44	0
54	MG	1A	3661	1/1	0.98	0.09	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3896	1/1	0.98	0.05	54,54,54,54	0
54	MG	1A	3111	1/1	0.98	0.13	32,32,32,32	0
54	MG	1A	3808	1/1	0.98	0.07	47,47,47,47	0
54	MG	1A	3809	1/1	0.98	0.08	50,50,50,50	0
54	MG	1A	3112	1/1	0.98	0.11	40,40,40,40	0
54	MG	2A	3110	1/1	0.98	0.05	31,31,31,31	0
54	MG	1A	3734	1/1	0.98	0.07	42,42,42,42	0
54	MG	1A	3194	1/1	0.98	0.13	39,39,39,39	0
54	MG	1a	3204	1/1	0.98	0.04	71,71,71,71	0
54	MG	1A	3264	1/1	0.98	0.17	33,33,33,33	0
54	MG	2A	3004	1/1	0.98	0.04	39,39,39,39	0
54	MG	1A	3539	1/1	0.98	0.06	31,31,31,31	0
54	MG	2E	305	1/1	0.98	0.13	39,39,39,39	0
54	MG	1A	3223	1/1	0.98	0.20	38,38,38,38	0
54	MG	1A	3052	1/1	0.98	0.25	36,36,36,36	0
54	MG	1a	3012	1/1	0.98	0.13	30,30,30,30	0
54	MG	1a	3210	1/1	0.98	0.08	65,65,65,65	0
54	MG	1A	3740	1/1	0.98	0.03	22,22,22,22	0
54	MG	1A	3365	1/1	0.98	0.07	32,32,32,32	0
54	MG	1A	3910	1/1	0.98	0.05	39,39,39,39	0
54	MG	1A	3268	1/1	0.98	0.18	53,53,53,53	0
54	MG	2A	3015	1/1	0.98	0.18	36,36,36,36	0
54	MG	1A	3367	1/1	0.98	0.08	49,49,49,49	0
54	MG	1A	3672	1/1	0.98	0.04	61,61,61,61	0
54	MG	1A	3101	1/1	0.98	0.27	34,34,34,34	0
54	MG	1A	3746	1/1	0.98	0.14	46,46,46,46	0
54	MG	2P	204	1/1	0.98	0.04	61,61,61,61	0
54	MG	1a	3219	1/1	0.98	0.08	50,50,50,50	0
54	MG	1a	3021	1/1	0.98	0.04	52,52,52,52	0
54	MG	1P	201	1/1	0.98	0.21	32,32,32,32	0
54	MG	1A	3171	1/1	0.98	0.15	29,29,29,29	0
54	MG	1P	203	1/1	0.98	0.10	32,32,32,32	0
54	MG	2A	3642	1/1	0.98	0.04	48,48,48,48	0
54	MG	2A	3246	1/1	0.98	0.36	38,38,38,38	0
54	MG	2A	3645	1/1	0.98	0.05	56,56,56,56	0
54	MG	2A	3646	1/1	0.98	0.07	41,41,41,41	0
54	MG	2A	3247	1/1	0.98	0.23	41,41,41,41	0
54	MG	2A	3374	1/1	0.98	0.09	62,62,62,62	0
54	MG	1A	3675	1/1	0.98	0.09	26,26,26,26	0
54	MG	2A	3376	1/1	0.98	0.07	48,48,48,48	0
54	MG	1A	3826	1/1	0.98	0.05	53,53,53,53	0
54	MG	2A	3250	1/1	0.98	0.19	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3676	1/1	0.98	0.07	48,48,48,48	0
54	MG	2A	3380	1/1	0.98	0.04	71,71,71,71	0
54	MG	1A	3423	1/1	0.98	0.04	15,15,15,15	0
54	MG	1A	3317	1/1	0.98	0.06	24,24,24,24	0
54	MG	2a	3147	1/1	0.98	0.10	53,53,53,53	0
54	MG	2a	3148	1/1	0.98	0.09	71,71,71,71	0
54	MG	1A	3150	1/1	0.98	0.25	33,33,33,33	0
54	MG	1A	3487	1/1	0.98	0.07	23,23,23,23	0
54	MG	1A	3229	1/1	0.98	0.18	31,31,31,31	0
54	MG	1A	3230	1/1	0.98	0.21	38,38,38,38	0
54	MG	2A	3663	1/1	0.98	0.12	42,42,42,42	0
54	MG	1A	3274	1/1	0.98	0.05	35,35,35,35	0
54	MG	1a	3234	1/1	0.98	0.10	68,68,68,68	0
54	MG	2A	3147	1/1	0.98	0.14	37,37,37,37	0
54	MG	2A	3261	1/1	0.98	0.15	43,43,43,43	0
54	MG	1A	3929	1/1	0.98	0.05	63,63,63,63	0
54	MG	1A	3115	1/1	0.98	0.14	28,28,28,28	0
54	MG	2A	3670	1/1	0.98	0.04	56,56,56,56	0
54	MG	1A	3276	1/1	0.98	0.05	30,30,30,30	0
54	MG	1A	3493	1/1	0.98	0.07	46,46,46,46	0
54	MG	2A	3395	1/1	0.98	0.11	43,43,43,43	0
54	MG	1A	3233	1/1	0.98	0.15	37,37,37,37	0
54	MG	1A	3934	1/1	0.98	0.05	58,58,58,58	0
54	MG	2A	3043	1/1	0.98	0.03	22,22,22,22	0
54	MG	1A	3840	1/1	0.98	0.05	45,45,45,45	0
54	MG	2a	3016	1/1	0.98	0.11	49,49,49,49	0
54	MG	1A	3234	1/1	0.98	0.19	36,36,36,36	0
54	MG	1A	3235	1/1	0.98	0.24	28,28,28,28	0
54	MG	1A	3236	1/1	0.98	0.14	24,24,24,24	0
54	MG	1A	3116	1/1	0.98	0.21	35,35,35,35	0
54	MG	1A	3438	1/1	0.98	0.03	30,30,30,30	0
54	MG	1A	3133	1/1	0.98	0.23	31,31,31,31	0
54	MG	2A	3535	1/1	0.98	0.09	44,44,44,44	0
54	MG	1A	3332	1/1	0.98	0.10	32,32,32,32	0
54	MG	2A	3537	1/1	0.98	0.04	60,60,60,60	0
54	MG	1A	3384	1/1	0.98	0.09	43,43,43,43	0
54	MG	1A	3202	1/1	0.98	0.17	36,36,36,36	0
54	MG	1A	3176	1/1	0.98	0.08	28,28,28,28	0
54	MG	2a	3184	1/1	0.98	0.05	63,63,63,63	0
54	MG	1A	3242	1/1	0.98	0.25	33,33,33,33	0
54	MG	1A	3852	1/1	0.98	0.04	44,44,44,44	0
54	MG	1A	3445	1/1	0.98	0.08	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3702	1/1	0.98	0.18	42,42,42,42	0
54	MG	1A	3177	1/1	0.98	0.09	33,33,33,33	0
54	MG	2A	3697	1/1	0.98	0.07	46,46,46,46	0
54	MG	1A	3287	1/1	0.98	0.09	23,23,23,23	0
54	MG	1B	222	1/1	0.98	0.04	55,55,55,55	0
54	MG	1A	3005	1/1	0.98	0.09	23,23,23,23	0
54	MG	1A	3778	1/1	0.98	0.06	28,28,28,28	0
54	MG	1A	3859	1/1	0.98	0.10	33,33,33,33	0
54	MG	2A	3292	1/1	0.98	0.07	56,56,56,56	0
54	MG	2A	3552	1/1	0.98	0.09	32,32,32,32	0
54	MG	2A	3554	1/1	0.98	0.04	22,22,22,22	0
54	MG	1A	3091	1/1	0.98	0.05	37,37,37,37	0
54	MG	2A	3294	1/1	0.98	0.08	38,38,38,38	0
54	MG	1A	3291	1/1	0.98	0.09	33,33,33,33	0
54	MG	1A	3957	1/1	0.98	0.07	49,49,49,49	0
54	MG	1A	3007	1/1	0.98	0.08	38,38,38,38	0
54	MG	2A	3298	1/1	0.98	0.12	45,45,45,45	0
54	MG	1A	3452	1/1	0.98	0.06	60,60,60,60	0
54	MG	2A	3713	1/1	0.98	0.04	55,55,55,55	0
54	MG	1A	3293	1/1	0.98	0.10	42,42,42,42	0
54	MG	1a	3268	1/1	0.98	0.06	61,61,61,61	0
54	MG	2A	3716	1/1	0.98	0.04	76,76,76,76	0
54	MG	2A	3072	1/1	0.98	0.19	38,38,38,38	0
54	MG	2A	3431	1/1	0.98	0.07	39,39,39,39	0
54	MG	2A	3073	1/1	0.98	0.07	46,46,46,46	0
54	MG	2A	3567	1/1	0.98	0.05	50,50,50,50	0
54	MG	1A	3181	1/1	0.98	0.15	35,35,35,35	0
54	MG	1A	3786	1/1	0.98	0.04	68,68,68,68	0
59	ZN	26	501	1/1	0.98	0.04	60,60,60,60	0
59	ZN	29	501	1/1	0.98	0.05	68,68,68,68	0
54	MG	2A	3306	1/1	0.98	0.07	31,31,31,31	0
60	SF4	1d	305	8/8	0.98	0.06	60,63,70,73	0
54	MG	1A	3157	1/1	0.98	0.24	31,31,31,31	0
54	MG	1A	3303	1/1	0.99	0.07	17,17,17,17	0
54	MG	2a	3137	1/1	0.99	0.10	63,63,63,63	0
54	MG	1a	3135	1/1	0.99	0.09	44,44,44,44	0
54	MG	2A	3553	1/1	0.99	0.05	64,64,64,64	0
54	MG	1A	3353	1/1	0.99	0.03	24,24,24,24	0
54	MG	1F	310	1/1	0.99	0.11	35,35,35,35	0
54	MG	1A	3678	1/1	0.99	0.04	44,44,44,44	0
54	MG	1A	3927	1/1	0.99	0.06	43,43,43,43	0
54	MG	1A	3504	1/1	0.99	0.05	19,19,19,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3505	1/1	0.99	0.07	23,23,23,23	0
54	MG	1A	3837	1/1	0.99	0.06	25,25,25,25	0
54	MG	1A	3327	1/1	0.99	0.04	21,21,21,21	0
54	MG	2A	3491	1/1	0.99	0.06	45,45,45,45	0
54	MG	1A	3240	1/1	0.99	0.18	33,33,33,33	0
54	MG	1A	3105	1/1	0.99	0.14	34,34,34,34	0
54	MG	1A	3224	1/1	0.99	0.14	36,36,36,36	0
54	MG	1A	3331	1/1	0.99	0.08	38,38,38,38	0
54	MG	1A	3762	1/1	0.99	0.04	43,43,43,43	0
54	MG	2A	3643	1/1	0.99	0.03	66,66,66,66	0
54	MG	1A	3009	1/1	0.99	0.08	30,30,30,30	0
54	MG	2A	3030	1/1	0.99	0.07	37,37,37,37	0
54	MG	1A	3888	1/1	0.99	0.03	50,50,50,50	0
54	MG	2A	3647	1/1	0.99	0.07	42,42,42,42	0
54	MG	2A	3571	1/1	0.99	0.04	51,51,51,51	0
54	MG	1A	3889	1/1	0.99	0.09	48,48,48,48	0
54	MG	1a	3274	1/1	0.99	0.05	61,61,61,61	0
54	MG	1a	3152	1/1	0.99	0.04	61,61,61,61	0
54	MG	1A	3006	1/1	0.99	0.03	25,25,25,25	0
54	MG	2A	3366	1/1	0.99	0.06	42,42,42,42	0
54	MG	2A	3654	1/1	0.99	0.12	53,53,53,53	0
54	MG	1A	3891	1/1	0.99	0.05	51,51,51,51	0
54	MG	2a	3167	1/1	0.99	0.05	66,66,66,66	0
54	MG	1A	3892	1/1	0.99	0.07	33,33,33,33	0
54	MG	1A	3334	1/1	0.99	0.04	22,22,22,22	0
54	MG	1A	3265	1/1	0.99	0.23	28,28,28,28	0
54	MG	1A	3041	1/1	0.99	0.09	17,17,17,17	0
54	MG	1A	3288	1/1	0.99	0.10	17,17,17,17	0
54	MG	1A	3655	1/1	0.99	0.04	46,46,46,46	0
54	MG	1A	3042	1/1	0.99	0.13	30,30,30,30	0
54	MG	15	105	1/1	0.99	0.10	26,26,26,26	0
54	MG	1A	3043	1/1	0.99	0.15	34,34,34,34	0
54	MG	2a	3177	1/1	0.99	0.05	68,68,68,68	0
54	MG	1D	303	1/1	0.99	0.17	38,38,38,38	0
54	MG	1A	3695	1/1	0.99	0.03	41,41,41,41	0
54	MG	2A	3589	1/1	0.99	0.08	39,39,39,39	0
54	MG	1A	3139	1/1	0.99	0.11	27,27,27,27	0
54	MG	2a	3182	1/1	0.99	0.05	61,61,61,61	0
54	MG	1Q	201	1/1	0.99	0.06	43,43,43,43	0
54	MG	1D	306	1/1	0.99	0.06	15,15,15,15	0
54	MG	1A	3902	1/1	0.99	0.03	52,52,52,52	0
54	MG	1A	3231	1/1	0.99	0.17	33,33,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	1A	3025	1/1	0.99	0.21	34,34,34,34	0
54	MG	1A	3045	1/1	0.99	0.06	23,23,23,23	0
54	MG	2A	3675	1/1	0.99	0.04	42,42,42,42	0
54	MG	1A	3100	1/1	0.99	0.11	32,32,32,32	0
54	MG	1A	3253	1/1	0.99	0.20	26,26,26,26	0
54	MG	2A	3678	1/1	0.99	0.07	61,61,61,61	0
54	MG	1A	3013	1/1	0.99	0.07	22,22,22,22	0
54	MG	2A	3600	1/1	0.99	0.03	40,40,40,40	0
54	MG	1A	3080	1/1	0.99	0.22	33,33,33,33	0
54	MG	1A	3071	1/1	0.99	0.12	33,33,33,33	0
54	MG	1A	3117	1/1	0.99	0.05	21,21,21,21	0
54	MG	1A	3258	1/1	0.99	0.17	35,35,35,35	0
54	MG	1E	303	1/1	0.99	0.10	30,30,30,30	0
54	MG	1A	3784	1/1	0.99	0.09	44,44,44,44	0
54	MG	1A	3463	1/1	0.99	0.03	56,56,56,56	0
54	MG	1E	306	1/1	0.99	0.02	34,34,34,34	0
54	MG	2A	3609	1/1	0.99	0.08	49,49,49,49	0
54	MG	1A	3867	1/1	0.99	0.04	51,51,51,51	0
54	MG	1A	3464	1/1	0.99	0.08	33,33,33,33	0
54	MG	2A	3262	1/1	0.99	0.07	40,40,40,40	0
54	MG	1A	3869	1/1	0.99	0.05	31,31,31,31	0
54	MG	1A	3433	1/1	0.99	0.03	13,13,13,13	0
54	MG	1A	3969	1/1	0.99	0.05	33,33,33,33	0
54	MG	2A	3266	1/1	0.99	0.07	22,22,22,22	0
54	MG	1A	3092	1/1	0.99	0.02	14,14,14,14	0
59	ZN	1Y	501	1/1	0.99	0.04	63,63,63,63	0
54	MG	1V	202	1/1	0.99	0.10	32,32,32,32	0
59	ZN	15	110	1/1	0.99	0.03	44,44,44,44	0
54	MG	2A	3137	1/1	0.99	0.07	36,36,36,36	0
54	MG	1A	3406	1/1	0.99	0.02	26,26,26,26	0
54	MG	1A	3921	1/1	0.99	0.06	54,54,54,54	0
59	ZN	25	103	1/1	0.99	0.03	63,63,63,63	0
54	MG	2A	3011	1/1	0.99	0.05	36,36,36,36	0
54	MG	1A	3436	1/1	0.99	0.04	46,46,46,46	0
54	MG	1A	3639	1/1	0.99	0.11	33,33,33,33	0
54	MG	2a	3134	1/1	0.99	0.05	63,63,63,63	0
54	MG	2A	3480	1/1	0.99	0.05	47,47,47,47	0
54	MG	2A	3365	1/1	1.00	0.05	36,36,36,36	0
59	ZN	16	501	1/1	1.00	0.06	42,42,42,42	0
59	ZN	19	103	1/1	1.00	0.04	42,42,42,42	0
54	MG	1A	3614	1/1	1.00	0.11	32,32,32,32	0
54	MG	1A	3470	1/1	1.00	0.07	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
54	MG	2A	3361	1/1	1.00	0.07	43,43,43,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.