Full wwPDB EM Validation Report (i)

Sep 19, 2026 – 11:38 AM JST

PDB ID	:	7D80 / pdb_00007d80
EMDB ID	:	EMD-30611
Title	:	Molecular model of the cryo-EM structure of 70S ribosome in complex with peptide deformylase, trigger factor, and methionine aminopeptidase
Authors	:	Akbar, S.; Bhakta, S.; Sengupta, J.
Deposited on	:	2020-10-06
Resolution	:	4.10 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

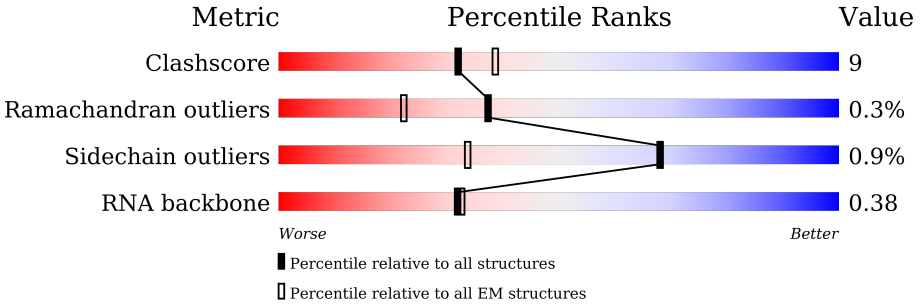
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

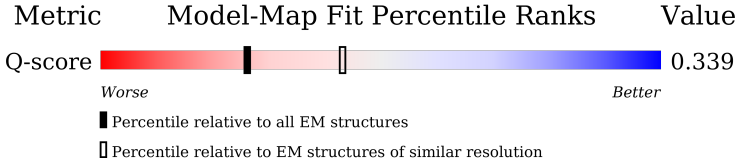
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.10 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)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	6458 (3.60 - 4.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	46	78% 22%
2	1	65	75% 18% • • •
3	2	38	61% 37% •

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Mol	Chain	Length	Quality of chain
4	3	169	71% 28%
5	5	432	28% 88% 12%
6	6	57	84% 14%
7	A	2903	56% 37% 7%
8	B	1539	49% 41% 9%
9	C	241	75% 16% 10%
10	D	233	65% 22% 12%
11	E	206	63% 37%
12	F	167	66% 24% 10%
13	G	135	54% 20% 26%
14	H	179	60% 24% 16%
15	I	130	66% 33%
16	J	130	65% 32%
17	K	103	68% 26% 5%
18	L	129	69% 22% 9%
19	M	124	73% 26%
20	N	118	67% 28%
21	O	101	57% 38% 5%
22	P	89	78% 21%
23	Q	82	72% 27%
24	R	84	52% 42% 5%
25	S	75	52% 21% 27%
26	T	92	67% 18% 14%
27	U	87	64% 31%
28	V	71	54% 17% 28%

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Mol	Chain	Length	Quality of chain
29	W	100	72% 22%
30	X	73	29% 36% 25% 11%
31	Z	76	32% 42% 34% 11% 13%
32	a	118	64% 35%
33	b	273	71% 27%
34	c	209	78% 21%
35	d	201	84% 16%
36	e	179	63% 36%
37	f	177	81% 17%
38	g	149	26% 6% 68%
39	h	142	10% 77% 22%
40	i	142	81% 18%
41	j	123	72% 27%
42	k	144	83% 15%
43	l	136	81% 18%
44	m	127	76% 19% 6%
45	n	117	83% 16%
46	o	115	77% 23%
47	p	118	78% 21%
48	q	103	83% 17%
49	r	110	81% 18%
50	s	104	78% 17%
51	t	94	86% 13%
52	u	85	81% 7% 12%
53	v	78	74% 24%

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Mol	Chain	Length	Quality of chain
54	w	63	78% 22%
55	x	59	85% 14%
56	y	77	45% 39% 6% 9%
57	z	55	73% 18% 9%

2 Entry composition (i)

There are 57 unique types of molecules in this entry. The entry contains 150808 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	46	377	228	90	57	2	0	0

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	64	504	323	105	74	2	0	0

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	38	302	185	65	48	4	0	0

- Molecule 4 is a protein called Peptide deformylase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	168	1346	844	241	255	6	0	0

- Molecule 5 is a protein called Trigger factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	5	432	3386	2119	582	674	11	0	0

- Molecule 6 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	6	56	444	269	94	80	1	0	0

- Molecule 7 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
7	A	2903	62317	27801	11467	20147	2902	0	0

- Molecule 8 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
8	B	1539	33015	14725	6052	10699	1539	0	0

- Molecule 9 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	C	218	1704	1081	305	311	7	0	0

- Molecule 10 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	D	206	1624	1028	305	288	3	0	0

- Molecule 11 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	E	205	1643	1026	315	298	4	0	0

- Molecule 12 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	F	150	1105	687	211	201	6	0	0

- Molecule 13 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	G	100	817	515	148	148	6	0	0

- Molecule 14 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	H	151	1181	735	227	215	4	0	0

- Molecule 15 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	I	129	979	616	173	184	6	0	0

- Molecule 16 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	J	127	1022	634	206	179	3	0	0

- Molecule 17 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	K	98	786	493	150	142	1	0	0

- Molecule 18 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	L	117	877	540	174	160	3	0	0

- Molecule 19 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	M	123	955	590	196	165	4	0	0

- Molecule 20 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	N	114	883	546	178	156	3	0	0

- Molecule 21 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	O	96	774	483	160	128	3	0	0

- Molecule 22 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	P	88	710	437	143	129	1	0	0

- Molecule 23 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	Q	82	649	406	128	114	1	0	0

- Molecule 24 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	R	80	648	411	121	113	3	0	0

- Molecule 25 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
25	S	55	455	288	86	81	0	0

- Molecule 26 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	T	79	637	408	120	107	2	0	0

- Molecule 27 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	U	85	665	411	137	114	3	0	0

- Molecule 28 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	V	51	425	265	86	73	1	0	0

- Molecule 29 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	W	96	764	484	142	136	2	0	0

- Molecule 30 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
30	X	65	1392	621	258	449	64	0	0

- Molecule 31 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
31	Z	66	1406	629	255	457	65	0	0

- Molecule 32 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
32	a	118	2529	1126	464	821	118	0	0

- Molecule 33 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	b	271	2082	1288	423	364	7	0	0

- Molecule 34 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	c	209	1565	979	288	294	4	0	0

- Molecule 35 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	d	201	1552	974	283	290	5	0	0

- Molecule 36 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	e	177	1410	899	249	256	6	0	0

- Molecule 37 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	f	176	1323	832	243	246	2	0	0

- Molecule 38 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	g	47	359	233	62	63	1	0	0

- Molecule 39 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	h	141	1032	651	179	196	6	0	0

- Molecule 40 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	i	142	1129	714	212	199	4	0	0

- Molecule 41 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	j	122	938	587	180	165	6	0	0

- Molecule 42 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	k	143	1045	649	206	189	1	0	0

- Molecule 43 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	l	136	1074	686	205	177	6	0	0

- Molecule 44 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	m	120	960	593	196	166	5	0	0

- Molecule 45 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
45	n	116	892	552	178	162	0	0

- Molecule 46 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	o	114	917	574	179	163	1	0	0

- Molecule 47 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
47	p	117	947	604	192	151	0	0

- Molecule 48 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	q	103	816	516	153	145	2	0	0

- Molecule 49 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	r	110	857	532	166	156	3	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
50	s	102	779	492	146	141	0	0

- Molecule 51 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	t	94	753	479	137	134	3	0	0

- Molecule 52 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	u	75	569	353	113	102	1	0	0

- Molecule 53 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	v	77	625	388	129	106	2	0	0

- Molecule 54 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	w	63	509	313	99	95	2	0	0

- Molecule 55 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	x	58	449	281	87	79	2	0	0

- Molecule 56 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
56	y	70	1496	665	267	494	70	0	0

- Molecule 57 is a protein called 50S ribosomal protein L33.

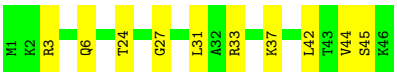
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
57	z	50	409	263	75	71	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

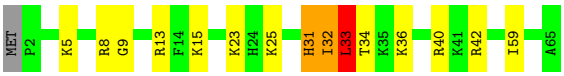
- Molecule 1: 50S ribosomal protein L34

Chain 0:



- Molecule 2: 50S ribosomal protein L35

Chain 1:

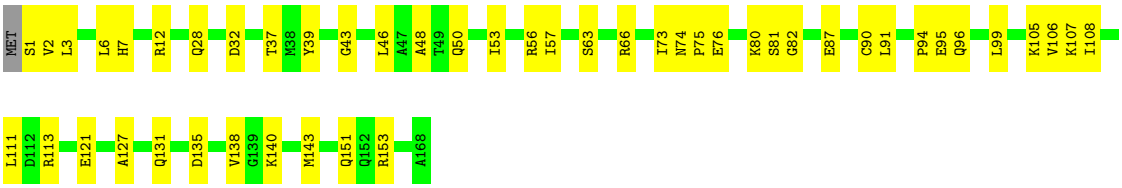


- Molecule 3: 50S ribosomal protein L36

Chain 2:

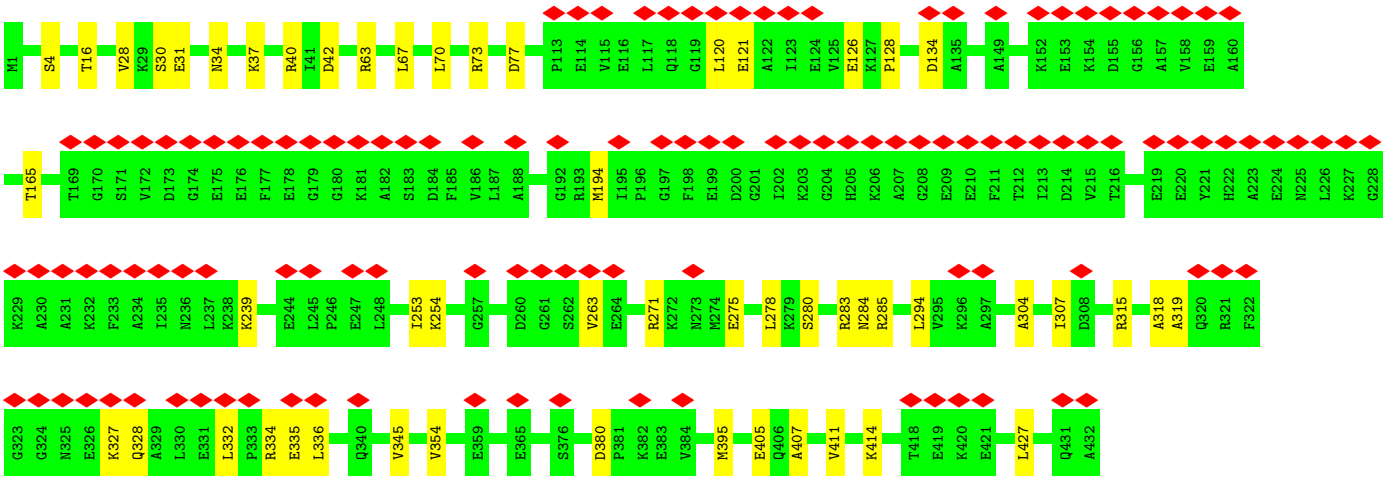
- Molecule 4: Peptide deformylase

Chain 3:



- Molecule 5: Trigger factor

Chain 5:

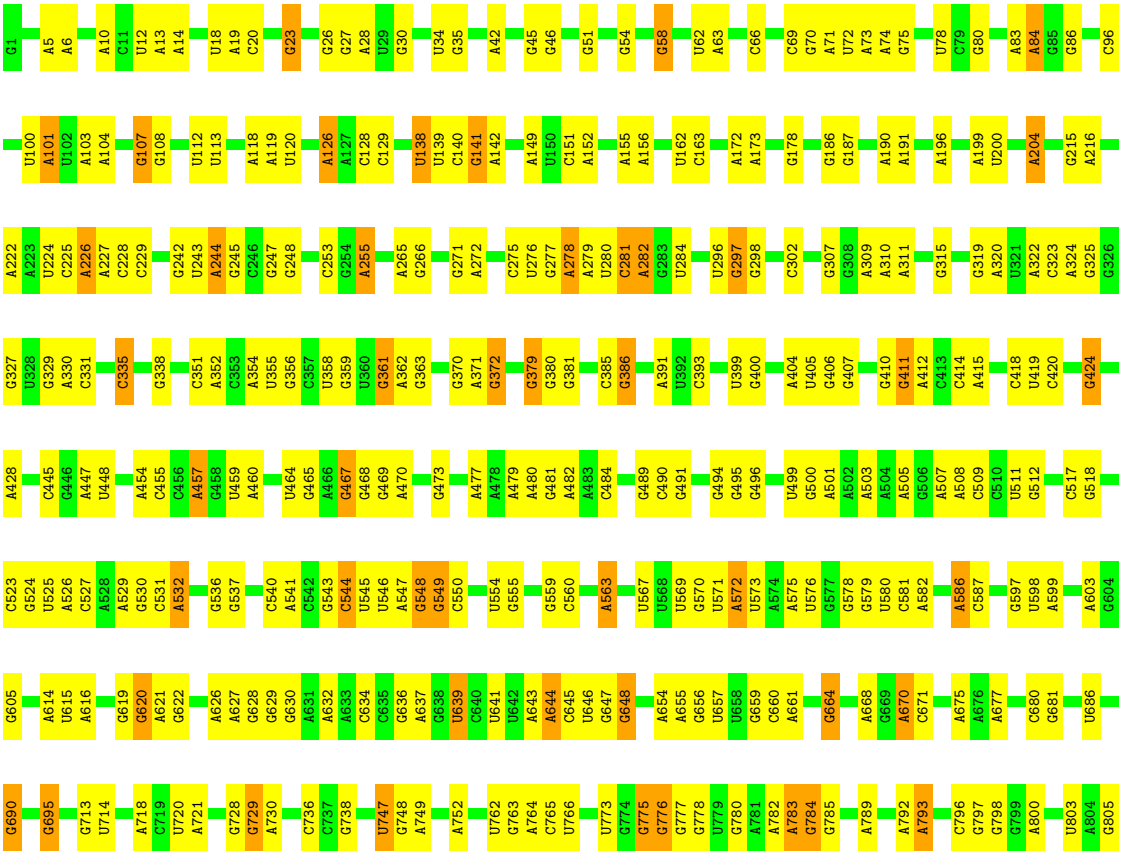


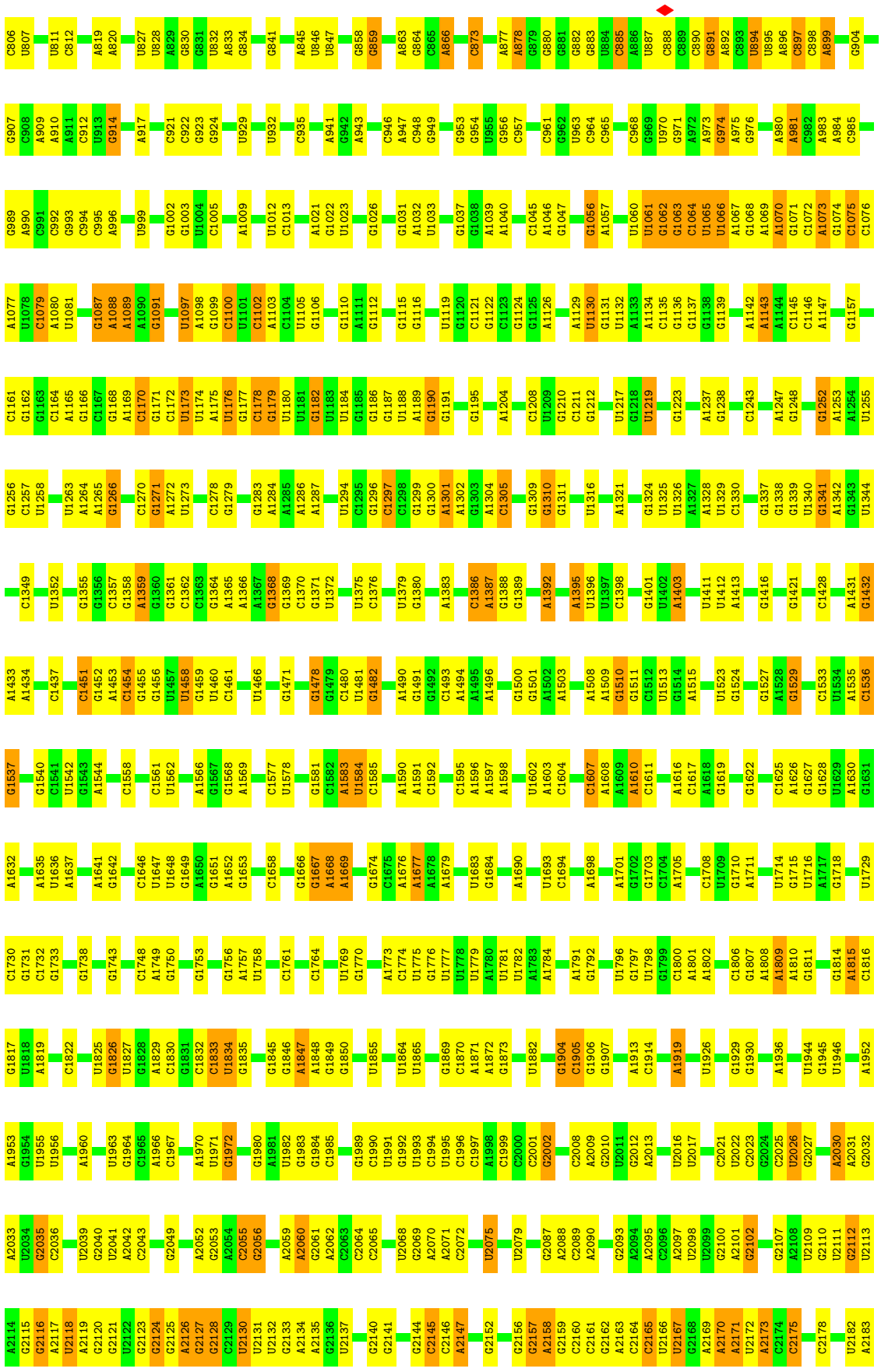
- Molecule 6: 50S ribosomal protein L32

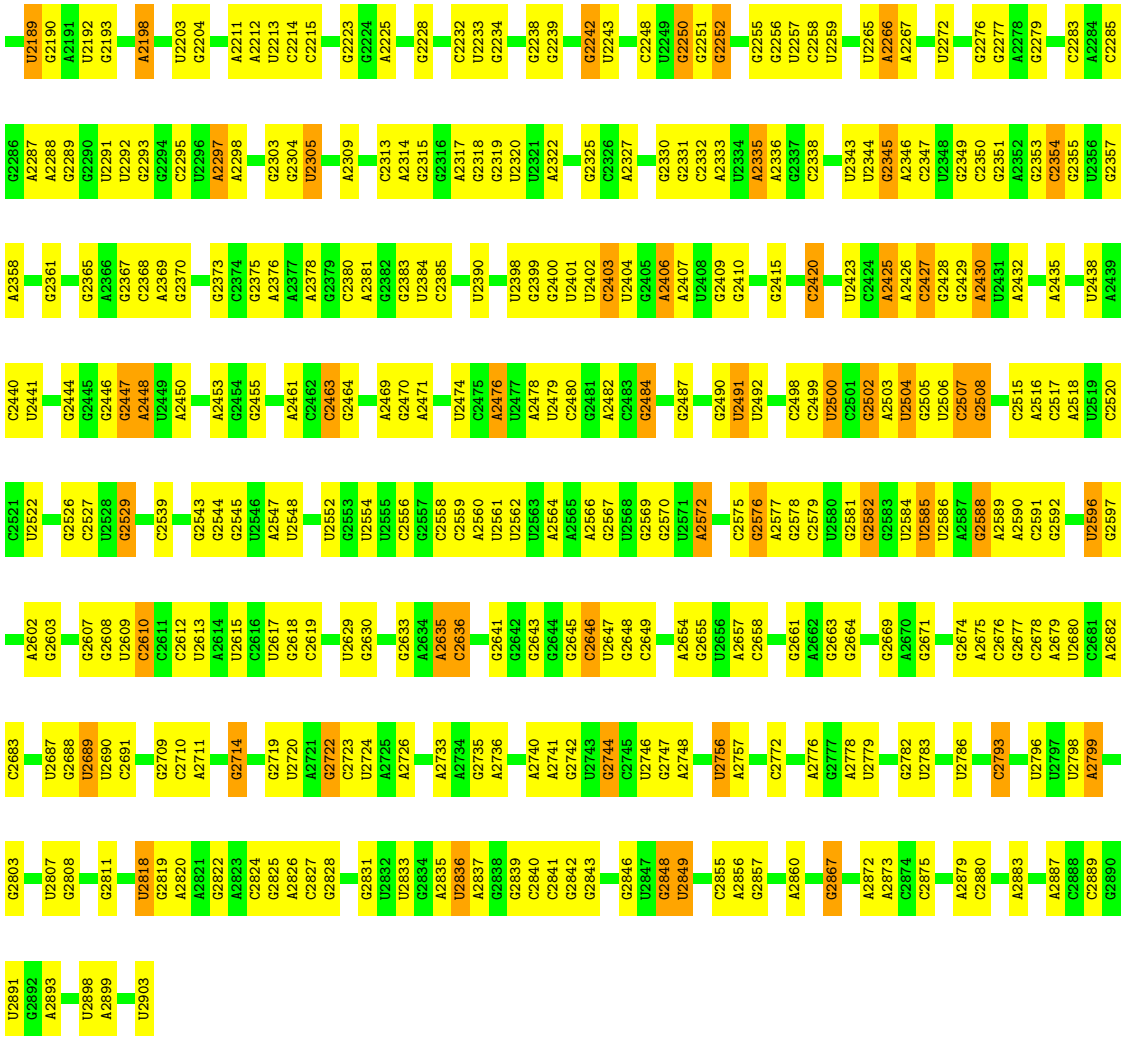
Chain 6:

- Molecule 7: 23S ribosomal RNA

Chain A:

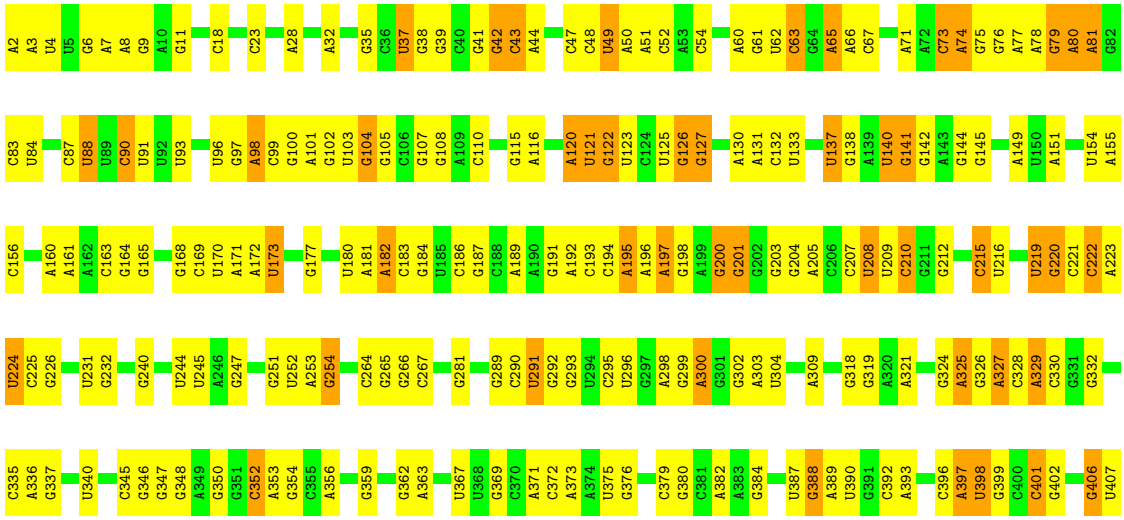


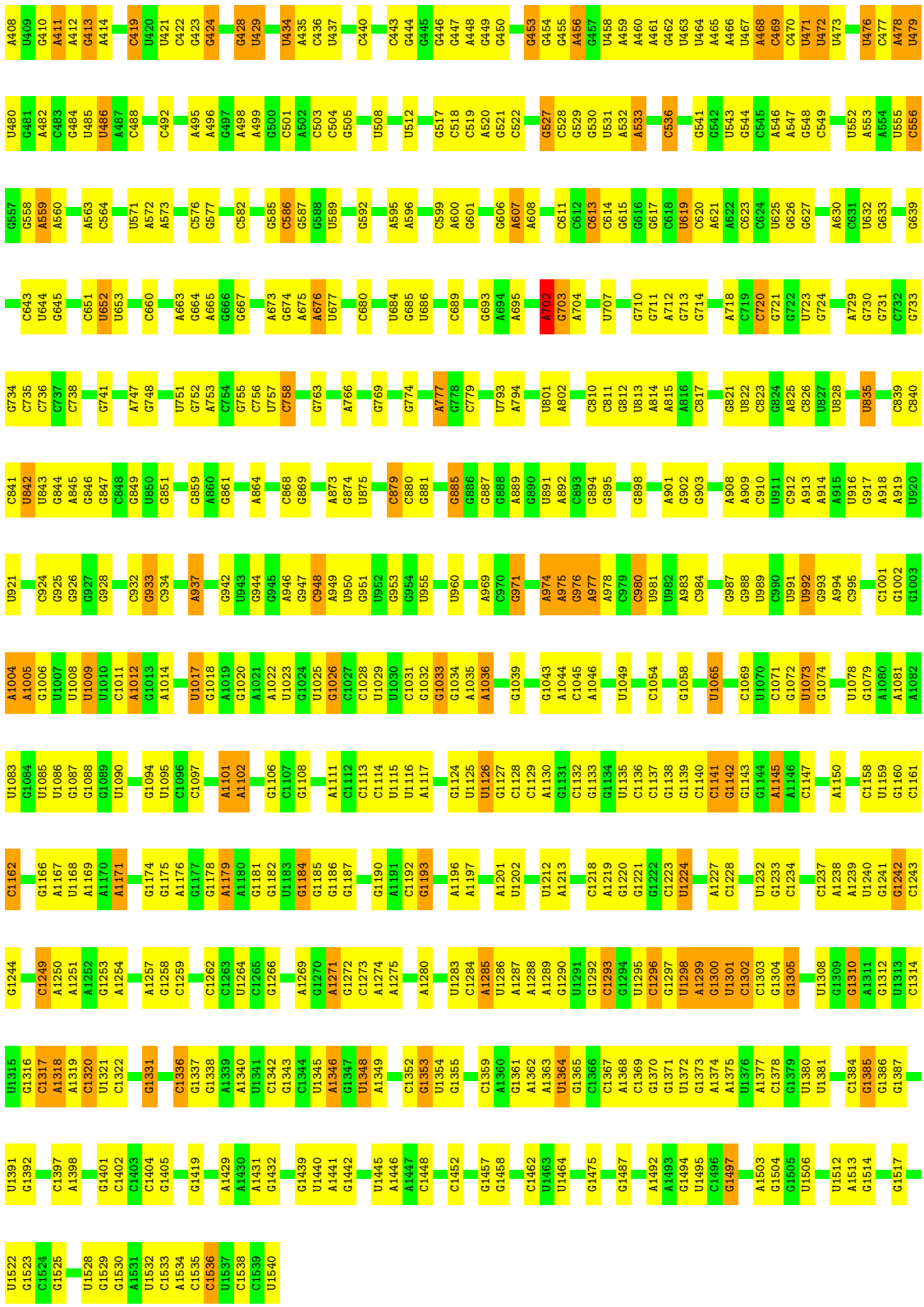

A2114 G2115 G2116 A2117 U2118 A2119 G2120 G2121 U2122 G2123 G2124 G2125 A2126 G2127 G2128 C2129 U2130 U2131 U2132 G2133 A2134 A2135 G2136 U2137 G2140 G2141 G2144 G2145 C2146 A2147 G2152 G2156 G2157 A2158 G2159 C2160 C2161 G2162 A2163 C2164 C2165 U2166 U2167 G2168 A2169 A2170 A2171 U2172 A2173 C2174 C2175 C2178 U2182 A2183
A2033 U2034 G2035 C2036 U2039 G2040 U2041 A2042 C2043 G2049 A2052 G2053 A2054 C2055 G2056 A2059 A2060 G2061 A2062 C2063 C2064 C2065 U2068 G2069 A2070 A2071 C2072 U2075 U2079 G2087 A2088 C2089 A2090 G2093 A2094 A2095 C2096 A2097 U2098 U2099 G2100 A2101 G2102 G2107 A2108 U2109 G2110 U2111 G2112 U2113
A1953 G1954 U1955 U1956 A1960 U1963 G1964 C1965 A1966 C1967 A1970 U1971 G1972 G1980 A1981 U1982 G1983 G1984 C1985 G1989 C1990 U1991 U1992 G1993 U1993 C1994 U1995 C1996 C1997 A1998 C1999 C2000 C2001 G2002 C2008 A2009 G2010 U2011 G2012 A2013 U2016 U2017 C2021 U2022 C2023 G2024 C2025 U2026 G2027 A2030 A2031 G2032
G1817 U1818 A1819 C1822 U1825 G1826 U1827 G1828 A1829 C1830 G1831 C1832 C1833 U1834 G1835 G1845 G1846 A1847 A1848 G1849 G1850 U1855 U1864 U1865 G1869 C1870 A1871 A1872 G1873 U1882 G1904 C1905 G1906 G1907 A1913 C1914 A1919 U1926 G1929 G1930 A1936 U1944 G1945 U1946 A1952
C1730 G1731 C1732 G1733 G1738 G1743 C1748 A1749 G1750 G1753 G1756 A1757 U1758 C1761 C1764 U1769 G1770 A1773 C1774 U1775 G1776 U1777 U1778 U1779 A1780 U1781 U1782 A1783 A1784 A1791 G1792 U1796 G1797 U1798 G1799 C1800 A1801 A1802 C1806 G1807 A1808 A1809 A1810 G1811 G1814 A1815 C1816
A1632 A1635 U1636 A1637 A1641 G1642 C1646 U1647 U1648 G1649 A1650 G1651 A1652 G1653 C1658 G1666 G1667 A1668 A1669 G1674 C1675 A1676 A1677 A1678 A1679 U1683 G1684 A1690 U1693 C1694 A1698 A1701 G1702 G1703 C1704 A1705 C1708 U1709 G1710 A1711 U1714 G1715 U1716 A1717 G1718 U1729
G1537 G1540 C1541 U1542 G1543 A1544 C1558 C1561 U1562 A1566 G1567 G1568 A1569 C1577 U1578 G1581 C1582 A1583 U1584 C1585 A1590 A1591 C1592 C1595 A1596 A1597 A1598 U1602 A1603 C1604 C1607 A1608 A1609 A1610 C1611 A1616 C1617 A1618 G1619 G1622 C1625 A1626 G1627 G1628 U1629 A1630 G1631
A1433 A1434 C1437 C1451 G1452 A1453 C1454 G1455 G1456 U1457 U1458 G1459 U1460 C1461 U1466 G1471 G1478 G1479 C1480 U1481 G1482 A1490 G1491 C1492 C1493 A1494 A1495 A1496 C1500 G1501 A1502 A1503 A1508 A1509 G1510 G1511 C1512 U1513 G1514 A1515 U1523 G1524 G1527 A1528 G1529 C1533 U1534 A1535 C1536
C1349 U1352 G1355 G1356 C1357 G1358 A1359 G1360 G1361 C1362 C1363 G1364 A1365 A1366 A1367 G1368 G1369 C1370 G1371 U1372 U1375 C1376 U1379 G1380 A1383 C1386 A1387 G1388 G1389 A1392 A1395 U1396 U1397 C1398 G1401 U1402 A1403 U1411 U1412 A1413 G1416 G1421 C1428 A1431 G1432
U1256 C1257 U1258 U1263 A1264 A1265 G1266 C1270 G1271 A1272 U1273 C1278 G1279 G1283 A1284 A1285 A1286 A1287 U1294 C1295 G1296 C1297 C1298 G1299 G1300 A1301 A1302 C1303 A1304 C1305 G1309 G1310 G1311 U1316 A1321 G1324 U1325 U1326 A1327 A1328 U1329 C1330 G1337 G1338 G1339 U1340 G1341 A1342 G1343 U1344
C1161 G1162 G1163 C1164 A1165 G1166 C1167 G1168 A1169 C1170 G1171 C1172 U1173 U1174 A1175 U1176 G1177 C1178 G1179 U1180 U1181 G1182 U1183 U1184 G1185 G1186 G1187 U1188 A1189 G1190 G1191 G1195 A1204 C1208 U1209 G1210 C1211 G1212 U1217 G1218 U1219 G1223 A1237 G1238 C1243 A1247 G1248 G1252 A1253 A1254 U1255
A1077 U1078 C1079 A1080 U1081 G1087 A1088 A1089 A1090 G1091 U1097 A1098 G1099 C1100 U1101 C1102 A1103 C1104 U1105 G1106 G1110 A1111 G1112 G1115 G1116 U1119 G1120 C1121 G1122 C1123 C1124 G1125 A1126 A1129 U1130 G1131 U1132 A1133 A1134 C1135 G1136 G1137 G1138 G1139 A1142 A1143 A1144 C1145 C1146 A1147 G1157
G989 A990 C991 C992 G993 C994 C995 A996 U999 G1002 G1003 U1004 C1005 A1009 U1012 C1013 A1021 G1022 U1023 G1026 G1031 A1032 U1033 G1037 G1038 A1039 A1040 C1045 A1046 G1047 G1056 A1057 U1060 U1061 G1062 G1063 C1064 U1065 U1066 A1067 G1068 A1069 A1070 G1071 C1072 A1073 G1074 C1075 C1076
G907 C908 A909 A910 A911 C912 U913 G914 A917 C921 C922 G923 G924 U929 U932 C935 A941 G942 A943 C946 A947 C948 G949 G953 G954 U955 G956 C957 C961 G962 U963 C964 C965 C968 G969 U970 G971 A972 A973 G974 A975 G976 A980 A981 C982 A983 A984 C985
C806 U807 U811 C812 A819 A820 U827 U828 A829 G830 G831 U832 A833 G834 G841 A845 U846 U847 G858 G859 A863 G864 C865 A866 C873 A877 A878 G879 G880 G881 G882 G883 U884 C885 A886 U887 C888 C889 C890 G891 A892 C893 U894 U895 A896 C897 C898 A899 G904



- Molecule 8: 16S ribosomal RNA

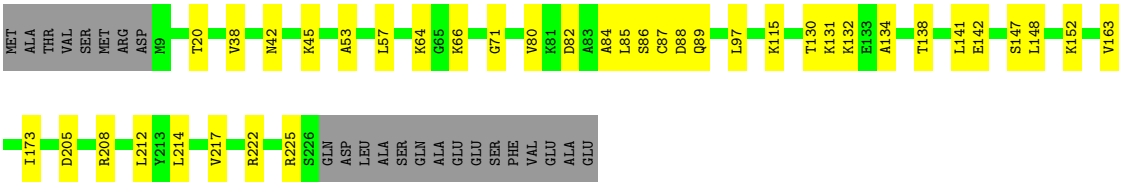
Chain B:





- Molecule 9: 30S ribosomal protein S2

Chain C: 75% 16% 10%



- Molecule 10: 30S ribosomal protein S3

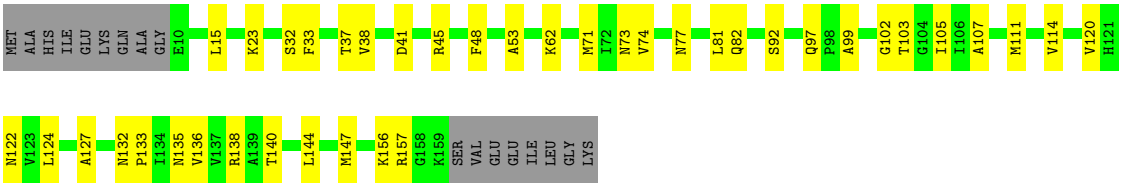
Chain D:

- Molecule 11: 30S ribosomal protein S4

Chain E:

- Molecule 12: 30S ribosomal protein S5

Chain F:



- Molecule 13: 30S ribosomal protein S6, fully modified isoform

Chain G:

ASP ASP PHE ALA ASN GLU THR ALA ASP ASP ALA GLU ALA GLY ASP SER GLU GLU GLU GLU GLU GLU

• Molecule 14: 30S ribosomal protein S7

Chain H: 60% 24% 16%

MET P2 R3 R4 R5 V6 I7 P16 E21 A24 K25 F26 V27 N28 M31 K35 V43 L47 A51 S57 E58 A65 N68 V69 R70 P71 K76 R79 V89 R96 N97 A108 R111 G112 D113 K114 S115 M116 A117 L118 R119 L120 A121

N122 E123 D126 A127 A128 E129 N130 D140 R143 A152 HIS TYR ARG TRP LEU SER LEU ARG SER PHE SER HIS GLN ALA GLY ALA SER SER LYS GLN PRO ALA LEU GLY TYR LEU ASN

• Molecule 15: 30S ribosomal protein S8

Chain I: 66% 33% •

MET S2 M3 Q4 D5 P6 I7 A8 D9 M10 L11 I14 R15 N16 M27 P28 S29 S30 K31 L32 K33 V34 K41 F45 F49 L59 K64 Q67 G68 K69 A70 V71 S74 I75 Q76 R77 R84 K87 R88 A102 V103 V104 S105 D113 R117

E124 I125 I126 C127 Y128 V129 A130

• Molecule 16: 30S ribosomal protein S9

Chain J: 65% 32% • •

MET ALA GLU N4 Q5 Y6 T9 R12 K13 R18 V19 K22 P23 G24 N25 G26 K27 I28 V29 I30 R45 R49 L52 E53 L54 V55 D56 M57 V58 E59 K60 L61 D62 L63 Y64 I65 T66 G74 I83 T84 R85 E89 Y90 D91 R95 L98 G102

R106 D107 K120 A121 R122 R123 R124 P125 Q126 F127 S128 K129 R130

• Molecule 17: 30S ribosomal protein S10

Chain K: 68% 26% • 5%

MET GLN ASN GLN R5 I6 R7 A12 F13 D14 H15 I18 P41 L42 P43 T44 R45 K46 E47 S54 P55 H56 V57 N58 R62 D63 Q64 Y65 E66 T69 H70 L71 R72 T80 T83 V84 D85 M88 R89 L102 GLY

• Molecule 18: 30S ribosomal protein S11

Chain L: 69% 22% 9%

MET ALA LYS ALA PRO ILE ARG ALA ARG LYS ARG VAL R13 S17 V20 A21 H22 I23 V32 T33 N40 W44 R53 G54 S55 S58 E76 I79 E83 V84 M85 V86 K87 R93 N101 R106 I107 D112 V113 P117 R122 K126 R127

R128 V129

• Molecule 19: 30S ribosomal protein S12

Chain M: 73% 26%

MET A2 N5 R12 A23 L24 C27 P28 Q29 K30 R36 V37 N46 R50 K51 V52 Y66 I67 E70 G71 E76 H77 L81 I82 R83 R86 Y95 H96 T97 V98 R99 G106 V107 K108 D109 R110 S115 V119 A124

• Molecule 20: 30S ribosomal protein S13

Chain N: 67% 28%

MET A2 R3 I4 N8 D11 H12 A15 V16 I17 A18 L19 I22 Y23 S30 L34 D42 I45 E50 I53 V65 E66 G67 D68 L69 E72 S76 R79 L80 M81 R87 G88 L89 R90 H91 R92 R93 V97 N105 R109 P115

ILE LYS LYS

• Molecule 21: 30S ribosomal protein S14

Chain O: 57% 38% 5%

MET A2 K3 Q4 S5 M6 K7 A8 R9 R13 L16 A17 D18 K19 Y20 K23 R24 L27 K28 A29 I30 I31 S32 D33 V34 N35 A36 SER ASP GLU ASP R41 L51 P52 R53 D54 S55 S56 R59 Q60 R61 N62 R63 C64 R65 R69 R75 K76 F77 R81

L96 K97 K98 A99 S100 W101

• Molecule 22: 30S ribosomal protein S15

Chain P: 78% 21%

MET S2 L3 S4 T8 A9 K10 S13 R17 D18 A19 S24 T25 E26 L32 I36 K47 K48 D49 S61 K65 L66 L67 D74 R77 L87 R88 R89

• Molecule 23: 30S ribosomal protein S16

Chain Q: 72% 27%

M1 V2 T3 I4 R5 L6 G10 P15 Q18 V21 A22 D23 S24 R28 R35 V36 G37 F38 I42 K46 I67 R70 V71 I75 K76 E77 K80 A81 A82

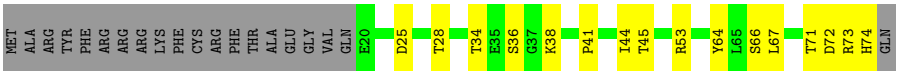
• Molecule 24: 30S ribosomal protein S17

Chain R: 52% 42% 5%

MET THR ASP K4 I5 R6 T7 L8 R11 V12 V13 S14 D15 K16 M17 E18 K19 V22 H31 P32 I33 K36 H45 V46 H47 D48 E49 E52 G56 D57 V58 I61 R62 E63 P66 L67 S68 K69 T70 K71 S72 V76 R77 V78 V79 E80 K81 A82 V83 LEU

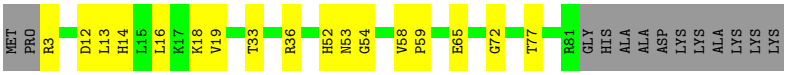
• Molecule 25: 30S ribosomal protein S18

Chain S: 52% 21% 27%



• Molecule 26: 30S ribosomal protein S19

Chain T:



• Molecule 27: 30S ribosomal protein S20

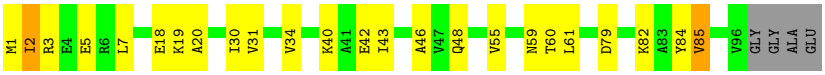
Chain U:

• Molecule 28: 30S ribosomal protein S21

Chain V:

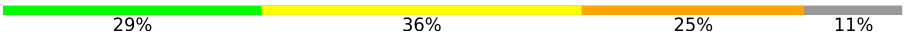
• Molecule 29: 50S ribosomal protein L23

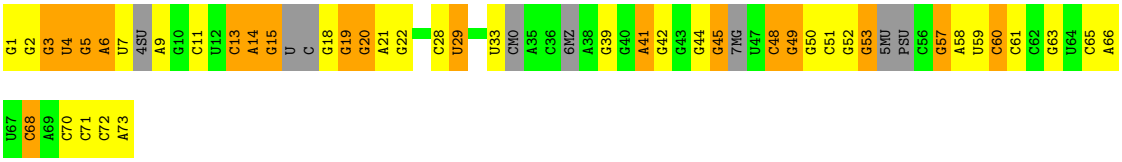
Chain W:



• Molecule 30: E-site tRNA

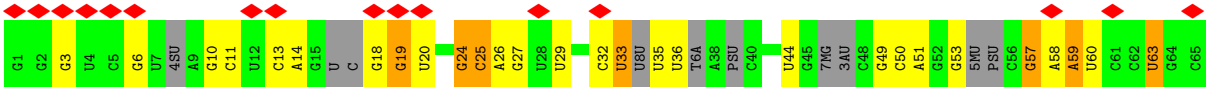
Chain X:

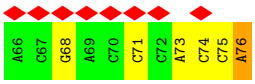




• Molecule 31: A-site tRNA

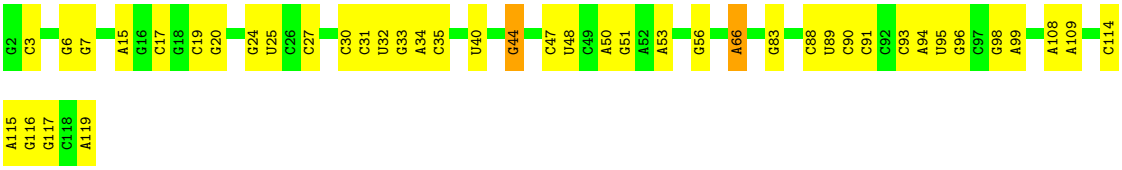
Chain Z:





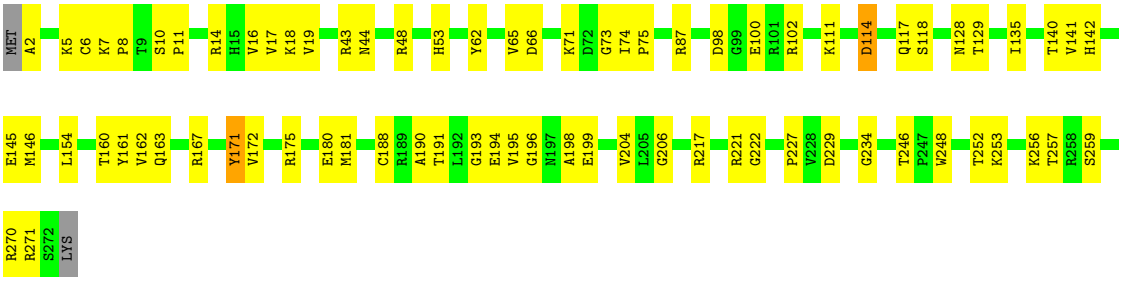
• Molecule 32: 5S ribosomal RNA

Chain a:



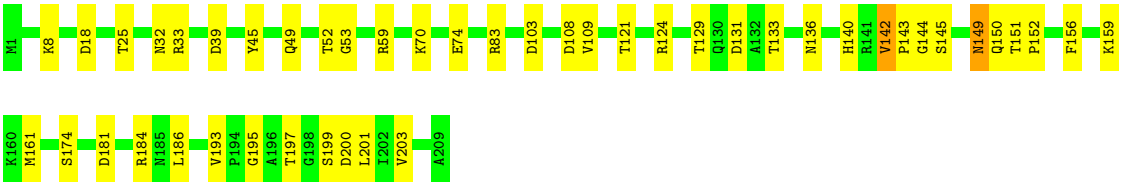
• Molecule 33: 50S ribosomal protein L2

Chain b:



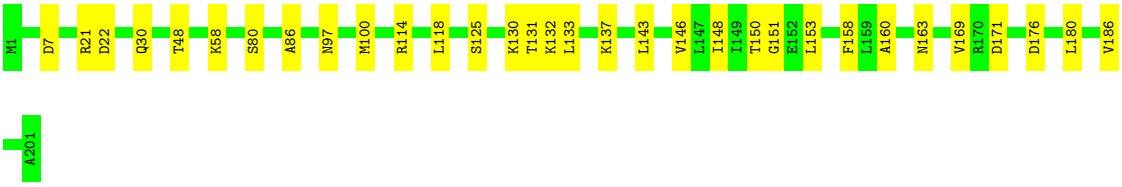
• Molecule 34: 50S ribosomal protein L3

Chain c:



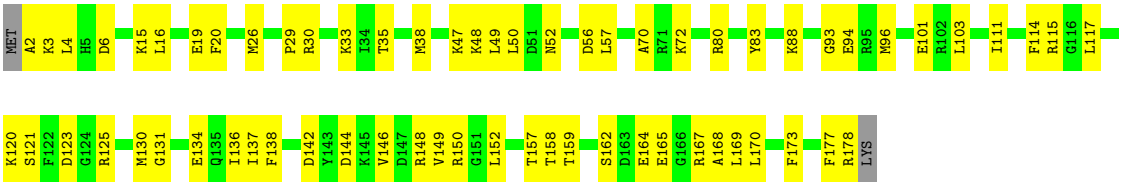
• Molecule 35: 50S ribosomal protein L4

Chain d:



• Molecule 36: 50S ribosomal protein L5

Chain e:

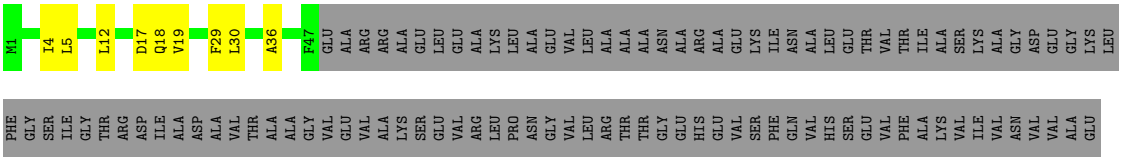


• Molecule 37: 50S ribosomal protein L6

Chain f:

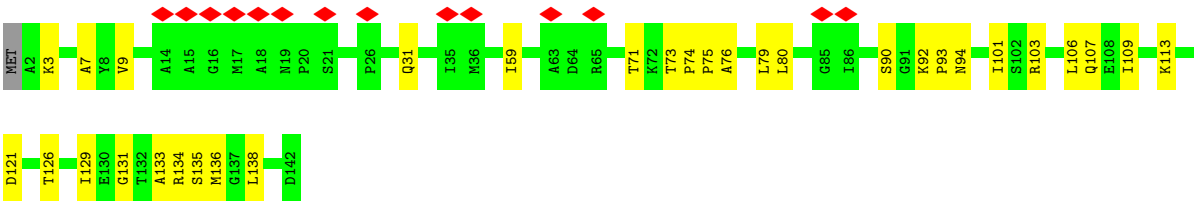
• Molecule 38: 50S ribosomal protein L9

Chain g:



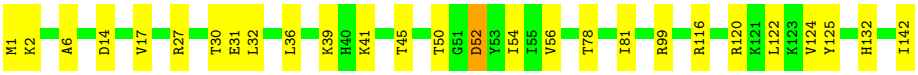
• Molecule 39: 50S ribosomal protein L11

Chain h:



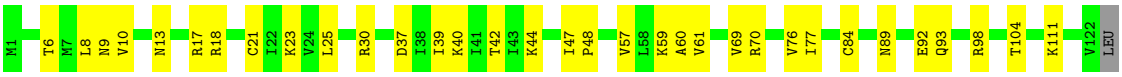
• Molecule 40: 50S ribosomal protein L13

Chain i:



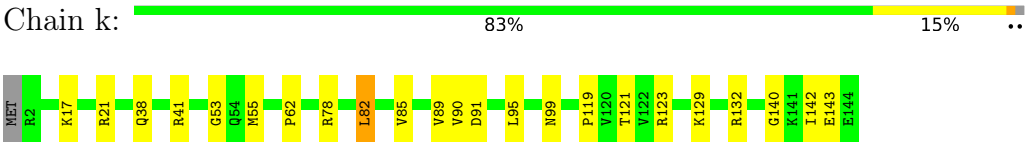
• Molecule 41: 50S ribosomal protein L14

Chain j:



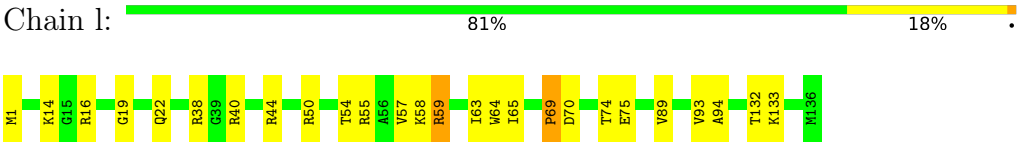
• Molecule 42: 50S ribosomal protein L15

Chain k:



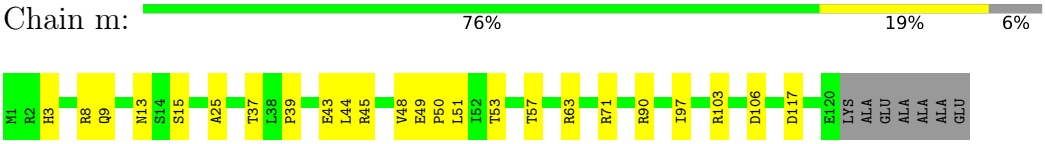
• Molecule 43: 50S ribosomal protein L16

Chain l:



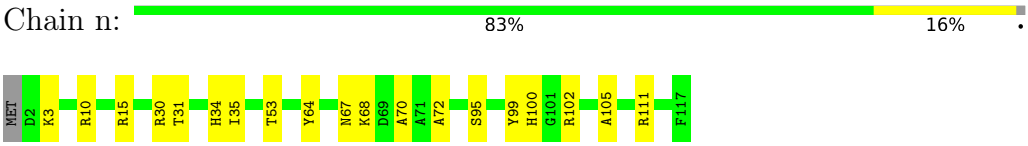
• Molecule 44: 50S ribosomal protein L17

Chain m:



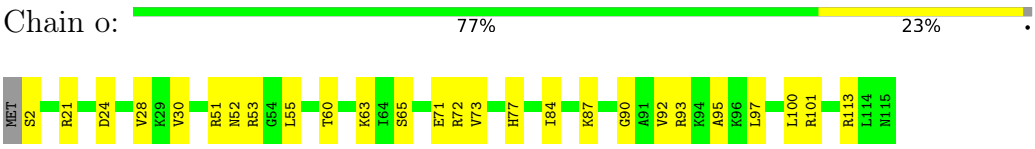
• Molecule 45: 50S ribosomal protein L18

Chain n:



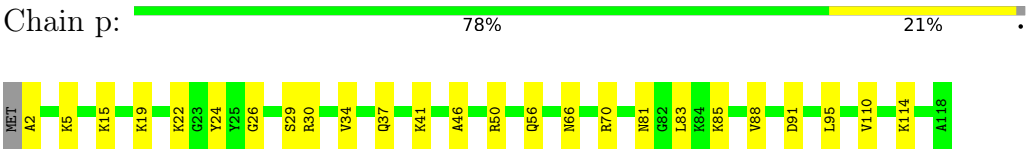
• Molecule 46: 50S ribosomal protein L19

Chain o:



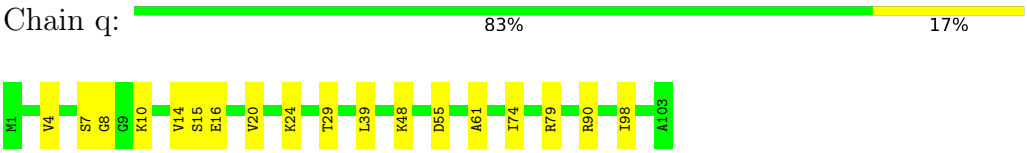
• Molecule 47: 50S ribosomal protein L20

Chain p:



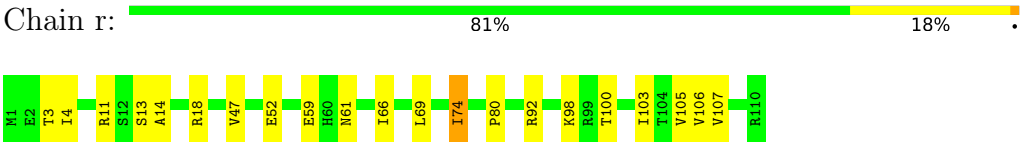
• Molecule 48: 50S ribosomal protein L21

Chain q:



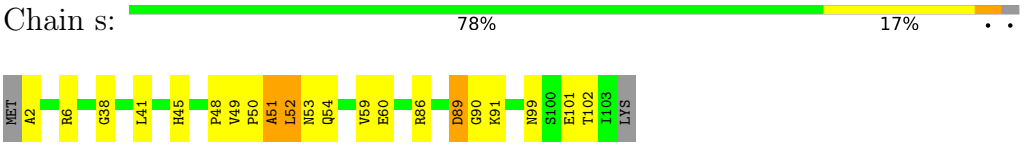
• Molecule 49: 50S ribosomal protein L22

Chain r:



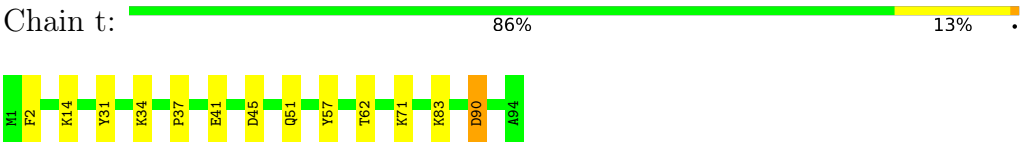
- Molecule 50: 50S ribosomal protein L24

Chain s:



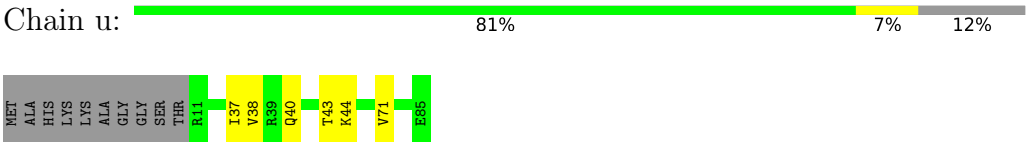
- Molecule 51: 50S ribosomal protein L25

Chain t:



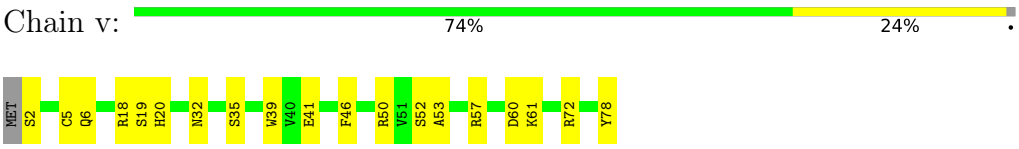
- Molecule 52: 50S ribosomal protein L27

Chain u:



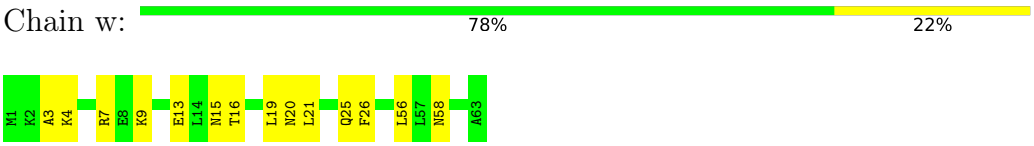
- Molecule 53: 50S ribosomal protein L28

Chain v:



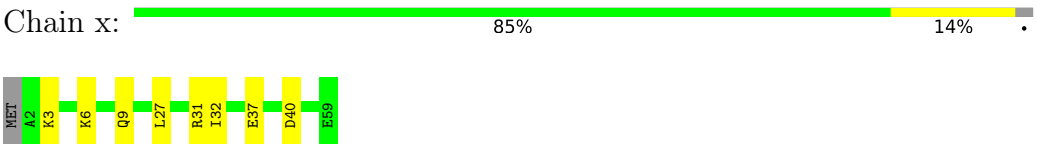
- Molecule 54: 50S ribosomal protein L29

Chain w:



- Molecule 55: 50S ribosomal protein L30

Chain x:

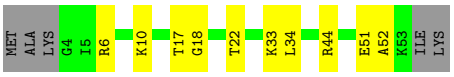


- Molecule 56: P-site tRNA

Chain y: 45% 39% 6% 9%

- Molecule 57: 50S ribosomal protein L33

Chain z: 73% 18% 9%



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	54875	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	32.57	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.093	Depositor
Minimum map value	-0.024	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	441.6, 441.6, 441.6	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.38, 1.38, 1.38	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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	0	0.79	0/380	0.76	0/498
2	1	0.66	0/513	0.86	1/676 (0.1%)
3	2	0.57	0/303	0.66	0/397
4	3	0.25	0/1361	0.58	0/1830
5	5	0.21	0/3426	0.52	0/4605
6	6	0.66	0/450	0.76	0/599
7	A	0.72	0/69796	0.52	0/108888
8	B	0.36	0/36966	0.40	1/57666 (0.0%)
9	C	0.32	0/1735	0.57	0/2338
10	D	0.27	0/1651	0.57	0/2225
11	E	0.27	0/1665	0.61	0/2227
12	F	0.36	0/1118	0.71	2/1504 (0.1%)
13	G	0.29	0/835	0.66	0/1128
14	H	0.24	0/1195	0.54	0/1602
15	I	0.33	0/989	0.55	0/1326
16	J	0.24	0/1034	0.60	0/1375
17	K	0.26	0/796	0.64	0/1077
18	L	0.31	0/893	0.60	0/1205
19	M	0.35	0/969	0.65	0/1300
20	N	0.25	0/892	0.62	1/1193 (0.1%)
21	O	0.25	0/785	0.58	0/1043
22	P	0.34	0/718	0.61	0/959
23	Q	0.30	0/659	0.59	0/884
24	R	0.33	0/657	0.66	0/881
25	S	0.30	0/462	0.64	2/621 (0.3%)
26	T	0.23	0/652	0.50	0/877
27	U	0.31	0/671	0.61	0/888
28	V	0.35	0/430	0.87	0/570
29	W	0.63	0/771	0.76	0/1031
30	X	0.20	0/1551	0.38	0/2404
31	Z	0.23	0/1565	0.37	0/2421
32	a	0.51	0/2828	0.40	0/4410
33	b	0.70	0/2121	0.72	0/2852
34	c	0.67	0/1586	0.69	0/2134

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	d	0.69	0/1571	0.65	0/2113
36	e	0.31	0/1434	0.56	0/1926
37	f	0.43	0/1343	0.56	0/1816
38	g	0.41	0/364	0.74	0/490
39	h	0.28	0/1046	0.65	1/1410 (0.1%)
40	i	0.71	0/1152	0.68	2/1551 (0.1%)
41	j	0.65	0/947	0.77	0/1268
42	k	0.66	0/1054	0.82	0/1403
43	l	0.63	0/1093	0.73	0/1460
44	m	0.71	0/973	0.86	0/1301
45	n	0.45	0/902	0.58	0/1209
46	o	0.61	0/929	0.69	0/1242
47	p	0.78	0/960	0.71	0/1278
48	q	0.64	0/829	0.68	0/1107
49	r	0.71	0/864	0.70	0/1156
50	s	0.56	0/787	0.69	0/1051
51	t	0.53	0/766	0.54	0/1025
52	u	0.63	0/576	0.61	0/762
53	v	0.67	0/635	0.66	0/848
54	w	0.56	0/510	0.65	0/677
55	x	0.65	0/453	0.71	0/605
56	y	0.21	0/1664	0.35	0/2577
57	z	0.41	0/416	0.57	0/554
All	All	0.57	0/163691	0.53	10/244463 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	1	0	1
3	2	0	1
9	C	0	1
11	E	0	2
12	F	0	2
13	G	0	1
16	J	0	2
17	K	0	1
19	M	0	1
20	N	0	1
23	Q	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
24	R	0	2
28	V	0	2
29	W	0	1
34	c	0	1
37	f	0	2
41	j	0	1
42	k	0	1
43	l	0	1
50	s	0	3
All	All	0	28

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
25	S	67	LEU	CA-C-N	7.08	138.87	122.31
25	S	67	LEU	C-N-CA	7.08	138.87	122.31
39	h	109	ILE	N-CA-C	-6.89	105.78	111.91
2	1	32	ILE	N-CA-C	6.32	122.49	109.34
12	F	77	ASN	CA-C-N	5.89	132.78	121.54
12	F	77	ASN	C-N-CA	5.89	132.78	121.54
8	B	702	A	C4'-C3'-O3'	5.55	121.33	113.00
20	N	67	GLY	N-CA-C	5.23	125.58	113.18
40	i	99	ARG	CA-C-N	-5.18	117.89	122.97
40	i	99	ARG	C-N-CA	-5.18	117.89	122.97

There are no chirality outliers.

All (28) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1	31	HIS	Peptide
3	2	20	ASP	Peptide
9	C	84	ALA	Peptide
11	E	173	VAL	Peptide
11	E	20	PHE	Peptide
12	F	102	GLY	Peptide
12	F	105	ILE	Peptide
13	G	53	LYS	Peptide
16	J	55	VAL	Peptide
16	J	60	LYS	Peptide
17	K	57	VAL	Peptide

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Mol	Chain	Res	Type	Group
19	M	24	LEU	Peptide
20	N	66	GLU	Peptide
23	Q	46	LYS	Peptide
24	R	68	SER	Peptide
24	R	70	THR	Peptide
28	V	34	ARG	Peptide
28	V	9	ASN	Peptide
29	W	2	ILE	Peptide
34	c	151	THR	Peptide
37	f	46	ALA	Peptide
37	f	47	ASP	Peptide
41	j	92	GLU	Peptide
42	k	53	GLY	Peptide
43	l	58	LYS	Peptide
50	s	52	LEU	Peptide
50	s	6	ARG	Peptide
50	s	89	ASP	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	377	0	418	7	0
2	1	504	0	572	13	0
3	2	302	0	343	13	0
4	3	1346	0	1394	31	0
5	5	3386	0	3403	34	0
6	6	444	0	458	7	0
7	A	62317	0	31343	644	0
8	B	33015	0	16617	383	0
9	C	1704	0	1732	26	0
10	D	1624	0	1696	34	0
11	E	1643	0	1707	59	0
12	F	1105	0	1148	29	0
13	G	817	0	808	18	0
14	H	1181	0	1238	34	0
15	I	979	0	1031	33	0
16	J	1022	0	1070	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	K	786	0	828	22	0
18	L	877	0	887	22	0
19	M	955	0	1016	23	0
20	N	883	0	941	26	0
21	O	774	0	824	33	0
22	P	710	0	728	13	0
23	Q	649	0	666	18	0
24	R	648	0	691	25	0
25	S	455	0	478	15	0
26	T	637	0	665	13	0
27	U	665	0	714	17	0
28	V	425	0	449	9	0
29	W	764	0	829	19	0
30	X	1392	0	714	24	0
31	Z	1406	0	722	25	0
32	a	2529	0	1281	17	0
33	b	2082	0	2154	50	0
34	c	1565	0	1616	33	0
35	d	1552	0	1619	21	0
36	e	1410	0	1444	47	0
37	f	1323	0	1371	18	0
38	g	359	0	381	6	0
39	h	1032	0	1085	22	0
40	i	1129	0	1162	18	0
41	j	938	0	1012	22	0
42	k	1045	0	1117	18	0
43	l	1074	0	1157	16	0
44	m	960	0	1000	18	0
45	n	892	0	923	16	0
46	o	917	0	962	21	0
47	p	947	0	1019	19	0
48	q	816	0	839	14	0
49	r	857	0	922	14	0
50	s	779	0	831	12	0
51	t	753	0	780	10	0
52	u	569	0	581	3	0
53	v	625	0	652	14	0
54	w	509	0	543	13	0
55	x	449	0	488	5	0
56	y	1496	0	764	14	0
57	z	409	0	440	7	0
All	All	150808	0	102273	1872	0

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

All (1872) 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)
7:A:2506:U:O2'	7:A:2507:C:O4'	1.56	1.19
8:B:98:A:H2'	8:B:99:C:C6	1.85	1.11
7:A:2572:A:N6	34:c:150:GLN:OE1	1.93	1.02
7:A:2508:G:OP1	31:Z:76:A:O5'	1.82	0.95
7:A:2507:C:O2'	31:Z:76:A:C1'	2.14	0.95
8:B:98:A:H2'	8:B:99:C:C5	2.00	0.95
7:A:2711:A:N6	7:A:2714:G:N7	2.14	0.95
7:A:1358:G:N2	7:A:1372:U:OP2	2.02	0.93
7:A:576:U:O2'	7:A:2502:G:C6	2.22	0.92
7:A:2267:A:N6	7:A:2272:U:H3	1.66	0.92
7:A:2711:A:C6	7:A:2714:G:C8	2.59	0.91
7:A:2060:A:C5	7:A:2502:G:N2	2.40	0.90
7:A:2267:A:H61	7:A:2272:U:H3	0.99	0.90
7:A:2507:C:O2'	31:Z:76:A:H1'	1.70	0.89
7:A:1846:G:O2'	8:B:702:A:C2	2.24	0.89
7:A:2722:G:N7	7:A:2723:C:C4	2.42	0.87
7:A:2507:C:HO2'	31:Z:76:A:C1'	1.87	0.87
7:A:2711:A:N6	7:A:2714:G:C8	2.42	0.87
7:A:2453:A:C2	7:A:2504:U:N3	2.43	0.87
7:A:2508:G:C6	7:A:2582:G:O6	2.28	0.86
7:A:2576:G:H21	7:A:2576:G:P	1.98	0.86
7:A:963:U:O2'	7:A:2250:G:C6	2.34	0.81
8:B:98:A:C2'	8:B:99:C:C6	2.63	0.80
7:A:576:U:O2'	7:A:2502:G:C5	2.36	0.79
7:A:2722:G:C8	7:A:2723:C:C4	2.70	0.79
7:A:1846:G:O2'	8:B:702:A:H2	1.60	0.79
7:A:2576:G:OP2	7:A:2576:G:N2	2.15	0.79
7:A:2060:A:C6	7:A:2502:G:N2	2.51	0.78
7:A:2689:U:OP2	7:A:2719:G:N2	2.15	0.78
7:A:284:U:H3	7:A:356:G:H1	1.33	0.77
8:B:84:U:H3	8:B:88:U:HO2'	1.33	0.76
7:A:2572:A:N7	34:c:150:GLN:HB2	2.01	0.75
8:B:203:G:H1	8:B:215:C:H42	1.33	0.75
7:A:783:A:H2'	7:A:784:G:H4'	1.68	0.74
7:A:2297:A:N7	7:A:2320:U:N3	2.35	0.74
7:A:2720:U:H5"	46:o:53:ARG:HH22	1.52	0.74
7:A:2060:A:C5	7:A:2502:G:C2	2.75	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:2576:G:O2'	7:A:2579:C:OP2	2.05	0.74
7:A:2508:G:OP1	31:Z:76:A:P	2.46	0.73
7:A:1847:A:H4'	8:B:702:A:H1'	1.71	0.72
7:A:1814:G:C8	7:A:1815:A:C8	2.78	0.72
7:A:2516:A:N6	7:A:2517:C:H42	1.88	0.72
7:A:2008:C:H2'	7:A:2009:A:H8	1.55	0.71
8:B:1305:G:H22	8:B:1331:G:H1'	1.55	0.71
7:A:1368:G:H2'	7:A:1369:G:C8	2.26	0.71
7:A:2060:A:C6	7:A:2502:G:C2	2.79	0.71
7:A:1358:G:C8	7:A:1371:G:O6	2.44	0.71
7:A:1270:C:H5"	7:A:1271:G:H5'	1.73	0.70
7:A:2276:G:H2'	7:A:2277:G:H8	1.56	0.70
7:A:1529:G:H1	7:A:1542:U:H3	1.39	0.70
7:A:1849:G:H2'	7:A:1850:G:H8	1.56	0.70
7:A:2297:A:N3	7:A:2297:A:H2'	2.06	0.70
7:A:2267:A:H3'	7:A:2267:A:N3	2.07	0.69
7:A:2500:U:O2	7:A:2504:U:C5	2.44	0.69
7:A:2506:U:O2'	7:A:2507:C:C1'	2.40	0.69
7:A:2087:G:H2'	7:A:2088:A:H8	1.58	0.69
7:A:1770:G:C6	7:A:1983:G:C6	2.81	0.69
31:Z:10:G:H1	31:Z:25:C:H42	1.41	0.68
7:A:571:U:N3	7:A:2030:A:N1	2.41	0.68
7:A:2064:C:C5	7:A:2065:C:N4	2.62	0.68
7:A:2267:A:N6	7:A:2272:U:C2	2.60	0.68
7:A:2507:C:O2'	31:Z:76:A:O4'	2.10	0.68
8:B:1264:U:H3	8:B:1271:A:H61	1.39	0.68
46:o:60:THR:HG22	46:o:73:VAL:HG12	1.74	0.68
7:A:2711:A:C6	7:A:2714:G:N9	2.62	0.68
7:A:2097:A:H61	7:A:2192:U:H3	1.42	0.68
7:A:2711:A:N6	7:A:2714:G:C5	2.61	0.68
7:A:2087:G:H2'	7:A:2088:A:C8	2.29	0.67
8:B:196:A:H2'	8:B:197:A:H2'	1.75	0.67
7:A:956:G:N7	43:l:14:LYS:NZ	2.42	0.67
7:A:2723:C:O5'	7:A:2723:C:H6	1.78	0.67
7:A:2722:G:C5	7:A:2723:C:N3	2.63	0.67
7:A:2453:A:H2	7:A:2504:U:N3	1.89	0.67
8:B:460:A:N6	8:B:472:U:O4	2.27	0.67
31:Z:18:G:N2	31:Z:57:G:N7	2.44	0.66
14:H:114:LYS:H	14:H:118:LEU:HD23	1.60	0.66
7:A:1482:G:H1'	7:A:1509:A:H61	1.61	0.66
7:A:1846:G:HO2'	8:B:702:A:H2	0.80	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:1373:G:H4'	14:H:31:MET:HE1	1.78	0.66
39:h:80:LEU:HD13	39:h:133:ALA:HB2	1.77	0.66
7:A:381:G:OP1	53:v:18:ARG:NH1	2.28	0.66
53:v:19:SER:OG	53:v:20:HIS:N	2.29	0.65
6:6:2:ALA:HA	7:A:2056:G:N2	2.11	0.65
7:A:2711:A:C6	7:A:2714:G:C4	2.84	0.65
7:A:1368:G:H2'	7:A:1369:G:H8	1.61	0.65
5:5:120:LEU:HD23	5:5:294:LEU:HD13	1.76	0.65
7:A:2250:G:H8	7:A:2250:G:OP2	1.79	0.65
7:A:2305:U:H5"	36:e:131:GLY:HA3	1.79	0.65
8:B:1033:G:N7	8:B:1035:A:N6	2.45	0.65
34:c:32:ASN:ND2	34:c:52:THR:OG1	2.30	0.65
41:j:37:ASP:N	41:j:37:ASP:OD1	2.28	0.65
7:A:18:U:O2'	7:A:554:U:OP1	2.14	0.64
37:f:88:GLN:HE21	37:f:163:ARG:HD2	1.61	0.64
7:A:2500:U:O2	7:A:2504:U:C4	2.51	0.64
8:B:1004:A:H1'	8:B:1035:A:H61	1.62	0.64
8:B:448:A:N6	8:B:486:U:O2	2.30	0.64
7:A:627:A:OP1	42:k:78:ARG:NH1	2.30	0.64
34:c:199:SER:OG	34:c:200:ASP:N	2.30	0.64
12:F:45:ARG:H	12:F:73:ASN:HA	1.61	0.64
7:A:2643:G:N2	7:A:2772:C:O2	2.31	0.64
8:B:101:A:N6	8:B:102:G:C6	2.66	0.64
7:A:2722:G:N7	7:A:2723:C:N3	2.46	0.63
4:3:127:ALA:O	4:3:131:GLN:NE2	2.32	0.63
7:A:2746:U:H2'	7:A:2747:G:H8	1.63	0.63
9:C:86:SER:OG	9:C:222:ARG:NH2	2.32	0.63
33:b:141:VAL:HG11	33:b:190:ALA:HB1	1.80	0.63
7:A:883:G:H1	7:A:894:U:H1'	1.63	0.63
7:A:2008:C:H2'	7:A:2009:A:C8	2.33	0.63
39:h:133:ALA:HA	39:h:136:MET:HB3	1.80	0.63
7:A:2711:A:N1	7:A:2714:G:C4	2.67	0.63
8:B:468:A:OP2	8:B:470:C:N4	2.31	0.63
8:B:756:C:O2	15:I:4:GLN:NE2	2.31	0.63
7:A:1172:C:N4	7:A:1177:G:O6	2.32	0.63
8:B:182:A:OP2	8:B:193:C:N4	2.31	0.63
39:h:133:ALA:HB1	39:h:138:LEU:HB3	1.81	0.63
7:A:1500:G:H2'	7:A:1501:G:H8	1.64	0.62
7:A:1361:G:HO2'	7:A:2215:C:HO2'	1.44	0.62
8:B:197:A:O2'	8:B:220:G:N2	2.32	0.62
5:5:40:ARG:HH22	7:A:1337:G:H1'	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:1026:G:OP2	8:B:1028:C:N4	2.32	0.62
5:5:73:ARG:NH1	5:5:77:ASP:OD2	2.32	0.62
7:A:2087:G:N2	7:A:2233:U:O2	2.33	0.62
8:B:406:G:N2	8:B:436:C:N3	2.47	0.62
39:h:76:ALA:HA	39:h:79:LEU:HB3	1.81	0.62
4:3:143:MET:HB3	4:3:151:GLN:HE21	1.63	0.62
7:A:559:G:N3	47:p:56:GLN:NE2	2.48	0.62
7:A:963:U:O2'	7:A:2250:G:N1	2.33	0.62
8:B:291:U:H2'	8:B:292:G:H8	1.64	0.62
7:A:1849:G:H8	7:A:1849:G:O5'	1.81	0.62
7:A:2008:C:N4	7:A:2009:A:H62	1.97	0.62
7:A:1077:A:H4'	39:h:94:ASN:HB2	1.81	0.62
12:F:97:GLN:HB3	12:F:124:LEU:HB2	1.81	0.62
33:b:17:VAL:HG22	33:b:204:VAL:HG22	1.81	0.62
8:B:587:G:OP1	15:I:84:ARG:NH2	2.33	0.62
7:A:2516:A:N6	7:A:2517:C:N4	2.46	0.62
8:B:99:C:O5'	8:B:99:C:H6	1.83	0.62
36:e:148:ARG:HH11	36:e:150:ARG:HG2	1.64	0.61
8:B:352:C:O2	8:B:356:A:N6	2.33	0.61
50:s:50:PRO:HA	50:s:54:GLN:HE22	1.65	0.61
2:1:42:ARG:NH2	7:A:2349:G:OP2	2.34	0.61
7:A:2079:U:O2	7:A:2242:G:N2	2.34	0.61
7:A:2118:U:N3	7:A:2145:C:N3	2.48	0.61
8:B:908:A:H2'	8:B:909:A:H8	1.66	0.61
8:B:1114:C:H42	8:B:1186:G:H1	1.48	0.61
4:3:50:GLN:NE2	4:3:90:CYS:SG	2.73	0.61
7:A:1009:A:OP2	40:i:39:LYS:NZ	2.32	0.61
7:A:2646:C:O5'	7:A:2646:C:H6	1.83	0.61
8:B:1266:G:N2	8:B:1269:A:OP2	2.34	0.61
12:F:107:ALA:HB1	12:F:111:MET:HE3	1.81	0.61
26:T:36:ARG:NH1	26:T:52:HIS:O	2.34	0.61
7:A:320:A:N3	35:d:163:ASN:ND2	2.48	0.61
7:A:999:U:O2	7:A:1157:G:N2	2.34	0.61
19:M:50:ARG:NH2	19:M:67:ILE:O	2.33	0.61
31:Z:11:C:H42	31:Z:24:G:H1	1.49	0.61
19:M:70:GLU:H	19:M:107:VAL:HG11	1.65	0.61
7:A:864:G:OP2	43:l:22:GLN:NE2	2.33	0.61
7:A:1266:G:H22	7:A:2012:G:H2'	1.65	0.61
8:B:823:C:HO2'	15:I:2:SER:N	1.98	0.61
10:D:22:TRP:HB3	10:D:59:ARG:H	1.66	0.61
3:2:27:CYS:HG	3:2:33:HIS:HD1	1.47	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:1298:U:O2	8:B:1299:A:N6	2.34	0.61
23:Q:5:ARG:HH12	23:Q:22:ALA:HB3	1.66	0.61
49:r:13:SER:OG	49:r:14:ALA:N	2.32	0.61
7:A:993:G:OP1	47:p:50:ARG:NH2	2.32	0.60
7:A:1796:U:H2'	7:A:1797:G:H8	1.66	0.60
8:B:101:A:C5	8:B:102:G:C5	2.89	0.60
8:B:340:U:O2	8:B:350:G:N2	2.34	0.60
17:K:15:HIS:HA	17:K:18:ILE:HG22	1.83	0.60
7:A:2336:A:H61	52:u:43:THR:HG21	1.66	0.60
30:X:15:G:N2	30:X:48:C:O2'	2.34	0.60
45:n:31:THR:O	45:n:102:ARG:NH1	2.34	0.60
7:A:2582:G:H2'	31:Z:76:A:H61	1.65	0.60
8:B:105:G:N2	8:B:379:C:O2'	2.35	0.60
8:B:546:A:OP2	11:E:62:ARG:NH2	2.34	0.60
8:B:606:G:N2	8:B:632:U:OP1	2.31	0.60
7:A:1056:G:H5'	7:A:1057:A:H5'	1.82	0.60
7:A:1364:G:N7	53:v:2:SER:OG	2.33	0.60
7:A:1798:U:OP2	33:b:271:ARG:NH2	2.34	0.60
8:B:201:G:N2	8:B:469:C:O2'	2.34	0.60
29:W:3:ARG:O	29:W:3:ARG:NE	2.34	0.60
7:A:1252:G:H1	47:p:37:GLN:HE21	1.48	0.60
7:A:2267:A:N6	7:A:2272:U:N3	2.32	0.60
26:T:53:ASN:HB2	26:T:77:THR:HA	1.82	0.60
6:6:13:ARG:NH1	7:A:1263:U:OP1	2.35	0.60
7:A:2130:U:O2'	7:A:2159:G:N2	2.35	0.60
8:B:898:G:N2	8:B:901:A:OP2	2.34	0.60
8:B:1162:C:H42	8:B:1174:G:H1	1.49	0.60
9:C:42:ASN:HD22	9:C:45:LYS:HB2	1.66	0.60
30:X:60:C:H5'	30:X:61:C:H5	1.66	0.60
7:A:2233:U:H2'	7:A:2234:G:H8	1.67	0.60
52:u:37:ILE:HG22	52:u:38:VAL:HG23	1.84	0.60
7:A:1358:G:C8	7:A:1371:G:C6	2.89	0.59
8:B:80:A:N6	8:B:90:C:O2	2.35	0.59
18:L:23:ILE:HG22	18:L:32:VAL:HG13	1.84	0.59
7:A:2722:G:N7	7:A:2723:C:N4	2.49	0.59
8:B:140:U:O2'	8:B:223:A:N6	2.35	0.59
6:6:2:ALA:N	7:A:2612:C:HO2'	2.00	0.59
7:A:2506:U:O2'	7:A:2507:C:C4'	2.51	0.59
8:B:913:A:OP2	19:M:86:ARG:NH2	2.36	0.59
8:B:1014:A:H4'	26:T:14:HIS:HB2	1.85	0.59
21:O:20:TYR:HA	21:O:24:ARG:HH21	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:G:44:ARG:O	13:G:56:LYS:NZ	2.35	0.59
15:I:15:ARG:NH1	15:I:75:ILE:O	2.35	0.59
8:B:880:C:OP1	19:M:5:ASN:ND2	2.35	0.59
8:B:1125:U:H4'	17:K:7:ARG:HH12	1.67	0.59
40:i:31:GLU:HG2	40:i:142:ILE:HG12	1.84	0.59
7:A:58:G:N3	7:A:70:G:N2	2.50	0.59
7:A:1283:G:N2	7:A:1286:A:OP2	2.36	0.59
7:A:2070:A:H2'	7:A:2071:A:C8	2.37	0.59
33:b:71:LYS:O	33:b:118:SER:OG	2.20	0.59
7:A:1357:C:H2'	7:A:1358:G:H5'	1.83	0.59
7:A:2711:A:C6	7:A:2714:G:C5	2.91	0.59
10:D:30:ALA:O	21:O:65:ARG:NH1	2.32	0.59
15:I:49:PHE:HB2	15:I:59:LEU:HD11	1.84	0.59
37:f:11:VAL:HB	37:f:48:ASN:HB2	1.84	0.59
7:A:1708:C:H42	7:A:1750:G:H1	1.49	0.59
39:h:103:ARG:NH1	39:h:107:GLN:OE1	2.36	0.59
8:B:519:C:N4	8:B:529:G:O2'	2.35	0.59
21:O:31:ILE:O	21:O:35:ASN:ND2	2.36	0.59
30:X:1:G:H22	30:X:72:C:H2'	1.66	0.59
2:1:8:ARG:NH1	7:A:243:U:OP2	2.36	0.58
18:L:23:ILE:HD11	18:L:86:VAL:HG22	1.83	0.58
18:L:86:VAL:HG11	18:L:93:ARG:HG3	1.83	0.58
27:U:59:ASP:OD1	27:U:69:LYS:NZ	2.35	0.58
7:A:587:C:OP2	42:k:21:ARG:NH2	2.35	0.58
7:A:2507:C:O3'	31:Z:76:A:C4'	2.51	0.58
8:B:182:A:N6	8:B:223:A:O2'	2.36	0.58
7:A:2052:A:H2'	7:A:2053:G:H8	1.66	0.58
8:B:101:A:N7	8:B:102:G:N7	2.51	0.58
8:B:108:G:OP2	8:B:325:A:N6	2.36	0.58
30:X:20:G:OP2	30:X:60:C:N4	2.34	0.58
35:d:125:SER:O	35:d:137:LYS:NZ	2.36	0.58
54:w:16:THR:HA	54:w:19:LEU:HB2	1.84	0.58
5:5:63:ARG:NH1	5:5:63:ARG:O	2.37	0.58
6:6:13:ARG:NH2	7:A:517:C:OP1	2.37	0.58
7:A:296:U:H2'	7:A:297:G:H8	1.67	0.58
7:A:2848:G:O2'	7:A:2867:G:N2	2.36	0.58
8:B:324:G:N2	8:B:327:A:OP2	2.36	0.58
8:B:450:G:N2	8:B:482:A:N1	2.51	0.58
29:W:7:LEU:HD12	29:W:46:ALA:HA	1.86	0.58
33:b:140:THR:HG22	33:b:163:GLN:HG2	1.85	0.58
7:A:747:U:O2'	49:r:92:ARG:NH2	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:H:143:ARG:NH1	30:X:42:G:OP1	2.37	0.58
16:J:28:ILE:HG23	16:J:63:LEU:HD23	1.84	0.58
5:5:30:SER:O	5:5:34:ASN:ND2	2.37	0.58
7:A:2657:A:H62	7:A:2664:G:H21	1.50	0.58
8:B:1305:G:N1	8:B:1331:G:N3	2.51	0.58
40:i:36:LEU:HD11	40:i:122:LEU:HD13	1.84	0.58
41:j:8:LEU:HD23	41:j:84:CYS:HB3	1.85	0.58
50:s:86:ARG:NH1	50:s:102:THR:OG1	2.36	0.58
8:B:60:A:N1	8:B:107:G:O2'	2.31	0.58
8:B:408:A:H61	8:B:434:U:H3	1.50	0.58
21:O:20:TYR:HB3	21:O:51:LEU:HD13	1.86	0.58
26:T:36:ARG:NH2	26:T:72:GLY:O	2.35	0.58
49:r:11:ARG:HH21	49:r:98:LYS:HD2	1.68	0.58
7:A:659:G:N2	35:d:30:GLN:OE1	2.36	0.58
8:B:614:C:OP2	11:E:81:ARG:NH1	2.36	0.58
11:E:62:ARG:HH21	11:E:69:GLU:H	1.52	0.58
35:d:22:ASP:N	35:d:22:ASP:OD1	2.35	0.58
32:a:30:C:OP1	45:n:3:LYS:NZ	2.36	0.58
7:A:532:A:N7	7:A:2021:C:O2'	2.36	0.58
7:A:660:C:H2'	7:A:661:A:H8	1.69	0.58
7:A:2266:A:H5'	7:A:2267:A:C8	2.39	0.58
7:A:2507:C:HO2'	31:Z:76:A:H1'	1.56	0.58
8:B:1271:A:H5'	8:B:1314:C:H5"	1.86	0.58
10:D:19:ASN:HB3	10:D:40:ARG:HH22	1.68	0.58
11:E:2:ALA:N	11:E:66:GLY:O	2.37	0.58
7:A:1451:C:H42	7:A:1459:G:H1	1.52	0.57
7:A:2351:G:N2	7:A:2367:G:O6	2.37	0.57
8:B:196:A:OP1	27:U:64:LYS:NZ	2.36	0.57
6:6:38:HIS:HB3	6:6:44:THR:HG22	1.86	0.57
7:A:1173:U:O2	7:A:1176:U:N3	2.37	0.57
20:N:3:ARG:HH22	36:e:142:ASP:HB2	1.69	0.57
36:e:15:LYS:NZ	36:e:19:GLU:OE2	2.37	0.57
7:A:1219:U:OP2	47:p:19:LYS:NZ	2.36	0.57
7:A:2248:C:H42	7:A:2256:G:H1	1.50	0.57
56:y:9:A:N3	56:y:21:A:N6	2.52	0.57
5:5:28:VAL:HG22	5:5:63:ARG:HD3	1.86	0.57
7:A:1481:U:H3	7:A:1510:G:H1	1.53	0.57
8:B:1088:G:H21	8:B:1167:A:H62	1.52	0.57
8:B:1250:A:H61	8:B:1354:U:H1'	1.70	0.57
33:b:135:ILE:O	33:b:167:ARG:NH1	2.37	0.57
7:A:2508:G:P	31:Z:76:A:O5'	2.61	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:2578:G:N2	7:A:2579:C:O2	2.37	0.57
8:B:937:A:N6	8:B:1345:U:O4	2.38	0.57
11:E:103:TYR:HB3	11:E:111:ARG:HH11	1.69	0.57
47:p:46:ALA:O	47:p:50:ARG:NH1	2.36	0.57
4:3:73:ILE:HG23	4:3:111:LEU:HB2	1.85	0.57
7:A:1817:G:OP1	33:b:87:ARG:NH2	2.37	0.57
7:A:2117:A:H61	7:A:2170:A:H61	1.53	0.57
8:B:142:G:O2'	8:B:195:A:N6	2.37	0.57
8:B:181:A:N6	8:B:195:A:OP2	2.38	0.57
31:Z:19:G:OP1	31:Z:59:A:N6	2.37	0.57
42:k:85:VAL:HG11	42:k:90:VAL:HG22	1.85	0.57
7:A:1368:G:N3	7:A:1369:G:N7	2.53	0.57
8:B:376:G:H1	8:B:387:U:H3	1.52	0.57
8:B:974:A:OP1	21:O:69:ARG:NH2	2.36	0.57
8:B:976:G:N1	8:B:1362:A:O2'	2.37	0.57
8:B:1145:A:H2	8:B:1147:C:H41	1.52	0.57
7:A:355:U:H2'	7:A:356:G:H8	1.68	0.57
7:A:1070:A:H2'	7:A:1097:U:H4'	1.87	0.57
8:B:401:C:N4	8:B:548:G:OP1	2.38	0.57
8:B:522:C:H1'	8:B:536:C:H5"	1.87	0.57
49:r:59:GLU:HB2	49:r:66:ILE:HD11	1.86	0.57
1:0:24:THR:OG1	1:0:27:GLY:N	2.34	0.57
7:A:1364:G:OP2	53:v:2:SER:N	2.37	0.57
7:A:2711:A:C5	7:A:2714:G:C8	2.92	0.57
9:C:86:SER:H	9:C:89:GLN:HE21	1.51	0.57
46:o:90:GLY:O	46:o:113:ARG:NH1	2.35	0.57
48:q:7:SER:OG	48:q:8:GLY:N	2.37	0.57
49:r:14:ALA:O	49:r:18:ARG:NH1	2.38	0.57
7:A:2144:G:O2'	7:A:2147:A:N6	2.38	0.56
8:B:544:G:OP2	11:E:14:ARG:NH2	2.38	0.56
13:G:63:ASN:ND2	13:G:96:VAL:O	2.38	0.56
30:X:49:G:H22	30:X:66:A:H1'	1.69	0.56
7:A:302:C:H42	7:A:315:G:H1	1.53	0.56
8:B:707:U:OP1	18:L:87:LYS:NZ	2.37	0.56
14:H:71:PRO:O	14:H:96:ARG:NH1	2.38	0.56
29:W:3:ARG:HH11	29:W:5:GLU:HA	1.69	0.56
39:h:9:VAL:H	39:h:59:ILE:HD13	1.70	0.56
7:A:84:A:H62	7:A:101:A:H2	1.53	0.56
7:A:563:A:OP2	48:q:79:ARG:NH1	2.37	0.56
7:A:1057:A:N6	7:A:1087:G:OP2	2.38	0.56
7:A:1779:U:OP2	7:A:1784:A:N6	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:2711:A:C8	7:A:2714:G:O4'	2.58	0.56
8:B:520:A:H61	8:B:533:A:H61	1.53	0.56
8:B:1126:U:OP1	17:K:7:ARG:NH2	2.39	0.56
8:B:1166:G:O2'	8:B:1169:A:N6	2.38	0.56
8:B:1220:G:N2	26:T:54:GLY:O	2.35	0.56
33:b:246:THR:HG23	33:b:248:TRP:H	1.70	0.56
6:6:16:ARG:NH1	7:A:1264:A:OP1	2.39	0.56
7:A:576:U:H4'	7:A:2502:G:N7	2.21	0.56
7:A:668:A:H2'	7:A:670:A:H62	1.70	0.56
7:A:1597:A:H5"	7:A:1598:A:H5'	1.86	0.56
8:B:160:A:H2'	8:B:161:A:H8	1.69	0.56
10:D:47:LEU:HD11	10:D:76:VAL:HG12	1.88	0.56
32:a:98:G:H1	51:t:14:LYS:HB3	1.71	0.56
37:f:10:VAL:HG23	37:f:49:THR:HG22	1.87	0.56
45:n:64:TYR:O	45:n:67:ASN:ND2	2.38	0.56
53:v:60:ASP:OD1	53:v:60:ASP:N	2.38	0.56
8:B:599:C:H2'	8:B:600:A:H8	1.69	0.56
8:B:1012:A:H61	8:B:1017:U:H3	1.53	0.56
15:I:11:LEU:HD22	15:I:75:ILE:HD11	1.88	0.56
16:J:123:ARG:NH1	16:J:124:ARG:O	2.38	0.56
40:i:41:LYS:NZ	40:i:50:THR:O	2.38	0.56
7:A:570:G:C4	7:A:2030:A:N7	2.74	0.56
7:A:571:U:C4	7:A:2030:A:C6	2.94	0.56
7:A:1668:A:H4'	7:A:1669:A:H5'	1.87	0.56
7:A:2584:U:H2'	7:A:2585:U:H2'	1.88	0.56
7:A:2722:G:H3'	7:A:2723:C:C6	2.41	0.56
8:B:101:A:N6	8:B:102:G:N1	2.54	0.56
10:D:35:SER:HA	10:D:38:LYS:HB2	1.87	0.56
10:D:63:SER:HA	10:D:97:VAL:HG11	1.88	0.56
51:t:45:ASP:N	51:t:45:ASP:OD1	2.37	0.56
8:B:66:A:H1'	8:B:173:U:H2'	1.88	0.56
8:B:674:G:H2'	8:B:675:A:H8	1.69	0.56
8:B:1223:C:H5"	8:B:1224:U:H5"	1.86	0.56
11:E:85:ASN:ND2	11:E:88:GLU:OE2	2.38	0.56
23:Q:1:MET:HE3	23:Q:24:SER:HB2	1.88	0.56
7:A:2646:C:N4	7:A:2675:A:C2	2.74	0.56
7:A:2683:C:O2	41:j:70:ARG:NH2	2.38	0.56
8:B:126:G:OP1	8:B:633:G:N2	2.38	0.56
8:B:684:U:O2'	18:L:40:ASN:O	2.21	0.56
11:E:85:ASN:O	11:E:89:ASN:ND2	2.39	0.56
13:G:91:ARG:NH1	13:G:92:THR:O	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:y:9:A:O2'	56:y:10:G:N7	2.36	0.56
5:5:126:GLU:HG2	5:5:128:PRO:HD3	1.88	0.56
7:A:626:A:H2'	42:k:78:ARG:HH22	1.69	0.56
7:A:948:C:H2'	7:A:949:G:H8	1.70	0.56
8:B:586:C:OP1	24:R:36:LYS:NZ	2.39	0.56
8:B:976:G:H1	8:B:1362:A:HO2'	1.51	0.56
10:D:64:ILE:HG23	10:D:99:ALA:HA	1.88	0.56
17:K:54:SER:O	21:O:81:ARG:NH1	2.38	0.56
32:a:93:C:H2'	32:a:94:A:H8	1.71	0.56
2:1:25:LYS:HB3	42:k:62:PRO:HG2	1.88	0.56
4:3:48:ALA:HB2	4:3:57:ILE:HG22	1.87	0.56
7:A:1412:U:H2'	7:A:1413:A:H8	1.71	0.56
8:B:407:U:OP1	11:E:3:ARG:NH2	2.38	0.56
21:O:16:LEU:HA	21:O:19:LYS:HB3	1.88	0.56
36:e:2:ALA:N	36:e:94:GLU:OE2	2.39	0.56
36:e:29:PRO:HG2	36:e:165:GLU:HB3	1.86	0.56
1:0:3:ARG:O	1:0:6:GLN:NE2	2.39	0.55
7:A:2561:U:O3'	41:j:40:LYS:NZ	2.38	0.55
7:A:2633:G:N2	7:A:2786:U:O2	2.39	0.55
8:B:434:U:H2'	8:B:435:A:H8	1.71	0.55
40:i:41:LYS:NZ	40:i:52:ASP:OD1	2.38	0.55
7:A:571:U:C4	7:A:2030:A:N6	2.73	0.55
8:B:437:U:O2'	11:E:120:HIS:ND1	2.39	0.55
34:c:142:VAL:HG13	34:c:144:GLY:H	1.72	0.55
43:l:40:ARG:HD3	43:l:93:VAL:HG21	1.86	0.55
5:5:278:LEU:HD21	5:5:427:LEU:HD21	1.89	0.55
7:A:247:G:OP1	7:A:386:G:O2'	2.24	0.55
7:A:2516:A:C6	7:A:2517:C:N4	2.74	0.55
8:B:902:G:H2'	8:B:903:G:H8	1.70	0.55
8:B:1045:C:H2'	8:B:1046:A:H8	1.70	0.55
7:A:1666:G:O2'	41:j:6:THR:OG1	2.25	0.55
12:F:156:LYS:O	15:I:64:LYS:NZ	2.39	0.55
50:s:99:ASN:ND2	50:s:101:GLU:OE2	2.40	0.55
2:1:8:ARG:NH2	7:A:244:A:OP2	2.39	0.55
7:A:629:G:N3	7:A:639:U:O2'	2.40	0.55
7:A:2126:A:N6	7:A:2171:A:OP2	2.40	0.55
8:B:546:A:OP1	11:E:70:ARG:N	2.38	0.55
8:B:585:G:H21	8:B:879:C:H1'	1.72	0.55
8:B:1078:U:O2	12:F:135:ASN:ND2	2.37	0.55
8:B:1439:G:H1	8:B:1462:C:H42	1.54	0.55
20:N:88:GLY:HA2	20:N:91:HIS:HD2	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:c:108:ASP:HB3	34:c:174:SER:H	1.72	0.55
47:p:26:GLY:O	47:p:30:ARG:NH1	2.40	0.55
2:1:23:LYS:NZ	7:A:630:G:OP2	2.38	0.55
7:A:885:C:O2'	7:A:891:G:N2	2.38	0.55
7:A:2171:A:H3'	7:A:2173:A:H62	1.72	0.55
8:B:208:U:O2	8:B:210:C:O2'	2.24	0.55
11:E:105:MET:HE2	11:E:171:LEU:HD22	1.89	0.55
13:G:21:MET:HA	13:G:24:ARG:HE	1.71	0.55
35:d:80:SER:O	35:d:80:SER:OG	2.24	0.55
54:w:16:THR:O	54:w:20:ASN:ND2	2.33	0.55
5:5:275:GLU:HA	5:5:278:LEU:HD12	1.87	0.55
7:A:1753:G:OP1	46:o:93:ARG:NH1	2.40	0.55
19:M:71:GLY:O	19:M:99:ARG:NH1	2.40	0.55
8:B:75:G:H22	8:B:93:U:H3	1.54	0.55
8:B:428:G:OP2	11:E:10:LYS:NZ	2.40	0.55
30:X:4:U:O4	30:X:6:A:N6	2.39	0.55
34:c:8:LYS:NZ	34:c:195:GLY:O	2.36	0.55
41:j:76:VAL:H	46:o:73:VAL:HG22	1.71	0.55
42:k:91:ASP:OD1	42:k:91:ASP:N	2.36	0.55
5:5:134:ASP:OD1	5:5:271:ARG:NH1	2.40	0.55
7:A:2484:G:OP1	43:l:44:ARG:NH2	2.37	0.55
8:B:35:G:N3	19:M:115:SER:OG	2.40	0.55
8:B:140:U:O4	8:B:221:C:N4	2.40	0.55
8:B:1342:C:H2'	8:B:1343:G:H8	1.71	0.55
8:B:1532:U:O4	28:V:47:ARG:NH1	2.40	0.55
11:E:44:ARG:NH1	11:E:45:LYS:O	2.40	0.55
16:J:12:ARG:HG3	16:J:13:LYS:HG2	1.88	0.55
56:y:10:G:H22	56:y:26:A:H1'	1.72	0.55
7:A:2002:G:OP2	44:m:9:GLN:NE2	2.40	0.55
15:I:2:SER:OG	15:I:3:MET:N	2.41	0.55
18:L:13:ARG:N	18:L:76:GLU:O	2.40	0.55
19:M:27:CYS:SG	19:M:30:LYS:NZ	2.70	0.55
22:P:26:GLU:OE2	22:P:77:ARG:NE	2.40	0.55
36:e:49:LEU:HA	36:e:52:ASN:HB2	1.89	0.55
37:f:17:VAL:HG12	37:f:26:ILE:HG12	1.89	0.55
7:A:325:G:O6	7:A:338:G:N2	2.40	0.54
7:A:1658:C:OP1	34:c:140:HIS:NE2	2.40	0.54
7:A:2849:U:O4	46:o:21:ARG:NH1	2.40	0.54
8:B:151:A:OP2	8:B:169:C:N4	2.40	0.54
12:F:32:SER:OG	12:F:33:PHE:N	2.38	0.54
13:G:2:ARG:NH2	13:G:92:THR:OG1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:X:28:C:N4	30:X:42:G:O6	2.40	0.54
43:l:19:GLY:O	43:l:38:ARG:NH1	2.40	0.54
7:A:605:G:N3	7:A:657:U:O2'	2.38	0.54
7:A:1088:A:N6	39:h:131:GLY:O	2.40	0.54
8:B:663:A:O3'	25:S:53:ARG:NH2	2.40	0.54
8:B:1359:C:H4'	8:B:1362:A:H62	1.72	0.54
48:q:15:SER:OG	48:q:16:GLU:N	2.38	0.54
7:A:370:G:O2'	7:A:424:G:OP1	2.26	0.54
33:b:6:CYS:SG	33:b:18:LYS:NZ	2.70	0.54
7:A:83:A:OP1	50:s:2:ALA:N	2.40	0.54
7:A:2258:C:O2'	7:A:2427:C:OP2	2.20	0.54
24:R:68:SER:OG	24:R:69:LYS:N	2.41	0.54
45:n:31:THR:OG1	45:n:34:HIS:O	2.26	0.54
7:A:2522:U:O2'	7:A:2647:U:OP1	2.21	0.54
7:A:2875:C:HO2'	46:o:2:SER:N	2.04	0.54
8:B:980:C:O2'	21:O:13:ARG:NH2	2.40	0.54
9:C:131:LYS:HA	9:C:134:ALA:HB3	1.88	0.54
45:n:67:ASN:OD1	45:n:70:ALA:N	2.40	0.54
57:z:17:THR:OG1	57:z:18:GLY:N	2.38	0.54
7:A:141:G:N1	29:W:1:MET:SD	2.72	0.54
7:A:1368:G:C2	7:A:1369:G:C5	2.95	0.54
8:B:18:C:OP1	12:F:132:ASN:ND2	2.40	0.54
8:B:73:C:O2'	8:B:75:G:N7	2.36	0.54
14:H:16:PRO:O	16:J:45:ARG:NH2	2.41	0.54
34:c:124:ARG:NH1	34:c:161:MET:O	2.40	0.54
43:l:1:MET:SD	43:l:1:MET:N	2.75	0.54
7:A:1129:A:N6	7:A:2491:U:OP1	2.40	0.54
7:A:1792:G:O2'	7:A:1830:C:OP1	2.26	0.54
8:B:974:A:H4'	8:B:975:A:H3'	1.89	0.54
8:B:1249:C:N4	8:B:1288:A:OP2	2.38	0.54
14:H:113:ASP:HB2	14:H:119:ARG:HB3	1.90	0.54
20:N:8:ASN:HD21	20:N:22:ILE:HD12	1.73	0.54
33:b:160:THR:OG1	33:b:161:TYR:N	2.41	0.54
44:m:117:ASP:OD1	44:m:117:ASP:N	2.33	0.54
56:y:18:G:N1	56:y:57:G:OP2	2.41	0.54
7:A:636:G:OP1	42:k:129:LYS:NZ	2.41	0.54
7:A:2507:C:O3'	31:Z:76:A:H4'	2.08	0.54
7:A:30:G:N1	7:A:511:U:O2	2.39	0.54
7:A:151:C:H2'	7:A:152:A:H8	1.73	0.54
7:A:379:G:O2'	7:A:2232:C:OP1	2.26	0.54
7:A:776:G:N2	7:A:2072:C:OP1	2.36	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:140:U:N3	8:B:141:G:O6	2.40	0.54
8:B:318:G:H1	8:B:335:C:H42	1.56	0.54
8:B:419:C:N4	8:B:424:G:O6	2.41	0.54
9:C:82:ASP:OD1	9:C:82:ASP:N	2.40	0.54
15:I:64:LYS:HB3	15:I:71:VAL:HG11	1.90	0.54
15:I:87:LYS:NZ	15:I:88:ARG:O	2.41	0.54
17:K:85:ASP:OD1	17:K:85:ASP:N	2.41	0.54
20:N:50:GLU:HA	20:N:53:ILE:HB	1.90	0.54
50:s:48:PRO:HB2	50:s:54:GLN:HB3	1.90	0.54
7:A:242:G:N2	7:A:255:A:OP2	2.40	0.54
7:A:572:A:OP2	48:q:79:ARG:NH2	2.41	0.54
7:A:2635:A:O2'	34:c:49:GLN:NE2	2.41	0.54
8:B:1237:C:O2'	8:B:1300:G:N2	2.33	0.54
14:H:57:SER:OG	14:H:58:GLU:N	2.41	0.54
3:2:20:ASP:O	3:2:22:VAL:N	2.41	0.53
7:A:2529:G:OP2	37:f:172:LYS:NZ	2.33	0.53
7:A:2857:G:N2	7:A:2860:A:OP2	2.41	0.53
8:B:1320:C:O2	26:T:36:ARG:NH2	2.37	0.53
20:N:76:SER:O	20:N:80:LEU:N	2.37	0.53
29:W:79:ASP:OD1	29:W:79:ASP:N	2.41	0.53
7:A:319:G:OP2	35:d:132:LYS:NZ	2.40	0.53
7:A:2060:A:N7	7:A:2502:G:N2	2.55	0.53
7:A:2840:C:H5"	44:m:53:THR:HG21	1.91	0.53
8:B:1011:C:O2	8:B:1018:G:N2	2.42	0.53
7:A:880:G:OP2	7:A:892:A:N6	2.42	0.53
8:B:673:A:O3'	13:G:86:ARG:NH2	2.41	0.53
16:J:9:THR:HB	16:J:85:ARG:HH11	1.74	0.53
21:O:4:GLN:O	21:O:8:ALA:N	2.39	0.53
36:e:111:ILE:HD13	36:e:137:ILE:HD13	1.90	0.53
52:u:40:GLN:OE1	52:u:44:LYS:N	2.42	0.53
4:3:95:GLU:O	4:3:96:GLN:NE2	2.42	0.53
7:A:690:G:O2'	7:A:780:G:OP1	2.23	0.53
7:A:1358:G:H2'	7:A:1359:A:OP2	2.09	0.53
8:B:402:G:O2'	8:B:620:C:N4	2.42	0.53
10:D:191:THR:HG23	10:D:193:TYR:H	1.73	0.53
3:2:1:MET:HE2	3:2:36:ARG:HB2	1.91	0.53
5:5:253:ILE:HD11	5:5:263:VAL:HG22	1.91	0.53
7:A:414:C:N4	7:A:2409:G:O6	2.38	0.53
9:C:20:THR:HB	9:C:38:VAL:HG22	1.90	0.53
21:O:65:ARG:NH2	21:O:77:PHE:O	2.42	0.53
29:W:20:ALA:HA	29:W:31:VAL:HG21	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:3:ARG:NH1	7:A:752:A:OP1	2.38	0.53
5:5:304:ALA:HA	5:5:307:ILE:HG22	1.90	0.53
7:A:20:C:OP1	47:p:22:LYS:NZ	2.42	0.53
7:A:1065:U:OP2	39:h:92:LYS:NZ	2.41	0.53
8:B:582:C:OP2	8:B:758:C:N4	2.32	0.53
28:V:40:LYS:O	28:V:44:GLU:N	2.36	0.53
7:A:833:A:H2'	7:A:834:G:H8	1.73	0.53
7:A:963:U:O2'	7:A:2250:G:O6	2.24	0.53
10:D:120:ILE:HA	10:D:123:GLN:HE21	1.72	0.53
19:M:36:ARG:NH1	19:M:37:VAL:O	2.42	0.53
24:R:31:HIS:HD2	24:R:33:ILE:H	1.57	0.53
1:0:33:ARG:NH2	7:A:467:G:OP1	2.41	0.53
7:A:578:G:OP1	7:A:1255:U:O2'	2.25	0.53
7:A:1683:U:H2'	7:A:1684:G:H8	1.74	0.53
7:A:2124:G:H1	7:A:2175:C:H1'	1.73	0.53
8:B:1178:G:N2	8:B:1181:G:OP2	2.34	0.53
37:f:27:LYS:NZ	37:f:28:GLY:O	2.41	0.53
7:A:2461:A:H1'	7:A:2492:U:H3	1.73	0.53
7:A:2720:U:OP1	46:o:53:ARG:NH2	2.41	0.53
8:B:811:C:O2'	8:B:901:A:N1	2.42	0.53
9:C:89:GLN:HE22	9:C:222:ARG:HH22	1.57	0.53
14:H:113:ASP:OD2	14:H:122:ASN:ND2	2.42	0.53
43:l:69:PRO:HA	43:l:94:ALA:HB2	1.90	0.53
7:A:544:C:N4	7:A:547:A:O2'	2.42	0.53
7:A:1091:G:H22	7:A:1100:C:H42	1.56	0.53
7:A:2746:U:C5	7:A:2747:G:N7	2.77	0.53
7:A:2782:G:N2	7:A:2783:U:C2	2.77	0.53
8:B:504:C:H42	8:B:541:G:H1	1.57	0.53
8:B:944:G:N1	8:B:1338:G:OP2	2.42	0.53
14:H:28:ASN:ND2	14:H:31:MET:SD	2.76	0.53
23:Q:35:ARG:HH22	23:Q:38:PHE:HD2	1.56	0.53
30:X:48:C:H5"	30:X:49:G:H5"	1.90	0.53
44:m:15:SER:O	44:m:15:SER:OG	2.27	0.53
47:p:83:LEU:HD22	47:p:88:VAL:HB	1.90	0.53
7:A:1392:A:N6	29:W:18:GLU:OE1	2.41	0.52
7:A:2482:A:O3'	31:Z:63:U:O2'	2.27	0.52
8:B:651:C:N4	8:B:753:A:OP2	2.41	0.52
8:B:953:G:O6	8:B:1228:C:N4	2.41	0.52
9:C:87:CYS:H	9:C:89:GLN:HE21	1.55	0.52
46:o:52:ASN:N	46:o:52:ASN:OD1	2.41	0.52
46:o:63:LYS:HE3	46:o:65:SER:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1064:C:H2'	7:A:1066:U:H4'	1.90	0.52
7:A:243:U:H2'	7:A:244:A:H8	1.74	0.52
7:A:576:U:O2'	7:A:2502:G:O6	2.25	0.52
7:A:1031:G:N3	7:A:1124:G:N2	2.57	0.52
7:A:1782:U:O2	7:A:2608:G:O2'	2.26	0.52
17:K:66:GLU:OE2	21:O:97:LYS:NZ	2.42	0.52
3:2:6:SER:HB2	7:A:1031:G:H4'	1.92	0.52
5:5:126:GLU:OE2	5:5:285:ARG:NH1	2.42	0.52
7:A:922:C:H2'	7:A:923:G:H8	1.73	0.52
7:A:1403:A:HO2'	7:A:1471:G:HO2'	1.52	0.52
7:A:2304:G:H4'	36:e:130:MET:HA	1.91	0.52
8:B:981:U:H1'	21:O:61:ARG:HE	1.73	0.52
15:I:76:GLN:HG3	15:I:128:TYR:HB2	1.90	0.52
36:e:148:ARG:HB3	36:e:150:ARG:HG3	1.90	0.52
54:w:21:LEU:HA	54:w:25:GLN:HB3	1.91	0.52
7:A:381:G:H1	7:A:393:C:H42	1.57	0.52
7:A:1536:C:O2	7:A:1537:G:N2	2.43	0.52
7:A:2291:U:OP1	7:A:2380:C:O2'	2.28	0.52
7:A:2297:A:N3	7:A:2297:A:C2'	2.73	0.52
8:B:585:G:O2'	8:B:879:C:OP1	2.25	0.52
8:B:1116:U:H3	8:B:1184:G:H1	1.57	0.52
8:B:1295:U:O2'	20:N:42:ASP:OD2	2.28	0.52
11:E:58:LYS:HE3	11:E:203:LEU:HD23	1.92	0.52
11:E:150:LYS:O	11:E:152:GLN:NE2	2.43	0.52
16:J:30:ILE:HA	16:J:65:ILE:HB	1.91	0.52
21:O:64:CYS:SG	21:O:65:ARG:N	2.82	0.52
39:h:126:THR:HA	39:h:129:ILE:HG22	1.91	0.52
41:j:13:ASN:OD1	41:j:98:ARG:N	2.40	0.52
7:A:18:U:H2'	7:A:19:A:C8	2.45	0.52
7:A:1119:U:OP1	51:t:83:LYS:NZ	2.42	0.52
7:A:1649:G:N1	7:A:2009:A:C6	2.78	0.52
7:A:1796:U:H2'	7:A:1797:G:C8	2.45	0.52
7:A:2375:G:N2	7:A:2378:A:OP2	2.38	0.52
7:A:2688:G:N1	7:A:2720:U:OP2	2.42	0.52
8:B:446:G:H21	8:B:488:C:H41	1.56	0.52
11:E:100:ASN:HD21	11:E:104:ARG:HE	1.57	0.52
23:Q:4:ILE:HG12	23:Q:21:VAL:HG12	1.91	0.52
39:h:90:SER:HB2	39:h:93:PRO:HA	1.92	0.52
5:5:334:ARG:NH1	5:5:335:GLU:OE2	2.42	0.52
7:A:1223:G:OP2	48:q:90:ARG:NH1	2.40	0.52
7:A:1865:U:OP1	7:A:2409:G:N2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:885:G:H1	8:B:912:C:H42	1.57	0.52
18:L:20:VAL:HG12	18:L:83:GLU:HB2	1.92	0.52
2:1:9:GLY:O	2:1:13:ARG:NH2	2.43	0.52
4:3:6:LEU:HD11	4:3:12:ARG:HH21	1.74	0.52
4:3:80:LYS:HA	4:3:106:VAL:HG12	1.92	0.52
7:A:1718:G:O6	7:A:1743:G:N2	2.42	0.52
8:B:335:C:H2'	8:B:336:A:H8	1.75	0.52
8:B:842:U:O2'	8:B:845:A:OP2	2.26	0.52
8:B:1049:U:OP1	21:O:2:ALA:N	2.43	0.52
8:B:1314:C:N4	26:T:3:ARG:O	2.43	0.52
10:D:28:GLU:O	10:D:32:ASN:ND2	2.42	0.52
21:O:35:ASN:HD22	21:O:41:ARG:HH22	1.58	0.52
55:x:3:LYS:NZ	55:x:40:ASP:OD2	2.36	0.52
7:A:1952:A:OP1	41:j:44:LYS:NZ	2.39	0.52
8:B:1106:G:O2'	10:D:169:ARG:NH1	2.43	0.52
11:E:44:ARG:HH12	11:E:47:ARG:HB2	1.74	0.52
33:b:10:SER:O	33:b:10:SER:OG	2.26	0.52
7:A:280:U:O4	7:A:361:G:N2	2.43	0.52
7:A:445:C:OP1	47:p:2:ALA:N	2.43	0.52
7:A:1653:G:OP1	7:A:2822:G:N1	2.31	0.52
7:A:2163:A:O3'	7:A:2170:A:O2'	2.27	0.52
7:A:2591:C:H42	7:A:2603:G:H1	1.57	0.52
33:b:5:LYS:HD2	33:b:17:VAL:HG12	1.92	0.52
33:b:180:GLU:OE2	33:b:270:ARG:NH1	2.43	0.52
36:e:48:LYS:O	36:e:52:ASN:ND2	2.39	0.52
5:5:165:THR:HB	5:5:239:LYS:HG3	1.92	0.51
7:A:540:C:H2'	7:A:541:A:H8	1.75	0.51
7:A:576:U:H4'	7:A:2502:G:C8	2.45	0.51
7:A:1904:G:N2	7:A:1905:C:O2	2.43	0.51
7:A:2576:G:N3	7:A:2576:G:C5'	2.73	0.51
8:B:428:G:O2'	11:E:33:LYS:NZ	2.43	0.51
8:B:1372:U:OP2	16:J:13:LYS:NZ	2.42	0.51
14:H:65:ALA:HB2	14:H:128:ALA:HA	1.92	0.51
7:A:1395:A:N6	7:A:1398:C:O2	2.42	0.51
7:A:1814:G:C5	7:A:1815:A:N7	2.79	0.51
7:A:2295:C:OP1	45:n:10:ARG:NH2	2.44	0.51
7:A:2343:U:O2'	7:A:2373:G:O2'	2.28	0.51
7:A:2649:C:H42	7:A:2671:G:H1	1.59	0.51
8:B:1058:G:H22	17:K:55:PRO:HG3	1.75	0.51
11:E:194:ASP:OD1	11:E:194:ASP:N	2.44	0.51
11:E:198:HIS:HE2	12:F:103:THR:HG1	1.52	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:J:91:ASP:OD1	16:J:91:ASP:N	2.43	0.51
7:A:2447:G:N2	7:A:2450:A:OP2	2.32	0.51
8:B:559:A:H4'	8:B:560:A:H3'	1.93	0.51
8:B:1302:C:N4	20:N:42:ASP:OD1	2.41	0.51
10:D:138:VAL:HA	10:D:149:ILE:HD11	1.91	0.51
15:I:5:ASP:OD2	15:I:77:ARG:NE	2.42	0.51
17:K:41:PRO:O	17:K:72:ARG:NH1	2.43	0.51
24:R:52:GLU:O	24:R:81:LYS:NZ	2.44	0.51
47:p:81:ASN:OD1	47:p:85:LYS:NZ	2.37	0.51
7:A:410:G:N2	7:A:418:C:O2	2.44	0.51
8:B:571:U:O4	8:B:864:A:N6	2.44	0.51
8:B:948:C:H2'	8:B:949:A:H8	1.75	0.51
8:B:977:A:O2'	8:B:981:U:N3	2.36	0.51
8:B:1218:C:H2'	8:B:1219:A:H8	1.75	0.51
8:B:1348:U:H2'	8:B:1349:A:H8	1.76	0.51
12:F:82:GLN:N	12:F:147:MET:SD	2.79	0.51
15:I:15:ARG:HH11	15:I:75:ILE:HG23	1.73	0.51
39:h:101:ILE:HG12	39:h:138:LEU:HD11	1.92	0.51
1:0:31:LEU:HD22	1:0:42:LEU:HD23	1.92	0.51
7:A:2127:G:H22	7:A:2161:C:H2'	1.75	0.51
8:B:137:U:H2'	8:B:138:G:H8	1.76	0.51
11:E:144:SER:OG	11:E:145:ILE:N	2.43	0.51
15:I:113:ASP:O	15:I:117:ARG:NH1	2.43	0.51
16:J:52:LEU:HB3	16:J:57:MET:HG2	1.91	0.51
7:A:385:C:H42	7:A:411:G:H1	1.58	0.51
7:A:776:G:N7	7:A:793:A:O2'	2.42	0.51
7:A:2798:U:H4'	7:A:2799:A:H5'	1.93	0.51
8:B:127:G:O2'	24:R:6:ARG:NH2	2.43	0.51
8:B:254:G:N2	24:R:18:GLU:OE1	2.42	0.51
8:B:456:A:N6	8:B:476:U:O4	2.44	0.51
8:B:1242:G:N2	8:B:1296:C:O2'	2.44	0.51
14:H:76:LYS:HE2	14:H:89:VAL:HG11	1.93	0.51
21:O:16:LEU:HD12	21:O:54:ASP:HB2	1.92	0.51
35:d:7:ASP:OD1	35:d:7:ASP:N	2.41	0.51
39:h:74:PRO:HD2	39:h:113:LYS:HE3	1.93	0.51
5:5:315:ARG:HA	5:5:318:ALA:HB3	1.93	0.51
7:A:690:G:N2	7:A:773:U:O2	2.43	0.51
34:c:18:ASP:OD1	34:c:18:ASP:N	2.37	0.51
7:A:775:G:OP1	7:A:777:G:O2'	2.24	0.51
8:B:28:A:O2'	8:B:296:U:OP1	2.22	0.51
8:B:738:C:OP1	13:G:2:ARG:NE	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:932:C:H5”	14:H:5:ARG:HH12	1.76	0.51
8:B:1345:U:OP1	16:J:122:ARG:NH1	2.44	0.51
38:g:5:LEU:HD12	38:g:17:ASP:HB2	1.93	0.51
7:A:807:U:OP2	42:k:41:ARG:NH1	2.43	0.51
8:B:54:C:H2’	8:B:352:C:H41	1.75	0.51
8:B:1445:U:H3	8:B:1457:G:H1	1.57	0.51
36:e:170:LEU:HG	36:e:173:PHE:HB2	1.92	0.51
7:A:2065:C:O2	7:A:2446:G:N2	2.43	0.51
7:A:2112:G:N2	30:X:19:G:O4’	2.44	0.51
7:A:2131:U:H5’	7:A:2158:A:H62	1.76	0.51
7:A:2564:A:OP1	7:A:2648:G:O2’	2.24	0.51
8:B:1193:G:OP1	10:D:167:TRP:NE1	2.39	0.51
8:B:1372:U:OP1	16:J:74:GLY:N	2.38	0.51
11:E:19:LEU:HA	11:E:64:ILE:HG12	1.91	0.51
14:H:113:ASP:O	14:H:119:ARG:NH2	2.44	0.51
16:J:120:LYS:HB2	16:J:123:ARG:HB3	1.92	0.51
19:M:29:GLN:HG2	19:M:81:LEU:HD23	1.93	0.51
34:c:103:ASP:N	34:c:103:ASP:OD1	2.42	0.51
3:2:19:ARG:NE	7:A:2756:U:OP2	2.44	0.50
4:3:46:LEU:HD21	4:3:91:LEU:HD23	1.93	0.50
7:A:2285:C:OP2	57:z:6:ARG:NH1	2.39	0.50
7:A:2403:C:C4	7:A:2415:G:N1	2.79	0.50
8:B:1250:A:N1	8:B:1353:G:N2	2.50	0.50
10:D:24:ALA:HB1	10:D:28:GLU:HG2	1.94	0.50
32:a:27:C:OP1	45:n:34:HIS:NE2	2.40	0.50
50:s:38:GLY:HA2	50:s:41:LEU:HD21	1.92	0.50
7:A:18:U:H6	7:A:18:U:H3’	1.77	0.50
7:A:2041:U:H2’	7:A:2042:A:H8	1.77	0.50
7:A:2368:C:H2’	7:A:2369:A:H8	1.77	0.50
8:B:933:G:O6	14:H:3:ARG:NH2	2.44	0.50
18:L:33:THR:HG22	18:L:44:TRP:HB3	1.92	0.50
19:M:106:GLY:HA3	19:M:119:VAL:HG22	1.91	0.50
22:P:24:SER:OG	22:P:26:GLU:OE1	2.28	0.50
4:3:56:ARG:NH2	4:3:74:ASN:OD1	2.41	0.50
7:A:680:C:N3	7:A:798:G:N2	2.60	0.50
7:A:2658:C:OP1	37:f:158:LYS:NZ	2.44	0.50
8:B:613:C:OP2	11:E:81:ARG:NE	2.44	0.50
8:B:1097:C:O2’	8:B:1169:A:O2’	2.28	0.50
8:B:1128:C:O2’	8:B:1147:C:N3	2.39	0.50
21:O:33:ASP:H	21:O:35:ASN:HD21	1.57	0.50
26:T:16:LEU:HA	26:T:19:VAL:HG12	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:2579:C:H3'	7:A:2579:C:H6	1.76	0.50
11:E:161:LEU:O	11:E:165:ARG:N	2.43	0.50
32:a:114:C:H2'	32:a:115:A:H8	1.77	0.50
33:b:146:MET:HE3	33:b:154:LEU:HD11	1.93	0.50
36:e:33:LYS:HE2	36:e:157:THR:HG21	1.92	0.50
51:t:41:GLU:N	51:t:41:GLU:OE1	2.44	0.50
53:v:39:TRP:HB2	53:v:46:PHE:HE1	1.75	0.50
5:5:411:VAL:HA	5:5:414:LYS:HE2	1.93	0.50
8:B:632:U:H5"	8:B:633:G:H8	1.75	0.50
11:E:73:ARG:O	11:E:77:LYS:NZ	2.38	0.50
16:J:26:GLY:HA3	16:J:58:VAL:HA	1.94	0.50
39:h:7:ALA:HB3	39:h:31:GLN:HE21	1.76	0.50
53:v:35:SER:O	53:v:35:SER:OG	2.26	0.50
57:z:10:LYS:HB3	57:z:52:ALA:HB3	1.94	0.50
7:A:1146:C:H2'	7:A:1147:A:H8	1.77	0.50
7:A:1296:G:OP1	7:A:2709:G:O2'	2.26	0.50
7:A:2796:U:H3	7:A:2799:A:H61	1.59	0.50
8:B:589:U:H5"	15:I:30:SER:HB2	1.93	0.50
8:B:928:G:O2'	8:B:1533:C:OP1	2.27	0.50
8:B:1078:U:O2'	12:F:138:ARG:NH1	2.45	0.50
8:B:1237:C:N4	8:B:1336:C:O2	2.44	0.50
11:E:118:VAL:HG22	11:E:123:ILE:HD12	1.93	0.50
32:a:48:U:H4'	45:n:100:HIS:HD2	1.76	0.50
7:A:1069:A:O2'	7:A:1073:A:OP2	2.29	0.50
7:A:1357:C:C2'	7:A:1358:G:H5'	2.41	0.50
7:A:1432:G:O6	7:A:1561:C:N4	2.43	0.50
7:A:1834:U:O2	7:A:1972:G:N2	2.44	0.50
7:A:2292:U:H2'	7:A:2293:G:H8	1.77	0.50
8:B:410:G:N7	8:B:429:U:O2'	2.37	0.50
8:B:1251:A:N3	8:B:1369:C:O2'	2.42	0.50
29:W:3:ARG:O	29:W:5:GLU:N	2.45	0.50
30:X:5:G:N1	30:X:68:C:N3	2.58	0.50
41:j:59:LYS:NZ	41:j:89:ASN:O	2.45	0.50
41:j:77:ILE:HG12	46:o:72:ARG:HD2	1.94	0.50
7:A:13:A:C2	7:A:526:A:C5	2.99	0.50
7:A:13:A:C6	7:A:525:U:C2	3.00	0.50
8:B:54:C:N4	8:B:353:A:OP2	2.43	0.50
8:B:74:A:C5	8:B:75:G:H1'	2.47	0.50
8:B:874:G:N2	15:I:16:ASN:OD1	2.44	0.50
12:F:99:ALA:HB3	12:F:122:ASN:HB3	1.92	0.50
30:X:53:G:N2	30:X:57:G:OP1	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:c:129:THR:OG1	34:c:140:HIS:O	2.28	0.50
56:y:7:G:N2	56:y:67:C:O2	2.45	0.50
7:A:2017:U:O2	7:A:2017:U:H2'	2.11	0.49
8:B:689:C:OP2	18:L:53:ARG:NH2	2.45	0.49
8:B:1310:G:OP2	20:N:87:ARG:NH2	2.45	0.49
9:C:138:THR:HA	9:C:141:LEU:HB2	1.94	0.49
19:M:23:ALA:HB2	19:M:95:TYR:HE1	1.75	0.49
22:P:13:SER:HA	22:P:19:ALA:HA	1.94	0.49
25:S:71:THR:O	25:S:74:HIS:NE2	2.45	0.49
34:c:131:ASP:O	34:c:136:ASN:ND2	2.45	0.49
35:d:150:THR:OG1	35:d:151:GLY:N	2.46	0.49
36:e:121:SER:O	36:e:121:SER:OG	2.28	0.49
37:f:104:ASN:ND2	37:f:114:ASP:OD1	2.44	0.49
7:A:372:G:OP2	53:v:61:LYS:NZ	2.45	0.49
7:A:1999:C:O2	7:A:2687:U:O2'	2.27	0.49
7:A:2117:A:N6	7:A:2166:U:O2	2.44	0.49
8:B:41:G:N3	8:B:402:G:N1	2.58	0.49
8:B:1308:U:OP1	20:N:97:VAL:N	2.41	0.49
12:F:114:VAL:HG11	12:F:140:THR:HG21	1.94	0.49
18:L:126:LYS:O	28:V:34:ARG:NE	2.29	0.49
23:Q:35:ARG:NH2	23:Q:37:GLY:O	2.45	0.49
49:r:80:PRO:O	49:r:100:THR:OG1	2.27	0.49
2:1:31:HIS:O	2:1:33:LEU:N	2.41	0.49
7:A:307:G:N2	7:A:310:A:OP2	2.43	0.49
7:A:457:A:H61	7:A:470:A:H5"	1.77	0.49
7:A:1849:G:H2'	7:A:1850:G:C8	2.42	0.49
7:A:2072:C:O2	7:A:2440:C:N4	2.45	0.49
7:A:2303:G:O2'	36:e:121:SER:O	2.28	0.49
8:B:1238:A:H2'	8:B:1239:A:H8	1.75	0.49
10:D:19:ASN:O	10:D:40:ARG:NH2	2.44	0.49
24:R:11:ARG:HH21	24:R:56:GLY:HA3	1.76	0.49
43:l:50:ARG:HG3	43:l:65:ILE:HD11	1.93	0.49
54:w:3:ALA:O	54:w:7:ARG:NH2	2.46	0.49
7:A:1102:C:H2'	7:A:1103:A:C8	2.47	0.49
8:B:252:U:O4	8:B:253:A:N6	2.46	0.49
8:B:470:C:H2'	8:B:471:U:H4'	1.94	0.49
10:D:11:ARG:NH2	10:D:177:THR:O	2.45	0.49
15:I:8:ALA:HB2	15:I:77:ARG:HD3	1.94	0.49
40:i:14:ASP:OD1	40:i:14:ASP:N	2.34	0.49
51:t:2:PHE:O	51:t:62:THR:OG1	2.30	0.49
7:A:2313:C:H2'	7:A:2314:A:H8	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:2711:A:C5	7:A:2714:G:O4'	2.66	0.49
11:E:67:VAL:HG11	11:E:75:TYR:HE2	1.77	0.49
15:I:30:SER:OG	15:I:31:LYS:N	2.45	0.49
44:m:57:THR:O	44:m:57:THR:OG1	2.29	0.49
5:5:67:LEU:HD23	5:5:70:LEU:HD23	1.93	0.49
7:A:224:U:O4	7:A:419:U:O2'	2.30	0.49
7:A:2267:A:N3	7:A:2267:A:C3'	2.74	0.49
7:A:2446:G:H4'	7:A:2448:A:N7	2.28	0.49
8:B:98:A:H8	8:B:99:C:C5	2.31	0.49
17:K:71:LEU:O	17:K:72:ARG:NH1	2.39	0.49
23:Q:3:THR:OG1	23:Q:24:SER:OG	2.31	0.49
25:S:34:THR:HG23	25:S:36:SER:H	1.77	0.49
35:d:21:ARG:O	35:d:114:ARG:NH2	2.34	0.49
36:e:38:MET:HG3	36:e:57:LEU:HD11	1.95	0.49
49:r:47:VAL:HG12	49:r:103:ILE:HG21	1.93	0.49
5:5:121:GLU:HG2	5:5:414:LYS:HB2	1.94	0.49
7:A:495:G:H21	49:r:61:ASN:HD21	1.59	0.49
7:A:571:U:C4	7:A:2030:A:N1	2.80	0.49
7:A:598:U:H2'	7:A:599:A:H8	1.77	0.49
7:A:1143:A:OP1	40:i:27:ARG:NH2	2.40	0.49
7:A:1748:C:H2'	7:A:1749:A:H8	1.78	0.49
7:A:2009:A:H2'	7:A:2010:G:H8	1.77	0.49
7:A:2133:G:N2	7:A:2158:A:O5'	2.44	0.49
8:B:677:U:H3	8:B:713:G:H22	1.61	0.49
8:B:978:A:N7	8:B:1318:A:N6	2.60	0.49
11:E:174:ASP:OD1	11:E:174:ASP:N	2.45	0.49
16:J:106:ARG:NH1	16:J:107:ASP:O	2.45	0.49
32:a:66:A:O4'	32:a:108:A:N6	2.46	0.49
36:e:70:ALA:N	36:e:83:TYR:O	2.46	0.49
46:o:55:LEU:HA	46:o:77:HIS:HD2	1.76	0.49
3:2:3:VAL:HG21	7:A:2539:C:H5'	1.95	0.49
4:3:81:SER:OG	4:3:82:GLY:N	2.45	0.49
7:A:27:G:N2	7:A:512:G:H1'	2.28	0.49
7:A:729:G:N2	33:b:11:PRO:O	2.45	0.49
7:A:1458:U:H4'	7:A:1459:G:H5'	1.95	0.49
7:A:2128:G:O6	7:A:2160:C:N4	2.46	0.49
7:A:1652:A:OP1	44:m:8:ARG:NH2	2.46	0.49
7:A:1945:G:N2	7:A:1963:U:O4	2.46	0.49
7:A:2026:U:H2'	7:A:2027:G:H8	1.78	0.49
8:B:1445:U:O2	8:B:1457:G:N2	2.35	0.49
13:G:51:ILE:HD13	13:G:86:ARG:HH21	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Q:75:ILE:HD11	23:Q:80:LYS:HE2	1.94	0.49
7:A:500:G:N1	7:A:503:A:OP2	2.42	0.49
7:A:780:G:N1	33:b:229:ASP:OD2	2.42	0.49
7:A:1130:U:OP2	7:A:2570:G:N2	2.41	0.49
7:A:1826:G:OP2	33:b:222:GLY:N	2.46	0.49
8:B:1074:G:O2'	8:B:1101:A:N1	2.36	0.49
12:F:15:LEU:HA	12:F:37:THR:HG22	1.94	0.49
31:Z:27:G:H22	31:Z:44:U:H3	1.61	0.49
48:q:55:ASP:N	48:q:55:ASP:OD1	2.36	0.49
56:y:38:C:H3'	56:y:39:G:H8	1.77	0.49
7:A:1607:C:N4	7:A:1622:G:OP2	2.42	0.48
7:A:2252:G:N2	56:y:75:C:N3	2.61	0.48
8:B:729:A:H2'	8:B:730:G:H8	1.79	0.48
17:K:45:ARG:NH1	17:K:47:GLU:OE2	2.38	0.48
20:N:23:TYR:HD2	20:N:66:GLU:HA	1.78	0.48
39:h:121:ASP:N	39:h:121:ASP:OD1	2.45	0.48
41:j:60:ALA:HB1	41:j:84:CYS:HB2	1.95	0.48
7:A:537:G:N2	7:A:555:G:N3	2.61	0.48
7:A:1368:G:C2	7:A:1369:G:N7	2.81	0.48
8:B:667:G:N2	22:P:49:ASP:OD2	2.45	0.48
8:B:1009:U:H3	8:B:1020:G:H1	1.61	0.48
14:H:126:ASP:OD1	14:H:126:ASP:N	2.44	0.48
24:R:4:LYS:NZ	24:R:5:ILE:O	2.44	0.48
27:U:76:LYS:O	27:U:80:THR:OG1	2.24	0.48
33:b:114:ASP:OD1	33:b:114:ASP:N	2.44	0.48
47:p:110:VAL:O	47:p:114:LYS:N	2.46	0.48
7:A:548:G:O2'	7:A:549:G:N7	2.43	0.48
7:A:2087:G:C2	7:A:2088:A:C5	3.00	0.48
7:A:2298:A:H5"	36:e:72:LYS:HZ1	1.78	0.48
7:A:2581:G:H1	7:A:2610:C:HO2'	1.59	0.48
12:F:136:VAL:O	12:F:140:THR:N	2.46	0.48
14:H:70:ARG:HE	14:H:97:ASN:HB3	1.78	0.48
17:K:80:THR:O	17:K:83:THR:OG1	2.30	0.48
27:U:31:PHE:O	27:U:34:LYS:NZ	2.44	0.48
31:Z:58:A:O2'	31:Z:60:U:OP2	2.30	0.48
3:2:23:ILE:HB	3:2:38:GLY:HA3	1.95	0.48
5:5:280:SER:O	5:5:284:ASN:N	2.46	0.48
7:A:414:C:H2'	7:A:415:A:H8	1.78	0.48
7:A:1171:G:N1	7:A:1179:G:O6	2.46	0.48
7:A:1190:G:H2'	7:A:1191:G:H8	1.78	0.48
7:A:2167:U:N3	7:A:2170:A:N7	2.60	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:2831:G:OP2	34:c:59:ARG:NH1	2.41	0.48
8:B:1073:U:OP1	12:F:62:LYS:NZ	2.46	0.48
11:E:126:ASN:ND2	11:E:141:ASP:OD1	2.46	0.48
25:S:44:ILE:HG23	25:S:45:THR:HG23	1.96	0.48
53:v:72:ARG:NH1	53:v:78:TYR:OH	2.44	0.48
56:y:74:C:N3	56:y:75:C:N4	2.61	0.48
7:A:2588:G:O6	7:A:2607:G:N1	2.46	0.48
7:A:2827:C:H2'	7:A:2828:G:H8	1.78	0.48
8:B:231:U:H2'	8:B:232:G:H8	1.78	0.48
9:C:85:LEU:HA	9:C:89:GLN:HG3	1.96	0.48
19:M:110:ARG:HD2	19:M:119:VAL:HB	1.95	0.48
22:P:61:SER:O	22:P:65:LYS:NZ	2.43	0.48
7:A:391:A:O2'	7:A:410:G:OP1	2.30	0.48
7:A:548:G:H4'	7:A:549:G:C4	2.48	0.48
7:A:644:A:H61	7:A:2349:G:H21	1.61	0.48
7:A:1061:U:O2'	7:A:1064:C:N4	2.45	0.48
7:A:1806:C:O2	33:b:44:ASN:ND2	2.46	0.48
7:A:2315:G:OP1	36:e:33:LYS:NZ	2.45	0.48
7:A:2589:A:H2'	7:A:2590:A:C8	2.49	0.48
7:A:2641:G:H5"	40:i:78:THR:HB	1.94	0.48
8:B:461:A:H2'	8:B:462:G:H8	1.79	0.48
8:B:942:G:H21	16:J:126:GLN:HE22	1.61	0.48
8:B:949:A:N7	20:N:105:ASN:ND2	2.61	0.48
8:B:1288:A:N3	8:B:1352:C:O2'	2.45	0.48
17:K:85:ASP:O	17:K:89:ARG:NH1	2.37	0.48
30:X:29:U:H3	30:X:41:A:H61	1.60	0.48
7:A:833:A:H2'	7:A:834:G:C8	2.48	0.48
7:A:1358:G:C2	7:A:1372:U:OP2	2.65	0.48
7:A:2353:G:N2	7:A:2354:C:O2	2.46	0.48
7:A:2855:C:H2'	7:A:2856:A:H8	1.78	0.48
8:B:1243:C:H2'	8:B:1244:G:H8	1.77	0.48
11:E:151:LYS:HE3	11:E:178:MET:HE3	1.95	0.48
32:a:34:A:N6	32:a:44:G:O2'	2.47	0.48
5:5:34:ASN:HA	5:5:37:LYS:HE3	1.95	0.48
7:A:970:U:O2	7:A:984:A:O2'	2.29	0.48
7:A:1176:U:H2'	7:A:1177:G:C5	2.49	0.48
7:A:2008:C:N4	7:A:2009:A:N6	2.60	0.48
8:B:434:U:H2'	8:B:435:A:C8	2.49	0.48
9:C:71:GLY:HA3	9:C:80:VAL:HG21	1.94	0.48
9:C:147:SER:OG	9:C:148:LEU:N	2.47	0.48
10:D:113:ALA:HA	10:D:116:VAL:HG12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:H:111:ARG:NH1	14:H:123:GLU:OE1	2.47	0.48
29:W:19:LYS:NZ	29:W:84:TYR:OH	2.46	0.48
30:X:13:C:N3	30:X:14:A:N6	2.61	0.48
45:n:72:ALA:HB2	45:n:105:ALA:HB1	1.94	0.48
4:3:43:GLY:HA3	4:3:91:LEU:HD22	1.95	0.48
7:A:1105:U:H2'	7:A:1106:G:C8	2.48	0.48
7:A:2500:U:C2	7:A:2504:U:C4	3.01	0.48
11:E:58:LYS:NZ	11:E:69:GLU:OE2	2.42	0.48
33:b:227:PRO:HG3	33:b:234:GLY:HA3	1.95	0.48
3:2:24:ARG:NH1	7:A:2742:G:OP2	2.43	0.48
7:A:482:A:H4'	50:s:45:HIS:CD2	2.48	0.48
7:A:1326:U:HO2'	7:A:2010:G:HO2'	1.59	0.48
7:A:2591:C:N4	7:A:2592:G:O6	2.46	0.48
8:B:103:U:H2'	8:B:172:A:H61	1.79	0.48
8:B:408:A:O4'	11:E:154:ARG:NH2	2.47	0.48
8:B:1034:G:OP2	8:B:1036:A:N6	2.47	0.48
33:b:16:VAL:HB	33:b:206:GLY:HA3	1.96	0.48
42:k:132:ARG:HG3	42:k:142:ILE:HD12	1.96	0.48
56:y:1:G:H22	56:y:73:G:H21	1.61	0.48
3:2:3:VAL:HG12	3:2:36:ARG:HB3	1.96	0.47
4:3:50:GLN:HE22	4:3:90:CYS:HG	1.60	0.47
5:5:307:ILE:HG13	5:5:345:VAL:HG21	1.95	0.47
7:A:680:C:H2'	7:A:681:G:H8	1.78	0.47
7:A:1358:G:C2'	7:A:1359:A:OP2	2.61	0.47
7:A:2746:U:C4	7:A:2747:G:N7	2.82	0.47
8:B:2:A:N1	8:B:627:G:N2	2.62	0.47
8:B:1179:A:OP1	16:J:95:ARG:NH2	2.47	0.47
42:k:95:LEU:O	42:k:99:ASN:N	2.47	0.47
7:A:883:G:N2	7:A:894:U:O2'	2.47	0.47
7:A:1136:G:H2'	7:A:1137:G:H8	1.79	0.47
7:A:2354:C:H2'	7:A:2355:G:H8	1.79	0.47
10:D:12:LEU:HA	10:D:16:LYS:HB2	1.96	0.47
24:R:58:VAL:HB	24:R:79:VAL:HG23	1.95	0.47
28:V:34:ARG:HB3	28:V:35:ARG:HG2	1.95	0.47
30:X:11:C:H42	30:X:45:G:H21	1.62	0.47
33:b:252:THR:OG1	33:b:253:LYS:N	2.45	0.47
34:c:181:ASP:OD2	34:c:184:ARG:NH2	2.47	0.47
53:v:5:CYS:HB2	53:v:52:SER:HB3	1.96	0.47
5:5:327:LYS:NZ	50:s:60:GLU:OE1	2.47	0.47
7:A:1864:U:OP1	7:A:2410:G:O2'	2.30	0.47
7:A:2049:G:N2	7:A:2619:C:O2	2.36	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:2101:A:N6	7:A:2102:G:O6	2.48	0.47
7:A:2313:C:H5"	36:e:88:LYS:HD3	1.95	0.47
8:B:924:C:N4	8:B:925:G:O6	2.47	0.47
10:D:73:PRO:HG3	10:D:105:GLU:HB2	1.96	0.47
27:U:35:VAL:HG11	27:U:79:LEU:HD21	1.96	0.47
30:X:5:G:O6	30:X:68:C:N4	2.41	0.47
34:c:181:ASP:HB3	34:c:186:LEU:HB2	1.97	0.47
55:x:6:LYS:HG2	55:x:37:GLU:HB3	1.95	0.47
55:x:9:GLN:HG2	55:x:32:ILE:HA	1.96	0.47
1:0:37:LYS:NZ	7:A:468:G:OP2	2.48	0.47
7:A:2060:A:N6	7:A:2502:G:N2	2.62	0.47
7:A:2898:U:H2'	7:A:2899:A:C8	2.49	0.47
8:B:517:G:N2	8:B:530:G:OP1	2.42	0.47
8:B:693:G:OP1	18:L:127:ARG:NH1	2.44	0.47
8:B:1083:U:O2'	8:B:1102:A:OP2	2.32	0.47
8:B:1158:C:O2'	9:C:132:LYS:NZ	2.37	0.47
10:D:113:ALA:HB3	10:D:185:ASN:HB2	1.97	0.47
10:D:118:ASP:HA	10:D:121:THR:HG22	1.95	0.47
20:N:22:ILE:HG13	20:N:66:GLU:HG3	1.96	0.47
33:b:141:VAL:O	33:b:162:VAL:N	2.48	0.47
44:m:45:ARG:HD3	44:m:97:ILE:HD11	1.96	0.47
7:A:1039:A:H61	7:A:1116:G:H1	1.63	0.47
7:A:1776:G:N2	7:A:1777:U:O2	2.47	0.47
8:B:543:U:OP1	11:E:14:ARG:NH2	2.48	0.47
8:B:714:G:N2	8:B:777:A:N3	2.63	0.47
8:B:1111:A:N6	10:D:176:HIS:O	2.47	0.47
11:E:105:MET:HG2	11:E:171:LEU:HB3	1.96	0.47
14:H:2:PRO:HA	14:H:5:ARG:HB2	1.97	0.47
27:U:15:GLU:HA	27:U:18:ARG:HB3	1.96	0.47
34:c:109:VAL:HG11	34:c:193:VAL:HG23	1.95	0.47
36:e:117:LEU:H	36:e:177:PHE:N	2.13	0.47
3:2:1:MET:N	7:A:2526:G:N3	2.62	0.47
7:A:598:U:H2'	7:A:599:A:C8	2.50	0.47
7:A:970:U:H2'	7:A:971:G:H8	1.78	0.47
7:A:1079:C:O2'	39:h:134:ARG:NH1	2.48	0.47
7:A:2056:G:O6	7:A:2612:C:N3	2.47	0.47
7:A:2134:A:N6	7:A:2157:G:O2'	2.46	0.47
7:A:2722:G:C5	7:A:2723:C:C2	3.03	0.47
8:B:141:G:N2	8:B:222:C:O2'	2.47	0.47
8:B:625:U:H2'	8:B:626:G:H8	1.79	0.47
11:E:69:GLU:O	11:E:73:ARG:NH1	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:W:30:ILE:HG13	29:W:85:VAL:HG13	1.97	0.47
7:A:690:G:H21	33:b:43:ARG:HH21	1.61	0.47
7:A:877:A:H2'	7:A:878:A:C8	2.50	0.47
7:A:895:U:H2'	7:A:899:A:H61	1.80	0.47
7:A:1073:A:OP1	7:A:1075:C:N4	2.42	0.47
7:A:1649:G:N1	7:A:2009:A:N6	2.63	0.47
7:A:2370:G:O2'	57:z:44:ARG:NH1	2.47	0.47
7:A:2575:C:OP1	34:c:149:ASN:ND2	2.48	0.47
7:A:2674:G:H4'	41:j:30:ARG:HD2	1.96	0.47
8:B:164:G:H2'	8:B:165:G:H8	1.80	0.47
8:B:436:C:H4'	11:E:154:ARG:HG2	1.97	0.47
8:B:477:C:N3	8:B:478:A:N6	2.62	0.47
8:B:564:C:OP1	19:M:12:ARG:NH1	2.48	0.47
8:B:971:G:O2'	8:B:1365:G:O2'	2.31	0.47
12:F:74:VAL:HG21	12:F:144:LEU:HB3	1.95	0.47
14:H:51:ALA:HB2	14:H:58:GLU:HG3	1.96	0.47
23:Q:18:GLN:HB3	23:Q:35:ARG:HH21	1.80	0.47
26:T:13:LEU:HD12	26:T:16:LEU:HB3	1.96	0.47
28:V:18:ARG:HA	28:V:21:ARG:HD3	1.96	0.47
35:d:143:LEU:HD13	35:d:146:VAL:HG11	1.97	0.47
36:e:47:LYS:HA	36:e:50:LEU:HD12	1.96	0.47
38:g:30:LEU:HD22	38:g:36:ALA:HB2	1.97	0.47
51:t:90:ASP:N	51:t:90:ASP:OD1	2.46	0.47
57:z:34:LEU:N	57:z:51:GLU:OE1	2.45	0.47
7:A:69:C:HO2'	7:A:73:A:HO2'	1.56	0.47
7:A:581:C:H2'	7:A:582:A:C8	2.50	0.47
7:A:2068:U:H3	7:A:2430:A:H62	1.62	0.47
7:A:2189:U:H2'	7:A:2190:G:H8	1.80	0.47
7:A:2746:U:C2	7:A:2747:G:C8	3.02	0.47
13:G:86:ARG:NH1	25:S:64:TYR:O	2.48	0.47
20:N:91:HIS:CE1	20:N:97:VAL:HG21	2.50	0.47
23:Q:18:GLN:HA	23:Q:38:PHE:HA	1.97	0.47
28:V:41:PRO:HA	28:V:45:ARG:HB2	1.97	0.47
31:Z:53:G:OP1	43:l:55:ARG:NH2	2.48	0.47
33:b:98:ASP:OD1	33:b:98:ASP:N	2.41	0.47
34:c:108:ASP:OD1	34:c:108:ASP:N	2.48	0.47
4:3:48:ALA:HB1	4:3:53:ILE:HG23	1.97	0.47
7:A:459:U:H2'	7:A:460:A:H8	1.80	0.47
7:A:1266:G:N2	7:A:2012:G:H2'	2.28	0.47
7:A:2267:A:N3	7:A:2267:A:C2'	2.77	0.47
8:B:101:A:C8	8:B:102:G:N7	2.82	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:779:C:O2'	18:L:122:ARG:NE	2.32	0.47
8:B:1166:G:N1	8:B:1169:A:OP2	2.46	0.47
11:E:187:GLU:OE1	11:E:189:SER:OG	2.32	0.47
21:O:5:SER:O	21:O:9:ARG:N	2.47	0.47
33:b:161:TYR:HD2	33:b:194:GLU:HG2	1.80	0.47
36:e:6:ASP:N	36:e:6:ASP:OD1	2.46	0.47
46:o:24:ASP:OD1	46:o:90:GLY:N	2.41	0.47
7:A:190:A:N6	7:A:191:A:N1	2.63	0.47
7:A:1496:A:N3	7:A:1577:C:O2'	2.48	0.47
7:A:2314:A:H5'	36:e:35:THR:HG21	1.96	0.47
8:B:104:G:O2'	8:B:105:G:O4'	2.33	0.47
8:B:369:G:OP2	8:B:388:G:N1	2.37	0.47
8:B:619:U:N3	11:E:131:ASN:OD1	2.43	0.47
9:C:138:THR:O	9:C:142:GLU:N	2.46	0.47
12:F:111:MET:HE1	12:F:127:ALA:HB2	1.96	0.47
16:J:24:GLY:N	16:J:60:LYS:O	2.47	0.47
29:W:48:GLN:HG3	29:W:55:VAL:HG12	1.96	0.47
37:f:56:ASP:OD1	37:f:56:ASP:N	2.48	0.47
44:m:106:ASP:OD1	44:m:106:ASP:N	2.45	0.47
4:3:135:ASP:HA	4:3:138:VAL:HG12	1.97	0.46
7:A:974:G:OP1	7:A:1187:G:O2'	2.31	0.46
7:A:1184:U:OP2	55:x:31:ARG:NH2	2.47	0.46
8:B:138:G:H1	8:B:225:C:H42	1.62	0.46
8:B:390:U:O3'	23:Q:28:ARG:NH1	2.48	0.46
10:D:88:ARG:HG2	10:D:99:ALA:HB3	1.96	0.46
19:M:52:VAL:HG12	19:M:66:TYR:HA	1.96	0.46
29:W:34:VAL:HG11	29:W:43:ILE:HD12	1.97	0.46
38:g:12:LEU:HD13	38:g:19:VAL:HG21	1.96	0.46
4:3:153:ARG:NH1	49:r:52:GLU:OE2	2.48	0.46
7:A:1667:G:H21	7:A:1994:C:H42	1.62	0.46
7:A:2508:G:OP1	31:Z:76:A:OP1	2.32	0.46
8:B:411:A:H5"	11:E:31:LYS:HD3	1.97	0.46
8:B:801:U:H2'	8:B:802:A:C8	2.50	0.46
8:B:861:G:O6	8:B:869:G:N2	2.49	0.46
24:R:46:VAL:HG21	24:R:61:ILE:HD12	1.96	0.46
31:Z:19:G:O6	31:Z:57:G:N2	2.48	0.46
7:A:954:G:OP2	43:l:16:ARG:NH1	2.48	0.46
7:A:1301:A:H62	7:A:1641:A:H61	1.64	0.46
7:A:1583:A:H4'	7:A:1584:U:H5	1.79	0.46
8:B:517:G:N1	8:B:533:A:OP1	2.39	0.46
8:B:1218:C:H2'	8:B:1219:A:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:1273:C:H2'	8:B:1274:A:H8	1.80	0.46
8:B:1536:C:N3	8:B:1538:C:N4	2.64	0.46
15:I:11:LEU:HD23	15:I:14:ILE:HD12	1.97	0.46
25:S:71:THR:HG22	25:S:73:ARG:H	1.80	0.46
27:U:43:ASP:OD1	27:U:46:ALA:N	2.45	0.46
43:l:54:THR:HG22	43:l:63:ILE:HD12	1.97	0.46
49:r:66:ILE:HA	49:r:69:LEU:HD12	1.98	0.46
54:w:21:LEU:O	54:w:26:PHE:N	2.49	0.46
4:3:75:PRO:HB2	4:3:108:ILE:HD11	1.97	0.46
5:5:31:GLU:HA	5:5:34:ASN:HD21	1.80	0.46
7:A:281:C:H2'	7:A:282:A:H8	1.80	0.46
7:A:980:A:N6	7:A:981:A:N1	2.63	0.46
8:B:49:U:H3	8:B:362:G:H1'	1.80	0.46
8:B:413:G:O3'	8:B:428:G:N2	2.48	0.46
19:M:76:GLU:O	19:M:77:HIS:ND1	2.48	0.46
27:U:7:ALA:O	27:U:11:ALA:N	2.49	0.46
34:c:121:THR:O	34:c:121:THR:OG1	2.29	0.46
35:d:130:LYS:HB2	35:d:133:LEU:HD13	1.97	0.46
7:A:327:G:H1	7:A:335:C:H42	1.64	0.46
7:A:1454:C:OP1	44:m:63:ARG:NH2	2.48	0.46
7:A:2060:A:C4	7:A:2502:G:N3	2.84	0.46
8:B:18:C:H1'	8:B:1079:G:H21	1.80	0.46
9:C:214:LEU:HA	9:C:217:VAL:HG12	1.98	0.46
13:G:10:VAL:HB	13:G:58:HIS:HB3	1.97	0.46
14:H:119:ARG:HA	14:H:122:ASN:HB2	1.98	0.46
45:n:15:ARG:NH2	45:n:95:SER:OG	2.48	0.46
54:w:13:GLU:HA	54:w:16:THR:HG22	1.96	0.46
7:A:12:U:O5'	7:A:12:U:H6	1.99	0.46
7:A:2403:C:C4	7:A:2415:G:C2	3.03	0.46
9:C:130:THR:HG23	9:C:132:LYS:H	1.80	0.46
24:R:13:VAL:HB	24:R:22:VAL:HG23	1.98	0.46
33:b:66:ASP:OD2	33:b:102:ARG:NH1	2.48	0.46
42:k:119:PRO:HB3	42:k:140:GLY:H	1.81	0.46
5:5:319:ALA:HA	5:5:328:GLN:HE22	1.81	0.46
7:A:586:A:O2'	7:A:671:C:O2	2.34	0.46
7:A:1590:A:H2'	7:A:1591:A:C8	2.51	0.46
7:A:2039:U:H2'	7:A:2040:G:C8	2.51	0.46
7:A:2403:C:N4	7:A:2415:G:N1	2.64	0.46
7:A:2786:U:H5'	34:c:70:LYS:HD3	1.97	0.46
8:B:891:U:H2'	8:B:892:A:H8	1.81	0.46
9:C:66:LYS:HG3	9:C:88:ASP:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:d:176:ASP:N	35:d:176:ASP:OD1	2.49	0.46
36:e:158:THR:OG1	36:e:159:THR:N	2.49	0.46
7:A:400:G:O6	53:v:57:ARG:NH1	2.48	0.46
7:A:460:A:H62	7:A:469:G:H21	1.62	0.46
7:A:619:G:OP2	7:A:620:G:N2	2.48	0.46
7:A:953:G:H2'	7:A:954:G:H8	1.80	0.46
7:A:2824:C:N4	7:A:2825:G:N7	2.64	0.46
8:B:303:A:HO2'	8:B:555:U:HO2'	1.62	0.46
8:B:1391:U:H2'	8:B:1392:G:C8	2.50	0.46
10:D:157:LEU:O	10:D:164:ARG:NH2	2.49	0.46
18:L:112:ASP:HB3	28:V:4:ILE:HG13	1.97	0.46
20:N:89:LEU:O	20:N:93:ARG:NE	2.48	0.46
24:R:7:THR:OG1	24:R:8:LEU:N	2.49	0.46
50:s:89:ASP:N	50:s:89:ASP:OD1	2.48	0.46
7:A:2507:C:H4'	31:Z:76:A:H4'	1.97	0.46
8:B:198:G:H1	8:B:219:U:H2'	1.81	0.46
8:B:685:G:N2	8:B:704:A:OP2	2.37	0.46
8:B:757:U:O2'	8:B:879:C:O2	2.27	0.46
8:B:801:U:H2'	8:B:802:A:H8	1.81	0.46
8:B:992:U:N3	8:B:1043:G:N7	2.64	0.46
17:K:56:HIS:HD2	17:K:57:VAL:HG12	1.81	0.46
3:2:2:LYS:HE2	3:2:2:LYS:HB3	1.82	0.46
7:A:664:G:OP1	42:k:17:LYS:NZ	2.40	0.46
7:A:1388:G:H2'	7:A:1389:G:H8	1.81	0.46
7:A:2559:C:H2'	7:A:2560:A:H8	1.81	0.46
7:A:2722:G:C8	7:A:2723:C:C5	3.04	0.46
8:B:101:A:N7	8:B:102:G:C5	2.84	0.46
8:B:123:U:O2'	8:B:290:C:O2	2.30	0.46
8:B:769:G:H4'	8:B:1513:A:H4'	1.97	0.46
10:D:189:ALA:HB3	10:D:196:ILE:HB	1.98	0.46
21:O:54:ASP:HA	21:O:59:ARG:HD3	1.98	0.46
33:b:129:THR:HB	33:b:191:THR:HB	1.98	0.46
41:j:9:ASN:OD1	41:j:18:ARG:NH1	2.48	0.46
41:j:42:THR:O	41:j:42:THR:OG1	2.33	0.46
44:m:13:ASN:OD1	44:m:13:ASN:N	2.40	0.46
2:1:34:THR:OG1	57:z:22:THR:O	2.34	0.45
5:5:283:ARG:NE	5:5:405:GLU:OE1	2.44	0.45
7:A:2529:G:H4'	37:f:175:LYS:HG3	1.97	0.45
7:A:2691:C:C4	7:A:2719:G:N2	2.84	0.45
7:A:2841:C:H2'	7:A:2842:G:H8	1.82	0.45
8:B:108:G:N2	8:B:326:G:O6	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:G:48:ALA:N	25:S:66:SER:OG	2.49	0.45
16:J:61:LEU:HD11	16:J:63:LEU:HD13	1.97	0.45
33:b:2:ALA:N	33:b:199:GLU:OE2	2.49	0.45
36:e:123:ASP:O	36:e:125:ARG:NH1	2.48	0.45
7:A:629:G:N2	7:A:639:U:O3'	2.40	0.45
7:A:1342:A:O2'	7:A:1344:U:OP2	2.26	0.45
8:B:63:C:H42	8:B:104:G:H22	1.65	0.45
8:B:875:U:O2	15:I:16:ASN:ND2	2.45	0.45
8:B:1083:U:O3'	8:B:1086:U:N3	2.49	0.45
8:B:1381:U:O2'	14:H:79:ARG:NH1	2.49	0.45
16:J:128:SER:OG	16:J:129:LYS:N	2.49	0.45
17:K:13:PHE:HE1	17:K:69:THR:HG22	1.81	0.45
18:L:21:ALA:HB3	18:L:84:VAL:HG12	1.97	0.45
23:Q:3:THR:N	23:Q:22:ALA:O	2.45	0.45
35:d:97:ASN:ND2	35:d:100:MET:SD	2.90	0.45
36:e:136:ILE:HD13	36:e:146:VAL:HG11	1.98	0.45
4:3:135:ASP:HB2	4:3:140:LYS:HB2	1.98	0.45
7:A:580:U:H2'	7:A:581:C:H6	1.80	0.45
7:A:1341:G:H21	29:W:59:ASN:HD22	1.64	0.45
7:A:1421:G:H21	7:A:1494:A:H61	1.65	0.45
7:A:1595:C:H2'	7:A:1596:A:H8	1.81	0.45
9:C:64:LYS:HE2	9:C:225:ARG:HB2	1.98	0.45
14:H:27:VAL:HG12	14:H:43:VAL:HG11	1.97	0.45
35:d:118:LEU:HD12	35:d:186:VAL:HB	1.98	0.45
40:i:6:ALA:H	40:i:45:THR:HG21	1.81	0.45
40:i:32:LEU:HD22	40:i:54:ILE:HG21	1.98	0.45
7:A:820:A:C2	7:A:943:A:H4'	2.52	0.45
7:A:1807:G:O2'	7:A:1809:A:N6	2.38	0.45
8:B:318:G:H2'	8:B:319:G:H8	1.81	0.45
8:B:1316:G:N1	8:B:1319:A:OP2	2.49	0.45
14:H:21:GLU:O	14:H:25:LYS:N	2.44	0.45
29:W:61:LEU:HD21	29:W:82:LYS:HE3	1.98	0.45
45:n:99:TYR:OH	45:n:111:ARG:NH1	2.49	0.45
47:p:66:ASN:OD1	47:p:70:ARG:NH1	2.49	0.45
7:A:355:U:H2'	7:A:356:G:C8	2.50	0.45
7:A:1846:G:N2	7:A:1848:A:H61	2.13	0.45
8:B:65:A:H5'	8:B:200:G:H4'	1.98	0.45
8:B:408:A:H5'	11:E:113:GLU:HB2	1.99	0.45
8:B:585:G:N1	8:B:757:U:O2	2.49	0.45
8:B:1374:A:H2'	8:B:1375:A:H8	1.82	0.45
11:E:151:LYS:HA	11:E:155:VAL:HG23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:N:15:ALA:HB1	20:N:34:LEU:HD11	1.98	0.45
21:O:53:ARG:O	21:O:56:SER:OG	2.31	0.45
56:y:17(A):G:O2'	56:y:19:U:OP2	2.35	0.45
3:2:6:SER:O	3:2:6:SER:OG	2.29	0.45
5:5:332:LEU:HB3	5:5:336:LEU:HD22	1.98	0.45
7:A:523:C:H2'	7:A:524:G:H8	1.81	0.45
7:A:897:C:OP2	7:A:899:A:N6	2.38	0.45
8:B:1343:G:H4'	16:J:124:ARG:HB3	1.98	0.45
9:C:53:ALA:O	9:C:57:LEU:N	2.42	0.45
14:H:108:ALA:HA	14:H:111:ARG:HD2	1.98	0.45
19:M:37:VAL:N	19:M:76:GLU:OE2	2.49	0.45
26:T:18:LYS:HD2	26:T:33:THR:HB	1.98	0.45
1:0:45:SER:OG	7:A:126:A:OP1	2.32	0.45
7:A:621:A:OP2	42:k:99:ASN:ND2	2.49	0.45
7:A:1217:U:OP2	47:p:15:LYS:NZ	2.40	0.45
7:A:2588:G:C6	7:A:2607:G:C2	3.05	0.45
7:A:2655:G:O2'	7:A:2664:G:O6	2.30	0.45
27:U:35:VAL:HG21	27:U:54:MET:HG2	1.99	0.45
33:b:73:GLY:O	33:b:117:GLN:NE2	2.50	0.45
4:3:135:ASP:OD1	4:3:135:ASP:N	2.35	0.45
5:5:42:ASP:O	7:A:1337:G:O2'	2.23	0.45
7:A:1089:A:O2'	7:A:1091:G:N7	2.41	0.45
7:A:2678:C:H2'	7:A:2679:A:H8	1.81	0.45
8:B:79:G:N2	8:B:90:C:O2	2.50	0.45
8:B:680:C:H42	8:B:710:G:H1	1.63	0.45
8:B:1069:C:O2'	8:B:1192:C:O2	2.34	0.45
8:B:1234:C:O2'	8:B:1364:U:O2	2.30	0.45
15:I:67:GLN:HB2	15:I:69:LYS:HG3	1.99	0.45
22:P:48:LYS:HE2	22:P:48:LYS:HB2	1.84	0.45
33:b:145:GLU:HB2	33:b:188:CYS:HB2	1.99	0.45
39:h:3:LYS:HD3	39:h:3:LYS:HA	1.75	0.45
40:i:116:ARG:O	40:i:120:ARG:NH2	2.50	0.45
7:A:141:G:H22	29:W:1:MET:HE1	1.82	0.45
7:A:172:A:H2'	7:A:173:A:C8	2.52	0.45
7:A:351:C:H2'	7:A:352:A:C8	2.52	0.45
7:A:2055:C:H5'	7:A:2056:G:OP1	2.17	0.45
7:A:2446:G:O2'	7:A:2448:A:C8	2.70	0.45
8:B:1386:G:H2'	8:B:1387:G:H8	1.82	0.45
15:I:74:SER:H	15:I:130:ALA:HB2	1.82	0.45
21:O:18:ASP:O	21:O:23:LYS:NZ	2.47	0.45
41:j:17:ARG:HD3	41:j:17:ARG:HA	1.72	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:358:U:H2'	7:A:359:G:H8	1.81	0.45
7:A:695:G:OP1	7:A:1380:G:O2'	2.34	0.45
7:A:2315:G:H1'	36:e:125:ARG:HH21	1.82	0.45
8:B:453:G:N7	8:B:479:U:N3	2.65	0.45
8:B:1391:U:H2'	8:B:1392:G:H8	1.82	0.45
16:J:4:ASN:OD1	16:J:4:ASN:N	2.49	0.45
19:M:83:ARG:HB2	19:M:98:VAL:HG22	1.99	0.45
22:P:67:LEU:HD21	22:P:87:LEU:HD23	1.99	0.45
34:c:25:THR:HG21	34:c:193:VAL:HG11	1.98	0.45
45:n:3:LYS:HE3	45:n:3:LYS:HB2	1.85	0.45
49:r:69:LEU:HD22	49:r:107:VAL:HG22	1.98	0.45
5:5:354:VAL:HB	5:5:407:ALA:HB1	2.00	0.44
5:5:380:ASP:OD1	5:5:380:ASP:N	2.49	0.44
7:A:138:U:H5'	29:W:1:MET:HG2	2.00	0.44
7:A:641:U:O2	7:A:648:G:N2	2.50	0.44
7:A:923:G:H2'	7:A:924:G:H8	1.82	0.44
7:A:1063:G:N2	7:A:1075:C:O2'	2.45	0.44
7:A:2562:U:H4'	41:j:25:LEU:HD22	1.99	0.44
7:A:2711:A:C5	7:A:2714:G:N9	2.85	0.44
7:A:2735:G:H2'	7:A:2736:A:H8	1.81	0.44
8:B:41:G:N2	8:B:42:G:N7	2.59	0.44
14:H:47:LEU:HG	14:H:58:GLU:HG2	1.99	0.44
37:f:5:ALA:HB2	37:f:66:GLY:HA2	1.99	0.44
45:n:34:HIS:ND1	45:n:53:THR:O	2.50	0.44
48:q:48:LYS:HB3	48:q:48:LYS:HE3	1.84	0.44
5:5:194:MET:HE2	5:5:194:MET:HB3	1.90	0.44
7:A:1069:A:O2'	7:A:1097:U:OP1	2.29	0.44
7:A:1386:C:H2'	7:A:1387:A:C8	2.52	0.44
7:A:2400:G:N2	7:A:2401:U:O2	2.50	0.44
8:B:410:G:H2'	8:B:429:U:C4	2.52	0.44
23:Q:70:ARG:HA	23:Q:70:ARG:HD2	1.83	0.44
44:m:90:ARG:HA	44:m:90:ARG:HD3	1.83	0.44
50:s:49:VAL:HG22	50:s:51:ALA:H	1.81	0.44
4:3:87:GLU:HA	4:3:99:LEU:HA	2.00	0.44
7:A:23:G:C2	7:A:518:G:C2	3.06	0.44
7:A:1287:A:O4'	44:m:103:ARG:NH1	2.50	0.44
7:A:2438:U:O2'	7:A:2440:C:OP1	2.34	0.44
7:A:2793:C:H42	7:A:2803:G:H1	1.64	0.44
8:B:37:U:H2'	8:B:38:G:H8	1.83	0.44
8:B:617:G:H1	8:B:623:C:H42	1.65	0.44
8:B:1232:U:H5"	16:J:126:GLN:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:E:151:LYS:HB3	11:E:156:LYS:HG3	1.99	0.44
27:U:5:LYS:HB3	27:U:8:LYS:HB2	2.00	0.44
40:i:125:TYR:OH	40:i:132:HIS:NE2	2.49	0.44
41:j:42:THR:HG22	41:j:57:VAL:HG12	2.00	0.44
50:s:52:LEU:HD12	50:s:53:ASN:H	1.82	0.44
3:2:26:ILE:HD13	3:2:26:ILE:HA	1.88	0.44
7:A:190:A:H5"	7:A:204:A:H61	1.83	0.44
7:A:873:C:O2'	43:l:64:TRP:NE1	2.43	0.44
7:A:2112:G:N2	30:X:19:G:OP2	2.50	0.44
7:A:2508:G:H1'	7:A:2582:G:H22	1.81	0.44
7:A:2515:C:H42	7:A:2569:G:H1	1.64	0.44
7:A:2516:A:C5	7:A:2517:C:N4	2.86	0.44
8:B:81:A:H61	8:B:88:U:H3	1.66	0.44
8:B:446:G:H21	8:B:488:C:N4	2.16	0.44
13:G:3:HIS:HB3	13:G:95:ALA:HB2	1.99	0.44
41:j:21:CYS:HB2	41:j:39:ILE:HD12	2.00	0.44
7:A:1527:G:N1	7:A:1544:A:OP2	2.48	0.44
7:A:1748:C:H2'	7:A:1749:A:C8	2.52	0.44
7:A:2543:G:C6	7:A:2544:G:C6	3.06	0.44
8:B:501:C:H1'	8:B:549:C:H1'	1.99	0.44
30:X:7:U:H3'	30:X:13:C:H5	1.82	0.44
30:X:51:C:H2'	30:X:52:G:H8	1.82	0.44
33:b:8:PRO:HB3	33:b:14:ARG:HG3	2.00	0.44
33:b:74:ILE:HA	33:b:75:PRO:HD3	1.88	0.44
34:c:39:ASP:OD1	34:c:39:ASP:N	2.51	0.44
47:p:24:TYR:O	47:p:29:SER:OG	2.30	0.44
7:A:2446:G:O2'	7:A:2448:A:H8	2.01	0.44
7:A:2516:A:C5	7:A:2517:C:C4	3.05	0.44
8:B:363:A:N6	19:M:27:CYS:SG	2.90	0.44
8:B:1342:C:H2'	8:B:1343:G:C8	2.50	0.44
8:B:1384:C:H2'	8:B:1385:G:C8	2.53	0.44
36:e:93:GLY:H	36:e:96:MET:HE2	1.82	0.44
47:p:50:ARG:HH22	48:q:74:ILE:HG13	1.83	0.44
55:x:27:LEU:HA	55:x:27:LEU:HD23	1.83	0.44
7:A:1316:U:O2	7:A:1337:G:N2	2.51	0.44
7:A:1339:G:N2	7:A:1603:A:N3	2.66	0.44
7:A:1432:G:N2	7:A:1562:U:O2	2.51	0.44
7:A:2089:C:H2'	7:A:2090:A:H8	1.82	0.44
7:A:2292:U:H2'	7:A:2293:G:C8	2.53	0.44
7:A:2722:G:H3'	7:A:2723:C:C5	2.52	0.44
8:B:1175:G:H2'	8:B:1176:A:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:1512:U:H2'	8:B:1513:A:H8	1.83	0.44
12:F:38:VAL:HA	12:F:48:PHE:HA	1.98	0.44
17:K:88:MET:SD	17:K:89:ARG:NH1	2.82	0.44
20:N:12:HIS:H	20:N:45:ILE:HB	1.83	0.44
37:f:159:GLY:O	37:f:163:ARG:NH1	2.50	0.44
42:k:82:LEU:HD22	42:k:90:VAL:HG21	1.99	0.44
43:l:54:THR:HA	43:l:57:VAL:HG12	2.00	0.44
4:3:39:TYR:HB3	4:3:66:ARG:HH11	1.82	0.44
7:A:954:G:N1	7:A:964:C:N3	2.65	0.44
7:A:1749:A:H2'	7:A:1750:G:H8	1.82	0.44
8:B:302:G:N2	8:B:556:C:O2'	2.51	0.44
8:B:522:C:H42	8:B:528:C:H42	1.64	0.44
8:B:644:U:H2'	8:B:645:G:H8	1.82	0.44
8:B:880:C:H2'	8:B:881:G:H8	1.82	0.44
8:B:1025:U:O2'	8:B:1033:G:O6	2.35	0.44
8:B:1150:A:H4'	17:K:43:PRO:HG3	2.00	0.44
8:B:1513:A:H2'	8:B:1514:G:H8	1.83	0.44
13:G:64:VAL:HG12	13:G:66:ALA:HB2	2.00	0.44
15:I:7:ILE:HG21	15:I:126:ILE:HD11	1.99	0.44
20:N:19:LEU:HB2	20:N:30:SER:HB2	1.99	0.44
33:b:53:HIS:O	33:b:217:ARG:N	2.47	0.44
33:b:111:LYS:HE2	33:b:111:LYS:HB2	1.86	0.44
36:e:142:ASP:OD1	36:e:142:ASP:N	2.46	0.44
56:y:64:G:N2	56:y:66:C:OP1	2.49	0.44
4:3:107:LYS:NZ	4:3:121:GLU:OE1	2.47	0.44
7:A:992:C:H2'	7:A:993:G:C8	2.53	0.44
7:A:994:C:H1'	48:q:10:LYS:HE2	1.98	0.44
7:A:1636:U:H2'	7:A:1637:A:H8	1.83	0.44
8:B:182:A:H8	8:B:193:C:H42	1.65	0.44
8:B:552:U:O4	8:B:553:A:N6	2.51	0.44
8:B:751:U:OP1	22:P:17:ARG:NH2	2.41	0.44
32:a:6:G:H2'	32:a:7:G:H8	1.82	0.44
36:e:26:MET:O	36:e:30:ARG:NH1	2.50	0.44
42:k:55:MET:HB3	42:k:55:MET:HE2	1.69	0.44
42:k:123:ARG:NH1	42:k:143:GLU:OE2	2.51	0.44
44:m:25:ALA:HB1	44:m:48:VAL:HG13	1.99	0.44
53:v:39:TRP:NE1	53:v:41:GLU:OE2	2.40	0.44
7:A:277:G:H2'	7:A:361:G:C6	2.53	0.43
7:A:2070:A:C2	7:A:2071:A:C5	3.05	0.43
7:A:2471:A:N6	7:A:2476:A:O2'	2.51	0.43
7:A:2499:C:N4	7:A:2500:U:O4	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:2508:G:C4	7:A:2582:G:N1	2.82	0.43
8:B:120:A:O2'	8:B:122:G:N7	2.49	0.43
8:B:530:G:H5"	8:B:531:U:H5"	1.99	0.43
8:B:586:C:P	24:R:36:LYS:HZ1	2.41	0.43
11:E:151:LYS:NZ	11:E:176:GLY:O	2.34	0.43
4:3:63:SER:HA	5:5:395:MET:HE1	2.01	0.43
8:B:140:U:H2'	8:B:141:G:C8	2.53	0.43
23:Q:46:LYS:HB3	23:Q:46:LYS:HE2	1.77	0.43
23:Q:77:GLU:OE1	23:Q:77:GLU:N	2.52	0.43
24:R:22:VAL:HG12	24:R:45:HIS:HA	1.99	0.43
27:U:10:ARG:HG3	27:U:13:GLN:HE21	1.81	0.43
29:W:2:ILE:HG12	29:W:42:GLU:HG2	1.99	0.43
48:q:61:ALA:HB2	48:q:98:ILE:HD13	1.99	0.43
7:A:26:G:H8	7:A:26:G:O5'	2.01	0.43
7:A:467:G:O2'	7:A:796:C:O2'	2.25	0.43
7:A:1161:C:H2'	7:A:1162:G:H8	1.83	0.43
7:A:1170:C:H42	7:A:1178:C:N4	2.16	0.43
7:A:1297:C:OP1	7:A:2710:C:H4'	2.18	0.43
7:A:1980:G:O2'	7:A:1982:U:OP2	2.33	0.43
7:A:2711:A:C5	7:A:2714:G:C1'	3.01	0.43
8:B:859:G:OP2	8:B:869:G:N1	2.43	0.43
24:R:76:VAL:HG12	24:R:77:ARG:H	1.83	0.43
33:b:259:SER:O	33:b:259:SER:OG	2.26	0.43
35:d:171:ASP:OD1	35:d:171:ASP:N	2.46	0.43
2:1:36:LYS:HB3	2:1:40:ARG:HD3	1.99	0.43
7:A:5:A:H2'	7:A:6:A:C8	2.54	0.43
7:A:499:U:H3	7:A:503:A:H62	1.66	0.43
7:A:1062:G:N2	39:h:135:SER:O	2.45	0.43
7:A:1845:G:OP1	33:b:256:LYS:NZ	2.41	0.43
7:A:2578:G:C5	34:c:145:SER:HB3	2.52	0.43
13:G:49:TYR:CZ	25:S:66:SER:HB2	2.53	0.43
14:H:21:GLU:HA	14:H:24:ALA:HB3	2.01	0.43
15:I:41:LYS:HB3	15:I:41:LYS:HE2	1.82	0.43
19:M:50:ARG:HD2	19:M:50:ARG:HA	1.75	0.43
23:Q:10:GLY:HA3	23:Q:15:PRO:HA	2.00	0.43
48:q:14:VAL:HG12	48:q:20:VAL:HG11	2.01	0.43
7:A:1168:G:N3	7:A:1182:G:N1	2.66	0.43
7:A:1411:U:N3	7:A:1592:C:O2	2.51	0.43
7:A:1676:A:N6	7:A:1677:A:N1	2.67	0.43
7:A:2740:A:N6	7:A:2741:A:N1	2.65	0.43
8:B:676:A:H1'	18:L:117:PRO:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:825:A:O2'	15:I:9:ASP:OD2	2.29	0.43
8:B:835:U:H3	8:B:851:G:H1	1.66	0.43
16:J:49:ARG:O	16:J:53:GLU:N	2.50	0.43
20:N:81:MET:HE3	20:N:92:ARG:HG3	1.99	0.43
24:R:15:ASP:O	24:R:17:MET:N	2.52	0.43
24:R:19:LYS:NZ	24:R:48:ASP:O	2.46	0.43
24:R:31:HIS:CD2	24:R:33:ILE:H	2.36	0.43
29:W:40:LYS:HB3	29:W:60:THR:HG21	1.99	0.43
54:w:9:LYS:HA	54:w:9:LYS:HD2	1.85	0.43
7:A:720:U:H2'	7:A:721:A:H8	1.82	0.43
7:A:1814:G:C4	7:A:1815:A:N7	2.86	0.43
8:B:861:G:H1	8:B:868:C:H42	1.66	0.43
9:C:64:LYS:HD3	9:C:64:LYS:HA	1.91	0.43
12:F:157:ARG:HB2	15:I:45:PHE:HE1	1.83	0.43
16:J:52:LEU:HD22	16:J:57:MET:HB3	2.01	0.43
23:Q:42:ILE:H	23:Q:42:ILE:HG13	1.70	0.43
26:T:12:ASP:O	26:T:16:LEU:N	2.51	0.43
44:m:25:ALA:HB2	44:m:44:LEU:HD11	2.00	0.43
5:5:254:LYS:HE2	5:5:254:LYS:HB3	1.82	0.43
6:6:4:GLN:HA	7:A:2615:U:C2	2.53	0.43
7:A:1627:G:H2'	7:A:1628:G:H8	1.83	0.43
7:A:1846:G:C2'	8:B:702:A:H2	2.31	0.43
8:B:223:A:N6	8:B:224:U:O2	2.52	0.43
8:B:1090:U:HO2'	8:B:1171:A:HO2'	1.64	0.43
8:B:1367:C:OP1	17:K:62:ARG:NH2	2.52	0.43
10:D:49:LYS:HD2	10:D:49:LYS:HA	1.82	0.43
12:F:41:ASP:N	12:F:41:ASP:OD1	2.52	0.43
20:N:53:ILE:HD13	20:N:53:ILE:HA	1.90	0.43
21:O:33:ASP:O	21:O:35:ASN:ND2	2.51	0.43
22:P:32:LEU:O	22:P:36:ILE:N	2.40	0.43
48:q:24:LYS:HB3	48:q:24:LYS:HE2	1.84	0.43
7:A:1278:C:H2'	7:A:1279:G:H8	1.84	0.43
7:A:1368:G:C2	7:A:1369:G:C6	3.07	0.43
7:A:1368:G:N1	7:A:1369:G:O6	2.52	0.43
7:A:1649:G:H1	7:A:2009:A:N6	2.17	0.43
7:A:2453:A:C2	7:A:2504:U:C4	3.06	0.43
8:B:375:U:H4'	23:Q:6:LEU:HD12	1.99	0.43
8:B:607:A:H2'	8:B:608:A:C8	2.53	0.43
11:E:3:ARG:HG3	11:E:115:ARG:NH2	2.33	0.43
15:I:10:MET:HG3	15:I:27:MET:HE2	2.01	0.43
16:J:6:TYR:CG	16:J:89:GLU:HB2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:d:131:THR:HG22	35:d:160:ALA:HA	2.00	0.43
36:e:30:ARG:H	36:e:159:THR:HG22	1.82	0.43
40:i:81:ILE:HD12	40:i:81:ILE:HA	1.81	0.43
51:t:31:TYR:HB3	51:t:37:PRO:HB3	2.00	0.43
8:B:981:U:H5"	21:O:63:ARG:HH21	1.84	0.43
8:B:1300:G:N2	8:B:1301:U:O4	2.38	0.43
12:F:53:ALA:HB2	12:F:62:LYS:HD3	2.00	0.43
15:I:28:PRO:O	15:I:33:LYS:NZ	2.42	0.43
19:M:67:ILE:HD13	19:M:97:THR:HG21	2.00	0.43
20:N:11:ASP:N	20:N:11:ASP:OD1	2.51	0.43
20:N:79:ARG:NH2	26:T:65:GLU:O	2.51	0.43
20:N:91:HIS:HA	20:N:109:ARG:HH22	1.84	0.43
36:e:80:ARG:HD3	36:e:80:ARG:HA	1.70	0.43
39:h:101:ILE:HD11	39:h:106:LEU:HD21	2.01	0.43
2:1:5:LYS:NZ	7:A:253:C:OP2	2.33	0.43
7:A:806:C:O2	7:A:2444:G:O2'	2.31	0.43
7:A:1604:C:O2'	7:A:1610:A:N1	2.49	0.43
7:A:2543:G:C6	7:A:2544:G:C5	3.07	0.43
7:A:2617:U:H2'	7:A:2618:G:H8	1.83	0.43
7:A:2711:A:C4	7:A:2714:G:C1'	3.02	0.43
7:A:2839:G:H4'	44:m:49:GLU:HB3	2.00	0.43
8:B:459:A:H61	8:B:473:U:H3	1.67	0.43
8:B:1404:C:H42	8:B:1497:G:H1	1.66	0.43
11:E:97:ARG:HA	11:E:134:SER:HA	2.01	0.43
11:E:102:VAL:HG23	11:E:114:ALA:HB1	2.01	0.43
20:N:69:LEU:HD12	20:N:72:GLU:HB3	2.01	0.43
32:a:50:A:OP1	45:n:68:LYS:N	2.52	0.43
33:b:167:ARG:HG3	33:b:172:VAL:HG22	2.01	0.43
7:A:1984:G:N2	7:A:1985:C:O2	2.52	0.42
7:A:2345:G:O2'	7:A:2381:A:N3	2.43	0.42
8:B:231:U:H2'	8:B:232:G:C8	2.54	0.42
8:B:664:G:H22	8:B:741:G:H1	1.67	0.42
8:B:720:C:H5'	25:S:41:PRO:HB3	2.01	0.42
9:C:205:ASP:OD1	9:C:205:ASP:N	2.47	0.42
10:D:139:GLN:O	10:D:143:ARG:N	2.41	0.42
11:E:177:LYS:HD3	11:E:177:LYS:HA	1.80	0.42
11:E:206:LYS:HB3	11:E:206:LYS:HE2	1.81	0.42
14:H:35:LYS:HD2	14:H:35:LYS:HA	1.64	0.42
15:I:102:ALA:N	15:I:113:ASP:OD1	2.52	0.42
16:J:19:VAL:HG11	16:J:83:ILE:HA	2.01	0.42
16:J:98:LEU:O	16:J:102:GLY:N	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:62:TYR:HE1	33:b:87:ARG:HH22	1.67	0.42
36:e:16:LEU:HD22	36:e:20:PHE:HE2	1.84	0.42
51:t:51:GLN:OE1	51:t:57:TYR:OH	2.32	0.42
53:v:6:GLN:OE1	53:v:50:ARG:N	2.44	0.42
2:1:31:HIS:HA	7:A:2420:C:H5	1.84	0.42
4:3:1:SER:OG	4:3:2:VAL:N	2.50	0.42
7:A:1992:G:N2	7:A:1996:C:O2	2.52	0.42
8:B:41:G:N2	8:B:43:C:N3	2.67	0.42
8:B:1124:G:O2'	8:B:1145:A:N6	2.49	0.42
8:B:1221:G:OP1	8:B:1321:U:N3	2.52	0.42
8:B:1259:C:O2'	8:B:1283:U:O2	2.33	0.42
10:D:47:LEU:HD12	10:D:47:LEU:HA	1.75	0.42
15:I:34:VAL:HG12	15:I:59:LEU:HD13	2.01	0.42
21:O:75:ARG:HD3	21:O:75:ARG:HA	1.88	0.42
22:P:4:SER:O	22:P:8:THR:OG1	2.33	0.42
26:T:58:VAL:HA	26:T:59:PRO:HD3	1.86	0.42
31:Z:53:G:N2	31:Z:57:G:OP1	2.52	0.42
50:s:91:LYS:HB2	50:s:91:LYS:HE3	1.78	0.42
7:A:1369:G:N3	7:A:1810:A:H2	2.17	0.42
7:A:2636:C:O2'	34:c:45:TYR:OH	2.34	0.42
7:A:2848:G:N7	46:o:95:ALA:HB2	2.34	0.42
8:B:1237:C:H42	8:B:1337:G:H1	1.68	0.42
11:E:198:HIS:CE1	12:F:103:THR:HG1	2.38	0.42
15:I:74:SER:O	15:I:130:ALA:N	2.53	0.42
17:K:65:TYR:HB3	21:O:96:LEU:HD11	2.00	0.42
18:L:106:ARG:HH12	28:V:8:GLU:HG3	1.85	0.42
19:M:83:ARG:HE	19:M:96:HIS:HB2	1.84	0.42
24:R:12:VAL:HB	24:R:56:GLY:H	1.84	0.42
27:U:45:ALA:O	27:U:49:LYS:N	2.49	0.42
32:a:40:U:N3	32:a:44:G:OP2	2.36	0.42
36:e:117:LEU:HB3	36:e:177:PHE:H	1.84	0.42
7:A:579:G:C8	7:A:2017:U:O4	2.73	0.42
7:A:2075:U:O2'	7:A:2596:U:N3	2.53	0.42
7:A:2544:G:H2'	7:A:2545:G:H8	1.84	0.42
8:B:220:G:H2'	8:B:221:C:O4'	2.20	0.42
8:B:300:A:O2'	8:B:564:C:N3	2.52	0.42
8:B:1005:A:H3'	8:B:1006:G:C8	2.54	0.42
8:B:1065:U:H5"	8:B:1190:G:H22	1.85	0.42
8:B:1401:G:O6	8:B:1504:G:N2	2.51	0.42
33:b:196:GLY:O	33:b:198:ALA:N	2.52	0.42
39:h:74:PRO:HA	39:h:75:PRO:HD3	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:p:91:ASP:OD1	47:p:91:ASP:N	2.45	0.42
7:A:411:G:OP2	7:A:2406:A:O2'	2.28	0.42
7:A:641:U:O2'	7:A:2350:C:OP1	2.36	0.42
7:A:1636:U:H2'	7:A:1637:A:C8	2.55	0.42
7:A:2463:C:H42	7:A:2487:G:H1	1.68	0.42
7:A:2683:C:OP1	46:o:51:ARG:NH2	2.40	0.42
8:B:186:C:H5"	27:U:77:ALA:HB2	2.01	0.42
8:B:1441:A:H3'	8:B:1442:G:H8	1.85	0.42
10:D:5:VAL:HG11	10:D:10:ILE:HD12	2.00	0.42
10:D:22:TRP:HD1	10:D:58:GLU:HA	1.85	0.42
11:E:117:LEU:HD21	11:E:155:VAL:HG11	2.02	0.42
12:F:97:GLN:N	12:F:124:LEU:O	2.52	0.42
36:e:4:LEU:HD12	36:e:101:GLU:HB3	2.02	0.42
41:j:111:LYS:HE3	41:j:111:LYS:HB2	1.80	0.42
49:r:74:ILE:HD12	49:r:105:VAL:HG22	2.01	0.42
4:3:81:SER:N	4:3:105:LYS:O	2.51	0.42
7:A:1625:C:N4	7:A:1626:A:N1	2.67	0.42
7:A:1995:U:N3	7:A:1996:C:N3	2.68	0.42
7:A:2016:U:H2'	7:A:2017:U:C6	2.54	0.42
8:B:1078:U:H1'	12:F:135:ASN:HD21	1.85	0.42
8:B:1115:U:H3	8:B:1185:G:H1	1.67	0.42
8:B:1244:G:H1	8:B:1293:C:H42	1.67	0.42
11:E:10:LYS:HA	11:E:13:ARG:HB2	2.01	0.42
30:X:2:G:H2'	30:X:3:G:C8	2.55	0.42
35:d:153:LEU:HD11	35:d:158:PHE:HB2	2.02	0.42
40:i:56:VAL:HB	40:i:124:VAL:HG22	2.02	0.42
48:q:4:VAL:HG23	48:q:39:LEU:HB2	2.01	0.42
54:w:15:ASN:OD1	54:w:16:THR:N	2.50	0.42
7:A:859:G:N2	7:A:917:A:OP2	2.33	0.42
7:A:1999:C:H5"	7:A:2723:C:O2'	2.19	0.42
8:B:108:G:P	8:B:326:G:H22	2.42	0.42
8:B:121:U:H3'	8:B:122:G:H8	1.83	0.42
8:B:193:C:N3	8:B:194:C:N4	2.67	0.42
8:B:632:U:H5"	8:B:633:G:C8	2.54	0.42
8:B:977:A:OP1	21:O:61:ARG:NH2	2.53	0.42
8:B:1343:G:H5"	16:J:124:ARG:HH21	1.85	0.42
12:F:92:SER:OG	12:F:135:ASN:O	2.24	0.42
13:G:19:PRO:HA	13:G:22:ILE:HB	2.01	0.42
16:J:45:ARG:HD3	16:J:45:ARG:H	1.84	0.42
34:c:33:ARG:NH2	34:c:74:GLU:O	2.53	0.42
36:e:144:ASP:N	36:e:144:ASP:OD1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:o:87:LYS:HA	46:o:87:LYS:HD3	1.69	0.42
51:t:71:LYS:HA	51:t:71:LYS:HD2	1.92	0.42
4:3:107:LYS:HD2	4:3:107:LYS:HA	1.75	0.42
7:A:35:G:O2'	7:A:454:A:O4'	2.36	0.42
7:A:882:G:H2'	7:A:883:G:C8	2.54	0.42
7:A:1165:A:H2'	7:A:1166:G:H8	1.85	0.42
8:B:11:G:H1	8:B:23:C:H42	1.67	0.42
8:B:65:A:OP1	8:B:382:A:N6	2.52	0.42
8:B:1354:U:H2'	8:B:1355:G:H8	1.84	0.42
27:U:21:ASN:O	27:U:25:ARG:N	2.43	0.42
30:X:18:G:H21	30:X:53:G:H21	1.66	0.42
32:a:19:C:H2'	32:a:20:G:H8	1.84	0.42
36:e:3:LYS:HD3	36:e:3:LYS:HA	1.76	0.42
48:q:29:THR:O	48:q:29:THR:OG1	2.35	0.42
4:3:32:ASP:OD1	4:3:32:ASP:N	2.46	0.42
7:A:626:A:H2'	42:k:78:ARG:HH12	1.84	0.42
7:A:2192:U:H2'	7:A:2193:G:C8	2.55	0.42
8:B:464:U:C2	8:B:466:A:H5"	2.55	0.42
10:D:108:LYS:HE2	10:D:144:LEU:HD13	2.02	0.42
14:H:116:MET:HE3	14:H:120:LEU:HG	2.02	0.42
17:K:64:GLN:O	21:O:99:ALA:N	2.48	0.42
21:O:3:LYS:HB3	21:O:6:MET:HG2	2.02	0.42
32:a:33:G:H2'	32:a:34:A:H8	1.83	0.42
35:d:180:LEU:HD23	35:d:180:LEU:HA	1.84	0.42
39:h:73:THR:HA	39:h:113:LYS:HG3	2.02	0.42
46:o:92:VAL:HG11	46:o:97:LEU:HD11	2.02	0.42
7:A:965:C:HO2'	7:A:2272:U:HO2'	1.66	0.42
7:A:1062:G:N2	39:h:93:PRO:HG2	2.35	0.42
7:A:1595:C:H2'	7:A:1596:A:C8	2.54	0.42
7:A:1651:G:H4'	44:m:39:PRO:HG2	2.02	0.42
8:B:735:C:H2'	8:B:736:C:H6	1.85	0.42
8:B:757:U:OP1	8:B:822:U:O2'	2.37	0.42
8:B:950:U:H2'	8:B:951:G:H8	1.83	0.42
8:B:1317:C:C2	21:O:53:ARG:HD3	2.54	0.42
11:E:95:GLU:HG3	11:E:104:ARG:HE	1.85	0.42
24:R:62:ARG:NH1	24:R:63:GLU:O	2.53	0.42
25:S:25:ASP:HB3	25:S:28:THR:HB	2.01	0.42
33:b:7:LYS:HE3	33:b:7:LYS:HB3	1.86	0.42
34:c:156:PHE:CG	40:i:81:ILE:HG12	2.55	0.42
38:g:5:LEU:HA	38:g:5:LEU:HD23	1.87	0.42
57:z:33:LYS:HD2	57:z:51:GLU:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1919:A:N1	8:B:1495:U:O2'	2.45	0.41
7:A:2198:A:C4	38:g:29:PHE:HB2	2.54	0.41
7:A:2351:G:H2'	7:A:2365:G:H22	1.84	0.41
7:A:2559:C:H2'	7:A:2560:A:C8	2.55	0.41
7:A:2676:C:H2'	7:A:2677:G:H8	1.85	0.41
8:B:101:A:C6	8:B:102:G:C5	3.08	0.41
8:B:711:G:H2'	8:B:712:A:C8	2.55	0.41
11:E:51:TYR:O	11:E:55:LEU:N	2.45	0.41
25:S:34:THR:HG22	25:S:38:LYS:H	1.84	0.41
30:X:49:G:H2'	30:X:50:G:H8	1.84	0.41
7:A:186:G:H2'	7:A:187:G:H8	1.85	0.41
7:A:1710:G:H2'	7:A:1711:A:C8	2.54	0.41
8:B:98:A:C8	8:B:99:C:C5	3.08	0.41
9:C:115:LYS:NZ	9:C:152:LYS:O	2.43	0.41
11:E:9:LEU:HD13	11:E:34:ILE:HD11	2.02	0.41
11:E:139:PRO:HA	11:E:182:PHE:HB2	2.03	0.41
15:I:105:SER:HB3	15:I:124:GLU:HG3	2.02	0.41
16:J:9:THR:H	16:J:85:ARG:HD2	1.84	0.41
24:R:72:SER:O	24:R:72:SER:OG	2.31	0.41
27:U:67:ILE:HG13	27:U:71:LYS:HD3	2.00	0.41
30:X:1:G:H2'	30:X:2:G:C5	2.55	0.41
51:t:34:LYS:HA	51:t:34:LYS:HD2	1.87	0.41
7:A:832:U:OP1	42:k:38:GLN:N	2.50	0.41
7:A:1037:G:H22	7:A:1119:U:H1'	1.85	0.41
8:B:303:A:O2'	8:B:555:U:O2'	2.35	0.41
8:B:1288:A:N6	8:B:1371:G:O2'	2.43	0.41
8:B:1522:U:H2'	8:B:1523:G:H8	1.85	0.41
14:H:140:ASP:HA	14:H:143:ARG:HG3	2.01	0.41
21:O:24:ARG:HA	21:O:27:LEU:HB2	2.02	0.41
33:b:142:HIS:ND1	33:b:193:GLY:O	2.53	0.41
37:f:23:VAL:HB	37:f:36:THR:HG23	2.01	0.41
37:f:95:ARG:HD3	37:f:95:ARG:HA	1.91	0.41
46:o:100:LEU:HD23	46:o:100:LEU:HA	1.89	0.41
56:y:67:C:H2'	56:y:68:G:H8	1.85	0.41
7:A:1491:G:O2'	33:b:100:GLU:OE1	2.38	0.41
7:A:1832:C:N4	7:A:1833:C:N3	2.69	0.41
7:A:2035:G:H5"	7:A:2036:C:H5	1.84	0.41
8:B:264:C:O2'	24:R:66:PRO:O	2.32	0.41
8:B:916:U:H2'	8:B:917:G:H8	1.85	0.41
8:B:978:A:OP1	8:B:1361:G:N1	2.53	0.41
8:B:1025:U:H5"	8:B:1026:G:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:1086:U:O2'	8:B:1087:G:O4'	2.38	0.41
8:B:1297:G:C2	14:H:114:LYS:HB3	2.56	0.41
13:G:40:GLU:HB3	13:G:42:TRP:NE1	2.35	0.41
16:J:22:LYS:HB3	16:J:62:ASP:HB2	2.03	0.41
32:a:116:G:H2'	32:a:117:G:C8	2.55	0.41
34:c:142:VAL:HG22	34:c:143:PRO:HD2	2.01	0.41
36:e:38:MET:HE2	36:e:38:MET:HB3	1.91	0.41
40:i:142:ILE:HD12	40:i:142:ILE:HA	1.90	0.41
54:w:21:LEU:HA	54:w:21:LEU:HD23	1.82	0.41
7:A:72:U:O4	54:w:58:ASN:ND2	2.53	0.41
7:A:447:A:OP1	47:p:5:LYS:NZ	2.54	0.41
7:A:882:G:H2'	7:A:883:G:H8	1.85	0.41
7:A:1278:C:H2'	7:A:1279:G:C8	2.55	0.41
7:A:1305:C:N4	7:A:1607:C:OP1	2.53	0.41
7:A:2297:A:C5	7:A:2320:U:C2	3.08	0.41
7:A:2332:C:O2'	7:A:2335:A:N3	2.45	0.41
7:A:2398:U:H2'	7:A:2399:G:H8	1.84	0.41
8:B:449:G:H2'	8:B:450:G:C8	2.55	0.41
8:B:946:A:H2'	8:B:947:G:C8	2.55	0.41
10:D:31:ASP:OD1	10:D:31:ASP:N	2.49	0.41
16:J:18:ARG:HE	16:J:66:THR:HG22	1.86	0.41
18:L:101:ASN:HB3	18:L:107:ILE:HD12	2.03	0.41
22:P:10:LYS:O	22:P:13:SER:OG	2.31	0.41
22:P:74:ASP:OD2	22:P:77:ARG:NH1	2.54	0.41
33:b:175:ARG:HD3	33:b:181:MET:HE2	2.02	0.41
33:b:195:VAL:H	33:b:195:VAL:HG12	1.68	0.41
36:e:115:ARG:HB2	36:e:178:ARG:HD3	2.03	0.41
7:A:28:A:O2'	7:A:582:A:O2'	2.31	0.41
7:A:86:G:O2'	7:A:104:A:O2'	2.33	0.41
7:A:1508:A:O2'	7:A:1509:A:O4'	2.30	0.41
7:A:2128:G:N1	7:A:2161:C:O2'	2.49	0.41
8:B:186:C:N4	8:B:187:G:O6	2.53	0.41
8:B:527:G:O6	19:M:46:ASN:ND2	2.54	0.41
8:B:1071:C:H2'	8:B:1072:G:H8	1.86	0.41
17:K:7:ARG:H	17:K:102:LEU:HA	1.85	0.41
17:K:57:VAL:HG22	17:K:58:ASN:H	1.85	0.41
18:L:55:SER:O	18:L:58:SER:OG	2.37	0.41
36:e:103:LEU:HD12	36:e:138:PHE:HZ	1.85	0.41
45:n:30:ARG:HD3	45:n:102:ARG:HE	1.86	0.41
53:v:32:ASN:HD22	53:v:53:ALA:HB2	1.85	0.41
2:1:15:LYS:HB2	2:1:23:LYS:HE2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1171:G:O6	7:A:1178:C:N4	2.44	0.41
7:A:1395:A:O2'	7:A:1396:U:H5"	2.21	0.41
7:A:1480:C:H42	7:A:1511:G:H1	1.69	0.41
7:A:1769:U:H2'	7:A:1770:G:C8	2.55	0.41
7:A:2548:U:O2	41:j:23:LYS:NZ	2.48	0.41
7:A:2818:U:H2'	7:A:2819:G:C8	2.56	0.41
8:B:191:G:H2'	8:B:192:A:H8	1.86	0.41
8:B:253:A:OP1	24:R:69:LYS:NZ	2.47	0.41
8:B:1284:C:H3'	8:B:1285:A:H8	1.84	0.41
11:E:18:ASP:OD1	11:E:18:ASP:N	2.54	0.41
12:F:71:MET:HE2	12:F:71:MET:HB3	1.96	0.41
12:F:133:PRO:HA	12:F:136:VAL:HG22	2.03	0.41
13:G:47:LEU:HD12	25:S:66:SER:HB3	2.01	0.41
18:L:113:VAL:HA	25:S:73:ARG:HD2	2.03	0.41
22:P:47:LYS:HA	22:P:47:LYS:HD3	1.86	0.41
32:a:44:G:N3	32:a:47:C:N4	2.58	0.41
35:d:148:ILE:HB	35:d:169:VAL:HG22	2.03	0.41
37:f:123:ALA:HA	37:f:133:LEU:HA	2.03	0.41
4:3:28:GLN:NE2	4:3:113:ARG:O	2.54	0.41
7:A:778:G:H5'	33:b:48:ARG:HH11	1.85	0.41
7:A:909:A:N6	7:A:912:C:O2	2.53	0.41
7:A:1358:G:N7	7:A:1371:G:C6	2.89	0.41
7:A:1369:G:N2	7:A:1370:C:C2	2.89	0.41
7:A:1666:G:O6	7:A:1667:G:N2	2.54	0.41
8:B:389:A:N6	8:B:390:U:O2	2.54	0.41
8:B:398:U:H2'	8:B:399:G:C8	2.55	0.41
8:B:1113:C:H42	8:B:1187:G:H1	1.68	0.41
9:C:97:LEU:HD23	9:C:97:LEU:HA	1.92	0.41
10:D:54:ARG:HE	10:D:54:ARG:HB3	1.68	0.41
11:E:77:LYS:HA	11:E:77:LYS:HD3	1.87	0.41
18:L:17:SER:HA	18:L:79:ILE:HA	2.02	0.41
18:L:113:VAL:HG23	25:S:73:ARG:HD2	2.01	0.41
30:X:9:A:H1'	30:X:45:G:H2'	2.02	0.41
34:c:33:ARG:NH1	34:c:53:GLY:O	2.46	0.41
34:c:159:LYS:HA	34:c:159:LYS:HD2	1.87	0.41
35:d:48:THR:HG22	35:d:86:ALA:HB2	2.02	0.41
41:j:69:VAL:HG11	41:j:104:THR:HG21	2.01	0.41
43:l:74:THR:OG1	43:l:75:GLU:N	2.54	0.41
43:l:132:THR:OG1	43:l:133:LYS:N	2.54	0.41
4:3:7:HIS:HD2	4:3:94:PRO:HD3	1.86	0.41
7:A:571:U:N3	7:A:2030:A:C6	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:675:A:OP1	35:d:58:LYS:NZ	2.47	0.41
7:A:762:U:N3	7:A:1431:A:OP1	2.54	0.41
7:A:866:A:N6	7:A:914:G:N7	2.69	0.41
7:A:2116:G:O4'	7:A:2165:C:N4	2.38	0.41
7:A:2265:U:H3'	7:A:2266:A:H8	1.85	0.41
7:A:2403:C:N3	7:A:2415:G:C2	2.89	0.41
7:A:2811:G:N2	7:A:2889:C:O2	2.41	0.41
8:B:729:A:H2'	8:B:730:G:C8	2.56	0.41
8:B:1081:A:H5'	12:F:23:LYS:HG3	2.03	0.41
8:B:1116:U:H2'	8:B:1117:A:C8	2.55	0.41
8:B:1141:C:H1'	8:B:1142:G:H5'	2.03	0.41
9:C:87:CYS:H	9:C:89:GLN:NE2	2.18	0.41
9:C:208:ARG:HH12	9:C:212:LEU:HD13	1.86	0.41
17:K:12:ALA:HB3	17:K:18:ILE:HD12	2.03	0.41
27:U:35:VAL:HG12	27:U:39:ILE:HD11	2.02	0.41
27:U:36:TYR:HA	27:U:39:ILE:HD12	2.03	0.41
36:e:134:GLU:HB3	36:e:149:VAL:HG22	2.02	0.41
38:g:4:ILE:HD13	38:g:18:GLN:HG2	2.02	0.41
47:p:41:LYS:HA	47:p:41:LYS:HD2	1.86	0.41
54:w:56:LEU:HD23	54:w:56:LEU:HA	1.87	0.41
4:3:3:LEU:HD23	4:3:37:THR:HG21	2.03	0.41
7:A:107:G:H2'	7:A:108:G:H8	1.86	0.41
7:A:2156:G:C5	7:A:2157:G:H1'	2.56	0.41
7:A:2354:C:H2'	7:A:2355:G:C8	2.56	0.41
7:A:2744:G:H21	37:f:143:GLN:HE22	1.68	0.41
8:B:643:C:H5'	15:I:32:LEU:HD13	2.02	0.41
8:B:839:C:O2	8:B:847:G:N2	2.48	0.41
8:B:1116:U:H2'	8:B:1117:A:H8	1.86	0.41
14:H:68:ASN:HB3	14:H:130:ASN:HB3	2.03	0.41
18:L:21:ALA:N	18:L:83:GLU:O	2.54	0.41
24:R:19:LYS:HZ3	24:R:49:GLU:HA	1.86	0.41
31:Z:53:G:H5'	43:l:59:ARG:HH12	1.86	0.41
36:e:120:LYS:HA	36:e:167:ARG:HH21	1.86	0.41
49:r:4:ILE:HA	49:r:106:VAL:HG12	2.03	0.41
4:3:56:ARG:NH2	4:3:76:GLU:OE2	2.45	0.40
7:A:277:G:H1'	7:A:278:A:C6	2.56	0.40
7:A:1188:U:H2'	7:A:1189:A:H8	1.86	0.40
7:A:1769:U:H2'	7:A:1770:G:H8	1.86	0.40
7:A:2577:A:O5'	7:A:2577:A:H8	2.04	0.40
8:B:652:U:O4	8:B:752:G:O2'	2.36	0.40
8:B:894:G:H2'	8:B:895:G:H8	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:1071:C:H2'	8:B:1072:G:C8	2.55	0.40
9:C:163:VAL:HG11	9:C:173:ILE:HD11	2.03	0.40
19:M:108:LYS:HA	19:M:108:LYS:HD3	1.94	0.40
20:N:90:ARG:HA	20:N:93:ARG:HE	1.87	0.40
31:Z:33:U:H1'	31:Z:35:U:H5"	2.03	0.40
33:b:117:GLN:N	33:b:128:ASN:OD1	2.50	0.40
33:b:161:TYR:CD2	33:b:194:GLU:HG2	2.56	0.40
33:b:171:TYR:HD1	33:b:171:TYR:HA	1.73	0.40
36:e:111:ILE:HG23	36:e:114:PHE:HB2	2.02	0.40
40:i:1:MET:HE3	40:i:1:MET:HB3	1.74	0.40
40:i:2:LYS:HB2	40:i:2:LYS:HE3	1.93	0.40
46:o:71:GLU:OE2	46:o:101:ARG:NE	2.52	0.40
49:r:3:THR:O	49:r:3:THR:OG1	2.32	0.40
7:A:2579:C:C3'	7:A:2579:C:C6	3.04	0.40
7:A:2836:U:H2'	7:A:2837:A:H8	1.87	0.40
8:B:2:A:O2'	11:E:83:LYS:NZ	2.41	0.40
8:B:327:A:O2'	8:B:329:A:O4'	2.40	0.40
8:B:1253:G:H2'	8:B:1254:A:C8	2.56	0.40
13:G:62:MET:HB3	13:G:64:VAL:HG23	2.02	0.40
14:H:31:MET:HB2	14:H:31:MET:HE3	1.85	0.40
21:O:29:ALA:HA	21:O:32:SER:HB3	2.02	0.40
36:e:164:GLU:O	36:e:168:ALA:N	2.48	0.40
37:f:126:PRO:HD3	37:f:132:VAL:HG12	2.03	0.40
46:o:28:VAL:HG23	46:o:84:ILE:HG12	2.04	0.40
54:w:4:LYS:HA	54:w:7:ARG:HH21	1.86	0.40
54:w:15:ASN:O	54:w:19:LEU:N	2.53	0.40
7:A:281:C:H2'	7:A:282:A:C8	2.56	0.40
7:A:1091:G:N2	7:A:1099:G:O6	2.54	0.40
7:A:1478:G:H1	7:A:1513:U:H3	1.69	0.40
7:A:2252:G:N2	56:y:74:C:O2	2.43	0.40
7:A:2425:A:H4'	7:A:2426:A:H5"	2.03	0.40
8:B:522:C:H42	8:B:528:C:N4	2.20	0.40
8:B:686:U:O2'	8:B:703:G:N2	2.52	0.40
8:B:702:A:H8	8:B:702:A:C5'	2.34	0.40
25:S:72:ASP:OD1	25:S:72:ASP:N	2.51	0.40
28:V:40:LYS:HA	28:V:40:LYS:HD2	1.78	0.40
34:c:8:LYS:HB2	34:c:201:LEU:HD11	2.03	0.40
34:c:83:ARG:HD2	34:c:83:ARG:HA	1.88	0.40
36:e:56:ASP:OD1	36:e:57:LEU:N	2.55	0.40
56:y:29:U:H2'	56:y:30:G:H8	1.86	0.40
2:1:59:ILE:HD12	2:1:59:ILE:HA	1.91	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:5:4:SER:OG	5:5:16:THR:O	2.35	0.40
7:A:155:A:H2'	7:A:156:A:C8	2.57	0.40
7:A:226:A:N6	7:A:227:A:N1	2.69	0.40
7:A:863:A:H2'	7:A:864:G:H8	1.87	0.40
7:A:1164:C:H2'	7:A:1165:A:H8	1.85	0.40
8:B:397:A:O2'	8:B:399:G:OP2	2.33	0.40
8:B:1377:A:C5	14:H:7:ILE:HD13	2.56	0.40
14:H:117:ALA:O	14:H:121:ALA:N	2.48	0.40
20:N:80:LEU:HB3	20:N:88:GLY:HA3	2.04	0.40
23:Q:67:ILE:HG23	23:Q:71:VAL:HB	2.03	0.40
32:a:95:U:H2'	32:a:96:G:C8	2.57	0.40
36:e:162:SER:OG	36:e:165:GLU:OE1	2.26	0.40
37:f:137:ASP:OD2	37:f:140:VAL:N	2.43	0.40
44:m:8:ARG:HD2	44:m:43:GLU:HB2	2.03	0.40
44:m:50:PRO:O	44:m:53:THR:OG1	2.35	0.40
46:o:30:VAL:HG11	46:o:72:ARG:HH21	1.87	0.40
7:A:1310:G:O6	7:A:1311:G:N2	2.54	0.40
7:A:1340:U:OP1	29:W:84:TYR:OH	2.31	0.40
7:A:1814:G:N7	7:A:1815:A:C8	2.89	0.40
8:B:1346:A:OP1	16:J:122:ARG:NH1	2.43	0.40
10:D:155:GLY:HA2	10:D:163:ALA:HB1	2.02	0.40
12:F:81:LEU:HD12	12:F:120:VAL:HG11	2.03	0.40
20:N:4:ILE:HD12	20:N:4:ILE:HA	1.97	0.40
21:O:4:GLN:HA	21:O:7:LYS:HB2	2.04	0.40
21:O:9:ARG:O	21:O:13:ARG:NH1	2.55	0.40
24:R:17:MET:HE1	24:R:45:HIS:CE1	2.57	0.40
32:a:33:G:H2'	32:a:34:A:C8	2.56	0.40
33:b:142:HIS:CE1	33:b:191:THR:HG23	2.56	0.40
41:j:47:ILE:HA	41:j:48:PRO:HD3	1.96	0.40
45:n:35:ILE:N	45:n:53:THR:OG1	2.52	0.40
47:p:95:LEU:HD23	47:p:95:LEU:HA	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	
1	0	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
2	1	62/65 (95%)	51 (82%)	9 (14%)	2 (3%)	3	24
3	2	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	27
4	3	166/169 (98%)	145 (87%)	21 (13%)	0	100	100
5	5	430/432 (100%)	387 (90%)	43 (10%)	0	100	100
6	6	54/57 (95%)	45 (83%)	8 (15%)	1 (2%)	6	34
9	C	216/241 (90%)	178 (82%)	38 (18%)	0	100	100
10	D	204/233 (88%)	176 (86%)	28 (14%)	0	100	100
11	E	203/206 (98%)	179 (88%)	24 (12%)	0	100	100
12	F	148/167 (89%)	114 (77%)	34 (23%)	0	100	100
13	G	98/135 (73%)	84 (86%)	14 (14%)	0	100	100
14	H	149/179 (83%)	138 (93%)	11 (7%)	0	100	100
15	I	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
16	J	125/130 (96%)	111 (89%)	14 (11%)	0	100	100
17	K	96/103 (93%)	84 (88%)	12 (12%)	0	100	100
18	L	115/129 (89%)	92 (80%)	23 (20%)	0	100	100
19	M	121/124 (98%)	95 (78%)	26 (22%)	0	100	100
20	N	112/118 (95%)	97 (87%)	13 (12%)	2 (2%)	6	35
21	O	92/101 (91%)	81 (88%)	11 (12%)	0	100	100
22	P	86/89 (97%)	78 (91%)	8 (9%)	0	100	100
23	Q	80/82 (98%)	66 (82%)	14 (18%)	0	100	100
24	R	78/84 (93%)	58 (74%)	19 (24%)	1 (1%)	9	41
25	S	53/75 (71%)	51 (96%)	2 (4%)	0	100	100
26	T	77/92 (84%)	69 (90%)	8 (10%)	0	100	100
27	U	83/87 (95%)	78 (94%)	4 (5%)	1 (1%)	10	42
28	V	49/71 (69%)	37 (76%)	12 (24%)	0	100	100
29	W	94/100 (94%)	80 (85%)	14 (15%)	0	100	100
33	b	269/273 (98%)	230 (86%)	39 (14%)	0	100	100
34	c	207/209 (99%)	187 (90%)	18 (9%)	2 (1%)	12	46
35	d	199/201 (99%)	185 (93%)	14 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	e	175/179 (98%)	153 (87%)	22 (13%)	0	100	100
37	f	174/177 (98%)	159 (91%)	13 (8%)	2 (1%)	11	44
38	g	45/149 (30%)	34 (76%)	11 (24%)	0	100	100
39	h	139/142 (98%)	115 (83%)	24 (17%)	0	100	100
40	i	140/142 (99%)	126 (90%)	14 (10%)	0	100	100
41	j	120/123 (98%)	89 (74%)	30 (25%)	1 (1%)	16	52
42	k	141/144 (98%)	121 (86%)	19 (14%)	1 (1%)	18	55
43	l	134/136 (98%)	118 (88%)	13 (10%)	3 (2%)	5	31
44	m	118/127 (93%)	99 (84%)	17 (14%)	2 (2%)	7	36
45	n	114/117 (97%)	103 (90%)	11 (10%)	0	100	100
46	o	112/115 (97%)	97 (87%)	15 (13%)	0	100	100
47	p	115/118 (98%)	109 (95%)	6 (5%)	0	100	100
48	q	101/103 (98%)	85 (84%)	16 (16%)	0	100	100
49	r	108/110 (98%)	99 (92%)	9 (8%)	0	100	100
50	s	100/104 (96%)	81 (81%)	17 (17%)	2 (2%)	6	33
51	t	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
52	u	73/85 (86%)	62 (85%)	11 (15%)	0	100	100
53	v	75/78 (96%)	64 (85%)	11 (15%)	0	100	100
54	w	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
55	x	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
57	z	48/55 (87%)	42 (88%)	6 (12%)	0	100	100
All	All	6114/6586 (93%)	5314 (87%)	779 (13%)	21 (0%)	37	70

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	1	32	ILE
20	N	67	GLY
37	f	48	ASN
2	1	33	LEU
3	2	21	GLY
6	6	55	ILE
24	R	71	LYS
27	U	69	LYS
37	f	47	ASP

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Mol	Chain	Res	Type
42	k	82	LEU
43	l	59	ARG
50	s	90	GLY
34	c	152	PRO
20	N	66	GLU
34	c	149	ASN
43	l	70	ASP
44	m	3	HIS
44	m	71	ARG
41	j	93	GLN
43	l	69	PRO
50	s	51	ALA

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	
1	0	38/38 (100%)	37 (97%)	1 (3%)	40	61
2	1	51/52 (98%)	50 (98%)	1 (2%)	48	66
3	2	34/34 (100%)	34 (100%)	0	100	100
4	3	148/149 (99%)	148 (100%)	0	100	100
5	5	359/359 (100%)	359 (100%)	0	100	100
6	6	47/48 (98%)	46 (98%)	1 (2%)	47	65
9	C	180/199 (90%)	180 (100%)	0	100	100
10	D	170/190 (90%)	166 (98%)	4 (2%)	43	63
11	E	172/173 (99%)	171 (99%)	1 (1%)	78	80
12	F	113/126 (90%)	113 (100%)	0	100	100
13	G	87/116 (75%)	86 (99%)	1 (1%)	65	74
14	H	124/147 (84%)	124 (100%)	0	100	100
15	I	104/105 (99%)	103 (99%)	1 (1%)	68	76
16	J	105/107 (98%)	105 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	K	86/90 (96%)	85 (99%)	1 (1%)	63	73
18	L	90/99 (91%)	90 (100%)	0	100	100
19	M	103/104 (99%)	103 (100%)	0	100	100
20	N	92/96 (96%)	90 (98%)	2 (2%)	45	64
21	O	79/84 (94%)	79 (100%)	0	100	100
22	P	75/77 (97%)	75 (100%)	0	100	100
23	Q	65/65 (100%)	65 (100%)	0	100	100
24	R	74/78 (95%)	74 (100%)	0	100	100
25	S	48/65 (74%)	48 (100%)	0	100	100
26	T	70/79 (89%)	70 (100%)	0	100	100
27	U	65/66 (98%)	64 (98%)	1 (2%)	57	70
28	V	44/61 (72%)	43 (98%)	1 (2%)	44	64
29	W	83/84 (99%)	82 (99%)	1 (1%)	63	73
33	b	216/218 (99%)	210 (97%)	6 (3%)	38	59
34	c	164/164 (100%)	160 (98%)	4 (2%)	43	63
35	d	165/165 (100%)	165 (100%)	0	100	100
36	e	148/150 (99%)	146 (99%)	2 (1%)	59	71
37	f	137/138 (99%)	136 (99%)	1 (1%)	76	79
38	g	38/114 (33%)	38 (100%)	0	100	100
39	h	109/110 (99%)	108 (99%)	1 (1%)	70	76
40	i	116/116 (100%)	113 (97%)	3 (3%)	40	61
41	j	103/104 (99%)	101 (98%)	2 (2%)	50	67
42	k	102/103 (99%)	100 (98%)	2 (2%)	48	66
43	l	109/109 (100%)	108 (99%)	1 (1%)	70	76
44	m	100/103 (97%)	98 (98%)	2 (2%)	48	66
45	n	86/87 (99%)	86 (100%)	0	100	100
46	o	99/100 (99%)	99 (100%)	0	100	100
47	p	89/90 (99%)	88 (99%)	1 (1%)	65	74
48	q	84/84 (100%)	84 (100%)	0	100	100
49	r	93/93 (100%)	92 (99%)	1 (1%)	65	74
50	s	83/85 (98%)	82 (99%)	1 (1%)	63	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	t	78/78 (100%)	77 (99%)	1 (1%)	61	72
52	u	56/63 (89%)	55 (98%)	1 (2%)	51	67
53	v	67/68 (98%)	67 (100%)	0	100	100
54	w	55/55 (100%)	55 (100%)	0	100	100
55	x	48/49 (98%)	48 (100%)	0	100	100
57	z	45/49 (92%)	45 (100%)	0	100	100
All	All	5096/5386 (95%)	5051 (99%)	45 (1%)	68	76

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	44	VAL
2	1	33	LEU
6	6	25	VAL
10	D	15	VAL
10	D	19	ASN
10	D	144	LEU
10	D	149	ILE
11	E	129	VAL
13	G	18	VAL
15	I	104	VAL
17	K	14	ASP
20	N	17	ILE
20	N	65	VAL
27	U	39	ILE
28	V	32	VAL
29	W	85	VAL
33	b	19	VAL
33	b	65	VAL
33	b	114	ASP
33	b	171	TYR
33	b	221	ARG
33	b	257	THR
34	c	133	THR
34	c	142	VAL
34	c	197	THR
34	c	203	VAL
36	e	152	LEU
36	e	169	LEU
37	f	98	VAL

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Mol	Chain	Res	Type
39	h	71	THR
40	i	17	VAL
40	i	30	THR
40	i	52	ASP
41	j	10	VAL
41	j	61	VAL
42	k	89	VAL
42	k	121	THR
43	l	89	VAL
44	m	37	THR
44	m	51	LEU
47	p	34	VAL
49	r	74	ILE
50	s	59	VAL
51	t	90	ASP
52	u	71	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (83) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	13	ASN
2	1	28	ASN
3	2	13	ASN
3	2	37	GLN
4	3	7	HIS
5	5	2	GLN
5	5	34	ASN
5	5	236	ASN
5	5	298	ASN
5	5	328	GLN
5	5	358	ASN
5	5	400	ASN
5	5	406	GLN
9	C	42	ASN
9	C	89	GLN
9	C	177	ASN
10	D	19	ASN
10	D	123	GLN
11	E	74	ASN
12	F	148	ASN
13	G	3	HIS
15	I	18	GLN

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Mol	Chain	Res	Type
15	I	67	GLN
16	J	4	ASN
16	J	25	ASN
16	J	75	GLN
17	K	56	HIS
18	L	119	ASN
19	M	59	ASN
19	M	96	HIS
21	O	4	GLN
21	O	35	ASN
21	O	62	ASN
22	P	37	ASN
22	P	62	GLN
23	Q	63	GLN
23	Q	79	ASN
24	R	31	HIS
26	T	69	HIS
27	U	70	ASN
27	U	82	GLN
28	V	9	ASN
29	W	70	HIS
29	W	91	GLN
29	W	92	ASN
34	c	32	ASN
34	c	49	GLN
35	d	9	GLN
35	d	136	GLN
35	d	165	HIS
36	e	37	ASN
36	e	63	GLN
37	f	22	GLN
37	f	45	HIS
37	f	88	GLN
37	f	104	ASN
37	f	116	GLN
37	f	143	GLN
38	g	2	GLN
39	h	31	GLN
40	i	47	HIS
40	i	86	GLN
40	i	130	HIS
41	j	3	GLN

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Mol	Chain	Res	Type
41	j	93	GLN
42	k	35	HIS
43	l	22	GLN
44	m	3	HIS
44	m	11	ASN
44	m	73	ASN
45	n	38	GLN
45	n	43	ASN
46	o	77	HIS
47	p	37	GLN
47	p	71	GLN
49	r	7	HIS
50	s	54	GLN
50	s	69	ASN
51	t	5	ASN
51	t	49	ASN
54	w	27	ASN
54	w	31	GLN
54	w	38	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	X	58/73 (79%)	30 (51%)	0
31	Z	58/76 (76%)	24 (41%)	1 (1%)
32	a	117/118 (99%)	21 (17%)	0
56	y	63/77 (81%)	19 (30%)	0
7	A	2902/2903 (99%)	740 (25%)	13 (0%)
8	B	1538/1539 (99%)	427 (27%)	3 (0%)
All	All	4736/4786 (98%)	1261 (26%)	17 (0%)

All (1261) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A	10	A
7	A	14	A
7	A	23	G
7	A	34	U
7	A	42	A
7	A	45	G
7	A	46	G

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Mol	Chain	Res	Type
7	A	51	G
7	A	54	G
7	A	58	G
7	A	62	U
7	A	63	A
7	A	66	C
7	A	71	A
7	A	74	A
7	A	75	G
7	A	78	U
7	A	80	G
7	A	84	A
7	A	96	C
7	A	100	U
7	A	101	A
7	A	103	A
7	A	107	G
7	A	112	U
7	A	113	U
7	A	118	A
7	A	119	A
7	A	120	U
7	A	126	A
7	A	128	C
7	A	129	C
7	A	138	U
7	A	139	U
7	A	140	C
7	A	141	G
7	A	142	A
7	A	149	A
7	A	162	U
7	A	163	C
7	A	178	G
7	A	196	A
7	A	199	A
7	A	200	U
7	A	204	A
7	A	215	G
7	A	216	A
7	A	222	A
7	A	225	C

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Mol	Chain	Res	Type
7	A	226	A
7	A	228	C
7	A	229	C
7	A	245	G
7	A	248	G
7	A	255	A
7	A	265	A
7	A	266	G
7	A	271	G
7	A	272	A
7	A	275	C
7	A	276	U
7	A	278	A
7	A	279	A
7	A	281	C
7	A	282	A
7	A	298	G
7	A	309	A
7	A	311	A
7	A	322	A
7	A	323	C
7	A	324	A
7	A	329	G
7	A	330	A
7	A	331	C
7	A	335	C
7	A	354	A
7	A	361	G
7	A	362	A
7	A	363	G
7	A	371	A
7	A	372	G
7	A	379	G
7	A	380	G
7	A	386	G
7	A	399	U
7	A	404	A
7	A	405	U
7	A	406	G
7	A	407	G
7	A	411	G
7	A	412	A

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Mol	Chain	Res	Type
7	A	420	C
7	A	424	G
7	A	428	A
7	A	448	U
7	A	455	C
7	A	457	A
7	A	464	U
7	A	465	G
7	A	467	G
7	A	473	G
7	A	477	A
7	A	479	A
7	A	480	A
7	A	481	G
7	A	484	C
7	A	489	G
7	A	490	C
7	A	491	G
7	A	494	G
7	A	496	G
7	A	501	A
7	A	505	A
7	A	507	A
7	A	508	A
7	A	509	C
7	A	527	C
7	A	529	A
7	A	530	G
7	A	531	C
7	A	532	A
7	A	536	G
7	A	543	G
7	A	544	C
7	A	545	U
7	A	546	U
7	A	548	G
7	A	549	G
7	A	550	C
7	A	560	C
7	A	563	A
7	A	567	U
7	A	569	U

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Mol	Chain	Res	Type
7	A	572	A
7	A	573	U
7	A	575	A
7	A	586	A
7	A	597	G
7	A	603	A
7	A	614	A
7	A	615	U
7	A	616	A
7	A	620	G
7	A	622	G
7	A	628	G
7	A	632	A
7	A	634	C
7	A	637	A
7	A	639	U
7	A	643	A
7	A	644	A
7	A	645	C
7	A	646	U
7	A	647	G
7	A	648	G
7	A	654	A
7	A	655	A
7	A	656	G
7	A	664	G
7	A	670	A
7	A	677	A
7	A	686	U
7	A	690	G
7	A	695	G
7	A	713	G
7	A	714	U
7	A	718	A
7	A	728	G
7	A	729	G
7	A	730	A
7	A	736	C
7	A	738	G
7	A	747	U
7	A	748	G
7	A	749	A

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Mol	Chain	Res	Type
7	A	763	G
7	A	764	A
7	A	765	C
7	A	766	U
7	A	775	G
7	A	776	G
7	A	782	A
7	A	783	A
7	A	784	G
7	A	785	G
7	A	789	A
7	A	792	A
7	A	793	A
7	A	797	G
7	A	800	A
7	A	803	U
7	A	805	G
7	A	811	U
7	A	812	C
7	A	819	A
7	A	827	U
7	A	828	U
7	A	830	G
7	A	841	G
7	A	845	A
7	A	846	U
7	A	847	U
7	A	858	G
7	A	859	G
7	A	866	A
7	A	873	C
7	A	878	A
7	A	885	C
7	A	887	U
7	A	888	C
7	A	890	C
7	A	891	G
7	A	894	U
7	A	896	A
7	A	898	C
7	A	899	A
7	A	904	G

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Mol	Chain	Res	Type
7	A	907	G
7	A	910	A
7	A	914	G
7	A	921	C
7	A	929	U
7	A	932	U
7	A	935	C
7	A	941	A
7	A	946	C
7	A	947	A
7	A	957	C
7	A	961	C
7	A	968	C
7	A	973	A
7	A	974	G
7	A	975	A
7	A	976	G
7	A	981	A
7	A	983	A
7	A	985	C
7	A	989	G
7	A	990	A
7	A	995	C
7	A	996	A
7	A	1002	G
7	A	1003	G
7	A	1005	C
7	A	1012	U
7	A	1013	C
7	A	1021	A
7	A	1022	G
7	A	1023	U
7	A	1026	G
7	A	1032	A
7	A	1033	U
7	A	1040	A
7	A	1045	C
7	A	1046	A
7	A	1047	G
7	A	1056	G
7	A	1060	U
7	A	1061	U

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Mol	Chain	Res	Type
7	A	1062	G
7	A	1063	G
7	A	1064	C
7	A	1065	U
7	A	1066	U
7	A	1067	A
7	A	1068	G
7	A	1070	A
7	A	1071	G
7	A	1072	C
7	A	1073	A
7	A	1074	G
7	A	1075	C
7	A	1076	C
7	A	1079	C
7	A	1080	A
7	A	1081	U
7	A	1087	G
7	A	1088	A
7	A	1089	A
7	A	1091	G
7	A	1097	U
7	A	1098	A
7	A	1100	C
7	A	1102	C
7	A	1110	G
7	A	1112	G
7	A	1115	G
7	A	1121	C
7	A	1122	G
7	A	1126	A
7	A	1130	U
7	A	1131	G
7	A	1132	U
7	A	1134	A
7	A	1135	C
7	A	1139	G
7	A	1142	A
7	A	1143	A
7	A	1145	C
7	A	1169	A
7	A	1170	C

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Mol	Chain	Res	Type
7	A	1173	U
7	A	1174	U
7	A	1175	A
7	A	1176	U
7	A	1178	C
7	A	1179	G
7	A	1180	U
7	A	1182	G
7	A	1186	G
7	A	1190	G
7	A	1195	G
7	A	1204	A
7	A	1208	C
7	A	1210	G
7	A	1211	C
7	A	1212	G
7	A	1219	U
7	A	1237	A
7	A	1238	G
7	A	1243	C
7	A	1247	A
7	A	1248	G
7	A	1252	G
7	A	1253	A
7	A	1256	G
7	A	1257	C
7	A	1258	U
7	A	1265	A
7	A	1266	G
7	A	1271	G
7	A	1272	A
7	A	1273	U
7	A	1284	A
7	A	1294	U
7	A	1297	C
7	A	1299	G
7	A	1300	G
7	A	1301	A
7	A	1302	A
7	A	1304	A
7	A	1305	C
7	A	1309	G

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Mol	Chain	Res	Type
7	A	1310	G
7	A	1321	A
7	A	1324	G
7	A	1325	U
7	A	1328	A
7	A	1329	U
7	A	1330	C
7	A	1338	G
7	A	1341	G
7	A	1349	C
7	A	1352	U
7	A	1355	G
7	A	1359	A
7	A	1362	C
7	A	1365	A
7	A	1366	A
7	A	1368	G
7	A	1375	U
7	A	1376	C
7	A	1379	U
7	A	1383	A
7	A	1386	C
7	A	1387	A
7	A	1392	A
7	A	1395	A
7	A	1401	G
7	A	1403	A
7	A	1416	G
7	A	1428	C
7	A	1432	G
7	A	1433	A
7	A	1434	A
7	A	1437	C
7	A	1451	C
7	A	1452	G
7	A	1453	A
7	A	1454	C
7	A	1455	G
7	A	1456	G
7	A	1458	U
7	A	1460	U
7	A	1461	C

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Mol	Chain	Res	Type
7	A	1466	U
7	A	1478	G
7	A	1482	G
7	A	1490	A
7	A	1493	C
7	A	1503	A
7	A	1510	G
7	A	1515	A
7	A	1523	U
7	A	1524	G
7	A	1529	G
7	A	1533	C
7	A	1535	A
7	A	1536	C
7	A	1537	G
7	A	1540	G
7	A	1558	C
7	A	1566	A
7	A	1568	G
7	A	1569	A
7	A	1578	U
7	A	1581	G
7	A	1583	A
7	A	1584	U
7	A	1585	C
7	A	1602	U
7	A	1607	C
7	A	1608	A
7	A	1610	A
7	A	1611	C
7	A	1616	A
7	A	1617	C
7	A	1619	G
7	A	1630	A
7	A	1632	A
7	A	1635	A
7	A	1642	G
7	A	1646	C
7	A	1647	U
7	A	1648	U
7	A	1667	G
7	A	1668	A

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Mol	Chain	Res	Type
7	A	1669	A
7	A	1674	G
7	A	1677	A
7	A	1679	A
7	A	1690	A
7	A	1693	U
7	A	1694	C
7	A	1698	A
7	A	1701	A
7	A	1703	G
7	A	1705	A
7	A	1714	U
7	A	1715	G
7	A	1716	U
7	A	1729	U
7	A	1731	G
7	A	1732	C
7	A	1733	G
7	A	1738	G
7	A	1756	G
7	A	1757	A
7	A	1758	U
7	A	1761	C
7	A	1764	C
7	A	1773	A
7	A	1774	C
7	A	1775	U
7	A	1781	U
7	A	1791	A
7	A	1800	C
7	A	1801	A
7	A	1802	A
7	A	1808	A
7	A	1809	A
7	A	1811	G
7	A	1815	A
7	A	1816	C
7	A	1819	A
7	A	1822	C
7	A	1825	U
7	A	1826	G
7	A	1827	U

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Mol	Chain	Res	Type
7	A	1829	A
7	A	1833	C
7	A	1834	U
7	A	1835	G
7	A	1847	A
7	A	1855	U
7	A	1869	G
7	A	1870	C
7	A	1871	A
7	A	1872	A
7	A	1873	G
7	A	1882	U
7	A	1905	C
7	A	1906	G
7	A	1907	G
7	A	1913	A
7	A	1914	C
7	A	1919	A
7	A	1926	U
7	A	1929	G
7	A	1930	G
7	A	1936	A
7	A	1944	U
7	A	1946	U
7	A	1953	A
7	A	1955	U
7	A	1956	U
7	A	1960	A
7	A	1964	G
7	A	1966	A
7	A	1967	C
7	A	1970	A
7	A	1971	U
7	A	1972	G
7	A	1989	G
7	A	1990	C
7	A	1991	U
7	A	1993	U
7	A	1997	C
7	A	2001	C
7	A	2002	G
7	A	2013	A

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Mol	Chain	Res	Type
7	A	2022	U
7	A	2023	C
7	A	2025	C
7	A	2026	U
7	A	2030	A
7	A	2031	A
7	A	2032	G
7	A	2033	A
7	A	2035	G
7	A	2043	C
7	A	2055	C
7	A	2056	G
7	A	2059	A
7	A	2060	A
7	A	2061	G
7	A	2062	A
7	A	2069	G
7	A	2075	U
7	A	2093	G
7	A	2095	A
7	A	2098	U
7	A	2100	G
7	A	2102	G
7	A	2107	G
7	A	2109	U
7	A	2110	G
7	A	2111	U
7	A	2112	G
7	A	2113	U
7	A	2115	G
7	A	2116	G
7	A	2118	U
7	A	2119	A
7	A	2120	G
7	A	2121	G
7	A	2123	G
7	A	2124	G
7	A	2125	G
7	A	2126	A
7	A	2127	G
7	A	2128	G
7	A	2130	U

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Mol	Chain	Res	Type
7	A	2132	U
7	A	2135	A
7	A	2137	U
7	A	2140	G
7	A	2141	G
7	A	2145	C
7	A	2146	C
7	A	2147	A
7	A	2152	G
7	A	2157	G
7	A	2158	A
7	A	2162	G
7	A	2164	C
7	A	2165	C
7	A	2167	U
7	A	2169	A
7	A	2170	A
7	A	2171	A
7	A	2172	U
7	A	2173	A
7	A	2175	C
7	A	2178	C
7	A	2182	U
7	A	2183	A
7	A	2189	U
7	A	2198	A
7	A	2203	U
7	A	2204	G
7	A	2211	A
7	A	2212	A
7	A	2213	U
7	A	2214	C
7	A	2223	G
7	A	2225	A
7	A	2228	G
7	A	2238	G
7	A	2239	G
7	A	2242	G
7	A	2243	U
7	A	2250	G
7	A	2251	G
7	A	2252	G

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Mol	Chain	Res	Type
7	A	2255	G
7	A	2257	U
7	A	2259	U
7	A	2266	A
7	A	2279	G
7	A	2283	C
7	A	2287	A
7	A	2288	A
7	A	2289	G
7	A	2297	A
7	A	2305	U
7	A	2309	A
7	A	2318	G
7	A	2319	G
7	A	2322	A
7	A	2325	G
7	A	2327	A
7	A	2330	G
7	A	2331	G
7	A	2333	A
7	A	2335	A
7	A	2338	C
7	A	2344	U
7	A	2345	G
7	A	2346	A
7	A	2347	C
7	A	2354	C
7	A	2357	G
7	A	2358	A
7	A	2361	G
7	A	2376	A
7	A	2383	G
7	A	2384	U
7	A	2385	C
7	A	2390	U
7	A	2402	U
7	A	2403	C
7	A	2404	U
7	A	2406	A
7	A	2407	A
7	A	2420	C
7	A	2423	U

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Mol	Chain	Res	Type
7	A	2425	A
7	A	2427	C
7	A	2428	G
7	A	2429	G
7	A	2430	A
7	A	2432	A
7	A	2435	A
7	A	2441	U
7	A	2447	G
7	A	2448	A
7	A	2455	G
7	A	2463	C
7	A	2464	G
7	A	2469	A
7	A	2470	G
7	A	2474	U
7	A	2476	A
7	A	2478	A
7	A	2479	U
7	A	2480	C
7	A	2484	G
7	A	2490	G
7	A	2491	U
7	A	2498	C
7	A	2500	U
7	A	2502	G
7	A	2503	A
7	A	2504	U
7	A	2505	G
7	A	2507	C
7	A	2508	G
7	A	2518	A
7	A	2520	C
7	A	2527	C
7	A	2529	G
7	A	2547	A
7	A	2552	U
7	A	2554	U
7	A	2556	C
7	A	2558	C
7	A	2566	A
7	A	2567	G

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Mol	Chain	Res	Type
7	A	2572	A
7	A	2576	G
7	A	2582	G
7	A	2585	U
7	A	2586	U
7	A	2588	G
7	A	2596	U
7	A	2597	G
7	A	2602	A
7	A	2609	U
7	A	2610	C
7	A	2613	U
7	A	2629	U
7	A	2630	G
7	A	2635	A
7	A	2636	C
7	A	2645	G
7	A	2646	C
7	A	2654	A
7	A	2661	G
7	A	2663	G
7	A	2669	G
7	A	2680	U
7	A	2682	A
7	A	2689	U
7	A	2690	U
7	A	2714	G
7	A	2722	G
7	A	2724	U
7	A	2726	A
7	A	2733	A
7	A	2744	G
7	A	2748	A
7	A	2757	A
7	A	2776	A
7	A	2778	A
7	A	2779	U
7	A	2793	C
7	A	2799	A
7	A	2807	U
7	A	2808	G
7	A	2818	U

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Mol	Chain	Res	Type
7	A	2820	A
7	A	2826	A
7	A	2833	U
7	A	2835	A
7	A	2836	U
7	A	2843	G
7	A	2846	G
7	A	2848	G
7	A	2849	U
7	A	2867	G
7	A	2872	A
7	A	2873	A
7	A	2879	A
7	A	2880	C
7	A	2883	A
7	A	2887	A
7	A	2891	U
7	A	2893	A
7	A	2903	U
8	B	3	A
8	B	4	U
8	B	6	G
8	B	7	A
8	B	8	A
8	B	9	G
8	B	32	A
8	B	37	U
8	B	39	G
8	B	42	G
8	B	43	C
8	B	44	A
8	B	47	C
8	B	48	C
8	B	49	U
8	B	50	A
8	B	51	A
8	B	52	C
8	B	61	G
8	B	62	U
8	B	63	C
8	B	65	A
8	B	67	C

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Mol	Chain	Res	Type
8	B	71	A
8	B	73	C
8	B	74	A
8	B	76	G
8	B	77	A
8	B	78	A
8	B	79	G
8	B	80	A
8	B	81	A
8	B	83	C
8	B	87	C
8	B	88	U
8	B	90	C
8	B	91	U
8	B	96	U
8	B	97	G
8	B	98	A
8	B	100	G
8	B	104	G
8	B	110	C
8	B	115	G
8	B	116	A
8	B	120	A
8	B	121	U
8	B	122	G
8	B	125	U
8	B	126	G
8	B	127	G
8	B	130	A
8	B	131	A
8	B	132	C
8	B	133	U
8	B	137	U
8	B	140	U
8	B	141	G
8	B	144	G
8	B	145	G
8	B	149	A
8	B	154	U
8	B	155	A
8	B	156	C
8	B	163	C

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Mol	Chain	Res	Type
8	B	168	G
8	B	170	U
8	B	171	A
8	B	173	U
8	B	177	G
8	B	180	U
8	B	182	A
8	B	183	C
8	B	184	G
8	B	189	A
8	B	195	A
8	B	197	A
8	B	200	G
8	B	201	G
8	B	204	G
8	B	205	A
8	B	207	C
8	B	208	U
8	B	209	U
8	B	210	C
8	B	212	G
8	B	215	C
8	B	216	U
8	B	219	U
8	B	220	G
8	B	222	C
8	B	224	U
8	B	226	G
8	B	240	G
8	B	244	U
8	B	245	U
8	B	247	G
8	B	251	G
8	B	254	G
8	B	265	G
8	B	266	G
8	B	267	C
8	B	281	G
8	B	289	G
8	B	291	U
8	B	293	G
8	B	295	C

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Mol	Chain	Res	Type
8	B	298	A
8	B	299	G
8	B	300	A
8	B	304	U
8	B	309	A
8	B	321	A
8	B	325	A
8	B	327	A
8	B	328	C
8	B	329	A
8	B	330	C
8	B	332	G
8	B	337	G
8	B	345	C
8	B	346	G
8	B	347	G
8	B	348	G
8	B	352	C
8	B	354	G
8	B	359	G
8	B	367	U
8	B	371	A
8	B	372	C
8	B	373	A
8	B	380	G
8	B	384	G
8	B	388	G
8	B	392	C
8	B	393	A
8	B	396	C
8	B	397	A
8	B	398	U
8	B	401	C
8	B	406	G
8	B	411	A
8	B	412	A
8	B	413	G
8	B	414	A
8	B	419	C
8	B	421	U
8	B	422	C
8	B	423	G

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Mol	Chain	Res	Type
8	B	424	G
8	B	428	G
8	B	429	U
8	B	434	U
8	B	440	C
8	B	443	C
8	B	444	G
8	B	447	G
8	B	453	G
8	B	454	G
8	B	455	G
8	B	456	A
8	B	458	U
8	B	463	U
8	B	465	A
8	B	467	U
8	B	468	A
8	B	469	C
8	B	471	U
8	B	472	U
8	B	476	U
8	B	478	A
8	B	479	U
8	B	480	U
8	B	484	G
8	B	485	U
8	B	486	U
8	B	492	C
8	B	495	A
8	B	496	A
8	B	498	A
8	B	499	A
8	B	503	C
8	B	505	G
8	B	508	U
8	B	512	U
8	B	518	C
8	B	521	G
8	B	527	G
8	B	532	A
8	B	533	A
8	B	536	C

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Mol	Chain	Res	Type
8	B	547	A
8	B	556	C
8	B	558	G
8	B	559	A
8	B	563	A
8	B	572	A
8	B	573	A
8	B	576	C
8	B	577	G
8	B	586	C
8	B	592	G
8	B	595	A
8	B	596	A
8	B	601	G
8	B	607	A
8	B	611	C
8	B	613	C
8	B	615	G
8	B	619	U
8	B	621	A
8	B	630	A
8	B	639	G
8	B	652	U
8	B	653	U
8	B	660	C
8	B	665	A
8	B	676	A
8	B	695	A
8	B	702	A
8	B	703	G
8	B	718	A
8	B	720	C
8	B	721	G
8	B	723	U
8	B	724	G
8	B	731	G
8	B	733	G
8	B	734	G
8	B	747	A
8	B	748	G
8	B	755	G
8	B	758	C

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Mol	Chain	Res	Type
8	B	763	G
8	B	766	A
8	B	774	G
8	B	777	A
8	B	793	U
8	B	794	A
8	B	810	C
8	B	812	G
8	B	813	U
8	B	814	A
8	B	815	A
8	B	817	C
8	B	821	G
8	B	826	C
8	B	828	U
8	B	835	U
8	B	840	C
8	B	841	C
8	B	842	U
8	B	843	U
8	B	844	G
8	B	846	G
8	B	849	G
8	B	873	A
8	B	879	C
8	B	885	G
8	B	887	G
8	B	889	A
8	B	910	C
8	B	914	A
8	B	918	A
8	B	919	A
8	B	921	U
8	B	926	G
8	B	933	G
8	B	934	C
8	B	937	A
8	B	948	C
8	B	955	U
8	B	960	U
8	B	969	A
8	B	971	G

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Mol	Chain	Res	Type
8	B	974	A
8	B	975	A
8	B	976	G
8	B	977	A
8	B	980	C
8	B	983	A
8	B	984	C
8	B	987	G
8	B	988	G
8	B	989	U
8	B	991	U
8	B	992	U
8	B	993	G
8	B	994	A
8	B	995	C
8	B	1001	C
8	B	1002	G
8	B	1004	A
8	B	1005	A
8	B	1008	U
8	B	1009	U
8	B	1012	A
8	B	1017	U
8	B	1022	A
8	B	1023	U
8	B	1026	G
8	B	1029	U
8	B	1031	C
8	B	1032	G
8	B	1033	G
8	B	1036	A
8	B	1039	G
8	B	1044	A
8	B	1054	C
8	B	1065	U
8	B	1073	U
8	B	1085	U
8	B	1094	G
8	B	1095	U
8	B	1101	A
8	B	1102	A
8	B	1108	G

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Mol	Chain	Res	Type
8	B	1126	U
8	B	1127	G
8	B	1129	C
8	B	1130	A
8	B	1132	C
8	B	1133	G
8	B	1135	U
8	B	1136	C
8	B	1137	C
8	B	1138	G
8	B	1139	G
8	B	1140	C
8	B	1141	C
8	B	1142	G
8	B	1143	G
8	B	1145	A
8	B	1159	U
8	B	1160	G
8	B	1161	C
8	B	1162	C
8	B	1168	U
8	B	1171	A
8	B	1179	A
8	B	1182	G
8	B	1184	G
8	B	1193	G
8	B	1196	A
8	B	1197	A
8	B	1202	U
8	B	1212	U
8	B	1213	A
8	B	1224	U
8	B	1227	A
8	B	1233	G
8	B	1240	U
8	B	1241	G
8	B	1242	G
8	B	1249	C
8	B	1257	A
8	B	1258	G
8	B	1262	C
8	B	1271	A

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Mol	Chain	Res	Type
8	B	1272	G
8	B	1275	A
8	B	1280	A
8	B	1285	A
8	B	1286	U
8	B	1287	A
8	B	1289	A
8	B	1290	G
8	B	1292	G
8	B	1293	C
8	B	1296	C
8	B	1298	U
8	B	1299	A
8	B	1300	G
8	B	1301	U
8	B	1302	C
8	B	1303	C
8	B	1304	G
8	B	1305	G
8	B	1310	G
8	B	1312	G
8	B	1317	C
8	B	1318	A
8	B	1320	C
8	B	1322	C
8	B	1331	G
8	B	1336	C
8	B	1340	A
8	B	1346	A
8	B	1348	U
8	B	1353	G
8	B	1363	A
8	B	1364	U
8	B	1368	A
8	B	1370	G
8	B	1378	C
8	B	1380	U
8	B	1385	G
8	B	1397	C
8	B	1398	A
8	B	1402	C
8	B	1405	G

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Mol	Chain	Res	Type
8	B	1419	G
8	B	1429	A
8	B	1431	A
8	B	1432	G
8	B	1440	U
8	B	1446	A
8	B	1448	C
8	B	1452	C
8	B	1458	G
8	B	1464	U
8	B	1475	G
8	B	1487	G
8	B	1492	A
8	B	1494	G
8	B	1497	G
8	B	1503	A
8	B	1506	U
8	B	1517	G
8	B	1525	G
8	B	1528	U
8	B	1529	G
8	B	1530	G
8	B	1534	A
8	B	1535	C
8	B	1536	C
8	B	1540	U
30	X	3	G
30	X	4	U
30	X	5	G
30	X	6	A
30	X	13	C
30	X	14	A
30	X	15	G
30	X	19	G
30	X	20	G
30	X	21	A
30	X	22	G
30	X	29	U
30	X	33	U
30	X	39	G
30	X	41	A
30	X	44	G

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Mol	Chain	Res	Type
30	X	45	G
30	X	48	C
30	X	49	G
30	X	53	G
30	X	57	G
30	X	58	A
30	X	59	U
30	X	60	C
30	X	63	G
30	X	65	C
30	X	68	C
30	X	70	C
30	X	71	C
30	X	73	A
31	Z	3	G
31	Z	6	G
31	Z	14	A
31	Z	19	G
31	Z	20	U
31	Z	24	G
31	Z	25	C
31	Z	26	A
31	Z	29	U
31	Z	32	C
31	Z	33	U
31	Z	36	U
31	Z	49	G
31	Z	50	C
31	Z	51	A
31	Z	57	G
31	Z	59	A
31	Z	63	U
31	Z	68	G
31	Z	71	C
31	Z	73	A
31	Z	74	C
31	Z	75	C
31	Z	76	A
32	a	3	C
32	a	15	A
32	a	17	C
32	a	24	G

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Mol	Chain	Res	Type
32	a	25	U
32	a	31	C
32	a	32	U
32	a	35	C
32	a	44	G
32	a	51	G
32	a	53	A
32	a	56	G
32	a	66	A
32	a	83	G
32	a	88	C
32	a	89	U
32	a	90	C
32	a	91	C
32	a	99	A
32	a	109	A
32	a	119	A
56	y	3	A
56	y	7	G
56	y	13	C
56	y	16	U
56	y	17	C
56	y	18	G
56	y	19	U
56	y	20	U
56	y	21	A
56	y	22	G
56	y	33	U
56	y	36	C
56	y	48	C
56	y	49	G
56	y	51	G
56	y	69	U
56	y	71	C
56	y	75	C
56	y	76	A

All (17) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	A	141	G
7	A	244	A

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Mol	Chain	Res	Type
7	A	271	G
7	A	297	G
7	A	404	A
7	A	897	C
7	A	975	A
7	A	1730	C
7	A	1904	G
7	A	1913	A
7	A	2317	A
7	A	2346	A
7	A	2756	U
8	B	115	G
8	B	428	G
8	B	1201	A
31	Z	13	C

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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.

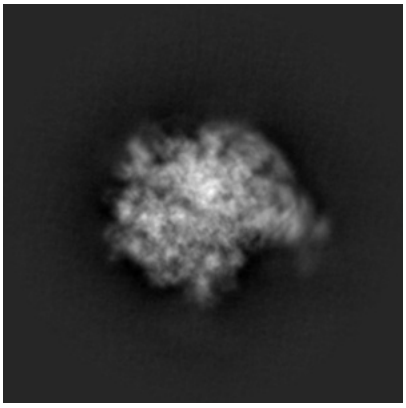
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-30611. These allow visual inspection of the internal detail of the map and identification of artifacts.

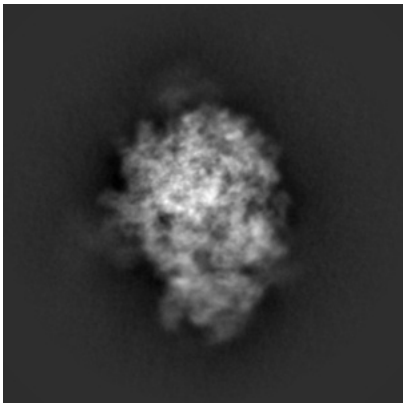
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

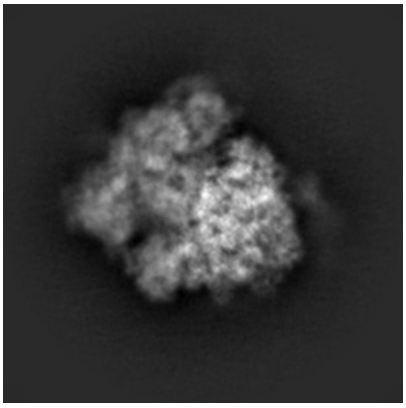
6.1.1 Primary map



X



Y

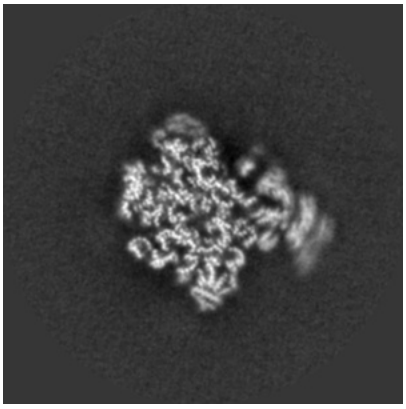


Z

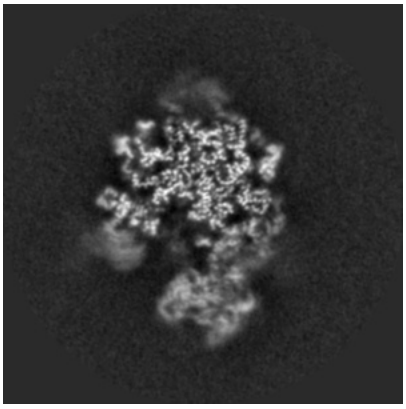
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

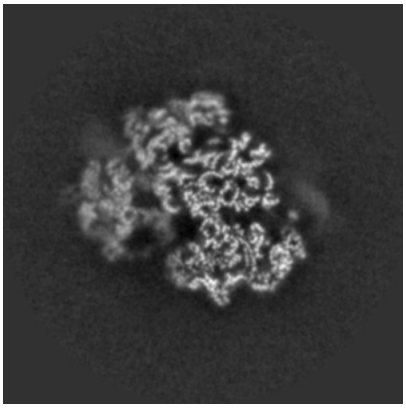
6.2.1 Primary map



X Index: 160



Y Index: 160

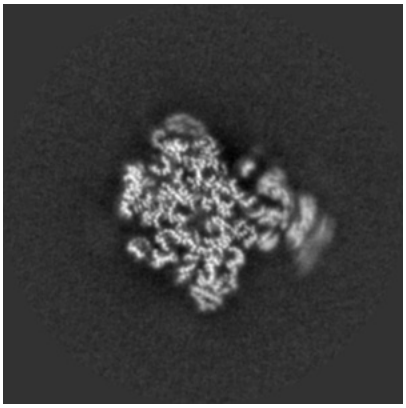


Z Index: 160

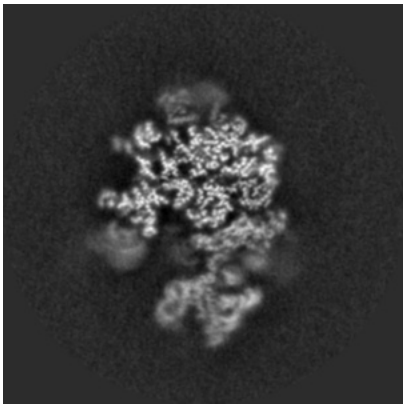
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

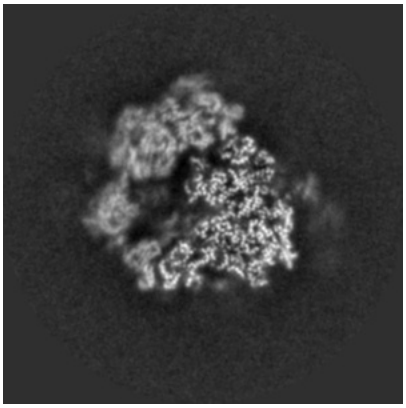
6.3.1 Primary map



X Index: 161



Y Index: 165

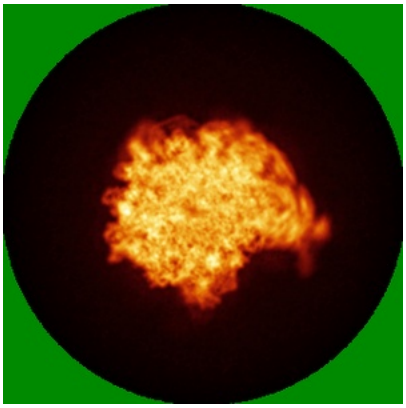


Z Index: 147

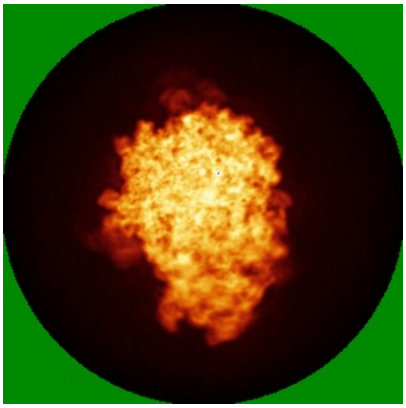
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

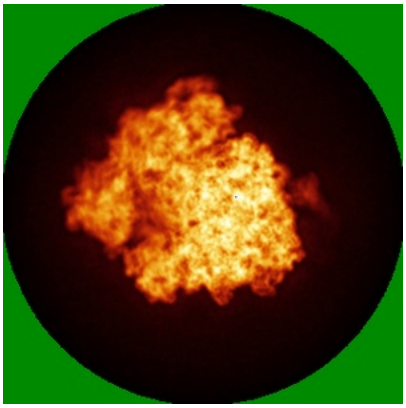
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

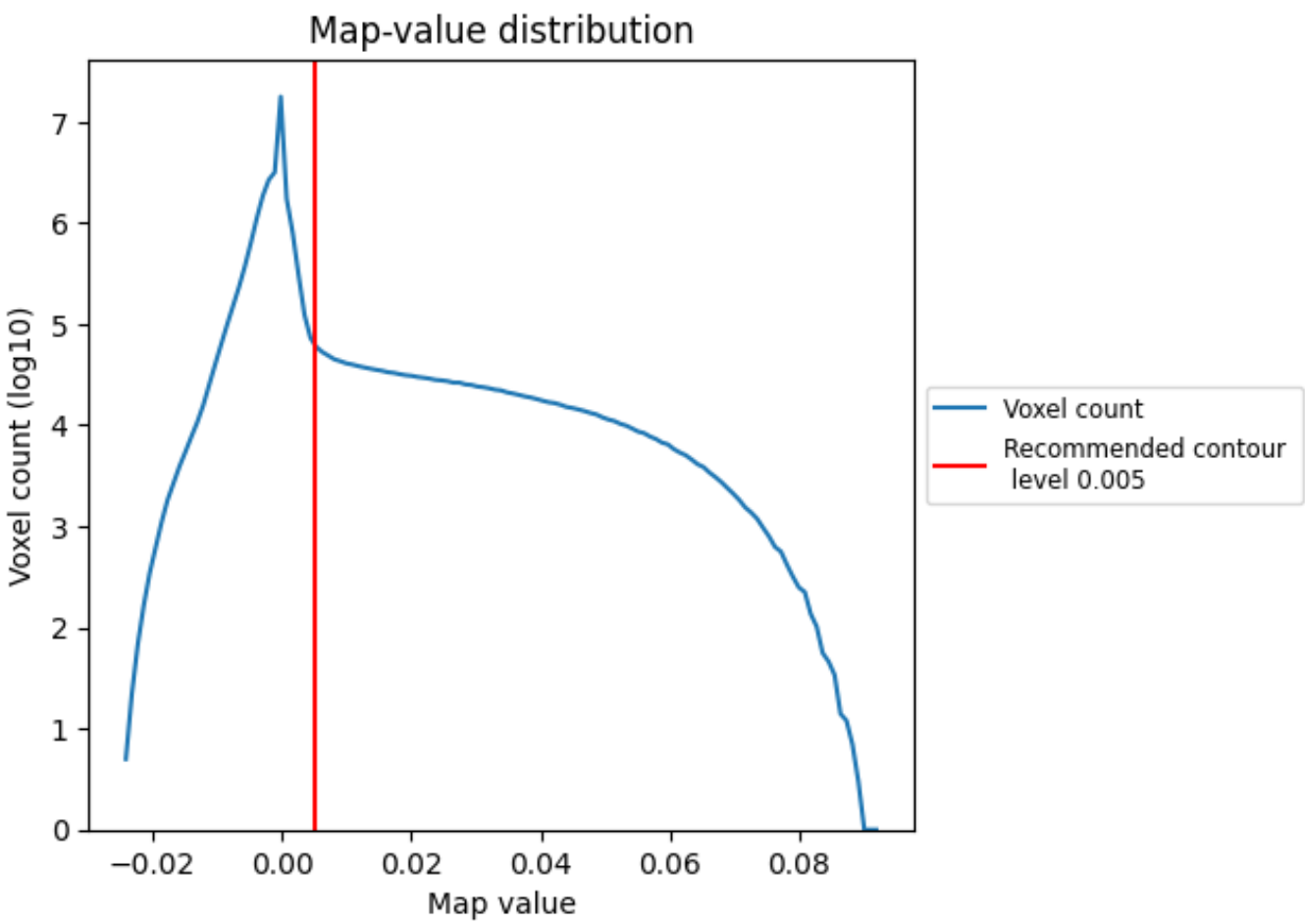
6.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis (i)

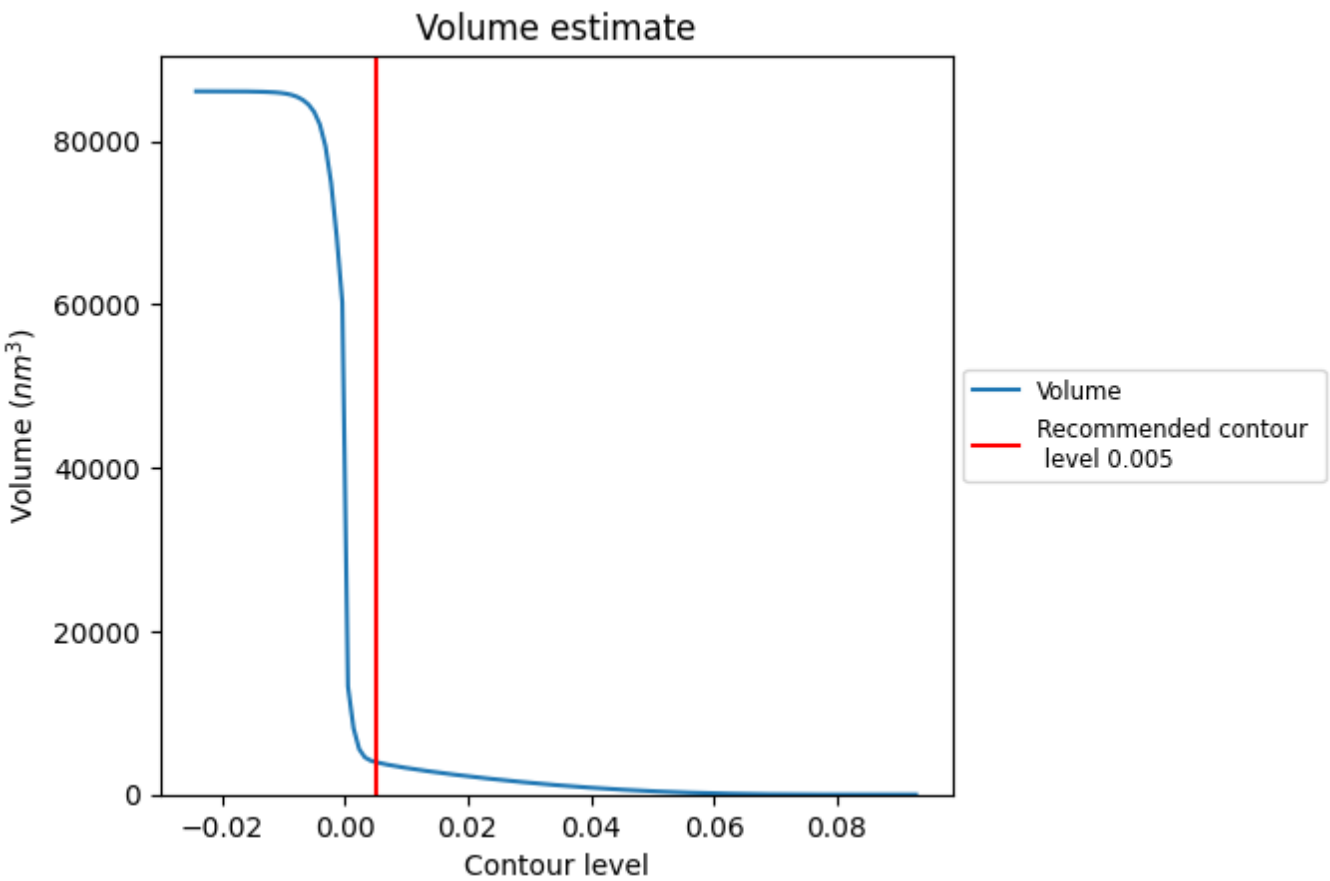
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

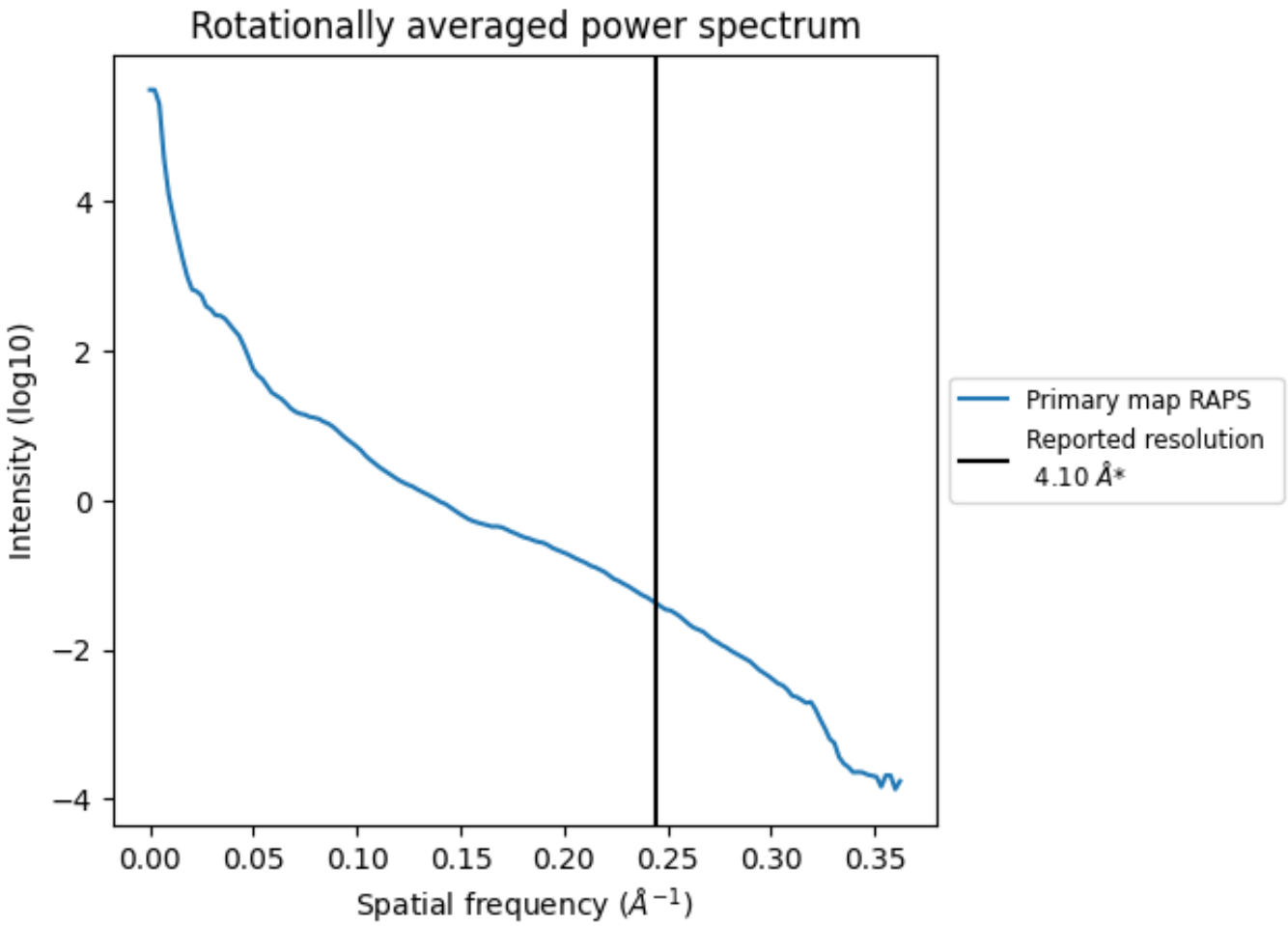
7.2 Volume estimate (i)



The volume at the recommended contour level is 3991 nm^3; this corresponds to an approximate mass of 3605 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

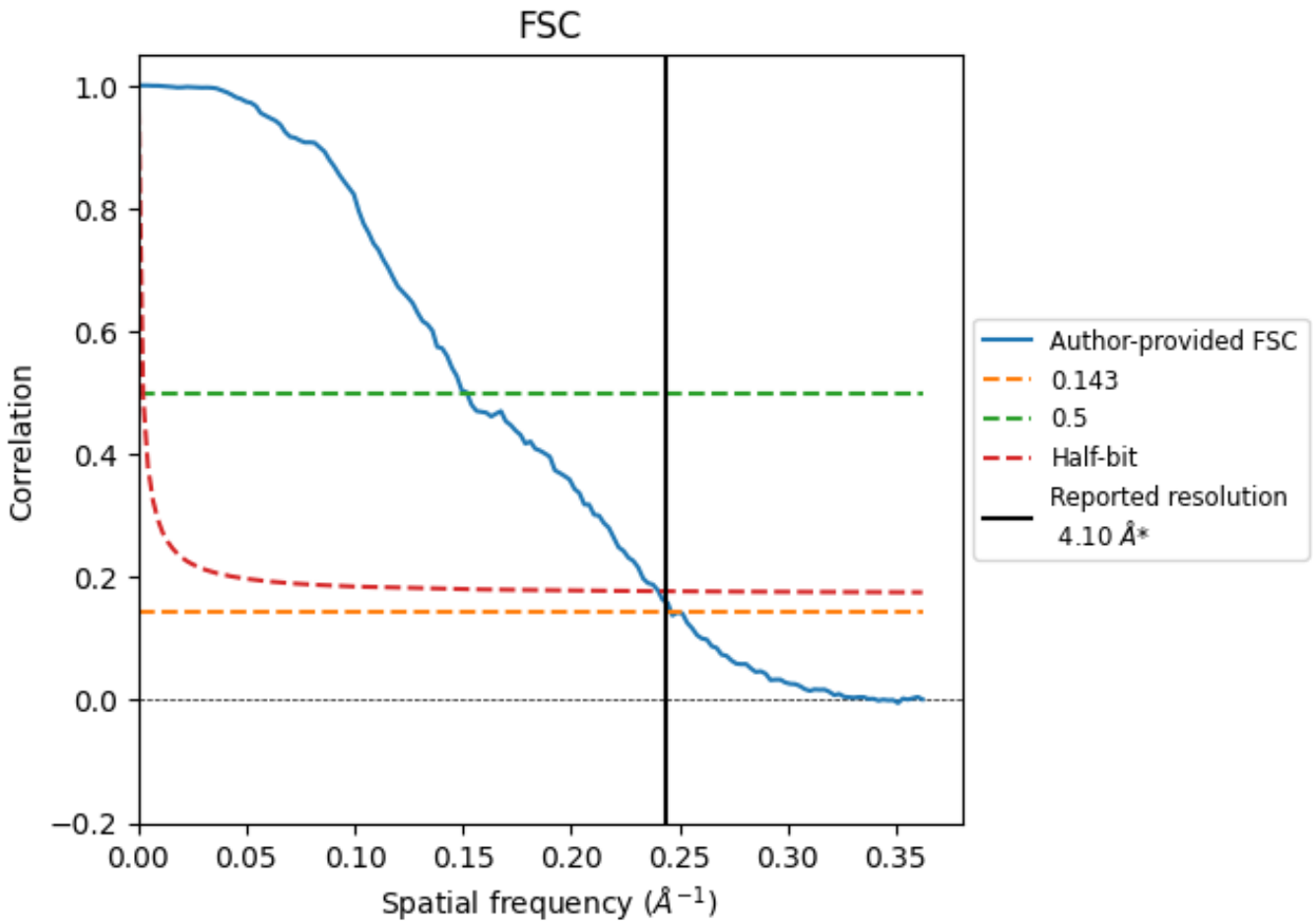


*Reported resolution corresponds to spatial frequency of 0.244 Å^{-1}

8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.244 Å^{-1}

8.2 Resolution estimates (i)

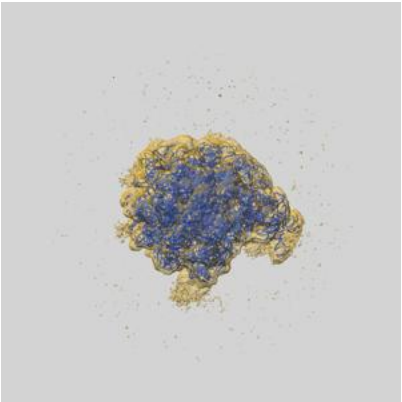
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.06	6.59	4.16
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

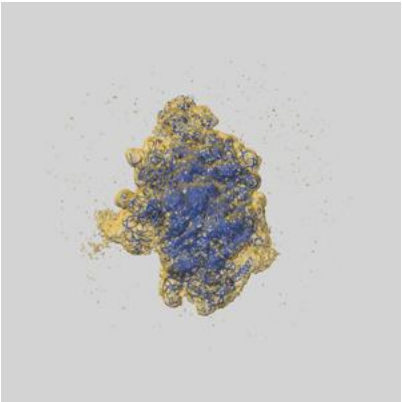
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-30611 and PDB model 7D80. Per-residue inclusion information can be found in section 3 on page 15.

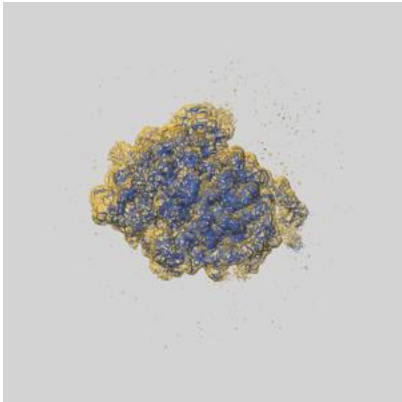
9.1 Map-model overlay (i)



X



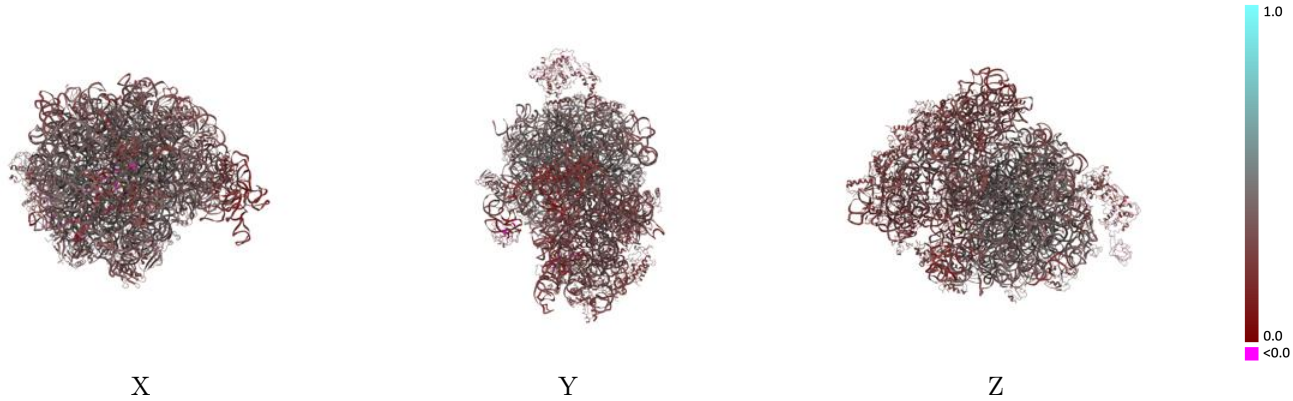
Y



Z

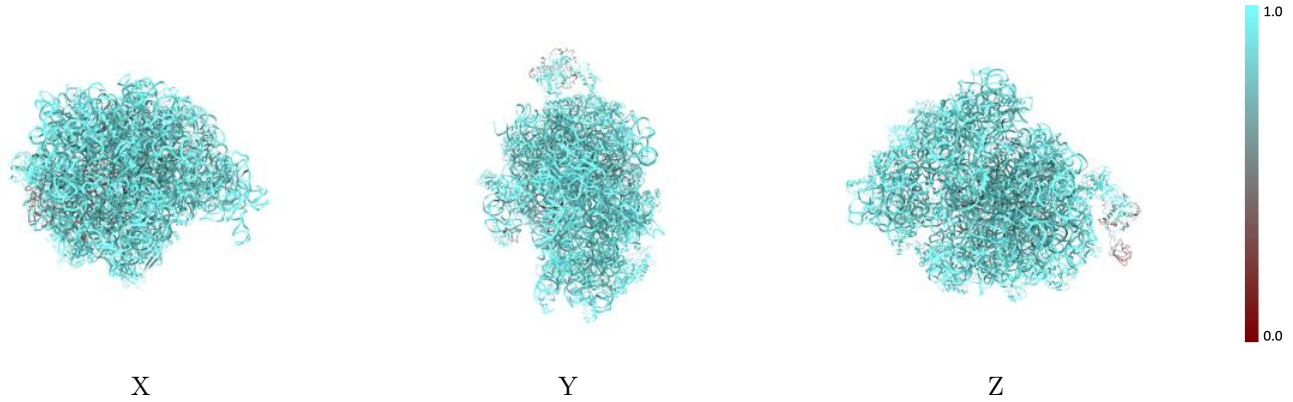
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



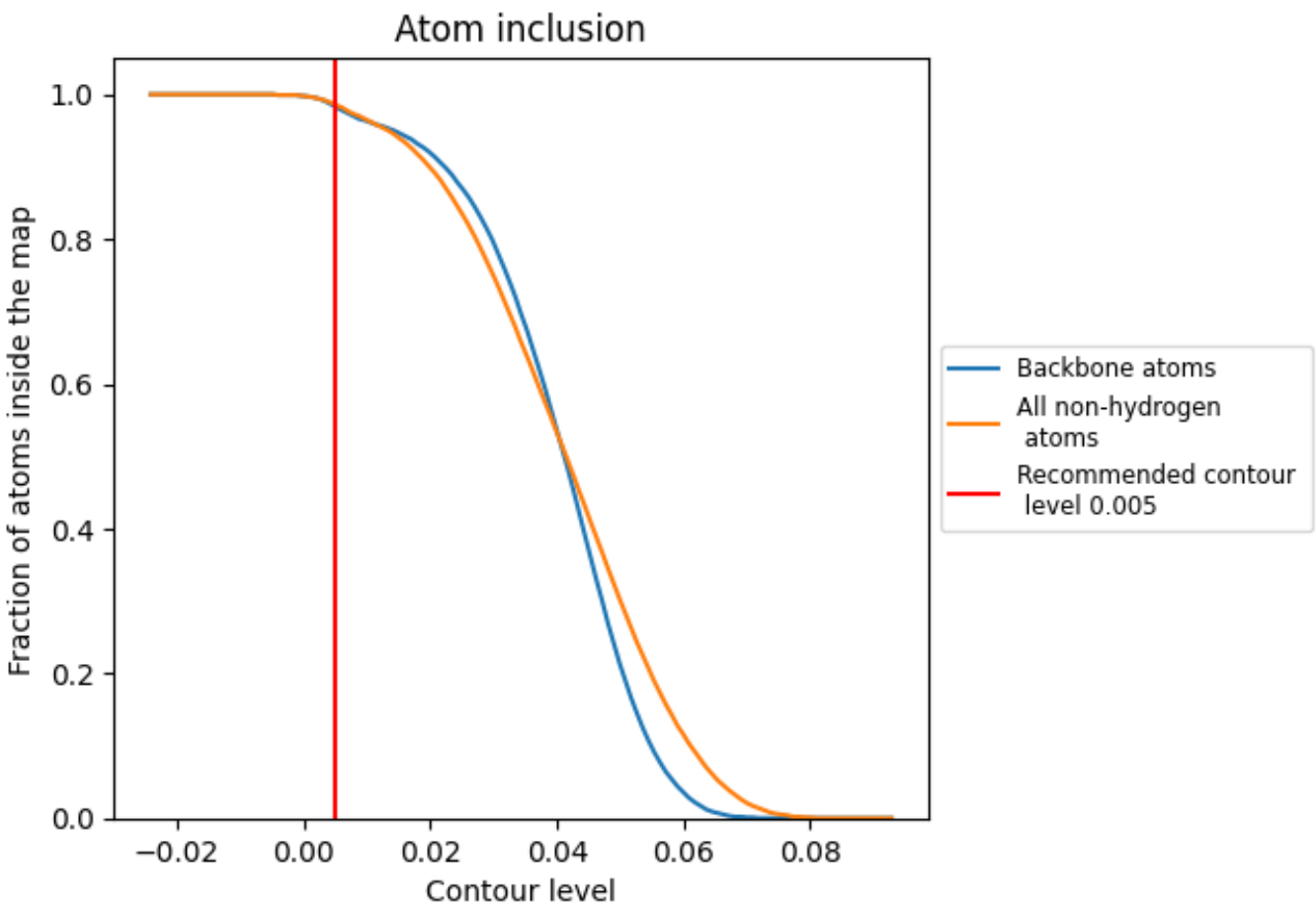
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.005).

9.4 Atom inclusion (i)



At the recommended contour level, 98% of all backbone atoms, 99% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9860	0.3390
0	0.9750	0.3790
1	0.9940	0.3960
2	1.0000	0.3610
3	0.9890	0.2710
5	0.6750	0.2400
6	1.0000	0.3920
A	0.9990	0.3870
B	1.0000	0.3000
C	1.0000	0.2690
D	0.9980	0.2850
E	1.0000	0.2120
F	0.9980	0.3040
G	0.9940	0.2860
H	0.9990	0.2410
I	0.9990	0.2790
J	1.0000	0.2260
K	0.9970	0.2560
L	0.9970	0.2910
M	0.9940	0.2620
N	0.9980	0.2210
O	1.0000	0.2350
P	0.9960	0.2560
Q	0.9980	0.2510
R	1.0000	0.2680
S	1.0000	0.3140
T	0.9980	0.2050
U	0.9970	0.2250
V	0.9930	0.2600
W	0.9950	0.3610
X	0.9980	0.2180
Z	0.5280	0.2640
a	1.0000	0.3520
b	0.9910	0.4030
c	0.9940	0.4000

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Chain	Atom inclusion	Q-score
d	0.9970	0.3740
e	0.9990	0.2550
f	1.0000	0.3330
g	1.0000	0.3360
h	0.8800	0.1720
i	0.9960	0.3910
j	0.9910	0.4010
k	0.9950	0.3920
l	0.9970	0.3940
m	0.9980	0.3800
n	1.0000	0.3220
o	0.9930	0.3830
p	0.9990	0.3670
q	0.9960	0.4020
r	0.9920	0.3850
s	0.9960	0.3580
t	1.0000	0.3620
u	0.9980	0.4010
v	0.9970	0.3730
w	1.0000	0.2840
x	0.9950	0.3850
y	0.9700	0.2890
z	0.9880	0.3580