



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 04:47 PM UTC

PDB ID : 6SPF / pdb_00006spf
EMDB ID : EMD-10284
Title : Pseudomonas aeruginosa 70s ribosome from an aminoglycoside resistant clinical isolate
Authors : Halfon, Y.; Jimenez-Fernande, A.; La Ros, R.; Espinos, R.; Krogh Johansen, H.; Matzov, D.; Eyal, Z.; Bashan, A.; Zimmerman, E.; Belousoff, M.; Molin, S.; Yonath, A.
Deposited on : 2019-09-01
Resolution : 2.89 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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

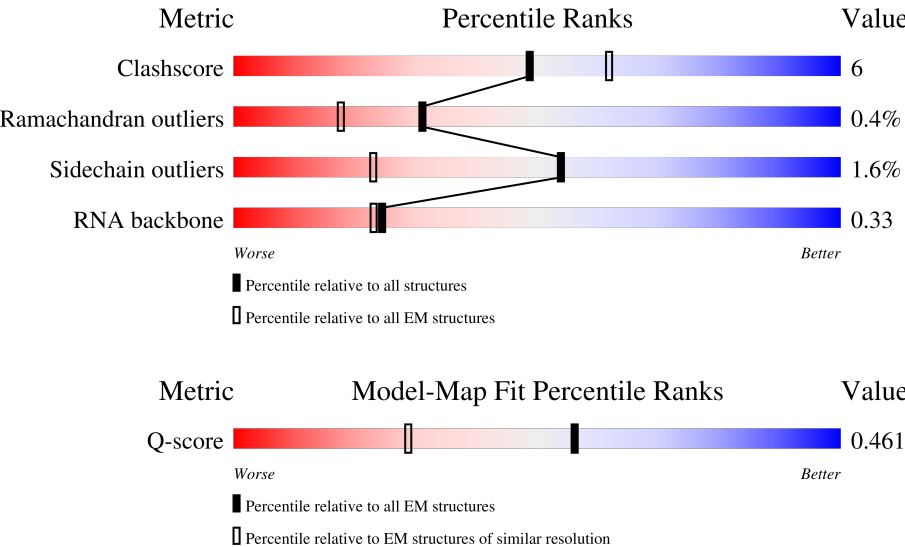
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 2.89 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	12148 (2.39 - 3.39)

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 $\leq 5\%$. 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	A	2888	
2	B	117	
3	C	271	

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Mol	Chain	Length	Quality of chain
4	D	207	
5	E	199	
6	F	174	
7	G	169	
8	H	78	
9	I	140	
10	J	141	
11	K	120	
12	L	144	
13	M	136	
14	N	120	
15	O	115	
16	P	114	
17	Q	117	
18	R	102	
19	S	110	
20	T	94	
21	U	103	
22	V	188	
23	W	76	
24	X	77	
25	Y	60	
26	Z	57	
27	1	31	
28	2	53	

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Mol	Chain	Length	Quality of chain
29	3	50	44% 90% 8%
30	4	44	80% 20%
31	5	63	79% 21%
32	6	38	76% 24%
33	a	1521	32% 41% 40% 10% 9%
34	b	226	80% 76% 22%
35	c	203	99% 84% 16%
36	d	204	76% 87% 13%
37	e	150	70% 85% 13%
38	f	100	87% 89% 11%
39	g	154	97% 89% 11%
40	h	129	58% 71% 27%
41	i	126	91% 80% 19%
42	j	96	99% 79% 21%
43	k	115	83% 77% 23%
44	l	120	72% 79% 20%
45	m	110	93% 75% 25%
46	n	98	98% 77% 23%
47	o	87	59% 67% 33%
48	p	78	46% 73% 27%
49	q	76	34% 78% 22%
50	r	56	82% 73% 27%
51	s	80	95% 82% 16%
52	t	86	29% 73% 27%
53	u	34	97% 74% 26%

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 138296 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 RNA chain called Pseudomonas aeruginosa strain PAO1 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2885	Total	C	N	O	P	0	0
			61899	27618	11351	20046	2884		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	117	Total	C	N	O	P	0	0
			2495	1114	448	816	117		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	271	Total	C	N	O	S	0	0
			2048	1258	422	362	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	207	Total	C	N	O	S	0	0
			1549	960	297	287	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	199	Total	C	N	O	S	0	0
			1509	948	281	278	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	174	Total	C	N	O	S	0	0
			1278	806	225	244	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	7	LEU	ILE	conflict	UNP A0A072ZMU2

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	169	Total	C	N	O	S	0	0
			1264	795	233	234	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	?	-	GLY	deletion	UNP A0A2V3F3S9
G	?	-	TYR	deletion	UNP A0A2V3F3S9
G	?	-	LYS	deletion	UNP A0A2V3F3S9
G	?	-	ALA	deletion	UNP A0A2V3F3S9

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	78	Total	C	N	O		0	0
			577	363	104	110			

- Molecule 9 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	140	Total	C	N	O	S	0	0
			1026	642	183	198	3		

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	141	Total	C	N	O	S	0	0
			1122	713	205	201	3		

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	120	Total	C	N	O	S	0	0
			922	576	178	162	6		

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	144	Total	C	N	O	S	0	0
			1063	653	214	193	3		

- Molecule 13 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	136	Total	C	N	O	S	0	0
			1076	684	210	179	3		

- Molecule 14 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	120	Total	C	N	O	S	0	0
			959	600	192	162	5		

- Molecule 15 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	115	Total	C	N	O	S	0	0
			881	544	174	161	2		

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	114	Total	C	N	O	S	0	0
			901	567	171	162	1		

- Molecule 17 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	Q	117	Total	C	N	O	0	0
			936	592	196	148		

- Molecule 18 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	102	Total	C	N	O	S	0	0
			801	509	154	136	2		

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	110	Total	C	N	O	S	0	0
			833	515	161	153	4		

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	94	Total	C	N	O	S	0	0
			732	469	132	130	1		

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	103	Total	C	N	O	S	0	0
			801	503	152	144	2		

- Molecule 22 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	188	Total	C	N	O	S	0	0
			1397	888	254	253	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	6	VAL	LEU	conflict	UNP A0A072ZBM5
V	71	VAL	ALA	conflict	UNP A0A072ZBM5

- Molecule 23 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	W	76	Total	C	N	O	0	0
			574	365	110	99		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
W	40	LEU	GLN	conflict	UNP A0A071LFT4

- Molecule 24 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	77	Total	C	N	O	S	0	0
			626	389	134	101	2		

- Molecule 25 is a protein called Ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	60	Total	C	N	O	S	0	0
			468	286	96	85	1		

- Molecule 26 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	57	Total	C	N	O	S	0	0
			445	277	87	79	2		

- Molecule 27 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	1	31	Total	C	N	O	S	0	0
			232	144	40	45	3		

- Molecule 28 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	2	53	Total	C	N	O	S	0	0
			419	251	89	78	1		

- Molecule 29 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	3	50	Total	C	N	O	0	0
			408	262	74	72		

- Molecule 30 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	44	Total	C	N	O	S	0	0
			364	222	87	53	2		

- Molecule 31 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	5	63	Total	C	N	O	S	0	0
			502	311	107	81	3		

- Molecule 32 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	6	38	Total	C	N	O	S	0	0
			303	184	69	46	4		

- Molecule 33 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	a	1390	Total	C	N	O	P	0	0
			29826	13303	5479	9654	1390		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	101	A	G	conflict	GB 1378074500

- Molecule 34 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	221	Total	C	N	O	S	0	0
			1698	1070	309	310	9		

- Molecule 35 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	c	203	Total	C	N	O	S	0	0
			1609	1017	303	284	5		

- Molecule 36 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	d	204	Total	C	N	O	S	0	0
			1596	988	310	293	5		

- Molecule 37 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	e	149	Total	C	N	O	S	0	0
			1092	687	202	197	6		

- Molecule 38 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	f	100	Total	C	N	O	S	0	0
			802	497	152	149	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
f	80	ALA	TYR	conflict	UNP A0A069Q263

- Molecule 39 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	g	154	Total	C	N	O	S	0	0
			1190	747	227	211	5		

- Molecule 40 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	h	129	Total	C	N	O	S	0	0
			965	608	171	180	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
h	94	ALA	LYS	conflict	UNP E2RXT9

- Molecule 41 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	i	126	Total	C	N	O	S	0	0
			994	616	198	179	1		

- Molecule 42 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	j	96	Total	C	N	O	S	0	0
			763	479	143	140	1		

- Molecule 43 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	k	115	Total	C	N	O	S	0	0
			832	514	160	156	2		

- Molecule 44 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	l	120	Total	C	N	O	S	0	0
			942	577	195	166	4		

- Molecule 45 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	m	109	Total	C	N	O	S	0	0
			847	515	173	155	4		

- Molecule 46 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	n	98	Total	C	N	O	S	0	0
			776	479	163	131	3		

- Molecule 47 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	o	87	Total	C	N	O	S	0	0
			691	428	135	127	1		

- Molecule 48 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	p	78	Total	C	N	O	S	0	0
			609	381	120	107	1		

- Molecule 49 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	q	76	Total	C	N	O	S	0	0
			619	387	120	110	2		

- Molecule 50 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	r	56	Total	C	N	O	0	0
			443	283	79	81		

- Molecule 51 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	s	80	Total	C	N	O	S	0	0
			635	405	121	106	3		

- Molecule 52 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	t	86	Total	C	N	O	S	0	0
			662	410	137	113	2		

- Molecule 53 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	u	34	Total	C	N	O	0	0
			295	178	70	47		

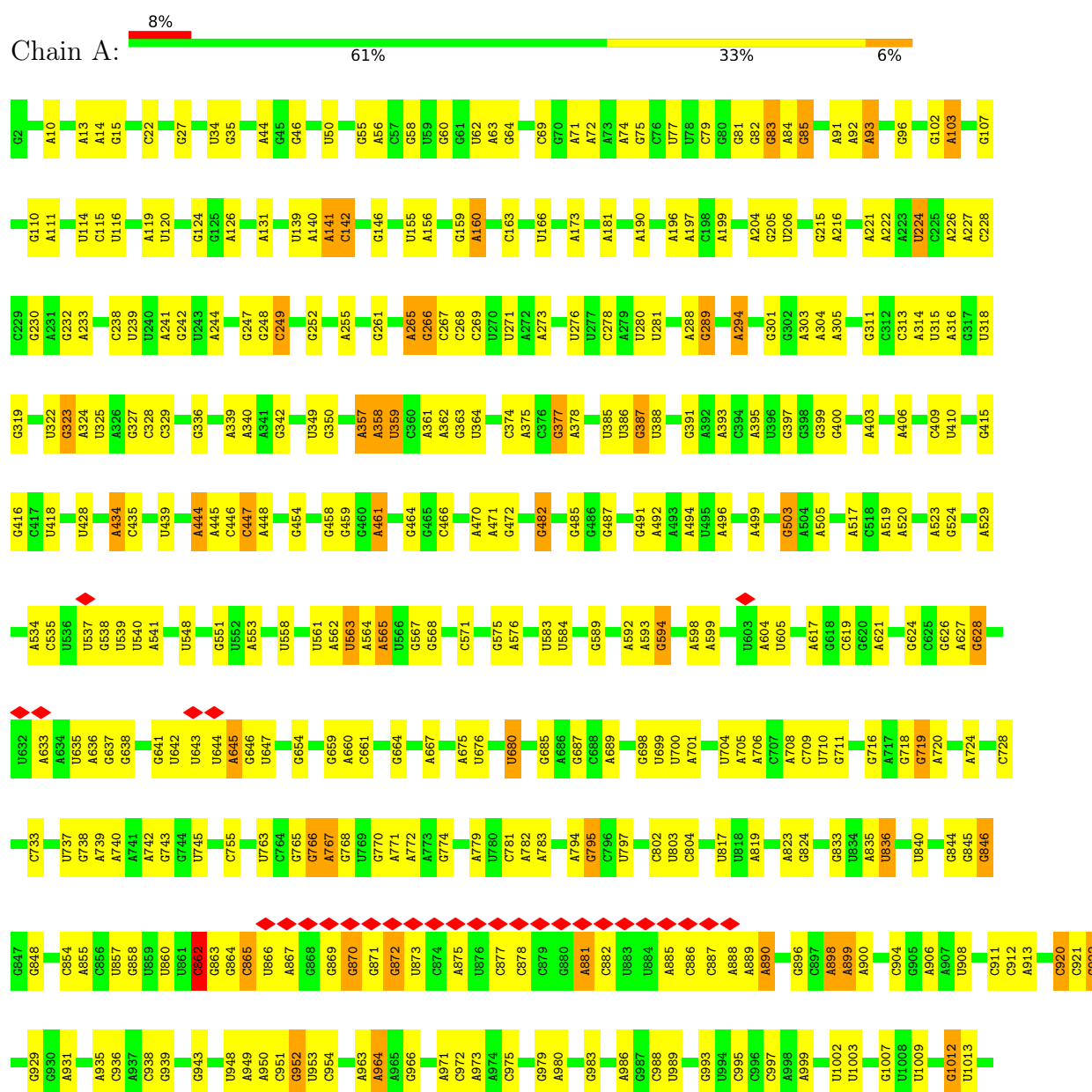
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u	46	ARG	LYS	conflict	UNP A0A069QC99

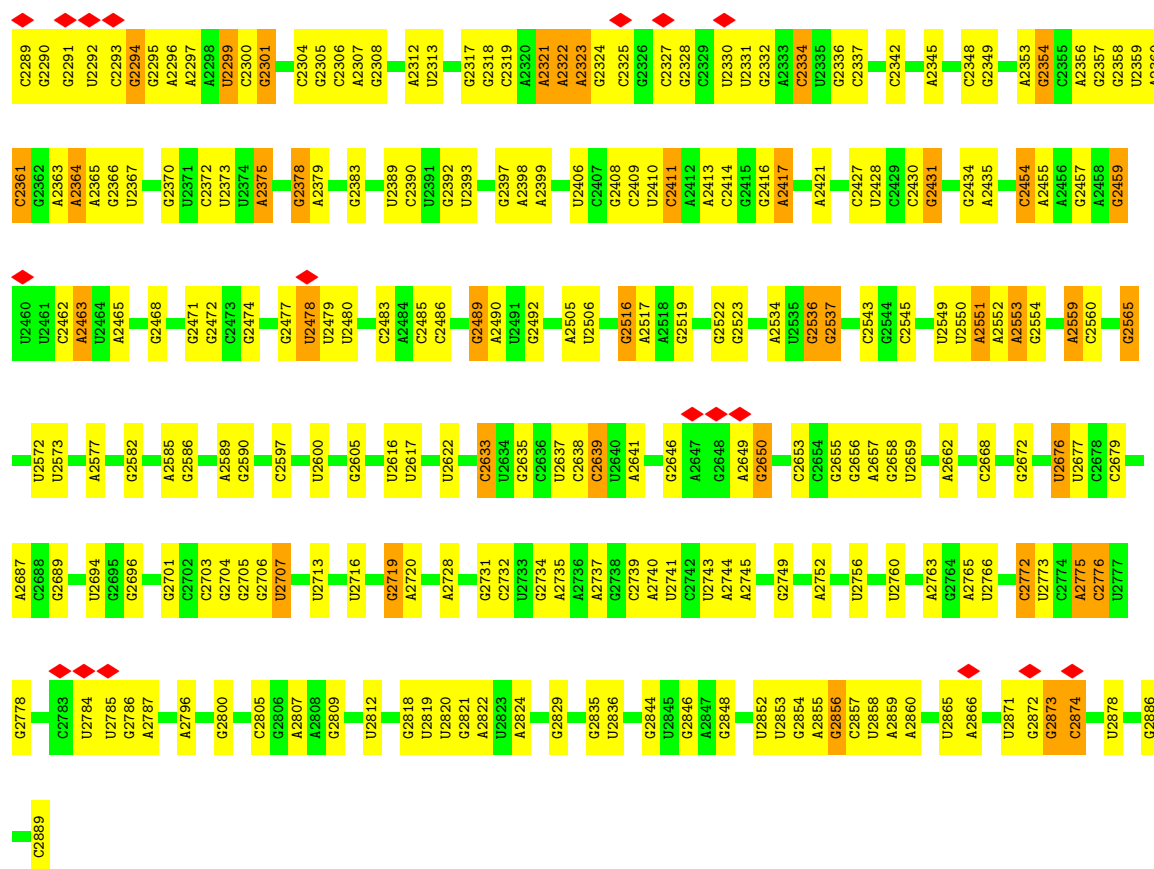
3 Residue-property plots

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

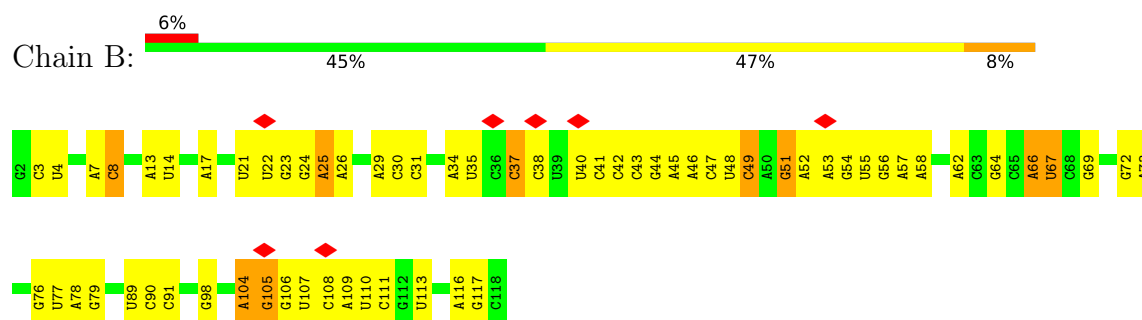
- Molecule 1: *Pseudomonas aeruginosa* strain PAO1 23S ribosomal RNA



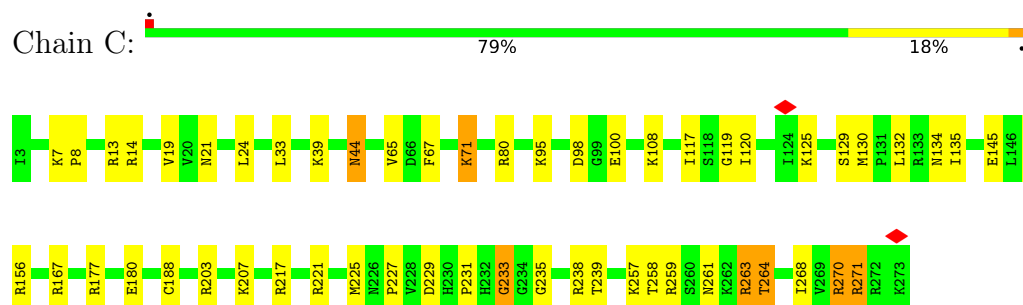
U1016	A1017	A1018	A1019	C1020	U1023	G1024	A1088	U1025	A1029	A1030	U1034	U1035	A1036	G1037	A1038	G1041	C1042	U1043	A1044	G1045	G1046	A1047	G1048	G1049	U1050	U1051	G1052	G1053	G1054	U1055	U1056	A1057	G1058	A1059	A1060	G1061	C1062	A1063	G1064	C1065	C1066	A1067	C1068	C1069	C1070	U1071	U1072	U1073	A1074	A1075	A1076	G1077	A1078	A1079	A1080	G1081			
C1082	G1083	U1084	A1085	A1086	U1087	A1088	G1089	C1090	U1091	C1092	A1093	C1094	U1095	A1096	G1097	U1098	C1099	G1100	A1101	G1102	U1103	C1104	G1105	G1106	G1114	G1115	A1116	A1117	G1118	A1119	U1120	G1121	U1122	A1123	A1124	C1125	G1126	G1129	C1132	A1133	A1138	A1142	C1143	C1144	G1145	A1146	A1147	G1148	G1154	G1155	U1156	G1157							
U1163	A1164	A1165	G1166	U1167	G1168	A1169	C1170	G1174	U1186	A1192	G1193	G1199	U1204	G1205	G1210	A1213	A1214	G1223	A1224	G1225	G1226	U1227	U1228	U1229	A1233	A1234	G1235	U1236	G1237	C1238	G1239	A1240	A1241	U1242	G1243	A1249	U1250	G1251	A1252	G1253	G1258	A1259	G1260	A1261	A1262	U1263	A1271												
C1276	A1277	A1281	U1288	C1292	U1299	G1306	C1307	A1308	A1309	U1313	U1316	U1327	U1328	U1331	C1332	G1333	G1334	U1335	U1339	A1346	G1347	G1348	C1349	U1350	G1351	A1352	A1355	G1361	U1362	U1366	G1367	A1372	C1373	U1381	A1382	U1383	U1384	C1385	U1395	G1396	G1397																		
G1403	C1404	A1405	A1406	U1407	G1408	A1414	C1415	A1420	A1421	A1426	C1430	A1431	U1432	C1433	G1437	C1438	G1439	U1440	U1441	G1442	U1447	U1454	G1461	G1462	U1463	G1466	G1469	A1470	A1471	A1472	U1475	G1478	G1479	U1480	A1481	A1482	A1483	U1484	G1488	U1492	U1493	C1494	A1495	A1496															
G1497	G1498	C1499	G1500	G1501	A1502	G1503	U1507	G1508	A1509	U1510	G1511	A1515	G1516	U1517	C1518	G1519	U1520	C1521	U1522	U	U	U	A1526	G1527	A1528	U1529	G1530	A1531	C1532	U1537	G1542	U1549	C1555	A1556	A1557	G1558	A1559	A1560	C1567	U1568	G1571	C1572	U1573	U1574	C1575	A1576	G1577	A1580	A1587										
A1588	C1597	A1598	A1599	A1600	C1601	C1602	G1603	A1604	C1605	G1616	G1621	A1624	C1629	G1635	C1636	U1637	U1638	G1639	A1640	G1641	A1642	G1643	U1647	C1648	G1649	G1656	G1657	A1658	A1659	C1660	G1664	C1665	G1671	U1683	C1684	G1685	G1686	G1700	U1708	G1709	A1710	G1711	G1712	G1713	A1714	U1715													
U1716	U1717	A1718	C1719	U1720	C1721	C1722	U1724	A1725	G1736	C1739	G1740	A1741	A1742	U1745	A1746	A1749	G1750	G1751	U1756	A1760	G1763	U1766	A1767	U1768	U1769	A1770	A1771	C1775	A1776	G1779	C1784	U1785	G1786	C1787	A1788	A1789	A1790	A1795	A1796	A1797	G1798	U1799	C1803	G1804															
U1807	A1808	G1809	C1817	A1814	A1815	G1816	C1820	C1824	A1829	U1830	C1831	A1834	A1835	U1838	U1839	A1840	A1841	A1853	C1854	C1855	G1856	C1857	A1858	A1859	C1861	G1862	A1863	A1864	G1865	G1871	G1875	A1876	A1877	G1890	G1893	G1894	C1895	C1896	G1897	U1898	A1899	A1900	C1901	U1902	A1903	U1904	A1905	A1906	C1907	G1908									
G1909	U1910	C1911	A1914	A1915	G1916	G1917	A1924	A1925	U1926	U1927	G1932	U1942	C1945	U1950	G1951	C1952	A1953	C1954	A1957	U1958	G1959	U1969	U1978	G1979	A1983	A1984	G1985	C1987	A1987	A1977	G1890	G1893	G1894	C1895	C1896	G1897	U1898	A1899	A1900	C1901	U1902	A1903	U1904	A1905	A1906	C1907	G1908												
G2025	U2026	G2027	U2030	U2038	A2039	C2042	C2043	A2047	G2048	A2049	G2054	U2055	G2056	C2060	U2063	A2064	U2074	G2075	U2079	G2080	G2081	A2082	C2083	U2084	G2087	A2088	G2089	C2090	C2091	U2092	G2093	C2094	U2095	U2096	G2097	U2098	G2099	U2100	A2101	G2102	U2153	U2154	G2155	A2104	U2105	A2106	G2107	U2108	U2109	G2110	G2111								
G2112	A2113	G2114	G2115	C2116	U2117	U2118	U2119	G2120	A2121	A2122	G2123	G2124	G2125	U2126	G2127	G2128	A2129	C2130	G2131	C2132	C2133	A2134	G2135	U2136	U2137	C2138	G2139	C2140	G2141	U2142	G2143	G2144	A2145	G2146	C2147	C2148	A2149	U2150	C2151	C2152	U2153	U2154	G2155	A2156	A2157	A2158	U2159	A2160	C2161	C2162	A2163	C2164	C2165	C2166	U2167	G2168	G2169	G2170	A2171
U2172	G2173	C2174	U2175	U2176	G2177	A2178	A2185	A2186	U2190	G2191	C2195	A2199	C2202	A2212	G2225	G2226	C2227	G2228	C2227	G2237	G2238	C2245	U2246	C2251	U2252	A2253	A2254	A2255	A2260	A2261	A2265	G2266	G2267	U2270	A2274	C2275	G2276	G2277	U2278	G2279	C2280	G2281	C2282	U2283															



- Molecule 2: 5S rRNA

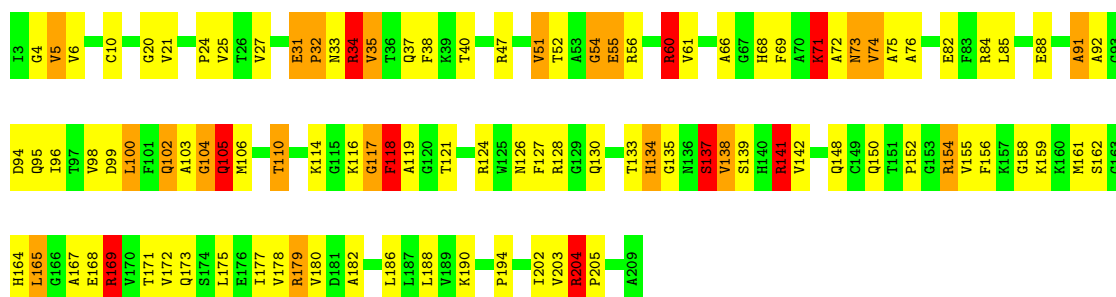


- Molecule 3: 50S ribosomal protein L2



- Molecule 4: 50S ribosomal protein L3

Chain D: 



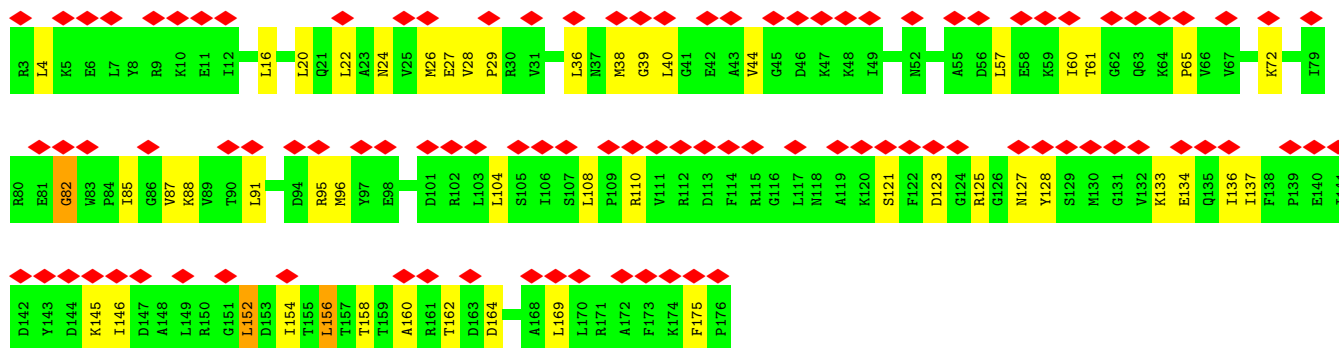
- Molecule 5: 50S ribosomal protein L4

Chain E: 



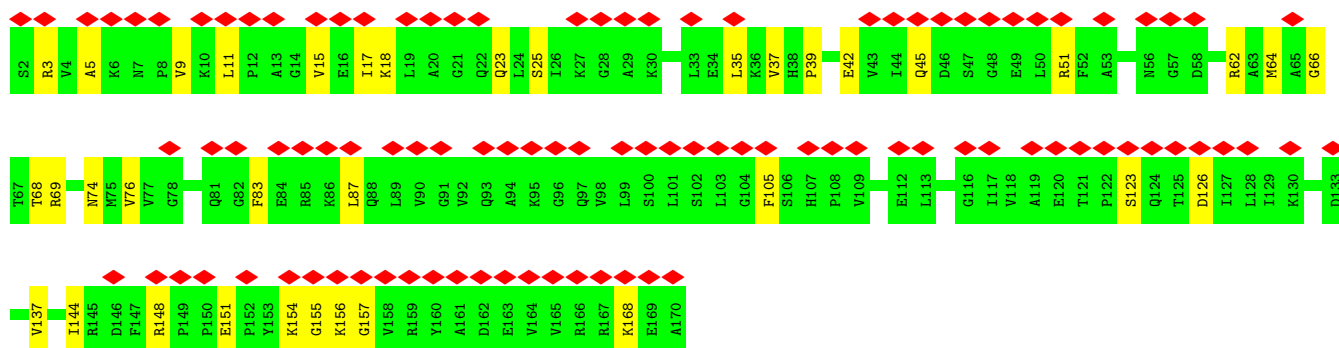
- Molecule 6: 50S ribosomal protein L5

Chain F: 

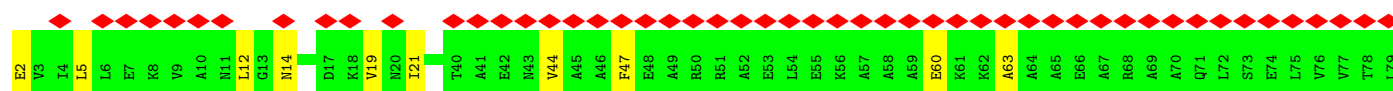
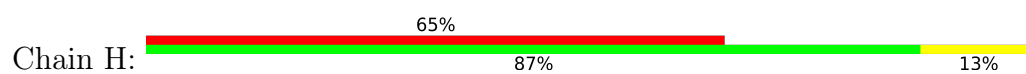


- Molecule 7: 50S ribosomal protein L6

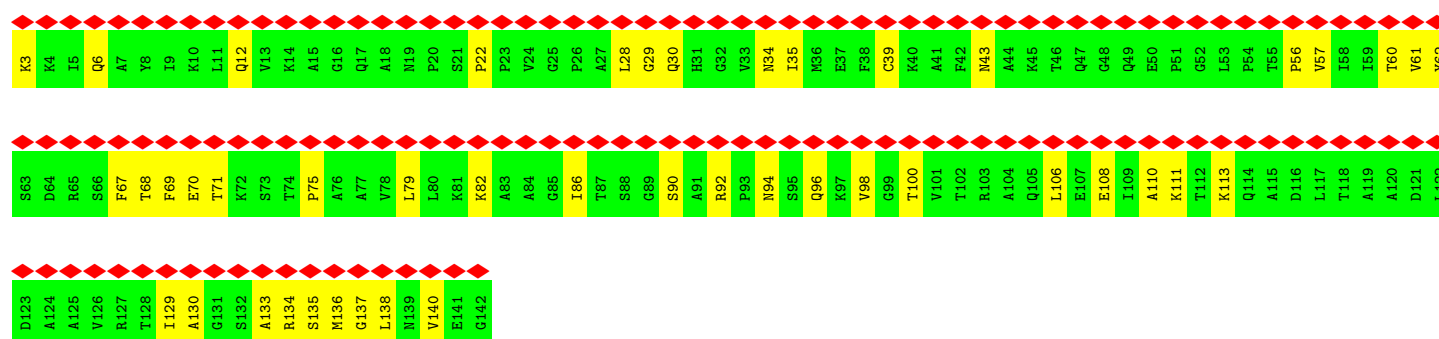
Chain G: 



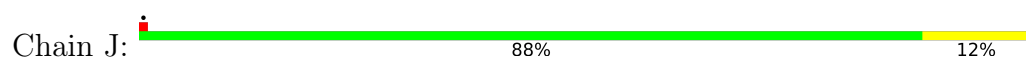
- Molecule 8: 50S ribosomal protein L9



• Molecule 9: 50S ribosomal protein L11



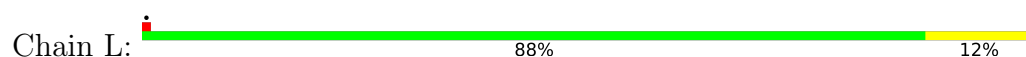
• Molecule 10: 50S ribosomal protein L13



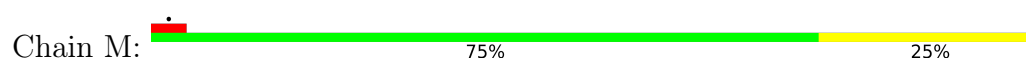
• Molecule 11: 50S ribosomal protein L14



• Molecule 12: 50S ribosomal protein L15



• Molecule 13: 50S ribosomal protein L16





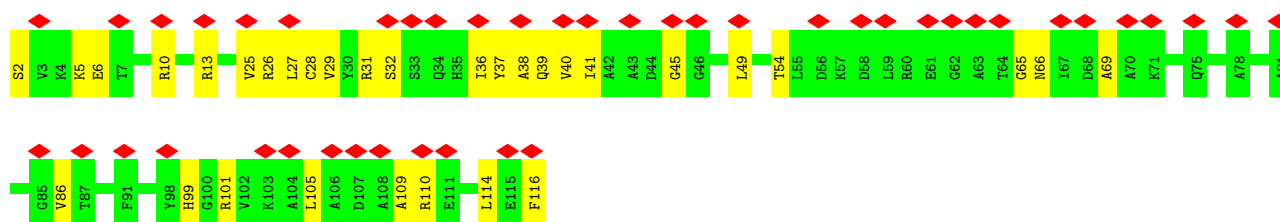
- Molecule 14: 50S ribosomal protein L17

Chain N: 87% 12%



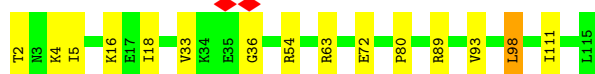
- Molecule 15: 50S ribosomal protein L18

Chain O: 38% 72% 28%



- Molecule 16: 50S ribosomal protein L19

Chain P: 87% 12%



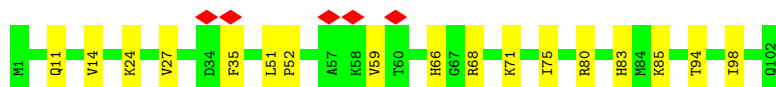
- Molecule 17: 50S ribosomal protein L20

Chain Q: 87% 11%



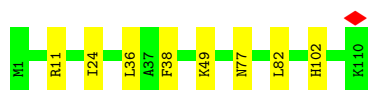
- Molecule 18: 50S ribosomal protein L21

Chain R: 5% 83% 17%

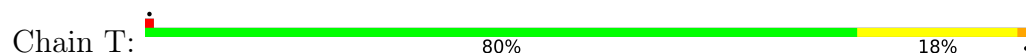


- Molecule 19: 50S ribosomal protein L22

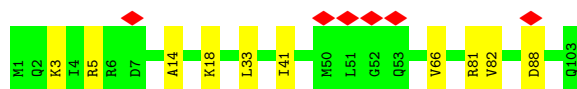
Chain S: 93% 7%



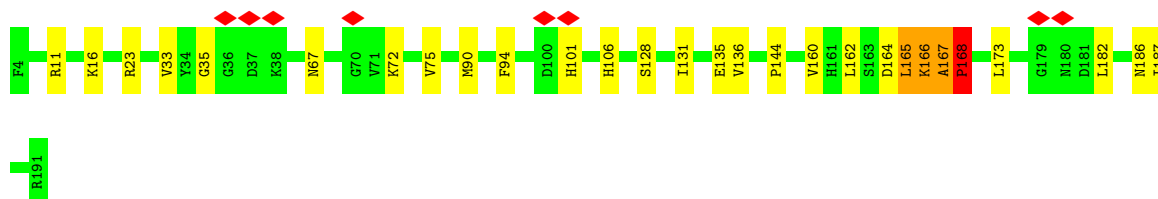
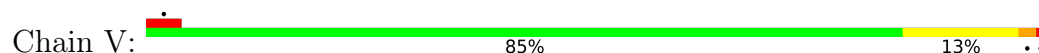
- Molecule 20: 50S ribosomal protein L23



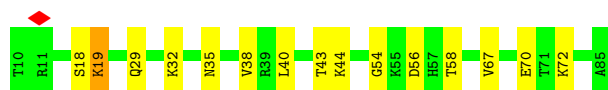
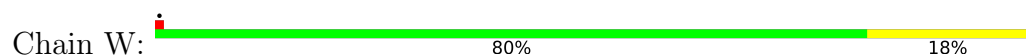
- Molecule 21: 50S ribosomal protein L24



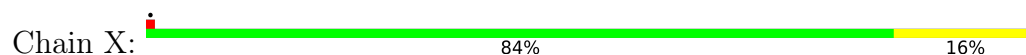
- Molecule 22: 50S ribosomal protein L25



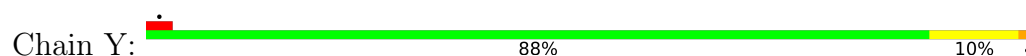
- Molecule 23: 50S ribosomal protein L27

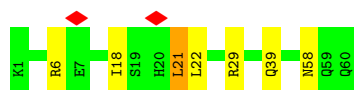


- Molecule 24: 50S ribosomal protein L28

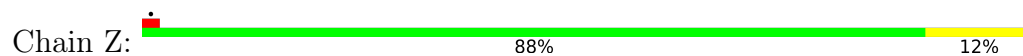


- Molecule 25: Ribosomal protein uL29

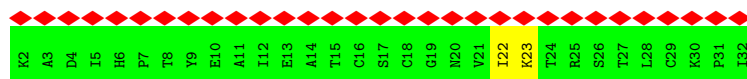




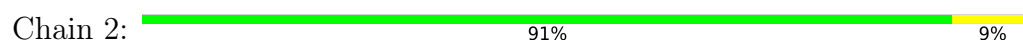
- Molecule 26: 50S ribosomal protein L30



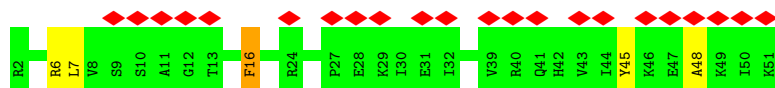
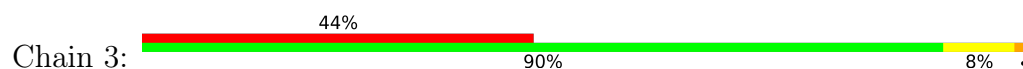
- Molecule 27: 50S ribosomal protein L31



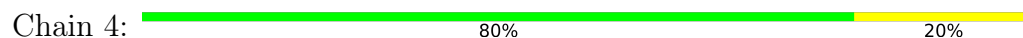
- Molecule 28: 50S ribosomal protein L32



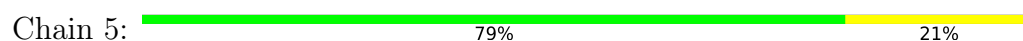
- Molecule 29: 50S ribosomal protein L33



- Molecule 30: 50S ribosomal protein L34



- Molecule 31: 50S ribosomal protein L35

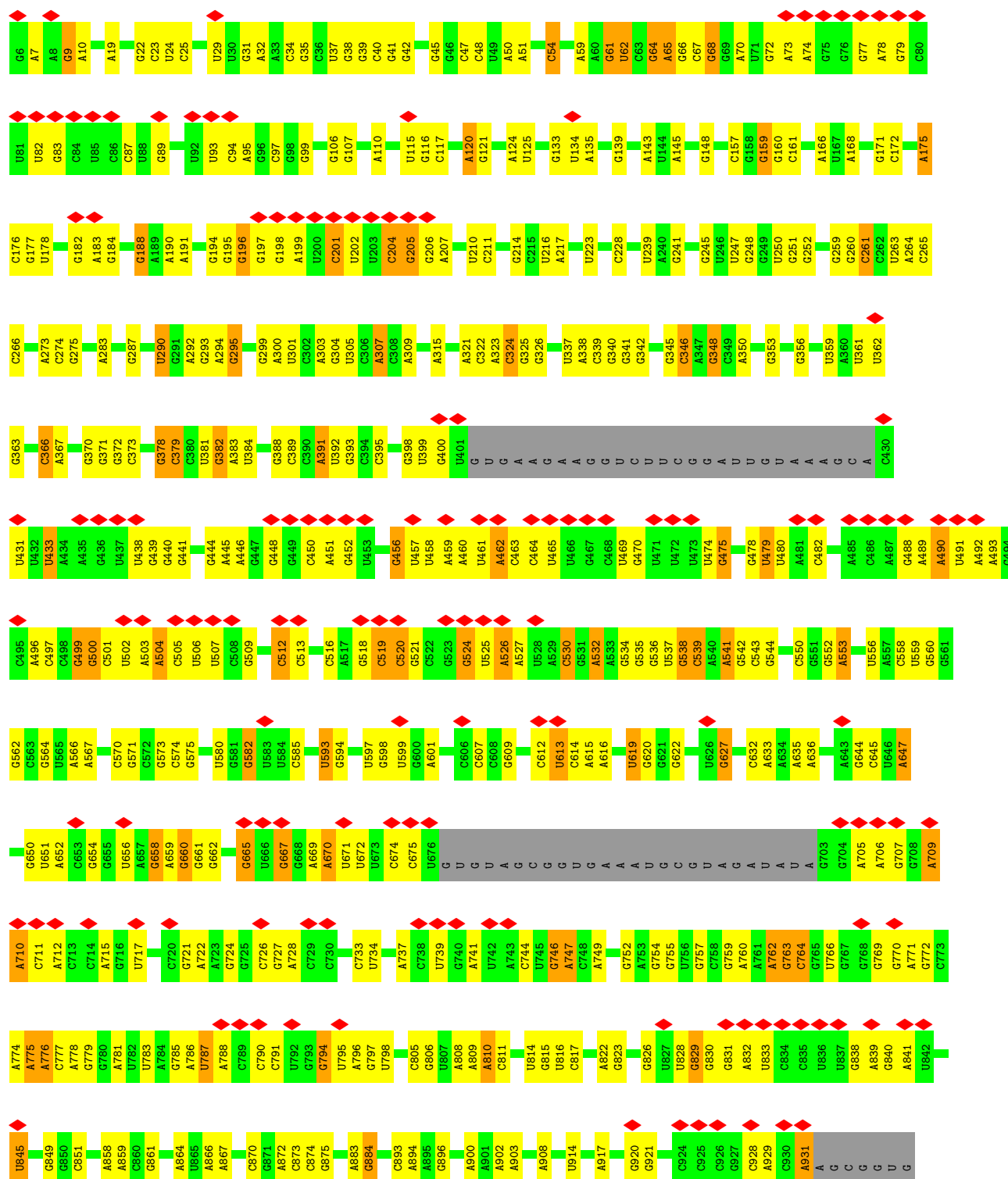


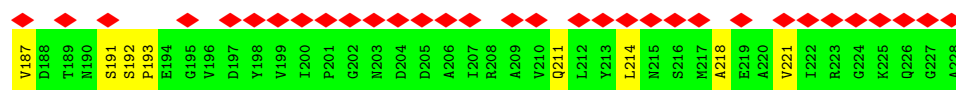
- Molecule 32: 50S ribosomal protein L36



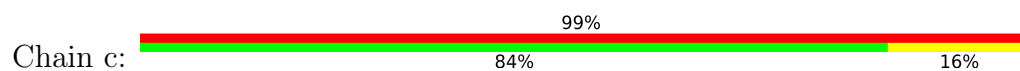


• Molecule 33: 16S rRNA

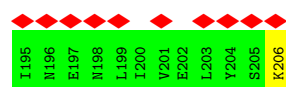
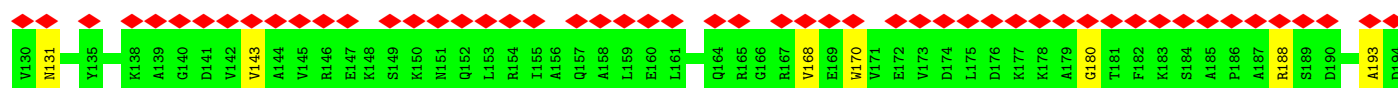
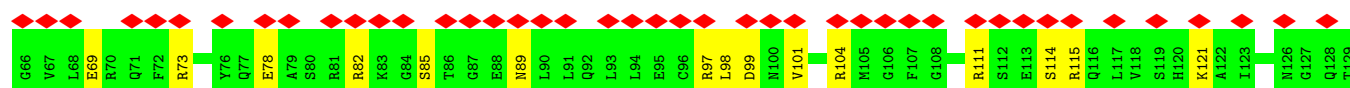
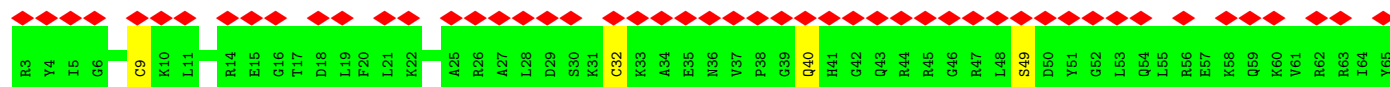
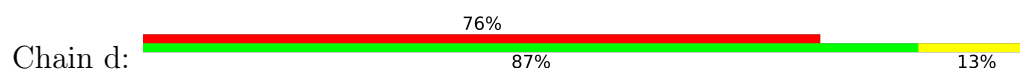




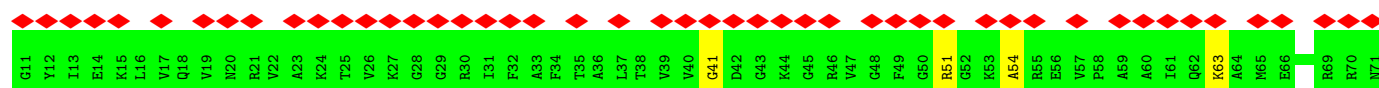
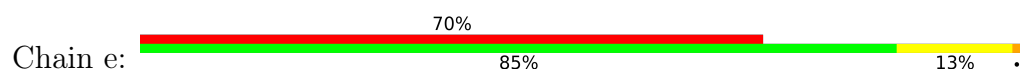
• Molecule 35: 30S ribosomal protein S3

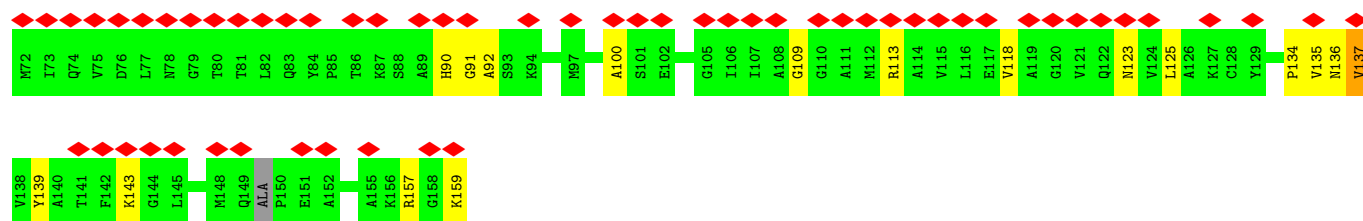


• Molecule 36: 30S ribosomal protein S4

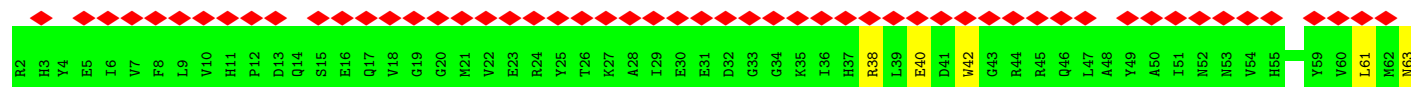
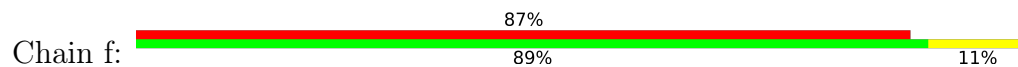


• Molecule 37: 30S ribosomal protein S5

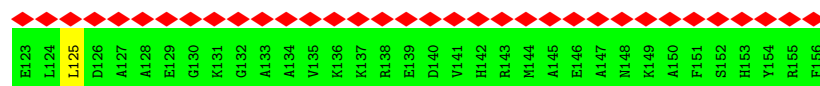
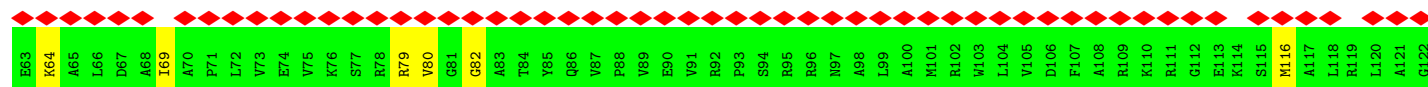
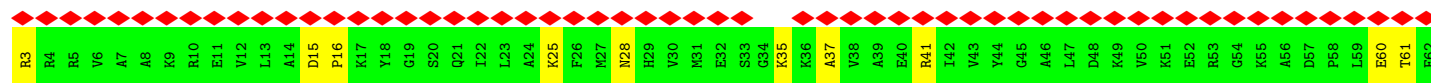
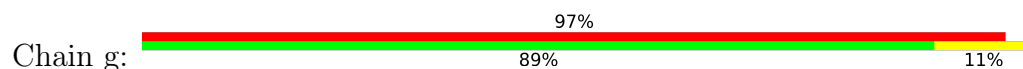




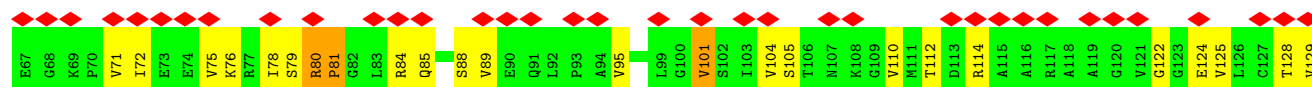
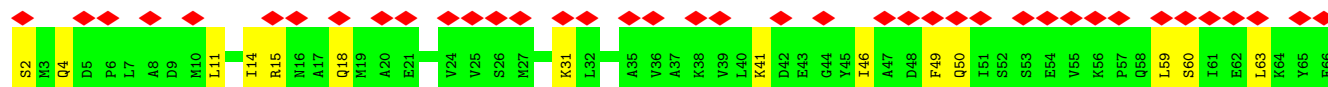
• Molecule 38: 30S ribosomal protein S6



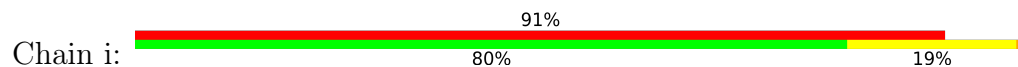
• Molecule 39: 30S ribosomal protein S7

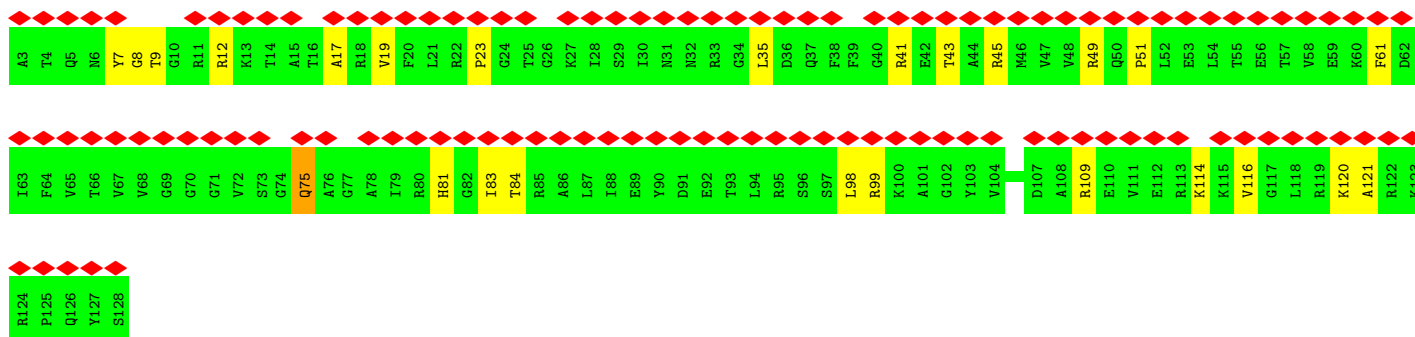


• Molecule 40: 30S ribosomal protein S8

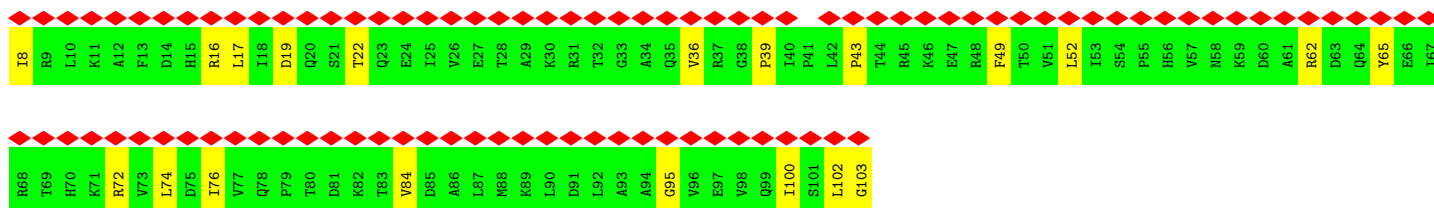
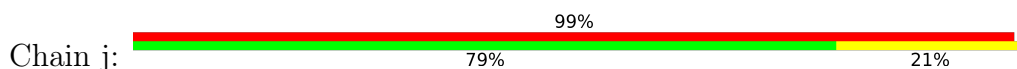


• Molecule 41: 30S ribosomal protein S9

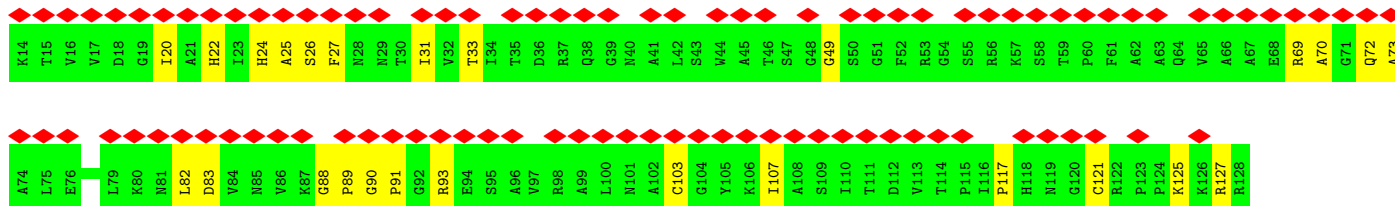
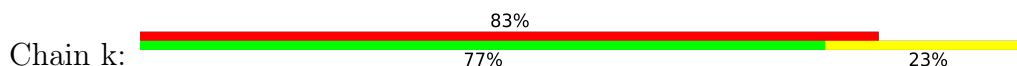




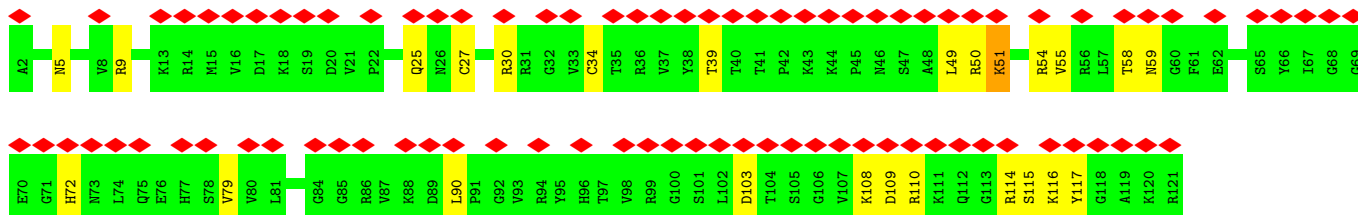
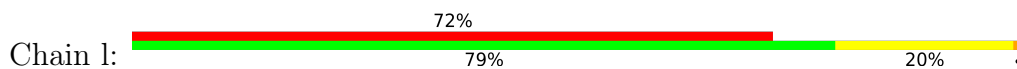
• Molecule 42: 30S ribosomal protein S10



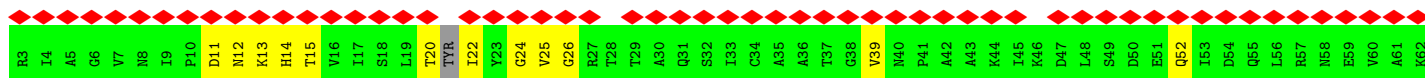
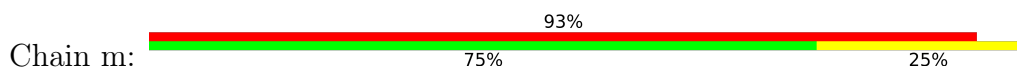
• Molecule 43: 30S ribosomal protein S11



• Molecule 44: 30S ribosomal protein S12

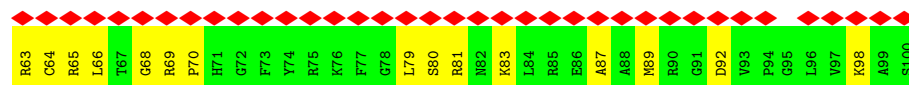
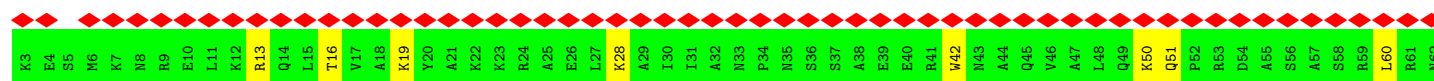
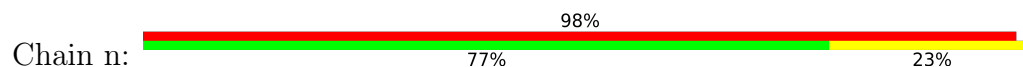


• Molecule 45: 30S ribosomal protein S13

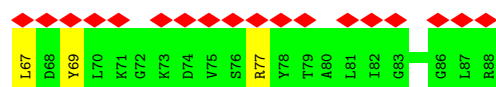
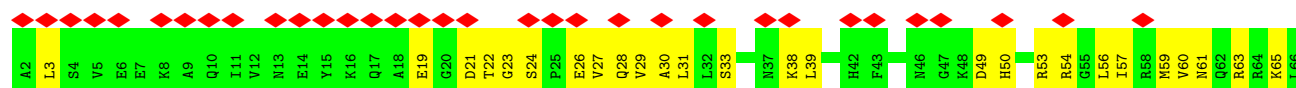




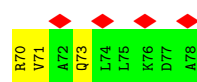
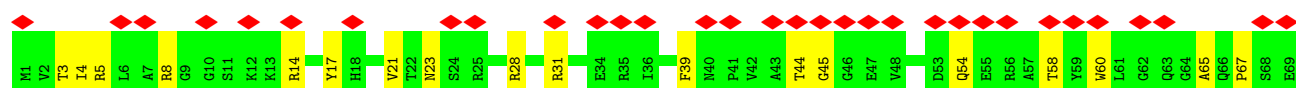
• Molecule 46: 30S ribosomal protein S14



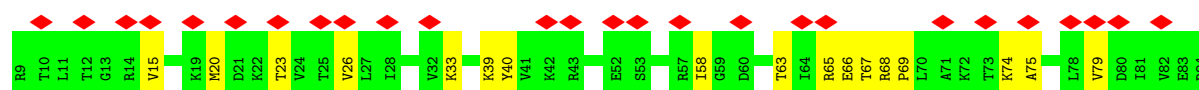
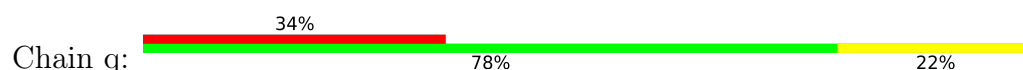
• Molecule 47: 30S ribosomal protein S15



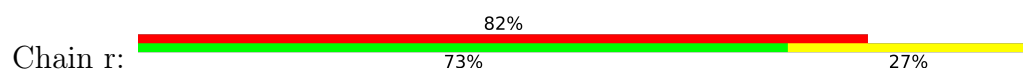
• Molecule 48: 30S ribosomal protein S16

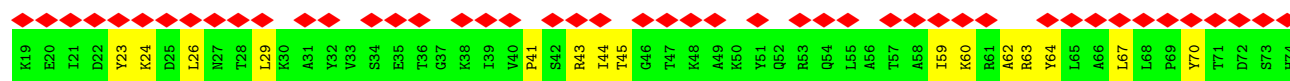


• Molecule 49: 30S ribosomal protein S17

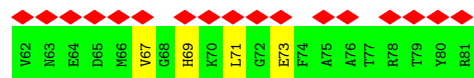
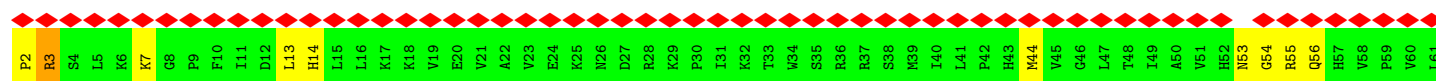
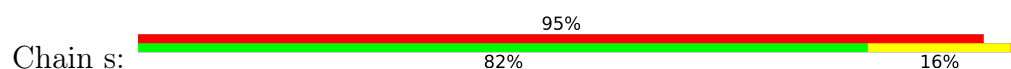


• Molecule 50: 30S ribosomal protein S18

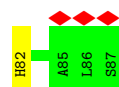
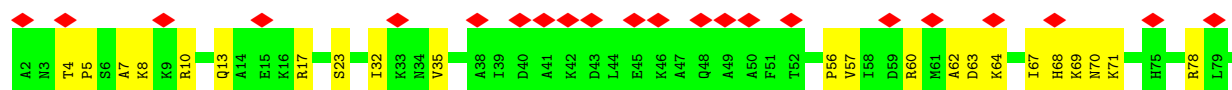
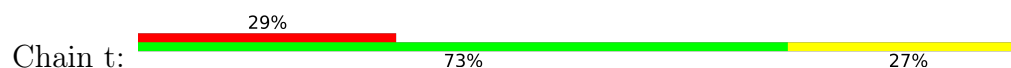




- Molecule 51: 30S ribosomal protein S19



- Molecule 52: 30S ribosomal protein S20



- Molecule 53: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	319022	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.788	Depositor
Minimum map value	-0.478	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.0491	Depositor
Map size ($\text{\AA}$)	440.0, 440.0, 440.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	A	0.46	0/69320	0.51	9/108135 (0.0%)
2	B	0.31	0/2789	0.52	1/4345 (0.0%)
3	C	0.58	0/2084	0.84	0/2800
4	D	0.84	0/1572	1.25	16/2118 (0.8%)
5	E	0.45	0/1529	0.78	1/2060 (0.0%)
6	F	0.31	0/1294	0.80	2/1754 (0.1%)
7	G	0.24	0/1280	0.63	0/1726
8	H	0.25	0/580	0.60	0/781
9	I	0.34	0/1041	0.85	1/1408 (0.1%)
10	J	0.51	1/1148 (0.1%)	0.71	0/1549
11	K	0.56	0/931	0.79	2/1247 (0.2%)
12	L	0.48	0/1075	0.72	0/1432
13	M	0.32	0/1096	0.60	0/1466
14	N	0.51	0/975	0.80	0/1304
15	O	0.33	0/888	0.83	0/1183
16	P	0.47	0/910	0.79	0/1218
17	Q	0.54	0/946	0.78	0/1257
18	R	0.45	0/814	0.73	0/1091
19	S	0.47	0/837	0.65	0/1114
20	T	0.46	0/742	0.75	0/993
21	U	0.35	0/809	0.73	0/1079
22	V	0.32	0/1420	0.77	4/1927 (0.2%)
23	W	0.48	0/582	1.01	4/773 (0.5%)
24	X	0.43	0/637	0.68	0/849
25	Y	0.38	0/471	0.70	1/630 (0.2%)
26	Z	0.45	0/449	0.70	0/602
27	1	0.24	0/235	0.62	0/318
28	2	0.46	0/425	0.72	0/568
29	3	0.33	0/415	0.82	0/554
30	4	0.61	0/367	0.89	1/482 (0.2%)
31	5	0.41	0/507	0.79	0/664
32	6	0.35	0/304	0.73	0/399
33	a	0.32	10/33391 (0.0%)	0.45	12/52073 (0.0%)
34	b	0.27	0/1724	0.76	2/2319 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	c	0.23	0/1638	0.61	0/2209
36	d	0.25	0/1615	0.72	0/2163
37	e	0.29	0/1106	0.75	0/1488
38	f	0.30	0/815	0.76	0/1098
39	g	0.31	0/1207	0.79	1/1616 (0.1%)
40	h	0.28	0/976	0.77	0/1314
41	i	0.28	0/1006	0.78	0/1347
42	j	0.24	0/773	0.61	0/1045
43	k	0.26	0/848	0.70	0/1152
44	l	0.30	0/955	0.75	0/1280
45	m	0.27	0/853	0.77	1/1144 (0.1%)
46	n	0.24	0/786	0.68	0/1047
47	o	0.28	0/698	0.85	1/933 (0.1%)
48	p	0.26	0/620	0.76	0/835
49	q	0.26	0/627	0.65	0/844
50	r	0.22	0/450	0.61	0/608
51	s	4.25	1/649 (0.2%)	0.74	1/874 (0.1%)
52	t	0.27	0/669	0.70	0/891
53	u	0.22	0/298	0.61	0/391
All	All	0.50	12/150176 (0.0%)	0.58	60/224497 (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
3	C	0	2
4	D	0	10
5	E	0	1
6	F	0	2
9	I	0	2
16	P	0	1
17	Q	0	1
18	R	0	1
22	V	0	3
29	3	0	1
36	d	0	1
40	h	0	3
41	i	0	1
44	l	0	1
45	m	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
46	n	0	1
47	o	0	1
48	p	0	1
51	s	0	1
All	All	0	36

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	s	3	ARG	CB-CG	108.14	4.76	1.52
33	a	1313	A	C6-N1	18.20	1.72	1.35
33	a	1313	A	N3-C4	17.09	1.69	1.34
33	a	1313	A	N1-C2	17.07	1.68	1.34
33	a	1313	A	C2-N3	16.74	1.67	1.33
33	a	1313	A	C5-C6	16.10	1.73	1.41
33	a	1313	A	C5-C4	14.56	1.67	1.38
33	a	1219	A	N9-C4	13.06	1.64	1.37
33	a	1219	A	N9-C8	-10.33	1.17	1.37
10	J	131	PRO	CA-CB	6.70	1.60	1.53
33	a	1219	A	N3-C4	6.12	1.47	1.34
33	a	1219	A	C8-N7	5.02	1.41	1.31

All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	a	1219	A	N7-C8-N9	-24.32	40.83	113.80
33	a	1219	A	C4-C5-N7	-22.90	42.00	110.70
33	a	1219	A	C8-N9-C4	-17.62	52.95	105.80
33	a	1219	A	C5-N7-C8	9.77	133.21	103.90
33	a	1219	A	C4-N9-C1'	9.23	153.98	126.30
33	a	1219	A	C8-N9-C1'	-8.88	101.05	127.70
33	a	1219	A	C6-C5-N7	8.71	158.44	132.30
22	V	166	LYS	CA-C-N	8.40	142.31	121.80
22	V	166	LYS	C-N-CA	8.40	142.31	121.80
5	E	180	ILE	N-CA-C	-8.33	105.20	113.20
23	W	19	LYS	CA-C-O	-7.72	109.47	120.51
4	D	74	VAL	CA-C-O	-7.31	113.43	120.30
22	V	35	GLY	N-CA-C	6.51	118.97	111.36
1	A	862	C	O3'-P-O5'	6.24	113.36	104.00
34	b	23	TRP	CA-C-N	6.12	131.37	121.83
34	b	23	TRP	C-N-CA	6.12	131.37	121.83
22	V	168	PRO	N-CA-C	6.06	124.95	112.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	m	24	GLY	N-CA-C	5.94	127.25	113.18
4	D	165	LEU	CA-C-N	-5.93	109.79	121.41
4	D	165	LEU	C-N-CA	-5.93	109.79	121.41
4	D	165	LEU	N-CA-C	-5.92	100.35	109.76
33	a	1313	A	N1-C2-N3	-5.89	111.62	129.30
4	D	31	GLU	CA-C-N	5.88	127.18	119.84
4	D	31	GLU	C-N-CA	5.88	127.18	119.84
11	K	91	GLN	CA-C-N	5.75	138.70	122.21
11	K	91	GLN	C-N-CA	5.75	138.70	122.21
23	W	18	SER	CA-C-N	5.69	132.41	121.54
23	W	18	SER	C-N-CA	5.69	132.41	121.54
4	D	118	PHE	CA-CB-CG	5.53	119.33	113.80
30	4	42	LEU	CA-CB-CG	5.50	135.56	116.30
33	a	1219	A	N3-C4-N9	5.50	143.91	127.40
1	A	1166	G	P-O3'-C3'	5.44	128.36	120.20
51	s	3	ARG	CB-CG-CD	5.42	123.78	111.30
33	a	159	G	P-O3'-C3'	5.41	128.31	120.20
1	A	1088	A	O5'-C5'-C4'	5.38	119.58	111.50
1	A	1088	A	C5'-C4'-C3'	5.34	124.01	116.00
1	A	920	C	P-O3'-C3'	5.32	128.19	120.20
4	D	71	LYS	N-CA-C	-5.31	105.18	110.97
9	I	22	PRO	N-CA-C	5.28	117.14	110.70
1	A	2536	G	C2'-C3'-O3'	5.24	121.56	113.70
23	W	18	SER	N-CA-C	5.23	117.03	110.91
39	g	69	ILE	N-CA-C	-5.22	107.62	112.43
4	D	204	ARG	CA-C-N	5.20	126.34	119.84
4	D	204	ARG	C-N-CA	5.20	126.34	119.84
4	D	54	GLY	CA-C-N	5.19	131.46	121.54
4	D	54	GLY	C-N-CA	5.19	131.46	121.54
47	o	31	LEU	CA-CB-CG	5.19	134.45	116.30
2	B	25	A	P-O3'-C3'	5.18	127.97	120.20
1	A	920	C	C2'-C3'-O3'	5.18	117.27	109.50
6	F	82	GLY	CA-C-N	5.17	127.15	120.44
6	F	82	GLY	C-N-CA	5.17	127.15	120.44
1	A	444	A	C2'-C3'-O3'	5.13	121.40	113.70
1	A	1642	A	C2'-C3'-O3'	5.12	121.37	113.70
4	D	73	ASN	CA-C-N	-5.12	117.70	122.66
4	D	73	ASN	C-N-CA	-5.12	117.70	122.66
4	D	91	ALA	CA-C-N	-5.10	114.35	122.66
4	D	91	ALA	C-N-CA	-5.10	114.35	122.66
33	a	34	C	C2'-C3'-O3'	5.06	121.29	113.70
25	Y	21	LEU	CA-CB-CG	5.04	133.93	116.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	a	1313	A	C2-N3-C4	5.03	125.69	110.60

There are no chirality outliers.

All (36) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
29	3	16	PHE	Peptide
3	C	270	ARG	Sidechain
3	C	271	ARG	Sidechain
4	D	124	ARG	Sidechain
4	D	128	ARG	Sidechain
4	D	141	ARG	Sidechain
4	D	154	ARG	Sidechain
4	D	169	ARG	Sidechain
4	D	179	ARG	Sidechain
4	D	204	ARG	Sidechain
4	D	34	ARG	Sidechain
4	D	60	ARG	Sidechain
4	D	84	ARG	Sidechain
5	E	163	LEU	Peptide
6	F	24	ASN	Peptide
6	F	72	LYS	Peptide
9	I	34	ASN	Peptide
9	I	68	THR	Peptide
16	P	36	GLY	Peptide
17	Q	83	LEU	Peptide
18	R	51	LEU	Peptide
22	V	101	HIS	Peptide
22	V	165	LEU	Peptide
22	V	167	ALA	Peptide
36	d	49	SER	Peptide
40	h	110	VAL	Peptide
40	h	79	SER	Peptide
40	h	80	ARG	Peptide
41	i	75	GLN	Peptide
44	l	108	LYS	Peptide
45	m	101	ARG	Peptide
45	m	26	GLY	Peptide
46	n	51	GLN	Peptide
47	o	30	ALA	Peptide
48	p	73	GLN	Peptide
51	s	44	MET	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	61899	0	31128	340	0
2	B	2495	0	1263	21	0
3	C	2048	0	2097	39	0
4	D	1549	0	1560	95	0
5	E	1509	0	1563	16	0
6	F	1278	0	1239	27	0
7	G	1264	0	1314	22	0
8	H	577	0	606	4	0
9	I	1026	0	1063	32	0
10	J	1122	0	1148	11	0
11	K	922	0	992	24	0
12	L	1063	0	1108	15	0
13	M	1076	0	1148	23	0
14	N	959	0	1005	10	0
15	O	881	0	920	22	0
16	P	901	0	958	12	0
17	Q	936	0	1025	12	0
18	R	801	0	830	11	0
19	S	833	0	897	5	0
20	T	732	0	778	11	0
21	U	801	0	864	7	0
22	V	1397	0	1417	16	0
23	W	574	0	601	8	0
24	X	626	0	649	10	0
25	Y	468	0	489	6	0
26	Z	445	0	472	5	0
27	1	232	0	238	1	0
28	2	419	0	409	7	0
29	3	408	0	430	3	0
30	4	364	0	409	6	0
31	5	502	0	558	13	0
32	6	303	0	339	5	0
33	a	29826	0	15021	256	0
34	b	1698	0	1708	30	0
35	c	1609	0	1636	22	0
36	d	1596	0	1619	19	0
37	e	1092	0	1139	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	f	802	0	771	11	0
39	g	1190	0	1227	14	0
40	h	965	0	1009	24	0
41	i	994	0	1031	20	0
42	j	763	0	801	16	0
43	k	832	0	819	18	0
44	l	942	0	989	16	0
45	m	847	0	888	17	0
46	n	776	0	818	18	0
47	o	691	0	714	17	0
48	p	609	0	613	15	0
49	q	619	0	659	9	0
50	r	443	0	460	13	0
51	s	635	0	662	25	0
52	t	662	0	715	16	0
53	u	295	0	313	8	0
All	All	138296	0	93129	1169	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 6.

All (1169) 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)
33:a:1313:A:N1	33:a:1313:A:C2	1.68	1.60
33:a:1313:A:C4	33:a:1313:A:N3	1.69	1.59
33:a:1313:A:N1	33:a:1313:A:C6	1.72	1.53
4:D:34:ARG:HH22	4:D:54:GLY:CA	1.49	1.25
4:D:34:ARG:HH22	4:D:54:GLY:HA2	1.06	1.18
4:D:34:ARG:NH2	4:D:54:GLY:HA2	1.58	1.17
4:D:69:PHE:O	4:D:72:ALA:O	1.75	1.05
3:C:71:LYS:HE2	3:C:100:GLU:HG2	1.04	1.01
3:C:71:LYS:CE	3:C:100:GLU:HG2	1.91	1.00
4:D:133:THR:O	4:D:135:GLY:N	1.96	0.99
33:a:817:C:HO2'	40:h:2:SER:N	1.64	0.95
4:D:34:ARG:NH2	4:D:54:GLY:CA	2.23	0.93
4:D:34:ARG:HH22	4:D:54:GLY:HA3	1.35	0.89
4:D:52:THR:HG21	4:D:76:ALA:CB	2.03	0.88
4:D:52:THR:HG21	4:D:76:ALA:HB1	1.56	0.87
4:D:110:THR:HG23	4:D:202:ILE:HB	1.58	0.84
1:A:2605:G:H21	4:D:155:VAL:HG21	1.42	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:32:PRO:HB2	4:D:95:GLN:HE21	1.43	0.82
4:D:34:ARG:HD2	4:D:74:VAL:HG22	1.65	0.78
3:C:71:LYS:HE2	3:C:100:GLU:CG	2.00	0.77
4:D:148:GLN:HE21	4:D:152:PRO:HD3	1.51	0.76
1:A:2818:G:OP2	4:D:60:ARG:NH1	2.18	0.76
33:a:651:U:H1'	47:o:28:GLN:HE21	1.51	0.75
9:I:94:ASN:H	9:I:137:GLY:HA2	1.53	0.73
33:a:64:G:H4'	33:a:65:A:H3'	1.71	0.72
4:D:69:PHE:CD1	4:D:76:ALA:HB3	2.24	0.72
1:A:2321:A:H4'	15:O:13:ARG:HB3	1.73	0.71
4:D:10:CYS:HG	16:P:2:THR:N	1.87	0.71
14:N:2:ARG:HA	14:N:5:LYS:HD3	1.72	0.71
1:A:2679:C:H5''	1:A:2856:G:H22	1.56	0.71
4:D:179:ARG:HG2	4:D:188:LEU:HD13	1.72	0.70
13:M:42:LEU:HD11	13:M:127:LEU:HD11	1.74	0.70
1:A:1239:G:H1	17:Q:37:GLN:HE21	1.36	0.70
1:A:872:G:N3	1:A:885:A:N6	2.40	0.69
37:e:134:PRO:HA	37:e:137:VAL:HB	1.75	0.69
1:A:1426:A:H62	1:A:1542:G:H8	1.41	0.68
1:A:1029:A:H61	1:A:1106:G:H1	1.41	0.68
1:A:2299:U:H3	6:F:39:GLY:HA2	1.59	0.68
4:D:102:GLN:O	4:D:180:VAL:CG2	2.41	0.68
1:A:1288:A:H2	1:A:1616:G:H21	1.40	0.67
1:A:1049:G:H5''	9:I:69:PHE:HB2	1.76	0.67
1:A:1253:G:OP1	28:2:16:ARG:NH2	2.28	0.67
4:D:172:VAL:HG12	4:D:175:LEU:HD21	1.77	0.67
3:C:261:ASN:ND2	3:C:264:THR:OG1	2.28	0.66
7:G:148:ARG:HG2	7:G:157:GLY:HA3	1.77	0.66
1:A:1647:U:H5''	4:D:138:VAL:O	1.95	0.66
1:A:771:A:OP1	3:C:217:ARG:NH2	2.28	0.66
15:O:2:SER:HB2	15:O:5:LYS:H	1.62	0.65
4:D:34:ARG:HD2	4:D:74:VAL:CG2	2.25	0.65
4:D:52:THR:HG21	4:D:76:ALA:HB2	1.79	0.65
15:O:66:ASN:H	15:O:69:ALA:HB3	1.59	0.65
33:a:1341:G:N7	41:i:109:ARG:NH1	2.45	0.65
40:h:15:ARG:HD3	40:h:75:VAL:H	1.62	0.65
33:a:828:U:H2'	33:a:829:G:H8	1.62	0.65
1:A:1466:G:H1	1:A:1499:C:H42	1.44	0.64
1:A:2291:G:N1	1:A:2294:G:N7	2.45	0.64
33:a:1157:G:H1	33:a:1167:C:H42	1.43	0.64
7:G:23:GLN:HE22	7:G:35:LEU:HB2	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:m:98:ARG:HB2	45:m:100:GLN:HE22	1.63	0.64
1:A:626:G:H5''	12:L:128:THR:HB	1.78	0.64
1:A:1253:G:OP2	28:2:17:ARG:NH2	2.29	0.64
33:a:661:G:H22	33:a:733:C:H42	1.45	0.64
33:a:833:U:H3	33:a:841:A:H61	1.46	0.64
1:A:362:A:H62	1:A:393:A:H2	1.43	0.64
1:A:2392:G:O2'	1:A:2398:A:N6	2.32	0.63
1:A:2278:U:H2'	1:A:2279:G:H8	1.62	0.63
4:D:52:THR:CG2	4:D:76:ALA:HB1	2.26	0.63
23:W:70:GLU:OE1	23:W:72:LYS:NZ	2.31	0.63
37:e:157:ARG:HG3	37:e:159:LYS:H	1.63	0.63
47:o:23:GLY:HA2	47:o:28:GLN:HE22	1.63	0.63
33:a:10:A:H61	33:a:24:U:H3	1.46	0.63
1:A:1078:A:N6	9:I:135:SER:OG	2.32	0.62
45:m:88:GLY:HA2	45:m:91:HIS:HB3	1.81	0.62
1:A:265:A:N6	1:A:418:U:O2'	2.32	0.62
1:A:1144:C:OP1	17:Q:92:ARG:NH2	2.31	0.62
41:i:9:THR:HG23	41:i:17:ALA:H	1.64	0.62
1:A:1017:A:O2'	1:A:1116:A:N6	2.30	0.62
38:f:38:ARG:HB3	38:f:63:ASN:HD22	1.65	0.62
48:p:4:ILE:HG12	48:p:21:VAL:HG22	1.80	0.62
1:A:244:A:H5''	12:L:67:VAL:HG21	1.82	0.62
1:A:2091:C:H1'	1:A:2173:G:H1	1.64	0.62
17:Q:43:GLY:HA3	18:R:75:ILE:HD13	1.82	0.62
43:k:125:LYS:HA	53:u:38:TYR:H	1.64	0.61
35:c:153:VAL:HB	35:c:166:GLU:HB2	1.83	0.61
4:D:102:GLN:O	4:D:180:VAL:HG21	1.99	0.61
42:j:8:ILE:HB	42:j:74:LEU:HB2	1.81	0.61
43:k:88:GLY:O	43:k:93:ARG:NH1	2.34	0.61
46:n:13:ARG:HD2	46:n:60:LEU:HD23	1.81	0.61
1:A:1251:G:OP1	28:2:16:ARG:NH1	2.27	0.61
1:A:911:C:O2'	23:W:29:GLN:NE2	2.34	0.61
4:D:103:ALA:O	4:D:105:GLN:N	2.33	0.61
1:A:619:C:O2'	1:A:628:G:N2	2.33	0.61
1:A:929:G:OP1	31:5:64:ARG:NH1	2.33	0.61
4:D:177:ILE:O	4:D:177:ILE:HG22	2.01	0.61
37:e:109:GLY:HA2	37:e:113:ARG:HH21	1.65	0.61
43:k:125:LYS:HG2	53:u:38:TYR:HB3	1.82	0.61
42:j:52:LEU:HB3	46:n:81:ARG:HD2	1.83	0.61
47:o:56:LEU:HA	47:o:59:MET:HE3	1.83	0.60
1:A:2707:U:OP1	16:P:54:ARG:NH1	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:a:500:G:N2	33:a:519:C:N3	2.49	0.60
33:a:1082:G:H21	33:a:1161:A:H61	1.49	0.60
10:J:17:VAL:HG23	10:J:137:PRO:HB2	1.83	0.60
1:A:575:G:N7	17:Q:6:ARG:NH1	2.50	0.60
1:A:1521:C:H42	1:A:1527:G:H1	1.49	0.60
3:C:135:ILE:O	3:C:167:ARG:NH2	2.32	0.60
6:F:158:THR:HG22	6:F:160:ALA:H	1.67	0.60
11:K:70:ARG:HG2	11:K:76:ILE:HG22	1.84	0.60
20:T:60:LEU:HB2	20:T:81:LYS:HB3	1.83	0.60
34:b:3:GLN:HG3	34:b:4:VAL:HG13	1.83	0.60
37:e:51:ARG:HH22	37:e:135:VAL:HG13	1.66	0.60
3:C:263:ARG:O	3:C:263:ARG:HG2	2.01	0.60
3:C:227:PRO:HA	3:C:233:GLY:HA2	1.84	0.60
1:A:1776:A:OP2	3:C:221:ARG:NH1	2.35	0.59
5:E:175:ASP:OD1	5:E:175:ASP:N	2.34	0.59
6:F:4:LEU:HD21	6:F:96:MET:HB3	1.82	0.59
34:b:113:ARG:HD2	34:b:144:LEU:HD22	1.83	0.59
34:b:211:GLN:HA	34:b:214:LEU:HB2	1.84	0.59
33:a:534:G:H22	36:d:40:GLN:HE21	1.50	0.59
3:C:8:PRO:HB3	3:C:14:ARG:HE	1.67	0.59
12:L:109:LYS:HE2	12:L:128:THR:HG22	1.83	0.59
2:B:48:U:OP1	15:O:31:ARG:NH1	2.35	0.59
33:a:669:A:H61	33:a:709:A:H61	1.51	0.59
1:A:1573:U:H4'	1:A:1574:U:H4'	1.83	0.59
1:A:1766:U:OP2	1:A:1771:A:N6	2.35	0.59
1:A:1385:C:OP1	20:T:56:ARG:NH2	2.36	0.59
6:F:36:LEU:HD13	6:F:152:LEU:HD23	1.85	0.59
37:e:100:ALA:HB3	37:e:123:ASN:HB2	1.85	0.59
1:A:434:A:N6	5:E:35:MET:O	2.35	0.59
1:A:461:A:OP1	5:E:73:ARG:NH1	2.36	0.59
4:D:35:VAL:HG22	4:D:92:ALA:HA	1.84	0.59
11:K:64:ARG:NH2	11:K:99:PHE:O	2.36	0.59
20:T:9:VAL:HG13	20:T:42:ILE:HG22	1.85	0.59
33:a:45:G:H5''	33:a:301:U:H1'	1.83	0.59
33:a:535:G:H21	36:d:40:GLN:HB2	1.68	0.59
1:A:2800:G:H22	1:A:2873:G:H1	1.50	0.58
4:D:6:VAL:H	4:D:33:ASN:HD21	1.50	0.58
6:F:121:SER:O	6:F:127:ASN:ND2	2.35	0.58
1:A:1853:A:N6	1:A:1862:G:O2'	2.36	0.58
20:T:5:ARG:NH2	20:T:36:ASP:O	2.35	0.58
33:a:1241:U:H5''	33:a:1243:C:H41	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:9:VAL:HA	7:G:69:ARG:HH21	1.68	0.58
33:a:762:A:O2'	33:a:1517:G:N2	2.36	0.58
1:A:840:U:H5''	26:Z:49:LYS:HG3	1.84	0.58
1:A:1051:U:H3'	9:I:56:PRO:HA	1.85	0.58
4:D:32:PRO:CB	4:D:95:GLN:HE21	2.15	0.58
4:D:154:ARG:HH12	4:D:156:PHE:HE1	1.52	0.58
21:U:33:LEU:HD13	21:U:66:VAL:HG12	1.86	0.58
1:A:654:G:N2	31:5:64:ARG:O	2.37	0.58
32:6:11:CYS:SG	32:6:14:CYS:N	2.76	0.58
4:D:61:VAL:HG12	4:D:66:ALA:HB2	1.84	0.58
4:D:116:LYS:HD3	4:D:116:LYS:N	2.18	0.58
13:M:11:LYS:HD3	13:M:87:LYS:HD3	1.85	0.58
33:a:293:G:N2	33:a:559:U:O2	2.36	0.58
33:a:1095:A:OP2	34:b:95:ARG:NH1	2.37	0.58
39:g:15:ASP:O	41:i:49:ARG:NH2	2.37	0.58
1:A:96:G:H4'	25:Y:39:GLN:HA	1.84	0.58
46:n:89:MET:SD	46:n:89:MET:N	2.76	0.58
1:A:1313:U:HO2'	1:A:1997:G:HO2'	1.44	0.58
1:A:357:A:H2	1:A:415:G:H21	1.51	0.58
1:A:971:A:H8	1:A:2014:G:H21	1.51	0.57
11:K:1:MET:HE3	11:K:65:THR:HG22	1.85	0.57
17:Q:83:LEU:HD11	17:Q:88:ILE:HG12	1.86	0.57
35:c:111:LEU:HB3	35:c:204:LYS:HD3	1.87	0.57
33:a:398:G:OP2	36:d:115:ARG:NH2	2.37	0.57
1:A:1210:G:OP1	18:R:68:ARG:NH2	2.38	0.57
9:I:110:ALA:HA	9:I:113:LYS:HE3	1.85	0.57
1:A:870:G:N2	1:A:871:G:O6	2.37	0.57
34:b:27:MET:HG2	34:b:193:PRO:HD3	1.87	0.57
1:A:870:G:N7	1:A:881:A:N6	2.51	0.57
33:a:593:U:H4'	40:h:122:GLY:H	1.69	0.57
1:A:249:C:O2	31:5:12:LYS:NZ	2.37	0.57
1:A:2349:G:OP1	31:5:39:ARG:NH2	2.33	0.57
33:a:1127:A:H61	33:a:1135:U:H3	1.52	0.57
45:m:11:ASP:O	45:m:13:LYS:NZ	2.38	0.57
6:F:145:LYS:HG3	6:F:146:ILE:HD12	1.86	0.57
15:O:32:SER:O	15:O:101:ARG:NH1	2.38	0.57
31:5:58:GLU:HG3	31:5:64:ARG:HG2	1.86	0.57
33:a:1067:U:O2	34:b:103:ASN:ND2	2.37	0.57
33:a:1173:A:N6	41:i:81:HIS:O	2.35	0.57
1:A:126:A:H5'	30:4:19:ARG:HG2	1.86	0.57
4:D:116:LYS:O	4:D:117:GLY:O	2.22	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:V:144:PRO:HB3	22:V:168:PRO:HG2	1.87	0.57
33:a:499:G:N2	33:a:520:C:O2	2.37	0.57
1:A:862:C:O2'	13:M:65:TRP:NE1	2.34	0.57
13:M:12:GLN:O	13:M:87:LYS:NZ	2.38	0.57
1:A:301:G:N1	1:A:304:A:OP2	2.36	0.56
1:A:718:G:H4'	3:C:13:ARG:HD3	1.87	0.56
1:A:1404:C:HO2'	1:A:1577:G:HO2'	1.52	0.56
1:A:2773:U:OP1	4:D:71:LYS:HE3	2.05	0.56
10:J:117:ASP:OD1	10:J:120:ARG:NH2	2.37	0.56
52:t:5:PRO:HA	52:t:8:LYS:HB2	1.86	0.56
1:A:2106:A:O2'	1:A:2108:G:OP2	2.23	0.56
1:A:2459:G:H2'	1:A:2462:C:H42	1.69	0.56
4:D:103:ALA:O	4:D:104:GLY:C	2.48	0.56
18:R:27:VAL:O	18:R:66:HIS:NE2	2.38	0.56
20:T:14:HIS:HD2	20:T:32:LYS:HE3	1.71	0.56
33:a:120:A:OP1	33:a:627:G:N2	2.38	0.56
33:a:672:U:H4'	33:a:772:G:H5'	1.86	0.56
33:a:931:A:N6	33:a:1372:C:N3	2.53	0.56
41:i:8:GLY:H	41:i:19:VAL:HG12	1.70	0.56
1:A:83:G:H21	1:A:103:A:H2	1.52	0.56
1:A:269:C:H42	1:A:361:A:H61	1.52	0.56
1:A:1091:U:O2	32:6:12:ARG:NH1	2.37	0.56
1:A:2716:U:H5'	4:D:24:PRO:HG2	1.86	0.56
3:C:152:ALA:O	3:C:156:ARG:NH1	2.38	0.56
22:V:128:SER:HB3	22:V:186:ASN:HB2	1.88	0.56
33:a:488:G:H21	33:a:490:A:H62	1.52	0.56
33:a:1139:C:OP1	33:a:1143:C:N4	2.37	0.56
41:i:12:ARG:HB2	41:i:75:GLN:HG2	1.86	0.56
2:B:57:A:H2'	2:B:58:A:H8	1.70	0.56
33:a:444:G:N1	33:a:479:U:O4	2.39	0.56
33:a:1315:U:H5'	51:s:67:VAL:H	1.71	0.56
39:g:61:THR:HG21	39:g:125:LEU:HA	1.86	0.56
47:o:29:VAL:O	47:o:33:SER:N	2.36	0.56
1:A:997:C:OP1	10:J:37:ARG:NH2	2.38	0.56
1:A:1250:U:OP1	28:2:13:ARG:NH1	2.38	0.56
1:A:2283:U:O2	1:A:2322:A:N6	2.38	0.56
33:a:1371:A:N7	39:g:3:ARG:NH2	2.53	0.56
35:c:125:GLU:HG2	35:c:191:THR:HA	1.87	0.56
1:A:1841:A:H62	1:A:1875:G:H8	1.52	0.56
4:D:100:LEU:O	4:D:100:LEU:HG	2.05	0.56
34:b:67:ILE:HG12	34:b:160:ALA:HB3	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:h:11:LEU:HD22	40:h:75:VAL:HG11	1.87	0.56
1:A:1683:U:O2	3:C:14:ARG:NH1	2.39	0.56
33:a:1233:A:N6	33:a:1291:G:O2'	2.39	0.56
42:j:8:ILE:N	42:j:74:LEU:O	2.39	0.56
33:a:875:G:OP1	44:l:9:ARG:NH1	2.36	0.56
33:a:1160:G:N2	33:a:1163:A:O2'	2.39	0.56
38:f:40:GLU:HB2	38:f:61:LEU:HB3	1.88	0.56
14:N:32:GLU:HG2	14:N:115:LEU:HD12	1.88	0.56
1:A:865:C:H42	1:A:890:A:H61	1.52	0.55
1:A:2074:U:H2'	1:A:2075:G:H8	1.72	0.55
1:A:2245:C:O2'	1:A:2414:C:OP2	2.24	0.55
1:A:2577:A:H5''	3:C:238:ARG:HG3	1.87	0.55
4:D:110:THR:CG2	4:D:202:ILE:HB	2.35	0.55
40:h:101:VAL:HG12	40:h:129:VAL:HG21	1.87	0.55
1:A:1030:A:H61	1:A:1105:G:H1	1.53	0.55
4:D:10:CYS:SG	16:P:2:THR:N	2.79	0.55
4:D:154:ARG:NH1	4:D:156:PHE:CE1	2.74	0.55
33:a:504:A:N3	33:a:537:U:O2'	2.39	0.55
33:a:1399:G:H1	33:a:1490:C:H42	1.54	0.55
1:A:592:A:HO2'	1:A:594:G:HO2'	1.53	0.55
1:A:2459:G:H1'	1:A:2465:A:H61	1.71	0.55
17:Q:50:ARG:O	17:Q:54:LYS:NZ	2.39	0.55
33:a:391:A:H62	33:a:541:A:H1'	1.71	0.55
1:A:680:U:O2'	1:A:770:G:OP1	2.23	0.55
1:A:1327:U:OP1	20:T:83:TYR:OH	2.25	0.55
13:M:78:PRO:HG2	13:M:81:VAL:HG21	1.88	0.55
33:a:1068:G:O2'	33:a:1095:A:N1	2.40	0.55
1:A:85:G:O2'	1:A:103:A:N6	2.40	0.55
12:L:51:GLU:OE2	31:5:56:ARG:NH1	2.39	0.55
22:V:67:ASN:HB3	22:V:72:LYS:HG2	1.89	0.55
33:a:770:G:N2	33:a:796:A:OP2	2.38	0.55
1:A:459:G:N7	30:4:39:ARG:NH2	2.54	0.55
6:F:16:LEU:HD12	6:F:28:VAL:HG22	1.89	0.55
13:M:48:GLU:OE2	13:M:51:ARG:NH1	2.38	0.55
40:h:71:VAL:HG23	40:h:72:ILE:HG13	1.88	0.55
1:A:797:U:O2'	1:A:2047:A:N1	2.39	0.55
3:C:119:GLY:O	3:C:134:ASN:ND2	2.39	0.55
33:a:178:U:H3	33:a:188:G:H22	1.55	0.55
1:A:491:G:N1	1:A:494:A:OP2	2.39	0.55
13:M:39:ARG:HB3	13:M:99:PRO:HD3	1.88	0.55
32:6:16:ILE:HG12	32:6:25:VAL:HG22	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:b:120:GLN:NE2	34:b:130:THR:OG1	2.39	0.55
46:n:87:ALA:HB1	46:n:92:ASP:HB2	1.88	0.55
1:A:374:C:N4	1:A:377:G:OP2	2.40	0.55
33:a:500:G:H1	33:a:518:G:H1	1.55	0.55
4:D:69:PHE:CE1	4:D:76:ALA:HB3	2.41	0.55
33:a:1283:A:H62	33:a:1365:G:H21	1.55	0.55
1:A:1784:C:HO2'	3:C:258:THR:HG1	1.51	0.54
33:a:1168:G:H2'	33:a:1169:G:H8	1.72	0.54
37:e:139:TYR:HB3	37:e:143:LYS:HZ1	1.72	0.54
1:A:2336:G:H22	1:A:2354:G:H1	1.56	0.54
4:D:158:GLY:O	4:D:159:LYS:C	2.50	0.54
22:V:33:VAL:HG12	22:V:94:PHE:HB2	1.90	0.54
33:a:67:C:H2'	33:a:68:G:H8	1.72	0.54
37:e:90:HIS:ND1	37:e:136:ASN:OD1	2.40	0.54
40:h:105:SER:HB3	40:h:124:GLU:HB2	1.90	0.54
42:j:16:ARG:HD2	42:j:17:LEU:HG	1.89	0.54
45:m:39:VAL:HG22	45:m:52:GLN:HB3	1.87	0.54
52:t:56:PRO:O	52:t:60:ARG:NH1	2.40	0.54
1:A:1051:U:H1'	9:I:12:GLN:HG3	1.89	0.54
4:D:102:GLN:O	4:D:177:ILE:HG21	2.07	0.54
9:I:28:LEU:HD12	9:I:35:ILE:HD13	1.89	0.54
33:a:580:U:OP1	49:q:39:LYS:NZ	2.40	0.54
43:k:49:GLY:O	43:k:69:ARG:NH1	2.41	0.54
1:A:1088:A:O5'	9:I:30:GLN:N	2.36	0.54
1:A:2191:G:H4'	3:C:150:LYS:HD3	1.89	0.54
14:N:24:MET:HE2	14:N:44:LEU:HD22	1.90	0.54
33:a:25:C:H41	33:a:553:A:H61	1.54	0.54
1:A:1587:A:H5''	1:A:1588:A:H5'	1.90	0.54
14:N:106:ASP:OD1	14:N:106:ASP:N	2.40	0.54
41:i:9:THR:HA	41:i:17:ALA:HB3	1.90	0.54
6:F:44:VAL:HG13	6:F:82:GLY:HA3	1.90	0.54
15:O:36:ILE:HG22	15:O:65:GLY:HA2	1.89	0.54
44:l:50:ARG:HH11	44:l:90:LEU:HG	1.73	0.54
4:D:27:VAL:HG12	4:D:188:LEU:HG	1.90	0.54
33:a:195:G:N3	33:a:464:C:O2'	2.39	0.54
33:a:774:A:OP1	43:k:127:ARG:NH1	2.40	0.54
1:A:447:C:OP1	20:T:71:ARG:NH2	2.41	0.54
1:A:1078:A:N6	9:I:134:ARG:O	2.40	0.54
1:A:2237:G:O2'	1:A:2483:C:OP1	2.26	0.54
6:F:128:TYR:OH	6:F:175:PHE:O	2.26	0.54
33:a:667:G:O2'	38:f:86:ARG:NH1	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:l:27:CYS:SG	44:l:30:ARG:NH2	2.81	0.54
33:a:744:C:O2'	47:o:21:ASP:OD1	2.26	0.54
33:a:1374:U:O2	33:a:1376:C:N4	2.41	0.54
38:f:90:MET:O	38:f:92:ARG:NH1	2.40	0.54
43:k:24:HIS:HB3	43:k:31:ILE:HB	1.89	0.54
1:A:1786:G:OP1	3:C:259:ARG:NH1	2.33	0.54
22:V:165:LEU:HD23	22:V:166:LYS:H	1.72	0.54
33:a:752:G:H4'	33:a:874:C:H4'	1.90	0.54
47:o:38:LYS:HG3	47:o:39:LEU:HD22	1.89	0.54
1:A:358:A:O2'	1:A:359:U:O2	2.26	0.53
1:A:2121:A:H62	1:A:2140:C:H2'	1.71	0.53
4:D:119:ALA:O	4:D:162:SER:HB2	2.08	0.53
4:D:186:LEU:HD21	16:P:5:ILE:HD12	1.89	0.53
9:I:39:CYS:O	9:I:43:ASN:ND2	2.41	0.53
49:q:23:THR:OG1	49:q:74:LYS:NZ	2.41	0.53
50:r:23:TYR:HB2	50:r:62:ALA:HB2	1.90	0.53
50:r:44:ILE:HG22	50:r:45:THR:HG23	1.89	0.53
1:A:529:A:H5''	10:J:7:LYS:HE3	1.91	0.53
1:A:2122:A:OP2	1:A:2140:C:N4	2.40	0.53
1:A:2327:C:H2'	1:A:2328:G:H8	1.74	0.53
6:F:57:LEU:HD12	6:F:65:PRO:HG3	1.89	0.53
7:G:3:ARG:NH1	7:G:62:ARG:O	2.42	0.53
33:a:1370:U:O4	39:g:25:LYS:NZ	2.40	0.53
45:m:86:TYR:HB3	51:s:73:GLU:HG2	1.89	0.53
1:A:1210:G:N7	18:R:71:LYS:NZ	2.55	0.53
1:A:1715:U:O2'	1:A:1717:U:OP2	2.24	0.53
7:G:23:GLN:HG2	7:G:37:VAL:HA	1.90	0.53
15:O:109:ALA:HB1	15:O:114:LEU:HB3	1.90	0.53
33:a:110:A:H61	33:a:307:A:H1'	1.72	0.53
1:A:303:A:N3	1:A:323:G:O2'	2.38	0.53
1:A:2278:U:O2'	1:A:2361:C:O2	2.26	0.53
33:a:1313:A:C6	51:s:3:ARG:CG	2.91	0.53
1:A:733:C:OP1	4:D:135:GLY:HA2	2.09	0.53
1:A:1441:U:O2'	1:A:1442:G:N7	2.41	0.53
1:A:1831:C:H5''	3:C:257:LYS:HG2	1.90	0.53
4:D:51:VAL:HG21	4:D:96:ILE:HD11	1.91	0.53
33:a:816:U:H3	33:a:872:A:H61	1.55	0.53
33:a:1173:A:O2'	41:i:98:LEU:O	2.27	0.53
40:h:41:LYS:HZ1	40:h:49:PHE:HB3	1.71	0.53
15:O:37:TYR:HE1	15:O:54:THR:HG22	1.73	0.53
33:a:1315:U:OP1	51:s:69:HIS:N	2.35	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:h:78:ILE:HG22	40:h:85:GLN:HG3	1.89	0.53
42:j:19:ASP:OD1	42:j:72:ARG:NH2	2.42	0.53
1:A:391:G:N7	24:X:57:ARG:NH1	2.56	0.53
1:A:1012:G:N2	1:A:1013:U:O4	2.40	0.53
1:A:1238:C:OP2	17:Q:6:ARG:NH2	2.41	0.53
33:a:769:G:N2	33:a:798:U:O4	2.40	0.53
33:a:1160:G:O2'	33:a:1163:A:N6	2.40	0.53
35:c:92:THR:HA	35:c:95:MET:HB3	1.91	0.53
36:d:101:VAL:HA	36:d:104:ARG:HB2	1.91	0.53
1:A:27:G:N2	1:A:503:G:O2'	2.25	0.53
1:A:2301:G:OP1	6:F:88:LYS:NZ	2.42	0.53
1:A:2465:A:O2'	1:A:2523:G:N2	2.42	0.53
2:B:79:G:N7	22:V:16:LYS:NZ	2.57	0.53
3:C:67:PHE:HB3	3:C:152:ALA:H	1.73	0.53
4:D:116:LYS:O	4:D:165:LEU:O	2.27	0.53
33:a:1369:A:H2	39:g:28:ASN:HB2	1.74	0.53
33:a:1373:G:N2	33:a:1375:U:O4	2.34	0.53
39:g:79:ARG:NH1	39:g:82:GLY:O	2.42	0.53
42:j:22:THR:HG21	42:j:72:ARG:HD2	1.90	0.53
1:A:1471:A:H2'	1:A:1472:A:H8	1.73	0.53
4:D:74:VAL:HG13	4:D:76:ALA:HB2	1.91	0.53
33:a:1313:A:C4	51:s:3:ARG:CB	2.92	0.53
33:a:204:C:OP2	33:a:205:G:N2	2.43	0.52
33:a:763:G:N2	33:a:805:C:O2	2.41	0.52
33:a:1215:G:H2'	51:s:53:ASN:HB3	1.91	0.52
35:c:22:TRP:HA	42:j:95:GLY:HA3	1.91	0.52
6:F:91:LEU:HA	6:F:95:ARG:HH21	1.75	0.52
48:p:17:TYR:HB2	48:p:39:PHE:HB3	1.91	0.52
1:A:1009:U:H5	1:A:1133:A:H62	1.56	0.52
1:A:2653:C:H41	7:G:105:PHE:HA	1.75	0.52
33:a:783:U:N3	33:a:786:A:OP2	2.36	0.52
1:A:1756:U:O2'	1:A:1945:C:OP1	2.28	0.52
1:A:2622:U:O2'	4:D:82:GLU:OE1	2.21	0.52
33:a:304:G:H5''	48:p:31:ARG:HB2	1.91	0.52
33:a:1145:A:H2	33:a:1146:A:H62	1.57	0.52
34:b:42:ASN:O	34:b:46:THR:OG1	2.26	0.52
34:b:42:ASN:OD1	34:b:45:LYS:NZ	2.41	0.52
1:A:197:A:N6	1:A:2417:A:O2'	2.43	0.52
33:a:582:G:N2	33:a:647:A:N7	2.50	0.52
1:A:1352:A:OP2	24:X:2:SER:OG	2.26	0.52
1:A:2646:G:N2	1:A:2649:A:OP2	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:664:G:H2'	1:A:794:A:H61	1.75	0.52
33:a:433:U:H4'	36:d:121:LYS:HD3	1.91	0.52
33:a:456:G:H1	33:a:465:U:H5	1.57	0.52
33:a:810:A:OP2	33:a:1520:G:O2'	2.27	0.52
1:A:1437:G:N2	1:A:1439:G:O6	2.43	0.52
1:A:2119:U:H5	1:A:2121:A:H4'	1.75	0.52
11:K:25:LEU:HD12	11:K:38:ILE:HG22	1.91	0.52
20:T:40:LEU:HG	20:T:44:LYS:HE2	1.91	0.52
33:a:914:U:O2'	33:a:1075:G:O2'	2.28	0.52
33:a:1247:G:O6	33:a:1277:C:N4	2.40	0.52
1:A:1478:G:O2'	3:C:100:GLU:OE1	2.27	0.52
1:A:1804:G:OP2	3:C:156:ARG:NH2	2.43	0.52
1:A:2336:G:OP1	31:5:44:ARG:NH2	2.43	0.52
4:D:172:VAL:HG23	4:D:194:PRO:HD3	1.91	0.52
18:R:24:LYS:HA	18:R:94:THR:HG23	1.92	0.52
35:c:57:ILE:HG12	35:c:66:ILE:HG12	1.92	0.52
1:A:1116:A:H4'	1:A:1117:A:H5''	1.91	0.52
39:g:16:PRO:HA	41:i:49:ARG:HH21	1.75	0.52
1:A:92:A:O2'	1:A:93:A:O5'	2.28	0.51
1:A:899:A:N3	1:A:2251:C:O2'	2.42	0.51
1:A:1250:U:O2'	28:2:4:GLN:NE2	2.35	0.51
1:A:1683:U:H5''	1:A:1684:C:H5	1.74	0.51
1:A:1839:U:O2	1:A:1877:A:N6	2.42	0.51
33:a:667:G:O6	33:a:710:A:N6	2.43	0.51
33:a:1020:G:OP2	33:a:1021:C:N4	2.38	0.51
52:t:60:ARG:O	52:t:64:LYS:NZ	2.42	0.51
1:A:2096:U:O4	1:A:2097:G:N2	2.42	0.51
23:W:40:LEU:HD11	23:W:44:LYS:HB3	1.91	0.51
33:a:1236:G:N1	33:a:1289:U:O4	2.42	0.51
52:t:63:ASP:HA	52:t:69:LYS:HE2	1.91	0.51
1:A:238:C:O2'	1:A:598:A:N3	2.42	0.51
1:A:1348:G:HO2'	1:A:2202:C:HO2'	1.55	0.51
45:m:90:ARG:NH2	45:m:97:VAL:O	2.44	0.51
1:A:27:G:H22	1:A:503:G:HO2'	1.50	0.51
14:N:32:GLU:OE2	14:N:86:ARG:NH2	2.44	0.51
31:5:6:THR:HG22	31:5:62:ARG:H	1.75	0.51
35:c:175:LEU:HD22	35:c:182:ILE:HG23	1.91	0.51
4:D:91:ALA:N	4:D:94:ASP:OD2	2.39	0.51
19:S:38:PHE:O	28:2:25:ASN:ND2	2.43	0.51
4:D:172:VAL:CG1	4:D:175:LEU:HD21	2.39	0.51
9:I:106:LEU:HD22	9:I:129:ILE:HD12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:38:ILE:HD11	11:K:111:PHE:HZ	1.76	0.51
38:f:38:ARG:HH12	50:r:24:LYS:HE2	1.76	0.51
1:A:2455:A:OP2	1:A:2463:A:N6	2.44	0.51
33:a:574:C:H42	33:a:755:G:H1	1.59	0.51
33:a:786:A:H4'	33:a:787:U:H5'	1.92	0.51
47:o:57:ILE:HA	47:o:60:VAL:HG12	1.93	0.51
48:p:54:GLN:NE2	48:p:58:THR:OG1	2.44	0.51
1:A:1641:G:H4'	14:N:39:PRO:HG2	1.93	0.51
10:J:9:GLU:HG2	10:J:10:THR:HG23	1.93	0.51
33:a:107:G:H1'	33:a:348:G:H5'	1.92	0.51
3:C:19:VAL:HG23	3:C:203:ARG:HB3	1.93	0.51
33:a:223:U:O2'	48:p:23:ASN:OD1	2.27	0.51
33:a:1426:G:O2'	33:a:1462:A:N6	2.43	0.51
1:A:1047:A:OP2	9:I:62:TYR:OH	2.29	0.51
1:A:2356:A:H2'	1:A:2357:G:C8	2.46	0.51
3:C:231:PRO:C	3:C:233:GLY:H	2.18	0.51
4:D:102:GLN:O	4:D:180:VAL:HG23	2.11	0.51
1:A:91:A:H4'	1:A:92:A:H5'	1.92	0.50
1:A:1199:G:O2'	1:A:1224:A:N6	2.44	0.50
1:A:2472:G:OP1	13:M:46:GLN:NE2	2.34	0.50
8:H:2:GLU:N	8:H:19:VAL:O	2.44	0.50
10:J:93:ILE:HA	10:J:97:PRO:HA	1.91	0.50
33:a:1195:A:O5'	33:a:1198:A:N6	2.42	0.50
33:a:1253:C:H4'	33:a:1350:A:H5'	1.94	0.50
33:a:1313:A:C6	51:s:3:ARG:CB	2.94	0.50
52:t:68:HIS:ND1	52:t:70:ASN:OD1	2.43	0.50
1:A:964:A:H8	1:A:980:A:H62	1.58	0.50
33:a:378:G:OP1	33:a:448:G:O2'	2.30	0.50
44:l:79:VAL:HG12	44:l:103:ASP:HB2	1.93	0.50
50:r:60:LYS:HA	50:r:63:ARG:HB2	1.93	0.50
1:A:529:A:H4'	10:J:7:LYS:HG3	1.93	0.50
49:q:33:LYS:HA	49:q:40:TYR:HA	1.94	0.50
1:A:505:A:N3	1:A:571:C:O2'	2.41	0.50
7:G:45:GLN:HE21	7:G:51:ARG:HE	1.60	0.50
9:I:79:LEU:HD23	9:I:82:LYS:HG3	1.92	0.50
33:a:305:U:OP1	48:p:31:ARG:NH2	2.44	0.50
33:a:1313:A:C4	51:s:3:ARG:CG	2.94	0.50
1:A:388:U:H5''	24:X:32:ASN:HB2	1.93	0.50
1:A:2734:G:OP1	7:G:74:ASN:ND2	2.44	0.50
4:D:102:GLN:HG3	4:D:105:GLN:HE21	1.77	0.50
34:b:32:PHE:HB2	34:b:42:ASN:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:o:3:LEU:HG	47:o:38:LYS:HD3	1.93	0.50
4:D:20:GLY:HA2	16:P:80:PRO:HG2	1.93	0.50
4:D:98:VAL:C	4:D:100:LEU:H	2.19	0.50
1:A:294:A:H2'	1:A:328:C:H1'	1.93	0.50
1:A:1199:G:O2'	1:A:1223:G:N2	2.44	0.50
1:A:2455:A:O2'	1:A:2468:G:N2	2.43	0.50
2:B:37:C:N4	2:B:48:U:O2	2.44	0.50
3:C:268:ILE:HG21	3:C:271:ARG:HD3	1.93	0.50
32:6:2:LYS:HB3	32:6:35:GLN:HG3	1.93	0.50
33:a:1019:U:H1'	33:a:1020:G:H8	1.75	0.50
1:A:1656:G:N3	11:K:3:GLN:NE2	2.60	0.50
7:G:39:PRO:HG3	7:G:64:MET:HE2	1.94	0.50
33:a:665:G:O2'	38:f:79:ARG:NH2	2.45	0.50
1:A:1372:A:O2'	1:A:1383:U:O2	2.30	0.50
7:G:83:PHE:HB2	7:G:137:VAL:HG21	1.94	0.50
33:a:478:G:OP2	33:a:478:G:N2	2.35	0.50
1:A:1018:A:H61	1:A:1115:G:H2'	1.77	0.49
1:A:1643:G:OP1	1:A:2809:G:N2	2.32	0.49
31:5:53:ASP:OD1	31:5:56:ARG:NH2	2.45	0.49
33:a:196:G:H21	33:a:462:A:H61	1.60	0.49
1:A:141:A:O2'	1:A:142:C:O4'	2.30	0.49
15:O:26:ARG:N	15:O:41:ILE:O	2.38	0.49
21:U:14:ALA:H	21:U:18:LYS:HG3	1.78	0.49
33:a:1071:G:N2	33:a:1074:A:OP2	2.41	0.49
33:a:1118:G:H1'	33:a:1274:A:H61	1.77	0.49
1:A:2392:G:O2'	1:A:2399:A:N6	2.45	0.49
33:a:1052:G:O2'	35:c:199:LYS:NZ	2.37	0.49
33:a:1313:A:C2	51:s:3:ARG:CG	2.96	0.49
1:A:1088:A:O5'	9:I:29:GLY:N	2.45	0.49
1:A:1713:G:H1	1:A:1721:C:H42	1.59	0.49
4:D:104:GLY:O	4:D:105:GLN:O	2.29	0.49
9:I:90:SER:HB2	9:I:137:GLY:HA3	1.94	0.49
21:U:3:LYS:HD2	21:U:82:VAL:HG23	1.94	0.49
33:a:1000:C:N4	33:a:1018:G:O6	2.46	0.49
1:A:1469:G:H1	1:A:1494:C:H42	1.59	0.49
1:A:2356:A:H2'	1:A:2357:G:H8	1.77	0.49
33:a:1215:G:OP2	51:s:54:GLY:N	2.45	0.49
35:c:186:THR:HG22	35:c:199:LYS:HG2	1.93	0.49
43:k:25:ALA:O	43:k:90:GLY:N	2.44	0.49
1:A:2125:G:N1	1:A:2140:C:O2	2.45	0.49
3:C:117:ILE:CB	3:C:129:SER:HB3	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:6:ASN:HD22	5:E:120:VAL:HG12	1.77	0.49
5:E:17:THR:HA	5:E:105:ARG:HG3	1.94	0.49
11:K:19:VAL:HG11	11:K:86:LEU:HD11	1.94	0.49
33:a:366:C:N4	33:a:382:G:OP2	2.42	0.49
33:a:632:C:H2'	33:a:633:A:H8	1.77	0.49
1:A:835:A:O2'	1:A:836:U:O2	2.30	0.49
1:A:900:A:N6	13:M:11:LYS:O	2.43	0.49
9:I:100:THR:HA	9:I:138:LEU:HD22	1.95	0.49
14:N:53:THR:HA	14:N:56:LYS:HE2	1.95	0.49
6:F:65:PRO:HB3	6:F:87:VAL:HG13	1.95	0.49
14:N:38:LEU:HD23	14:N:111:ALA:HB2	1.95	0.49
33:a:309:A:O2'	33:a:324:C:O2'	2.31	0.49
43:k:82:LEU:HB2	43:k:107:ILE:HG22	1.93	0.49
43:k:117:PRO:O	53:u:35:ARG:NH2	2.43	0.49
1:A:160:A:N3	1:A:2195:C:O2'	2.42	0.49
1:A:2772:C:O3'	4:D:71:LYS:HE3	2.13	0.49
4:D:35:VAL:CG2	4:D:92:ALA:HA	2.42	0.49
4:D:74:VAL:CG1	4:D:76:ALA:HB2	2.42	0.49
4:D:204:ARG:HB2	4:D:205:PRO:HD2	1.94	0.49
33:a:356:G:H5''	44:l:58:THR:HG21	1.95	0.49
33:a:917:A:N6	33:a:1386:G:O6	2.46	0.49
33:a:1303:G:N2	33:a:1321:G:O6	2.46	0.49
34:b:166:VAL:HG21	34:b:187:VAL:HG12	1.94	0.49
35:c:43:LEU:HD13	35:c:52:VAL:HG21	1.95	0.49
39:g:41:ARG:HG2	41:i:41:ARG:HH22	1.78	0.49
45:m:78:LYS:NZ	45:m:82:ASP:OD2	2.46	0.49
48:p:60:TRP:O	48:p:65:ALA:N	2.44	0.49
1:A:1089:G:OP1	9:I:3:LYS:NZ	2.41	0.49
4:D:99:ASP:OD1	4:D:182:ALA:HB2	2.13	0.49
33:a:539:C:H3'	36:d:69:GLU:HB2	1.95	0.49
1:A:1088:A:P	9:I:30:GLN:H	2.35	0.48
1:A:1795:A:H3'	1:A:1796:A:C8	2.48	0.48
35:c:66:ILE:HB	35:c:99:VAL:HG11	1.95	0.48
1:A:1049:G:H8	9:I:69:PHE:HB3	1.78	0.48
1:A:1253:G:O2'	1:A:1999:G:O6	2.31	0.48
2:B:31:C:H42	2:B:51:G:H1	1.61	0.48
33:a:760:A:N1	33:a:1519:G:N2	2.61	0.48
33:a:1015:U:H5'	33:a:1016:U:H5'	1.95	0.48
1:A:2553:A:N1	11:K:28:SER:OG	2.45	0.48
34:b:70:VAL:HG23	34:b:163:VAL:HA	1.94	0.48
53:u:40:LYS:HD2	53:u:41:PRO:HD2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:567:G:O2'	1:A:1241:A:OP1	2.31	0.48
1:A:1242:U:H5''	1:A:1243:G:H5''	1.96	0.48
1:A:1660:C:O2	4:D:134:HIS:NE2	2.42	0.48
2:B:55:U:O2'	2:B:57:A:N6	2.46	0.48
1:A:661:C:N4	12:L:40:SER:O	2.41	0.48
1:A:2087:G:H2'	1:A:2088:A:H8	1.78	0.48
4:D:133:THR:C	4:D:135:GLY:N	2.68	0.48
6:F:110:ARG:HA	6:F:137:ILE:HG12	1.96	0.48
9:I:130:ALA:HA	9:I:140:VAL:HG11	1.95	0.48
11:K:9:ASP:OD1	11:K:18:ARG:NH1	2.38	0.48
31:5:47:SER:OG	31:5:48:MET:N	2.46	0.48
33:a:1313:A:C5	51:s:3:ARG:CG	2.96	0.48
35:c:25:ASP:HB2	35:c:28:ASN:HD22	1.78	0.48
52:t:78:ARG:O	52:t:82:HIS:ND1	2.42	0.48
1:A:645:A:H4'	1:A:646:G:H5'	1.95	0.48
1:A:2323:A:H61	23:W:43:THR:HG21	1.79	0.48
33:a:110:A:N1	33:a:307:A:O2'	2.46	0.48
1:A:111:A:O3'	25:Y:58:ASN:ND2	2.47	0.48
1:A:1034:U:O3'	1:A:1101:A:N6	2.42	0.48
1:A:1787:C:H5	1:A:1804:G:H22	1.60	0.48
1:A:2805:C:OP1	1:A:2824:A:O2'	2.28	0.48
26:Z:15:ARG:HE	26:Z:53:LEU:HD21	1.78	0.48
1:A:482:G:O6	19:S:49:LYS:NZ	2.36	0.48
33:a:62:U:OP1	33:a:379:C:O2'	2.27	0.48
33:a:616:A:H61	48:p:14:ARG:HH22	1.62	0.48
33:a:873:C:H5''	44:l:5:ASN:HD22	1.78	0.48
33:a:1313:A:C2	51:s:3:ARG:CB	2.96	0.48
1:A:2378:G:O2'	1:A:2411:C:N4	2.41	0.48
33:a:1313:A:C5	51:s:3:ARG:CB	2.97	0.48
35:c:113:ALA:HA	35:c:202:ILE:HD12	1.95	0.48
36:d:188:ARG:HH22	36:d:193:ALA:HA	1.79	0.48
53:u:52:ALA:HA	53:u:55:ARG:HE	1.78	0.48
1:A:2191:G:OP2	3:C:147:LYS:NZ	2.39	0.48
15:O:27:LEU:HD12	15:O:40:VAL:HG22	1.96	0.48
33:a:1518:C:N4	33:a:1519:G:O6	2.47	0.48
42:j:49:PHE:HB2	42:j:65:TYR:HB2	1.96	0.48
1:A:294:A:OP2	21:U:81:ARG:NH2	2.48	0.47
4:D:25:VAL:HG11	4:D:188:LEU:HD23	1.94	0.47
5:E:82:THR:HB	5:E:85:ALA:HB2	1.96	0.47
20:T:2:ASN:O	20:T:4:GLU:N	2.47	0.47
29:3:7:LEU:HB3	29:3:45:TYR:HB3	1.94	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:d:85:SER:O	36:d:89:ASN:ND2	2.47	0.47
44:l:51:LYS:HG3	44:l:72:HIS:HE1	1.79	0.47
50:r:29:LEU:HD13	50:r:59:ILE:HD13	1.96	0.47
15:O:110:ARG:HH21	15:O:116:PHE:HD2	1.61	0.47
16:P:89:ARG:NH2	16:P:111:ILE:O	2.45	0.47
33:a:1257:G:H21	33:a:1267:G:H1'	1.80	0.47
23:W:32:LYS:H	23:W:35:ASN:ND2	2.12	0.47
40:h:88:SER:OG	40:h:89:VAL:N	2.46	0.47
1:A:224:U:O4	1:A:410:U:O2'	2.32	0.47
1:A:896:G:OP1	13:M:24:GLY:N	2.43	0.47
1:A:1126:G:O2'	1:A:2025:G:O2'	2.26	0.47
5:E:57:LYS:NZ	5:E:61:GLN:OE1	2.43	0.47
6:F:60:ILE:HG13	6:F:61:THR:HG23	1.96	0.47
32:6:4:ARG:O	32:6:37:GLN:NE2	2.47	0.47
34:b:6:MET:HA	34:b:9:MET:HB3	1.95	0.47
1:A:621:A:H5'	12:L:64:PHE:HE2	1.79	0.47
1:A:854:C:H42	1:A:898:A:H2	1.63	0.47
7:G:87:LEU:HD13	7:G:144:ILE:HG21	1.95	0.47
12:L:70:LYS:HG2	12:L:107:ARG:HH12	1.80	0.47
33:a:1078:G:H5''	33:a:1079:U:H2'	1.96	0.47
33:a:1152:C:H5	33:a:1176:G:H1'	1.79	0.47
33:a:1175:G:OP2	41:i:99:ARG:NH1	2.48	0.47
34:b:104:TYR:O	34:b:108:ARG:N	2.48	0.47
36:d:98:LEU:HA	36:d:101:VAL:HG22	1.97	0.47
36:d:111:ARG:HA	36:d:114:SER:HB2	1.96	0.47
42:j:76:ILE:HD11	42:j:102:LEU:HD12	1.96	0.47
1:A:2454:C:O2	13:M:124:LYS:NZ	2.41	0.47
1:A:2886:G:H4'	10:J:136:GLN:HE22	1.80	0.47
5:E:116:ARG:NH1	12:L:1:MET:O	2.45	0.47
33:a:259:G:N2	33:a:261:C:O4'	2.47	0.47
33:a:356:G:OP1	44:l:58:THR:OG1	2.31	0.47
1:A:1049:G:OP1	9:I:71:THR:OG1	2.32	0.47
1:A:1328:U:OP2	1:A:1381:U:O2'	2.29	0.47
1:A:2074:U:H2'	1:A:2075:G:C8	2.49	0.47
2:B:78:A:H62	2:B:98:G:H21	1.62	0.47
7:G:5:ALA:HB2	7:G:66:GLY:HA2	1.96	0.47
13:M:17:ASN:O	13:M:39:ARG:NH1	2.47	0.47
16:P:2:THR:HG22	16:P:4:LYS:H	1.79	0.47
16:P:93:VAL:HG11	16:P:98:LEU:HD11	1.97	0.47
33:a:106:G:H4'	33:a:383:A:H4'	1.96	0.47
33:a:747:A:OP1	47:o:69:TYR:OH	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:a:1300:A:H1'	45:m:109:ARG:HA	1.97	0.47
38:f:42:TRP:HE1	38:f:61:LEU:HB2	1.80	0.47
44:l:39:THR:HB	44:l:49:LEU:HD11	1.96	0.47
52:t:57:VAL:HG22	52:t:60:ARG:HH22	1.80	0.47
2:B:72:G:H1'	2:B:105:G:H22	1.80	0.47
11:K:2:ILE:HG23	11:K:32:TYR:HD1	1.80	0.47
24:X:47:VAL:HG21	24:X:68:LEU:HD11	1.96	0.47
33:a:1314:C:H41	51:s:71:LEU:HD11	1.80	0.47
36:d:168:VAL:HG23	36:d:170:TRP:H	1.80	0.47
46:n:16:THR:HA	46:n:19:LYS:HB2	1.97	0.47
1:A:1824:C:O2'	1:A:1914:A:N3	2.45	0.47
7:G:15:VAL:HG21	7:G:76:VAL:HG13	1.96	0.47
33:a:1315:U:OP1	51:s:69:HIS:ND1	2.48	0.47
1:A:1671:G:C8	1:A:1749:A:H2'	2.50	0.47
5:E:111:LEU:HB3	5:E:117:LEU:HB2	1.97	0.47
22:V:131:ILE:HD13	22:V:182:LEU:HD23	1.97	0.47
27:l:22:ILE:HG22	27:l:23:LYS:HD2	1.97	0.47
43:k:27:PHE:HA	43:k:91:PRO:HD2	1.97	0.47
4:D:72:ALA:O	4:D:74:VAL:N	2.48	0.46
5:E:74:SER:HB3	5:E:77:TRP:CD1	2.50	0.46
13:M:41:ARG:HE	13:M:94:VAL:HG11	1.80	0.46
1:A:562:A:OP2	18:R:80:ARG:NH1	2.41	0.46
9:I:133:ALA:HA	9:I:136:MET:HE3	1.96	0.46
15:O:38:ALA:HB2	15:O:105:LEU:HD21	1.96	0.46
33:a:1117:A:O2'	42:j:39:PRO:O	2.32	0.46
33:a:1122:C:H1'	33:a:1138:G:H22	1.80	0.46
48:p:8:ARG:HB2	48:p:28:ARG:HH12	1.80	0.46
6:F:22:LEU:HD13	6:F:27:GLU:HG3	1.98	0.46
15:O:26:ARG:HH12	15:O:45:GLY:HA2	1.80	0.46
24:X:70:ASP:OD1	24:X:70:ASP:N	2.49	0.46
33:a:1508:G:H1	33:a:1515:C:H42	1.61	0.46
35:c:95:MET:HE2	35:c:97:VAL:HG23	1.98	0.46
1:A:563:U:O2'	1:A:565:A:OP1	2.26	0.46
1:A:1932:G:N2	1:A:1950:U:O4	2.47	0.46
33:a:1316:C:OP2	51:s:69:HIS:ND1	2.44	0.46
1:A:1529:U:H2'	1:A:1530:G:C8	2.51	0.46
2:B:31:C:H4'	6:F:26:MET:HE1	1.98	0.46
33:a:544:G:O2'	44:l:116:LYS:NZ	2.34	0.46
48:p:67:PRO:HB3	48:p:71:VAL:HB	1.98	0.46
1:A:719:G:C6	3:C:207:LYS:HB2	2.51	0.46
1:A:857:U:H3	1:A:898:A:H62	1.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:148:VAL:HB	5:E:187:VAL:HG12	1.97	0.46
15:O:6:GLU:O	15:O:10:ARG:N	2.47	0.46
33:a:337:U:O2'	33:a:340:G:O6	2.32	0.46
33:a:1118:G:H2'	33:a:1143:C:H42	1.80	0.46
33:a:1118:G:O2'	33:a:1121:A:N1	2.49	0.46
35:c:35:ALA:HB1	35:c:95:MET:HG3	1.98	0.46
40:h:49:PHE:HB2	40:h:59:LEU:HD11	1.97	0.46
1:A:2772:C:O2'	4:D:68:HIS:HD2	1.98	0.46
1:A:2773:U:P	4:D:71:LYS:HE3	2.55	0.46
4:D:74:VAL:O	4:D:75:ALA:HB3	2.16	0.46
33:a:303:A:H2'	33:a:304:G:H8	1.80	0.46
33:a:651:U:H2'	33:a:652:A:H8	1.80	0.46
33:a:764:C:O2'	33:a:893:C:N3	2.47	0.46
33:a:1346:C:N4	33:a:1363:C:O2	2.49	0.46
1:A:1147:A:C8	17:Q:51:ARG:HG2	2.51	0.46
1:A:1712:G:H1	1:A:1722:C:H42	1.64	0.46
1:A:2516:G:OP1	7:G:168:LYS:NZ	2.41	0.46
1:A:2639:C:N4	1:A:2655:G:O6	2.48	0.46
20:T:7:PHE:O	25:Y:29:ARG:NH1	2.49	0.46
33:a:194:G:H2'	33:a:195:G:H8	1.81	0.46
33:a:754:G:H3'	33:a:755:G:H8	1.80	0.46
33:a:1302:C:H5''	45:m:87:ARG:HH21	1.81	0.46
2:B:31:C:H2'	2:B:53:A:H61	1.80	0.46
33:a:670:A:H2	43:k:121:CYS:H	1.62	0.46
40:h:95:VAL:HG11	40:h:128:THR:HG23	1.98	0.46
1:A:766:G:N2	1:A:783:A:O2'	2.48	0.45
1:A:1104:C:H2'	1:A:1105:G:C8	2.51	0.45
1:A:2379:A:N6	1:A:2411:C:O2	2.48	0.45
3:C:21:ASN:HB3	3:C:24:LEU:HG	1.97	0.45
9:I:86:ILE:HG21	9:I:98:VAL:HG21	1.98	0.45
33:a:175:A:H61	33:a:188:G:H2'	1.81	0.45
33:a:1257:G:N2	33:a:1267:G:N3	2.63	0.45
38:f:88:LEU:HD22	50:r:64:TYR:HD2	1.81	0.45
1:A:92:A:O2'	1:A:93:A:O4'	2.33	0.45
1:A:795:G:N2	1:A:819:A:OP1	2.48	0.45
1:A:1048:G:C6	9:I:70:GLU:HG3	2.52	0.45
4:D:33:ASN:HB2	4:D:96:ILE:HG13	1.97	0.45
33:a:1494:A:H5''	33:a:1502:G:H5'	1.97	0.45
44:l:110:ARG:HG2	44:l:117:TYR:HB2	1.97	0.45
53:u:52:ALA:HB1	53:u:55:ARG:HH21	1.81	0.45
1:A:387:G:OP2	24:X:10:LYS:NZ	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:48:U:H4'	15:O:99:HIS:HB3	1.97	0.45
33:a:884:G:O2'	33:a:900:A:N6	2.49	0.45
33:a:1263:A:OP2	33:a:1264:G:N2	2.48	0.45
36:d:9:CYS:HB3	36:d:32:CYS:HB3	1.71	0.45
38:f:99:GLN:HG2	50:r:24:LYS:HB3	1.97	0.45
42:j:8:ILE:HD11	42:j:76:ILE:HG23	1.98	0.45
53:u:53:VAL:O	53:u:57:ALA:N	2.43	0.45
1:A:733:C:O2'	1:A:1649:G:OP1	2.32	0.45
1:A:899:A:C8	13:M:13:MET:HG2	2.51	0.45
1:A:2238:G:OP1	13:M:82:ARG:NH1	2.49	0.45
1:A:2676:U:OP1	1:A:2706:G:N1	2.40	0.45
4:D:4:GLY:HA3	4:D:204:ARG:HB3	1.97	0.45
33:a:593:U:H2'	33:a:594:G:C8	2.52	0.45
33:a:774:A:H61	33:a:794:G:H3'	1.81	0.45
33:a:1123:C:H42	33:a:1137:G:H1	1.63	0.45
52:t:62:ALA:HB1	52:t:69:LYS:HA	1.97	0.45
1:A:1047:A:H2'	9:I:60:THR:HG21	1.99	0.45
1:A:2559:A:N7	4:D:150:GLN:HB2	2.31	0.45
2:B:98:G:H1	22:V:16:LYS:HB2	1.81	0.45
4:D:5:VAL:HG12	4:D:203:VAL:HB	1.99	0.45
4:D:148:GLN:NE2	4:D:152:PRO:HD3	2.25	0.45
25:Y:18:ILE:O	25:Y:22:LEU:N	2.48	0.45
33:a:139:G:N2	33:a:172:C:N3	2.65	0.45
35:c:187:TYR:O	35:c:198:VAL:N	2.49	0.45
46:n:64:CYS:SG	46:n:65:ARG:N	2.89	0.45
1:A:221:A:O2'	1:A:266:G:N7	2.45	0.45
2:B:66:A:H1'	2:B:67:U:H5	1.82	0.45
5:E:20:GLY:O	5:E:113:ARG:NH2	2.39	0.45
7:G:3:ARG:HD3	7:G:5:ALA:H	1.82	0.45
33:a:135:A:H1'	33:a:176:C:C4	2.51	0.45
1:A:190:A:H5''	1:A:204:A:H61	1.81	0.45
1:A:1461:G:N2	1:A:1503:G:N7	2.65	0.45
1:A:1462:G:O2'	1:A:1501:G:O6	2.29	0.45
33:a:474:U:H2'	33:a:475:G:C8	2.51	0.45
33:a:1310:G:OP1	46:n:28:LYS:NZ	2.46	0.45
37:e:54:ALA:HB2	37:e:63:LYS:HD3	1.99	0.45
41:i:51:PRO:HG2	41:i:83:ILE:HD13	1.99	0.45
43:k:22:HIS:HB2	43:k:33:THR:HB	1.99	0.45
52:t:4:THR:HG23	52:t:7:ALA:H	1.81	0.45
4:D:88:GLU:N	4:D:88:GLU:OE1	2.50	0.45
8:H:44:VAL:HA	8:H:47:PHE:HD2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:b:135:LEU:O	34:b:139:ARG:N	2.46	0.45
1:A:247:G:OP2	1:A:249:C:N4	2.47	0.45
1:A:1061:G:N2	9:I:6:GLN:OE1	2.50	0.45
1:A:1276:C:H2'	1:A:1277:A:H8	1.82	0.45
1:A:2760:U:H5''	4:D:169:ARG:HG2	1.99	0.45
2:B:49:C:O5'	15:O:101:ARG:NH2	2.50	0.45
8:H:5:LEU:HD22	8:H:14:ASN:H	1.80	0.45
11:K:104:ARG:HH11	11:K:107:ARG:NH1	2.14	0.45
15:O:28:CYS:N	15:O:39:GLN:O	2.50	0.45
33:a:645:C:N4	33:a:746:G:O2'	2.49	0.45
33:a:1283:A:C5	39:g:35:LYS:HD3	2.52	0.45
37:e:159:LYS:HE3	40:h:114:ARG:HH11	1.81	0.45
39:g:16:PRO:HG3	41:i:43:THR:HB	1.99	0.45
42:j:84:VAL:HB	42:j:100:ILE:HG12	1.98	0.45
1:A:77:U:O2'	25:Y:6:ARG:NH2	2.50	0.45
1:A:767:A:H2'	1:A:768:G:H8	1.82	0.45
1:A:2228:A:H2'	1:A:2229:G:C8	2.52	0.45
33:a:250:U:H2'	33:a:251:G:H8	1.81	0.45
33:a:1200:G:H2'	33:a:1201:G:H8	1.82	0.45
33:a:1509:G:H2'	33:a:1510:G:C8	2.52	0.45
34:b:73:LYS:HB3	34:b:76:ALA:HB3	1.99	0.45
46:n:50:LYS:HD3	51:s:14:HIS:HB2	1.98	0.45
1:A:471:A:H4'	21:U:41:ILE:HD13	1.98	0.44
1:A:1020:C:H5	1:A:1114:G:H1	1.64	0.44
1:A:1621:G:N1	1:A:1624:A:OP2	2.43	0.44
18:R:35:PHE:O	18:R:59:VAL:N	2.46	0.44
33:a:384:U:H4'	48:p:28:ARG:HH21	1.82	0.44
33:a:612:C:N4	33:a:615:A:OP2	2.36	0.44
33:a:1119:U:H3	42:j:103:GLY:HA3	1.82	0.44
33:a:1234:U:C2	39:g:116:MET:HG2	2.52	0.44
33:a:1312:A:OP1	51:s:7:LYS:NZ	2.41	0.44
49:q:20:MET:SD	49:q:20:MET:N	2.91	0.44
49:q:63:THR:HG23	49:q:79:VAL:HB	1.98	0.44
1:A:1132:C:H5''	1:A:1133:A:H8	1.82	0.44
1:A:1350:U:O2'	1:A:1796:A:N3	2.43	0.44
1:A:2150:U:H5'	1:A:2152:C:H41	1.82	0.44
4:D:102:GLN:CG	4:D:105:GLN:NE2	2.80	0.44
13:M:65:TRP:HB2	13:M:105:GLU:HB2	1.99	0.44
33:a:1323:G:O5'	45:m:25:VAL:N	2.44	0.44
37:e:41:GLY:HA3	37:e:118:VAL:HB	1.98	0.44
1:A:84:A:OP2	21:U:5:ARG:NH2	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1790:A:H8	1:A:1809:G:H21	1.64	0.44
33:a:99:G:OP1	52:t:17:ARG:NH2	2.50	0.44
33:a:148:G:H1	33:a:161:C:H42	1.64	0.44
36:d:78:GLU:O	36:d:82:ARG:N	2.48	0.44
1:A:72:A:H61	25:Y:58:ASN:HD22	1.65	0.44
1:A:1647:U:OP2	4:D:141:ARG:HG3	2.16	0.44
6:F:57:LEU:O	6:F:61:THR:OG1	2.31	0.44
14:N:71:ARG:HA	14:N:71:ARG:HD2	1.76	0.44
33:a:1315:U:O3'	45:m:87:ARG:NH1	2.51	0.44
33:a:1406:C:OP1	44:l:54:ARG:NH2	2.51	0.44
34:b:163:VAL:HG12	34:b:185:GLY:HA3	2.00	0.44
36:d:97:ARG:HD3	36:d:99:ASP:HB3	1.98	0.44
1:A:519:A:H5''	10:J:113:PRO:HG3	2.00	0.44
1:A:641:G:N7	1:A:642:U:N3	2.65	0.44
1:A:952:G:H21	1:A:2237:G:H1	1.66	0.44
3:C:132:LEU:HD23	3:C:135:ILE:HD12	1.98	0.44
6:F:44:VAL:HG21	6:F:85:ILE:HG22	2.00	0.44
17:Q:90:ILE:HA	18:R:11:GLN:HE22	1.83	0.44
22:V:23:ARG:HH11	22:V:90:MET:HB2	1.81	0.44
33:a:645:C:N4	33:a:747:A:OP2	2.51	0.44
35:c:6:HIS:HE1	46:n:98:LYS:HD2	1.83	0.44
46:n:79:LEU:HD13	46:n:83:LYS:HG2	2.00	0.44
1:A:2835:G:O2'	1:A:2854:G:N2	2.38	0.44
2:B:8:C:O2'	15:O:26:ARG:NH2	2.46	0.44
40:h:101:VAL:HG22	40:h:112:THR:HB	1.99	0.44
1:A:869:G:C5	1:A:870:G:H1'	2.52	0.44
1:A:1186:U:H1'	17:Q:4:VAL:HB	2.00	0.44
1:A:1237:G:N7	12:L:18:ARG:NH2	2.66	0.44
6:F:133:LYS:NZ	6:F:154:ILE:H	2.15	0.44
24:X:2:SER:OG	24:X:3:ARG:N	2.51	0.44
33:a:1215:G:H4'	51:s:56:GLN:H	1.82	0.44
33:a:1322:C:H3'	45:m:20:THR:HG23	2.00	0.44
43:k:26:SER:OG	43:k:27:PHE:N	2.50	0.44
1:A:548:U:OP1	10:J:112:ASN:HB3	2.18	0.44
1:A:2267:G:O2'	1:A:2375:A:N1	2.49	0.44
4:D:137:SER:HB3	4:D:138:VAL:H	1.68	0.44
5:E:26:LEU:HD11	5:E:99:MET:HG3	1.99	0.44
7:G:11:LEU:HD11	7:G:17:ILE:HD11	1.99	0.44
11:K:1:MET:HB2	11:K:8:LEU:HD22	2.00	0.44
11:K:24:VAL:HG13	11:K:33:ALA:HB2	2.00	0.44
14:N:1:MET:HE3	14:N:1:MET:HB2	1.74	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:c:112:ASP:HB2	35:c:115:LEU:HD12	2.00	0.44
40:h:104:VAL:HG22	40:h:125:VAL:HA	2.00	0.44
1:A:2373:U:H4'	23:W:56:ASP:HA	2.00	0.44
2:B:77:U:OP1	22:V:23:ARG:NH2	2.44	0.44
9:I:92:ARG:HB3	9:I:96:GLN:HB3	1.99	0.44
34:b:19:GLN:HA	34:b:38:ILE:HG22	2.00	0.44
34:b:144:LEU:HB2	34:b:148:LEU:HD12	1.99	0.44
43:k:20:ILE:HA	43:k:83:ASP:HB2	1.98	0.44
46:n:69:ARG:HD2	46:n:70:PRO:HD2	2.00	0.44
47:o:26:GLU:OE2	47:o:77:ARG:NH1	2.45	0.44
1:A:1799:U:O2	3:C:44:ASN:ND2	2.39	0.43
33:a:188:G:O2'	52:t:63:ASP:OD2	2.33	0.43
33:a:613:U:N3	36:d:131:ASN:OD1	2.47	0.43
33:a:1512:A:H2'	33:a:1513:A:C8	2.53	0.43
35:c:66:ILE:HD12	35:c:99:VAL:HG21	1.99	0.43
39:g:35:LYS:HG3	39:g:37:ALA:H	1.83	0.43
41:i:35:LEU:HG	41:i:45:ARG:HE	1.83	0.43
46:n:63:ARG:HA	46:n:70:PRO:HA	1.99	0.43
1:A:938:C:H2'	1:A:939:G:C8	2.53	0.43
1:A:1723:G:N2	1:A:1724:U:O2	2.51	0.43
2:B:66:A:OP2	2:B:108:C:N4	2.37	0.43
9:I:108:GLU:HA	9:I:111:LYS:HE2	1.99	0.43
12:L:78:ARG:HG3	12:L:113:SER:HB3	1.99	0.43
41:i:23:PRO:HA	41:i:61:PHE:HA	2.00	0.43
1:A:1018:A:N6	1:A:1115:G:H2'	2.33	0.43
1:A:2280:C:H2'	1:A:2281:G:H8	1.82	0.43
33:a:294:A:C5	33:a:295:G:H1'	2.53	0.43
33:a:512:C:H2'	33:a:524:G:H1'	2.00	0.43
1:A:2112:G:N2	1:A:2159:U:OP1	2.52	0.43
1:A:2186:A:OP1	24:X:37:ARG:NH1	2.51	0.43
4:D:60:ARG:HD2	4:D:60:ARG:HA	1.77	0.43
33:a:263:U:H2'	33:a:264:A:C8	2.53	0.43
33:a:356:G:N1	33:a:359:U:OP2	2.45	0.43
42:j:36:VAL:HG22	42:j:76:ILE:HG22	2.01	0.43
43:k:70:ALA:HA	43:k:73:ALA:HB3	1.99	0.43
52:t:10:ARG:HA	52:t:13:GLN:HB3	2.00	0.43
1:A:1897:G:H3'	1:A:1898:U:H5''	1.98	0.43
1:A:2279:G:H2'	1:A:2280:C:C6	2.54	0.43
3:C:145:GLU:HB2	3:C:188:CYS:HB2	2.01	0.43
6:F:134:GLU:HG2	6:F:136:ILE:H	1.82	0.43
23:W:54:GLY:N	23:W:58:THR:O	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:a:1407:A:H2	33:a:1481:G:H22	1.64	0.43
45:m:14:HIS:CD2	45:m:15:THR:H	2.37	0.43
1:A:2119:U:H3	1:A:2146:G:H1'	1.82	0.43
2:B:104:A:C5	2:B:105:G:H1'	2.54	0.43
3:C:130:MET:HE3	3:C:130:MET:HB2	1.80	0.43
6:F:38:MET:O	6:F:40:LEU:N	2.52	0.43
33:a:903:A:N3	33:a:1407:A:O2'	2.45	0.43
40:h:50:GLN:HB3	40:h:60:SER:HB2	2.01	0.43
49:q:65:ARG:HH11	49:q:66:GLU:H	1.65	0.43
1:A:1406:A:H61	1:A:1481:A:H62	1.66	0.43
1:A:1518:C:N4	1:A:1519:G:O6	2.52	0.43
33:a:516:C:H1'	33:a:530:C:H5''	2.01	0.43
34:b:162:PHE:HD1	34:b:184:ILE:HG23	1.84	0.43
35:c:37:LEU:HD13	46:n:66:LEU:HG	2.00	0.43
1:A:589:G:H21	5:E:99:MET:HE1	1.83	0.43
1:A:896:G:H5'	13:M:23:ARG:HB3	2.01	0.43
21:U:14:ALA:HA	21:U:18:LYS:HE2	2.00	0.43
29:3:6:ARG:HB3	29:3:48:ALA:HA	2.01	0.43
33:a:1311:C:N4	46:n:50:LYS:HG2	2.34	0.43
41:i:116:VAL:HG21	42:j:62:ARG:HB2	2.01	0.43
49:q:69:PRO:HA	49:q:75:ALA:HA	2.01	0.43
50:r:26:LEU:HD21	50:r:67:LEU:HD22	2.01	0.43
1:A:363:G:O2'	1:A:391:G:O6	2.34	0.43
1:A:1119:A:H61	1:A:2478:U:H5''	1.83	0.43
1:A:1488:G:H5''	3:C:95:LYS:HD2	2.00	0.43
41:i:83:ILE:HG23	41:i:84:THR:HG23	2.01	0.43
44:l:25:GLN:OE1	44:l:59:ASN:ND2	2.52	0.43
46:n:64:CYS:HB3	46:n:68:GLY:H	1.83	0.43
47:o:22:THR:HA	47:o:27:VAL:HG21	2.00	0.43
1:A:912:C:H2'	1:A:913:A:C8	2.54	0.43
1:A:1048:G:N2	9:I:71:THR:O	2.52	0.43
1:A:1051:U:H5'	9:I:57:VAL:HB	2.01	0.43
1:A:2489:G:H5''	1:A:2490:A:H5''	2.00	0.43
1:A:2550:U:O2'	1:A:2552:A:N7	2.44	0.43
33:a:24:U:O3'	33:a:518:G:O2'	2.36	0.43
33:a:67:C:H1'	33:a:166:A:H1'	2.00	0.43
33:a:661:G:H2'	33:a:662:G:C8	2.54	0.43
33:a:722:A:N7	47:o:54:ARG:NH2	2.66	0.43
34:b:56:PHE:HD1	34:b:59:ARG:HH21	1.66	0.43
53:u:48:LYS:O	53:u:52:ALA:N	2.47	0.43
1:A:938:C:H2'	1:A:939:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:61:LEU:O	31:5:13:ARG:NH1	2.52	0.42
22:V:75:VAL:HG13	22:V:94:PHE:HB3	2.01	0.42
33:a:40:C:H2'	33:a:41:G:C8	2.53	0.42
33:a:197:G:O2'	33:a:460:A:N1	2.52	0.42
33:a:1290:C:O2'	45:m:12:ASN:OD1	2.37	0.42
41:i:120:LYS:HG3	41:i:121:ALA:H	1.83	0.42
46:n:80:SER:OG	46:n:81:ARG:N	2.47	0.42
47:o:49:ASP:O	47:o:53:ARG:NH1	2.52	0.42
1:A:742:A:H3'	30:4:1:MET:HE3	2.01	0.42
1:A:1174:G:OP1	18:R:85:LYS:NZ	2.34	0.42
1:A:1276:C:H2'	1:A:1277:A:C8	2.54	0.42
1:A:2633:C:OP2	1:A:2719:G:O2'	2.37	0.42
1:A:2662:A:H4'	11:K:29:HIS:HB2	2.01	0.42
23:W:38:VAL:HG12	23:W:40:LEU:HB2	2.00	0.42
33:a:538:G:N2	33:a:543:C:O3'	2.52	0.42
37:e:91:GLY:HA3	37:e:136:ASN:HD21	1.84	0.42
43:k:26:SER:HA	43:k:89:PRO:HD2	2.00	0.42
1:A:568:G:OP1	1:A:1242:U:O2'	2.30	0.42
1:A:2582:G:N2	1:A:2585:A:OP2	2.41	0.42
3:C:225:MET:HB3	3:C:229:ASP:HB2	2.01	0.42
5:E:175:ASP:OD1	5:E:178:SER:OG	2.23	0.42
11:K:13:ASN:HB2	11:K:97:ARG:H	1.83	0.42
43:k:72:GLN:NE2	43:k:103:CYS:SG	2.92	0.42
44:l:34:CYS:HA	44:l:55:VAL:HG12	2.01	0.42
1:A:835:A:N1	1:A:922:G:N1	2.56	0.42
1:A:943:G:OP2	13:M:18:ARG:NH2	2.49	0.42
1:A:2079:U:OP1	1:A:2186:A:O2'	2.31	0.42
19:S:77:ASN:HB2	19:S:102:HIS:HB2	2.01	0.42
22:V:162:LEU:HD23	22:V:165:LEU:HD13	2.00	0.42
26:Z:16:LEU:HB2	26:Z:19:HIS:CD2	2.54	0.42
33:a:658:G:O2'	33:a:660:G:OP2	2.30	0.42
33:a:1012:G:OP1	33:a:1032:U:O2'	2.30	0.42
52:t:32:ILE:HA	52:t:35:VAL:HG22	2.00	0.42
1:A:1068:C:O2	1:A:1069:C:N4	2.48	0.42
1:A:1575:C:H3'	1:A:1576:A:H8	1.84	0.42
3:C:7:LYS:HA	3:C:8:PRO:HD3	1.88	0.42
4:D:152:PRO:HG3	4:D:156:PHE:CZ	2.55	0.42
22:V:106:HIS:CD2	22:V:135:GLU:HB3	2.54	0.42
33:a:77:G:H2'	33:a:78:A:H8	1.85	0.42
33:a:371:G:H5'	48:p:5:ARG:NH1	2.35	0.42
33:a:496:A:OP1	44:l:115:SER:N	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:a:739:U:OP1	33:a:845:U:O2'	2.32	0.42
36:d:73:ARG:HD3	36:d:73:ARG:HA	1.78	0.42
1:A:107:G:H21	1:A:340:A:H62	1.68	0.42
1:A:1807:U:H5	3:C:177:ARG:HH21	1.67	0.42
18:R:14:VAL:HG13	18:R:98:ILE:HG13	2.00	0.42
33:a:59:A:H5''	33:a:381:U:H5''	2.02	0.42
33:a:438:U:H2'	33:a:439:G:C8	2.55	0.42
33:a:597:U:H2'	33:a:598:G:C8	2.55	0.42
33:a:775:A:H5'	33:a:776:A:C8	2.54	0.42
33:a:1431:A:H2'	33:a:1432:G:H8	1.84	0.42
1:A:1515:A:C5	1:A:1516:G:H1'	2.54	0.42
1:A:2038:U:H3'	1:A:2565:G:H5''	2.00	0.42
13:M:34:LEU:HD13	13:M:118:PHE:HB3	2.02	0.42
33:a:831:G:H2'	33:a:832:A:C8	2.55	0.42
33:a:1444:G:H21	33:a:1447:A:H2	1.67	0.42
38:f:90:MET:HE1	50:r:23:TYR:HE1	1.84	0.42
50:r:62:ALA:HB1	50:r:67:LEU:HB2	2.01	0.42
1:A:2519:G:N2	1:A:2650:G:O2'	2.52	0.42
13:M:68:VAL:HG12	13:M:101:LYS:HE3	2.01	0.42
24:X:43:GLU:OE1	24:X:45:ARG:NH2	2.52	0.42
33:a:61:G:H1'	33:a:62:U:H5'	2.01	0.42
40:h:46:ILE:HG22	40:h:63:LEU:HA	2.02	0.42
40:h:81:PRO:O	40:h:84:ARG:NH1	2.52	0.42
47:o:61:ASN:O	47:o:65:LYS:N	2.45	0.42
52:t:67:ILE:HD12	52:t:71:LYS:HD2	2.02	0.42
4:D:10:CYS:HB3	4:D:27:VAL:HG23	2.02	0.42
4:D:172:VAL:CG2	4:D:194:PRO:HD3	2.50	0.42
9:I:61:VAL:HG13	9:I:67:PHE:HE1	1.85	0.42
12:L:59:ARG:HA	31:5:13:ARG:NH2	2.33	0.42
17:Q:27:ALA:HB1	17:Q:31:VAL:HG22	2.01	0.42
33:a:201:C:H42	33:a:207:A:H2	1.67	0.42
33:a:1452:G:H4'	52:t:23:SER:HB2	2.02	0.42
36:d:143:VAL:O	36:d:180:GLY:N	2.41	0.42
1:A:1483:A:N3	1:A:1567:C:O2'	2.51	0.42
1:A:1659:A:H5''	1:A:2537:G:OP1	2.20	0.42
7:G:123:SER:HB2	7:G:126:ASP:HB2	2.02	0.42
11:K:38:ILE:HD11	11:K:111:PHE:CZ	2.54	0.42
13:M:21:ALA:HB2	13:M:98:GLN:HB2	2.02	0.42
33:a:594:G:OP1	40:h:88:SER:OG	2.34	0.42
33:a:619:U:H2'	33:a:620:G:C8	2.55	0.42
39:g:60:GLU:OE2	39:g:64:LYS:NZ	2.39	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1658:A:H5''	11:K:5:GLN:HE21	1.83	0.41
1:A:2260:A:H2'	1:A:2261:A:C8	2.55	0.41
1:A:2796:A:OP1	1:A:2874:C:N4	2.52	0.41
3:C:98:ASP:OD1	3:C:98:ASP:N	2.50	0.41
33:a:67:C:H2'	33:a:68:G:C8	2.54	0.41
34:b:181:ILE:HA	34:b:182:PRO:HD3	1.95	0.41
1:A:633:A:N6	1:A:2357:G:O4'	2.53	0.41
4:D:102:GLN:HG3	4:D:105:GLN:NE2	2.35	0.41
4:D:179:ARG:HB3	4:D:188:LEU:HB2	2.02	0.41
11:K:7:MET:HE2	11:K:20:MET:HB2	2.02	0.41
15:O:25:VAL:HG21	15:O:86:VAL:HG11	2.02	0.41
30:4:22:MET:HG3	30:4:28:ARG:HG3	2.03	0.41
33:a:499:G:H1	33:a:500:G:H21	1.69	0.41
33:a:507:U:O4	33:a:532:A:N6	2.53	0.41
33:a:1249:G:O2'	33:a:1252:G:N3	2.46	0.41
34:b:104:TYR:HA	34:b:107:ILE:HG13	2.02	0.41
1:A:13:A:O4'	1:A:517:A:N6	2.53	0.41
1:A:288:A:O2'	1:A:289:G:O4'	2.29	0.41
1:A:2103:G:H22	1:A:2149:A:H8	1.68	0.41
2:B:66:A:O2'	2:B:67:U:O5'	2.34	0.41
2:B:76:G:OP1	22:V:11:ARG:NH1	2.53	0.41
7:G:42:GLU:OE2	7:G:68:THR:OG1	2.26	0.41
19:S:24:ILE:HD13	19:S:36:LEU:HD11	2.03	0.41
26:Z:16:LEU:HB2	26:Z:19:HIS:HD2	1.86	0.41
33:a:216:U:H2'	33:a:217:A:C8	2.55	0.41
33:a:1122:C:O2	33:a:1138:G:N1	2.54	0.41
46:n:83:LYS:HG3	46:n:87:ALA:HB2	2.01	0.41
47:o:21:ASP:OD1	47:o:24:SER:N	2.50	0.41
47:o:50:HIS:HA	47:o:53:ARG:HD3	2.02	0.41
1:A:740:A:OP1	1:A:1605:C:N4	2.45	0.41
1:A:2017:A:N3	1:A:2486:C:H5''	2.34	0.41
6:F:104:LEU:HA	6:F:108:LEU:HB2	2.01	0.41
7:G:18:LYS:HD2	7:G:25:SER:HB3	2.02	0.41
33:a:54:C:H2'	33:a:346:C:H41	1.84	0.41
33:a:931:A:H62	33:a:1372:C:H42	1.67	0.41
33:a:1018:G:H2'	33:a:1019:U:C2	2.55	0.41
33:a:1043:U:O2'	33:a:1208:C:N3	2.52	0.41
33:a:1216:G:N7	51:s:55:ARG:HG2	2.35	0.41
33:a:1376:C:H4'	39:g:79:ARG:HG2	2.02	0.41
34:b:218:ALA:HA	34:b:221:VAL:HG12	2.02	0.41
45:m:20:THR:O	45:m:22:ILE:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:r:41:PRO:HB2	50:r:43:ARG:HG3	2.01	0.41
1:A:1335:U:H3	1:A:1588:A:H61	1.68	0.41
4:D:56:ARG:HD2	4:D:56:ARG:HA	1.88	0.41
4:D:118:PHE:CD1	4:D:118:PHE:C	2.99	0.41
5:E:107:ILE:HA	12:L:1:MET:HE1	2.01	0.41
6:F:156:LEU:HD22	6:F:156:LEU:HA	1.94	0.41
7:G:18:LYS:HB3	7:G:25:SER:HB3	2.02	0.41
7:G:154:LYS:HD3	7:G:156:LYS:HE2	2.01	0.41
11:K:78:ARG:HB3	16:P:72:GLU:HB2	2.02	0.41
33:a:9:G:O2'	36:d:206:LYS:NZ	2.54	0.41
33:a:580:U:O2	40:h:4:GLN:NE2	2.54	0.41
33:a:585:C:OP1	40:h:31:LYS:NZ	2.51	0.41
33:a:706:A:N1	33:a:707:G:N2	2.69	0.41
33:a:1251:U:O2'	33:a:1354:A:OP2	2.26	0.41
33:a:1315:U:H3'	51:s:69:HIS:HE1	1.86	0.41
34:b:30:PHE:HA	34:b:42:ASN:HB2	2.02	0.41
48:p:3:THR:HG21	48:p:5:ARG:NH1	2.36	0.41
1:A:583:U:H2'	1:A:584:U:C6	2.56	0.41
1:A:803:U:H2'	1:A:804:C:C6	2.56	0.41
1:A:1119:A:N6	1:A:2478:U:H5''	2.35	0.41
3:C:235:GLY:HA3	3:C:239:THR:HG21	2.03	0.41
6:F:162:THR:OG1	6:F:164:ASP:OD1	2.30	0.41
7:G:151:GLU:HB3	7:G:155:GLY:H	1.85	0.41
12:L:55:GLN:O	12:L:60:ARG:NH1	2.54	0.41
13:M:1:MET:HE2	13:M:45:ARG:HB3	2.01	0.41
33:a:1002:U:O2'	33:a:1013:G:O6	2.38	0.41
33:a:1233:A:OP2	33:a:1292:U:O2'	2.37	0.41
40:h:76:LYS:H	40:h:128:THR:HB	1.85	0.41
45:m:77:ILE:HG22	45:m:81:MET:HE2	2.02	0.41
48:p:44:THR:HG22	48:p:45:GLY:H	1.86	0.41
1:A:823:A:H2'	1:A:824:G:C8	2.56	0.41
1:A:2430:C:H2'	1:A:2431:G:C8	2.56	0.41
8:H:60:GLU:HA	8:H:63:ALA:HB3	2.01	0.41
15:O:40:VAL:HB	15:O:49:LEU:HD22	2.03	0.41
26:Z:42:GLU:H	26:Z:42:GLU:HG2	1.73	0.41
33:a:828:U:H2'	33:a:829:G:C8	2.49	0.41
38:f:38:ARG:HH11	38:f:61:LEU:HD21	1.86	0.41
40:h:14:ILE:O	40:h:18:GLN:N	2.54	0.41
50:r:63:ARG:HB3	50:r:70:TYR:CE1	2.55	0.41
1:A:1779:G:O2'	1:A:1817:C:OP1	2.35	0.41
2:B:3:C:H2'	2:B:4:U:H6	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:98:VAL:C	4:D:100:LEU:N	2.78	0.41
11:K:1:MET:HB3	11:K:2:ILE:H	1.63	0.41
29:3:6:ARG:HG3	29:3:16:PHE:CD1	2.55	0.41
33:a:619:U:H2'	33:a:620:G:H8	1.85	0.41
33:a:721:G:N2	33:a:724:G:OP2	2.41	0.41
1:A:583:U:O2'	31:5:64:ARG:OXT	2.32	0.41
1:A:845:G:H2'	1:A:846:G:C8	2.56	0.41
1:A:1050:U:C4	9:I:75:PRO:HA	2.56	0.41
1:A:1060:A:H62	1:A:1087:U:H5'	1.85	0.41
1:A:1309:A:OP1	19:S:11:ARG:NH2	2.54	0.41
1:A:1395:U:H2'	1:A:1396:G:C8	2.56	0.41
1:A:2114:G:N2	1:A:2150:U:OP1	2.50	0.41
1:A:2327:C:H2'	1:A:2328:G:C8	2.54	0.41
1:A:2334:C:O2	1:A:2357:G:N2	2.53	0.41
4:D:121:THR:HB	4:D:127:PHE:CD2	2.56	0.41
22:V:160:VAL:HG23	22:V:164:ASP:HB3	2.02	0.41
33:a:41:G:H2'	33:a:42:G:C8	2.55	0.41
33:a:496:A:OP1	44:l:114:ARG:N	2.54	0.41
33:a:759:G:H3'	33:a:806:G:N2	2.36	0.41
33:a:1141:C:H5''	41:i:7:TYR:HB2	2.02	0.41
34:b:6:MET:HE3	34:b:10:LEU:HB2	2.02	0.41
34:b:191:SER:OG	34:b:192:SER:N	2.54	0.41
36:d:104:ARG:HD3	36:d:170:TRP:HZ2	1.85	0.41
40:h:15:ARG:HD3	40:h:75:VAL:N	2.34	0.41
47:o:63:ARG:O	47:o:67:LEU:N	2.49	0.41
1:A:155:U:H2'	1:A:156:A:C8	2.56	0.41
1:A:1263:U:OP2	1:A:1635:G:O2'	2.29	0.41
1:A:2775:A:H2'	1:A:2776:C:C6	2.56	0.41
11:K:35:ILE:HG13	11:K:65:THR:HG23	2.03	0.41
11:K:66:LYS:HE2	11:K:66:LYS:HB3	1.95	0.41
50:r:63:ARG:HB3	50:r:70:TYR:HE1	1.86	0.41
1:A:1349:C:O2'	1:A:1797:A:O2'	2.36	0.40
1:A:1602:C:H5'	30:4:7:PRO:HG3	2.02	0.40
1:A:2003:U:O2'	28:2:4:GLN:O	2.36	0.40
1:A:2026:U:H2'	1:A:2027:G:C8	2.56	0.40
1:A:2125:G:O2'	1:A:2141:G:N2	2.54	0.40
1:A:2364:A:O2'	15:O:116:PHE:OXT	2.39	0.40
4:D:38:PHE:HE1	4:D:85:LEU:CD1	2.34	0.40
6:F:123:ASP:O	6:F:125:ARG:N	2.49	0.40
13:M:3:GLN:HG2	13:M:93:TRP:CD1	2.57	0.40
30:4:24:THR:HG23	30:4:27:GLY:H	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:a:446:A:H1'	48:p:70:ARG:HE	1.86	0.40
33:a:671:U:O2'	43:k:121:CYS:SG	2.77	0.40
35:c:88:ARG:O	35:c:92:THR:OG1	2.33	0.40
35:c:149:ILE:HG12	35:c:202:ILE:HA	2.03	0.40
1:A:906:A:H5''	1:A:2255:A:H61	1.86	0.40
16:P:63:ARG:NH2	16:P:72:GLU:OE2	2.48	0.40
17:Q:41:LYS:HD2	17:Q:45:TYR:CZ	2.55	0.40
20:T:52:VAL:HG11	20:T:92:LEU:HD21	2.04	0.40
33:a:19:A:H5''	37:e:92:ALA:HB3	2.03	0.40
33:a:526:A:O4'	33:a:1049:A:N6	2.54	0.40
33:a:1094:U:O5'	34:b:95:ARG:NH2	2.54	0.40
33:a:1313:A:N1	51:s:3:ARG:CG	2.84	0.40
46:n:42:TRP:HE1	51:s:13:LEU:HD21	1.87	0.40
1:A:617:A:N6	12:L:112:LEU:O	2.49	0.40
1:A:950:A:H2'	1:A:952:G:H5'	2.03	0.40
1:A:1174:G:H5''	18:R:83:HIS:CE1	2.56	0.40
4:D:105:GLN:HE21	4:D:105:GLN:HB2	1.53	0.40
11:K:76:ILE:HD11	11:K:78:ARG:HH11	1.86	0.40
33:a:40:C:H2'	33:a:41:G:H8	1.86	0.40
33:a:1458:U:H2'	33:a:1459:A:C8	2.56	0.40
41:i:114:LYS:HZ2	41:i:120:LYS:HD2	1.86	0.40
45:m:85:CYS:HB2	51:s:73:GLU:HB3	2.03	0.40
1:A:2280:C:H2'	1:A:2281:G:C8	2.57	0.40
1:A:2551:A:OP1	1:A:2635:G:O2'	2.32	0.40
6:F:29:PRO:HD2	6:F:169:LEU:HG	2.02	0.40
10:J:98:GLU:HB2	10:J:124:VAL:HG23	2.01	0.40
11:K:104:ARG:NH2	16:P:33:VAL:HB	2.35	0.40
15:O:29:VAL:HG12	15:O:38:ALA:HA	2.04	0.40
33:a:107:G:O6	33:a:307:A:N6	2.54	0.40
33:a:290:U:O2'	33:a:550:C:O2	2.35	0.40
33:a:564:G:O6	33:a:859:A:N6	2.54	0.40
33:a:651:U:H2'	33:a:652:A:C8	2.56	0.40
33:a:1145:A:H4'	42:j:43:PRO:HB3	2.03	0.40
1:A:226:A:N1	1:A:409:C:O2'	2.50	0.40
1:A:1395:U:H2'	1:A:1396:G:H8	1.87	0.40
4:D:110:THR:HB	4:D:171:THR:OG1	2.22	0.40
16:P:16:LYS:HE3	16:P:18:ILE:HD11	2.04	0.40
22:V:136:VAL:HG12	22:V:173:LEU:HD13	2.04	0.40
24:X:10:LYS:HE3	24:X:54:LYS:HD3	2.03	0.40
33:a:303:A:H2'	33:a:304:G:C8	2.57	0.40
34:b:29:LYS:O	34:b:45:LYS:NZ	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:q:15:VAL:HA	49:q:26:VAL:HG12	2.04	0.40
49:q:67:THR:OG1	49:q:68:ARG:N	2.52	0.40
51:s:2:PRO:HB2	51:s:3:ARG:H	1.68	0.40
52:t:68:HIS:HD1	52:t:70:ASN:H	1.69	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	
3	C	269/271 (99%)	239 (89%)	28 (10%)	2 (1%)	18	48
4	D	205/207 (99%)	176 (86%)	19 (9%)	10 (5%)	1	6
5	E	197/199 (99%)	191 (97%)	6 (3%)	0	100	100
6	F	172/174 (99%)	138 (80%)	34 (20%)	0	100	100
7	G	167/169 (99%)	152 (91%)	15 (9%)	0	100	100
8	H	76/78 (97%)	70 (92%)	6 (8%)	0	100	100
9	I	138/140 (99%)	118 (86%)	20 (14%)	0	100	100
10	J	139/141 (99%)	129 (93%)	10 (7%)	0	100	100
11	K	118/120 (98%)	111 (94%)	7 (6%)	0	100	100
12	L	142/144 (99%)	132 (93%)	10 (7%)	0	100	100
13	M	134/136 (98%)	127 (95%)	7 (5%)	0	100	100
14	N	118/120 (98%)	109 (92%)	9 (8%)	0	100	100
15	O	113/115 (98%)	96 (85%)	17 (15%)	0	100	100
16	P	112/114 (98%)	97 (87%)	15 (13%)	0	100	100
17	Q	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
18	R	100/102 (98%)	91 (91%)	8 (8%)	1 (1%)	12	39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	S	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
20	T	92/94 (98%)	84 (91%)	7 (8%)	1 (1%)	11	36
21	U	101/103 (98%)	90 (89%)	10 (10%)	1 (1%)	12	39
22	V	186/188 (99%)	158 (85%)	26 (14%)	2 (1%)	11	36
23	W	74/76 (97%)	60 (81%)	13 (18%)	1 (1%)	9	30
24	X	75/77 (97%)	70 (93%)	5 (7%)	0	100	100
25	Y	58/60 (97%)	55 (95%)	3 (5%)	0	100	100
26	Z	55/57 (96%)	53 (96%)	2 (4%)	0	100	100
27	1	29/31 (94%)	26 (90%)	3 (10%)	0	100	100
28	2	51/53 (96%)	48 (94%)	3 (6%)	0	100	100
29	3	48/50 (96%)	36 (75%)	12 (25%)	0	100	100
30	4	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
31	5	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
32	6	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
34	b	217/226 (96%)	199 (92%)	18 (8%)	0	100	100
35	c	201/203 (99%)	174 (87%)	27 (13%)	0	100	100
36	d	202/204 (99%)	177 (88%)	25 (12%)	0	100	100
37	e	147/150 (98%)	138 (94%)	9 (6%)	0	100	100
38	f	98/100 (98%)	88 (90%)	10 (10%)	0	100	100
39	g	152/154 (99%)	134 (88%)	18 (12%)	0	100	100
40	h	127/129 (98%)	111 (87%)	14 (11%)	2 (2%)	7	27
41	i	124/126 (98%)	107 (86%)	17 (14%)	0	100	100
42	j	94/96 (98%)	81 (86%)	13 (14%)	0	100	100
43	k	113/115 (98%)	95 (84%)	18 (16%)	0	100	100
44	l	118/120 (98%)	100 (85%)	17 (14%)	1 (1%)	16	44
45	m	105/110 (96%)	92 (88%)	13 (12%)	0	100	100
46	n	96/98 (98%)	81 (84%)	15 (16%)	0	100	100
47	o	85/87 (98%)	78 (92%)	6 (7%)	1 (1%)	10	34
48	p	76/78 (97%)	68 (90%)	8 (10%)	0	100	100
49	q	74/76 (97%)	71 (96%)	3 (4%)	0	100	100
50	r	54/56 (96%)	50 (93%)	4 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	s	78/80 (98%)	59 (76%)	19 (24%)	0	100	100
52	t	84/86 (98%)	83 (99%)	1 (1%)	0	100	100
53	u	32/34 (94%)	32 (100%)	0	0	100	100
All	All	5608/5719 (98%)	5018 (90%)	568 (10%)	22 (0%)	31	59

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	120	ILE
4	D	105	GLN
4	D	134	HIS
20	T	3	GLN
22	V	167	ALA
22	V	168	PRO
40	h	80	ARG
4	D	117	GLY
4	D	167	ALA
21	U	88	ASP
4	D	73	ASN
4	D	164	HIS
40	h	81	PRO
47	o	19	GLU
4	D	55	GLU
18	R	52	PRO
23	W	19	LYS
44	l	109	ASP
3	C	233	GLY
4	D	32	PRO
4	D	137	SER
4	D	104	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	
3	C	206/212 (97%)	194 (94%)	12 (6%)	18	49
4	D	157/159 (99%)	125 (80%)	32 (20%)	1	4
5	E	155/157 (99%)	154 (99%)	1 (1%)	78	93
6	F	122/149 (82%)	119 (98%)	3 (2%)	42	74
7	G	131/135 (97%)	131 (100%)	0	100	100
8	H	55/55 (100%)	53 (96%)	2 (4%)	31	65
9	I	108/108 (100%)	108 (100%)	0	100	100
10	J	118/118 (100%)	117 (99%)	1 (1%)	73	90
11	K	100/100 (100%)	97 (97%)	3 (3%)	36	70
12	L	105/106 (99%)	105 (100%)	0	100	100
13	M	109/109 (100%)	108 (99%)	1 (1%)	70	90
14	N	99/99 (100%)	97 (98%)	2 (2%)	48	78
15	O	86/86 (100%)	86 (100%)	0	100	100
16	P	96/96 (100%)	95 (99%)	1 (1%)	68	89
17	Q	87/87 (100%)	86 (99%)	1 (1%)	65	88
18	R	82/86 (95%)	82 (100%)	0	100	100
19	S	87/87 (100%)	86 (99%)	1 (1%)	65	88
20	T	77/79 (98%)	75 (97%)	2 (3%)	40	73
21	U	88/88 (100%)	88 (100%)	0	100	100
22	V	144/153 (94%)	143 (99%)	1 (1%)	76	92
23	W	56/56 (100%)	55 (98%)	1 (2%)	51	80
24	X	65/66 (98%)	65 (100%)	0	100	100
25	Y	51/53 (96%)	50 (98%)	1 (2%)	48	78
26	Z	48/48 (100%)	47 (98%)	1 (2%)	47	77
27	1	27/27 (100%)	27 (100%)	0	100	100
28	2	45/46 (98%)	45 (100%)	0	100	100
29	3	44/46 (96%)	44 (100%)	0	100	100
30	4	37/37 (100%)	37 (100%)	0	100	100
31	5	53/54 (98%)	52 (98%)	1 (2%)	50	79
32	6	33/34 (97%)	33 (100%)	0	100	100
34	b	174/188 (93%)	173 (99%)	1 (1%)	78	93
35	c	163/169 (96%)	163 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	d	166/173 (96%)	166 (100%)	0	100	100
37	e	108/109 (99%)	106 (98%)	2 (2%)	50	79
38	f	81/85 (95%)	81 (100%)	0	100	100
39	g	116/120 (97%)	115 (99%)	1 (1%)	70	90
40	h	104/107 (97%)	103 (99%)	1 (1%)	68	89
41	i	102/102 (100%)	102 (100%)	0	100	100
42	j	85/85 (100%)	85 (100%)	0	100	100
43	k	83/87 (95%)	83 (100%)	0	100	100
44	l	104/104 (100%)	103 (99%)	1 (1%)	68	89
45	m	91/92 (99%)	91 (100%)	0	100	100
46	n	78/80 (98%)	78 (100%)	0	100	100
47	o	73/73 (100%)	73 (100%)	0	100	100
48	p	61/63 (97%)	61 (100%)	0	100	100
49	q	70/70 (100%)	69 (99%)	1 (1%)	59	85
50	r	46/48 (96%)	46 (100%)	0	100	100
51	s	69/71 (97%)	69 (100%)	0	100	100
52	t	68/68 (100%)	68 (100%)	0	100	100
53	u	28/28 (100%)	28 (100%)	0	100	100
All	All	4541/4658 (98%)	4467 (98%)	74 (2%)	54	83

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	33	LEU
3	C	39	LYS
3	C	44	ASN
3	C	65	VAL
3	C	71	LYS
3	C	80	ARG
3	C	108	LYS
3	C	125	LYS
3	C	180	GLU
3	C	263	ARG
3	C	264	THR
3	C	270	ARG
4	D	5	VAL

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Mol	Chain	Res	Type
4	D	21	VAL
4	D	31	GLU
4	D	34	ARG
4	D	35	VAL
4	D	37	GLN
4	D	40	THR
4	D	47	ARG
4	D	51	VAL
4	D	55	GLU
4	D	60	ARG
4	D	71	LYS
4	D	100	LEU
4	D	102	GLN
4	D	105	GLN
4	D	106	MET
4	D	110	THR
4	D	114	LYS
4	D	118	PHE
4	D	126	ASN
4	D	130	GLN
4	D	137	SER
4	D	138	VAL
4	D	139	SER
4	D	141	ARG
4	D	142	VAL
4	D	161	MET
4	D	168	GLU
4	D	169	ARG
4	D	173	GLN
4	D	178	VAL
4	D	190	LYS
5	E	179	LEU
6	F	20	LEU
6	F	152	LEU
6	F	156	LEU
8	H	12	LEU
8	H	21	ILE
10	J	80	PHE
11	K	2	ILE
11	K	8	LEU
11	K	77	ILE
13	M	6	ARG

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Mol	Chain	Res	Type
14	N	2	ARG
14	N	95	LEU
16	P	98	LEU
17	Q	4	VAL
19	S	82	LEU
20	T	9	VAL
20	T	83	TYR
22	V	187	ILE
23	W	67	VAL
25	Y	21	LEU
26	Z	43	ASN
31	5	50	ASN
34	b	117	LEU
37	e	125	LEU
37	e	137	VAL
39	g	80	VAL
40	h	101	VAL
44	l	51	LYS
49	q	58	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (93) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	90	HIS
4	D	33	ASN
4	D	37	GLN
4	D	68	HIS
4	D	73	ASN
4	D	95	GLN
4	D	105	GLN
4	D	130	GLN
4	D	132	ASN
4	D	148	GLN
4	D	150	GLN
4	D	173	GLN
5	E	6	ASN
7	G	23	GLN
7	G	45	GLN
7	G	59	GLN
7	G	74	ASN
7	G	97	GLN
7	G	135	GLN

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Mol	Chain	Res	Type
7	G	139	GLN
8	H	28	ASN
10	J	76	HIS
10	J	77	HIS
10	J	135	GLN
10	J	136	GLN
11	K	5	GLN
11	K	67	HIS
14	N	9	HIS
15	O	66	ASN
17	Q	37	GLN
17	Q	72	ASN
17	Q	101	ASN
18	R	83	HIS
19	S	61	ASN
20	T	14	HIS
21	U	68	ASN
22	V	106	HIS
22	V	113	ASN
22	V	129	HIS
22	V	175	GLN
23	W	46	HIS
24	X	16	ASN
24	X	34	GLN
24	X	35	HIS
24	X	36	HIS
25	Y	27	ASN
25	Y	58	ASN
26	Z	13	ASN
26	Z	19	HIS
26	Z	33	HIS
26	Z	43	ASN
26	Z	48	ASN
29	3	42	HIS
31	5	50	ASN
34	b	36	ASN
34	b	51	ASN
34	b	120	GLN
34	b	190	ASN
35	c	18	HIS
35	c	28	ASN
36	d	89	ASN

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Mol	Chain	Res	Type
36	d	116	GLN
36	d	136	GLN
37	e	83	GLN
38	f	37	HIS
38	f	58	HIS
39	g	21	GLN
39	g	28	ASN
39	g	148	ASN
40	h	50	GLN
40	h	107	ASN
41	i	126	GLN
42	j	58	ASN
43	k	64	GLN
43	k	72	GLN
44	l	5	ASN
44	l	25	GLN
44	l	59	ASN
44	l	72	HIS
45	m	40	ASN
45	m	76	ASN
45	m	100	GLN
46	n	49	GLN
47	o	28	GLN
47	o	35	ASN
47	o	42	HIS
47	o	61	ASN
47	o	62	GLN
48	p	54	GLN
51	s	57	HIS
52	t	21	ASN
53	u	61	GLN
53	u	64	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2883/2888 (99%)	818 (28%)	36 (1%)
2	B	116/117 (99%)	48 (41%)	4 (3%)
33	a	1383/1521 (90%)	574 (41%)	0
All	All	4382/4526 (96%)	1440 (32%)	40 (0%)

All (1440) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	10	A
1	A	14	A
1	A	15	G
1	A	22	C
1	A	34	U
1	A	35	G
1	A	44	A
1	A	46	G
1	A	50	U
1	A	55	G
1	A	56	A
1	A	58	G
1	A	60	G
1	A	62	U
1	A	63	A
1	A	64	G
1	A	69	C
1	A	71	A
1	A	74	A
1	A	75	G
1	A	79	C
1	A	82	G
1	A	83	G
1	A	85	G
1	A	93	A
1	A	102	G
1	A	103	A
1	A	110	G
1	A	114	U
1	A	115	C
1	A	116	U
1	A	119	A
1	A	120	U
1	A	124	G
1	A	131	A
1	A	139	U
1	A	140	A
1	A	141	A
1	A	142	C
1	A	146	G
1	A	160	A
1	A	163	C
1	A	166	U

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Mol	Chain	Res	Type
1	A	173	A
1	A	181	A
1	A	196	A
1	A	199	A
1	A	205	G
1	A	206	U
1	A	215	G
1	A	216	A
1	A	222	A
1	A	224	U
1	A	227	A
1	A	228	C
1	A	230	G
1	A	232	G
1	A	233	A
1	A	239	U
1	A	241	A
1	A	242	G
1	A	248	G
1	A	249	C
1	A	252	G
1	A	255	A
1	A	261	G
1	A	265	A
1	A	266	G
1	A	267	C
1	A	268	C
1	A	271	U
1	A	273	A
1	A	276	U
1	A	278	C
1	A	280	U
1	A	281	U
1	A	289	G
1	A	294	A
1	A	305	A
1	A	311	G
1	A	313	C
1	A	315	U
1	A	316	A
1	A	318	U
1	A	319	G

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Mol	Chain	Res	Type
1	A	322	U
1	A	323	G
1	A	324	A
1	A	325	U
1	A	327	G
1	A	329	C
1	A	336	G
1	A	339	A
1	A	342	G
1	A	349	U
1	A	350	G
1	A	357	A
1	A	358	A
1	A	359	U
1	A	364	U
1	A	375	A
1	A	377	G
1	A	378	A
1	A	385	U
1	A	386	U
1	A	387	G
1	A	395	A
1	A	397	G
1	A	400	G
1	A	403	A
1	A	406	A
1	A	416	G
1	A	428	U
1	A	435	C
1	A	439	U
1	A	445	A
1	A	446	C
1	A	447	C
1	A	448	A
1	A	454	G
1	A	458	G
1	A	461	A
1	A	464	G
1	A	466	C
1	A	470	A
1	A	472	G
1	A	482	G

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Mol	Chain	Res	Type
1	A	485	G
1	A	487	G
1	A	492	A
1	A	496	A
1	A	499	A
1	A	520	A
1	A	523	A
1	A	524	G
1	A	534	A
1	A	535	C
1	A	537	U
1	A	538	G
1	A	539	U
1	A	540	U
1	A	541	A
1	A	553	A
1	A	558	U
1	A	561	U
1	A	563	U
1	A	564	A
1	A	565	A
1	A	576	A
1	A	593	A
1	A	594	G
1	A	599	A
1	A	604	A
1	A	605	U
1	A	624	G
1	A	627	A
1	A	628	G
1	A	635	U
1	A	636	A
1	A	637	G
1	A	638	G
1	A	643	U
1	A	644	U
1	A	645	A
1	A	647	U
1	A	659	G
1	A	660	A
1	A	667	A
1	A	675	A

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Mol	Chain	Res	Type
1	A	676	U
1	A	680	U
1	A	685	G
1	A	687	G
1	A	689	A
1	A	698	G
1	A	699	U
1	A	700	U
1	A	701	A
1	A	704	U
1	A	705	A
1	A	706	A
1	A	708	A
1	A	709	C
1	A	710	U
1	A	711	G
1	A	716	G
1	A	719	G
1	A	720	A
1	A	724	A
1	A	728	C
1	A	737	U
1	A	738	G
1	A	739	A
1	A	743	G
1	A	745	U
1	A	755	C
1	A	763	U
1	A	765	G
1	A	766	G
1	A	767	A
1	A	772	A
1	A	774	G
1	A	779	A
1	A	781	C
1	A	782	A
1	A	795	G
1	A	802	C
1	A	817	U
1	A	833	G
1	A	836	U
1	A	844	G

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Mol	Chain	Res	Type
1	A	846	G
1	A	848	G
1	A	855	A
1	A	858	G
1	A	860	U
1	A	862	C
1	A	863	G
1	A	864	G
1	A	865	C
1	A	866	U
1	A	867	A
1	A	870	G
1	A	872	G
1	A	873	U
1	A	875	A
1	A	877	C
1	A	878	C
1	A	881	A
1	A	882	C
1	A	886	C
1	A	887	C
1	A	888	A
1	A	889	A
1	A	890	A
1	A	898	A
1	A	899	A
1	A	904	C
1	A	908	U
1	A	921	C
1	A	922	G
1	A	931	A
1	A	935	A
1	A	936	C
1	A	948	U
1	A	949	A
1	A	951	C
1	A	952	G
1	A	954	C
1	A	963	A
1	A	964	A
1	A	966	G
1	A	972	C

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Mol	Chain	Res	Type
1	A	973	A
1	A	975	C
1	A	979	G
1	A	983	G
1	A	986	A
1	A	988	C
1	A	989	U
1	A	993	G
1	A	995	C
1	A	999	A
1	A	1002	U
1	A	1003	U
1	A	1007	G
1	A	1012	G
1	A	1016	U
1	A	1017	A
1	A	1023	U
1	A	1025	U
1	A	1029	A
1	A	1030	A
1	A	1034	U
1	A	1035	U
1	A	1036	A
1	A	1037	G
1	A	1038	A
1	A	1042	C
1	A	1043	U
1	A	1044	A
1	A	1045	G
1	A	1047	A
1	A	1049	G
1	A	1051	U
1	A	1052	G
1	A	1054	C
1	A	1055	U
1	A	1057	A
1	A	1058	G
1	A	1060	A
1	A	1062	C
1	A	1063	A
1	A	1064	G
1	A	1065	C

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Mol	Chain	Res	Type
1	A	1066	C
1	A	1067	A
1	A	1068	C
1	A	1069	C
1	A	1070	C
1	A	1071	U
1	A	1072	U
1	A	1073	U
1	A	1074	A
1	A	1075	A
1	A	1076	A
1	A	1077	G
1	A	1078	A
1	A	1079	A
1	A	1083	G
1	A	1084	U
1	A	1085	A
1	A	1086	A
1	A	1087	U
1	A	1088	A
1	A	1089	G
1	A	1090	C
1	A	1092	C
1	A	1093	A
1	A	1094	C
1	A	1097	G
1	A	1098	U
1	A	1099	C
1	A	1100	G
1	A	1101	A
1	A	1102	G
1	A	1103	U
1	A	1105	G
1	A	1117	A
1	A	1118	G
1	A	1119	A
1	A	1120	U
1	A	1121	G
1	A	1122	U
1	A	1123	A
1	A	1124	A
1	A	1125	C

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Mol	Chain	Res	Type
1	A	1129	G
1	A	1133	A
1	A	1138	A
1	A	1142	A
1	A	1146	A
1	A	1148	G
1	A	1154	G
1	A	1155	G
1	A	1156	U
1	A	1157	G
1	A	1163	U
1	A	1164	A
1	A	1165	A
1	A	1166	G
1	A	1167	U
1	A	1170	C
1	A	1192	A
1	A	1193	G
1	A	1199	G
1	A	1204	U
1	A	1205	G
1	A	1214	A
1	A	1223	G
1	A	1224	A
1	A	1225	G
1	A	1227	U
1	A	1228	A
1	A	1229	U
1	A	1233	A
1	A	1234	A
1	A	1235	G
1	A	1237	G
1	A	1238	C
1	A	1240	A
1	A	1242	U
1	A	1243	G
1	A	1249	A
1	A	1253	G
1	A	1258	G
1	A	1259	A
1	A	1261	A
1	A	1263	U

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Mol	Chain	Res	Type
1	A	1271	A
1	A	1276	C
1	A	1281	A
1	A	1288	A
1	A	1292	C
1	A	1299	U
1	A	1306	G
1	A	1308	A
1	A	1316	U
1	A	1327	U
1	A	1328	U
1	A	1331	U
1	A	1333	G
1	A	1334	G
1	A	1339	U
1	A	1346	A
1	A	1349	C
1	A	1352	A
1	A	1355	A
1	A	1361	G
1	A	1362	U
1	A	1366	U
1	A	1367	G
1	A	1372	A
1	A	1373	C
1	A	1382	A
1	A	1397	G
1	A	1403	G
1	A	1404	C
1	A	1406	A
1	A	1408	G
1	A	1414	A
1	A	1415	C
1	A	1420	A
1	A	1421	A
1	A	1430	C
1	A	1433	C
1	A	1439	G
1	A	1440	U
1	A	1441	U
1	A	1442	G
1	A	1447	U

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Mol	Chain	Res	Type
1	A	1454	U
1	A	1463	U
1	A	1469	G
1	A	1475	U
1	A	1480	U
1	A	1481	A
1	A	1484	U
1	A	1495	A
1	A	1496	A
1	A	1497	G
1	A	1503	G
1	A	1507	U
1	A	1509	A
1	A	1511	G
1	A	1515	A
1	A	1516	G
1	A	1517	U
1	A	1518	C
1	A	1519	G
1	A	1530	G
1	A	1537	U
1	A	1542	G
1	A	1549	U
1	A	1555	C
1	A	1556	A
1	A	1558	G
1	A	1559	A
1	A	1560	A
1	A	1568	U
1	A	1571	G
1	A	1573	U
1	A	1574	U
1	A	1576	A
1	A	1580	A
1	A	1597	C
1	A	1598	A
1	A	1600	A
1	A	1603	G
1	A	1624	A
1	A	1629	C
1	A	1636	C
1	A	1637	U

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Mol	Chain	Res	Type
1	A	1638	U
1	A	1639	G
1	A	1641	G
1	A	1643	G
1	A	1657	G
1	A	1664	G
1	A	1665	C
1	A	1683	U
1	A	1684	C
1	A	1685	G
1	A	1686	G
1	A	1700	G
1	A	1708	U
1	A	1710	A
1	A	1711	A
1	A	1717	U
1	A	1718	A
1	A	1720	U
1	A	1724	U
1	A	1725	A
1	A	1736	G
1	A	1739	C
1	A	1740	G
1	A	1741	A
1	A	1742	A
1	A	1745	U
1	A	1746	A
1	A	1750	G
1	A	1751	G
1	A	1756	U
1	A	1760	A
1	A	1763	G
1	A	1768	U
1	A	1769	U
1	A	1771	A
1	A	1775	C
1	A	1787	C
1	A	1788	A
1	A	1789	A
1	A	1795	A
1	A	1797	A
1	A	1798	G

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Mol	Chain	Res	Type
1	A	1803	C
1	A	1807	U
1	A	1820	C
1	A	1829	G
1	A	1834	A
1	A	1835	A
1	A	1838	U
1	A	1841	A
1	A	1853	A
1	A	1855	C
1	A	1861	C
1	A	1862	G
1	A	1863	A
1	A	1865	G
1	A	1871	G
1	A	1875	G
1	A	1890	G
1	A	1894	G
1	A	1895	C
1	A	1897	G
1	A	1898	U
1	A	1899	A
1	A	1901	C
1	A	1902	U
1	A	1903	A
1	A	1904	U
1	A	1905	A
1	A	1907	C
1	A	1908	G
1	A	1909	G
1	A	1911	C
1	A	1916	G
1	A	1917	G
1	A	1924	A
1	A	1925	A
1	A	1927	U
1	A	1942	U
1	A	1952	C
1	A	1953	A
1	A	1954	C
1	A	1957	A
1	A	1958	U

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Mol	Chain	Res	Type
1	A	1959	G
1	A	1969	U
1	A	1978	U
1	A	1980	U
1	A	1983	C
1	A	1984	C
1	A	1991	G
1	A	2007	A
1	A	2010	C
1	A	2018	A
1	A	2020	A
1	A	2021	U
1	A	2022	G
1	A	2030	U
1	A	2039	A
1	A	2042	C
1	A	2043	G
1	A	2047	A
1	A	2048	G
1	A	2049	A
1	A	2054	G
1	A	2055	U
1	A	2056	G
1	A	2060	C
1	A	2063	U
1	A	2064	A
1	A	2080	G
1	A	2082	A
1	A	2083	C
1	A	2084	U
1	A	2094	C
1	A	2095	U
1	A	2096	U
1	A	2098	U
1	A	2099	G
1	A	2104	A
1	A	2106	A
1	A	2110	G
1	A	2113	A
1	A	2114	G
1	A	2116	C
1	A	2117	U

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Mol	Chain	Res	Type
1	A	2118	U
1	A	2119	U
1	A	2120	G
1	A	2121	A
1	A	2132	C
1	A	2133	C
1	A	2134	A
1	A	2139	G
1	A	2140	C
1	A	2141	G
1	A	2143	G
1	A	2144	G
1	A	2145	A
1	A	2146	G
1	A	2147	C
1	A	2148	C
1	A	2150	U
1	A	2151	C
1	A	2152	C
1	A	2156	A
1	A	2157	A
1	A	2158	A
1	A	2159	U
1	A	2160	A
1	A	2169	G
1	A	2174	C
1	A	2175	U
1	A	2176	U
1	A	2178	A
1	A	2185	A
1	A	2190	U
1	A	2191	G
1	A	2199	A
1	A	2212	A
1	A	2225	G
1	A	2226	G
1	A	2228	A
1	A	2229	G
1	A	2237	G
1	A	2246	U
1	A	2253	A
1	A	2265	A

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Mol	Chain	Res	Type
1	A	2270	U
1	A	2274	A
1	A	2275	A
1	A	2276	G
1	A	2279	G
1	A	2281	G
1	A	2283	U
1	A	2289	C
1	A	2290	G
1	A	2292	U
1	A	2293	C
1	A	2294	G
1	A	2295	G
1	A	2296	A
1	A	2297	A
1	A	2299	U
1	A	2300	C
1	A	2301	G
1	A	2304	C
1	A	2305	G
1	A	2306	C
1	A	2307	A
1	A	2308	G
1	A	2312	A
1	A	2313	U
1	A	2318	G
1	A	2319	C
1	A	2321	A
1	A	2322	A
1	A	2323	A
1	A	2324	G
1	A	2325	C
1	A	2330	U
1	A	2331	U
1	A	2332	G
1	A	2334	C
1	A	2337	C
1	A	2342	C
1	A	2345	A
1	A	2348	C
1	A	2353	A
1	A	2354	G

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Mol	Chain	Res	Type
1	A	2358	G
1	A	2359	U
1	A	2360	A
1	A	2361	C
1	A	2363	A
1	A	2364	A
1	A	2365	A
1	A	2366	G
1	A	2367	U
1	A	2370	G
1	A	2372	C
1	A	2375	A
1	A	2378	G
1	A	2383	G
1	A	2389	U
1	A	2390	C
1	A	2393	U
1	A	2397	G
1	A	2406	U
1	A	2409	C
1	A	2410	U
1	A	2411	C
1	A	2413	A
1	A	2416	G
1	A	2417	A
1	A	2421	A
1	A	2427	C
1	A	2428	U
1	A	2431	G
1	A	2434	G
1	A	2435	A
1	A	2454	C
1	A	2457	G
1	A	2459	G
1	A	2463	A
1	A	2471	G
1	A	2474	G
1	A	2477	G
1	A	2478	U
1	A	2479	U
1	A	2480	U
1	A	2485	C

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Mol	Chain	Res	Type
1	A	2489	G
1	A	2492	G
1	A	2505	A
1	A	2506	U
1	A	2516	G
1	A	2517	A
1	A	2522	G
1	A	2534	A
1	A	2537	G
1	A	2543	C
1	A	2545	C
1	A	2549	U
1	A	2551	A
1	A	2553	A
1	A	2554	G
1	A	2559	A
1	A	2560	C
1	A	2565	G
1	A	2572	U
1	A	2573	U
1	A	2586	G
1	A	2589	A
1	A	2590	G
1	A	2597	C
1	A	2600	U
1	A	2616	U
1	A	2617	U
1	A	2633	C
1	A	2637	U
1	A	2638	C
1	A	2639	C
1	A	2641	A
1	A	2650	G
1	A	2656	G
1	A	2657	A
1	A	2658	G
1	A	2659	U
1	A	2668	C
1	A	2672	G
1	A	2676	U
1	A	2677	U
1	A	2687	A

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Mol	Chain	Res	Type
1	A	2689	G
1	A	2694	U
1	A	2696	G
1	A	2701	G
1	A	2704	G
1	A	2705	G
1	A	2707	U
1	A	2713	U
1	A	2719	G
1	A	2720	A
1	A	2728	A
1	A	2731	G
1	A	2732	C
1	A	2735	A
1	A	2737	A
1	A	2739	C
1	A	2740	A
1	A	2741	U
1	A	2744	A
1	A	2745	A
1	A	2749	G
1	A	2752	A
1	A	2756	U
1	A	2763	A
1	A	2765	A
1	A	2766	U
1	A	2772	C
1	A	2775	A
1	A	2776	C
1	A	2778	G
1	A	2784	U
1	A	2785	U
1	A	2786	G
1	A	2787	A
1	A	2807	A
1	A	2812	U
1	A	2819	U
1	A	2820	U
1	A	2821	G
1	A	2822	A
1	A	2829	G
1	A	2836	U

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Mol	Chain	Res	Type
1	A	2844	G
1	A	2846	G
1	A	2848	G
1	A	2852	U
1	A	2853	U
1	A	2855	A
1	A	2856	G
1	A	2857	C
1	A	2858	U
1	A	2859	A
1	A	2860	A
1	A	2865	U
1	A	2866	A
1	A	2871	U
1	A	2872	G
1	A	2873	G
1	A	2874	C
1	A	2878	U
1	A	2889	C
2	B	7	A
2	B	8	C
2	B	13	A
2	B	14	U
2	B	17	A
2	B	21	U
2	B	22	U
2	B	23	G
2	B	24	G
2	B	25	A
2	B	26	A
2	B	29	A
2	B	30	C
2	B	35	U
2	B	37	C
2	B	38	C
2	B	40	U
2	B	41	C
2	B	42	C
2	B	43	C
2	B	44	G
2	B	45	A
2	B	46	A

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Mol	Chain	Res	Type
2	B	47	C
2	B	49	C
2	B	51	G
2	B	52	A
2	B	54	G
2	B	56	G
2	B	62	A
2	B	64	G
2	B	66	A
2	B	67	U
2	B	69	G
2	B	73	A
2	B	89	U
2	B	90	C
2	B	91	C
2	B	104	A
2	B	105	G
2	B	106	G
2	B	107	U
2	B	109	A
2	B	110	U
2	B	111	C
2	B	113	U
2	B	116	A
2	B	117	G
33	a	7	A
33	a	9	G
33	a	22	G
33	a	23	C
33	a	29	U
33	a	31	G
33	a	32	A
33	a	35	G
33	a	37	U
33	a	38	G
33	a	39	G
33	a	47	C
33	a	48	C
33	a	50	A
33	a	51	A
33	a	54	C
33	a	61	G

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Mol	Chain	Res	Type
33	a	62	U
33	a	64	G
33	a	65	A
33	a	66	G
33	a	68	G
33	a	70	A
33	a	72	G
33	a	73	A
33	a	74	A
33	a	79	G
33	a	82	U
33	a	83	G
33	a	87	C
33	a	89	G
33	a	93	U
33	a	94	C
33	a	95	A
33	a	97	C
33	a	115	U
33	a	116	G
33	a	117	C
33	a	120	A
33	a	121	G
33	a	124	A
33	a	125	U
33	a	133	G
33	a	134	U
33	a	143	A
33	a	145	A
33	a	157	C
33	a	159	G
33	a	160	G
33	a	168	A
33	a	171	G
33	a	175	A
33	a	177	G
33	a	182	G
33	a	183	A
33	a	184	G
33	a	188	G
33	a	190	A
33	a	191	A

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Mol	Chain	Res	Type
33	a	196	G
33	a	198	G
33	a	199	A
33	a	201	C
33	a	202	U
33	a	204	C
33	a	205	G
33	a	206	G
33	a	210	U
33	a	211	C
33	a	214	G
33	a	228	C
33	a	239	U
33	a	241	G
33	a	245	G
33	a	247	U
33	a	248	G
33	a	252	G
33	a	260	G
33	a	261	C
33	a	265	C
33	a	266	C
33	a	273	A
33	a	274	C
33	a	275	G
33	a	283	A
33	a	287	G
33	a	290	U
33	a	292	A
33	a	295	G
33	a	299	G
33	a	300	A
33	a	307	A
33	a	315	A
33	a	321	A
33	a	322	C
33	a	323	A
33	a	324	C
33	a	325	G
33	a	326	G
33	a	338	A
33	a	339	C

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Mol	Chain	Res	Type
33	a	341	G
33	a	342	G
33	a	345	G
33	a	346	C
33	a	348	G
33	a	350	A
33	a	353	G
33	a	361	U
33	a	362	U
33	a	363	G
33	a	366	C
33	a	367	A
33	a	370	G
33	a	372	G
33	a	373	C
33	a	378	G
33	a	379	C
33	a	382	G
33	a	388	G
33	a	389	C
33	a	391	A
33	a	392	U
33	a	393	G
33	a	395	C
33	a	399	U
33	a	400	G
33	a	431	U
33	a	433	U
33	a	440	G
33	a	441	G
33	a	445	A
33	a	450	C
33	a	451	A
33	a	452	G
33	a	456	G
33	a	457	U
33	a	458	U
33	a	459	A
33	a	461	U
33	a	462	A
33	a	463	C
33	a	469	U

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Mol	Chain	Res	Type
33	a	470	G
33	a	475	G
33	a	479	U
33	a	480	U
33	a	482	C
33	a	489	A
33	a	490	A
33	a	491	U
33	a	492	A
33	a	493	A
33	a	497	C
33	a	499	G
33	a	500	G
33	a	501	C
33	a	502	U
33	a	503	A
33	a	504	A
33	a	505	C
33	a	506	U
33	a	509	G
33	a	512	C
33	a	513	C
33	a	519	C
33	a	520	C
33	a	521	G
33	a	524	G
33	a	525	U
33	a	526	A
33	a	527	A
33	a	530	C
33	a	532	A
33	a	536	G
33	a	538	G
33	a	539	C
33	a	541	A
33	a	542	G
33	a	552	G
33	a	553	A
33	a	556	U
33	a	558	C
33	a	560	G
33	a	562	G

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Mol	Chain	Res	Type
33	a	566	A
33	a	567	A
33	a	570	C
33	a	571	G
33	a	573	G
33	a	575	G
33	a	582	G
33	a	593	U
33	a	599	U
33	a	601	A
33	a	607	C
33	a	609	G
33	a	613	U
33	a	614	C
33	a	619	U
33	a	622	G
33	a	627	G
33	a	635	A
33	a	636	A
33	a	644	G
33	a	647	A
33	a	650	G
33	a	654	G
33	a	656	U
33	a	658	G
33	a	659	A
33	a	660	G
33	a	665	G
33	a	667	G
33	a	670	A
33	a	674	C
33	a	675	C
33	a	705	A
33	a	709	A
33	a	710	A
33	a	711	C
33	a	712	A
33	a	715	A
33	a	717	U
33	a	726	C
33	a	727	G
33	a	728	A

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Mol	Chain	Res	Type
33	a	734	U
33	a	737	A
33	a	741	A
33	a	746	G
33	a	747	A
33	a	749	A
33	a	757	G
33	a	762	A
33	a	763	G
33	a	764	C
33	a	766	U
33	a	771	A
33	a	775	A
33	a	776	A
33	a	777	C
33	a	778	A
33	a	779	G
33	a	781	A
33	a	785	G
33	a	787	U
33	a	788	A
33	a	790	C
33	a	791	C
33	a	794	G
33	a	795	U
33	a	797	G
33	a	808	A
33	a	809	A
33	a	810	A
33	a	811	C
33	a	814	U
33	a	815	G
33	a	822	A
33	a	823	G
33	a	826	G
33	a	829	G
33	a	830	G
33	a	838	G
33	a	839	A
33	a	840	G
33	a	845	U
33	a	849	G

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Mol	Chain	Res	Type
33	a	851	C
33	a	858	A
33	a	861	G
33	a	864	A
33	a	866	A
33	a	867	A
33	a	870	C
33	a	883	A
33	a	884	G
33	a	894	A
33	a	896	G
33	a	902	A
33	a	908	A
33	a	920	G
33	a	921	G
33	a	928	C
33	a	929	A
33	a	931	A
33	a	997	G
33	a	998	A
33	a	1004	C
33	a	1007	G
33	a	1008	A
33	a	1009	G
33	a	1011	U
33	a	1013	G
33	a	1015	U
33	a	1017	G
33	a	1019	U
33	a	1021	C
33	a	1025	C
33	a	1026	G
33	a	1028	G
33	a	1032	U
33	a	1039	C
33	a	1041	G
33	a	1043	U
33	a	1044	G
33	a	1046	U
33	a	1047	G
33	a	1048	C
33	a	1049	A

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Mol	Chain	Res	Type
33	a	1050	U
33	a	1051	G
33	a	1052	G
33	a	1053	C
33	a	1061	A
33	a	1062	G
33	a	1069	U
33	a	1073	G
33	a	1078	G
33	a	1079	U
33	a	1082	G
33	a	1088	G
33	a	1089	U
33	a	1090	C
33	a	1094	U
33	a	1095	A
33	a	1100	G
33	a	1101	C
33	a	1105	A
33	a	1113	C
33	a	1115	U
33	a	1116	U
33	a	1117	A
33	a	1118	G
33	a	1119	U
33	a	1120	U
33	a	1121	A
33	a	1123	C
33	a	1124	A
33	a	1125	G
33	a	1126	C
33	a	1127	A
33	a	1130	U
33	a	1132	G
33	a	1133	G
33	a	1134	G
33	a	1135	U
33	a	1137	G
33	a	1139	C
33	a	1140	A
33	a	1141	C
33	a	1142	U

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Mol	Chain	Res	Type
33	a	1143	C
33	a	1145	A
33	a	1146	A
33	a	1148	G
33	a	1149	A
33	a	1150	G
33	a	1151	A
33	a	1152	C
33	a	1153	U
33	a	1154	G
33	a	1159	U
33	a	1162	C
33	a	1163	A
33	a	1165	A
33	a	1167	C
33	a	1171	G
33	a	1172	G
33	a	1173	A
33	a	1174	A
33	a	1175	G
33	a	1176	G
33	a	1177	U
33	a	1189	C
33	a	1190	A
33	a	1191	A
33	a	1192	G
33	a	1193	U
33	a	1194	C
33	a	1195	A
33	a	1196	U
33	a	1197	C
33	a	1199	U
33	a	1200	G
33	a	1204	C
33	a	1205	U
33	a	1206	U
33	a	1207	A
33	a	1208	C
33	a	1209	G
33	a	1210	G
33	a	1211	C
33	a	1212	C

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Mol	Chain	Res	Type
33	a	1213	A
33	a	1214	G
33	a	1215	G
33	a	1217	C
33	a	1218	U
33	a	1219	A
33	a	1221	A
33	a	1224	C
33	a	1225	G
33	a	1227	G
33	a	1228	C
33	a	1229	U
33	a	1230	A
33	a	1231	C
33	a	1232	A
33	a	1233	A
33	a	1234	U
33	a	1235	G
33	a	1236	G
33	a	1237	U
33	a	1239	G
33	a	1240	G
33	a	1242	A
33	a	1243	C
33	a	1244	A
33	a	1245	A
33	a	1246	A
33	a	1247	G
33	a	1250	U
33	a	1251	U
33	a	1252	G
33	a	1254	C
33	a	1255	A
33	a	1256	A
33	a	1257	G
33	a	1258	C
33	a	1259	C
33	a	1260	G
33	a	1261	C
33	a	1263	A
33	a	1264	G
33	a	1265	G

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Mol	Chain	Res	Type
33	a	1266	U
33	a	1267	G
33	a	1268	G
33	a	1272	U
33	a	1273	A
33	a	1274	A
33	a	1275	U
33	a	1276	C
33	a	1277	C
33	a	1278	C
33	a	1279	A
33	a	1280	U
33	a	1282	A
33	a	1283	A
33	a	1286	C
33	a	1287	G
33	a	1291	G
33	a	1292	U
33	a	1293	A
33	a	1294	G
33	a	1295	U
33	a	1296	C
33	a	1297	C
33	a	1298	G
33	a	1299	G
33	a	1300	A
33	a	1301	U
33	a	1303	G
33	a	1304	C
33	a	1305	A
33	a	1307	U
33	a	1308	C
33	a	1309	U
33	a	1310	G
33	a	1311	C
33	a	1313	A
33	a	1314	C
33	a	1315	U
33	a	1316	C
33	a	1317	G
33	a	1318	A
33	a	1319	C

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Mol	Chain	Res	Type
33	a	1320	U
33	a	1321	G
33	a	1323	G
33	a	1324	U
33	a	1326	A
33	a	1330	C
33	a	1331	G
33	a	1332	G
33	a	1333	A
33	a	1334	A
33	a	1336	C
33	a	1337	G
33	a	1338	C
33	a	1339	U
33	a	1340	A
33	a	1341	G
33	a	1342	U
33	a	1344	A
33	a	1345	U
33	a	1346	C
33	a	1347	G
33	a	1348	U
33	a	1350	A
33	a	1351	A
33	a	1352	U
33	a	1353	C
33	a	1354	A
33	a	1355	G
33	a	1356	A
33	a	1357	A
33	a	1358	U
33	a	1359	G
33	a	1361	C
33	a	1362	A
33	a	1363	C
33	a	1364	G
33	a	1365	G
33	a	1366	U
33	a	1368	A
33	a	1370	U
33	a	1371	A
33	a	1372	C

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Mol	Chain	Res	Type
33	a	1373	G
33	a	1374	U
33	a	1375	U
33	a	1377	C
33	a	1378	C
33	a	1379	G
33	a	1380	G
33	a	1384	U
33	a	1388	A
33	a	1389	C
33	a	1391	C
33	a	1394	C
33	a	1395	G
33	a	1401	C
33	a	1413	G
33	a	1421	C
33	a	1422	U
33	a	1423	C
33	a	1428	A
33	a	1432	G
33	a	1435	A
33	a	1440	A
33	a	1441	A
33	a	1444	G
33	a	1445	C
33	a	1446	A
33	a	1447	A
33	a	1448	G
33	a	1454	C
33	a	1455	G
33	a	1458	U
33	a	1469	G
33	a	1481	G
33	a	1485	G
33	a	1487	A
33	a	1488	G
33	a	1491	G
33	a	1493	A
33	a	1497	A
33	a	1500	U
33	a	1501	A
33	a	1503	C

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Mol	Chain	Res	Type
33	a	1507	A
33	a	1511	G
33	a	1513	A
33	a	1514	C
33	a	1518	C
33	a	1519	G
33	a	1522	U
33	a	1523	G
33	a	1524	G
33	a	1525	A
33	a	1526	U

All (40) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	62	U
1	A	63	A
1	A	81	G
1	A	114	U
1	A	159	G
1	A	227	A
1	A	314	A
1	A	399	G
1	A	434	A
1	A	444	A
1	A	503	G
1	A	540	U
1	A	551	G
1	A	920	C
1	A	953	U
1	A	1016	U
1	A	1065	C
1	A	1070	C
1	A	1088	A
1	A	1166	G
1	A	1169	A
1	A	1213	A
1	A	1431	A
1	A	1441	U
1	A	1496	A
1	A	1642	A
1	A	1893	G

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Mol	Chain	Res	Type
1	A	2228	A
1	A	2274	A
1	A	2317	G
1	A	2389	U
1	A	2408	G
1	A	2536	G
1	A	2703	C
1	A	2731	G
1	A	2743	U
2	B	25	A
2	B	34	A
2	B	51	G
2	B	66	A

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
33	a	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	a	1376:C	O3'	1377:C	P	3.50

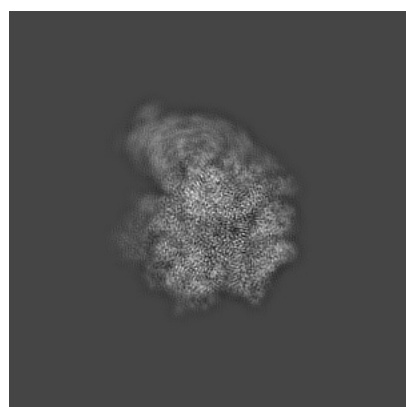
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10284. These allow visual inspection of the internal detail of the map and identification of artifacts.

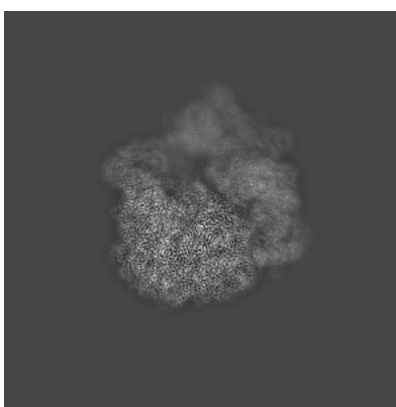
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

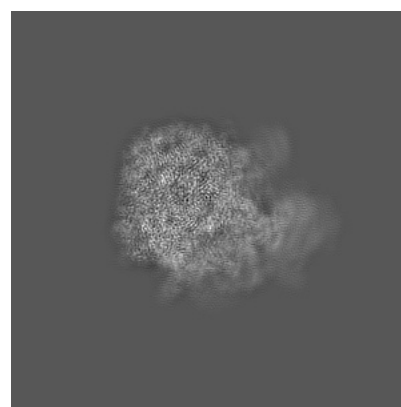
6.1.1 Primary map



X



Y

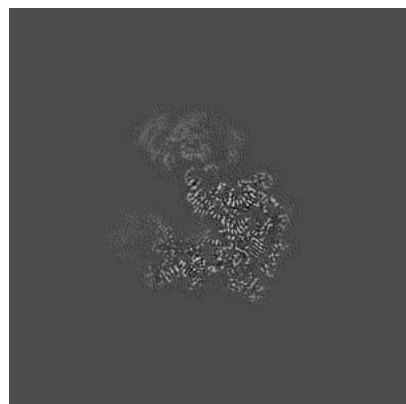


Z

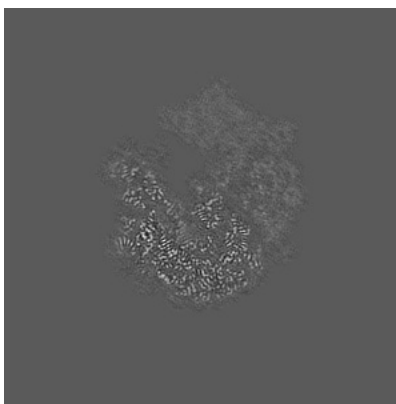
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

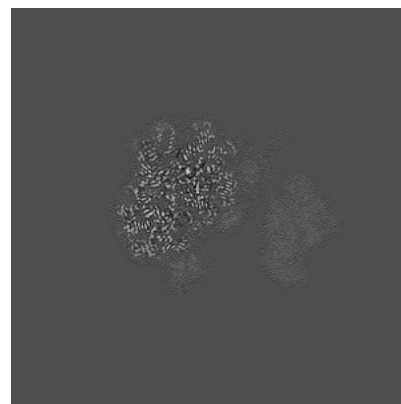
6.2.1 Primary map



X Index: 200



Y Index: 200

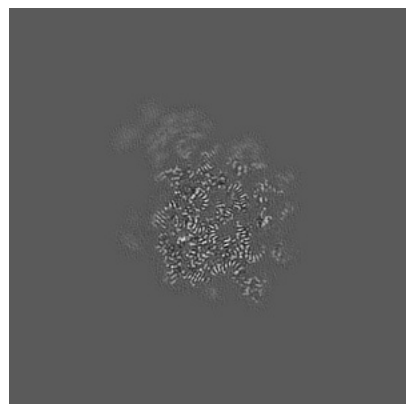


Z Index: 200

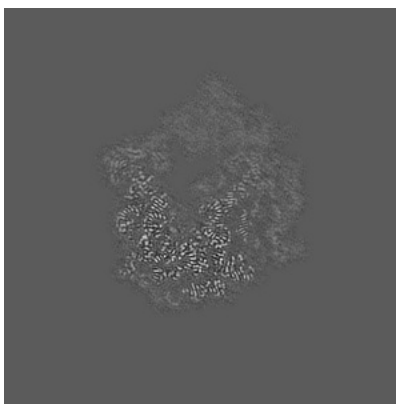
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

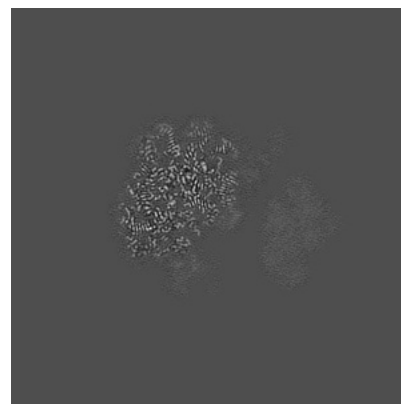
6.3.1 Primary map



X Index: 153



Y Index: 187

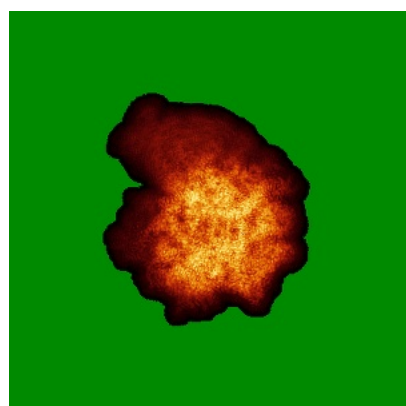


Z Index: 198

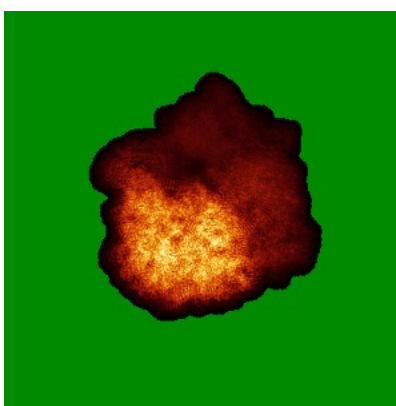
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

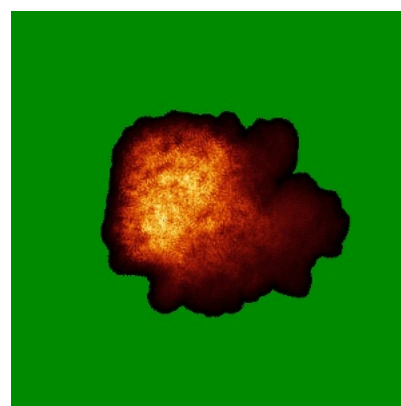
6.4.1 Primary map



X



Y

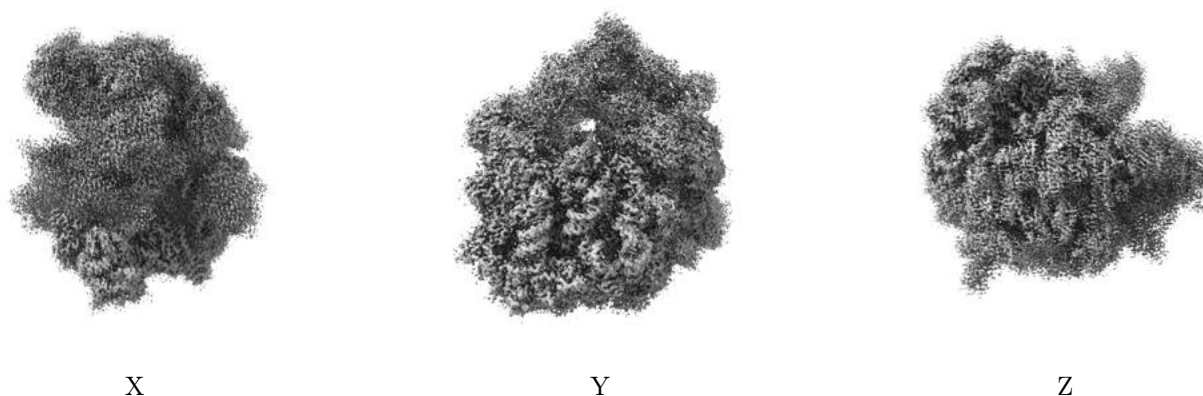


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.0491. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

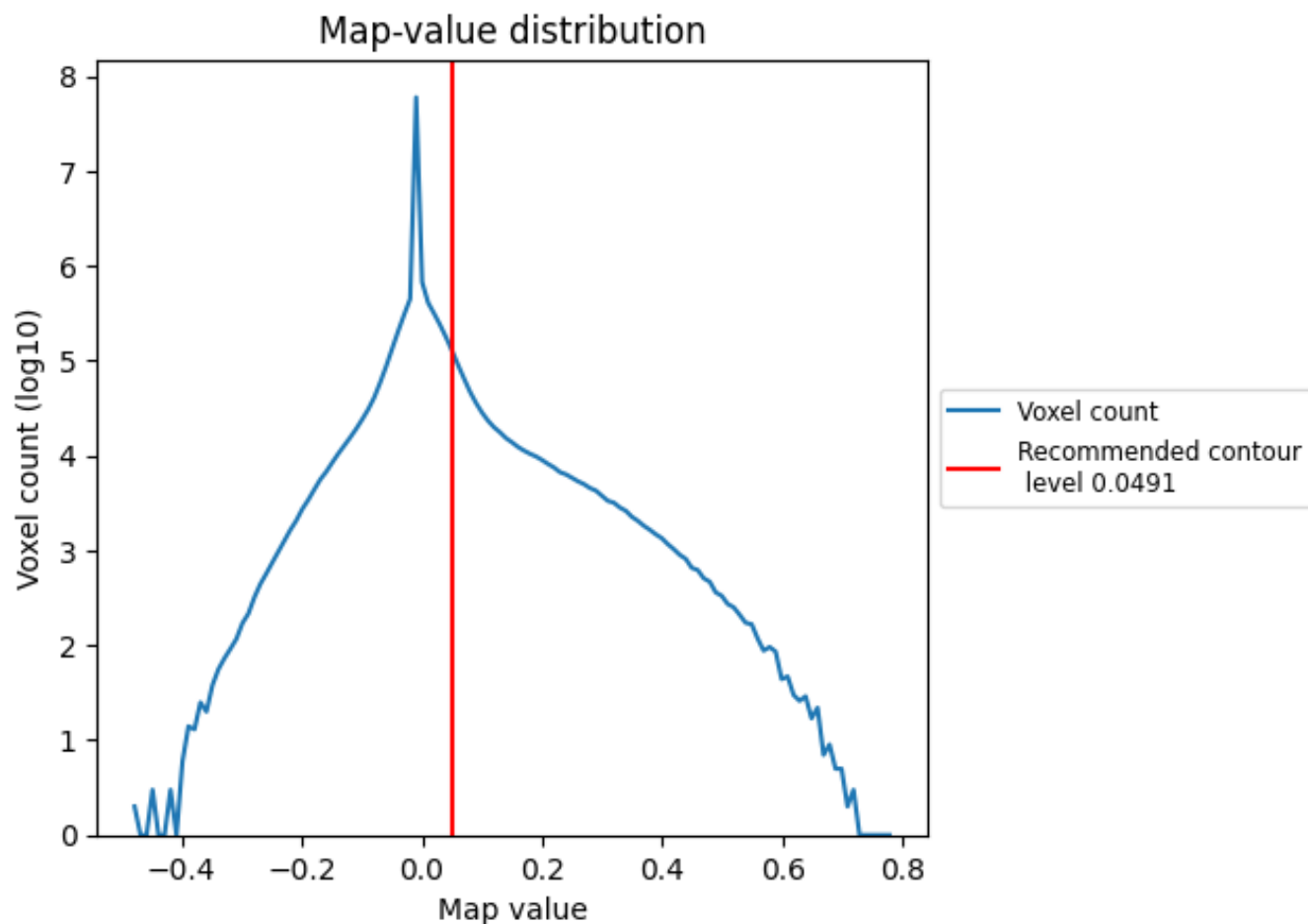
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

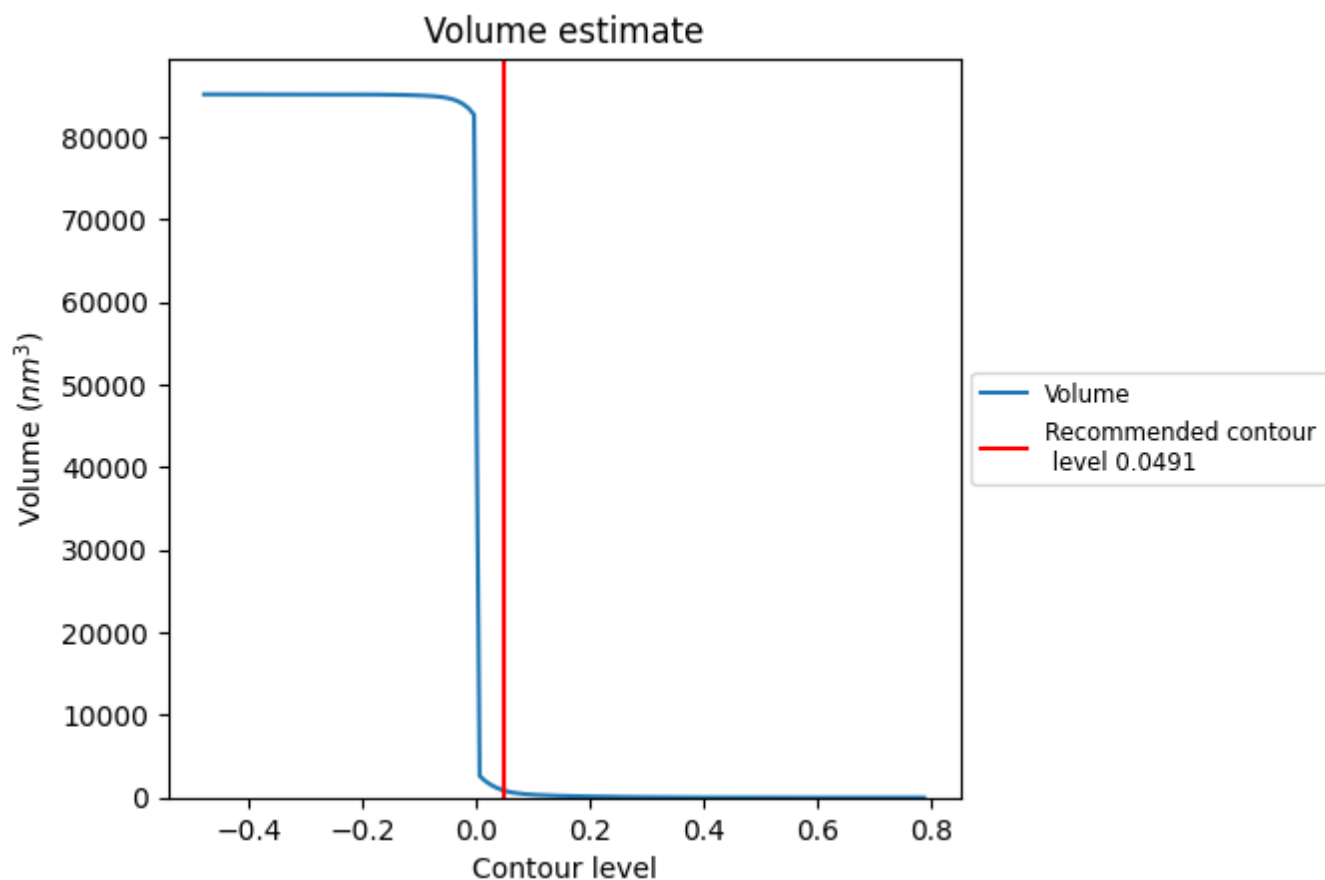
This section contains the results of statistical analysis of the map.

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.

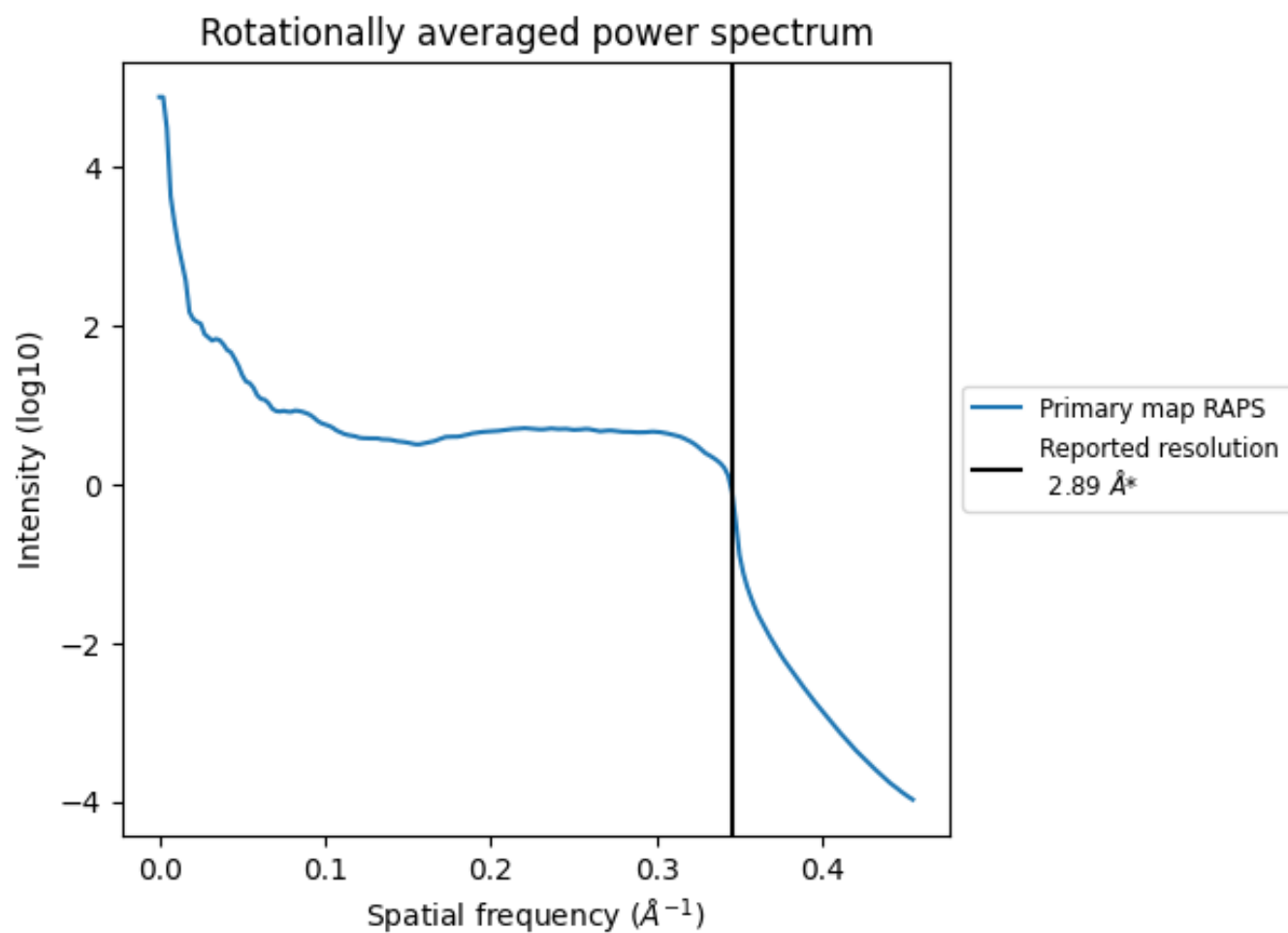
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 861 nm³; this corresponds to an approximate mass of 778 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.346 Å⁻¹

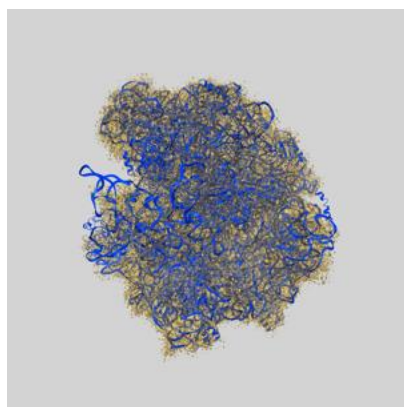
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

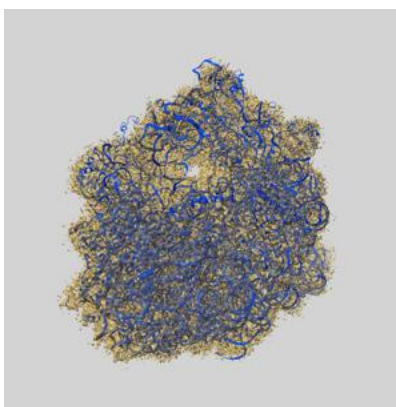
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10284 and PDB model 6SPF. Per-residue inclusion information can be found in section [3](#) on page [14](#).

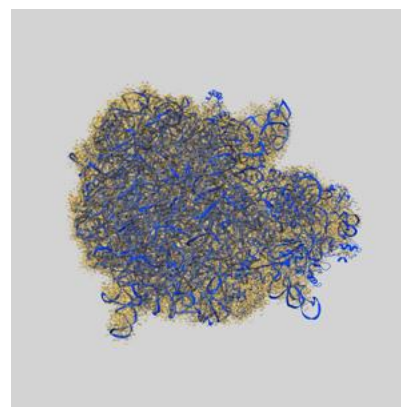
9.1 Map-model overlay [i](#)



X



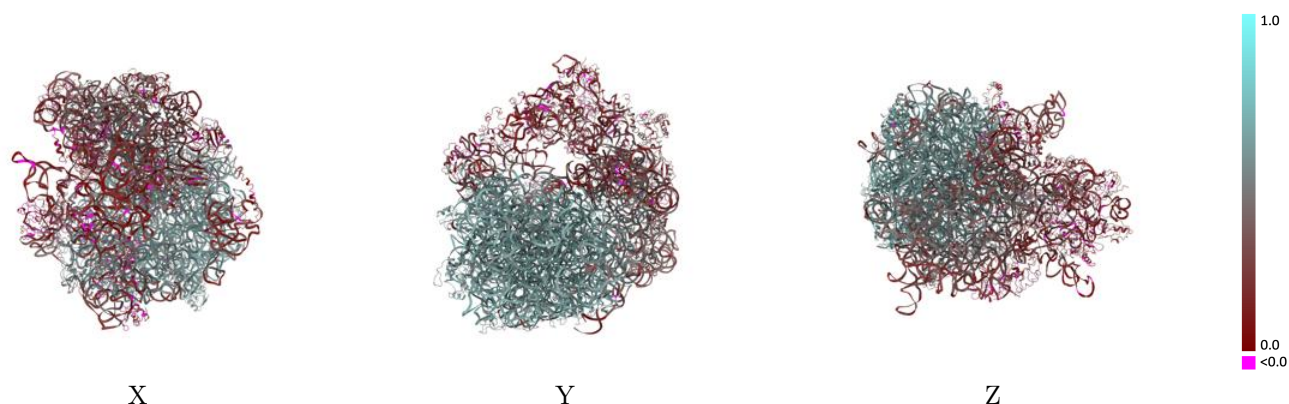
Y



Z

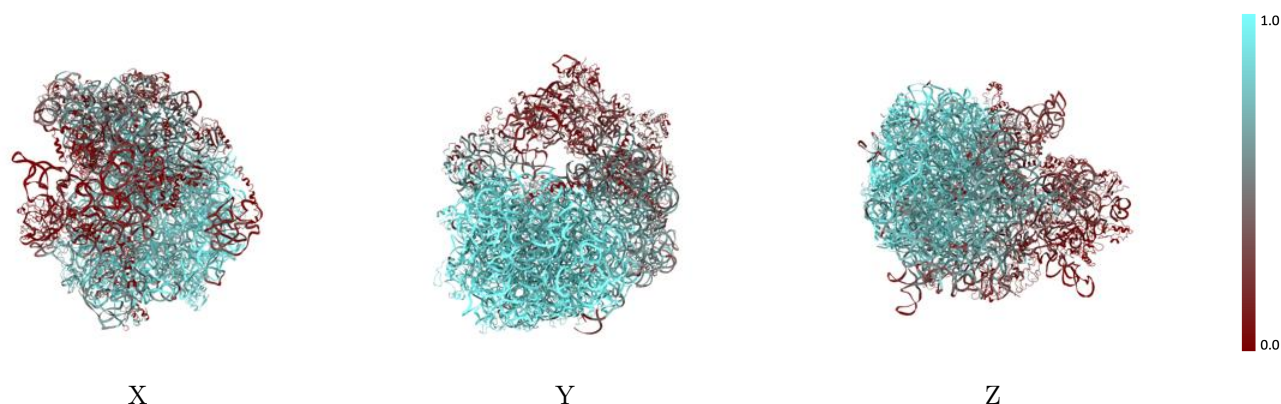
The images above show the 3D surface view of the map at the recommended contour level 0.0491 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



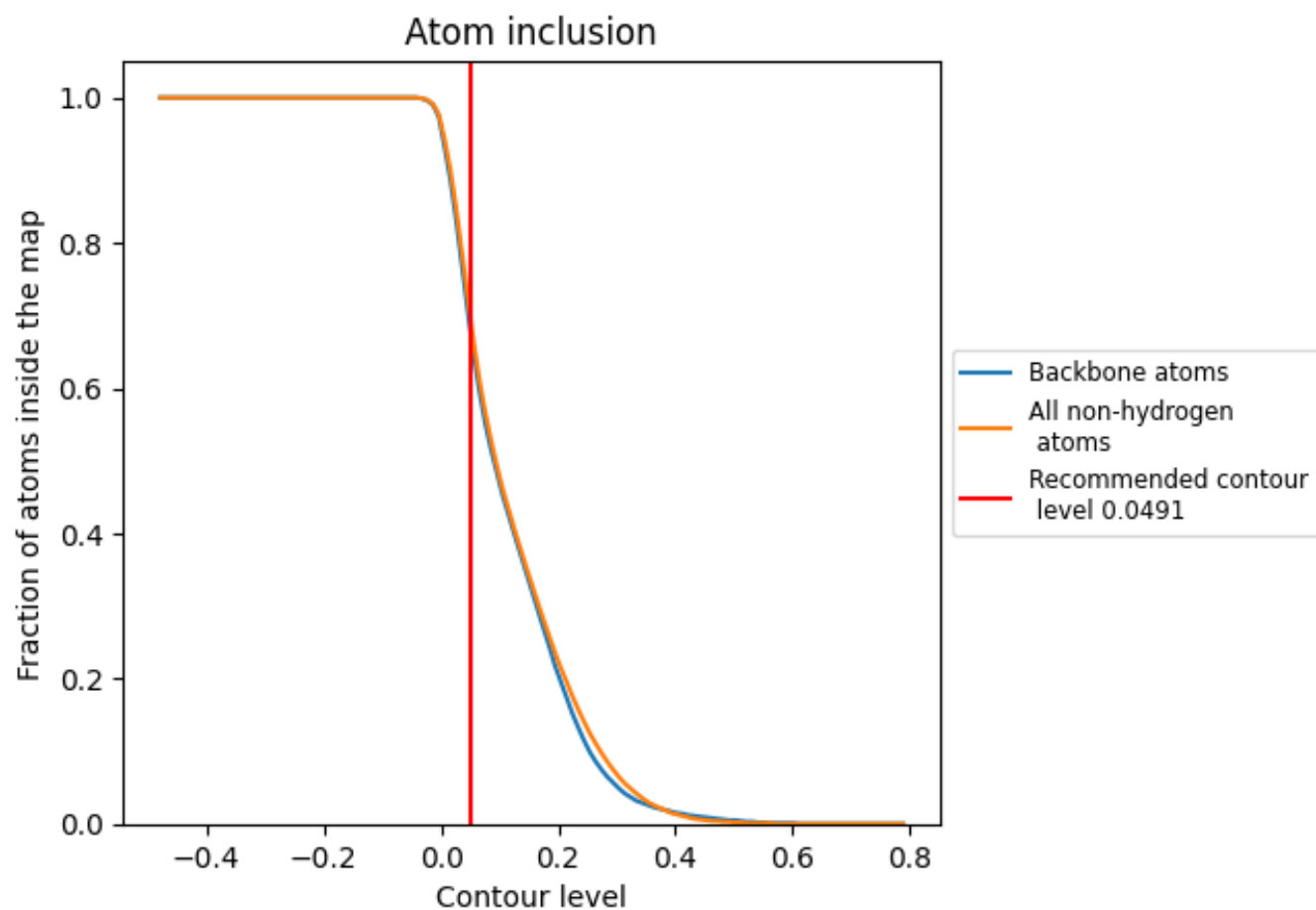
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0491).

9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 70% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0491) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7030	 0.4610
1	 0.0000	 0.1520
2	 0.9360	 0.6140
3	 0.5090	 0.3640
4	 0.9710	 0.6320
5	 0.8910	 0.5960
6	 0.8200	 0.5610
A	 0.8870	 0.5680
B	 0.7480	 0.3920
C	 0.9330	 0.6170
D	 0.9490	 0.6250
E	 0.9200	 0.5970
F	 0.3800	 0.2220
G	 0.3760	 0.3870
H	 0.3080	 0.2770
I	 0.0290	 0.1120
J	 0.9430	 0.6150
K	 0.9060	 0.6100
L	 0.9130	 0.5920
M	 0.8170	 0.5770
N	 0.9540	 0.6200
O	 0.5130	 0.2330
P	 0.8940	 0.5950
Q	 0.9230	 0.6060
R	 0.8800	 0.5620
S	 0.9230	 0.6200
T	 0.8990	 0.5870
U	 0.8310	 0.5470
V	 0.7330	 0.4960
W	 0.8950	 0.5910
X	 0.9100	 0.6020
Y	 0.8860	 0.5720
Z	 0.9310	 0.6070
a	 0.5370	 0.3220
b	 0.2520	 0.2730



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Chain	Atom inclusion	Q-score
c	 0.0560	 0.1670
d	 0.2680	 0.2390
e	 0.2910	 0.3050
f	 0.2170	 0.2100
g	 0.0940	 0.2300
h	 0.3720	 0.3130
i	 0.1350	 0.1730
j	 0.0630	 0.1880
k	 0.1990	 0.2160
l	 0.2990	 0.3490
m	 0.1090	 0.1710
n	 0.0580	 0.1730
o	 0.3770	 0.2550
p	 0.4440	 0.3410
q	 0.4800	 0.3650
r	 0.2210	 0.1440
s	 0.1340	 0.1910
t	 0.5600	 0.3880
u	 0.1230	 0.2450