



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 10:14 PM UTC

PDB ID : 7AQC / pdb_00007aqc
EMDB ID : EMD-11862
Title : Structure of the bacterial RQC complex (Decoding State)
Authors : Filbeck, S.; Pfeffer, S.
Deposited on : 2020-10-21
Resolution : 2.99 Å (reported)
Based on initial models : 1DM9, 3J9W, 5H3X, 5H3W

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:

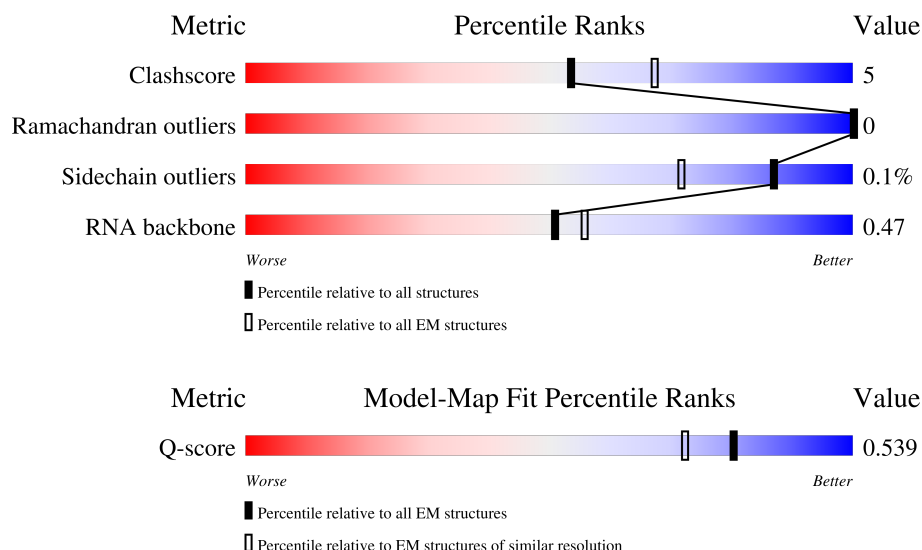
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.99 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.



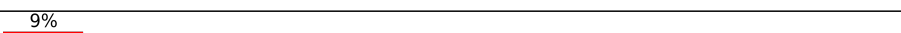
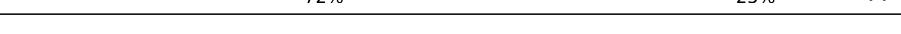
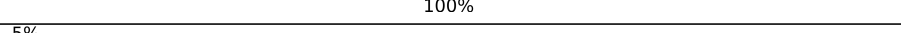
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13287 (2.49 - 3.49)

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	2820	
2	B	112	
3	C	277	

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Mol	Chain	Length	Quality of chain
4	D	209	
5	E	207	
6	F	179	
7	G	179	
8	I	141	
9	J	145	
10	K	122	
11	L	146	
12	M	144	
13	N	120	
14	O	120	
15	P	76	
15	T	76	
16	Q	119	
17	R	570	
18	S	113	
19	U	103	
20	V	94	
21	W	7	
22	X	62	
23	Y	86	
24	Z	59	
25	a	115	
26	b	59	
27	c	49	

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Mol	Chain	Length	Quality of chain
28	d	44	89% 11%
29	e	66	86% 11%
30	f	37	86% 11%
31	g	102	7% 89% 10%
32	h	95	83% 15%
33	i	66	5% 88% 11%

2 Entry composition

There are 33 unique types of molecules in this entry. The entry contains 95378 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 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2820	Total	C	N	O	P	0	0
			60561	27019	11193	19529	2820		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	112	Total	C	N	O	P	0	0
			2395	1068	435	780	112		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	275	Total	C	N	O	S	0	0
			2111	1312	416	377	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
			1575	988	290	292	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	178	Total	C	N	O	S	0	0
			1404	893	245	259	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	133	Total	C	N	O	S	0	0
			981	617	173	185	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	142	Total	C	N	O	S	0	0
			1123	710	206	202	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	146	Total	C	N	O	S	0	0
			1081	671	207	201	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	138	Total	C	N	O	S	0	0
			1097	703	208	181	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	119	Total	C	N	O	S	0	0
			953	583	186	180	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	120	Total	C	N	O	S	0	0
			912	564	176	171	1		

- Molecule 15 is a RNA chain called Ala-tRNA (P-site).

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	69	Total	C	N	O	P	0	0
			1477	657	268	483	69		
15	T	76	Total	C	N	O	P	0	0
			1622	722	290	534	76		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 17 is a protein called Rqc2 homolog RqcH.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	558	Total	C	N	O	S	0	0
			4498	2855	782	850	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 19 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	U	100	Total	C	N	O	S	0	0
			754	473	141	137	3		

- Molecule 20 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	82	Total	C	N	O		0	0
			630	390	123	117			

- Molecule 21 is a protein called nascent polyalanine.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	W	7	Total	C	N	O	0	0
			35	21	7	7		

- Molecule 22 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	58	Total	C	N	O	S	0	0
			444	275	92	75	2		

- Molecule 23 is a protein called Uncharacterized protein YabO.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	84	Total	C	N	O	S	0	0
			667	416	122	127	2		

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 25 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	a	114	Total	C	N	O	0	0
			936	595	184	157		

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 27 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c	48	Total	C	N	O	S	0	0
			401	244	80	73	4		

- Molecule 28 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	44	Total	C	N	O	S	0	0
			367	222	89	54	2		

- Molecule 29 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	e	64	Total	C	N	O	S	0	0
			512	321	107	82	2		

- Molecule 30 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	36	Total	C	N	O	S	0	0
			288	181	59	44	4		

- Molecule 31 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	g	101	Total	C	N	O		0	0
			786	501	139	146			

- Molecule 32 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	h	93	Total	C	N	O	S	0	0
			752	472	137	139	4		

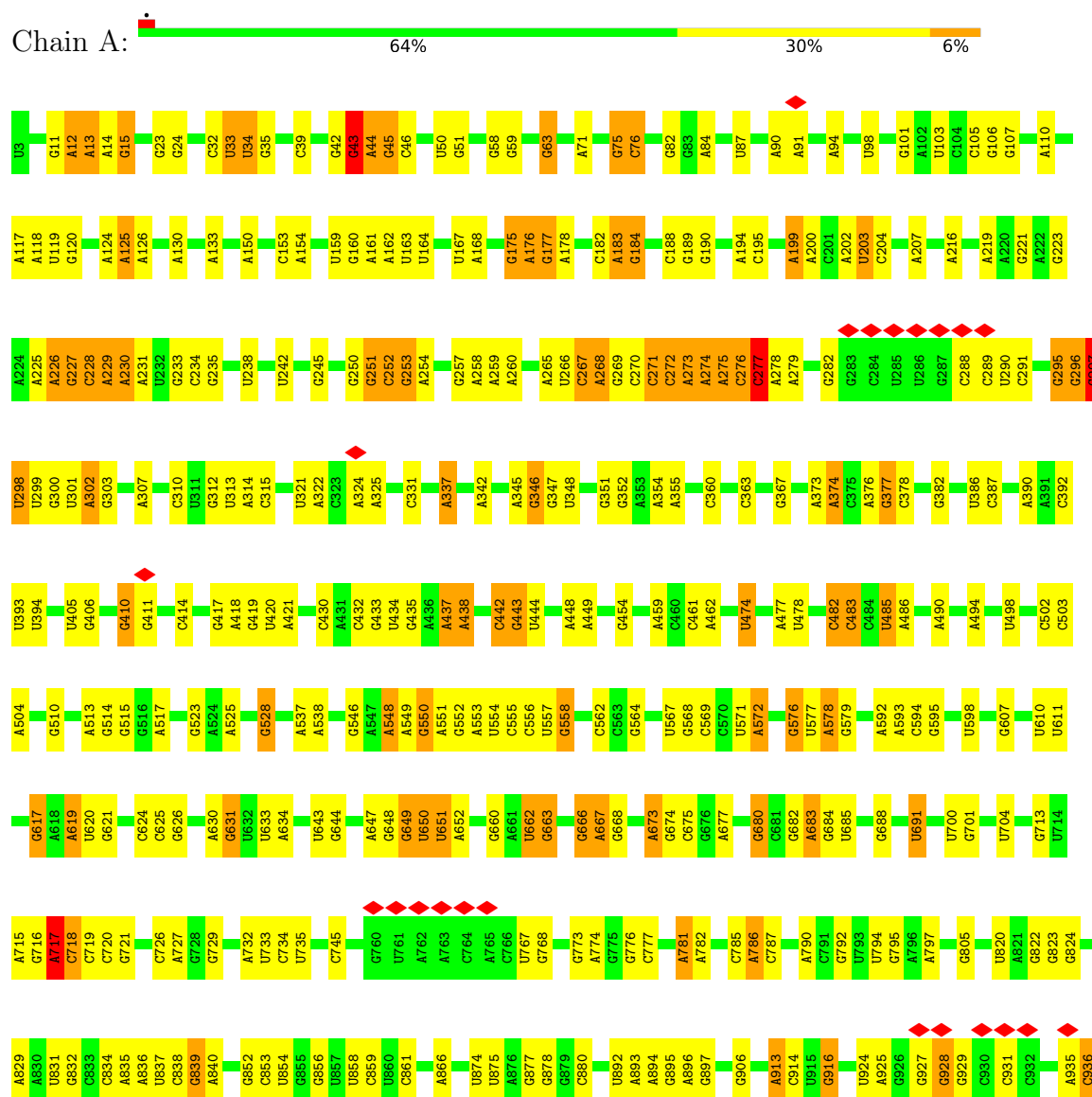
- Molecule 33 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	i	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

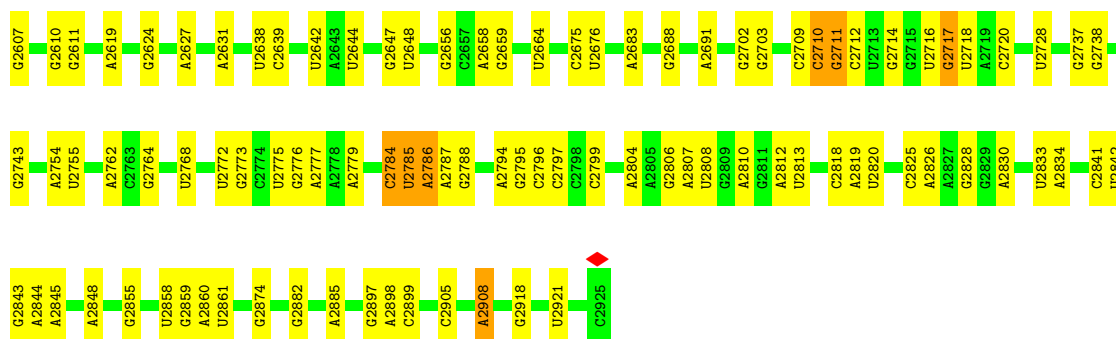
3 Residue-property plots

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: 23S ribosomal RNA



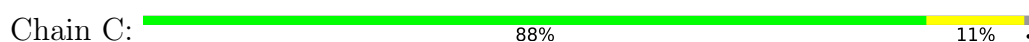
G2476	C2348	G2232	U2020	A1877	C1755	G1633	U1535	C1433	A1339	A1243	A1131	C1028	C937
A2477	A2349	C2233	G2021	U1881	U1756	U1634	A1536	C1444	A1340	A1244	A1132	A1029	G938
G2484	A2350	C2234	U2022	G1757	U1758	C1645	G1537	A1445	A1341	G1245	A1133	G1030	G939
C2485	G2352	C2235	U2023	G1758	U1759	C1646	G1538	C1450	U1345	G1246	A1134	C1031	G940
U2486	C2356	C2236	U2024	U1760	U1760	U1647	C1539	C1456	A1346	G1247	U1135	C1032	U941
U2487	A2357	C2237	A2025	G1769	A1648	A1648	A1553	U1457	A1347	G1250	U1136	A1034	U942
A2488	A2358	U2240	C2035	C1770	C1649	C1650	U1554	U1458	G1348	U1251	G1139	C1037	A943
U2489	A2241	U2242	G1898	G1771	C1651	G1651	A1555	U1459	G1349	U1252	A1140	C944	C944
G2501	C2361	A2243	U1899	A1774	A1652	C1652	G1561	A1461	U1350	G1256	A1142	A1042	C945
U2502	A2362	G2039	A1900	G1775	A1653	A1653	A1562	A1462	U1351	A1260	U1143	A1046	U947
C2503	G2040	G2041	G1901	G1776	A1654	A1655	G1563	C1463	U1352	A1264	A1144	A1046	A948
A2504	G2041	G1902	G1902	G1777	A1655	C1656	C1564	A1464	A1360	G1264	A1149	C1063	A952
A2505	A2047	G1912	G1912	A1778	U1565	C1657	U1565	G1463	A1361	U1274	C1150	A1054	A952
C2506	U2048	A1913	A1913	G1779	C1657	C1657	G1566	G1472	G1362	G1274	C1150	A1055	G952
A2507	A2049	A1914	A1914	C1780	U1568	A1658	U1567	A1473	G1363	G1275	U1151	A1058	G953
G2519	C2375	G1918	A1918	C1781	A1659	A1660	A1569	C1474	C1364	G1276	G1152	A1058	U954
U2520	U2377	A1918	A1918	C1782	A1661	A1661	U1570	G1475	U1365	G1277	G1156	A1059	A957
G2378	G2289	G1783	C1783	G1782	A1661	A1661	G1571	C1476	C1366	G1278	G1157	A1066	A958
C2379	G2287	A1784	G1785	G1782	G1664	G1664	G1572	A1477	G1367	C1279	A1157	A1067	A958
G2522	G2287	G1785	G1785	C1573	A1667	A1667	C1573	G1478	U1368	G1280	G1158	A1067	C959
G2523	G2287	A1788	G1785	G1578	A1667	A1667	G1578	G1479	C1370	C1281	U1159	U1069	U960
C2527	U2274	A1791	G1791	G1581	G1674	G1674	A1581	A1483	G1371	U1283	G1168	A1072	C961
C2528	G2275	G1792	G1792	U1581	A1674	A1674	U1581	U1484	G1376	A1284	U1176	A1072	C962
G2531	A2276	G1793	G1793	U1582	A1679	A1679	U1582	A1490	G1377	U1289	G1177	A1078	G963
A2532	G2067	A1941	A1941	A1583	A1680	A1680	A1583	A1491	U1380	G1290	G1178	A1079	A964
U2533	G2068	A1948	A1948	U1584	A1681	A1681	U1584	G1492	U1381	G1291	A1179	A1091	A970
G2534	C1949	C1949	C1949	A1585	C1682	C1682	A1585	C1493	A1381	G1292	C1181	A1092	A971
U2535	G1805	G1805	G1805	A1586	C1683	C1683	U1586	G1496	G1382	G1293	G1182	A1092	U972
A2542	U1808	U1808	U1808	U1587	A1691	A1691	U1587	G1497	C1384	U1295	G1185	A1094	G973
C2549	A1809	A1809	A1809	A1588	A1692	A1692	A1588	U1498	A1388	G1296	G1186	G1102	U977
G2556	G1810	G1810	G1810	A1592	C1693	C1693	A1592	U1499	A1302	A1302	U1187	A1103	A978
U2557	A1812	A1812	A1812	U1595	G1696	G1696	U1595	A1506	U1303	A1303	U1187	A1104	U979
C2558	A1813	A1813	A1813	U1596	A1697	A1697	U1596	U1507	A1404	G1304	A1188	G1105	C980
U2559	C1826	C1826	C1826	C1597	U1704	U1704	C1597	A1507	U1417	U1307	A1194	U1106	C981
A2560	U1827	U1827	U1827	C1598	C1705	C1705	C1598	G1512	U1418	U1307	U1107	G1108	A987
U2564	G1828	G1828	G1828	C1598	G1706	G1706	C1598	U1513	A1201	A1308	G1108	G1109	G988
G2564	C1829	C1829	C1829	C1598	A1709	A1709	C1598	C1514	A1202	A1308	G1109	G1110	U988
C2572	G1830	G1830	G1830	A1614	A1712	A1712	A1614	C1515	A1202	A1308	G1109	G1110	C990
G2577	A1845	A1845	A1845	A1617	A1714	A1714	A1617	C1516	G1209	A1312	U1111	U1111	A991
U2583	A1848	A1848	A1848	A1618	C1715	C1715	A1618	A1517	G1213	A1314	U1112	U1112	G992
A2593	G1853	G1853	G1853	A1619	G1719	G1719	A1619	C1519	G1213	A1315	G1114	G1114	A999
A2594	G1854	G1854	G1854	A1620	A1727	A1727	A1620	A1520	U1217	A1316	A1115	A1115	A1005
A2595	C1855	C1855	C1855	A1621	G1744	G1744	A1621	A1523	U1218	G1317	A1116	A1116	A1006
C2596	A1858	A1858	A1858	C1622	A1745	A1745	C1622	A1524	U1219	G1318	G1117	G1117	G1007
A2468	A1858	A1858	A1858	C1623	G1745	G1745	C1623	U1528	A1221	C1322	A1123	C1124	C1010
C2469	G1864	G1864	G1864	U1626	A1745	A1745	U1626	G1529	A1222	A1325	U1127	U1127	A1019
C2470	U1863	U1863	U1863	G1630	A1752	A1752	G1630	A1532	G1440	A1326	U1128	U1128	A1020
G2474	G1864	G1864	G1864	A1631	G1752	G1752	A1631	A1533	U1441	A1327	G1231	G1231	A1026
G2475	A1876	A1876	A1876	G1632	G1752	G1752	G1632	A1534	A1442	C1329	U1242	A1130	A1027



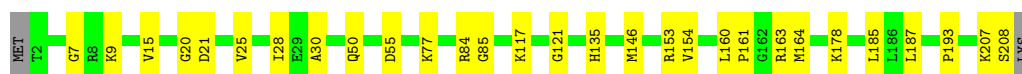
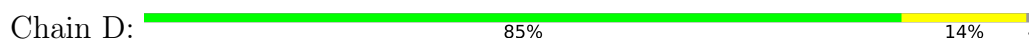
• Molecule 2: 5S ribosomal RNA



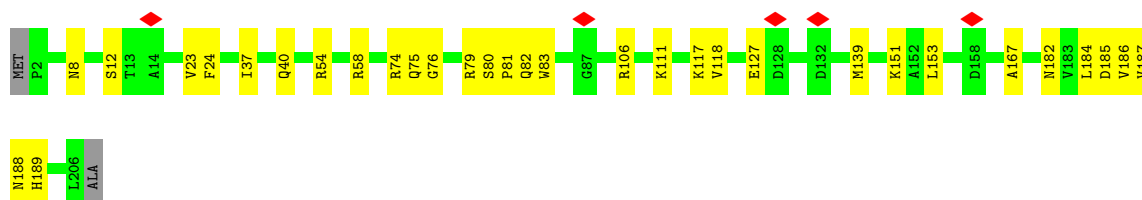
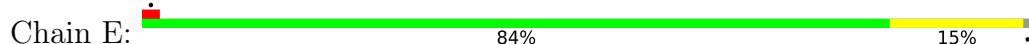
• Molecule 3: 50S ribosomal protein L2



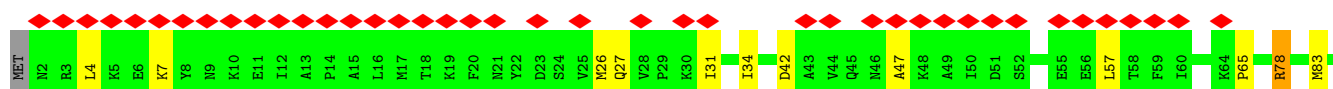
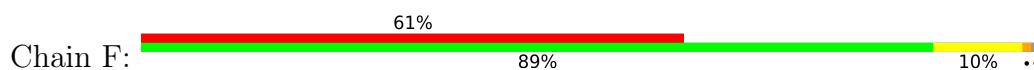
• Molecule 4: 50S ribosomal protein L3

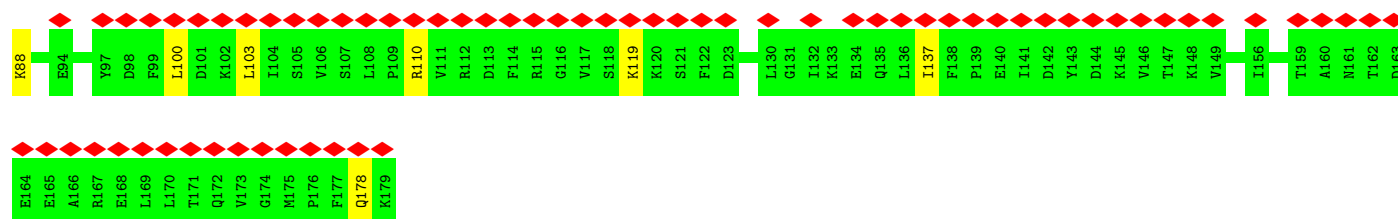


• Molecule 5: 50S ribosomal protein L4

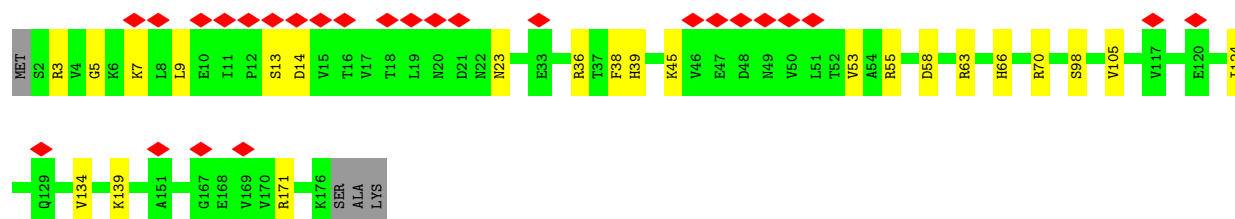
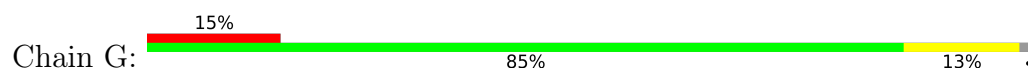


• Molecule 6: 50S ribosomal protein L5

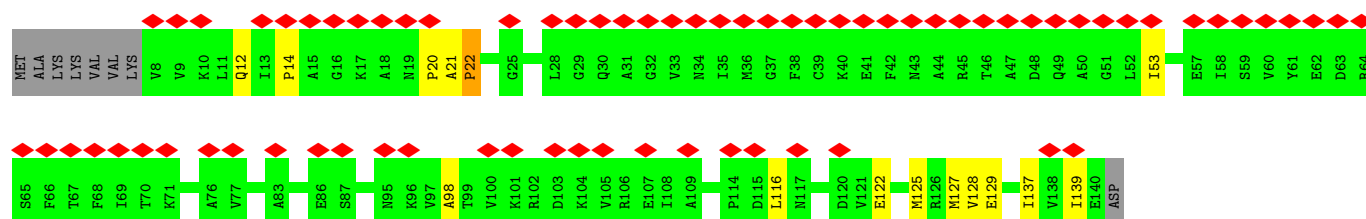
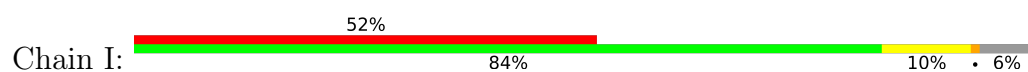




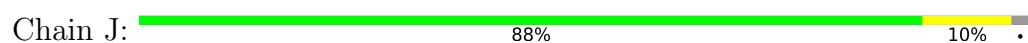
• Molecule 7: 50S ribosomal protein L6



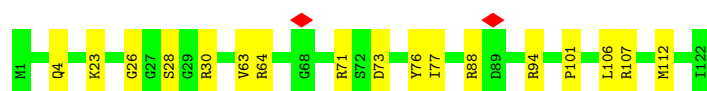
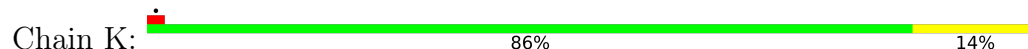
• Molecule 8: 50S ribosomal protein L11



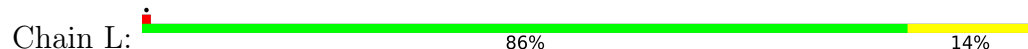
• Molecule 9: 50S ribosomal protein L13

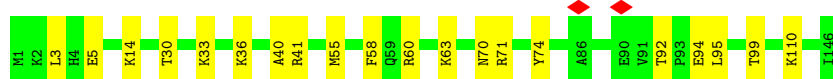


• Molecule 10: 50S ribosomal protein L14

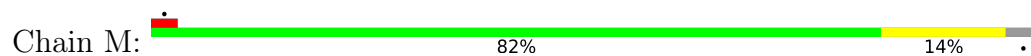


• Molecule 11: 50S ribosomal protein L15





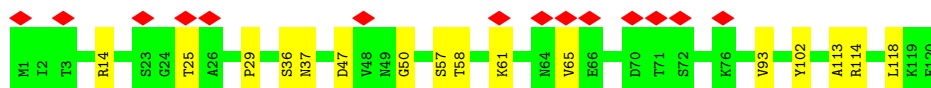
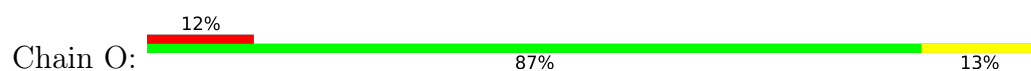
- Molecule 12: 50S ribosomal protein L16



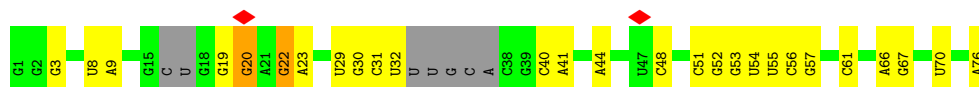
- Molecule 13: 50S ribosomal protein L17



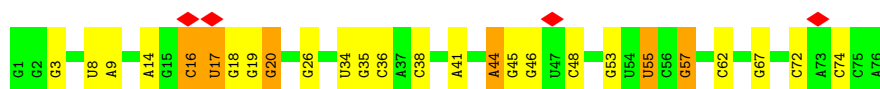
- Molecule 14: 50S ribosomal protein L18



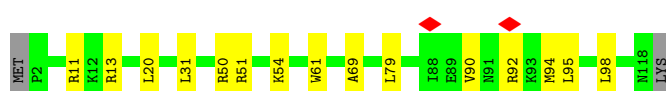
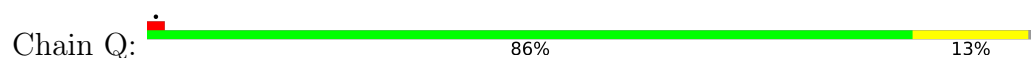
- Molecule 15: Ala-tRNA (P-site)



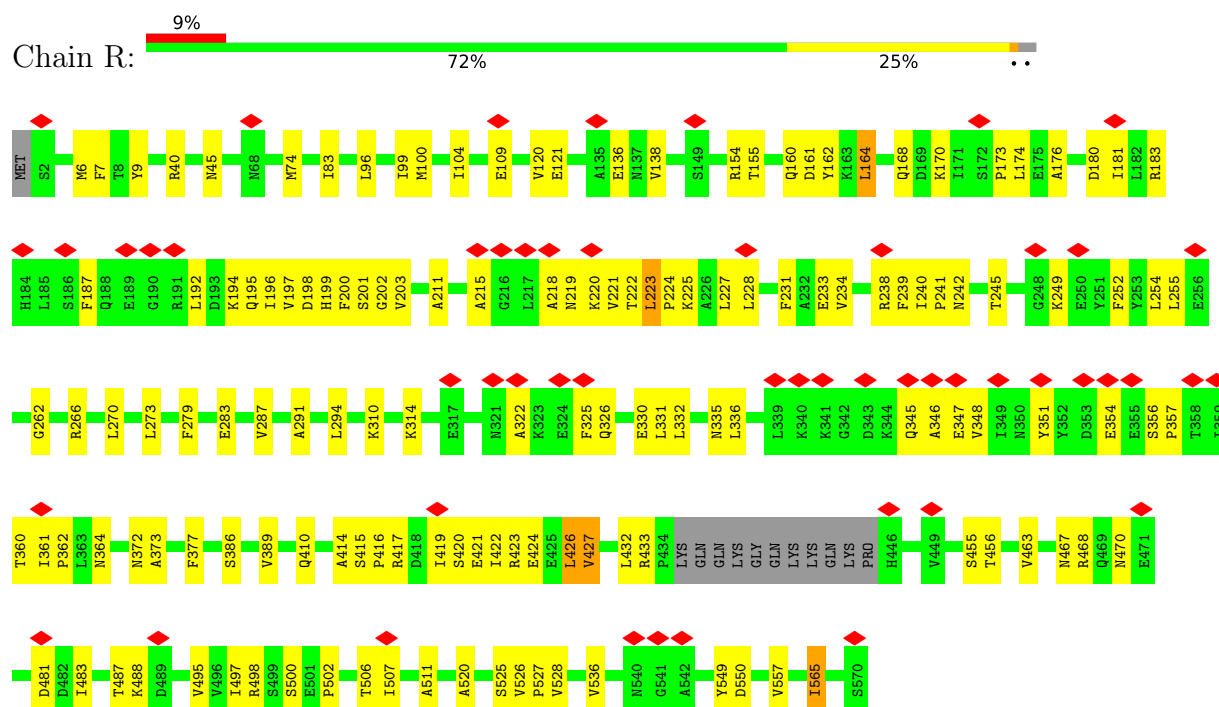
- Molecule 15: Ala-tRNA (P-site)



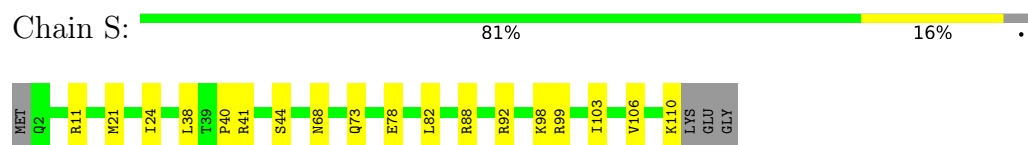
- Molecule 16: 50S ribosomal protein L20



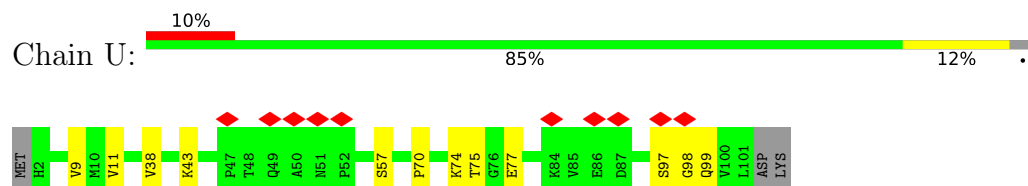
- Molecule 17: Rqc2 homolog RqcH



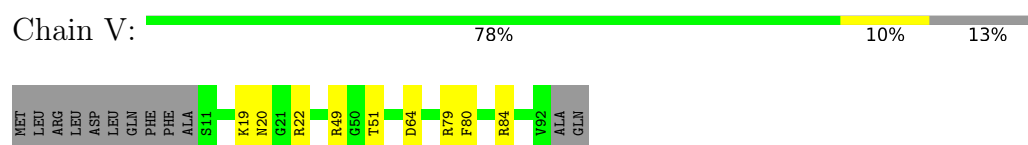
- Molecule 18: 50S ribosomal protein L22



- Molecule 19: 50S ribosomal protein L24



- Molecule 20: 50S ribosomal protein L27

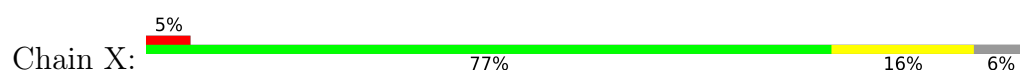


- Molecule 21: nascent polyalanine

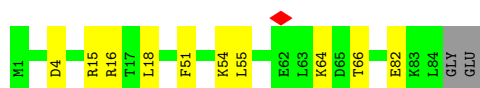
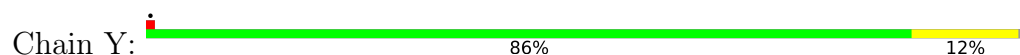


There are no outlier residues recorded for this chain.

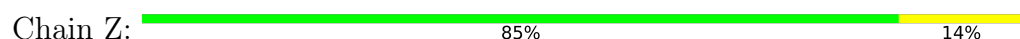
- Molecule 22: 50S ribosomal protein L28



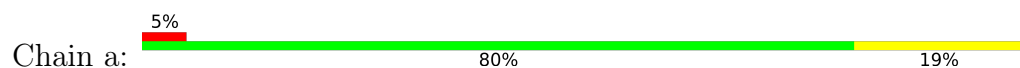
- Molecule 23: Uncharacterized protein YabO



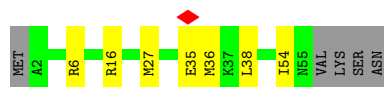
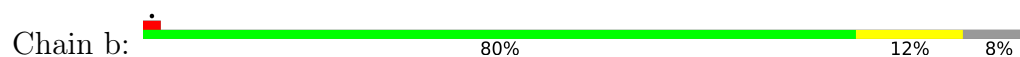
- Molecule 24: 50S ribosomal protein L30



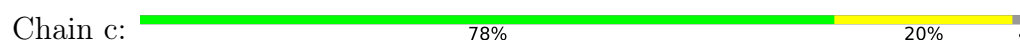
- Molecule 25: 50S ribosomal protein L19



- Molecule 26: 50S ribosomal protein L32



- Molecule 27: 50S ribosomal protein L33 1



- Molecule 28: 50S ribosomal protein L34



- Molecule 29: 50S ribosomal protein L35

Chain e:  86% 11% .

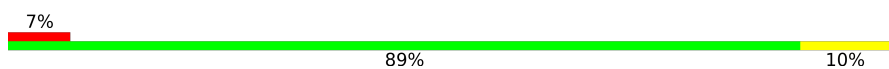


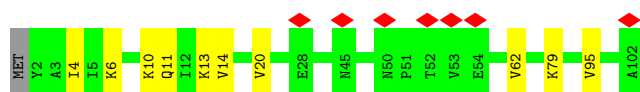
- Molecule 30: 50S ribosomal protein L36

Chain f:  86% 11% .



- Molecule 31: 50S ribosomal protein L21

Chain g:  7% 89% 10% .



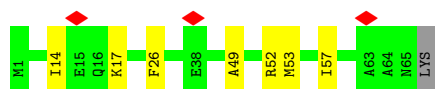
- Molecule 32: 50S ribosomal protein L23

Chain h:  83% 15% .



- Molecule 33: 50S ribosomal protein L29

Chain i:  5% 88% 11% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	138382	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.300	Depositor
Minimum map value	-0.042	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.011	Depositor
Map size (Å)	410.88, 410.88, 410.88	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.18	0/67837	0.39	15/105829 (0.0%)
2	B	0.17	0/2678	0.38	0/4174
3	C	0.19	0/2148	0.51	0/2881
4	D	0.20	0/1597	0.54	0/2140
5	E	0.22	0/1580	0.63	2/2132 (0.1%)
6	F	0.27	0/1423	0.75	3/1910 (0.2%)
7	G	0.22	0/1360	0.56	0/1832
8	I	0.25	0/995	0.59	0/1346
9	J	0.25	0/1146	0.60	3/1542 (0.2%)
10	K	0.23	0/927	0.62	2/1245 (0.2%)
11	L	0.20	0/1093	0.53	0/1457
12	M	0.21	0/1120	0.55	2/1496 (0.1%)
13	N	0.20	0/960	0.55	0/1284
14	O	0.23	0/921	0.62	2/1236 (0.2%)
15	P	0.20	0/1648	0.39	0/2564
15	T	0.16	0/1811	0.37	0/2822
16	Q	0.25	0/952	0.60	0/1266
17	R	0.59	0/4590	0.82	5/6195 (0.1%)
18	S	0.24	0/851	0.64	0/1146
19	U	0.20	0/764	0.55	0/1022
20	V	0.25	0/638	0.61	0/847
21	W	0.16	0/34	0.49	0/46
22	X	0.31	0/448	0.90	2/596 (0.3%)
23	Y	0.16	0/670	0.45	0/893
24	Z	0.23	0/457	0.58	0/613
25	a	0.17	0/949	0.48	0/1269
26	b	0.25	0/433	0.74	0/574
27	c	0.18	0/406	0.44	0/540
28	d	0.16	0/370	0.49	0/483
29	e	0.22	0/519	0.62	2/680 (0.3%)
30	f	0.17	0/291	0.40	0/383
31	g	0.24	0/797	0.70	0/1070
32	h	0.18	0/759	0.53	0/1011
33	i	0.25	0/531	0.60	0/707

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.22	0/103703	0.46	38/155231 (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	1
8	I	0	1
All	All	0	2

There are no bond length outliers.

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1351	U	C2'-C3'-O3'	7.55	120.82	109.50
1	A	43	G	C2'-C3'-O3'	7.29	124.64	113.70
1	A	297	G	C4'-C3'-O3'	7.27	123.90	113.00
22	X	23	ASN	CA-C-N	7.01	134.32	121.70
22	X	23	ASN	C-N-CA	7.01	134.32	121.70
14	O	65	VAL	CA-C-N	6.87	134.06	121.70
14	O	65	VAL	C-N-CA	6.87	134.06	121.70
12	M	137	ILE	CA-C-N	6.54	133.47	121.70
12	M	137	ILE	C-N-CA	6.54	133.47	121.70
1	A	717	A	C4'-C3'-O3'	6.53	119.19	109.40
1	A	649	G	C2'-C3'-O3'	6.50	123.46	113.70
6	F	78	ARG	CA-C-N	6.49	133.39	121.70
6	F	78	ARG	C-N-CA	6.49	133.39	121.70
17	R	223	LEU	CA-C-N	6.44	126.20	119.05
17	R	223	LEU	C-N-CA	6.44	126.20	119.05
9	J	26	LEU	N-CA-C	6.08	117.58	111.07
6	F	83	MET	CA-CB-CG	6.01	126.13	114.10
1	A	717	A	C2'-C3'-O3'	5.95	118.43	109.50
17	R	164	LEU	CA-C-N	5.95	126.51	120.38
17	R	164	LEU	C-N-CA	5.95	126.51	120.38
1	A	1245	G	C4'-C3'-O3'	5.91	118.26	109.40
29	e	20	GLY	CA-C-N	5.90	132.33	121.70
29	e	20	GLY	C-N-CA	5.90	132.33	121.70
10	K	28	SER	CA-C-N	5.69	131.95	121.70
10	K	28	SER	C-N-CA	5.69	131.95	121.70
1	A	1652	C	C2'-C3'-O3'	5.64	117.97	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2785	U	P-O3'-C3'	5.37	128.25	120.20
1	A	1245	G	C2'-C3'-O3'	5.34	117.51	109.50
1	A	1351	U	C4'-C3'-O3'	5.29	117.34	109.40
9	J	26	LEU	CA-C-N	5.22	131.09	121.70
9	J	26	LEU	C-N-CA	5.22	131.09	121.70
1	A	277	C	C4'-C3'-O3'	5.20	120.79	113.00
17	R	314	LYS	CB-CG-CD	5.17	123.20	111.30
1	A	377	G	P-O3'-C3'	5.09	127.84	120.20
1	A	936	C	P-O3'-C3'	5.08	127.81	120.20
5	E	127	GLU	CA-C-N	5.02	131.13	121.54
5	E	127	GLU	C-N-CA	5.02	131.13	121.54
1	A	683	A	P-O3'-C3'	5.01	127.71	120.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	154	LEU	Peptide
8	I	22	PRO	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	60561	0	30478	434	0
2	B	2395	0	1212	8	0
3	C	2111	0	2200	20	0
4	D	1575	0	1642	19	0
5	E	1561	0	1647	22	0
6	F	1404	0	1467	14	0
7	G	1342	0	1388	19	0
8	I	981	0	1020	14	0
9	J	1123	0	1162	7	0
10	K	920	0	977	12	0
11	L	1081	0	1132	15	0
12	M	1097	0	1165	10	0
13	N	953	0	983	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	O	912	0	947	9	0
15	P	1477	0	751	6	0
15	T	1622	0	823	8	0
16	Q	940	0	1005	27	0
17	R	4498	0	4514	137	0
18	S	842	0	899	15	0
19	U	754	0	809	6	0
20	V	630	0	644	7	0
21	W	35	0	37	0	0
22	X	444	0	487	6	0
23	Y	667	0	716	8	0
24	Z	455	0	491	5	0
25	a	936	0	1008	13	0
26	b	426	0	445	8	0
27	c	401	0	413	8	0
28	d	367	0	410	5	0
29	e	512	0	564	6	0
30	f	288	0	330	3	0
31	g	786	0	826	21	0
32	h	752	0	802	10	0
33	i	530	0	568	4	0
All	All	95378	0	63962	788	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 5.

All (788) 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)
16:Q:92:ARG:HH12	31:g:10:LYS:CA	1.28	1.46
16:Q:92:ARG:NH1	31:g:10:LYS:CA	1.86	1.32
16:Q:92:ARG:NH1	31:g:10:LYS:HA	0.96	1.27
16:Q:92:ARG:CZ	31:g:10:LYS:HA	1.96	0.95
1:A:2776:G:H21	1:A:2786:A:H62	1.18	0.91
1:A:1245:G:H1'	1:A:1246:G:H5'	1.54	0.89
1:A:1491:A:N6	1:A:1512:G:H1	1.71	0.88
1:A:1491:A:H62	1:A:1512:G:H1	0.88	0.86
1:A:12:A:H5''	1:A:12:A:H8	1.41	0.85
1:A:1246:G:H1'	1:A:1247:G:H5'	1.60	0.82
17:R:291:ALA:HB2	17:R:419:ILE:HD13	1.63	0.80
17:R:254:LEU:HD12	17:R:255:LEU:HG	1.63	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:138:VAL:HA	17:R:161:ASP:HA	1.65	0.78
1:A:12:A:H5''	1:A:12:A:C8	2.18	0.78
1:A:82:G:N2	1:A:103:U:O4	2.17	0.78
1:A:175:G:H8	1:A:175:G:H5''	1.46	0.78
1:A:1651:G:H5''	1:A:1651:G:N3	1.98	0.78
1:A:228:C:H5''	1:A:228:C:H6	1.47	0.78
17:R:419:ILE:HA	17:R:422:ILE:HD12	1.65	0.77
1:A:1516:A:C8	1:A:1516:A:H5''	2.20	0.76
1:A:1515:C:H2'	1:A:1516:A:H8	1.49	0.76
17:R:294:LEU:HD22	17:R:432:LEU:HD11	1.67	0.75
1:A:716:G:N3	1:A:716:G:H2'	1.99	0.75
17:R:223:LEU:HB2	17:R:224:PRO:HD3	1.71	0.73
16:Q:92:ARG:HG3	31:g:11:GLN:CD	2.12	0.73
1:A:2711:G:H5'	1:A:2711:G:H8	1.53	0.72
17:R:483:ILE:HG13	17:R:502:PRO:HG3	1.71	0.72
1:A:1348:G:H21	1:A:1656:C:H5'	1.54	0.72
17:R:219:ASN:HB3	17:R:222:THR:HB	1.72	0.72
17:R:7:PHE:HA	17:R:254:LEU:HD23	1.71	0.71
8:I:21:ALA:HB3	17:R:351:TYR:CD1	2.26	0.71
1:A:1516:A:H5''	1:A:1516:A:H8	1.56	0.69
1:A:1349:G:H1'	1:A:1656:C:H5''	1.74	0.69
1:A:1515:C:H2'	1:A:1516:A:C8	2.27	0.69
1:A:721:G:H5''	5:E:76:GLY:H	1.58	0.69
1:A:2776:G:N2	1:A:2786:A:H62	1.91	0.68
1:A:251:G:H4'	1:A:251:G:OP1	1.93	0.68
17:R:356:SER:N	17:R:357:PRO:HD3	2.09	0.68
17:R:423:ARG:HH11	17:R:432:LEU:HD13	1.59	0.67
1:A:175:G:H8	1:A:175:G:C5'	2.08	0.67
1:A:295:G:H2'	1:A:296:G:C8	2.28	0.67
16:Q:92:ARG:HH12	31:g:10:LYS:CB	2.05	0.67
1:A:271:C:H5''	1:A:271:C:H6	1.59	0.67
17:R:221:VAL:C	17:R:224:PRO:HD2	2.20	0.66
31:g:6:LYS:HB3	31:g:11:GLN:HG2	1.76	0.66
17:R:335:ASN:HB2	17:R:351:TYR:OH	1.95	0.66
1:A:442:C:C6	1:A:442:C:H5''	2.31	0.66
1:A:442:C:H5''	1:A:442:C:H6	1.59	0.66
1:A:443:G:C8	1:A:443:G:H5''	2.31	0.66
12:M:65:TRP:HB2	12:M:105:GLU:HB2	1.78	0.66
1:A:1363:G:H4'	1:A:1363:G:OP1	1.96	0.65
17:R:331:LEU:HB3	17:R:348:VAL:HG11	1.79	0.65
17:R:511:ALA:HB1	17:R:528:VAL:HG11	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:58:ARG:O	5:E:79:ARG:NH1	2.30	0.65
1:A:1706:G:N2	1:A:2717:G:OP1	2.30	0.65
17:R:415:SER:HB2	17:R:416:PRO:HD2	1.77	0.65
23:Y:51:PHE:HB2	23:Y:54:LYS:HB2	1.78	0.65
1:A:43:G:H8	1:A:43:G:H5''	1.61	0.64
1:A:1491:A:N7	1:A:1512:G:N2	2.37	0.64
1:A:271:C:H5''	1:A:271:C:C6	2.31	0.64
8:I:21:ALA:CB	17:R:351:TYR:CD1	2.81	0.64
17:R:294:LEU:HD11	17:R:423:ARG:HB2	1.80	0.64
20:V:80:PHE:HB2	20:V:84:ARG:HB3	1.80	0.64
7:G:3:ARG:HE	7:G:5:GLY:H	1.45	0.64
1:A:894:A:H62	1:A:979:U:H3	1.44	0.64
1:A:296:G:H2'	1:A:297:G:C8	2.33	0.63
1:A:717:A:H4'	1:A:718:C:H3'	1.81	0.63
17:R:218:ALA:HB1	17:R:223:LEU:HD11	1.80	0.63
16:Q:92:ARG:NH1	31:g:10:LYS:CB	2.61	0.63
1:A:251:G:H3'	1:A:251:G:H8	1.63	0.63
17:R:421:GLU:HB3	17:R:468:ARG:HH11	1.64	0.63
1:A:13:A:H61	1:A:571:U:H3'	1.63	0.63
1:A:916:G:H8	1:A:916:G:H5''	1.64	0.62
1:A:2776:G:H21	1:A:2786:A:N6	1.92	0.62
2:B:70:G:H21	2:B:102:A:H62	1.48	0.62
25:a:55:GLY:HA2	25:a:60:GLU:HG3	1.82	0.62
1:A:1808:U:OP2	1:A:1813:A:N6	2.33	0.62
1:A:250:G:H3'	1:A:252:C:O2	2.00	0.61
1:A:443:G:H5''	1:A:443:G:H8	1.65	0.61
6:F:110:ARG:HD2	6:F:137:ILE:HA	1.83	0.61
1:A:228:C:H5''	1:A:228:C:C6	2.32	0.61
1:A:1622:C:C6	1:A:1622:C:H5''	2.35	0.61
17:R:294:LEU:HD21	17:R:423:ARG:HD2	1.81	0.61
1:A:1565:U:O5'	1:A:1565:U:H6	1.83	0.61
15:T:26:G:H1	15:T:44:A:H61	1.49	0.61
1:A:1516:A:H3'	1:A:1517:A:C8	2.36	0.61
1:A:1516:A:H3'	1:A:1517:A:H8	1.66	0.60
1:A:1523:U:H4'	1:A:1523:U:OP1	2.00	0.60
1:A:517:A:OP1	5:E:79:ARG:NH2	2.34	0.60
1:A:1111:U:H3	1:A:1115:A:H5''	1.65	0.60
1:A:1279:C:H2'	1:A:1280:G:C8	2.36	0.60
17:R:155:THR:HB	17:R:160:GLN:HE22	1.66	0.60
1:A:251:G:H3'	1:A:251:G:C8	2.36	0.60
17:R:239:PHE:CD1	17:R:254:LEU:HD13	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1244:A:H4'	11:L:3:LEU:HD23	1.84	0.60
1:A:1368:U:H2'	1:A:1368:U:O2	2.02	0.60
3:C:241:ILE:HG21	3:C:246:PRO:HB3	1.84	0.60
1:A:1863:U:H5''	1:A:1864:G:H5'	1.84	0.60
1:A:2504:C:H42	1:A:2558:G:H22	1.50	0.60
3:C:273:ARG:HG2	3:C:274:ARG:HG2	1.84	0.60
17:R:361:ILE:HG13	17:R:361:ILE:O	2.02	0.60
1:A:2039:G:OP2	18:S:41:ARG:NH1	2.35	0.59
1:A:1582:U:H3	1:A:1585:A:H62	1.51	0.59
7:G:3:ARG:HH11	7:G:55:ARG:HH21	1.49	0.59
1:A:12:A:H8	1:A:12:A:C5'	2.14	0.59
1:A:199:A:H62	1:A:878:G:H21	1.50	0.59
1:A:1112:U:H3'	1:A:1112:U:H6	1.68	0.59
1:A:160:G:O2'	1:A:168:A:N6	2.34	0.59
1:A:515:G:N7	28:d:39:ARG:NH2	2.51	0.59
1:A:175:G:H5''	1:A:175:G:C8	2.35	0.59
5:E:8:ASN:H	5:E:12:SER:HB2	1.68	0.59
1:A:2374:G:H5'	1:A:2376:C:H5'	1.85	0.58
1:A:630:A:H62	1:A:1291:A:H2	1.50	0.58
1:A:1496:G:H1	1:A:1507:U:H3	1.50	0.58
6:F:42:ASP:HB3	6:F:47:ALA:H	1.68	0.58
29:e:54:ASP:OD1	29:e:57:ARG:NH2	2.36	0.58
1:A:1347:A:N6	1:A:1651:G:H1'	2.18	0.58
1:A:716:G:H21	1:A:717:A:H5'	1.69	0.58
1:A:2711:G:H8	1:A:2711:G:C5'	2.16	0.58
1:A:419:G:N2	1:A:448:A:OP2	2.37	0.58
7:G:5:GLY:HA2	7:G:70:ARG:HD3	1.85	0.57
10:K:107:ARG:HG3	10:K:112:MET:HE1	1.85	0.57
16:Q:90:VAL:O	31:g:11:GLN:NE2	2.35	0.57
19:U:11:VAL:HG21	19:U:38:VAL:HG11	1.85	0.57
17:R:240:ILE:O	17:R:240:ILE:HG22	2.03	0.57
1:A:880:C:O2'	29:e:57:ARG:NH1	2.37	0.57
5:E:139:MET:HG2	5:E:167:ALA:HB2	1.87	0.57
1:A:745:C:O2'	1:A:781:A:N6	2.37	0.57
1:A:1245:G:H2'	1:A:1245:G:N3	2.20	0.57
1:A:2041:G:OP1	18:S:11:ARG:NH2	2.38	0.57
5:E:153:LEU:HD21	5:E:185:ASP:HB3	1.87	0.57
17:R:219:ASN:HB3	17:R:222:THR:CB	2.32	0.57
17:R:287:VAL:HB	17:R:419:ILE:HG21	1.86	0.57
32:h:20:LEU:HD22	32:h:25:LYS:HD2	1.87	0.57
1:A:221:G:H1	1:A:238:U:H4'	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1367:G:O5'	1:A:1367:G:H8	1.88	0.57
1:A:229:A:H3'	1:A:230:A:C8	2.40	0.56
1:A:272:C:O2	1:A:272:C:H2'	2.05	0.56
17:R:322:ALA:HA	17:R:325:PHE:CD2	2.40	0.56
1:A:44:A:H8	1:A:44:A:H5''	1.70	0.56
1:A:194:A:H2'	1:A:195:C:C6	2.40	0.56
1:A:230:A:O5'	1:A:230:A:H8	1.88	0.56
1:A:1433:U:H5''	1:A:1648:A:H4'	1.86	0.56
1:A:1712:G:O2'	1:A:1714:A:N7	2.39	0.56
8:I:22:PRO:HD3	17:R:351:TYR:HB3	1.85	0.56
1:A:483:C:H5''	1:A:483:C:H6	1.71	0.56
1:A:633:U:H2'	1:A:634:A:H8	1.71	0.56
6:F:78:ARG:HD3	15:P:56:C:H1'	1.87	0.56
1:A:250:G:C5	1:A:252:C:H1'	2.40	0.56
17:R:345:GLN:N	17:R:362:PRO:O	2.38	0.56
19:U:43:LYS:HB3	19:U:57:SER:HB2	1.88	0.55
6:F:119:LYS:HB3	6:F:178:GLN:HB3	1.88	0.55
17:R:155:THR:HB	17:R:160:GLN:NE2	2.22	0.55
1:A:1568:G:N2	1:A:1569:A:O2'	2.40	0.55
12:M:1:MET:N	12:M:48:GLU:OE1	2.40	0.55
17:R:187:PHE:HZ	17:R:220:LYS:HG2	1.72	0.55
17:R:279:PHE:CZ	17:R:565:ILE:HG13	2.42	0.55
32:h:32:VAL:HA	32:h:77:ARG:HD3	1.88	0.55
1:A:1245:G:H1'	1:A:1246:G:C5'	2.34	0.55
17:R:294:LEU:CD2	17:R:432:LEU:HD11	2.36	0.55
1:A:200:A:N6	1:A:2459:A:O2'	2.40	0.55
1:A:1042:A:O2'	16:Q:92:ARG:NE	2.40	0.55
17:R:423:ARG:O	17:R:427:VAL:HG13	2.07	0.55
1:A:717:A:OP2	1:A:717:A:H2'	2.07	0.54
1:A:1828:G:OP1	3:C:260:ARG:NH1	2.37	0.54
1:A:2287:C:O2'	1:A:2456:C:OP2	2.25	0.54
17:R:223:LEU:N	17:R:224:PRO:CD	2.70	0.54
27:c:24:ARG:NH1	27:c:25:ASN:OD1	2.40	0.54
1:A:1971:C:H3'	1:A:1972:U:H2'	1.89	0.54
1:A:203:U:H2'	1:A:203:U:O2	2.07	0.54
1:A:790:A:O2'	1:A:1704:U:OP1	2.26	0.54
14:O:29:PRO:HG2	14:O:93:VAL:HG12	1.89	0.54
17:R:416:PRO:O	17:R:419:ILE:HG13	2.08	0.54
17:R:424:GLU:O	17:R:427:VAL:HG22	2.08	0.54
1:A:13:A:O4'	1:A:572:A:N6	2.41	0.54
18:S:38:LEU:HD13	26:b:38:LEU:HB3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:572:A:O2'	1:A:2072:C:O2	2.26	0.54
15:P:55:U:O2	15:P:57:G:N2	2.41	0.54
17:R:219:ASN:H	17:R:223:LEU:HG	1.72	0.54
22:X:45:LYS:HB3	22:X:46:LYS:HB2	1.88	0.54
1:A:175:G:C5'	1:A:175:G:C8	2.90	0.54
1:A:267:C:H6	1:A:267:C:OP2	1.91	0.54
1:A:1111:U:H6	1:A:1111:U:O5'	1.90	0.54
1:A:2788:G:O2'	7:G:36:ARG:NH2	2.40	0.54
1:A:33:U:H1'	1:A:34:U:C4	2.42	0.54
1:A:854:U:OP2	11:L:41:ARG:NH2	2.41	0.54
12:M:44:ASN:HB3	12:M:70:PRO:HG3	1.89	0.54
17:R:252:PHE:HB2	17:R:273:LEU:HD11	1.90	0.54
25:a:78:PRO:HG2	25:a:81:THR:HB	1.89	0.54
1:A:175:G:OP1	1:A:175:G:C4'	2.56	0.54
1:A:1111:U:H3	1:A:1115:A:C5'	2.21	0.54
1:A:2711:G:C5'	1:A:2711:G:C8	2.91	0.54
4:D:20:GLY:HA3	25:a:83:LYS:HE3	1.90	0.54
1:A:2421:A:OP2	1:A:2453:C:N4	2.41	0.54
6:F:78:ARG:NH2	15:P:20:G:O6	2.41	0.54
16:Q:92:ARG:HG3	31:g:11:GLN:NE2	2.23	0.54
10:K:63:VAL:HG12	10:K:106:LEU:HD11	1.90	0.53
1:A:2833:U:H2'	1:A:2834:A:H8	1.73	0.53
17:R:99:ILE:HD12	17:R:121:GLU:HG2	1.89	0.53
20:V:19:LYS:O	20:V:22:ARG:NH2	2.39	0.53
1:A:227:G:H1	1:A:234:C:H42	1.57	0.53
1:A:662:U:H2'	1:A:663:G:H8	1.74	0.53
1:A:840:A:OP2	1:A:2100:A:O2'	2.25	0.53
1:A:227:G:OP2	1:A:227:G:H3'	2.08	0.53
1:A:251:G:C8	1:A:251:G:C3'	2.91	0.53
17:R:520:ALA:HB3	17:R:526:VAL:HG21	1.90	0.53
27:c:31:GLU:OE2	27:c:46:ARG:NH1	2.41	0.53
32:h:24:LYS:HZ1	32:h:87:SER:H	1.56	0.53
4:D:146:MET:HE1	4:D:160:LEU:HD11	1.89	0.53
7:G:5:GLY:O	7:G:70:ARG:NH1	2.41	0.53
17:R:502:PRO:HB2	17:R:507:ILE:HD11	1.89	0.53
1:A:45:G:H8	1:A:45:G:H5''	1.73	0.53
1:A:1886:G:H21	1:A:1914:A:H62	1.56	0.53
1:A:2474:G:OP1	5:E:74:ARG:NH2	2.40	0.53
3:C:16:MET:HB3	3:C:206:GLY:HA3	1.90	0.53
16:Q:92:ARG:NH1	31:g:10:LYS:C	2.61	0.53
17:R:332:LEU:HG	17:R:336:LEU:HD23	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:716:G:N3	1:A:716:G:C2'	2.70	0.53
1:A:1151:U:H2'	1:A:1152:G:H8	1.74	0.53
1:A:2047:A:H3'	26:b:6:ARG:HH22	1.74	0.53
1:A:175:G:OP1	1:A:175:G:H4'	2.06	0.53
1:A:1067:A:H2'	1:A:1068:G:H4'	1.91	0.53
1:A:1425:C:H1'	1:A:1516:A:H1'	1.90	0.53
1:A:1433:U:O2	32:h:16:ARG:NH2	2.42	0.53
4:D:121:GLY:HA2	4:D:161:PRO:HB3	1.90	0.53
11:L:55:MET:O	11:L:60:ARG:NH1	2.42	0.53
17:R:233:GLU:OE1	17:R:238:ARG:HD2	2.09	0.53
17:R:536:VAL:HG12	17:R:549:TYR:HB3	1.91	0.53
1:A:1246:G:H2'	1:A:1246:G:N3	2.24	0.53
14:O:113:ALA:HB1	14:O:118:LEU:HD12	1.89	0.53
1:A:1513:U:H3	1:A:1572:G:H1	1.57	0.53
5:E:151:LYS:HB3	5:E:189:HIS:HD2	1.74	0.53
17:R:173:PRO:HD3	17:R:201:SER:HB2	1.90	0.53
1:A:1855:C:O2'	1:A:2000:A:OP2	2.27	0.52
1:A:11:G:H2'	1:A:12:A:C8	2.44	0.52
1:A:2787:A:O2'	7:G:39:HIS:NE2	2.36	0.52
1:A:1010:C:O2'	1:A:2302:A:N3	2.41	0.52
1:A:1033:C:O2'	1:A:1046:A:N3	2.41	0.52
1:A:2504:C:H42	1:A:2558:G:N2	2.06	0.52
14:O:102:TYR:OH	14:O:114:ARG:NH2	2.42	0.52
17:R:294:LEU:HD21	17:R:423:ARG:CD	2.40	0.52
1:A:680:G:O6	11:L:71:ARG:NH2	2.42	0.52
1:A:2315:A:OP2	27:c:25:ASN:ND2	2.41	0.52
22:X:44:PRO:HB2	22:X:45:LYS:HG3	1.91	0.52
1:A:861:C:O2'	1:A:1264:G:N2	2.41	0.52
1:A:1296:G:O2'	5:E:75:GLN:NE2	2.42	0.52
1:A:1444:C:H2'	1:A:1445:A:H8	1.75	0.52
1:A:1295:U:OP2	1:A:2531:G:N2	2.41	0.52
1:A:2105:U:OP2	1:A:2267:G:N2	2.43	0.52
17:R:455:SER:OG	17:R:456:THR:N	2.41	0.52
18:S:21:MET:HA	18:S:24:ILE:HG22	1.92	0.52
1:A:2709:C:H2'	1:A:2710:C:H6	1.74	0.52
6:F:78:ARG:NH1	15:P:56:C:O2'	2.43	0.52
1:A:229:A:H4'	1:A:229:A:OP1	2.10	0.52
1:A:1934:C:H4'	1:A:1958:G:H8	1.75	0.52
1:A:2048:U:OP2	26:b:6:ARG:NH2	2.43	0.52
1:A:2711:G:H5'	1:A:2711:G:C8	2.41	0.52
22:X:15:GLY:HA3	22:X:29:TRP:HE1	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1363:G:H1'	1:A:1661:A:N6	2.26	0.51
8:I:129:GLU:HG2	8:I:139:ILE:HG12	1.91	0.51
1:A:1715:C:O2	4:D:135:HIS:NE2	2.40	0.51
17:R:7:PHE:HA	17:R:254:LEU:CD2	2.37	0.51
19:U:75:THR:HG23	19:U:77:GLU:H	1.74	0.51
1:A:805:G:H21	1:A:2010:A:H62	1.57	0.51
1:A:2104:U:OP1	3:C:243:ARG:NH1	2.44	0.51
18:S:21:MET:HE1	18:S:103:ILE:HG23	1.92	0.51
1:A:275:A:H2'	1:A:276:C:C6	2.45	0.51
1:A:576:G:O2'	1:A:578:A:N7	2.44	0.51
1:A:839:G:N3	1:A:2101:G:O2'	2.44	0.51
1:A:2448:U:H5''	27:c:18:ILE:HD13	1.91	0.51
11:L:58:PHE:O	29:e:13:ARG:NE	2.42	0.51
1:A:33:U:H6	1:A:33:U:H5''	1.75	0.51
1:A:1783:C:OP1	25:a:97:ARG:NE	2.43	0.51
17:R:291:ALA:CB	17:R:419:ILE:HD13	2.37	0.51
1:A:182:C:H6	1:A:182:C:O5'	1.94	0.51
1:A:342:A:N3	1:A:363:C:O2'	2.37	0.51
1:A:2688:G:N2	1:A:2691:A:OP2	2.44	0.51
18:S:88:ARG:HB2	18:S:92:ARG:HB2	1.92	0.51
1:A:1279:C:H2'	1:A:1280:G:H8	1.75	0.51
1:A:2556:C:H5''	30:f:30:PRO:HB2	1.92	0.51
6:F:31:ILE:HD11	6:F:34:ILE:HD11	1.93	0.51
13:N:25:ILE:HD13	13:N:83:LEU:HD11	1.94	0.50
17:R:487:THR:HG23	17:R:527:PRO:O	2.11	0.50
1:A:644:G:N2	1:A:650:U:OP1	2.32	0.50
1:A:1078:A:H2	1:A:1168:G:H22	1.59	0.50
17:R:168:GLN:NE2	15:T:35:G:O4'	2.44	0.50
1:A:651:U:H2'	1:A:652:A:H8	1.77	0.50
16:Q:50:ARG:O	16:Q:54:LYS:NZ	2.43	0.50
17:R:417:ARG:O	17:R:421:GLU:HG3	2.11	0.50
1:A:1106:U:H4'	1:A:1107:U:H5'	1.92	0.50
1:A:2307:A:OP2	20:V:20:ASN:ND2	2.43	0.50
11:L:74:TYR:HB3	11:L:110:LYS:HB2	1.93	0.50
17:R:174:LEU:C	17:R:176:ALA:H	2.18	0.50
31:g:14:VAL:HG12	31:g:20:VAL:HG11	1.92	0.50
1:A:273:A:C2'	1:A:274:A:H5'	2.41	0.50
1:A:621:G:O2'	1:A:1294:A:OP1	2.30	0.50
1:A:1284:A:H5''	1:A:1284:A:H8	1.75	0.50
11:L:92:THR:HG22	11:L:94:GLU:H	1.76	0.50
12:M:75:THR:HA	12:M:90:PRO:HA	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:N:102:MET:HE1	26:b:54:ILE:HG12	1.93	0.50
17:R:170:LYS:HE2	17:R:198:ASP:HA	1.94	0.50
1:A:734:C:H5''	28:d:2:LYS:HE2	1.93	0.50
11:L:33:LYS:HE3	11:L:40:ALA:HA	1.93	0.50
17:R:330:GLU:HA	17:R:377:PHE:HZ	1.77	0.50
18:S:11:ARG:NH1	18:S:99:ARG:O	2.44	0.50
1:A:2035:C:O2'	1:A:2848:A:N3	2.44	0.50
1:A:732:A:H8	1:A:735:U:H3	1.58	0.50
4:D:21:ASP:HA	10:K:73:ASP:HA	1.92	0.50
7:G:9:LEU:HD13	7:G:70:ARG:HE	1.76	0.50
17:R:222:THR:HA	17:R:225:LYS:NZ	2.27	0.50
17:R:364:ASN:HB3	17:R:372:ASN:ND2	2.27	0.50
2:B:10:G:N2	20:V:79:ARG:O	2.44	0.50
16:Q:92:ARG:NH1	31:g:11:GLN:N	2.60	0.50
1:A:1351:U:H5''	1:A:1352:U:C6	2.46	0.49
1:A:1094:A:N6	1:A:1156:G:O2'	2.45	0.49
15:T:16:C:H4'	15:T:17:U:H4'	1.93	0.49
1:A:266:U:H1'	1:A:477:A:N3	2.28	0.49
1:A:1068:G:N2	1:A:1069:U:O4	2.43	0.49
1:A:1111:U:H2'	1:A:1112:U:C2	2.48	0.49
5:E:117:LYS:NZ	5:E:186:VAL:O	2.44	0.49
8:I:14:PRO:HA	8:I:53:ILE:HA	1.93	0.49
7:G:55:ARG:NH1	7:G:58:ASP:OD1	2.45	0.49
8:I:21:ALA:HB1	17:R:351:TYR:CE1	2.48	0.49
24:Z:19:GLN:HG2	24:Z:50:VAL:HG12	1.95	0.49
1:A:44:A:H5''	1:A:44:A:C8	2.48	0.49
1:A:295:G:O2'	1:A:296:G:H5'	2.13	0.49
1:A:677:A:OP2	29:e:23:LYS:NZ	2.38	0.49
32:h:62:LYS:H	32:h:73:THR:HB	1.77	0.49
1:A:75:G:H22	1:A:110:A:H2	1.60	0.49
1:A:528:G:O2'	1:A:553:A:N6	2.46	0.49
1:A:2315:A:N6	27:c:19:SER:OG	2.46	0.49
3:C:37:LEU:HG	3:C:62:TYR:HB2	1.95	0.49
8:I:98:ALA:HB3	8:I:137:ILE:HG12	1.94	0.49
17:R:40:ARG:NH2	17:R:45:ASN:OD1	2.45	0.49
1:A:12:A:C8	1:A:12:A:C5'	2.92	0.49
1:A:183:A:H3'	1:A:183:A:H8	1.77	0.49
17:R:197:VAL:HA	17:R:203:VAL:HG13	1.94	0.49
25:a:54:ARG:NH2	25:a:59:SER:O	2.42	0.49
1:A:1652:C:H4'	1:A:1653:A:O5'	2.12	0.49
1:A:253:G:H2'	1:A:254:A:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:C:HO2'	1:A:278:A:H8	1.61	0.49
1:A:675:C:O2	1:A:685:U:O2'	2.31	0.49
1:A:1478:G:H2'	1:A:1479:G:C8	2.48	0.49
6:F:100:LEU:HD23	6:F:103:LEU:HD12	1.95	0.49
10:K:76:TYR:HB2	25:a:76:THR:HB	1.95	0.49
17:R:254:LEU:CD1	17:R:255:LEU:HG	2.37	0.49
2:B:55:A:H1'	6:F:27:GLN:HG3	1.95	0.48
7:G:53:VAL:O	7:G:66:HIS:NE2	2.44	0.48
17:R:347:GLU:HA	17:R:360:THR:O	2.13	0.48
17:R:488:LYS:HB3	17:R:527:PRO:HB2	1.94	0.48
22:X:18:ARG:HE	22:X:22:MET:HB2	1.78	0.48
1:A:916:G:H5''	1:A:916:G:C8	2.47	0.48
1:A:1242:U:H2'	1:A:1243:A:H8	1.78	0.48
1:A:2251:G:H4'	3:C:185:LEU:HD11	1.93	0.48
1:A:2357:A:H2'	1:A:2358:A:C8	2.48	0.48
13:N:24:LEU:HD23	13:N:44:VAL:HG21	1.95	0.48
16:Q:92:ARG:NE	31:g:11:GLN:HG3	2.28	0.48
17:R:100:MET:HB3	17:R:120:VAL:HB	1.95	0.48
17:R:330:GLU:CA	17:R:377:PHE:HZ	2.25	0.48
17:R:497:ILE:HD13	17:R:506:THR:HG22	1.95	0.48
19:U:74:LYS:HD2	19:U:99:GLN:HB2	1.95	0.48
17:R:354:GLU:N	17:R:354:GLU:OE1	2.45	0.48
1:A:259:A:H2'	1:A:260:A:C8	2.49	0.48
1:A:644:G:H1	1:A:704:U:H3	1.59	0.48
1:A:1304:G:OP1	26:b:16:ARG:NH2	2.38	0.48
1:A:1359:G:C2	1:A:1368:U:H5''	2.48	0.48
1:A:1535:U:O2'	1:A:1537:G:N7	2.47	0.48
1:A:2841:C:O2	1:A:2908:A:O2'	2.30	0.48
9:J:24:LYS:HB2	9:J:29:LEU:HD23	1.94	0.48
16:Q:92:ARG:HD2	31:g:11:GLN:HB2	1.96	0.48
17:R:294:LEU:CD2	17:R:432:LEU:CD1	2.91	0.48
1:A:732:A:O2'	1:A:820:U:O4	2.29	0.48
1:A:1139:G:N2	1:A:1145:G:O6	2.46	0.48
1:A:1649:C:H2'	1:A:1650:C:H6	1.77	0.48
33:i:14:ILE:HG12	33:i:57:ILE:HD13	1.96	0.48
1:A:223:G:H1	1:A:474:U:H3'	1.79	0.48
1:A:1283:U:H1'	11:L:5:GLU:HA	1.95	0.48
1:A:2365:A:H61	20:V:51:THR:HG21	1.78	0.48
18:S:11:ARG:HH21	18:S:98:LYS:HD2	1.79	0.48
1:A:1578:G:O2'	1:A:1588:A:N6	2.47	0.48
1:A:2021:G:N2	1:A:2025:C:O2'	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:G:H5''	1:A:43:G:C8	2.45	0.48
1:A:569:C:O2	1:A:598:U:O2'	2.31	0.48
8:I:125:MET:HA	8:I:128:VAL:HG22	1.94	0.48
1:A:1053:C:OP1	9:J:38:ARG:NH1	2.43	0.48
4:D:117:LYS:HB2	4:D:164:MET:HB3	1.96	0.48
1:A:2342:C:H4'	6:F:88:LYS:HD3	1.96	0.47
17:R:426:LEU:HB2	17:R:432:LEU:HD12	1.96	0.47
1:A:1110:C:H3'	1:A:1111:U:C5	2.49	0.47
17:R:181:ILE:HG12	17:R:200:PHE:HE2	1.79	0.47
24:Z:5:GLU:OE1	24:Z:59:GLN:NE2	2.45	0.47
1:A:1939:G:N2	17:R:74:MET:SD	2.74	0.47
1:A:688:G:N2	1:A:691:U:OP2	2.41	0.47
1:A:1112:U:C3'	1:A:1112:U:C6	2.97	0.47
1:A:1462:G:HO2'	1:A:1633:G:HO2'	1.57	0.47
1:A:2728:U:H3	1:A:2737:G:H1	1.60	0.47
7:G:58:ASP:O	7:G:63:ARG:NH1	2.47	0.47
15:P:22:G:H2'	15:P:23:A:H8	1.78	0.47
16:Q:61:TRP:CD2	16:Q:94:MET:HB3	2.49	0.47
17:R:279:PHE:CG	17:R:565:ILE:HD11	2.49	0.47
16:Q:69:ALA:HB2	16:Q:79:LEU:HD22	1.97	0.47
17:R:326:GLN:HG2	17:R:377:PHE:HD1	1.79	0.47
15:T:26:G:H1	15:T:44:A:N6	2.12	0.47
1:A:617:G:O2'	1:A:619:A:OP1	2.31	0.47
2:B:52:G:H21	6:F:26:MET:HE3	1.80	0.47
17:R:197:VAL:HA	17:R:203:VAL:CG1	2.45	0.47
26:b:27:MET:HA	26:b:38:LEU:HA	1.97	0.47
1:A:177:G:OP2	1:A:177:G:H3'	2.14	0.47
1:A:482:C:O2	1:A:482:C:H3'	2.14	0.47
1:A:662:U:H5''	5:E:106:ARG:HD2	1.96	0.47
1:A:1664:G:N2	28:d:1:MET:O	2.40	0.47
1:A:1887:G:N2	1:A:1912:G:O2'	2.48	0.47
3:C:35:ALA:HB3	3:C:62:TYR:HB3	1.95	0.47
5:E:184:LEU:O	5:E:188:ASN:HB2	2.15	0.47
16:Q:95:LEU:HD23	31:g:4:ILE:HD12	1.96	0.47
17:R:136:GLU:HG2	17:R:138:VAL:HG13	1.97	0.47
25:a:28:THR:HA	25:a:49:VAL:HA	1.97	0.47
1:A:265:A:H2'	1:A:266:U:O4'	2.15	0.47
1:A:1493:C:O2'	1:A:1592:A:N3	2.42	0.47
1:A:1848:A:H5''	3:C:160:THR:HG21	1.97	0.47
7:G:124:ILE:HG13	7:G:134:VAL:HG23	1.96	0.47
17:R:220:LYS:O	17:R:224:PRO:HG2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:774:A:OP1	1:A:1477:A:O2'	2.33	0.47
1:A:1302:A:OP1	18:S:99:ARG:NH1	2.45	0.47
8:I:122:GLU:HA	8:I:125:MET:HG3	1.96	0.47
17:R:283:GLU:HA	17:R:283:GLU:OE1	2.14	0.47
1:A:1365:U:O4	1:A:1692:U:O2'	2.31	0.46
1:A:1759:U:H2'	1:A:1760:A:H8	1.80	0.46
1:A:1360:A:H3'	1:A:1361:A:H8	1.79	0.46
1:A:1956:A:H2'	1:A:1957:A:C8	2.50	0.46
1:A:2504:C:N4	1:A:2558:G:H22	2.12	0.46
10:K:26:GLY:HA3	10:K:30:ARG:HE	1.80	0.46
27:c:2:ARG:HD2	27:c:20:LYS:HB3	1.97	0.46
1:A:1030:G:OP2	1:A:1030:G:N2	2.41	0.46
1:A:2274:U:H5''	1:A:2275:G:H5'	1.98	0.46
1:A:2323:C:H5'	14:O:14:ARG:HD3	1.96	0.46
5:E:75:GLN:OE1	5:E:83:TRP:NE1	2.44	0.46
9:J:20:ASP:OD1	9:J:59:ASN:ND2	2.44	0.46
17:R:99:ILE:CD1	17:R:121:GLU:HG2	2.44	0.46
17:R:467:ASN:HA	17:R:470:ASN:HB2	1.97	0.46
1:A:50:U:H2'	1:A:176:A:C2	2.50	0.46
1:A:767:U:H2'	1:A:768:G:H8	1.81	0.46
4:D:9:LYS:HA	4:D:28:ILE:HA	1.96	0.46
17:R:420:SER:O	17:R:423:ARG:HB3	2.14	0.46
17:R:498:ARG:HG2	17:R:498:ARG:HH11	1.78	0.46
27:c:29:ARG:HG3	27:c:47:GLU:HB3	1.98	0.46
1:A:2532:A:O2'	1:A:2534:G:OP2	2.32	0.46
1:A:2577:G:O2'	10:K:4:GLN:OE1	2.34	0.46
1:A:1347:A:H61	1:A:1651:G:H1'	1.80	0.46
1:A:1649:C:H2'	1:A:1650:C:C6	2.51	0.46
1:A:2361:C:OP1	20:V:84:ARG:NH2	2.48	0.46
1:A:2624:G:N2	1:A:2627:A:OP2	2.42	0.46
4:D:55:ASP:HA	4:D:77:LYS:HA	1.98	0.46
5:E:24:PHE:HB3	5:E:118:VAL:HG21	1.97	0.46
18:S:82:LEU:HB2	18:S:98:LYS:HB2	1.96	0.46
1:A:726:C:H2'	1:A:727:A:H8	1.79	0.46
17:R:245:THR:O	17:R:262:GLY:HA3	2.15	0.46
17:R:421:GLU:CB	17:R:468:ARG:HH11	2.27	0.46
17:R:427:VAL:HG12	17:R:432:LEU:HB2	1.98	0.46
1:A:50:U:OP1	1:A:176:A:H1'	2.16	0.46
1:A:183:A:H3'	1:A:183:A:C8	2.51	0.46
1:A:2710:C:O2	1:A:2710:C:H2'	2.15	0.46
6:F:57:LEU:HB3	6:F:65:PRO:HG3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:U:97:SER:HA	19:U:98:GLY:HA2	1.78	0.46
1:A:557:U:H4'	1:A:1275:G:H4'	1.98	0.46
1:A:2709:C:H5'	4:D:193:PRO:HA	1.97	0.46
22:X:42:GLY:HA2	22:X:43:LYS:HA	1.60	0.46
4:D:207:LYS:HA	4:D:208:SER:HA	1.69	0.46
1:A:106:G:H2'	1:A:107:G:H8	1.81	0.45
1:A:611:U:H5''	11:L:36:LYS:HD2	1.97	0.45
1:A:720:C:OP1	5:E:54:ARG:NH1	2.47	0.45
1:A:717:A:OP2	1:A:717:A:H8	2.00	0.45
1:A:1826:C:O2'	3:C:259:THR:OG1	2.32	0.45
1:A:1954:C:OP2	23:Y:16:ARG:NH2	2.49	0.45
1:A:2772:U:OP2	1:A:2784:C:N4	2.48	0.45
4:D:7:GLY:HA3	4:D:30:ALA:HA	1.99	0.45
1:A:1110:C:H3'	1:A:1111:U:C6	2.51	0.45
13:N:34:GLU:HG2	13:N:115:ALA:HB2	1.97	0.45
16:Q:92:ARG:CD	31:g:11:GLN:HG3	2.46	0.45
25:a:38:GLY:HA2	25:a:39:ASN:HA	1.68	0.45
1:A:673:A:H61	1:A:682:G:H2'	1.81	0.45
1:A:1947:A:H3'	1:A:1948:A:H8	1.81	0.45
1:A:2258:U:H2'	1:A:2259:G:H8	1.81	0.45
3:C:130:LEU:HD13	3:C:134:ASN:HB2	1.98	0.45
17:R:356:SER:N	17:R:357:PRO:CD	2.79	0.45
1:A:420:U:H2'	1:A:421:A:H8	1.81	0.45
1:A:2093:C:H2'	1:A:2094:C:H6	1.81	0.45
17:R:386:SER:HA	17:R:389:VAL:HG12	1.99	0.45
18:S:40:PRO:O	18:S:44:SER:OG	2.27	0.45
1:A:184:G:H2'	1:A:184:G:OP1	2.17	0.45
1:A:720:C:H5''	5:E:81:PRO:HD2	1.99	0.45
1:A:896:A:H2'	1:A:897:G:H8	1.82	0.45
1:A:965:A:N3	2:B:78:U:O2'	2.48	0.45
1:A:1853:G:H5''	3:C:52:ARG:HH21	1.81	0.45
9:J:12:ILE:HD13	9:J:51:THR:HA	1.99	0.45
17:R:481:ASP:OD1	17:R:500:SER:HA	2.15	0.45
1:A:307:A:N6	1:A:410:G:O6	2.50	0.45
1:A:1444:C:H2'	1:A:1445:A:C8	2.52	0.45
1:A:1598:C:H5'	1:A:1769:G:H22	1.82	0.45
1:A:1565:U:H2'	1:A:1566:G:H8	1.82	0.45
8:I:116:LEU:HD11	8:I:127:MET:HE1	1.99	0.45
17:R:326:GLN:HG2	17:R:377:PHE:CD1	2.51	0.45
1:A:268:A:H8	1:A:268:A:OP1	2.00	0.45
1:A:273:A:H62	1:A:298:U:H3	1.63	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:15:VAL:HB	4:D:25:VAL:HG21	1.98	0.45
4:D:178:LYS:HB3	4:D:187:LEU:HD12	1.98	0.45
17:R:354:GLU:N	17:R:354:GLU:CD	2.75	0.45
18:S:68:ASN:OD1	18:S:110:LYS:NZ	2.45	0.45
25:a:25:PRO:HG3	25:a:53:ARG:HB2	1.98	0.45
25:a:107:ARG:HA	25:a:108:GLY:HA2	1.67	0.45
1:A:1845:A:OP2	3:C:40:LYS:NZ	2.46	0.45
17:R:162:TYR:CE2	17:R:164:LEU:HD12	2.52	0.45
17:R:203:VAL:HG13	17:R:203:VAL:O	2.17	0.45
17:R:336:LEU:O	17:R:336:LEU:HD12	2.17	0.45
17:R:520:ALA:CB	17:R:526:VAL:HG21	2.46	0.45
1:A:1348:G:N2	1:A:1656:C:H5'	2.29	0.44
1:A:1528:U:H4'	1:A:1529:G:H5'	1.99	0.44
1:A:2066:A:H2'	1:A:2067:G:C8	2.52	0.44
5:E:23:VAL:HG13	5:E:111:LYS:HG2	1.99	0.44
1:A:1107:U:H3	8:I:12:GLN:H	1.64	0.44
4:D:185:LEU:HD13	25:a:11:ILE:HD11	1.98	0.44
15:T:20:G:C6	15:T:57:G:H1'	2.53	0.44
25:a:12:THR:HG21	25:a:58:ILE:HG21	1.99	0.44
1:A:1046:A:O2'	24:Z:10:ARG:NH1	2.50	0.44
1:A:1221:A:H2'	1:A:1222:A:H8	1.82	0.44
1:A:1565:U:H2'	1:A:1566:G:C8	2.52	0.44
1:A:1619:A:H2'	1:A:1620:A:C8	2.53	0.44
1:A:1646:G:OP2	32:h:58:ASN:ND2	2.49	0.44
9:J:50:ASP:HB2	9:J:115:LEU:HD22	1.98	0.44
17:R:195:GLN:O	17:R:199:HIS:HB2	2.17	0.44
17:R:463:VAL:HG22	17:R:495:VAL:HG22	2.00	0.44
17:R:483:ILE:CG1	17:R:502:PRO:HG3	2.45	0.44
30:f:2:LYS:NZ	30:f:31:LYS:O	2.51	0.44
1:A:1360:A:H3'	1:A:1361:A:C8	2.53	0.44
1:A:2100:A:H2'	1:A:2101:G:H8	1.82	0.44
3:C:53:HIS:HA	3:C:217:ARG:HG2	1.99	0.44
7:G:13:SER:HA	7:G:14:ASP:HA	1.62	0.44
1:A:13:A:H1'	1:A:15:G:C6	2.52	0.44
1:A:257:G:N7	29:e:5:LYS:NZ	2.66	0.44
1:A:620:U:H2'	1:A:621:G:C8	2.52	0.44
1:A:662:U:H2'	1:A:663:G:C8	2.53	0.44
1:A:720:C:H4'	5:E:82:GLN:HE22	1.83	0.44
1:A:1220:G:H2'	1:A:1221:A:H8	1.82	0.44
1:A:1941:A:H8	1:A:1947:A:H61	1.64	0.44
1:A:2560:A:H61	1:A:2691:A:H61	1.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:180:ASP:O	17:R:183:ARG:HG2	2.18	0.44
1:A:351:G:H21	1:A:374:A:H62	1.65	0.44
1:A:2093:C:H2'	1:A:2094:C:C6	2.52	0.44
10:K:88:ARG:HG3	10:K:94:ARG:HD2	2.00	0.44
14:O:36:SER:OG	14:O:37:ASN:N	2.51	0.44
17:R:83:ILE:HG23	17:R:104:ILE:HG21	1.99	0.44
17:R:121:GLU:OE1	17:R:154:ARG:NH2	2.51	0.44
18:S:38:LEU:HD22	26:b:38:LEU:HD22	2.00	0.44
20:V:49:ARG:NH2	20:V:64:ASP:OD1	2.50	0.44
1:A:461:C:H2'	1:A:462:A:H8	1.82	0.44
7:G:7:LYS:O	7:G:70:ARG:NH2	2.50	0.44
17:R:6:MET:HE1	17:R:202:GLY:O	2.18	0.44
17:R:215:ALA:CB	17:R:223:LEU:HD23	2.47	0.44
1:A:235:G:OP2	1:A:235:G:H8	2.00	0.44
1:A:2100:A:H2'	1:A:2101:G:C8	2.52	0.44
12:M:103:LEU:HD11	12:M:127:ILE:HD11	1.99	0.44
17:R:219:ASN:CB	17:R:222:THR:HB	2.46	0.44
1:A:32:C:H2'	1:A:33:U:C6	2.52	0.44
1:A:63:G:H21	32:h:66:VAL:HG11	1.82	0.44
1:A:928:G:H2'	1:A:929:G:H8	1.83	0.44
10:K:23:LYS:HE2	10:K:23:LYS:HB2	1.83	0.44
17:R:433:ARG:NH2	15:T:14:A:O2'	2.51	0.44
1:A:84:A:N1	1:A:98:U:O2'	2.47	0.43
1:A:230:A:C8	1:A:230:A:O5'	2.70	0.43
1:A:234:C:H2'	1:A:234:C:O2	2.17	0.43
1:A:558:G:OP1	1:A:1274:U:O2'	2.31	0.43
1:A:1220:G:H2'	1:A:1221:A:C8	2.53	0.43
1:A:1282:U:H2'	1:A:1283:U:C6	2.53	0.43
1:A:1112:U:H6	1:A:1112:U:C3'	2.31	0.43
1:A:346:G:H2'	1:A:347:G:H8	1.83	0.43
1:A:1202:A:O4'	16:Q:51:ARG:NH1	2.51	0.43
1:A:1683:C:O3'	1:A:2738:G:N2	2.52	0.43
17:R:9:TYR:CD1	17:R:9:TYR:C	2.96	0.43
17:R:211:ALA:HB1	17:R:227:LEU:HD22	2.00	0.43
17:R:242:ASN:HA	17:R:266:ARG:HA	1.99	0.43
1:A:125:A:H61	28:d:42:LEU:HD12	1.83	0.43
1:A:630:A:N1	1:A:856:G:O2'	2.46	0.43
1:A:897:G:H1'	24:Z:25:THR:HG21	1.99	0.43
1:A:1094:A:H1'	1:A:1158:G:H21	1.84	0.43
1:A:1425:C:O2'	1:A:1515:C:O2'	2.32	0.43
5:E:184:LEU:HD23	5:E:184:LEU:HA	1.91	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:23:ASN:ND2	7:G:39:HIS:O	2.44	0.43
1:A:204:C:OP1	22:X:18:ARG:NH2	2.39	0.43
1:A:578:A:H4'	1:A:579:G:C8	2.54	0.43
1:A:625:C:H2'	1:A:626:G:H8	1.83	0.43
1:A:643:U:H2'	1:A:644:G:H8	1.83	0.43
1:A:1111:U:H2'	1:A:1112:U:N3	2.33	0.43
1:A:1212:U:H2'	1:A:1213:G:H8	1.84	0.43
3:C:131:PRO:HA	3:C:189:ARG:HA	2.00	0.43
5:E:80:SER:HB2	5:E:83:TRP:HD1	1.83	0.43
17:R:222:THR:HA	17:R:225:LYS:HZ1	1.84	0.43
1:A:1111:U:O5'	1:A:1111:U:C6	2.71	0.43
17:R:6:MET:O	17:R:9:TYR:HB3	2.18	0.43
17:R:332:LEU:HD23	17:R:373:ALA:HB2	2.00	0.43
17:R:346:ALA:O	17:R:362:PRO:HD2	2.18	0.43
17:R:421:GLU:HA	17:R:424:GLU:CD	2.44	0.43
23:Y:15:ARG:HH21	23:Y:18:LEU:HD21	1.83	0.43
1:A:2053:C:H5''	4:D:153:ARG:HD3	2.00	0.43
1:A:2656:G:N2	1:A:2806:G:OP2	2.52	0.43
18:S:73:GLN:HB2	18:S:106:VAL:HB	2.00	0.43
1:A:184:G:OP1	1:A:184:G:H8	2.01	0.43
1:A:1117:G:H1'	1:A:1135:G:H2'	2.00	0.43
1:A:1477:A:H2'	1:A:1478:G:C8	2.54	0.43
2:B:70:G:N2	2:B:102:A:H62	2.14	0.43
3:C:145:GLU:HB2	3:C:188:CYS:HB3	2.01	0.43
12:M:30:GLY:HA2	12:M:107:SER:HB3	2.00	0.43
17:R:279:PHE:CZ	17:R:565:ILE:CG1	3.01	0.43
17:R:422:ILE:O	17:R:426:LEU:HD13	2.19	0.43
17:R:525:SER:HA	17:R:557:VAL:O	2.18	0.43
15:T:55:U:O2	15:T:57:G:N2	2.52	0.43
1:A:666:G:H5'	1:A:667:A:H5'	2.00	0.43
1:A:1066:A:N1	1:A:1187:U:O2'	2.42	0.43
1:A:1133:G:N2	1:A:1136:U:O2	2.52	0.43
1:A:1231:G:OP1	11:L:30:THR:OG1	2.33	0.43
1:A:2314:C:OP2	27:c:2:ARG:NH2	2.41	0.43
6:F:100:LEU:HA	6:F:103:LEU:HB2	2.01	0.43
16:Q:98:LEU:HD13	31:g:13:LYS:HD3	2.01	0.43
26:b:35:GLU:HA	26:b:36:MET:HA	1.76	0.43
33:i:17:LYS:HG3	33:i:53:MET:HE1	2.01	0.43
1:A:1368:U:O2	1:A:1368:U:C2'	2.67	0.43
11:L:95:LEU:O	11:L:99:THR:OG1	2.30	0.43
17:R:194:LYS:HB3	17:R:194:LYS:HE3	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:A:H8	1:A:454:G:H21	1.67	0.42
1:A:1291:A:OP1	16:Q:13:ARG:NH2	2.51	0.42
1:A:1317:G:H2'	1:A:1318:G:C8	2.54	0.42
1:A:1380:U:OP2	1:A:1433:U:O2'	2.36	0.42
1:A:1425:C:H2'	1:A:1426:A:C8	2.53	0.42
1:A:1774:A:H3'	1:A:1775:G:H8	1.84	0.42
9:J:128:GLY:HA2	9:J:129:SER:HA	1.80	0.42
16:Q:92:ARG:HH11	31:g:11:GLN:H	1.67	0.42
17:R:173:PRO:HB2	17:R:231:PHE:CE1	2.54	0.42
17:R:287:VAL:HG11	17:R:414:ALA:O	2.19	0.42
1:A:461:C:H2'	1:A:462:A:C8	2.54	0.42
1:A:726:C:H2'	1:A:727:A:C8	2.54	0.42
32:h:8:LEU:HB2	33:i:26:PHE:HE2	1.84	0.42
1:A:272:C:H5''	1:A:298:U:O4	2.19	0.42
1:A:278:A:H2'	1:A:279:A:H8	1.83	0.42
1:A:485:U:H2'	1:A:486:A:C8	2.54	0.42
1:A:2076:C:H2'	1:A:2077:G:H8	1.83	0.42
13:N:4:ARG:NH1	13:N:39:GLU:OE1	2.46	0.42
15:P:3:G:H1	15:P:70:U:H3	1.67	0.42
17:R:6:MET:HG3	17:R:234:VAL:HG11	2.02	0.42
31:g:62:VAL:HG22	31:g:95:VAL:HG12	2.00	0.42
1:A:105:C:O2'	1:A:337:A:H4'	2.19	0.42
1:A:1322:G:N2	1:A:1325:A:OP2	2.52	0.42
1:A:2703:G:H4'	10:K:30:ARG:HD3	2.00	0.42
1:A:971:A:H2'	1:A:972:U:C6	2.54	0.42
1:A:1367:G:H2'	1:A:1369:C:C4	2.54	0.42
1:A:1514:C:H2'	1:A:1569:A:H61	1.84	0.42
1:A:2775:U:H5''	7:G:139:LYS:HE3	2.01	0.42
5:E:37:ILE:HD11	5:E:187:VAL:HG11	2.01	0.42
8:I:20:PRO:HB2	8:I:22:PRO:HD2	2.01	0.42
12:M:34:ILE:HD12	12:M:104:PHE:HD2	1.85	0.42
23:Y:64:LYS:HG3	23:Y:66:THR:HG23	2.01	0.42
1:A:776:G:C8	3:C:207:LYS:HE3	2.55	0.42
9:J:33:VAL:HG13	9:J:55:VAL:HG11	2.00	0.42
17:R:427:VAL:HA	17:R:432:LEU:O	2.20	0.42
1:A:153:C:H2'	1:A:154:A:H8	1.83	0.42
1:A:252:C:H4'	1:A:253:G:O5'	2.18	0.42
1:A:510:G:N2	1:A:513:A:OP2	2.39	0.42
1:A:1140:U:N3	1:A:1143:U:OP2	2.44	0.42
1:A:1371:G:N7	1:A:1654:A:O2'	2.40	0.42
1:A:2320:U:O2'	1:A:2403:C:O2	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:4:LEU:HA	6:F:7:LYS:HB3	2.02	0.42
17:R:502:PRO:CB	17:R:507:ILE:HD11	2.49	0.42
1:A:302:A:H2'	1:A:303:G:C8	2.55	0.42
1:A:437:A:O2'	1:A:438:A:O4'	2.37	0.42
1:A:999:A:OP1	12:M:18:ARG:NH2	2.44	0.42
1:A:1307:U:H2'	1:A:1308:A:H8	1.83	0.42
1:A:1536:A:N6	3:C:73:GLY:O	2.53	0.42
1:A:1645:C:OP1	32:h:77:ARG:NH1	2.53	0.42
1:A:2060:A:N3	1:A:2484:G:O2'	2.38	0.42
17:R:196:ILE:HA	17:R:200:PHE:CD1	2.54	0.42
17:R:211:ALA:HB1	17:R:227:LEU:CD2	2.50	0.42
1:A:23:G:OP1	1:A:550:G:N1	2.46	0.42
1:A:125:A:O2'	1:A:126:A:O4'	2.33	0.42
1:A:729:G:H5'	28:d:26:ASN:ND2	2.35	0.42
1:A:448:A:H2'	1:A:449:A:C8	2.55	0.42
1:A:786:A:H1'	1:A:787:C:H5	1.85	0.42
1:A:906:G:O2'	1:A:963:G:O6	2.35	0.42
1:A:1623:C:OP2	1:A:1623:C:H6	2.03	0.42
1:A:2610:G:OP2	1:A:2610:G:N2	2.42	0.42
17:R:109:GLU:HB3	23:Y:18:LEU:HD22	2.01	0.42
1:A:567:U:H2'	1:A:568:G:C8	2.55	0.41
1:A:1102:G:H21	1:A:1149:A:H62	1.66	0.41
1:A:2342:C:H2'	1:A:2343:A:C8	2.55	0.41
7:G:23:ASN:HB3	7:G:38:PHE:HB2	2.02	0.41
7:G:171:ARG:HH12	30:f:29:ASN:HA	1.85	0.41
10:K:26:GLY:HA3	10:K:30:ARG:HH21	1.84	0.41
16:Q:20:LEU:HD23	16:Q:20:LEU:HA	1.94	0.41
1:A:242:U:O2'	1:A:668:G:O2'	2.33	0.41
1:A:2275:G:H2'	1:A:2276:A:C8	2.55	0.41
1:A:2882:G:N2	1:A:2885:A:OP2	2.43	0.41
17:R:249:LYS:HE3	17:R:249:LYS:HB2	1.87	0.41
23:Y:55:LEU:HB3	23:Y:82:GLU:HB3	2.01	0.41
1:A:183:A:C8	1:A:183:A:C3'	3.03	0.41
1:A:523:G:H4'	1:A:548:A:H61	1.85	0.41
1:A:631:G:H1	11:L:33:LYS:HE2	1.84	0.41
1:A:1377:G:O2'	1:A:1432:A:N1	2.47	0.41
2:B:110:G:N2	14:O:50:GLY:O	2.51	0.41
10:K:71:ARG:HH21	10:K:77:ILE:HG21	1.84	0.41
17:R:241:PRO:HB3	17:R:270:LEU:HD23	2.03	0.41
1:A:14:A:O5'	1:A:14:A:H8	2.03	0.41
1:A:167:U:H2'	1:A:168:A:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:A:OP2	1:A:297:G:N1	2.43	0.41
1:A:1352:U:O2	1:A:1352:U:C2'	2.69	0.41
1:A:2099:G:H2'	1:A:2100:A:C8	2.56	0.41
14:O:57:SER:OG	14:O:58:THR:N	2.53	0.41
17:R:550:ASP:N	17:R:550:ASP:OD1	2.51	0.41
23:Y:4:ASP:OD1	23:Y:4:ASP:N	2.52	0.41
1:A:970:A:H2'	1:A:971:A:H8	1.85	0.41
1:A:1256:C:OP1	16:Q:11:ARG:NH1	2.54	0.41
1:A:1830:G:OP2	3:C:150:LYS:NZ	2.53	0.41
1:A:2489:U:H5	1:A:2521:U:H3	1.67	0.41
1:A:2664:U:O2'	4:D:50:GLN:NE2	2.51	0.41
13:N:40:LEU:HD23	13:N:117:ILE:HD13	2.02	0.41
17:R:96:LEU:HG	17:R:173:PRO:HD2	2.02	0.41
17:R:192:LEU:HD22	17:R:223:LEU:HD13	2.02	0.41
1:A:1221:A:H2'	1:A:1222:A:C8	2.55	0.41
1:A:1328:C:H2'	1:A:1329:C:H6	1.85	0.41
8:I:20:PRO:HG2	8:I:22:PRO:HG2	2.03	0.41
1:A:161:A:N3	1:A:2237:C:O2'	2.51	0.41
1:A:1281:C:O2	1:A:1281:C:O4'	2.38	0.41
1:A:1476:C:H2'	1:A:1477:A:C8	2.56	0.41
1:A:1483:A:H2'	1:A:1484:U:H6	1.85	0.41
1:A:2501:G:H5'	15:T:62:C:H4'	2.03	0.41
1:A:2843:G:H2'	1:A:2844:A:C8	2.56	0.41
8:I:21:ALA:HB1	17:R:351:TYR:CD1	2.53	0.41
13:N:21:THR:HG23	13:N:44:VAL:HG22	2.03	0.41
14:O:61:LYS:HE3	14:O:61:LYS:HB2	1.88	0.41
19:U:9:VAL:HG12	19:U:70:PRO:HA	2.03	0.41
1:A:1112:U:H3'	1:A:1112:U:C6	2.52	0.41
1:A:1317:G:H2'	1:A:1318:G:H8	1.84	0.41
1:A:2647:G:H21	4:D:154:VAL:HG21	1.85	0.41
2:B:34:C:H42	2:B:47:C:H1'	1.86	0.41
10:K:64:ARG:NH1	10:K:101:PRO:O	2.47	0.41
32:h:35:ASN:HB2	32:h:38:GLU:HG3	2.03	0.41
1:A:24:G:O2'	18:S:78:GLU:O	2.36	0.41
1:A:525:A:H61	1:A:546:G:HO2'	1.68	0.41
1:A:834:C:H5''	1:A:835:A:H5'	2.02	0.41
4:D:84:ARG:HA	4:D:85:GLY:HA2	1.61	0.41
7:G:45:LYS:HA	7:G:45:LYS:HD3	1.75	0.41
11:L:63:LYS:HG2	29:e:12:LYS:HB3	2.03	0.41
17:R:410:GLN:O	17:R:414:ALA:HB2	2.20	0.41
25:a:26:GLY:HA2	25:a:100:LEU:HD11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:75:G:H2'	1:A:76:C:H5'	2.02	0.41
1:A:805:G:N2	1:A:2010:A:H62	2.18	0.41
12:M:17:MET:HE1	12:M:40:SER:HA	2.02	0.41
12:M:116:GLU:OE2	12:M:119:ARG:NH2	2.46	0.41
17:R:138:VAL:HG12	17:R:161:ASP:HA	2.03	0.41
23:Y:64:LYS:HD3	23:Y:64:LYS:HA	1.91	0.41
1:A:120:G:H4'	1:A:150:A:H5'	2.03	0.40
1:A:229:A:H3'	1:A:230:A:H8	1.84	0.40
1:A:483:C:H6	1:A:483:C:C5'	2.32	0.40
1:A:625:C:H2'	1:A:626:G:C8	2.56	0.40
1:A:1650:C:H3'	1:A:1651:G:H21	1.86	0.40
14:O:25:THR:HB	14:O:47:ASP:HB2	2.04	0.40
17:R:174:LEU:C	17:R:176:ALA:N	2.79	0.40
1:A:624:C:H4'	16:Q:31:LEU:HD13	2.03	0.40
1:A:1042:A:O2'	16:Q:92:ARG:CZ	2.70	0.40
1:A:1439:U:H2'	1:A:1440:G:C8	2.56	0.40
1:A:2842:U:OP1	13:N:103:LYS:NZ	2.55	0.40
4:D:163:ARG:HE	4:D:163:ARG:HB2	1.74	0.40
24:Z:4:LEU:HD21	24:Z:56:VAL:HG13	2.02	0.40
33:i:49:ALA:HA	33:i:52:ARG:HG2	2.02	0.40
1:A:913:A:C5'	1:A:913:A:C8	3.04	0.40
1:A:1652:C:N4	1:A:1667:A:OP2	2.54	0.40
1:A:1886:G:N2	1:A:1914:A:H62	2.19	0.40
3:C:5:LYS:HG2	3:C:17:THR:HG22	2.02	0.40
5:E:40:GLN:HE22	5:E:182:ASN:HB2	1.86	0.40
17:R:224:PRO:O	17:R:228:LEU:HD23	2.22	0.40
1:A:189:G:H2'	1:A:190:G:H8	1.86	0.40
1:A:610:U:O4	31:g:79:LYS:NZ	2.55	0.40
1:A:1532:A:H2'	1:A:1533:A:H8	1.86	0.40
1:A:1681:U:H2'	1:A:1682:C:C6	2.57	0.40
7:G:98:SER:HB3	7:G:105:VAL:HB	2.04	0.40
17:R:310:LYS:HB2	17:R:310:LYS:HE2	1.94	0.40
1:A:633:U:H2'	1:A:634:A:C8	2.52	0.40
1:A:1462:G:O2'	1:A:1633:G:O2'	2.31	0.40
1:A:1524:A:H8	1:A:1524:A:H5''	1.85	0.40
1:A:2275:G:H2'	1:A:2276:A:H8	1.86	0.40
1:A:2656:G:O2'	1:A:2810:A:N1	2.53	0.40
11:L:14:LYS:HB3	11:L:14:LYS:HE3	1.82	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	273/277 (99%)	261 (96%)	12 (4%)	0	100	100
4	D	205/209 (98%)	197 (96%)	8 (4%)	0	100	100
5	E	203/207 (98%)	189 (93%)	14 (7%)	0	100	100
6	F	176/179 (98%)	163 (93%)	13 (7%)	0	100	100
7	G	173/179 (97%)	165 (95%)	8 (5%)	0	100	100
8	I	131/141 (93%)	126 (96%)	5 (4%)	0	100	100
9	J	140/145 (97%)	133 (95%)	7 (5%)	0	100	100
10	K	120/122 (98%)	112 (93%)	8 (7%)	0	100	100
11	L	144/146 (99%)	140 (97%)	4 (3%)	0	100	100
12	M	136/144 (94%)	133 (98%)	3 (2%)	0	100	100
13	N	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
14	O	118/120 (98%)	113 (96%)	5 (4%)	0	100	100
16	Q	115/119 (97%)	110 (96%)	5 (4%)	0	100	100
17	R	554/570 (97%)	520 (94%)	34 (6%)	0	100	100
18	S	107/113 (95%)	94 (88%)	13 (12%)	0	100	100
19	U	98/103 (95%)	87 (89%)	11 (11%)	0	100	100
20	V	80/94 (85%)	80 (100%)	0	0	100	100
21	W	5/7 (71%)	5 (100%)	0	0	100	100
22	X	56/62 (90%)	51 (91%)	5 (9%)	0	100	100
23	Y	82/86 (95%)	78 (95%)	4 (5%)	0	100	100
24	Z	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
25	a	112/115 (97%)	107 (96%)	5 (4%)	0	100	100
26	b	52/59 (88%)	48 (92%)	4 (8%)	0	100	100
27	c	46/49 (94%)	46 (100%)	0	0	100	100
28	d	42/44 (96%)	42 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	e	62/66 (94%)	59 (95%)	3 (5%)	0	100	100
30	f	34/37 (92%)	33 (97%)	1 (3%)	0	100	100
31	g	99/102 (97%)	86 (87%)	13 (13%)	0	100	100
32	h	91/95 (96%)	87 (96%)	4 (4%)	0	100	100
33	i	63/66 (96%)	59 (94%)	4 (6%)	0	100	100
All	All	3690/3835 (96%)	3492 (95%)	198 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	223/225 (99%)	223 (100%)	0	100	100
4	D	168/170 (99%)	168 (100%)	0	100	100
5	E	169/170 (99%)	169 (100%)	0	100	100
6	F	153/154 (99%)	153 (100%)	0	100	100
7	G	148/151 (98%)	148 (100%)	0	100	100
8	I	103/110 (94%)	103 (100%)	0	100	100
9	J	120/123 (98%)	120 (100%)	0	100	100
10	K	101/101 (100%)	101 (100%)	0	100	100
11	L	110/110 (100%)	109 (99%)	1 (1%)	70	85
12	M	111/116 (96%)	111 (100%)	0	100	100
13	N	99/100 (99%)	99 (100%)	0	100	100
14	O	93/93 (100%)	93 (100%)	0	100	100
16	Q	96/98 (98%)	96 (100%)	0	100	100
17	R	494/505 (98%)	491 (99%)	3 (1%)	78	88
18	S	90/93 (97%)	90 (100%)	0	100	100
19	U	84/87 (97%)	84 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	V	64/74 (86%)	64 (100%)	0	100	100
22	X	47/50 (94%)	47 (100%)	0	100	100
23	Y	74/75 (99%)	74 (100%)	0	100	100
24	Z	52/53 (98%)	52 (100%)	0	100	100
25	a	99/100 (99%)	99 (100%)	0	100	100
26	b	48/53 (91%)	48 (100%)	0	100	100
27	c	46/47 (98%)	46 (100%)	0	100	100
28	d	39/39 (100%)	39 (100%)	0	100	100
29	e	54/56 (96%)	54 (100%)	0	100	100
30	f	34/35 (97%)	34 (100%)	0	100	100
31	g	83/84 (99%)	83 (100%)	0	100	100
32	h	84/85 (99%)	84 (100%)	0	100	100
33	i	56/57 (98%)	56 (100%)	0	100	100
All	All	3142/3214 (98%)	3138 (100%)	4 (0%)	87	93

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	L	70	ASN
17	R	426	LEU
17	R	427	VAL
17	R	565	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	95	ASN
3	C	111	GLN
3	C	143	ASN
3	C	153	GLN
3	C	228	ASN
5	E	29	ASN
5	E	40	GLN
5	E	189	HIS
9	J	54	HIS
11	L	4	HIS

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Mol	Chain	Res	Type
11	L	17	ASN
11	L	27	ASN
13	N	57	HIS
14	O	39	HIS
16	Q	81	HIS
17	R	300	ASN
18	S	97	ASN
22	X	16	ASN
23	Y	33	ASN
23	Y	61	ASN
24	Z	19	GLN
31	g	83	HIS
33	i	65	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2817/2820 (99%)	647 (22%)	56 (1%)
15	P	66/76 (86%)	20 (30%)	1 (1%)
15	T	75/76 (98%)	22 (29%)	0
2	B	111/112 (99%)	30 (27%)	2 (1%)
All	All	3069/3084 (99%)	719 (23%)	59 (1%)

All (719) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	12	A
1	A	13	A
1	A	15	G
1	A	33	U
1	A	34	U
1	A	35	G
1	A	39	C
1	A	42	G
1	A	43	G
1	A	44	A
1	A	45	G
1	A	46	C
1	A	51	G
1	A	59	G
1	A	63	G

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Mol	Chain	Res	Type
1	A	71	A
1	A	75	G
1	A	76	C
1	A	87	U
1	A	91	A
1	A	94	A
1	A	101	G
1	A	117	A
1	A	118	A
1	A	119	U
1	A	124	A
1	A	125	A
1	A	130	A
1	A	133	A
1	A	159	U
1	A	162	A
1	A	163	U
1	A	164	U
1	A	175	G
1	A	176	A
1	A	177	G
1	A	178	A
1	A	183	A
1	A	184	G
1	A	188	C
1	A	199	A
1	A	202	A
1	A	203	U
1	A	207	A
1	A	216	A
1	A	219	A
1	A	225	A
1	A	226	A
1	A	227	G
1	A	228	C
1	A	229	A
1	A	230	A
1	A	231	A
1	A	233	G
1	A	245	G
1	A	251	G
1	A	252	C

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Mol	Chain	Res	Type
1	A	253	G
1	A	258	A
1	A	267	C
1	A	268	A
1	A	269	G
1	A	270	C
1	A	271	C
1	A	272	C
1	A	273	A
1	A	274	A
1	A	275	A
1	A	276	C
1	A	277	C
1	A	282	G
1	A	289	C
1	A	290	U
1	A	291	C
1	A	295	G
1	A	296	G
1	A	297	G
1	A	298	U
1	A	299	U
1	A	300	G
1	A	301	U
1	A	302	A
1	A	310	C
1	A	312	G
1	A	313	U
1	A	314	A
1	A	315	C
1	A	321	U
1	A	322	A
1	A	324	A
1	A	325	A
1	A	331	C
1	A	337	A
1	A	345	A
1	A	346	G
1	A	348	U
1	A	352	G
1	A	354	A
1	A	355	A

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Mol	Chain	Res	Type
1	A	360	C
1	A	367	G
1	A	373	A
1	A	374	A
1	A	376	A
1	A	378	C
1	A	382	G
1	A	386	U
1	A	387	C
1	A	390	A
1	A	392	C
1	A	393	U
1	A	394	U
1	A	405	U
1	A	406	G
1	A	410	G
1	A	411	G
1	A	414	C
1	A	417	G
1	A	418	A
1	A	430	C
1	A	432	C
1	A	433	G
1	A	434	U
1	A	435	G
1	A	438	A
1	A	442	C
1	A	443	G
1	A	444	U
1	A	459	A
1	A	474	U
1	A	478	U
1	A	482	C
1	A	483	C
1	A	485	U
1	A	490	A
1	A	494	A
1	A	498	U
1	A	502	C
1	A	503	C
1	A	504	A
1	A	514	G

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Mol	Chain	Res	Type
1	A	528	G
1	A	538	A
1	A	548	A
1	A	550	G
1	A	551	A
1	A	552	G
1	A	554	U
1	A	555	C
1	A	556	C
1	A	558	G
1	A	562	C
1	A	564	G
1	A	572	A
1	A	576	G
1	A	577	U
1	A	578	A
1	A	592	A
1	A	593	A
1	A	594	C
1	A	595	G
1	A	607	G
1	A	617	G
1	A	619	A
1	A	631	G
1	A	647	A
1	A	648	G
1	A	649	G
1	A	650	U
1	A	651	U
1	A	660	G
1	A	663	G
1	A	666	G
1	A	667	A
1	A	673	A
1	A	674	G
1	A	680	G
1	A	683	A
1	A	684	G
1	A	691	U
1	A	700	U
1	A	701	G
1	A	713	G

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Mol	Chain	Res	Type
1	A	715	A
1	A	717	A
1	A	718	C
1	A	719	C
1	A	733	U
1	A	773	G
1	A	777	C
1	A	781	A
1	A	782	A
1	A	786	A
1	A	792	G
1	A	794	U
1	A	795	G
1	A	797	A
1	A	822	G
1	A	823	G
1	A	824	G
1	A	829	A
1	A	831	U
1	A	832	G
1	A	836	A
1	A	837	U
1	A	838	C
1	A	839	G
1	A	852	G
1	A	853	C
1	A	858	U
1	A	859	C
1	A	866	A
1	A	874	U
1	A	875	U
1	A	877	G
1	A	892	U
1	A	893	A
1	A	895	G
1	A	913	A
1	A	914	C
1	A	916	G
1	A	924	U
1	A	925	A
1	A	927	G
1	A	928	G

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Mol	Chain	Res	Type
1	A	931	C
1	A	935	A
1	A	937	C
1	A	942	U
1	A	943	A
1	A	944	C
1	A	948	A
1	A	951	C
1	A	952	A
1	A	954	U
1	A	957	A
1	A	959	C
1	A	961	C
1	A	962	C
1	A	964	A
1	A	973	G
1	A	977	U
1	A	978	A
1	A	981	C
1	A	987	A
1	A	988	G
1	A	990	C
1	A	991	A
1	A	992	G
1	A	999	A
1	A	1005	A
1	A	1007	G
1	A	1019	A
1	A	1020	A
1	A	1025	A
1	A	1026	A
1	A	1027	A
1	A	1028	C
1	A	1029	A
1	A	1031	C
1	A	1034	A
1	A	1037	C
1	A	1055	A
1	A	1058	U
1	A	1059	A
1	A	1068	G
1	A	1072	A

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Mol	Chain	Res	Type
1	A	1079	U
1	A	1091	U
1	A	1092	A
1	A	1093	G
1	A	1102	G
1	A	1104	U
1	A	1105	G
1	A	1107	U
1	A	1108	G
1	A	1110	C
1	A	1112	U
1	A	1113	A
1	A	1115	A
1	A	1116	A
1	A	1117	G
1	A	1123	A
1	A	1124	C
1	A	1127	U
1	A	1128	U
1	A	1129	U
1	A	1131	A
1	A	1135	G
1	A	1139	G
1	A	1140	U
1	A	1141	A
1	A	1142	A
1	A	1143	U
1	A	1144	A
1	A	1152	G
1	A	1157	A
1	A	1158	G
1	A	1159	U
1	A	1176	U
1	A	1178	U
1	A	1179	A
1	A	1181	C
1	A	1182	G
1	A	1185	G
1	A	1187	U
1	A	1188	A
1	A	1194	A
1	A	1201	A

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Mol	Chain	Res	Type
1	A	1202	A
1	A	1209	G
1	A	1217	U
1	A	1218	U
1	A	1219	C
1	A	1220	G
1	A	1245	G
1	A	1246	G
1	A	1247	G
1	A	1251	U
1	A	1252	G
1	A	1260	A
1	A	1276	G
1	A	1278	G
1	A	1281	C
1	A	1283	U
1	A	1284	A
1	A	1289	U
1	A	1293	A
1	A	1295	U
1	A	1296	G
1	A	1311	G
1	A	1312	A
1	A	1313	A
1	A	1314	A
1	A	1315	G
1	A	1327	U
1	A	1339	A
1	A	1340	A
1	A	1345	U
1	A	1346	A
1	A	1351	U
1	A	1352	U
1	A	1359	G
1	A	1360	A
1	A	1361	A
1	A	1363	G
1	A	1364	C
1	A	1376	G
1	A	1381	A
1	A	1382	G
1	A	1384	C

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Mol	Chain	Res	Type
1	A	1388	A
1	A	1404	A
1	A	1417	A
1	A	1418	U
1	A	1423	A
1	A	1424	A
1	A	1425	C
1	A	1431	G
1	A	1433	U
1	A	1435	U
1	A	1436	U
1	A	1439	U
1	A	1441	U
1	A	1442	A
1	A	1450	C
1	A	1456	A
1	A	1460	G
1	A	1464	A
1	A	1472	G
1	A	1473	A
1	A	1474	C
1	A	1490	A
1	A	1497	G
1	A	1498	U
1	A	1499	A
1	A	1507	U
1	A	1513	U
1	A	1515	C
1	A	1516	A
1	A	1517	A
1	A	1519	C
1	A	1520	A
1	A	1523	U
1	A	1524	A
1	A	1528	U
1	A	1536	A
1	A	1539	C
1	A	1553	A
1	A	1555	A
1	A	1561	G
1	A	1563	G
1	A	1569	A

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Mol	Chain	Res	Type
1	A	1571	G
1	A	1572	G
1	A	1573	C
1	A	1581	A
1	A	1582	U
1	A	1584	U
1	A	1586	G
1	A	1596	U
1	A	1607	C
1	A	1608	A
1	A	1614	A
1	A	1617	A
1	A	1623	C
1	A	1626	U
1	A	1631	A
1	A	1632	G
1	A	1634	U
1	A	1651	G
1	A	1652	C
1	A	1653	A
1	A	1655	A
1	A	1657	C
1	A	1658	G
1	A	1660	C
1	A	1667	A
1	A	1674	G
1	A	1679	A
1	A	1691	A
1	A	1692	U
1	A	1693	C
1	A	1696	G
1	A	1697	A
1	A	1705	C
1	A	1709	A
1	A	1712	G
1	A	1719	G
1	A	1727	A
1	A	1744	G
1	A	1745	A
1	A	1752	G
1	A	1756	U
1	A	1757	G

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Mol	Chain	Res	Type
1	A	1758	U
1	A	1770	C
1	A	1774	A
1	A	1777	G
1	A	1778	A
1	A	1779	G
1	A	1780	C
1	A	1781	C
1	A	1782	G
1	A	1785	G
1	A	1788	A
1	A	1791	A
1	A	1792	G
1	A	1793	G
1	A	1802	A
1	A	1805	G
1	A	1809	A
1	A	1811	C
1	A	1829	C
1	A	1830	G
1	A	1845	A
1	A	1858	A
1	A	1877	A
1	A	1881	U
1	A	1895	A
1	A	1898	G
1	A	1901	A
1	A	1902	G
1	A	1912	G
1	A	1913	A
1	A	1918	A
1	A	1935	G
1	A	1941	A
1	A	1949	C
1	A	1958	G
1	A	1959	G
1	A	1966	A
1	A	1968	U
1	A	1972	U
1	A	1984	U
1	A	1990	C
1	A	1993	G

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Mol	Chain	Res	Type
1	A	1996	C
1	A	1999	A
1	A	2000	A
1	A	2001	G
1	A	2011	U
1	A	2020	U
1	A	2021	G
1	A	2022	U
1	A	2024	U
1	A	2026	A
1	A	2050	G
1	A	2052	A
1	A	2060	A
1	A	2061	G
1	A	2062	A
1	A	2068	G
1	A	2072	C
1	A	2084	C
1	A	2085	G
1	A	2088	A
1	A	2089	A
1	A	2090	G
1	A	2091	A
1	A	2098	G
1	A	2110	C
1	A	2111	A
1	A	2121	U
1	A	2123	A
1	A	2232	G
1	A	2233	C
1	A	2235	G
1	A	2240	U
1	A	2241	A
1	A	2243	C
1	A	2254	A
1	A	2255	C
1	A	2267	G
1	A	2268	G
1	A	2308	G
1	A	2311	G
1	A	2312	C
1	A	2315	A

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Mol	Chain	Res	Type
1	A	2317	A
1	A	2333	G
1	A	2334	U
1	A	2335	U
1	A	2336	G
1	A	2337	G
1	A	2338	A
1	A	2345	U
1	A	2346	C
1	A	2348	C
1	A	2349	A
1	A	2350	G
1	A	2351	A
1	A	2352	G
1	A	2356	A
1	A	2357	A
1	A	2363	C
1	A	2364	A
1	A	2374	G
1	A	2377	U
1	A	2379	C
1	A	2390	A
1	A	2408	G
1	A	2411	G
1	A	2412	G
1	A	2414	C
1	A	2420	G
1	A	2431	U
1	A	2435	C
1	A	2436	A
1	A	2454	A
1	A	2455	A
1	A	2457	G
1	A	2458	G
1	A	2459	A
1	A	2464	A
1	A	2468	A
1	A	2469	C
1	A	2470	C
1	A	2476	G
1	A	2477	A
1	A	2486	U

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Mol	Chain	Res	Type
1	A	2488	A
1	A	2502	U
1	A	2505	A
1	A	2507	A
1	A	2519	G
1	A	2523	G
1	A	2527	C
1	A	2528	C
1	A	2531	G
1	A	2532	A
1	A	2534	G
1	A	2535	U
1	A	2542	A
1	A	2549	C
1	A	2558	G
1	A	2564	G
1	A	2572	G
1	A	2577	G
1	A	2583	U
1	A	2593	A
1	A	2594	A
1	A	2595	A
1	A	2596	G
1	A	2598	G
1	A	2601	A
1	A	2607	G
1	A	2611	G
1	A	2619	A
1	A	2631	A
1	A	2638	U
1	A	2639	C
1	A	2642	U
1	A	2644	U
1	A	2648	U
1	A	2658	A
1	A	2659	G
1	A	2675	C
1	A	2676	U
1	A	2683	A
1	A	2702	G
1	A	2711	G
1	A	2712	C

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Mol	Chain	Res	Type
1	A	2714	G
1	A	2717	G
1	A	2718	U
1	A	2720	C
1	A	2743	G
1	A	2754	A
1	A	2755	U
1	A	2762	A
1	A	2764	G
1	A	2768	U
1	A	2773	G
1	A	2777	A
1	A	2779	A
1	A	2785	U
1	A	2786	A
1	A	2794	A
1	A	2795	G
1	A	2797	C
1	A	2799	C
1	A	2804	A
1	A	2807	A
1	A	2808	U
1	A	2813	U
1	A	2818	C
1	A	2819	A
1	A	2820	U
1	A	2825	C
1	A	2826	A
1	A	2828	G
1	A	2830	A
1	A	2845	A
1	A	2855	G
1	A	2858	U
1	A	2859	G
1	A	2860	A
1	A	2861	U
1	A	2874	G
1	A	2897	G
1	A	2898	A
1	A	2899	C
1	A	2905	C
1	A	2908	A

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Mol	Chain	Res	Type
1	A	2918	G
1	A	2921	U
2	B	10	G
2	B	11	A
2	B	12	U
2	B	13	A
2	B	14	G
2	B	19	G
2	B	20	A
2	B	23	U
2	B	28	C
2	B	33	U
2	B	38	U
2	B	39	A
2	B	40	C
2	B	41	C
2	B	42	G
2	B	48	G
2	B	49	G
2	B	51	A
2	B	54	U
2	B	55	A
2	B	59	U
2	B	60	C
2	B	64	A
2	B	85	U
2	B	86	U
2	B	87	U
2	B	88	C
2	B	97	A
2	B	107	G
2	B	110	G
15	P	8	U
15	P	9	A
15	P	19	G
15	P	20	G
15	P	22	G
15	P	29	U
15	P	30	G
15	P	31	C
15	P	32	U
15	P	40	C

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Mol	Chain	Res	Type
15	P	41	A
15	P	44	A
15	P	48	C
15	P	52	G
15	P	53	G
15	P	54	U
15	P	61	C
15	P	66	A
15	P	67	G
15	P	76	A
15	T	3	G
15	T	8	U
15	T	9	A
15	T	16	C
15	T	17	U
15	T	18	G
15	T	19	G
15	T	20	G
15	T	34	U
15	T	36	C
15	T	38	C
15	T	41	A
15	T	44	A
15	T	45	G
15	T	46	G
15	T	48	C
15	T	53	G
15	T	55	U
15	T	57	G
15	T	67	G
15	T	72	C
15	T	74	C

All (59) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	12	A
1	A	43	G
1	A	45	G
1	A	58	G
1	A	90	A
1	A	175	G

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Mol	Chain	Res	Type
1	A	177	G
1	A	183	A
1	A	229	A
1	A	252	C
1	A	272	C
1	A	274	A
1	A	275	A
1	A	276	C
1	A	288	C
1	A	295	G
1	A	296	G
1	A	377	G
1	A	405	U
1	A	437	A
1	A	442	C
1	A	537	A
1	A	549	A
1	A	649	G
1	A	662	U
1	A	683	A
1	A	717	A
1	A	785	C
1	A	837	U
1	A	936	C
1	A	1111	U
1	A	1245	G
1	A	1250	G
1	A	1351	U
1	A	1359	G
1	A	1438	C
1	A	1516	A
1	A	1595	U
1	A	1630	G
1	A	1652	C
1	A	1755	C
1	A	1779	G
1	A	1784	A
1	A	1948	A
1	A	2267	G
1	A	2334	U
1	A	2351	A
1	A	2454	A

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Mol	Chain	Res	Type
1	A	2468	A
1	A	2710	C
1	A	2711	G
1	A	2716	U
1	A	2784	C
1	A	2785	U
1	A	2796	C
1	A	2812	A
2	B	47	C
2	B	59	U
15	P	51	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	2124:A	O3'	2223:U	P	17.51

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1941:A	O3'	1947:A	P	13.89

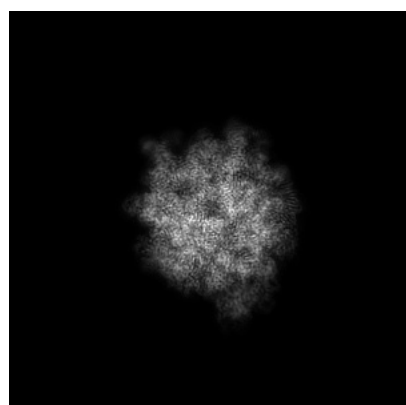
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11862. These allow visual inspection of the internal detail of the map and identification of artifacts.

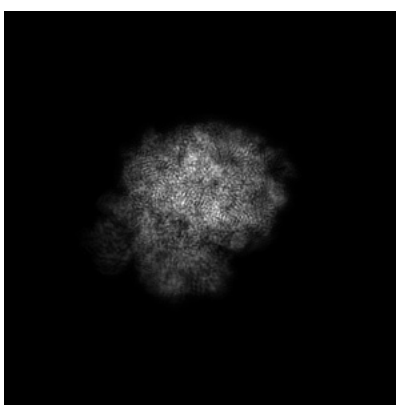
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

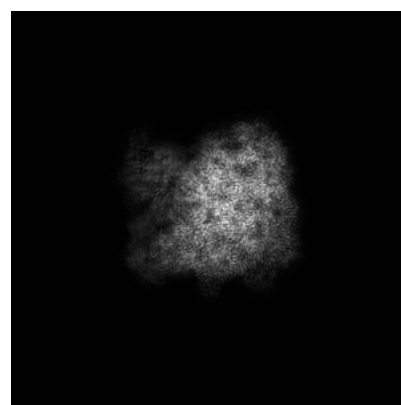
6.1.1 Primary map



X



Y



Z

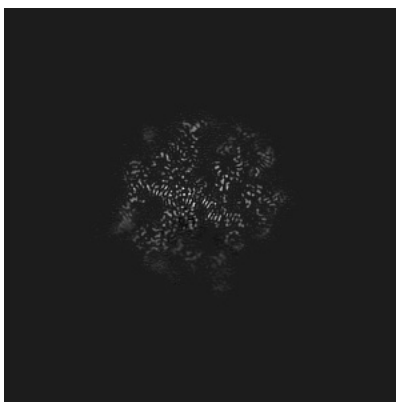
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

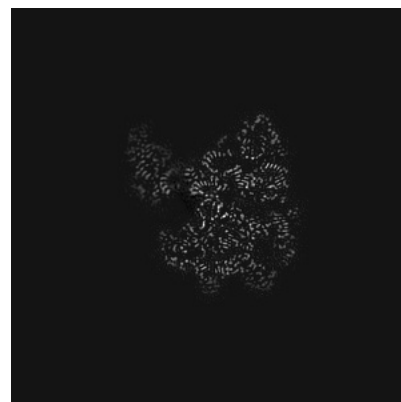
6.2.1 Primary map



X Index: 192



Y Index: 192

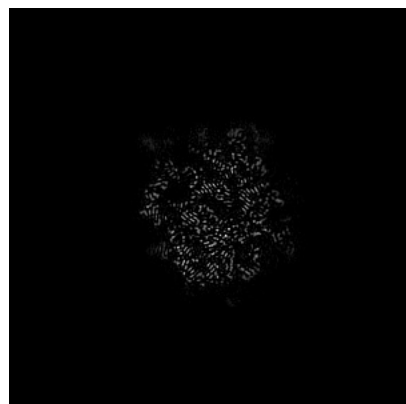


Z Index: 192

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

6.3 Largest variance slices [i](#)

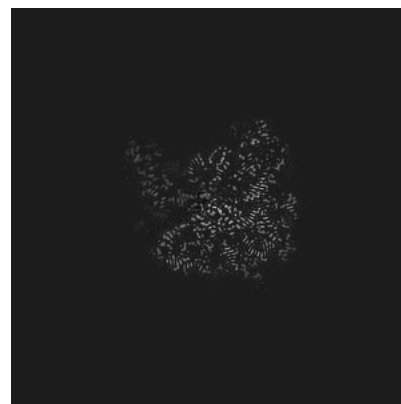
6.3.1 Primary map



X Index: 211



Y Index: 213

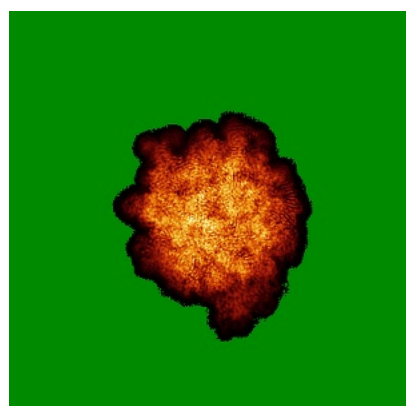


Z Index: 182

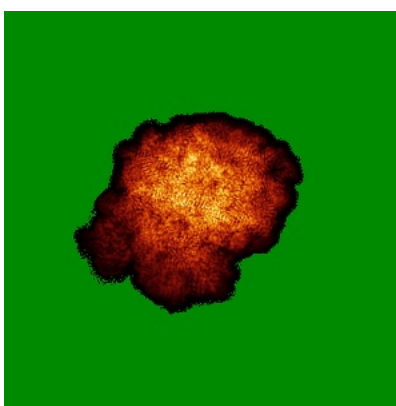
The images above show the largest variance slices of the map in three orthogonal directions.

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

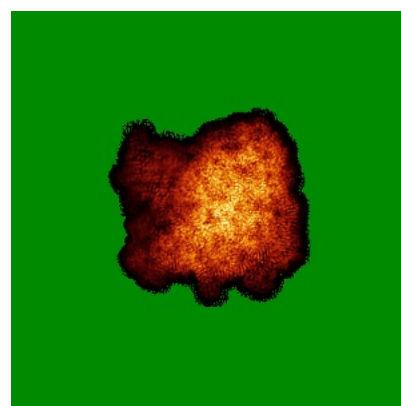
6.4.1 Primary map



X



Y

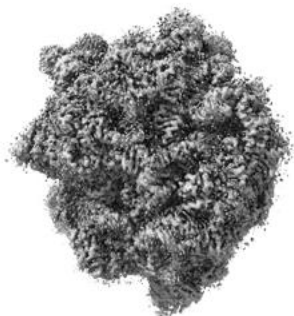


Z

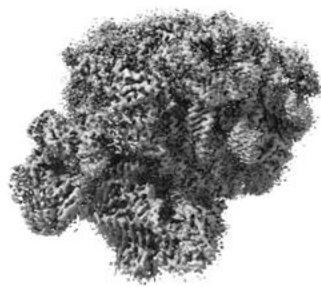
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

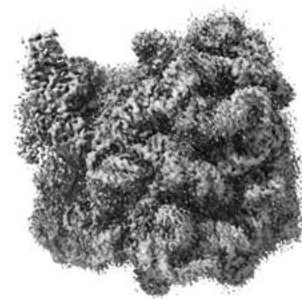
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.011. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

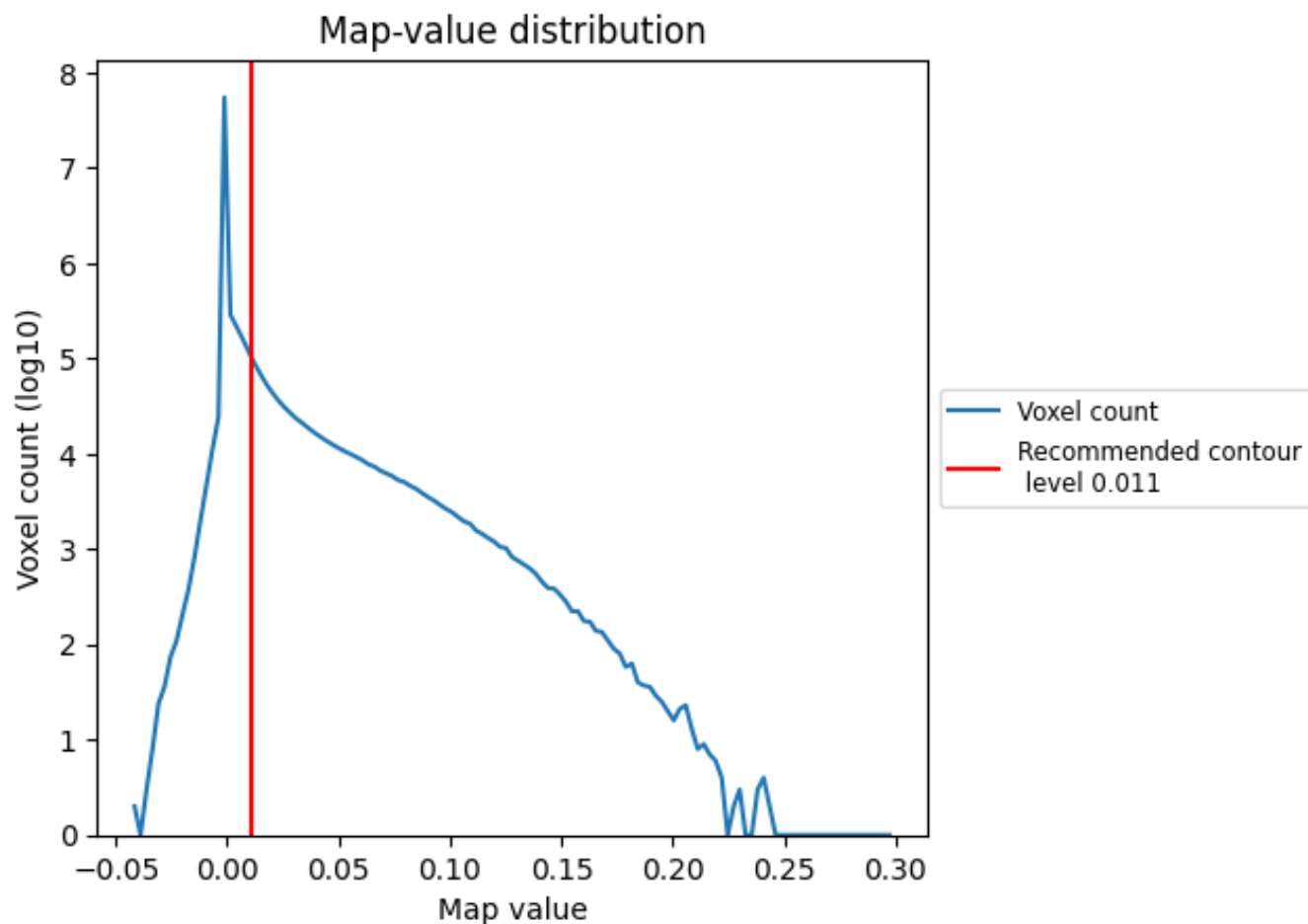
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

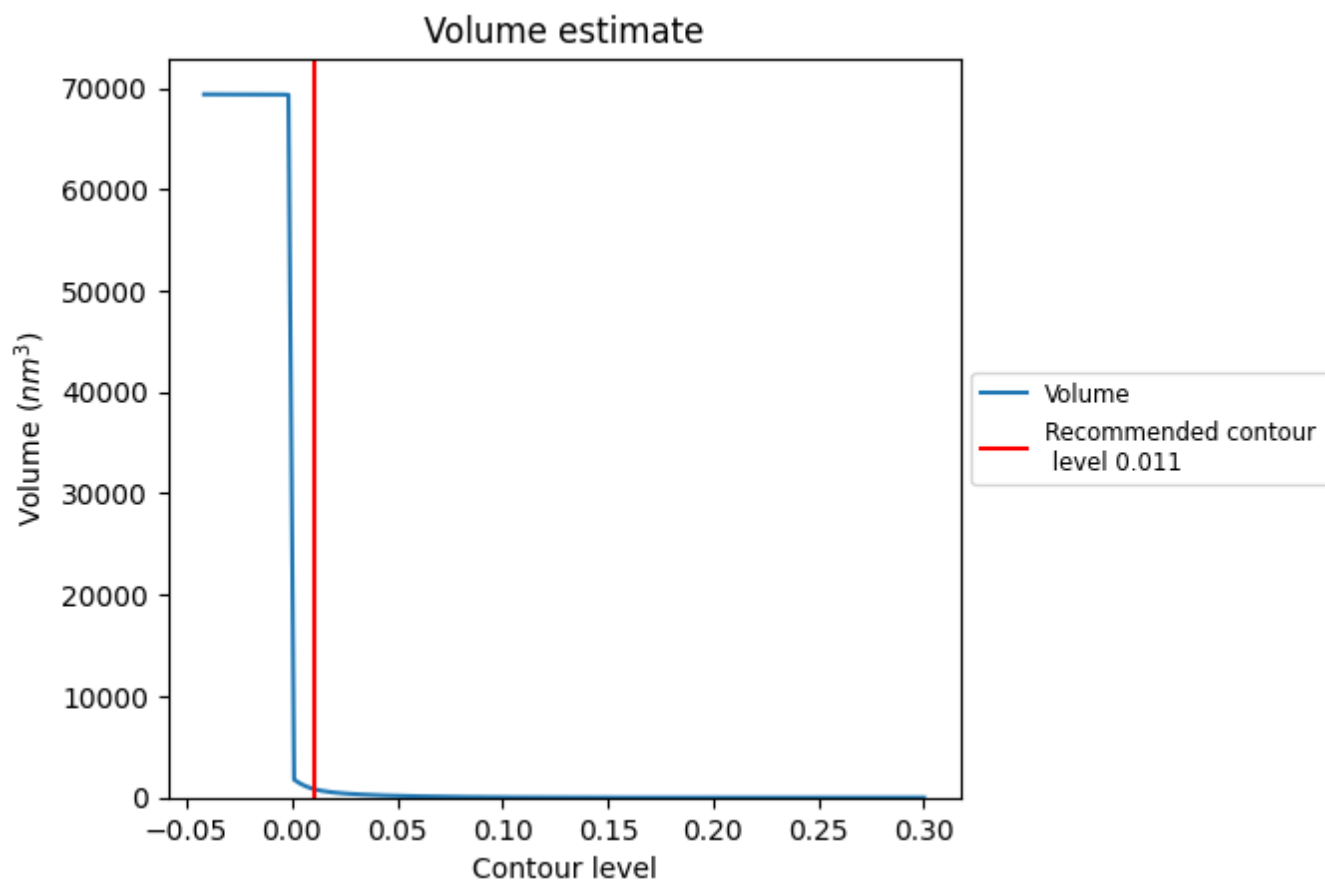
This section contains the results of statistical analysis of the map.

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.

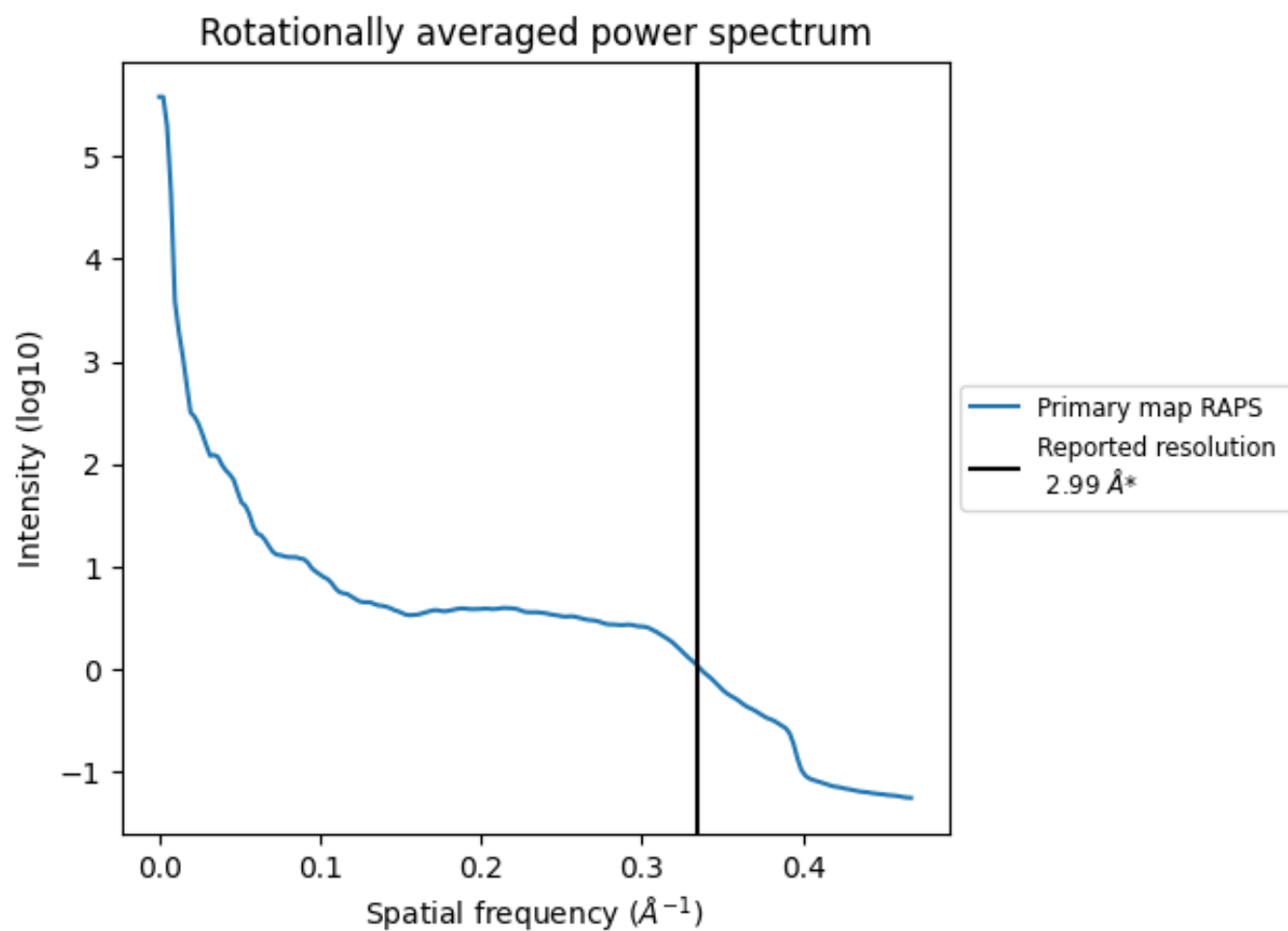
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 818 nm³; this corresponds to an approximate mass of 739 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 0.334 Å⁻¹

8 Fourier-Shell correlation

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

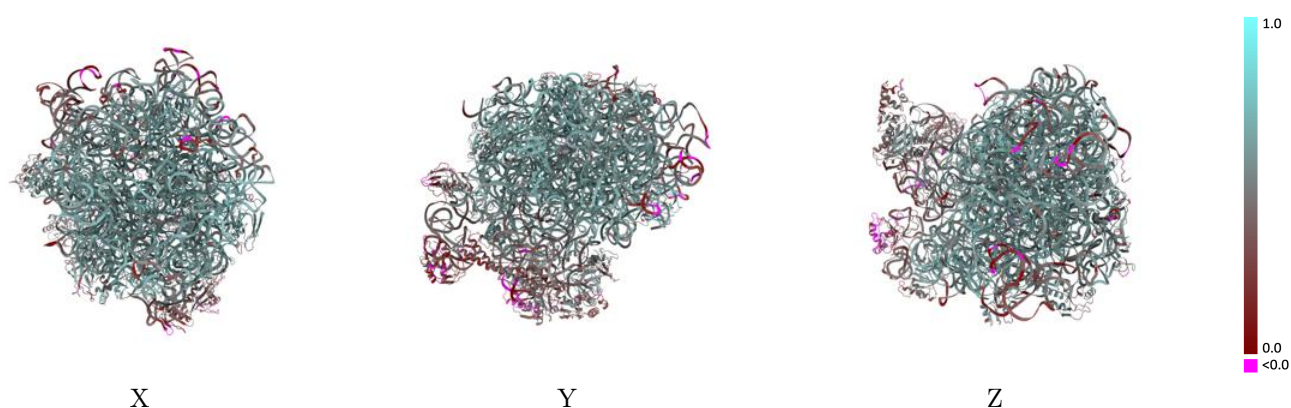
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11862 and PDB model 7AQC. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)

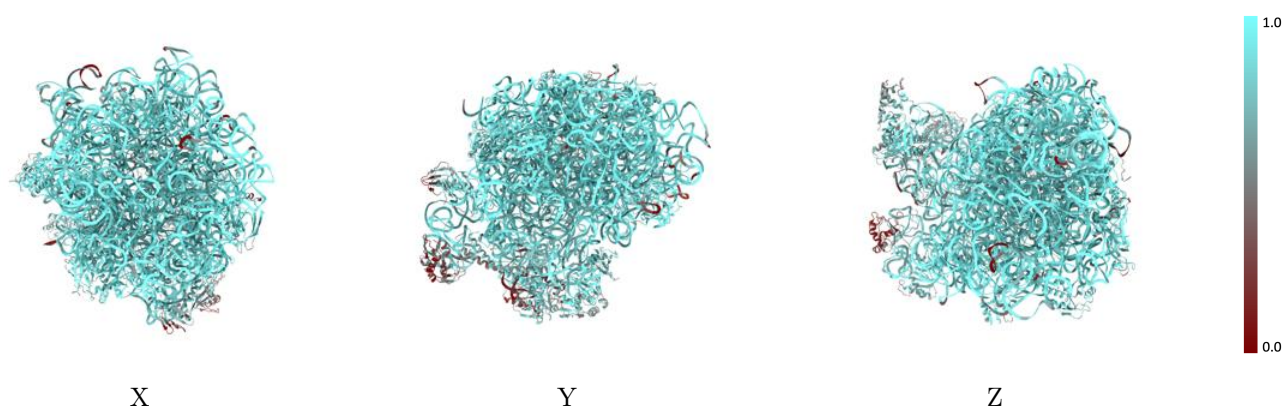
This section was not generated.

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



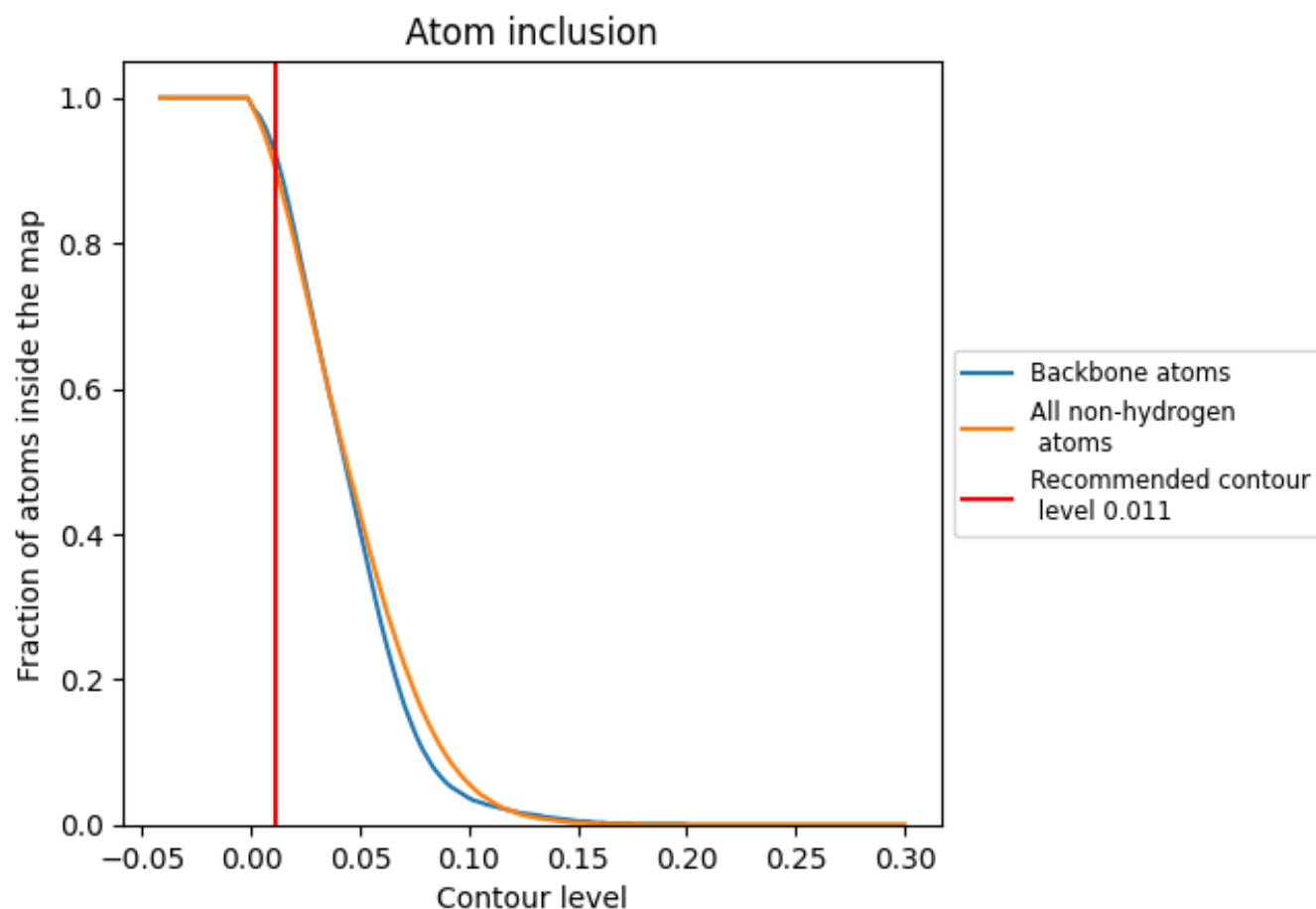
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.011).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 90% 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 (0.011) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9050	 0.5390
A	 0.9500	 0.5720
B	 0.9170	 0.4680
C	 0.9530	 0.6210
D	 0.9390	 0.6100
E	 0.8950	 0.5480
F	 0.2780	 0.0930
G	 0.6530	 0.3320
I	 0.3600	 0.2060
J	 0.9450	 0.6000
K	 0.9230	 0.5770
L	 0.9060	 0.5560
M	 0.9040	 0.5680
N	 0.9460	 0.6240
O	 0.7430	 0.4020
P	 0.8820	 0.4160
Q	 0.9350	 0.5900
R	 0.7260	 0.3900
S	 0.9500	 0.6020
T	 0.8220	 0.3780
U	 0.8060	 0.4840
V	 0.9460	 0.6040
W	 0.8000	 0.4750
X	 0.8450	 0.4720
Y	 0.7900	 0.4430
Z	 0.9170	 0.5850
a	 0.8590	 0.5370
b	 0.9100	 0.5730
c	 0.9300	 0.5900
d	 0.9940	 0.6850
e	 0.9680	 0.6270
f	 0.9400	 0.5950
g	 0.8530	 0.4880
h	 0.8750	 0.5400
i	 0.7940	 0.4210

