



wwPDB EM Validation Summary Report ⓘ

Mar 22, 2026 – 05:41 PM UTC

PDB ID : 7ASN / pdb_00007asn
EMDB ID : EMD-11901
Title : Staphylococcus aureus 50S after 30 minutes incubation a 37C
Authors : Camicata, G.; Bashan, A.; Yonath, A.
Deposited on : 2020-10-27
Resolution : 2.73 Å(reported)

This is a wwPDB EM Validation Summary 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
Mogul : 2022.3.0, CSD as543be (2022)
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

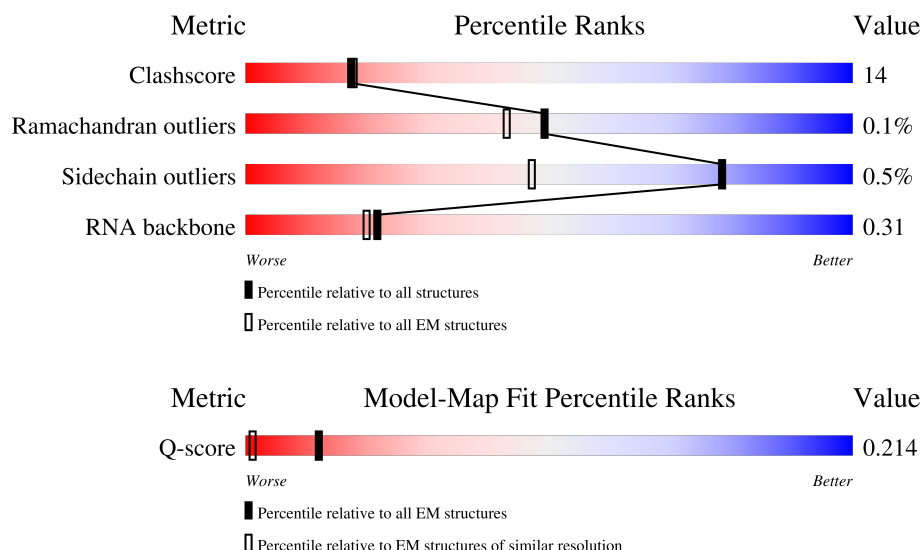
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.73 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	10432 (2.23 - 3.23)

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	2742	
2	B	106	
3	1	47	

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Mol	Chain	Length	Quality of chain
4	2	43	
5	3	64	
6	F	274	
7	D	215	
8	E	206	
9	H	144	
10	L	146	
11	Y	137	
12	G	122	
13	M	117	
14	N	114	
15	O	116	
16	P	102	
17	Q	112	
18	R	89	
19	S	103	
20	T	94	
21	a	79	
22	V	49	
23	W	67	
24	X	58	
25	b	48	

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 80694 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2742	Total	C	N	O	P	0	0
			58787	26244	10755	19046	2742		

- Molecule 2 is a RNA chain called 5S.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	106	Total	C	N	O	P	0	0
			2260	1010	407	737	106		

- Molecule 3 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1	47	Total	C	N	O	S	0	0
			390	238	78	70	4		

- Molecule 4 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	2	43	Total	C	N	O	S	0	0
			367	225	89	52	1		

- Molecule 5 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	3	64	Total	C	N	O	S	0	0
			521	324	113	82	2		

- Molecule 6 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	274	Total	C	N	O	S	0	0
			2094	1303	415	371	5		

- Molecule 7 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	215	Total	C	N	O	S	0	0
			1627	1018	299	305	5		

- Molecule 8 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	206	Total	C	N	O	S	0	0
			1572	986	288	296	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	144	Total	C	N	O	S	0	0
			1132	708	204	217	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	1	MET	-	initiating methionine	UNP W8TUE6

- Molecule 10 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	146	Total	C	N	O	S	0	0
			1086	674	214	197	1		

- Molecule 11 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Y	137	Total	C	N	O	S	0	0
			1071	689	203	175	4		

- Molecule 12 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	122	Total	C	N	O	S	0	0
			918	572	174	168	4		

- Molecule 13 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	M	117	Total	C	N	O	0	0
			872	543	172	157		

- Molecule 14 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	N	113	Total	C	N	O	0	0
			878	557	171	150		

- Molecule 15 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	116	Total	C	N	O	S	0	0
			942	593	189	156	4		

- Molecule 16 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	102	Total	C	N	O	S	0	0
			790	503	142	144	1		

- Molecule 17 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	112	Total	C	N	O	S	0	0
			854	534	164	153	3		

- Molecule 18 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	89	Total	C	N	O	S	0	0
			715	453	127	131	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	103	Total	C	N	O	S	0	0
			770	486	142	141	1		

- Molecule 20 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	T	94	Total	C	N	O	0	0
			722	463	130	129		

- Molecule 21 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	a	79	Total	C	N	O	0	0
			597	369	117	111		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
22	V	49	Total	C	N	O	0	0
			379	234	82	63		

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	W	67	Total	C	N	O	0	0
			541	333	102	106		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
24	X	58	Total	C	N	O	0	0
			449	280	85	84		

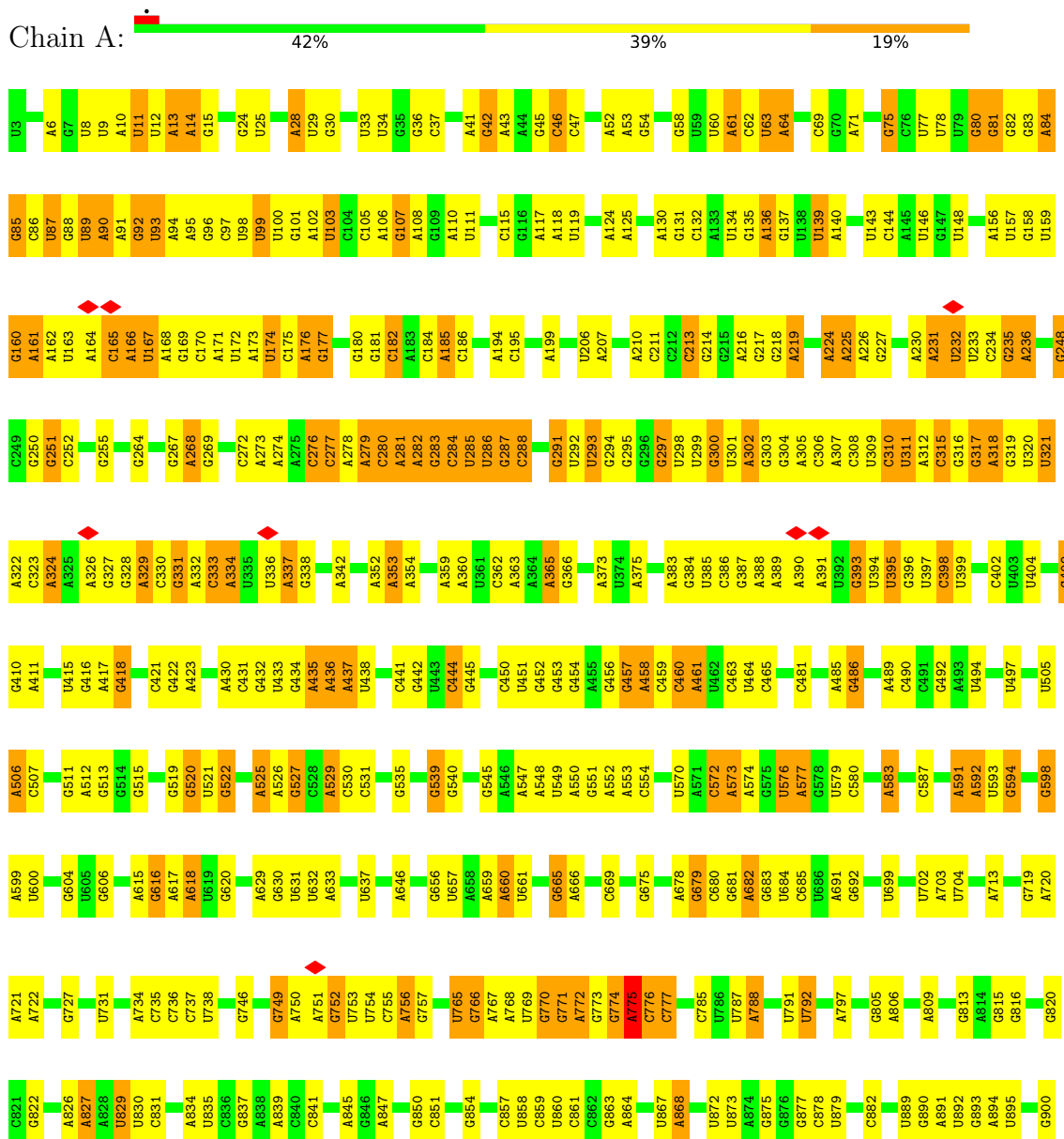
- Molecule 25 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	48	Total	C	N	O	S	0	0
			360	222	77	59	2		

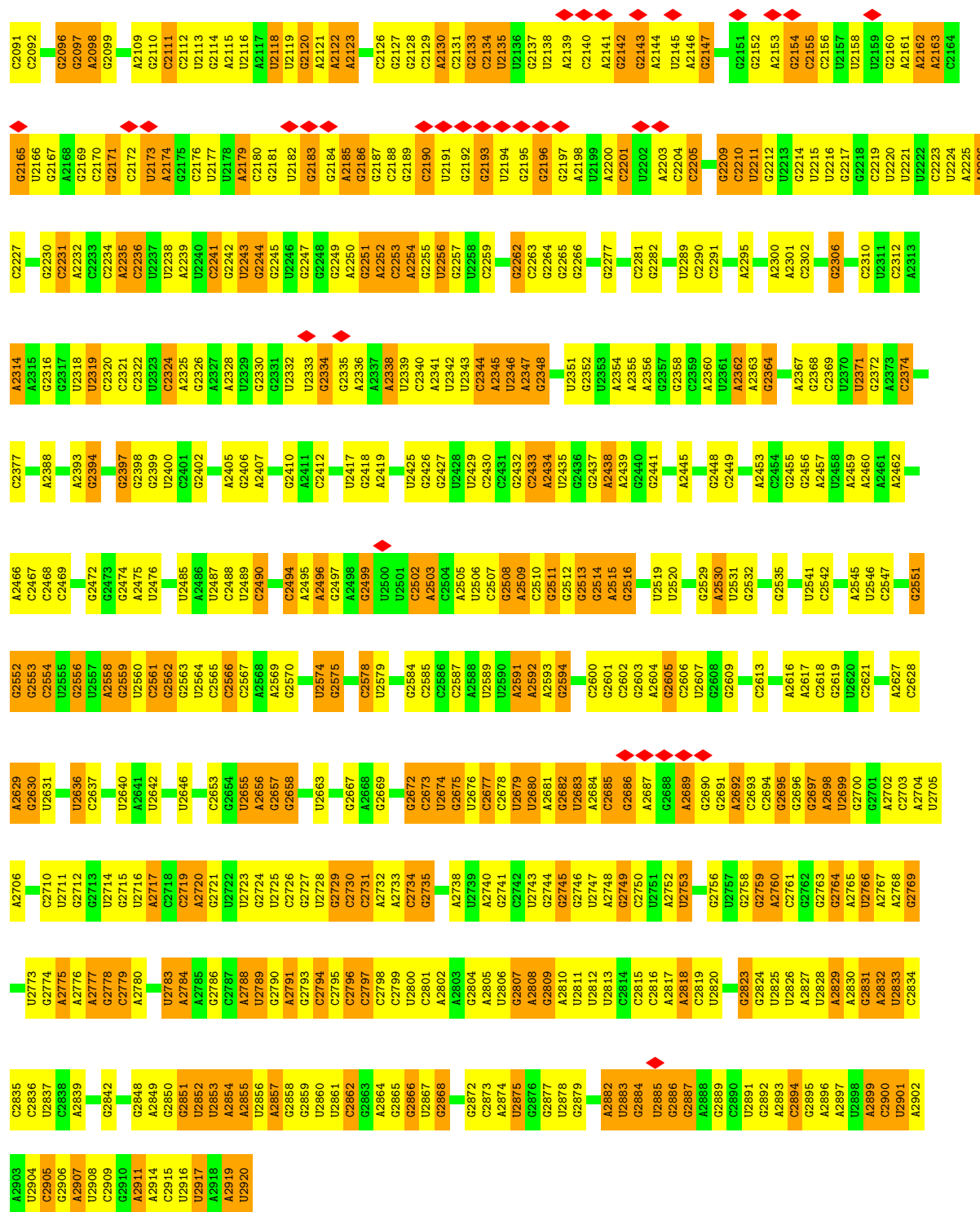
3 Residue-property plots

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.

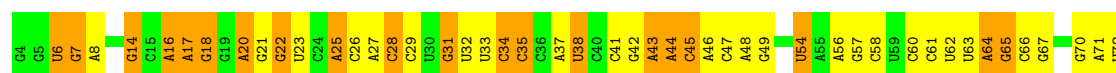
• Molecule 1: 23S



A2008	C1947	U1879	U1804	G1731	U1640	C1486	U1408	A1312	C1197	U1079	A973	G901
G2012	G1948	A1880	U1805	U1732	G1641	G1487	U1409	G1313	G1198	G1080	A977	A902
G2013	G1949	A1881	U1806	A1733	C1642	A1488	A1410	A1314	A1199	C1081	A977	G903
			A1807	A1734		A1489	U1416	C1315	G1201	C1082		G904
		G1882	U1808	C1735	G1645	G1490	U1417	G1316	C1202	U1084	G986	
		U1736	C1809	U1736	U1646	C1491	G1418	A1321	U1203	U1085	A989	A908
		A1883	A1810	U1737	A1647	U1493			G1204	U1086		G909
		A1954	A1811	C1738	G1650	G1494	A1421	A1324	A1208	C1087	A990	C910
		G1885	A1812	G1739	C1651	C1495	G1425		U1209	C1088	A991	A911
		A1886	A1813	G1740	A1652	U1496	G1426	G1336	U1210	C1089	A992	C912
		G1887	A1814	G1741	A1653	A1497	U1427	U1337	G1211	U1090		U913
		U1888	C1815	A1742	A1654	U1498	G1429	U1338	U1212	G1091		U917
		G1889	A1816	G1743	A1654	U1499	U1430		C1213	A1092	A1003	G918
		G1890	C1817	A1744		G1500	U1431	U1343	C1214	C1093	A1004	A920
		A1963	A1818	A1745	G1663	U1501	U1440	A1344	U1215	A1095	G1005	G921
		U1891	G1819	G1746	A1666	A1502	A1440	G1347	U1216	C1096	C1008	G922
		U1892	G1820	G1747			C1441	U1217	U1217	G1096		A923
		A1964	U1823	G1748	C1669	U1503	C1442	G1218	G1218	U1151	C1015	G924
		A1965	C1824	G1749	A1670	U1504	U1443	U1349	G1219	U1152		G925
		U1966		U1750	A1671	G1505	C1444	U1350	G1220	C1153	A1018	G926
		U1967		G1751		C1506	U1445	G1351	A1220	G1154	A1019	G927
		C1968	C1827	C1752	G1675	A1507	C1446	C1352	C1221	A1155	A1027	C928
		C1969	U1828	G1752	A1676	C1508	U1447		A1222	G1156		C929
		U1970	A1829	U1753	G1677	G1509	U1448	G1356	G1225	U1157	G1033	G937
		G1972	A1830	C1754	A1678	U1598	U1449	G1357	G1226	G1158		G938
		U1973		U1755	G1677	U1599	A1450	U1227	U1227	A1161	C1038	U940
		C1974	A1837	U1756	A1679	A1600	U1451	A1228	U1228	C1162	C1038	A941
		G1975	U1840	A1758	U1680		C1452	A1358		U1163	C1040	C942
		C1901		G1759	U1681	U1603	U1453	A1359	U1238	G1164	G1041	C943
		G1902	U1843	G1760	A1685	C1604	U1454	U1366	U1239	C1165	C1042	G944
		A1903	G1844	U1761	C1686	A1605	U1455	C1367	U1240	C1166	U1043	A945
		U1904	U1845	U1762	G1687	C1606		G1368	G1245	C1167	A1044	A946
		C1905	A1846	U1763		A1607	A1458	G1369		C1168	A1045	U947
		G1961		A1764	A1690	C1608	U1459	C1370	G1245	G1169	A1046	U948
		C1906		U1765	G1691	G1610	U1460	U1373	G1250	A1170		C949
		U1907	G1852	C1766	C1692		C1461	G1374	G1250	A1171		A950
		A1908	C1853	G1767		G1613	G1462		A1258	C1050	C1050	A951
		C1909	U1854	C1768	A1698	A1616	A1463	U1381	G1261	A1172	C1051	G951
		G1910	G1855	C1769	A1699	A1617	U1464	C1382	U1261	A1173	A1052	A952
		A1911	A1856	C1770	C1700	A1618	G1465	G1383	G1275	U1174	A1053	C953
		C1857	C1857	A1771	U1701		G1466	G1384	A1275	U1175	A1054	A954
				G1772	C1702	U1623	G1467	G1385	A1285	A1177	A1055	A955
					U1703	C1624	G1468	U1386	G1286	C1178	A1057	C957
					C1704	U1625	G1469	C1387	U1287	U1058	U1058	U958
					G1705	A1626		C1388	G1288	C1179		C959
					U1706	U1706	C1472	U1389	A1289	U1060	G1061	C960
					U1707	G1627	G1473		G1289	G1183	G1062	A962
						A1628	C1474	G1392	A1290	C1184	U1062	
					G1710	U1629	A1475		A1291	U1185	U1062	G965
						A1630	U1476	G1395	A1292	A1186	A1065	C966
					G1717	G1631	C1477	A1396	G1294	C1189	G1074	A968
					G1718	A1632	A1478			U1193	G1075	A969
						A1633	G1479	A1402	G1302	U1194	A1076	U970
					U1724	A1634	U1480	C1403		A1195	G1078	A972
					G1725	A1635	G1481	A1404		C1196		
					A1726	U1636	U1482	G1405	G1309			
					C1727	A1637	A1483	G1406	A1311			
						G1638	G1484	C1407				
					C1730	G1639	G1485					
							</					



• Molecule 2: 5S





• Molecule 3: 50S ribosomal protein L33



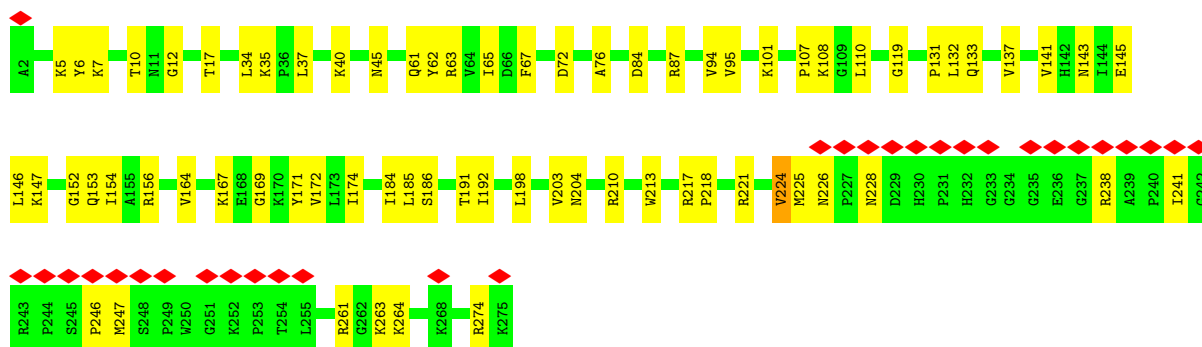
• Molecule 4: 50S ribosomal protein L34



• Molecule 5: 50S ribosomal protein L35

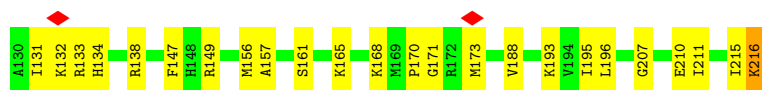


• Molecule 6: 50S ribosomal protein L2

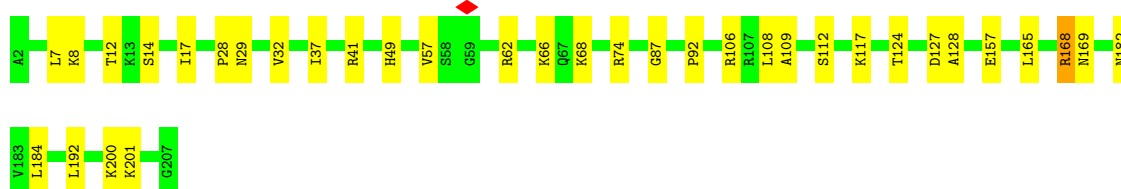
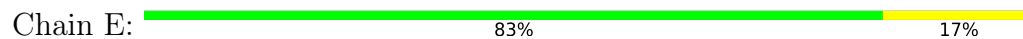


• Molecule 7: 50S ribosomal protein L3

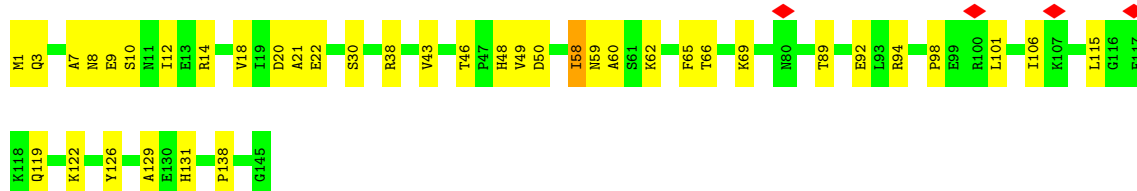




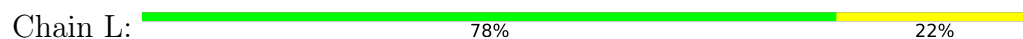
- Molecule 8: 50S ribosomal protein L4



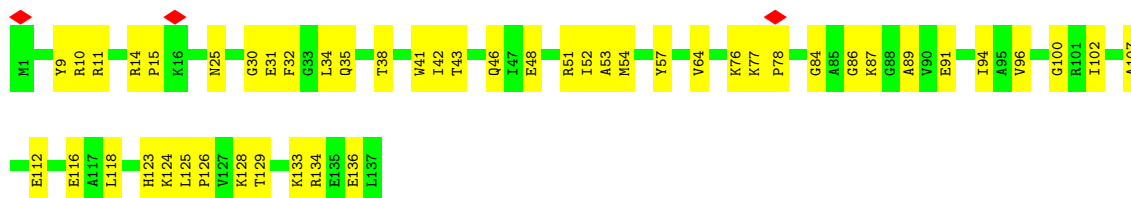
- Molecule 9: 50S ribosomal protein L13



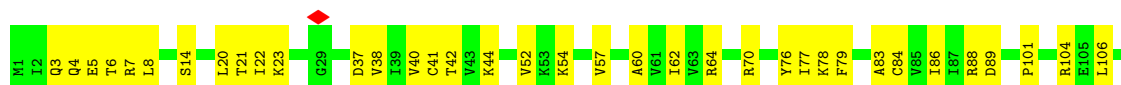
- Molecule 10: 50S ribosomal protein L15

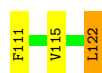


- Molecule 11: 50S ribosomal protein L16



- Molecule 12: 50S ribosomal protein L14





- Molecule 13: 50S ribosomal protein L18



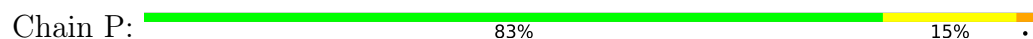
- Molecule 14: 50S ribosomal protein L19



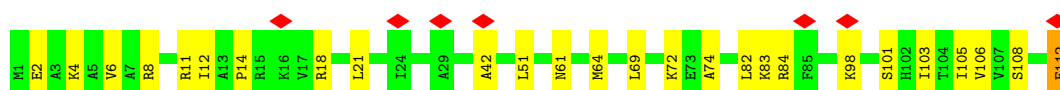
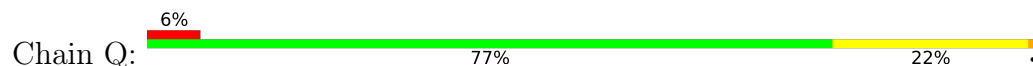
- Molecule 15: 50S ribosomal protein L20



- Molecule 16: 50S ribosomal protein L21

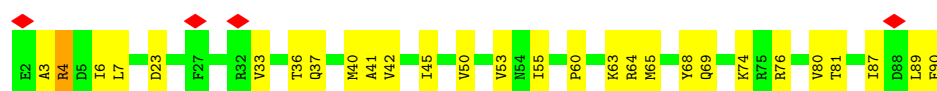


- Molecule 17: 50S ribosomal protein L22



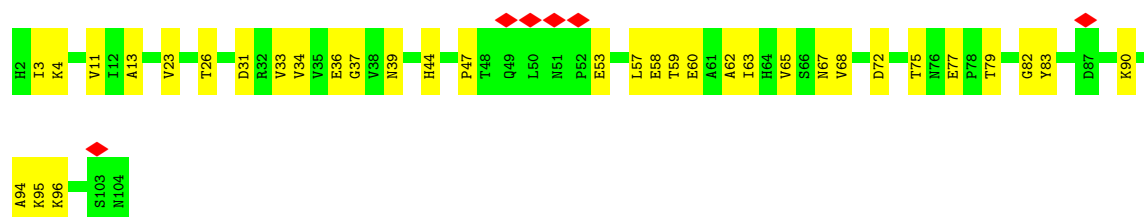
- Molecule 18: 50S ribosomal protein L23

Chain R:  69% 30%



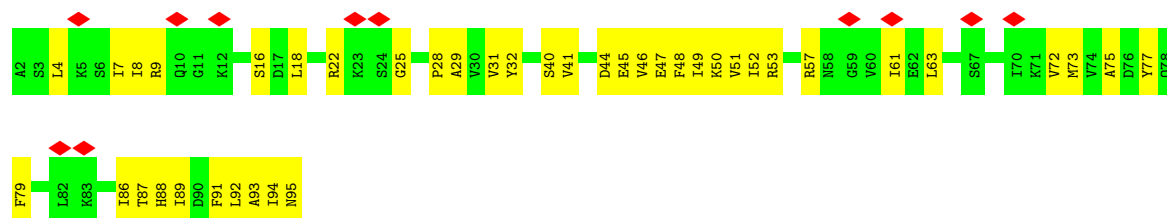
- Molecule 19: 50S ribosomal protein L24

Chain S:  6% 67% 33%



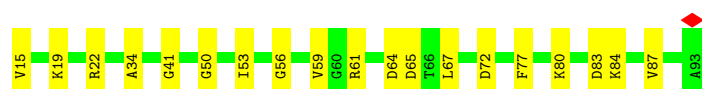
- Molecule 20: 50S ribosomal protein L25

Chain T:  12% 56% 44%



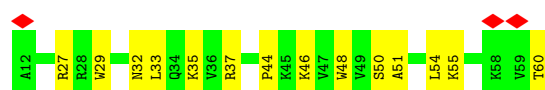
- Molecule 21: 50S ribosomal protein L27

Chain a:  76% 24%



- Molecule 22: 50S ribosomal protein L28

Chain V:  6% 71% 29%

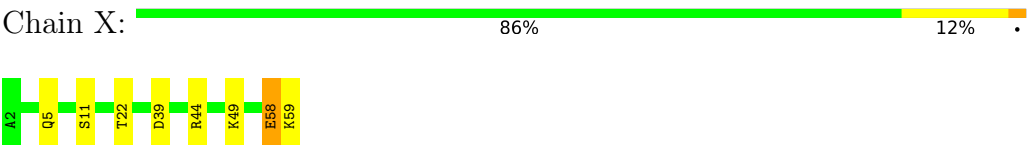


- Molecule 23: 50S ribosomal protein L29

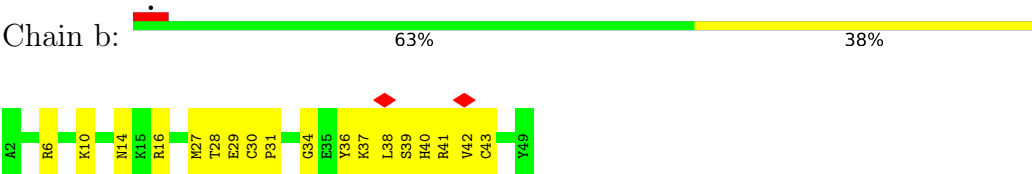
Chain W:  67% 33%



● Molecule 24: 50S ribosomal protein L30



● Molecule 25: 50S ribosomal protein L32



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	175844	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 ($e^-/\text{\AA}^2$)	47	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.029	Depositor
Minimum map value	-0.011	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0026	Depositor
Map size ($\text{\AA}$)	281.42398, 281.42398, 281.42398	wwPDB
Map dimensions	328, 328, 328	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.8579999, 0.8579999, 0.8579999	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 2MA, 5MU

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	0.38	0/65753	0.50	3/102527 (0.0%)
2	B	0.22	0/2523	0.44	0/3920
3	1	0.33	0/395	0.87	2/530 (0.4%)
4	2	0.47	0/371	0.96	0/484
5	3	0.36	0/526	0.73	0/690
6	F	0.38	0/2129	0.73	1/2858 (0.0%)
7	D	0.40	0/1651	0.78	1/2215 (0.0%)
8	E	0.40	0/1595	0.73	1/2154 (0.0%)
9	H	0.42	0/1153	0.69	0/1553
10	L	0.38	0/1100	0.80	1/1467 (0.1%)
11	Y	0.30	0/1095	0.65	0/1472
12	G	0.43	0/925	0.74	0/1242
13	M	0.24	0/881	0.67	1/1180 (0.1%)
14	N	0.40	0/889	0.73	0/1192
15	O	0.48	0/954	0.81	0/1264
16	P	0.47	0/800	0.79	0/1070
17	Q	0.40	0/862	0.69	0/1161
18	R	0.33	0/723	0.65	1/966 (0.1%)
19	S	0.33	0/779	0.71	0/1043
20	T	0.26	0/730	0.65	0/981
21	a	0.34	0/603	0.57	0/802
22	V	0.28	0/384	0.64	0/515
23	W	0.29	0/542	0.67	0/722
24	X	0.35	0/451	0.62	0/606
25	b	0.38	0/366	0.91	0/489
All	All	0.38	0/88180	0.55	11/133103 (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	1	0	1
7	D	0	2
8	E	0	1
9	H	0	1
All	All	0	5

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	1	12	CYS	CA-CB-SG	6.89	130.24	114.40
6	F	224	VAL	N-CA-C	-6.73	106.17	112.83
8	E	168	ARG	N-CA-C	-5.80	107.45	114.75
3	1	38	ARG	N-CA-C	-5.71	106.96	114.04
18	R	4	ARG	N-CA-C	-5.63	107.41	114.56

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	1	11	GLU	Peptide
7	D	53	PHE	Peptide
7	D	6	LEU	Peptide
8	E	12	THR	Peptide
9	H	58	ILE	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	58787	0	29564	1175	0
2	B	2260	0	1148	59	0
3	1	390	0	394	23	0
4	2	367	0	415	16	0
5	3	521	0	586	13	0
6	F	2094	0	2205	57	0
7	D	1627	0	1667	47	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	E	1572	0	1619	23	0
9	H	1132	0	1120	32	0
10	L	1086	0	1125	22	0
11	Y	1071	0	1123	39	0
12	G	918	0	981	36	0
13	M	872	0	893	33	0
14	N	878	0	923	34	0
15	O	942	0	1014	34	0
16	P	790	0	830	13	0
17	Q	854	0	914	20	0
18	R	715	0	748	23	0
19	S	770	0	809	32	0
20	T	722	0	766	32	0
21	a	597	0	604	15	0
22	V	379	0	400	10	0
23	W	541	0	563	18	0
24	X	449	0	491	5	0
25	b	360	0	358	25	0
All	All	80694	0	51260	1700	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 14.

The worst 5 of 1700 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2432:G:H21	1:A:2439:A:N6	1.39	1.21
1:A:2432:G:N2	1:A:2439:A:H62	1.44	1.14
1:A:2171:G:H21	1:A:2174:A:N6	1.50	1.09
1:A:2852:U:H1'	1:A:2853:U:H5'	1.38	1.05
1:A:307:A:N6	1:A:409:G:C6	2.26	1.04

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	1	45/47 (96%)	41 (91%)	4 (9%)	0	100	100
4	2	41/43 (95%)	40 (98%)	1 (2%)	0	100	100
5	3	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
6	F	272/274 (99%)	247 (91%)	25 (9%)	0	100	100
7	D	213/215 (99%)	172 (81%)	40 (19%)	1 (0%)	24	40
8	E	204/206 (99%)	188 (92%)	16 (8%)	0	100	100
9	H	141/144 (98%)	124 (88%)	17 (12%)	0	100	100
10	L	144/146 (99%)	128 (89%)	16 (11%)	0	100	100
11	Y	135/137 (98%)	119 (88%)	16 (12%)	0	100	100
12	G	120/122 (98%)	105 (88%)	15 (12%)	0	100	100
13	M	115/117 (98%)	101 (88%)	14 (12%)	0	100	100
14	N	109/114 (96%)	91 (84%)	18 (16%)	0	100	100
15	O	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
16	P	100/102 (98%)	88 (88%)	10 (10%)	2 (2%)	6	10
17	Q	110/112 (98%)	104 (94%)	6 (6%)	0	100	100
18	R	87/89 (98%)	77 (88%)	10 (12%)	0	100	100
19	S	101/103 (98%)	82 (81%)	19 (19%)	0	100	100
20	T	92/94 (98%)	76 (83%)	16 (17%)	0	100	100
21	a	77/79 (98%)	70 (91%)	7 (9%)	0	100	100
22	V	47/49 (96%)	44 (94%)	3 (6%)	0	100	100
23	W	65/67 (97%)	58 (89%)	7 (11%)	0	100	100
24	X	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
25	b	46/48 (96%)	35 (76%)	11 (24%)	0	100	100
All	All	2496/2546 (98%)	2212 (89%)	281 (11%)	3 (0%)	49	69

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	P	51	PRO
7	D	6	LEU
16	P	78	ARG

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	1	44/45 (98%)	44 (100%)	0	100	100
4	2	39/39 (100%)	39 (100%)	0	100	100
5	3	55/55 (100%)	55 (100%)	0	100	100
6	F	221/221 (100%)	221 (100%)	0	100	100
7	D	173/173 (100%)	172 (99%)	1 (1%)	78	87
8	E	168/168 (100%)	167 (99%)	1 (1%)	78	87
9	H	121/122 (99%)	121 (100%)	0	100	100
10	L	109/112 (97%)	109 (100%)	0	100	100
11	Y	108/114 (95%)	108 (100%)	0	100	100
12	G	100/100 (100%)	99 (99%)	1 (1%)	68	80
13	M	83/93 (89%)	83 (100%)	0	100	100
14	N	92/100 (92%)	91 (99%)	1 (1%)	65	79
15	O	96/96 (100%)	95 (99%)	1 (1%)	68	80
16	P	84/86 (98%)	83 (99%)	1 (1%)	63	77
17	Q	89/91 (98%)	88 (99%)	1 (1%)	65	79
18	R	78/80 (98%)	77 (99%)	1 (1%)	61	75
19	S	81/88 (92%)	81 (100%)	0	100	100
20	T	78/82 (95%)	78 (100%)	0	100	100
21	a	59/62 (95%)	59 (100%)	0	100	100
22	V	39/41 (95%)	38 (97%)	1 (3%)	40	62
23	W	58/60 (97%)	58 (100%)	0	100	100
24	X	52/52 (100%)	51 (98%)	1 (2%)	50	68
25	b	35/44 (80%)	35 (100%)	0	100	100
All	All	2062/2124 (97%)	2052 (100%)	10 (0%)	78	88

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	R	90	PHE
22	V	60	THR
24	X	58	GLU
14	N	113	GLN
15	O	88	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
10	L	38	GLN
11	Y	46	GLN
23	W	31	GLN
11	Y	12	GLN
13	M	15	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2728/2742 (99%)	948 (34%)	51 (1%)
2	B	101/106 (95%)	44 (43%)	3 (2%)
All	All	2829/2848 (99%)	992 (35%)	54 (1%)

5 of 992 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	11	U
1	A	14	A
1	A	15	G
1	A	24	G
1	A	25	U

5 of 54 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2003	U
1	A	2081	A
1	A	2883	U
1	A	2006	C
1	A	2020	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
1	5MU	A	792	1	19,22,23	4.96	7 (36%)	27,32,35	3.86	12 (44%)
1	2MA	A	2530	1	22,25,26	3.80	10 (45%)	32,37,40	2.71	11 (34%)
1	5MU	A	1966	1	19,22,23	5.18	7 (36%)	27,32,35	3.57	12 (44%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	5MU	A	792	1	-	0/7/25/26	0/2/2/2
1	2MA	A	2530	1	-	3/7/25/26	0/3/3/3
1	5MU	A	1966	1	-	2/7/25/26	0/2/2/2

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1966	5MU	C2-N1	12.85	1.58	1.38
1	A	792	5MU	C2-N1	11.90	1.57	1.38
1	A	2530	2MA	C4-N3	11.28	1.48	1.34
1	A	1966	5MU	C6-N1	10.81	1.56	1.38
1	A	1966	5MU	C4-C5	10.67	1.62	1.44

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	792	5MU	C5-C4-N3	12.26	125.98	115.32
1	A	1966	5MU	C5-C4-N3	11.38	125.21	115.32
1	A	792	5MU	C5-C6-N1	-9.84	112.62	123.31
1	A	1966	5MU	C5-C6-N1	-8.82	113.73	123.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2530	2MA	N9-C8-N7	-6.85	104.21	113.94

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	2530	2MA	O4'-C4'-C5'-O5'
1	A	1966	5MU	C2'-C1'-N1-C2
1	A	1966	5MU	C2'-C1'-N1-C6
1	A	2530	2MA	C3'-C4'-C5'-O5'
1	A	2530	2MA	C4'-C5'-O5'-P

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1966	5MU	2	0

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	11
2	B	4
9	H	1

The worst 5 of 16 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1067:U	O3'	1074:G	P	32.56
1	A	1509:G	O3'	1598:U	P	17.87
1	A	2911:A	O3'	2914:A	P	16.95
1	A	1096:C	O3'	1151:G	P	15.42
1	A	758:G	O3'	764:C	P	14.44

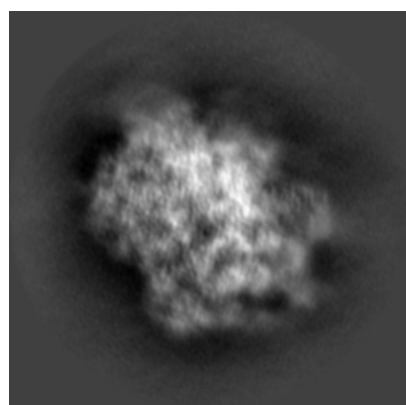
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11901. These allow visual inspection of the internal detail of the map and identification of artifacts.

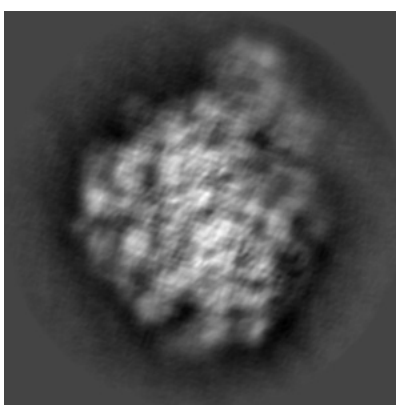
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

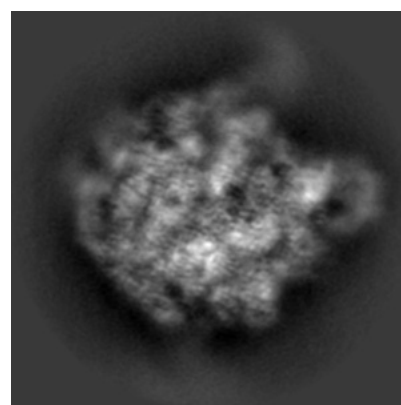
6.1.1 Primary map



X



Y

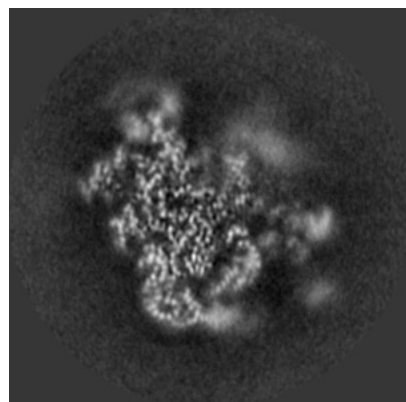


Z

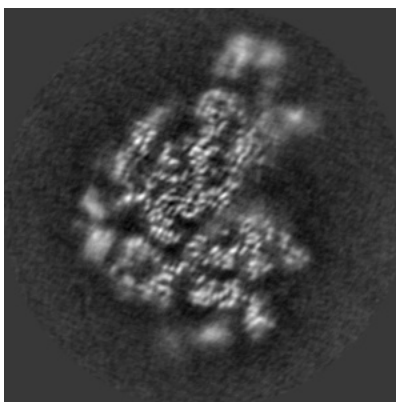
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

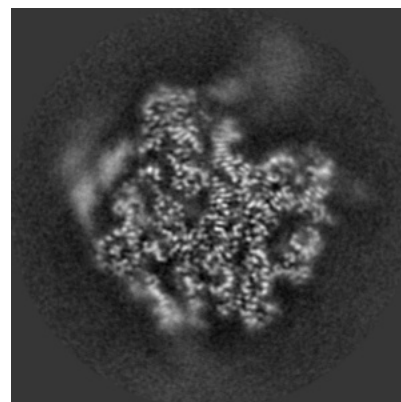
6.2.1 Primary map



X Index: 164



Y Index: 164

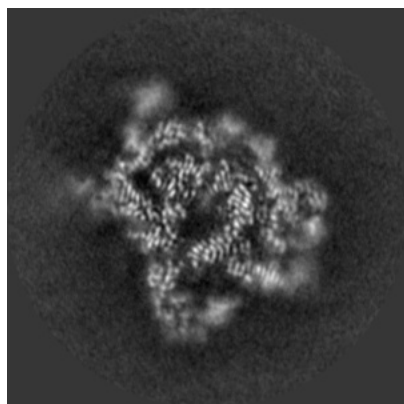


Z Index: 164

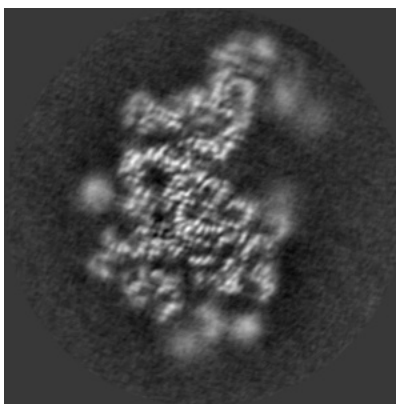
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

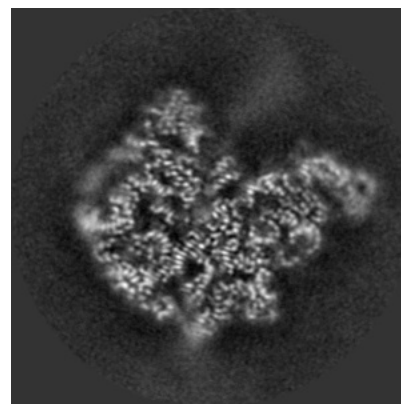
6.3.1 Primary map



X Index: 146



Y Index: 188

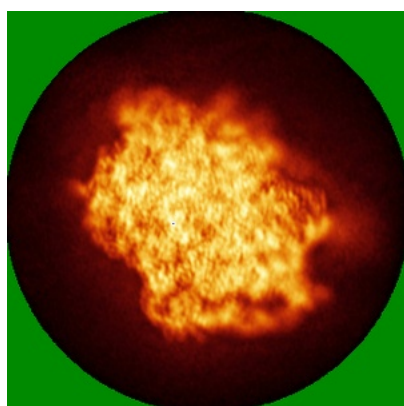


Z Index: 180

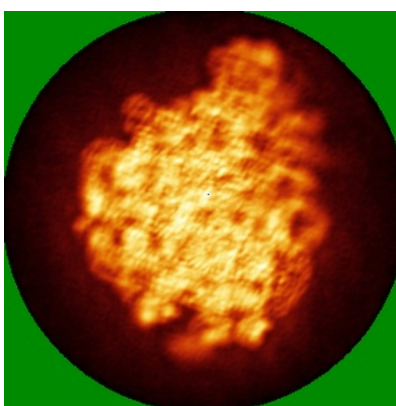
The images above show the largest variance slices of the map in three orthogonal directions.

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

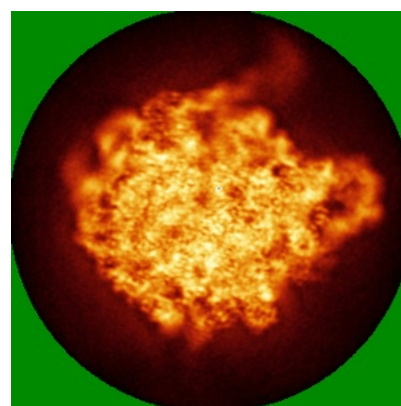
6.4.1 Primary map



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 0.0026. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

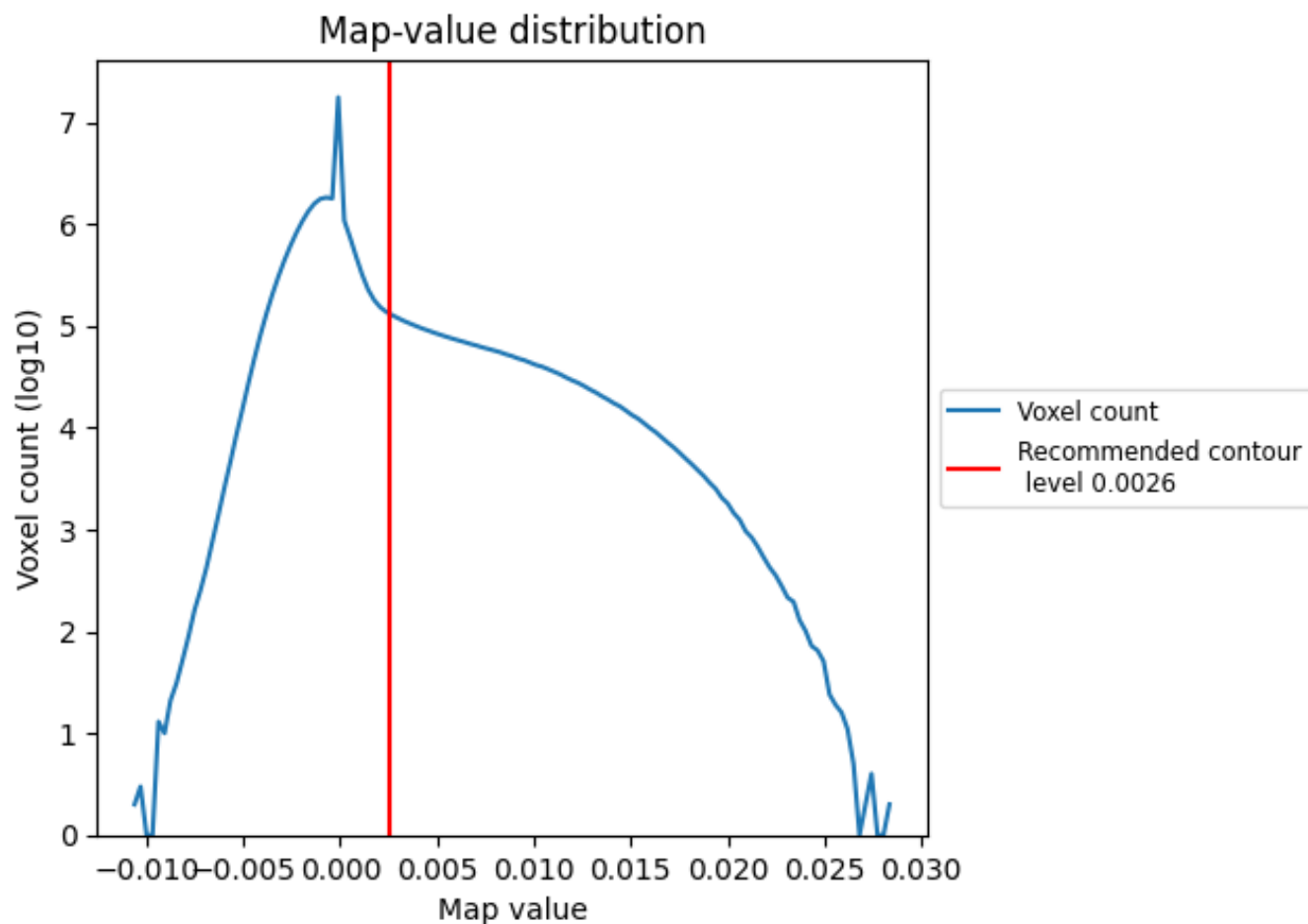
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

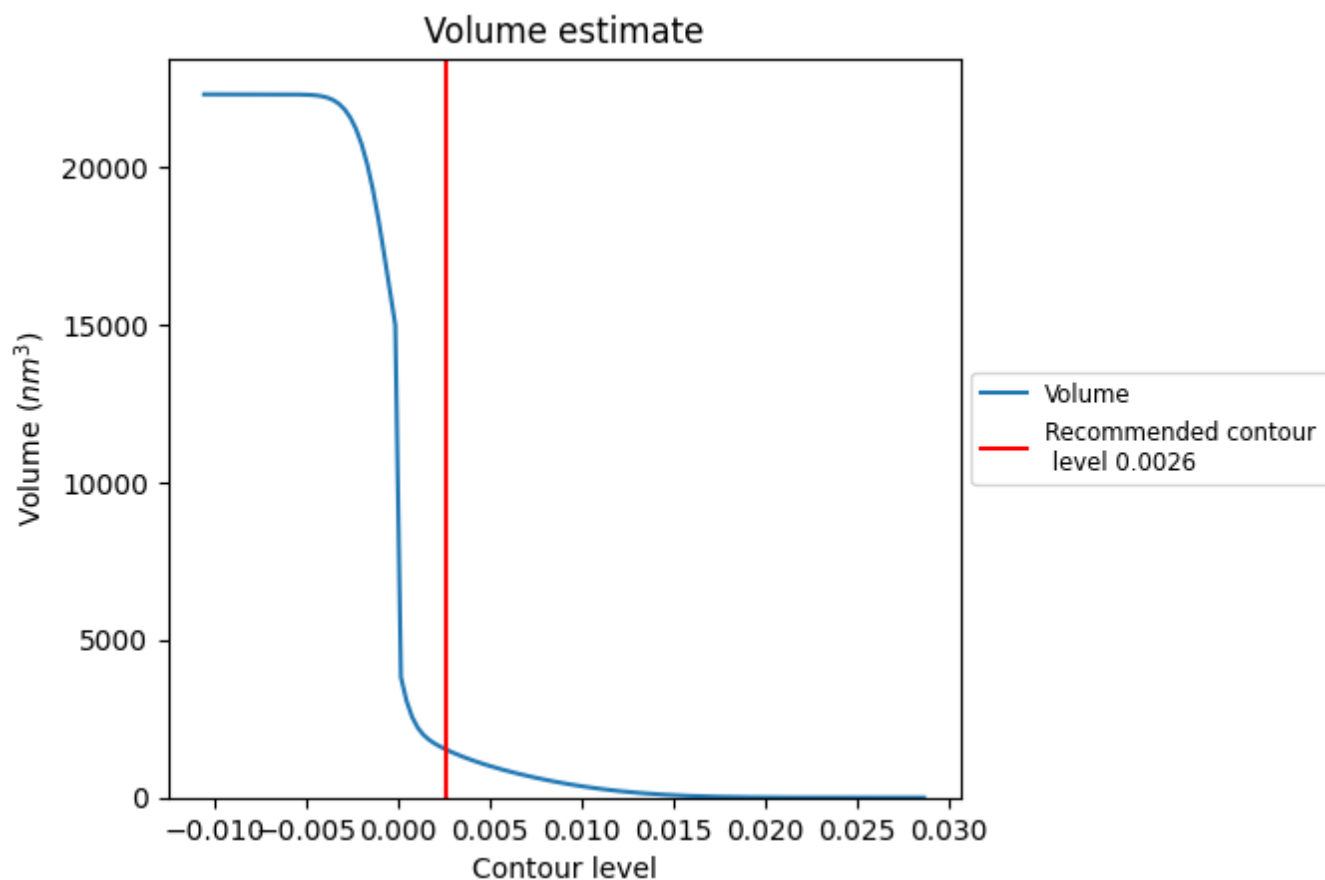
This section contains the results of statistical analysis of the map.

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.

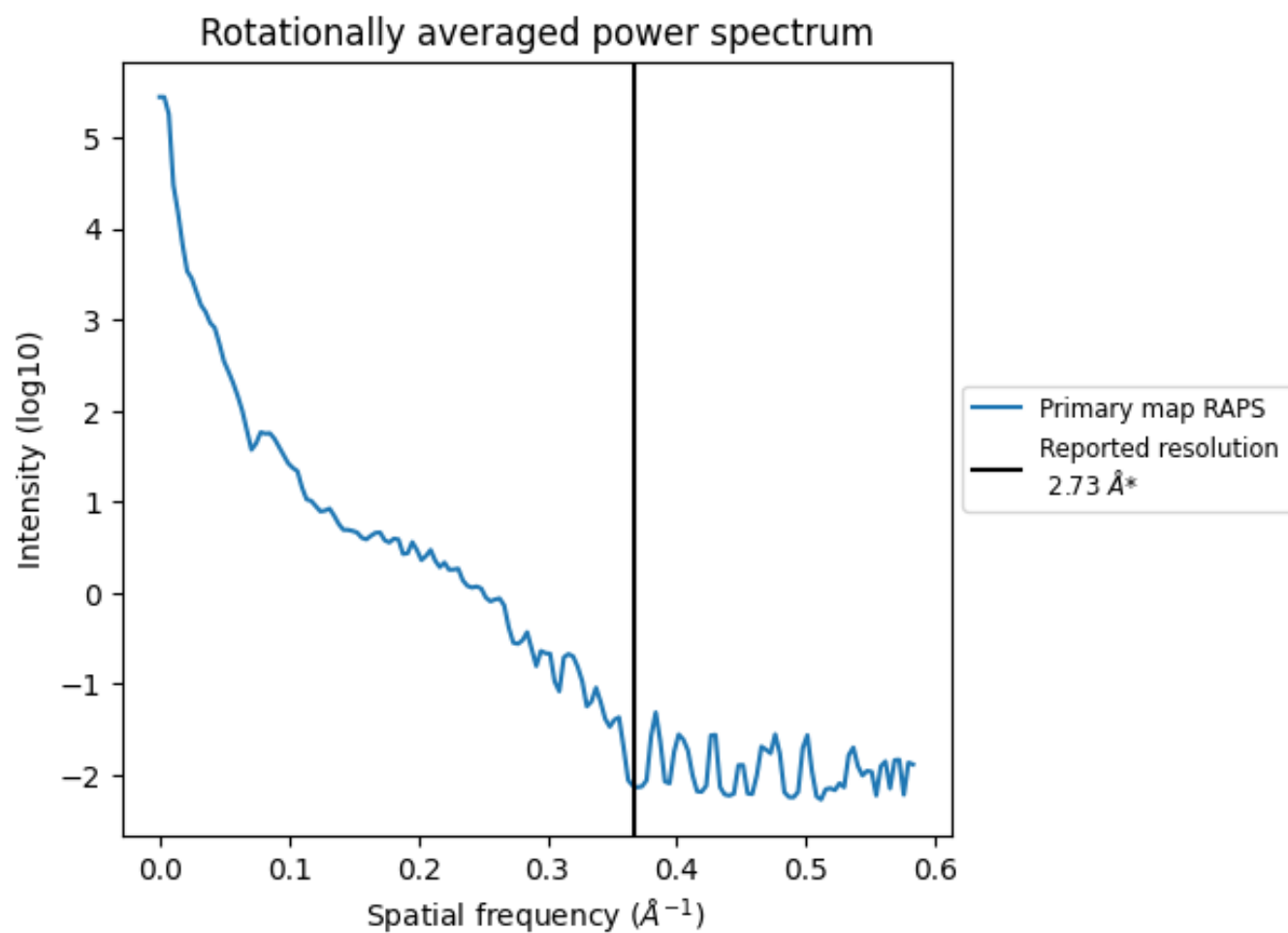
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1520 nm^3 ; this corresponds to an approximate mass of 1373 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 0.366 Å⁻¹

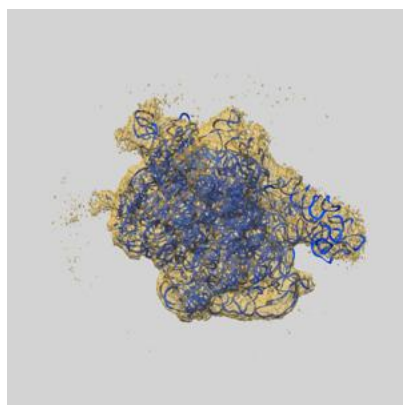
8 Fourier-Shell correlation

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

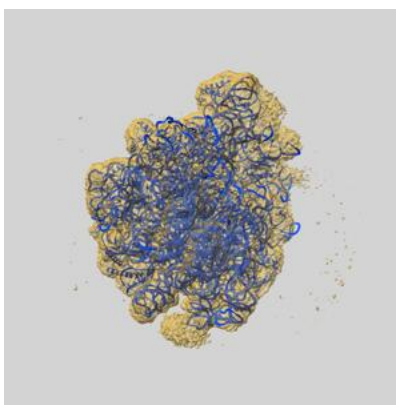
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11901 and PDB model 7ASN. Per-residue inclusion information can be found in section [3](#) on page [8](#).

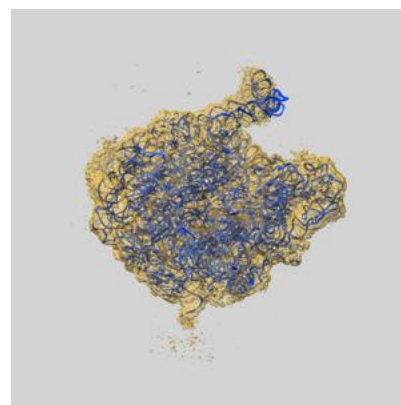
9.1 Map-model overlay [i](#)



X



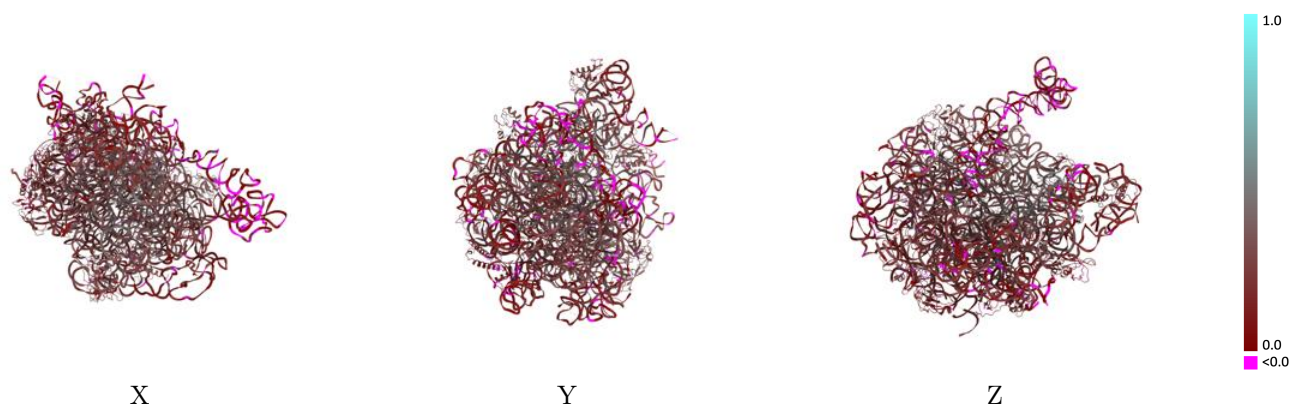
Y



Z

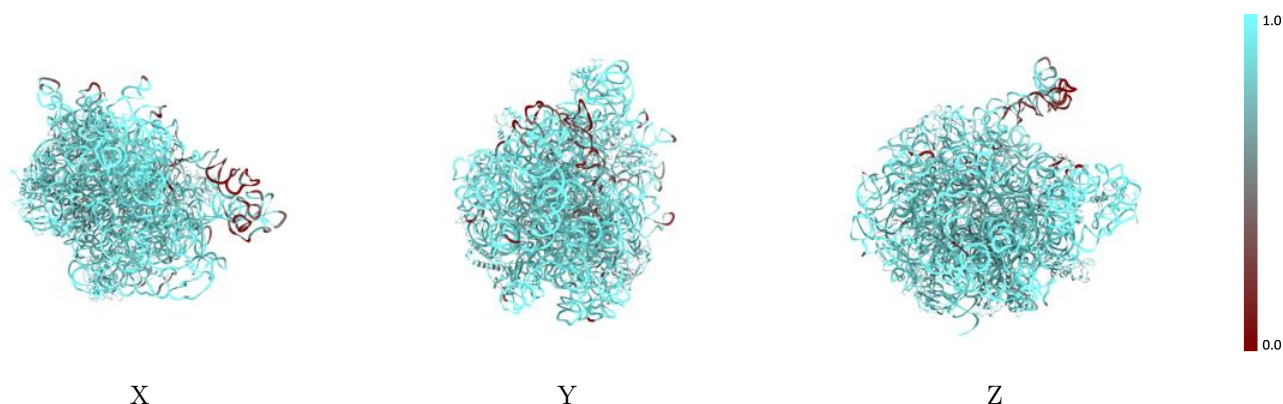
The images above show the 3D surface view of the map at the recommended contour level 0.0026 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



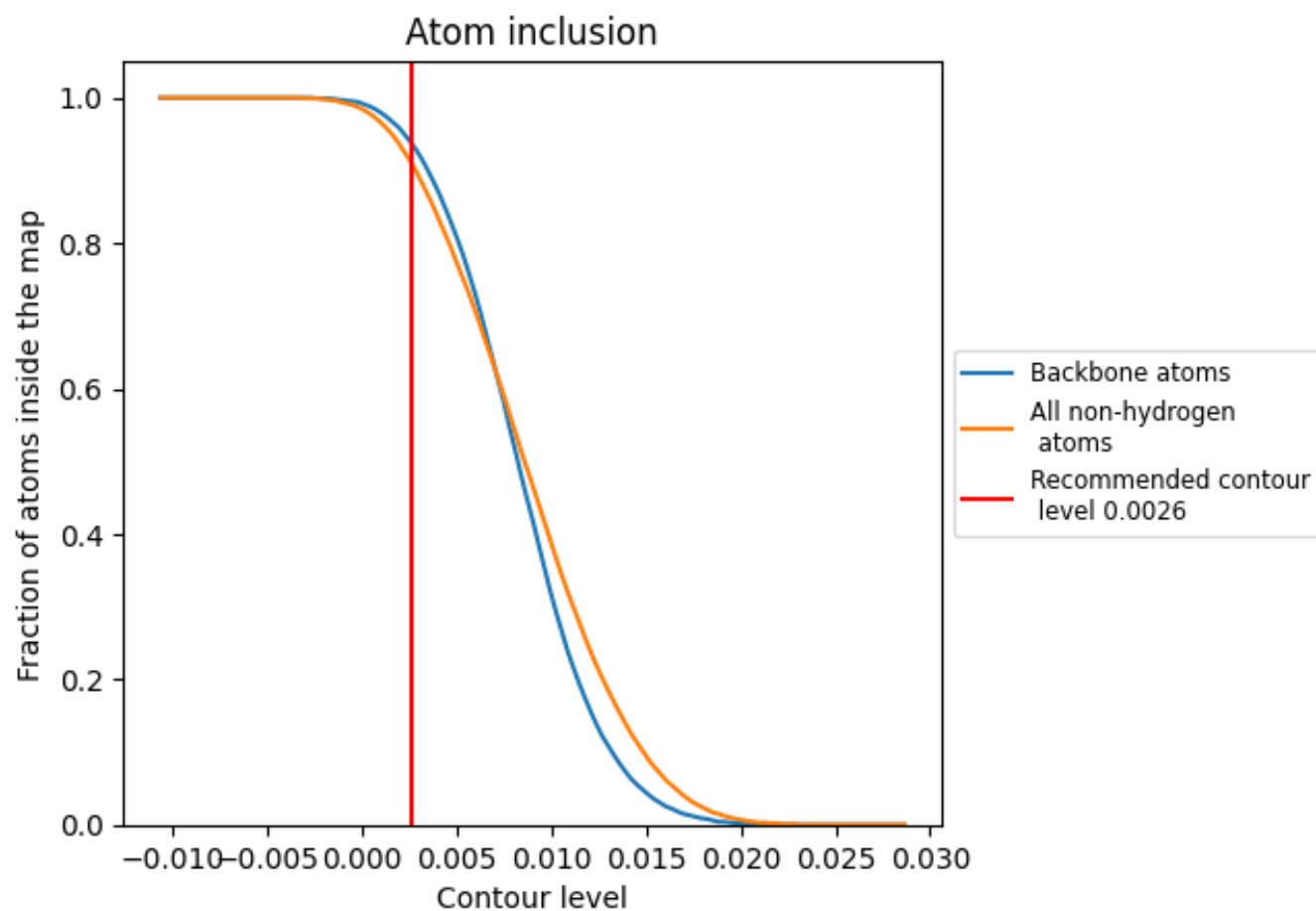
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0026).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 91% 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 (0.0026) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9120	 0.2140
1	 0.5330	 0.1980
2	 0.8090	 0.2330
3	 0.8650	 0.2920
A	 0.9330	 0.2160
B	 0.9850	 0.1650
D	 0.8370	 0.1770
E	 0.8880	 0.2570
F	 0.7900	 0.2430
G	 0.8560	 0.2280
H	 0.8290	 0.1950
L	 0.8880	 0.2940
M	 0.9230	 0.2080
N	 0.7810	 0.1890
O	 0.8310	 0.2050
P	 0.8680	 0.2180
Q	 0.8000	 0.1710
R	 0.8200	 0.1170
S	 0.8400	 0.1490
T	 0.7420	 0.1570
V	 0.8190	 0.2360
W	 0.8630	 0.1370
X	 0.8800	 0.2830
Y	 0.8820	 0.2480
a	 0.9270	 0.3170
b	 0.8100	 0.1200

