



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 11:40 PM UTC

PDB ID : 5GAG / pdb_00005gag
EMDB ID : EMD-8003
Title : RNC in complex with SRP-SR in the closed state
Authors : Jomaa, A.; Boehringer, D.; Leibundgut, M.; Ban, N.
Deposited on : 2015-11-26
Resolution : 3.80 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:

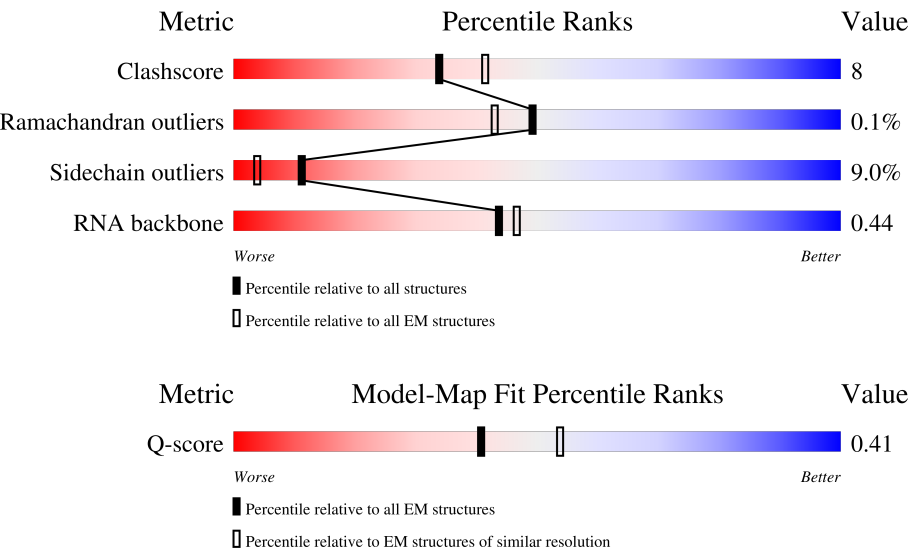
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.80 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.



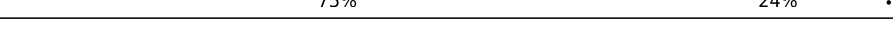
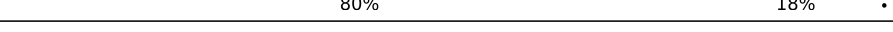
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	1	113	
2	2	3	
3	A	2903	

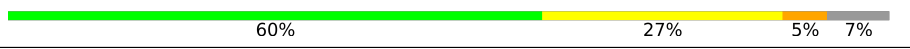
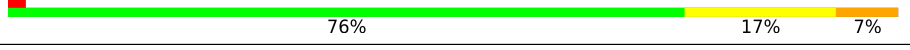
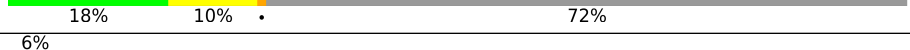
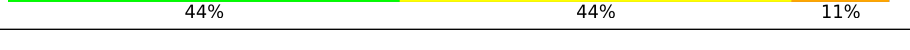
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Mol	Chain	Length	Quality of chain
4	B	120	
5	C	273	
6	D	209	
7	E	201	
8	F	179	
9	G	177	
10	H	149	
11	I	165	
12	J	142	
13	K	142	
14	L	123	
15	M	144	
16	N	136	
17	O	127	
18	P	117	
19	Q	115	
20	R	118	
21	S	103	
22	T	110	
23	U	100	
24	V	104	
25	W	94	
26	X	85	
27	Y	78	
28	Z	63	

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Mol	Chain	Length	Quality of chain
29	a	59	
30	b	57	
31	c	55	
32	d	46	
33	e	65	
34	f	38	
35	i	450	
36	k	18	

2 Entry composition [i](#)

There are 38 unique types of molecules in this entry. The entry contains 94030 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 SRP 4.5S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	43	Total	C	N	O	P	0	0
			926	413	174	296	43		

- Molecule 2 is a RNA chain called tRNA CCAend.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	3	Total	C	N	O	P	0	0
			62	28	11	20	3		

- Molecule 3 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	2883	Total	C	N	O	P	0	0
			61902	27613	11397	20009	2883		

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	272	Total	C	N	O	S	0	1
			2083	1288	424	364	7		

- Molecule 6 is a protein called 50S ribosomal protein L3.

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

- Molecule 7 is a protein called 50S ribosomal protein L4.

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

- Molecule 8 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	178	Total	C	N	O	S	0	1
			1411	899	250	256	6		

- Molecule 9 is a protein called 50S ribosomal protein L6.

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

- Molecule 10 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

- Molecule 11 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	125	Total	C	N	O	S	0	0
			946	599	169	175	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	85	VAL	SER	conflict	UNP P0A7J3
I	86	THR	MET	conflict	UNP P0A7J3

- Molecule 12 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	134	Total	C	N	O	S	0	0
			979	619	169	185	6		

- Molecule 13 is a protein called 50S ribosomal protein L13.

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

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 15 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 16 is a protein called 50S ribosomal protein L16.

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

- Molecule 17 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	125	Total	C	N	O	S	0	0
			993	613	202	173	5		

- Molecule 18 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 19 is a protein called 50S ribosomal protein L19.

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

- Molecule 20 is a protein called 50S ribosomal protein L20.

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

- Molecule 21 is a protein called 50S ribosomal protein L21.

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

- Molecule 22 is a protein called 50S ribosomal protein L22.

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

- Molecule 23 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	95	Total	C	N	O	S	0	0
			756	479	141	135	1		

- Molecule 24 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	V	103	Total	C	N	O	0	1
			780	492	147	141		

- Molecule 25 is a protein called 50S ribosomal protein L25.

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

- Molecule 26 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	76	Total	C	N	O	S	0	0
			580	359	117	103	1		

- Molecule 27 is a protein called 50S ribosomal protein L28.

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

- Molecule 28 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 29 is a protein called 50S ribosomal protein L30.

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

- Molecule 30 is a protein called 50S ribosomal protein L32.

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

- Molecule 31 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	c	51	Total	C	N	O	0	0
			414	266	76	72		

- Molecule 32 is a protein called 50S ribosomal protein L34.

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

- Molecule 33 is a protein called 50S ribosomal protein L35.

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

- Molecule 34 is a protein called 50S ribosomal protein L36.

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

- Molecule 35 is a protein called Signal recognition particle protein Ffh.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	126	Total	C	N	O	S	0	0
			916	575	169	161	11		

- Molecule 36 is a protein called 1A9L SS.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	18	Total	C	N	O	S	0	0
			137	94	20	22	1		

- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
37	2	1	Total	Mg	0
			1	1	
37	A	411	Total	Mg	0
			411	411	
37	B	12	Total	Mg	0
			12	12	
37	C	2	Total	Mg	0
			2	2	
37	D	1	Total	Mg	0
			1	1	
37	O	1	Total	Mg	0
			1	1	
37	R	1	Total	Mg	0
			1	1	
37	Y	1	Total	Mg	0
			1	1	
37	b	1	Total	Mg	0
			1	1	

- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

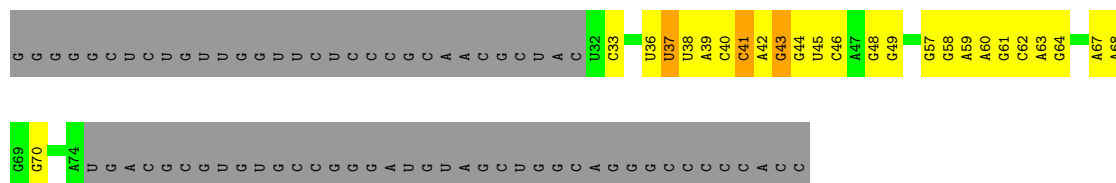
Mol	Chain	Residues	Atoms		AltConf
38	f	1	Total	Zn	0
			1	1	

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: SRP 4.5S RNA

Chain 1: 



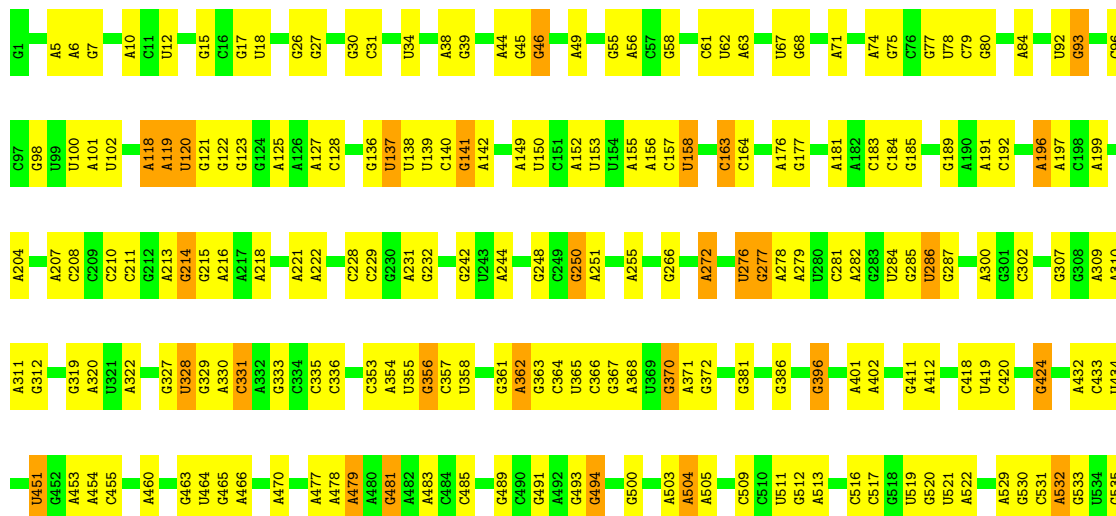
• Molecule 2: tRNA CCAend

Chain 2: 

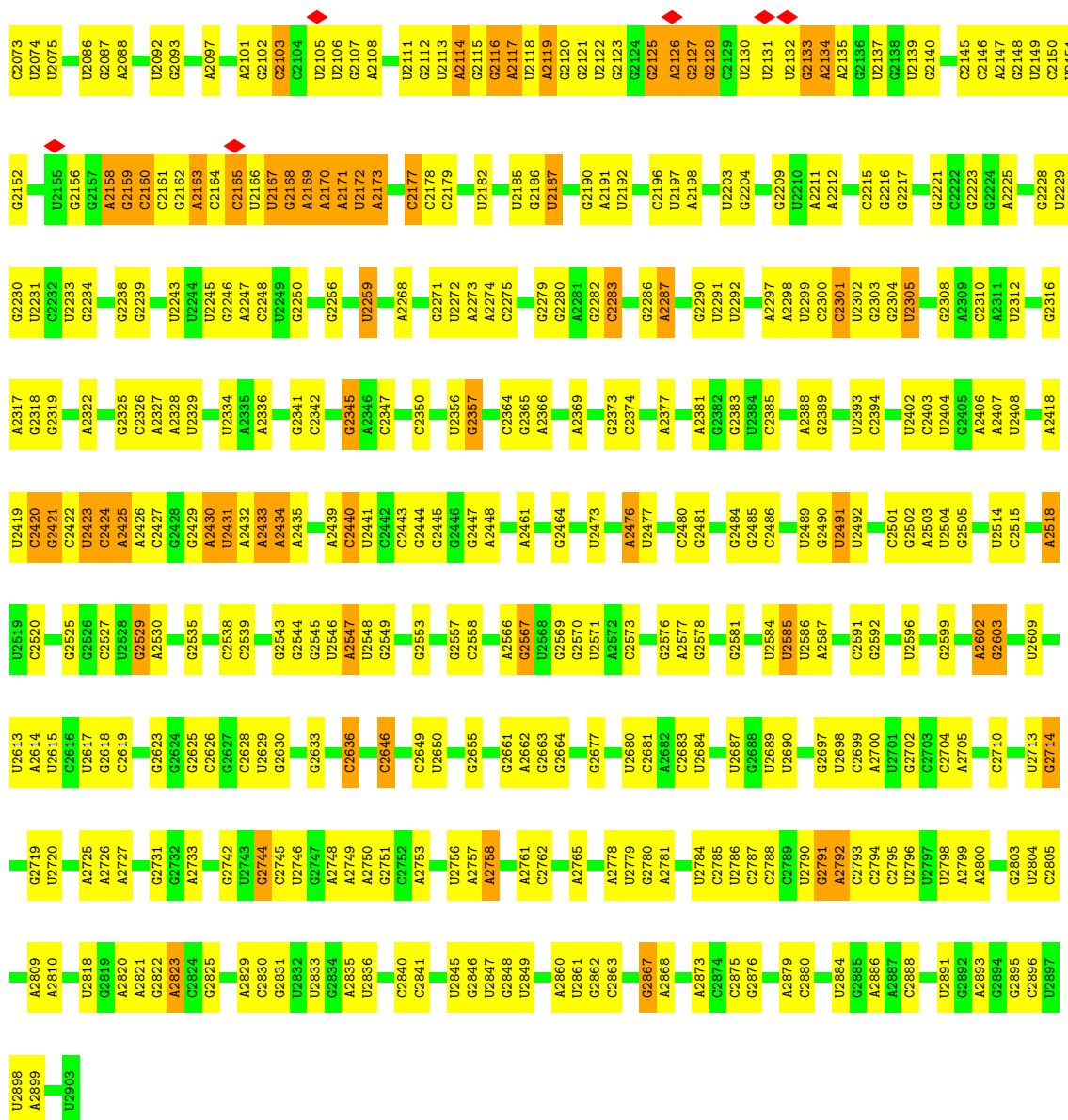


• Molecule 3: 23S rRNA

Chain A: 

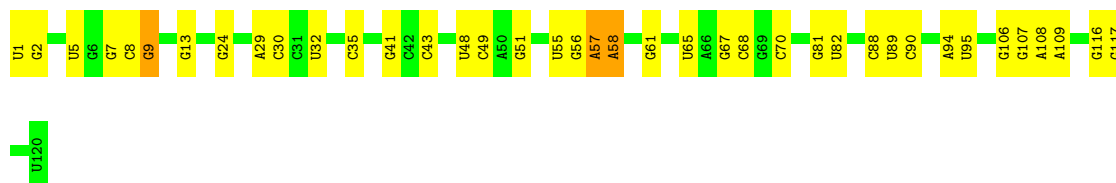


U1971	G1873	A1773	G1529	U1442	U1344	C1207	G1099	U1012	A999	C814	C717	A621	G536
G1972	C1874	A1783	A1532	U1443	C1345	C1208	C1100	C1013	A910	C815	C718	A627	G537
C1974	G1875	A1784	C1533	G1444	A1346	U1209	C1101	C1102	A911	C816	U720	G627	A538
U1982	C1880	A1789	U1534	G1448	U1352	G1212	C1103	A1020	G914	A819	A721	G629	C540
A1987	C1881	C1790	C1535	G1449	A1353	G1218	C1104	A1021	C915	U827	U724	A632	C542
G1988	U1882	A1791	G1537	G1450	A1354	U1223	C1105	G1022	C922	U828	G725	A633	G543
U1991	A1889	G1796	C1538	C1451	G1355	G1224	G1106	G1023	U927	G831	G726	G633	C544
G1992	A1890	G1797	U1539	G1452	G1361	U1227	G1110	G1025	A927	U832	A727	G635	U545
U1993	U1900	G1798	G1543	A1453	C1362	G1227	A1111	G1026	A927	A833	G729	A637	A
C1996	G1903	G1799	A1544	G1456	A1365	G1236	G1112	A1028	U932	G834	A730	G638	G548
C1997	G1904	A1801	A1545	U1457	A1366	A1237	U1119	U1033	A933	U839	G738	U639	G549
A1998	C1905	C1547	G1548	U1458	A1367	G1238	U1130	A1038	U934	C840	G739	A643	G559
C1999	G1906	A1548	U1460	G1461	G1369	C1251	U1131	A1039	C935	G843	U741	A644	A563
C2000	A1808	A1549	C1462	C1463	C1370	G1252	U1132	A1046	A943	A844	A743	U646	C564
G2012	C1909	A1553	G1464	G1465	G1377	A1253	A1133	A1047	C946	A845	U747	G647	C565
U2017	G1910	U1554	G1466	U1467	A1378	G1256	A1134	A1048	G956	U847	G748	G648	U566
C2023	A	A1566	U1468	U1469	A1384	G1266	A1135	C1052	C957	U848	U749	U653	G570
G2027	U1911	A1569	A1470	U1471	A1385	G1271	A1136	G1056	U958	A849	U753	A654	U573
U2028	A1912	U1570	C1472	G1473	A1386	A1272	C1140	A1057	A959	G857	U754	A655	A574
A2030	C1924	A1572	U1474	U1475	A1387	G1278	U1141	U1060	C961	G858	U755	A656	A575
C2031	U1923	U1578	G1478	G1479	A1394	C1279	U1142	U1061	G962	U860	U756	G659	U576
G2032	A1826	G1581	G1482	G1483	A1395	G1282	C1153	G1062	U967	A863	U757	A668	G577
A2037	U1827	C1582	U1484	U1485	A1403	G1283	G1154	G1063	C968	G864	U758	G669	U580
G2038	G1828	U1583	C1486	U1487	G1408	C1293	A1166	U1065	U973	G869	G775	G670	C581
U2039	U1720	U1584	A1490	U1491	U1409	U1294	C1167	A1067	G974	U870	G776	G672	G585
G2040	C1833	C1585	G1491	G1492	G1410	C1297	U1173	G1068	A975	U871	G777	A675	A586
U2041	G1842	G1587	C1493	U1494	A1413	G1300	A	A1069	G976	A878	G780	G681	C587
A2042	C1843	U1588	U1495	U1496	C1414	A1301	U	C1075	A980	G879	A781	G682	U589
C2043	G1846	A1590	A1497	C1498	U1415	A1302	U	C1076	A981	G880	A782	A590	A594
G2046	A1847	C1592	U1497	C1499	G1416	A1302	G1177	A1077	C982	G881	G783	A685	C595
U2049	G1848	A1603	U1498	U1508	C1417	G1317	G1182	U1078	A983	G882	G784	U686	U596
C2050	U1850	C1606	A1508	A1509	G1422	U1318	U1183	C1079	A984	G	A789	G690	G597
A2054	G1857	A1608	G1510	G1511	G1423	A1321	U1184	U1081	C985	U	U790	C691	G600
C2055	A1858	G1613	U1512	U1513	G1424	G1324	U1188	A1082	C986	C	C791	C692	A603
G2066	G1860	A1614	G1514	U1515	G1425	U1326	A1189	U1083	C987	A	A794	A693	U607
A2060	C1617	C1617	A1522	U1523	A1427	A1327	G1195	U1084	G988	C	G797	G697	C698
C2061	U1636	A1637	U1524	G1525	G1428	G1331	C1196	A1085	A996	C	A800	A705	A612
A2062	A1637	C1638	U1526	A1528	A1434	G1332	U1197	A1086	A1000	G	G805	A706	A613
G2069	U1638	A1637	A1528	A1529	A1434	U1340	U1198	G1087	A1001	C	U807	G707	A614
A2070	C1638	A1637	A1529	A1530	A1434	G1341	U1199	A1088	G1002	U894	G808	G708	U615
A2071	G1638	A1637	A1530	A1531	A1434	G1342	U1203	A1089	C1007	A896	U809	U709	A616
A2072	A1638	A1637	A1531	A1532	A1434	G1343	A1204	U1097	A1008	C897	C812	G712	G618
C2072	A1638	A1637	A1532	A1533	A1434	G1343	G1206	A1098	A1009	C898	U813	G713	



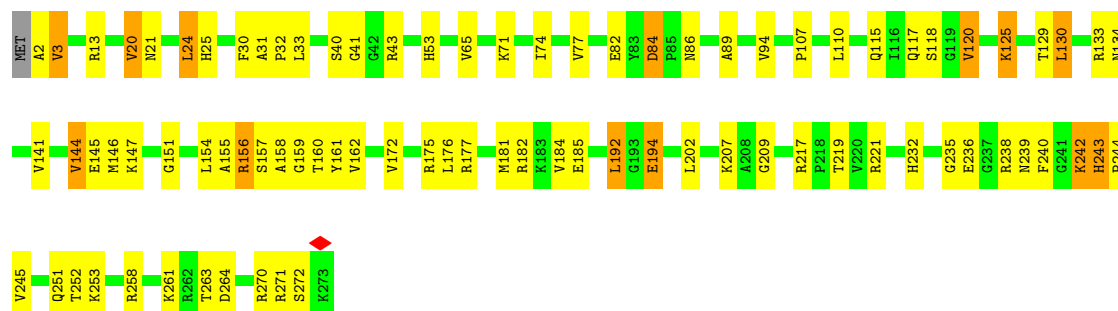
• Molecule 4: 5S rRNA

Chain B: 68% 30%



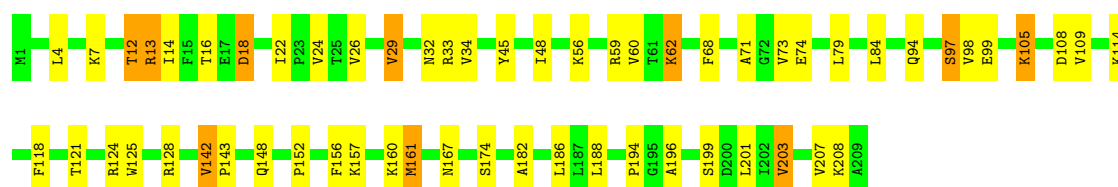
• Molecule 5: 50S ribosomal protein L2

Chain C: 68% 27% 5%



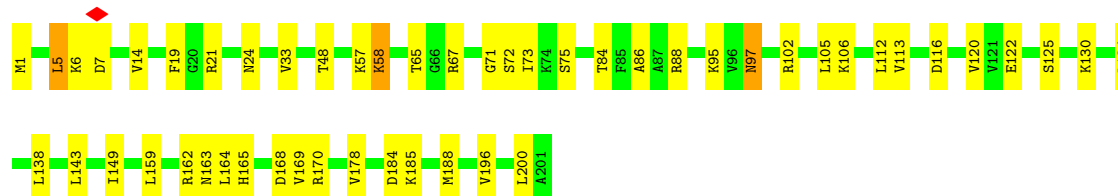
- Molecule 6: 50S ribosomal protein L3

Chain D: 72% 23% 5%



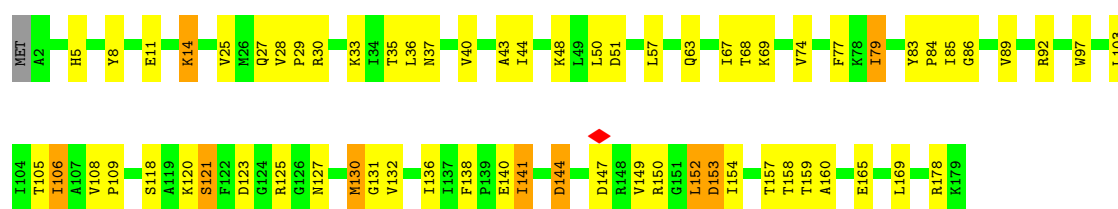
- Molecule 7: 50S ribosomal protein L4

Chain E: 75% 24% .



- Molecule 8: 50S ribosomal protein L5

Chain F: 63% 32% 5% .



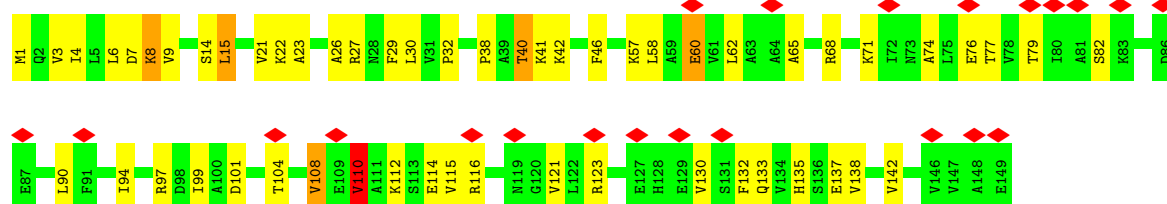
- Molecule 9: 50S ribosomal protein L6

Chain G: 76% 23% ..

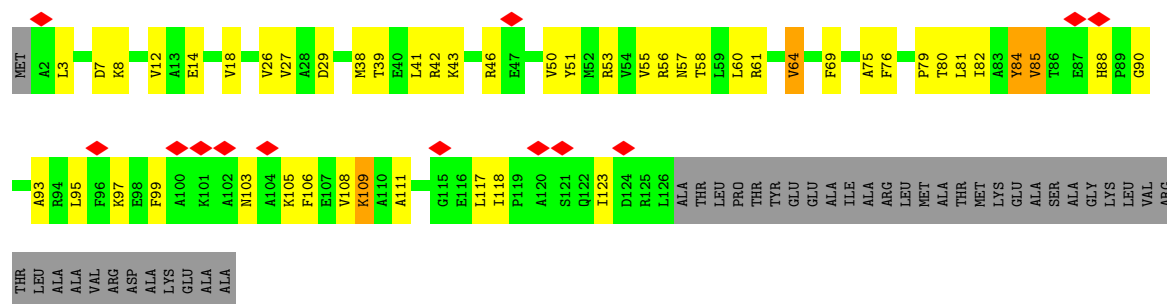




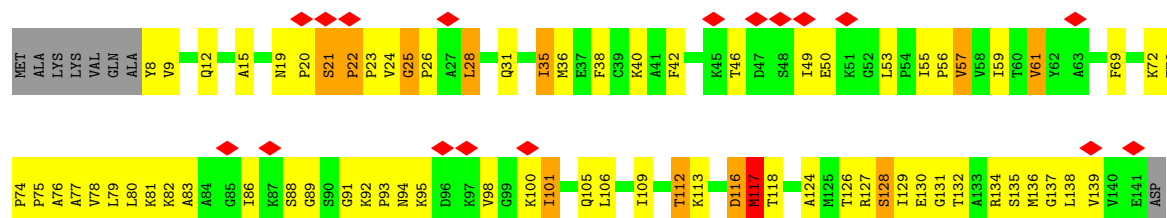
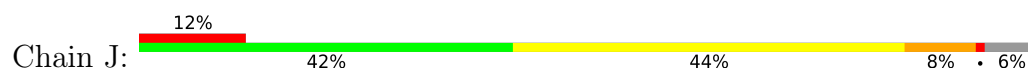
• Molecule 10: 50S ribosomal protein L9



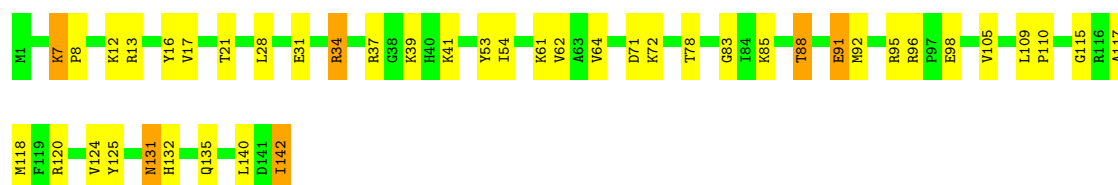
• Molecule 11: 50S ribosomal protein L10



• Molecule 12: 50S ribosomal protein L11

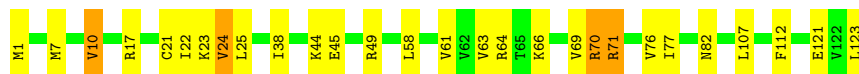


• Molecule 13: 50S ribosomal protein L13



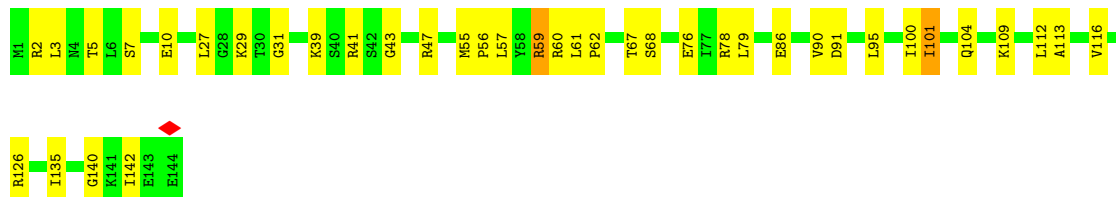
- Molecule 14: 50S ribosomal protein L14

Chain L:  77% 20% .



- Molecule 15: 50S ribosomal protein L15

Chain M:  73% 26% .



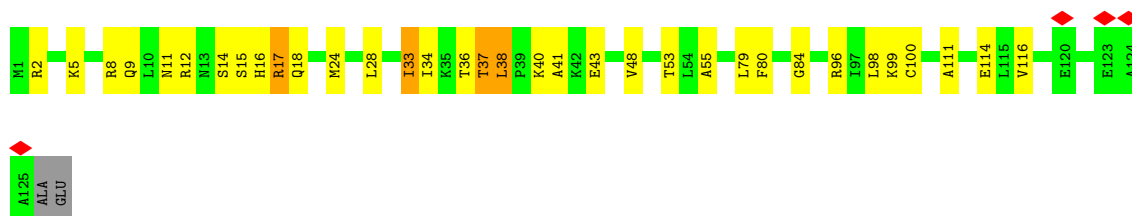
- Molecule 16: 50S ribosomal protein L16

Chain N:  79% 21% .



- Molecule 17: 50S ribosomal protein L17

Chain O:  72% 24% . .



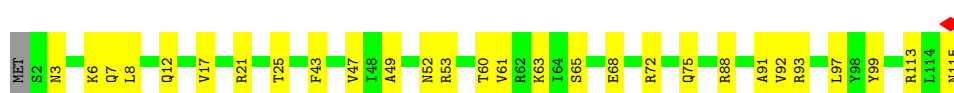
- Molecule 18: 50S ribosomal protein L18

Chain P:  72% 25% .



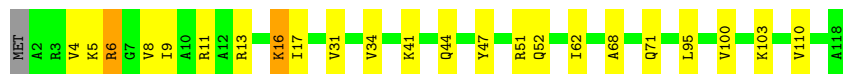
- Molecule 19: 50S ribosomal protein L19

Chain Q:  75% 24% .



- Molecule 20: 50S ribosomal protein L20

Chain R:  80% 18% ..



- Molecule 21: 50S ribosomal protein L21

Chain S:  76% 24%



- Molecule 22: 50S ribosomal protein L22

Chain T:  76% 23% .



- Molecule 23: 50S ribosomal protein L23

Chain U:  75% 18% . 5%



- Molecule 24: 50S ribosomal protein L24

Chain V:  73% 25% ..



- Molecule 25: 50S ribosomal protein L25

Chain W:  76% 21% .



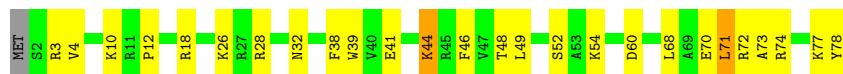
- Molecule 26: 50S ribosomal protein L27

Chain X:  66% 21% . 11%



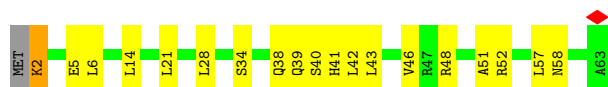
- Molecule 27: 50S ribosomal protein L28

Chain Y:  65% 31% ..



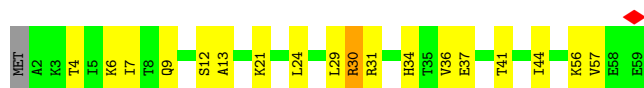
- Molecule 28: 50S ribosomal protein L29

Chain Z:  68% 29% ..



- Molecule 29: 50S ribosomal protein L30

Chain a:  68% 29% ..



- Molecule 30: 50S ribosomal protein L32

Chain b:  54% 37% 7% .



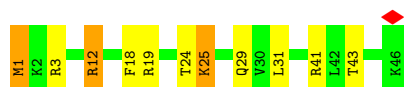
- Molecule 31: 50S ribosomal protein L33

Chain c:  60% 27% 5% 7%



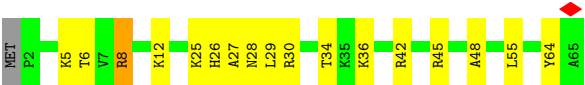
- Molecule 32: 50S ribosomal protein L34

Chain d:  76% 17% 7%

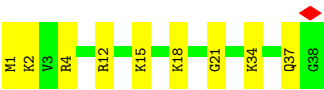


- Molecule 33: 50S ribosomal protein L35

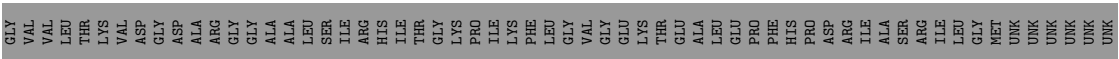
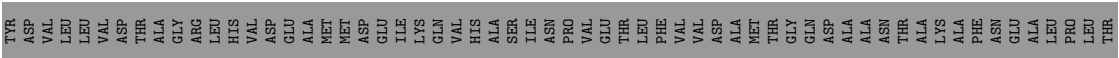
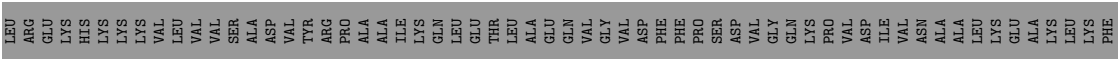
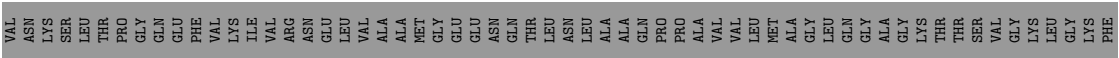
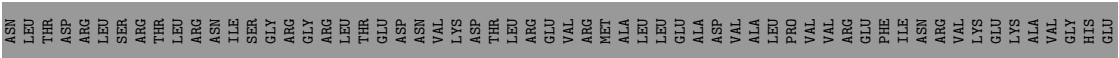
Chain e:  72% 25% ..



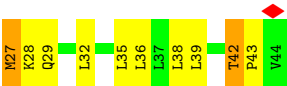
• Molecule 34: 50S ribosomal protein L36



• Molecule 35: Signal recognition particle protein Ffh



• Molecule 36: 1A9L SS



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	75942	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 ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.287	Depositor
Minimum map value	-0.121	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.032	Depositor
Map size (Å)	443.2, 443.2, 443.2	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.385, 1.385, 1.385	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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	1	0.45	0/1037	0.53	0/1616
2	2	0.28	0/68	0.52	0/103
3	A	0.32	0/69329	0.45	0/108152
4	B	0.27	0/2872	0.38	0/4478
5	C	0.56	1/2122 (0.0%)	0.97	6/2854 (0.2%)
6	D	0.54	0/1586	0.97	4/2134 (0.2%)
7	E	0.50	0/1571	0.91	4/2113 (0.2%)
8	F	0.50	1/1435 (0.1%)	0.88	0/1928
9	G	0.48	0/1343	0.90	2/1816 (0.1%)
10	H	0.66	0/1121	0.87	1/1515 (0.1%)
11	I	0.88	1/958 (0.1%)	0.98	2/1292 (0.2%)
12	J	1.05	1/993 (0.1%)	1.14	10/1341 (0.7%)
13	K	0.53	0/1152	0.89	3/1551 (0.2%)
14	L	0.54	0/955	0.90	0/1279
15	M	0.51	0/1062	0.92	1/1413 (0.1%)
16	N	0.52	0/1093	0.91	2/1460 (0.1%)
17	O	0.56	0/1006	0.94	2/1345 (0.1%)
18	P	0.51	0/910	0.92	0/1219
19	Q	0.50	0/929	0.90	2/1242 (0.2%)
20	R	0.61	0/960	0.85	0/1278
21	S	0.51	0/829	0.92	1/1107 (0.1%)
22	T	0.61	0/864	1.05	2/1156 (0.2%)
23	U	0.60	0/763	0.92	0/1021
24	V	0.57	1/788 (0.1%)	0.92	0/1053
25	W	0.44	0/766	0.83	0/1025
26	X	0.51	0/587	0.95	2/776 (0.3%)
27	Y	0.53	0/635	0.85	0/848
28	Z	0.52	0/502	0.95	0/667
29	a	0.48	0/453	0.84	0/605
30	b	0.58	0/450	0.89	0/599
31	c	0.50	0/421	0.99	2/561 (0.4%)
32	d	0.53	0/380	0.92	0/498

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.52	0/513	0.92	0/676
34	f	0.55	0/303	0.96	0/397
35	i	0.68	0/672	1.01	3/883 (0.3%)
36	k	1.19	1/137 (0.7%)	1.10	1/186 (0.5%)
All	All	0.41	6/101565 (0.0%)	0.61	50/152187 (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
5	C	0	1
35	i	0	1
All	All	0	2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	272	SER	C-N	-6.81	1.23	1.33
8	F	178	ARG	C-N	-6.75	1.23	1.33
24	V	103	ILE	C-N	-6.50	1.24	1.33
12	J	22	PRO	CA-C	5.97	1.57	1.52
36	k	42	THR	CA-C	5.74	1.58	1.52

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	142	VAL	CA-C-N	10.28	129.90	119.82
6	D	142	VAL	C-N-CA	10.28	129.90	119.82
35	i	390	LYS	CA-C-N	9.67	129.93	119.87
35	i	390	LYS	C-N-CA	9.67	129.93	119.87
12	J	116	ASP	N-CA-C	9.11	124.65	113.17

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	C	232	HIS	Peptide
35	i	367	UNK	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	1	926	0	467	18	0
2	2	62	0	34	0	0
3	A	61902	0	31133	695	0
4	B	2569	0	1301	22	0
5	C	2083	0	2154	53	0
6	D	1565	0	1616	37	0
7	E	1552	0	1619	31	0
8	F	1411	0	1444	42	0
9	G	1323	0	1371	25	0
10	H	1110	0	1148	32	0
11	I	946	0	978	32	0
12	J	979	0	1028	60	0
13	K	1129	0	1162	26	0
14	L	946	0	1023	19	0
15	M	1053	0	1129	23	0
16	N	1074	0	1157	15	0
17	O	993	0	1034	22	0
18	P	900	0	935	24	0
19	Q	917	0	962	17	0
20	R	947	0	1019	14	0
21	S	816	0	839	13	0
22	T	857	0	922	11	0
23	U	756	0	817	9	0
24	V	780	0	831	12	0
25	W	753	0	780	11	0
26	X	580	0	594	13	0
27	Y	625	0	652	16	0
28	Z	501	0	531	15	0
29	a	449	0	488	10	0
30	b	444	0	458	19	0
31	c	414	0	442	12	0
32	d	377	0	418	13	0
33	e	504	0	572	12	0
34	f	302	0	340	6	0
35	i	916	0	943	43	0
36	k	137	0	168	11	0
37	2	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	A	411	0	0	0	0
37	B	12	0	0	0	0
37	C	2	0	0	0	0
37	D	1	0	0	0	0
37	O	1	0	0	0	0
37	R	1	0	0	0	0
37	Y	1	0	0	0	0
37	b	1	0	0	0	0
38	f	1	0	0	0	0
All	All	94030	0	62509	1265	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 8.

The worst 5 of 1265 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)
12:J:86:ILE:HD13	12:J:138:LEU:HD21	1.51	0.93
3:A:276:U:O2	3:A:278:A:N6	2.03	0.91
3:A:2584:U:H3'	3:A:2585:U:H5''	1.52	0.89
3:A:2304:G:H22	3:A:2312:U:H3	1.18	0.88
3:A:2128:G:H1	3:A:2160:C:H42	1.19	0.88

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	
5	C	270/273 (99%)	263 (97%)	7 (3%)	0	100	100
6	D	207/209 (99%)	202 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	E	199/201 (99%)	191 (96%)	7 (4%)	1 (0%)	24	57
8	F	176/179 (98%)	172 (98%)	4 (2%)	0	100	100
9	G	174/177 (98%)	172 (99%)	2 (1%)	0	100	100
10	H	147/149 (99%)	138 (94%)	9 (6%)	0	100	100
11	I	123/165 (74%)	113 (92%)	9 (7%)	1 (1%)	16	48
12	J	132/142 (93%)	125 (95%)	7 (5%)	0	100	100
13	K	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
14	L	121/123 (98%)	116 (96%)	5 (4%)	0	100	100
15	M	142/144 (99%)	140 (99%)	2 (1%)	0	100	100
16	N	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
17	O	123/127 (97%)	119 (97%)	4 (3%)	0	100	100
18	P	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
19	Q	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
20	R	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
21	S	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
22	T	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
23	U	93/100 (93%)	89 (96%)	4 (4%)	0	100	100
24	V	101/104 (97%)	99 (98%)	2 (2%)	0	100	100
25	W	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
26	X	74/85 (87%)	73 (99%)	1 (1%)	0	100	100
27	Y	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
28	Z	60/63 (95%)	58 (97%)	2 (3%)	0	100	100
29	a	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
30	b	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
31	c	49/55 (89%)	48 (98%)	1 (2%)	0	100	100
32	d	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
33	e	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
34	f	36/38 (95%)	36 (100%)	0	0	100	100
35	i	84/450 (19%)	84 (100%)	0	0	100	100
36	k	16/18 (89%)	12 (75%)	4 (25%)	0	100	100
All	All	3535/4042 (88%)	3426 (97%)	107 (3%)	2 (0%)	49	79

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	E	6	LYS
11	I	108	VAL

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	
5	C	216/218 (99%)	196 (91%)	20 (9%)	8	30
6	D	164/164 (100%)	150 (92%)	14 (8%)	10	33
7	E	165/165 (100%)	149 (90%)	16 (10%)	8	29
8	F	148/150 (99%)	133 (90%)	15 (10%)	7	27
9	G	137/138 (99%)	128 (93%)	9 (7%)	15	41
10	H	114/114 (100%)	98 (86%)	16 (14%)	3	18
11	I	95/123 (77%)	88 (93%)	7 (7%)	13	38
12	J	104/110 (94%)	94 (90%)	10 (10%)	8	29
13	K	116/116 (100%)	103 (89%)	13 (11%)	6	24
14	L	104/104 (100%)	94 (90%)	10 (10%)	8	29
15	M	103/103 (100%)	94 (91%)	9 (9%)	9	33
16	N	109/109 (100%)	101 (93%)	8 (7%)	13	39
17	O	102/103 (99%)	93 (91%)	9 (9%)	9	33
18	P	87/87 (100%)	80 (92%)	7 (8%)	11	36
19	Q	99/100 (99%)	95 (96%)	4 (4%)	28	52
20	R	89/90 (99%)	80 (90%)	9 (10%)	7	27
21	S	84/84 (100%)	80 (95%)	4 (5%)	23	47
22	T	93/93 (100%)	85 (91%)	8 (9%)	10	33
23	U	82/84 (98%)	76 (93%)	6 (7%)	13	39
24	V	83/85 (98%)	76 (92%)	7 (8%)	10	34
25	W	78/78 (100%)	68 (87%)	10 (13%)	4	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	X	57/63 (90%)	51 (90%)	6 (10%)	6	26
27	Y	67/68 (98%)	61 (91%)	6 (9%)	9	32
28	Z	54/55 (98%)	48 (89%)	6 (11%)	6	24
29	a	48/49 (98%)	45 (94%)	3 (6%)	16	42
30	b	47/48 (98%)	38 (81%)	9 (19%)	1	9
31	c	45/49 (92%)	41 (91%)	4 (9%)	9	32
32	d	38/38 (100%)	33 (87%)	5 (13%)	4	19
33	e	51/52 (98%)	48 (94%)	3 (6%)	18	43
34	f	34/34 (100%)	33 (97%)	1 (3%)	37	58
35	i	71/313 (23%)	64 (90%)	7 (10%)	7	28
36	k	17/17 (100%)	16 (94%)	1 (6%)	18	43
All	All	2901/3204 (90%)	2639 (91%)	262 (9%)	11	32

5 of 262 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	a	36	VAL
30	b	32	LYS
35	i	430	MET
12	J	28	LEU
11	I	109	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
19	Q	7	GLN
21	S	66	HIS
19	Q	52	ASN
20	R	37	GLN
22	T	7	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	42/113 (37%)	12 (28%)	0
2	2	2/3 (66%)	1 (50%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	A	2878/2903 (99%)	488 (16%)	17 (0%)
4	B	119/120 (99%)	16 (13%)	0
All	All	3041/3139 (96%)	517 (17%)	17 (0%)

5 of 517 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	33	C
1	1	36	U
1	1	37	U
1	1	38	U
1	1	39	A

5 of 17 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	A	2430	A
3	A	2756	U
3	A	1110	G
3	A	1344	U
3	A	1494	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 432 ligands modelled in this entry, 432 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

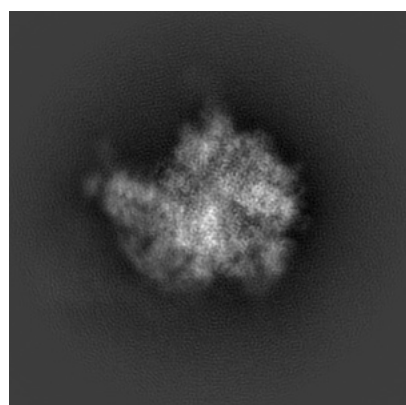
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8003. These allow visual inspection of the internal detail of the map and identification of artifacts.

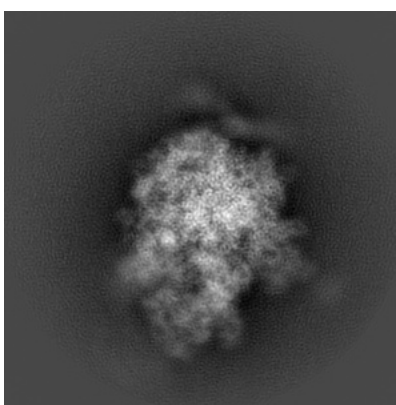
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

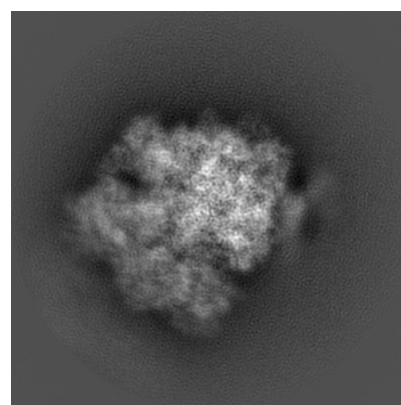
6.1.1 Primary map



X



Y

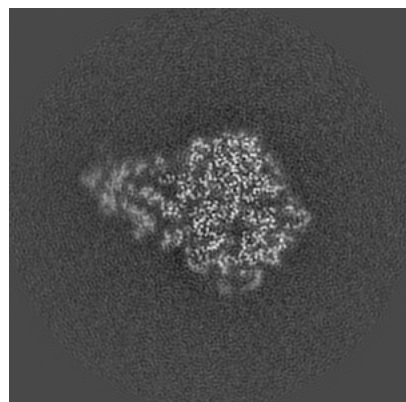


Z

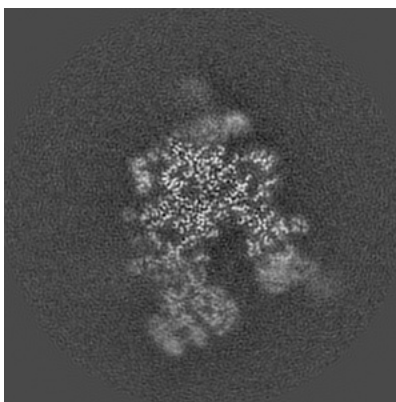
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

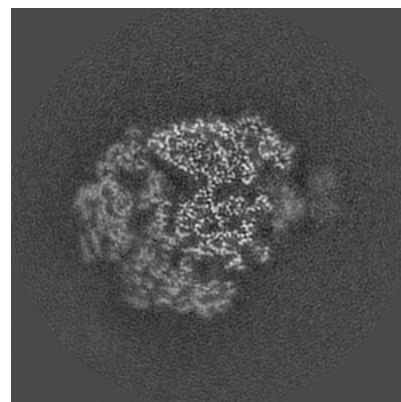
6.2.1 Primary map



X Index: 160



Y Index: 160

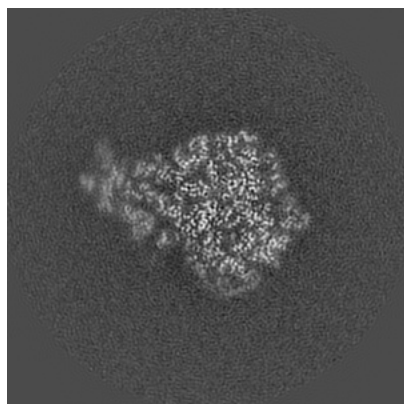


Z Index: 160

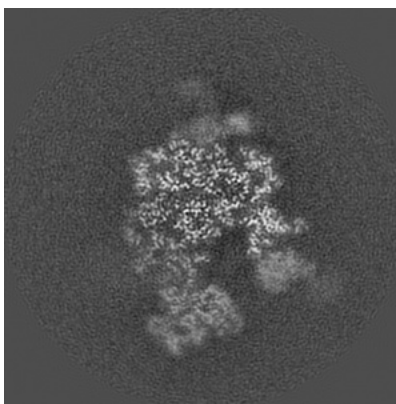
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

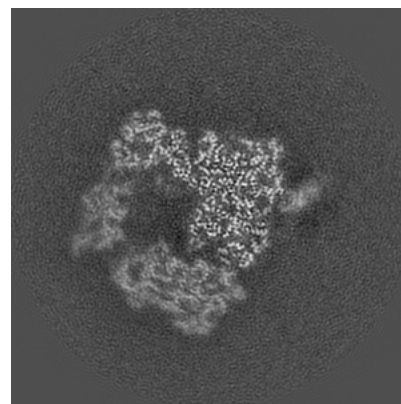
6.3.1 Primary map



X Index: 157



Y Index: 157

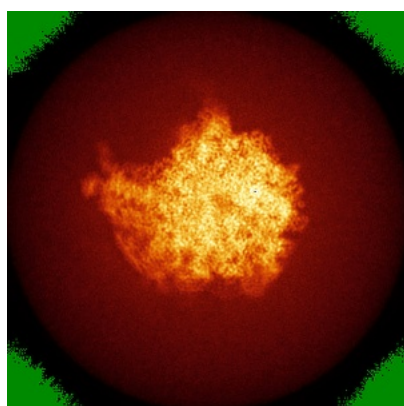


Z Index: 176

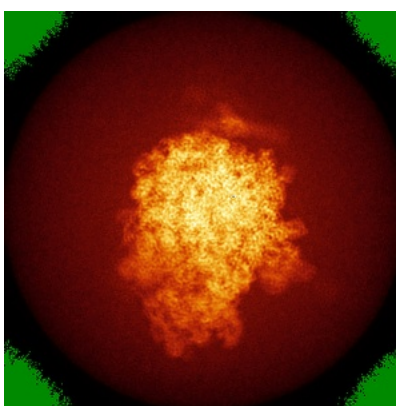
The images above show the largest variance slices of the map in three orthogonal directions.

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

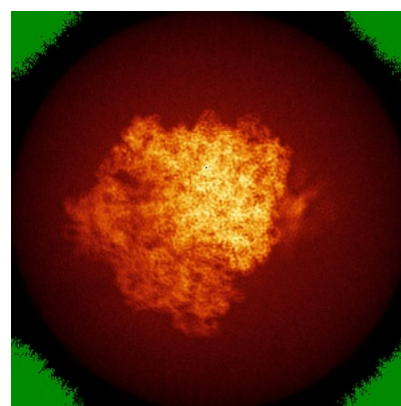
6.4.1 Primary map



X



Y

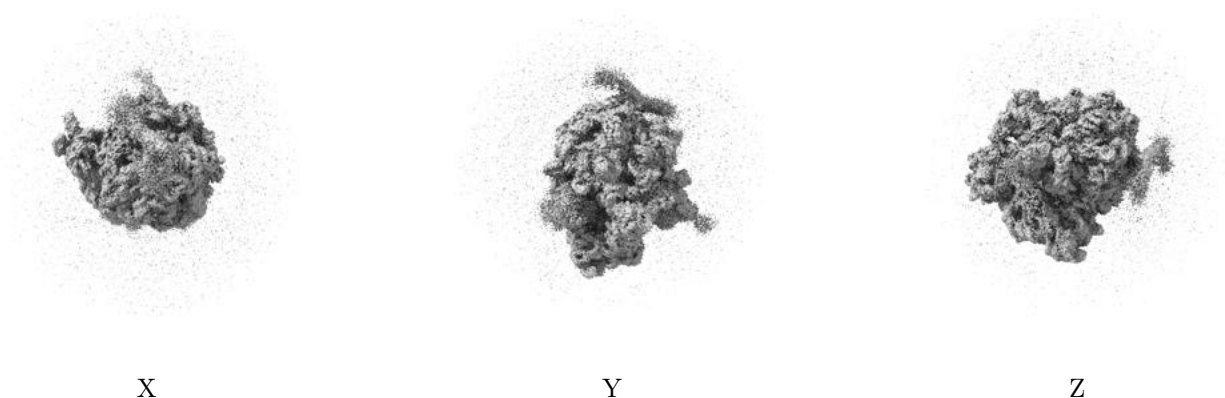


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.032. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

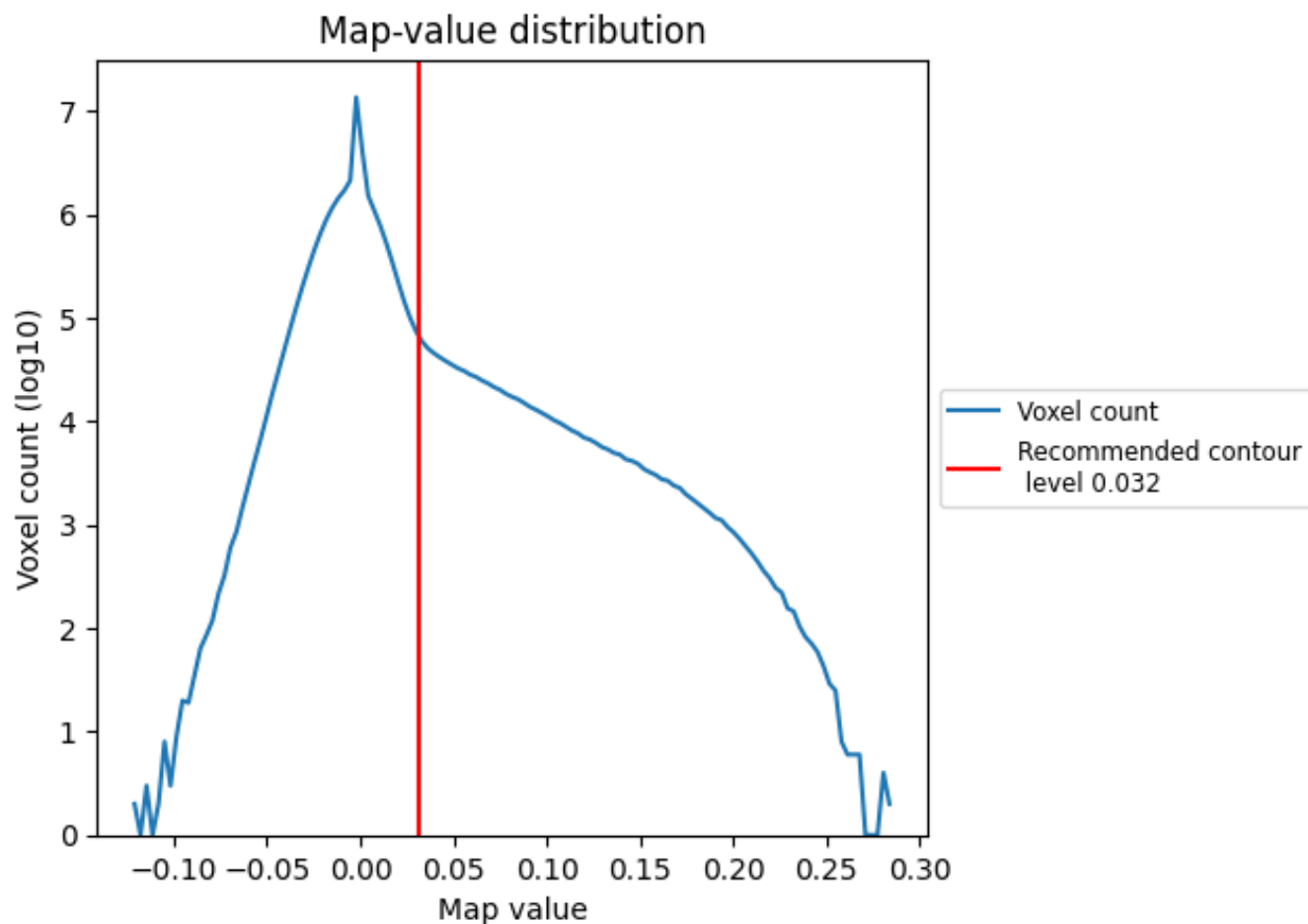
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

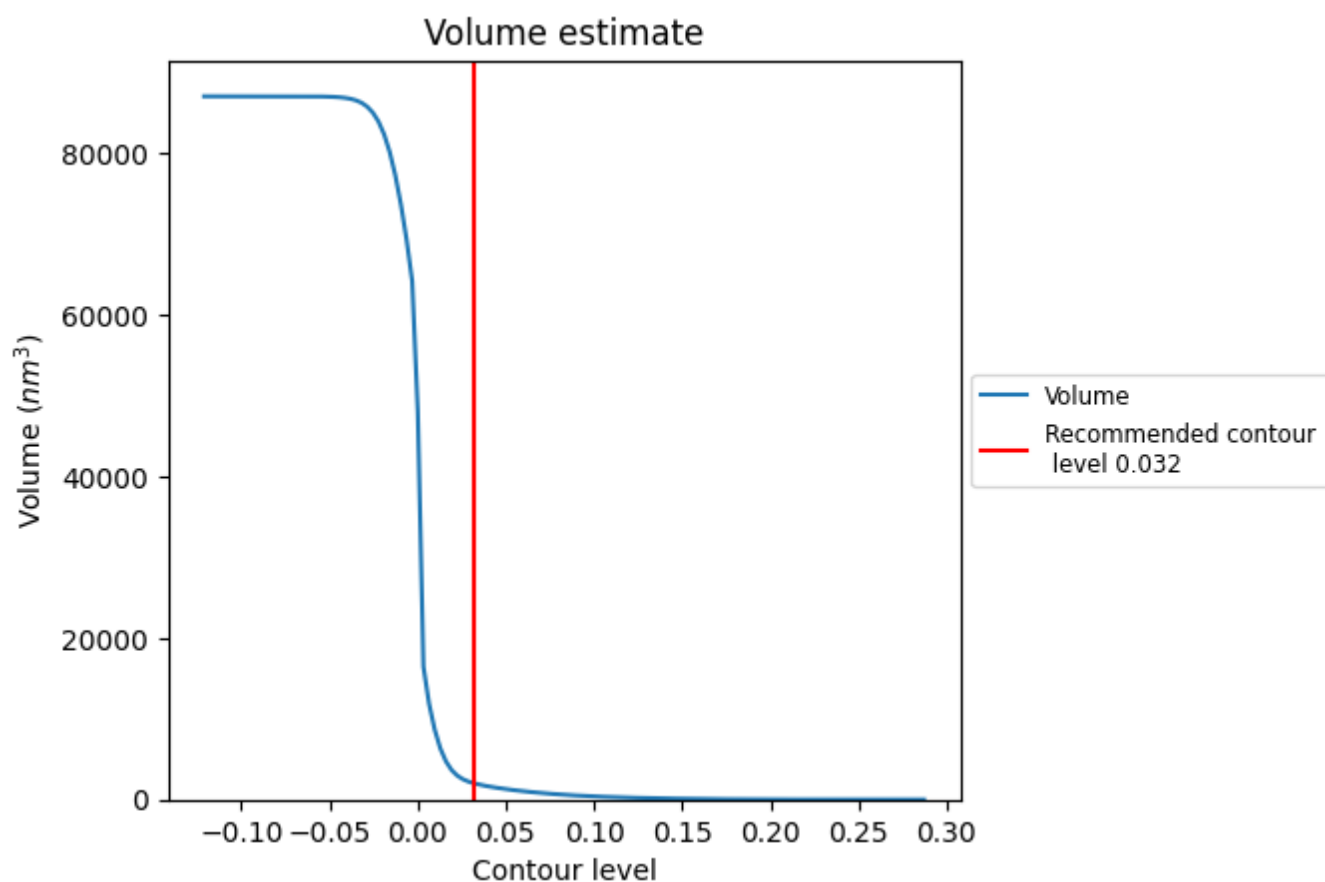
This section contains the results of statistical analysis of the map.

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.

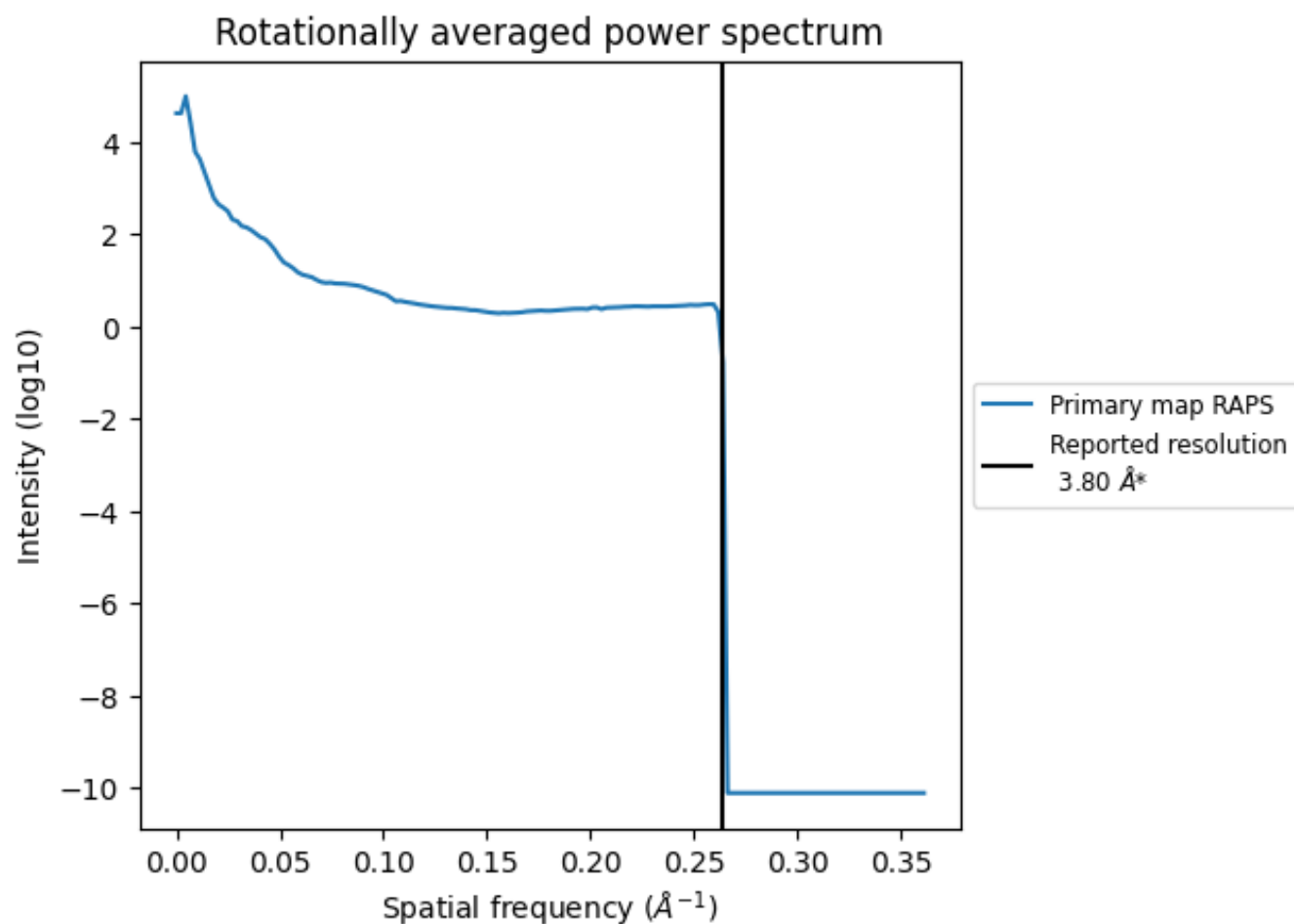
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2014 nm³; this corresponds to an approximate mass of 1819 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 0.263 Å⁻¹

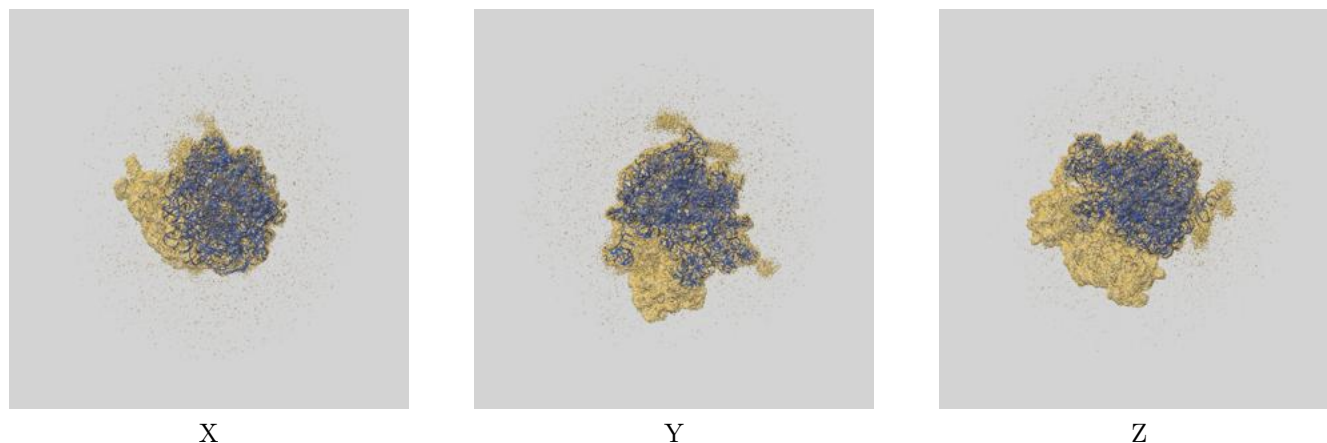
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

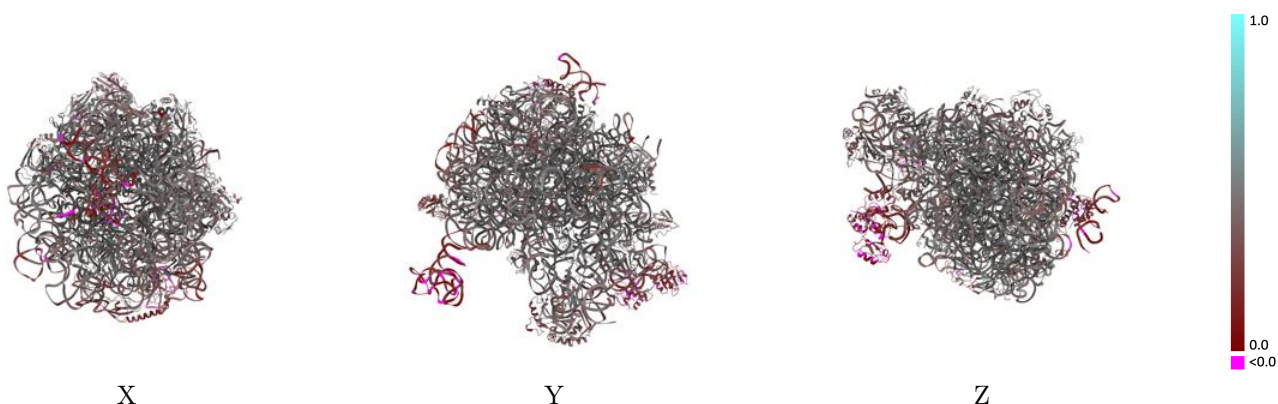
This section contains information regarding the fit between EMDB map EMD-8003 and PDB model 5GAG. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



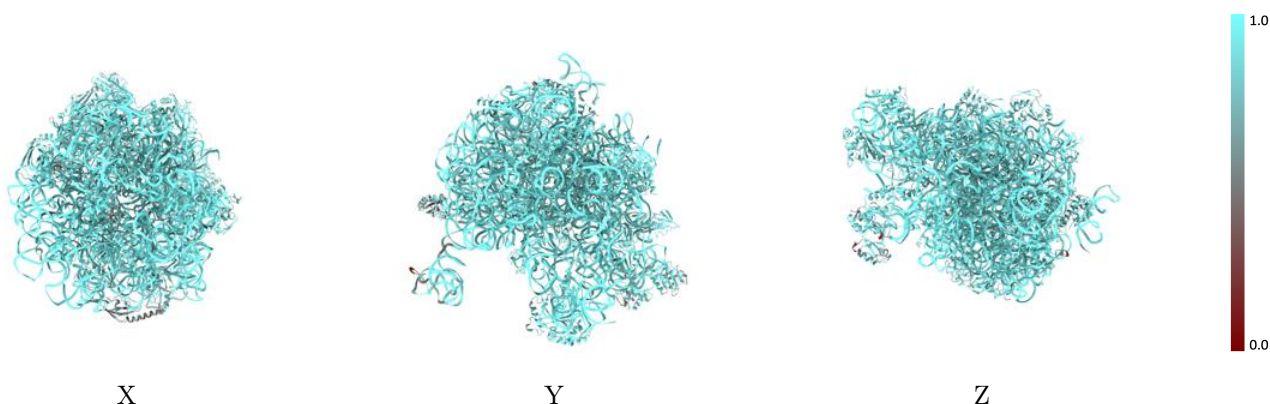
The images above show the 3D surface view of the map at the recommended contour level 0.032 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



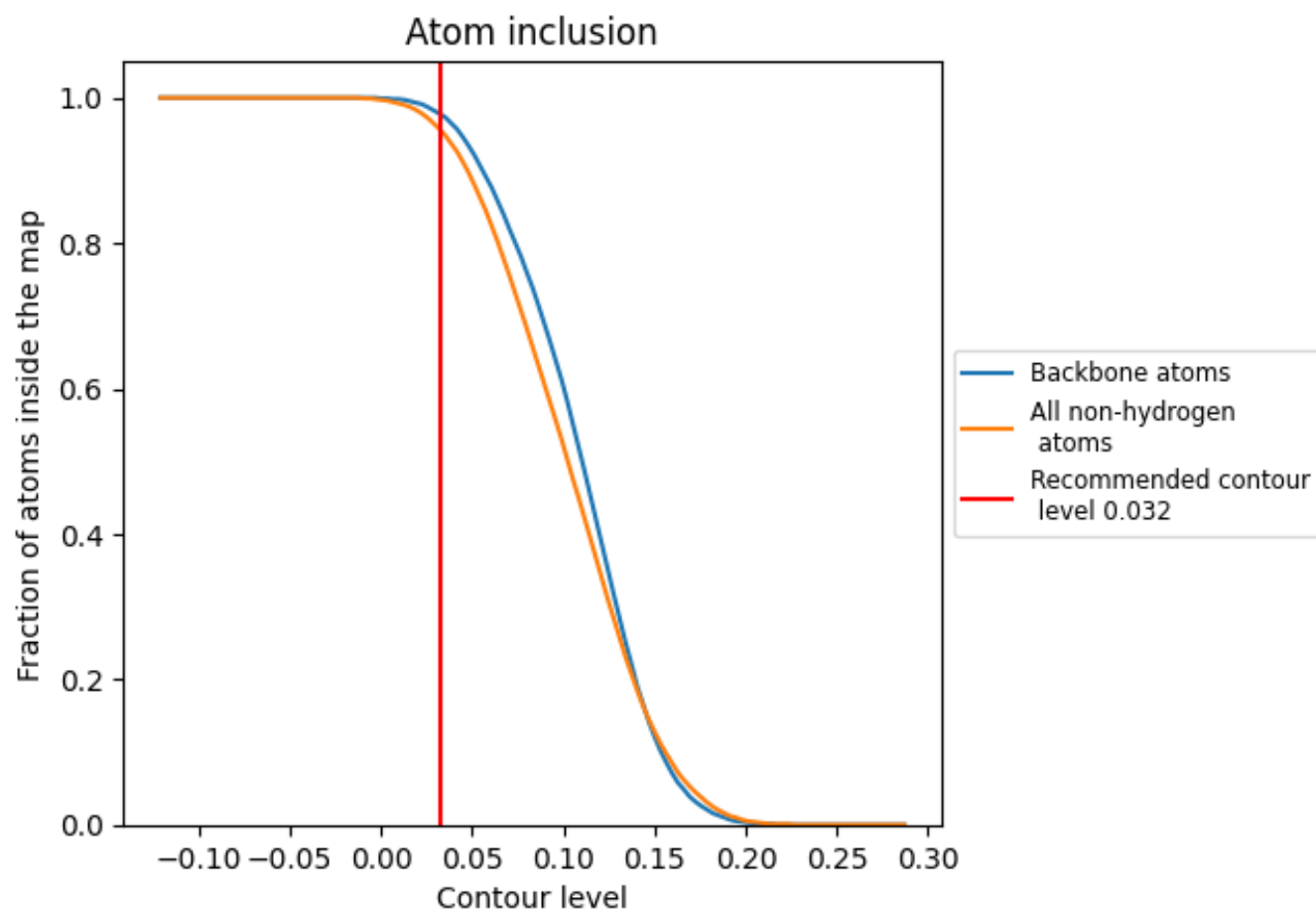
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.032).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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 (0.032) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9570	 0.4100
1	 0.9290	 0.1400
2	 0.9840	 0.4630
A	 0.9860	 0.4170
B	 0.9940	 0.4110
C	 0.9250	 0.4680
D	 0.9310	 0.4640
E	 0.8970	 0.4230
F	 0.8980	 0.3590
G	 0.9230	 0.4060
H	 0.6620	 0.2910
I	 0.7660	 0.1660
J	 0.7560	 0.0780
K	 0.9410	 0.4580
L	 0.8620	 0.4370
M	 0.9260	 0.4460
N	 0.9200	 0.4570
O	 0.9190	 0.4490
P	 0.9290	 0.4110
Q	 0.8870	 0.4290
R	 0.9540	 0.4600
S	 0.9080	 0.4370
T	 0.8780	 0.4510
U	 0.8920	 0.4380
V	 0.9130	 0.4260
W	 0.9170	 0.4270
X	 0.9330	 0.4650
Y	 0.9370	 0.4560
Z	 0.8920	 0.3930
a	 0.9310	 0.4460
b	 0.8950	 0.4400
c	 0.8970	 0.4320
d	 0.9180	 0.4610
e	 0.9180	 0.4720
f	 0.9320	 0.4560



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Chain	Atom inclusion	Q-score
i	 0.8060	 0.2190
k	 0.8470	 0.1090