



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 01:25 AM UTC

PDB ID : 5GAH / pdb_00005gah
EMDB ID : EMD-8004
Title : RNC in complex with SRP with detached NG domain
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

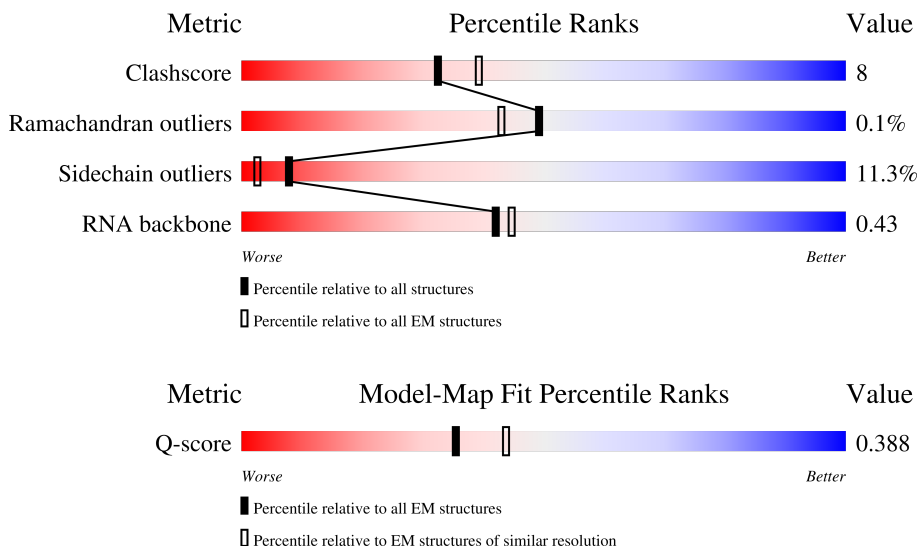
1 Overall quality at a glance

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.



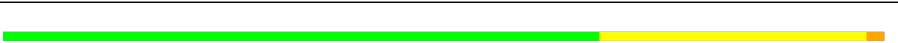
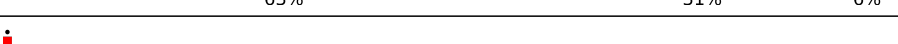
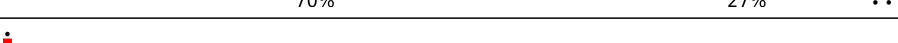
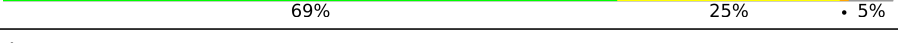
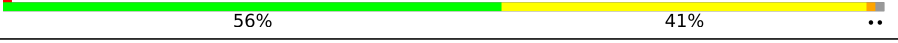
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	69%27%
30	b	57	56%32%11%
31	c	55	71%20%7%
32	d	46	70%26%
33	e	65	57%40%
34	f	38	68%24%8%
35	i	453	9%17%10%72%
36	k	18	22%56%33%11%

2 Entry composition [i](#)

There are 38 unique types of molecules in this entry. The entry contains 94027 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	271	Total	C	N	O	S	0	0
			2082	1288	423	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	177	Total	C	N	O	S	0	0
			1410	899	249	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	102	Total	C	N	O	0	0
			779	492	146	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	412	Total	Mg	0
			412	412	
37	B	11	Total	Mg	0
			11	11	
37	C	2	Total	Mg	0
			2	2	
37	D	1	Total	Mg	0
			1	1	
37	E	1	Total	Mg	0
			1	1	
37	P	1	Total	Mg	0
			1	1	
37	R	1	Total	Mg	0
			1	1	
37	b	1	Total	Mg	0
			1	1	

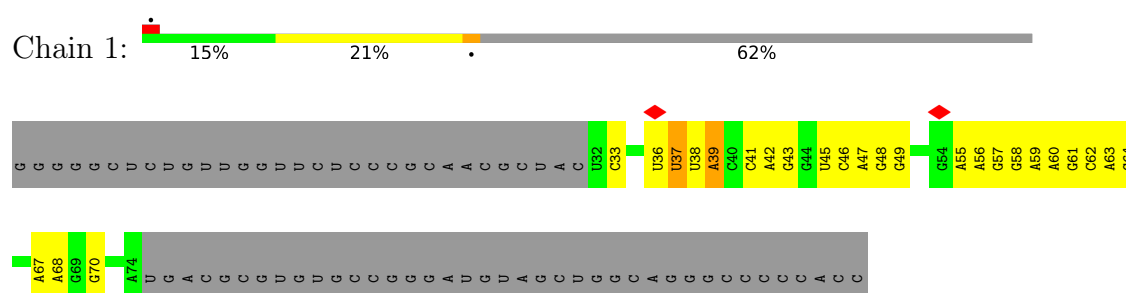
- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

3 Residue-property plots

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.

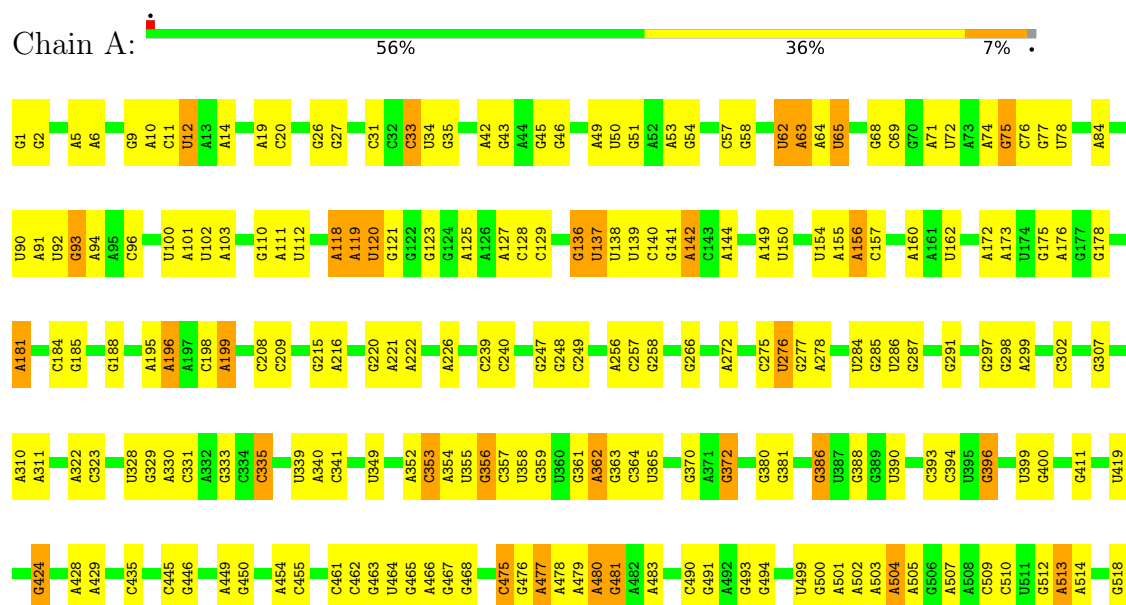
• Molecule 1: SRP 4.5S RNA



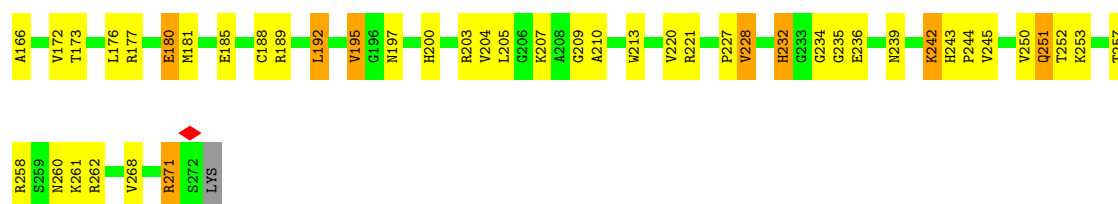
• Molecule 2: tRNA CCAend



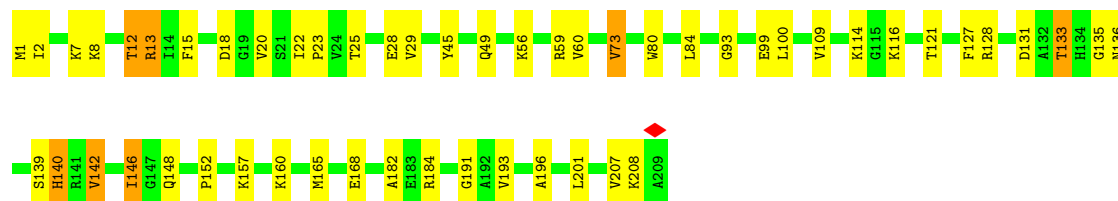
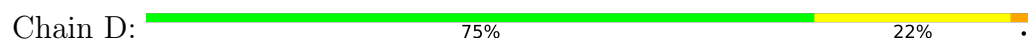
• Molecule 3: 23S rRNA



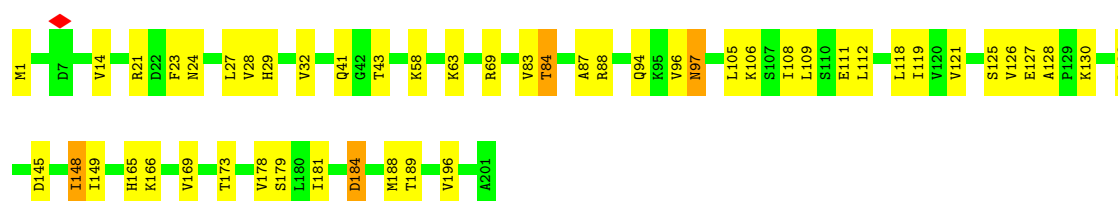
A1853	G1763	U1648	A1545	A1453	U1379	G1259	C1140	A1067	A983	G879	G799	A706	U519
A1858	C1764	G1649	G1546	C1463	U1379	A1262	U1141	G1068	A984	G880	A800	G707	G520
U1859	G1770	G1653	U1554	G1464	A1383	A1262	A1142	A1069	A981	G881	A609	C610	U521
G1869	A1773	A1655	G1560	U1466	C1386	U1267	G1149	G1071	C987	U	A804	G713	A526
C1870	C1774	G1660	U1563	U1467	A1387	A1268	C1150	A1070	A980	C	G805	A613	G527
A1871	U1775	G1667	C1564	U1468	G1388	A1269	G1154	A1073	C991	U	U807	A614	A528
A1872	U1780	G1677	C1566	U1469	U1394	A1272	A1155	C1076	C992	C	G808	U714	A529
C1873	U1781	G1673	U1568	G1473	A1395	A1272	A1169	A1077	C994	C	U811	C717	C531
C1874	U1782	G1674	U1570	U1474	U1396	A1275	G1170	U1078	A996	C	U812	A621	A532
G1875	A1785	A1672	A1569	G1482	U1397	A1275	A1169	C1079	G997	A	C814	A722	G533
A1877	U1786	G1674	A1570	G1483	C1398	A1287	C1170	U1082	C998	C	A819	A627	G543
G1878	A1786	A1677	A1572	U1484	C1399	G1288	U	U1083	U999	U894	G628	A627	C544
U1880	U1789	A1677	U1572	U1485	U1400	C1289	A	A1084	A1000	U895	G629	G630	U
C1881	C1790	G1681	U1576	C1489	U1402	C1290	U	A1085	A1001	A896	G630	A631	G548
G1888	A1791	A1689	C1577	G1490	A1403	U1294	G1177	A1086	A1002	C897	A822	A632	G549
A1794	U1794	A1689	U1578	G1491	C1404	U1294	G1177	A1087	C1005	U898	U824	A633	C550
C1795	C1795	A1700	G1581	U1492	U1405	G1300	G1178	A1088	C1006	U899	U825	A634	U552
U1796	U1796	G1706	C1582	C1493	U1406	A1301	U1180	A1089	C1007	A899	U826	G738	G551
G1797	G1797	G1707	U1583	A1494	U1406	A1302	U1181	A1090	A1008	G907	U827	U747	U552
U1798	U1798	G1707	U1584	A1495	G1410	A1302	G1182	A1090	A1009	C908	U828	A753	U558
G1799	C1708	A1689	C1585	A1496	C1414	A1308	G1182	G1093	A1009	A909	U829	A637	U558
C1800	U1709	U1709	U1497	U1497	U1415	A1308	G1187	U1094	U1012	A910	G830	U639	G561
A1801	G1710	G1710	C1498	U1498	G1416	U1313	G1187	A1095	C1013	A911	U831	G640	U562
A1802	A1711	A1711	A1591	C1499	C1417	U1313	U1199	A1096	U1013	G914	U832	C645	U562
G1906	G1906	G1715	C1592	G1501	U1418	G1324	U1199	U1097	A1021	C915	A833	U646	C564
A1807	U1807	G1715	C1592	G1501	A1419	G1324	U1199	A1098	A1022	G916	G647	G648	C565
A1808	A1808	G1715	C1592	G1501	A1419	G1324	U1199	A1098	A1022	A917	U839	G649	U566
A1809	A1809	G1715	C1592	G1501	A1419	G1324	U1199	A1098	A1022	G917	C840	C650	U567
C1810	C1810	G1715	C1592	G1501	A1419	G1324	U1199	A1098	A1022	G917	U839	C650	U568
U1811	U1811	G1715	C1592	G1501	A1419	G1324	U1199	A1098	A1022	G917	U839	C650	U569
A1816	U1917	U1725	A1603	C1507	U1506	G1332	G1210	C1102	A1026	G930	C840	C772	U570
G1817	U1817	U1729	C1606	U1507	G1421	A1327	G1211	U832	A1027	U931	A845	G774	A571
U1818	U1818	C1730	C1607	A1508	G1422	A1328	G1212	U832	A1028	U932	A846	A654	A572
A1819	U1819	C1732	A1609	U1510	G1423	U1329	G1212	A933	U1033	C946	U847	A655	U573
U1820	U1820	C1732	A1610	G1511	A1427	U1337	G1218	C947	U1033	U947	C848	G656	A574
A1821	U1821	C1732	A1611	G1516	C1428	U1338	G1218	C948	U1033	U948	U850	G657	A575
C1822	U1822	C1732	A1612	G1517	G1432	U1340	U1231	C949	U1033	U949	U851	G658	U576
U1825	U1825	U1735	C1614	G1524	A1434	U1342	U1231	G953	U1033	G953	G857	A668	G577
G1826	U1826	U1736	A1616	A1525	G1435	U1344	G1236	G953	U1033	G953	G858	G669	C581
U1827	U1827	G1737	A1616	A1526	G1436	U1344	A1237	C957	U1033	C957	U860	A670	G581
G1828	U1828	G1737	G1627	C1526	C1437	U1345	G1238	U958	U1046	U958	A861	C671	G585
A1829	U1829	U1743	G1628	G1527	U1438	G1346	C1243	A959	A1046	A959	G862	C672	G585
U1837	U1837	A1744	G1631	A1528	A1439	G1351	A1247	A960	A1048	A960	G864	A675	A586
C1838	U1751	U1751	G1631	G1529	U1442	A1354	A1247	C961	G1056	C961	C865	A675	U591
G1839	C1752	C1752	A1634	C1533	U1443	A1354	G1248	C968	G1057	C968	U790	A676	A592
G1846	U1756	G1756	A1637	U1534	C1446	G1355	U1249	G969	A1057	G969	U791	A677	A593
A1847	U1757	U1757	C1638	A1536	C1447	C1363	G1250	U970	U1060	U970	A792	C678	U594
U1848	U1758	U1758	C1639	G1537	G1448	A1365	G1251	U971	U1061	C971	A793	C679	C595
A1849	U1759	A1759	G1645	G1542	G1449	A1366	A1253	A972	G1062	A972	U871	C680	C801
U1850	C1760	C1760	G1646	U1542	U1450	A1367	G1256	A973	G1063	A973	U872	G681	A602
A1912	U1946	U1946	C1647	G1543	C1257	G1374	C1257	A974	U1064	A974	C876	U686	A603
A	C1947	C1947	U1647	A1544	G1452			G976	U1066	G976	A878	G798	G605



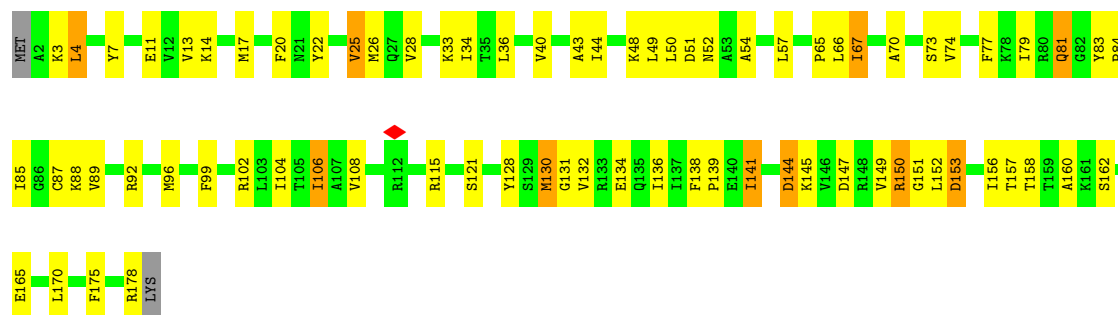
• Molecule 6: 50S ribosomal protein L3



• Molecule 7: 50S ribosomal protein L4



• Molecule 8: 50S ribosomal protein L5

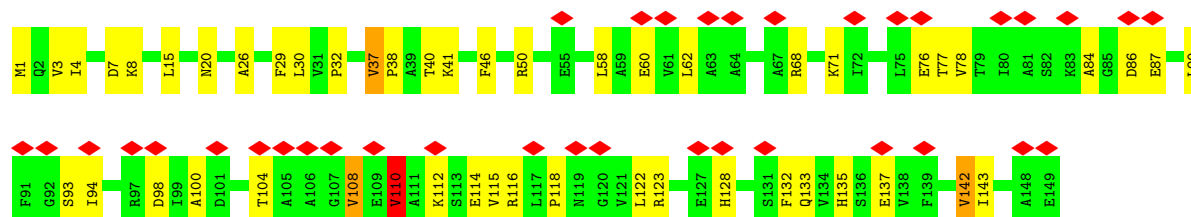


• Molecule 9: 50S ribosomal protein L6

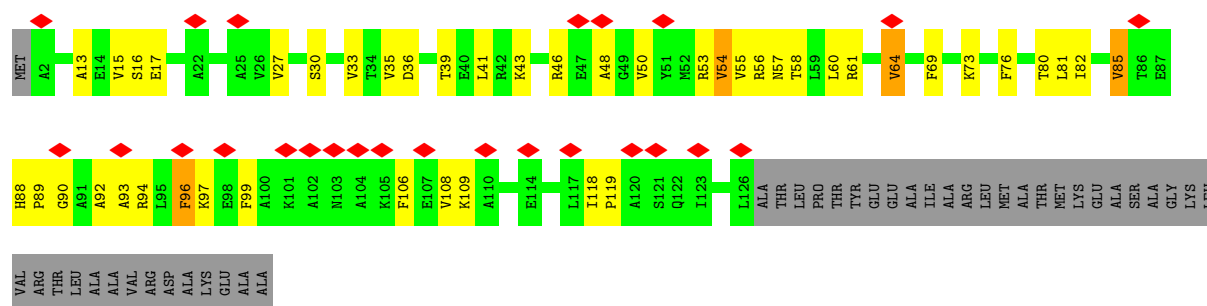




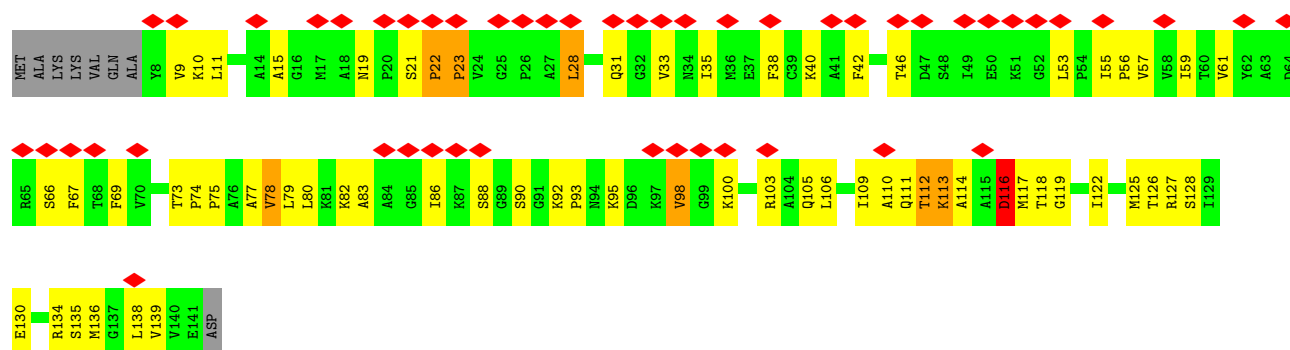
• Molecule 10: 50S ribosomal protein L9



• Molecule 11: 50S ribosomal protein L10

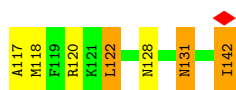


• Molecule 12: 50S ribosomal protein L11



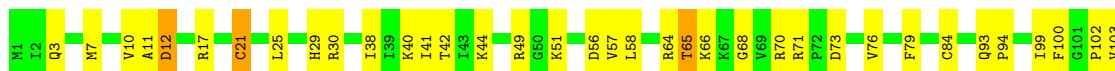
• Molecule 13: 50S ribosomal protein L13





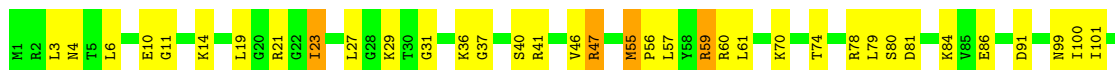
- Molecule 14: 50S ribosomal protein L14

Chain L: 67% 30%



- Molecule 15: 50S ribosomal protein L15

Chain M: 71% 26%



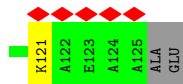
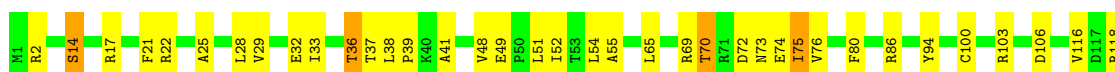
- Molecule 16: 50S ribosomal protein L16

Chain N: 68% 29%



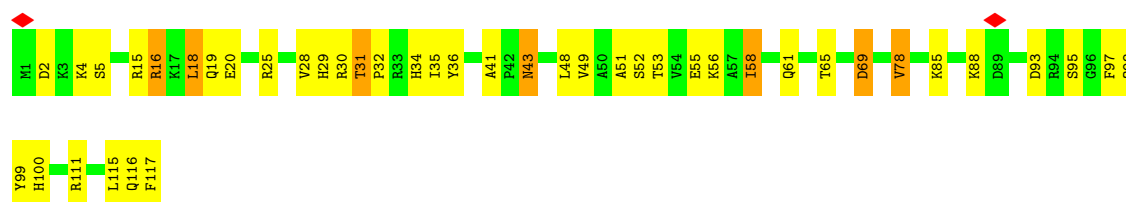
- Molecule 17: 50S ribosomal protein L17

Chain O: 69% 27%



- Molecule 18: 50S ribosomal protein L18

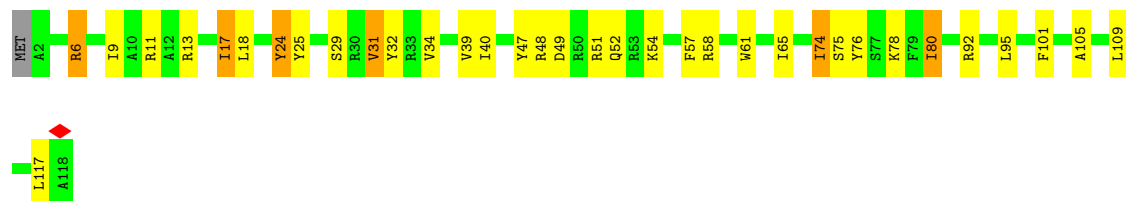
Chain P: 63% 31% 6%



- Molecule 19: 50S ribosomal protein L19



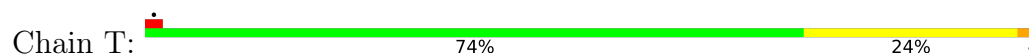
- Molecule 20: 50S ribosomal protein L20



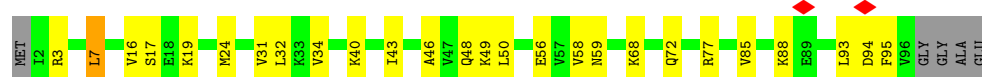
- Molecule 21: 50S ribosomal protein L21



- Molecule 22: 50S ribosomal protein L22

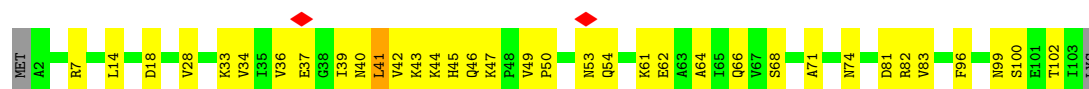


- Molecule 23: 50S ribosomal protein L23



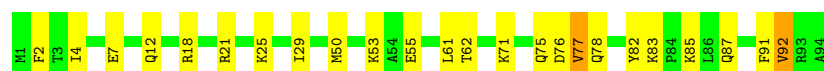
- Molecule 24: 50S ribosomal protein L24

Chain V:  64% 33% ..



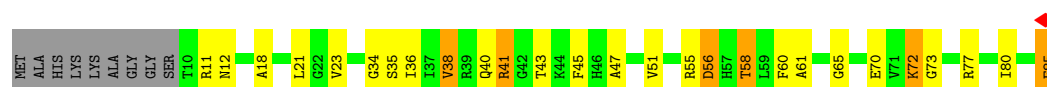
- Molecule 25: 50S ribosomal protein L25

Chain W:  74% 23% .



- Molecule 26: 50S ribosomal protein L27

Chain X:  58% 25% 7% 11%



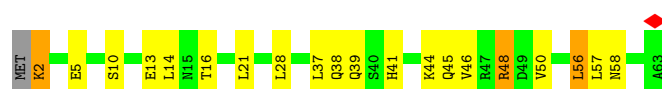
- Molecule 27: 50S ribosomal protein L28

Chain Y:  56% 41% ..



- Molecule 28: 50S ribosomal protein L29

Chain Z:  67% 27% 5% .



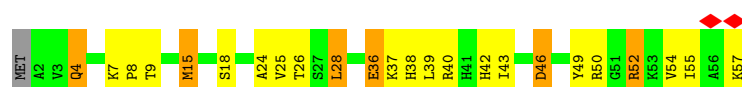
- Molecule 29: 50S ribosomal protein L30

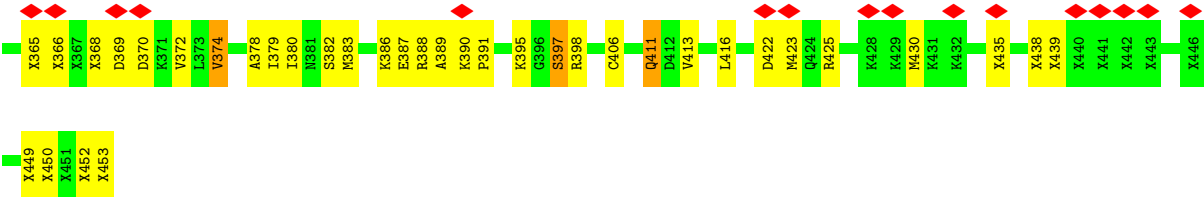
Chain a:  69% 27% ..



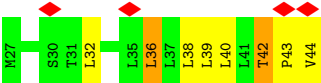
- Molecule 30: 50S ribosomal protein L32

Chain b:  56% 32% 11% .





● 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	46409	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	0.390	Depositor
Minimum map value	-0.215	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	398.88, 398.88, 398.88	wwPDB
Map dimensions	288, 288, 288	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	0.42	0/1037	0.52	0/1616
2	2	0.35	0/68	0.51	0/103
3	A	0.35	0/69329	0.48	1/108152 (0.0%)
4	B	0.27	0/2872	0.40	0/4478
5	C	0.60	0/2121	0.96	1/2852 (0.0%)
6	D	0.60	0/1586	0.95	5/2134 (0.2%)
7	E	0.57	0/1571	0.91	0/2113
8	F	0.51	1/1434 (0.1%)	0.93	5/1926 (0.3%)
9	G	0.51	0/1343	0.97	3/1816 (0.2%)
10	H	0.59	0/1121	0.89	1/1515 (0.1%)
11	I	0.72	0/958	0.95	0/1292
12	J	0.94	1/993 (0.1%)	1.13	8/1341 (0.6%)
13	K	0.58	0/1152	0.88	2/1551 (0.1%)
14	L	0.57	0/955	0.97	2/1279 (0.2%)
15	M	0.57	0/1062	0.98	3/1413 (0.2%)
16	N	0.58	0/1093	0.96	6/1460 (0.4%)
17	O	0.61	0/1006	0.95	1/1345 (0.1%)
18	P	0.50	0/910	0.93	0/1219
19	Q	0.54	0/929	0.94	2/1242 (0.2%)
20	R	0.73	0/960	0.91	1/1278 (0.1%)
21	S	0.57	0/829	0.95	0/1107
22	T	0.66	0/864	1.05	2/1156 (0.2%)
23	U	0.60	1/763 (0.1%)	0.95	0/1021
24	V	0.45	0/787	0.88	2/1051 (0.2%)
25	W	0.47	0/766	0.92	0/1025
26	X	0.59	0/587	0.98	2/776 (0.3%)
27	Y	0.61	0/635	0.92	0/848
28	Z	0.51	0/502	0.90	0/667
29	a	0.53	0/453	0.87	0/605
30	b	0.55	0/450	0.89	0/599
31	c	0.55	0/421	1.01	2/561 (0.4%)
32	d	0.66	0/380	0.95	0/498

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.62	0/513	0.97	0/676
34	f	0.60	0/303	0.99	0/397
35	i	0.61	0/672	0.90	2/883 (0.2%)
36	k	1.03	1/137 (0.7%)	1.04	1/186 (0.5%)
All	All	0.43	4/101562 (0.0%)	0.63	52/152181 (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
9	G	0	1
12	J	0	1
All	All	0	3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	J	22	PRO	CA-C	5.63	1.57	1.52
8	F	108	VAL	CA-CB	5.52	1.57	1.53
36	k	42	THR	CA-C	5.24	1.58	1.52
23	U	94	ASP	N-CA	5.13	1.52	1.46

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	G	155	GLU	CA-C-N	9.38	129.01	119.82
9	G	155	GLU	C-N-CA	9.38	129.01	119.82
12	J	116	ASP	N-CA-C	8.00	123.25	113.17
12	J	98	VAL	N-CA-C	7.57	120.32	112.83
12	J	22	PRO	N-CA-C	6.55	118.69	110.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	C	232	HIS	Peptide
9	G	47	ASP	Peptide
12	J	19	ASN	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	17	0
2	2	62	0	34	1	0
3	A	61902	0	31133	716	0
4	B	2569	0	1301	20	0
5	C	2082	0	2154	50	0
6	D	1565	0	1616	33	0
7	E	1552	0	1619	29	0
8	F	1410	0	1444	43	0
9	G	1323	0	1371	36	0
10	H	1110	0	1148	23	0
11	I	946	0	978	31	0
12	J	979	0	1028	42	0
13	K	1129	0	1162	24	0
14	L	946	0	1023	22	0
15	M	1053	0	1129	28	0
16	N	1074	0	1157	25	0
17	O	993	0	1034	26	0
18	P	900	0	935	23	0
19	Q	917	0	962	20	0
20	R	947	0	1019	26	0
21	S	816	0	839	23	0
22	T	857	0	922	16	0
23	U	756	0	817	15	0
24	V	779	0	831	21	0
25	W	753	0	780	16	0
26	X	580	0	594	16	0
27	Y	625	0	652	17	0
28	Z	501	0	531	13	0
29	a	449	0	488	9	0
30	b	444	0	458	18	0
31	c	414	0	442	5	0
32	d	377	0	418	7	0
33	e	504	0	572	15	0
34	f	302	0	340	13	0
35	i	916	0	945	48	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	412	0	0	0	0
37	B	11	0	0	0	0
37	C	2	0	0	0	0
37	D	1	0	0	0	0
37	E	1	0	0	0	0
37	P	1	0	0	0	0
37	R	1	0	0	0	0
37	b	1	0	0	0	0
38	f	1	0	0	0	0
All	All	94027	0	62511	1312	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 1312 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)
3:A:1818:U:OP2	5:C:156:ARG:NH1	2.00	0.95
3:A:1168:G:H1	3:A:1181:U:H3	1.20	0.90
3:A:63:A:H5'	35:i:449:UNK:HG1	1.54	0.89
3:A:276:U:O2	3:A:278:A:N6	2.08	0.87
3:A:1827:U:OP2	5:C:221:ARG:NH1	2.08	0.86

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	269/273 (98%)	261 (97%)	8 (3%)	0	100	100
6	D	207/209 (99%)	201 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	E	199/201 (99%)	190 (96%)	9 (4%)	0	100	100
8	F	175/179 (98%)	166 (95%)	9 (5%)	0	100	100
9	G	174/177 (98%)	171 (98%)	3 (2%)	0	100	100
10	H	147/149 (99%)	138 (94%)	8 (5%)	1 (1%)	18	51
11	I	123/165 (74%)	113 (92%)	9 (7%)	1 (1%)	16	48
12	J	132/142 (93%)	126 (96%)	6 (4%)	0	100	100
13	K	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
14	L	121/123 (98%)	117 (97%)	4 (3%)	0	100	100
15	M	142/144 (99%)	140 (99%)	2 (1%)	0	100	100
16	N	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
17	O	123/127 (97%)	118 (96%)	5 (4%)	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%)	114 (99%)	1 (1%)	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%)	90 (97%)	3 (3%)	0	100	100
24	V	100/104 (96%)	99 (99%)	1 (1%)	0	100	100
25	W	92/94 (98%)	89 (97%)	3 (3%)	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%)	55 (98%)	1 (2%)	0	100	100
30	b	54/57 (95%)	50 (93%)	4 (7%)	0	100	100
31	c	49/55 (89%)	48 (98%)	1 (2%)	0	100	100
32	d	44/46 (96%)	43 (98%)	1 (2%)	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	84/453 (18%)	84 (100%)	0	0	100	100
36	k	16/18 (89%)	12 (75%)	4 (25%)	0	100	100
All	All	3532/4045 (87%)	3415 (97%)	115 (3%)	2 (0%)	49	79

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	H	118	PRO
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%)	190 (88%)	26 (12%)	5	21
6	D	164/164 (100%)	148 (90%)	16 (10%)	7	29
7	E	165/165 (100%)	149 (90%)	16 (10%)	8	29
8	F	148/150 (99%)	127 (86%)	21 (14%)	3	17
9	G	137/138 (99%)	125 (91%)	12 (9%)	9	33
10	H	114/114 (100%)	100 (88%)	14 (12%)	4	21
11	I	95/123 (77%)	85 (90%)	10 (10%)	6	26
12	J	104/110 (94%)	88 (85%)	16 (15%)	2	15
13	K	116/116 (100%)	99 (85%)	17 (15%)	3	17
14	L	104/104 (100%)	96 (92%)	8 (8%)	12	37
15	M	103/103 (100%)	92 (89%)	11 (11%)	6	25
16	N	109/109 (100%)	99 (91%)	10 (9%)	8	31
17	O	102/103 (99%)	95 (93%)	7 (7%)	14	40
18	P	87/87 (100%)	70 (80%)	17 (20%)	1	9
19	Q	99/100 (99%)	88 (89%)	11 (11%)	6	24
20	R	89/90 (99%)	79 (89%)	10 (11%)	6	24
21	S	84/84 (100%)	73 (87%)	11 (13%)	4	20
22	T	93/93 (100%)	84 (90%)	9 (10%)	8	29
23	U	82/84 (98%)	77 (94%)	5 (6%)	17	43
24	V	83/85 (98%)	75 (90%)	8 (10%)	8	29
25	W	78/78 (100%)	72 (92%)	6 (8%)	12	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	X	57/63 (90%)	47 (82%)	10 (18%)	2	12
27	Y	67/68 (98%)	59 (88%)	8 (12%)	5	22
28	Z	54/55 (98%)	47 (87%)	7 (13%)	4	20
29	a	48/49 (98%)	45 (94%)	3 (6%)	16	42
30	b	47/48 (98%)	36 (77%)	11 (23%)	1	5
31	c	45/49 (92%)	40 (89%)	5 (11%)	6	24
32	d	38/38 (100%)	31 (82%)	7 (18%)	1	11
33	e	51/52 (98%)	47 (92%)	4 (8%)	11	36
34	f	34/34 (100%)	31 (91%)	3 (9%)	9	33
35	i	71/341 (21%)	64 (90%)	7 (10%)	7	28
36	k	17/17 (100%)	15 (88%)	2 (12%)	5	22
All	All	2901/3232 (90%)	2573 (89%)	328 (11%)	8	23

5 of 328 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	S	85	LYS
29	a	30	ARG
22	T	74	ILE
25	W	92	VAL
31	c	5	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
20	R	37	GLN
23	U	59	ASN
20	R	81	ASN
22	T	102	HIS
25	W	12	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	42/113 (37%)	13 (30%)	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%)	518 (17%)	19 (0%)
4	B	119/120 (99%)	13 (10%)	0
All	All	3041/3139 (96%)	545 (17%)	19 (0%)

5 of 545 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 19 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	A	2422	C
3	A	2602	A
3	A	2756	U
3	A	2430	A
3	A	1344	U

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.

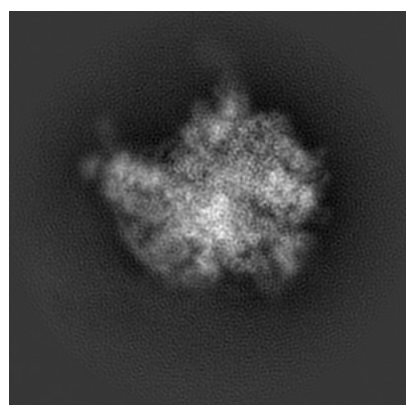
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8004. These allow visual inspection of the internal detail of the map and identification of artifacts.

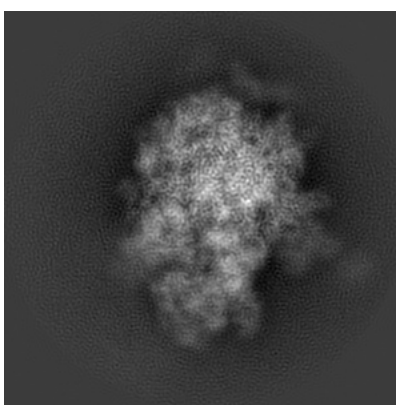
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

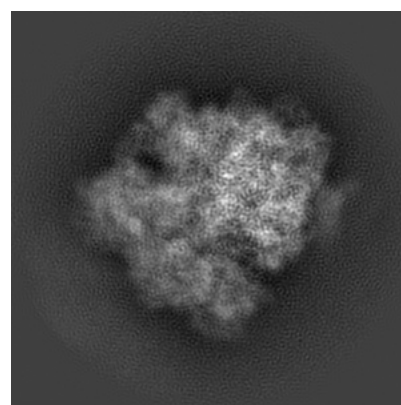
6.1.1 Primary map



X



Y

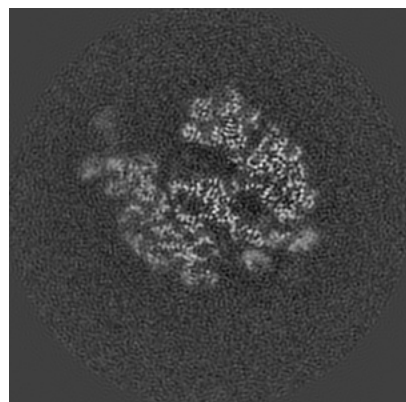


Z

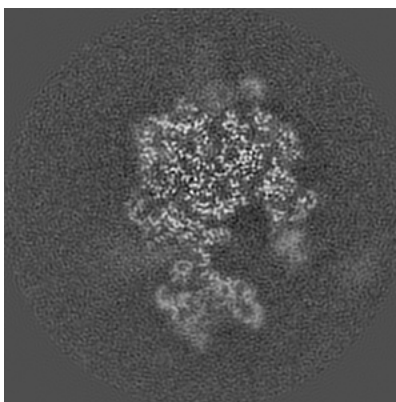
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

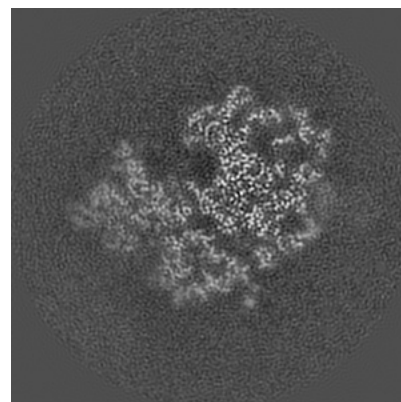
6.2.1 Primary map



X Index: 144



Y Index: 144

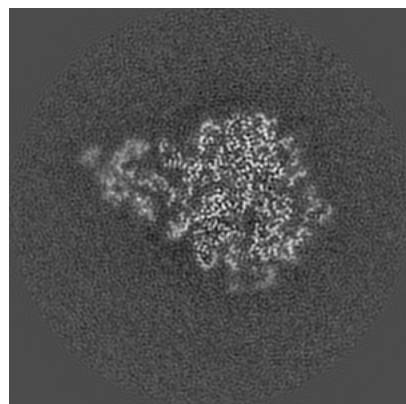


Z Index: 144

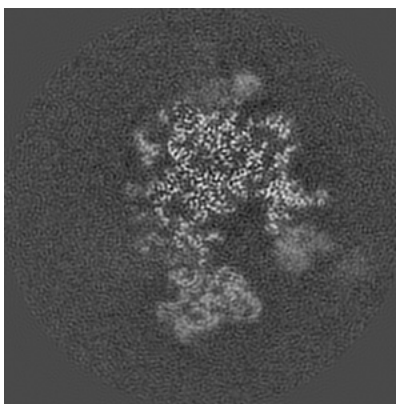
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

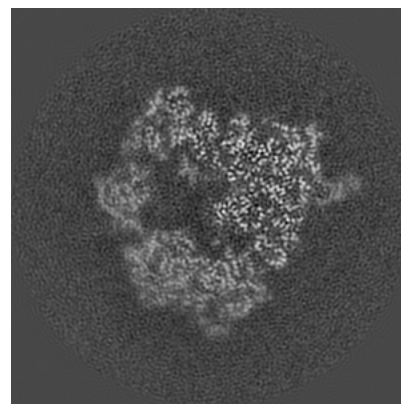
6.3.1 Primary map



X Index: 165



Y Index: 150

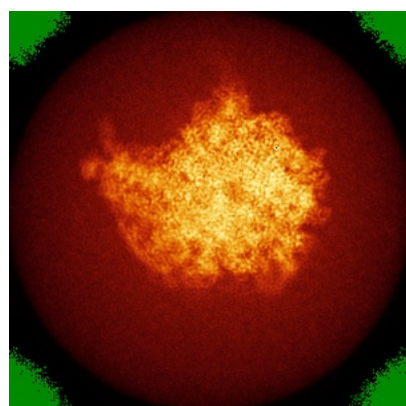


Z Index: 166

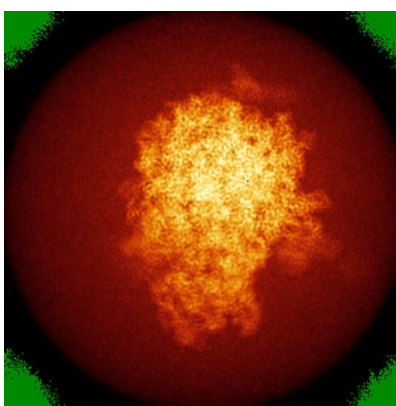
The images above show the largest variance slices of the map in three orthogonal directions.

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

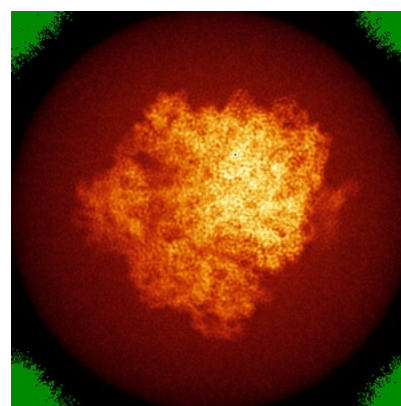
6.4.1 Primary map



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

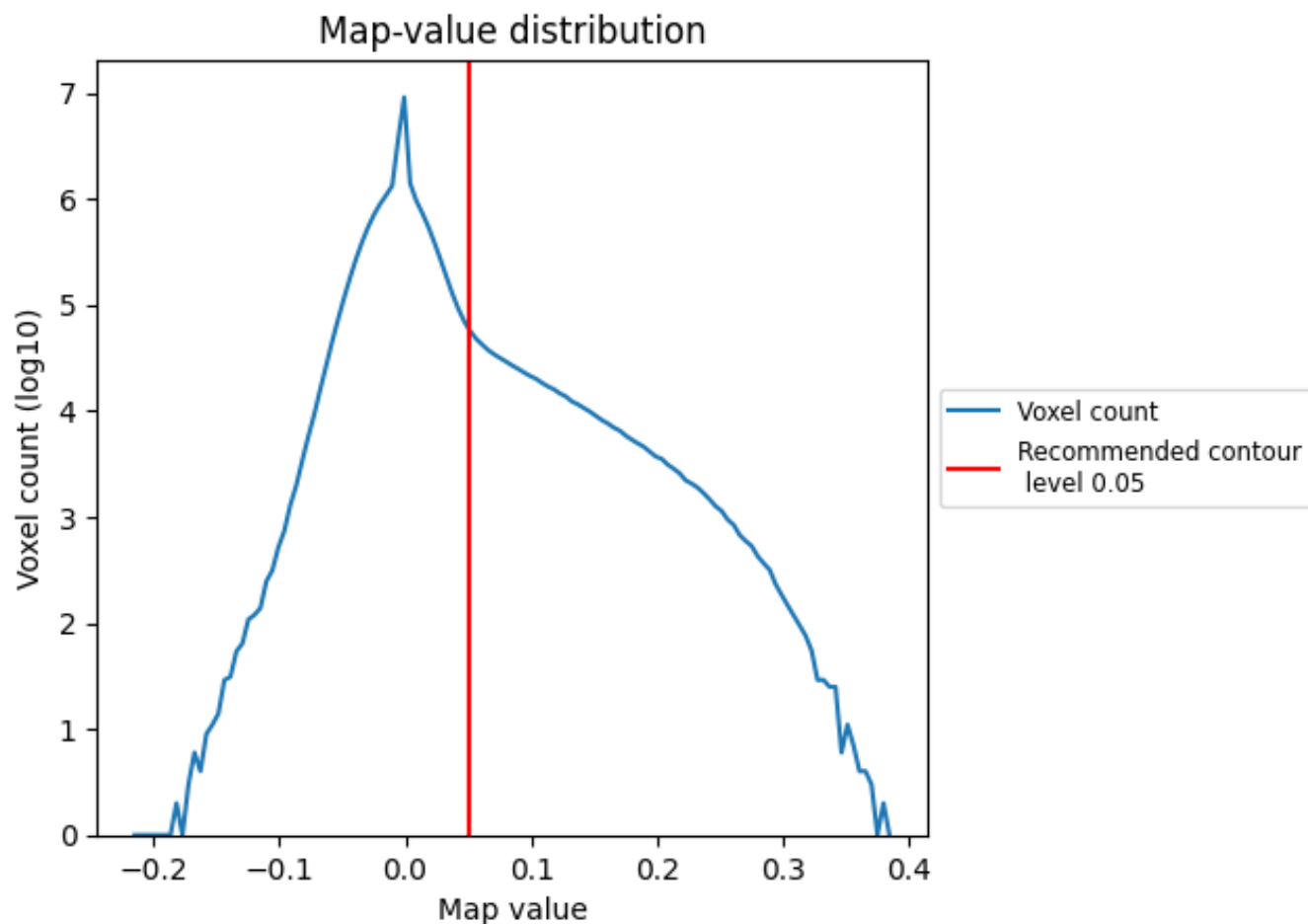
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

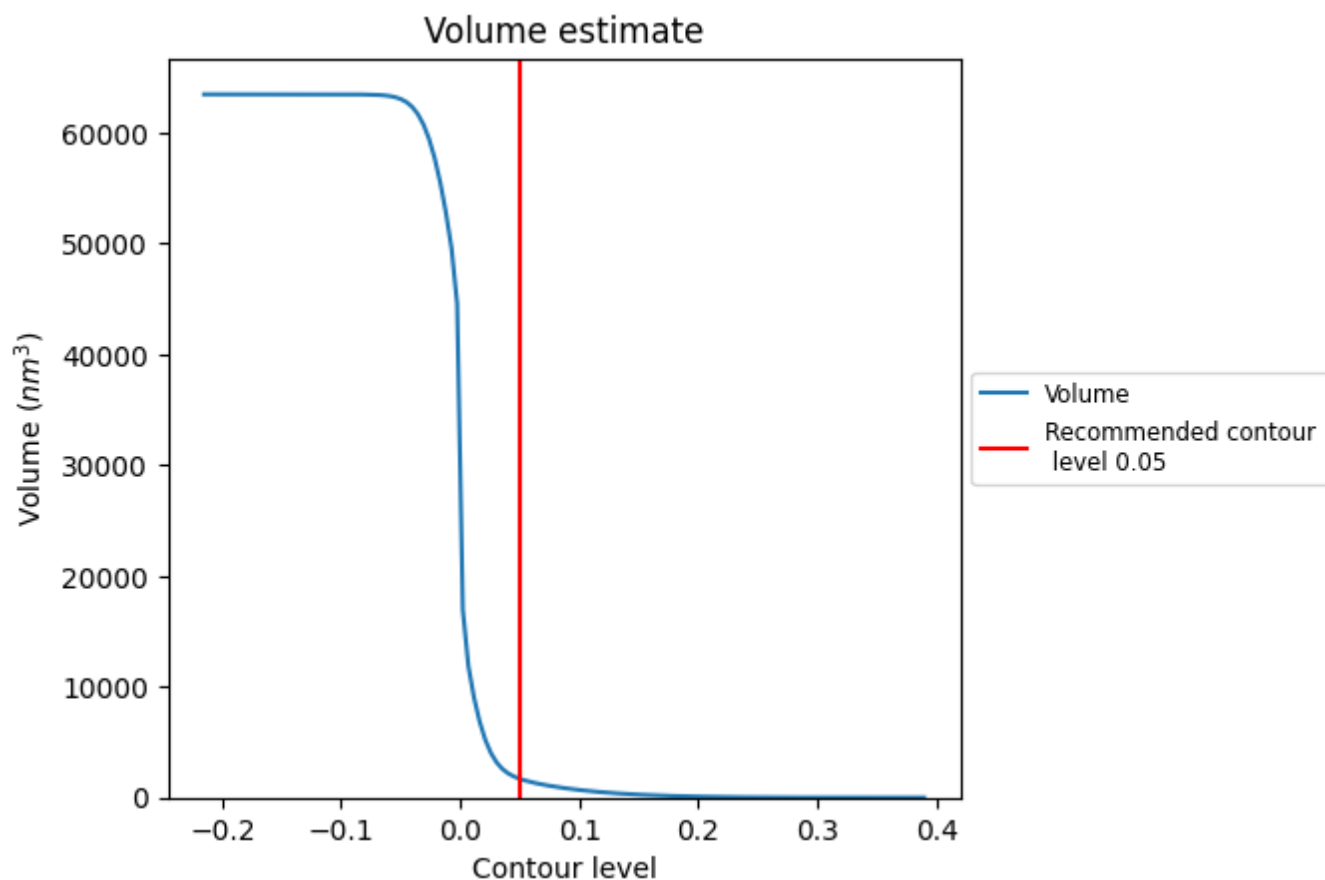
This section contains the results of statistical analysis of the map.

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.

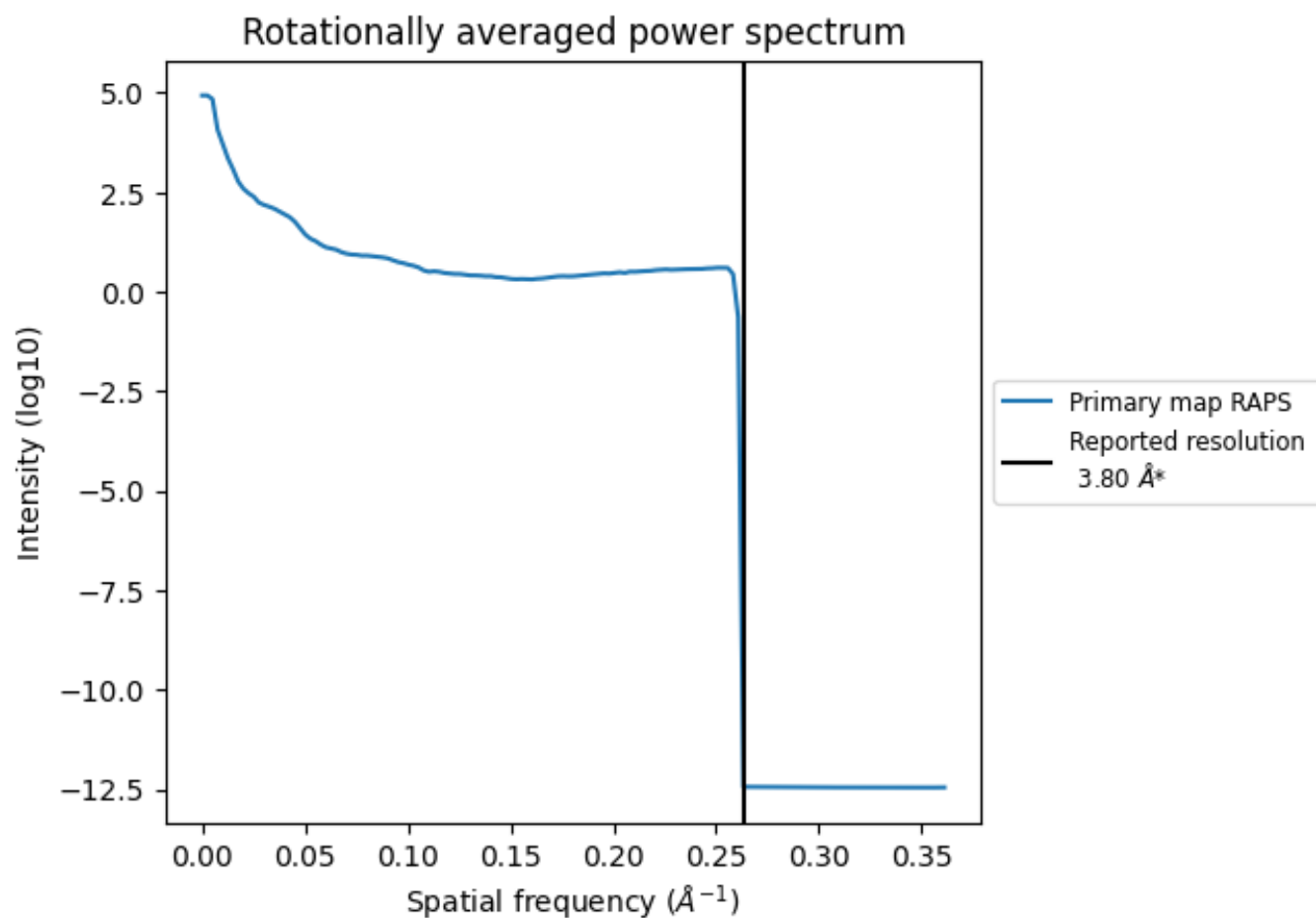
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1693 nm³; this corresponds to an approximate mass of 1530 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

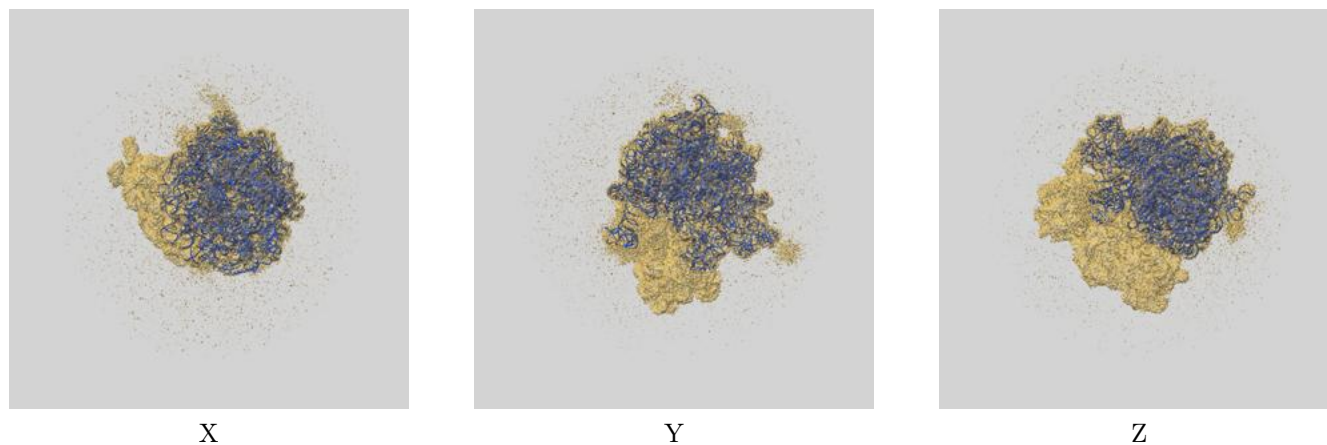
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

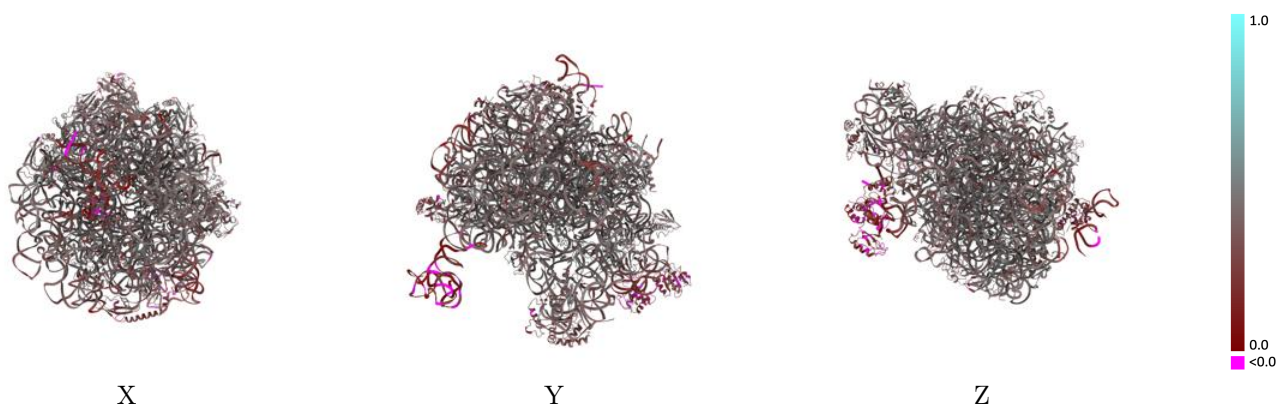
This section contains information regarding the fit between EMDB map EMD-8004 and PDB model 5GAH. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

9.1 Map-model overlay [i](#)



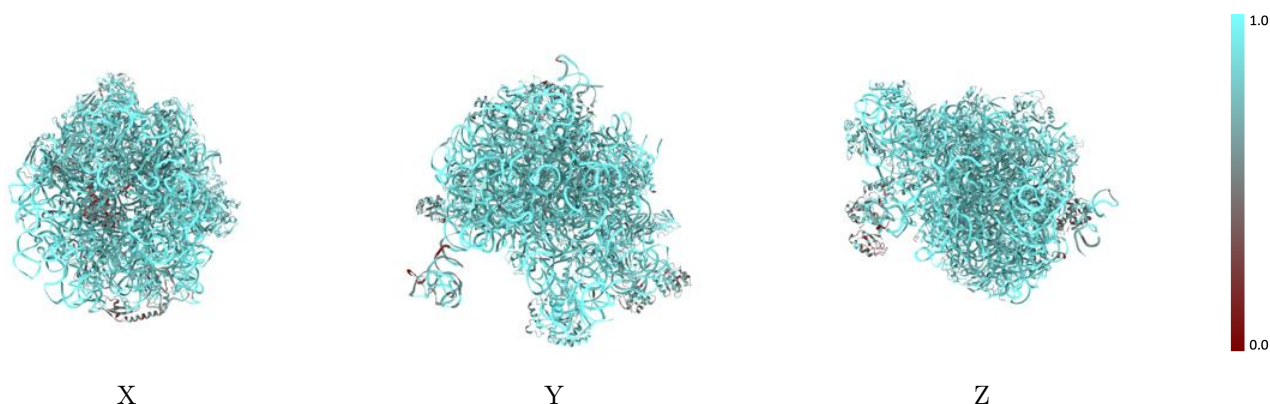
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



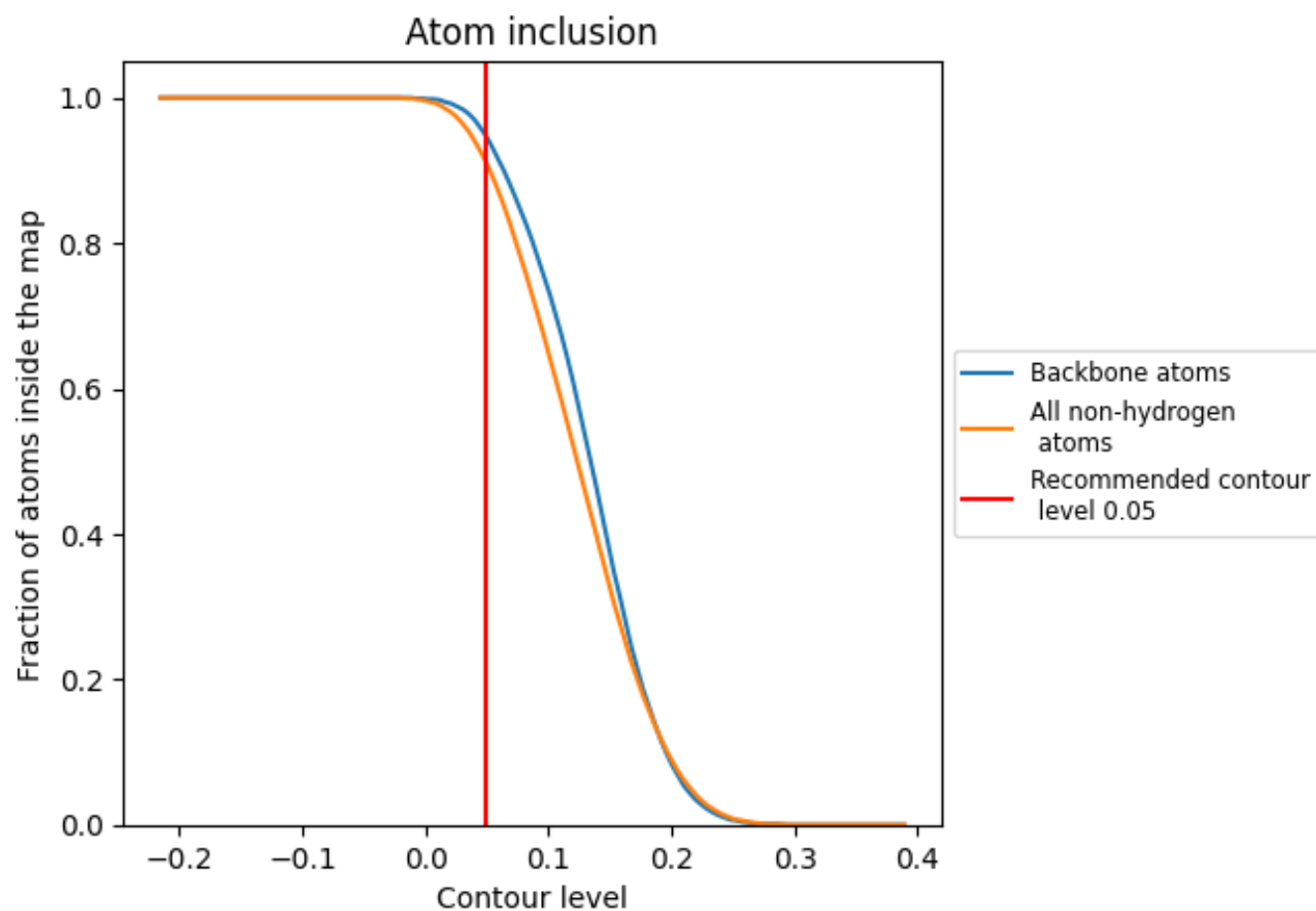
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9090	 0.3880
1	 0.7850	 0.1610
2	 0.9360	 0.4300
A	 0.9530	 0.3920
B	 0.9820	 0.3990
C	 0.8470	 0.4420
D	 0.8660	 0.4400
E	 0.8250	 0.4010
F	 0.8190	 0.3330
G	 0.8570	 0.3810
H	 0.5880	 0.2850
I	 0.6240	 0.1910
J	 0.5320	 0.1210
K	 0.8750	 0.4340
L	 0.7960	 0.4210
M	 0.8590	 0.4120
N	 0.8560	 0.4350
O	 0.8470	 0.4110
P	 0.8840	 0.4000
Q	 0.8260	 0.4050
R	 0.8740	 0.4190
S	 0.8770	 0.4320
T	 0.8130	 0.4270
U	 0.8080	 0.3860
V	 0.8360	 0.4030
W	 0.8740	 0.4250
X	 0.8650	 0.4480
Y	 0.8470	 0.4240
Z	 0.8020	 0.3690
a	 0.8700	 0.4200
b	 0.8390	 0.4110
c	 0.8180	 0.3950
d	 0.8650	 0.4380
e	 0.8720	 0.4570
f	 0.8800	 0.4360



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Chain	Atom inclusion	Q-score
i	 0.5820	 0.2390
k	 0.5330	 0.1660