



wwPDB EM Validation Summary Report ⓘ

Oct 13, 2024 – 10:00 am BST

PDB ID : 7PAT
EMDB ID : EMD-13285
Title : free 50S in untreated Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-07-30
Resolution : 9.20 Å (reported)
Based on initial model : 7OOD

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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

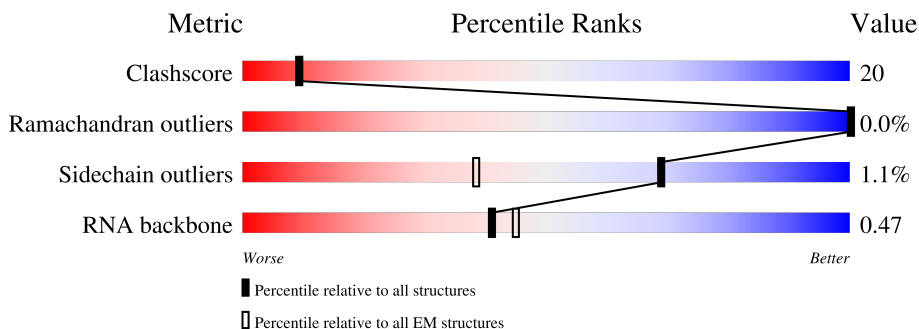
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.20 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	0	48	46% 52% .
2	1	59	54% 46%
3	2	37	51% 49%
4	a	287	99% .
5	b	287	80% 20%
6	c	212	99% .
7	d	180	17% 96% ..

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Mol	Chain	Length	Quality of chain
8	e	184	
9	f	149	
10	g	161	
11	h	137	
12	i	146	
13	j	122	
14	k	151	
15	l	139	
16	m	124	
17	n	116	
18	o	119	
19	p	127	
20	q	100	
21	r	159	
22	s	237	
23	t	111	
24	u	104	
25	v	65	
26	w	111	
27	x	97	
28	y	57	
29	z	53	
30	3	2907	
31	4	108	

2 Entry composition

There are 31 unique types of molecules in this entry. The entry contains 91293 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 protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	47	Total	C	N	O	S	0	0
			380	236	81	61	2		

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	59	Total	C	N	O	S	0	0
			477	300	99	77	1		

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	37	Total	C	N	O	S	0	0
			304	189	65	46	4		

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	a	285	Total	C	N	O	S	0	0
			2225	1385	437	397	6		

- Molecule 5 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	b	229	Total	C	N	O	S	0	0
			1762	1119	318	318	7		

- Molecule 6 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	c	210	Total	C	N	O	S	0	0
			1644	1047	297	297	3		

- Molecule 7 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	d	175	Total	C	N	O	S	0	0
			1388	893	245	246	4		

- Molecule 8 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	e	176	Total	C	N	O	S	0	0
			1396	899	247	250			

- Molecule 9 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	f	145	Total	C	N	O	S	0	0
			1160	746	204	207	3		

- Molecule 10 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	g	126	Total	C	N	O	S	0	0
			960	612	167	178	3		

- Molecule 11 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	h	128	Total	C	N	O	S	0	0
			959	616	160	177	6		

- Molecule 12 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	i	144	Total	C	N	O	S	0	0
			1164	737	213	209	5		

- Molecule 13 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	j	122	Total	C	N	O	S	0	0
			944	595	178	167	4		

- Molecule 14 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	k	148	Total	C	N	O	0	0
			1153	731	226	196		

- Molecule 15 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	l	136	Total	C	N	O	S	0	0
			1079	694	196	182	7		

- Molecule 16 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	m	119	Total	C	N	O	S	0	0
			958	609	175	171	3		

- Molecule 17 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	n	112	Total	C	N	O	S	0	0
			889	557	175	155	2		

- Molecule 18 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	o	115	Total	C	N	O	S	0	0
			938	592	180	165	1		

- Molecule 19 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	p	114	Total	C	N	O	S	0	0
			947	603	188	154	2		

- Molecule 20 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	q	99	Total	C	N	O	S	0	0
			811	525	148	134	4		

- Molecule 21 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	r	139	Total	C	N	O	S	0	0
			1068	663	207	191	7		

- Molecule 22 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	s	92	Total	C	N	O	S	0	0
			720	475	122	122	1		

- Molecule 23 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	t	111	Total	C	N	O	S	0	0
			872	550	166	153	3		

- Molecule 24 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	u	86	Total	C	N	O	S	0	0
			657	409	130	117	1		

- Molecule 25 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	v	63	Total	C	N	O	S	0	0
			513	317	108	87	1		

- Molecule 26 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	w	100	Total	C	N	O		0	0
			818	517	153	148			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	x	44	Total	C	N	O	S	0	0
			344	221	55	64	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	y	56	Total	C	N	O	S	0	0
			452	274	98	75	5		

- Molecule 29 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

- Molecule 30 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

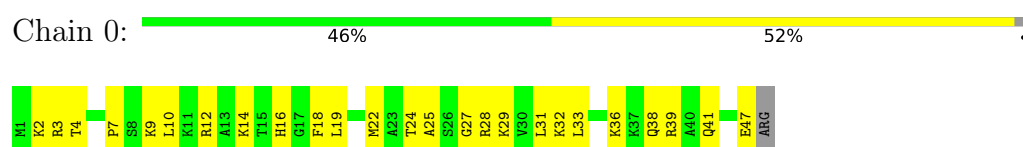
- Molecule 31 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

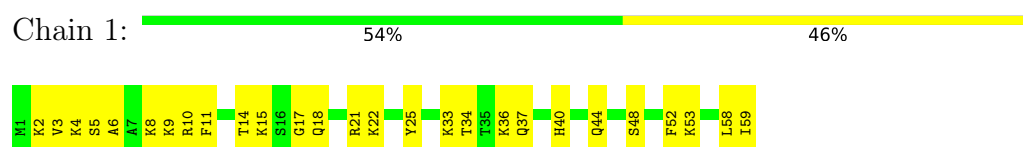
3 Residue-property plots [i](#)

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: 50S ribosomal protein L34



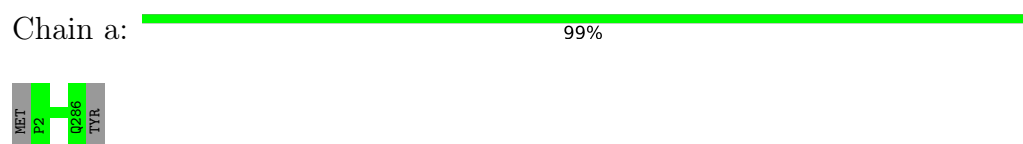
- Molecule 2: 50S ribosomal protein L35



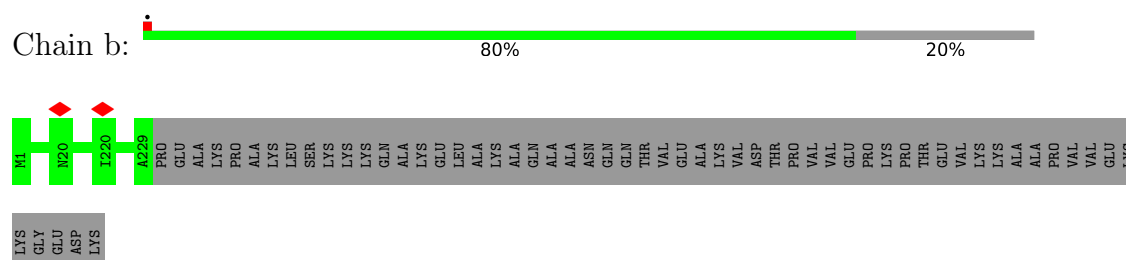
- Molecule 3: 50S ribosomal protein L36



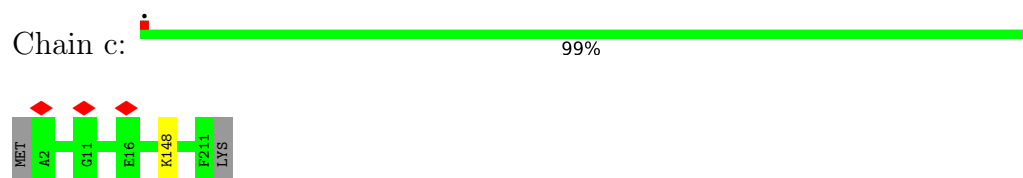
- Molecule 4: 50S ribosomal protein L2



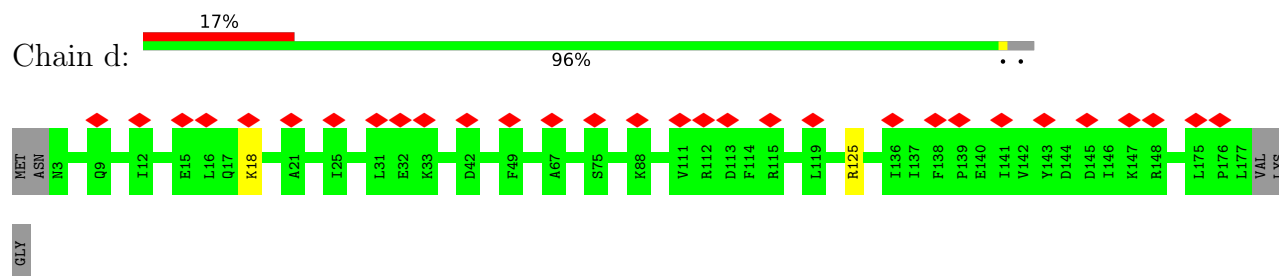
- Molecule 5: 50S ribosomal protein L3



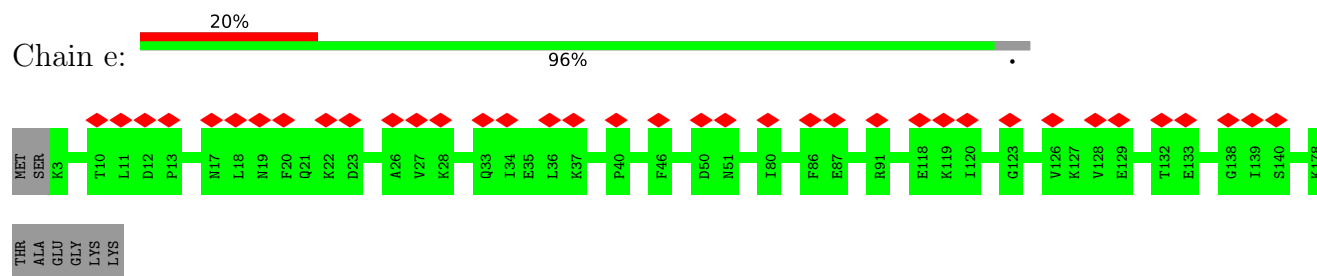
- Molecule 6: 50S ribosomal protein L4



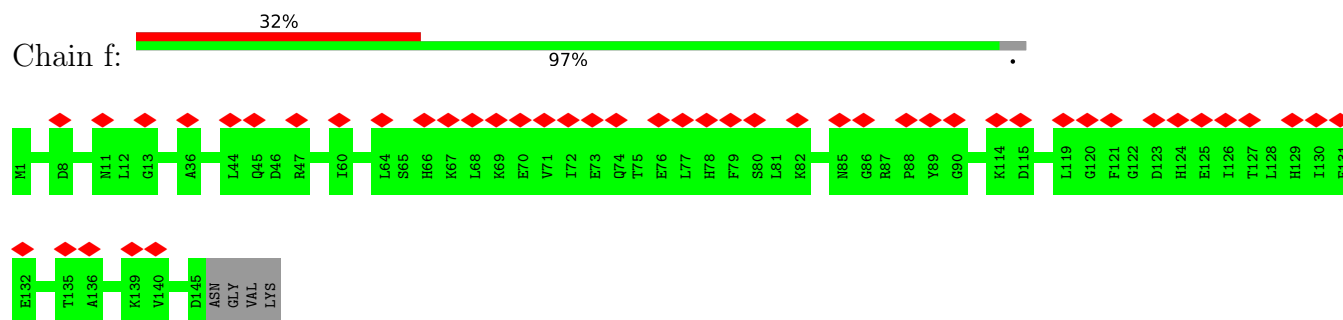
- Molecule 7: 50S ribosomal protein L5



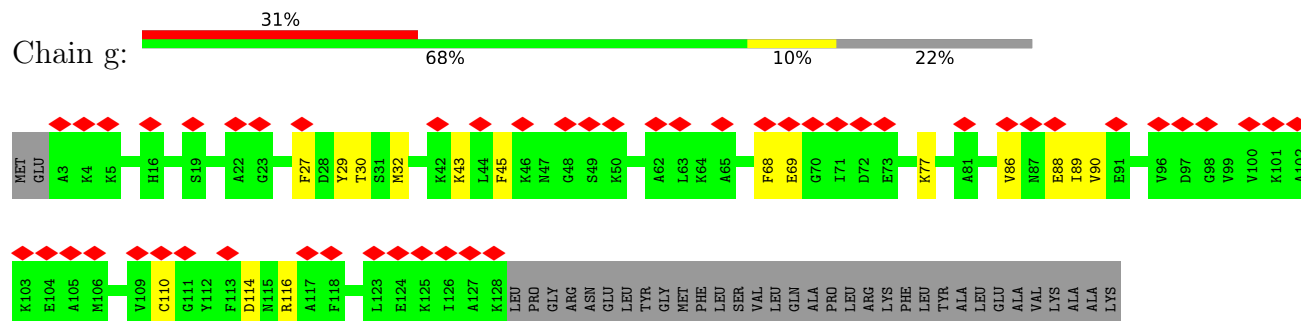
- Molecule 8: 50S ribosomal protein L6



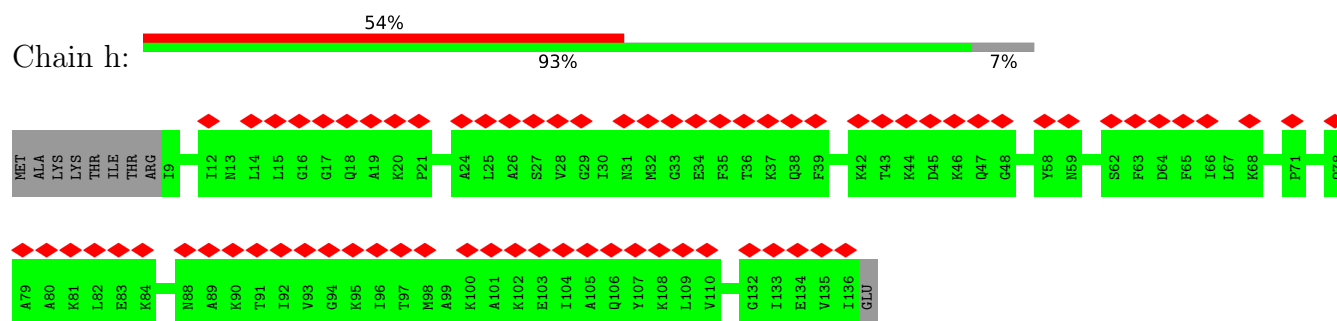
- Molecule 9: 50S ribosomal protein L9



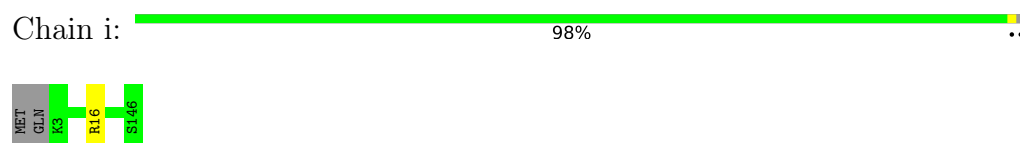
- Molecule 10: 50S ribosomal protein L10



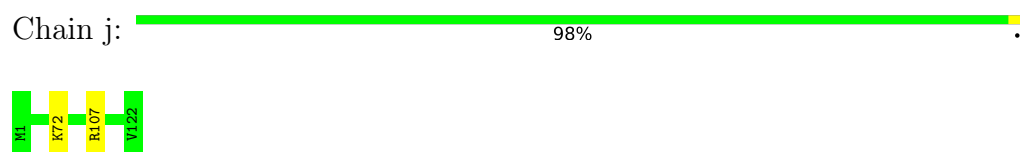
- Molecule 11: 50S ribosomal protein L11



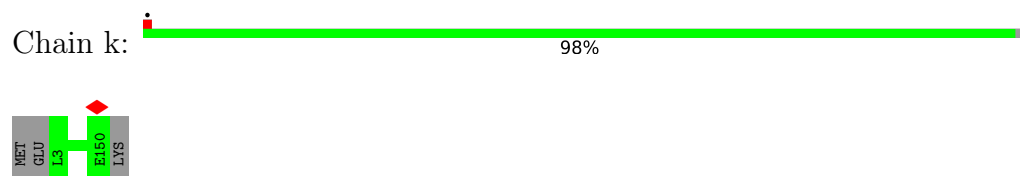
- Molecule 12: 50S ribosomal protein L13



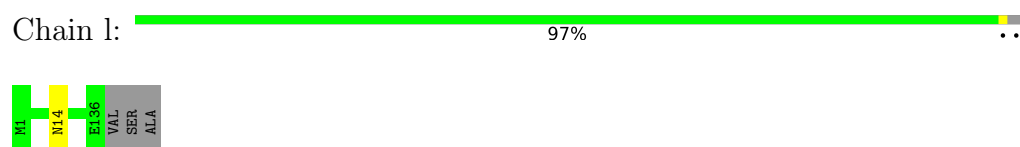
- Molecule 13: 50S ribosomal protein L14



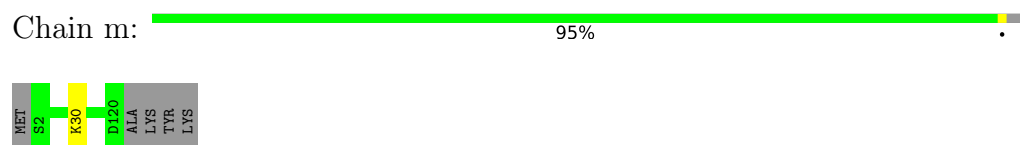
- Molecule 14: 50S ribosomal protein L15



- Molecule 15: 50S ribosomal protein L16

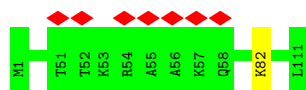


- Molecule 16: 50S ribosomal protein L17

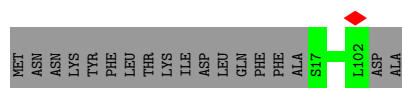
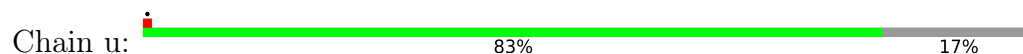


- Molecule 17: 50S ribosomal protein L18

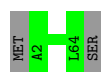




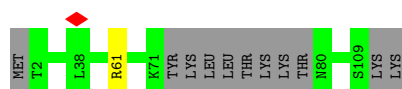
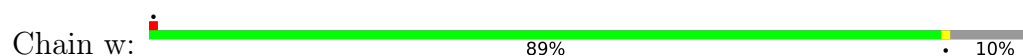
- Molecule 24: 50S ribosomal protein L27



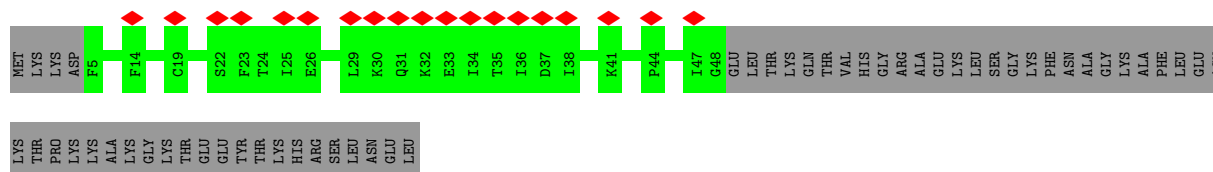
- Molecule 25: 50S ribosomal protein L28



- Molecule 26: 50S ribosomal protein L29



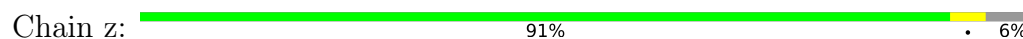
- Molecule 27: 50S ribosomal protein L31



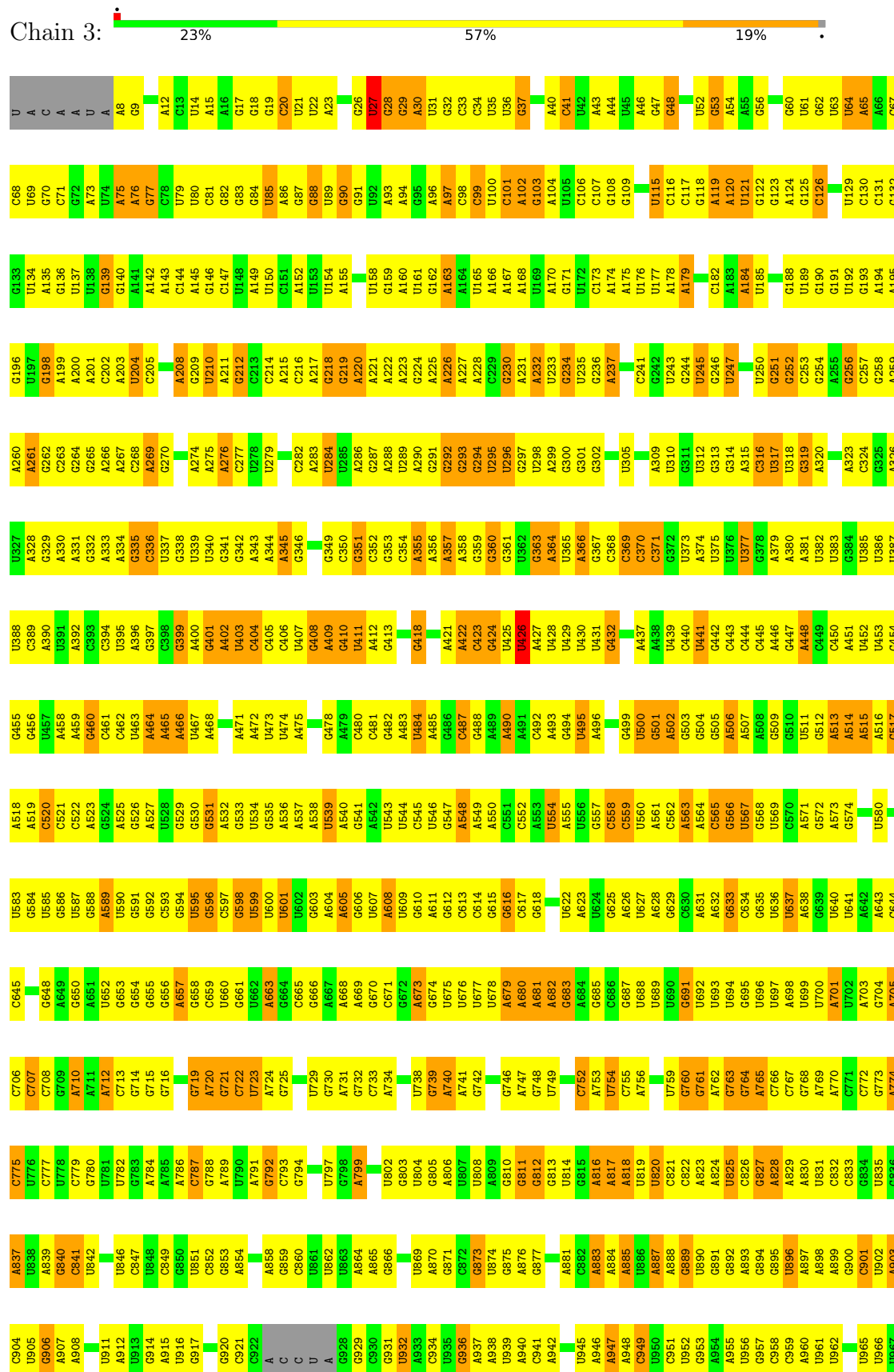
- Molecule 28: 50S ribosomal protein L32



- Molecule 29: 50S ribosomal protein L33 1

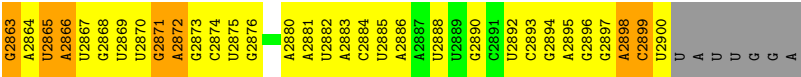


● Molecule 30: 23S ribosomal RNA

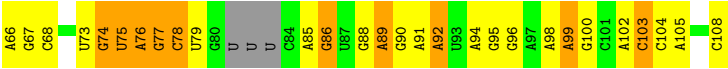
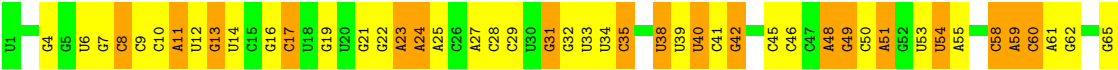


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G1870	U1743	C1808	G1837	G1905	G1485	A1420	U1357	G1295	U1235	A1168	U1101	U1035	U971
U1871	U1744	C1809	G1838	G1906	U1486	A1421	U1358	G1296	A1236	A1169	A1036	A1036	
A1872	U1745	C1812	G1839	G1907	U1487	A1422	U1359	G1297	G1237	G1170	G1103	A1037	C974
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G1885	U1748	C1815	G1842	G1910	G1490	U1428	C1362	G1300	U1240	G1174	C1041		A977
G1886	A1749	C1816	G1843	G1911	G1491	A1431	C1363	G1301	U1241	C1175	C1042		
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A1892	U1754	C1821	G1848	G1916	U1496	A1436	U1368	G1306	U1246		A1047		A985
C1893	U1755	C1822	G1849	G1917	A1497	C1437	U1369	G1307	C1247	U1182	A1048		A986
U1894	G1756	C1823	G1850	G1918		A1500	U1370	A1308	C1248	A1183	U1049		
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A1896	G1758	C1825	G1852	G1920	G	U1502	C1373	U1310	G1251	U1185			
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A1908	A1766	C1833	G1860	G1928	U1509	A1447	A1382	U1318	C1259	U1193			
C1909	U1767	C1834	G1861	G1929	U1510	U1448	U1383	G1319	A1259	U1194			
G1910	G1768	C1835	G1862	G1930	A1511	U1449	G1384	C1320	U1260	A1195			
G1911	C1769	C1836	G1863	G1931	U1512	G1450	C1385	C1321	U1261	U1196			
C1912	A1770	C1837	G1864	G1932	G1574	A1451	U1386	A1322	G1262	G1197			C1001
G1913	C1771	C1838	G1865	G1933	G1575	U1514	G1387	A1323	G1263	G1198			A1002
G1914	G1772	C1839	G1866	G1934	U1576	A1515	U1388	A1324	U1264	A1199			U1003
C1915		C1840	G1867	G1935	A1577		G1389	A1325	G1265	U1200			U1004
G1916	G1776	C1841	G1868	G1936	U1578	C1518	U1390	C1326	G1266				U1005
G1917	U1777	C1842	G1869	G1937	G1579	A1519	C1391	G1327	A1267	U1206			U1006
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A1920		C1845	G1872	G1940	U1582	U1522	U1394		A1271	U1209			A1009
C1921	U1780	C1846	G1873	G1941	G1583	C1523	A1395	U1334	A1272	U1210			G1075
U1922		C1847	G1874	G1942	U1584	C1524	A1396	A1335	U1273	A1211			G1077
A1923	G1783	C1848	G1875	G1943	U1585	U1525	C1398	A1336	A1274	U1212			A1011
	U1784	C1849	G1876	G1944	U1586	U1526	G1399	G1337	C1275	C1213			G1012
A1926	U1785	C1850	G1877	G1945	U1587	A1662	U1400	G1338	A1276	G1145			G1015
C1927	U1786	C1851	G1878	G1946	U1588	U1466	A1401	G1339	A1277	U1214			A1016
G1928	A1787	C1852	G1879	G1947	U1589	U1467	G1402	U1340	G1278	G1215			A1017
U1929	C1788	C1853	G1880	G1948	U1590	U1468	G1403	U1341	U1279	U1216			A1018
G1930	U1789	C1854	G1881	G1949	C1591	C1469	C1404	C1342	A1281	G1217			G1084
C1931	U1790	C1855	G1882	G1950	U1592	C1470	G1405	C1343	G1280	G1218			A1019
C1932	A1791	C1856	G1883	G1951	U1593	A1471	G1406	G1344	G1282	U1219			G1086
C1933	U1792	C1857	G1884	G1952	U1594	C1472	U1407	U1345	A1283	G1220			C1022
A1934		C1858	G1885	G1953		C1473	U1408	G1346	A1284	G1221			G1023
U1935	G1793	C1859	G1886	G1954	U1597	C1474	G1409	U1347	U1285				A1024
G1936	A1799	C1860	G1887	G1955	U1598	C1475	A1410	C1348	G1286	G1226			G1091
U1937	U1798	C1861	G1888	G1956	U1599	U1476		C1349	C1287	C1158			A1092
U1938	C1732	C1862	G1889	G1957	U1600	A1477		A1350	C1288	C1159			U1093
A1939	U1733	C1863	G1890	G1958	A1603	U1478	A1413	G1351	G1289	G1160			C1027
G1940	G1733	C1864	G1891	G1959	A1604	U1479	C1414	G1352	G1290	A1161			A1029
U1941	U1800	C1865	G1892	G1960	U1605	A1480	A1415	G1353	C1291	U1229			U1096
C1942	A1803	C1866	G1893	G1961	U1606	U1543	G1416	G1354	C1292	G1230			G1097
A1943	U1805	C1867	G1894	G1962		U1482	G1417	U1354	A1292	U1232			U1030





● Molecule 31: 5S ribosomal RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	15954	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 ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.419	Depositor
Minimum map value	-0.423	Depositor
Average map value	0.016	Depositor
Map value standard deviation	0.100	Depositor
Recommended contour level	0.41	Depositor
Map size (Å)	480.00003, 480.00003, 480.00003	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.4, 2.4, 2.4	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.23	0/383	0.42	0/504
2	1	0.23	0/484	0.42	0/637
3	2	0.21	0/306	0.45	0/401
4	a	0.24	0/2267	0.46	0/3044
5	b	0.25	0/1795	0.47	0/2412
6	c	0.24	0/1671	0.43	0/2246
7	d	0.25	0/1409	0.48	0/1894
8	e	0.25	0/1420	0.48	0/1912
9	f	0.24	0/1183	0.46	0/1587
10	g	0.38	0/969	0.57	0/1295
11	h	0.25	0/968	0.47	0/1298
12	i	0.23	0/1186	0.43	0/1592
13	j	0.24	0/953	0.47	0/1275
14	k	0.24	0/1170	0.46	0/1559
15	l	0.25	0/1104	0.46	0/1481
16	m	0.23	0/973	0.43	0/1309
17	n	0.23	0/897	0.45	0/1198
18	o	0.25	0/948	0.49	0/1262
19	p	0.24	0/961	0.40	0/1278
20	q	0.25	0/828	0.49	0/1111
21	r	0.24	0/1077	0.43	0/1441
22	s	0.24	0/732	0.47	0/988
23	t	0.23	0/879	0.44	0/1165
24	u	0.25	0/665	0.49	0/884
25	v	0.22	0/519	0.50	0/695
26	w	0.23	0/826	0.43	0/1104
27	x	0.26	0/353	0.42	0/474
28	y	0.30	0/457	0.55	0/601
29	z	0.23	0/412	0.43	0/547
30	3	0.20	0/69073	0.81	56/107710 (0.1%)
31	4	0.20	0/2505	0.82	3/3902 (0.1%)
All	All	0.21	0/99373	0.74	59/148806 (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
15	1	0	1

There are no bond length outliers.

The worst 5 of 59 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	3	370	C	N3-C2-O2	-10.97	114.22	121.90
30	3	559	C	N3-C2-O2	-9.31	115.38	121.90
30	3	99	C	N3-C2-O2	-9.23	115.44	121.90
30	3	371	C	N3-C2-O2	-8.74	115.78	121.90
30	3	1159	C	N3-C2-O2	-8.15	116.19	121.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	1	14	ASN	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	380	0	429	24	0
2	1	477	0	530	21	0
3	2	304	0	350	19	0
4	a	2225	0	2301	0	0
5	b	1762	0	1808	0	0
6	c	1644	0	1731	0	0
7	d	1388	0	1469	0	0
8	e	1396	0	1481	0	0
9	f	1160	0	1172	0	0
10	g	960	0	1014	0	0
11	h	959	0	1039	0	0
12	i	1164	0	1192	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	j	944	0	1019	0	0
14	k	1153	0	1256	0	0
15	l	1079	0	1134	0	0
16	m	958	0	1011	0	0
17	n	889	0	952	0	0
18	o	938	0	1008	0	0
19	p	947	0	1028	0	0
20	q	811	0	858	0	0
21	r	1068	0	1150	0	0
22	s	720	0	803	0	0
23	t	872	0	972	0	0
24	u	657	0	695	0	0
25	v	513	0	560	0	0
26	w	818	0	870	0	0
27	x	344	0	333	0	0
28	y	452	0	472	0	0
29	z	408	0	440	0	0
30	3	61664	0	30954	1849	0
31	4	2239	0	1137	51	0
All	All	91293	0	61168	1930	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 20.

The worst 5 of 1930 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)
30:3:535:G:C2	30:3:540:A:N6	2.14	1.15
30:3:341:G:N2	30:3:364:A:H61	1.44	1.13
30:3:341:G:H21	30:3:364:A:N6	1.51	1.08
30:3:1807:C:H42	30:3:1824:G:N2	1.49	1.07
30:3:2108:C:N4	30:3:2109:A:N6	2.01	1.06

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	45/48 (94%)	45 (100%)	0	0	100	100
2	1	57/59 (97%)	54 (95%)	3 (5%)	0	100	100
3	2	35/37 (95%)	35 (100%)	0	0	100	100
4	a	283/287 (99%)	260 (92%)	23 (8%)	0	100	100
5	b	227/287 (79%)	213 (94%)	14 (6%)	0	100	100
6	c	208/212 (98%)	199 (96%)	9 (4%)	0	100	100
7	d	173/180 (96%)	161 (93%)	12 (7%)	0	100	100
8	e	174/184 (95%)	164 (94%)	10 (6%)	0	100	100
9	f	143/149 (96%)	130 (91%)	13 (9%)	0	100	100
10	g	124/161 (77%)	114 (92%)	9 (7%)	1 (1%)	16	55
11	h	126/137 (92%)	121 (96%)	5 (4%)	0	100	100
12	i	142/146 (97%)	130 (92%)	12 (8%)	0	100	100
13	j	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
14	k	146/151 (97%)	137 (94%)	9 (6%)	0	100	100
15	l	134/139 (96%)	122 (91%)	12 (9%)	0	100	100
16	m	117/124 (94%)	112 (96%)	5 (4%)	0	100	100
17	n	108/116 (93%)	102 (94%)	6 (6%)	0	100	100
18	o	113/119 (95%)	104 (92%)	9 (8%)	0	100	100
19	p	112/127 (88%)	109 (97%)	3 (3%)	0	100	100
20	q	97/100 (97%)	83 (86%)	14 (14%)	0	100	100
21	r	137/159 (86%)	128 (93%)	9 (7%)	0	100	100
22	s	90/237 (38%)	85 (94%)	5 (6%)	0	100	100
23	t	109/111 (98%)	102 (94%)	7 (6%)	0	100	100
24	u	84/104 (81%)	77 (92%)	7 (8%)	0	100	100
25	v	61/65 (94%)	58 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	w	96/111 (86%)	88 (92%)	8 (8%)	0	100	100
27	x	42/97 (43%)	38 (90%)	4 (10%)	0	100	100
28	y	54/57 (95%)	50 (93%)	4 (7%)	0	100	100
29	z	48/53 (91%)	45 (94%)	3 (6%)	0	100	100
All	All	3405/3879 (88%)	3183 (94%)	221 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	g	32	MET

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	
1	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
4	a	241/243 (99%)	241 (100%)	0	100	100
5	b	186/233 (80%)	186 (100%)	0	100	100
6	c	182/184 (99%)	181 (100%)	1 (0%)	86	89
7	d	150/154 (97%)	148 (99%)	2 (1%)	65	77
8	e	153/159 (96%)	153 (100%)	0	100	100
9	f	123/134 (92%)	123 (100%)	0	100	100
10	g	101/129 (78%)	86 (85%)	15 (15%)	2	11
11	h	102/110 (93%)	102 (100%)	0	100	100
12	i	126/128 (98%)	125 (99%)	1 (1%)	79	85
13	j	103/103 (100%)	101 (98%)	2 (2%)	52	69
14	k	123/126 (98%)	123 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	l	113/115 (98%)	113 (100%)	0	100	100
16	m	105/109 (96%)	104 (99%)	1 (1%)	73	82
17	n	96/99 (97%)	95 (99%)	1 (1%)	73	82
18	o	101/105 (96%)	101 (100%)	0	100	100
19	p	100/108 (93%)	100 (100%)	0	100	100
20	q	90/91 (99%)	89 (99%)	1 (1%)	70	80
21	r	116/132 (88%)	115 (99%)	1 (1%)	75	83
22	s	82/208 (39%)	82 (100%)	0	100	100
23	t	96/96 (100%)	95 (99%)	1 (1%)	73	82
24	u	69/85 (81%)	69 (100%)	0	100	100
25	v	58/60 (97%)	58 (100%)	0	100	100
26	w	87/98 (89%)	86 (99%)	1 (1%)	70	80
27	x	41/86 (48%)	41 (100%)	0	100	100
28	y	48/49 (98%)	44 (92%)	4 (8%)	9	27
29	z	47/50 (94%)	45 (96%)	2 (4%)	25	46
All	All	2965/3321 (89%)	2932 (99%)	33 (1%)	69	80

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	y	47	MET
28	y	51	LEU
29	z	26	LYS
10	g	88	GLU
10	g	86	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
9	f	100	GLN
16	m	59	ASN
25	v	34	GLN
23	t	32	GLN
24	u	54	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	3	2875/2907 (98%)	844 (29%)	34 (1%)
31	4	103/108 (95%)	42 (40%)	3 (2%)
All	All	2978/3015 (98%)	886 (29%)	37 (1%)

5 of 886 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
30	3	12	A
30	3	14	U
30	3	15	A
30	3	20	C
30	3	27	U

5 of 37 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
30	3	2506	C
31	4	54	U
30	3	2668	A
30	3	2862	U
30	3	1048	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

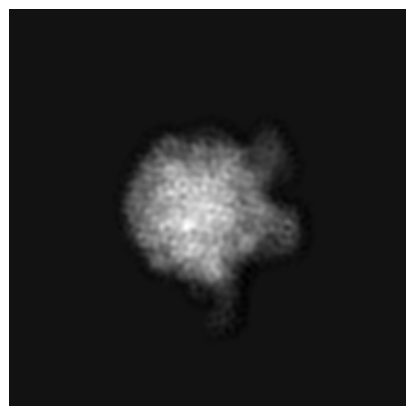
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13285. These allow visual inspection of the internal detail of the map and identification of artifacts.

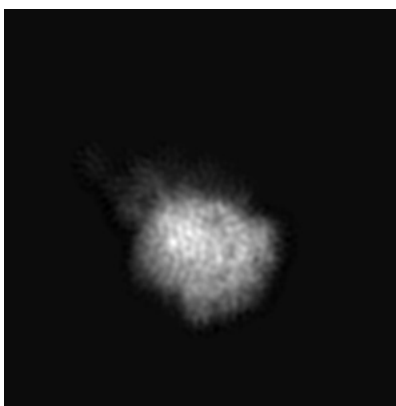
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

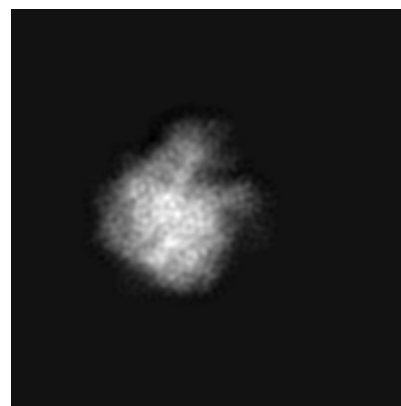
6.1.1 Primary map



X

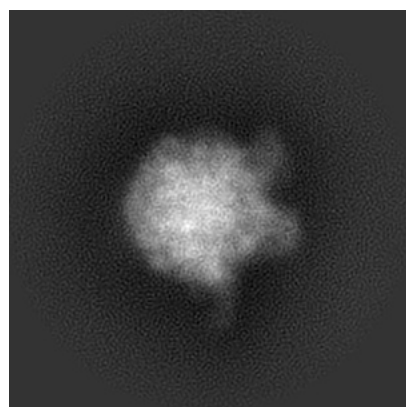


Y

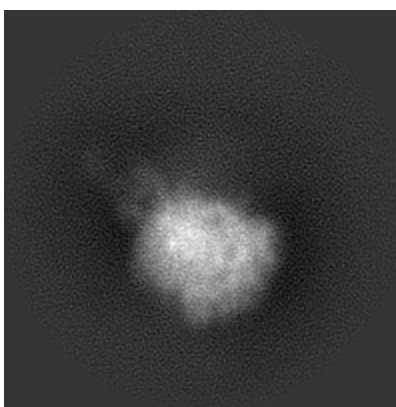


Z

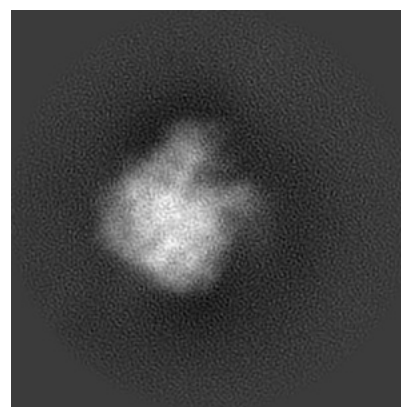
6.1.2 Raw map



X



Y

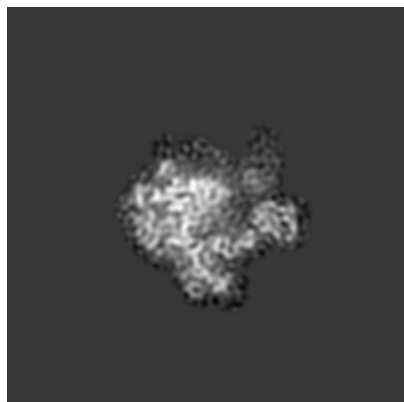


Z

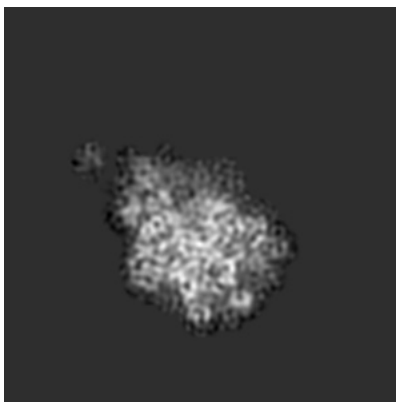
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

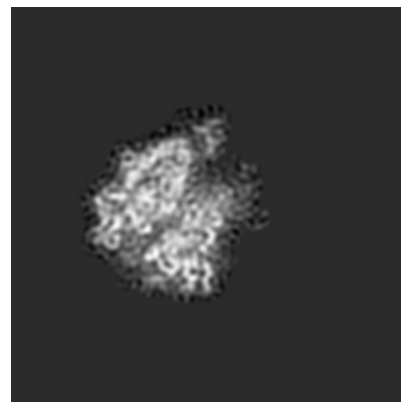
6.2.1 Primary map



X Index: 100

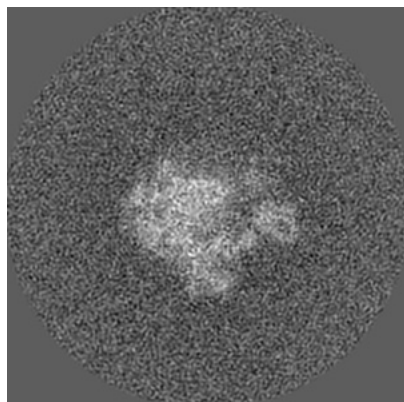


Y Index: 100

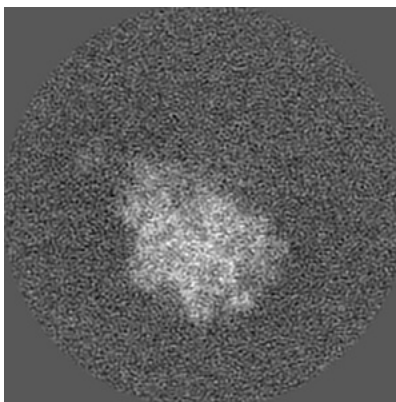


Z Index: 100

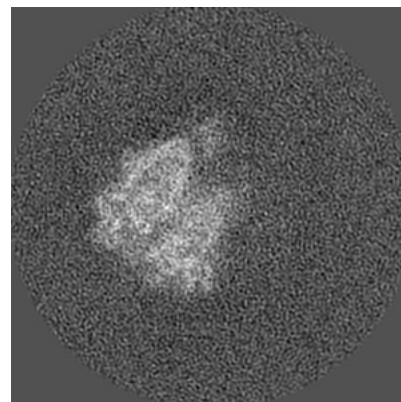
6.2.2 Raw map



X Index: 100



Y Index: 100

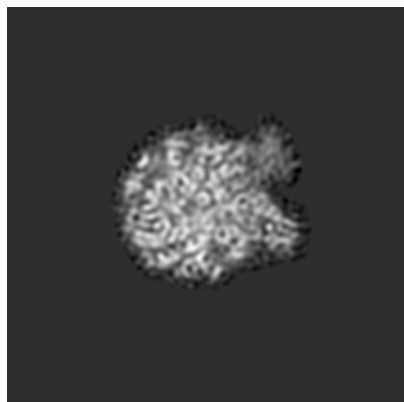


Z Index: 100

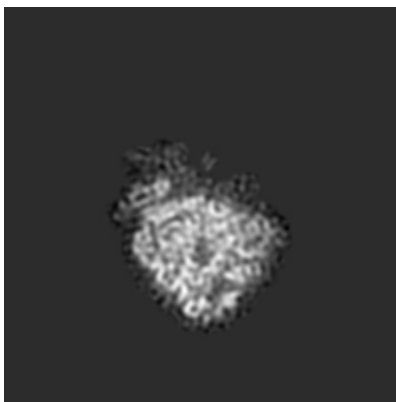
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

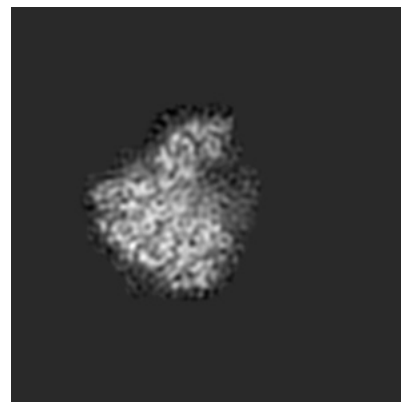
6.3.1 Primary map



X Index: 83

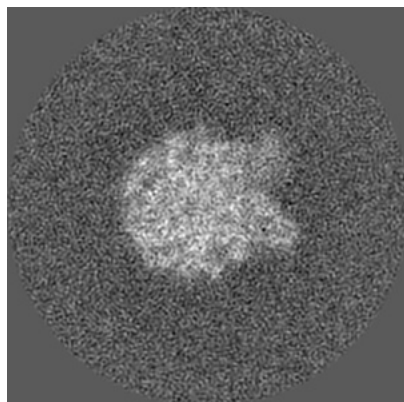


Y Index: 89

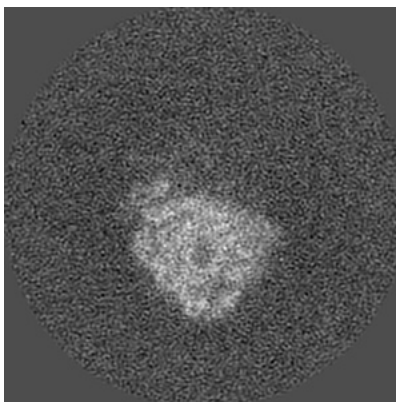


Z Index: 94

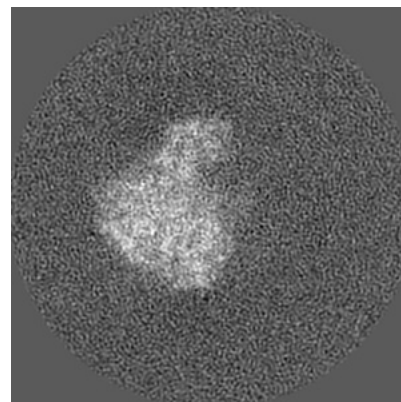
6.3.2 Raw map



X Index: 83



Y Index: 89

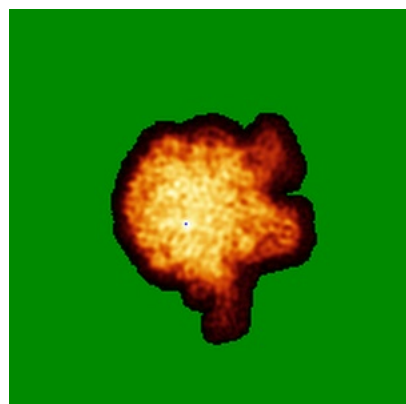


Z Index: 93

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

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

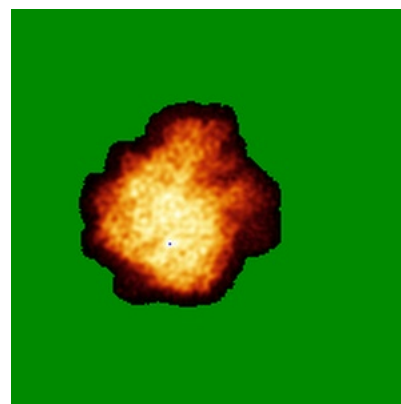
6.4.1 Primary map



X

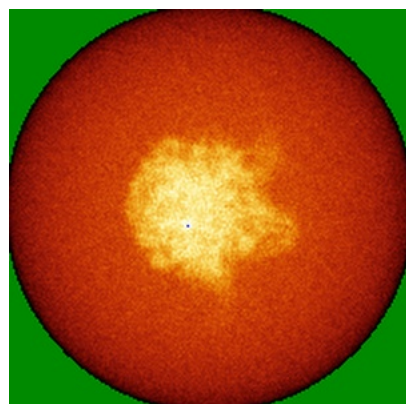


Y

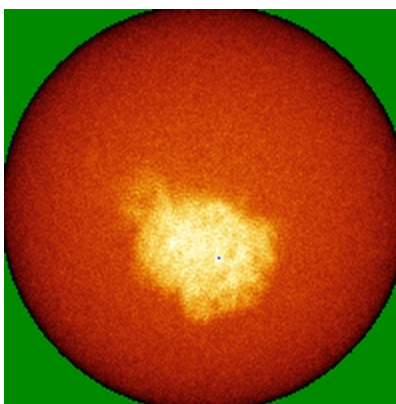


Z

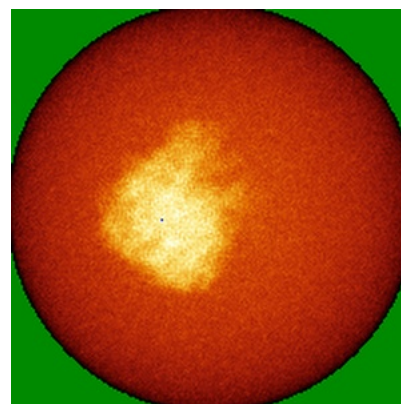
6.4.2 Raw map



X



Y

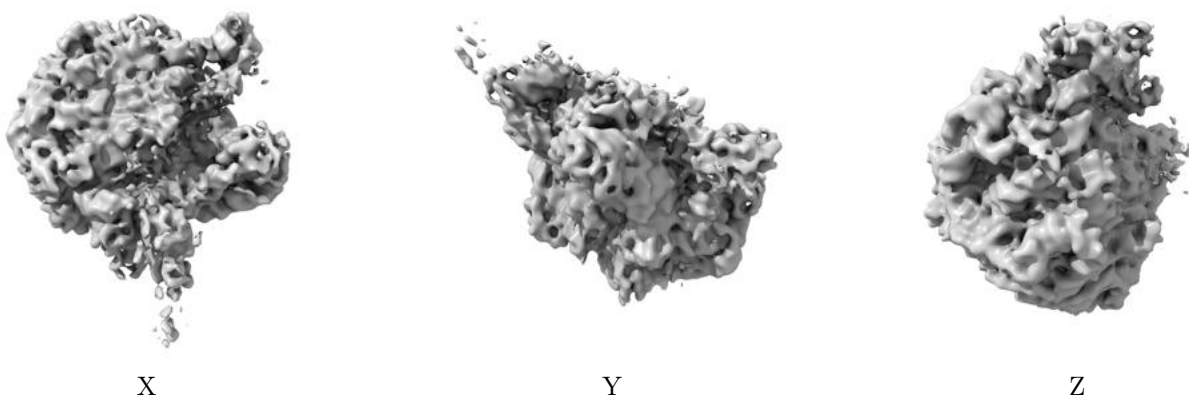


Z

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.

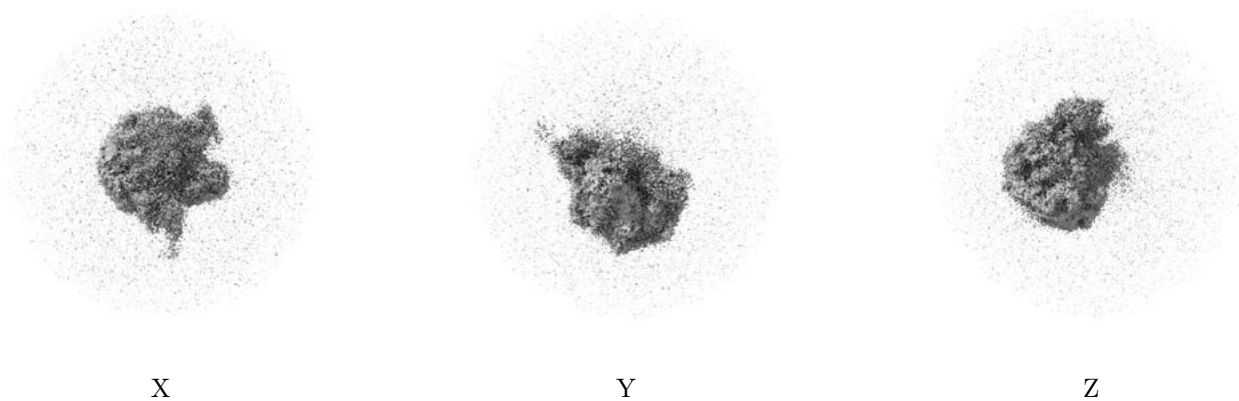
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.41. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

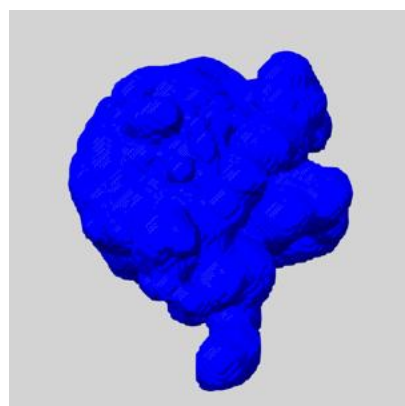
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

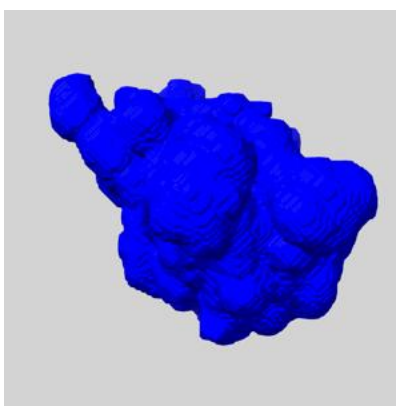
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

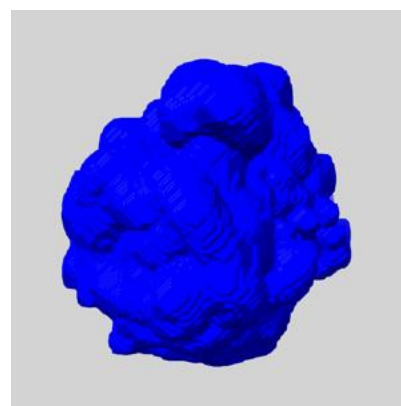
6.6.1 emd_13285_msk_1.map [i](#)



X



Y

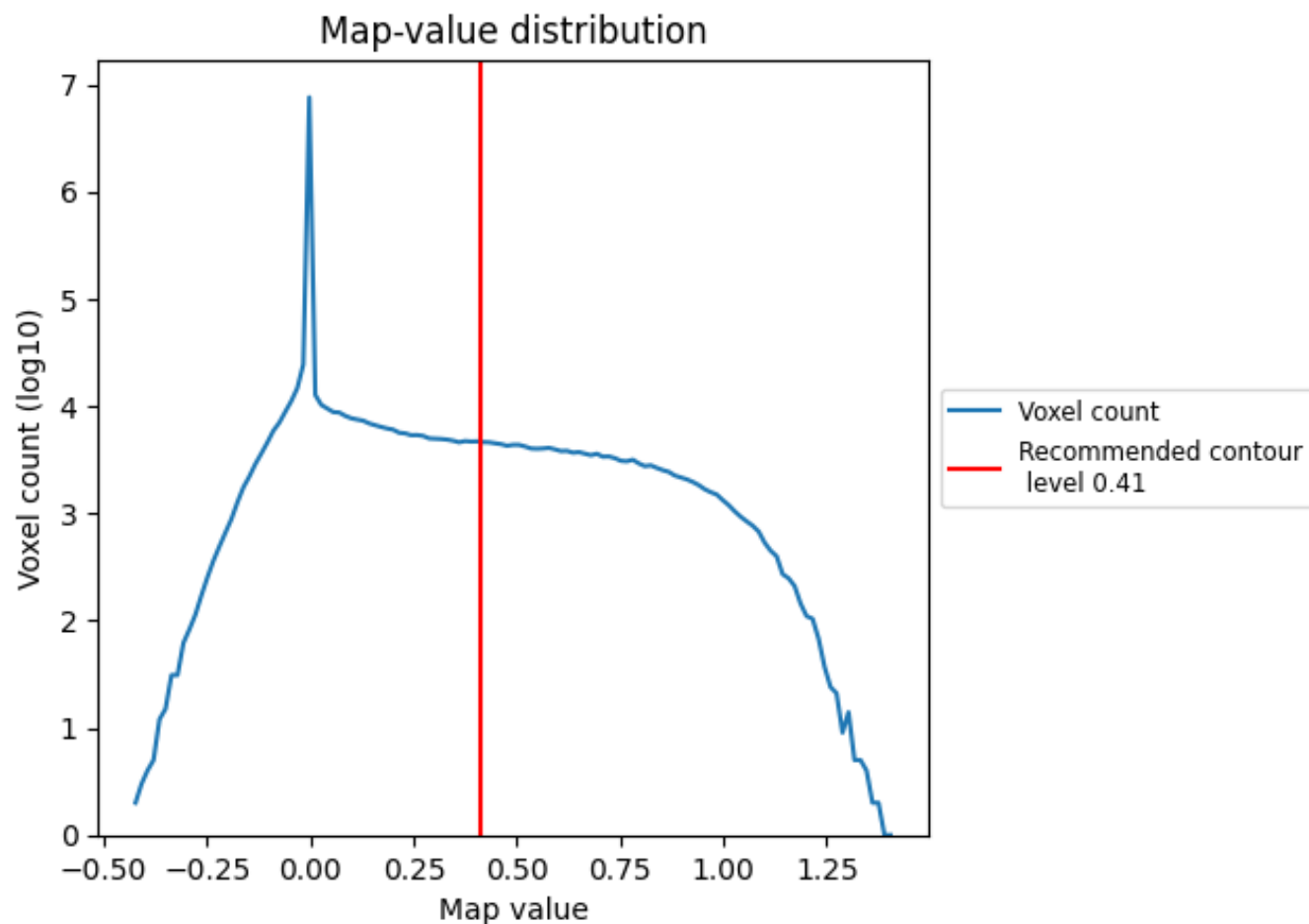


Z

7 Map analysis [i](#)

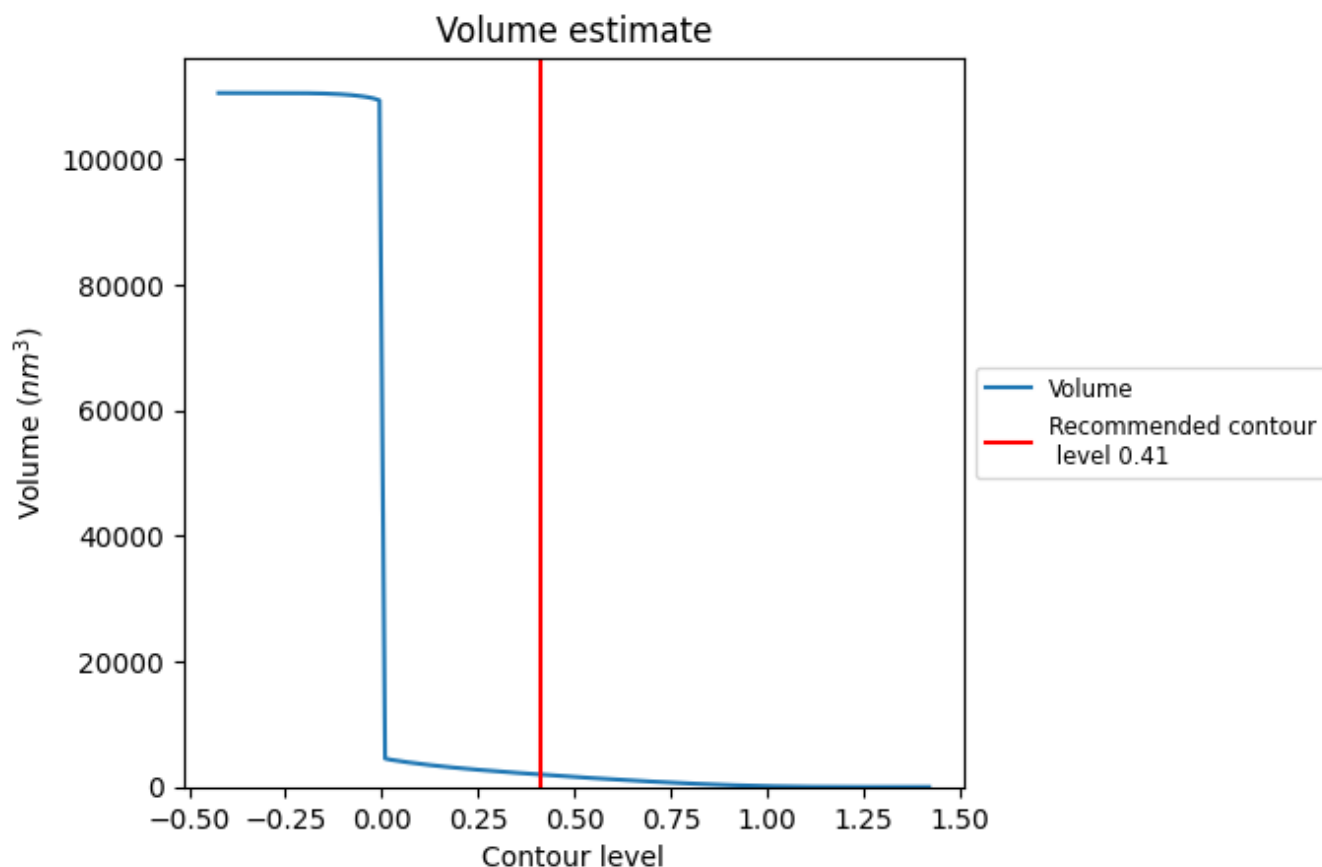
This section contains the results of statistical analysis of the map.

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.

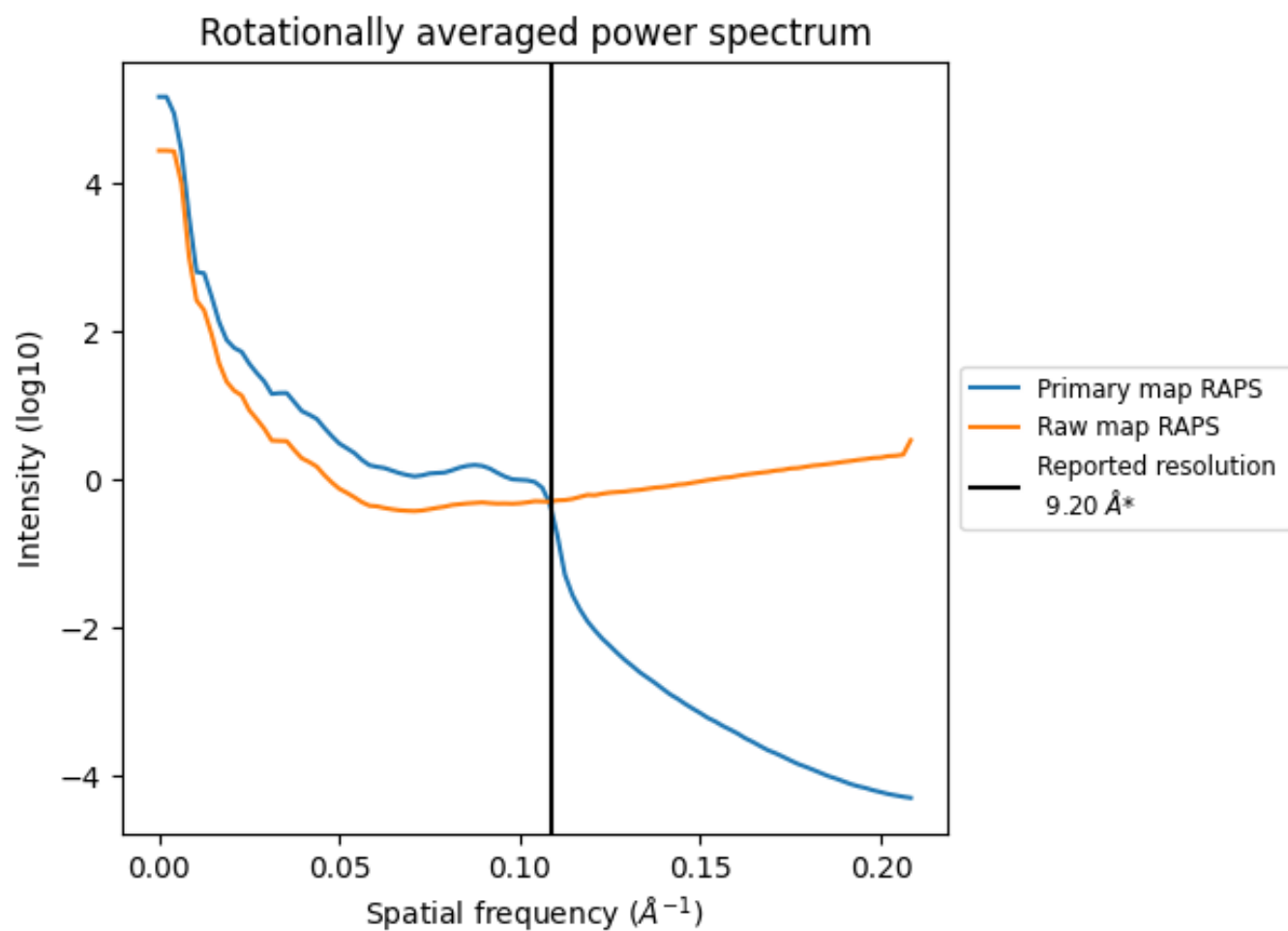
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1985 nm³; this corresponds to an approximate mass of 1793 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 ⓘ

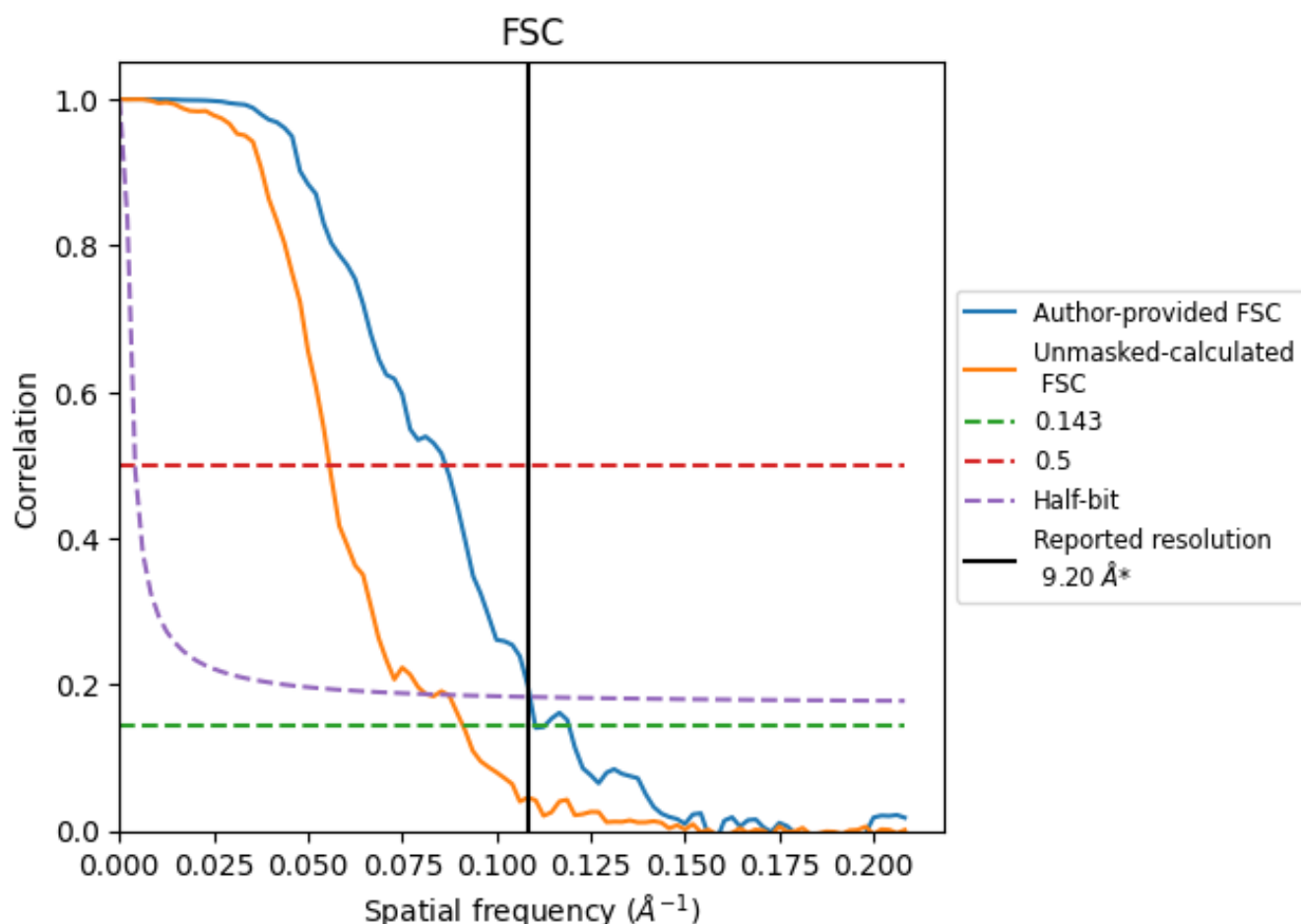


*Reported resolution corresponds to spatial frequency of 0.109 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.109 \AA^{-1}

8.2 Resolution estimates [i](#)

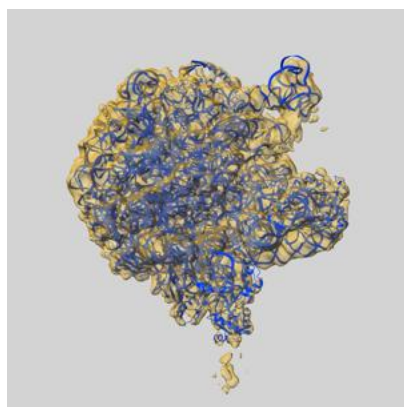
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.20	-	-
Author-provided FSC curve	9.07	11.56	9.18
Unmasked-calculated*	10.98	17.95	12.29

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 10.98 differs from the reported value 9.2 by more than 10 %

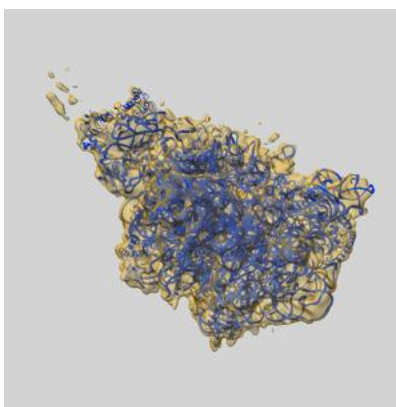
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13285 and PDB model 7PAT. Per-residue inclusion information can be found in section [3](#) on page [9](#).

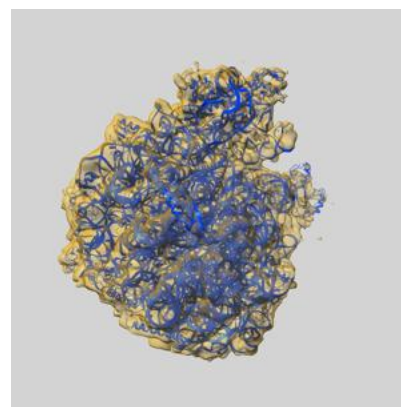
9.1 Map-model overlay [i](#)



X



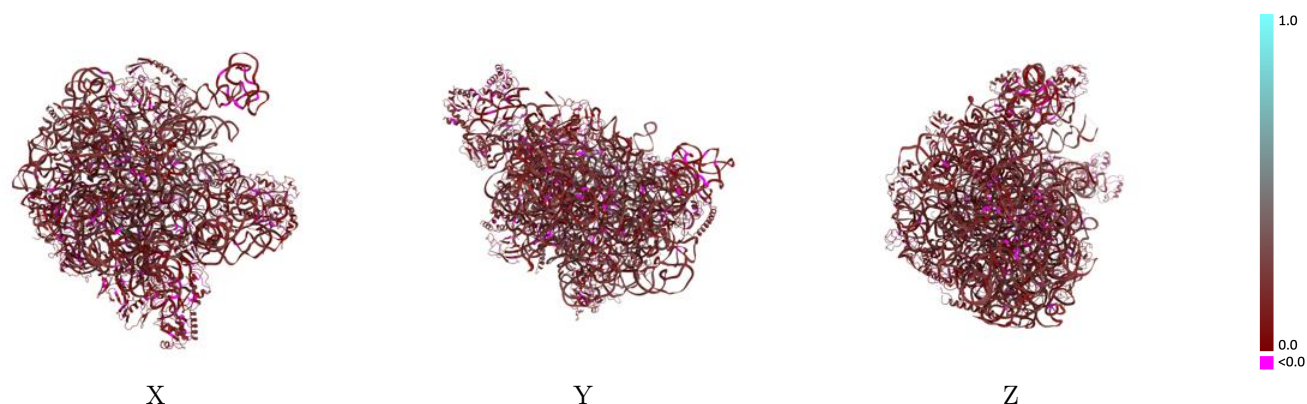
Y



Z

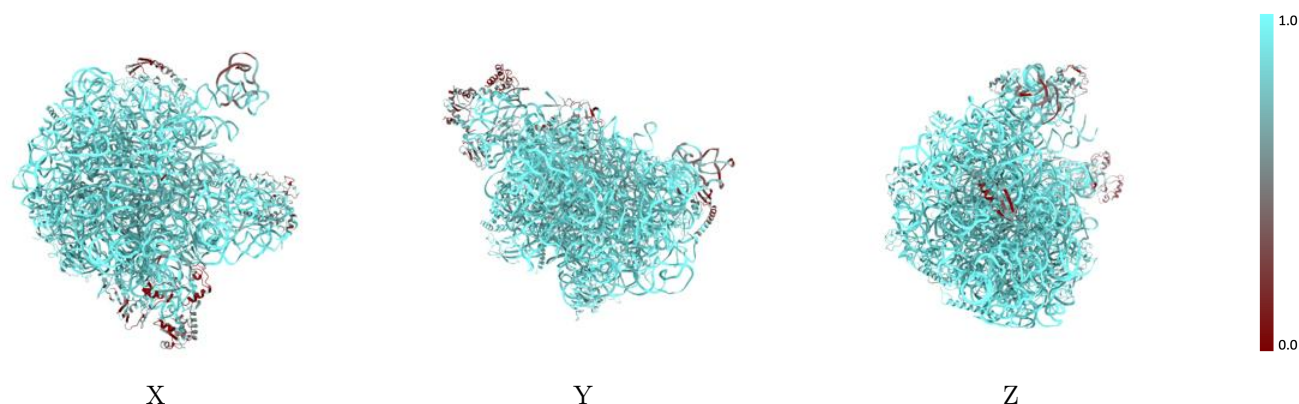
The images above show the 3D surface view of the map at the recommended contour level 0.41 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



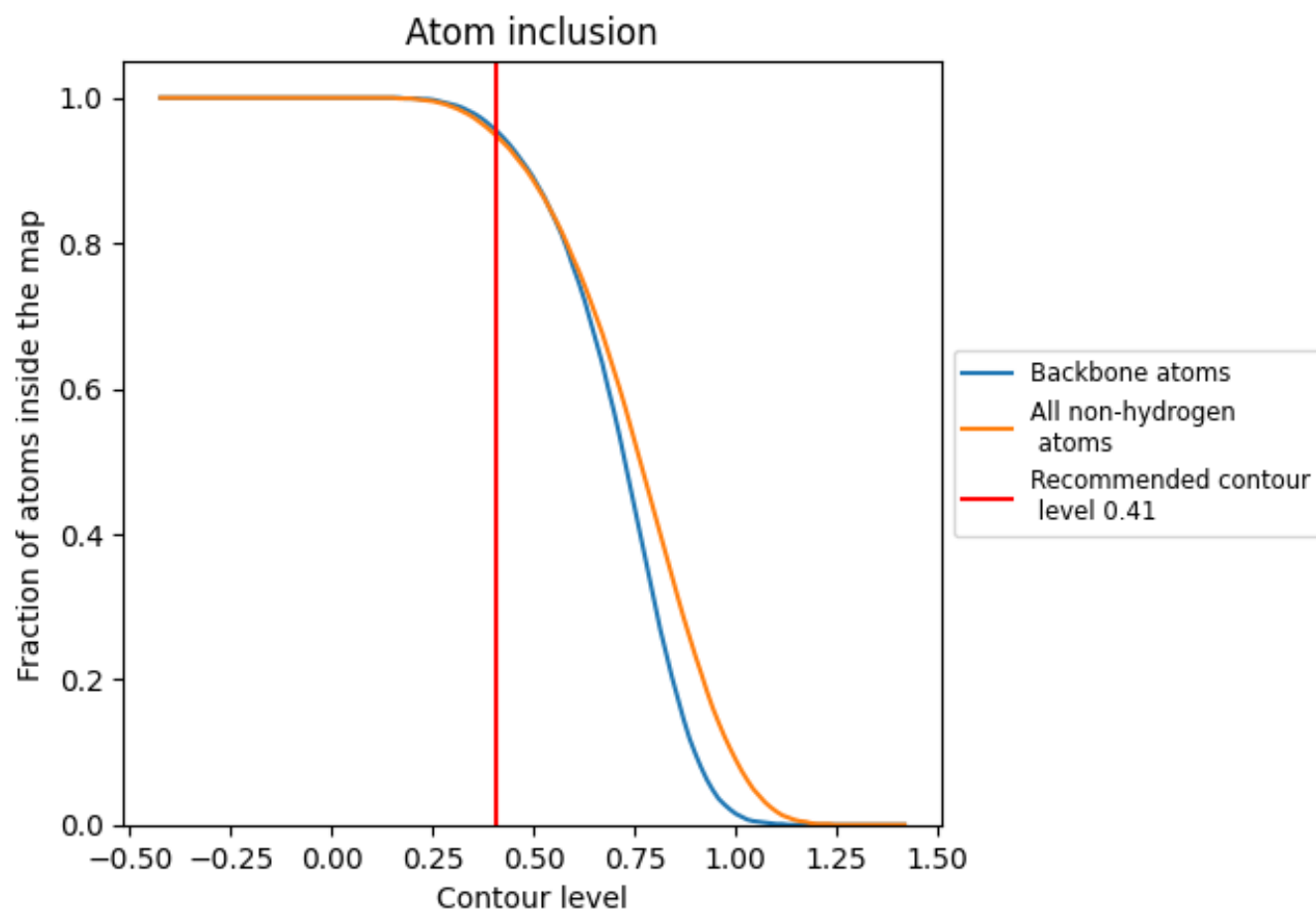
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.41).

































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 95% 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 (0.41) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9470	 0.1570
0	 0.9950	 0.1330
1	 0.9850	 0.1160
2	 0.9560	 0.0860
3	 0.9830	 0.1680
4	 0.9640	 0.1800
a	 0.9840	 0.1170
b	 0.9490	 0.1070
c	 0.9320	 0.1350
d	 0.7000	 0.1380
e	 0.6600	 0.1340
f	 0.5750	 0.1350
g	 0.4890	 0.1510
h	 0.3630	 0.1220
i	 0.9740	 0.1400
j	 0.9460	 0.1300
k	 0.9580	 0.1280
l	 0.9370	 0.1280
m	 0.9750	 0.1290
n	 0.8130	 0.1410
o	 0.9000	 0.1440
p	 0.9650	 0.1200
q	 0.9260	 0.1390
r	 0.9890	 0.1490
s	 0.9790	 0.1430
t	 0.8750	 0.1210
u	 0.9560	 0.1070
v	 0.9980	 0.1150
w	 0.9300	 0.1780
x	 0.4900	 0.1520
y	 0.9860	 0.1100
z	 0.9850	 0.1180

