



wwPDB EM Validation Summary Report ⓘ

Nov 6, 2022 – 07:23 PM EST

PDB ID : 6O8X
EMDB ID : EMD-0657
Title : Cryo-EM image reconstruction of the 70S Ribosome *Enterococcus faecalis* Class02
Authors : Jogl, G.; Khayat, R.
Deposited on : 2019-03-12
Resolution : 3.68 Å (reported)
Based on initial models : 4YBB, 5LI0

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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

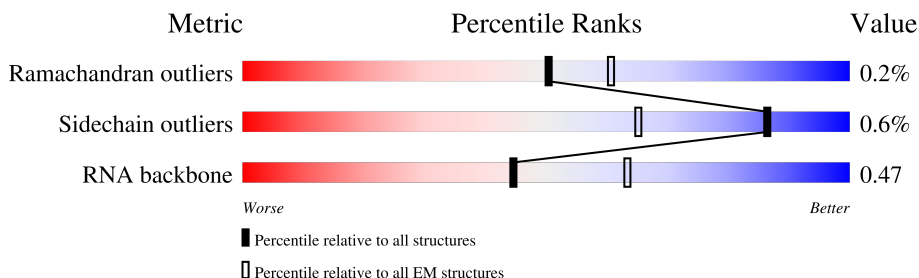
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.68 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.



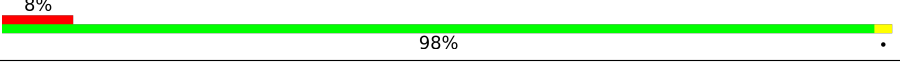
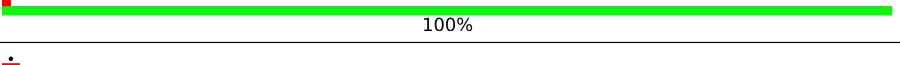
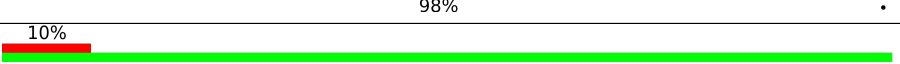
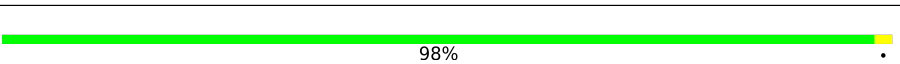
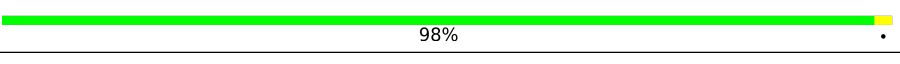
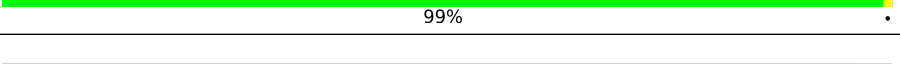
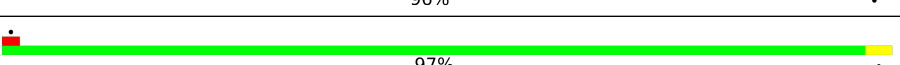
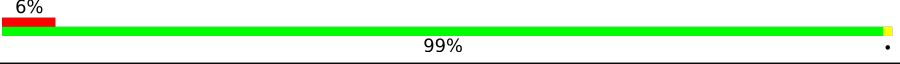
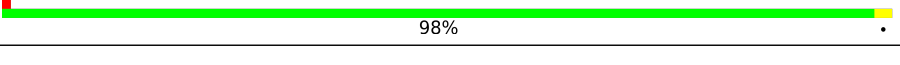

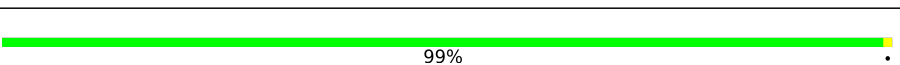
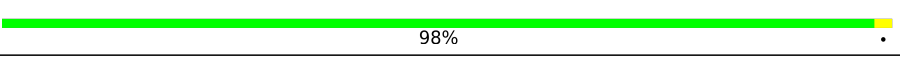
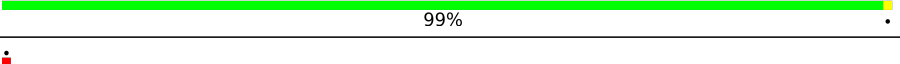
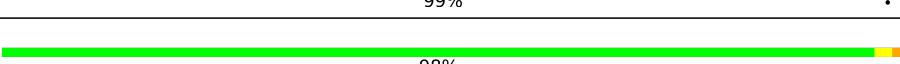
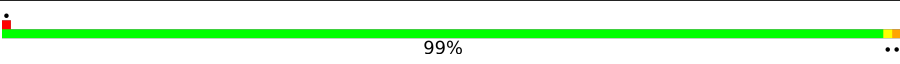
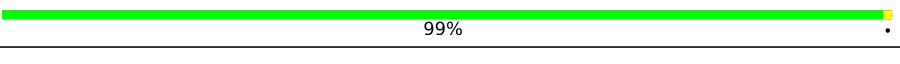
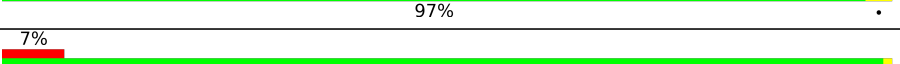
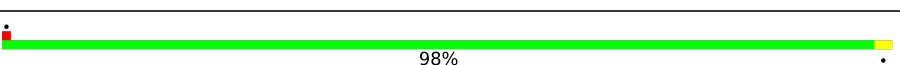
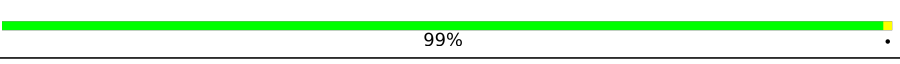
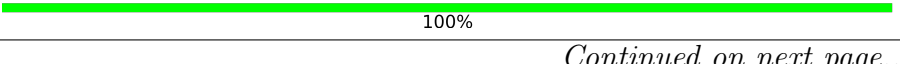



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	a	1528	
2	c	204	
3	d	201	
4	e	163	
5	f	97	
6	g	154	
7	h	131	
8	i	128	

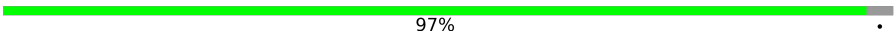

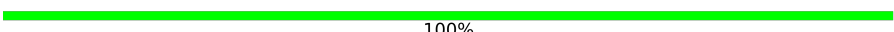
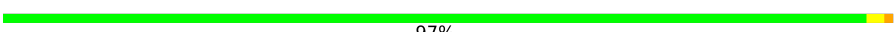
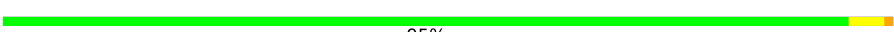








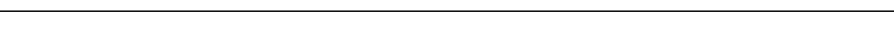
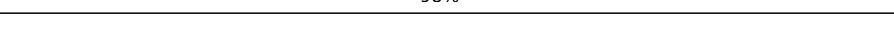
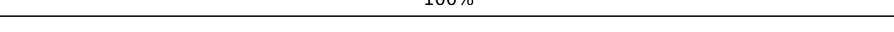
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Mol	Chain	Length	Quality of chain
9	j	99	
10	k	117	
11	l	136	
12	m	112	
13	n	60	
14	o	88	
15	p	89	
16	q	83	
17	r	66	
18	s	78	
19	t	81	
20	A	2903	
21	B	116	
22	C	275	
23	D	207	
24	E	206	
25	F	177	
26	G	176	
27	K	145	
28	L	122	
29	M	146	
30	N	141	
31	O	123	
32	P	117	
33	Q	114	

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Mol	Chain	Length	Quality of chain
34	R	118	 97%
35	S	102	 99%
36	T	112	 100%
37	U	89	 97%
38	V	101	 95%
39	W	94	 67%
40	X	76	 98%
41	Y	54	 94% 6%
42	Z	61	 100%
43	0	58	 98%
44	1	60	 5%
45	2	56	 100%
46	3	49	 100%
47	4	44	 98%
48	5	64	 100%
49	6	38	 100%

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 138230 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 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1528	Total	C	N	O	P	0	0
			32746	14609	5979	10630	1528		

- Molecule 2 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	204	Total	C	N	O	S	0	0
			1610	1012	303	292	3		

- Molecule 3 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d	201	Total	C	N	O	S	0	0
			1620	1016	303	297	4		

- Molecule 4 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	163	Total	C	N	O	S	0	0
			1204	759	222	221	2		

- Molecule 5 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	97	Total	C	N	O	S	0	0
			795	501	137	154	3		

- Molecule 6 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	154	Total	C	N	O	S	0	0
			1229	765	236	222	6		

- Molecule 7 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	131	Total	C	N	O	S	0	0
			1041	662	184	193	2		

- Molecule 8 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	128	Total	C	N	O	S	0	0
			990	615	197	177	1		

- Molecule 9 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	j	99	Total	C	N	O	S	0	0
			800	504	147	147	2		

- Molecule 10 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	117	Total	C	N	O	S	0	0
			863	533	165	161	4		

- Molecule 11 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	l	136	Total	C	N	O	S	0	0
			1065	661	214	188	2		

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	m	112	Total	C	N	O	S	0	0
			884	540	180	163	1		

- Molecule 13 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	60	Total	C	N	O	S	0	0
			492	310	100	77	5		

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	o	88	Total	C	N	O	S	0	0
			741	455	152	133	1		

- Molecule 15 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	p	89	Total	C	N	O	S	0	0
			708	448	131	127	2		

- Molecule 16 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	q	83	Total	C	N	O	S	0	0
			681	427	127	124	3		

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	r	66	Total	C	N	O	S	0	0
			537	343	99	94	1		

- Molecule 18 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	s	78	Total	C	N	O	S	0	0
			634	410	113	109	2		

- Molecule 19 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	t	81	Total	C	N	O	S	0	0
			610	372	119	117	2		

- Molecule 20 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	A	2898	Total	C	N	O	P	0	0
			62196	27761	11436	20101	2898		

- Molecule 21 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	B	116	Total	C	N	O	P	0	0
			2478	1105	444	813	116		

- Molecule 22 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	C	275	Total	C	N	O	S	0	0
			2114	1310	416	381	7		

- Molecule 23 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	D	207	Total	C	N	O	S	0	0
			1578	993	292	289	4		

- Molecule 24 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	E	206	Total	C	N	O	S	0	0
			1572	984	289	297	2		

- Molecule 25 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	F	177	Total	C	N	O	S	0	0
			1391	886	239	260	6		

- Molecule 26 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	G	176	Total	C	N	O	S	0	0
			1344	841	244	255	4		

- Molecule 27 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	K	145	Total	C	N	O	S	0	0
			1129	713	205	207	4		

- Molecule 28 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	L	122	Total	C	N	O	S	0	0
			922	574	176	170	2		

- Molecule 29 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	M	146	Total	C	N	O	S	0	0
			1094	676	212	205	1		

- Molecule 30 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	N	141	Total	C	N	O	S	0	0
			1117	709	216	185	7		

- Molecule 31 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	O	123	Total	C	N	O	S	0	0
			978	603	189	183	3		

- Molecule 32 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	P	117	Total	C	N	O	S	0	0
			898	555	175	167	1		

- Molecule 33 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	Q	114	Total	C	N	O	0	0
			924	582	185	157		

- Molecule 34 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	R	115	Total	C	N	O	S	0	0
			913	580	172	157	4		

- Molecule 35 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	S	102	Total	C	N	O	S	0	0
			783	500	138	143	2		

- Molecule 36 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	T	112	Total	C	N	O	S	0	0
			849	532	156	159	2		

- Molecule 37 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	U	89	Total	C	N	O	S	0	0
			719	457	127	132	3		

- Molecule 38 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	V	101	Total	C	N	O	S	0	0
			763	486	135	140	2		

- Molecule 39 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	W	94	Total	C	N	O	S	0	0
			757	478	135	140	4		

- Molecule 40 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	X	76	Total	C	N	O	0	0
			572	351	109	112		

- Molecule 41 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Y	54	Total	C	N	O	S	0	0
			424	265	86	71	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	51	ALA	THR	conflict	UNP A0A1B4XRZ8

- Molecule 42 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Z	61	Total	C	N	O	S	0	0
			504	314	94	95	1		

- Molecule 43 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	0	58	Total	C	N	O	S	0	0
			435	271	81	82	1		

- Molecule 44 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	1	60	Total	C	N	O	S	0	0
			475	301	75	97	2		

- Molecule 45 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	2	56	Total	C	N	O	S	0	0
			429	262	88	73	6		

- Molecule 46 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	3	49	Total	C	N	O	S	0	0
			419	253	86	76	4		

- Molecule 47 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	4	44	Total	C	N	O	S	0	0
			373	226	91	54	2		

- Molecule 48 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5	64	Total	C	N	O	S	0	0
			522	320	122	78	2		

- Molecule 49 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	6	38	Total	C	N	O	S	0	0
			304	188	66	44	6		

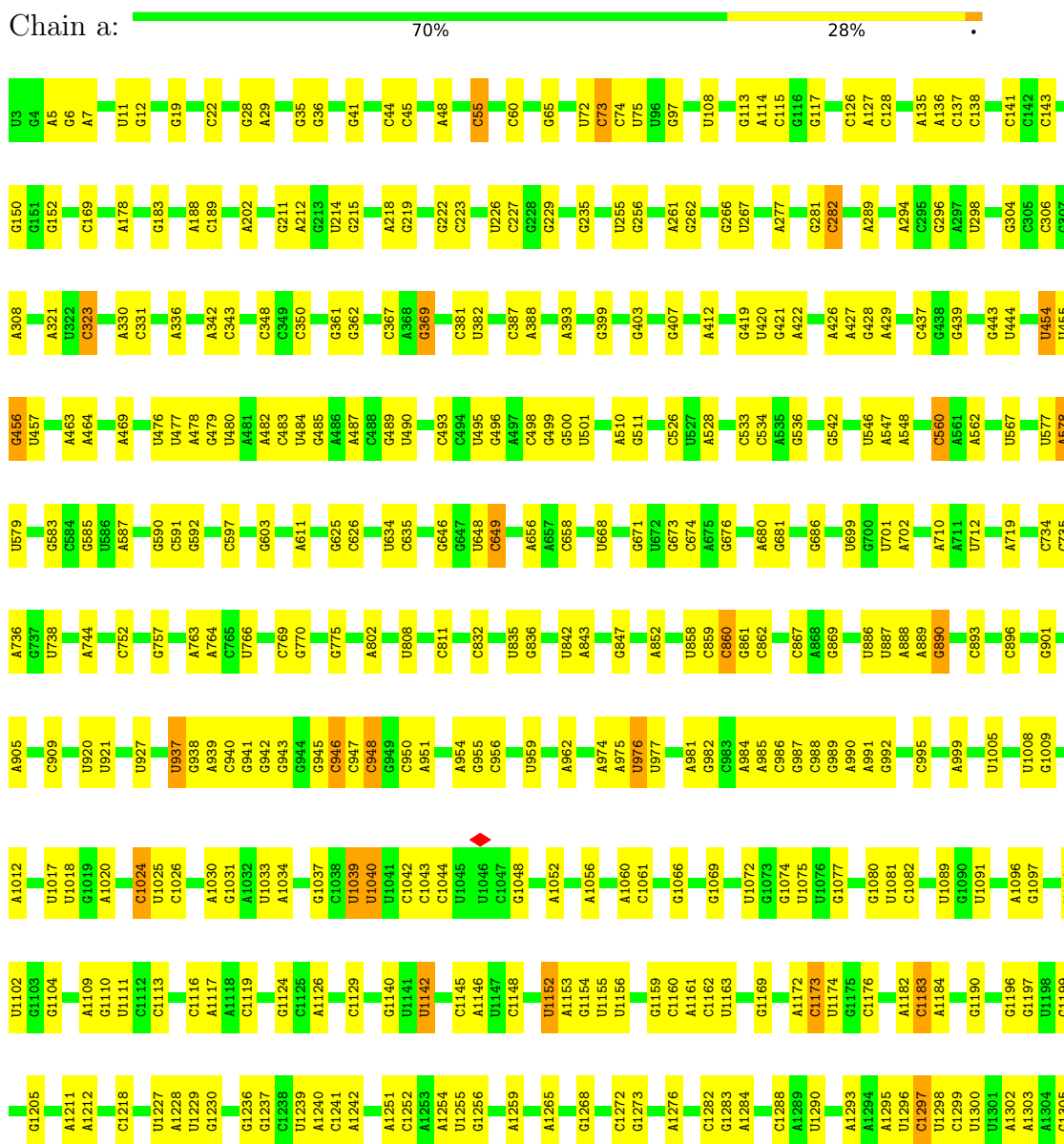
- Molecule 50 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

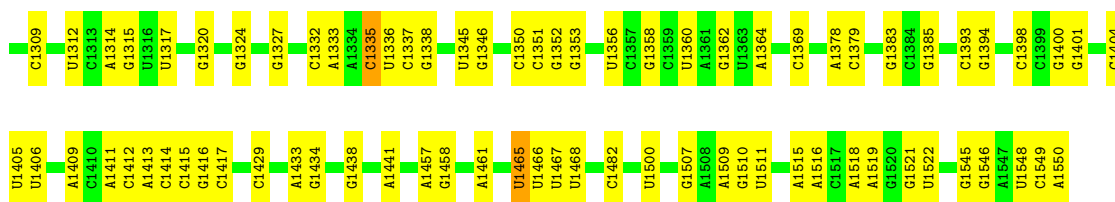
Mol	Chain	Residues	Atoms		AltConf
50	n	1	Total	Zn	0
			1	1	
50	2	1	Total	Zn	0
			1	1	
50	3	1	Total	Zn	0
			1	1	
50	6	1	Total	Zn	0
			1	1	

3 Residue-property plots

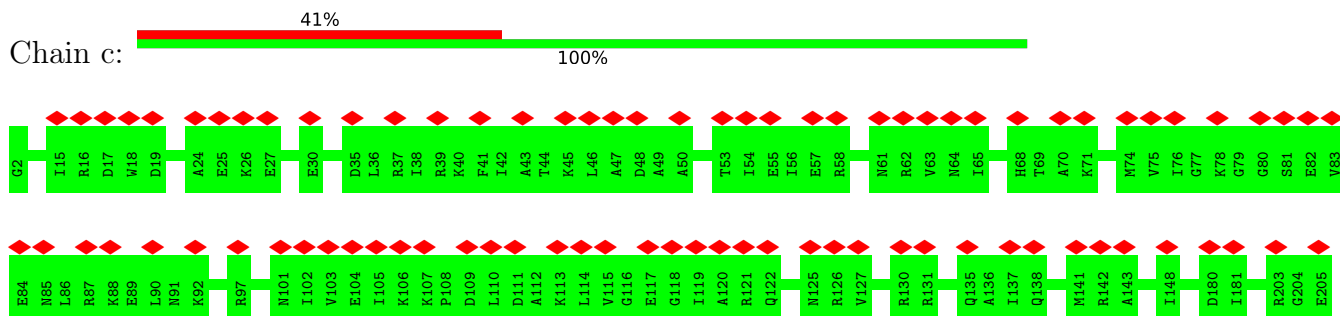
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S rRNA

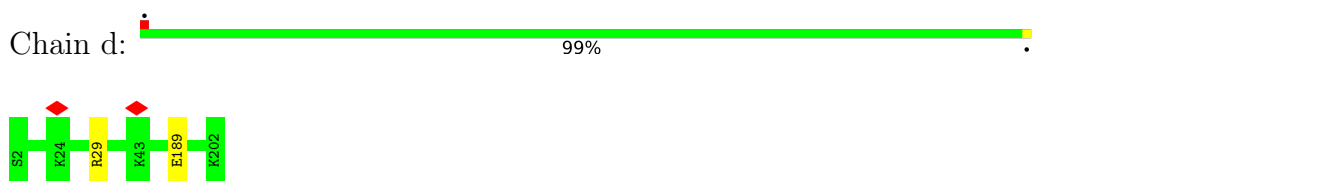




• Molecule 2: 30S ribosomal protein S3



• Molecule 3: 30S ribosomal protein S4



• Molecule 4: 30S ribosomal protein S5



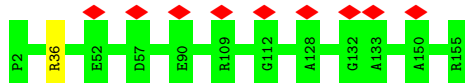
There are no outlier residues recorded for this chain.

• Molecule 5: 30S ribosomal protein S6



There are no outlier residues recorded for this chain.

• Molecule 6: 30S ribosomal protein S7



• Molecule 7: 30S ribosomal protein S8





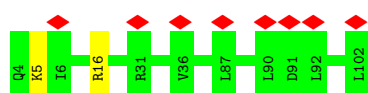
- Molecule 8: 30S ribosomal protein S9

Chain i: 99%



- Molecule 9: 30S ribosomal protein S10

Chain j: 8% 98%



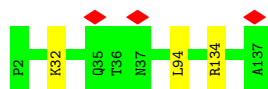
- Molecule 10: 30S ribosomal protein S11

Chain k: 100%



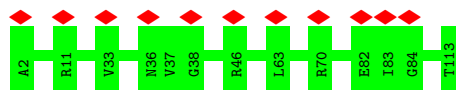
- Molecule 11: 30S ribosomal protein S12

Chain l: 98%



- Molecule 12: 30S ribosomal protein S13

Chain m: 10% 100%




- Molecule 13: 30S ribosomal protein S14 type Z

Chain n: 98%



- Molecule 14: 30S ribosomal protein S15

Chain o:  98%



- Molecule 15: 30S ribosomal protein S16

Chain p:  99%



- Molecule 16: 30S ribosomal protein S17

Chain q:  96%



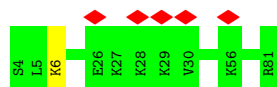
- Molecule 17: 30S ribosomal protein S18

Chain r:  97%



- Molecule 18: 30S ribosomal protein S19

Chain s:  6% 99%



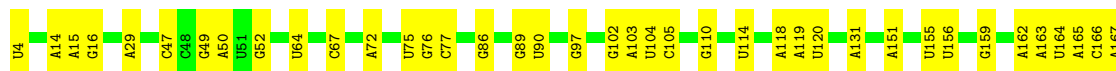
- Molecule 19: 30S ribosomal protein S20

Chain t:  98%

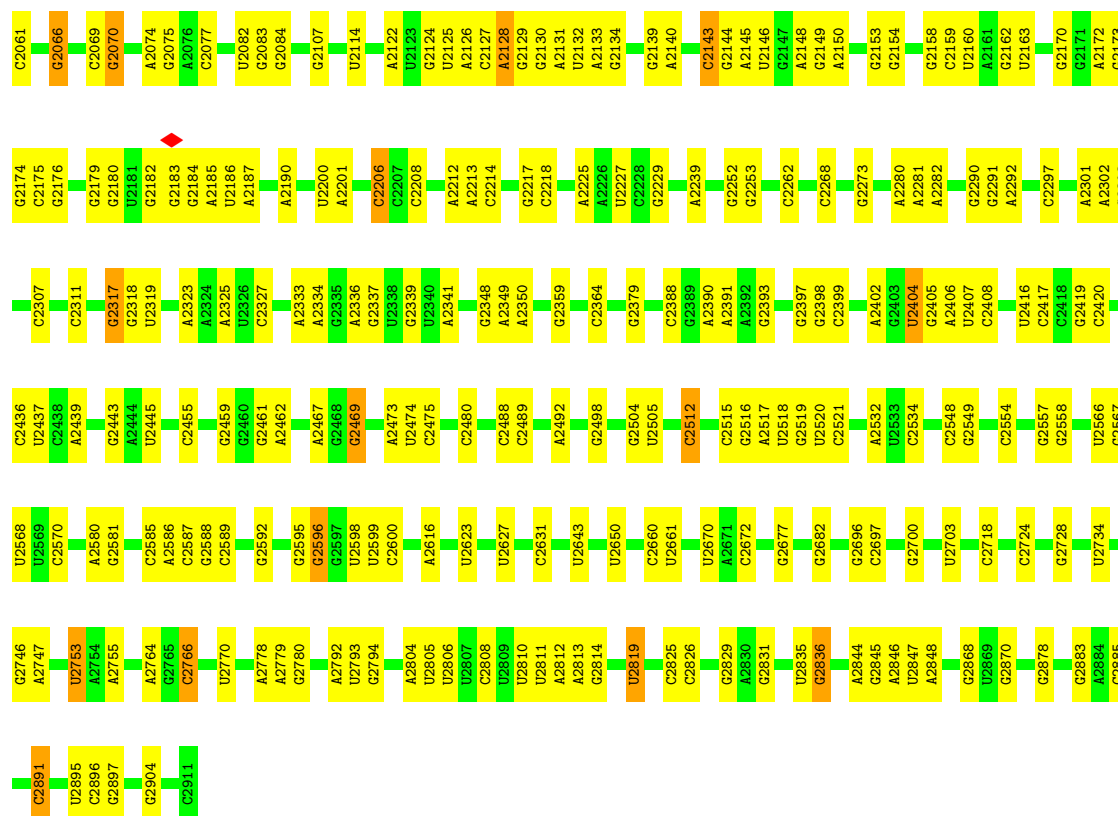


- Molecule 20: 23S rRNA

Chain A:  70% 27%



A	G1777	A1615	C1511	A1421	U1292	G1152	A1088	A964	U885	G741	G610	U989	U168
C	G1778	C1623	A1516	C1422	G1293	C1156	C1089	U965	U886	A755	A611	G300	A169
U	A1782	G1428	G1519	G1428	C1294	C1157	C1092	U966	G887	A756	A612	U301	A179
A	G1783	A1629	G1520	A1431	G1302	G1162	A1094	U975	A888	A758	C621	C309	G181
A1931	G1784	A1630	A1521	U1432	G1303	G1163	A1095	G978	G889	A759	G622	G310	U182
A1933	A1787	A1632	U1525	U1433	U1304	A1167	G1096	A985	A890	C759	A623	A311	A163
U1940	G1790	A1633	U1526	C1434	G1308	A1168	A1097	G986	U892	G766	A624	A313	G184
A1941	U1795	C1635	A1530	C1435	A1309	G1171	U1100	G992	U895	G769	C638	A318	A185
A1942	U1796	A1636	G1531	C1436	A1310	A1172	U1101	G993	G896	A770	G639	A189	A186
G1943	U1797	C1637	A1532	U1437	A1311	A1173	G1102	A993	G897	A496	A640	A188	A187
G1944	A1798	U1638	A1533	G1443	G1317	C1174	G1103	A997	G900	C780	U644	C321	A199
A1952	A1805	U1639	A1536	U1444	A1320	C1175	C1104	U998	U901	U786	U645	U322	A198
U1957	U1806	C1641	U1539	U1445	A1321	G1176	U1105	U999	U902	U787	A506	G323	A202
U1958	C1814	U1642	U1540	U1446	A1322	G1177	A1106	A999	A904	G788	C649	U324	A207
A1815	A1816	A1643	A1545	U1447	A1323	C1178	U1107	A1000	G905	A789	G650	U325	A208
U1969	A1817	C1644	C1548	G1451	U1336	C1179	G1108	G1001	G906	A790	A651	A326	G218
U1970	A1818	G1645	U1551	U1452	A1337	U1181	A1109	G1006	A907	A791	A652	G327	A219
C1976	U1821	G1646	U1552	U1453	U1338	A1182	G1110	A1013	G914	A801	G653	G332	A224
G1977	U1822	A1651	A1553	U1454	U1339	A1183	G1111	A1014	G915	A802	A654	G333	A225
G1978	A1823	U1652	A1554	G1455	U1340	A1184	G1112	A1015	G916	A803	A655	G334	A226
C1979	G1827	A1653	A1555	G1456	C1350	A1185	G1113	A1016	A919	G805	A656	G335	A227
A1980	U1828	U1677	A1556	A1457	A1357	C1183	C1115	G1016	G922	G806	C657	G344	A228
C1981	G1829	U1678	G1560	G1458	A1358	A1196	C1116	G1017	G923	G807	G658	C352	A229
A1819	A1820	A1679	A1566	A1459	U1362	G1197	A1117	G1018	G924	G808	G659	C353	A230
A1821	A1822	C1680	C1567	A1460	U1363	G1198	C1118	A1009	C925	G809	A660	C354	U232
A1823	U1832	G1681	G1568	U1461	U1364	C1200	C1119	G1010	C926	G810	A661	C355	U233
A1833	A1834	C1682	G1569	G1462	U1365	C1201	C1120	A1011	C927	G811	A662	A367	C234
U1941	G1841	G1717	G1570	C1463	C1366	C1211	U1121	A1012	A927	A822	G673	A383	C235
G1842	A1843	C1718	A1571	C1464	U1376	C1212	C1122	A1013	U928	A823	A676	G386	A244
A1843	U1844	A1719	A1572	U1475	U1377	G1213	C1123	A1014	U929	U824	C548	C387	A245
U1862	U1723	U1724	U1573	U1476	U1378	G1214	C1124	A1015	U930	U825	C549	C388	U246
C1872	C1726	C1727	U1574	C1477	U1379	G1215	C1125	A1016	G931	A826	A683	C391	G251
U1878	C1737	G1738	C1588	G1488	U1388	G1216	C1126	A1017	G932	G827	U684	C396	A254
G1881	A1741	A1742	C1589	C1489	U1389	G1217	C1127	A1018	U933	G828	G693	A399	G255
C1882	U1756	U1757	A1590	C1490	C1396	G1218	C1128	A1019	G934	G829	A694	G400	C256
G1886	U1758	C1759	C1591	U1496	G1397	U1219	C1129	A1020	U935	G830	U695	G404	A268
A1896	U1760	U1761	C1592	U1497	U1401	G1220	C1130	A1021	U936	G831	G708	G410	G269
C1907	G1767	G1768	C1593	A1500	A1402	G1221	C1131	A1022	U937	G832	A709	A411	C270
U2048	A1769	A1770	C1594	A1501	U1403	G1222	C1132	A1023	A937	G833	G694	A399	A254
G2049	G1770	U1771	C1595	G1502	A1404	G1223	C1133	A1024	C938	G834	A710	G400	G255
C2050	U1772	U1773	C1596	G1503	A1405	G1224	C1134	A1025	C939	G835	C711	G404	C256
A2056	U1774	A1775	C1597	G1504	U1415	A1284	C1135	A1026	A942	G836	A716	G404	A268
C2057	U1775	U1776	A1612	G1505	A1416	G1285	C1136	A1027	U943	G837	U580	G410	G269
A	U1925	A1777	A1613	U1509	C1419	A1290	C1137	A1028	U944	G838	U581	A411	C270
	A	A1778	G1614	C1510	A1420	A1291	C1138	A1029	A946	G839	A585	A412	C271
							C1139	A1030	U949	U850	A586	U413	C272
							C1140	A1031	A950	U851	U587	A421	A278
							C1141	A1032	A951	C852	G588	A421	A278
							C1142	A1033	A952	U591	U591	A424	C284
							C1143	A1034	A953	U592	U592	A424	C284
							C1144	A1035	A954	U593	U593	A424	C284
							C1145	A1036	A955	U594	U594	A424	C284
							C1146	A1037	A956	U595	U595	A424	C284
							C1147	A1038	A957	U596	U596	A424	C284
							C1148	A1039	A958	U597	U597	A424	C284
							C1149	A1040	A959	U598	U598	A424	C284
							C1150	A1041	A960	U599	U599	A424	C284
							C1151	A1042	A961	U600	U600	A427	U285
							C1152	A1043	A962	U601	U601	A427	U285
							C1153	A1044	A963	U602	U602	A427	U285
							C1154	A1045	A964	U603	U603	A427	U285
							C1155	A1046	A965	U604	U604	A427	U285
							C1156	A1047	A966	U605	U605	A427	U285
							C1157	A1048	A967	U606	U606	A427	U285
							C1158	A1049	A968	U607	U607	A427	U285
							C1159	A1050	A969	U608	U608	A427	U285
							C1160	A1051	A970	U609	U609	A427	U285
							C1161	A1052	A971	U610	U610	A427	U285
							C1162	A1053	A972	U611	U611	A427	U285
							C1163	A1054	A973	U612	U612	A427	U285
							C1164	A1055	A974	U613	U613	A427	U285
							C1165	A1056	A975	U614	U614	A427	U285
							C1166	A1057	A976	U615	U615	A427	U285
							C1167	A1058	A977	U616	U616	A427	U285
							C1168	A1059	A978	U617	U617	A427	U285
							C1169	A1060	A979	U618	U618	A427	U285
							C1170	A1061	A980	U619	U619	A427	U285
							C1171	A1062	A981	U620	U620	A427	U285
							C1172	A1063	A982	U621	U621	A427	U285
							C1173	A1064	A983	U622	U622	A427	U285
							C1174	A1065	A984	U623	U623	A427	U285
							C1175	A1066	A985	U624	U624	A427	U285
							C1176	A1067	A986	U625	U625	A427	U285
							C1177	A1068	A987	U626	U626	A427	U285
							C1178	A1069	A988	U627	U627	A427	U285
							C1179	A1070	A989	U628	U628	A427	U285
							C1180	A1071	A990	U629	U629	A427	U285
							C1181	A1072	A991	U630	U630	A427	U285
							C1182	A1073	A992	U631	U631	A427	U285
							C1183	A1074	A993	U632	U632	A427	U285
							C1184	A1075	A994	U633	U633	A427	U285
							C1185	A1076	A995	U634	U634	A427	U285
							C1186	A1077	A996	U635	U635	A427	U285
							C1187	A1078	A997	U636	U636	A427	U285
							C1188	A1079	A998	U637	U637	A427	U285
							C1189	A1080	A999	U638	U638	A427	U285
							C1190	A1081	A1000	U639	U639	A427	U285
							C1191	A1082	A1001	U640	U640	A427	U285
							C1192	A1083	A1002	U641	U641	A427	U285
							C1193	A1084	A1003	U642	U642	A427	U285
							C1194	A1085	A1004	U643	U643	A427	U285
							C1195	A1086	A1005	U644	U644	A427	U285
							C1196	A1087	A1006	U645	U645	A427	U285
							C1197	A1088	A1007	U646	U646	A427	U285
							C1198	A1089	A1008	U647	U647	A427	U285
							C1199	A1090	A1009	U648	U648	A427	U285
							C1200	A1091	A1010	U649	U649	A427	U285
							C1201	A1092	A1011	U650	U650	A427	U285
							C1202	A1093	A1012	U651	U651	A427	U285
							C1203	A1094	A1013	U652	U652	A427	U285
							C1204	A1095	A1014	U653	U653	A427	U285
							C1205	A1096	A1015	U654	U654	A427	U285
							C1206	A1097	A1016	U655	U655</		





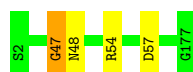
- Molecule 25: 50S ribosomal protein L5

Chain F: 99%



- Molecule 26: 50S ribosomal protein L6

Chain G: 98%



- Molecule 27: 50S ribosomal protein L13

Chain K: 99%



- Molecule 28: 50S ribosomal protein L14

Chain L: 99%



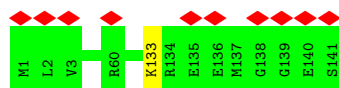
- Molecule 29: 50S ribosomal protein L15

Chain M: 97%



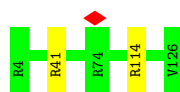
- Molecule 30: 50S ribosomal protein L16

Chain N: 7% 99%



- Molecule 31: 50S ribosomal protein L17

Chain O: 98%



- Molecule 32: 50S ribosomal protein L18

Chain P: 99%



- Molecule 33: 50S ribosomal protein L19

Chain Q: 100%

There are no outlier residues recorded for this chain.

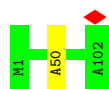
- Molecule 34: 50S ribosomal protein L20

Chain R: 97%



- Molecule 35: 50S ribosomal protein L21

Chain S: 99%



- Molecule 36: 50S ribosomal protein L22

Chain T: 100%

There are no outlier residues recorded for this chain.

- Molecule 37: 50S ribosomal protein L23

Chain U: 97%

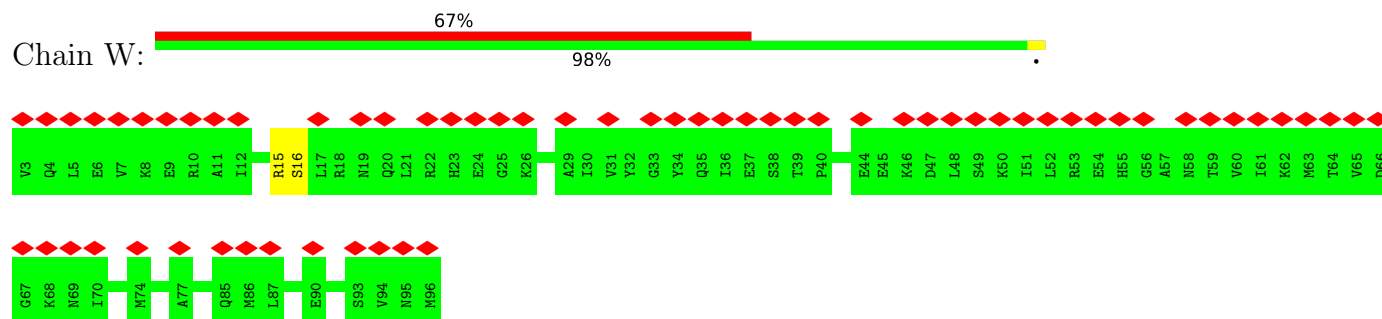


- Molecule 38: 50S ribosomal protein L24

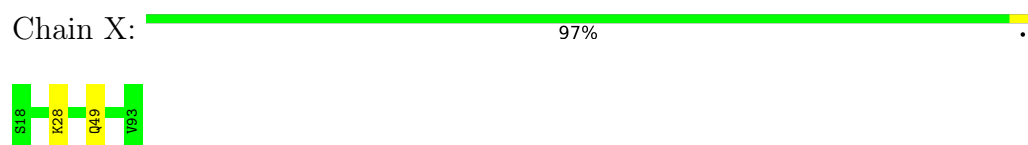
Chain V: 95%



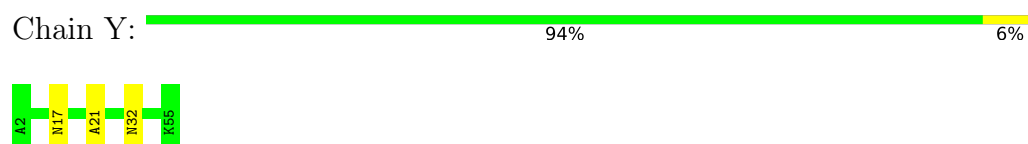
- Molecule 39: 50S ribosomal protein L25



- Molecule 40: 50S ribosomal protein L27



- Molecule 41: 50S ribosomal protein L28

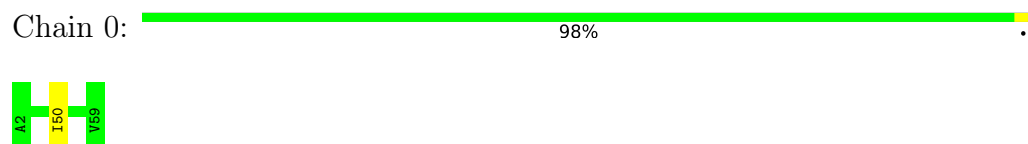


- Molecule 42: 50S ribosomal protein L29

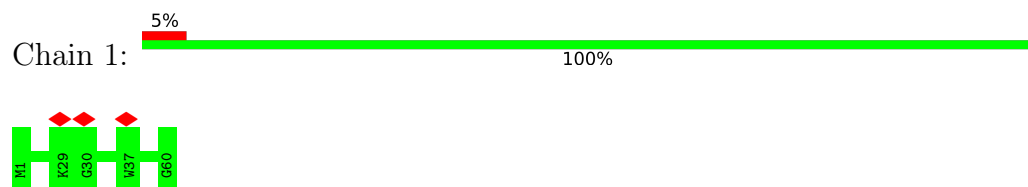


There are no outlier residues recorded for this chain.

- Molecule 43: 50S ribosomal protein L30



- Molecule 44: 50S ribosomal protein L31 type B



- Molecule 45: 50S ribosomal protein L32



There are no outlier residues recorded for this chain.

- Molecule 46: 50S ribosomal protein L33

Chain 3:  100%

There are no outlier residues recorded for this chain.

- Molecule 47: 50S ribosomal protein L34

Chain 4:  98%



- Molecule 48: 50S ribosomal protein L35

Chain 5:  100%

There are no outlier residues recorded for this chain.

- Molecule 49: 50S ribosomal protein L36

Chain 6:  100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	32689	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 ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	1.890	Depositor
Minimum map value	-0.723	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.088	Depositor
Recommended contour level	0.238	Depositor
Map size (Å)	482.68, 482.68, 482.68	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.097, 1.097, 1.097	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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	a	0.66	1/36657 (0.0%)	1.14	181/57173 (0.3%)
2	c	0.28	0/1635	0.57	0/2197
3	d	0.35	0/1650	0.57	0/2217
4	e	0.32	0/1217	0.60	0/1641
5	f	0.36	0/807	0.55	0/1087
6	g	0.30	0/1249	0.55	0/1682
7	h	0.38	0/1054	0.58	0/1417
8	i	0.28	0/1003	0.56	0/1343
9	j	0.28	0/812	0.60	0/1093
10	k	0.34	0/878	0.59	0/1185
11	l	0.33	0/1082	0.65	1/1453 (0.1%)
12	m	0.28	0/890	0.54	0/1195
13	n	0.30	0/504	0.54	0/669
14	o	0.38	0/751	0.58	0/1001
15	p	0.40	0/720	0.61	0/966
16	q	0.38	0/689	0.62	0/920
17	r	0.35	0/544	0.63	0/728
18	s	0.31	0/650	0.55	0/872
19	t	0.33	0/612	0.52	0/818
20	A	0.88	4/69661 (0.0%)	1.20	425/108645 (0.4%)
21	B	0.76	1/2769 (0.0%)	1.22	20/4310 (0.5%)
22	C	0.48	0/2147	0.69	1/2885 (0.0%)
23	D	0.51	0/1598	0.72	0/2145
24	E	0.45	0/1594	0.62	0/2155
25	F	0.35	0/1408	0.57	0/1890
26	G	0.39	0/1362	0.67	1/1833 (0.1%)
27	K	0.49	0/1148	0.71	0/1549
28	L	0.49	0/929	0.68	1/1247 (0.1%)
29	M	0.42	0/1103	0.70	0/1470
30	N	0.46	0/1140	0.69	0/1518
31	O	0.45	0/985	0.76	2/1318 (0.2%)
32	P	0.46	0/907	0.61	0/1214

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Q	0.50	0/938	0.67	0/1262
34	R	0.50	0/923	0.62	0/1227
35	S	0.45	0/794	0.65	0/1064
36	T	0.45	0/858	0.64	0/1157
37	U	0.44	0/724	0.70	0/966
38	V	0.39	0/772	0.71	1/1035 (0.1%)
39	W	0.28	0/766	0.61	0/1030
40	X	0.53	0/578	0.67	0/773
41	Y	0.32	0/430	0.55	0/573
42	Z	0.40	0/505	0.58	0/672
43	0	0.42	0/437	0.66	1/589 (0.2%)
44	1	0.37	0/487	0.64	0/662
45	2	0.47	0/436	0.62	0/578
46	3	0.35	0/423	0.55	0/563
47	4	0.42	0/374	0.68	0/485
48	5	0.42	0/528	0.63	0/689
49	6	0.47	0/309	0.60	0/409
All	All	0.72	6/150437 (0.0%)	1.07	634/225570 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	d	0	2
7	h	0	1
16	q	0	1
19	t	0	1
22	C	0	2
23	D	0	2
24	E	0	1
25	F	0	1
26	G	0	2
27	K	0	2
29	M	0	2
30	N	0	1
32	P	0	1
35	S	0	1
37	U	0	2
38	V	0	2
39	W	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
40	X	0	2
41	Y	0	1
47	4	0	1
All	All	0	29

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	B	1	U	OP3-P	-10.68	1.48	1.61
20	A	897	G	N9-C4	-5.90	1.33	1.38
20	A	1418	A	N9-C4	-5.32	1.34	1.37
20	A	1805	A	N9-C4	-5.29	1.34	1.37
1	a	939	A	N9-C4	-5.24	1.34	1.37

The worst 5 of 634 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	a	1335	C	N1-C2-O2	13.14	126.78	118.90
20	A	1130	U	N1-C2-O2	12.36	131.45	122.80
20	A	1130	U	C2-N1-C1'	12.03	132.14	117.70
1	a	1335	C	C2-N1-C1'	11.30	131.22	118.80
20	A	897	G	N3-C4-N9	-11.05	119.37	126.00

There are no chirality outliers.

5 of 29 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	d	189	GLU	Peptide
3	d	29	ARG	Peptide
7	h	22	HIS	Peptide
16	q	73	THR	Peptide
19	t	66	ILE	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
2	c	202/204 (99%)	177 (88%)	25 (12%)	0	100	100
3	d	199/201 (99%)	175 (88%)	24 (12%)	0	100	100
4	e	161/163 (99%)	146 (91%)	15 (9%)	0	100	100
5	f	95/97 (98%)	87 (92%)	8 (8%)	0	100	100
6	g	152/154 (99%)	138 (91%)	14 (9%)	0	100	100
7	h	129/131 (98%)	119 (92%)	10 (8%)	0	100	100
8	i	126/128 (98%)	107 (85%)	19 (15%)	0	100	100
9	j	97/99 (98%)	85 (88%)	12 (12%)	0	100	100
10	k	115/117 (98%)	93 (81%)	22 (19%)	0	100	100
11	l	134/136 (98%)	107 (80%)	27 (20%)	0	100	100
12	m	110/112 (98%)	90 (82%)	20 (18%)	0	100	100
13	n	58/60 (97%)	52 (90%)	6 (10%)	0	100	100
14	o	86/88 (98%)	76 (88%)	10 (12%)	0	100	100
15	p	87/89 (98%)	78 (90%)	9 (10%)	0	100	100
16	q	81/83 (98%)	69 (85%)	12 (15%)	0	100	100
17	r	64/66 (97%)	56 (88%)	8 (12%)	0	100	100
18	s	76/78 (97%)	69 (91%)	7 (9%)	0	100	100
19	t	79/81 (98%)	72 (91%)	7 (9%)	0	100	100
22	C	271/275 (98%)	228 (84%)	43 (16%)	0	100	100
23	D	205/207 (99%)	177 (86%)	27 (13%)	1 (0%)	29	66
24	E	204/206 (99%)	170 (83%)	34 (17%)	0	100	100
25	F	174/177 (98%)	153 (88%)	21 (12%)	0	100	100
26	G	172/176 (98%)	147 (86%)	23 (13%)	2 (1%)	13	49
27	K	141/145 (97%)	123 (87%)	18 (13%)	0	100	100
28	L	120/122 (98%)	102 (85%)	18 (15%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	M	144/146 (99%)	109 (76%)	33 (23%)	2 (1%)	11	45
30	N	139/141 (99%)	121 (87%)	18 (13%)	0	100	100
31	O	119/123 (97%)	94 (79%)	25 (21%)	0	100	100
32	P	115/117 (98%)	98 (85%)	17 (15%)	0	100	100
33	Q	112/114 (98%)	97 (87%)	15 (13%)	0	100	100
34	R	110/118 (93%)	104 (94%)	6 (6%)	0	100	100
35	S	98/102 (96%)	88 (90%)	10 (10%)	0	100	100
36	T	110/112 (98%)	94 (86%)	16 (14%)	0	100	100
37	U	86/89 (97%)	71 (83%)	13 (15%)	2 (2%)	6	36
38	V	99/101 (98%)	75 (76%)	21 (21%)	3 (3%)	4	32
39	W	92/94 (98%)	71 (77%)	20 (22%)	1 (1%)	14	50
40	X	74/76 (97%)	62 (84%)	12 (16%)	0	100	100
41	Y	52/54 (96%)	41 (79%)	11 (21%)	0	100	100
42	Z	59/61 (97%)	54 (92%)	5 (8%)	0	100	100
43	0	56/58 (97%)	47 (84%)	9 (16%)	0	100	100
44	1	58/60 (97%)	39 (67%)	19 (33%)	0	100	100
45	2	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
46	3	47/49 (96%)	41 (87%)	6 (13%)	0	100	100
47	4	42/44 (96%)	39 (93%)	3 (7%)	0	100	100
48	5	62/64 (97%)	53 (86%)	9 (14%)	0	100	100
49	6	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
All	All	5102/5212 (98%)	4375 (86%)	716 (14%)	11 (0%)	50	78

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
26	G	48	ASN
26	G	47	GLY
29	M	95	VAL
38	V	73	PRO
39	W	16	SER

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	
2	c	162/162 (100%)	162 (100%)	0	100	100
3	d	175/175 (100%)	175 (100%)	0	100	100
4	e	126/126 (100%)	126 (100%)	0	100	100
5	f	86/86 (100%)	86 (100%)	0	100	100
6	g	131/131 (100%)	130 (99%)	1 (1%)	81	89
7	h	112/112 (100%)	112 (100%)	0	100	100
8	i	101/101 (100%)	100 (99%)	1 (1%)	76	86
9	j	90/90 (100%)	88 (98%)	2 (2%)	52	72
10	k	91/91 (100%)	91 (100%)	0	100	100
11	l	118/118 (100%)	116 (98%)	2 (2%)	60	79
12	m	95/95 (100%)	95 (100%)	0	100	100
13	n	51/51 (100%)	50 (98%)	1 (2%)	55	74
14	o	78/78 (100%)	76 (97%)	2 (3%)	46	69
15	p	79/79 (100%)	78 (99%)	1 (1%)	69	83
16	q	76/76 (100%)	74 (97%)	2 (3%)	46	69
17	r	57/57 (100%)	55 (96%)	2 (4%)	36	63
18	s	68/68 (100%)	67 (98%)	1 (2%)	65	81
19	t	62/62 (100%)	61 (98%)	1 (2%)	62	79
22	C	225/225 (100%)	224 (100%)	1 (0%)	91	95
23	D	169/170 (99%)	167 (99%)	2 (1%)	71	84
24	E	172/172 (100%)	170 (99%)	2 (1%)	71	84
25	F	153/154 (99%)	153 (100%)	0	100	100
26	G	146/146 (100%)	146 (100%)	0	100	100
27	K	122/122 (100%)	121 (99%)	1 (1%)	81	89
28	L	98/98 (100%)	98 (100%)	0	100	100
29	M	111/112 (99%)	111 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	N	111/112 (99%)	111 (100%)	0	100	100
31	O	104/105 (99%)	103 (99%)	1 (1%)	76	86
32	P	91/91 (100%)	91 (100%)	0	100	100
33	Q	97/97 (100%)	97 (100%)	0	100	100
34	R	88/94 (94%)	88 (100%)	0	100	100
35	S	83/83 (100%)	83 (100%)	0	100	100
36	T	95/95 (100%)	95 (100%)	0	100	100
37	U	80/80 (100%)	80 (100%)	0	100	100
38	V	85/85 (100%)	85 (100%)	0	100	100
39	W	84/85 (99%)	84 (100%)	0	100	100
40	X	61/61 (100%)	61 (100%)	0	100	100
41	Y	46/47 (98%)	44 (96%)	2 (4%)	29	58
42	Z	55/55 (100%)	55 (100%)	0	100	100
43	0	49/49 (100%)	49 (100%)	0	100	100
44	1	54/55 (98%)	54 (100%)	0	100	100
45	2	46/46 (100%)	46 (100%)	0	100	100
46	3	49/49 (100%)	49 (100%)	0	100	100
47	4	38/39 (97%)	38 (100%)	0	100	100
48	5	51/51 (100%)	51 (100%)	0	100	100
49	6	35/35 (100%)	35 (100%)	0	100	100
All	All	4356/4371 (100%)	4331 (99%)	25 (1%)	86	93

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	s	6	LYS
23	D	119	PHE
41	Y	32	ASN
22	C	257	TYR
23	D	168	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
25	F	2	ASN
34	R	81	HIS
48	5	4	GLN
25	F	37	ASN
32	P	20	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1526/1528 (99%)	392 (25%)	0
20	A	2890/2903 (99%)	708 (24%)	24 (0%)
21	B	113/116 (97%)	30 (26%)	1 (0%)
All	All	4529/4547 (99%)	1130 (24%)	25 (0%)

5 of 1130 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	5	A
1	a	6	G
1	a	7	A
1	a	11	U
1	a	12	G

5 of 25 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
20	A	1502	G
20	A	1585	U
21	B	101	U
20	A	1584	G
20	A	1604	A

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
20	A	2
1	a	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	928:U	O3'	931:C	P	12.58
1	a	75:U	O3'	96:U	P	12.00
1	A	1579:U	O3'	1583:A	P	10.23

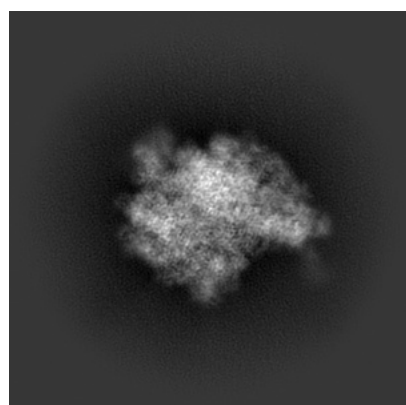
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0657. These allow visual inspection of the internal detail of the map and identification of artifacts.

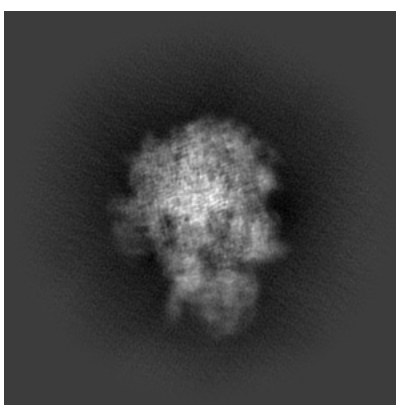
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

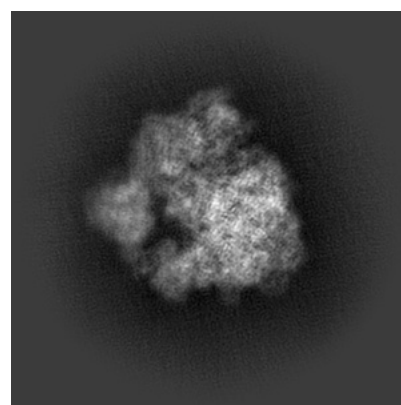
6.1.1 Primary map



X



Y

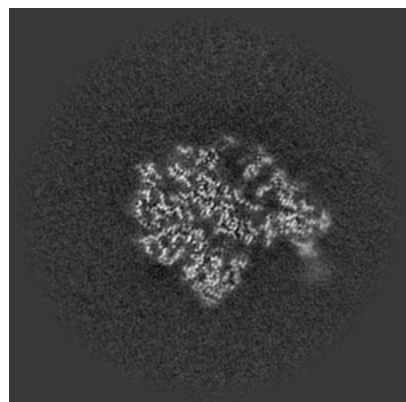


Z

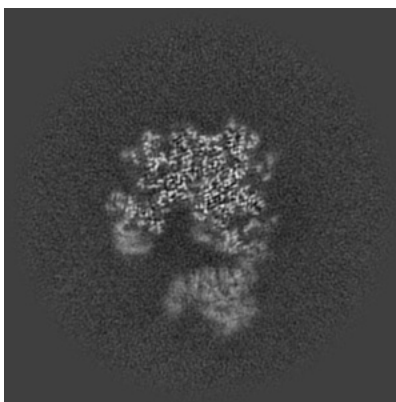
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

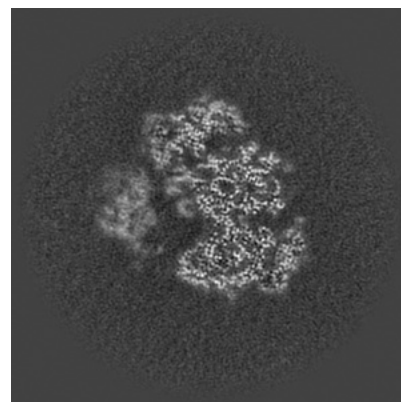
6.2.1 Primary map



X Index: 220



Y Index: 220

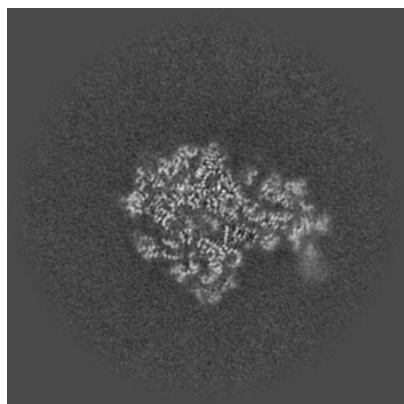


Z Index: 220

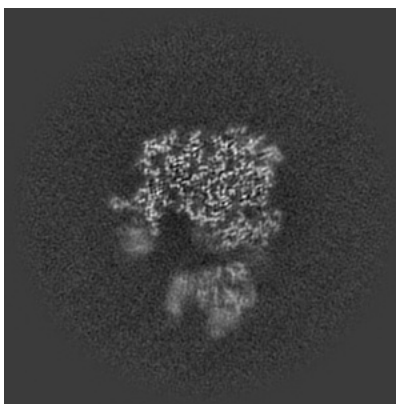
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

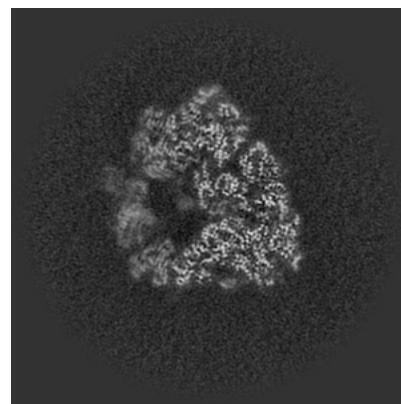
6.3.1 Primary map



X Index: 228



Y Index: 231



Z Index: 209

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.238. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

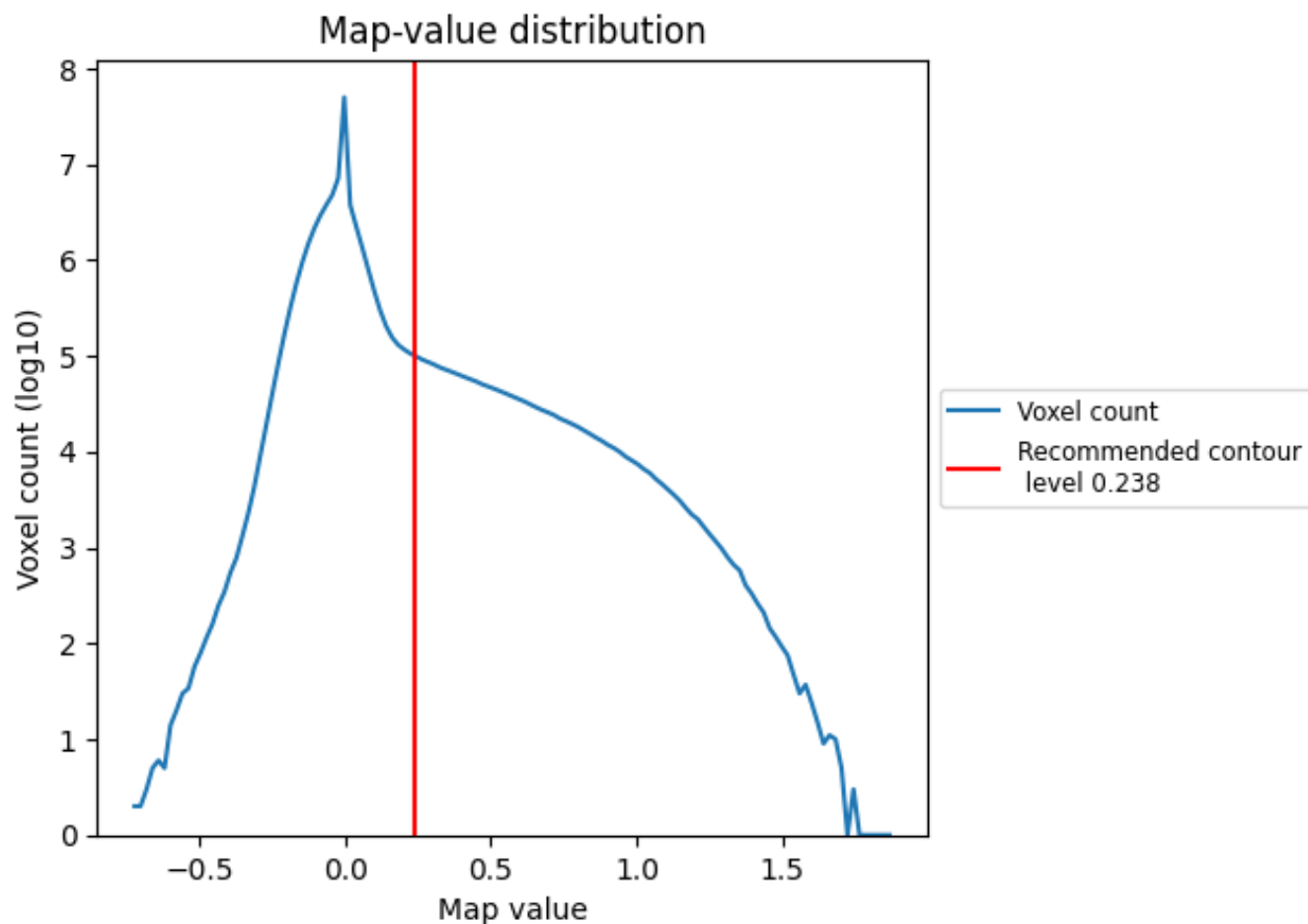
6.5 Mask visualisation

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

7 Map analysis [i](#)

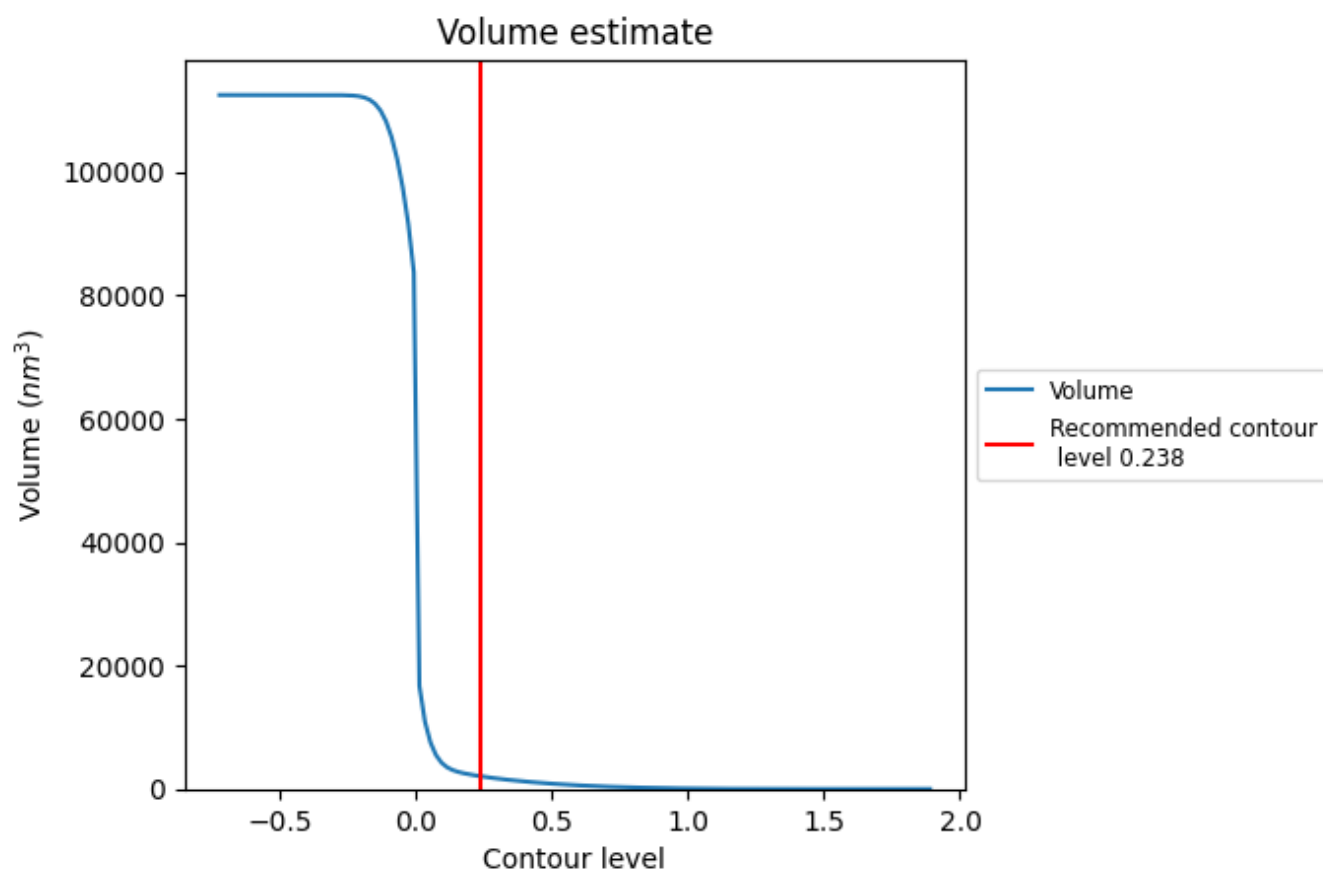
This section contains the results of statistical analysis of the map.

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.

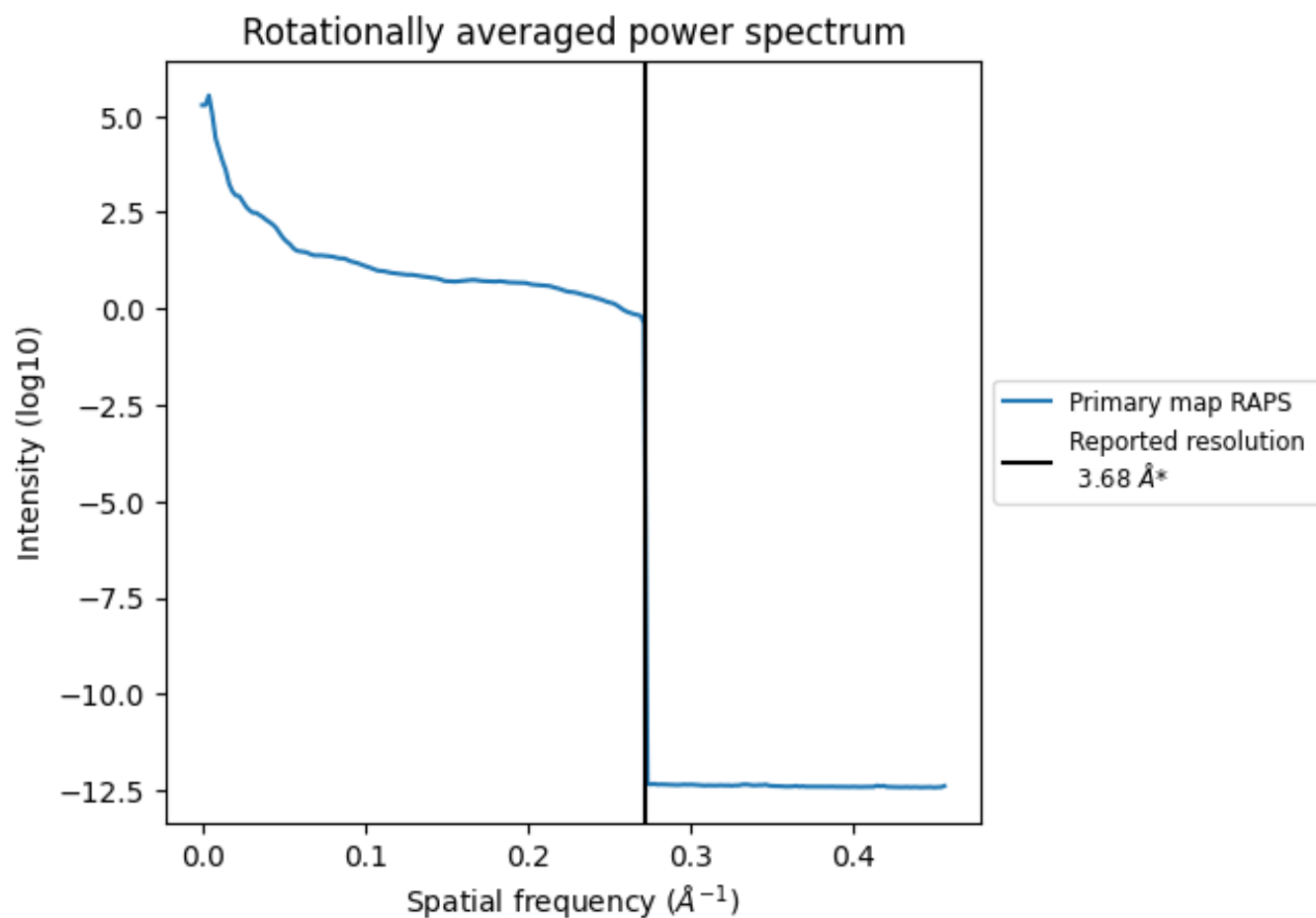
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2048 nm^3 ; this corresponds to an approximate mass of 1850 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 0.272 Å⁻¹

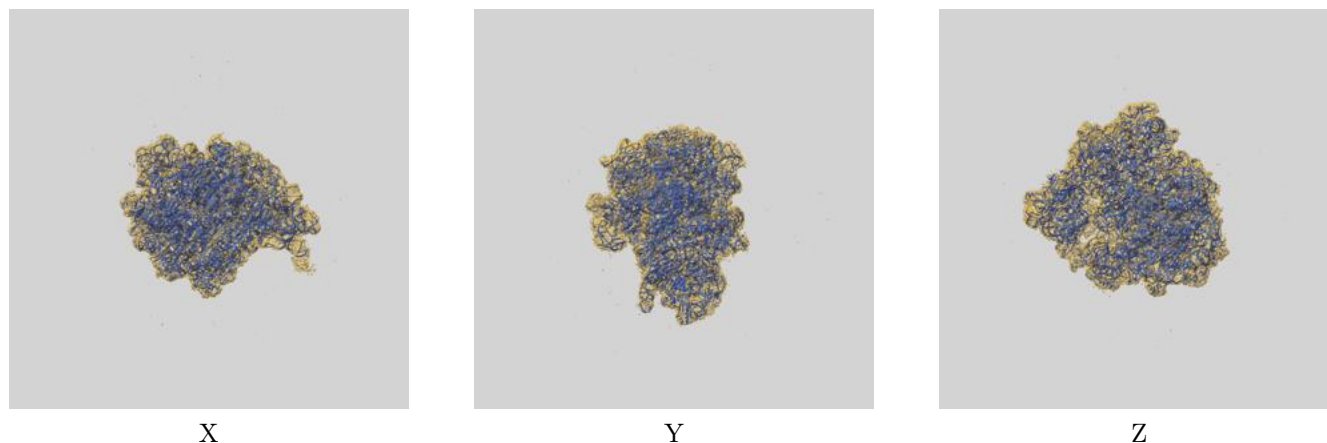
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

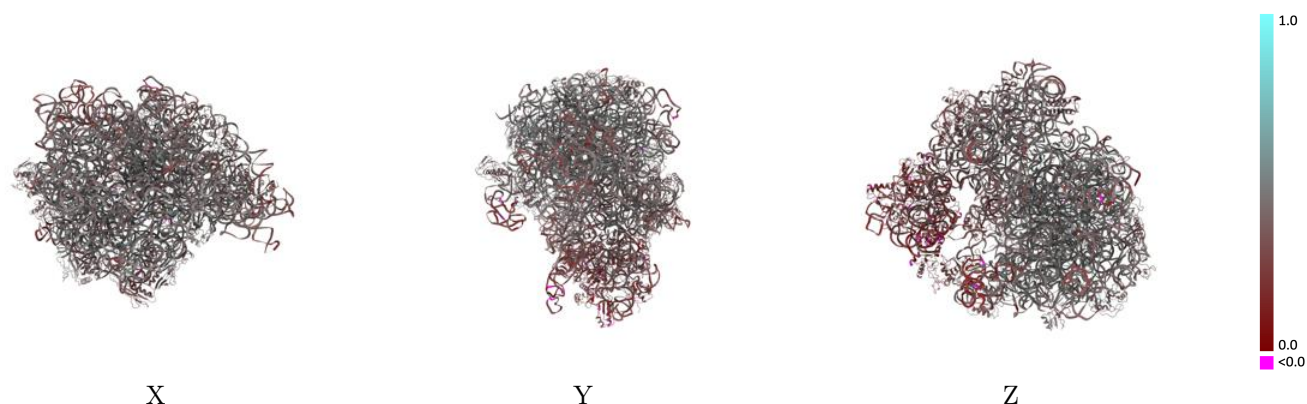
This section contains information regarding the fit between EMDB map EMD-0657 and PDB model 6O8X. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



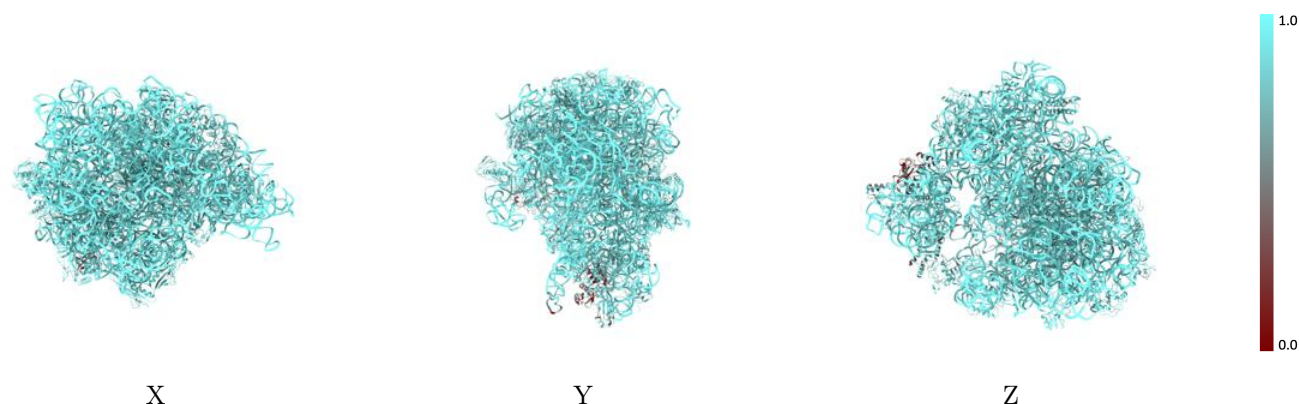
The images above show the 3D surface view of the map at the recommended contour level 0.238 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



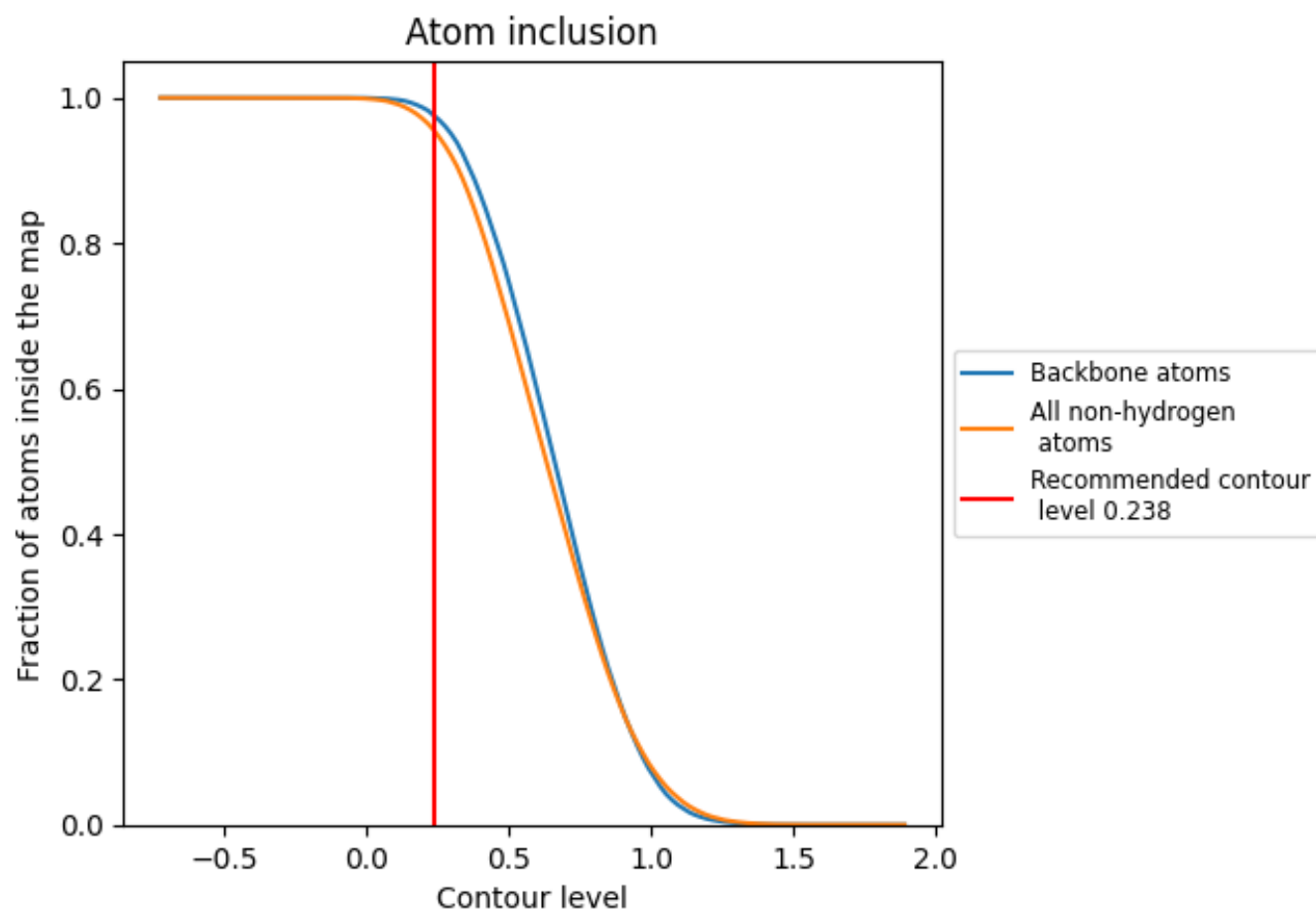
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.238).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% 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 (0.238) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9546	 0.4020
0	 0.9091	 0.4630
1	 0.8827	 0.2890
2	 0.9571	 0.4650
3	 0.8762	 0.4560
4	 0.9229	 0.4470
5	 0.9135	 0.4770
6	 0.9559	 0.4600
A	 0.9898	 0.4290
B	 0.9956	 0.4020
C	 0.9261	 0.4520
D	 0.9297	 0.4690
E	 0.9220	 0.4370
F	 0.8602	 0.3250
G	 0.8871	 0.3780
K	 0.9303	 0.4550
L	 0.9041	 0.4720
M	 0.9317	 0.4460
N	 0.8181	 0.4070
O	 0.9183	 0.4350
P	 0.8923	 0.3700
Q	 0.9153	 0.4560
R	 0.9018	 0.4120
S	 0.9239	 0.4500
T	 0.9232	 0.4500
U	 0.9148	 0.4240
V	 0.8647	 0.3960
W	 0.3154	 0.2990
X	 0.9459	 0.4660
Y	 0.8908	 0.4570
Z	 0.9045	 0.3750
a	 0.9879	 0.3700
c	 0.5307	 0.2820
d	 0.8957	 0.3340
e	 0.8848	 0.3640



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Chain	Atom inclusion	Q-score
f	 0.8814	 0.3990
g	 0.8562	 0.2080
h	 0.9154	 0.4090
i	 0.8956	 0.2830
j	 0.8100	 0.2520
k	 0.9092	 0.3700
l	 0.8566	 0.3950
m	 0.7680	 0.2210
n	 0.8926	 0.2790
o	 0.8822	 0.4010
p	 0.9291	 0.3930
q	 0.8763	 0.4040
r	 0.8942	 0.3900
s	 0.8484	 0.2450
t	 0.8865	 0.3680