



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:52 PM UTC

PDB ID : 8BH6 / pdb_00008bh6
EMDB ID : EMD-16048
Title : Mature 30S ribosomal subunit from Staphylococcus aureus
Authors : Garaeva, N.; Fatkhullin, B.; Jenner, L.; Soufari, H.; Yusupov, M.; Usachev, K.
Deposited on : 2022-10-30
Resolution : 3.70 Å(reported)

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A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

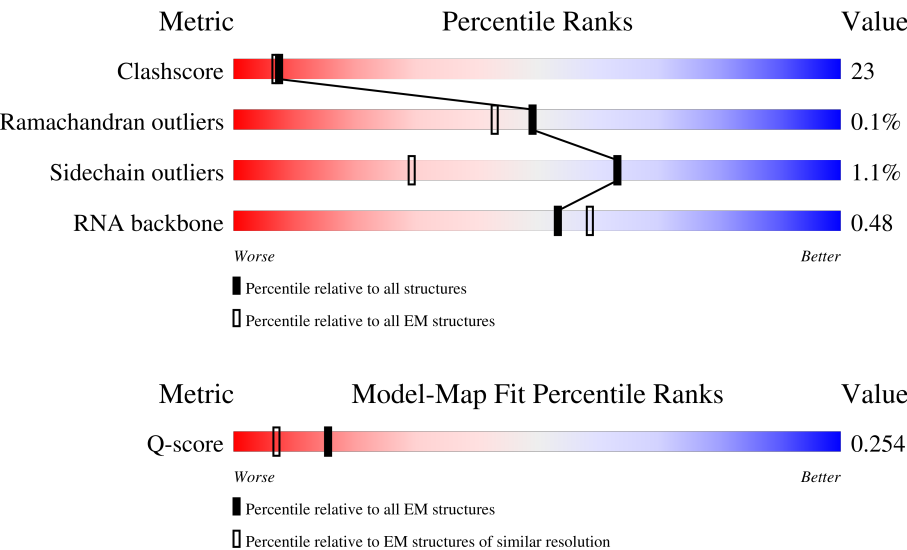
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



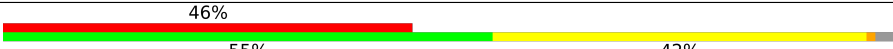
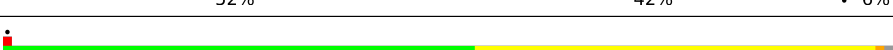
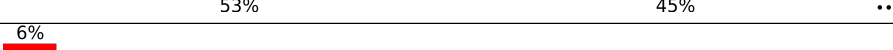
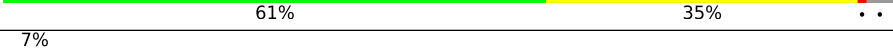
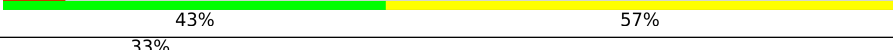
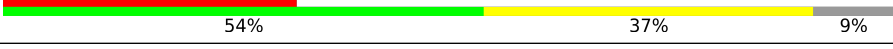
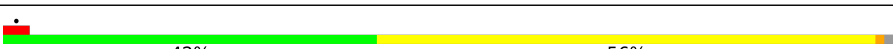
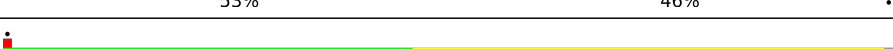
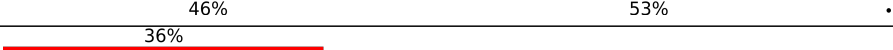
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	1547	27%63%10%
2	b	255	51% 54%33%12%
3	c	217	11% 69%27%5%

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Mol	Chain	Length	Quality of chain
4	d	200	
5	e	166	
6	f	98	
7	g	156	
8	h	132	
9	i	132	
10	j	102	
11	k	129	
12	l	137	
13	m	121	
14	n	61	
15	o	89	
16	p	91	
17	q	87	
18	r	80	
19	s	92	
20	t	83	

2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 51548 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 ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1547	Total	C	N	O	P	0	0
			33126	14790	6036	10753	1547		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	224	Total	C	N	O	S	0	0
			1802	1147	315	333	7		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	c	207	Total	C	N	O	S	0	0
			1634	1030	305	297	2		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	192	Total	C	N	O	S	0	0
			1570	992	294	282	2		

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	164	Total	C	N	O	S	0	0
			1234	772	228	232	2		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	96	Total	C	N	O	S	0	0
			798	503	139	153	3		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	147	Total	C	N	O	S	0	0
			1189	744	227	214	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	131	Total	C	N	O	S	0	0
			1032	652	183	193	4		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	i	128	Total	C	N	O	S	0	0
			1017	629	203	184	1		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	j	102	Total	C	N	O	S	0	0
			813	512	148	150	3		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	118	Total	C	N	O	S	0	0
			880	543	169	165	3		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	135	Total	C	N	O	S	0	0
			1062	658	218	184	2		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	109	Total	C	N	O	S	0	0
			873	535	174	163	1		

- Molecule 14 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	60	Total	C	N	O	S	0	0
			493	309	99	80	5		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	88	Total	C	N	O	S	0	0
			738	454	153	130	1		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	90	Total	C	N	O	S	0	0
			712	448	132	131	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	86	Total	C	N	O	S	0	0
			707	447	126	133	1		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	r	70	Total	C	N	O	S	0	0
			585	370	114	98	3		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	84	Total	C	N	O	S	0	0
			677	434	120	121	2		

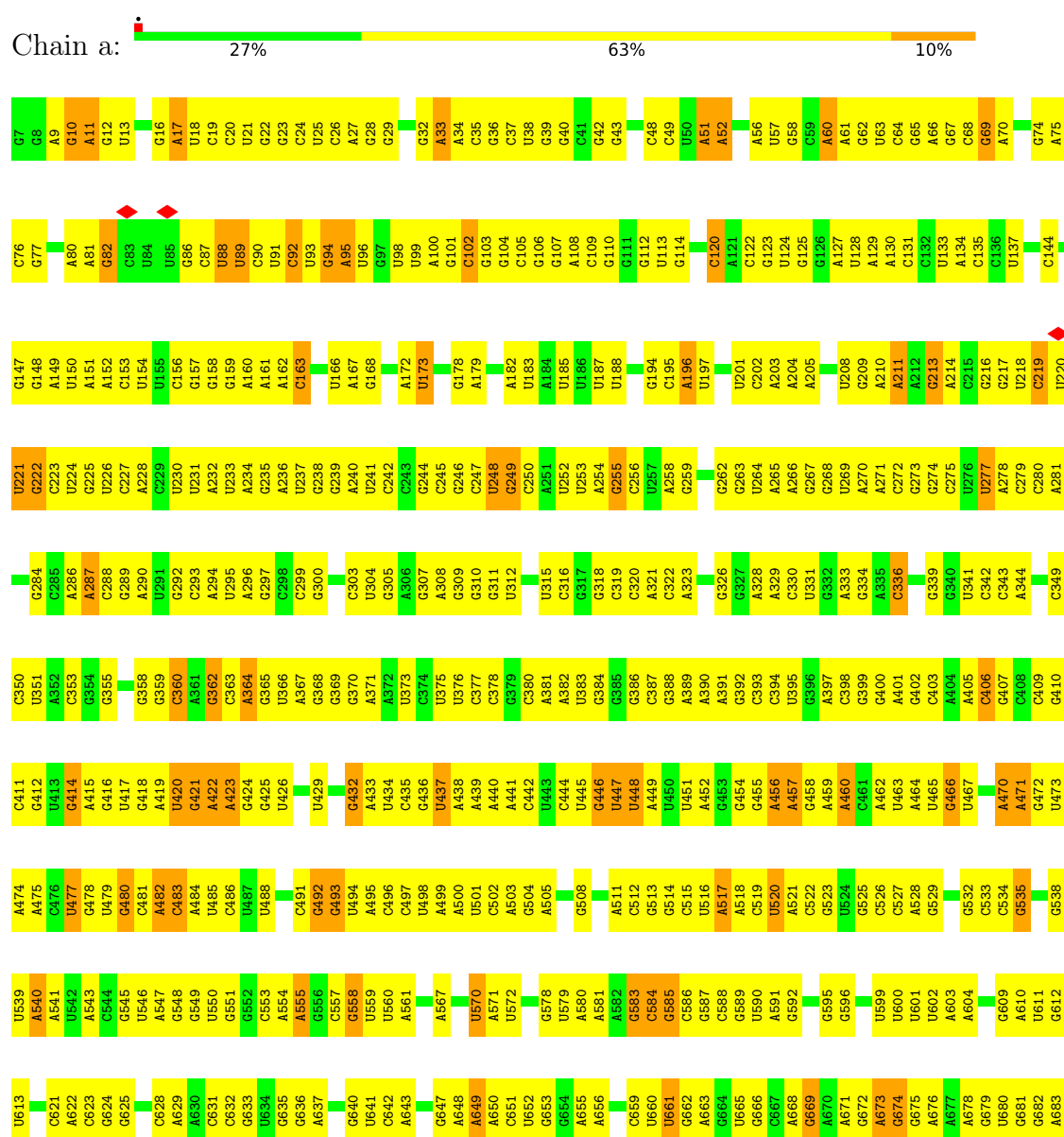
- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	80	Total	C	N	O	S	0	0
			606	367	119	118	2		

3 Residue-property plots

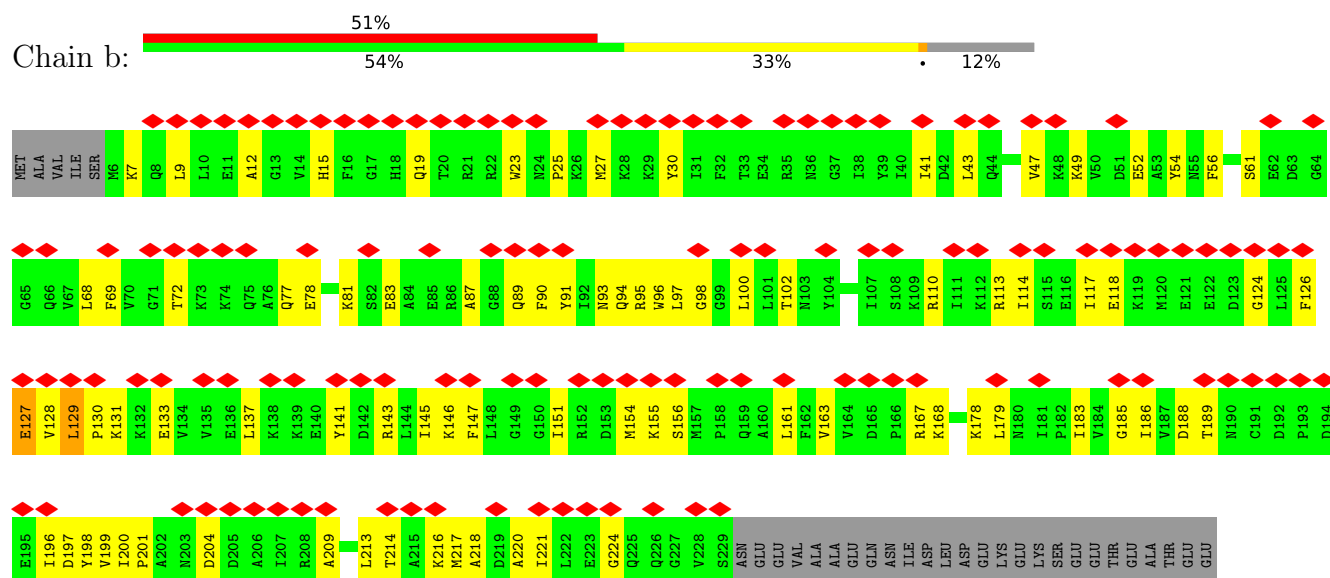
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S ribosomal RNA

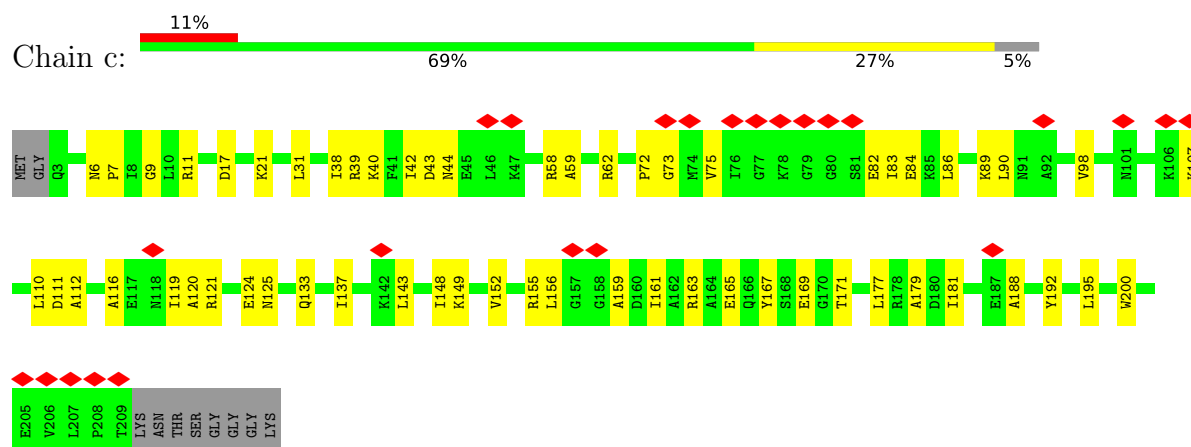


A1546	C1547	C1548	U1549	C1550	C1551	U1552	U1553	A1481	G1482	G1483	U1484	G1485	G1486	U1487	A1488	G1489	A1490	G1491	G1492	U1493	G1494	A1495	U1496	G1497	G1498	G1499	G1500	G1501	U1502	G1503	G1506	U1507	C1508	G1509	U1510	A1511	A1514	A1515	U1518	A1519	A1520	U1524	A1525	U1526	C1527	G1528	G1529	A1530	G1531	G1532	G1533	U1534	G1535	C1536	G1537	G1538	C1539	U1540	G1541	G1542	A1543	G1478	U1544	C1545	A1418	A1419	G1420	A1421	G1422	G1423	A1424	G1425	G1426	A1427	G1428	A1491	A1492	G1430	U1431	U1432	U1433	G1434	U1435	A1436	A1437	G1438	A1439	G1440	G1441	G1442	G1443	G1446	G1447	G1450	U1451	G1452	G1453	A1454	A1457	A1458	C1459	U1461	U1462	U1463	U1464	A1465	G1466	G1467	A1468	G1469	G1470	U1471	A1472	G1473	C1474	G1475	G1476	U1477	U1543	G1478	G1479	A1480	G1349	A1350	C1353	G1354	C1355	U1356	A1357	G1358	U1359	A1360	A1361	U1362	C1363	G1364	U1365	A1366	G1367	A1368	U1369	C1370	A1371	G1372	G1373	U1374	U1375	G1376	G1377	U1378	A1379	C1380	G1381	G1382	U1383	G1384	A1385	U1386	U1387	G1397	G1398	U1399	C1400	U1401	U1402	G1403	A1404	A1405	C1406	A1407	U1408	A1409	C1410	G1411	G1412	C1413	G1414	C1415	G1416	U1417	U1418	A1419	G1420	A1421	G1422	G1423	A1424	G1425	G1426	A1427	G1428	A1283	C1284	A1286	A1289	A1290	A1291	U1292	G1293	C1294	U1297	A1298	A1299	U1302	U1303	G1304	U1305	U1306	C1307	A1310	G1311	U1312	U1313	G1314	G1315	G1316	A1317	G1320	U1321	A1322	G1323	U1324	C1325	U1326	G1327	C1328	A1329	A1330	C1331	U1332	C1333	G1334	U1337	A1338	C1339	A1340	U1341	G1342	A1343	A1344	G1345	C1346	U1347	G1348	G1283	C1284	A1286	A1289	A1290	A1291	U1292	G1293	C1294	U1297	A1298	A1299	U1302	U1303	G1304	U1305	U1306	C1307	A1310	G1311	U1312	U1313	G1314	G1315	G1316	A1317	G1320	U1321	A1322	G1323	U1324	C1325	U1326	G1327	C1328	A1329	A1330	C1331	U1332	C1333	G1334	U1337	A1338	C1339	A1340	U1341	G1342	A1343	A1344	G1345	C1346	U1347	G1348	G1260	C1261	A1262	A1263	G1266	C1267	A1268	G1269	C1270	G1271	A1272	A1273	G1276	G1277	G1278	A1279	A1280	G1281	G1282	G1185	G1186	G1187	G1188	G1189	A1190	G1191	G1192	G1195	G1196	G1197	G1198	A1199	U1200	G1201	G1204	A1207	A1208	A1209	U1210	U1211	U1147	A1148	A1149	G1150	U1151	U1152	G1153	G1154	G1155	C1158	U1159	C1160	A1163	G1164	U1165	U1166	G1167	A1168	C1169	U1170	G1171	C1172	C1173	G1174	G1175	U1176	G1177	A1178	C1179	A1180	A1181	A1182	G1185	G1186	G1187	G1188	G1189	A1190	G1191	G1192	G1195	G1196	G1197	G1198	A1199	U1200	G1201	G1204	A1207	A1208	A1209	U1210	U1211	C1083	G1084	U1085	G1086	U1087	G1088	U1089	G1090	G1091	U1092	G1093	A1094	U1095	G1096	U1097	U1098	A1099	G1100	G1101	U1102	U1103	G1106	U1107	C1108	C1109	C1110	G1111	G1112	U1113	A1114	C1115	G1116	A1117	G1118	C1119	G1120	A1123	C1124	C1125	C1126	U1127	U1128	A1129	A1130	G1131	C1132	U1133	U1134	A1135	G1136	U1137	G1138	G1139	G1140	C1141	A1142	C1144	C1020	U1021	G1022	G1023	U1024	G1025	A1026	U1027	U1028	G1029	U1030	G1031	U1032	C1033	U1034	A1035	C1036	G1037	G1038	C1039	U1040	U1041	G1042	G1043	U1044	G1045	G1046	G1047	A1048	C1049	A1050	A1051	A1052	G1053	U1054	G1055	A1056	C1057	A1058	G1059	G1060	U1061	G1065	C1066	A1067	U1068	G1069	U1070	U1071	U1072	G1073	U1074	C1075	G1076	U1077	G1080	C1081	U1082	A956	G957	C958	C959	U960	G961	U962	G963	G964	U966	U970	G973	A974	G975	C976	C977	A978	C980	G981	G982	G983	A984	A985	G986	A987	U988	C989	U990	U991	U992	A993	C994	C995	A996	A997	A998	U999	C1000	U1001	U1002	G1003	A1004	C1005	A1006	U1007	C1008	C1009	U1012	G1013	A1014	C1015	A1016	A1017	C1018	U1019	C887	U888	C889	C890	U891	C892	C893	U894	A899	G900	U901	A902	C903	G904	A905	C906	C907	G908	C909	A910	U911	G912	G913	G916	A917	A918	U919	C920	U921	C922	G926	G927	A928	C929	U930	U931	G932	A933	G934	G935	C936	G937	G938	A939	G943	C944	A945	C946	A947	A948	G949	C950	G951	G954	G955	C818	C819	U821	C825	G826	A827	U828	G829	A830	G833	C834	U835	A836	A837	G838	U839	G840	U841	A910	U842	G844	G847	G848	U851	C852	C854	G855	C856	C857	U858	C859	U860	U861	A862	G863	U864	G865	C866	U867	G868	C869	A870	C871	C872	U873	C804	C805	U806	G807	G808	A742	C743	U744	C814	A815	C816	G817	A886	C747	A834	U885	C886	C887	C888	U889	G890	G891	U892	G893	U894	A895	G896	C897	G898	C899	U900	G701	U702	A703	A704	C707	G708	G711	A712	G713	U714	U715	A716	U717	G718	U719	A720	G721	G722	A723	U724	C725	A726	C727	G728	A729	G730	U731	G732	G733	C734	C740	C741	A742	C743	U744	C745	U746	C747	A748	G749	U750	G751	C752	U753	G754	U755	A756	U757	G758	U759	A760	G761	C762	G763	U764	G765	U766	A767	U770	G771	G772	G773	A774	U775	G776	U777	G781	G782	U783	A784	U785	C786	U787	A788	U789	A790	C791	A792	G793	C794	G795	U796	U797	A800	C804	C805	U806	G807	G808	A874	A875	C876	G877	C878	A882	A886
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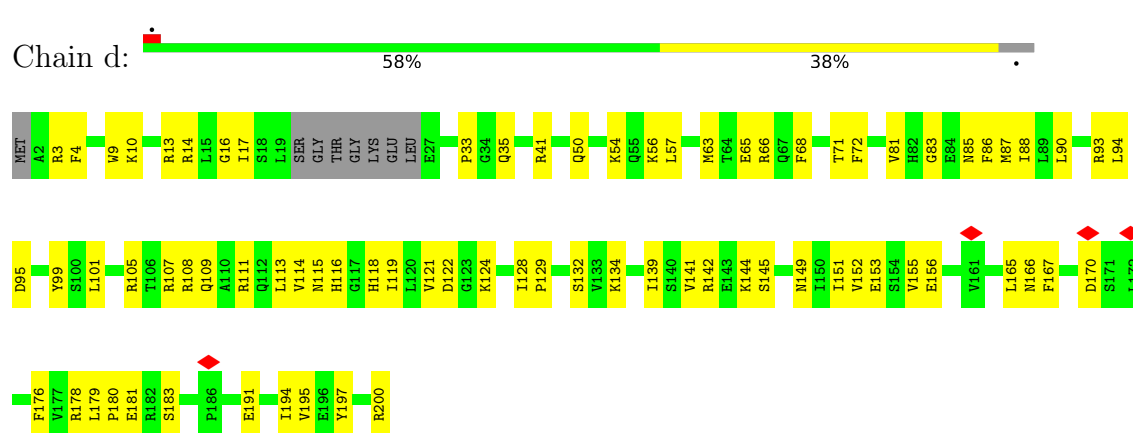
- Molecule 2: 30S ribosomal protein S2



- Molecule 3: 30S ribosomal protein S3

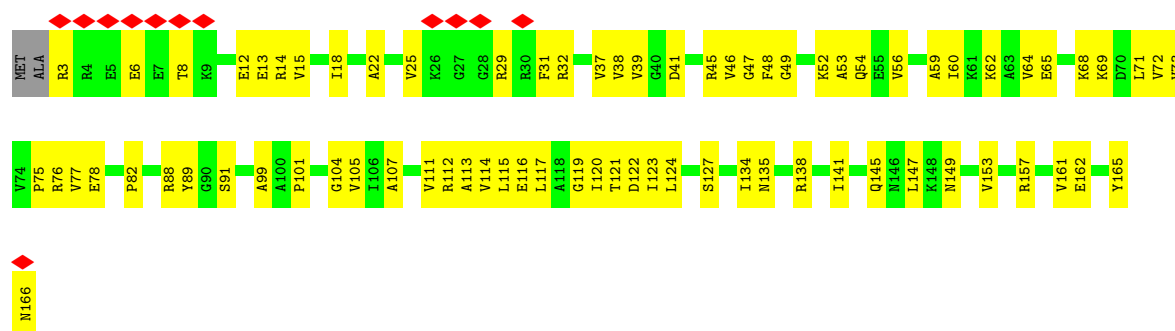


- Molecule 4: 30S ribosomal protein S4



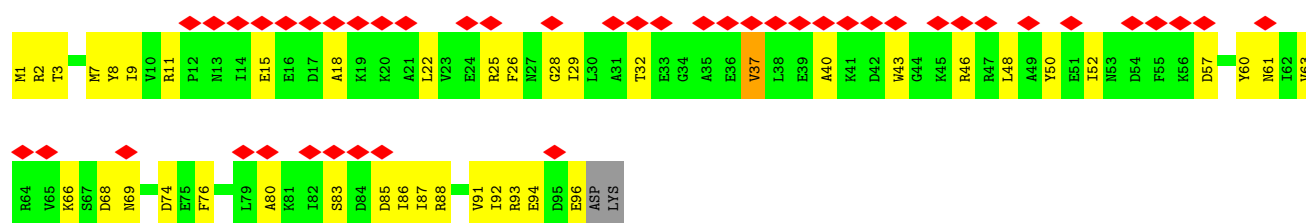
- Molecule 5: 30S ribosomal protein S5

Chain e: 



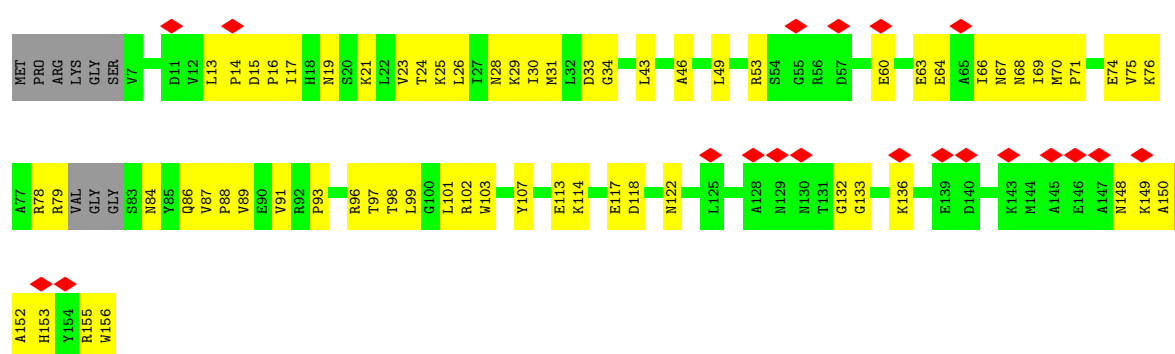
• Molecule 6: 30S ribosomal protein S6

Chain f: 



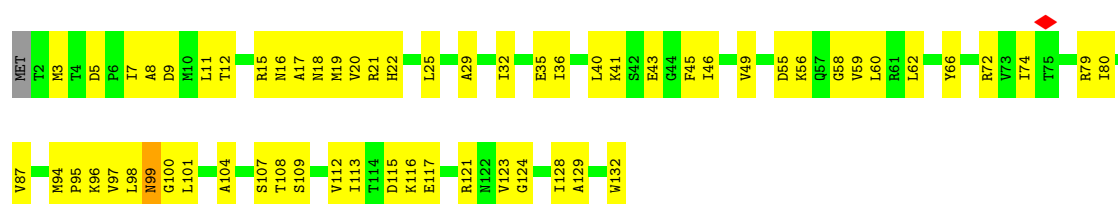
• Molecule 7: 30S ribosomal protein S7

Chain g: 

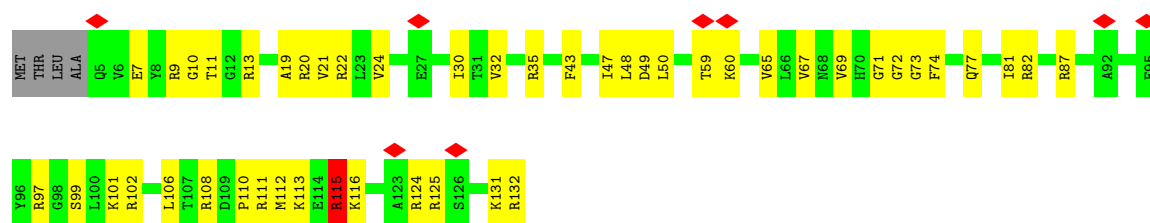


• Molecule 8: 30S ribosomal protein S8

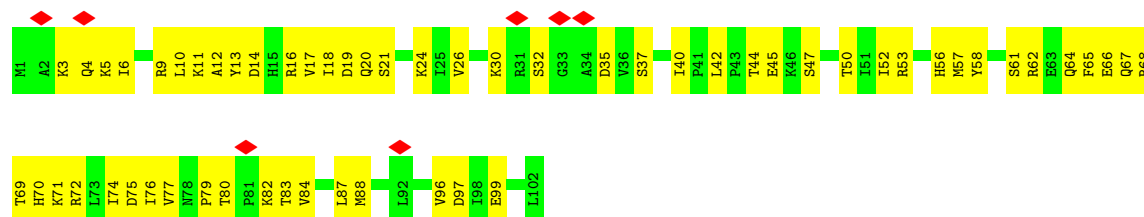
Chain h: 



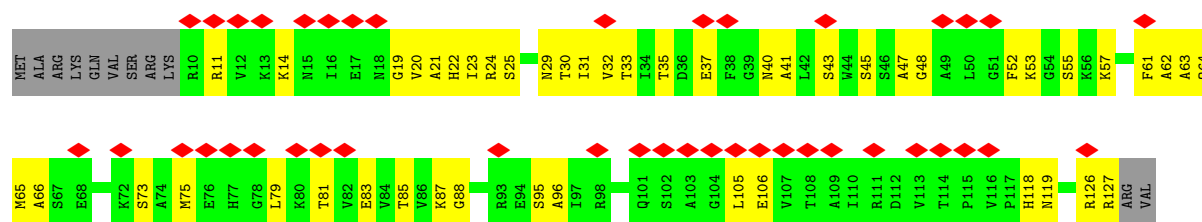
• Molecule 9: 30S ribosomal protein S9



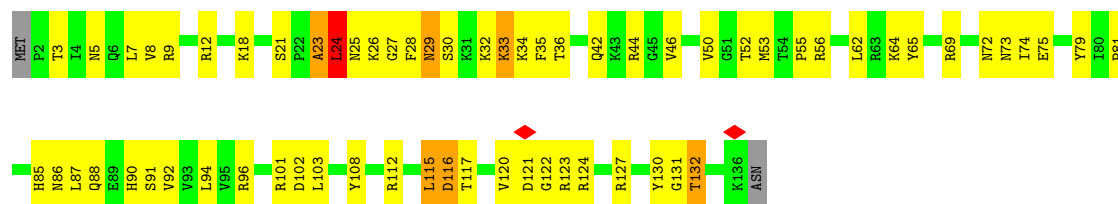
- Molecule 10: 30S ribosomal protein S10



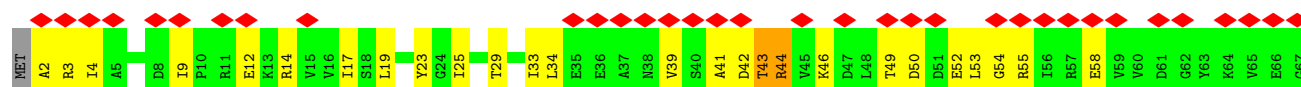
- Molecule 11: 30S ribosomal protein S11

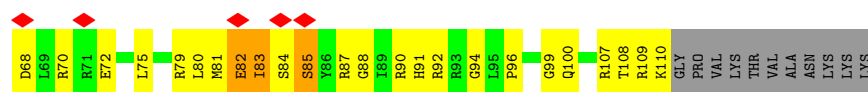


- Molecule 12: 30S ribosomal protein S12



- Molecule 13: 30S ribosomal protein S13

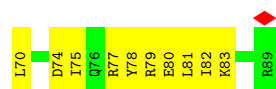
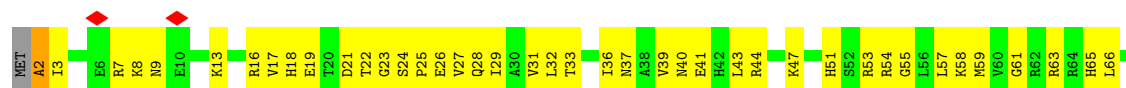




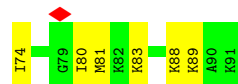
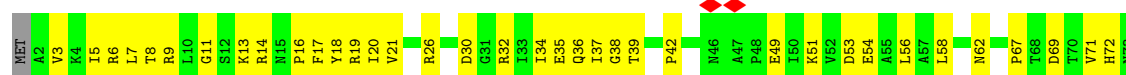
- Molecule 14: 30S ribosomal protein S14 type Z



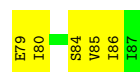
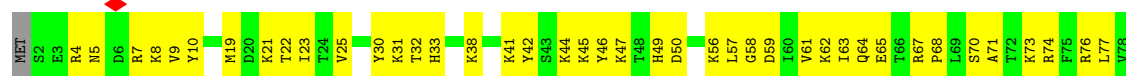
- Molecule 15: 30S ribosomal protein S15



- Molecule 16: 30S ribosomal protein S16

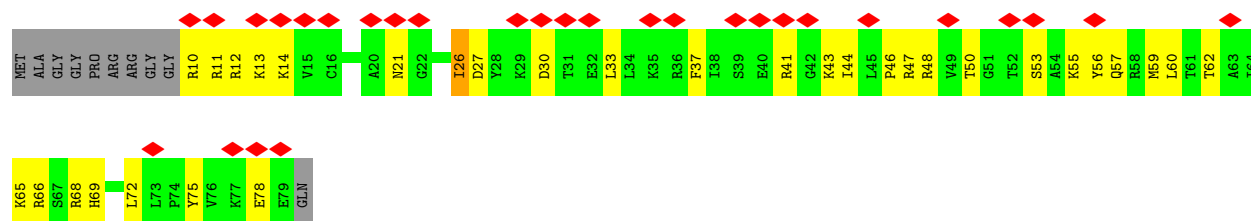


- Molecule 17: 30S ribosomal protein S17

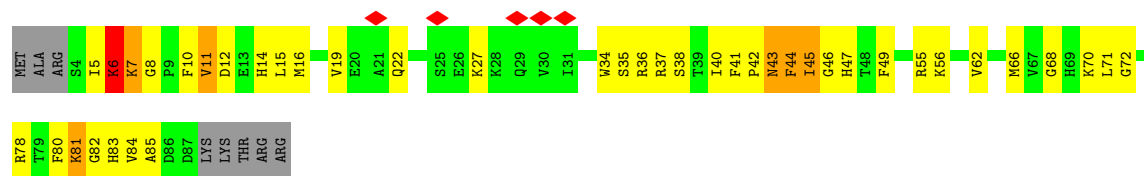


- Molecule 18: 30S ribosomal protein S18

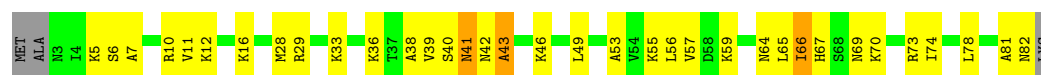




• Molecule 19: 30S ribosomal protein S19



• Molecule 20: 30S ribosomal protein S20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	326920	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	3.7	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	3.439	Depositor
Minimum map value	-1.008	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.108	Depositor
Recommended contour level	0.423	Depositor
Map size ($\text{\AA}$)	460.80002, 460.80002, 460.80002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.2, 1.2, 1.2	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.19	0/37086	0.32	0/57833
2	b	0.21	0/1829	0.54	0/2454
3	c	0.19	0/1657	0.48	0/2228
4	d	0.22	0/1599	0.49	0/2146
5	e	0.23	0/1248	0.47	0/1680
6	f	0.19	0/809	0.51	1/1085 (0.1%)
7	g	0.20	0/1207	0.56	1/1625 (0.1%)
8	h	0.24	0/1044	0.57	1/1401 (0.1%)
9	i	0.31	1/1033 (0.1%)	0.58	2/1386 (0.1%)
10	j	0.30	0/825	0.60	0/1110
11	k	0.22	0/895	0.50	0/1207
12	l	0.34	1/1079 (0.1%)	0.66	2/1445 (0.1%)
13	m	0.24	0/879	0.82	2/1177 (0.2%)
14	n	0.25	0/501	0.85	3/662 (0.5%)
15	o	0.19	0/747	0.59	2/996 (0.2%)
16	p	0.22	0/723	0.58	0/971
17	q	0.21	0/715	0.50	0/955
18	r	0.17	0/594	0.56	2/792 (0.3%)
19	s	0.22	0/695	0.67	3/934 (0.3%)
20	t	0.27	0/606	0.71	4/810 (0.5%)
All	All	0.21	2/55771 (0.0%)	0.42	23/82897 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	i	115	ARG	CA-C	-5.40	1.45	1.53
12	l	131	GLY	C-N	-5.29	1.26	1.33

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	m	43	THR	N-CA-C	-15.06	83.62	108.48
12	l	24	LEU	N-CA-C	-11.98	97.93	112.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	n	19	ARG	N-CA-C	-10.69	98.52	112.41
13	m	43	THR	CB-CA-C	9.62	131.93	114.52
20	t	43	ALA	CB-CA-C	-8.99	93.62	111.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	33126	0	16679	1200	0
2	b	1802	0	1861	70	0
3	c	1634	0	1699	45	0
4	d	1570	0	1597	66	0
5	e	1234	0	1293	61	0
6	f	798	0	794	40	0
7	g	1189	0	1218	54	0
8	h	1032	0	1082	63	0
9	i	1017	0	1039	43	0
10	j	813	0	859	60	0
11	k	880	0	899	58	0
12	l	1062	0	1130	67	0
13	m	873	0	916	53	0
14	n	493	0	519	40	0
15	o	738	0	769	45	0
16	p	712	0	744	41	0
17	q	707	0	749	47	0
18	r	585	0	625	31	0
19	s	677	0	672	53	0
20	t	606	0	650	44	0
All	All	51548	0	35794	1955	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 23.

The worst 5 of 1955 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)
20:t:43:ALA:O	20:t:46:LYS:HG2	1.38	1.23
1:a:673:A:H62	1:a:732:G:H1	1.08	0.98
1:a:602:U:H3	1:a:653:G:H1	1.13	0.96
1:a:901:U:H2'	1:a:902:A:H8	1.32	0.95
19:s:12:ASP:H	19:s:38:SER:HB3	1.29	0.95

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	b	222/255 (87%)	207 (93%)	15 (7%)	0	100	100
3	c	205/217 (94%)	195 (95%)	10 (5%)	0	100	100
4	d	188/200 (94%)	179 (95%)	9 (5%)	0	100	100
5	e	162/166 (98%)	157 (97%)	5 (3%)	0	100	100
6	f	94/98 (96%)	88 (94%)	6 (6%)	0	100	100
7	g	143/156 (92%)	132 (92%)	11 (8%)	0	100	100
8	h	129/132 (98%)	125 (97%)	3 (2%)	1 (1%)	16	48
9	i	126/132 (96%)	118 (94%)	8 (6%)	0	100	100
10	j	100/102 (98%)	91 (91%)	9 (9%)	0	100	100
11	k	116/129 (90%)	112 (97%)	4 (3%)	0	100	100
12	l	133/137 (97%)	118 (89%)	14 (10%)	1 (1%)	16	48
13	m	107/121 (88%)	100 (94%)	6 (6%)	1 (1%)	14	45
14	n	58/61 (95%)	50 (86%)	8 (14%)	0	100	100
15	o	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
16	p	88/91 (97%)	82 (93%)	6 (7%)	0	100	100
17	q	84/87 (97%)	70 (83%)	14 (17%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	r	68/80 (85%)	64 (94%)	4 (6%)	0	100	100
19	s	82/92 (89%)	74 (90%)	8 (10%)	0	100	100
20	t	78/83 (94%)	76 (97%)	2 (3%)	0	100	100
All	All	2269/2428 (94%)	2118 (93%)	148 (6%)	3 (0%)	49	78

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	h	116	LYS
12	l	29	ASN
13	m	83	ILE

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	b	194/221 (88%)	192 (99%)	2 (1%)	68	74
3	c	169/175 (97%)	169 (100%)	0	100	100
4	d	169/175 (97%)	169 (100%)	0	100	100
5	e	130/131 (99%)	130 (100%)	0	100	100
6	f	84/86 (98%)	84 (100%)	0	100	100
7	g	126/132 (96%)	126 (100%)	0	100	100
8	h	112/113 (99%)	112 (100%)	0	100	100
9	i	106/109 (97%)	105 (99%)	1 (1%)	70	75
10	j	91/91 (100%)	91 (100%)	0	100	100
11	k	94/104 (90%)	94 (100%)	0	100	100
12	l	117/119 (98%)	111 (95%)	6 (5%)	21	47
13	m	94/104 (90%)	91 (97%)	3 (3%)	34	56
14	n	51/53 (96%)	49 (96%)	2 (4%)	28	53
15	o	80/81 (99%)	80 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	p	76/77 (99%)	76 (100%)	0	100	100
17	q	81/82 (99%)	81 (100%)	0	100	100
18	r	63/68 (93%)	63 (100%)	0	100	100
19	s	73/80 (91%)	67 (92%)	6 (8%)	10	36
20	t	67/69 (97%)	66 (98%)	1 (2%)	57	68
All	All	1977/2070 (96%)	1956 (99%)	21 (1%)	63	73

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	s	6	LYS
19	s	43	ASN
20	t	41	ASN
19	s	44	PHE
19	s	11	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
12	l	77	ASN
20	t	82	ASN
15	o	9	ASN
20	t	41	ASN
13	m	76	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1546/1547 (99%)	258 (16%)	0

5 of 258 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	10	G
1	a	11	A
1	a	17	A
1	a	32	G
1	a	33	A

There are no RNA pucker outliers to report.

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 [i](#)

There are no chain breaks in this entry.

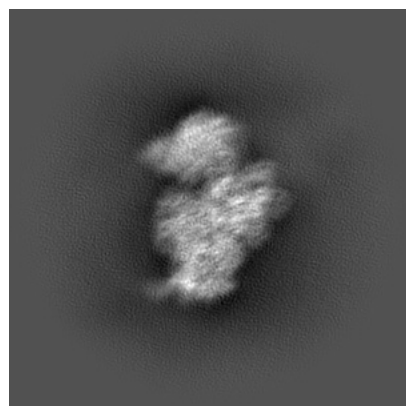
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16048. These allow visual inspection of the internal detail of the map and identification of artifacts.

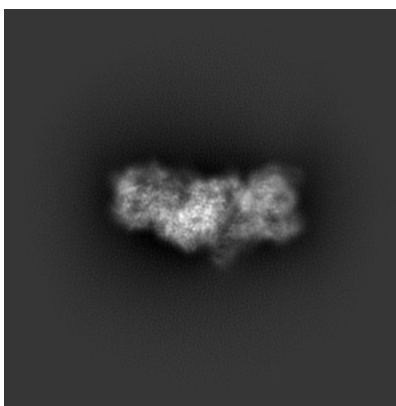
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

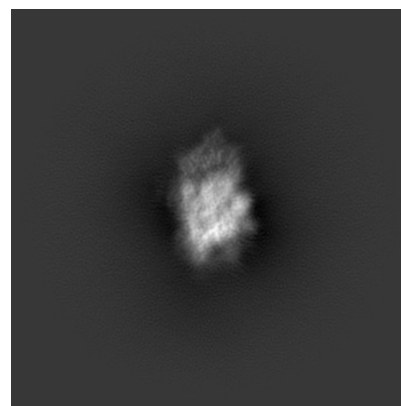
6.1.1 Primary map



X

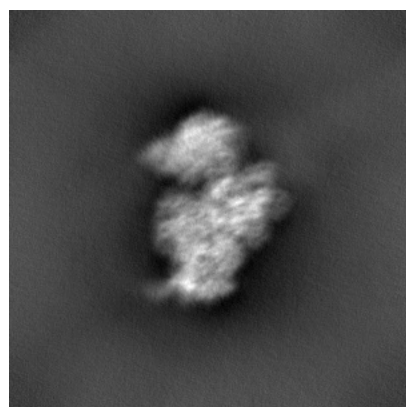


Y

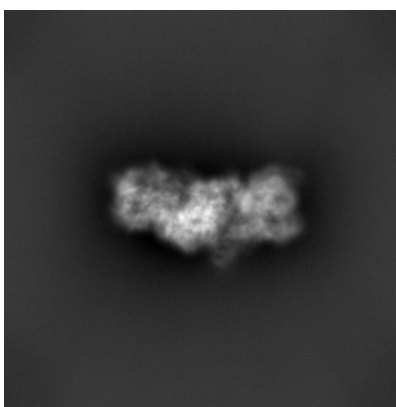


Z

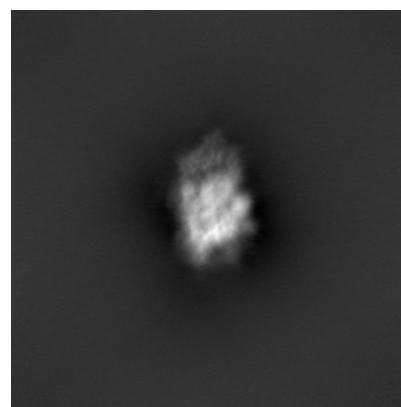
6.1.2 Raw map



X



Y

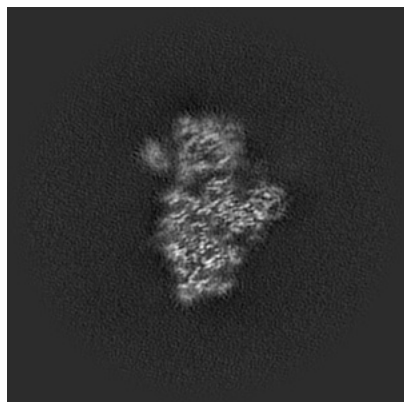


Z

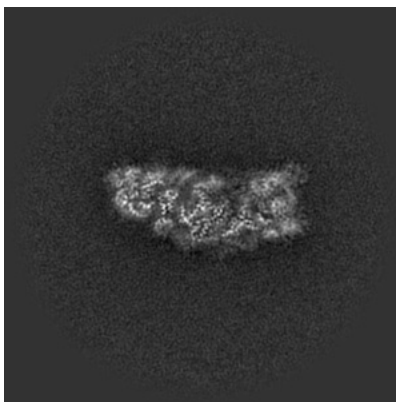
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

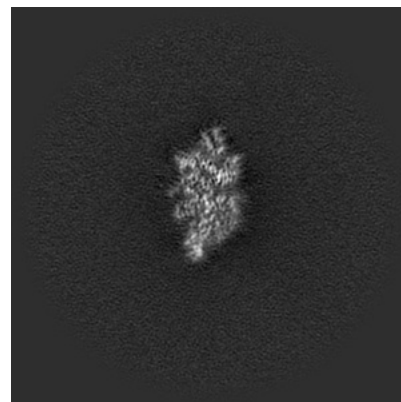
6.2.1 Primary map



X Index: 192

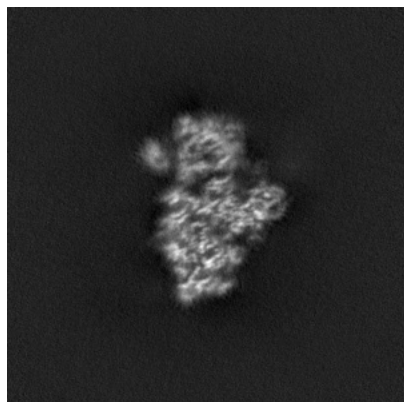


Y Index: 192

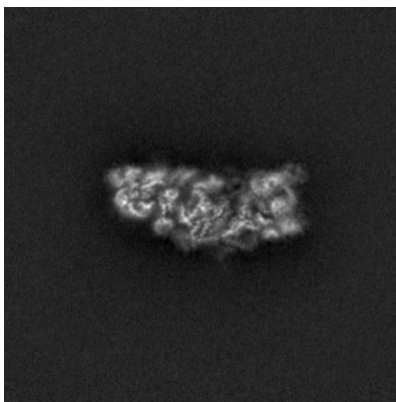


Z Index: 192

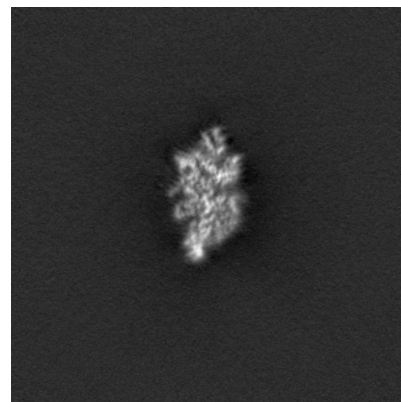
6.2.2 Raw map



X Index: 192



Y Index: 192

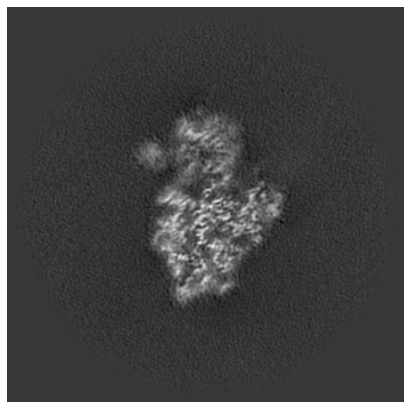


Z Index: 192

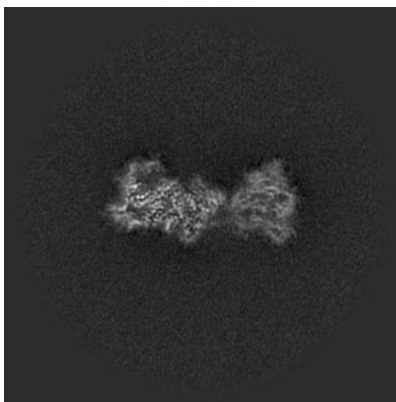
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

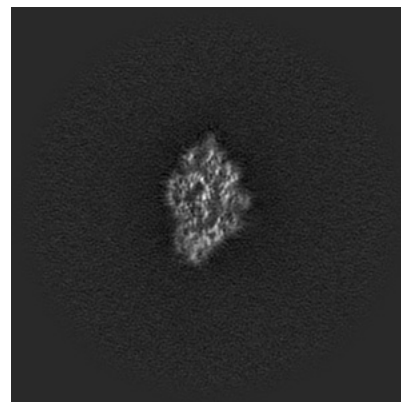
6.3.1 Primary map



X Index: 188

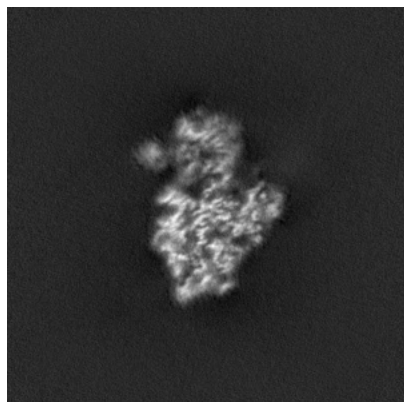


Y Index: 170

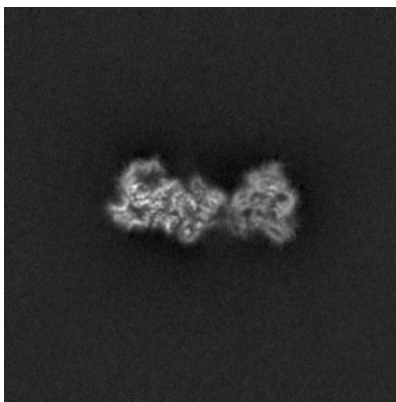


Z Index: 181

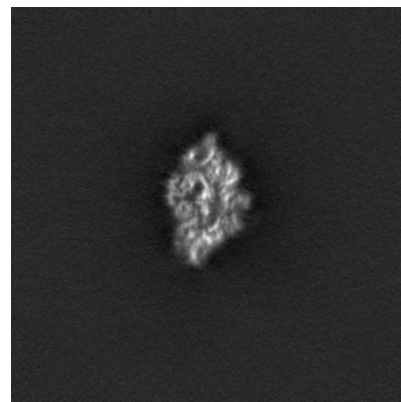
6.3.2 Raw map



X Index: 188



Y Index: 171

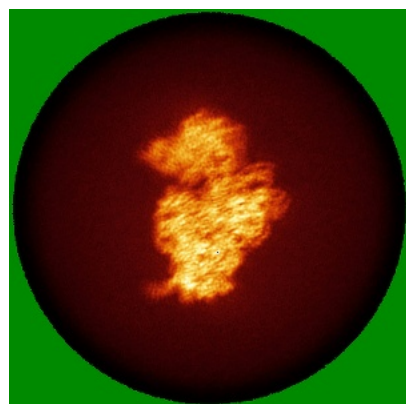


Z Index: 182

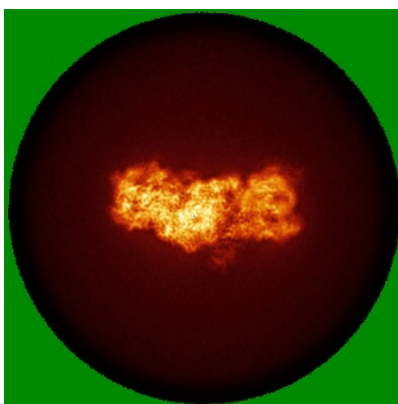
The images above show the largest variance slices of the map in three orthogonal directions.

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

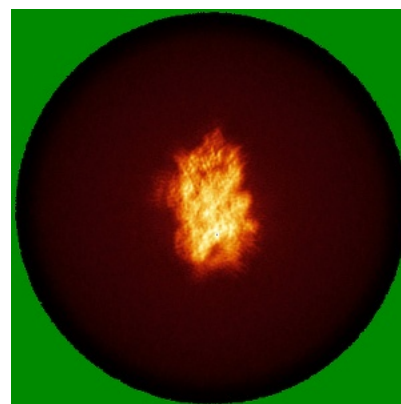
6.4.1 Primary map



X



Y

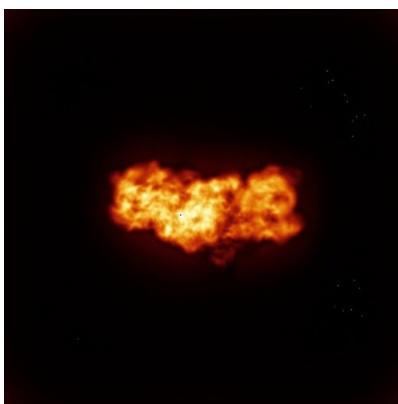


Z

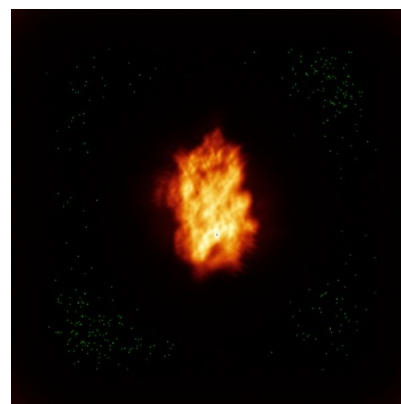
6.4.2 Raw map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.423. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

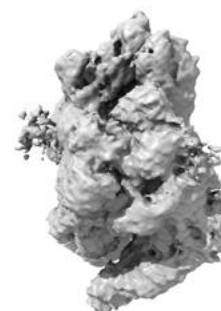
6.5.2 Raw map



X



Y



Z

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.

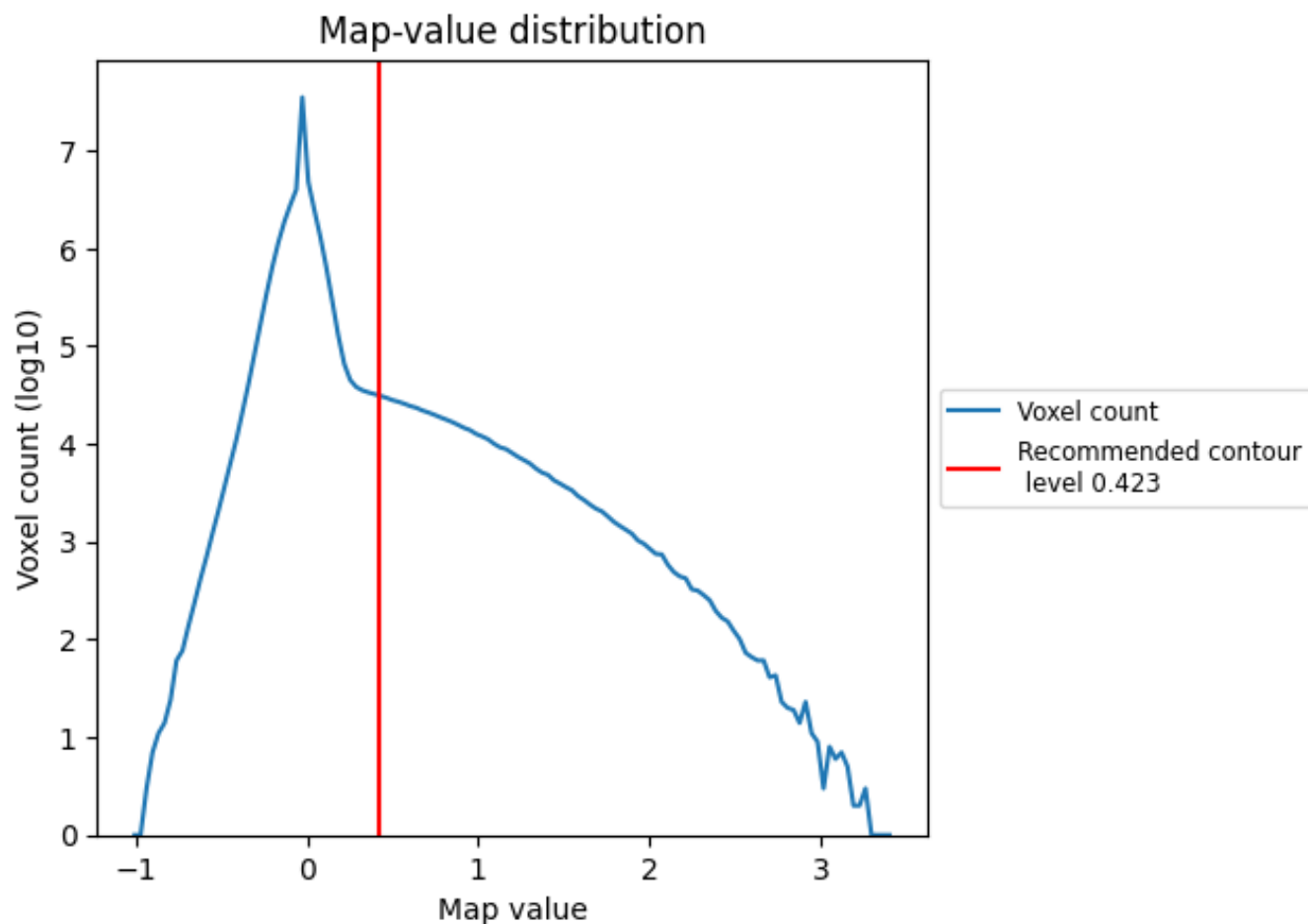
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

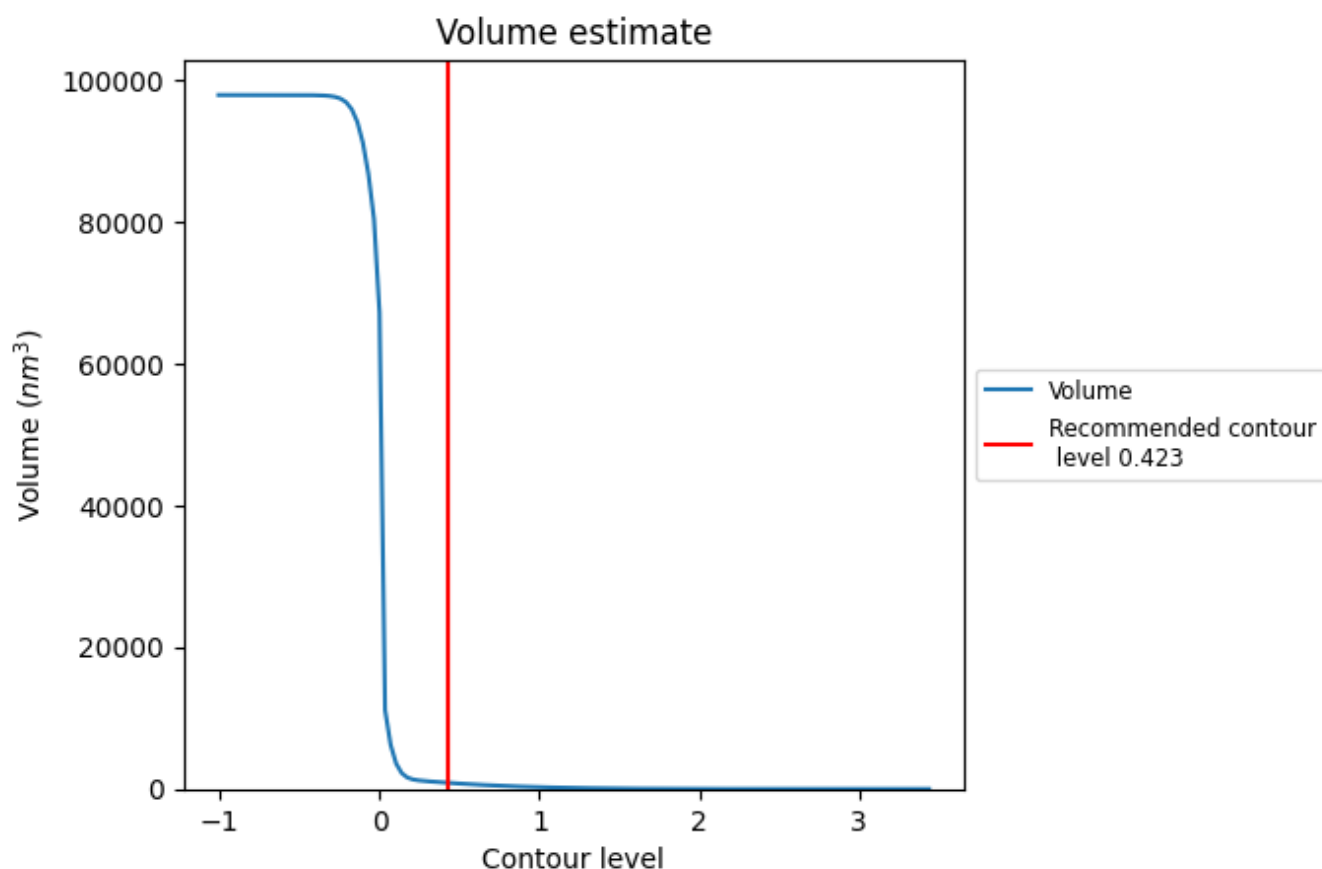
This section contains the results of statistical analysis of the map.

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.

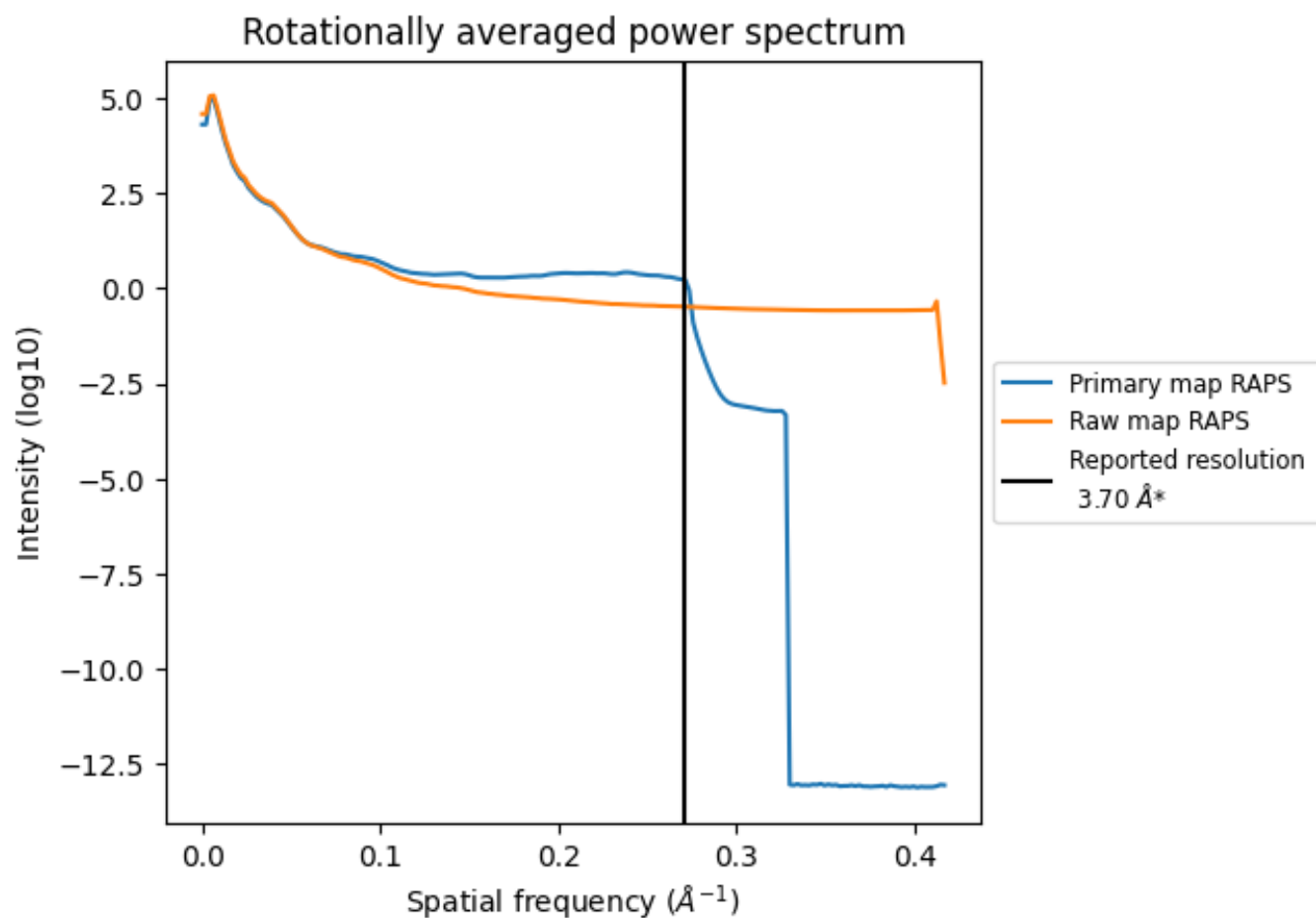
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 874 nm^3 ; this corresponds to an approximate mass of 789 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 ⓘ

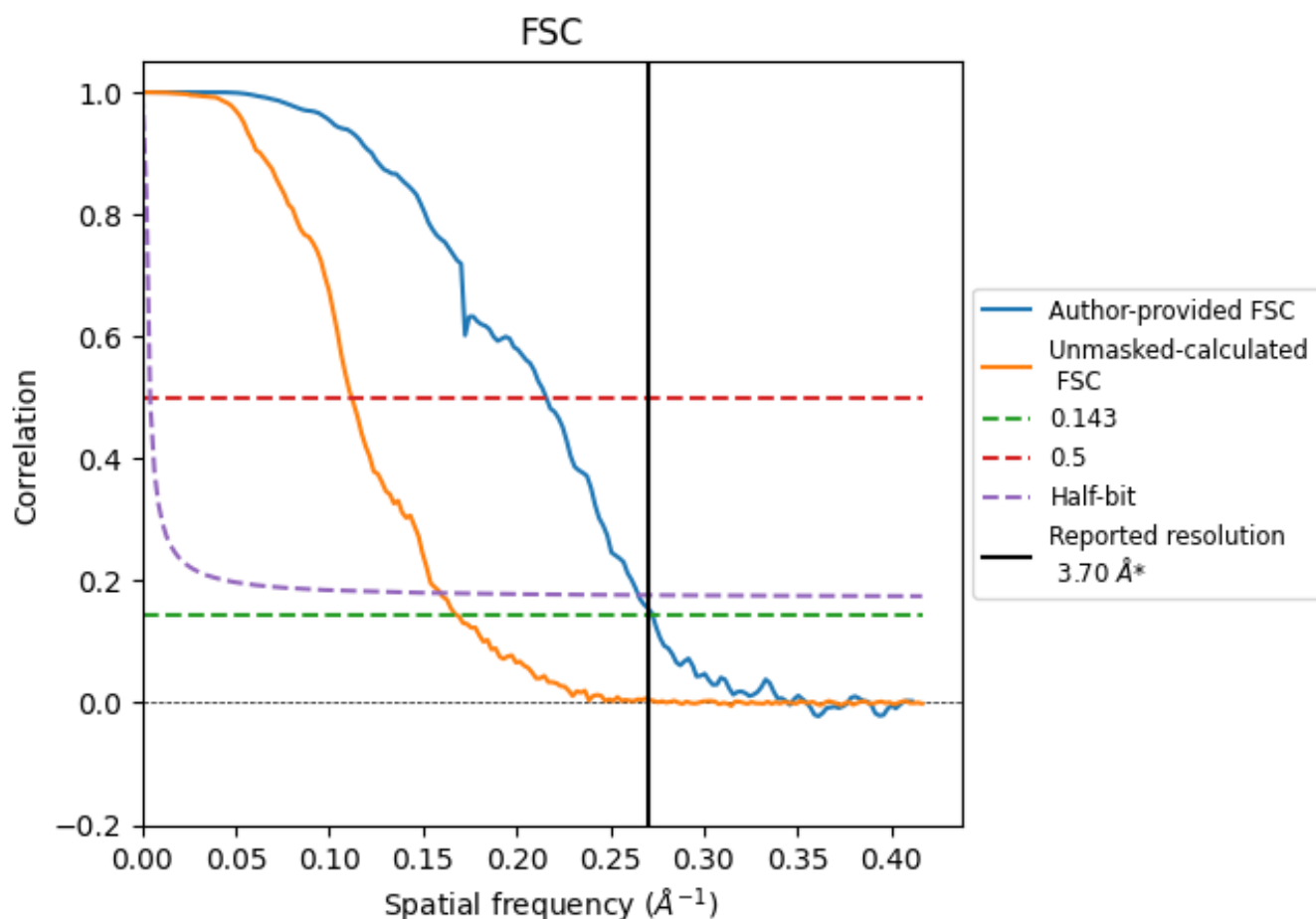


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

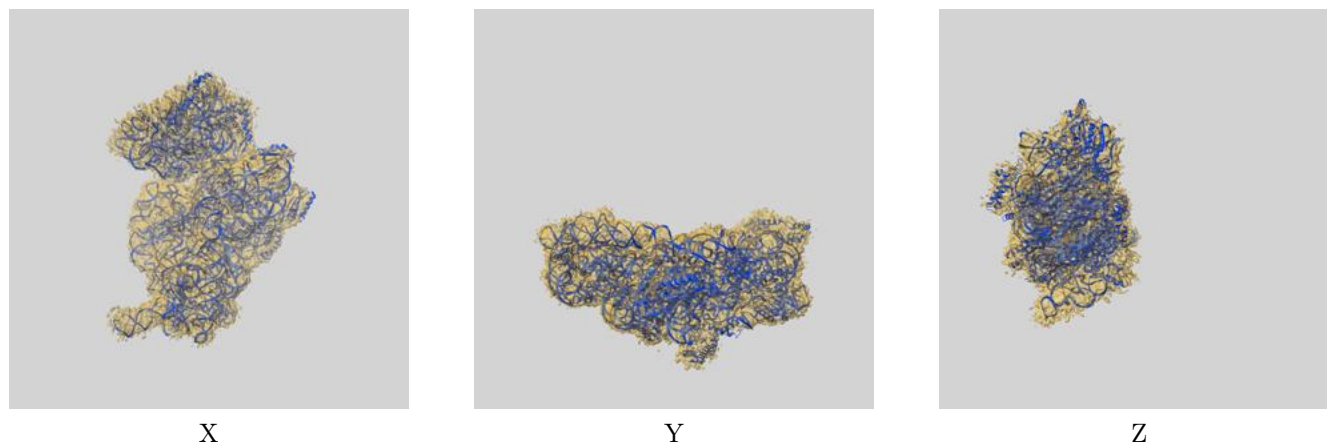
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.67	4.63	3.77
Unmasked-calculated*	5.94	8.94	6.28

*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 5.94 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

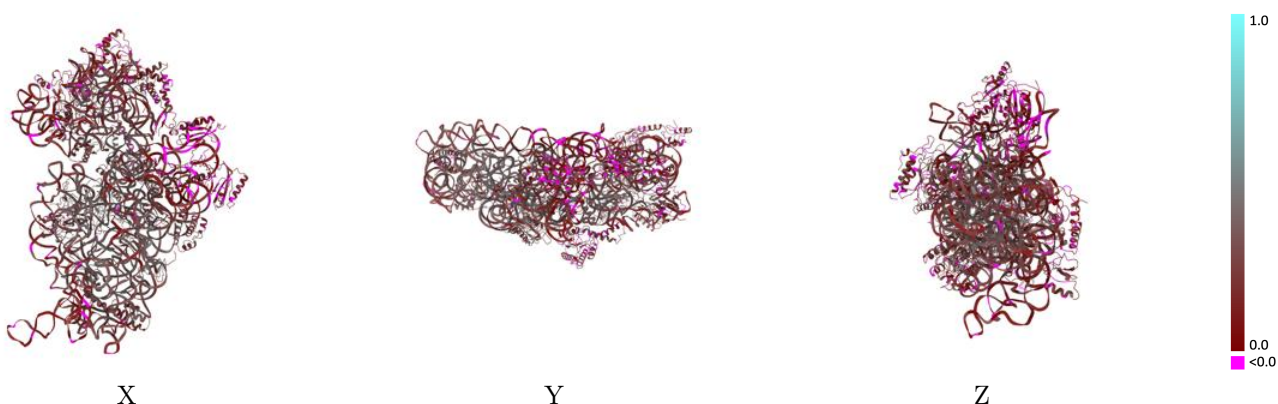
This section contains information regarding the fit between EMDB map EMD-16048 and PDB model 8BH6. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



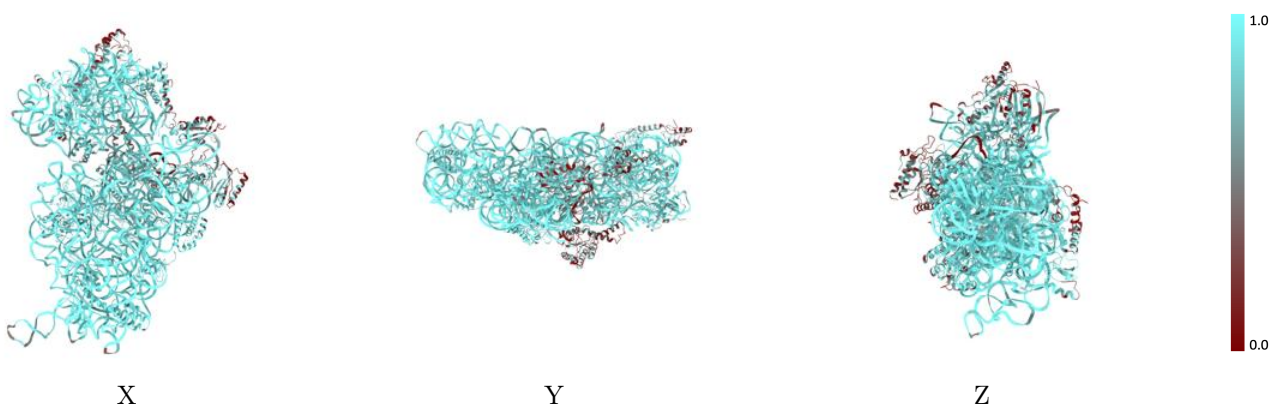
The images above show the 3D surface view of the map at the recommended contour level 0.423 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



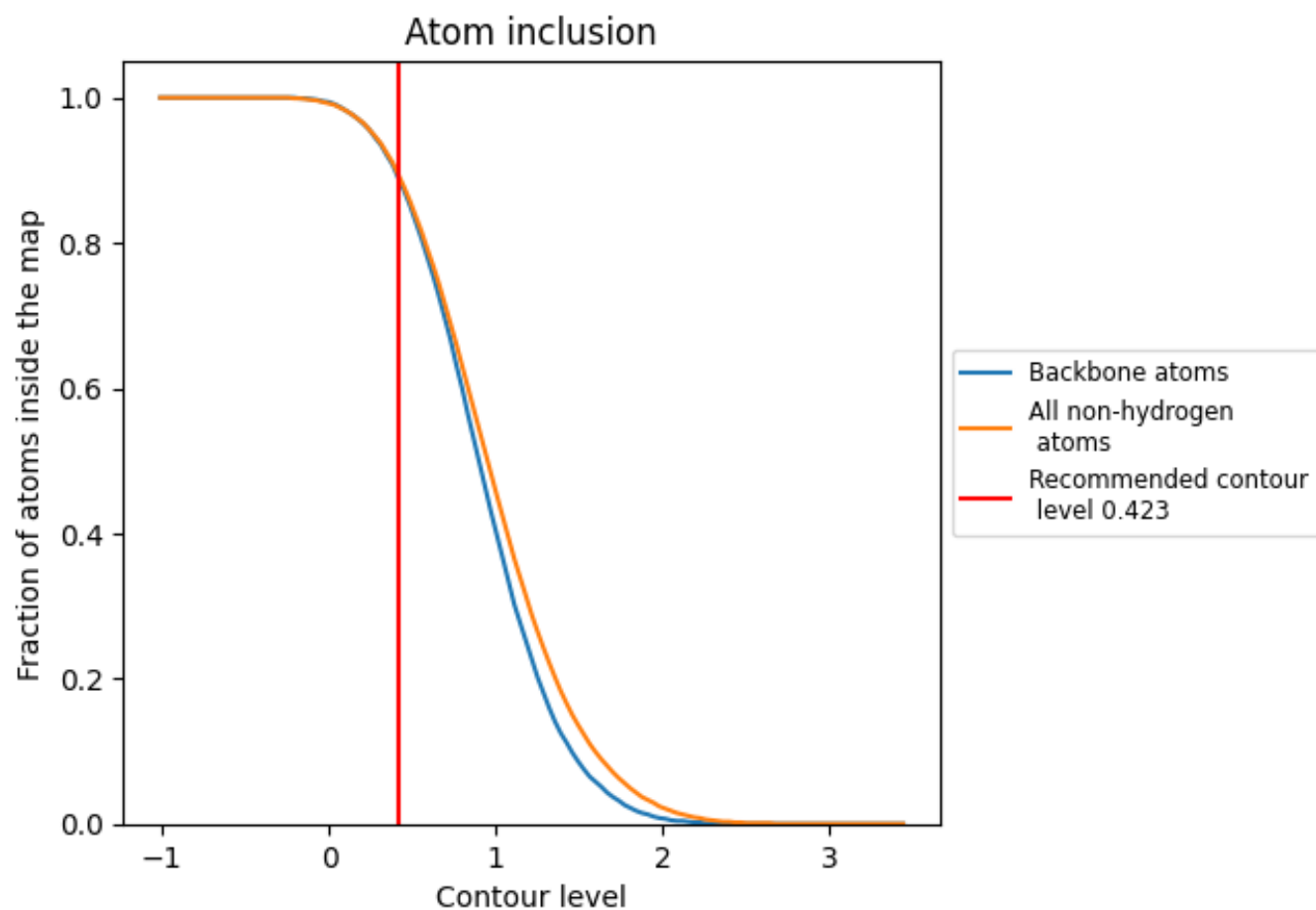
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.423).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 89% 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 (0.423) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8910	 0.2540
a	 0.9540	 0.2660
b	 0.3760	 0.1820
c	 0.7810	 0.2580
d	 0.9250	 0.2630
e	 0.8510	 0.3470
f	 0.4860	 0.1080
g	 0.7930	 0.1780
h	 0.9370	 0.3300
i	 0.8470	 0.2060
j	 0.8790	 0.2450
k	 0.5530	 0.0970
l	 0.9390	 0.3400
m	 0.5780	 0.1400
n	 0.9790	 0.2830
o	 0.9180	 0.2380
p	 0.9440	 0.3100
q	 0.9390	 0.3380
r	 0.5120	 0.0660
s	 0.8680	 0.1810
t	 0.9600	 0.2890

