



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 01:34 PM UTC

PDB ID : 6FAI / pdb_00006fai
EMDB ID : EMD-4214
Title : Structure of a eukaryotic cytoplasmic pre-40S ribosomal subunit
Authors : Scaiola, A.; Pena, C.; Weisser, M.; Boehringer, D.; Leibundgut, M.; Klingauf-Nerurkar, P.; Gerhardy, S.; Panse, V.G.; Ban, N.
Deposited on : 2017-12-15
Resolution : 3.40 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

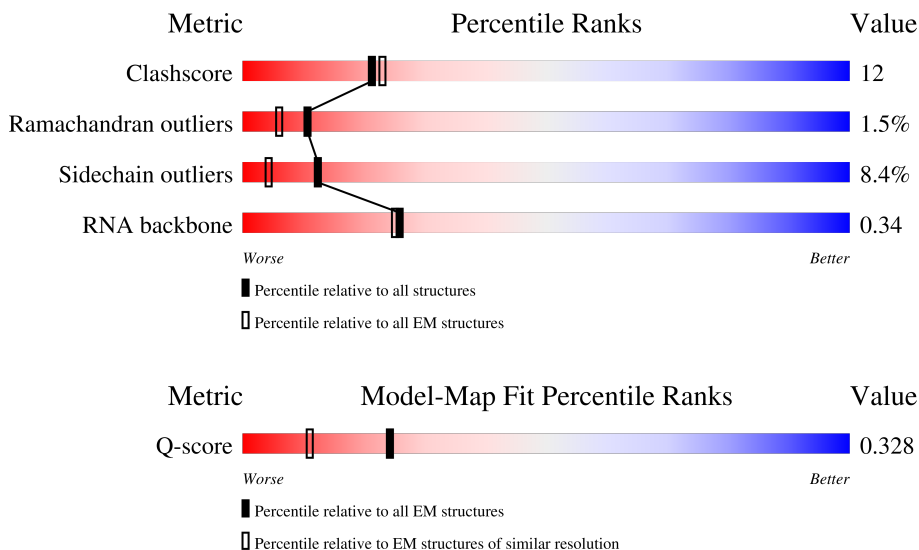
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.40 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.





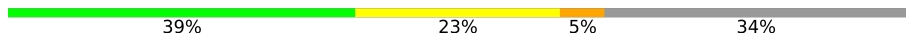



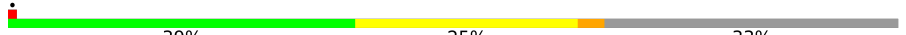
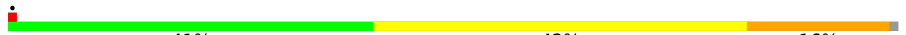

















Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	b	82	
2	c	67	
3	d	56	









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Mol	Chain	Length	Quality of chain
4	e	63	
5	g	319	
6	h	274	
7	i	483	
8	j	463	
9	k	788	
10	l	425	
11	2	1800	
12	A	252	
13	B	255	
14	C	254	
15	D	240	
16	E	261	
17	F	225	
18	G	236	
19	H	190	
20	I	200	
21	J	197	
22	L	156	
23	M	143	
24	N	151	
25	O	137	
26	P	142	
27	Q	143	
28	R	136	

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Mol	Chain	Length	Quality of chain
29	S	146	 60% 31% 8%
30	T	144	 65% 31%
31	U	121	 5% 63% 19% 15%
32	V	87	 64% 29% 7%
33	W	130	 62% 28% 6%
34	X	145	 59% 36%
35	Y	135	 69% 26%
36	Z	108	 36% 20% 42%

2 Entry composition [i](#)

There are 38 unique types of molecules in this entry. The entry contains 84964 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 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	b	81	610	382	110	113	5	0	0

- Molecule 2 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	c	63	497	306	99	91	1	0	0

- Molecule 3 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	d	37	302	186	62	50	4	0	0

- Molecule 4 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	e	48	384	242	81	59	2	0	0

- Molecule 5 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	g	317	2431	1538	417	468	8	0	0

- Molecule 6 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	h	181	1436	917	261	254	4	0	0

- Molecule 7 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	i	262	2133	1388	364	378	3	0	0

- Molecule 8 is a protein called Protein LTV1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	j	46	396	242	57	95	2	0	0

- Molecule 9 is a protein called Ribosome biogenesis protein TSR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	k	670	5402	3449	937	1002	14	0	0

- Molecule 10 is a protein called Serine/threonine-protein kinase RIO2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	l	286	2322	1464	410	430	18	0	0

- Molecule 11 is a RNA chain called 20S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
11	2	1775	37824	16909	6694	12446	1775	0	0

- Molecule 12 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	A	206	1611	1036	285	288	2	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	206	PHE	ASP	conflict	UNP P32905

- Molecule 13 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	B	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 14 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	C	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 15 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	D	202	Total	C	N	O	S	0	0
			1576	998	290	282	6		

- Molecule 16 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	E	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 17 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	F	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 18 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	G	232	Total	C	N	O	S	0	0
			1873	1172	366	332	3		

- Molecule 19 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	H	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 20 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	I	188	1489	925	298	264	2	0	0

- Molecule 21 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	J	185	1494	943	289	261	1	0	0

- Molecule 22 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	L	140	1129	724	215	187	3	0	0

- Molecule 23 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	M	125	941	591	166	182	2	0	0

- Molecule 24 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	N	150	1192	759	224	207	2	0	0

- Molecule 25 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	O	127	926	569	185	169	3	0	0

- Molecule 26 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	P	127	1001	637	186	171	7	0	0

- Molecule 27 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	Q	127	Total	C	N	O	0	0
			993	640	177	176		

- Molecule 28 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	R	125	Total	C	N	O	S	0	0
			1000	625	188	185	2		

- Molecule 29 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	S	135	Total	C	N	O	S	0	0
			1110	696	215	197	2		

- Molecule 30 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	T	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 31 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	U	103	Total	C	N	O	S	0	0
			819	519	148	151	1		

- Molecule 32 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	V	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 33 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	W	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 34 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	X	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 35 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	Y	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 36 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	Z	63	Total	C	N	O	0	0
			512	328	94	90		

- Molecule 37 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
37	b	1	Total	Zn	0
			1	1	
37	d	1	Total	Zn	0
			1	1	

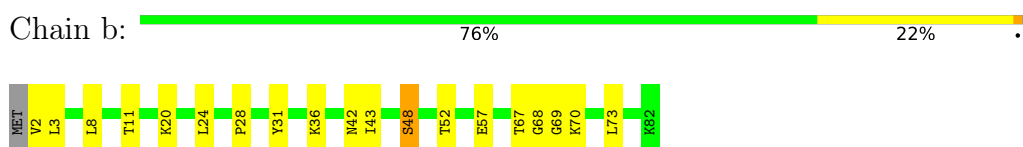
- Molecule 38 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
38	2	46	Total	Mg	0
			46	46	

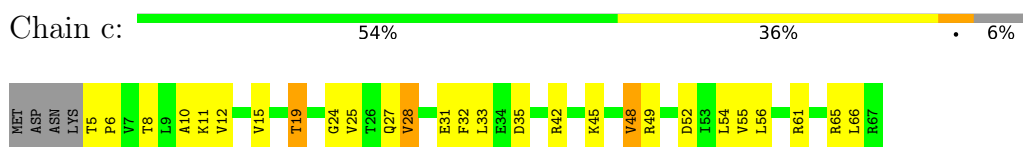
3 Residue-property plots [i](#)

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.

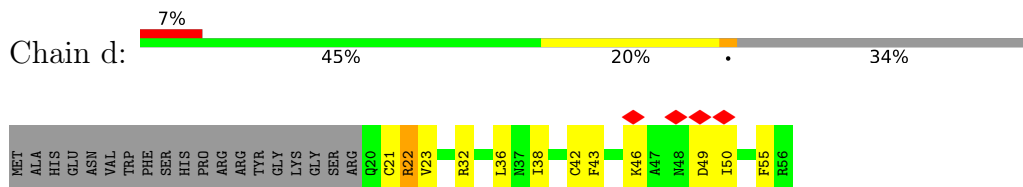
- Molecule 1: 40S ribosomal protein S27-A



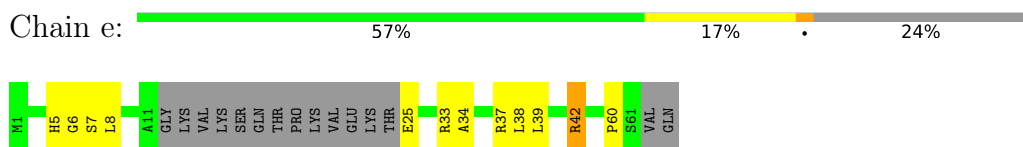
- Molecule 2: 40S ribosomal protein S28-A



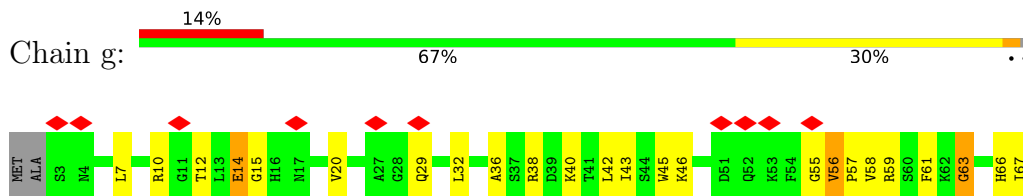
- Molecule 3: 40S ribosomal protein S29-A

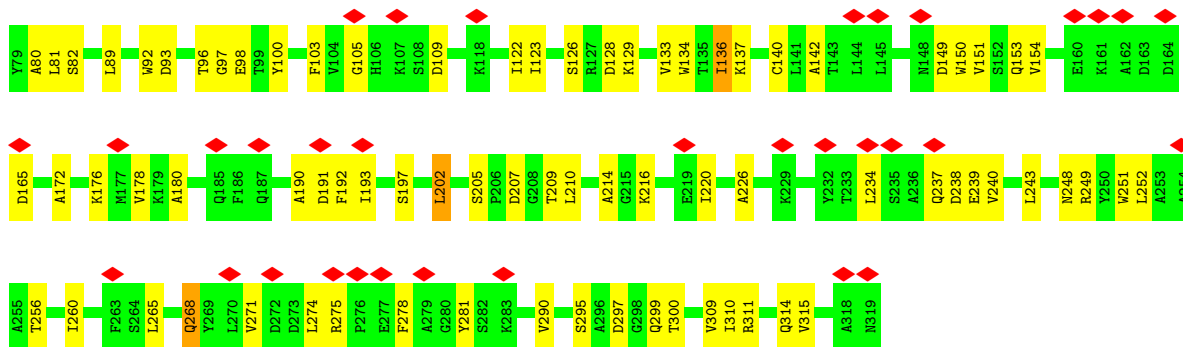


- Molecule 4: 40S ribosomal protein S30-A

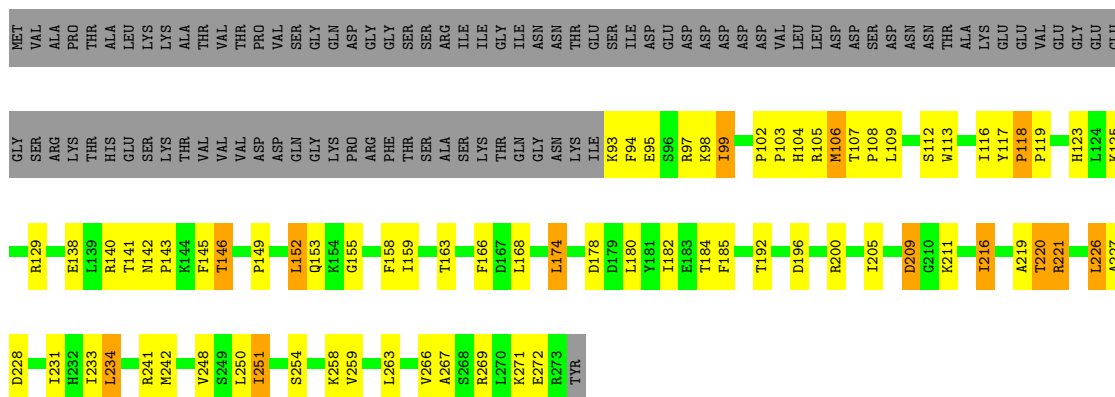


- Molecule 5: Guanine nucleotide-binding protein subunit beta-like protein

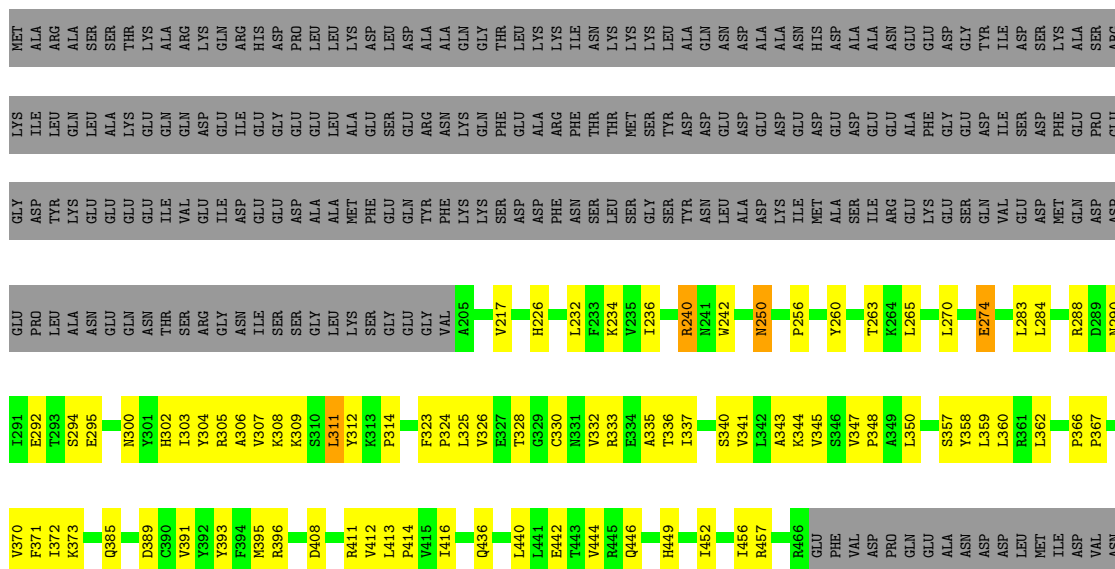
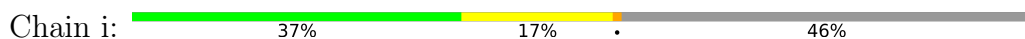




• Molecule 6: Pre-rRNA-processing protein PNO1



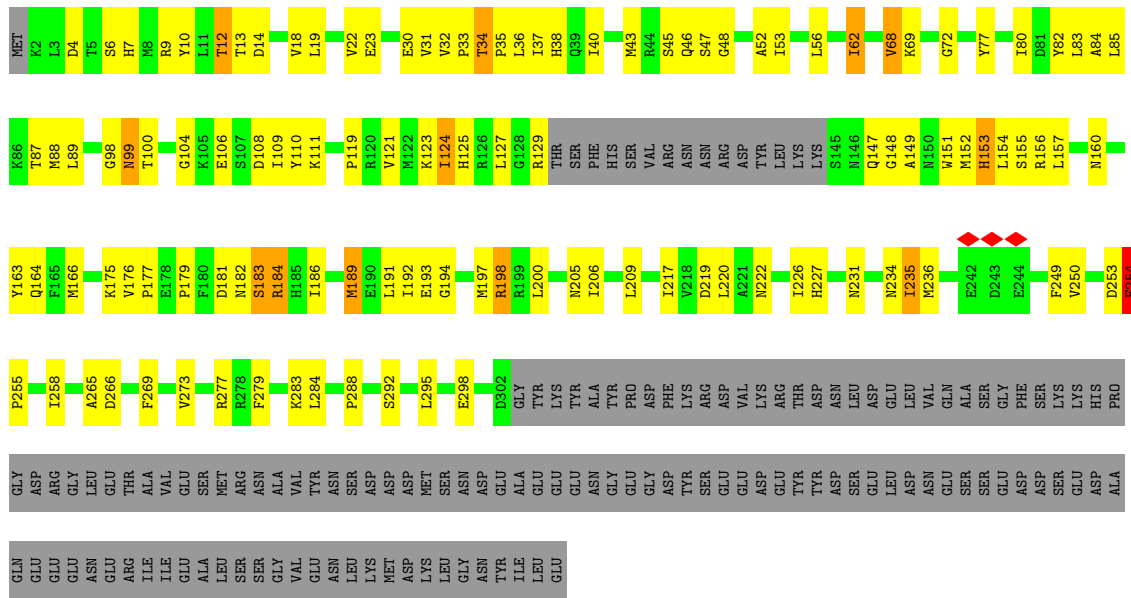
• Molecule 7: Essential nuclear protein 1



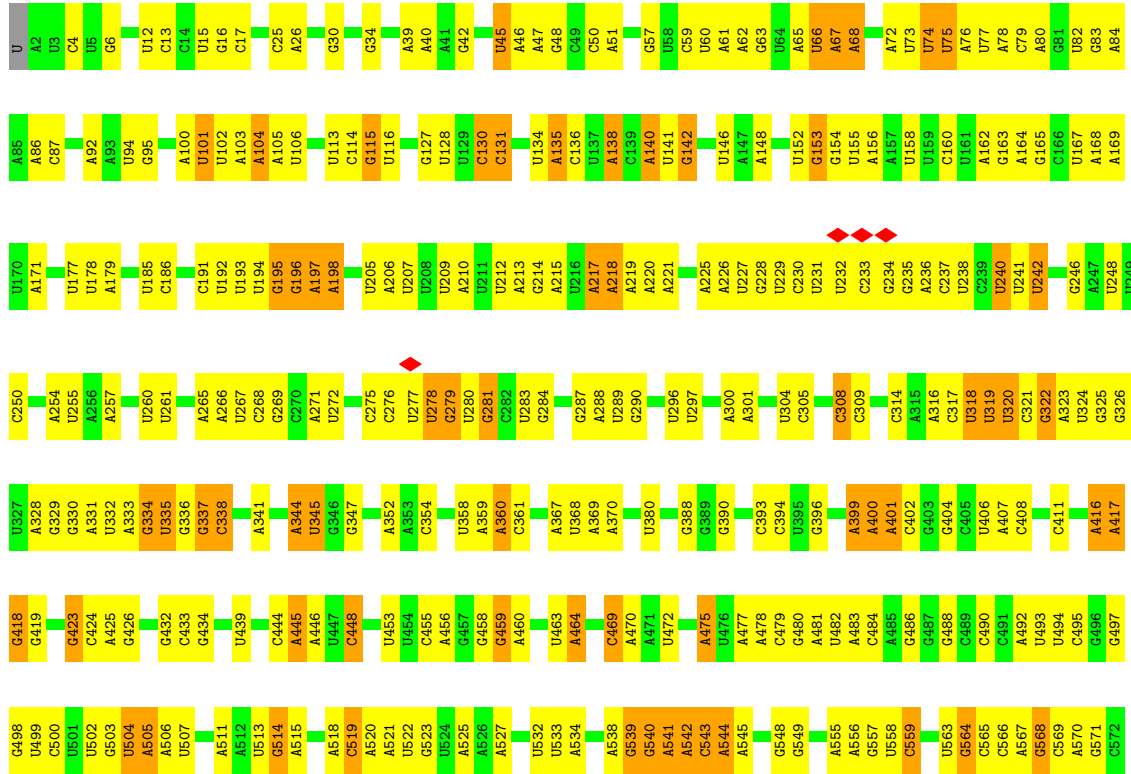
• Molecule 8: Protein LTV1



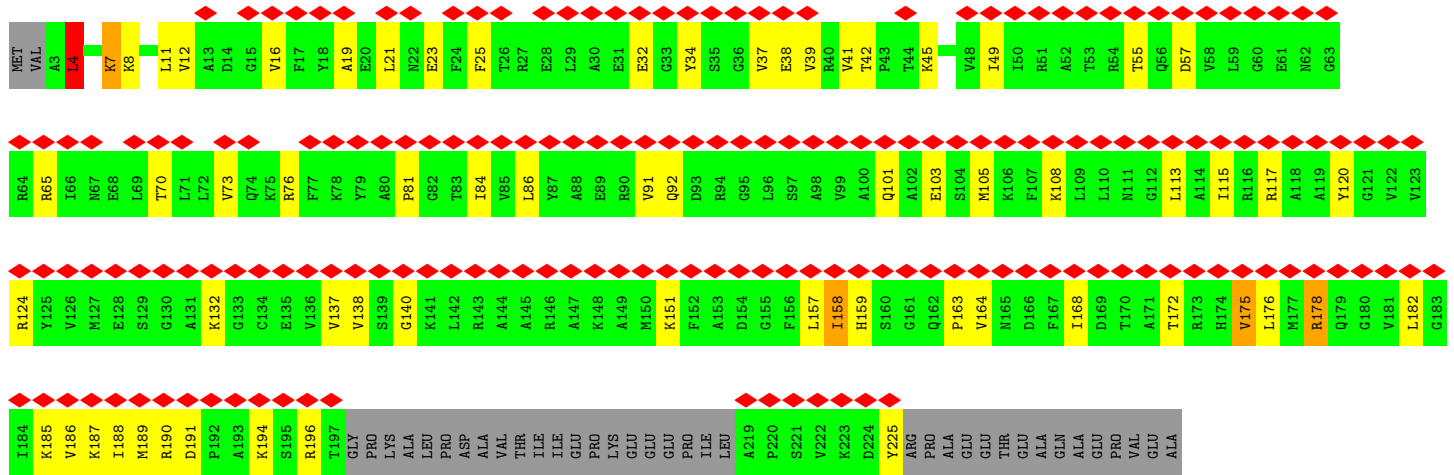
• Molecule 10: Serine/threonine-protein kinase RIO2



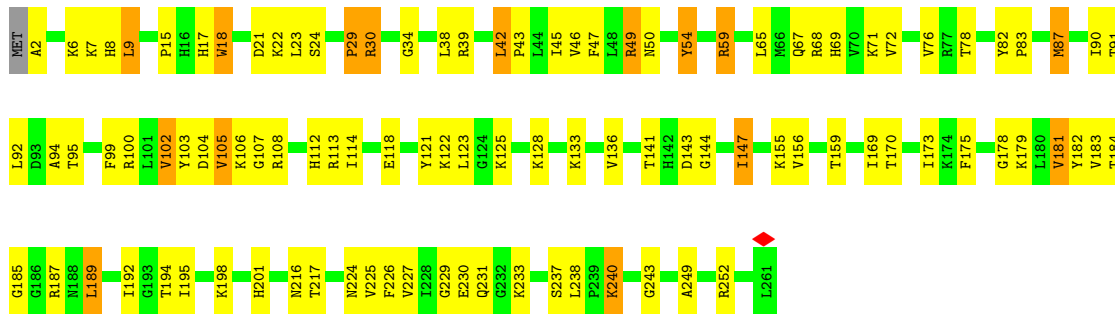
• Molecule 11: 20S ribosomal RNA



U1657	U1585	C1500	U1439	G1354	U1276	G1213	A1143	G1045	U958	A887	A814	C736	C653	C573	
G1658	A1596	C1501	C1431	C1355	G1277	U1214	A1146	G1046	U959	U888	G815	A737	C654	G574	
A1659	A1587	G1502	G1432	U1356	C1278	C1215	G1147	U1049	U960	U894	G816	G738	G655	C575	
G1660	C1593	A1503	U1433	A1357	C1279	G1216	C1148	G1053	A963	G895	G819	G739	G656	G576	
G1662	G1590	G1504	G1434	U1360	C1280	A1217	C1149	U1054	U964	G896	U820	A740	U657	G577	
G1663	C1591	G1506	A1436	U1361	G1281	A1219	G1150	U1055	U965	C897	U821	C741	C658	U578	
A1671	A1592	U1511	U1437	U1362	C1284	A1221	A1151	U1056	A966	A898	G823	U743	C	A579	
G1672	A1593	G1438	U1438	U1363	U1285	C1221	A1152	U1057	C969	G899	G824	U749	G	A580	
G1673	C1439	U1512	C1439	U1364	A1286	A1222	G1153	U1058	U900	A900	U825	U750	A	U581	
C1674	U1594	G1513	C1440	C1365	U1287	C1223	A1154	U1059	G901	G901	U826	U751	U	U582	
A1681	C1596	U1514	C1441	U1366	A1288	A1224	G1155	U1060	G902	G902	U827	A753	U	C583	
U1682	A1597	A1515	U1442	G1367	U1289	U1225	C1156	U1061	G903	G903	C827	U754	U	C584	
U1676	U1598	A1516	U1443	U1367	U1290	A1226	A1157	A1061	G904	G904	U828	A754	U	G586	
C1677	C1599	U1521	A1444	U1370	G1291	A1227	C1158	A1062	A905	A905	A829	A755	U	C589	
A1678	G1600	U1522	G1445	A1371	U1292	G1228	C1159	U1063	A906	A906	U830	A756	U	C590	
G1679	G1601	G1523	A1446	U1372	U1293	G1229	A1160	G1064	A907	A907	U831	A757	C	A591	
G1680	U1602	U1524	C1447	G1373	G1294	C1230	C1161	A1065	G908	U908	U832	U758	U	A592	
U1682	G1607	A1525	U1448	C1376	G1295	U1231	G1162	C1066	A992	U909	U833	U	U	U593	
C1683	U1608	A1526	U1449	U1379	U1298	U1232	G1164	C1067	A993	C910	U834	A762	U	U594	
U1684	U1609	C1533	C1451	C1379	A1300	G1233	G1165	C1072	C997	U912	G763	G764	U	G595	
C1686	A1611	U1534	U1452	U1380	A1301	A1234	G1166	G1073	A998	G913	U839	U765	U	U602	
U1687	G1615	G1535	G1455	A1382	U1301	C1235	G1167	A1076	C1000	G914	U840	U766	G676	U603	
U1688	C1618	U1536	C1456	A1384	C1309	G1237	A1171	C1077	A1001	U916	G842	C768	A677	A606	
A1689	C1619	C1537	G1457	U1385	U1310	U1239	G1172	C1078	G1002	U917	U843	G772	A678	A607	
G1690	U1620	U1538	C1458	G1386	G1311	U1240	U1175	U1079	A1003	U918	U844	G773	U680	U608	
G1696	C1621	G1539	U1459	U1387	U1314	G1241	G1176	U1080	U1004	A919	G846	A774	U681	U609	
U1697	U1622	C1541	A1460	A1388	A1315	A1242	U1181	A1081	A1005	U920	A847	A775	A684	G610	
G1698	G1623	G1542	C1461	C1389	G1316	G1243	U1182	C1082	C1006	U921	G850	G776	A685	G611	
G1699	C1624	A1543	G1462	U1390	U1316	A1244	U1183	G1083	C1007	A924	A851	C777	C686	U612	
A1700	U1627	G1548	C1467	U1397	C1321	C1245	A1184	A1092	G1008	G925	U852	G778	A679	G613	
U1701	U1628	U1549	A1468	U1398	C1322	U1246	U1185	A1093	U1009	U926	G853	G779	G690	C614	
C1706	G1629	U1551	A1469	C1399	G1324	G1247	U1186	G1094	A927	C927	U854	A780	C696	A619	
A1707	U1630	U1552	A1471	A1400	U1327	U1248	U1187	U1095	U1012	A929	A855	U781	C697	A620	
A1712	A1631	G1553	C1472	A1401	G1328	C1252	A1189	C1096	C1016	A930	U857	U782	U698	A621	
G1713	C1632	U1554	G1473	G1409	A1329	U1253	C	U1097	U1017	C931	G784	G785	U699	A622	
A1714	A1633	A1555	G1474	A1410	G1330	U1254	U	U1098	U1018	U932	U860	U786	C700	A623	
G1715	C1634	U1556	A1475	A1411	A1331	G1255	A	U1099	A1019	A933	U861	C786	U699	G624	
C1635	A1635	U1557	G1476	G1412	C1332	A1256	A	G1101	A1020	C934	A862	G787	C708	C625	
C1637	C1636	U1558	A1479	U1413	C1333	U1257	C	G1102	C1021	U935	A863	A788	C709	U626	
G1638	A1589	A1589	G1480	U1414	U1334	U1258	A	U1098	C1022	A944	U864	A789	A630	A630	
C1639	C1481	U1560	C1481	U1415	U1335	U1259	C1197	U1098	A1025	A939	A865	U790	G712	A631	
C1641	A1483	U1561	C1482	G1416	A1336	U1260	G1198	U1099	A1026	A940	G866	A791	A713	G632	
A1730	G1486	C1563	A1487	A1417	A1337	G1261	G1199	U1100	A1027	A941	G867	U792	G714	U632	
A1731	G1487	U1568	G1487	G1418	C1338	U1262	G1200	U1120	C1028	C943	G868	U793	G715	A635	
A1732	A1648	C1569	A1488	C1420	U1340	G1263	A1201	C1121	U1031	U945	G870	U795	U715	U638	
C1733	G1649	A1570	G1488	A1421	U1341	U1264	A1202	A1125	A1031	U946	G871	A789	C717	U639	
U1734	U1650	C1571	C1490	A1422	G1267	U1265	U1206	A1126	A1036	U947	G872	U799	U718	U640	
U1735	A1651	G1572	U1491	A1424	A1344	G1266	C1207	G1130	C1037	G948	U873	A804	U719	C645	
G1736	C1652	A1573	A1424	A1424	U1345	U1268	A1208	U1136	G1041	C949	G876	U719	U719	C645	
G1737	C1653	G1574	A1493	C1426	U1347	G1270	C1209	U1135	G1041	A955	U884	G810	G720	C645	
U1738	A1654	U1575	U1427	A1428	U1348	G1271	C1210	A1137	G1042	A956	A884	A811	U721	U649	
C1739	U1655	G1584	G1428	C1429	U1349	U1271	A1211	A1138	U1044	C957	U886	A812	G722	U650	
A1740	U1656	G1584	G1499	C1429	U1349	A1275	G1212	A1138	U1044			U813	G723		
													U728		



• Molecule 16: 40S ribosomal protein S4-A

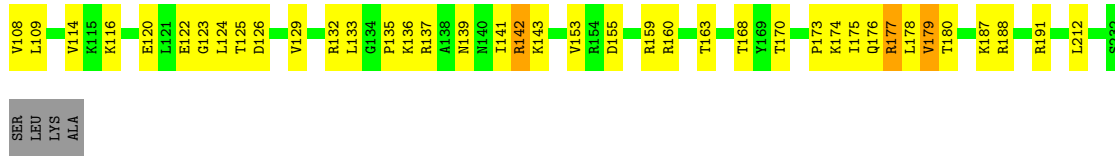


• Molecule 17: 40S ribosomal protein S5

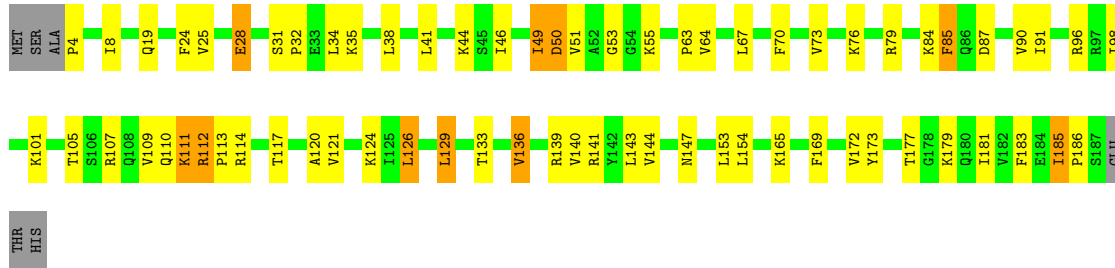


• Molecule 18: 40S ribosomal protein S6-A

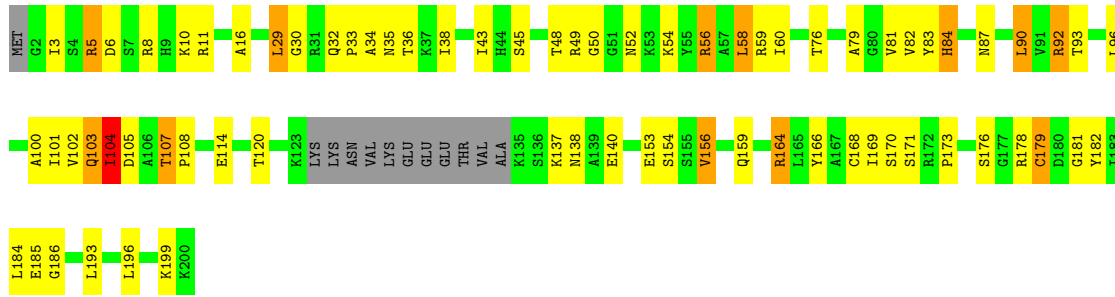




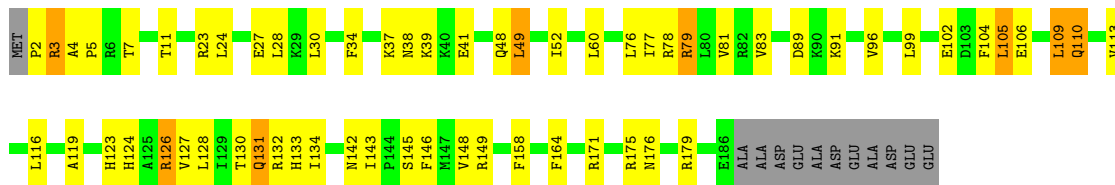
• Molecule 19: 40S ribosomal protein S7-A



• Molecule 20: 40S ribosomal protein S8-A

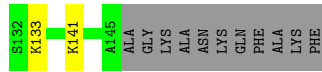


• Molecule 21: 40S ribosomal protein S9-A

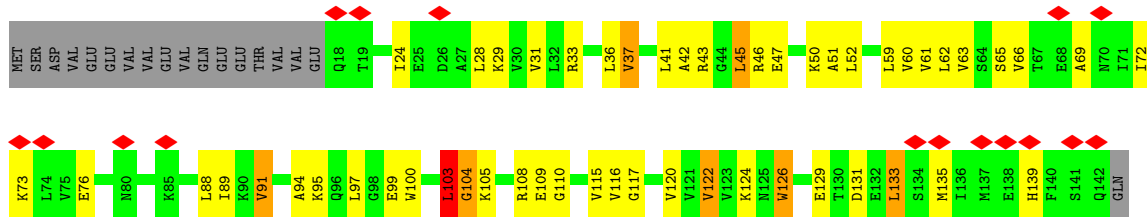


• Molecule 22: 40S ribosomal protein S11-A

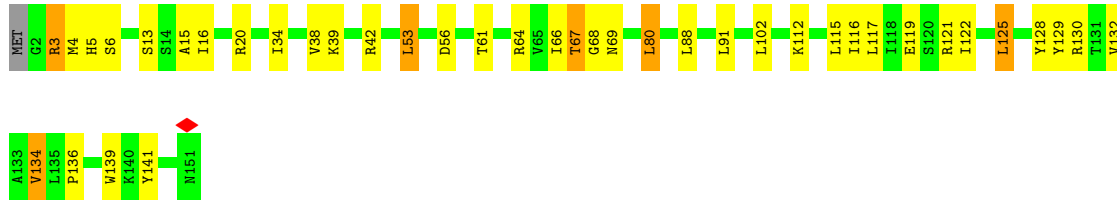
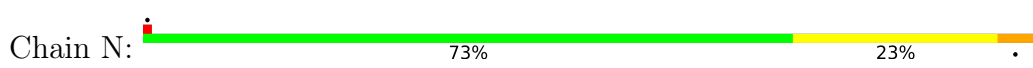




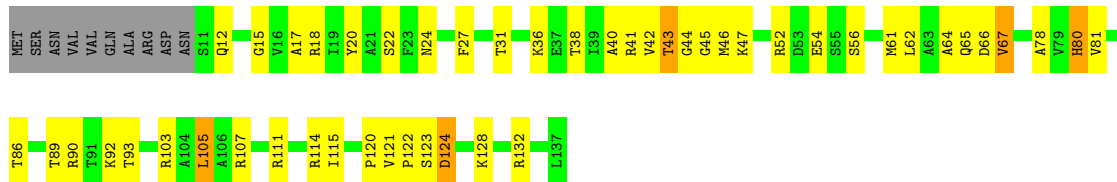
• Molecule 23: 40S ribosomal protein S12



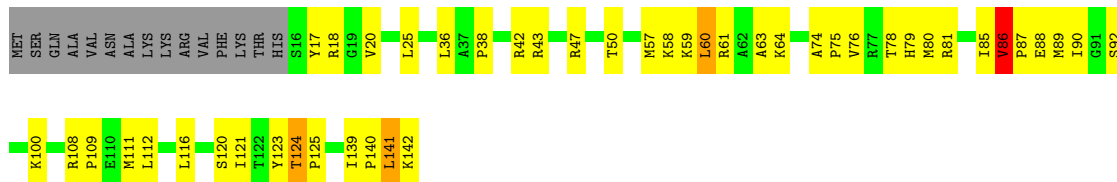
• Molecule 24: 40S ribosomal protein S13



• Molecule 25: 40S ribosomal protein S14-A

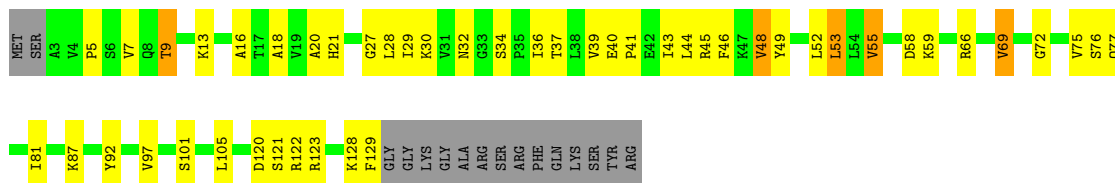


• Molecule 26: 40S ribosomal protein S15

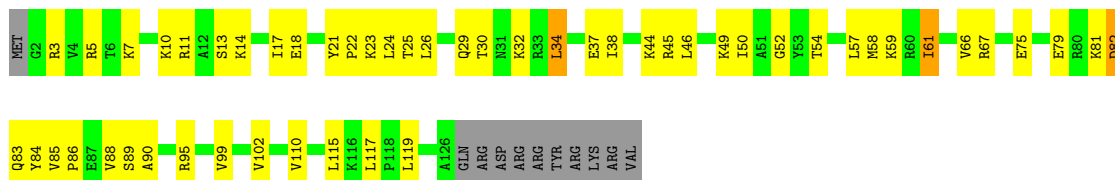


• Molecule 27: 40S ribosomal protein S16-A

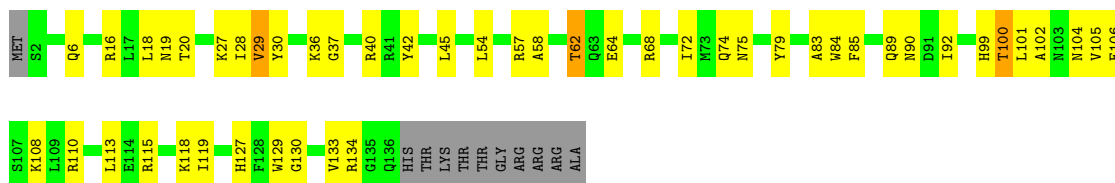




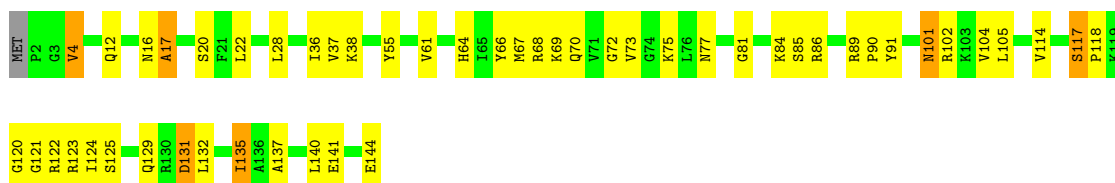
- Molecule 28: 40S ribosomal protein S17-A



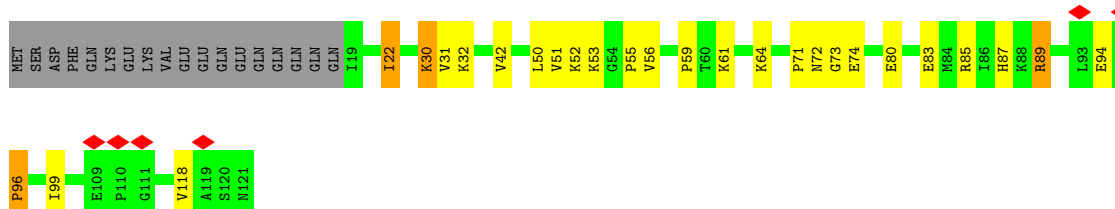
- Molecule 29: 40S ribosomal protein S18-A



- Molecule 30: 40S ribosomal protein S19-A



- Molecule 31: 40S ribosomal protein S20



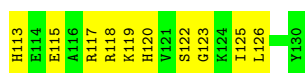
- Molecule 32: 40S ribosomal protein S21-A

Chain V:  64% 29% 7%



• Molecule 33: 40S ribosomal protein S22-A

Chain W:  62% 28% 6% ..



• Molecule 34: 40S ribosomal protein S23-A

Chain X:  59% 36% ..




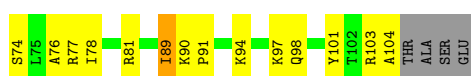
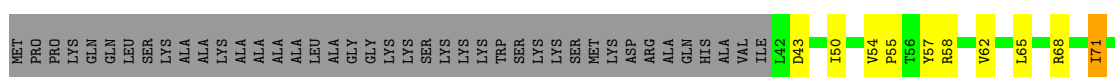
• Molecule 35: 40S ribosomal protein S24-A

Chain Y:  69% 26% ..



• Molecule 36: 40S ribosomal protein S25-A

Chain Z:  36% 20% . 42%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	165168	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.393	Depositor
Minimum map value	-0.144	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	444.8, 444.8, 444.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.39, 1.39, 1.39	Depositor

5 Model quality i

5.1 Standard geometry i

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	b	0.46	0/620	0.84	0/838
2	c	0.47	0/499	0.75	0/670
3	d	0.47	0/306	0.82	0/404
4	e	0.45	0/390	0.84	0/517
5	g	0.50	0/2484	0.77	1/3382 (0.0%)
6	h	0.41	0/1462	0.86	2/1969 (0.1%)
7	i	0.52	0/2188	0.78	2/2970 (0.1%)
8	j	0.49	0/403	0.65	0/543
9	k	0.37	0/5528	0.83	8/7477 (0.1%)
10	l	0.46	0/2368	0.83	5/3181 (0.2%)
11	2	0.30	0/42303	0.42	2/65912 (0.0%)
12	A	0.50	0/1653	0.97	8/2261 (0.4%)
13	B	0.45	0/1735	0.86	2/2335 (0.1%)
14	C	0.58	0/1665	0.94	2/2263 (0.1%)
15	D	0.54	0/1596	0.77	1/2142 (0.0%)
16	E	0.60	0/2109	0.94	8/2839 (0.3%)
17	F	0.47	0/1629	0.84	2/2202 (0.1%)
18	G	0.38	0/1897	0.83	5/2532 (0.2%)
19	H	0.42	0/1506	0.80	3/2028 (0.1%)
20	I	0.48	0/1514	0.88	2/2021 (0.1%)
21	J	0.56	0/1519	0.93	1/2035 (0.0%)
22	L	0.60	0/1155	0.92	3/1557 (0.2%)
23	M	0.57	0/949	0.81	0/1284
24	N	0.52	0/1215	0.85	0/1638
25	O	0.40	0/937	0.88	2/1261 (0.2%)
26	P	0.40	0/1022	0.84	2/1373 (0.1%)
27	Q	0.51	0/1011	0.85	4/1362 (0.3%)
28	R	0.50	0/1010	0.82	0/1355
29	S	0.44	0/1128	0.76	0/1518
30	T	0.45	0/1130	0.85	3/1517 (0.2%)
31	U	0.55	0/829	0.81	0/1121
32	V	0.48	0/693	0.89	1/935 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	W	0.76	0/1038	1.06	2/1395 (0.1%)
34	X	0.59	0/1139	0.92	5/1518 (0.3%)
35	Y	0.52	0/1087	0.86	0/1449
36	Z	0.52	0/519	0.84	0/696
All	All	0.41	0/90236	0.67	76/130500 (0.1%)

There are no bond length outliers.

The worst 5 of 76 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	W	76	SER	CA-C-N	-10.29	106.98	119.84
33	W	76	SER	C-N-CA	-10.29	106.98	119.84
11	2	1185	U	OP2-P-O3'	-8.65	82.04	108.00
9	k	392	VAL	CA-C-N	-7.98	111.52	119.90
9	k	392	VAL	C-N-CA	-7.98	111.52	119.90

There are no chirality outliers.

There are no planarity outliers.

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	b	610	0	629	13	0
2	c	497	0	535	14	0
3	d	302	0	297	9	0
4	e	384	0	423	9	0
5	g	2431	0	2381	48	0
6	h	1436	0	1515	53	0
7	i	2133	0	2172	59	0
8	j	396	0	322	10	0
9	k	5402	0	5276	104	0
10	l	2322	0	2305	78	0
11	2	37824	0	19031	638	0
12	A	1611	0	1616	76	0
13	B	1709	0	1784	52	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	C	1635	0	1723	59	0
15	D	1576	0	1650	41	0
16	E	2068	0	2154	66	0
17	F	1609	0	1675	72	0
18	G	1873	0	1980	51	0
19	H	1481	0	1572	45	0
20	I	1489	0	1525	55	0
21	J	1494	0	1573	42	0
22	L	1129	0	1196	19	0
23	M	941	0	982	42	0
24	N	1192	0	1255	26	0
25	O	926	0	950	39	0
26	P	1001	0	1042	36	0
27	Q	993	0	1051	37	0
28	R	1000	0	1063	38	0
29	S	1110	0	1134	33	0
30	T	1112	0	1124	33	0
31	U	819	0	885	19	0
32	V	684	0	672	22	0
33	W	1021	0	1060	35	0
34	X	1121	0	1196	43	0
35	Y	1073	0	1132	33	0
36	Z	512	0	551	20	0
37	b	1	0	0	0	0
37	d	1	0	0	0	0
38	2	46	0	0	0	0
All	All	84964	0	67431	1770	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 12.

The worst 5 of 1770 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)
7:i:444:VAL:HG11	7:i:457:ARG:HB2	1.54	0.89
11:2:885:G:N2	25:O:124:ASP:OD2	2.06	0.88
23:M:43:ARG:HD2	23:M:103:LEU:HD21	1.54	0.88
19:H:177:THR:HG23	19:H:179:LYS:H	1.40	0.86
9:k:486:ILE:HD11	9:k:701:ALA:HB1	1.57	0.86

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	79/82 (96%)	69 (87%)	9 (11%)	1 (1%)	9	33
2	c	61/67 (91%)	53 (87%)	7 (12%)	1 (2%)	7	29
3	d	35/56 (62%)	32 (91%)	2 (6%)	1 (3%)	3	19
4	e	44/63 (70%)	36 (82%)	7 (16%)	1 (2%)	5	23
5	g	315/319 (99%)	279 (89%)	30 (10%)	6 (2%)	6	26
6	h	179/274 (65%)	165 (92%)	12 (7%)	2 (1%)	11	38
7	i	260/483 (54%)	247 (95%)	12 (5%)	1 (0%)	30	59
8	j	44/463 (10%)	42 (96%)	2 (4%)	0	100	100
9	k	664/788 (84%)	599 (90%)	54 (8%)	11 (2%)	7	28
10	l	282/425 (66%)	253 (90%)	21 (7%)	8 (3%)	4	19
12	A	204/252 (81%)	181 (89%)	17 (8%)	6 (3%)	3	19
13	B	212/255 (83%)	184 (87%)	24 (11%)	4 (2%)	6	26
14	C	215/254 (85%)	196 (91%)	15 (7%)	4 (2%)	6	26
15	D	198/240 (82%)	182 (92%)	14 (7%)	2 (1%)	12	40
16	E	258/261 (99%)	235 (91%)	20 (8%)	3 (1%)	10	35
17	F	204/225 (91%)	184 (90%)	19 (9%)	1 (0%)	24	54
18	G	230/236 (98%)	216 (94%)	14 (6%)	0	100	100
19	H	182/190 (96%)	162 (89%)	16 (9%)	4 (2%)	5	24
20	I	184/200 (92%)	160 (87%)	19 (10%)	5 (3%)	4	20
21	J	183/197 (93%)	163 (89%)	18 (10%)	2 (1%)	11	38
22	L	138/156 (88%)	129 (94%)	9 (6%)	0	100	100
23	M	123/143 (86%)	110 (89%)	9 (7%)	4 (3%)	3	17
24	N	148/151 (98%)	137 (93%)	10 (7%)	1 (1%)	18	47
25	O	125/137 (91%)	113 (90%)	10 (8%)	2 (2%)	7	29
26	P	125/142 (88%)	116 (93%)	8 (6%)	1 (1%)	16	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	Q	125/143 (87%)	112 (90%)	11 (9%)	2 (2%)	7	29
28	R	123/136 (90%)	114 (93%)	9 (7%)	0	100	100
29	S	133/146 (91%)	122 (92%)	11 (8%)	0	100	100
30	T	141/144 (98%)	131 (93%)	7 (5%)	3 (2%)	5	24
31	U	101/121 (84%)	93 (92%)	4 (4%)	4 (4%)	2	15
32	V	85/87 (98%)	77 (91%)	8 (9%)	0	100	100
33	W	127/130 (98%)	110 (87%)	11 (9%)	6 (5%)	2	12
34	X	142/145 (98%)	128 (90%)	12 (8%)	2 (1%)	9	31
35	Y	132/135 (98%)	119 (90%)	12 (9%)	1 (1%)	16	44
36	Z	61/108 (56%)	56 (92%)	5 (8%)	0	100	100
All	All	5862/7354 (80%)	5305 (90%)	468 (8%)	89 (2%)	11	30

5 of 89 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	k	483	PRO
12	A	189	VAL
13	B	81	PHE
23	M	104	GLY
23	M	109	GLU

5.3.2 Protein sidechains [i](#)

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	b	70/71 (99%)	66 (94%)	4 (6%)	18	45
2	c	56/60 (93%)	48 (86%)	8 (14%)	3	13
3	d	33/49 (67%)	33 (100%)	0	100	100
4	e	40/54 (74%)	36 (90%)	4 (10%)	7	26
5	g	259/262 (99%)	239 (92%)	20 (8%)	12	37
6	h	158/238 (66%)	144 (91%)	14 (9%)	9	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	i	234/424 (55%)	222 (95%)	12 (5%)	21	48
8	j	44/419 (10%)	42 (96%)	2 (4%)	24	51
9	k	580/703 (82%)	556 (96%)	24 (4%)	27	52
10	l	260/384 (68%)	245 (94%)	15 (6%)	18	45
12	A	171/210 (81%)	153 (90%)	18 (10%)	6	23
13	B	191/224 (85%)	175 (92%)	16 (8%)	10	34
14	C	176/205 (86%)	153 (87%)	23 (13%)	4	16
15	D	164/195 (84%)	148 (90%)	16 (10%)	7	27
16	E	221/222 (100%)	200 (90%)	21 (10%)	8	29
17	F	173/191 (91%)	162 (94%)	11 (6%)	16	42
18	G	198/201 (98%)	174 (88%)	24 (12%)	5	19
19	H	165/170 (97%)	150 (91%)	15 (9%)	9	30
20	I	150/161 (93%)	131 (87%)	19 (13%)	4	17
21	J	158/166 (95%)	136 (86%)	22 (14%)	3	14
22	L	125/137 (91%)	111 (89%)	14 (11%)	6	21
23	M	101/119 (85%)	94 (93%)	7 (7%)	14	40
24	N	127/128 (99%)	115 (91%)	12 (9%)	8	29
25	O	91/105 (87%)	81 (89%)	10 (11%)	6	22
26	P	105/118 (89%)	98 (93%)	7 (7%)	15	41
27	Q	107/119 (90%)	100 (94%)	7 (6%)	15	42
28	R	113/124 (91%)	103 (91%)	10 (9%)	9	31
29	S	120/129 (93%)	114 (95%)	6 (5%)	22	49
30	T	115/116 (99%)	106 (92%)	9 (8%)	11	37
31	U	96/114 (84%)	90 (94%)	6 (6%)	16	42
32	V	74/74 (100%)	63 (85%)	11 (15%)	3	12
33	W	110/111 (99%)	94 (86%)	16 (14%)	3	13
34	X	119/120 (99%)	110 (92%)	9 (8%)	12	38
35	Y	112/113 (99%)	99 (88%)	13 (12%)	5	20
36	Z	56/89 (63%)	54 (96%)	2 (4%)	31	56
All	All	5072/6325 (80%)	4645 (92%)	427 (8%)	12	34

5 of 427 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	G	212	LEU
21	J	131	GLN
33	W	106	THR
19	H	87	ASP
20	I	140	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 95 such sidechains are listed below:

Mol	Chain	Res	Type
19	H	5	GLN
24	N	58	HIS
19	H	108	GLN
21	J	123	HIS
26	P	128	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	2	1771/1800 (98%)	632 (35%)	20 (1%)

5 of 632 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	2	4	C
11	2	17	C
11	2	25	C
11	2	26	A
11	2	34	G

5 of 20 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	2	1458	G
11	2	1573	A
11	2	1652	C
11	2	1631	A
11	2	779	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 48 ligands modelled in this entry, 48 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
11	2	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	1377:U	O3'	1378:U	P	3.76
1	2	902:G	O3'	903:U	P	3.04

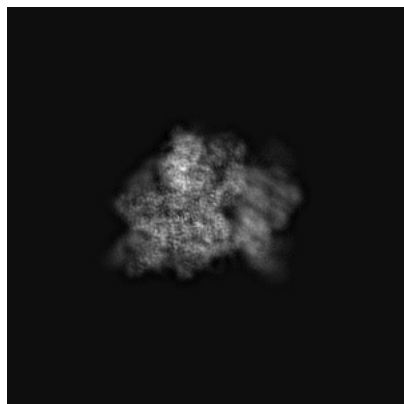
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4214. These allow visual inspection of the internal detail of the map and identification of artifacts.

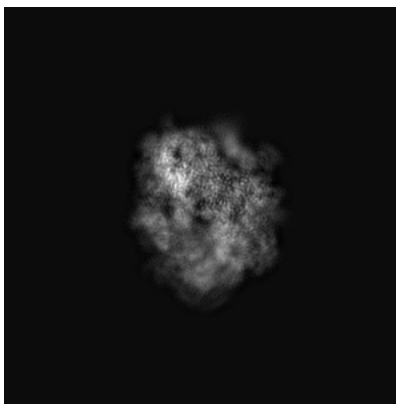
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

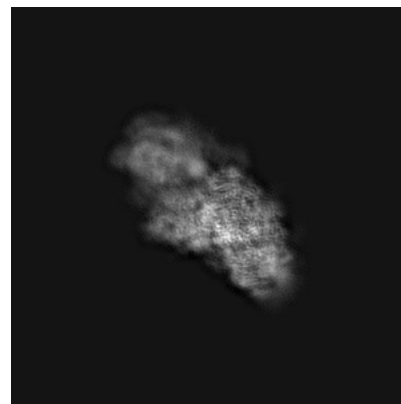
6.1.1 Primary map



X

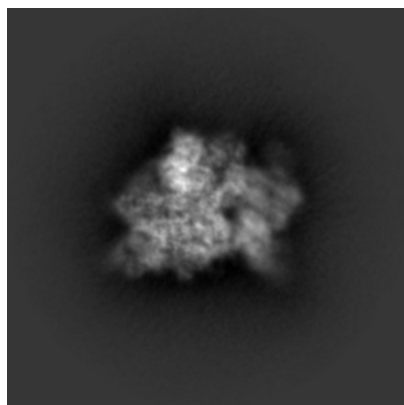


Y

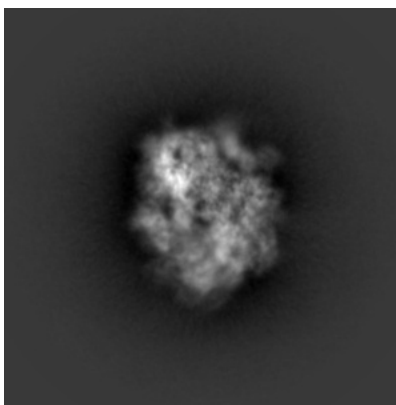


Z

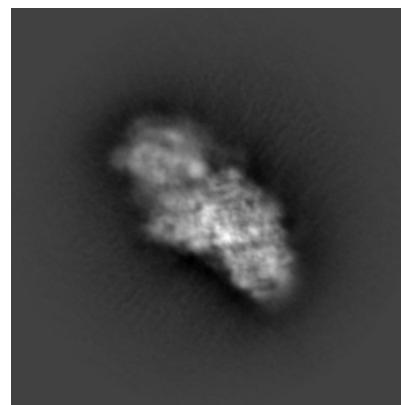
6.1.2 Raw map



X



Y

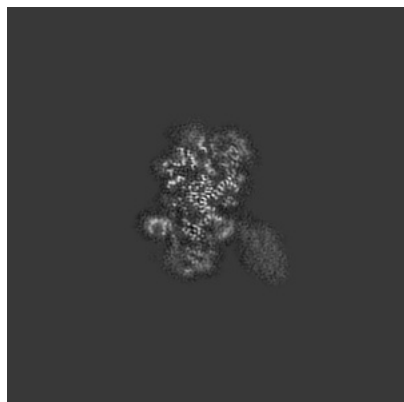


Z

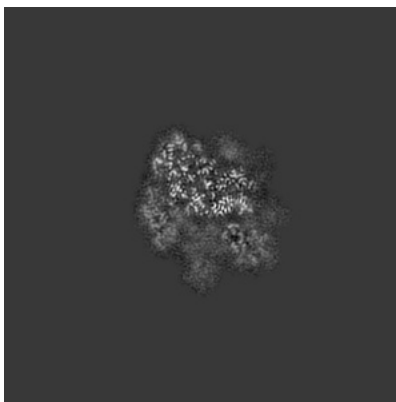
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

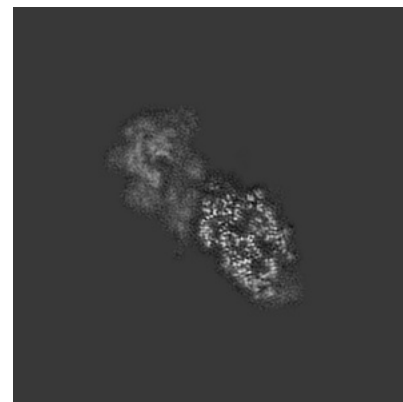
6.2.1 Primary map



X Index: 160

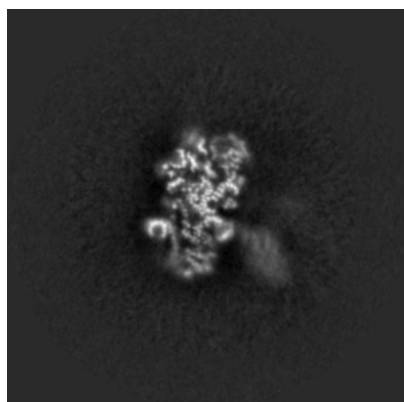


Y Index: 160

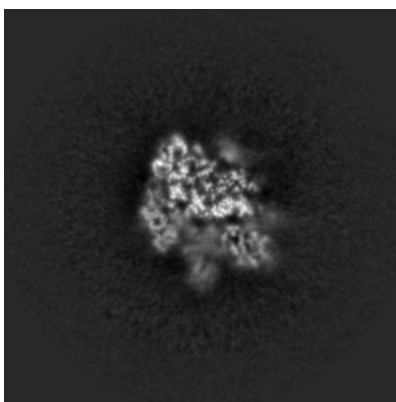


Z Index: 160

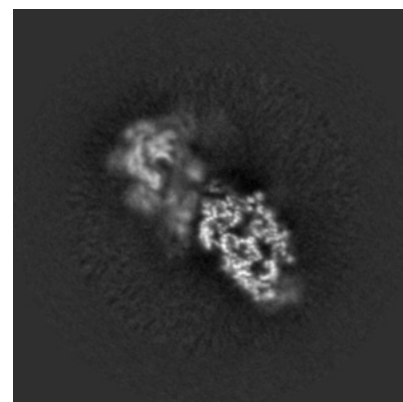
6.2.2 Raw map



X Index: 160



Y Index: 160

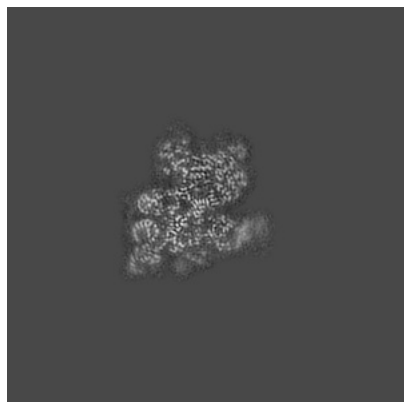


Z Index: 160

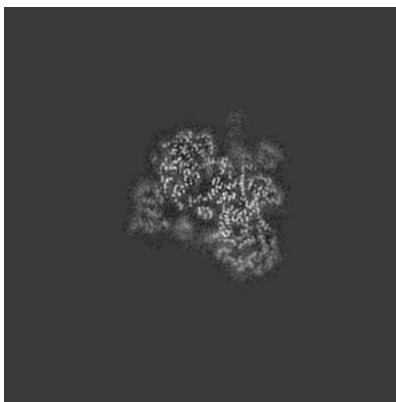
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

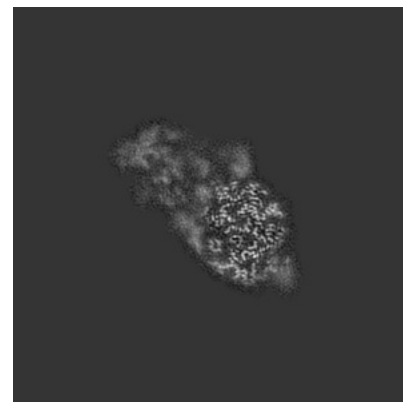
6.3.1 Primary map



X Index: 178

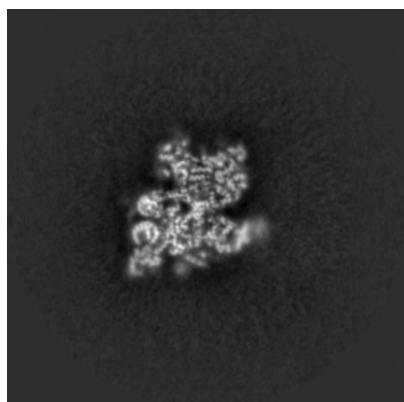


Y Index: 141

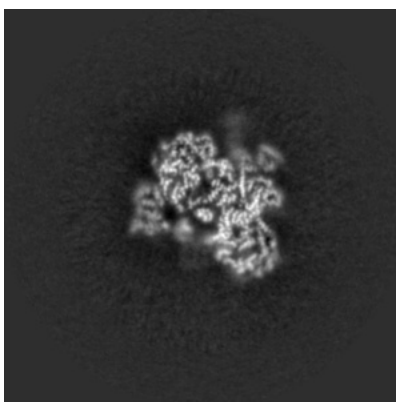


Z Index: 144

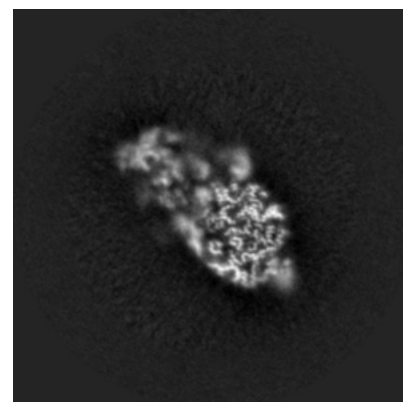
6.3.2 Raw map



X Index: 178



Y Index: 141

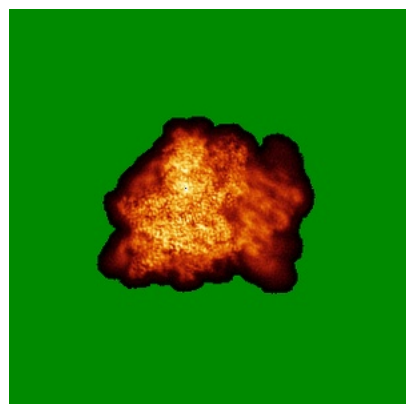


Z Index: 144

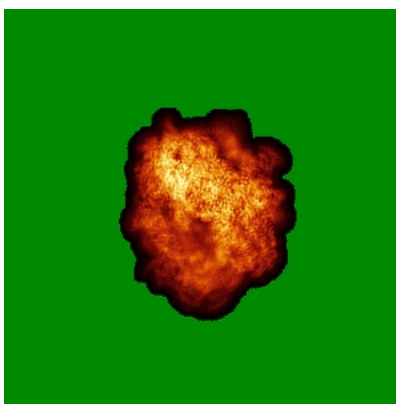
The images above show the largest variance slices of the map in three orthogonal directions.

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

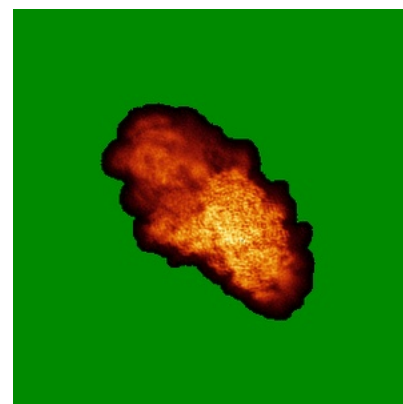
6.4.1 Primary map



X

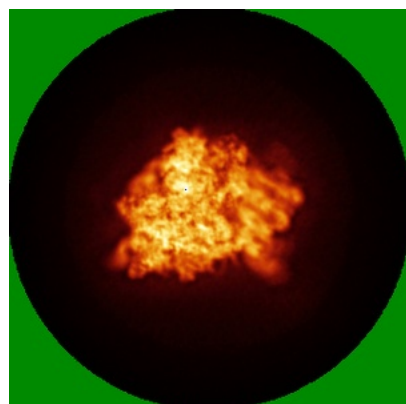


Y

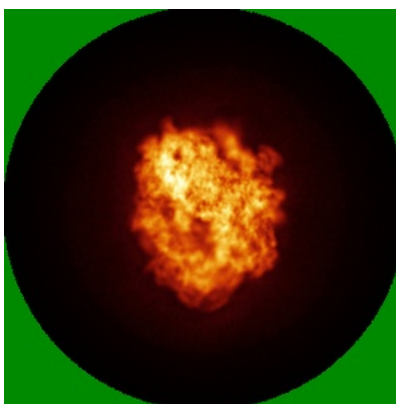


Z

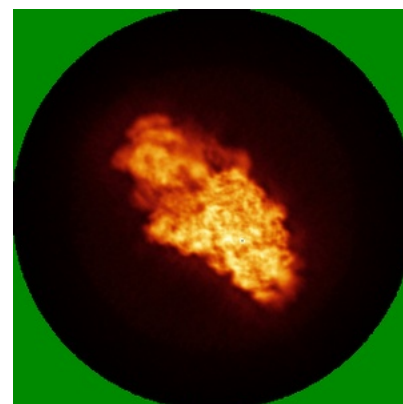
6.4.2 Raw map



X



Y

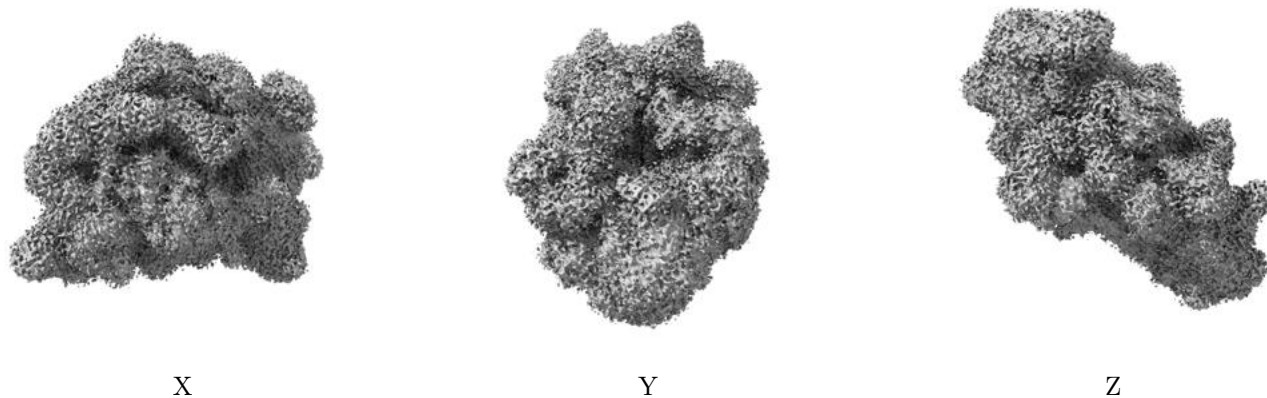


Z

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.

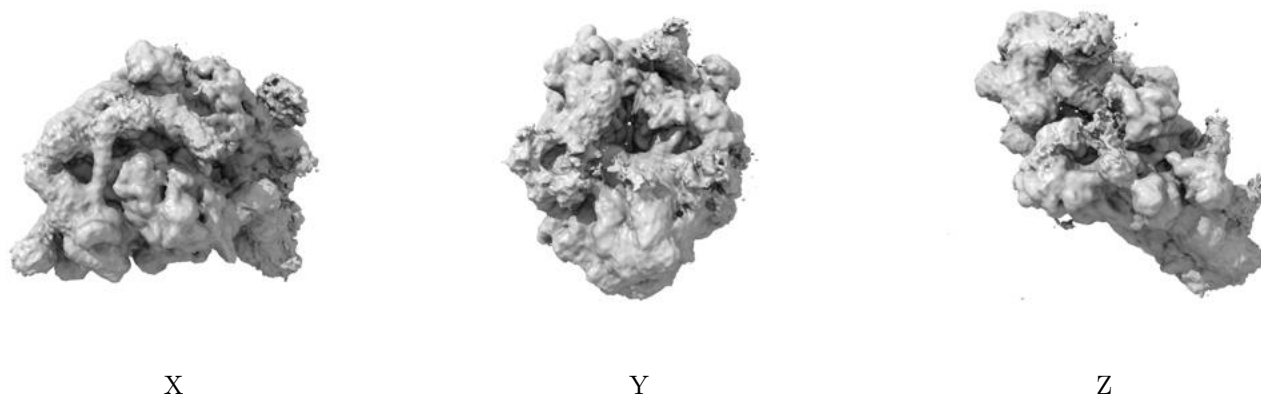
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. 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.

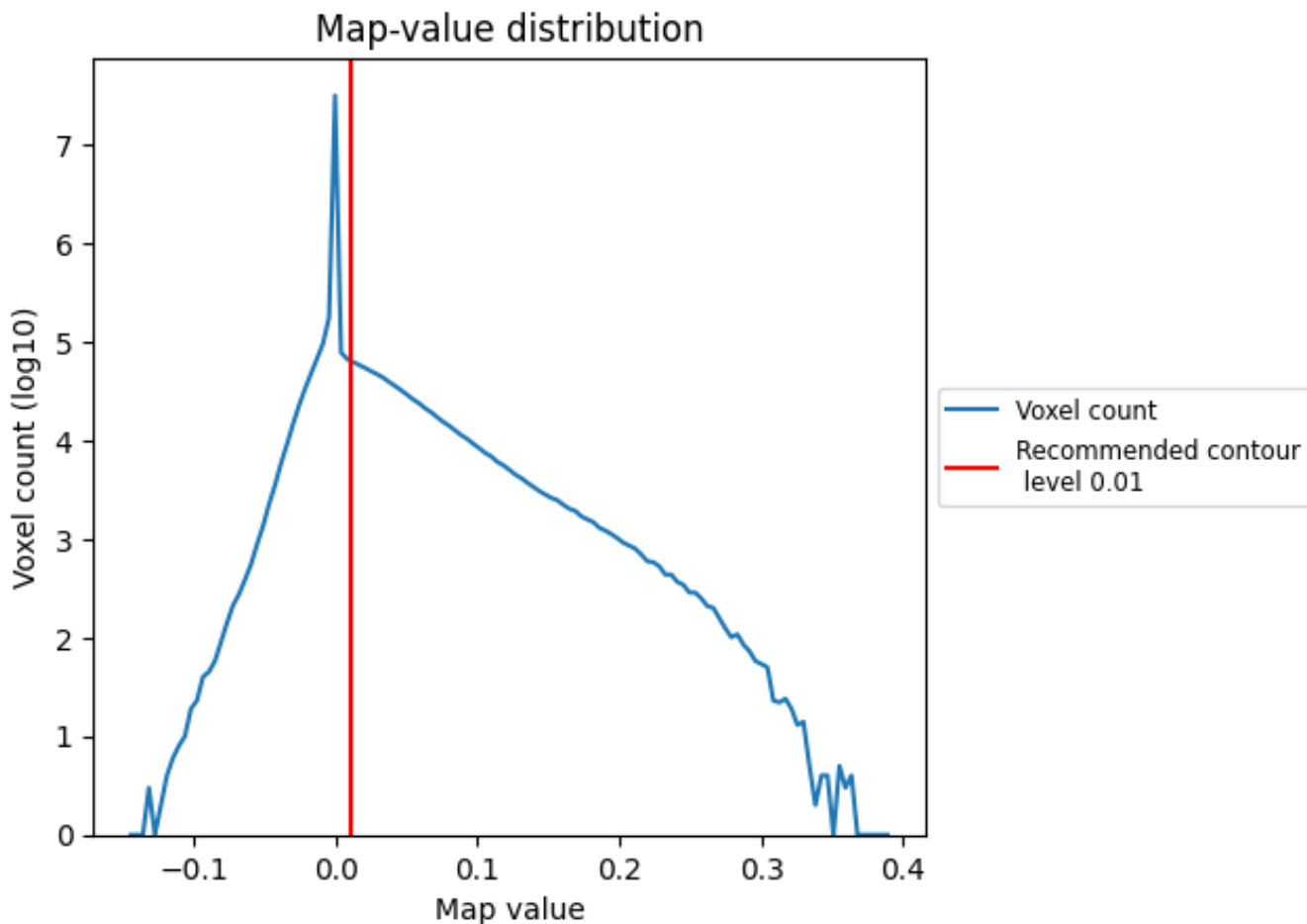
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

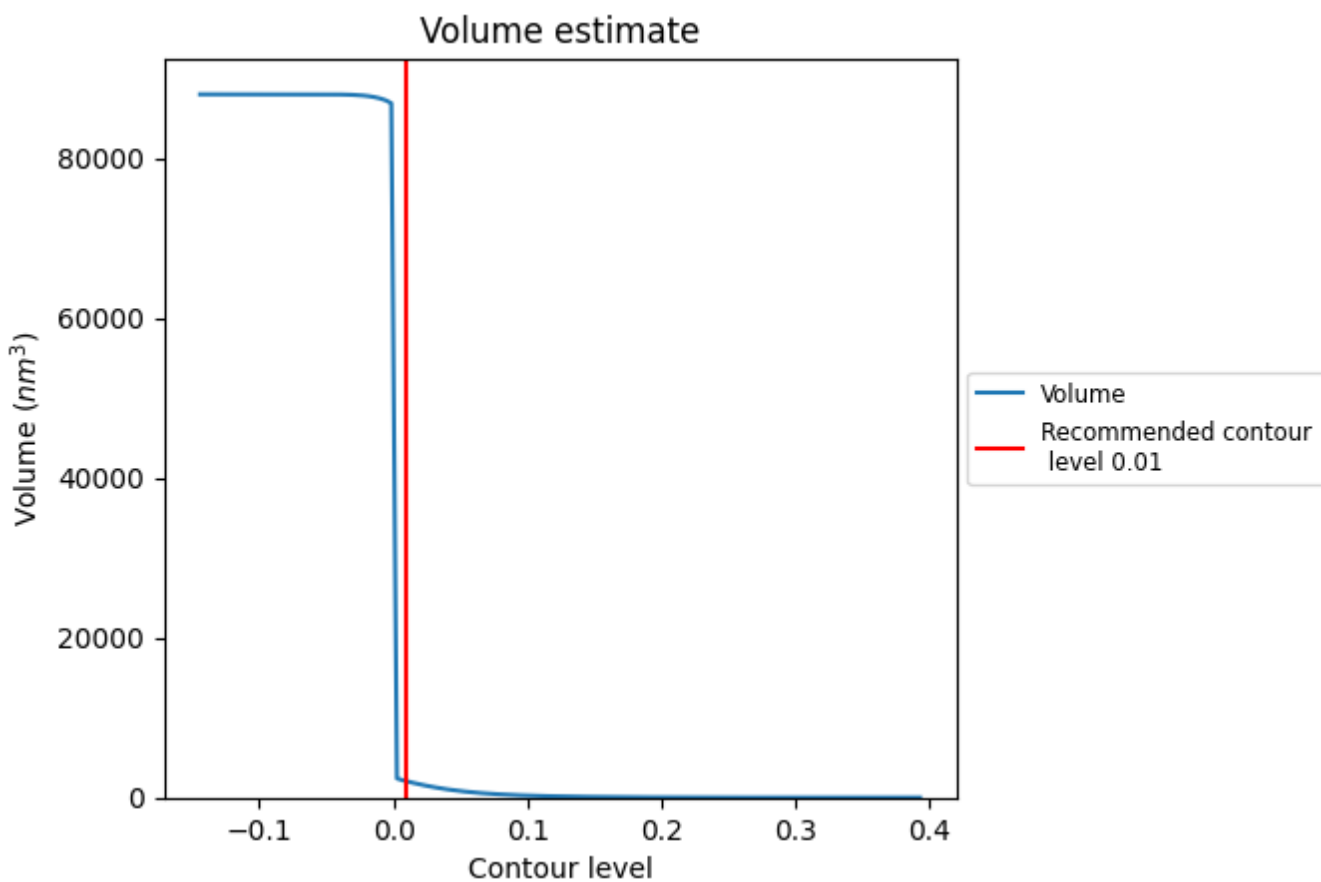
This section contains the results of statistical analysis of the map.

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.

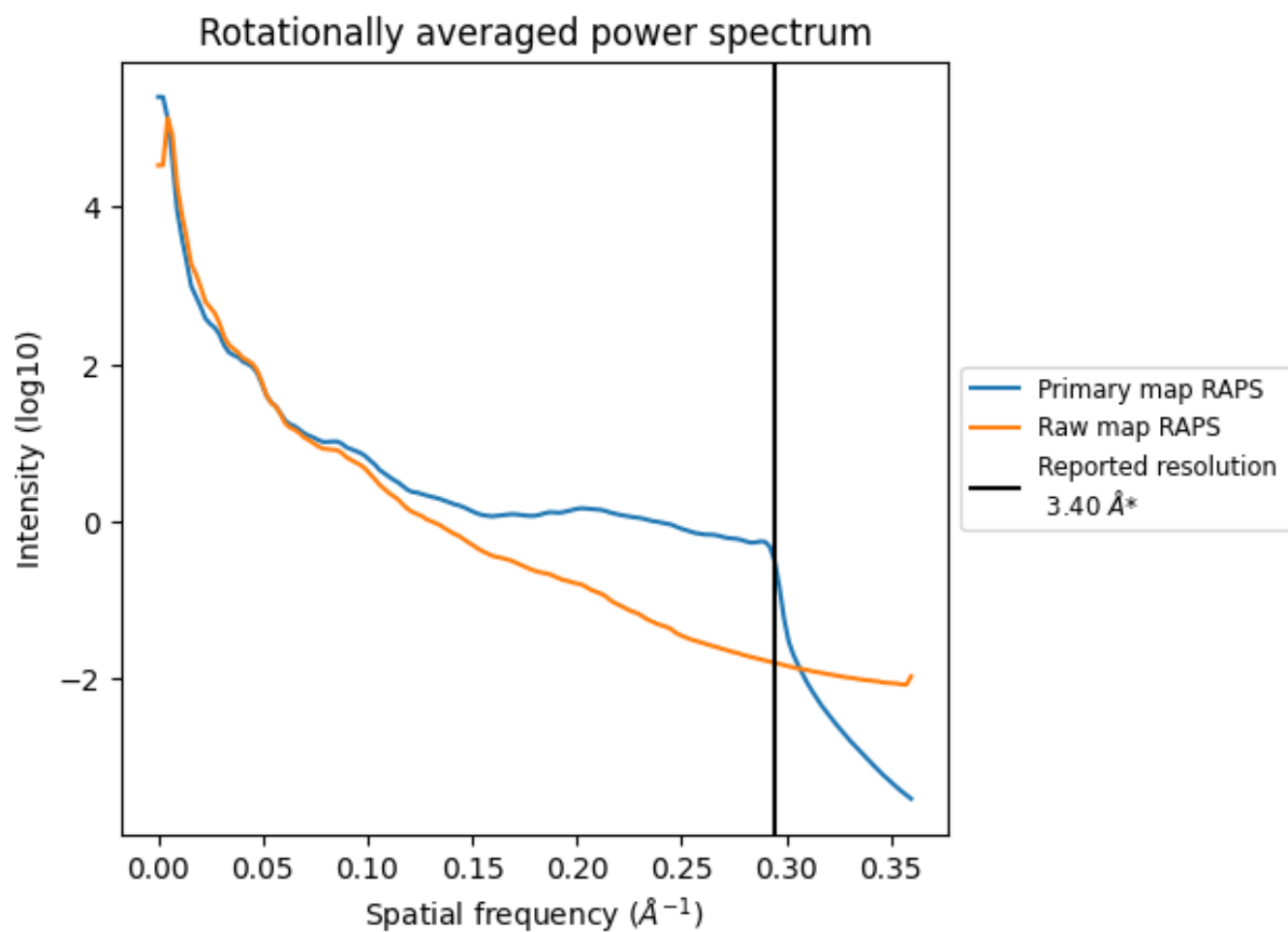
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2041 nm^3 ; this corresponds to an approximate mass of 1844 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 i

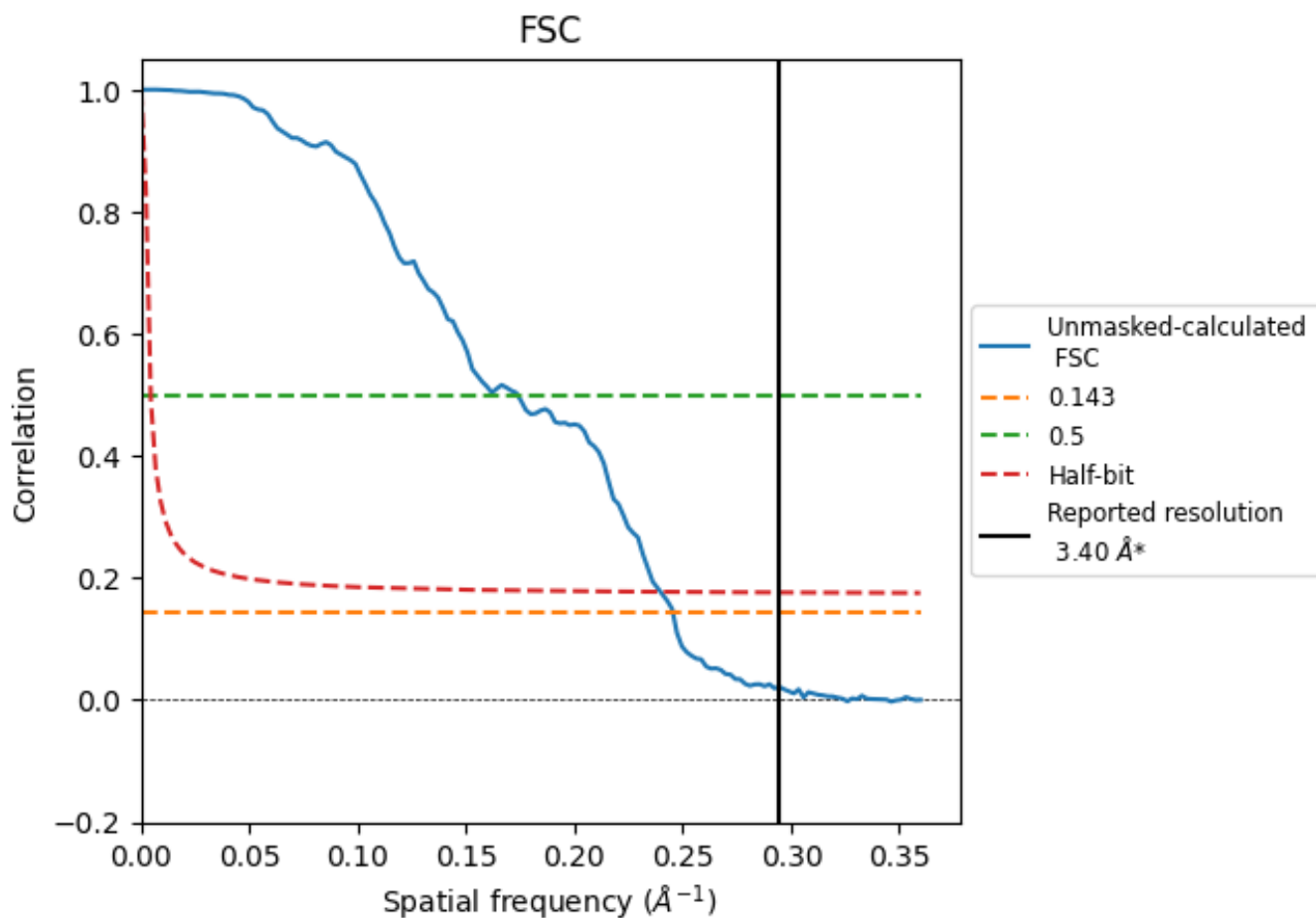


*Reported resolution corresponds to spatial frequency of 0.294 \AA^{-1}

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

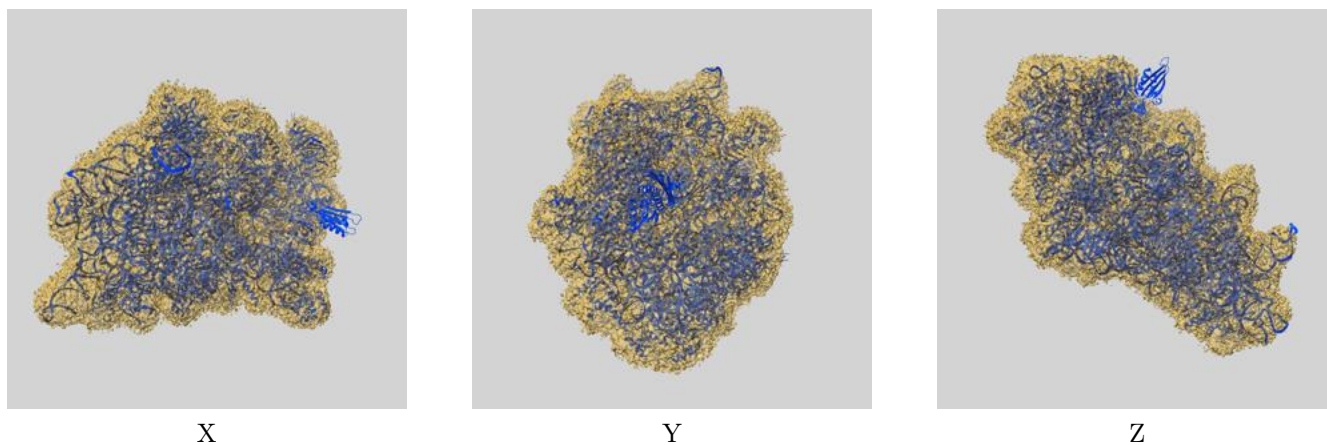
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.07	5.76	4.17

*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 4.07 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

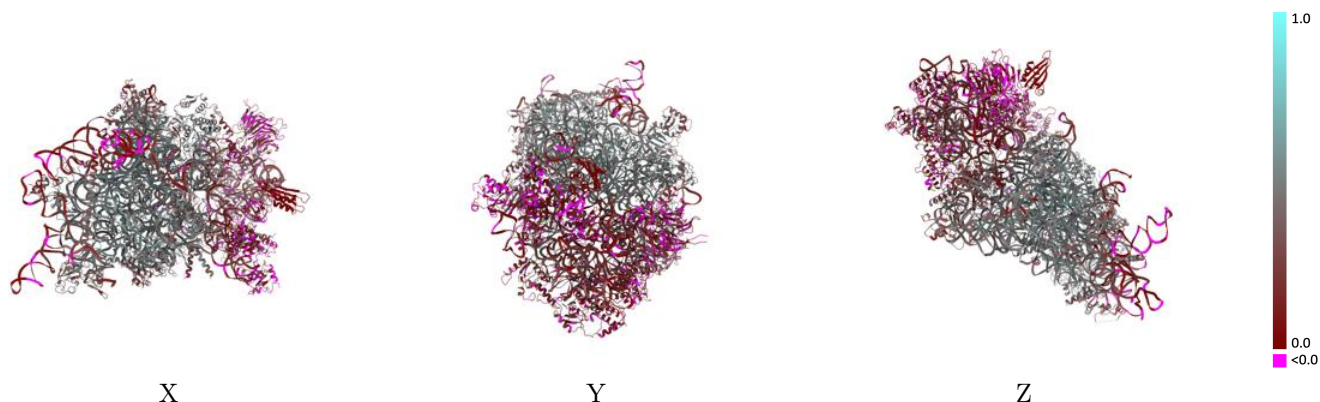
This section contains information regarding the fit between EMDB map EMD-4214 and PDB model 6FAI. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



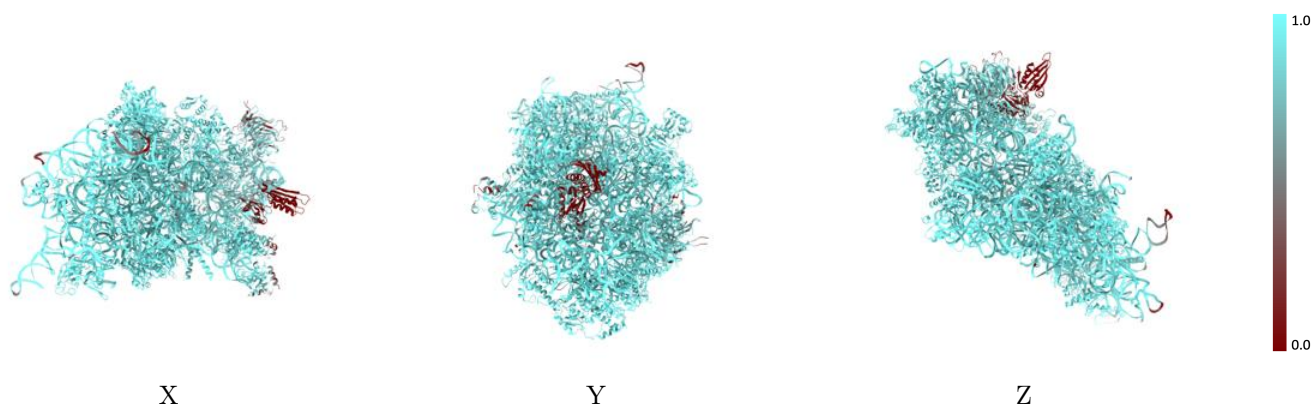
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



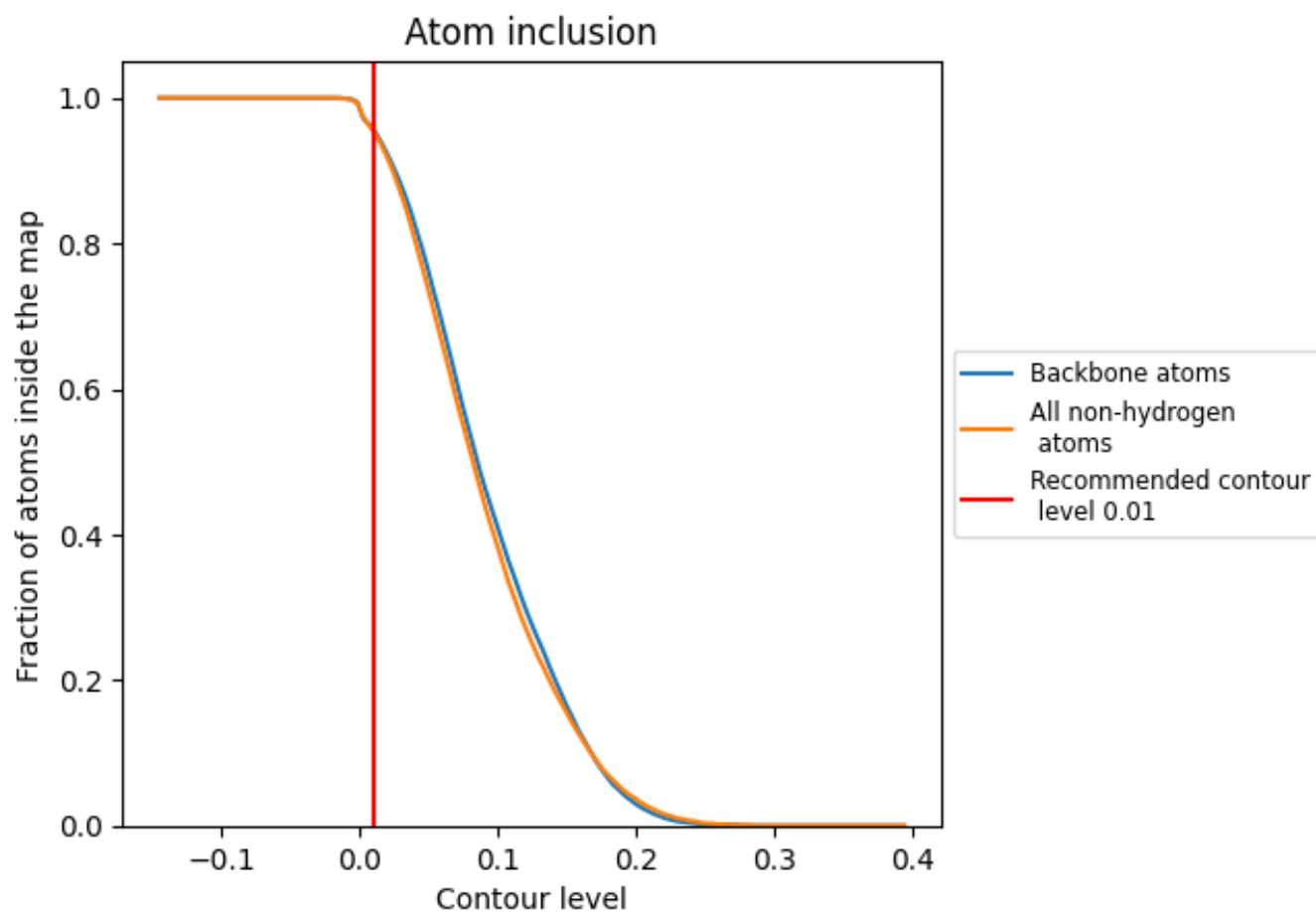
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9540	 0.3280
2	 0.9860	 0.3450
A	 0.9940	 0.4650
B	 0.9870	 0.4070
C	 0.9910	 0.4910
D	 0.1160	 0.0110
E	 0.9910	 0.5140
F	 0.9810	 0.1790
G	 0.9930	 0.4050
H	 0.9880	 0.3830
I	 0.9940	 0.4530
J	 0.9900	 0.4900
L	 0.9950	 0.5100
M	 0.7850	 0.0600
N	 0.9860	 0.4620
O	 0.9920	 0.3990
P	 0.9730	 0.2270
Q	 0.9770	 0.1420
R	 0.9750	 0.2020
S	 0.9820	 0.1630
T	 0.9900	 0.1610
U	 0.8000	 0.0910
V	 0.9930	 0.4870
W	 0.9940	 0.5380
X	 0.9650	 0.4560
Y	 0.9920	 0.4780
Z	 0.9680	 0.1420
b	 0.9920	 0.4760
c	 0.9730	 0.1660
d	 0.8290	 0.0570
e	 0.9590	 0.3900
g	 0.7240	 0.0850
h	 0.9820	 0.3650
i	 0.9610	 0.0920
j	 0.6560	 0.0400



Continued on next page...

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Chain	Atom inclusion	Q-score
k	 0.9780	 0.3780
l	 0.9550	 0.1840