



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 03:23 AM UTC

PDB ID : 8I7J / pdb_00008i7j
EMDB ID : EMD-35216
Title : Yeast 40S-eIF4B - partially open conformation of the 40S head
Authors : Datey, A.; Khaja, F.T.; Hussain, T.
Deposited on : 2023-01-31
Resolution : 4.60 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:

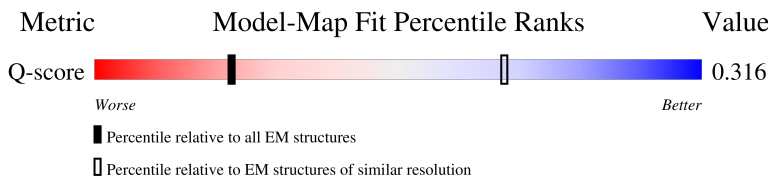
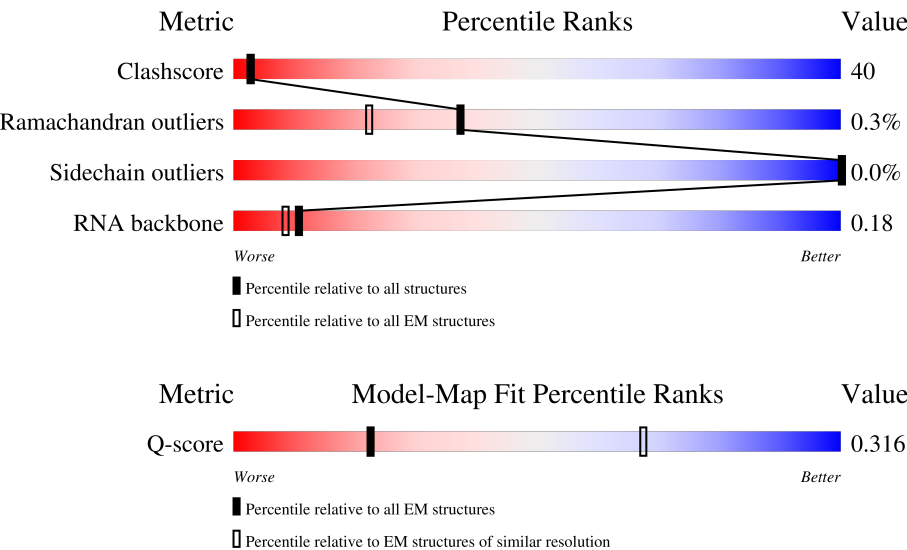
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.60 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.



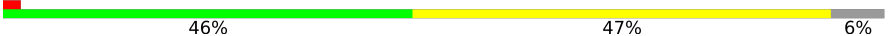
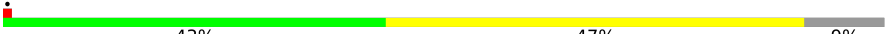
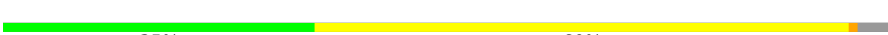
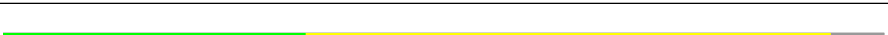
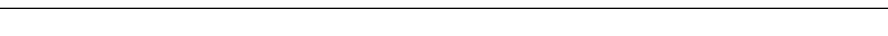
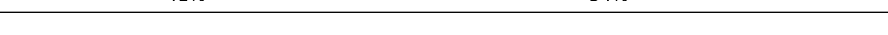
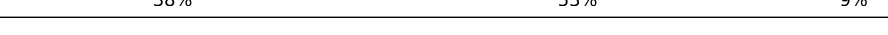
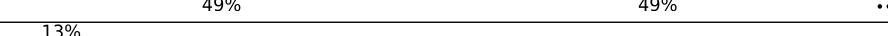
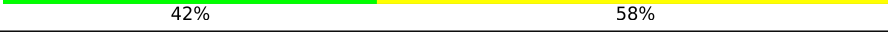
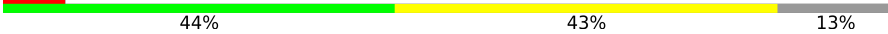
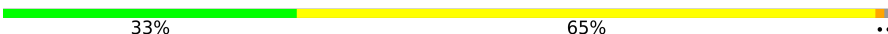
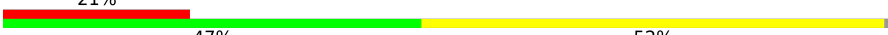
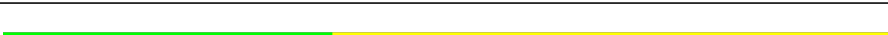
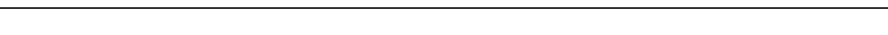
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	2407 (4.10 - 5.10)

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	2	1799	5% 47% 47% .
2	A	254	32% 50% 18%
3	B	255	31% 56% 13%

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Mol	Chain	Length	Quality of chain
4	C	259	
5	D	237	
6	E	261	
7	F	227	
8	G	236	
9	H	190	
10	I	201	
11	J	188	
12	K	106	
13	L	156	
14	M	134	
15	N	151	
16	O	137	
17	P	142	
18	Q	143	
19	R	136	
20	S	146	
21	T	144	
22	U	117	
23	V	87	
24	W	130	
25	X	145	
26	Y	135	
27	Z	108	
28	a	119	

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Mol	Chain	Length	Quality of chain
29	b	82	52% 46%
30	c	67	30% 64% 6%
31	d	56	36% 59% 5%
32	e	63	51% 33% 16%
33	f	150	6% 19% 27% 54%
34	g	326	37% 60%
35	h	25	36% 64%

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 76299 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 RNA (1780-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1780	Total	C	N	O	P	0	0
			37797	16892	6658	12467	1780		

- Molecule 2 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	208	Total	C	N	O	S	0	0
			1626	1040	286	298	2		

- Molecule 3 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	223	Total	C	N	O	S	0	0
			1774	1120	325	326	3		

- Molecule 4 is a protein called KLLA0F09812p.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	217	Total	C	N	O	S	0	0
			1629	1041	287	297	4		

- Molecule 5 is a protein called KLLA0D08305p.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	223	Total	C	N	O	S	0	0
			1744	1108	313	318	5		

- Molecule 6 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	260	Total	C	N	O	S	0	0
			2078	1322	393	359	4		

- Molecule 7 is a protein called KLLA0D10659p.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	206	Total	C	N	O	S	0	0
			1609	1008	298	300	3		

- Molecule 8 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	226	Total	C	N	O	S	0	0
			1812	1134	348	326	4		

- Molecule 9 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	184	Total	C	N	O	S	0	0
			1483	950	270	263			

- Molecule 10 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	188	Total	C	N	O	S	0	0
			1489	923	300	265	1		

- Molecule 11 is a protein called KLLA0E23673p.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	182	Total	C	N	O	S	0	0
			1471	929	287	254	1		

- Molecule 12 is a protein called KLLA0B08173p.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	96	Total	C	N	O	S	0	0
			809	533	129	146	1		

- Molecule 13 is a protein called KLLA0A10483p.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	155	Total	C	N	O	S	0	0
			1248	798	237	210	3		

- Molecule 14 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	M	122	Total	C	N	O	0	0
			922	575	167	180		

- Molecule 15 is a protein called KLLA0F18040p.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	150	Total	C	N	O	S	0	0
			1187	756	223	206	2		

- Molecule 16 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	127	Total	C	N	O	S	0	0
			942	578	188	173	3		

- Molecule 17 is a protein called KLLA0F07843p.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	123	Total	C	N	O	S	0	0
			980	628	179	168	5		

- Molecule 18 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Q	141	Total	C	N	O	0	0
			1105	709	204	192		

- Molecule 19 is a protein called KLLA0B01474p.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	125	Total	C	N	O	S	0	0
			991	619	182	187	3		

- Molecule 20 is a protein called KLLA0B01562p.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	145	Total	C	N	O	S	0	0
			1193	741	240	210	2		

- Molecule 21 is a protein called KLLA0A07194p.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	T	143	Total	C	N	O	0	0
			1110	693	210	207		

- Molecule 22 is a protein called KLLA0F25542p.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	106	Total	C	N	O	S	0	0
			845	540	152	152	1		

- Molecule 23 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	87	Total	C	N	O	S	0	0
			687	424	126	135	2		

- Molecule 24 is a protein called KLLA0B07931p.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	129	Total	C	N	O	S	0	0
			1021	651	187	180	3		

- Molecule 25 is a protein called KLLA0B11231p.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	144	Total	C	N	O	S	0	0
			1119	708	218	191	2		

- Molecule 26 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	Y	134	Total	C	N	O	0	0
			1061	665	207	189		

- Molecule 27 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	70	Total	C	N	O	S	0	0
			558	355	104	98	1		

- Molecule 28 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	98	Total	C	N	O	S	0	0
			779	480	165	129	5		

- Molecule 29 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	81	Total	C	N	O	S	0	0
			609	379	112	113	5		

- Molecule 30 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	63	Total	C	N	O	S	0	0
			494	305	98	90	1		

- Molecule 31 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	53	Total	C	N	O	S	0	0
			446	280	89	76	1		

- Molecule 32 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	53	Total	C	N	O	S	0	0
			428	268	87	72	1		

- Molecule 33 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	69	Total	C	N	O	S	0	0
			549	352	102	91	4		

- Molecule 34 is a protein called KLLA0E12277p.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	318	Total	C	N	O	S	0	0
			2466	1561	430	470	5		

- Molecule 35 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 36 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
36	2	2	Total	Mg	0
			2	2	

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

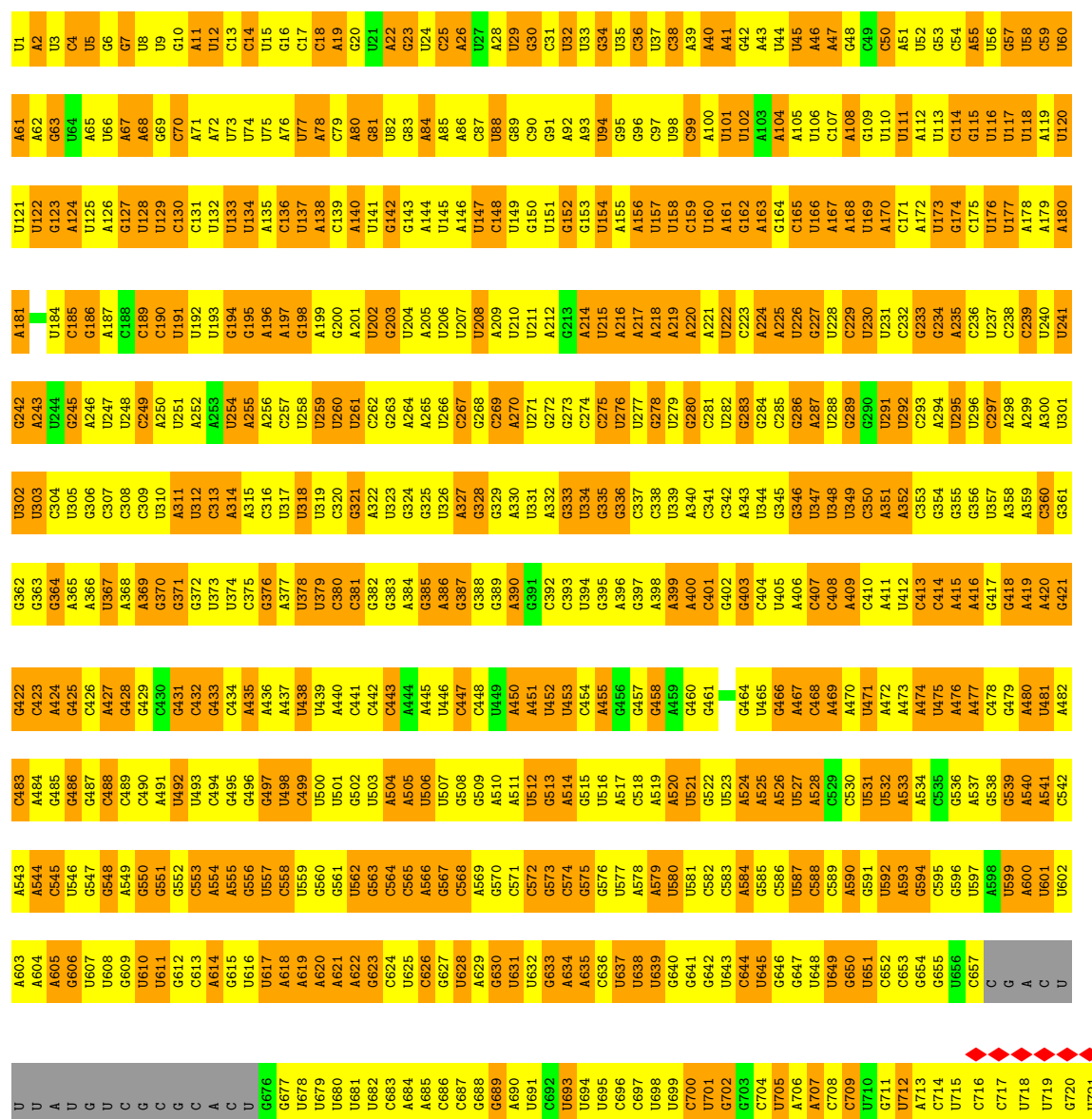
Mol	Chain	Residues	Atoms		AltConf
37	a	1	Total	Zn	0
			1	1	
37	b	1	Total	Zn	0
			1	1	
37	f	1	Total	Zn	0
			1	1	

3 Residue-property plots

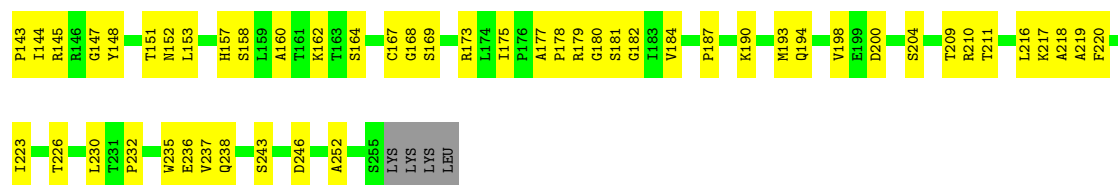
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: RNA (1780-MER)

Chain 2:  5%  47%  47% 

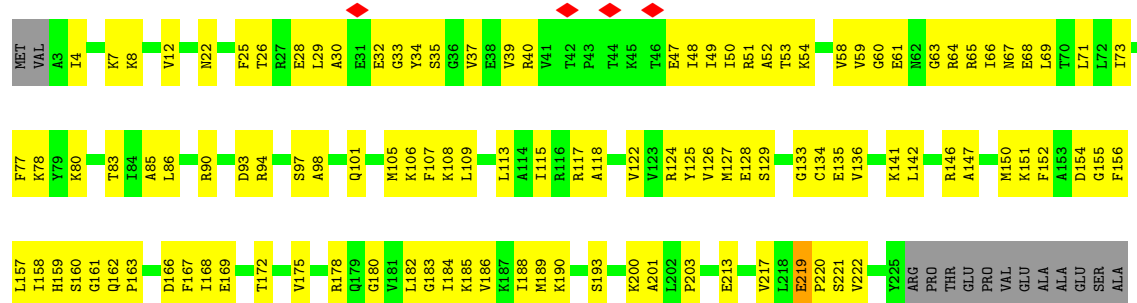


A1631	G1570	G1507	U1447	G1387	G1327	U1265	U1205	G1145	A1085	A1025	U963	G903	A843	G782	G722
C1632	A1571	U1508	U1448	U1388	A1328	G1266	C1206	A1146	A1086	A1026	U964	A904	G844	C783	G723
A1633	G1572	G1509	C1449	A1389	G1329	G1267	C1208	G1147	A1087	C1027	U965	A905	G845	U784	G724
C1634	G1573	G1510	U1450	U1390	A1330	U1268	C1209	G1148	U1088	U1028	A966	A906	A846	C785	U725
C1635	A1574	G1511	G1451	C1391	C1331	G1269	G1210	G1149	C1089	A1029	U967	U907	C947	G786	U726
G1636	A1575	U1512	G1452	G1392	C1332	G1270	G1211	A1150	A1090	U1030	C968	U908	A849	A787	G727
C1637	U1576	A1513	G1453	G1393	U1333	U1271	G1212	A1151	A1091	G1031	A969	C909	U849	A788	G728
C1638	U1577	A1514	C1454	U1394	U1334	G1272	G1213	A1152	A1092	C1032	A970	U910	U850	U789	G729
C1639	C1578	U1515	C1455	U1395	A1335	G1273	U1213	G1153	G1093	C1033	C971	U911	C851	U790	G730
G1640	U1579	C1516	G1456	U1396	A1336	A1274	C1214	G1154	U1094	A1034	A972	G912	U852	U791	G731
U1641	U1580	U1517	C1457	C1397	C1337	U1275	C1215	C1155	C1095	A1035	A973	G913	U853	A792	G732
C1642	A1581	G1518	A1458	A1398	C1338	G1276	A1216	A1156	U1096	A1036	C974	A914	A854	U793	G733
G1643	G1582	U1519	C1459	A1399	U1339	G1277	G1217	C1157	U1097	U1037	C975	U915	A855	U794	G734
C1644	U1583	G1520	G1460	G1400	A1340	C1278	A1218	C1158	U1098	A1038	A976	U916	U856	A795	G735
U1645	A1584	G1521	C1461	C1401	C1341	G1279	C1219	A1159	G1099	G1039	A977	U917	G857	G796	C736
A1646	A1585	A1522	G1462	C1402	U1342	G1280	U1220	A1160	U1100	G1040	A978	A918	U858	C797	A737
G1647	G1586	A1523	G1463	G1403	A1343	U1281	C1221	G1161	G1101	A1041	C979	U919	U859	A798	A738
U1648	C1587	A1524	G1464	A1404	A1344	U1282	A1222	A1162	U1102	G1042	U980	U920	U860	U799	G739
A1649	U1588	C1525	C1465	U1405	A1345	C1283	A1223	G1163	U1103	U1043	U981	G921	A861	G800	A740
C1650	C1589	G1529	U1466	G1406	U1346	U1284	U1224	G1164	C1104	C1044	A982	A922	A862	A801	A741
C1651	A1590	G1530	A1467	G1407	A1347	U1285	A1225	A1165	U1105	G1045	C983	A923	U863	A802	U742
G1652	A1591	U1530	C1468	A1408	G1348	A1286	A1226	G1166	G1106	G1046	C984	G924	A864	A803	U743
A1653	G1592	C1531	A1469	A1409	G1349	U1287	G1227	U1167	G1107	G1047	C985	A925	G865	U804	U744
U1654	U1593	G1532	C1470	G1410	G1350	U1288	G1228	G1168	G1108	U1048	G986	C926	G866	U805	U745
U1655	C1594	U1533	U1471	U1411	U1351	U1289	A1229	G1169	G1109	G1049	A987	U927	G867	G806	U746
G1656	A1595	G1534	G1472	U1412	U1352	G1290	U1230	A1170	G1110	G1050	U988	A928	A868	G808	A747
A1657	U1596	C1535	A1473	U1413	G1353	G1291	U1231	G1171	G1111	U1051	C989	A929	C869	G809	C747
C1658	C1597	U1536	C1474	G1414	C1354	U1292	C1232	C1172	U1112	G1052	C990	C930	G870	A810	U748
U1659	A1598	G1537	G1475	A1415	U1355	G1293	A1233	C1173	G1113	U1053	A991	U931	G871	A811	U749
G1660	G1599	G1538	G1476	G1416	G1356	U1294	C1234	U1174	U1114	U1054	A992	A932	U872	U812	U750
C1661	C1600	U1539	A1477	G1417	G1357	G1295	A1235	G1175	U1115	U1055	C993	C933	C873	A813	G751
G1662	U1601	G1540	G1478	G1418	C1358	U1297	G1236	C1176	U1116	U1056	A994	U934	G874	G814	A752
U1663	A1602	A1541	C1479	A1419	A1359	G1298	A1237	G1177	G1117	U1057	U995	G935	G875	G815	A753
G1664	G1603	U1542	A1480	C1420	C1360	U1299	U1238	G1178	U1118	C1058	C996	C936	G876	A816	A754
A1665	C1604	A1543	A1481	U1421	U1361	U1300	U1239	C1179	U1119	U1059	A997	G937	G877	C817	A755
G1666	G1605	G1544	G1482	A1422	U1362	U1301	G1240	U1180	C1120	U1060	U998	A938	G878	U818	A756
U1667	U1606	A1545	C1483	A1423	G1363	U1302	A1241	U1181	G1121	A1061	C999	A939	C879	U819	A757
G1668	G1607	G1546	G1484	C1424	C1364	G1303	G1242	A1182	C1122	U1062	A1000	A940	A880	U820	U758
A1669	A1609	G1547	A1485	A1425	C1365	U1304	A1243	A1183	A1123	G1063	G1001	C941	U881	U821	U759
G1670	U1610	U1548	G1486	G1426	G1366	C1305	G1244	U1184	A1124	A1064	A1002	C942	C882	G822	A760
C1671	U1611	U1550	U1487	G1427	G1367	U1306	C1245	U1185	G1125	C1065	U1003	A943	A883	G823	G761
C1672	A1612	G1551	A1488	U1428	U1368	G1307	U1246	U1186	G1126	C1066	A1004	U944	G884	U824	A762
G1673	G1613	U1552	C1489	C1429	U1369	C1308	G1247	G1187	G1127	C1067	C1005	U945	U885	U825	G763
U1674	G1614	A1553	A1490	U1430	G1370	U1309	U1248	A1188	U1128	A1068	C1006	U946	A886	C826	U764
U1675	U1615	A1554	A1491	G1431	C1371	U1310	U1249	G1189	G1129	C1069	G1007	C947	U887	U827	G765
A1676	C1616	U1555	C1492	U1432	C1372	A1311	U1250	U1190	A1130	U1070	G1010	C949	U888	U828	G766
G1677	G1617	U1556	C1493	G1433	C1373	U1312	C1251	C1191	A1131	C1071	U1011	A950	C889	U829	G767
C1678	U1618	A1557	A1494	A1434	C1374	U1313	U1252	A1192	A1132	G1072	U1012	A951	U830	U831	A769
A1679	U1619	U1558	U1495	U1435	U1375	U1314	U1253	A1193	C1133	G1073	A952	A951	U831	U832	A770
U1680	G1620	U1559	G1496	G1436	U1376	G1315	G1254	C1194	U1134	C1074	G1013	G952	U832	U833	A771
G1681	C1621	G1560	C1497	C1437	C1377	C1316	A1255	A1195	U1135	A1075	U1014	G953	G894	U834	G772
U1682	C1622	C1561	C1498	C1438	U1378	G1317	U1256	G1197	A1136	C1076	C1015	A954	U895	U835	A773
C1683	C1623	U1562	C1499	C1439	U1379	U1318	U1257	G1198	A1137	C1077	U1016	G955	C896	G836	G774
G1684	U1624	C1563	G1500	U1440	A1380	U1319	U1258	G1199	U1138	U1078	U1017	G956	C897	G837	A775
U1685	U1625	U1564	A1501	U1441	G1381	A1320	U1259	G1199	G1139	U1079	G1020	U957	A897	U838	G776
C1686	G1626	U1565	G1502	A1442	A1382	A1321	G1260	G1200	G1140	A1080	C1021	U958	G898	U839	G777
A1687	G1627	C1566	A1503	G1443	G1383	C1322	U1261	A1201	A1141	C1081	C1022	U959	A899	U840	A778
G1688	U1628	A1567	G1504	A1444	G1384	G1323	G1262	A1202	A1142	G1082	U1023	C961	G900	U841	A779
A1689	C1629	U1568	G1505	A1445	G1385	G1324	G1263	A1203	U1143	A1083	U1024	C962	U902	U842	A781
G1690	C1630	C1569	U1506	G1446	A1386	C1326	G1264	C1204	U1144	G1084		A962			



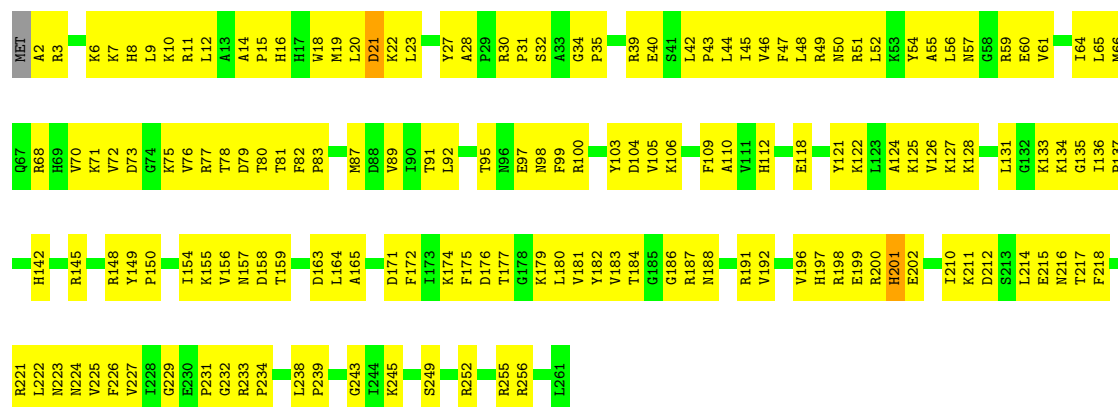
• Molecule 5: KLLA0D08305p

Chain D: 46% 47% 6%



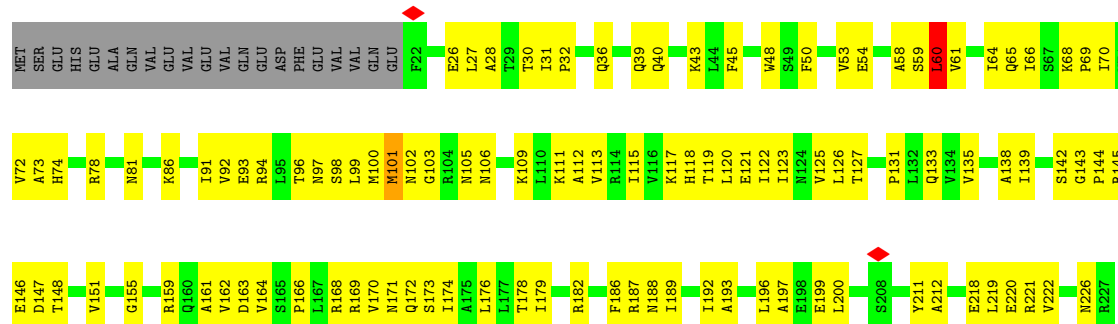
• Molecule 6: 40S ribosomal protein S4

Chain E: 39% 60%

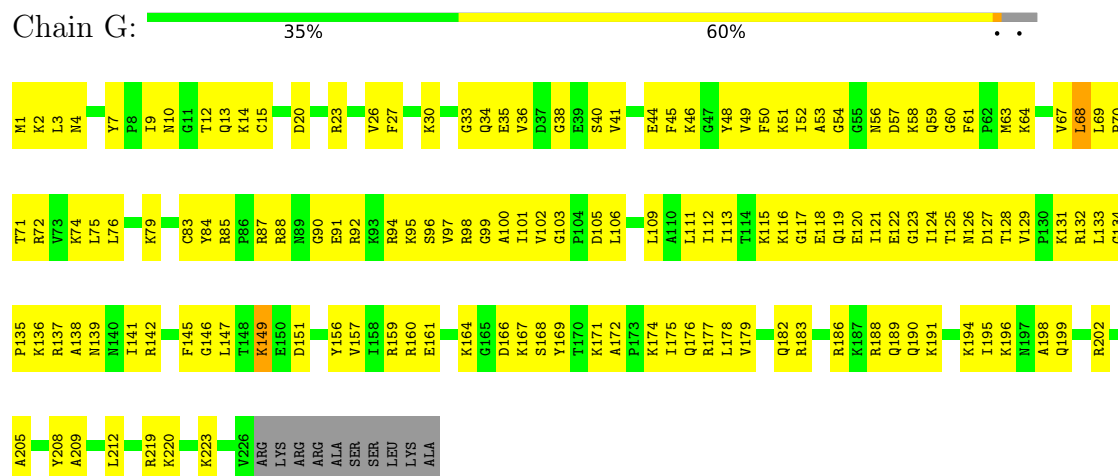


• Molecule 7: KLLA0D10659p

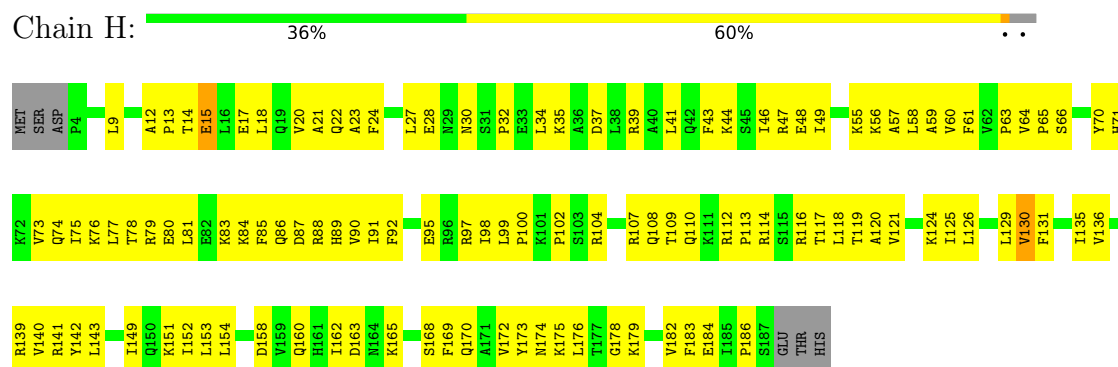
Chain F: 43% 47% 9%



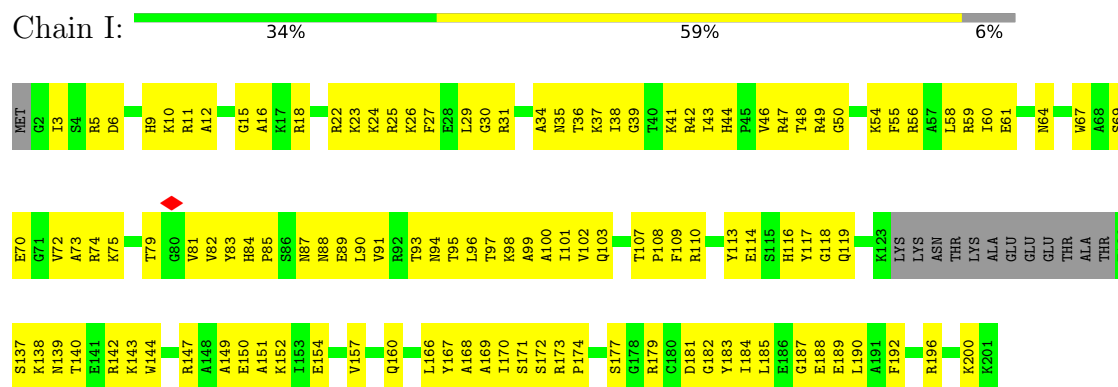
- Molecule 8: 40S ribosomal protein S6



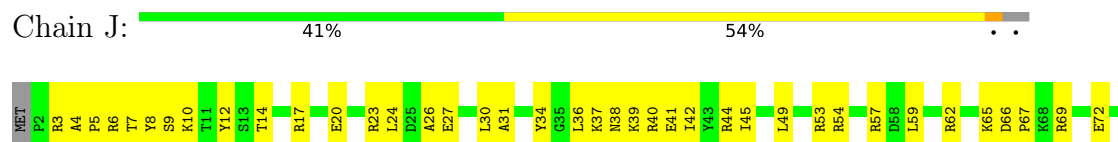
- Molecule 9: 40S ribosomal protein S7



- Molecule 10: 40S ribosomal protein S8



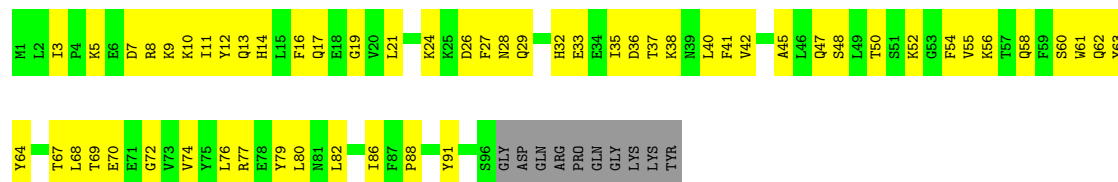
- Molecule 11: KLLA0E23673p





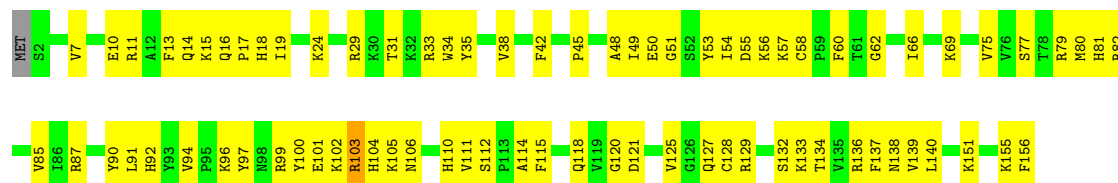
• Molecule 12: KLLA0B08173p

Chain K: 38% 53% 9%



• Molecule 13: KLLA0A10483p

Chain L: 49% 49% ..



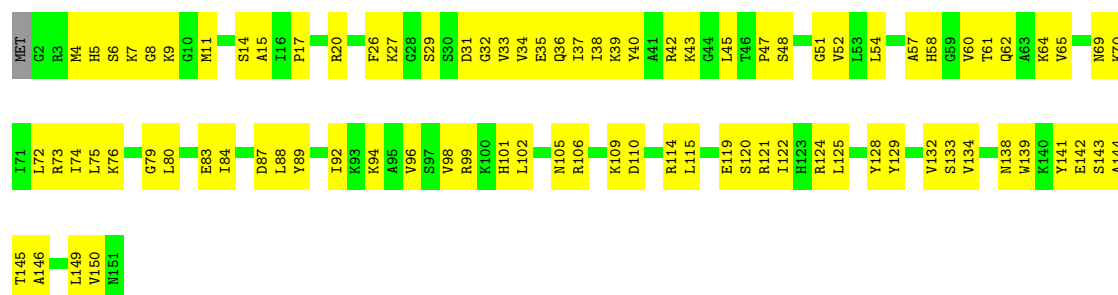
• Molecule 14: 40S ribosomal protein S12

Chain M: 13% 46% 44% 9%

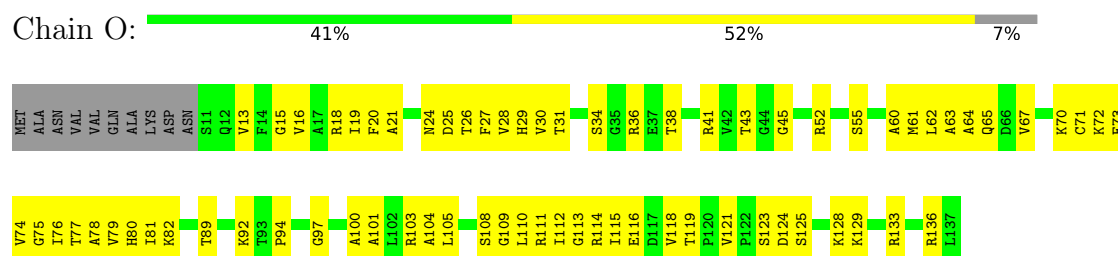


• Molecule 15: KLLA0F18040p

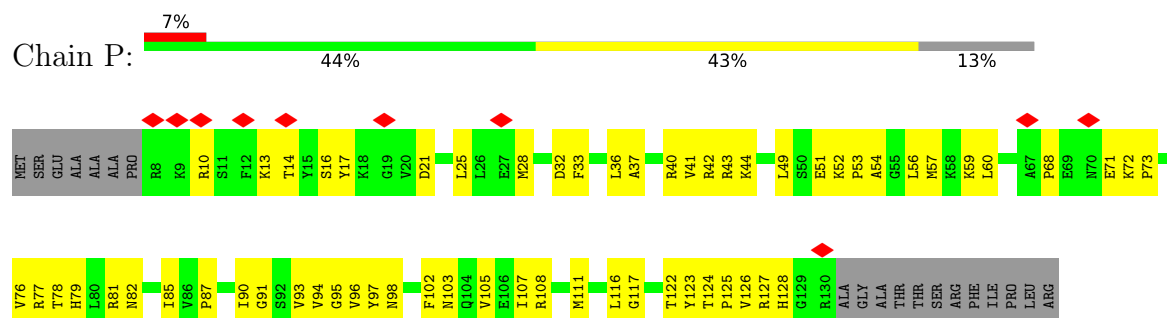
Chain N: 42% 58%



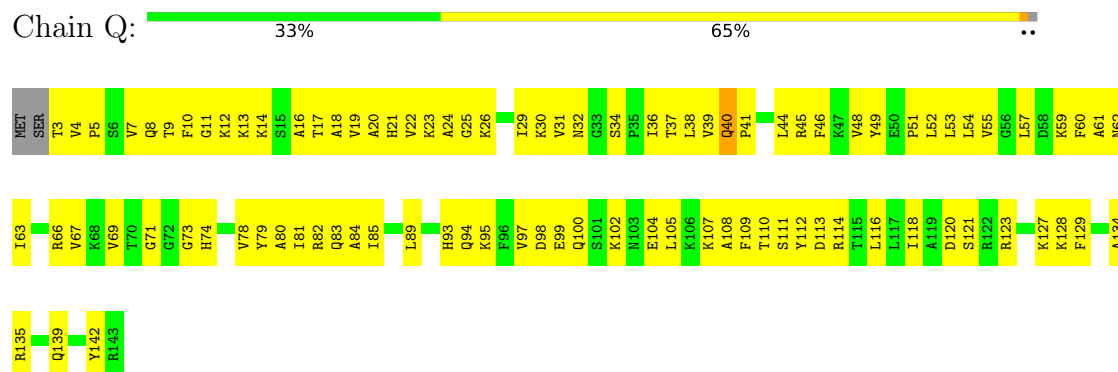
- Molecule 16: 40S ribosomal protein S14



- Molecule 17: KLLA0F07843p



- Molecule 18: 40S ribosomal protein S16

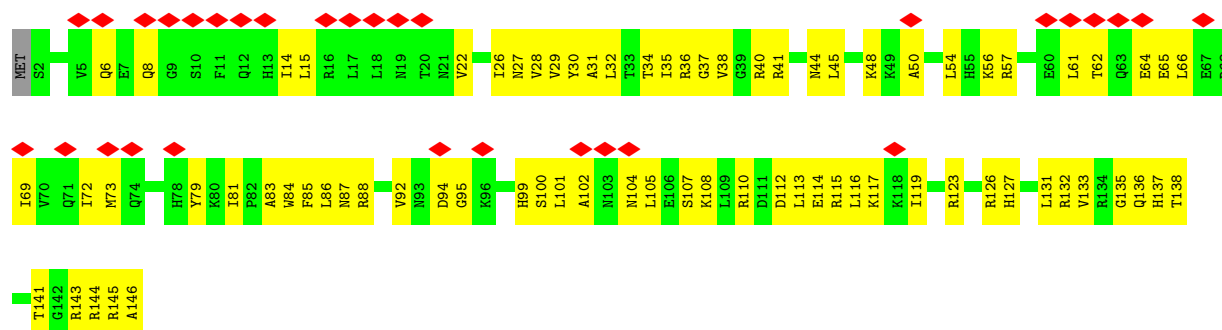


- Molecule 19: KLLA0B01474p



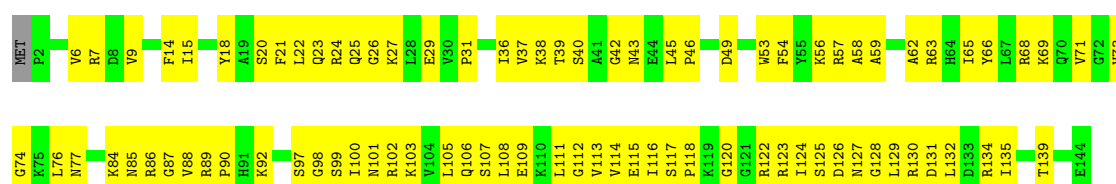
- Molecule 20: KLLA0B01562p





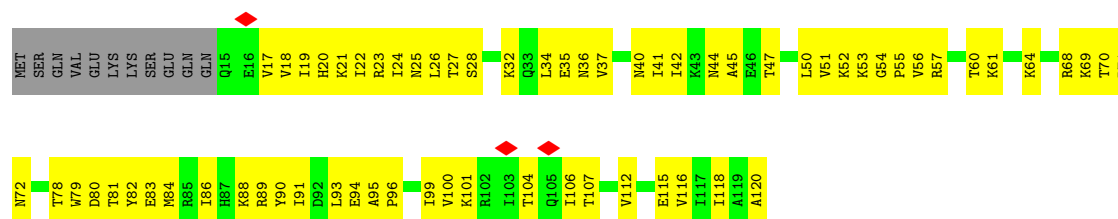
• Molecule 21: KLLA0A07194p

Chain T: 40% 60%



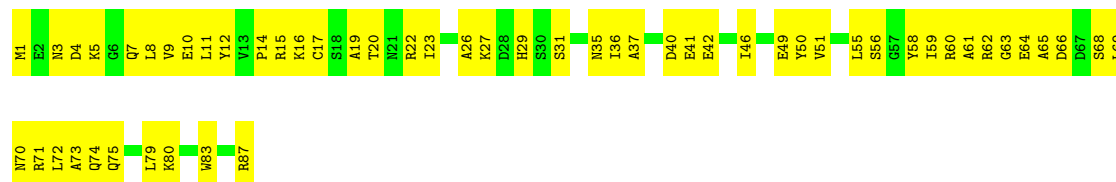
• Molecule 22: KLLA0F25542p

Chain U: 34% 56% 9%



• Molecule 23: 40S ribosomal protein S21

Chain V: 37% 63%



• Molecule 24: KLLA0B07931p

Chain W: 35% 65%





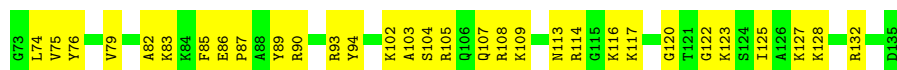
• Molecule 25: KLLA0B11231p

Chain X: 44% 54%



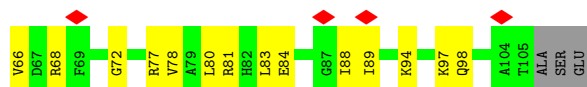
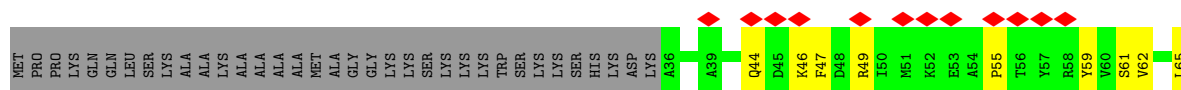
• Molecule 26: 40S ribosomal protein S24

Chain Y: 44% 53%



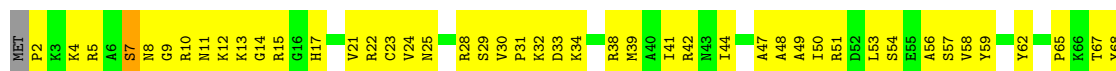
• Molecule 27: 40S ribosomal protein S25

Chain Z: 15% 44% 21% 35%



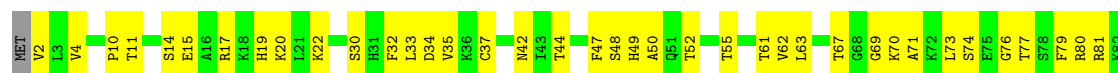
• Molecule 28: 40S ribosomal protein S26

Chain a: 30% 51% 18%



• Molecule 29: 40S ribosomal protein S27

Chain b: 52% 46%



- Molecule 30: 40S ribosomal protein S28



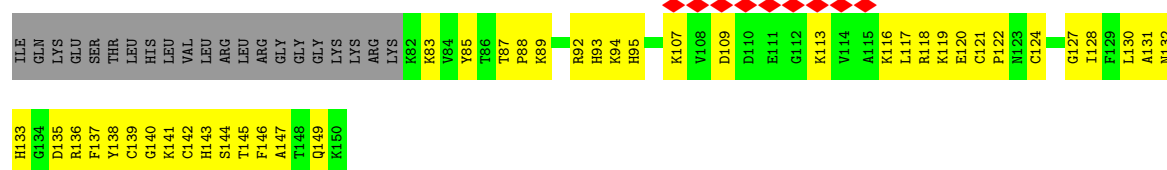
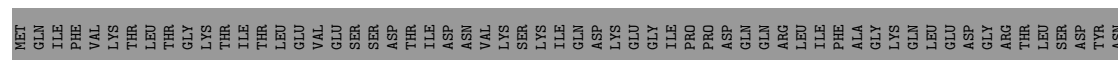
- Molecule 31: 40S ribosomal protein S29



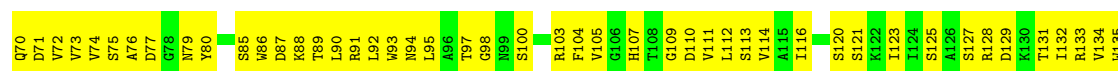
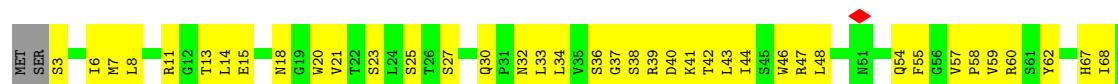
- Molecule 32: 40S ribosomal protein S30

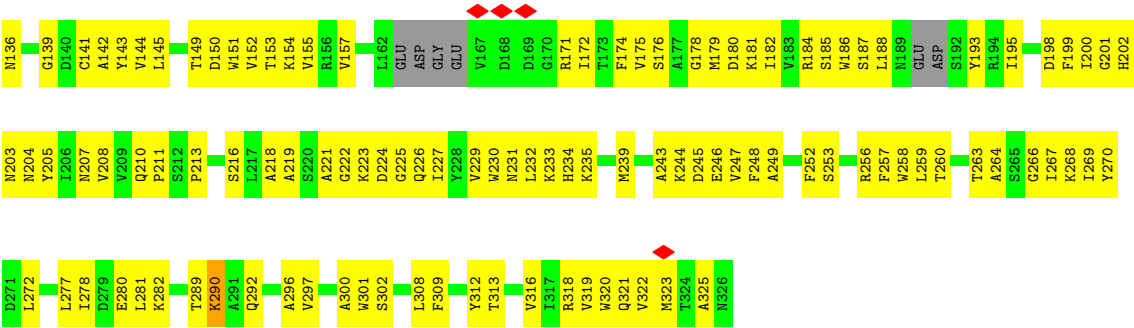


- Molecule 33: Ubiquitin-40S ribosomal protein S27a

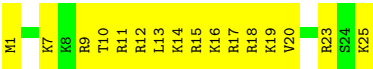
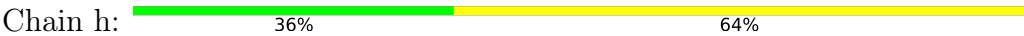


- Molecule 34: KLLA0E12277p





• Molecule 35: 60S ribosomal protein L41-A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	108616	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	42000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.075	Depositor
Minimum map value	-0.023	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.006	Depositor
Map size (Å)	421.19998, 421.19998, 421.19998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.17, 1.17, 1.17	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: MG, 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	2	0.34	0/42269	0.48	2/65862 (0.0%)
2	A	0.36	0/1666	0.61	0/2279
3	B	0.33	0/1798	0.62	0/2421
4	C	0.36	0/1659	0.61	0/2252
5	D	0.25	0/1769	0.56	0/2378
6	E	0.34	0/2122	0.62	2/2861 (0.1%)
7	F	0.24	0/1628	0.60	0/2198
8	G	0.27	0/1835	0.54	0/2451
9	H	0.30	0/1507	0.59	0/2028
10	I	0.32	0/1515	0.58	0/2029
11	J	0.32	0/1495	0.65	0/2001
12	K	0.28	0/831	0.56	0/1123
13	L	0.34	0/1276	0.59	0/1718
14	M	0.21	0/929	0.60	0/1255
15	N	0.31	0/1210	0.57	0/1628
16	O	0.31	0/953	0.65	0/1279
17	P	0.25	0/1000	0.63	0/1343
18	Q	0.23	0/1125	0.51	0/1510
19	R	0.31	0/1002	0.68	0/1346
20	S	0.20	0/1212	0.59	0/1629
21	T	0.26	0/1129	0.55	0/1520
22	U	0.26	0/857	0.57	0/1158
23	V	0.33	0/696	0.57	0/938
24	W	0.42	0/1039	0.69	0/1399
25	X	0.33	0/1137	0.62	0/1516
26	Y	0.30	0/1075	0.57	0/1433
27	Z	0.21	0/567	0.62	0/762
28	a	0.39	1/791 (0.1%)	0.60	0/1059
29	b	0.31	0/619	0.60	0/837
30	c	0.24	0/496	0.61	0/666
31	d	0.29	0/457	0.57	0/607
32	e	0.31	0/435	0.64	0/579

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.23	0/562	0.62	0/751
34	g	0.23	0/2521	0.52	0/3431
35	h	0.25	0/234	0.67	0/300
All	All	0.32	1/81416 (0.0%)	0.54	4/118547 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	A	0	1
3	B	0	1
5	D	0	1
7	F	0	2
8	G	0	1
9	H	0	1
11	J	0	2
13	L	0	1
14	M	0	1
18	Q	0	1
19	R	0	3
25	X	0	2
26	Y	0	1
34	g	0	1
All	All	0	19

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	a	7	SER	CA-C	-5.67	1.42	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1624	U	C1'-C2'-O2'	-7.31	97.44	108.40
1	2	1623	C	C2'-C3'-O3'	-6.13	100.30	109.50
6	E	21	ASP	CA-C-N	-5.10	112.20	122.55
6	E	21	ASP	C-N-CA	-5.10	112.20	122.55

There are no chirality outliers.

5 of 19 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	26	ALA	Peptide
3	B	213	ARG	Peptide
5	D	219	GLU	Peptide
7	F	101	MET	Peptide
7	F	60	LEU	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	37797	0	19014	3015	0
2	A	1626	0	1633	126	0
3	B	1774	0	1834	153	0
4	C	1629	0	1710	109	0
5	D	1744	0	1826	111	0
6	E	2078	0	2157	170	0
7	F	1609	0	1679	134	0
8	G	1812	0	1911	182	0
9	H	1483	0	1579	128	0
10	I	1489	0	1504	141	0
11	J	1471	0	1554	119	0
12	K	809	0	810	56	0
13	L	1248	0	1311	87	0
14	M	922	0	953	54	0
15	N	1187	0	1251	74	0
16	O	942	0	979	98	0
17	P	980	0	1026	74	0
18	Q	1105	0	1170	108	0
19	R	991	0	1039	87	0
20	S	1193	0	1217	72	0
21	T	1110	0	1124	103	0
22	U	845	0	913	83	0
23	V	687	0	682	65	0
24	W	1021	0	1056	93	0
25	X	1119	0	1198	93	0
26	Y	1061	0	1111	85	0
27	Z	558	0	585	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	a	779	0	828	101	0
29	b	609	0	630	37	0
30	c	494	0	534	48	0
31	d	446	0	436	55	0
32	e	428	0	468	25	0
33	f	549	0	563	47	0
34	g	2466	0	2406	192	0
35	h	233	0	284	23	0
36	2	2	0	0	0	0
37	a	1	0	0	0	0
37	b	1	0	0	0	0
37	f	1	0	0	0	0
All	All	76299	0	58975	5379	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 40.

The worst 5 of 5379 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)
1:2:363:G:N2	1:2:757:A:C2	1.68	1.59
1:2:1178:G:N2	1:2:1458:A:C2	1.77	1.44
1:2:1178:G:N2	1:2:1458:A:H2	1.11	1.38
1:2:96:G:H1	1:2:386:A:N6	1.35	1.21
1:2:1469:A:N6	1:2:1536:U:C2	2.14	1.14

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	A	206/254 (81%)	164 (80%)	42 (20%)	0	100	100
3	B	219/255 (86%)	183 (84%)	36 (16%)	0	100	100
4	C	215/259 (83%)	181 (84%)	33 (15%)	1 (0%)	24	63
5	D	221/237 (93%)	188 (85%)	33 (15%)	0	100	100
6	E	258/261 (99%)	195 (76%)	62 (24%)	1 (0%)	30	67
7	F	204/227 (90%)	164 (80%)	39 (19%)	1 (0%)	24	63
8	G	224/236 (95%)	186 (83%)	37 (16%)	1 (0%)	30	67
9	H	182/190 (96%)	144 (79%)	36 (20%)	2 (1%)	11	45
10	I	184/201 (92%)	147 (80%)	36 (20%)	1 (0%)	24	63
11	J	180/188 (96%)	135 (75%)	43 (24%)	2 (1%)	11	45
12	K	94/106 (89%)	78 (83%)	16 (17%)	0	100	100
13	L	153/156 (98%)	117 (76%)	36 (24%)	0	100	100
14	M	120/134 (90%)	97 (81%)	23 (19%)	0	100	100
15	N	148/151 (98%)	126 (85%)	22 (15%)	0	100	100
16	O	125/137 (91%)	95 (76%)	30 (24%)	0	100	100
17	P	121/142 (85%)	102 (84%)	19 (16%)	0	100	100
18	Q	139/143 (97%)	120 (86%)	19 (14%)	0	100	100
19	R	123/136 (90%)	91 (74%)	29 (24%)	3 (2%)	4	27
20	S	143/146 (98%)	116 (81%)	27 (19%)	0	100	100
21	T	141/144 (98%)	124 (88%)	17 (12%)	0	100	100
22	U	104/117 (89%)	90 (86%)	14 (14%)	0	100	100
23	V	85/87 (98%)	65 (76%)	20 (24%)	0	100	100
24	W	127/130 (98%)	101 (80%)	26 (20%)	0	100	100
25	X	142/145 (98%)	97 (68%)	43 (30%)	2 (1%)	9	39
26	Y	132/135 (98%)	109 (83%)	22 (17%)	1 (1%)	16	53
27	Z	68/108 (63%)	53 (78%)	15 (22%)	0	100	100
28	a	96/119 (81%)	67 (70%)	29 (30%)	0	100	100
29	b	79/82 (96%)	57 (72%)	22 (28%)	0	100	100
30	c	61/67 (91%)	50 (82%)	11 (18%)	0	100	100
31	d	51/56 (91%)	39 (76%)	12 (24%)	0	100	100
32	e	51/63 (81%)	41 (80%)	10 (20%)	0	100	100
33	f	67/150 (45%)	46 (69%)	21 (31%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	g	312/326 (96%)	267 (86%)	45 (14%)	0	100	100
35	h	23/25 (92%)	23 (100%)	0	0	100	100
All	All	4798/5313 (90%)	3858 (80%)	925 (19%)	15 (0%)	37	71

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
19	R	98	ASP
4	C	45	LYS
19	R	72	LYS
25	X	4	GLY
26	Y	35	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	174/211 (82%)	174 (100%)	0	100	100
3	B	198/228 (87%)	198 (100%)	0	100	100
4	C	176/203 (87%)	176 (100%)	0	100	100
5	D	185/196 (94%)	185 (100%)	0	100	100
6	E	223/224 (100%)	223 (100%)	0	100	100
7	F	174/194 (90%)	174 (100%)	0	100	100
8	G	192/200 (96%)	192 (100%)	0	100	100
9	H	164/170 (96%)	164 (100%)	0	100	100
10	I	147/159 (92%)	147 (100%)	0	100	100
11	J	153/158 (97%)	153 (100%)	0	100	100
12	K	88/96 (92%)	88 (100%)	0	100	100
13	L	136/137 (99%)	136 (100%)	0	100	100
14	M	97/109 (89%)	96 (99%)	1 (1%)	68	76
15	N	127/128 (99%)	127 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	O	96/104 (92%)	96 (100%)	0	100	100
17	P	105/119 (88%)	105 (100%)	0	100	100
18	Q	117/119 (98%)	117 (100%)	0	100	100
19	R	112/124 (90%)	112 (100%)	0	100	100
20	S	128/129 (99%)	128 (100%)	0	100	100
21	T	117/118 (99%)	117 (100%)	0	100	100
22	U	96/107 (90%)	96 (100%)	0	100	100
23	V	73/73 (100%)	73 (100%)	0	100	100
24	W	110/111 (99%)	110 (100%)	0	100	100
25	X	119/120 (99%)	119 (100%)	0	100	100
26	Y	108/109 (99%)	108 (100%)	0	100	100
27	Z	60/88 (68%)	60 (100%)	0	100	100
28	a	83/100 (83%)	83 (100%)	0	100	100
29	b	71/72 (99%)	71 (100%)	0	100	100
30	c	55/59 (93%)	55 (100%)	0	100	100
31	d	46/48 (96%)	46 (100%)	0	100	100
32	e	47/55 (86%)	47 (100%)	0	100	100
33	f	58/133 (44%)	58 (100%)	0	100	100
34	g	265/272 (97%)	264 (100%)	1 (0%)	84	82
35	h	23/23 (100%)	23 (100%)	0	100	100
All	All	4123/4496 (92%)	4121 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	M	116	ASN
34	g	54	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
21	T	77	ASN
27	Z	95	HIS
21	T	85	ASN

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Mol	Chain	Res	Type
24	W	42	GLN
34	g	189	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1778/1799 (98%)	979 (55%)	57 (3%)

5 of 979 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	3	U
1	2	4	C
1	2	5	U
1	2	7	G

5 of 57 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	898	G
1	2	1788	A
1	2	1067	C
1	2	1765	G
1	2	1566	C

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 5 ligands modelled in this entry, 5 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

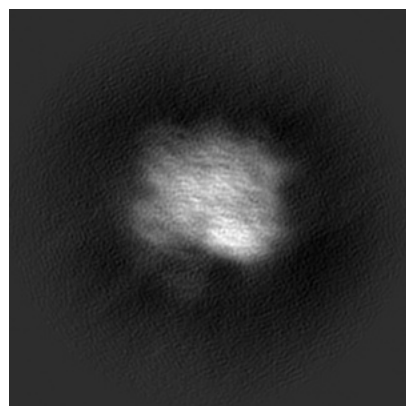
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35216. These allow visual inspection of the internal detail of the map and identification of artifacts.

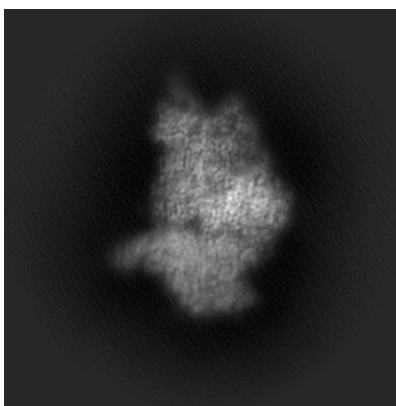
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

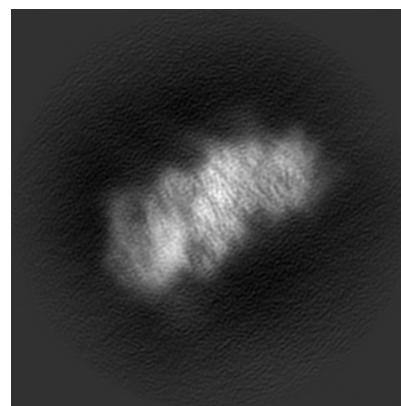
6.1.1 Primary map



X

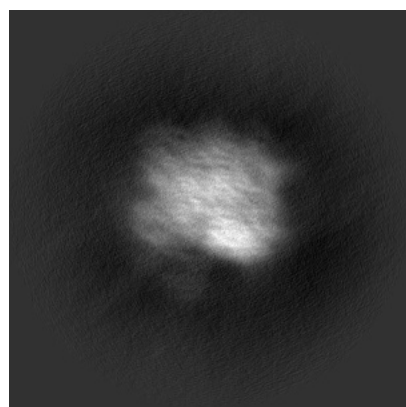


Y

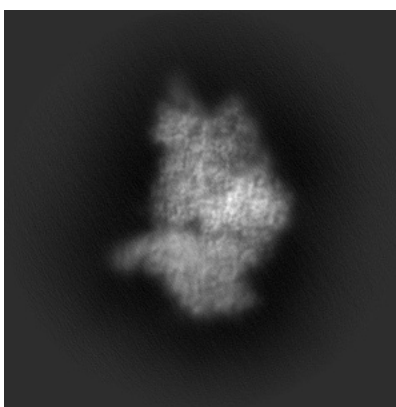


Z

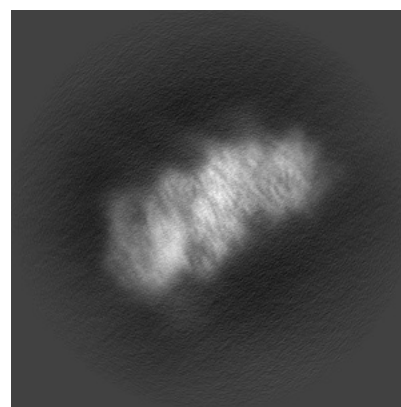
6.1.2 Raw map



X



Y

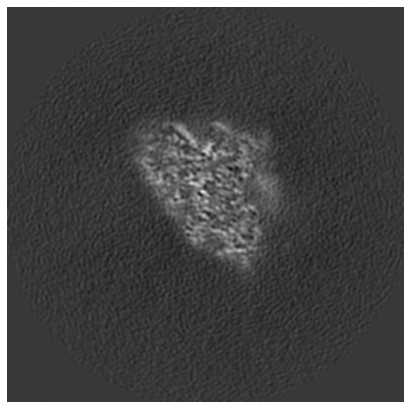


Z

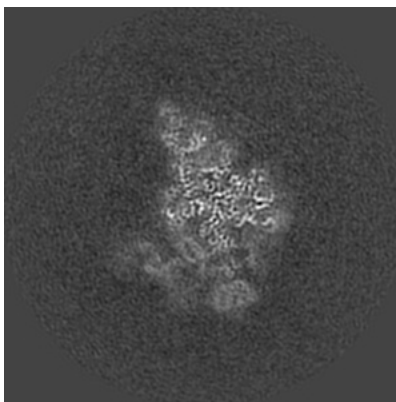
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

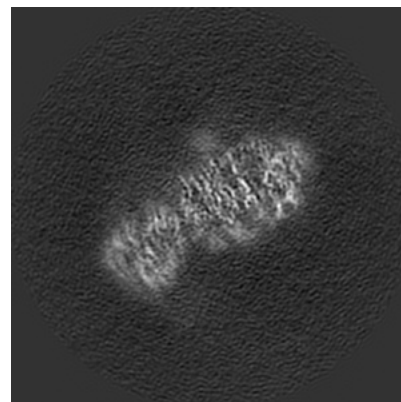
6.2.1 Primary map



X Index: 180

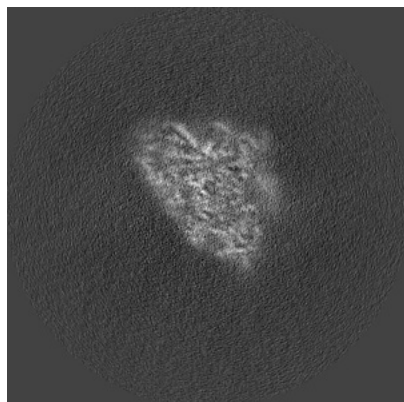


Y Index: 180

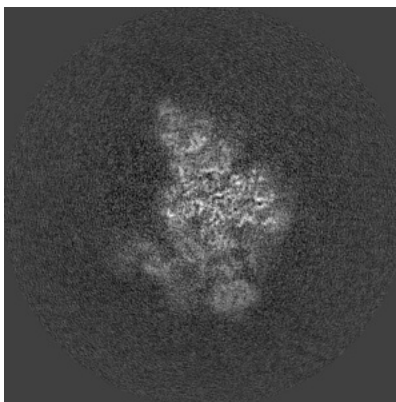


Z Index: 180

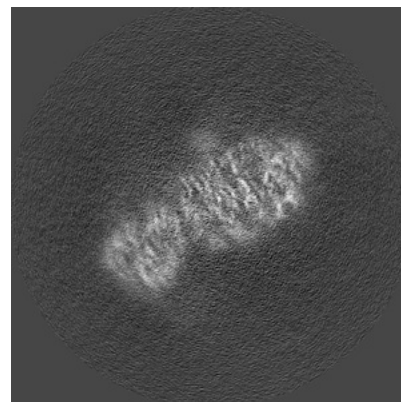
6.2.2 Raw map



X Index: 180



Y Index: 180

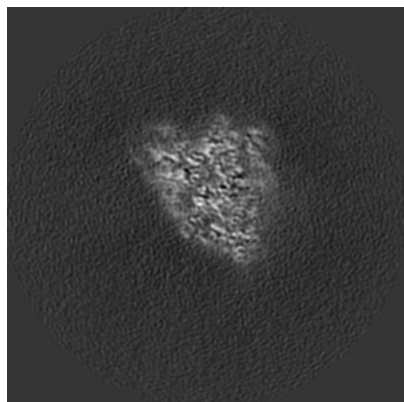


Z Index: 180

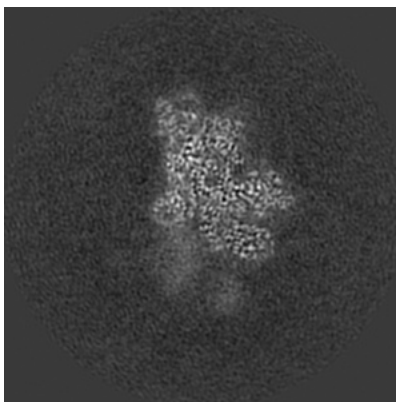
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

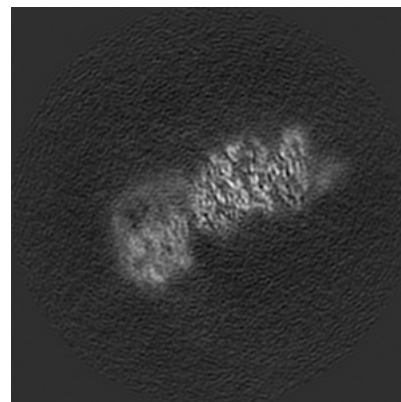
6.3.1 Primary map



X Index: 187

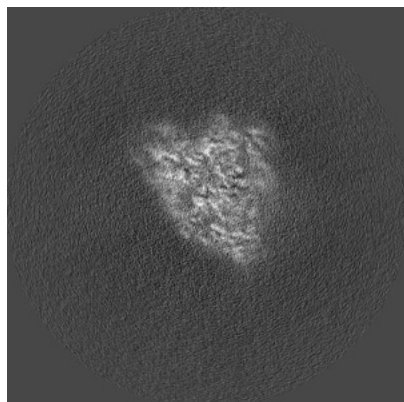


Y Index: 195

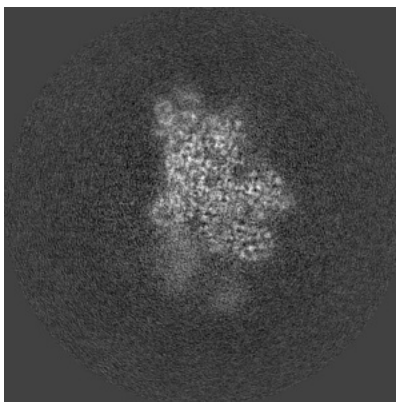


Z Index: 160

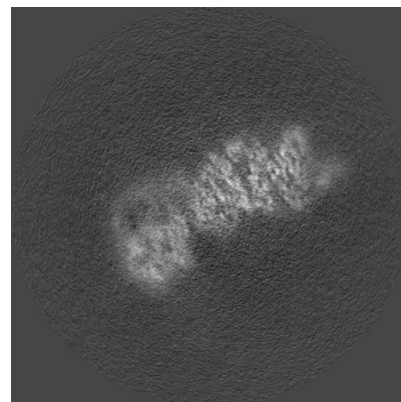
6.3.2 Raw map



X Index: 187



Y Index: 196

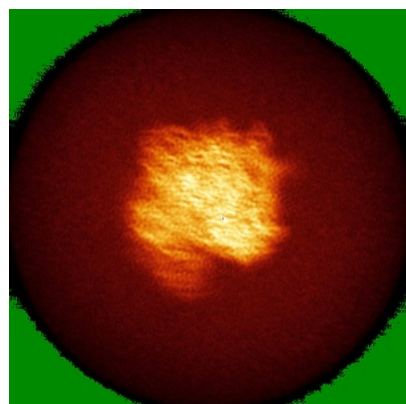


Z Index: 159

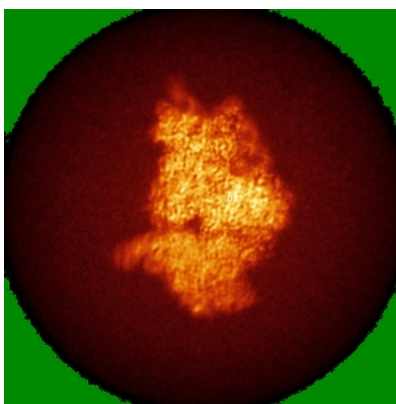
The images above show the largest variance slices of the map in three orthogonal directions.

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

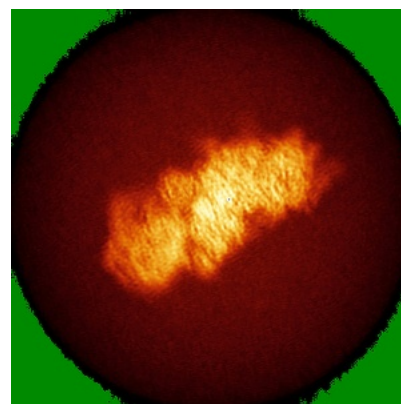
6.4.1 Primary map



X

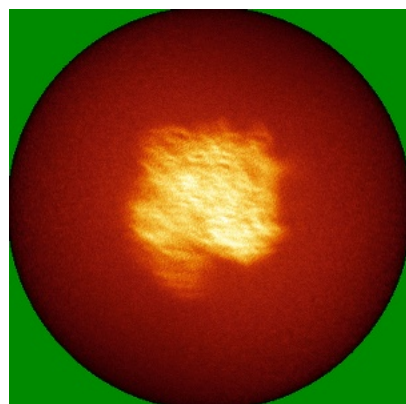


Y

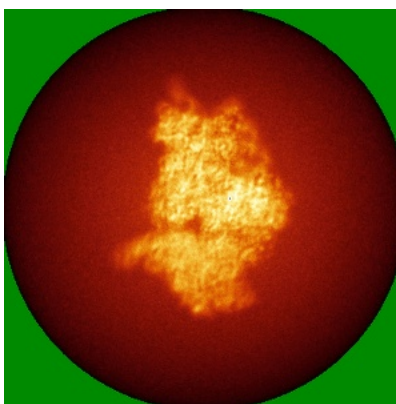


Z

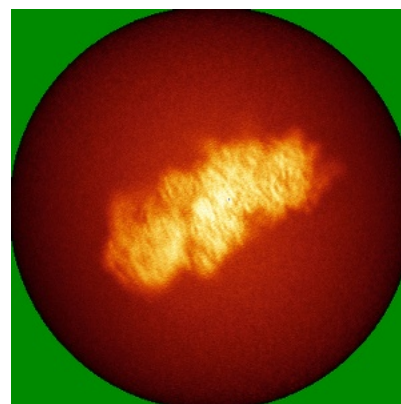
6.4.2 Raw map



X



Y

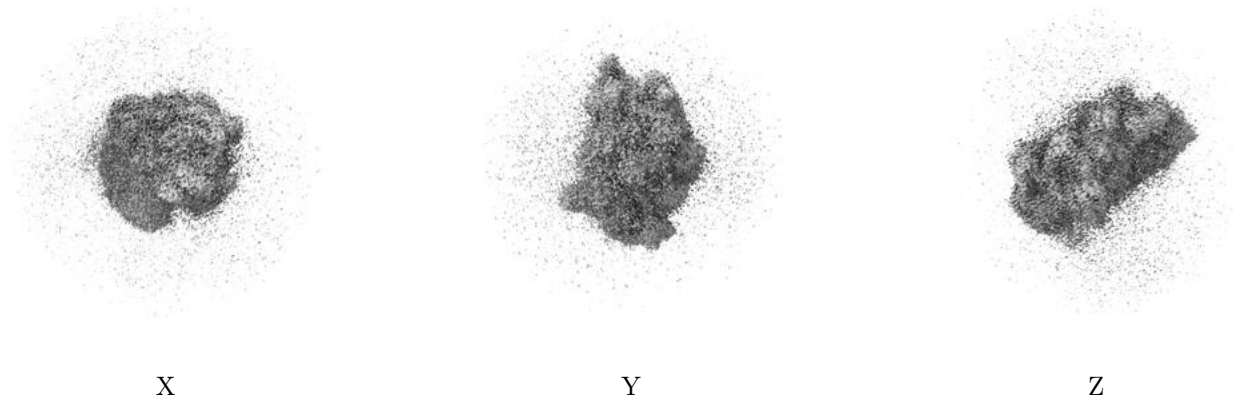


Z

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.

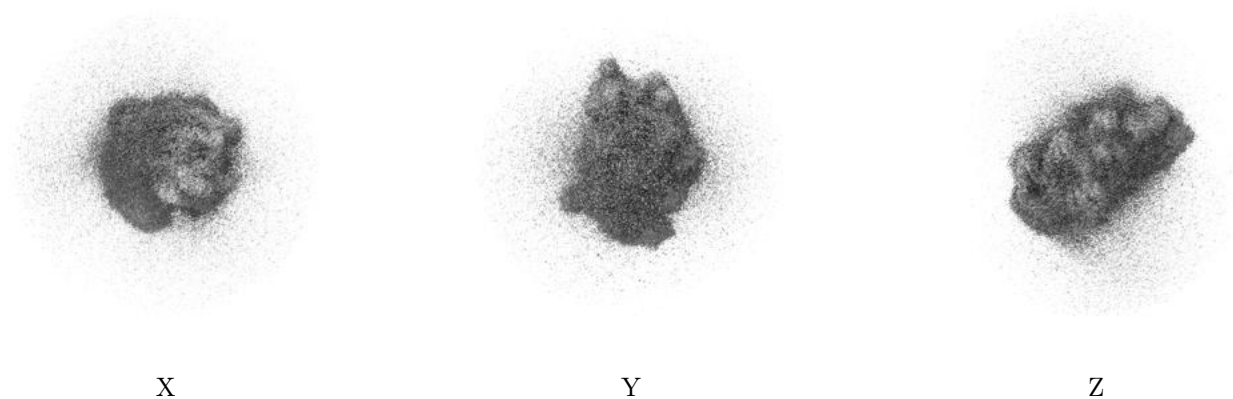
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.006. 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.

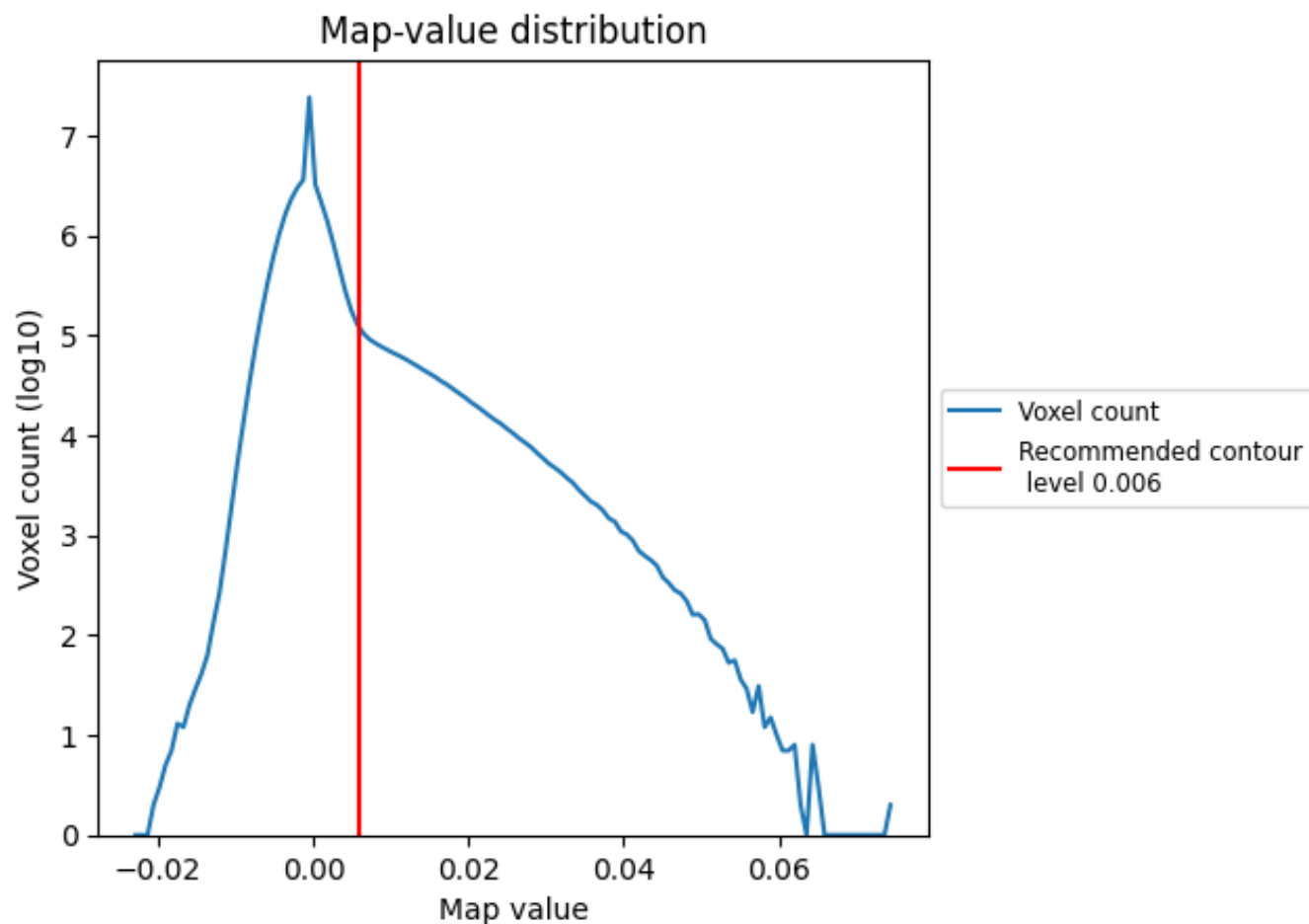
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

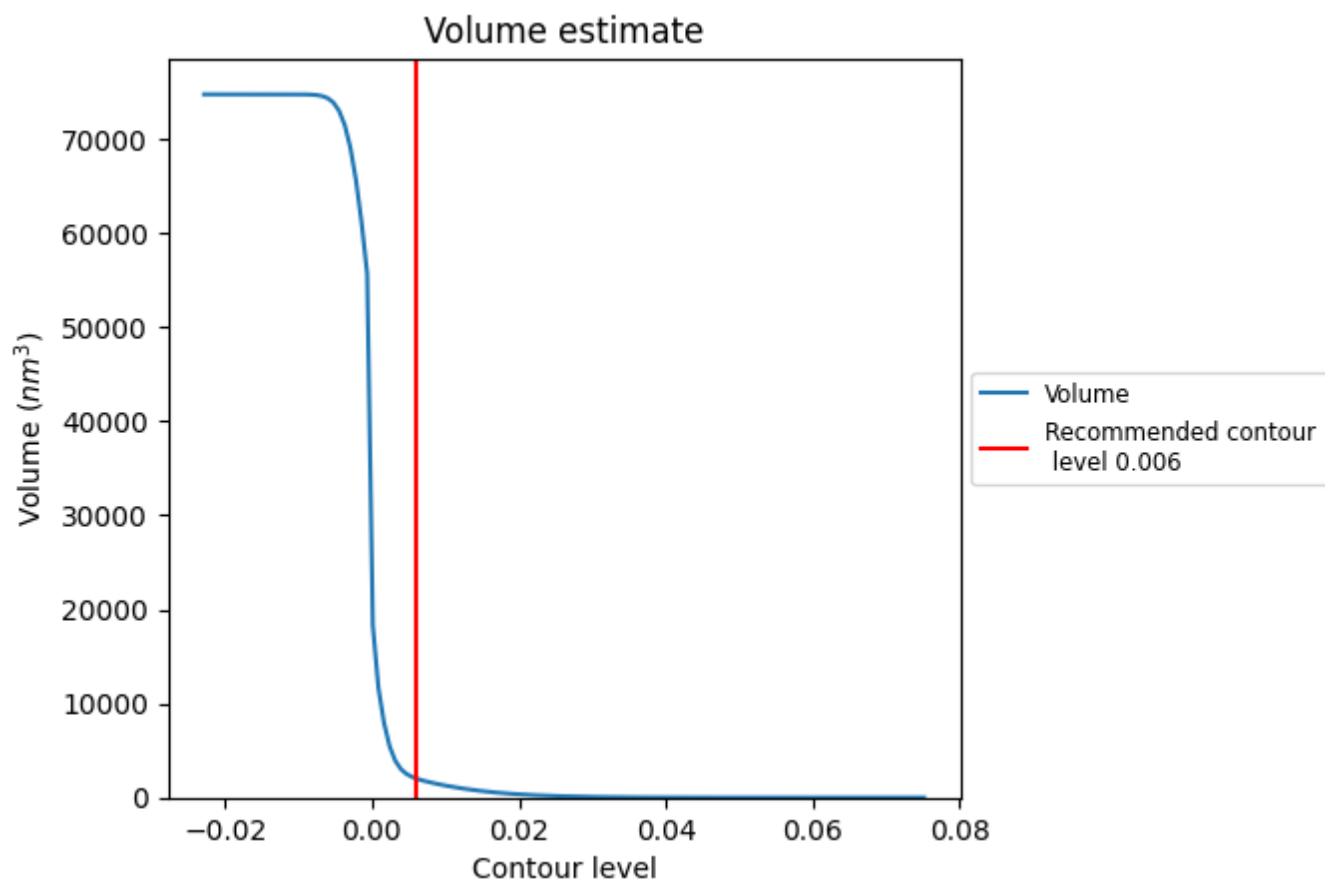
This section contains the results of statistical analysis of the map.

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.

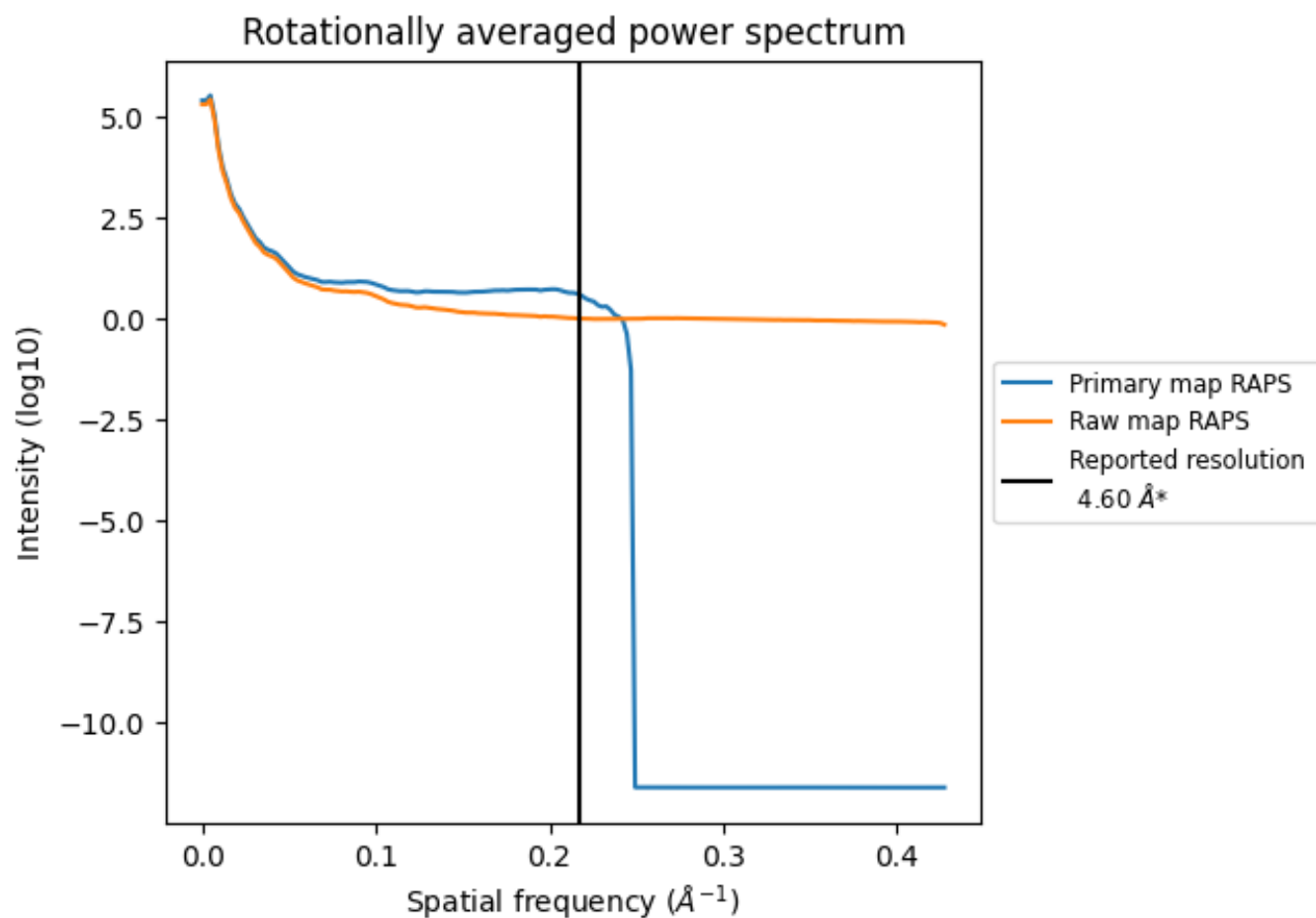
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2040 nm^3 ; this corresponds to an approximate mass of 1843 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 ⓘ

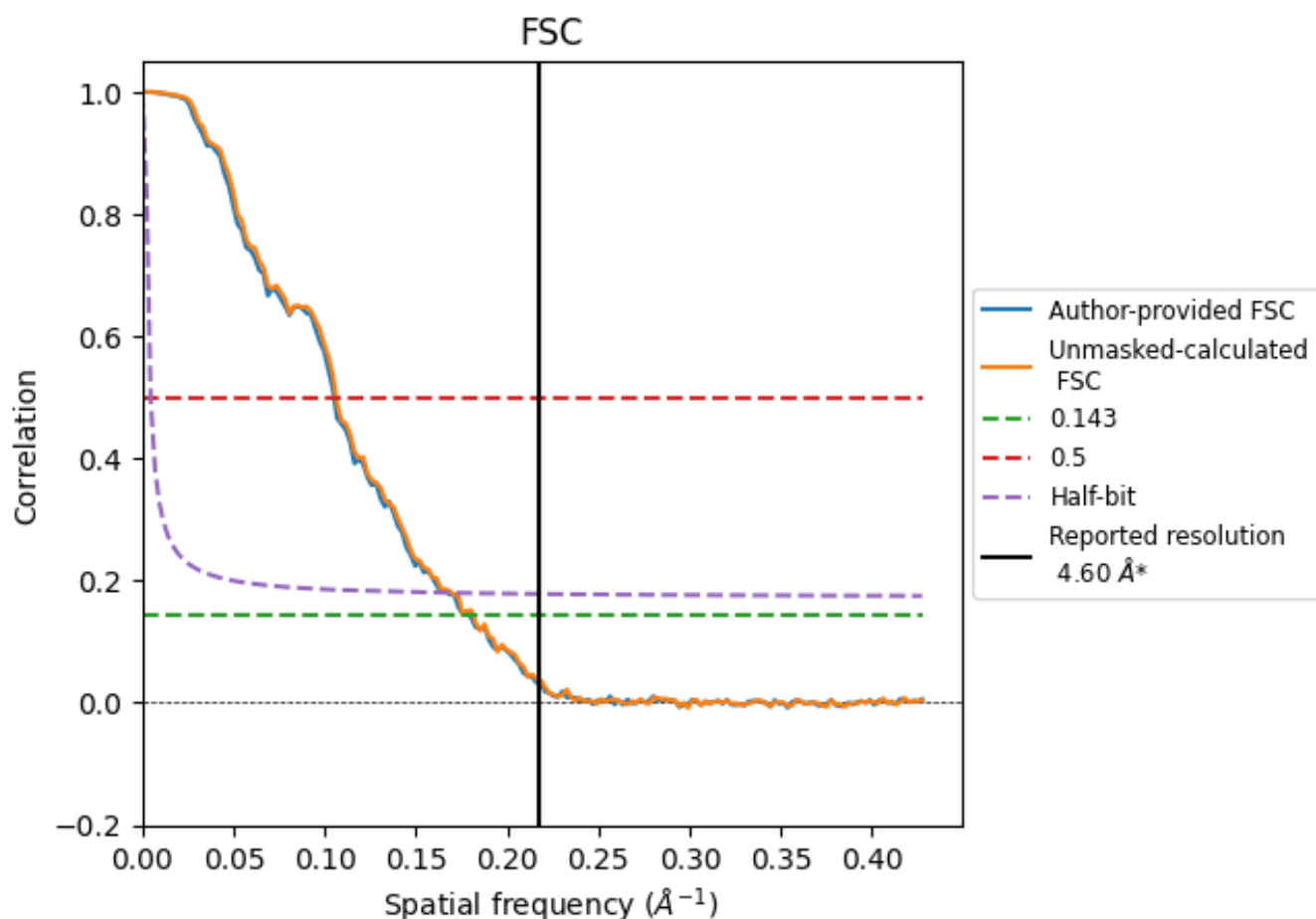


*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

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 0.217 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	5.57	9.51	5.97
Unmasked-calculated*	5.51	9.41	5.89

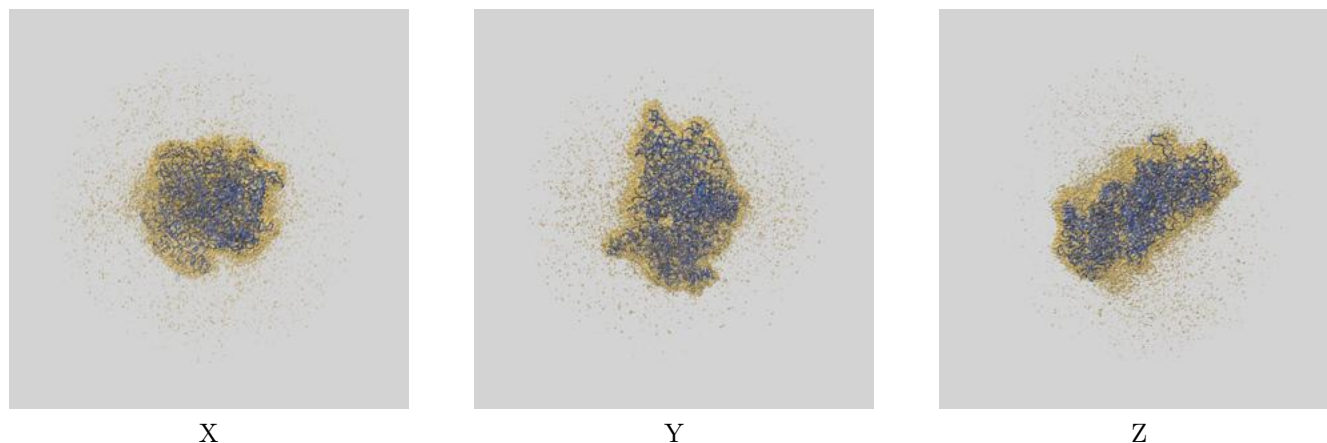
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 5.57 differs from the reported value 4.6 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.51 differs from the reported value 4.6 by more than 10 %

9 Map-model fit [i](#)

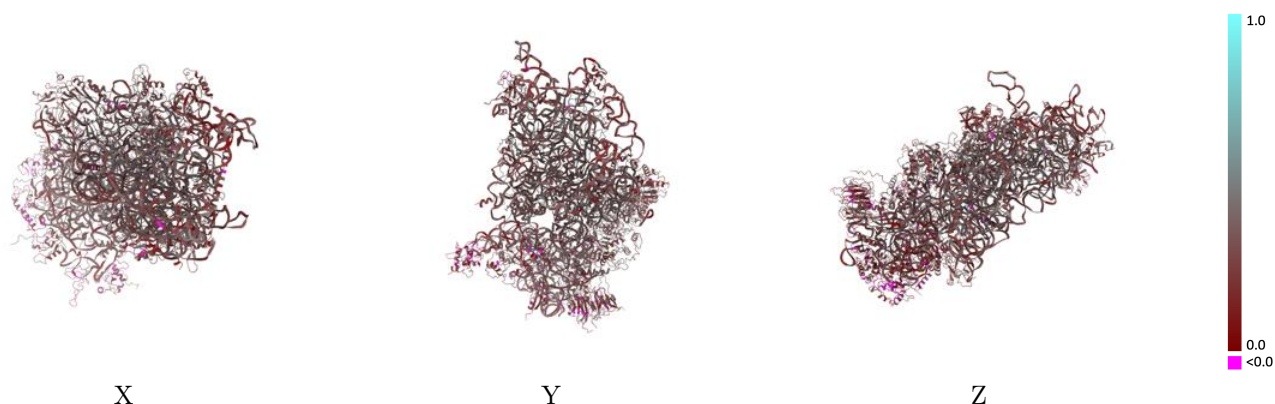
This section contains information regarding the fit between EMDB map EMD-35216 and PDB model 8I7J. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



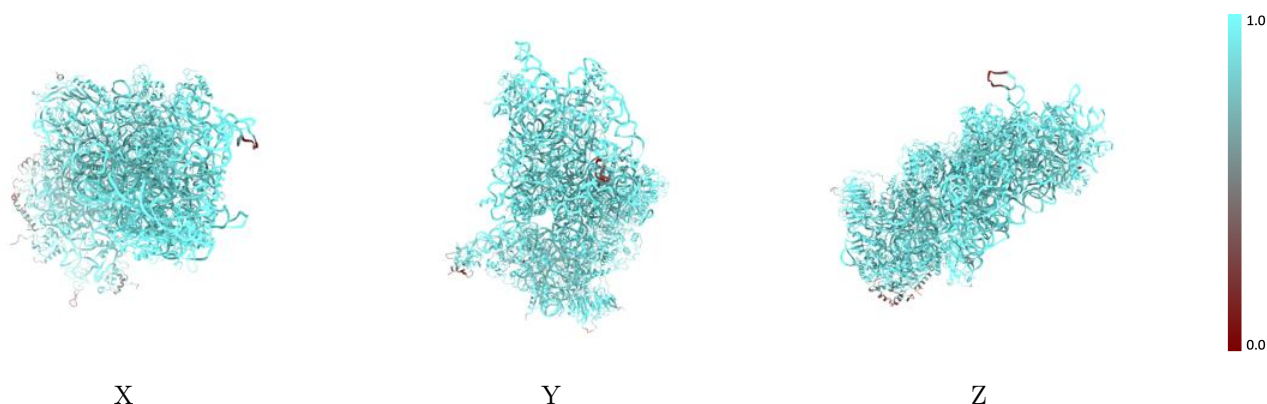
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



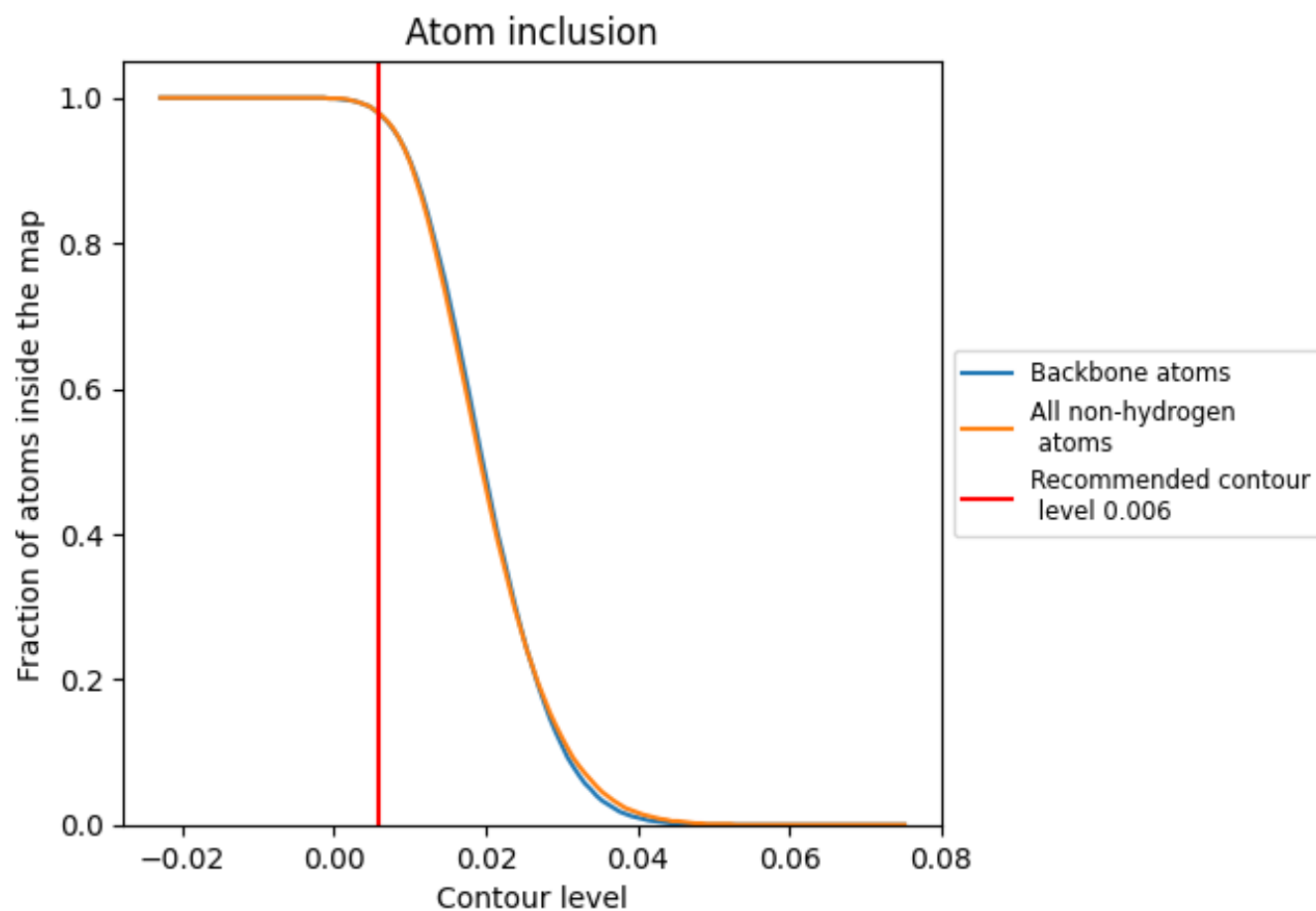
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.006).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9780	 0.3160
2	 0.9950	 0.3290
A	 0.9870	 0.3510
B	 0.9700	 0.3220
C	 0.9930	 0.3530
D	 0.9460	 0.2720
E	 0.9970	 0.3640
F	 0.9770	 0.2430
G	 0.9940	 0.3160
H	 0.9830	 0.3310
I	 0.9920	 0.3490
J	 0.9950	 0.3530
K	 0.9790	 0.2530
L	 0.9840	 0.3780
M	 0.8200	 0.1930
N	 0.9890	 0.3600
O	 0.9910	 0.3180
P	 0.8770	 0.2160
Q	 1.0000	 0.2870
R	 0.9790	 0.3240
S	 0.7490	 0.1600
T	 0.9970	 0.2510
U	 0.9140	 0.2590
V	 0.9930	 0.3530
W	 0.9910	 0.3810
X	 0.9910	 0.3920
Y	 0.9990	 0.3400
Z	 0.6630	 0.1020
a	 0.9960	 0.3620
b	 0.9970	 0.3760
c	 0.9680	 0.2080
d	 1.0000	 0.2730
e	 1.0000	 0.3180
f	 0.8200	 0.1190
g	 0.9640	 0.2700
h	 0.9430	 0.1670

