



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 02:48 AM UTC

PDB ID : 8P09 / pdb_00008p09
EMDB ID : EMD-17330
Title : 48S late-stage initiation complex with non methylated mRNA
Authors : Guca, E.; Lima, L.H.F.; Boissier, F.; Hashem, Y.
Deposited on : 2023-05-09
Resolution : 3.30 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:

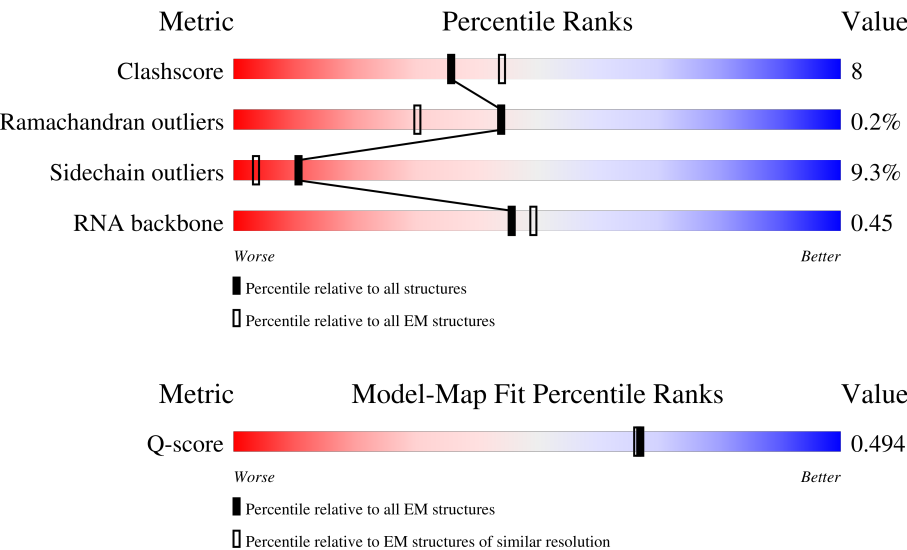
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 3.30 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	15087 (2.80 - 3.80)

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	1	75	
2	2	1863	
3	3	9	

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Mol	Chain	Length	Quality of chain
4	A	284	
5	C	207	
6	D	215	
7	E	270	
8	F	227	
9	G	263	
10	H	191	
11	I	237	
12	J	190	
13	K	206	
14	L	194	
15	M	98	
16	N	158	
17	O	132	
18	P	150	
19	Q	151	
20	R	145	
21	S	141	
22	T	135	
23	U	152	
24	V	141	
25	W	119	
26	X	83	
27	Y	130	
28	Z	143	

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Mol	Chain	Length	Quality of chain
29	a	133	 5% 79% 13% 5%
30	b	115	 63% 19% 14%
31	c	84	 6% 86% 13%
32	d	69	 62% 28% 7%
33	e	56	 82% 12% 5%
34	f	71	 18% 79% 17%
35	g	313	 70% 26%
36	i	133	 7% 41% 56%
37	j	111	 25% 81% 15%
38	k	595	 87% 73% 23%
39	l	25	 12% 72% 28%
40	n	124	 6% 36% 24% 40%

2 Entry composition

There are 41 unique types of molecules in this entry. The entry contains 86284 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 initiator methionylated tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	75	Total	C	N	O	P	0	0
			1617	722	299	521	75		

- Molecule 2 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1741	Total	C	N	O	P	0	0
			37147	16585	6650	12172	1740		

- Molecule 3 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	9	Total	C	N	O	P	0	0
			192	86	36	61	9		

- Molecule 4 is a protein called Eukaryotic translation initiation factor 2 subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	266	Total	C	N	O	S	0	0
			2146	1354	376	405	11		

- Molecule 5 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	207	Total	C	N	O	S	0	0
			1637	1042	288	299	8		

- Molecule 6 is a protein called ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	215	Total	C	N	O	S	0	0
			1741	1107	309	310	15		

- Molecule 7 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	226	Total	C	N	O	S	0	0
			1754	1139	298	310	7		

- Molecule 8 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	227	Total	C	N	O	S	0	0
			1764	1124	317	315	8		

- Molecule 9 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	263	Total	C	N	O	S	0	0
			2083	1329	385	359	10		

- Molecule 10 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	187	Total	C	N	O	S	0	0
			1482	928	279	268	7		

- Molecule 11 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	237	Total	C	N	O	S	0	0
			1924	1199	387	331	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	130	THR	PRO	conflict	UNP A0A5K1UJS7

- Molecule 12 is a protein called ribosomal protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	190	Total	C	N	O	S	0	0
			1530	975	281	273	1		

- Molecule 13 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	K	206	Total	C	N	O	S	0	0
			1680	1054	329	292	5		

- Molecule 14 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	188	Total	C	N	O	S	0	0
			1542	979	309	251	3		

- Molecule 15 is a protein called 40S ribosomal protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	98	Total	C	N	O	S	0	0
			828	539	148	135	6		

- Molecule 16 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	158	Total	C	N	O	S	0	0
			1296	827	241	221	7		

- Molecule 17 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	124	Total	C	N	O	S	0	0
			958	600	170	179	9		

- Molecule 18 is a protein called ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 19 is a protein called 40S ribosomal protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 20 is a protein called 40S ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R	140	Total	C	N	O	S	0	0
			1154	733	219	195	7		

- Molecule 21 is a protein called 40S ribosomal protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 22 is a protein called 40S ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T	126	Total	C	N	O	S	0	0
			1019	639	188	187	5		

- Molecule 23 is a protein called 40S ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	145	Total	C	N	O	S	0	0
			1194	747	243	203	1		

- Molecule 24 is a protein called 40S ribosomal protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	141	Total	C	N	O	S	0	0
			1113	701	213	196	3		

- Molecule 25 is a protein called 40S ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	104	Total	C	N	O	S	0	0
			822	514	156	148	4		

- Molecule 26 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 27 is a protein called Ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 28 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	142	Total	C	N	O	S	0	0
			1106	698	220	184	4		

- Molecule 29 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	126	Total	C	N	O	S	0	0
			1021	645	198	173	5		

- Molecule 30 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	99	Total	C	N	O	S	0	0
			789	491	162	130	6		

- Molecule 31 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	84	Total	C	N	O	S	0	0
			659	413	122	116	8		

- Molecule 32 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 33 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	53	Total	C	N	O	S	0	0
			444	278	90	71	5		

- Molecule 34 is a protein called ribosomal protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	71	Total	C	N	O	S	0	0
			582	367	109	99	7		

- Molecule 35 is a protein called Ribosomal protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	313	Total	C	N	O	S	0	0
			2437	1535	424	466	12		

- Molecule 36 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	58	Total	C	N	O	S	0	0
			464	287	102	74	1		

- Molecule 37 is a protein called Eukaryotic translation initiation factor 4C.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	108	Total	C	N	O	S	0	0
			874	543	166	161	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
j	39	ILE	VAL	conflict	UNP G1SYS4
j	76	ILE	VAL	conflict	UNP G1SYS4

- Molecule 38 is a protein called ATP binding cassette subfamily E member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	595	Total	C	N	O	S	0	0
			4693	2995	802	865	31		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	538	ILE	VAL	conflict	UNP G1SG72

- Molecule 39 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	25	Total	C	N	O	S	0	0
			240	145	64	28	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	n	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

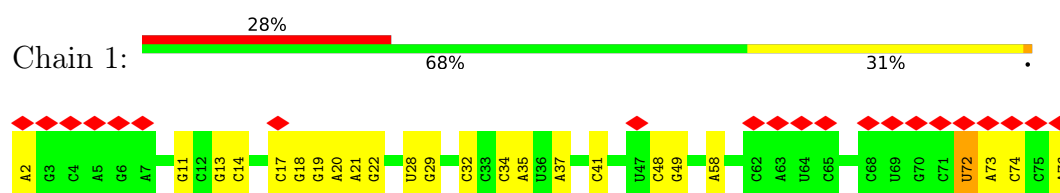
- Molecule 41 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
41	2	220	Total	Mg	0
			220	220	
41	3	3	Total	Mg	0
			3	3	
41	G	2	Total	Mg	0
			2	2	
41	I	2	Total	Mg	0
			2	2	
41	K	1	Total	Mg	0
			1	1	
41	L	1	Total	Mg	0
			1	1	
41	Z	1	Total	Mg	0
			1	1	

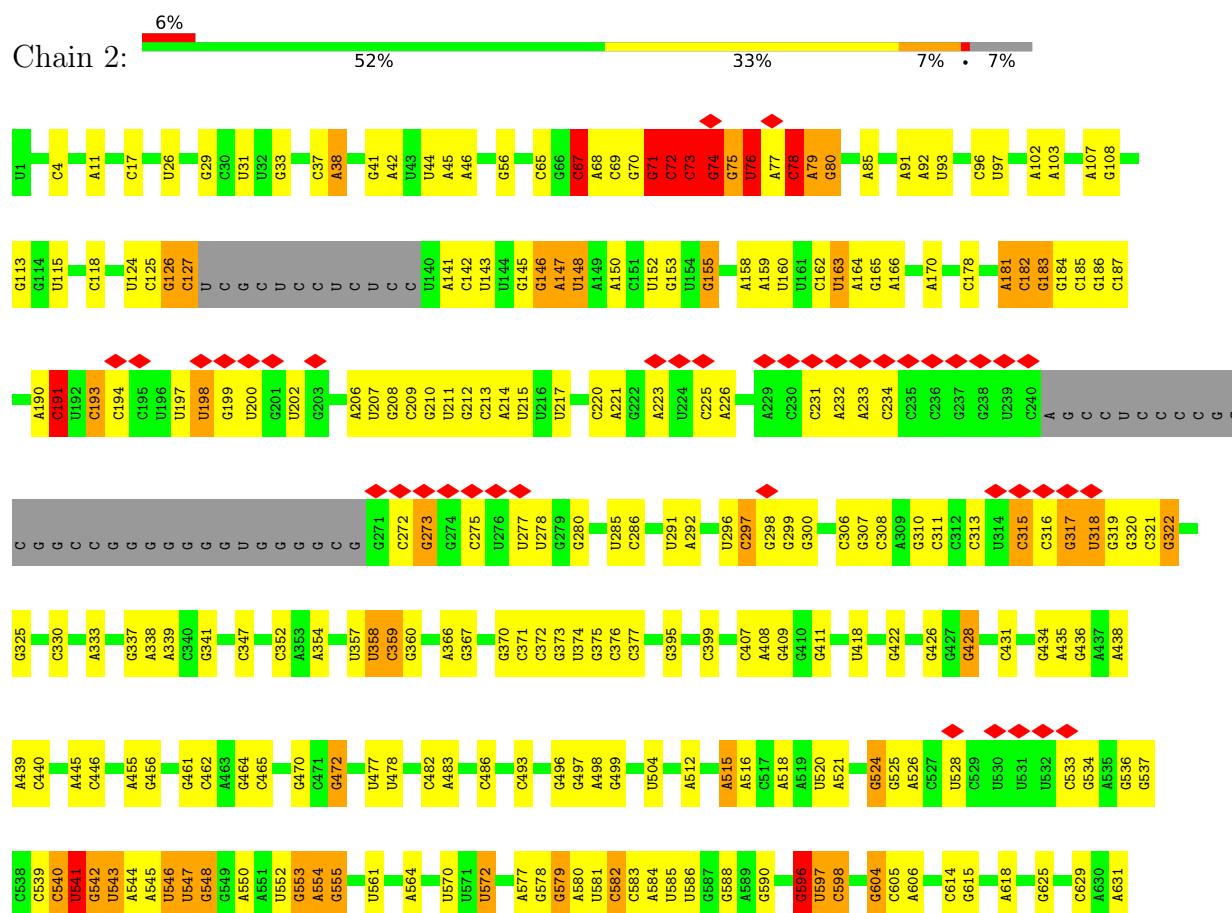
3 Residue-property plots [i](#)

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: initiator methionylated tRNA

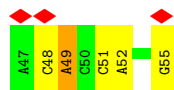
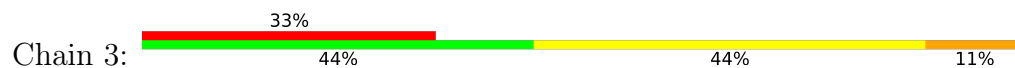


- Molecule 2: 18S ribosomal RNA

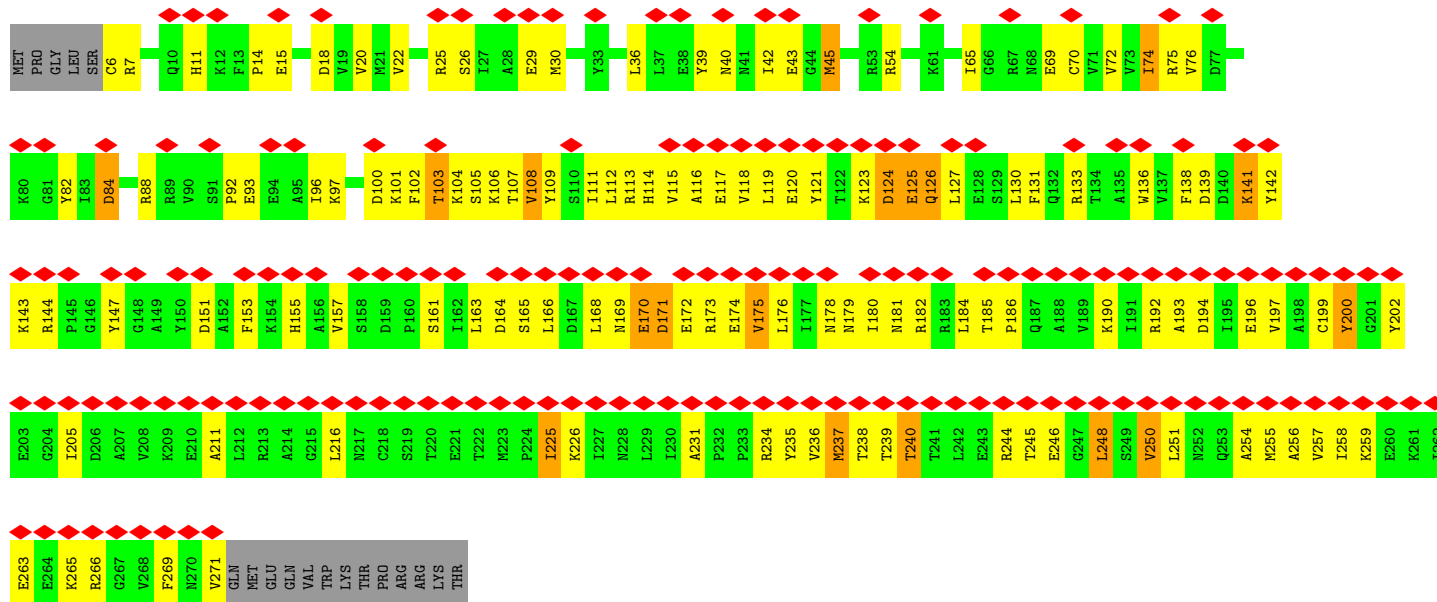


U1815	A1726	G1635	G1543	G1447	U1367	A1254	A1140	A1030	G929	A865	U829	U	C	U632
A1816	G1727	G1643	U1546	A1448	C1370	A1255	A1141	A1031	G932	A866	G	G	G	A633
A1818	G1731	G1643	U1546	C1449	G1370	A1256	A1145	A1032	C933	U867	U	U	A	G649
A1819	G1732	A1450	C1547	A1450	G1371	C1260	U1150	G1030	C934	A868	C	C	G	C650
G1820	C1733	A1451	C1548	A1451	A1372	A1261	U1151	G1039	U935	G870	C	C	C	U651
A1828	G1739	G1650	C1549	G1452	U1373	C1267	U1151	A1045	U936	A871	C	A	A	G652
A1829	A1740	C1651	U1550	U1453	A1374	C1267	G1154	A1045	C937	C872	C	C	C	C653
G1830	U1741	C1652	A1551	G1454	A1375	G1270	G1160	U1052	U938	C873	C	C	C	A654
G1831	C1742	G1653	C1552	G1455	A1376	G1271	G1161	A1054	U940	G874	G	G	G	G655
U1832	C1742	G1653	C1553	G1456	G1377	A1272	G1162	A1055	U941	C875	C	C	C	A656
C1835	G1747	C1655	C1557	U1457	C1380	A1273	G1166	A1056	G945	G876	C	C	C	A657
C1836	G1748	A1656	G1558	U1458	G1381	A1274	A1166	U1057	C946	C786	C	C	C	A661
C1837	C1749	C1660	C1559	C1460	A1382	C1275	G1167	A1058	U946	C787	U	U	G	A662
G1843	G1751	G1661	G1561	A1461	G1383	G1276	U1168	C1059	A951	C788	C	C	C	C663
A1844	G1752	C1662	G1562	C1464	A1392	A1277	U1169	C1060	G954	C789	C	C	C	C664
A1845	G1753	U1663	C1563	G1464	U1393	G1278	U1170	G1061	G954	A790	U	U	U	U665
C1846	C1754	G1666	A1564	A1472	U1394	C1279	U1170	G1061	G954	A882	C	C	C	U668
G1852	U1755	U1667	G1565	U1473	G1399	G1280	A1177	C1074	G957	U883	C	C	C	G673
A1853	C	U1668	G1566	A1476	U1400	G1281	A1178	C1075	C957	U883	C	C	C	G673
A1854	G	G1669	G1570	A1480	A1401	G1282	A1179	A1076	A958	C792	C	C	C	C732
G1855	U1671	U1670	G1571	G1480	G1402	G1286	G1183	U1077	A959	C793	C	C	C	C734
G1856	U1672	U1671	G1572	A1483	U1403	A1289	G1183	A1078	U961	C794	C	C	C	C735
A1857	C	C1684	A1574	C1484	A1404	G1298	A1191	A1079	U962	U887	C	C	C	C736
U1858	C	C1684	U1573	G1486	A1405	G1299	A1195	A1081	G966	U889	C	C	C	C737
C1859	C	C1684	C1575	G1486	G1407	U1300	A1195	C1090	G967	U890	C	C	C	C738
A1860	C	U1688	C1576	G1486	G1408	U1300	G1203	C1090	A968	A807	C	C	C	U739
U1861	G	U1689	U1581	G1491	C1409	U1304	G1203	G1095	G968	A807	C	C	C	C740
U1862	C1766	U1690	G1582	U1492	A1410	C1305	G1206	A1096	A977	U810	C	C	C	C741
A1863	C1767	A1583	A1584	A1494	C1411	U1306	G1207	U1097	G978	U811	C	C	C	C742
C1768	C1768	A1694	A1584	A1494	C1412	U1306	G1208	G1098	G981	A812	C	C	C	C743
U1769	G1768	G1697	U1590	A1502	C1414	U1310	G1211	G1103	G981	U817	C	C	C	C744
G1770	U1769	U1697	U1591	G1503	C1415	C1312	G1212	G1104	C985	U818	C	C	C	U745
C1771	C1770	G1700	C1592	G1506	G1416	U1313	G1217	C1105	A986	U819	C	C	C	C746
G1772	C1771	U1702	G1593	U1507	G1417	U1313	G1217	G1106	G987	C820	C	C	C	C747
G1773	C1772	U1702	G1593	C1508	A1418	G1317	G1220	U1110	A988	U819	C	C	C	C748
G1774	C1773	G1705	U1596	G1509	C1419	G1317	G1220	U1111	C901	G827	C	C	C	C749
A1775	U1706	U1706	G1597	G1510	G1420	G1321	G1223	C1112	G903	G828	C	C	C	C750
G1776	A1707	C1708	G1598	G1511	G1420	U1322	A1224	C1113	A904	C829	C	C	C	C751
C1777	C1708	C1708	G1599	G1511	G1420	U1322	G1225	C1114	G905	C830	C	C	C	C752
G1778	U1709	C1708	G1600	G1515	U1422	U1325	G1231	A1115	G906	C831	C	C	C	C
C1782	A1710	A1710	A1502	C1516	C1423	G1326	G1231	U1116	C907	G832	C	C	C	C
A1795	U1715	U1715	U1611	A1517	G1424	A1328	A1236	U1116	A1004	A833	C	C	C	C
G1799	U1716	U1716	G1612	A1526	C1426	U1329	A1237	C1120	A1005	A834	C	C	C	C
A1800	G1717	G1717	C1527	C1527	G1427	U1329	U1237	C1121	G1006	G834	C	C	C	C
A1803	A1718	A1718	U1616	A1528	U1428	G1334	U1238	G1126	A1007	C835	C	C	C	C
U1804	G1719	G1719	C1529	C1529	C1429	U1339	I2T1244	G1126	U1009	G837	C	C	C	C
C1805	U1720	U1720	U1617	U1530	C1430	U1339	A1246	U1133	U1012	C838	C	C	C	C
G1722	G1721	G1721	U1618	G1531	C1431	U1343	A1247	C1134	U1013	C839	C	C	C	C
U1806	G1722	G1722	A1625	A1532	C1432	U1343	A1247	C1134	U1013	G841	C	C	C	C
A1807	U1724	U1724	G1536	G1536	C1433	G1344	G1252	G1136	A1019	G842	C	C	C	C
G1808	U1725	U1725	A1632	U1536	C1436	U1346	G1253	G1136	G1029	A843	C	C	C	C
G1814	G1814	G1814	A1632	U1536	C1436	U1346	G1253	G1136	G1029	C847	C	C	C	C
										G848	C	C	C	C
										G864	C	C	C	C

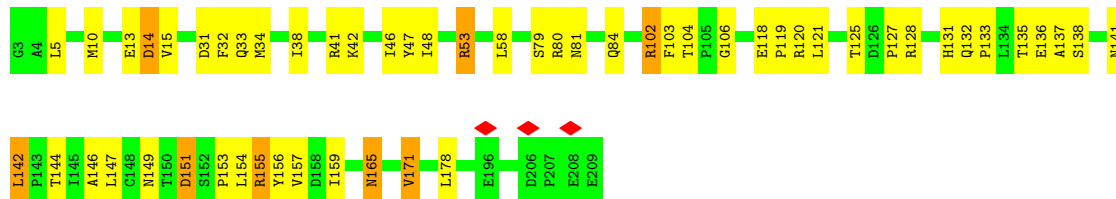
- Molecule 3: mRNA



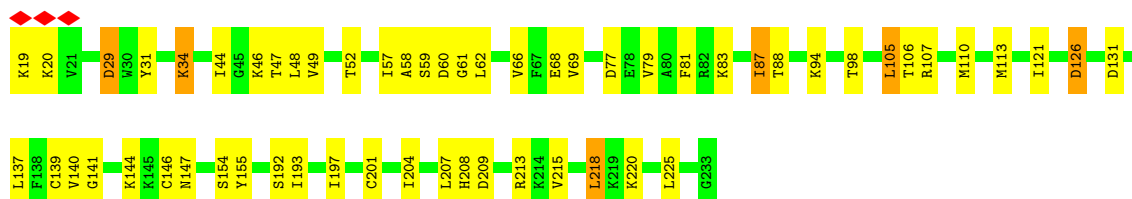
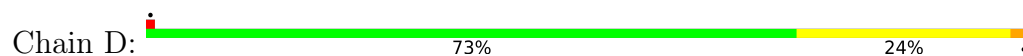
- Molecule 4: Eukaryotic translation initiation factor 2 subunit 1



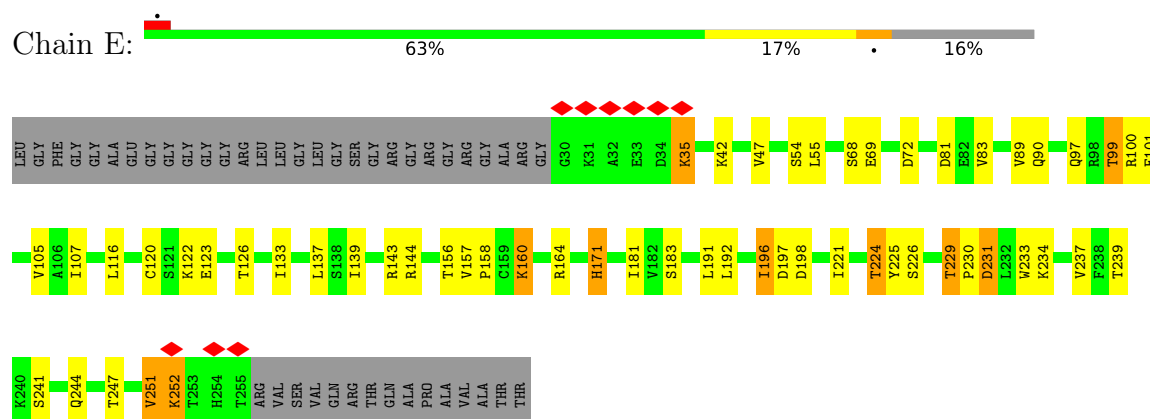
- Molecule 5: 40S ribosomal protein SA



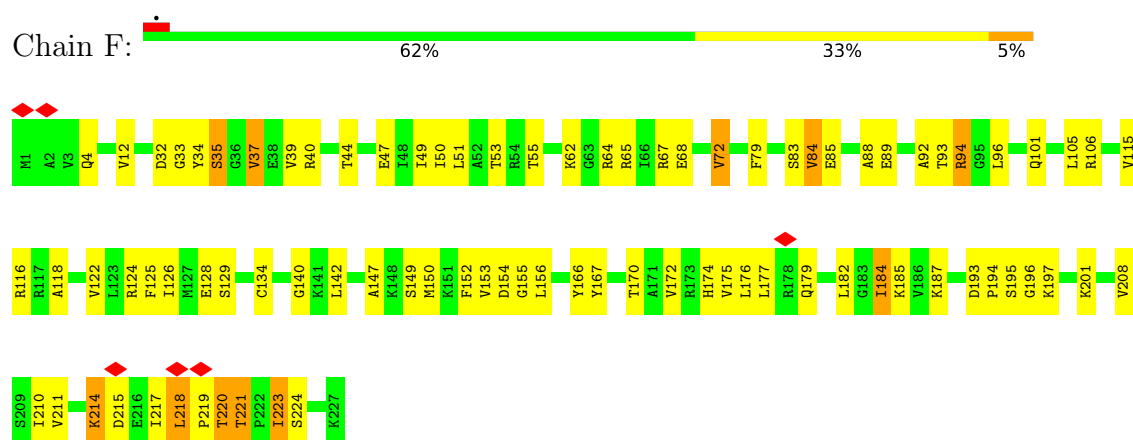
- Molecule 6: ribosomal protein eS1



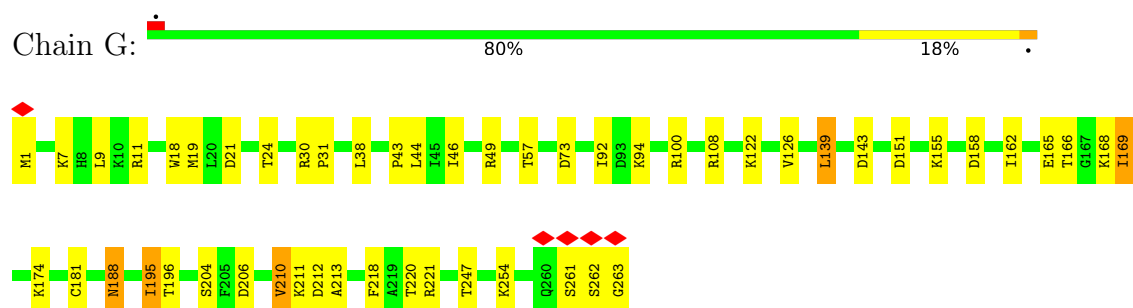
- Molecule 7: 40S ribosomal protein S2



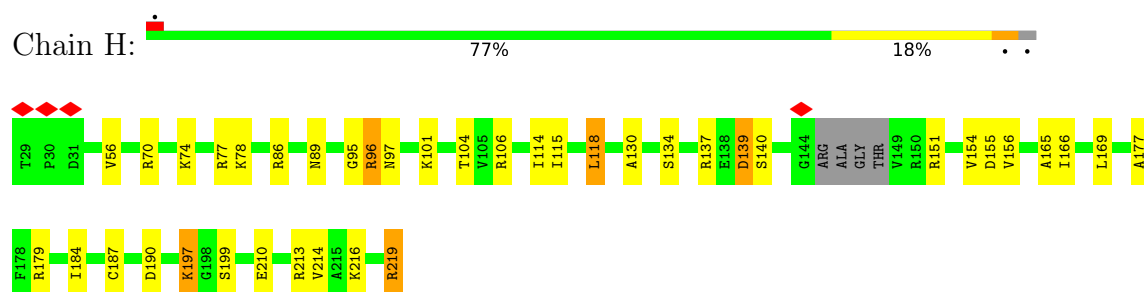
- Molecule 8: Ribosomal protein S3



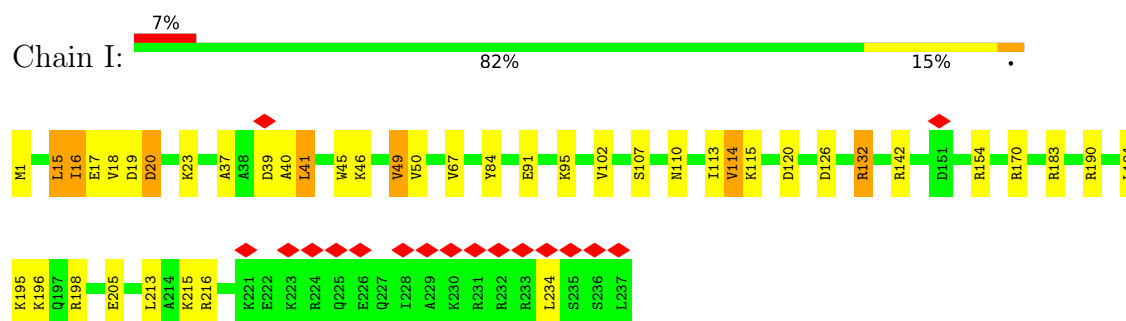
- Molecule 9: 40S ribosomal protein S4



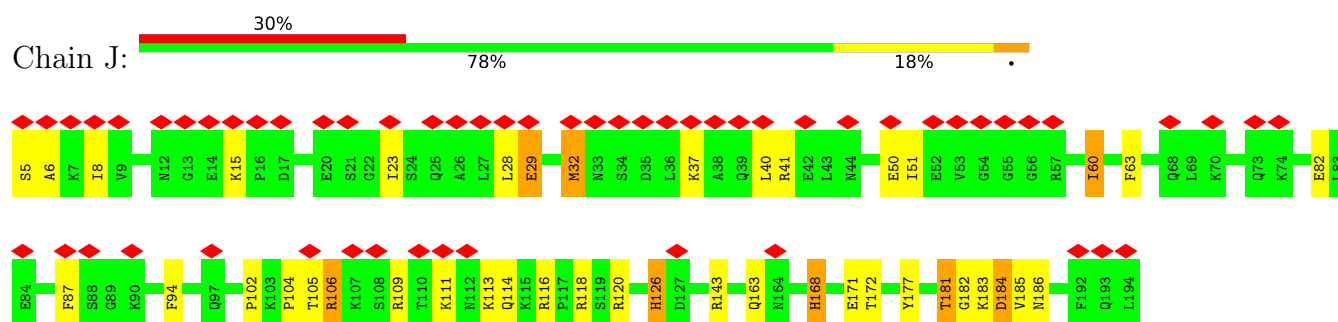
- Molecule 10: Ribosomal protein S5



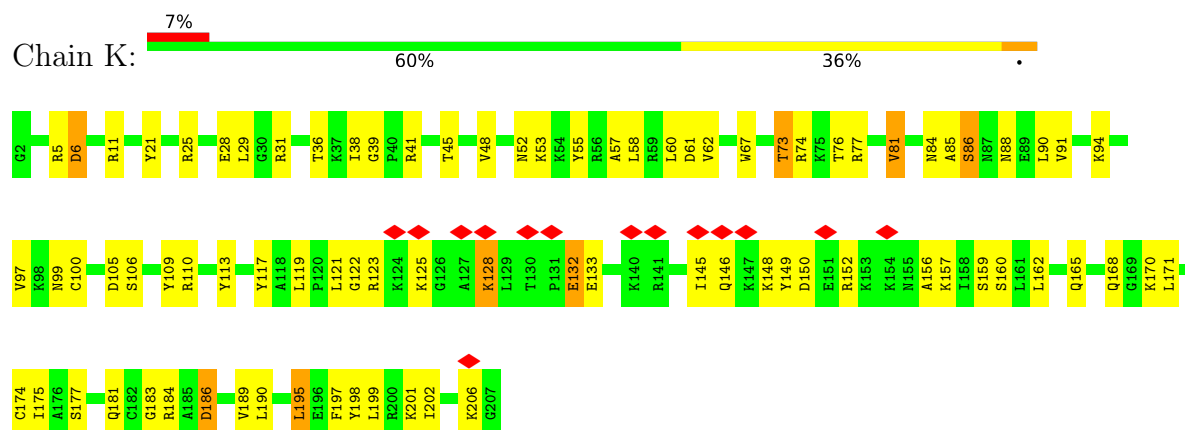
- Molecule 11: 40S ribosomal protein S6



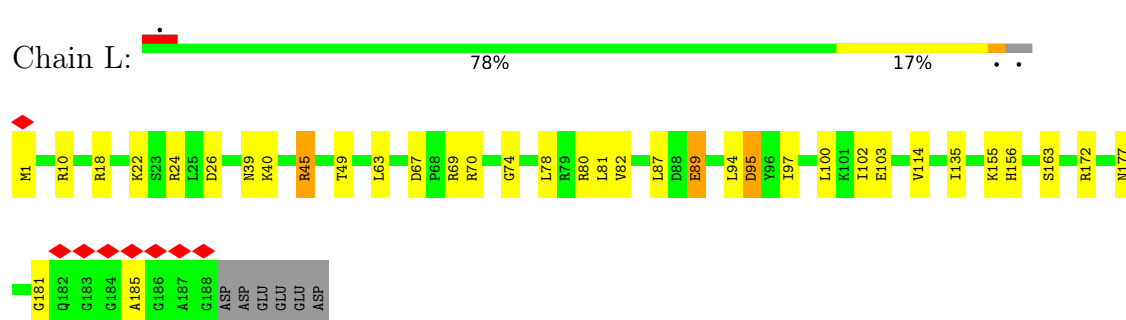
- Molecule 12: ribosomal protein eS7



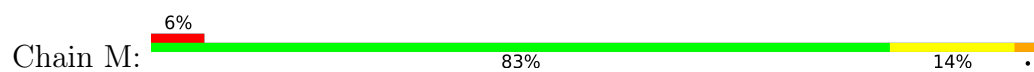
- Molecule 13: 40S ribosomal protein S8



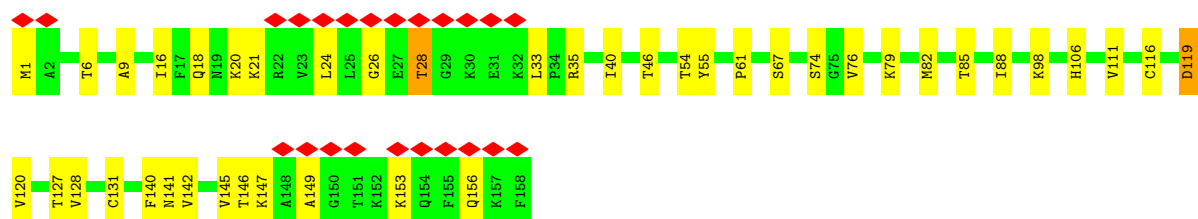
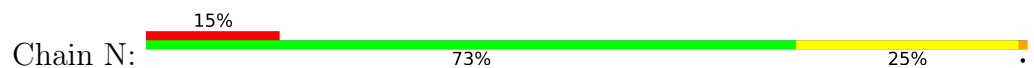
- Molecule 14: 40S ribosomal protein S9



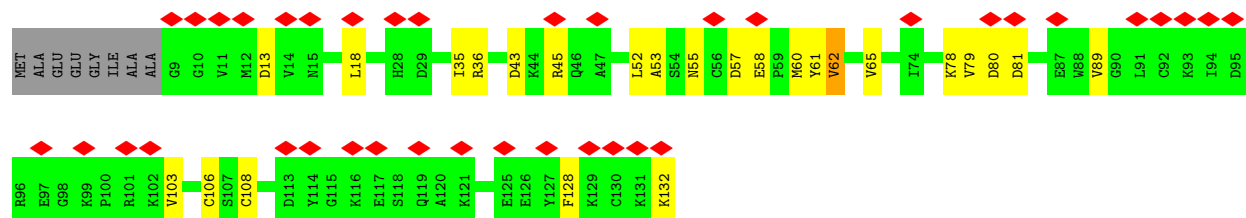
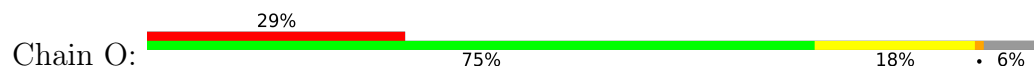
- Molecule 15: 40S ribosomal protein eS10



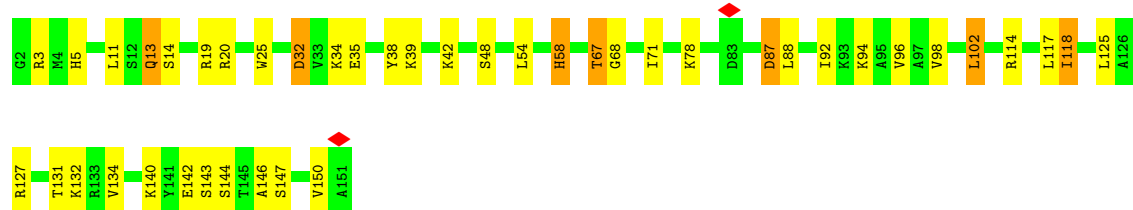
- Molecule 16: 40S ribosomal protein S11



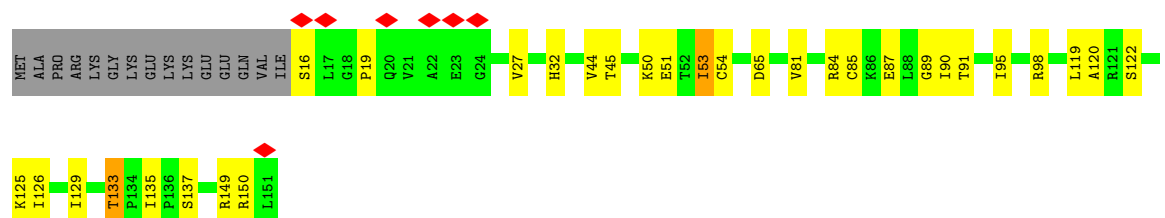
- Molecule 17: 40S ribosomal protein S12



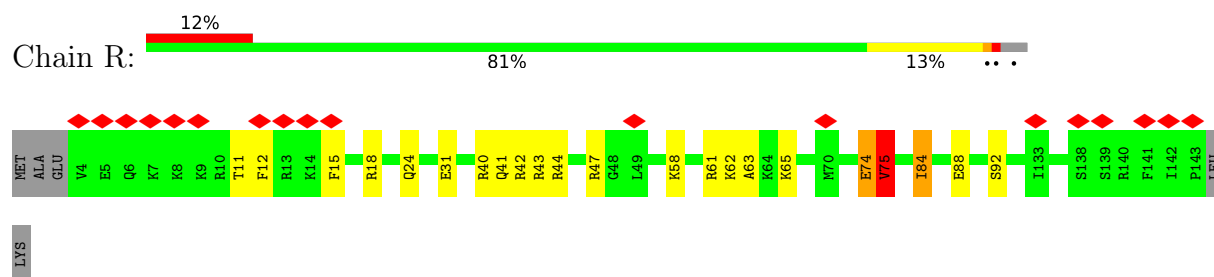
- Molecule 18: ribosomal protein uS15



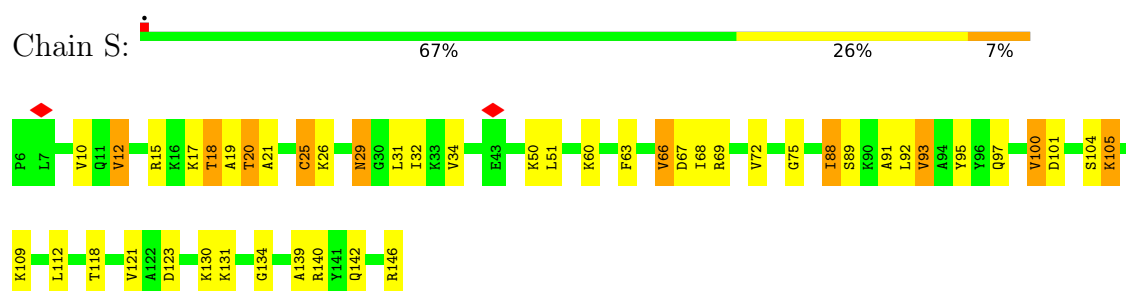
- Molecule 19: 40S ribosomal protein uS11



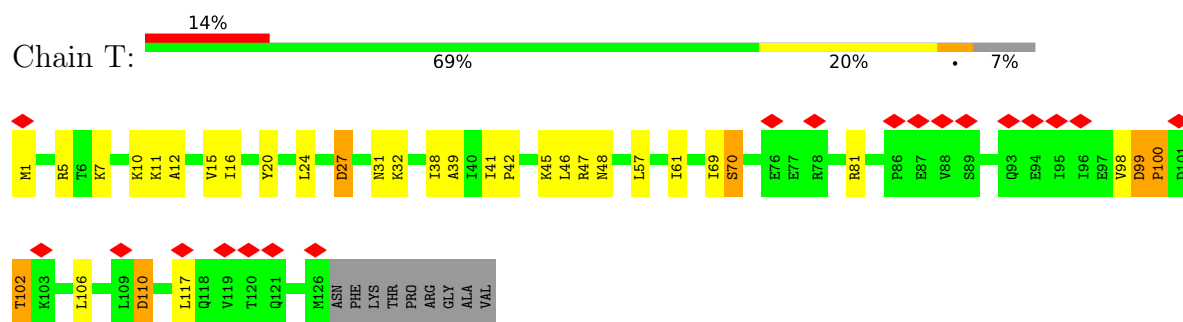
- Molecule 20: 40S ribosomal protein uS19



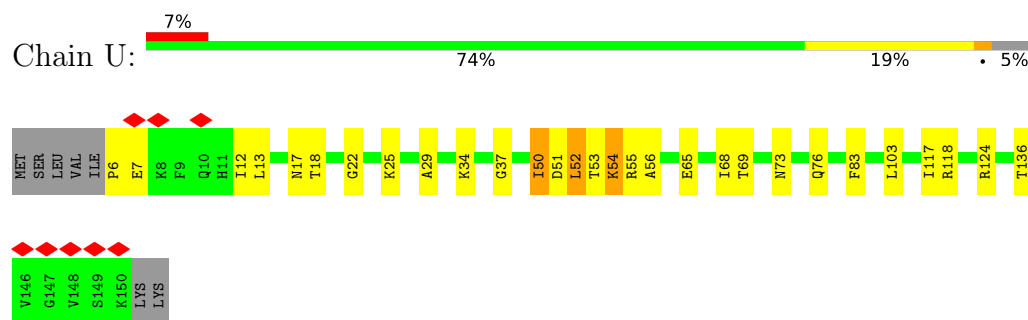
- Molecule 21: 40S ribosomal protein uS9



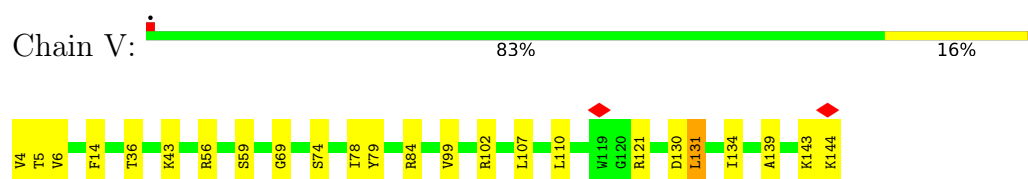
- Molecule 22: 40S ribosomal protein eS17



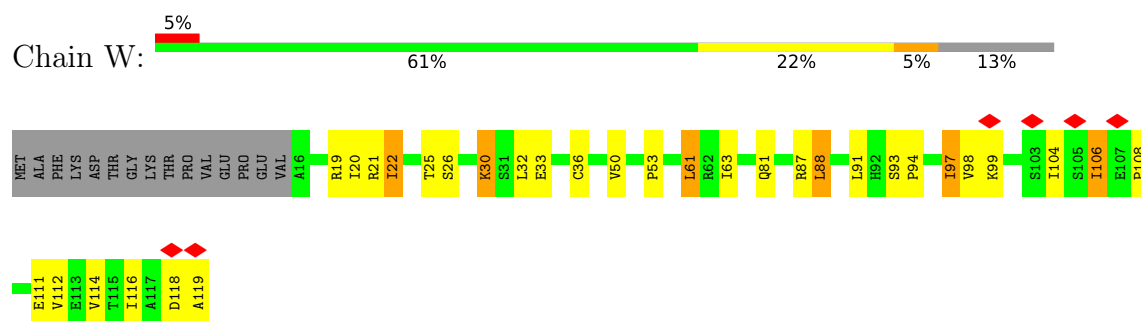
- Molecule 23: 40S ribosomal protein uS13



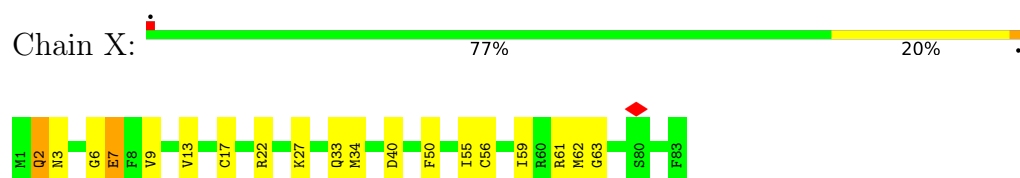
- Molecule 24: 40S ribosomal protein eS19



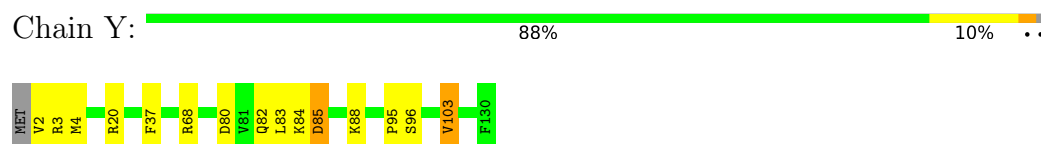
- Molecule 25: 40S ribosomal protein uS10



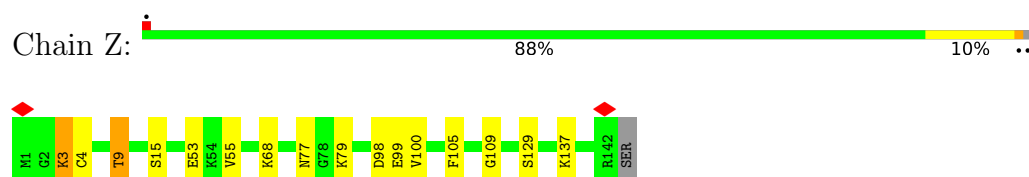
- Molecule 26: 40S ribosomal protein S21



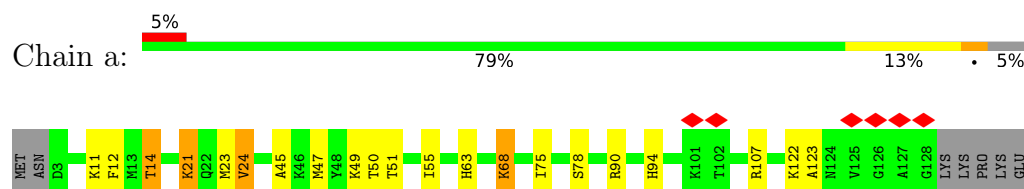
- Molecule 27: Ribosomal protein S15a



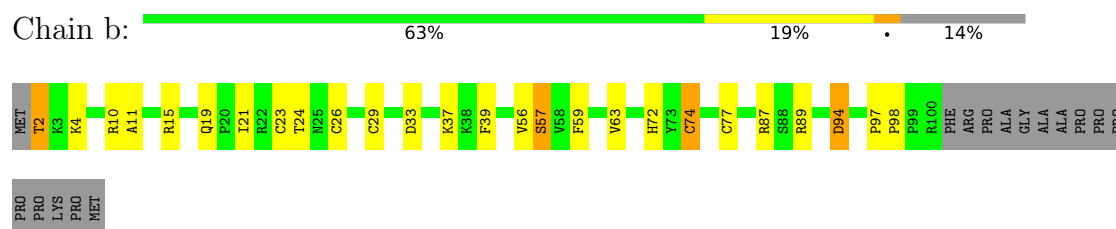
- Molecule 28: 40S ribosomal protein S23



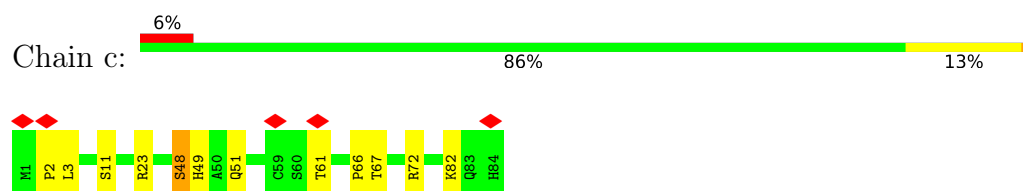
- Molecule 29: 40S ribosomal protein S24



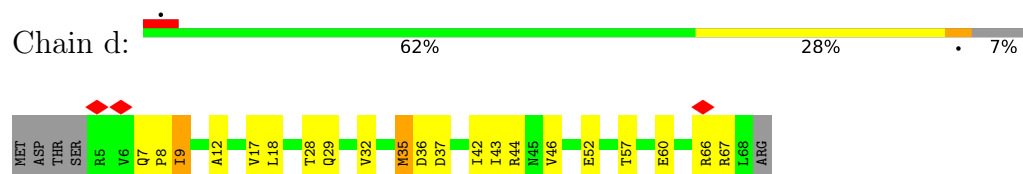
- Molecule 30: 40S ribosomal protein S26



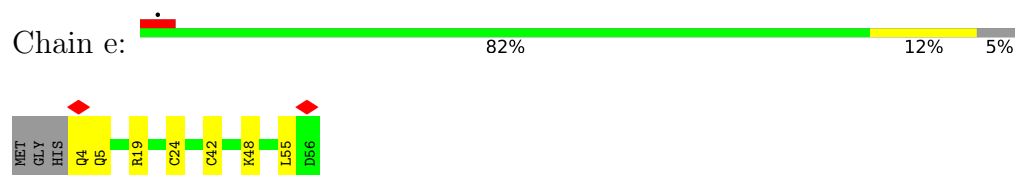
- Molecule 31: 40S ribosomal protein S27



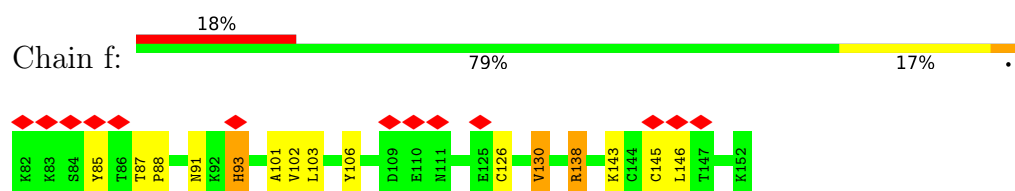
- Molecule 32: 40S ribosomal protein S28



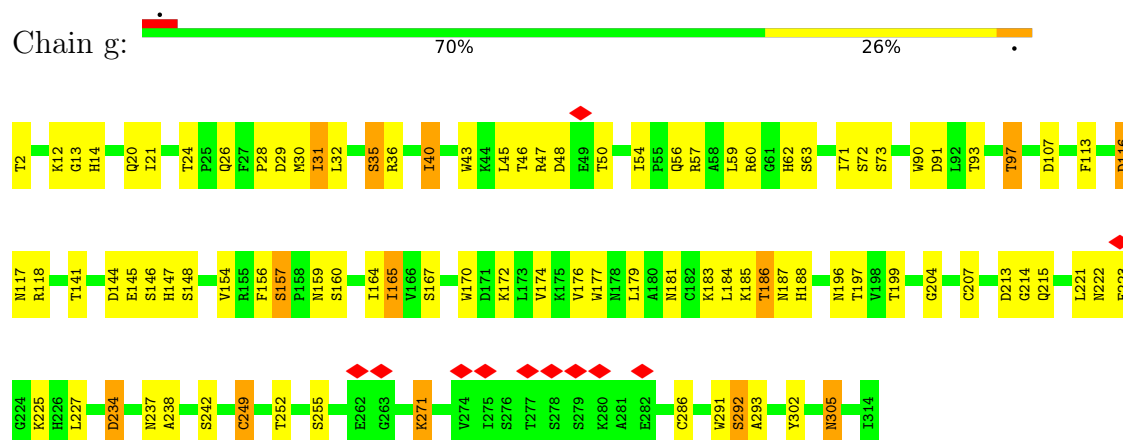
- Molecule 33: 40S ribosomal protein S29



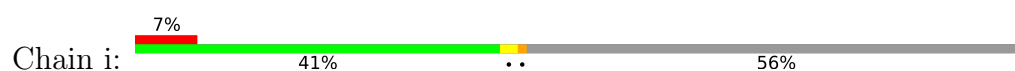
- Molecule 34: ribosomal protein eS31

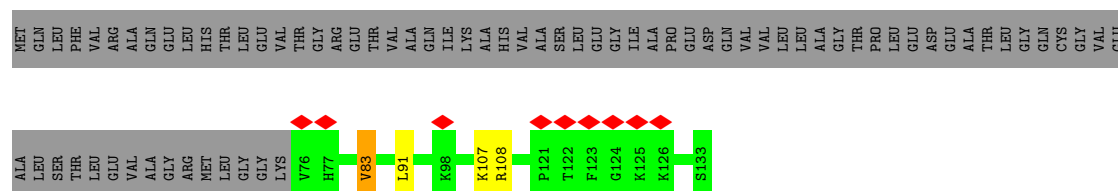


- Molecule 35: Ribosomal protein RACK1

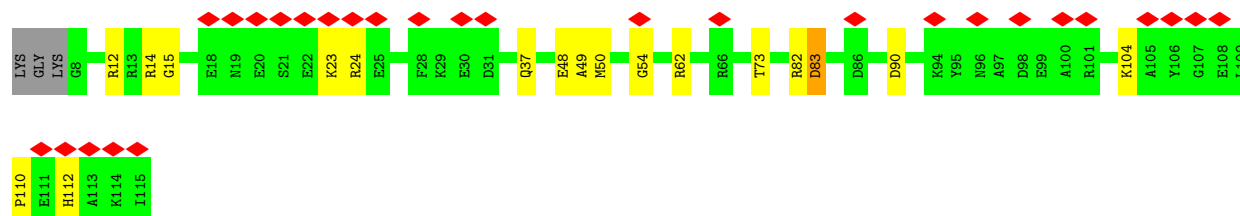
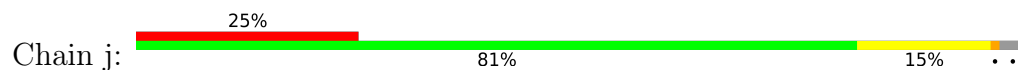


- Molecule 36: 40S ribosomal protein S30

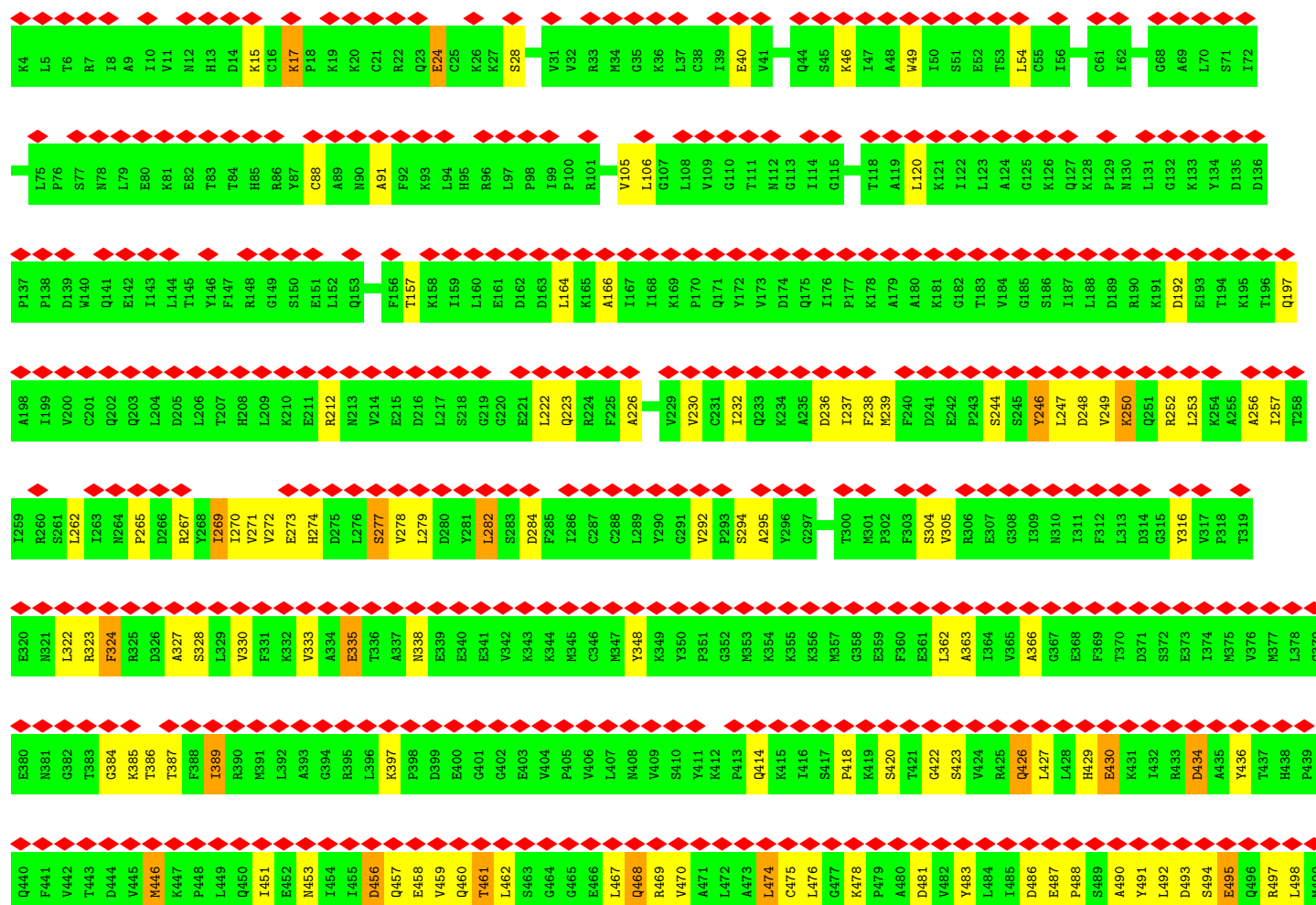
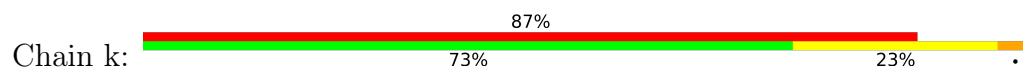


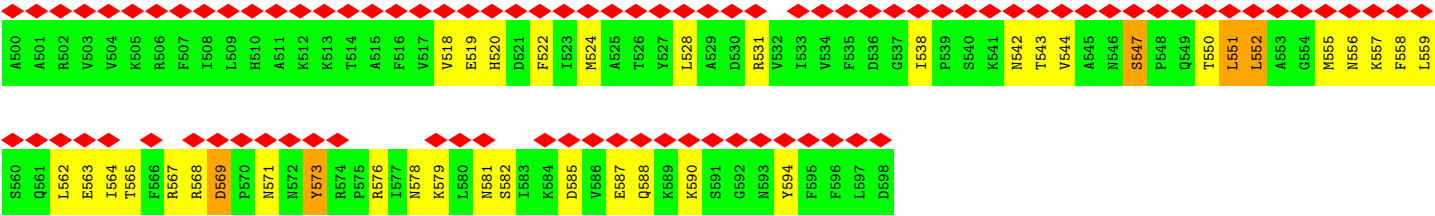


• Molecule 37: Eukaryotic translation initiation factor 4C



• Molecule 38: ATP binding cassette subfamily E member 1

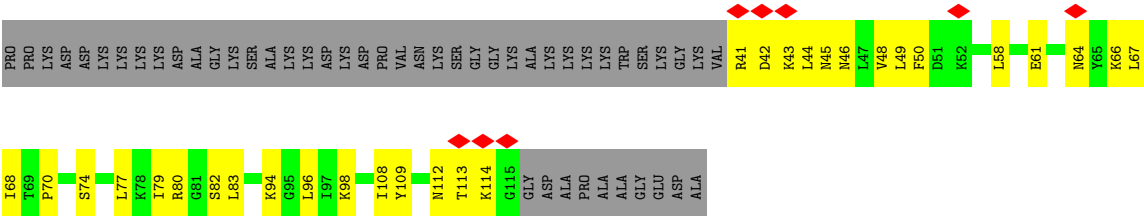




• Molecule 39: 60S ribosomal protein L41



• Molecule 40: 40S ribosomal protein S25



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	74515	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 ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.112	Depositor
Minimum map value	-0.060	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.013	Depositor
Map size (Å)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	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: T6A, MG, I2T

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	1	0.60	3/1773 (0.2%)	0.91	10/2763 (0.4%)
2	2	0.67	2/41502 (0.0%)	0.78	86/64679 (0.1%)
3	3	0.89	0/214	1.26	1/331 (0.3%)
4	A	0.36	0/2177	0.67	1/2935 (0.0%)
5	C	0.64	0/1674	0.93	3/2275 (0.1%)
6	D	0.50	0/1769	0.73	3/2367 (0.1%)
7	E	0.61	0/1794	0.87	3/2430 (0.1%)
8	F	0.47	0/1792	0.67	0/2412
9	G	0.54	0/2125	0.77	3/2856 (0.1%)
10	H	0.62	0/1503	0.98	4/2020 (0.2%)
11	I	0.60	0/1946	0.98	2/2588 (0.1%)
12	J	0.53	0/1553	1.01	3/2079 (0.1%)
13	K	0.59	0/1709	0.93	7/2278 (0.3%)
14	L	0.69	0/1567	1.03	4/2092 (0.2%)
15	M	0.58	0/852	1.05	0/1147
16	N	0.51	0/1319	0.59	0/1761
17	O	0.66	0/968	1.26	0/1296
18	P	0.54	0/1232	0.74	2/1656 (0.1%)
19	Q	0.62	0/1029	1.00	2/1380 (0.1%)
20	R	0.76	0/1177	1.30	6/1571 (0.4%)
21	S	0.58	0/1142	0.82	1/1528 (0.1%)
22	T	0.61	0/1031	1.06	5/1383 (0.4%)
23	U	0.47	0/1212	0.76	0/1621
24	V	0.62	0/1133	0.99	2/1517 (0.1%)
25	W	0.49	0/832	0.71	0/1117
26	X	0.57	0/643	0.85	0/860
27	Y	0.69	0/1051	0.95	0/1406
28	Z	0.67	0/1124	1.13	1/1500 (0.1%)
29	a	0.71	0/1038	1.13	2/1380 (0.1%)
30	b	0.71	0/802	1.06	2/1076 (0.2%)
31	c	0.62	0/673	1.12	3/902 (0.3%)
32	d	0.54	0/508	0.83	0/680

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.67	0/454	1.07	1/603 (0.2%)
34	f	0.63	0/594	1.09	1/786 (0.1%)
35	g	0.47	0/2494	0.79	0/3394
36	i	0.79	0/469	1.38	0/617
37	j	0.63	0/884	1.19	5/1175 (0.4%)
38	k	0.63	0/4780	1.15	13/6452 (0.2%)
39	l	0.51	0/241	0.59	0/305
40	n	0.35	0/604	0.56	0/810
All	All	0.63	5/91384 (0.0%)	0.87	176/132028 (0.1%)

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
1	1	0	1
2	2	0	131
3	3	0	1
4	A	0	1
5	C	0	1
7	E	0	1
9	G	0	1
10	H	0	1
11	I	0	3
13	K	0	3
19	Q	0	2
24	V	0	2
27	Y	0	1
29	a	0	1
32	d	0	1
34	f	0	1
38	k	0	4
All	All	0	156

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	72	U	O3'-P	-12.66	1.42	1.61
2	2	1245	C	O3'-P	-12.24	1.42	1.61
2	2	1708	C	P-OP1	6.26	1.61	1.49
1	1	2	A	P-OP1	6.22	1.61	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2	A	P-OP2	6.17	1.61	1.49

The worst 5 of 176 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	72	U	OP2-P-O3'	-29.25	20.26	108.00
1	1	28	U	P-O3'-C3'	-9.55	105.87	120.20
2	2	73	C	C2'-C3'-O3'	9.47	123.71	109.50
1	1	2	A	P-O5'-C5'	-9.34	106.88	120.90
24	V	143	LYS	O-C-N	-9.32	110.99	122.55

There are no chirality outliers.

5 of 156 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	32	C	Sidechain
2	2	26	U	Sidechain
2	2	38	A	Sidechain
2	2	44	U	Sidechain
2	2	45	A	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	1617	0	821	0	0
2	2	37147	0	18655	431	0
3	3	192	0	99	0	0
4	A	2146	0	2191	91	0
5	C	1637	0	1641	30	0
6	D	1741	0	1815	27	0
7	E	1754	0	1834	28	0
8	F	1764	0	1863	57	0
9	G	2083	0	2189	33	0
10	H	1482	0	1534	20	0
11	I	1924	0	2089	23	0
12	J	1530	0	1627	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	K	1680	0	1762	46	0
14	L	1542	0	1659	19	0
15	M	828	0	854	11	0
16	N	1296	0	1374	22	0
17	O	958	0	993	16	0
18	P	1208	0	1294	26	0
19	Q	1016	0	1039	14	0
20	R	1154	0	1213	11	0
21	S	1124	0	1193	29	0
22	T	1019	0	1075	22	0
23	U	1194	0	1253	16	0
24	V	1113	0	1149	9	0
25	W	822	0	887	16	0
26	X	636	0	637	10	0
27	Y	1034	0	1080	8	0
28	Z	1106	0	1179	8	0
29	a	1021	0	1085	13	0
30	b	789	0	839	15	0
31	c	659	0	683	8	0
32	d	506	0	536	9	0
33	e	444	0	442	4	0
34	f	582	0	599	8	0
35	g	2437	0	2393	55	0
36	i	464	0	511	3	0
37	j	874	0	893	6	0
38	k	4693	0	4826	88	0
39	l	240	0	289	5	0
40	n	598	0	656	22	0
41	2	220	0	0	0	0
41	3	3	0	0	0	0
41	G	2	0	0	0	0
41	I	2	0	0	0	0
41	K	1	0	0	0	0
41	L	1	0	0	0	0
41	Z	1	0	0	0	0
All	All	86284	0	68751	1175	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 8.

The worst 5 of 1175 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:E:247:THR:O	7:E:251:VAL:HG23	1.45	1.16
2:2:1417:A:N6	2:2:1423:C:N4	2.13	0.96
2:2:124:U:H3	2:2:330:C:N4	1.63	0.95
6:D:49:VAL:HG11	6:D:62:LEU:HD11	1.47	0.95
2:2:1407:G:N1	2:2:1431:C:N3	2.14	0.95

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	A	264/284 (93%)	238 (90%)	26 (10%)	0	100	100
5	C	205/207 (99%)	179 (87%)	26 (13%)	0	100	100
6	D	213/215 (99%)	185 (87%)	28 (13%)	0	100	100
7	E	224/270 (83%)	192 (86%)	30 (13%)	2 (1%)	14	43
8	F	225/227 (99%)	200 (89%)	25 (11%)	0	100	100
9	G	261/263 (99%)	232 (89%)	29 (11%)	0	100	100
10	H	183/191 (96%)	162 (88%)	21 (12%)	0	100	100
11	I	235/237 (99%)	211 (90%)	24 (10%)	0	100	100
12	J	188/190 (99%)	163 (87%)	25 (13%)	0	100	100
13	K	204/206 (99%)	178 (87%)	25 (12%)	1 (0%)	24	55
14	L	186/194 (96%)	172 (92%)	14 (8%)	0	100	100
15	M	96/98 (98%)	84 (88%)	11 (12%)	1 (1%)	12	40
16	N	156/158 (99%)	140 (90%)	16 (10%)	0	100	100
17	O	122/132 (92%)	105 (86%)	16 (13%)	1 (1%)	16	45
18	P	148/150 (99%)	137 (93%)	11 (7%)	0	100	100
19	Q	134/151 (89%)	111 (83%)	22 (16%)	1 (1%)	18	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	R	138/145 (95%)	125 (91%)	12 (9%)	1 (1%)	18	49
21	S	139/141 (99%)	126 (91%)	13 (9%)	0	100	100
22	T	124/135 (92%)	106 (86%)	18 (14%)	0	100	100
23	U	143/152 (94%)	128 (90%)	15 (10%)	0	100	100
24	V	139/141 (99%)	122 (88%)	16 (12%)	1 (1%)	18	49
25	W	102/119 (86%)	93 (91%)	9 (9%)	0	100	100
26	X	81/83 (98%)	62 (76%)	19 (24%)	0	100	100
27	Y	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
28	Z	140/143 (98%)	128 (91%)	11 (8%)	1 (1%)	18	49
29	a	124/133 (93%)	109 (88%)	15 (12%)	0	100	100
30	b	97/115 (84%)	86 (89%)	11 (11%)	0	100	100
31	c	82/84 (98%)	70 (85%)	12 (15%)	0	100	100
32	d	62/69 (90%)	50 (81%)	12 (19%)	0	100	100
33	e	51/56 (91%)	43 (84%)	8 (16%)	0	100	100
34	f	69/71 (97%)	58 (84%)	11 (16%)	0	100	100
35	g	311/313 (99%)	275 (88%)	36 (12%)	0	100	100
36	i	56/133 (42%)	50 (89%)	6 (11%)	0	100	100
37	j	106/111 (96%)	91 (86%)	15 (14%)	0	100	100
38	k	593/595 (100%)	512 (86%)	81 (14%)	0	100	100
39	l	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
40	n	73/124 (59%)	66 (90%)	7 (10%)	0	100	100
All	All	5824/6191 (94%)	5129 (88%)	686 (12%)	9 (0%)	44	71

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	E	252	LYS
20	R	75	VAL
7	E	251	VAL
15	M	33	PRO
17	O	103	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	
4	A	238/255 (93%)	203 (85%)	35 (15%)	3	14
5	C	173/173 (100%)	153 (88%)	20 (12%)	5	21
6	D	196/196 (100%)	175 (89%)	21 (11%)	6	24
7	E	190/214 (89%)	166 (87%)	24 (13%)	4	18
8	F	190/190 (100%)	163 (86%)	27 (14%)	3	14
9	G	225/225 (100%)	211 (94%)	14 (6%)	16	45
10	H	159/161 (99%)	145 (91%)	14 (9%)	9	32
11	I	207/207 (100%)	189 (91%)	18 (9%)	9	32
12	J	170/170 (100%)	154 (91%)	16 (9%)	8	30
13	K	177/177 (100%)	154 (87%)	23 (13%)	4	17
14	L	162/168 (96%)	150 (93%)	12 (7%)	13	38
15	M	89/89 (100%)	84 (94%)	5 (6%)	19	47
16	N	142/142 (100%)	127 (89%)	15 (11%)	6	24
17	O	104/108 (96%)	100 (96%)	4 (4%)	29	57
18	P	130/130 (100%)	118 (91%)	12 (9%)	8	30
19	Q	106/119 (89%)	94 (89%)	12 (11%)	5	21
20	R	126/130 (97%)	120 (95%)	6 (5%)	23	52
21	S	117/117 (100%)	101 (86%)	16 (14%)	3	16
22	T	114/121 (94%)	107 (94%)	7 (6%)	17	45
23	U	125/132 (95%)	113 (90%)	12 (10%)	8	29
24	V	113/113 (100%)	105 (93%)	8 (7%)	13	40
25	W	94/107 (88%)	80 (85%)	14 (15%)	3	13
26	X	67/67 (100%)	60 (90%)	7 (10%)	7	25
27	Y	112/113 (99%)	105 (94%)	7 (6%)	16	44
28	Z	114/115 (99%)	110 (96%)	4 (4%)	32	58
29	a	108/115 (94%)	103 (95%)	5 (5%)	24	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	b	87/99 (88%)	77 (88%)	10 (12%)	5	21
31	c	76/76 (100%)	73 (96%)	3 (4%)	28	56
32	d	57/62 (92%)	47 (82%)	10 (18%)	2	9
33	e	47/49 (96%)	46 (98%)	1 (2%)	47	67
34	f	64/64 (100%)	58 (91%)	6 (9%)	8	30
35	g	272/272 (100%)	241 (89%)	31 (11%)	5	21
36	i	48/106 (45%)	46 (96%)	2 (4%)	26	55
37	j	91/93 (98%)	87 (96%)	4 (4%)	25	54
38	k	523/523 (100%)	477 (91%)	46 (9%)	9	32
39	l	24/24 (100%)	22 (92%)	2 (8%)	10	34
40	n	66/102 (65%)	63 (96%)	3 (4%)	24	53
All	All	5103/5324 (96%)	4627 (91%)	476 (9%)	11	30

5 of 476 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	N	24	LEU
38	k	385	LYS
21	S	51	LEU
38	k	282	LEU
40	n	44	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 97 such sidechains are listed below:

Mol	Chain	Res	Type
21	S	24	HIS
31	c	51	GLN
22	T	74	GLN
28	Z	77	ASN
33	e	37	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	74/75 (98%)	16 (21%)	1 (1%)
2	2	1734/1863 (93%)	300 (17%)	24 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	3	8/9 (88%)	4 (50%)	0
All	All	1816/1947 (93%)	320 (17%)	25 (1%)

5 of 320 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	11	G
1	1	13	G
1	1	14	C
1	1	17	C
1	1	18	G

5 of 25 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	1310	U
2	2	1472	A
2	2	1855	G
2	2	1433	C
2	2	1515	G

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	I2T	2	1244	2	25,29,30	2.70	4 (16%)	28,42,45	1.26	4 (14%)
1	T6A	1	37	1	31,34,35	0.95	3 (9%)	43,49,52	1.62	9 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	I2T	2	1244	2	-	1/16/34/35	0/2/2/2
1	T6A	1	37	1	-	5/23/41/42	0/3/3/3

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1244	I2T	CN1-N1	-9.62	1.27	1.46
2	2	1244	I2T	O2'-C2'	-7.53	1.24	1.43
2	2	1244	I2T	C33-N34	-4.08	1.27	1.48
1	1	37	T6A	ODA-C13	2.66	1.30	1.22
1	1	37	T6A	ODB-C13	-2.47	1.22	1.30

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	37	T6A	C14-C12-C13	3.85	116.75	110.03
1	1	37	T6A	ODB-C13-C12	3.69	126.95	114.15
2	2	1244	I2T	O3'-C3'-C4'	-3.63	100.65	111.08
1	1	37	T6A	C12-N11-C10	3.35	127.55	121.99
1	1	37	T6A	N6-C10-N11	3.24	118.23	113.77

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1	37	T6A	N11-C12-C13-ODA
1	1	37	T6A	N11-C12-C13-ODB
1	1	37	T6A	C14-C12-C13-ODA
1	1	37	T6A	C14-C12-C13-ODB
1	1	37	T6A	C14-C12-N11-C10

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 230 ligands modelled in this entry, 230 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
2	2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	730:C	O3'	731:C	P	9.63

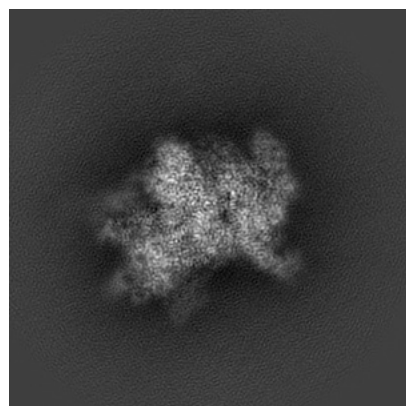
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17330. These allow visual inspection of the internal detail of the map and identification of artifacts.

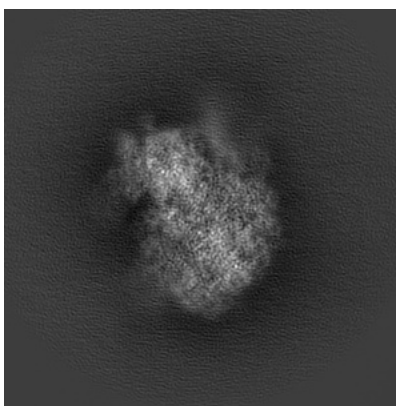
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

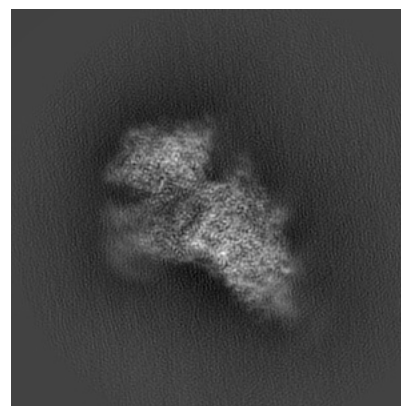
6.1.1 Primary map



X

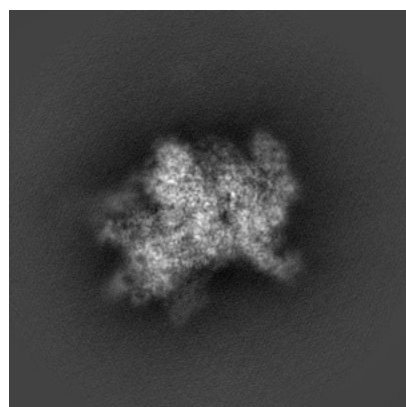


Y

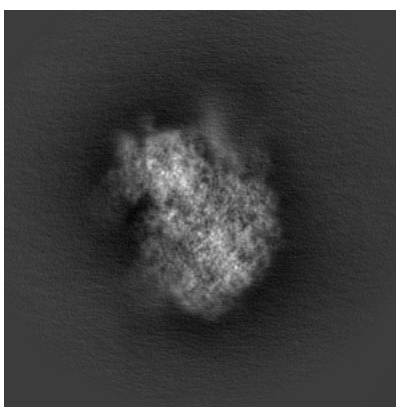


Z

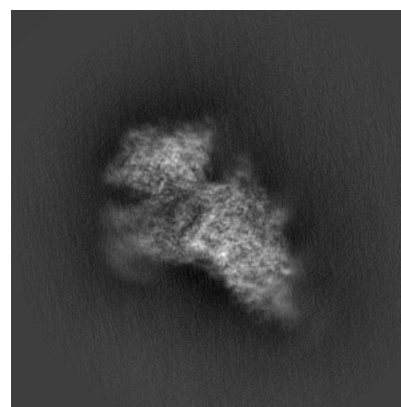
6.1.2 Raw map



X



Y

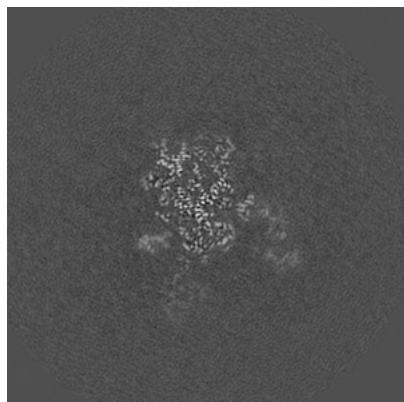


Z

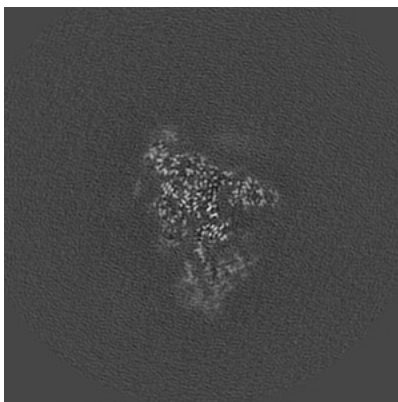
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

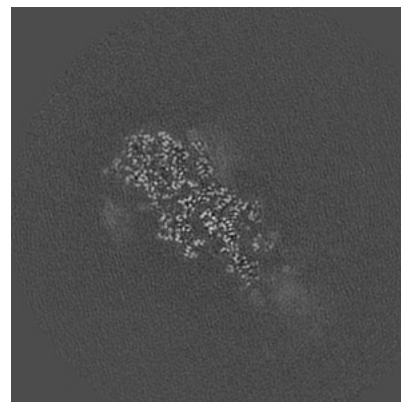
6.2.1 Primary map



X Index: 192

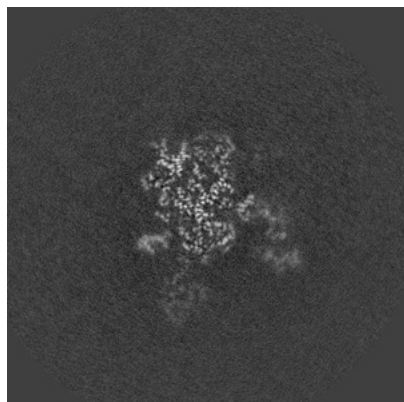


Y Index: 192

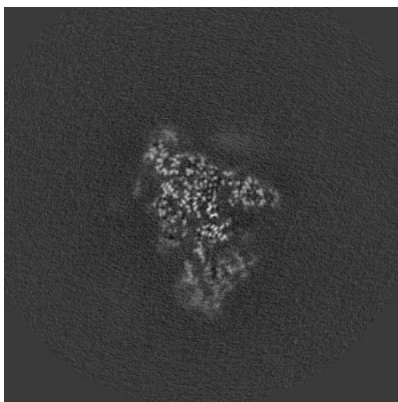


Z Index: 192

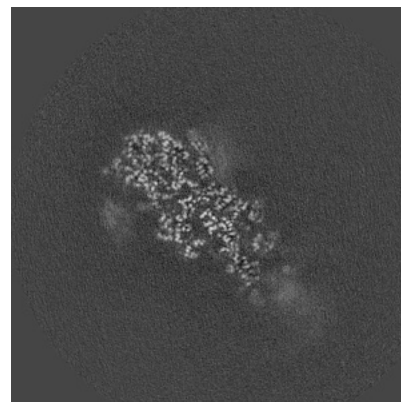
6.2.2 Raw map



X Index: 192



Y Index: 192

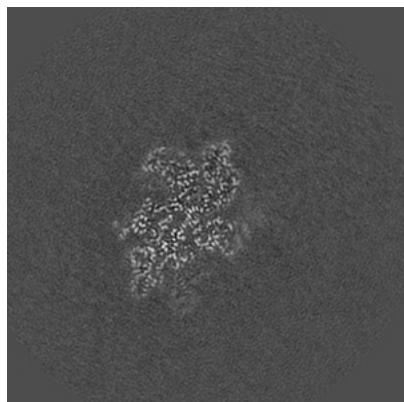


Z Index: 192

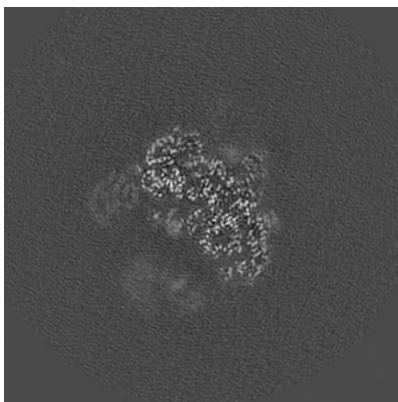
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

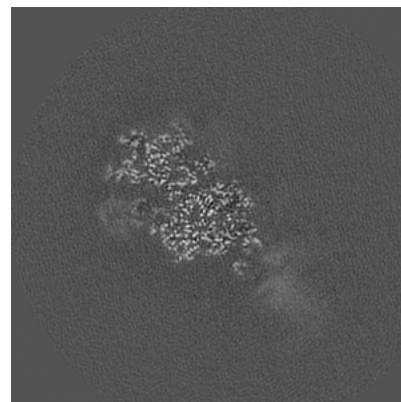
6.3.1 Primary map



X Index: 213

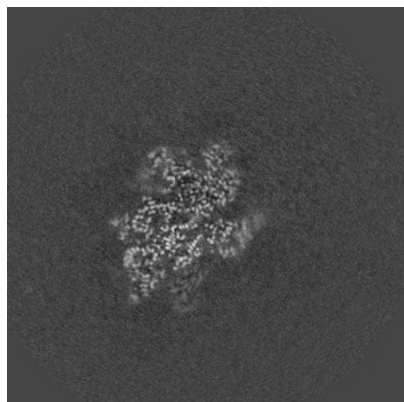


Y Index: 160

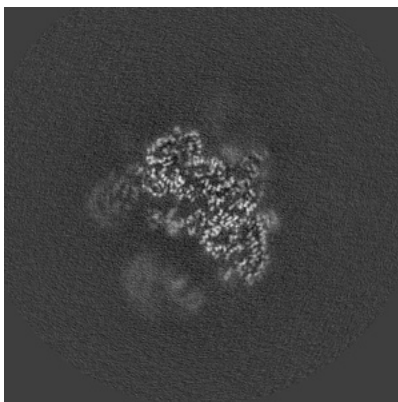


Z Index: 200

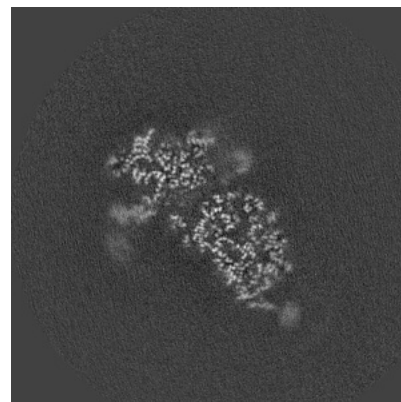
6.3.2 Raw map



X Index: 216



Y Index: 159

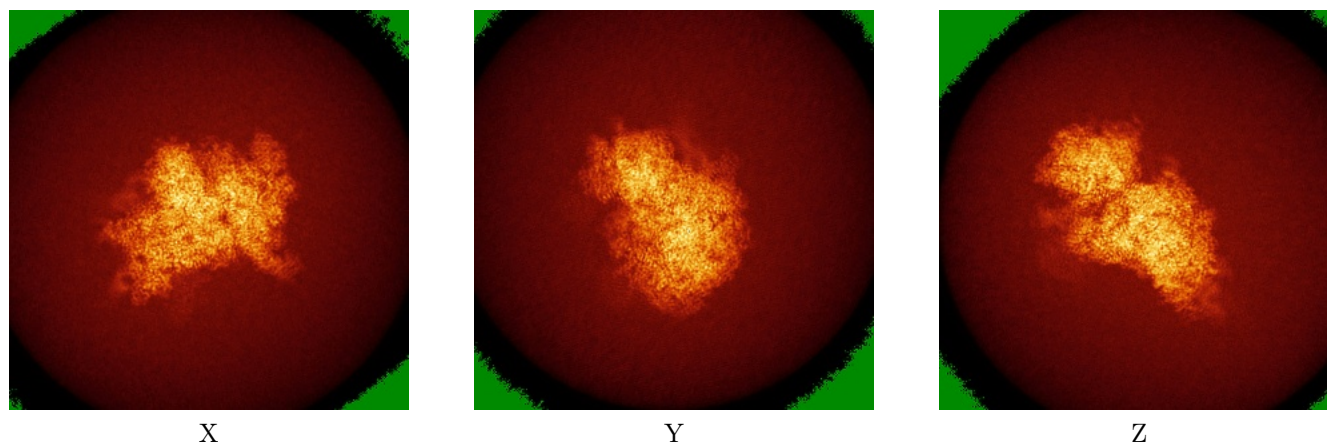


Z Index: 180

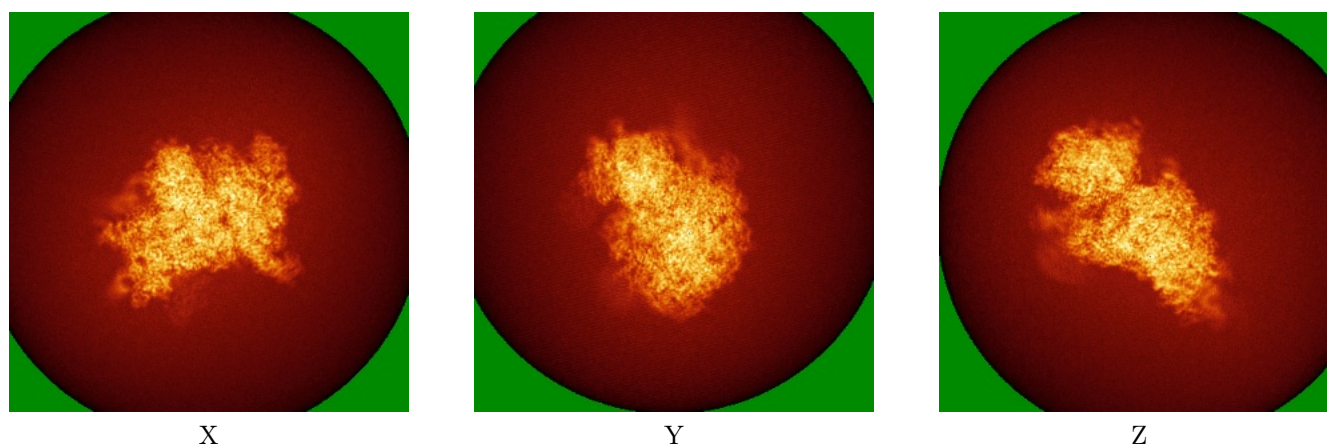
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

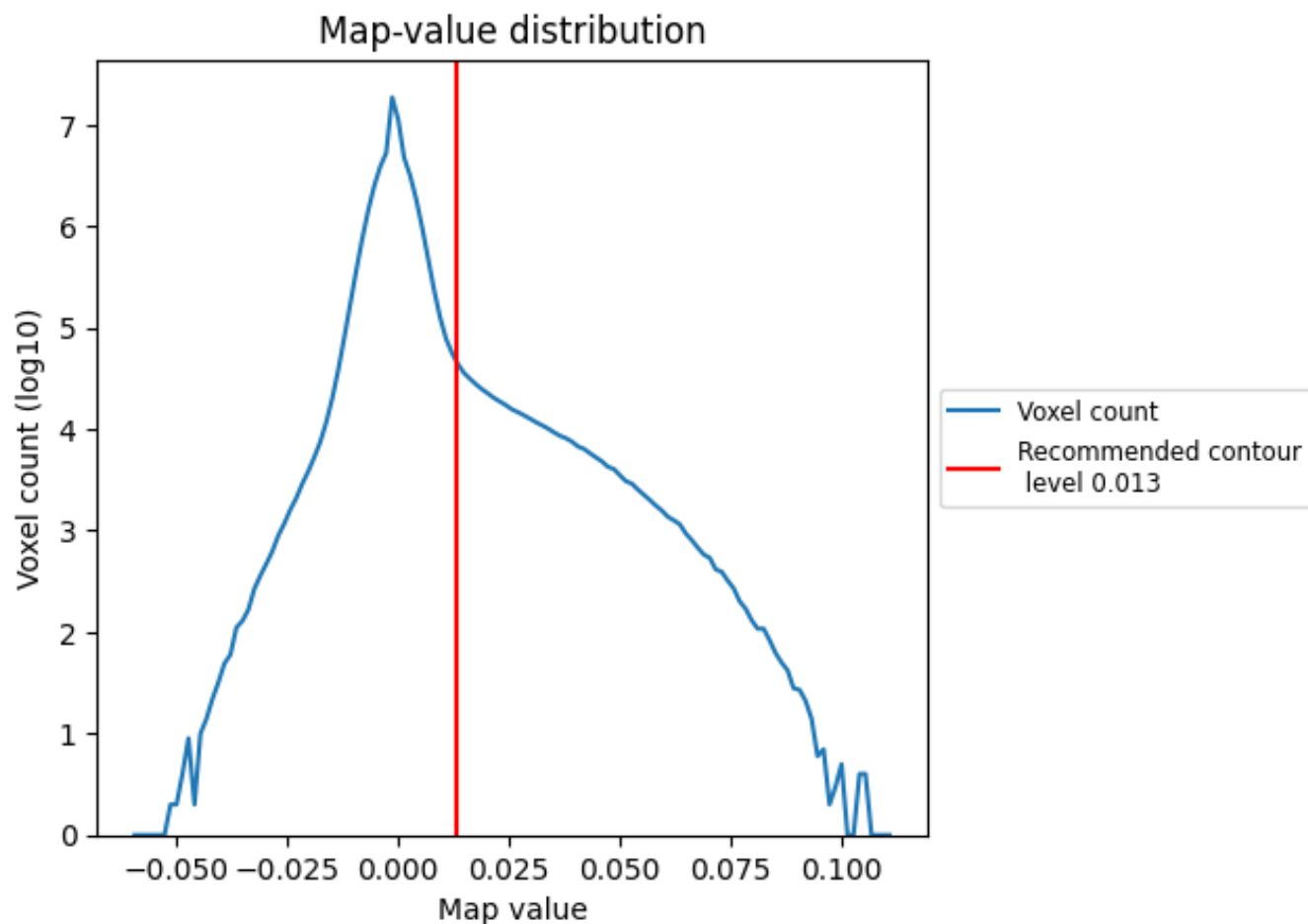
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

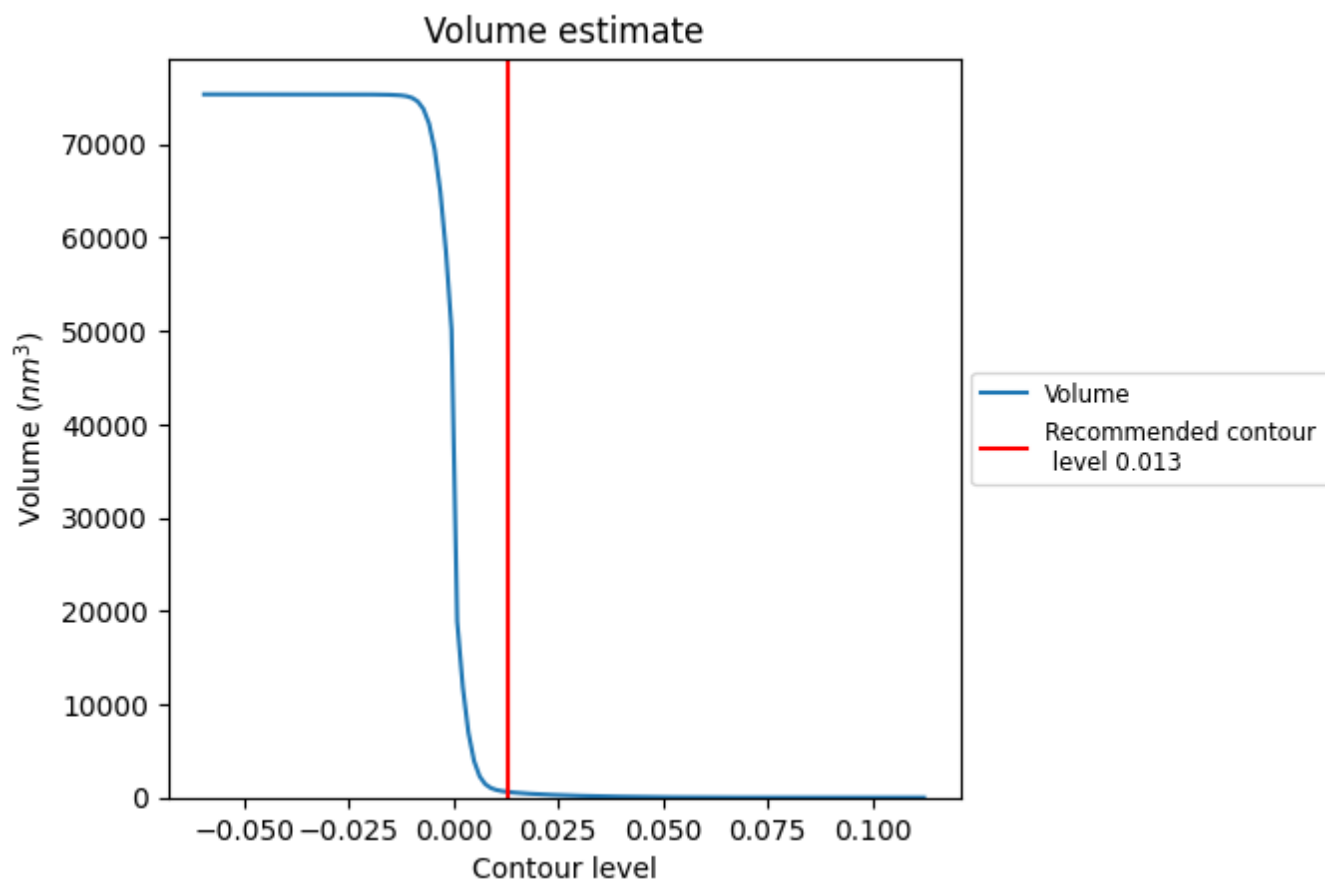
This section contains the results of statistical analysis of the map.

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.

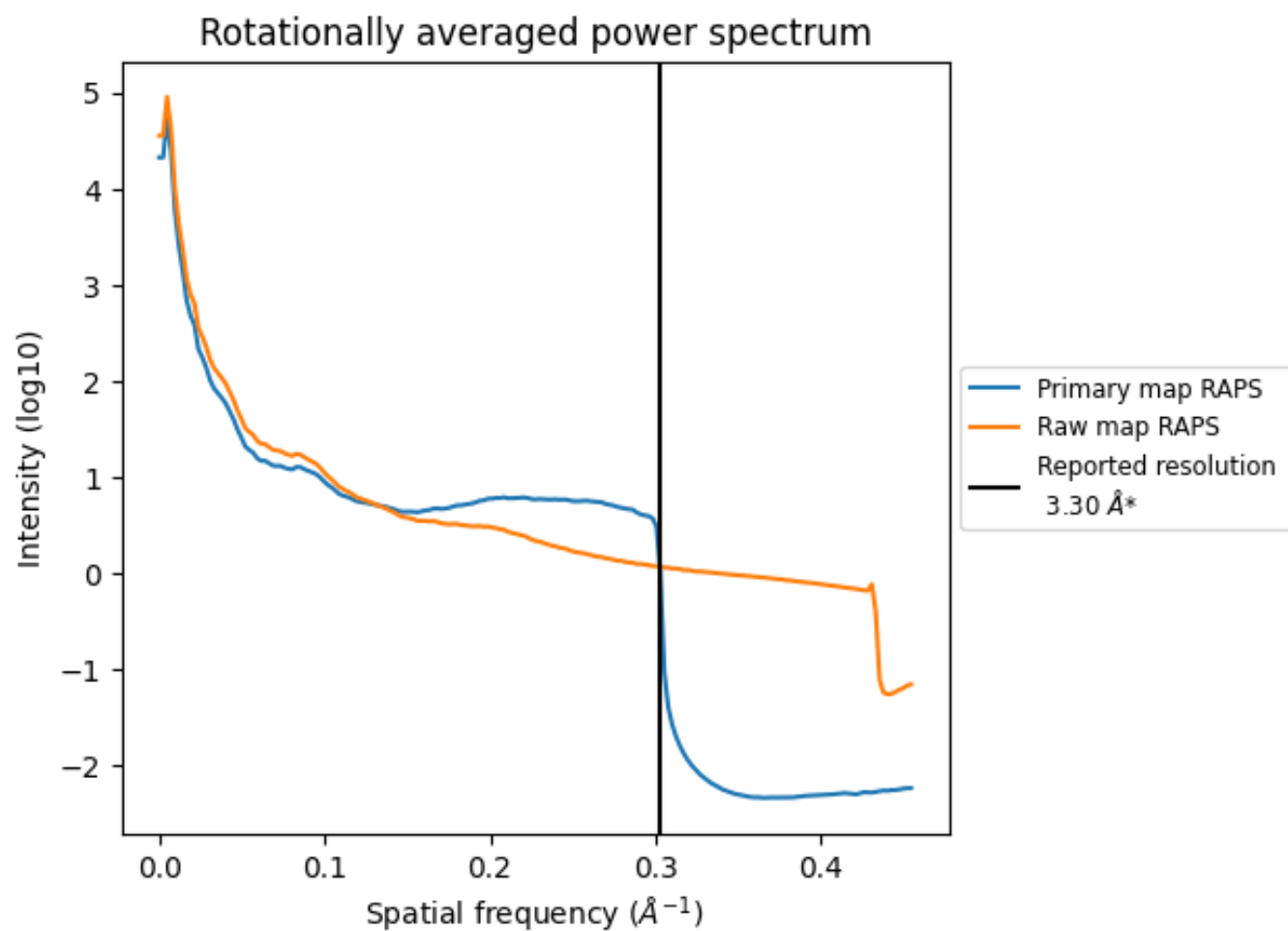
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 603 nm³; this corresponds to an approximate mass of 544 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 ⓘ

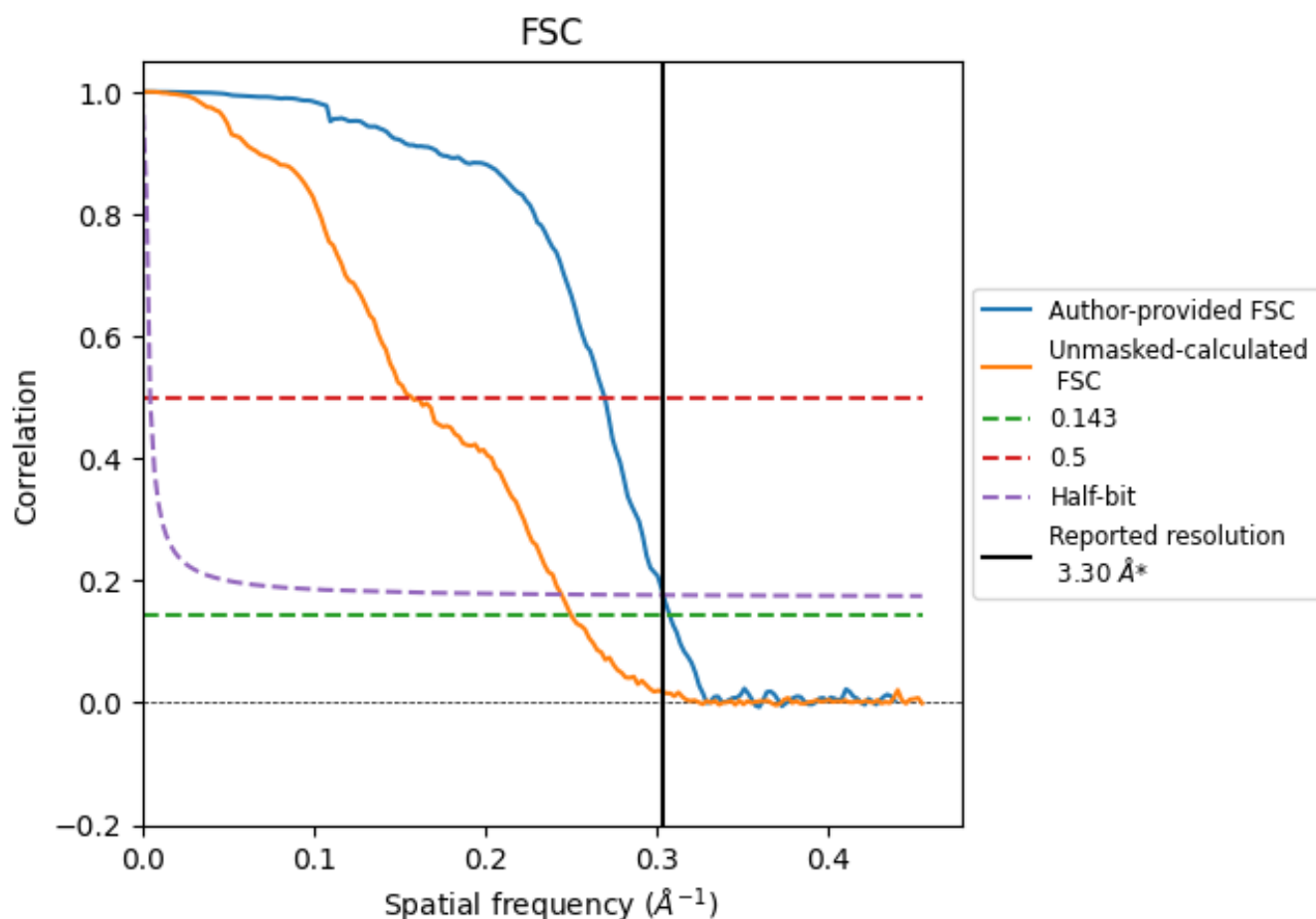


*Reported resolution corresponds to spatial frequency of 0.303 $\text{\AA}^{-1}$

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 0.303 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

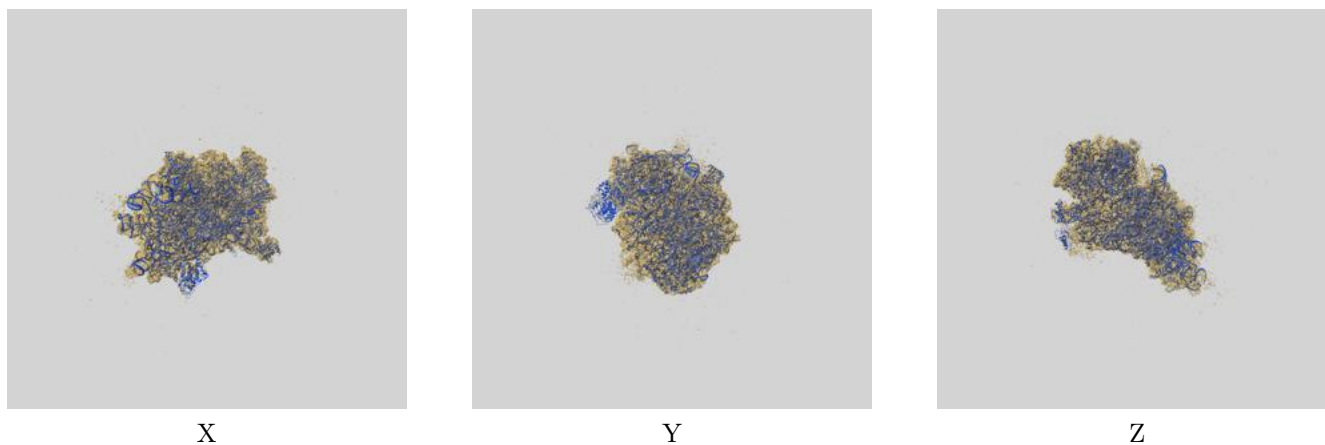
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.25	3.71	3.29
Unmasked-calculated*	4.00	6.37	4.09

*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 4.00 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

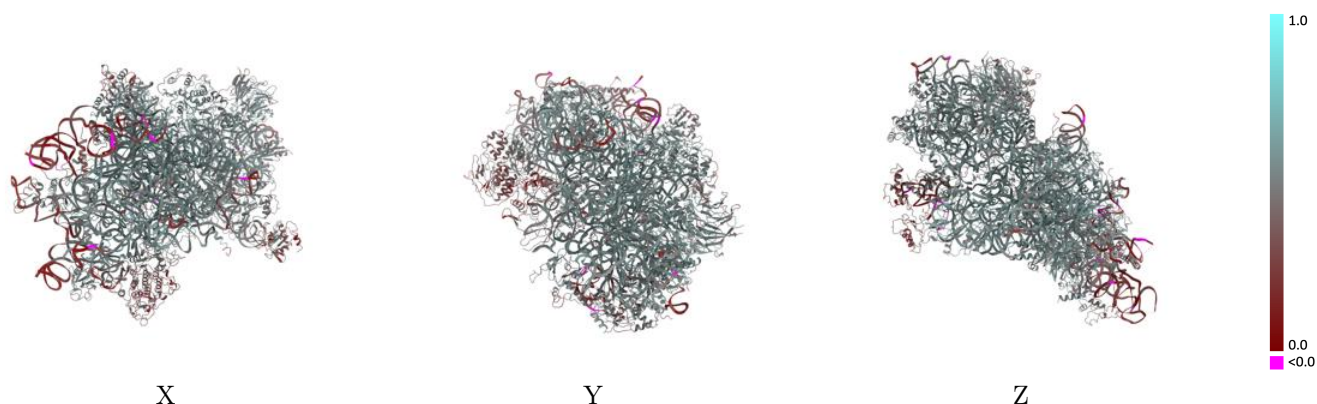
This section contains information regarding the fit between EMDB map EMD-17330 and PDB model 8P09. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.013 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](#)

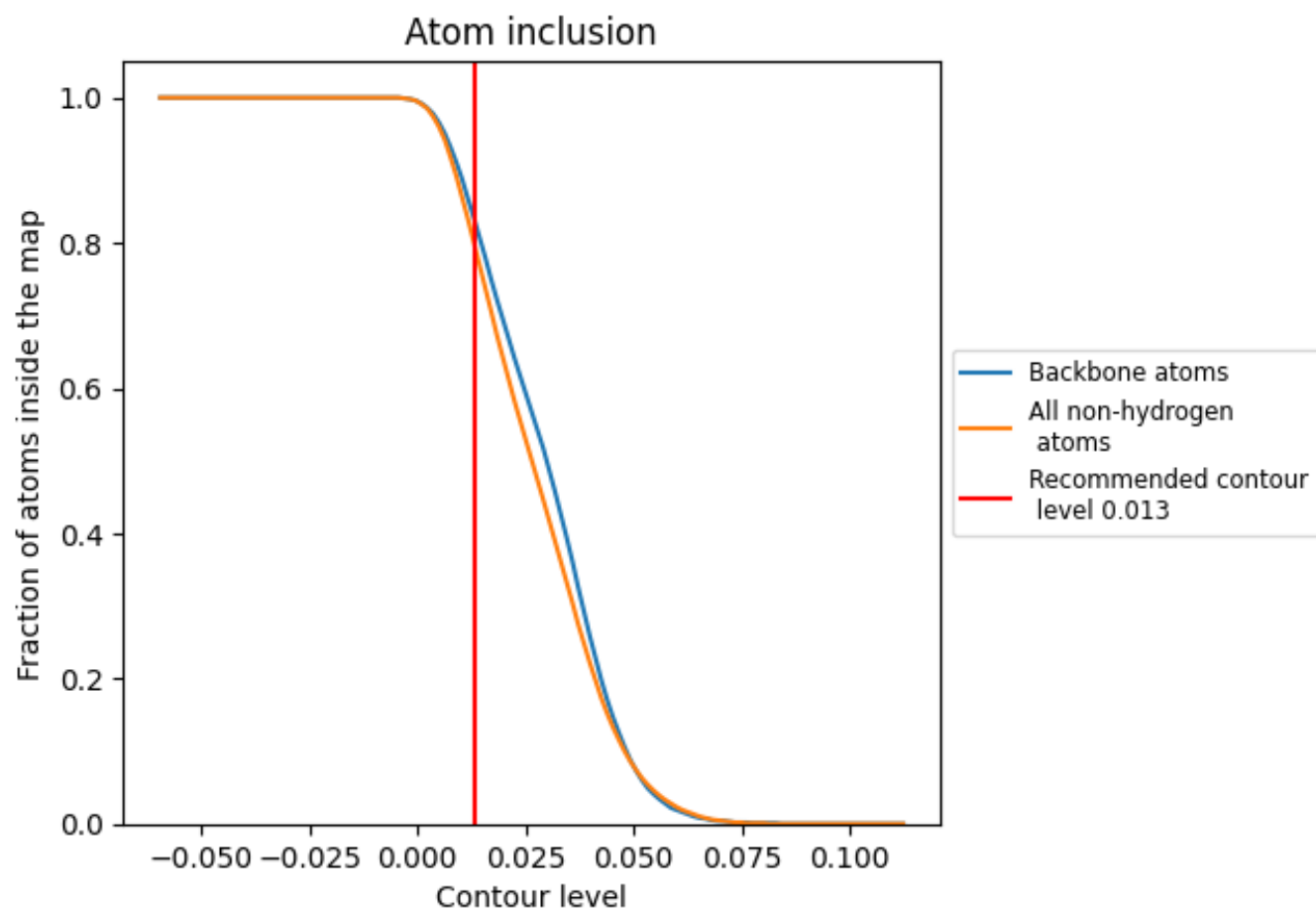


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 80% 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 (0.013) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8010	 0.4940
1	 0.5970	 0.2440
2	 0.9010	 0.5010
3	 0.6260	 0.4820
A	 0.2940	 0.3580
C	 0.8810	 0.5450
D	 0.8800	 0.5410
E	 0.8680	 0.5550
F	 0.8340	 0.5270
G	 0.8870	 0.5530
H	 0.8610	 0.5370
I	 0.7990	 0.4960
J	 0.5520	 0.4490
K	 0.8280	 0.5050
L	 0.8820	 0.5450
M	 0.8330	 0.4970
N	 0.7810	 0.5240
O	 0.5090	 0.3430
P	 0.8750	 0.5470
Q	 0.8610	 0.5390
R	 0.7510	 0.4870
S	 0.9010	 0.5570
T	 0.7390	 0.4960
U	 0.8110	 0.5090
V	 0.8670	 0.5310
W	 0.7790	 0.5130
X	 0.8790	 0.5490
Y	 0.9060	 0.5780
Z	 0.8810	 0.5610
a	 0.8670	 0.5140
b	 0.8960	 0.5640
c	 0.8130	 0.5130
d	 0.8090	 0.5440
e	 0.9080	 0.5580
f	 0.6630	 0.4080



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Chain	Atom inclusion	Q-score
g	 0.8490	 0.5080
i	 0.7340	 0.4940
j	 0.5250	 0.4800
k	 0.1650	 0.3790
l	 0.7900	 0.5400
n	 0.7500	 0.4900