



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 03:12 PM UTC

PDB ID : 7QP7 / pdb_00007qp7
EMDB ID : EMD-14114
Title : Structure of the human 48S initiation complex in closed state (h48S AUG closed)
Authors : Yi, S.-H.; Petrychenko, V.; Schliep, J.E.; Goyal, A.; Linden, A.; Chari, A.; Urlaub, H.; Stark, H.; Rodnina, M.V.; Adio, S.; Fischer, N.
Deposited on : 2022-01-03
Resolution : 3.70 Å (reported)
Based on initial model : 6ZMW

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:

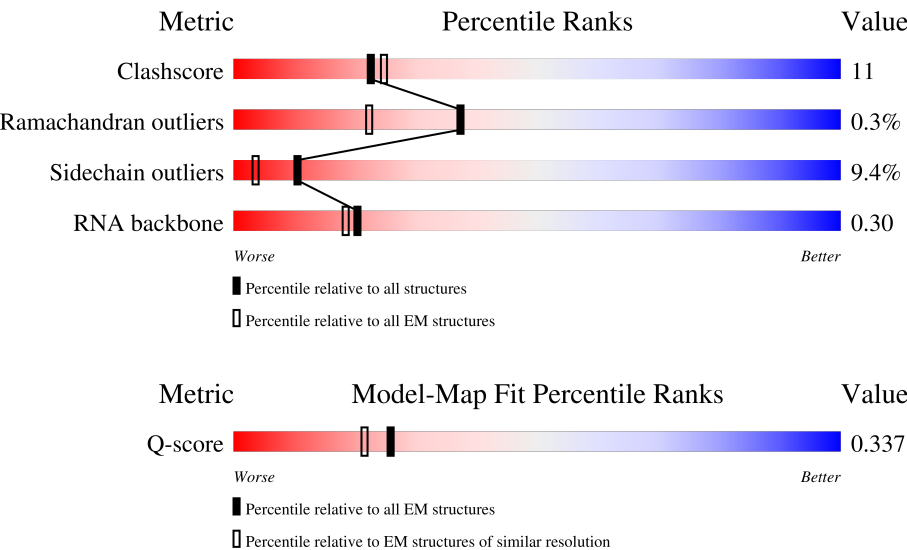
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

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



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

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

Mol	Chain	Length	Quality of chain
1	1	813	19% 47% 7% 45%
2	3	218	64% 89% 9% .
3	4	357	15% 64% 8% 28%

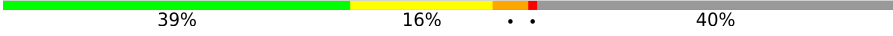
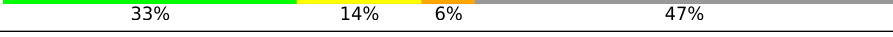
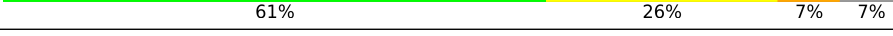
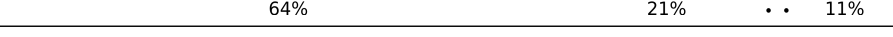
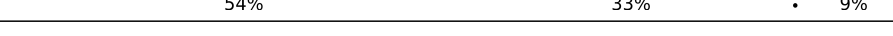
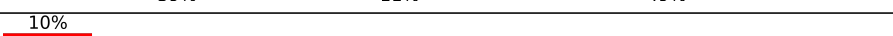
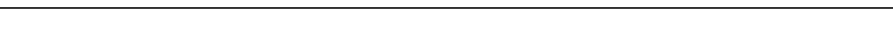
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Mol	Chain	Length	Quality of chain
4	5	564	
5	6	374	
6	7	255	
7	8	352	
8	9	25	
9	A	1869	
10	B	158	
11	C	263	
12	D	194	
13	E	143	
14	F	59	
15	G	194	
16	H	84	
17	I	151	
18	J	130	
19	K	83	
20	L	293	
21	M	135	
22	N	295	
23	O	264	
24	P	151	
25	Q	115	
26	R	208	
27	S	249	
28	T	133	

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Mol	Chain	Length	Quality of chain
29	V	204	
30	Y	146	
31	Z	243	
32	a	165	
33	b	145	
34	c	317	
35	d	145	
36	e	125	
37	f	152	
38	h	119	
39	i	56	
40	k	156	
41	m	132	
42	n	69	
43	o	320	
44	q	144	
45	r	315	
46	t	472	
47	u	1382	
48	v	445	
49	w	75	
50	x	548	
51	y	913	

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 108194 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Eukaryotic translation initiation factor 3 subunit B.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	447	Total	C	N	O	S	0	0
			2560	1570	492	493	5		

- Molecule 2 is a protein called Eukaryotic translation initiation factor 3 subunit K.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	3	213	Total	C	N	O	0	0
			1057	631	213	213		

- Molecule 3 is a protein called Eukaryotic translation initiation factor 3 subunit F.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	4	257	Total	C	N	O	0	0
			1272	757	257	258		

- Molecule 4 is a protein called Eukaryotic translation initiation factor 3 subunit L.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	5	319	Total	C	N	O	0	0
			1581	943	319	319		

- Molecule 5 is a protein called Eukaryotic translation initiation factor 3 subunit M.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	6	350	Total	C	N	O	S	0	0
			1917	1159	376	380	2		

- Molecule 6 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	7	21	Total	C	N	O	P	0	0
			441	199	78	144	20		

- Molecule 7 is a protein called Eukaryotic translation initiation factor 3 subunit H.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	8	317	Total	C	N	O	0	0
			1571	936	317	318		

- Molecule 8 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	9	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 9 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	1719	Total	C	N	O	P	0	0
			36668	16378	6574	11998	1718		

- Molecule 10 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	142	Total	C	N	O	S	0	0
			1166	743	218	199	6		

- Molecule 11 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	256	Total	C	N	O	S	0	0
			2035	1302	378	347	8		

- Molecule 12 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	177	Total	C	N	O	S	0	0
			1477	941	295	239	2		

- Molecule 13 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	140	Total	C	N	O	S	0	0
			1087	687	215	182	3		

- Molecule 14 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	47	Total	C	N	O	S	0	0
			378	231	85	61	1		

- Molecule 15 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	177	Total	C	N	O	S	0	0
			1430	917	260	252	1		

- Molecule 16 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H	81	Total	C	N	O	S	0	0
			631	397	116	111	7		

- Molecule 17 is a protein called 40S ribosomal protein S13.

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

- Molecule 18 is a protein called 40S ribosomal protein S15a.

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

- Molecule 19 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	81	Total	C	N	O	S	0	0
			617	380	114	118	5		

- Molecule 20 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	220	Total	C	N	O	S	0	0
			1707	1104	292	301	10		

- Molecule 21 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	125	Total	C	N	O	S	0	0
			1015	639	185	187	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	207	Total	C	N	O	S	0	0
			1633	1040	288	297	8		

- Molecule 23 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	211	Total	C	N	O	S	0	0
			1715	1088	307	306	14		

- Molecule 24 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	133	Total	C	N	O	S	0	0
			997	610	196	185	6		

- Molecule 25 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	99	Total	C	N	O	S	0	0
			792	492	165	130	5		

- Molecule 26 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	198	Total	C	N	O	S	0	0
			1627	1021	322	279	5		

- Molecule 27 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	S	230	Total	C	N	O	S	0	0
			1862	1164	371	320	7		

- Molecule 28 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	125	Total	C	N	O	S	0	0
			1015	642	199	169	5		

- Molecule 29 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	V	184	Total	C	N	O	S	0	0
			1461	914	276	264	7		

- Molecule 30 is a protein called 40S ribosomal protein S16.

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

- Molecule 31 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 32 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	99	Total	C	N	O	S	0	0
			834	544	149	135	6		

- Molecule 33 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	110	Total	C	N	O	S	0	0
			913	580	168	158	7		

- Molecule 34 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 35 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	142	Total	C	N	O	S	0	0
			1105	692	213	197	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	66	Total	C	N	O	S	0	0
			523	338	93	91	1		

- Molecule 37 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	142	Total	C	N	O	S	0	0
			1176	737	239	199	1		

- Molecule 38 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	103	Total	C	N	O	S	0	0
			817	511	155	147	4		

- Molecule 39 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	50	Total	C	N	O	S	0	0
			419	262	85	67	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	53	Total	C	N	O	S	0	0
			435	276	82	70	7		

- Molecule 41 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	122	Total	C	N	O	S	0	0
			950	596	168	177	9		

- Molecule 42 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	63	Total	C	N	O	S	0	0
			498	302	101	93	2		

- Molecule 43 is a protein called Eukaryotic translation initiation factor 3 subunit G.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	77	Total	C	N	O		0	0
			616	389	111	116			

- Molecule 44 is a protein called Eukaryotic translation initiation factor 1A, X-chromosomal.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	101	Total	C	N	O	S	0	0
			782	494	141	143	4		

- Molecule 45 is a protein called Eukaryotic translation initiation factor 2 subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	275	Total	C	N	O	S	0	0
			2215	1398	387	418	12		

- Molecule 46 is a protein called Eukaryotic translation initiation factor 2 subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	t	356	Total	C	N	O	0	0
			1750	1038	356	356		

- Molecule 47 is a protein called Eukaryotic translation initiation factor 3 subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	u	706	Total	C	N	O	S	1	0
			5383	3379	982	999	23		

- Molecule 48 is a protein called Eukaryotic translation initiation factor 3 subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	v	384	Total	C	N	O	S	0	0
			2635	1657	477	489	12		

- Molecule 49 is a RNA chain called Initiator Met-tRNA-i.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	w	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 50 is a protein called Eukaryotic translation initiation factor 3 subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	x	421	Total	C	N	O	S	0	0
			2831	1746	521	555	9		

- Molecule 51 is a protein called Eukaryotic translation initiation factor 3 subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	y	642	Total	C	N	O	S	0	0
			5197	3274	925	963	35		

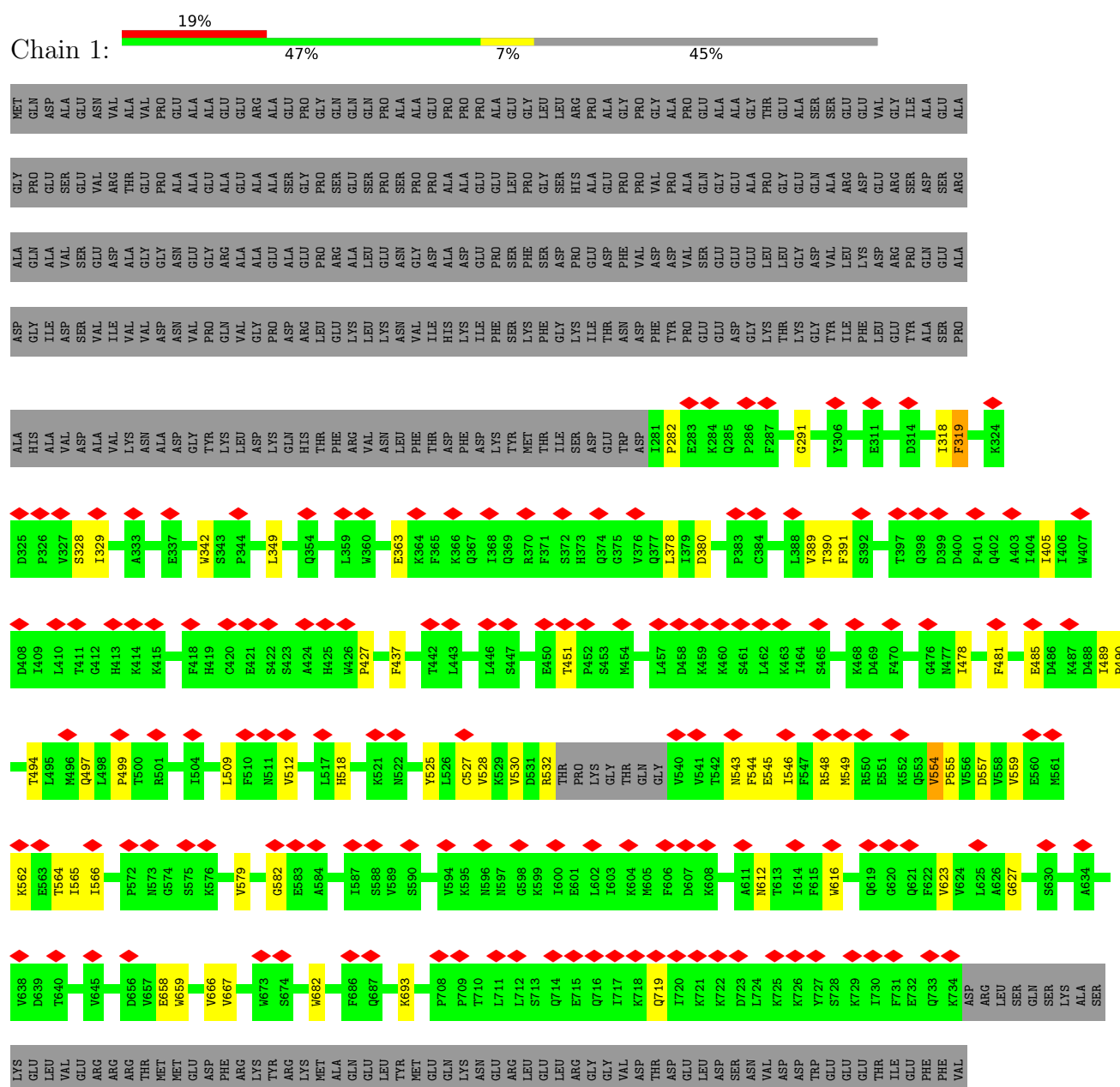
- Molecule 52 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
52	Q	1	Total	Zn	0
			1	1	
52	k	1	Total	Zn	0
			1	1	

3 Residue-property plots

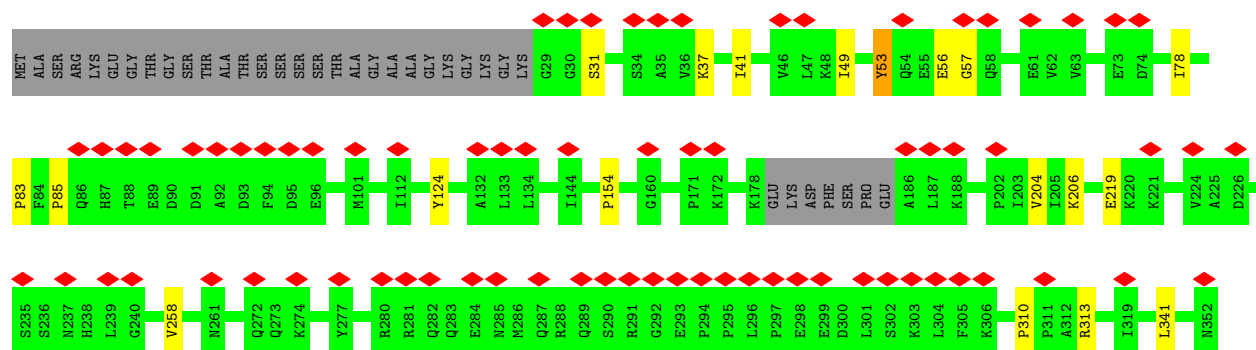
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Eukaryotic translation initiation factor 3 subunit B



[illegible]

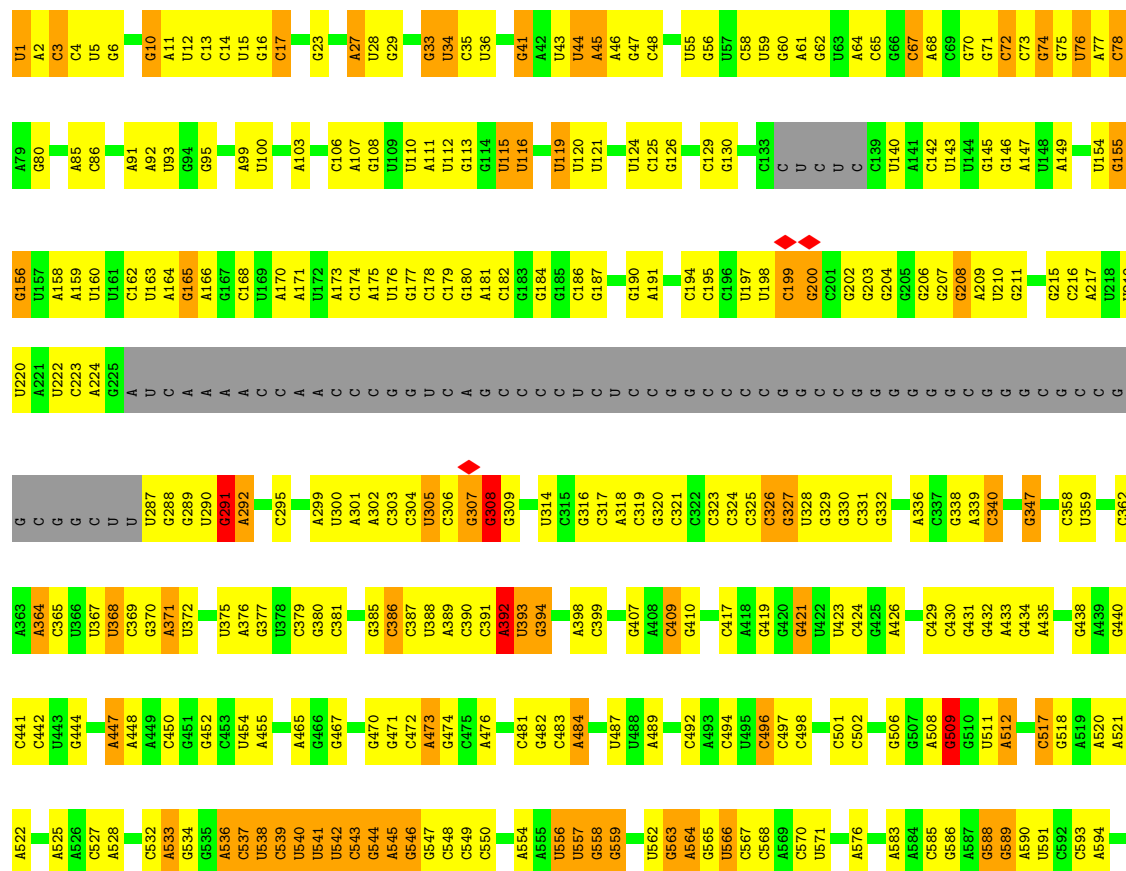
Chain 8:



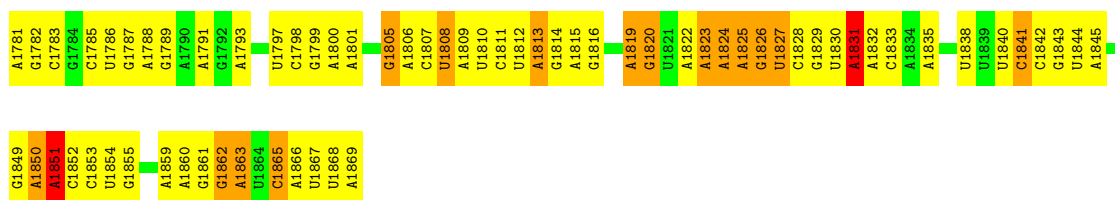
Chain 9: 68% 20% 8% .



Chain A: 39% 40% 12% 8%

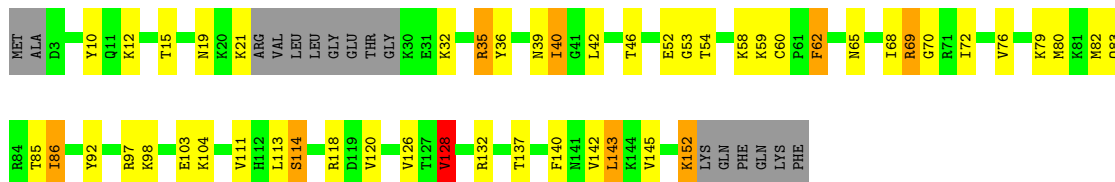


G1703	A1621	C1538	G1456	G1290	A1220	C1125	G1037	C950	U883	A811	C	G683	A599
G1704	U1622	U1539	U1457	G1294	G1221	C1132	G1043	G958	C884	U814	C746	G684	G600
A1712	A1623	G1541	G1458	A1295	A1378	A1133	G1044	G959	U885	U814	U747	G602	G601
G1713	U1624	G1542	U1459	U1296	A1295	A1223	U1045	G960	U886	A818	U749	G603	A604
G1714	U1625	C1543	U1463	U1297	G1224	G1134	U1046	G961	U887	G819	C750	U669	G604
A1715	C1627	C1544	A1464	A1301	G1225	C1135	C1047	A862	U888	U820	G751	G690	A605
A1719	G1628	G1550	G1465	G1302	G1226	C1138	G1048	A863	U889	G821	G752	G691	G606
U1720	C1629	U1551	G1466	G1303	A1227	C1139	A1049	A964	U890	U822	C753	U607	U607
U1721	G1636	C1470	U1471	U1304	G1228	G1140	U1049	U965	G891	A964	G	U608	C608
G1722	A1637	C1552	C1471	C1305	C1230	C1053	C1053	U966	U892	C824	C	A693	U609
G1638	G1638	C1553	U1392	U1306	C1231	A1144	G1054	G969	U893	A825	C	G694	G610
G1639	U1555	C1554	U1397	U1307	C1232	A1145	A1058	G970	G894	A826	C	G695	G611
U1728	G1475	A1474	U1397	U1308	G1233	A1149	A1059	G971	U895	A827	C	G696	U612
U1729	A1476	A1476	U1397	C1309	C1234	A1150	G1060	C972	U897	G828	C	G697	G613
U1733	U1643	C1557	A1402	C1310	C1234	A1150	U1061	C973	U898	C829	C	G	C614
G1737	C1644	A1483	A1405	C1311	C1237	G1153	U1062	A981	U899	A830	C	G	C615
G1646	G1645	U1484	U1406	G1312	U1238	U1154	C1063	G981	C900	C833	C	G	A616
A1647	U1485	U1485	U1407	A1313	U1239	U1154	C1063	G982	A903	C834	A	G	G617
A1647	A1486	U1486	U1408	U1314	A1240	U1155	C1064	A983	A904	C835	U	C	C624
A1650	U1487	U1487	U1409	U1315	A1241	U1156	G1071	G985	A905	C836	G	G	G625
U1741	C1488	C1488	C1410	C1316	U1242	G1157	U1072	G986	C905	A837	C	G	G626
C1742	A1489	C1317	C1411	C1317	U1243	G1158	U1073	A987	U906	G838	C	C	U627
G1743	G1490	G1318	G1411	G1318	U1244	U1158	C1074	C988	A908	C839	C	C	A628
G1744	G1497	G1322	A1414	G1322	U1245	C1163	C1074	C989	G909	C840	U	G	A629
A1745	G1497	G1323	C1415	G1323	A1246	G1164	C1075	C990	G910	C841	U	G	U630
U1746	U1498	U1324	C1416	G1324	C1249	G1166	U1081	A990	G911	C842	A	C	U631
C1747	U1499	G1325	C1417	G1325	U1250	U1167	A1082	A991	C912	C843	C	C	C632
U1663	G1500	G1326	C1418	G1326	A1251	A1170	A1083	A992	C913	G845	C	G	C633
C1750	C1501	U1326	C1419	U1326	A1252	A1171	A1084	A993	U914	G846	U	G	A634
G1665	C1502	A1332	G1420	A1332	G1253	U1174	C1085	A994	G915	A847	A	A	G635
C1666	U1507	U1333	A1421	U1333	C1254	G1175	C1085	A995	A916	U848	G	G	C636
U1667	G1507	G1334	G1422	G1334	G1255	U1176	G1089	A996	U917	U849	U	G	C638
U1668	U1508	U1335	C1423	G1335	G1256	A1181	G1092	A997	U918	C851	U	C	C639
G1671	U1509	C1336	G1424	C1336	G1257	A1182	A1093	A998	A919	G852	U	G	A640
U1672	G1510	C1337	U1425	C1337	U1258	A1183	A1093	U1002	A920	U857	C	A	A641
U1673	U1511	G1338	G1425	G1338	A1259	A1184	A1093	U1003	G921	U858	C	G	U642
G1674	C1512	U1339	G1433	U1339	C1260	A1185	G1096	U1004	A922	A859	C	C	A643
A1675	C1513	U1340	C1434	U1340	C1261	A1189	G1097	A1008	G923	A860	C	C	G644
U	G1514	C1341	C1435	C1341	U1262	A1190	G1097	A1009	G924	A861	C	A	U652
C	U1515	U1342	C1436	U1342	C1263	C1191	U1101	U1013	G925	A862	C	C	A653
C	G1520	U1343	C1437	U1343	C1264	U1192	G1102	G1014	A926	U866	G	G	A654
C	C1521	G1348	A1438	G1348	G1265	A1193	G1105	U1015	G927	G867	C	C	A655
C	C1522	G1349	U1441	U1350	C1266	U1194	G1109	U1016	G928	G868	C	C	G656
C	G1524	U1351	U1442	U1351	C1267	A1195	C1109	U1017	G929	A869	C	C	C
A	U1524	G1352	U1443	G1352	C1268	A1199	G1112	A1020	C931	A870	G	G	C660
U1690	G1524	C1353	U1444	C1353	G1269	A1200	U1112	U1021	G932	U871	U	U	U666
U1691	C1527	U1354	U1445	U1354	C1270	G1203	U1113	U1022	G933	A872	C	C	U667
U1692	G1528	G1355	U1446	G1355	C1271	A1204	U1114	A1023	G934	G873	C	C	A668
G1693	U1529	U1356	U1447	U1356	C1272	G1204	U1115	U1024	G935	A874	C	C	A669
U1694	C1530	A1357	U1448	A1357	C1273	A1205	C1116	A1025	U940	A875	U	U	A670
C1695	U1530	U1362	U1449	U1362	C1274	G1206	C1117	A1026	U941	C876	C	C	A671
C1696	G1531	C1363	U1450	C1363	C1275	A1207	C1118	A1027	G942	G877	U	U	A672
U1697	A1531	U1364	U1451	U1364	C1276	A1208	C1119	A1028	U943	G878	C	C	G673
C1698	G1532	U1365	U1452	U1365	C1277	A1209	A1119	A1029	A944	C879	U	U	U674
A1699	C1533	U1366	U1453	U1366	C1278	G1210	C1120	A1030	G945	G880	C	C	C675
C1700	U1534	U1367	U1454	U1367	C1279	G1211	C1121	C1032	G946	U881	U	U	U676
G1778	C1535	U1368	U1455	U1368	C1280	G1212	C1122	A1033	G947	U882	C	C	C
C1779	U1536	U1369	U1456	U1369	C1281	G1213	C1123	A1034	G948	A810	C	C	C
G1780	A1537	U1370	U1457	U1370	C1282	G1214	C1124	G949	G949	A810	C	C	C



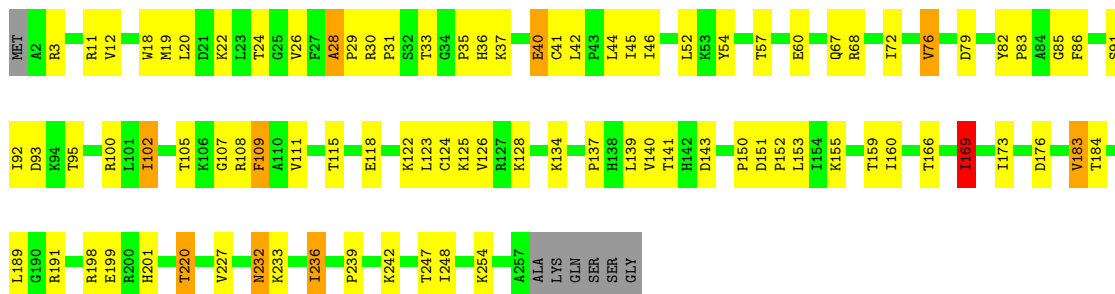
• Molecule 10: 40S ribosomal protein S11

Chain B: 58% 26% 5% 10%



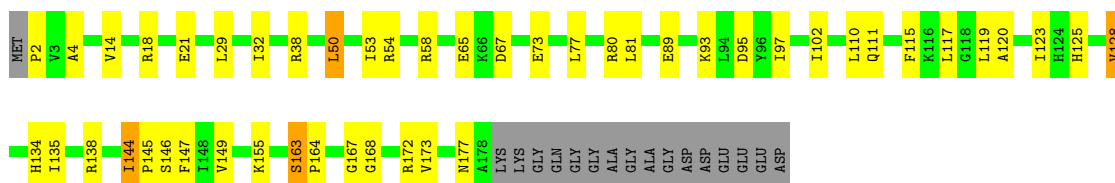
• Molecule 11: 40S ribosomal protein S4, X isoform

Chain C: 63% 30% 7%



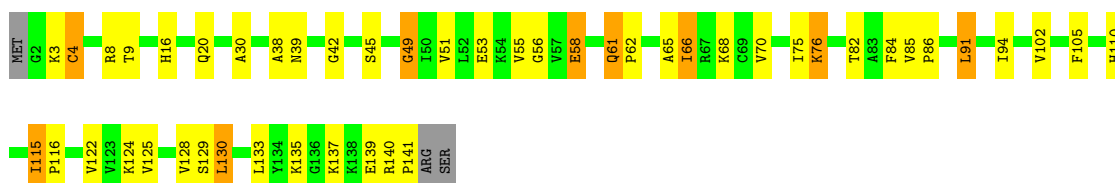
• Molecule 12: 40S ribosomal protein S9

Chain D: 66% 23% 9%



• Molecule 13: 40S ribosomal protein S23

Chain E: 64% 27% 6%



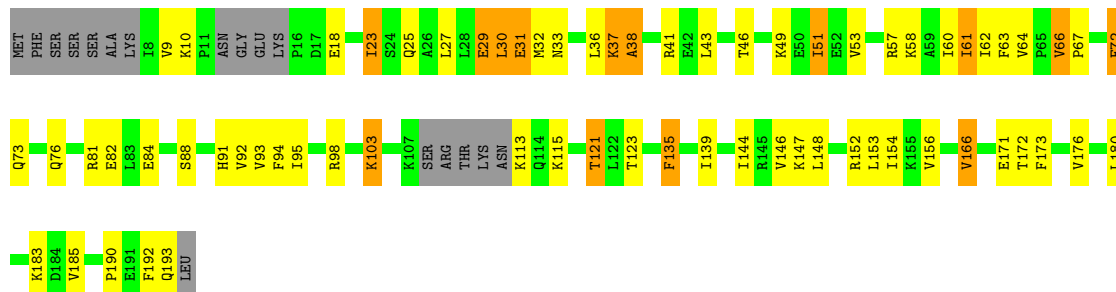
- Molecule 14: 40S ribosomal protein S30

Chain F: 



- Molecule 15: 40S ribosomal protein S7

Chain G: 



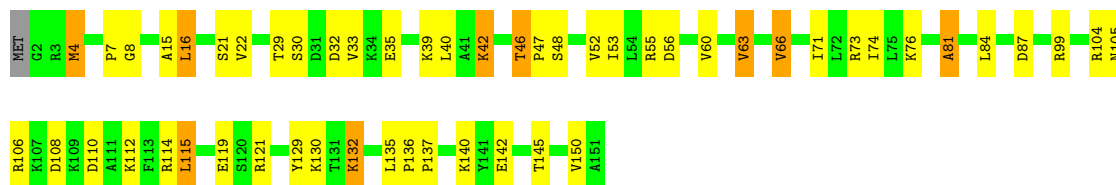
- Molecule 16: 40S ribosomal protein S27

Chain H: 



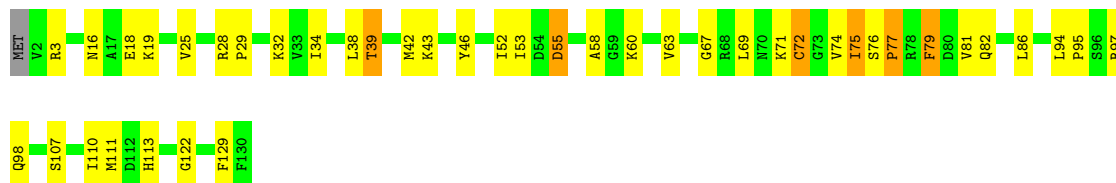
- Molecule 17: 40S ribosomal protein S13

Chain I: 



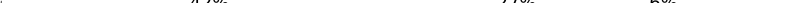
- Molecule 18: 40S ribosomal protein S15a

Chain J: 



- Molecule 19: 40S ribosomal protein S21

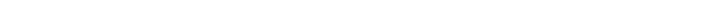
M1	Q2	N3	D4	V9	V13	P14	R15	A19	R22	T23	T24	D28	I29	A30	S31	T32	Q33	N34	V39	V42	T43	G44	R45	F50	K51	T52	M62	G63	E64	D67	S68	V79	S80	K81	ASN	PHF
----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Chain L: 

[illegible]

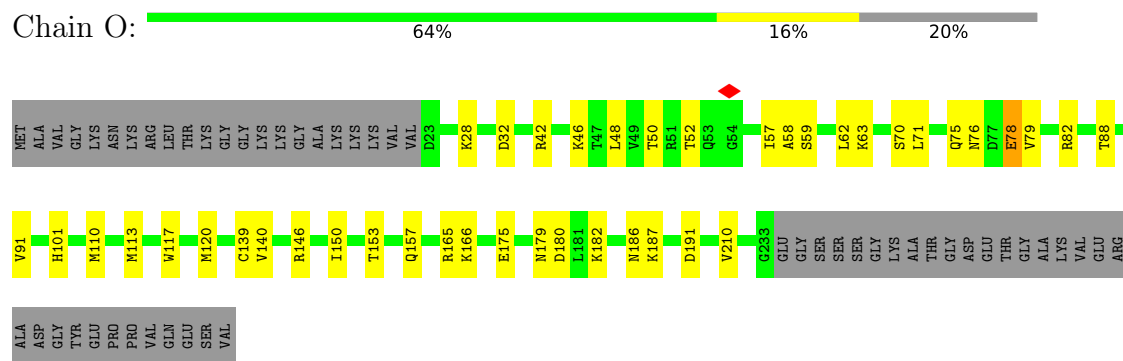
- Chain M: 59% 28% 7%

MET
GLY
ARG
VAL
ARG
THR
LYS
T8
V9
E18
K19
R23
K32
R33
V34
C35
I38
I41
R47
N48
L57
N58
I61
G64
P65
V66
I69
S70
I71
K72
L73
Q74
E77
P86
S87
V88
S89
A90
L91
D92
Q93
E94
I95
D99
P100
D101
T102
L106
K107
L108
L109
D110
F111
S115
N116
T120
M127
F128
K132
GLY
PRO
VAL

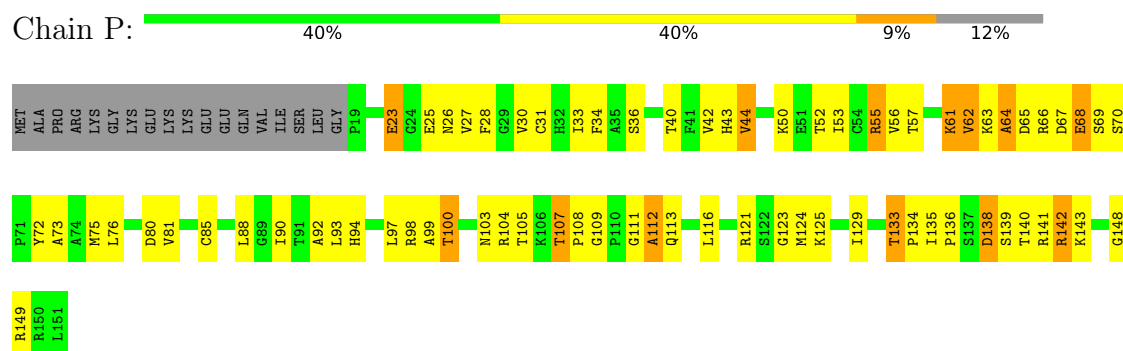
- Chain N:  38% 25% 6% 30%

[illegible]

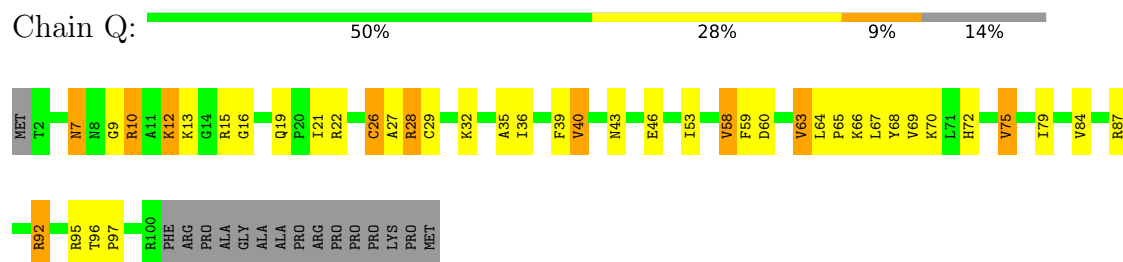
- 
- WORLDWIDE
PDB
PROTEIN DATA BANK



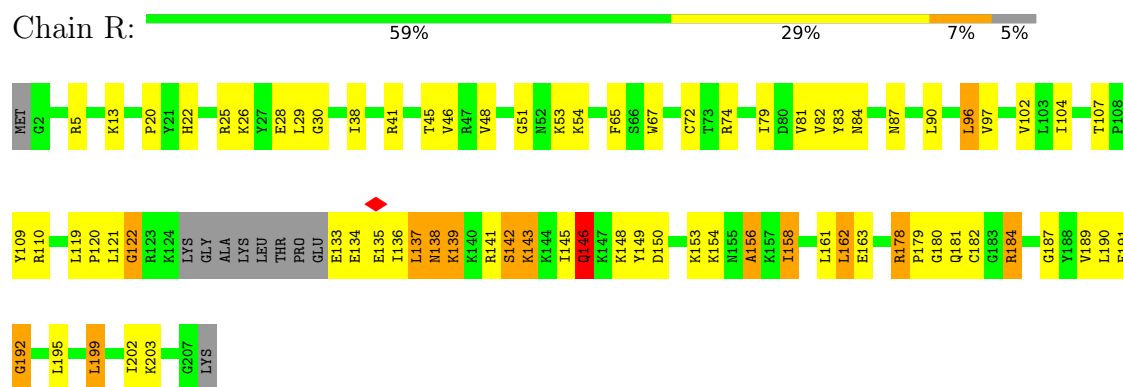
• Molecule 24: 40S ribosomal protein S14



• Molecule 25: 40S ribosomal protein S26

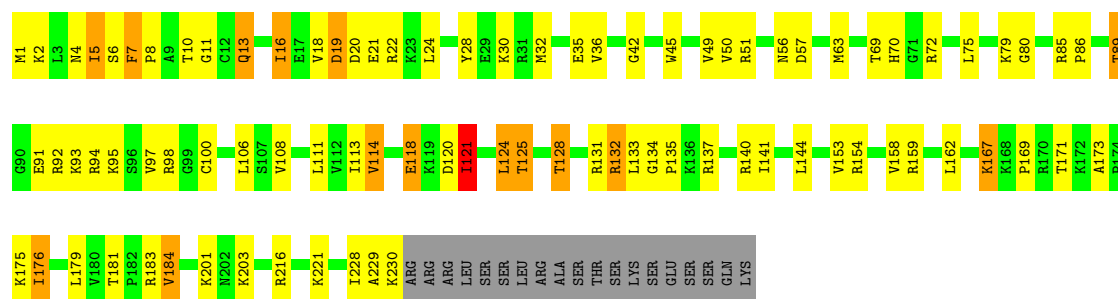


• Molecule 26: 40S ribosomal protein S8



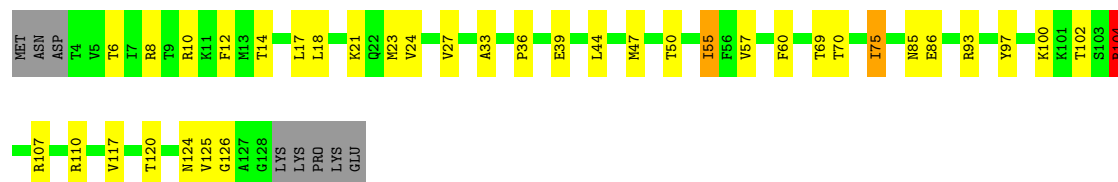
• Molecule 27: 40S ribosomal protein S6

Chain S: 



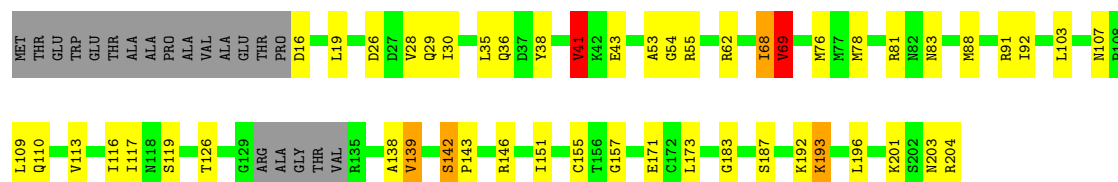
• Molecule 28: 40S ribosomal protein S24

Chain T: 



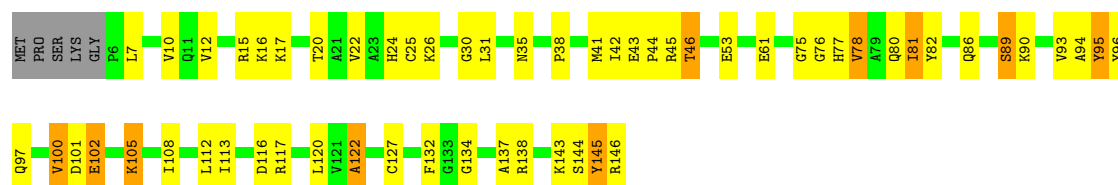
• Molecule 29: 40S ribosomal protein S5

Chain V: 



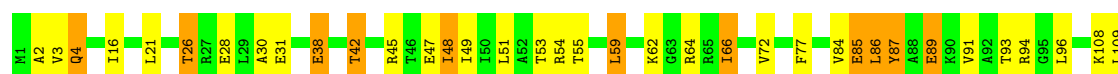
• Molecule 30: 40S ribosomal protein S16

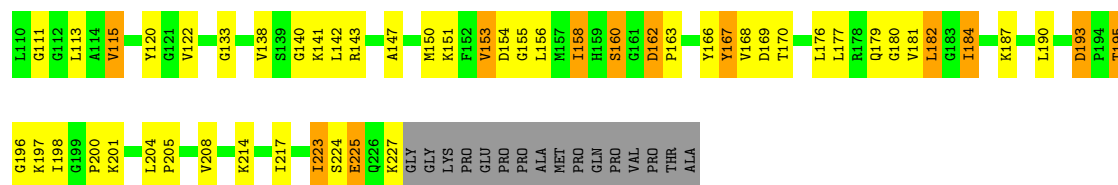
Chain Y: 



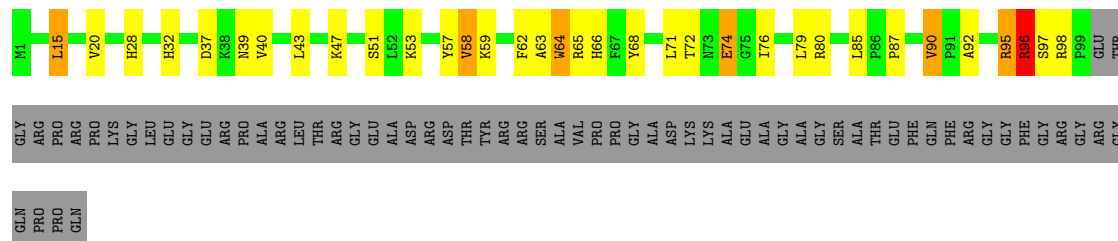
• Molecule 31: 40S ribosomal protein S3

Chain Z: 

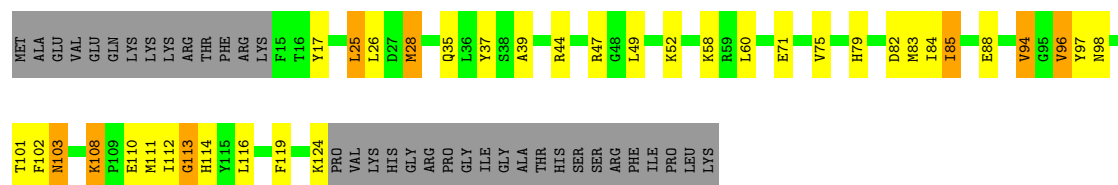




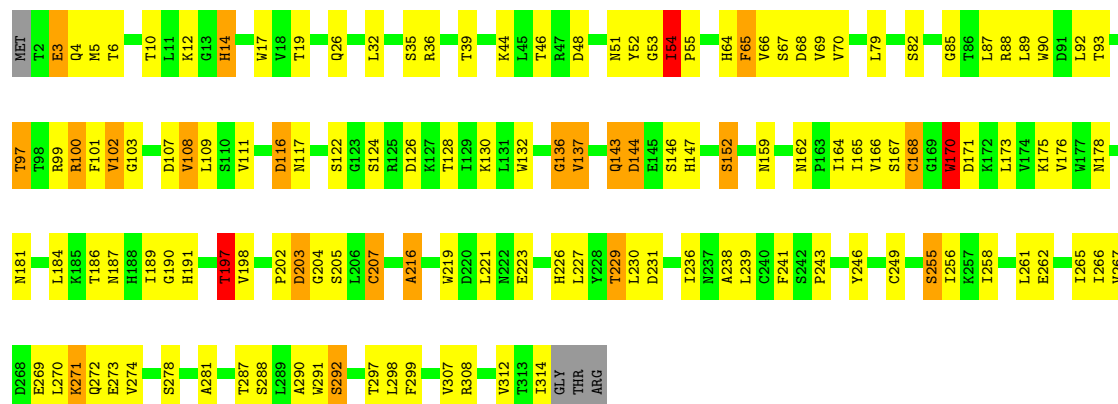
• Molecule 32: 40S ribosomal protein S10



• Molecule 33: 40S ribosomal protein S15

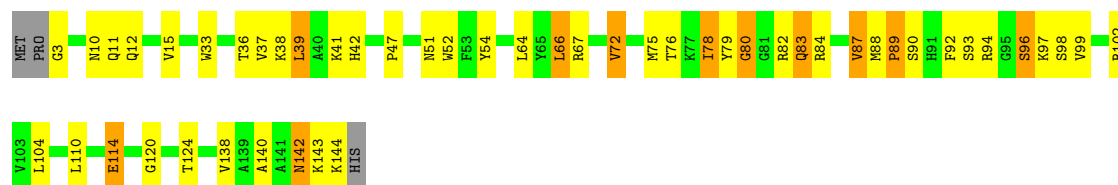


• Molecule 34: Receptor of activated protein C kinase 1

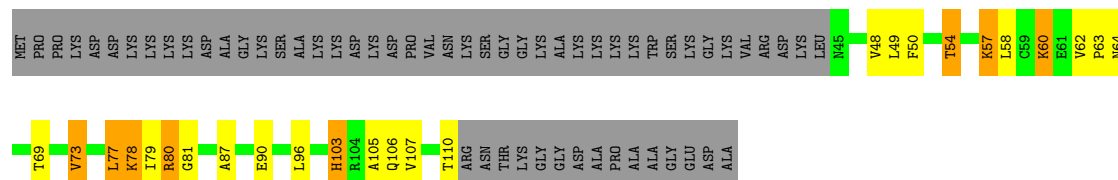
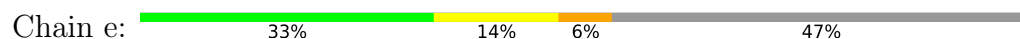


• Molecule 35: 40S ribosomal protein S19

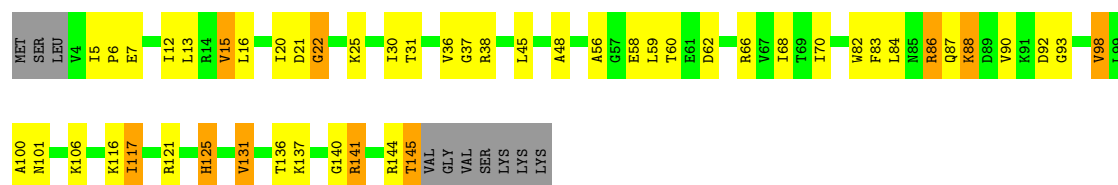




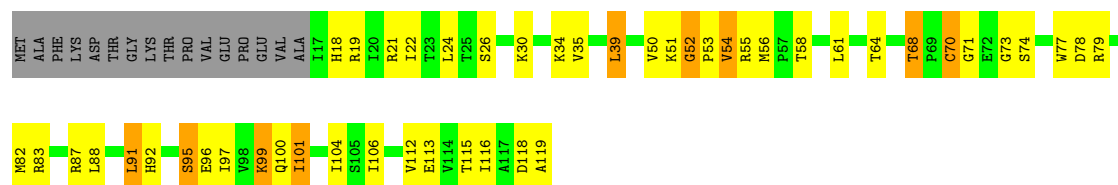
- Molecule 36: 40S ribosomal protein S25



- Molecule 37: 40S ribosomal protein S18



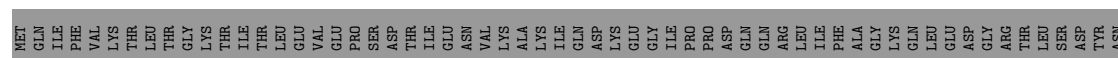
- Molecule 38: 40S ribosomal protein S20

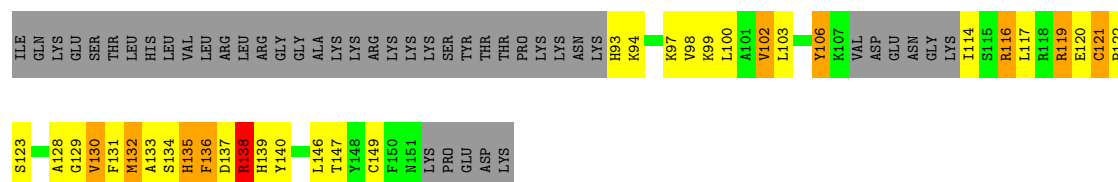


- Molecule 39: 40S ribosomal protein S29

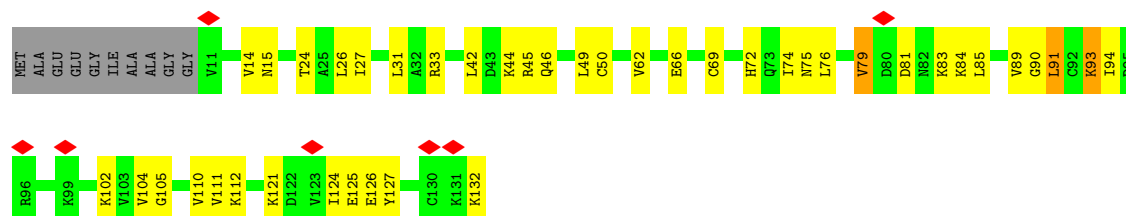


- Molecule 40: Ubiquitin-40S ribosomal protein S27a

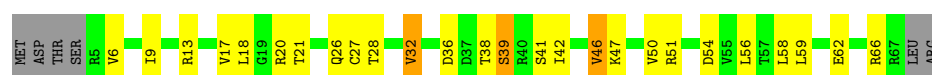




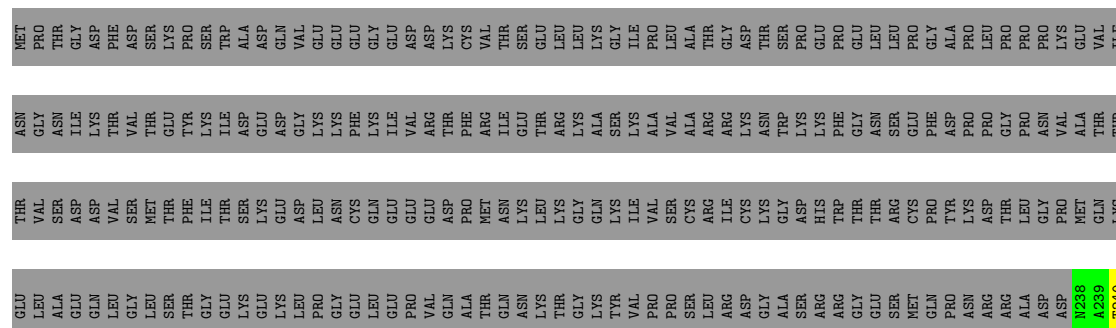
• Molecule 41: 40S ribosomal protein S12



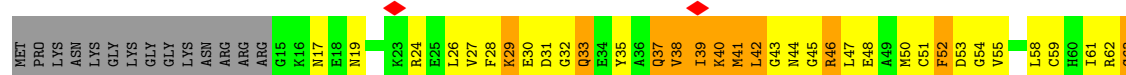
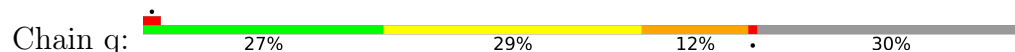
• Molecule 42: 40S ribosomal protein S28



• Molecule 43: Eukaryotic translation initiation factor 3 subunit G

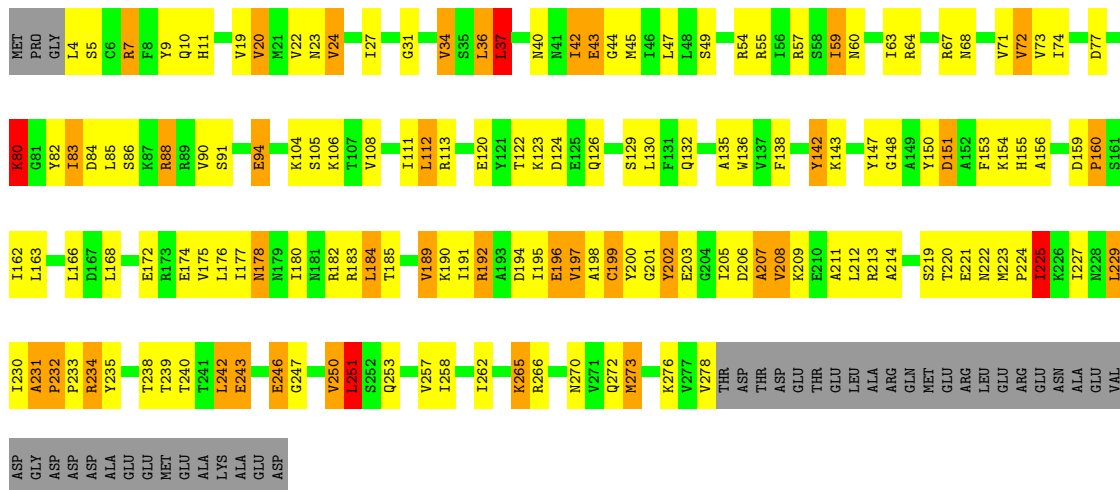


• Molecule 44: Eukaryotic translation initiation factor 1A, X-chromosomal



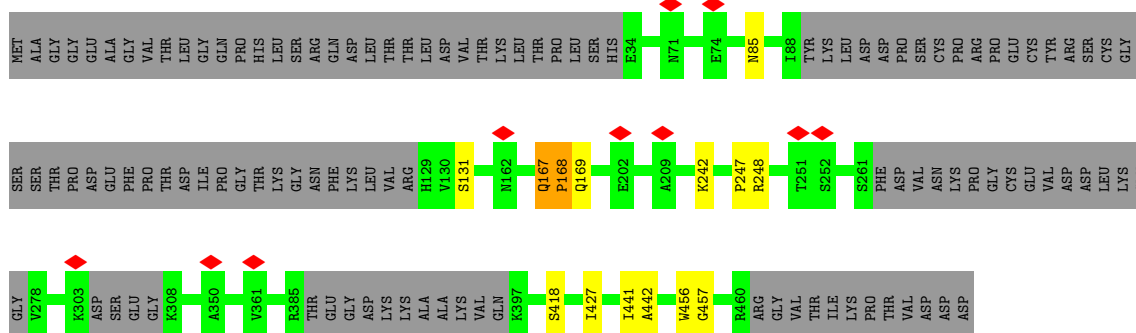
- Molecule 45: Eukaryotic translation initiation factor 2 subunit 1

Chain r:

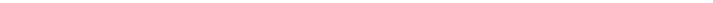


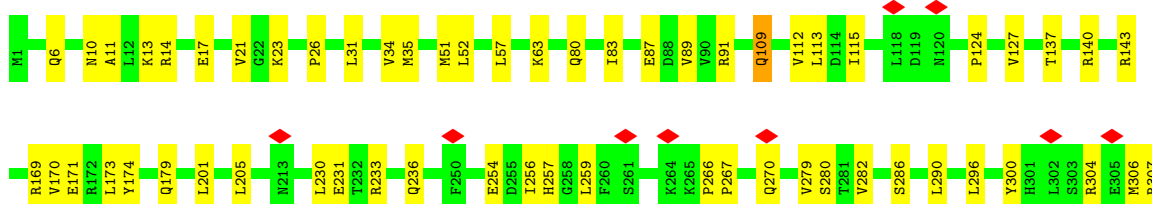
- Molecule 46: Eukaryotic translation initiation factor 2 subunit 3

Chain t: 72% . 25%

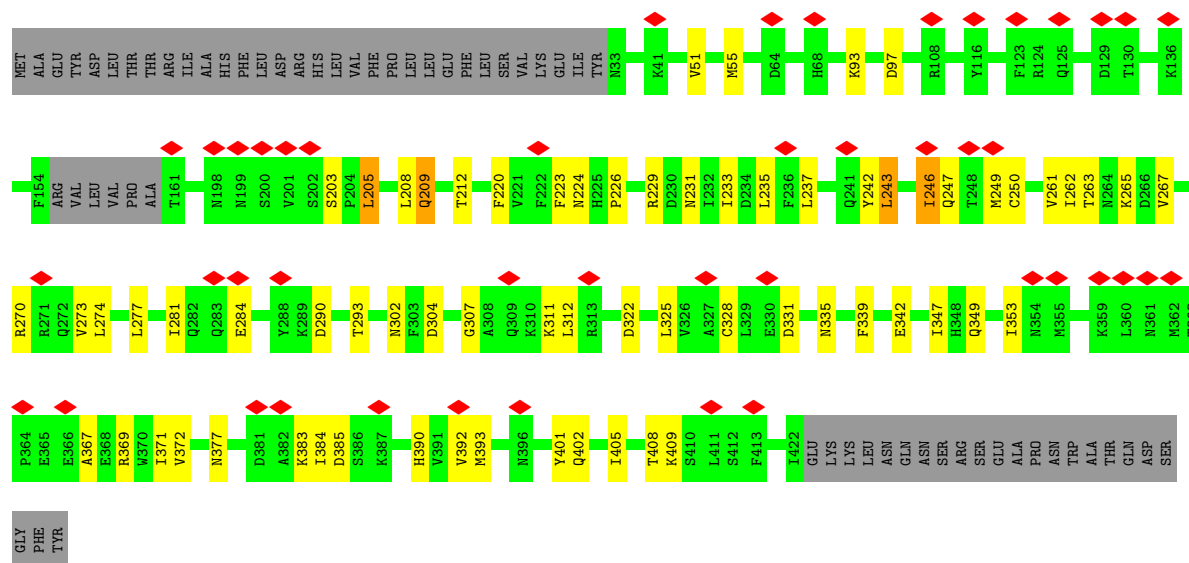


- Molecule 47: Eukaryotic translation initiation factor 3 subunit A

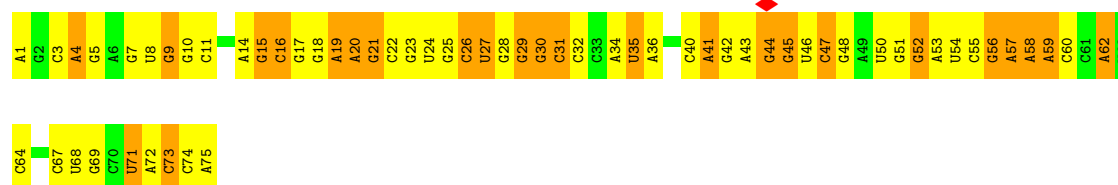
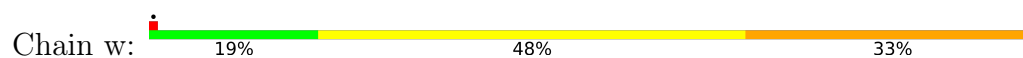
Chain u: 



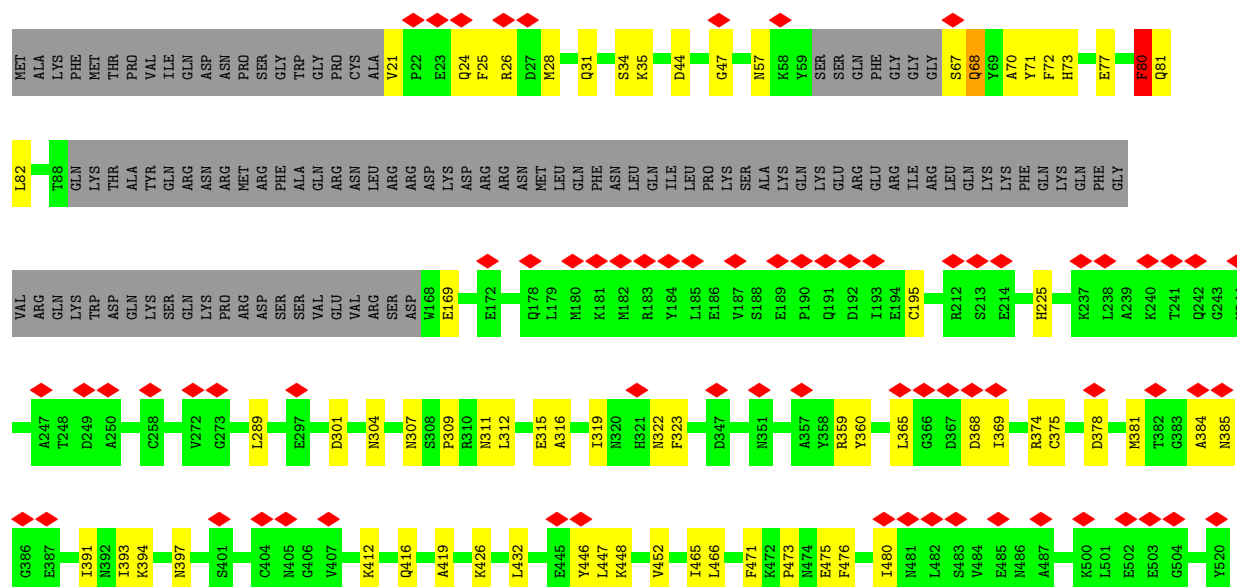
- Molecule 48: Eukaryotic translation initiation factor 3 subunit E



• Molecule 49: Initiator Met-tRNA-i

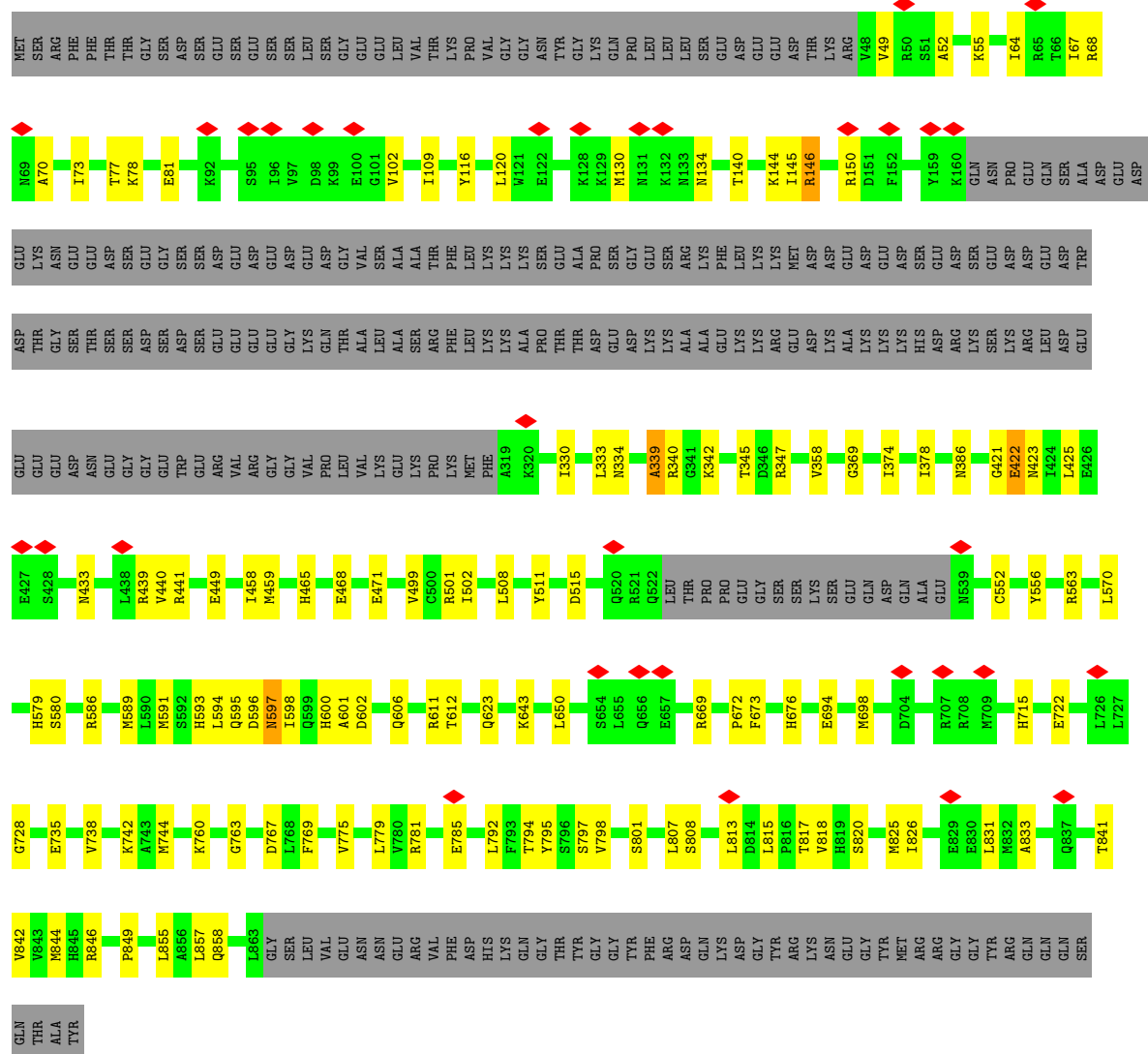


• Molecule 50: Eukaryotic translation initiation factor 3 subunit D





• Molecule 51: Eukaryotic translation initiation factor 3 subunit C



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	364950	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	24.271	Depositor
Minimum map value	-11.101	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.15	Depositor
Map size (Å)	417.59998, 417.59998, 417.59998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MA6, 5MC, OMU, 5MU, A2M, UR3, OMC, PSU, OMC

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	0.61	0/2581	1.01	7/3561 (0.2%)
2	3	0.55	0/1055	0.98	1/1469 (0.1%)
3	4	0.70	0/1269	1.03	3/1762 (0.2%)
4	5	0.54	0/1575	0.93	3/2187 (0.1%)
5	6	0.62	0/1926	1.04	9/2669 (0.3%)
6	7	0.68	2/492 (0.4%)	0.96	1/764 (0.1%)
7	8	0.67	0/1569	1.08	6/2183 (0.3%)
8	9	1.60	1/231 (0.4%)	1.19	2/294 (0.7%)
9	A	0.44	0/40362	0.72	39/62905 (0.1%)
10	B	1.34	3/1186 (0.3%)	1.37	16/1585 (1.0%)
11	C	1.33	3/2077 (0.1%)	1.25	23/2796 (0.8%)
12	D	1.39	6/1502 (0.4%)	1.28	20/2008 (1.0%)
13	E	1.56	4/1105 (0.4%)	1.50	21/1476 (1.4%)
14	F	1.35	0/380	1.42	6/496 (1.2%)
15	G	1.23	1/1451 (0.1%)	1.37	22/1942 (1.1%)
16	H	1.30	2/644 (0.3%)	1.30	9/864 (1.0%)
17	I	1.38	2/1232 (0.2%)	1.36	25/1656 (1.5%)
18	J	1.67	3/1051 (0.3%)	1.56	23/1406 (1.6%)
19	K	1.48	0/623	1.45	14/833 (1.7%)
20	L	1.62	8/1743 (0.5%)	1.37	20/2354 (0.8%)
21	M	1.33	2/1029 (0.2%)	1.30	8/1383 (0.6%)
22	N	1.53	7/1670 (0.4%)	1.51	36/2271 (1.6%)
23	O	0.39	0/1742	0.70	0/2330
24	P	1.59	8/1010 (0.8%)	1.65	24/1353 (1.8%)
25	Q	1.43	4/805 (0.5%)	1.51	13/1079 (1.2%)
26	R	1.12	2/1654 (0.1%)	1.26	23/2203 (1.0%)
27	S	1.01	0/1885	1.28	19/2510 (0.8%)
28	T	1.30	2/1032 (0.2%)	1.21	6/1371 (0.4%)
29	V	1.54	3/1481 (0.2%)	1.36	20/1988 (1.0%)
30	Y	1.46	3/1142 (0.3%)	1.40	15/1528 (1.0%)
31	Z	1.43	1/1793 (0.1%)	1.44	25/2414 (1.0%)
32	a	1.27	2/859 (0.2%)	1.29	11/1159 (0.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	b	1.17	2/929 (0.2%)	1.29	12/1241 (1.0%)
34	c	1.15	4/2493 (0.2%)	1.36	30/3394 (0.9%)
35	d	1.42	2/1123 (0.2%)	1.29	10/1504 (0.7%)
36	e	1.29	0/529	1.44	9/712 (1.3%)
37	f	1.29	1/1194 (0.1%)	1.39	20/1599 (1.3%)
38	h	1.40	2/827 (0.2%)	1.43	10/1110 (0.9%)
39	i	1.40	1/429 (0.2%)	1.35	5/568 (0.9%)
40	k	0.92	0/444	1.48	11/588 (1.9%)
41	m	0.53	0/960	0.92	1/1286 (0.1%)
42	n	1.36	0/500	1.39	5/669 (0.7%)
43	o	0.56	0/628	0.89	0/846
44	q	1.02	2/792 (0.3%)	1.63	24/1062 (2.3%)
45	r	0.94	0/2247	1.35	31/3029 (1.0%)
46	t	0.58	0/1745	0.98	2/2417 (0.1%)
47	u	0.55	0/5475	0.89	8/7432 (0.1%)
48	v	0.59	0/2672	0.94	2/3647 (0.1%)
49	w	0.40	0/1795	0.71	1/2798 (0.0%)
50	x	0.56	0/2874	0.90	4/3925 (0.1%)
51	y	0.51	0/5284	0.84	8/7123 (0.1%)
All	All	0.88	83/113096 (0.1%)	1.03	663/161749 (0.4%)

The worst 5 of 83 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	9	2	ARG	CA-C	-6.93	1.44	1.52
20	L	172	ASN	CA-C	-6.45	1.44	1.52
20	L	170	TRP	CA-C	-6.23	1.45	1.52
34	c	168	CYS	CA-C	-6.23	1.45	1.52
20	L	229	CYS	CA-C	-6.22	1.45	1.52

The worst 5 of 663 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	N	7	VAL	N-CA-C	-19.27	77.15	108.95
10	B	53	GLY	N-CA-C	18.38	136.07	112.54
37	f	100	ALA	N-CA-C	15.19	127.32	111.07
44	q	45	GLY	N-CA-C	-14.93	94.82	112.73
44	q	42	LEU	N-CA-C	-14.18	86.14	109.24

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	2560	0	1609	29	0
2	3	1057	0	475	9	0
3	4	1272	0	564	26	0
4	5	1581	0	689	8	0
5	6	1917	0	1096	56	0
6	7	441	0	228	14	0
7	8	1571	0	683	12	0
8	9	230	0	276	5	0
9	A	36668	0	18551	747	0
10	B	1166	0	1233	60	0
11	C	2035	0	2138	34	0
12	D	1477	0	1589	15	0
13	E	1087	0	1154	16	0
14	F	378	0	417	4	0
15	G	1430	0	1520	27	0
16	H	631	0	657	13	0
17	I	1208	0	1294	21	0
18	J	1034	0	1080	20	0
19	K	617	0	622	9	0
20	L	1707	0	1794	46	0
21	M	1015	0	1060	26	0
22	N	1633	0	1640	50	0
23	O	1715	0	1785	32	0
24	P	997	0	1021	37	0
25	Q	792	0	841	33	0
26	R	1627	0	1706	39	0
27	S	1862	0	2018	81	0
28	T	1015	0	1086	21	0
29	V	1461	0	1511	26	0
30	Y	1124	0	1193	37	0
31	Z	1765	0	1865	65	0
32	a	834	0	861	21	0
33	b	913	0	952	17	0
34	c	2436	0	2393	61	0
35	d	1105	0	1138	37	0
36	e	523	0	573	12	0
37	f	1176	0	1233	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	h	817	0	882	29	0
39	i	419	0	415	13	0
40	k	435	0	434	22	0
41	m	950	0	987	28	0
42	n	498	0	525	12	0
43	o	616	0	600	29	0
44	q	782	0	773	43	0
45	r	2215	0	2266	120	0
46	t	1750	0	806	5	0
47	u	5383	0	5085	140	0
48	v	2635	0	2207	58	0
49	w	1604	0	816	48	0
50	x	2831	0	2199	45	0
51	y	5197	0	5201	91	0
52	Q	1	0	0	0	0
52	k	1	0	0	0	0
All	All	108194	0	83741	2158	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 11.

The worst 5 of 2158 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)
10:B:86:ILE:HD11	10:B:113:LEU:CB	1.58	1.32
6:7:23:A:C2	31:Z:108:LYS:NZ	1.98	1.30
10:B:86:ILE:CD1	10:B:113:LEU:HB2	1.61	1.29
10:B:86:ILE:CD1	10:B:113:LEU:HD13	1.63	1.27
10:B:80:MET:HG2	10:B:86:ILE:CG2	1.68	1.24

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	443/813 (54%)	414 (94%)	26 (6%)	3 (1%)	18	50
2	3	209/218 (96%)	205 (98%)	3 (1%)	1 (0%)	24	56
3	4	251/357 (70%)	229 (91%)	19 (8%)	3 (1%)	10	40
4	5	307/564 (54%)	301 (98%)	6 (2%)	0	100	100
5	6	348/374 (93%)	318 (91%)	30 (9%)	0	100	100
7	8	313/352 (89%)	276 (88%)	35 (11%)	2 (1%)	21	52
8	9	22/25 (88%)	22 (100%)	0	0	100	100
10	B	138/158 (87%)	136 (99%)	2 (1%)	0	100	100
11	C	254/263 (97%)	249 (98%)	5 (2%)	0	100	100
12	D	175/194 (90%)	174 (99%)	1 (1%)	0	100	100
13	E	138/143 (96%)	134 (97%)	3 (2%)	1 (1%)	18	50
14	F	43/59 (73%)	43 (100%)	0	0	100	100
15	G	171/194 (88%)	163 (95%)	7 (4%)	1 (1%)	21	52
16	H	79/84 (94%)	76 (96%)	2 (2%)	1 (1%)	9	38
17	I	148/151 (98%)	147 (99%)	1 (1%)	0	100	100
18	J	127/130 (98%)	124 (98%)	2 (2%)	1 (1%)	16	48
19	K	79/83 (95%)	77 (98%)	2 (2%)	0	100	100
20	L	218/293 (74%)	215 (99%)	2 (1%)	1 (0%)	24	56
21	M	123/135 (91%)	121 (98%)	2 (2%)	0	100	100
22	N	205/295 (70%)	201 (98%)	3 (2%)	1 (0%)	24	56
23	O	209/264 (79%)	193 (92%)	16 (8%)	0	100	100
24	P	131/151 (87%)	123 (94%)	7 (5%)	1 (1%)	16	48
25	Q	97/115 (84%)	93 (96%)	4 (4%)	0	100	100
26	R	194/208 (93%)	194 (100%)	0	0	100	100
27	S	228/249 (92%)	223 (98%)	5 (2%)	0	100	100
28	T	123/133 (92%)	122 (99%)	1 (1%)	0	100	100
29	V	180/204 (88%)	175 (97%)	5 (3%)	0	100	100
30	Y	139/146 (95%)	136 (98%)	3 (2%)	0	100	100
31	Z	225/243 (93%)	223 (99%)	2 (1%)	0	100	100
32	a	97/165 (59%)	97 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	b	108/145 (74%)	107 (99%)	1 (1%)	0	100	100
34	c	311/317 (98%)	301 (97%)	10 (3%)	0	100	100
35	d	140/145 (97%)	136 (97%)	4 (3%)	0	100	100
36	e	64/125 (51%)	64 (100%)	0	0	100	100
37	f	140/152 (92%)	134 (96%)	6 (4%)	0	100	100
38	h	101/119 (85%)	97 (96%)	4 (4%)	0	100	100
39	i	48/56 (86%)	47 (98%)	0	1 (2%)	5	31
40	k	49/156 (31%)	44 (90%)	4 (8%)	1 (2%)	6	32
41	m	120/132 (91%)	118 (98%)	2 (2%)	0	100	100
42	n	61/69 (88%)	59 (97%)	1 (2%)	1 (2%)	7	35
43	o	75/320 (23%)	73 (97%)	2 (3%)	0	100	100
44	q	99/144 (69%)	83 (84%)	12 (12%)	4 (4%)	2	21
45	r	273/315 (87%)	255 (93%)	17 (6%)	1 (0%)	30	60
46	t	346/472 (73%)	337 (97%)	5 (1%)	4 (1%)	10	40
47	u	705/1382 (51%)	672 (95%)	32 (4%)	1 (0%)	48	78
48	v	380/445 (85%)	350 (92%)	30 (8%)	0	100	100
50	x	415/548 (76%)	386 (93%)	29 (7%)	0	100	100
51	y	636/913 (70%)	610 (96%)	25 (4%)	1 (0%)	43	72
All	All	9485/12718 (75%)	9077 (96%)	378 (4%)	30 (0%)	37	65

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	282	PRO
1	1	427	PRO
3	4	264	GLY
16	H	56	CYS
24	P	136	PRO

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	
1	1	97/701 (14%)	95 (98%)	2 (2%)	47	64
5	6	49/335 (15%)	48 (98%)	1 (2%)	48	64
8	9	23/24 (96%)	23 (100%)	0	100	100
10	B	129/142 (91%)	117 (91%)	12 (9%)	8	32
11	C	220/225 (98%)	195 (89%)	25 (11%)	5	24
12	D	158/168 (94%)	149 (94%)	9 (6%)	18	45
13	E	112/115 (97%)	101 (90%)	11 (10%)	7	30
14	F	38/48 (79%)	35 (92%)	3 (8%)	11	37
15	G	159/174 (91%)	135 (85%)	24 (15%)	3	16
16	H	73/76 (96%)	61 (84%)	12 (16%)	2	14
17	I	130/131 (99%)	121 (93%)	9 (7%)	14	41
18	J	112/113 (99%)	108 (96%)	4 (4%)	31	54
19	K	65/67 (97%)	57 (88%)	8 (12%)	4	22
20	L	186/225 (83%)	157 (84%)	29 (16%)	2	15
21	M	114/122 (93%)	98 (86%)	16 (14%)	3	18
22	N	173/243 (71%)	159 (92%)	14 (8%)	11	36
23	O	192/231 (83%)	190 (99%)	2 (1%)	68	74
24	P	104/119 (87%)	84 (81%)	20 (19%)	1	9
25	Q	86/98 (88%)	74 (86%)	12 (14%)	3	18
26	R	172/180 (96%)	154 (90%)	18 (10%)	6	28
27	S	200/218 (92%)	174 (87%)	26 (13%)	4	20
28	T	107/115 (93%)	96 (90%)	11 (10%)	7	29
29	V	156/170 (92%)	144 (92%)	12 (8%)	12	38
30	Y	117/121 (97%)	107 (92%)	10 (8%)	10	35
31	Z	190/202 (94%)	153 (80%)	37 (20%)	1	9
32	a	90/136 (66%)	83 (92%)	7 (8%)	11	37
33	b	100/130 (77%)	89 (89%)	11 (11%)	6	26
34	c	272/275 (99%)	229 (84%)	43 (16%)	2	15
35	d	112/115 (97%)	99 (88%)	13 (12%)	5	24
36	e	58/103 (56%)	50 (86%)	8 (14%)	3	19
37	f	123/132 (93%)	108 (88%)	15 (12%)	5	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	h	94/107 (88%)	82 (87%)	12 (13%)	4	21
39	i	44/49 (90%)	41 (93%)	3 (7%)	14	42
40	k	47/140 (34%)	34 (72%)	13 (28%)	0	3
41	m	104/108 (96%)	95 (91%)	9 (9%)	9	34
42	n	56/62 (90%)	46 (82%)	10 (18%)	2	12
43	o	64/277 (23%)	59 (92%)	5 (8%)	11	37
44	q	77/123 (63%)	61 (79%)	16 (21%)	1	8
45	r	247/280 (88%)	199 (81%)	48 (19%)	1	9
47	u	528/1259 (42%)	518 (98%)	10 (2%)	50	65
48	v	206/406 (51%)	198 (96%)	8 (4%)	28	53
50	x	206/494 (42%)	197 (96%)	9 (4%)	25	50
51	y	563/811 (69%)	554 (98%)	9 (2%)	55	68
All	All	6153/9370 (66%)	5577 (91%)	576 (9%)	10	32

5 of 576 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	n	17	VAL
51	y	597	ASN
44	q	27	VAL
42	n	9	ILE
45	r	178	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 104 such sidechains are listed below:

Mol	Chain	Res	Type
38	h	18	HIS
47	u	79	GLN
51	y	520	GLN
38	h	81	GLN
43	o	311	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
49	w	74/75 (98%)	42 (56%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
6	7	21/255 (8%)	11 (52%)	3 (14%)
9	A	1710/1869 (91%)	510 (29%)	69 (4%)
All	All	1805/2199 (82%)	563 (31%)	72 (3%)

5 of 563 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	7	4	G
6	7	5	A
6	7	8	A
6	7	11	A
6	7	15	U

5 of 72 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	1600	G
9	A	1831	A
9	A	1637	A
9	A	1757	G
9	A	839	C

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

26 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	$\# Z > 2$
9	5MU	A	814	9	19,22,23	1.55	5 (26%)	27,32,35	2.38	9 (33%)
9	OMU	A	116	9	19,22,23	1.36	3 (15%)	25,31,34	1.94	5 (20%)
9	UR3	A	1830	9	19,22,23	1.04	2 (10%)	26,32,35	2.27	8 (30%)
9	OMC	A	517	9	19,22,23	0.95	1 (5%)	25,31,34	1.18	2 (8%)
9	OMG	A	644	9	23,26,27	1.36	4 (17%)	32,38,41	2.15	9 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	PSU	A	823	9	18,21,22	1.60	5 (27%)	21,30,33	2.18	4 (19%)
9	A2M	A	159	9	22,25,26	1.50	4 (18%)	30,36,39	2.20	9 (30%)
9	PSU	A	1081	9	18,21,22	1.73	5 (27%)	21,30,33	2.49	6 (28%)
9	A2M	A	1031	9	22,25,26	1.55	6 (27%)	30,36,39	2.34	9 (30%)
9	PSU	A	822	9	18,21,22	1.55	4 (22%)	21,30,33	2.39	5 (23%)
9	MA6	A	1850	9	23,26,27	1.53	4 (17%)	33,38,41	2.53	13 (39%)
9	5MC	A	1374	9	19,22,23	1.70	3 (15%)	26,32,35	1.51	6 (23%)
9	OMG	A	683	9	23,26,27	1.33	4 (17%)	32,38,41	2.21	6 (18%)
9	A2M	A	484	9	22,25,26	1.53	4 (18%)	30,36,39	2.32	8 (26%)
9	A2M	A	1678	9	22,25,26	1.54	6 (27%)	30,36,39	2.13	10 (33%)
9	MA6	A	1851	9	23,26,27	1.57	5 (21%)	33,38,41	2.38	14 (42%)
9	PSU	A	1243	9	18,21,22	1.54	5 (27%)	21,30,33	2.20	4 (19%)
9	OMC	A	1703	9	19,22,23	1.04	2 (10%)	25,31,34	1.20	1 (4%)
9	PSU	A	612	9	18,21,22	1.51	5 (27%)	21,30,33	2.18	4 (19%)
9	PSU	A	119	9	18,21,22	1.47	4 (22%)	21,30,33	2.32	5 (23%)
9	A2M	A	27	9	22,25,26	1.55	6 (27%)	30,36,39	2.31	10 (33%)
9	A2M	A	166	9	22,25,26	1.53	5 (22%)	30,36,39	2.25	9 (30%)
9	OMU	A	121	9	19,22,23	1.46	4 (21%)	25,31,34	1.96	6 (24%)
9	OMC	A	174	9	19,22,23	0.91	0	25,31,34	1.17	2 (8%)
9	OMG	A	509	9	23,26,27	1.38	4 (17%)	32,38,41	2.15	6 (18%)
9	A2M	A	668	9	22,25,26	1.53	6 (27%)	30,36,39	2.06	11 (36%)

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
9	5MU	A	814	9	-	0/7/25/26	0/2/2/2
9	OMU	A	116	9	-	1/9/27/28	0/2/2/2
9	UR3	A	1830	9	-	2/7/25/26	0/2/2/2
9	OMC	A	517	9	-	1/9/27/28	0/2/2/2
9	OMG	A	644	9	-	2/9/27/28	0/3/3/3
9	PSU	A	823	9	-	1/7/25/26	0/2/2/2
9	A2M	A	159	9	-	1/9/27/28	0/3/3/3
9	PSU	A	1081	9	-	2/7/25/26	0/2/2/2
9	A2M	A	1031	9	-	1/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	PSU	A	822	9	-	0/7/25/26	0/2/2/2
9	MA6	A	1850	9	-	1/11/29/30	0/3/3/3
9	5MC	A	1374	9	-	0/7/25/26	0/2/2/2
9	OMG	A	683	9	-	1/9/27/28	0/3/3/3
9	A2M	A	484	9	-	1/9/27/28	0/3/3/3
9	A2M	A	1678	9	-	0/9/27/28	0/3/3/3
9	MA6	A	1851	9	-	4/11/29/30	0/3/3/3
9	PSU	A	1243	9	-	0/7/25/26	0/2/2/2
9	OMC	A	1703	9	-	2/9/27/28	0/2/2/2
9	PSU	A	612	9	-	1/7/25/26	0/2/2/2
9	PSU	A	119	9	-	1/7/25/26	0/2/2/2
9	A2M	A	27	9	-	1/9/27/28	0/3/3/3
9	A2M	A	166	9	-	0/9/27/28	0/3/3/3
9	OMU	A	121	9	-	0/9/27/28	0/2/2/2
9	OMC	A	174	9	-	0/9/27/28	0/2/2/2
9	OMG	A	509	9	-	2/9/27/28	0/3/3/3
9	A2M	A	668	9	-	3/9/27/28	0/3/3/3

The worst 5 of 106 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	1374	5MC	C5-C4	5.90	1.48	1.44
9	A	159	A2M	C5-C4	4.54	1.47	1.39
9	A	166	A2M	C5-C4	4.46	1.47	1.39
9	A	484	A2M	C5-C4	4.22	1.46	1.39
9	A	1031	A2M	C5-C4	4.19	1.46	1.39

The worst 5 of 181 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	822	PSU	N1-C2-N3	7.03	122.58	115.17
9	A	1830	UR3	C4-N3-C2	-7.00	118.95	124.58
9	A	1081	PSU	N1-C2-N3	6.92	122.47	115.17
9	A	119	PSU	N1-C2-N3	6.54	122.07	115.17
9	A	484	A2M	C2'-C1'-N9	-6.54	102.99	113.75

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	A	27	A2M	C1'-C2'-O2'-CM'

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Mol	Chain	Res	Type	Atoms
9	A	116	OMU	C1'-C2'-O2'-CM2
9	A	159	A2M	C1'-C2'-O2'-CM'
9	A	484	A2M	C1'-C2'-O2'-CM'
9	A	517	OMC	C1'-C2'-O2'-CM2

There are no ring outliers.

12 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	116	OMU	3	0
9	A	517	OMC	2	0
9	A	644	OMG	1	0
9	A	1031	A2M	2	0
9	A	1850	MA6	2	0
9	A	683	OMG	1	0
9	A	484	A2M	1	0
9	A	1851	MA6	1	0
9	A	1703	OMC	1	0
9	A	119	PSU	1	0
9	A	27	A2M	4	0
9	A	509	OMG	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 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](#)

There are no chain breaks in this entry.

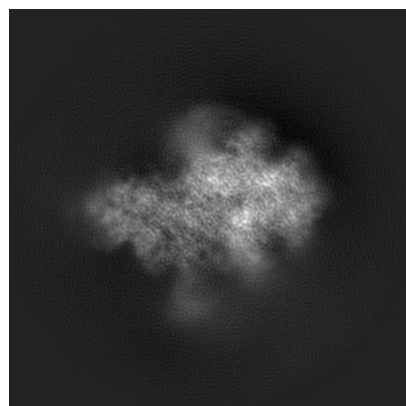
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14114. These allow visual inspection of the internal detail of the map and identification of artifacts.

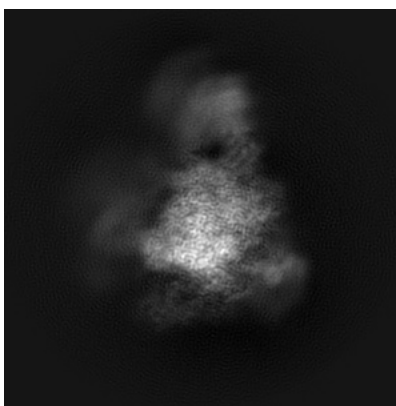
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

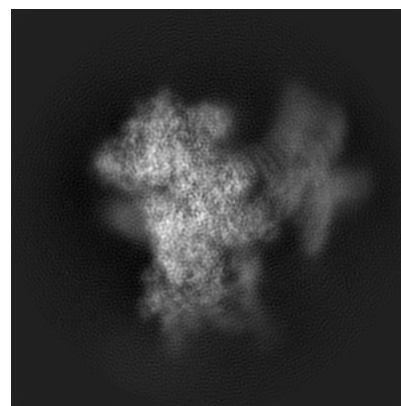
6.1.1 Primary map



X

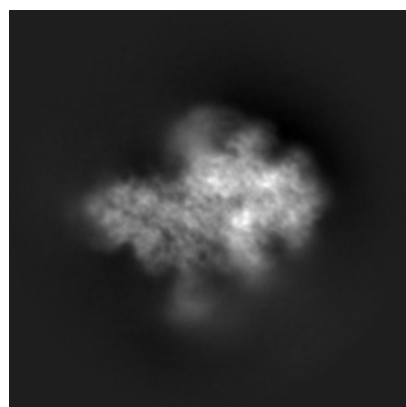


Y

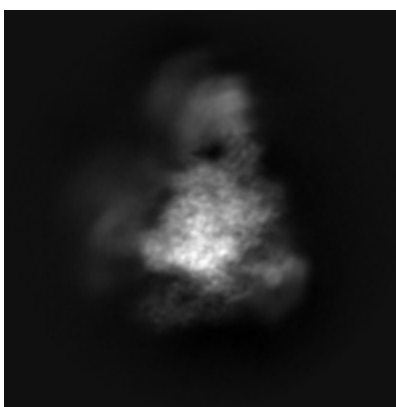


Z

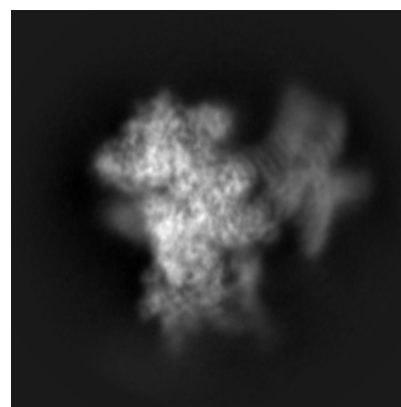
6.1.2 Raw map



X



Y

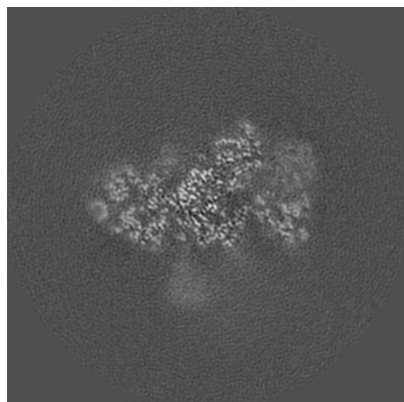


Z

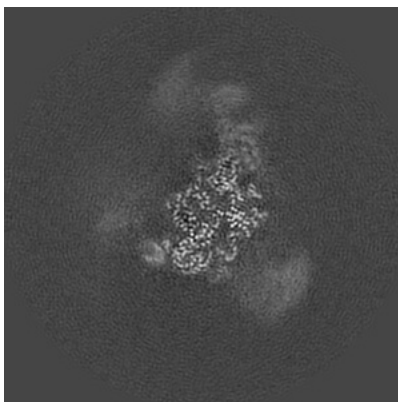
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

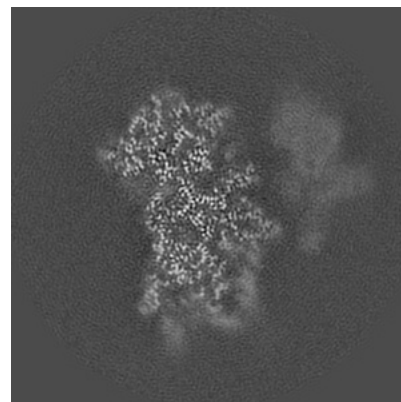
6.2.1 Primary map



X Index: 180

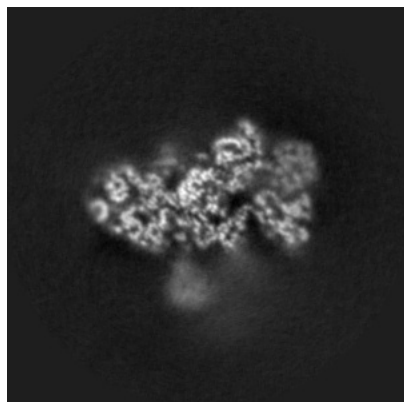


Y Index: 180

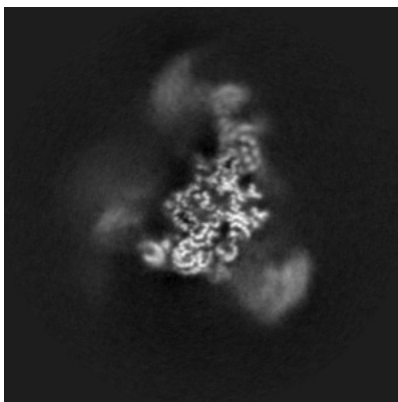


Z Index: 180

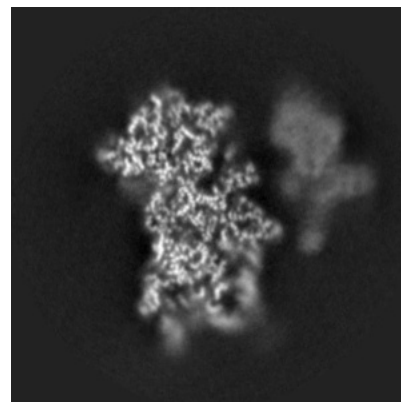
6.2.2 Raw map



X Index: 180



Y Index: 180

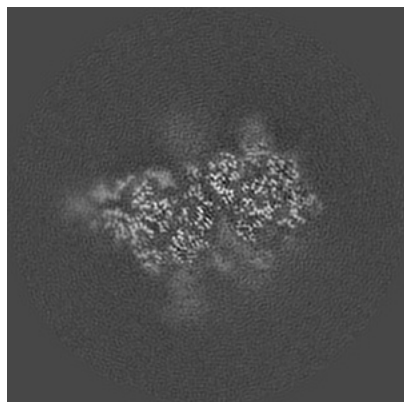


Z Index: 180

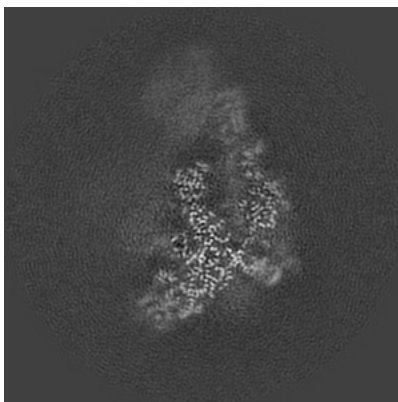
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

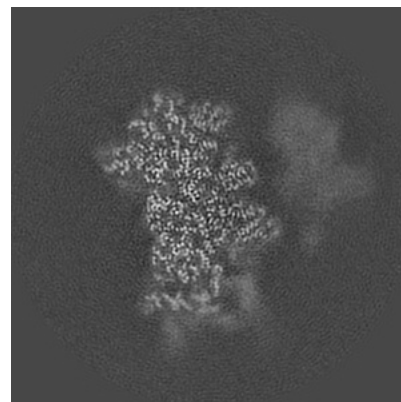
6.3.1 Primary map



X Index: 149

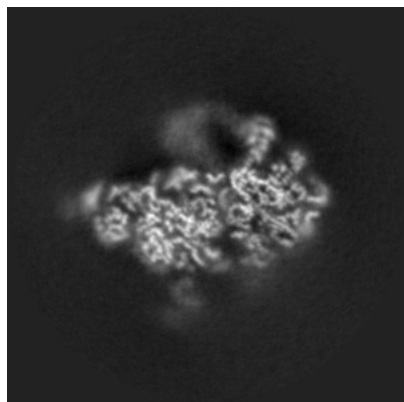


Y Index: 213

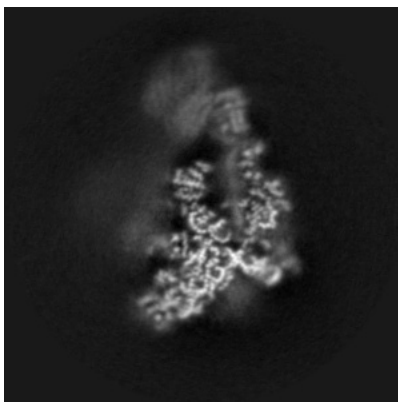


Z Index: 176

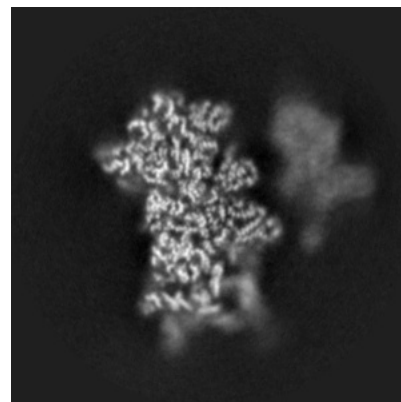
6.3.2 Raw map



X Index: 139



Y Index: 213

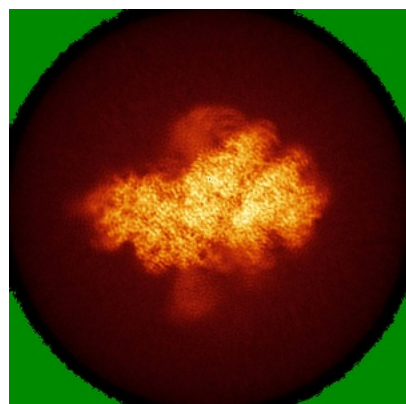


Z Index: 176

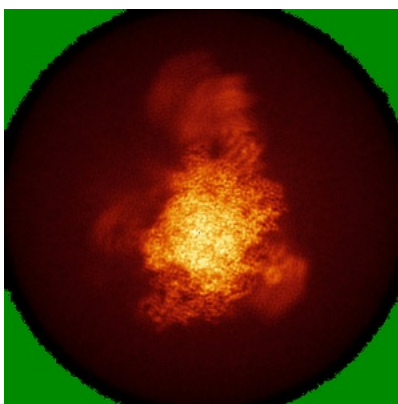
The images above show the largest variance slices of the map in three orthogonal directions.

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

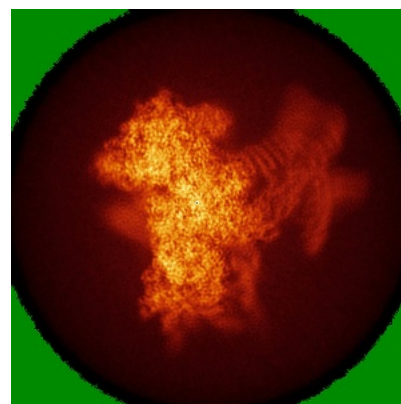
6.4.1 Primary map



X

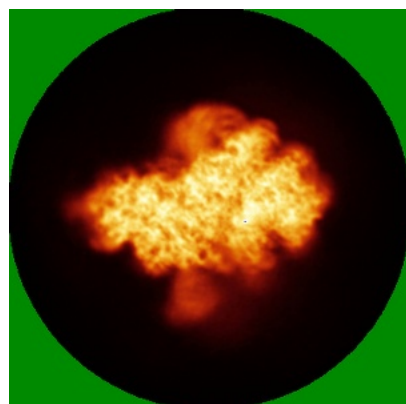


Y

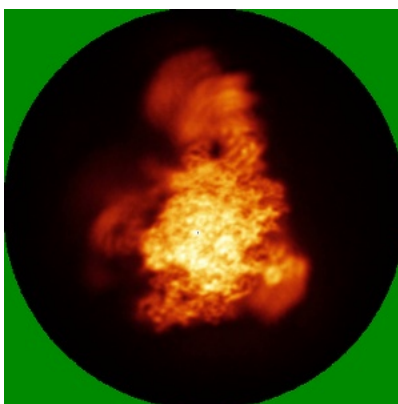


Z

6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

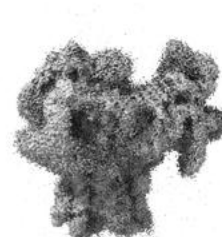
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.15. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

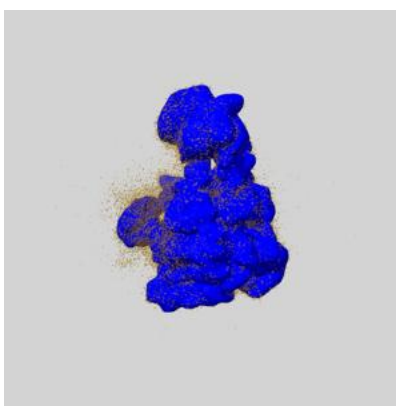
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

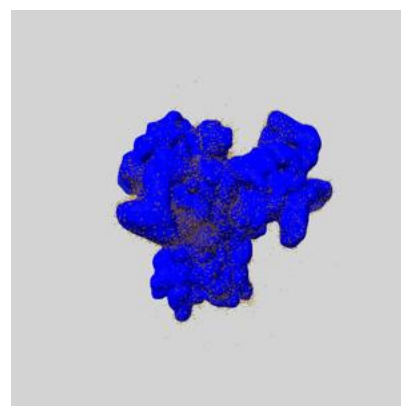
6.6.1 emd_14114_msk_1.map [i](#)



X



Y

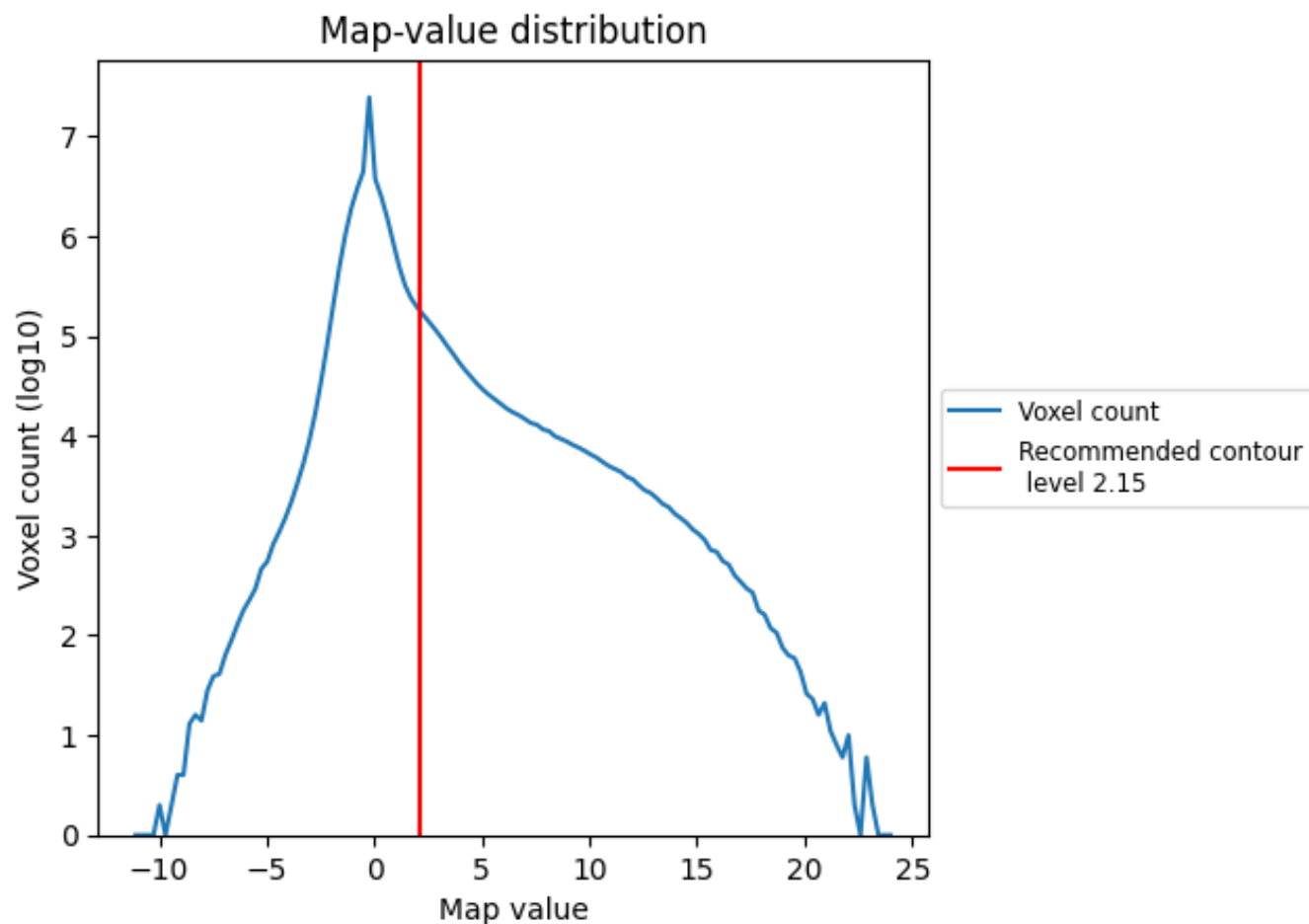


Z

7 Map analysis [i](#)

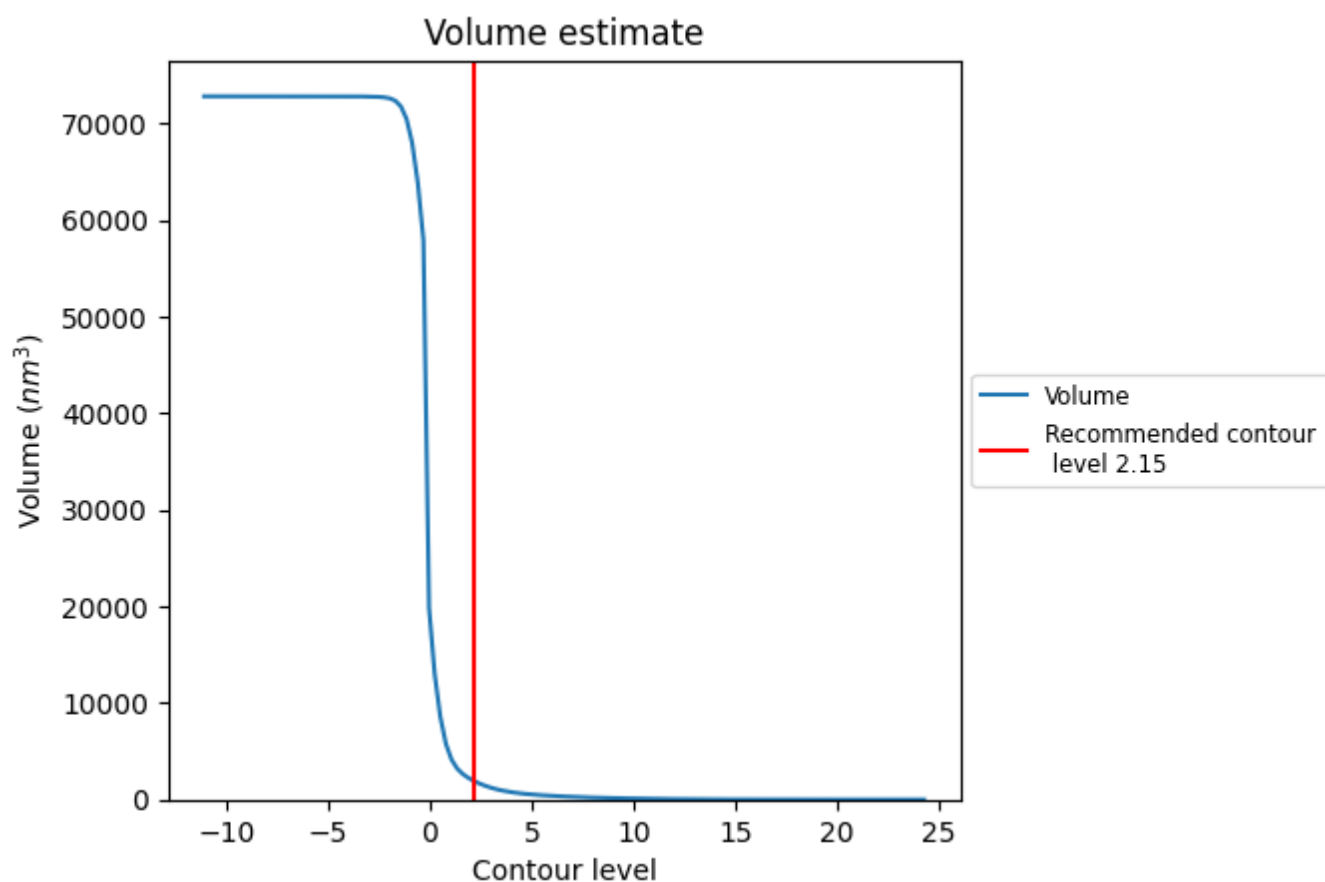
This section contains the results of statistical analysis of the map.

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.

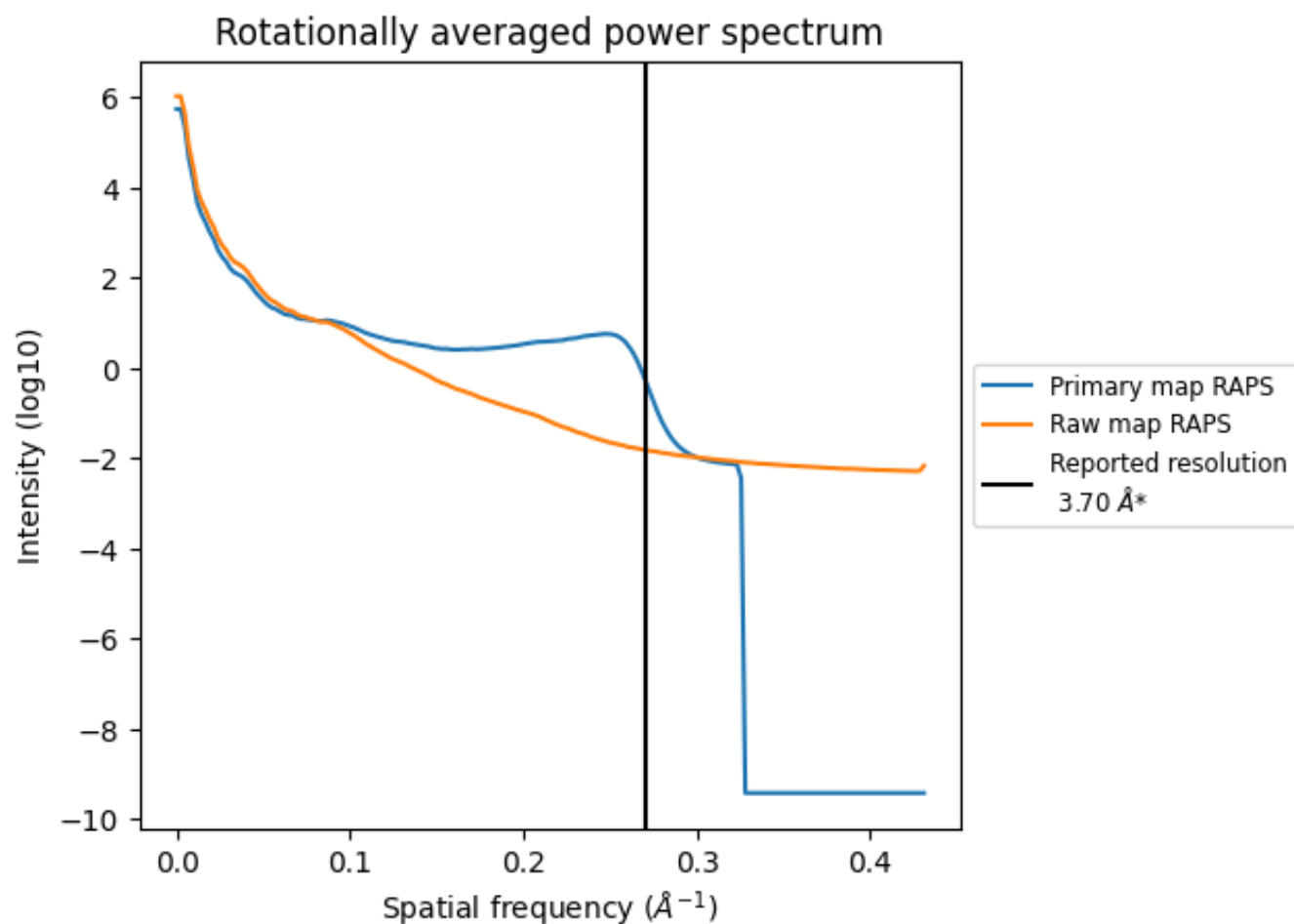
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1935 nm³; this corresponds to an approximate mass of 1748 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

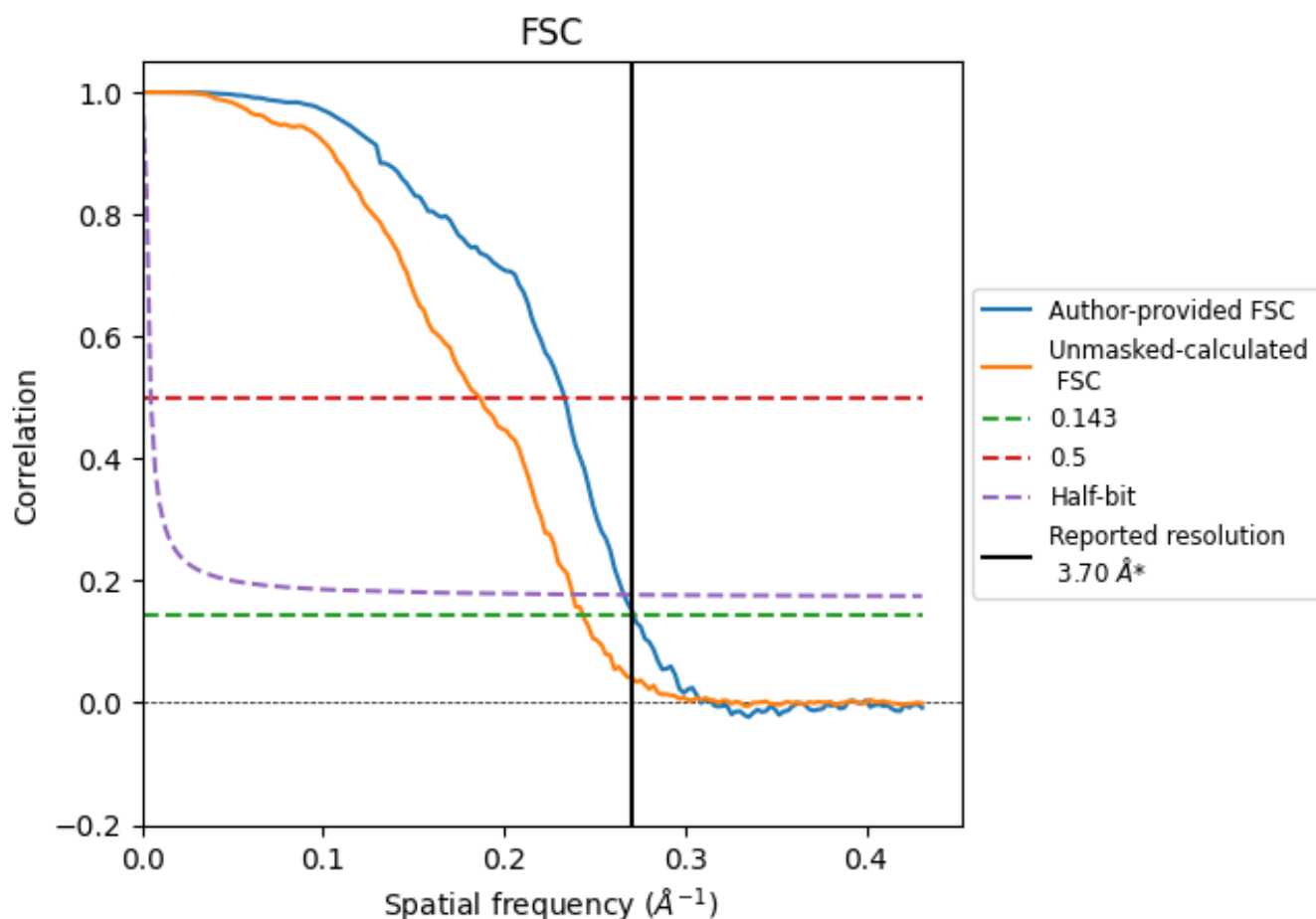


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.270 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

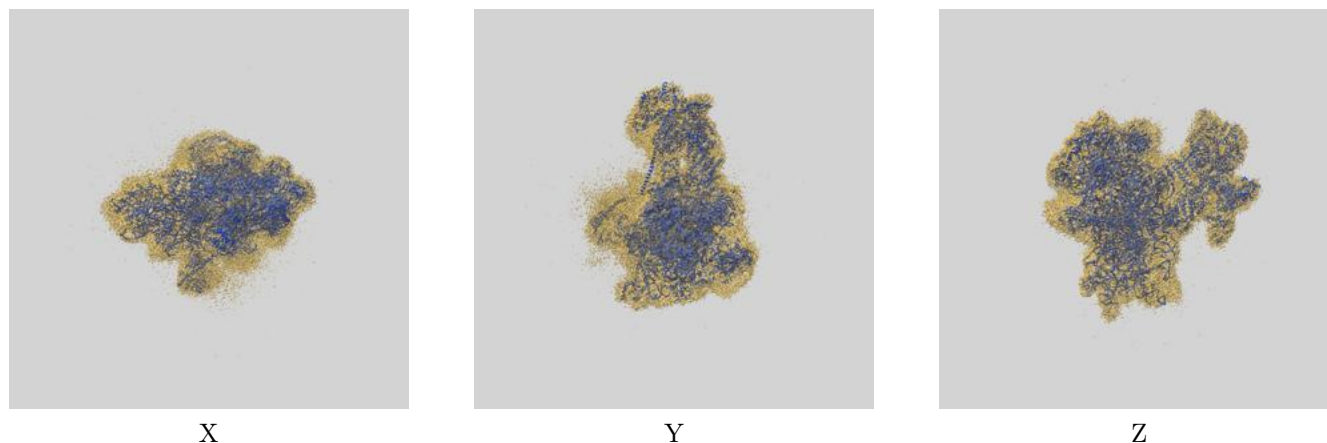
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.68	4.29	3.76
Unmasked-calculated*	4.11	5.36	4.20

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

9 Map-model fit [i](#)

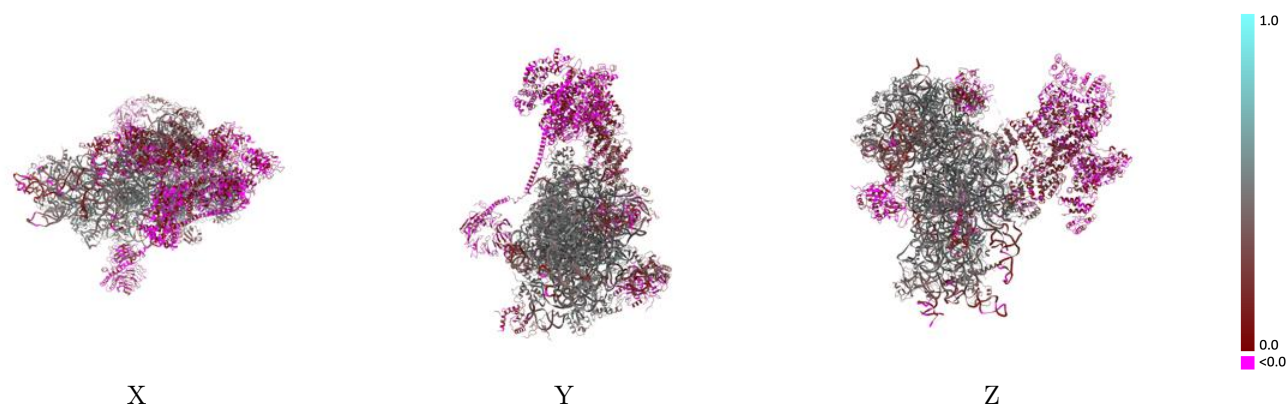
This section contains information regarding the fit between EMDB map EMD-14114 and PDB model 7QP7. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



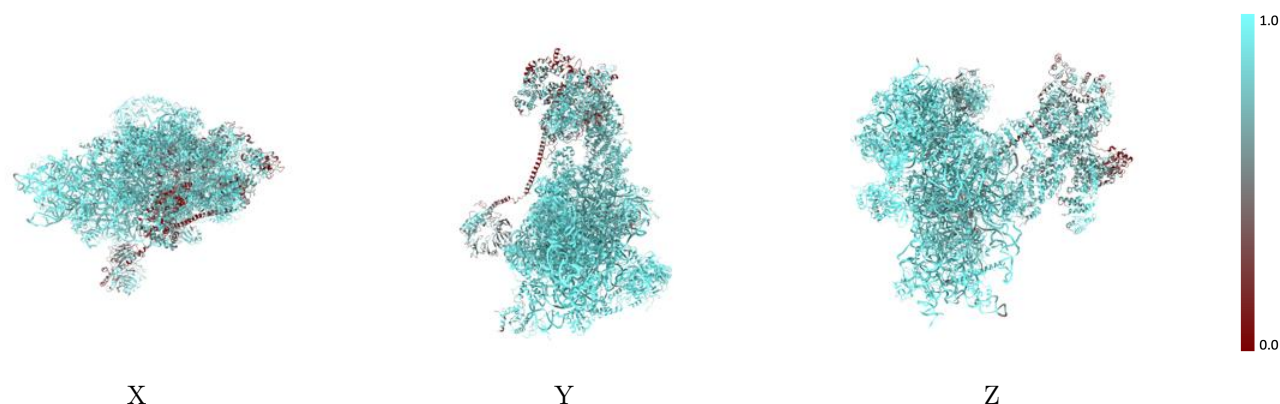
The images above show the 3D surface view of the map at the recommended contour level 2.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



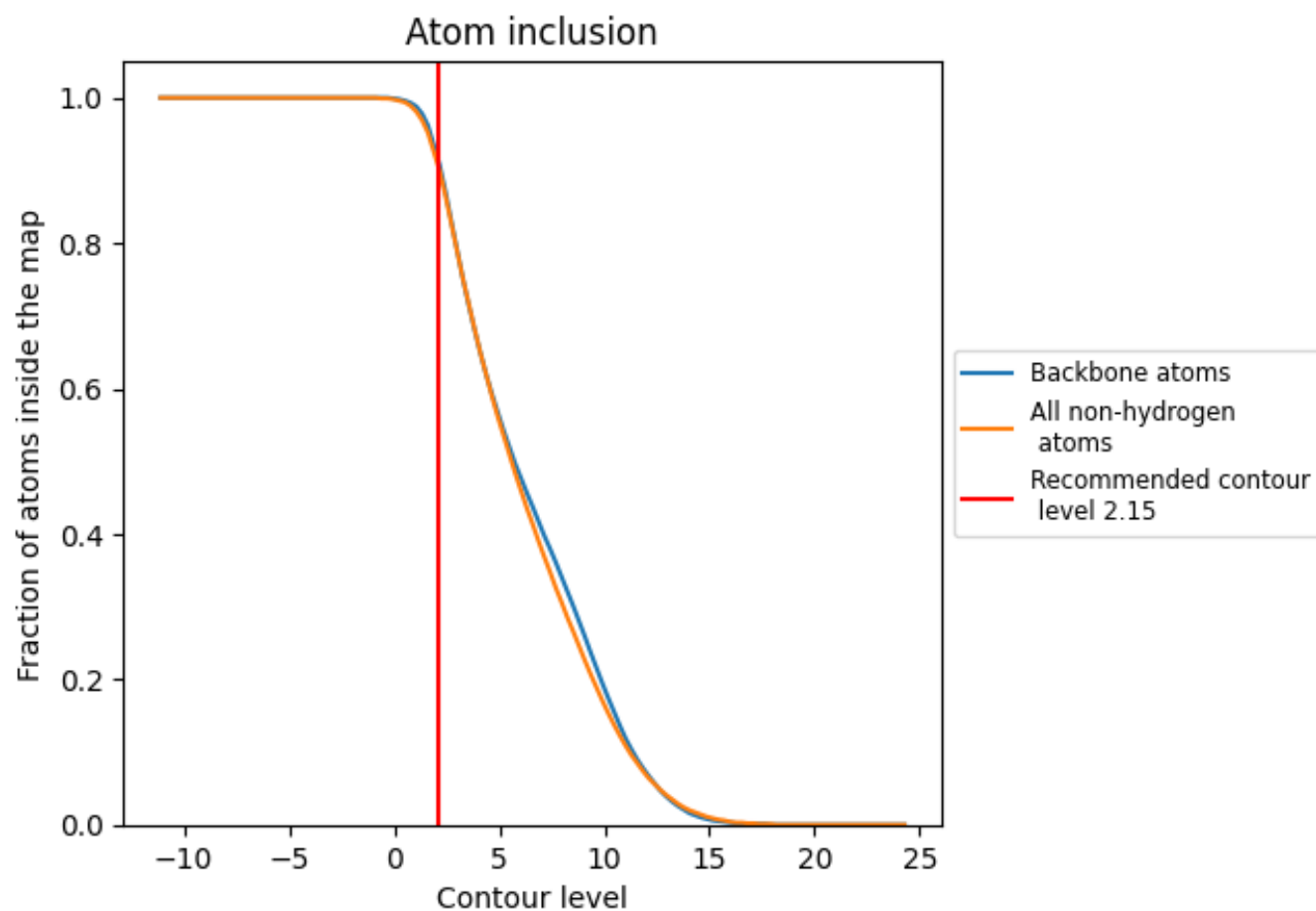
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 90% 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 (2.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9010	 0.3370
1	 0.5900	 0.0480
3	 0.4050	 0.0230
4	 0.7400	 0.0390
5	 0.6400	 0.0290
6	 0.6270	 0.0200
7	 0.8870	 0.2360
8	 0.6980	 0.0350
9	 0.9710	 0.4920
A	 0.9850	 0.4050
B	 0.9680	 0.4940
C	 0.9720	 0.4950
D	 0.9680	 0.4890
E	 0.9700	 0.5100
F	 0.9730	 0.4820
G	 0.9300	 0.4390
H	 0.9440	 0.4800
I	 0.9800	 0.4910
J	 0.9610	 0.5170
K	 0.9720	 0.5040
L	 0.9490	 0.5010
M	 0.9250	 0.4600
N	 0.9540	 0.4940
O	 0.9210	 0.3930
P	 0.9660	 0.4860
Q	 0.9590	 0.5090
R	 0.9640	 0.4350
S	 0.9660	 0.4150
T	 0.9850	 0.4700
V	 0.9650	 0.4930
Y	 0.9650	 0.4950
Z	 0.9400	 0.4750
a	 0.9580	 0.4660
b	 0.9610	 0.4650
c	 0.9590	 0.4390



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Chain	Atom inclusion	Q-score
d	 0.9780	 0.4840
e	 0.9590	 0.4570
f	 0.9580	 0.4520
h	 0.9670	 0.4650
i	 0.9530	 0.4940
k	 0.9430	 0.3350
m	 0.8100	 0.1540
n	 0.9370	 0.4830
o	 0.8600	 0.2190
q	 0.8380	 0.3450
r	 0.9560	 0.3330
t	 0.9320	 0.0370
u	 0.7040	 0.1200
v	 0.7640	 0.0480
w	 0.9740	 0.2120
x	 0.7010	 0.1440
y	 0.7970	 0.1610