



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 02:50 AM UTC

PDB ID : 3J80 / pdb_00003j80
EMDB ID : EMD-2764
Title : CryoEM structure of 40S-eIF1-eIF1A preinitiation complex
Authors : Hussain, T.; Llacer, J.L.; Fernandez, I.S.; Savva, C.G.; Ramakrishnan, V.
Deposited on : 2014-08-28
Resolution : 3.75 Å(reported)
Based on initial models : 3U5B, 3U5C

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

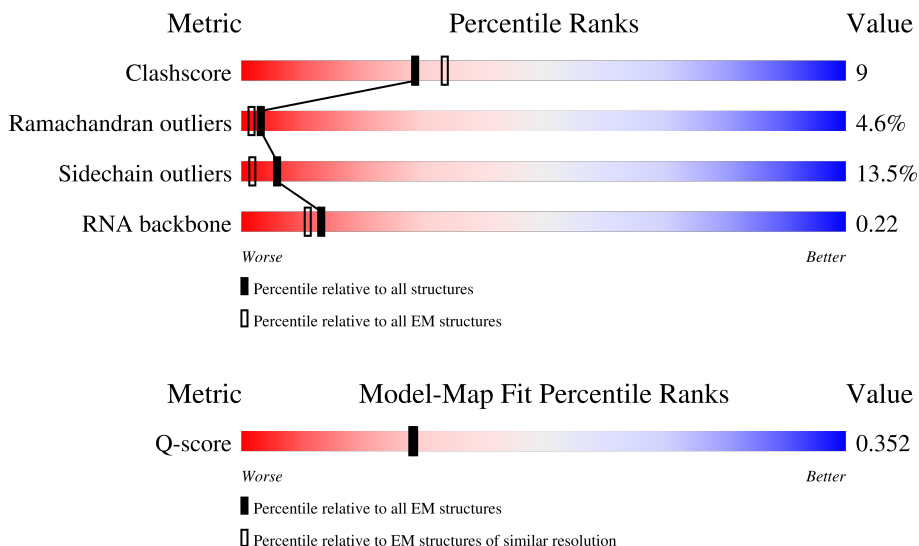
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.75 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.



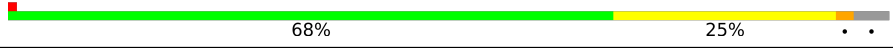
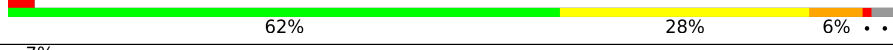
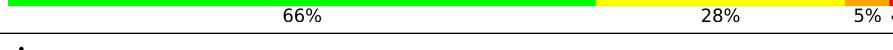
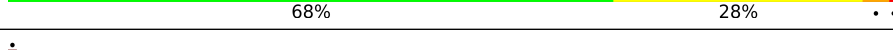
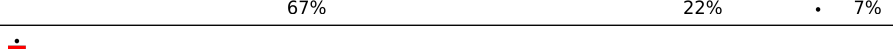
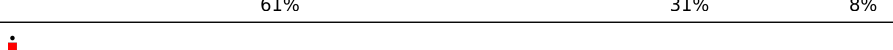
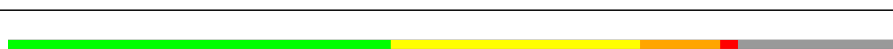
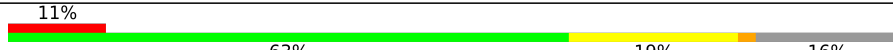
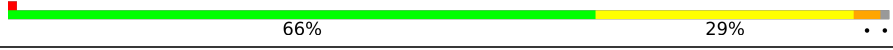
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10301 (3.25 - 4.25)

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

Mol	Chain	Length	Quality of chain
1	2	1799	
2	A	254	
3	B	255	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	C	259	
5	E	261	
6	G	236	
7	H	190	
8	I	201	
9	J	188	
10	L	156	
11	N	151	
12	O	137	
13	V	87	
14	W	130	
15	X	145	
16	Y	135	
17	a	119	
18	b	82	
19	e	63	
20	D	237	
21	F	227	
22	K	106	
23	M	134	
24	P	140	
25	Q	143	
26	R	136	
27	S	146	
28	T	144	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	U	117	
30	Z	108	
31	c	67	
32	d	56	
33	f	150	
34	g	326	
35	h	25	
36	i	153	
37	j	108	

2 Entry composition

There are 39 unique types of molecules in this entry. The entry contains 77716 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 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1779	Total	C	N	O	P	0	0
			37775	16882	6653	12461	1779		

- Molecule 2 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	206	Total	C	N	O	S	0	0
			1616	1035	285	294	2		

- Molecule 3 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	214	Total	C	N	O	S	0	0
			1722	1089	313	317	3		

- Molecule 4 is a protein called uS5.

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

- Molecule 5 is a protein called eS4.

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

- Molecule 6 is a protein called eS6.

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

- Molecule 7 is a protein called eS7.

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

- Molecule 8 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	188	Total	C	N	O	S	0	0
			1493	926	301	265	1		

- Molecule 9 is a protein called uS4.

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

- Molecule 10 is a protein called uS17.

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

- Molecule 11 is a protein called uS15.

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

- Molecule 12 is a protein called uS11.

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

- Molecule 13 is a protein called eS21.

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

- Molecule 14 is a protein called uS8.

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

- Molecule 15 is a protein called uS12.

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

- Molecule 16 is a protein called eS24.

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

- Molecule 17 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	a	97	Total	C	N	O	S	0	0
			770	475	163	127	5		

- Molecule 18 is a protein called eS27.

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

- Molecule 19 is a protein called eS30.

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

- Molecule 20 is a protein called uS3.

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

- Molecule 21 is a protein called uS7.

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

- Molecule 22 is a protein called eS10.

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

- Molecule 23 is a protein called eS12.

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

- Molecule 24 is a protein called uS19.

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

- Molecule 25 is a protein called uS9.

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

- Molecule 26 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	120	Total	C	N	O	S	0	0
			959	598	178	180	3		

- Molecule 27 is a protein called uS13.

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

- Molecule 28 is a protein called eS19.

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

- Molecule 29 is a protein called uS10.

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

- Molecule 30 is a protein called eS25.

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

- Molecule 31 is a protein called eS28.

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

- Molecule 32 is a protein called uS14.

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

- Molecule 33 is a protein called eS31.

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

- Molecule 34 is a protein called RACK1.

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

- Molecule 35 is a protein called eL41.

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

- Molecule 36 is a protein called eIF1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	96	Total	C	N	O	S	0	0
			778	482	144	147	5		

- Molecule 37 is a protein called eIF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	86	Total	C	N	O	S	0	0
			695	439	128	124	4		

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

Mol	Chain	Residues	Atoms		AltConf
38	2	67	Total	Mg	0
			67	67	

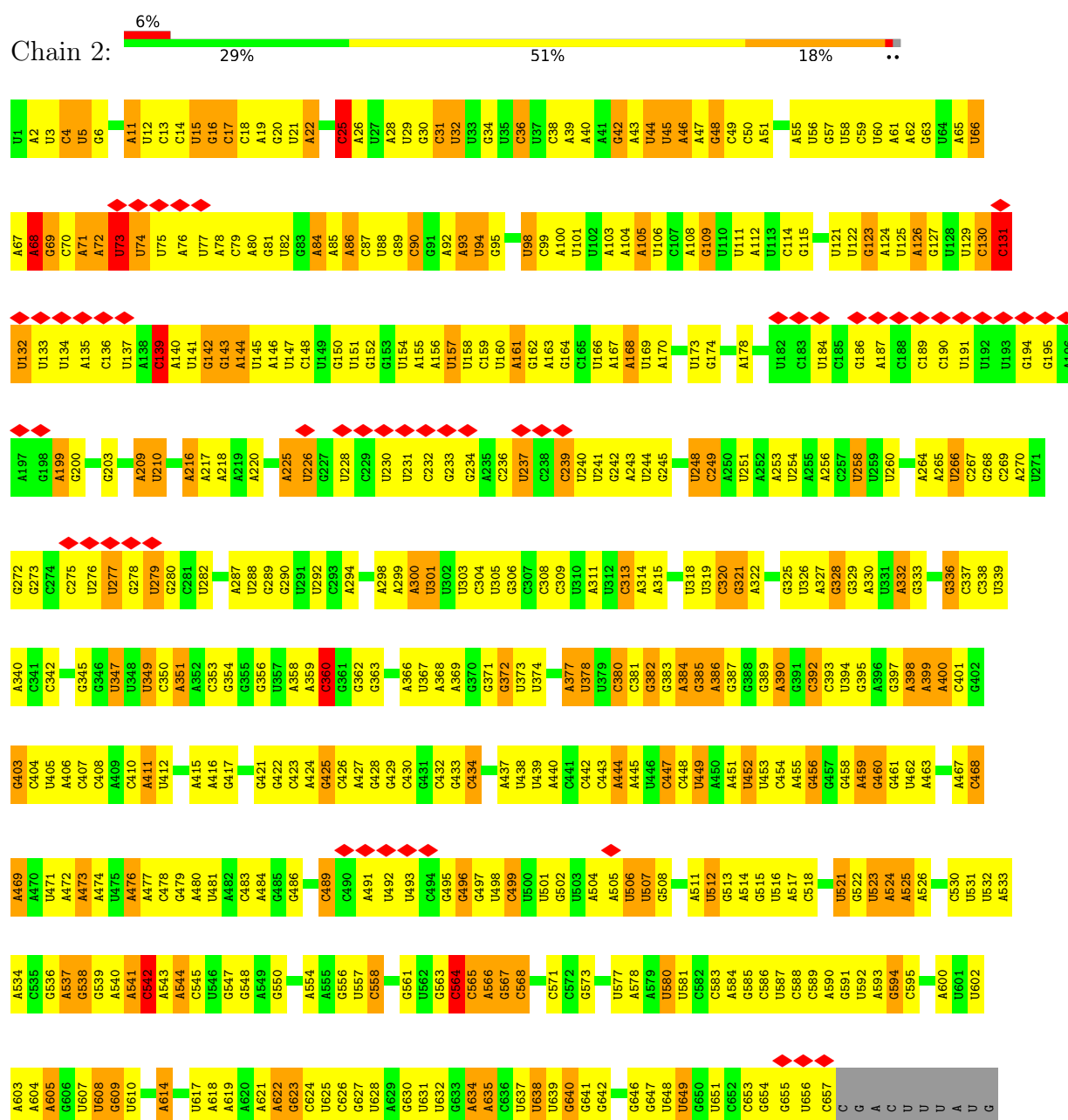
- Molecule 39 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

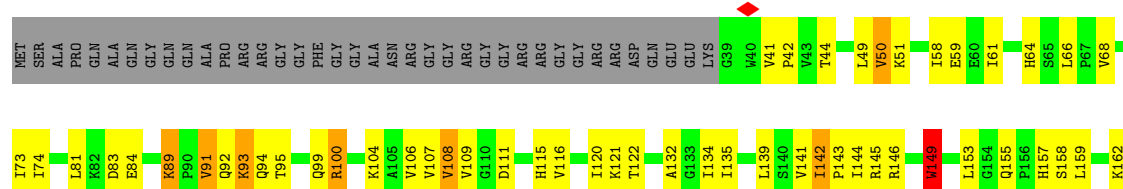
3 Residue-property plots

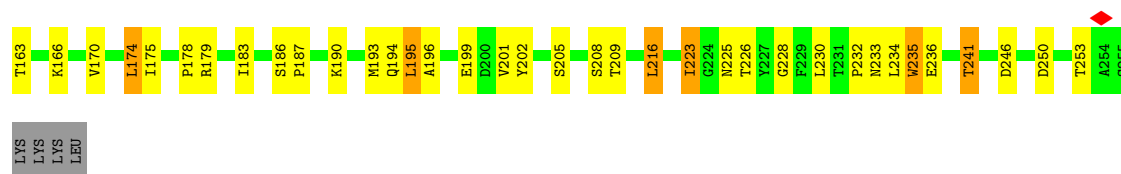
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 18S rRNA

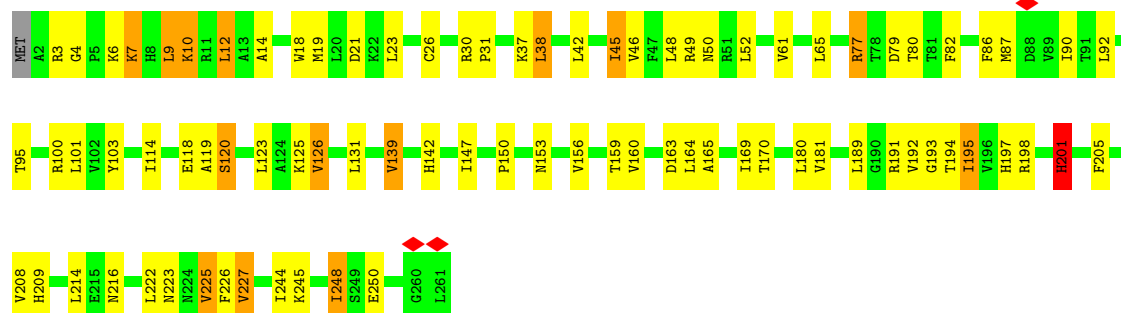


U1558	U1559	U1495	U1432	U1289	A1223	C1158	A1019	G953	U881	A811	G738	U
G1496	G1497	G1496	G1433	G1290	U1224	A1159	C1020	G954	C882	A811	G739	C
G1498	G1499	G1291	U1434	G1291	A1225	C1160	C1021	A954	G883	A812	A740	G
G1500	G1501	G1292	U1435	G1292	A1226	C1161	U1096	C955	G884	A813	C741	C
A1501	A1502	G1293	U1436	G1293	G1227	U1097	U1098	C956	U885	G814	U742	G
U1502	U1503	G1294	U1437	G1294	G1228	G1163	G1099	U957	A886	G815	U743	C
U1503	U1504	A1295	U1438	A1295	A1229	G1164	G1100	U958	U887	A816	C747	A
U1504	U1505	G1296	U1439	G1296	G1232	A1165	A1026	U959	C888	C817		U
U1505	U1506	G1297	U1440	G1297	U1233	G1166	A1027	U960	U889	G818	A753	G576
U1506	U1507	A1300	U1441	A1300	C1234	U1167	A1028	C961	U890	U819	A754	A584
U1507	U1508	U1306	U1442	U1306	U1235	A1170	U1030	U962	U893	U821	A755	C887
U1508	U1509	U1307	U1443	U1307	A1237	G1171	G1031	U963	G894	U822	A756	
U1509	U1510	U1308	U1444	U1308	U1238	C1172	C1032	U964	U895	U823	A757	
U1510	U1511	A1311	U1445	A1311	U1239	C1173	G1033	U965	C896	U824	U758	
U1511	U1512	A1312	U1446	A1312	G1240	U1174	G1034	U966	G897	C826	G765	U691
U1512	U1513	U1313	U1447	U1313	A1241	U1175	G1035	U967	G898	U827	U766	C592
U1513	U1514	A1314	U1448	A1314	C1242	C1176	C1036	U968	G899	A828	U767	U694
U1514	U1515	G1315	U1449	G1315	U1243	G1177	U1037	U969	G900	U829	U768	U695
U1515	U1516	C1316	U1450	C1316	A1244	C1178	A1038	G971	A904	U830	C769	C596
U1516	U1517	G1317	U1451	G1317	G1247	U1180	G1039	A972	A905	U831	A770	C597
U1517	U1518	A1320	U1452	A1320	U1248	U1181	U1040	A973	A906	U832	A771	U698
U1518	U1519	C1321	U1453	C1321	U1249	A1182	G1041	A974	U907	G837	G772	U699
U1519	U1520	G1322	U1454	G1322	U1250	A1183	U1042	A975	U908	U838	G773	C700
U1520	U1521	A1323	U1455	A1323	C1251	U1184	U1043	A976	C909	U839	A774	U701
U1521	U1522	G1324	U1456	G1324	U1252	U1185	U1044	A977	U910	U840	G775	G702
U1522	U1523	A1325	U1457	A1325	C1253	U1186	U1045	A978	U911	U841	G776	G703
U1523	U1524	G1326	U1458	G1326	U1254	G1187	G1046	A979	G912	C843	G777	C704
U1524	U1525	C1327	U1459	C1327	U1255	U1188	U1047	A980	G913	G844	G778	G705
U1525	U1526	A1330	U1460	A1330	U1256	C1189	U1048	A981	A914	G845	A779	A706
U1526	U1527	C1331	U1461	C1331	U1257	U1190	U1049	A982	U915	A846	A780	A707
U1527	U1528	G1332	U1462	G1332	U1258	U1191	U1050	A983	U916	U853	A781	C708
U1528	U1529	A1333	U1463	A1333	U1259	U1192	G1051	A984	U917	U854	A782	C709
U1529	U1530	U1334	U1464	U1334	U1260	U1193	U1052	A985	U918	C844	G783	U710
U1530	U1531	A1335	U1465	A1335	U1261	C1194	U1053	A986	U919	A855	U784	G711
U1531	U1532	C1336	U1466	C1336	U1262	U1195	U1054	A987	U920	G857	C785	G712
U1532	U1533	A1337	U1467	A1337	U1263	U1196	U1055	A988	U921	U860	A787	U713
U1533	U1534	G1338	U1468	G1338	U1264	U1197	U1056	A989	U922	U861	A788	C714
U1534	U1535	C1339	U1469	C1339	U1265	U1198	U1057	A990	U923	A862	U789	C715
U1535	U1536	A1340	U1470	A1340	U1266	U1199	C1058	A991	U924	U863	A790	U716
U1536	U1537	U1341	U1471	U1341	U1267	U1200	U1059	A992	U925	U864	C792	C717
U1537	U1538	G1410	U1472	G1410	U1268	U1201	U1060	A993	U926	G865	U793	U718
U1538	U1539	U1411	U1473	U1411	U1269	A1202	U1061	A994	U927	G866	U794	U719
U1539	U1540	U1412	U1474	U1412	G1272	U1203	A1075	A995	U928	U867	A795	G720
U1540	U1541	A1343	U1475	A1343	C1273	U1204	C1074	A996	U929	A868	C797	U721
U1541	U1542	A1344	U1476	A1344	U1274	U1205	A1076	A997	U930	G869	U798	G722
U1542	U1543	U1345	U1477	U1345	U1275	U1206	U1077	A998	U931	U870	A799	U723
U1543	U1544	A1346	U1478	A1346	U1276	U1207	U1078	A999	U932	G871	G800	G724
U1544	U1545	U1347	U1479	U1347	G1277	C1208	U1079	A1000	U933	U872	G801	A802
U1545	U1546	G1348	U1480	G1348	U1278	U1209	U1080	A1001	U934	C873	A803	U725
U1546	U1547	U1349	U1481	U1349	C1279	U1210	U1081	A1002	U935	G874	A804	G726
U1547	U1548	G1350	U1482	G1350	U1280	U1211	U1082	A1003	U936	G875	A805	C727
U1548	U1549	U1351	U1483	U1351	U1281	G1212	U1083	U1011	U937	G876	A806	C728
U1549	U1550	A1352	U1484	A1352	U1282	U1213	U1084	U1012	U938	G877	U807	A729
U1550	U1551	G1353	U1485	G1353	U1283	U1214	U1085	A1013	U939	G878	G808	G730
U1551	U1552	C1354	U1486	C1354	U1284	U1215	U1086	A1014	U940	C879	A809	G731
U1552	U1553	U1355	U1487	U1355	C1285	U1216	U1087	U1015	U941	G880	A810	G732
U1553	U1554	G1356	U1488	G1356	U1286	U1217	U1088	U1016	U942	G881	A811	G733
U1554	U1555	U1428	U1489	U1428	U1287	U1218	U1089	U1017	U943	C882	A812	G734
U1555	U1556	A1359	U1490	A1359	U1288	U1219	U1090	U1018	U944	U883	A813	G735
U1556	U1557	C1360	U1491	C1360	U1289	U1220	U1091	U1019	U945	G884	A814	G736
U1557	U1558	U1431	U1492	U1431	U1290	U1221	U1092	U1020	U946	C885	A815	G737
U1558	U1559	G1432	U1493	G1432	U1291	U1222	U1093	U1021	U947	G886	A816	G738
U1559	U1560	A1433	U1494	A1433	U1292	U1223	U1094	U1022	U948	U887	A817	G739
U1560	U1561	C1434	U1495	C1434	U1293	U1224	U1095	U1023	U949	G888	A818	G740
U1561	U1562	U1435	U1496	U1435	U1294	U1225	U1096	U1024	U950	U889	A819	G741
U1562	U1563	G1436	U1497	G1436	U1295	U1226	U1097	U1025	U951	U890	A820	G742
U1563	U1564	A1437	U1498	A1437	U1296	U1227	U1098	U1026	U952	U891	A821	G743
U1564	U1565	U1438	U1499	U1438	U1297	U1228	U1099	U1027	U953	U892	A822	G744
U1565	U1566	G1439	U1500	G1439	U1298	U1229	U1100	U1028	U954	U893	A823	G745
U1566	U1567	U1440	U1501	U1440	U1299	U1230	G1101	U1029	U955	U894	A824	G746
U1567	U1568	A1441	U1502	A1441	U1300	U1231	G1102	A1030	U956	U895	A825	G747
U1568	U1569	G1442	U1503	G1442	U1301	U1232	U1103	A1031	U957	U896	A826	G748
U1569	U1570	U1443	U1504	U1443	U1302	U1233	U1104	A1032	U958	U897	A827	G749
U1570	U1571	A1444	U1505	A1444	U1303	U1234	U1105	A1033	U959	U898	A828	G750
U1571	U1572	G1445	U1506	G1445	U1304	U1235	G1106	A1034	U960	U899	A829	G751
U1572	U1573	U1446	U1507	U1446	U1305	U1236	U1107	A1035	U961	U900	A830	G752
U1573	U1574	C1447	U1508	C1447	U1306	U1237	G1108	A1036	U962	U901	A831	G753
U1574	U1575	U1448	U1509	U1448	U1307	U1238	G1109	A1037	U963	U902	A832	G754
U1575	U1576	A1449	U1510	A1449	U1308	U1239	G1110	A1038	U964	U903	A833	G755
U1576	U1577	G1450	U1511	G1450	U1309	U1240	G1111	A1039	U965	U904	A834	G756
U1577	U1578	U1451	U1512	U1451	U1310	U1241	G1112	A1040	U966	U905	A835	G757
U1578	U1579	G1452	U1513	G1452	U1311	U1242	G1113	A1041	U967	U906	A836	G758
U1579	U1580	U1453	U1514	U1453	U1312	U1243	U1114	A1042	U968	U907	A837	G759
U1580	U1581	C1454	U1515	C1454	U1313	U1244	U1115	A1043	U969	U908	A838	G760
U1581	U1582	U1455	U1516	U1455	U1314	U1245	U1116	A1044	U970	U909	A839	G761
U1582	U1583	G1456	U1517	G1456	U1315	U1246	U1117	A1045	U971	U910	A840	G762
U1583	U1584	U1457	U1518	U1457	U1316	U1247	U1118	A1046	U972	U911	A841	G763
U1584	U1585	C1458	U1519	C1458	U1317	U1248	U1119	A1047	U973	U912	A842	G764
U1585	U1586	U1459	U1520	U1459	U1318	U1249	U1120	A1048	U974	U913	A843	G765
U1586	U1587	G1460	U1521	G1460	U1319	U1250	G1121	U1049	U975	U914	A844	G766
U1587	U1588	C1461	U1522	C1461	U1320	U1251	G1122	U1050	U976	U915	A845	G767
U1588	U1589	U1462	U1523	U1462	U1321	U1252	G1123	U1051	U977	U916	A846	G768
U1589	U1590	G1463	U1524	G1463	U1322	U1253	G1124	U1052	U978	U917	A847	G769
U1590	U1591	U1464	U1525	U1464	U1323	U1254	G1125	U1053	U979	U918	A848	G770
U1591	U1592	C1465	U1526	C1465	U1324	U1255	G1126	U1054	U980	U919	A849	G771
U1592	U1593	U1466	U1527	U1466	U1325	U1256	G1127	U1055	U981	U920	A850	G772
U1593	U1594	A1467	U1528	A1467	U1326	U1257	U1128	U1056	U982	U921	A851	G773
U1594	U1595	G1468	U									

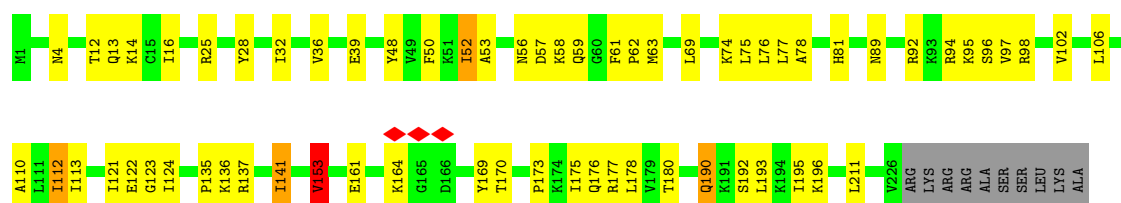




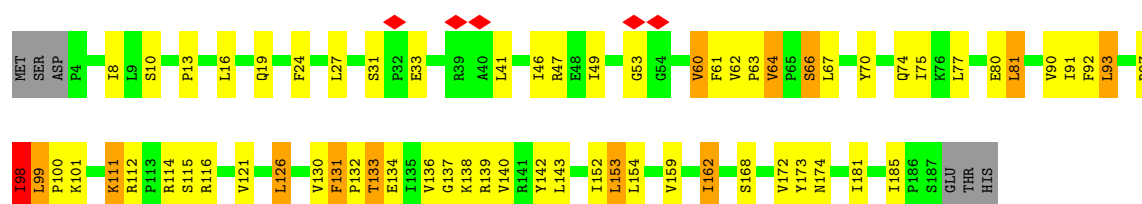
• Molecule 5: eS4



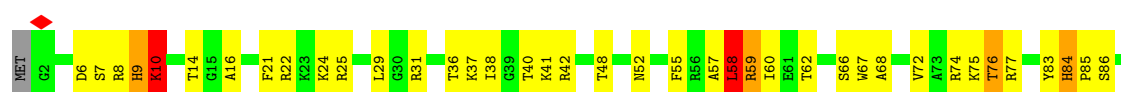
• Molecule 6: eS6

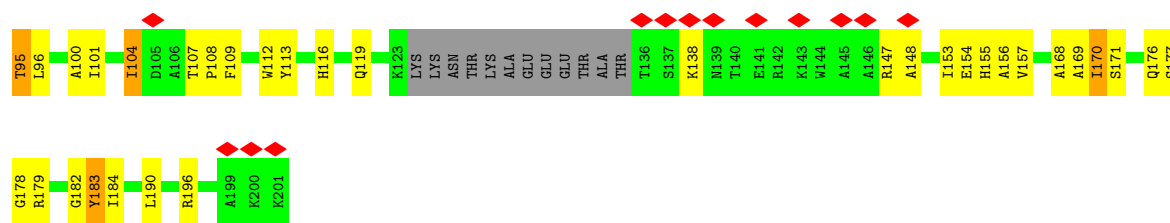


• Molecule 7: eS7

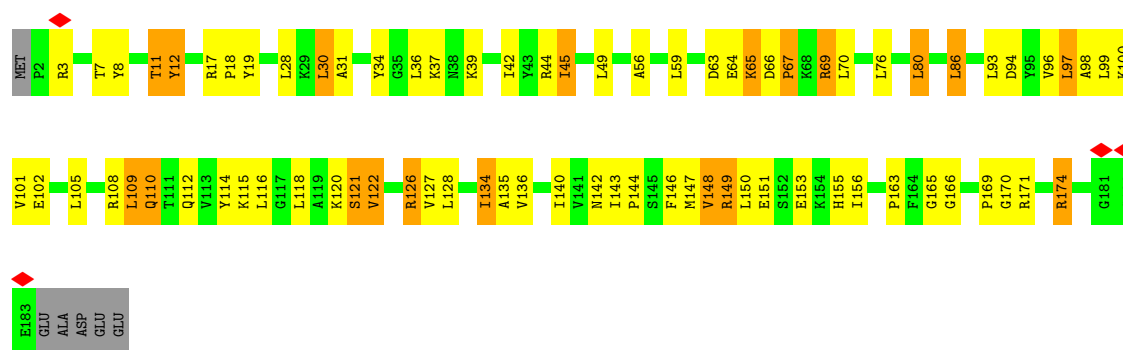


• Molecule 8: eS8

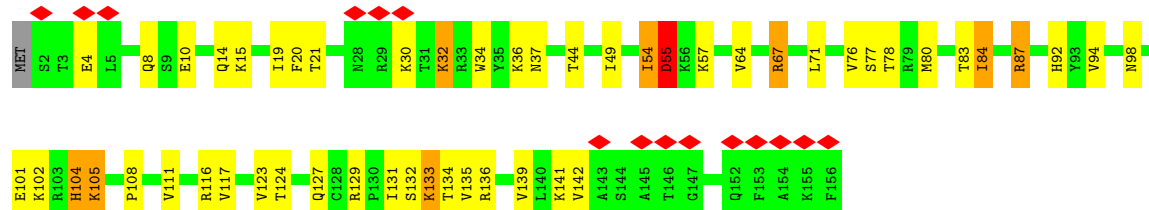




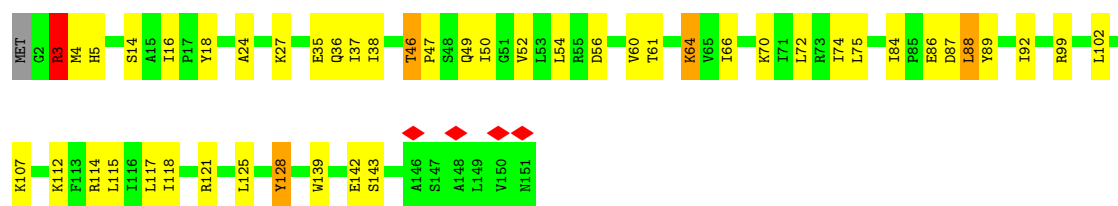
• Molecule 9: uS4



• Molecule 10: uS17



• Molecule 11: uS15

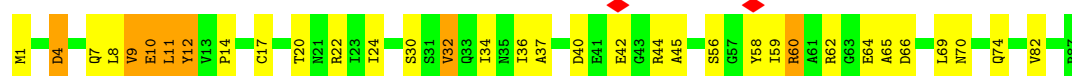


• Molecule 12: uS11

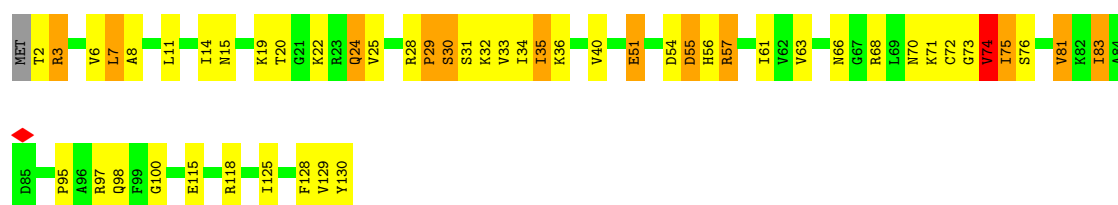




• Molecule 13: eS21



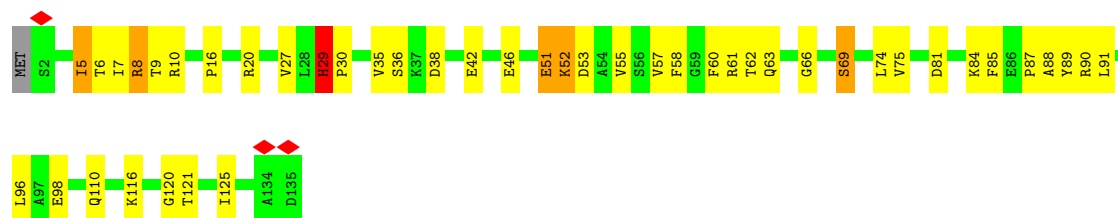
• Molecule 14: uS8



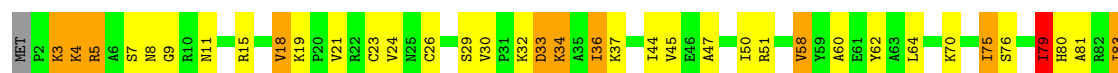
• Molecule 15: uS12

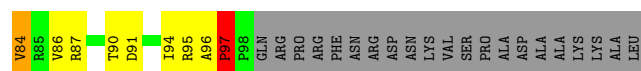


• Molecule 16: eS24

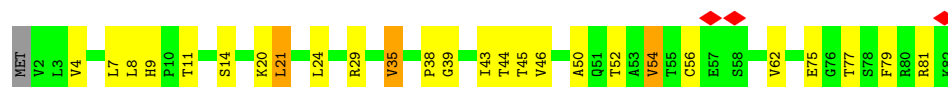


• Molecule 17: eS26





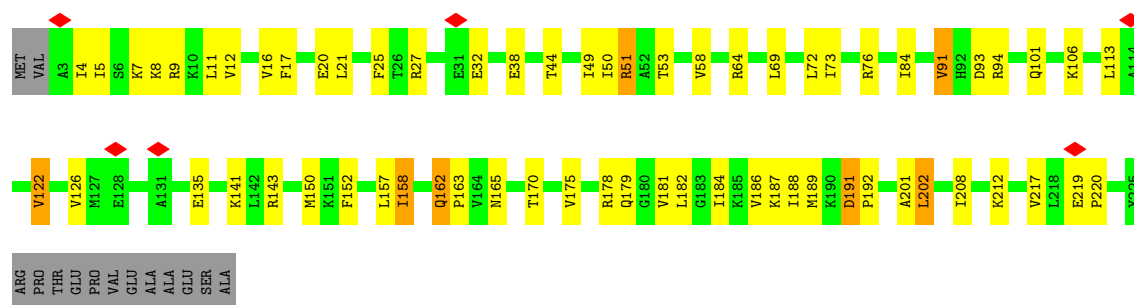
• Molecule 18: eS27



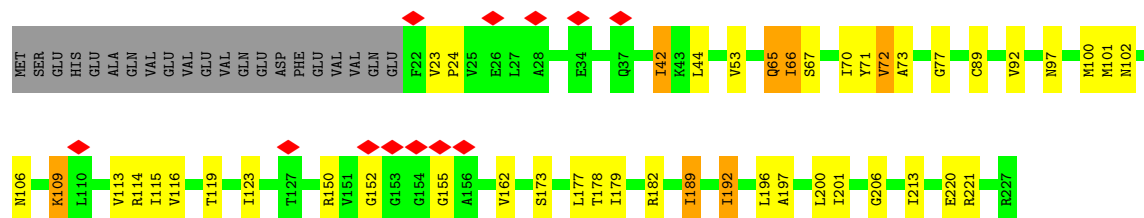
• Molecule 19: eS30



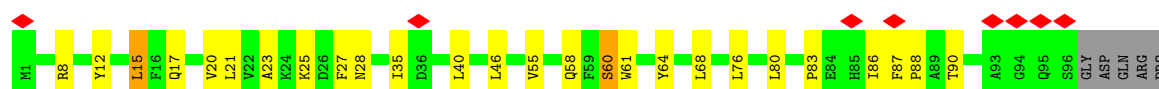
• Molecule 20: uS3



• Molecule 21: uS7



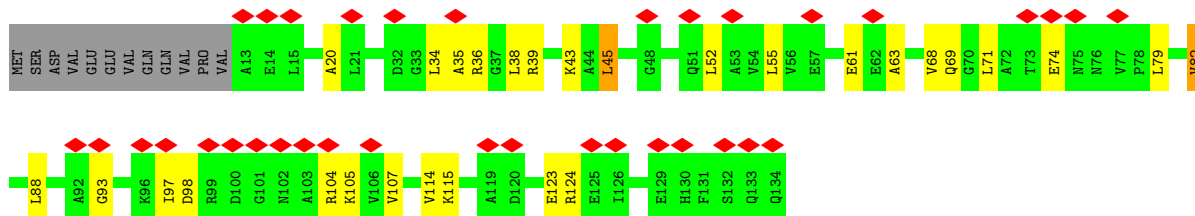
• Molecule 22: eS10



GLN
GLY
LYS
TYR

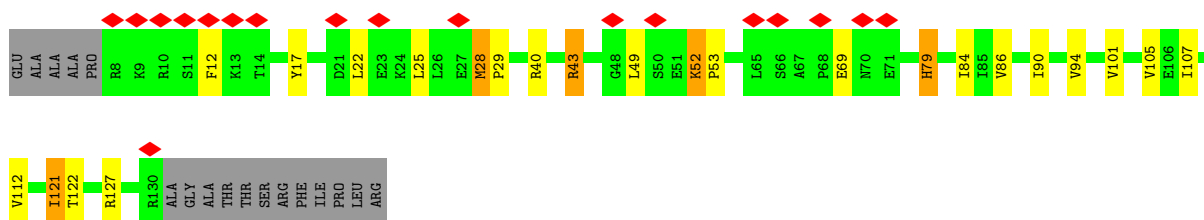
• Molecule 23: eS12

Chain M: 



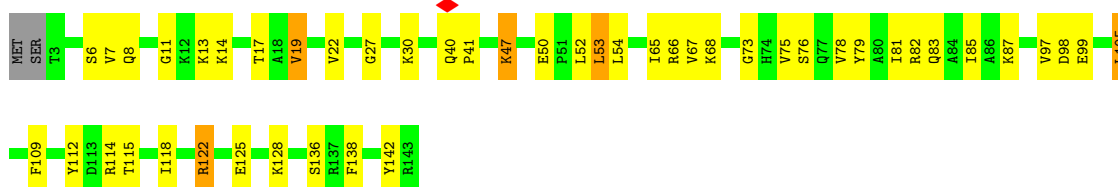
• Molecule 24: uS19

Chain P: 



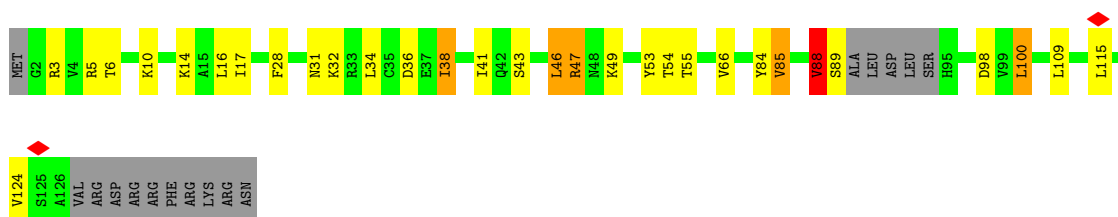
• Molecule 25: uS9

Chain Q: 



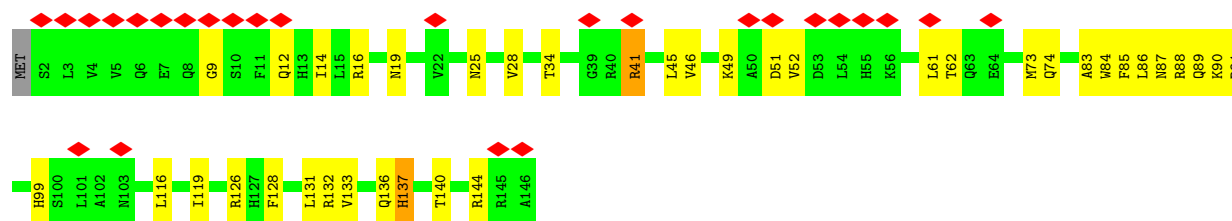
• Molecule 26: eS17

Chain R: 

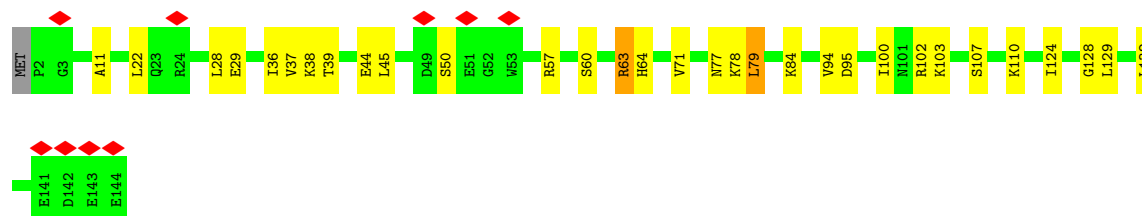
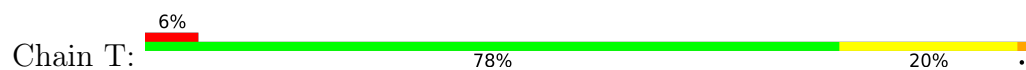


• Molecule 27: uS13

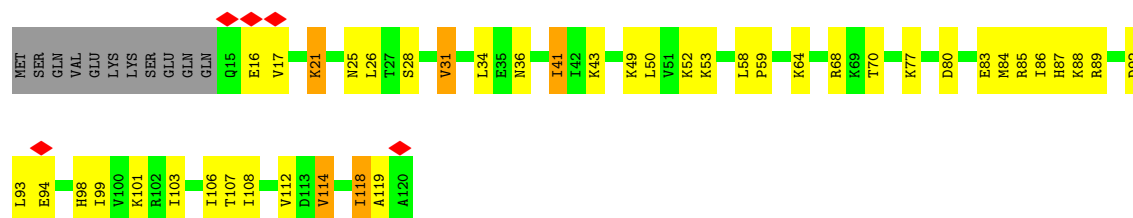
Chain S: 



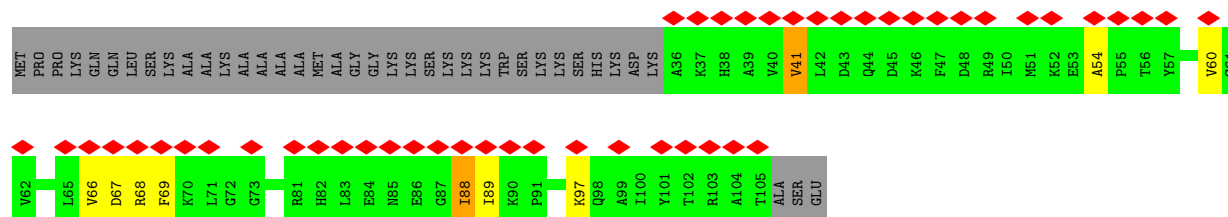
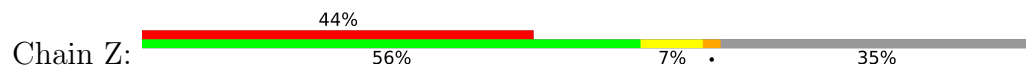
• Molecule 28: eS19



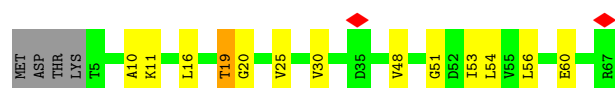
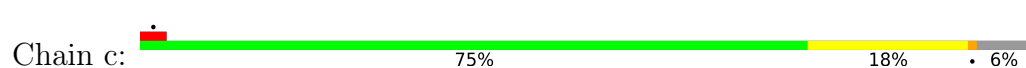
• Molecule 29: uS10



• Molecule 30: eS25

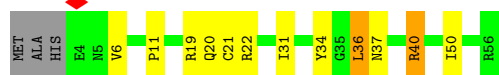


• Molecule 31: eS28



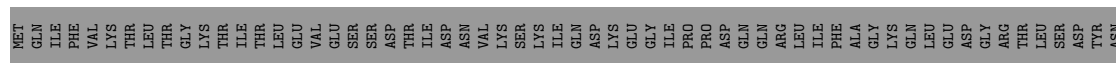
• Molecule 32: uS14

Chain d: 



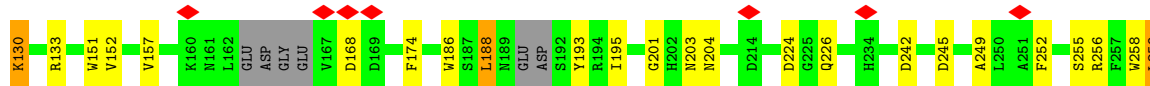
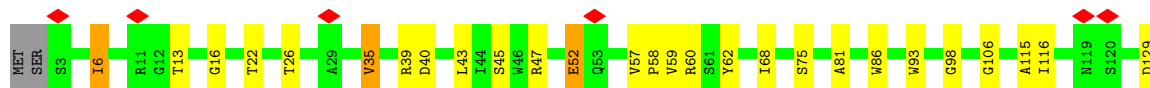
• Molecule 33: eS31

Chain f: 



• Molecule 34: RACK1

Chain g: 



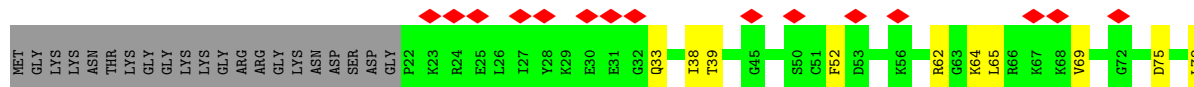
• Molecule 35: eL41

Chain h: 



• Molecule 36: eIF1A

Chain i: 



● Molecule 37: eIF1



MET	SER	ILE	GLU	ASN	LEU	LYS	SER	PHE	ASP	PRO	PHE	ALA	ASP	THR	GLY	ASP	ASP	GLU	THR	ALA	THR	S23	N24	H27	I28	R29	I30	T40	T41	V42	Q43	K70	D71	P72	E73	M74	G75	E76	I77	I78	Q79	R85	A86	K87	E90	L98	Q99	K100	K101	G107	F108
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	100709	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	104478	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.602	Depositor
Minimum map value	-0.221	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.065	Depositor
Map size ($\text{\AA}$)	402.0, 402.0, 402.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.34, 1.34, 1.34	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	2	0.41	0/42244	0.81	52/65823 (0.1%)
2	A	0.55	0/1656	1.13	6/2264 (0.3%)
3	B	0.52	0/1747	1.02	3/2353 (0.1%)
4	C	0.55	0/1659	1.08	0/2252
5	E	0.50	0/2122	0.97	4/2861 (0.1%)
6	G	0.52	0/1835	0.97	1/2451 (0.0%)
7	H	0.57	0/1507	1.05	1/2028 (0.0%)
8	I	0.52	0/1519	1.04	5/2033 (0.2%)
9	J	0.56	0/1495	1.12	0/2001
10	L	0.57	0/1276	0.97	0/1718
11	N	0.54	0/1210	1.21	6/1628 (0.4%)
12	O	0.54	0/953	1.03	1/1279 (0.1%)
13	V	0.56	0/696	0.99	1/938 (0.1%)
14	W	0.59	0/1039	1.20	4/1399 (0.3%)
15	X	0.59	0/1137	1.14	4/1516 (0.3%)
16	Y	0.50	0/1075	1.07	2/1433 (0.1%)
17	a	0.64	1/782 (0.1%)	1.06	1/1047 (0.1%)
18	b	0.53	0/619	0.96	1/837 (0.1%)
19	e	0.51	0/435	0.96	0/579
20	D	0.55	0/1769	1.04	2/2378 (0.1%)
21	F	0.53	0/1628	1.11	2/2198 (0.1%)
22	K	0.53	0/831	1.08	2/1123 (0.2%)
23	M	0.59	0/929	1.05	0/1255
24	P	0.58	0/1000	0.99	2/1343 (0.1%)
25	Q	0.53	0/1125	1.05	0/1510
26	R	0.59	0/969	1.07	1/1299 (0.1%)
27	S	0.53	0/1212	1.02	0/1629
28	T	0.50	0/1129	1.07	0/1520
29	U	0.58	0/857	1.00	0/1158
30	Z	0.61	0/567	1.03	0/762
31	c	0.58	0/496	0.93	0/666
32	d	0.54	0/457	0.87	0/607

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.66	0/562	0.98	0/751
34	g	0.55	0/2521	0.85	0/3431
35	h	0.45	0/234	1.14	0/300
36	i	0.54	0/788	0.88	0/1051
37	j	0.55	0/703	1.03	2/938 (0.2%)
All	All	0.48	1/82783 (0.0%)	0.92	103/120359 (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
7	H	0	1
9	J	0	1
14	W	0	1
15	X	0	2
16	Y	0	1
17	a	0	1
25	Q	0	1
All	All	0	8

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	a	97	PRO	CA-C	5.22	1.57	1.52

The worst 5 of 103 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	X	41	SER	CA-C-N	9.02	131.12	119.84
15	X	41	SER	C-N-CA	9.02	131.12	119.84
17	a	97	PRO	N-CA-C	8.92	121.58	110.70
8	I	183	TYR	N-CA-C	8.78	123.39	108.02
1	2	828	A	C2'-C3'-O3'	8.59	122.39	109.50

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	H	131	PHE	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
9	J	12	TYR	Peptide
14	W	75	ILE	Peptide
15	X	11	SER	Peptide
15	X	63	GLN	Peptide

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	2	37775	0	19004	720	0
2	A	1616	0	1636	36	0
3	B	1722	0	1795	27	0
4	C	1629	0	1710	43	0
5	E	2078	0	2157	38	0
6	G	1812	0	1911	33	0
7	H	1483	0	1579	29	0
8	I	1493	0	1515	29	0
9	J	1471	0	1554	43	0
10	L	1248	0	1311	25	0
11	N	1187	0	1251	18	0
12	O	942	0	979	16	0
13	V	687	0	682	15	0
14	W	1021	0	1056	36	0
15	X	1119	0	1198	22	0
16	Y	1061	0	1111	17	0
17	a	770	0	822	28	0
18	b	609	0	631	10	0
19	e	428	0	468	7	0
20	D	1744	0	1826	28	0
21	F	1609	0	1679	20	0
22	K	809	0	810	10	0
23	M	922	0	953	10	0
24	P	980	0	1026	10	0
25	Q	1105	0	1170	22	0
26	R	959	0	1006	13	0
27	S	1193	0	1217	21	0
28	T	1110	0	1124	16	0
29	U	845	0	913	14	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	Z	558	0	585	3	0
31	c	494	0	534	5	0
32	d	446	0	436	3	0
33	f	549	0	564	4	0
34	g	2466	0	2406	35	0
35	h	233	0	284	6	0
36	i	778	0	779	7	0
37	j	695	0	729	5	0
38	2	67	0	0	0	0
39	a	1	0	0	0	0
39	b	1	0	0	0	0
39	f	1	0	0	0	0
All	All	77716	0	60411	1281	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 9.

The worst 5 of 1281 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1037:U:H3	1:2:1091:A:N6	1.23	1.32
1:2:1290:G:N2	1:2:1323:G:H22	1.28	1.28
1:2:991:A:N1	1:2:1011:U:O4	1.78	1.15
1:2:991:A:N1	1:2:1011:U:C4	2.17	1.12
1:2:1290:G:H22	1:2:1323:G:N2	1.56	1.03

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	204/254 (80%)	167 (82%)	24 (12%)	13 (6%)	1	13
3	B	212/255 (83%)	175 (82%)	25 (12%)	12 (6%)	1	14
4	C	215/259 (83%)	182 (85%)	23 (11%)	10 (5%)	2	17
5	E	258/261 (99%)	215 (83%)	36 (14%)	7 (3%)	4	26
6	G	224/236 (95%)	196 (88%)	24 (11%)	4 (2%)	6	32
7	H	182/190 (96%)	152 (84%)	15 (8%)	15 (8%)	0	9
8	I	184/201 (92%)	146 (79%)	26 (14%)	12 (6%)	1	13
9	J	180/188 (96%)	148 (82%)	20 (11%)	12 (7%)	1	13
10	L	153/156 (98%)	129 (84%)	18 (12%)	6 (4%)	2	20
11	N	148/151 (98%)	127 (86%)	17 (12%)	4 (3%)	4	26
12	O	125/137 (91%)	98 (78%)	20 (16%)	7 (6%)	1	15
13	V	85/87 (98%)	67 (79%)	11 (13%)	7 (8%)	0	9
14	W	127/130 (98%)	109 (86%)	13 (10%)	5 (4%)	2	20
15	X	142/145 (98%)	115 (81%)	13 (9%)	14 (10%)	0	7
16	Y	132/135 (98%)	114 (86%)	10 (8%)	8 (6%)	1	14
17	a	95/119 (80%)	64 (67%)	21 (22%)	10 (10%)	0	6
18	b	79/82 (96%)	62 (78%)	12 (15%)	5 (6%)	1	13
19	e	51/63 (81%)	47 (92%)	3 (6%)	1 (2%)	6	31
20	D	221/237 (93%)	197 (89%)	18 (8%)	6 (3%)	4	26
21	F	204/227 (90%)	169 (83%)	25 (12%)	10 (5%)	1	17
22	K	94/106 (89%)	81 (86%)	11 (12%)	2 (2%)	5	30
23	M	120/134 (90%)	96 (80%)	20 (17%)	4 (3%)	3	23
24	P	121/140 (86%)	99 (82%)	16 (13%)	6 (5%)	1	16
25	Q	139/143 (97%)	120 (86%)	15 (11%)	4 (3%)	3	25
26	R	116/136 (85%)	93 (80%)	18 (16%)	5 (4%)	2	19
27	S	143/146 (98%)	113 (79%)	23 (16%)	7 (5%)	1	17
28	T	141/144 (98%)	123 (87%)	15 (11%)	3 (2%)	5	30
29	U	104/117 (89%)	91 (88%)	5 (5%)	8 (8%)	1	11
30	Z	68/108 (63%)	53 (78%)	10 (15%)	5 (7%)	1	11
31	c	61/67 (91%)	55 (90%)	6 (10%)	0	100	100
32	d	51/56 (91%)	41 (80%)	9 (18%)	1 (2%)	6	31
33	f	67/150 (45%)	43 (64%)	17 (25%)	7 (10%)	0	6

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	g	312/326 (96%)	256 (82%)	48 (15%)	8 (3%)	4	27
35	h	23/25 (92%)	23 (100%)	0	0	100	100
36	i	94/153 (61%)	86 (92%)	8 (8%)	0	100	100
37	j	84/108 (78%)	75 (89%)	8 (10%)	1 (1%)	10	39
All	All	4959/5572 (89%)	4127 (83%)	603 (12%)	229 (5%)	3	18

5 of 229 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	26	ALA
2	A	95	ALA
3	B	100	PHE
3	B	117	TRP
4	C	141	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	174/211 (82%)	143 (82%)	31 (18%)	2	12
3	B	196/228 (86%)	176 (90%)	20 (10%)	7	27
4	C	176/203 (87%)	145 (82%)	31 (18%)	2	12
5	E	223/224 (100%)	189 (85%)	34 (15%)	3	16
6	G	192/200 (96%)	171 (89%)	21 (11%)	6	25
7	H	164/170 (96%)	139 (85%)	25 (15%)	3	16
8	I	148/159 (93%)	122 (82%)	26 (18%)	2	12
9	J	153/158 (97%)	122 (80%)	31 (20%)	1	8
10	L	136/137 (99%)	115 (85%)	21 (15%)	2	15
11	N	127/128 (99%)	108 (85%)	19 (15%)	3	16
12	O	96/104 (92%)	89 (93%)	7 (7%)	13	38
13	V	73/73 (100%)	57 (78%)	16 (22%)	1	6

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	W	110/111 (99%)	93 (84%)	17 (16%)	2	15
15	X	119/120 (99%)	100 (84%)	19 (16%)	2	14
16	Y	108/109 (99%)	86 (80%)	22 (20%)	1	8
17	a	82/100 (82%)	61 (74%)	21 (26%)	0	4
18	b	71/72 (99%)	60 (84%)	11 (16%)	2	15
19	e	47/55 (86%)	43 (92%)	4 (8%)	10	33
20	D	185/196 (94%)	160 (86%)	25 (14%)	4	18
21	F	174/194 (90%)	155 (89%)	19 (11%)	6	25
22	K	88/96 (92%)	77 (88%)	11 (12%)	4	21
23	M	97/109 (89%)	88 (91%)	9 (9%)	8	31
24	P	105/117 (90%)	96 (91%)	9 (9%)	10	33
25	Q	117/119 (98%)	99 (85%)	18 (15%)	2	15
26	R	109/124 (88%)	93 (85%)	16 (15%)	3	17
27	S	128/129 (99%)	112 (88%)	16 (12%)	4	21
28	T	117/118 (99%)	108 (92%)	9 (8%)	12	36
29	U	96/107 (90%)	81 (84%)	15 (16%)	2	15
30	Z	60/88 (68%)	58 (97%)	2 (3%)	33	54
31	c	55/59 (93%)	49 (89%)	6 (11%)	6	25
32	d	46/48 (96%)	37 (80%)	9 (20%)	1	8
33	f	58/133 (44%)	52 (90%)	6 (10%)	7	27
34	g	265/272 (97%)	243 (92%)	22 (8%)	10	34
35	h	23/23 (100%)	19 (83%)	4 (17%)	2	12
36	i	83/130 (64%)	81 (98%)	2 (2%)	43	61
37	j	77/96 (80%)	72 (94%)	5 (6%)	15	41
All	All	4278/4720 (91%)	3699 (86%)	579 (14%)	6	18

5 of 579 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
25	Q	122	ARG
36	i	97	LEU
26	R	54	THR
25	Q	118	ILE
29	U	103	ILE

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

Mol	Chain	Res	Type
19	e	57	ASN
27	S	27	ASN
20	D	195	ASN
23	M	76	ASN
28	T	25	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1777/1799 (98%)	850 (47%)	132 (7%)

5 of 850 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	3	U
1	2	4	C
1	2	5	U
1	2	11	A

5 of 132 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	1570	G
1	2	1613	C
1	2	1788	A
1	2	577	U
1	2	566	A

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 70 ligands modelled in this entry, 70 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

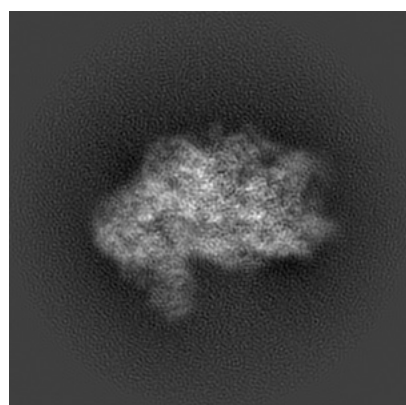
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2764. These allow visual inspection of the internal detail of the map and identification of artifacts.

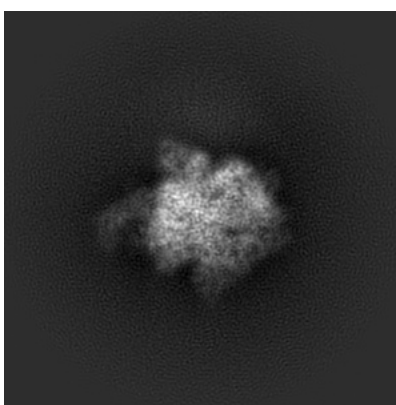
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

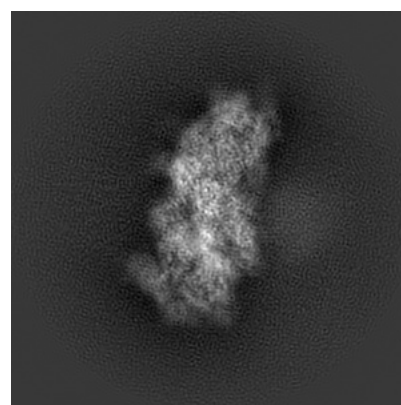
6.1.1 Primary map



X



Y

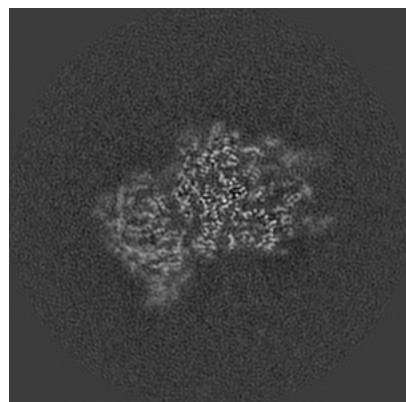


Z

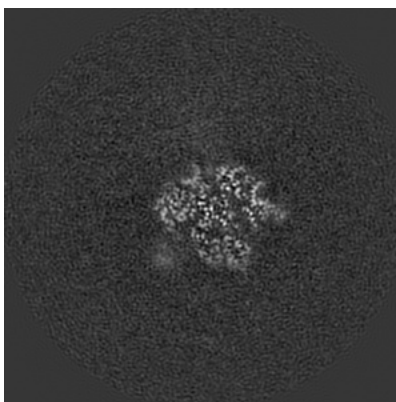
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

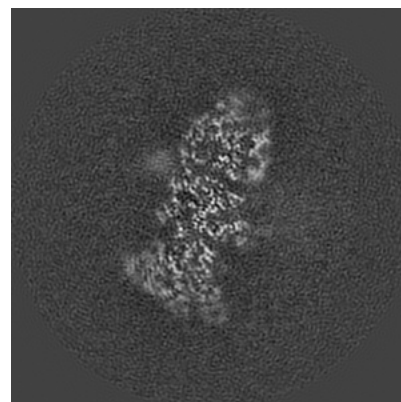
6.2.1 Primary map



X Index: 150



Y Index: 150

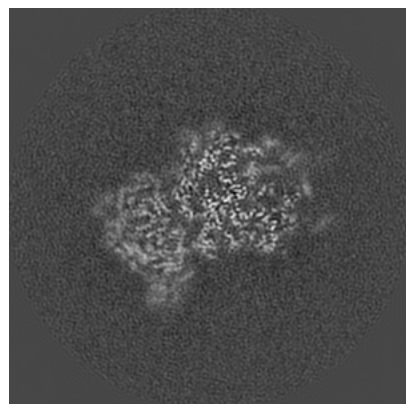


Z Index: 150

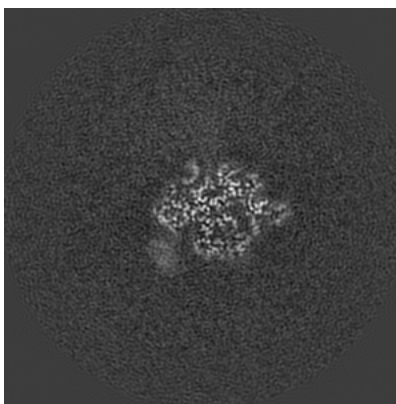
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

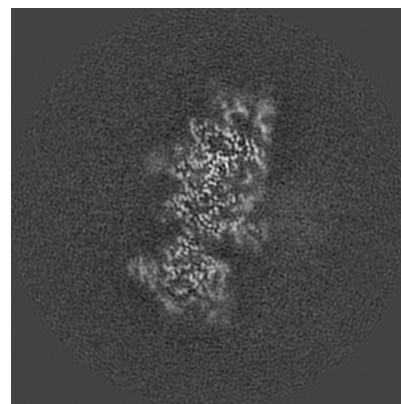
6.3.1 Primary map



X Index: 149



Y Index: 153

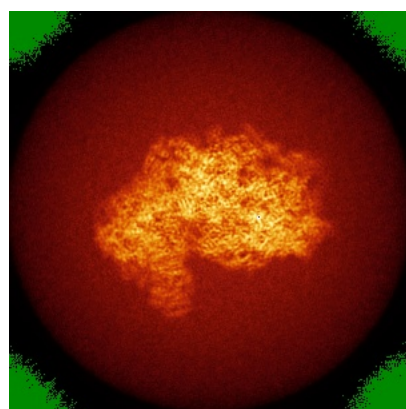


Z Index: 145

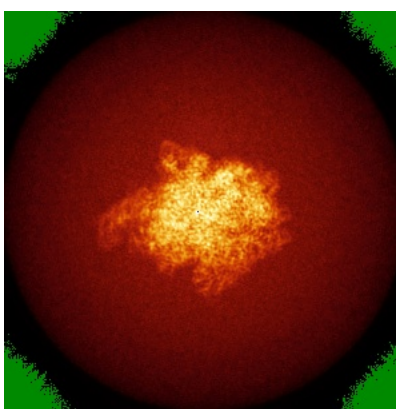
The images above show the largest variance slices of the map in three orthogonal directions.

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

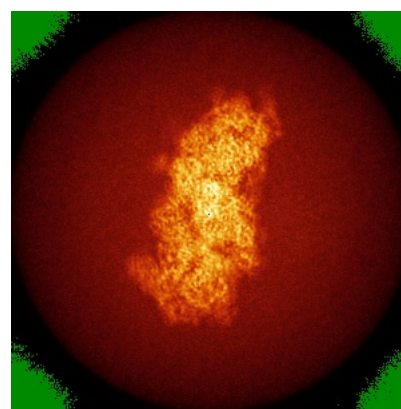
6.4.1 Primary map



X



Y

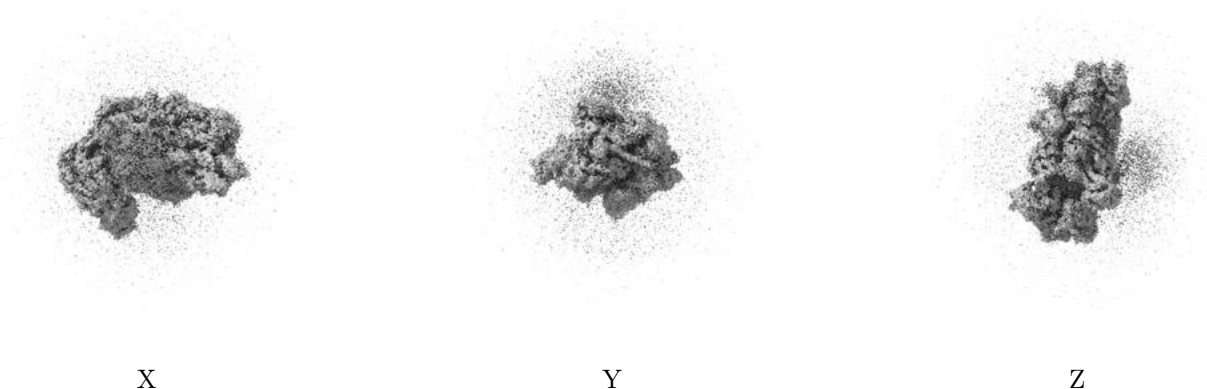


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.065. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

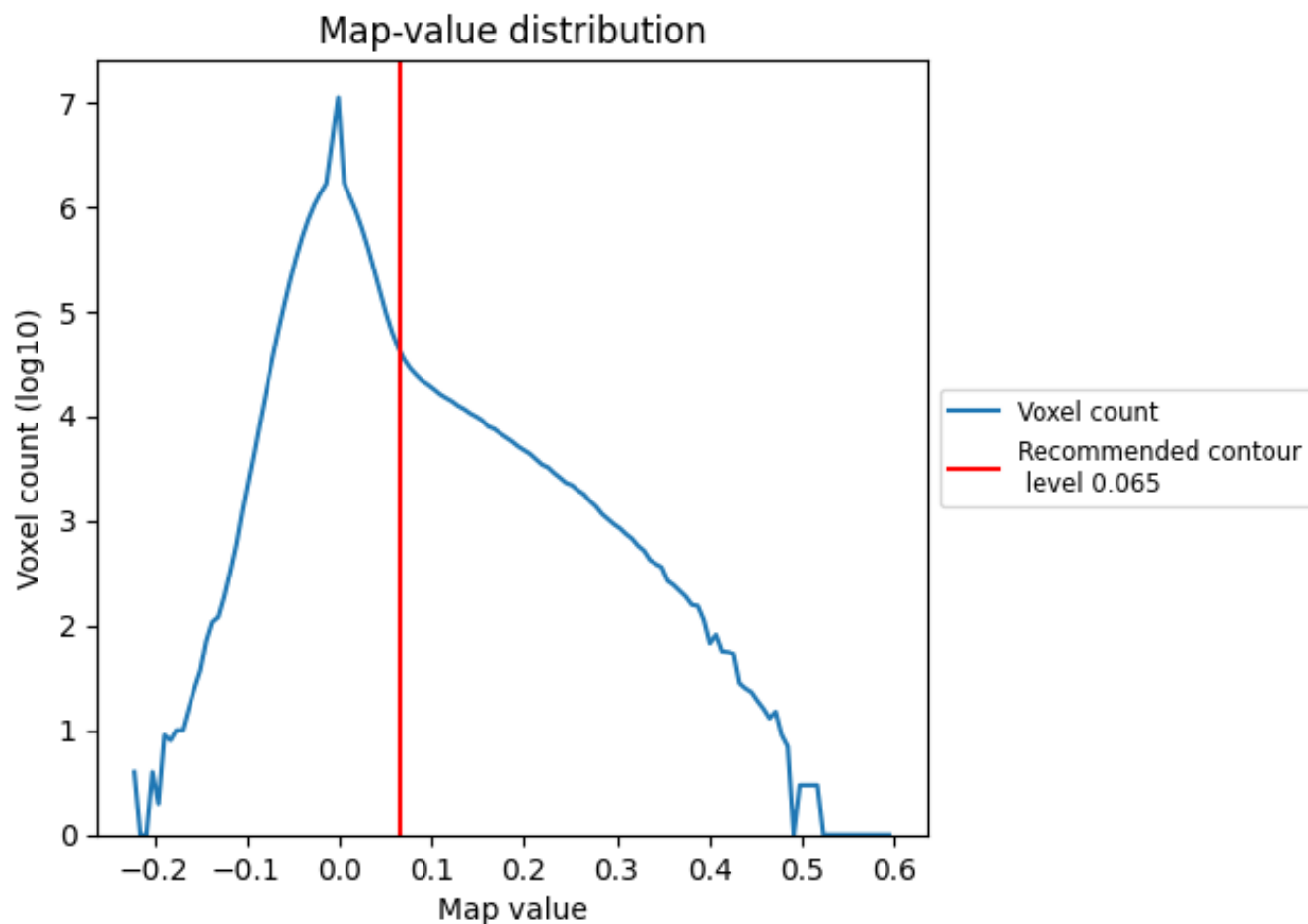
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

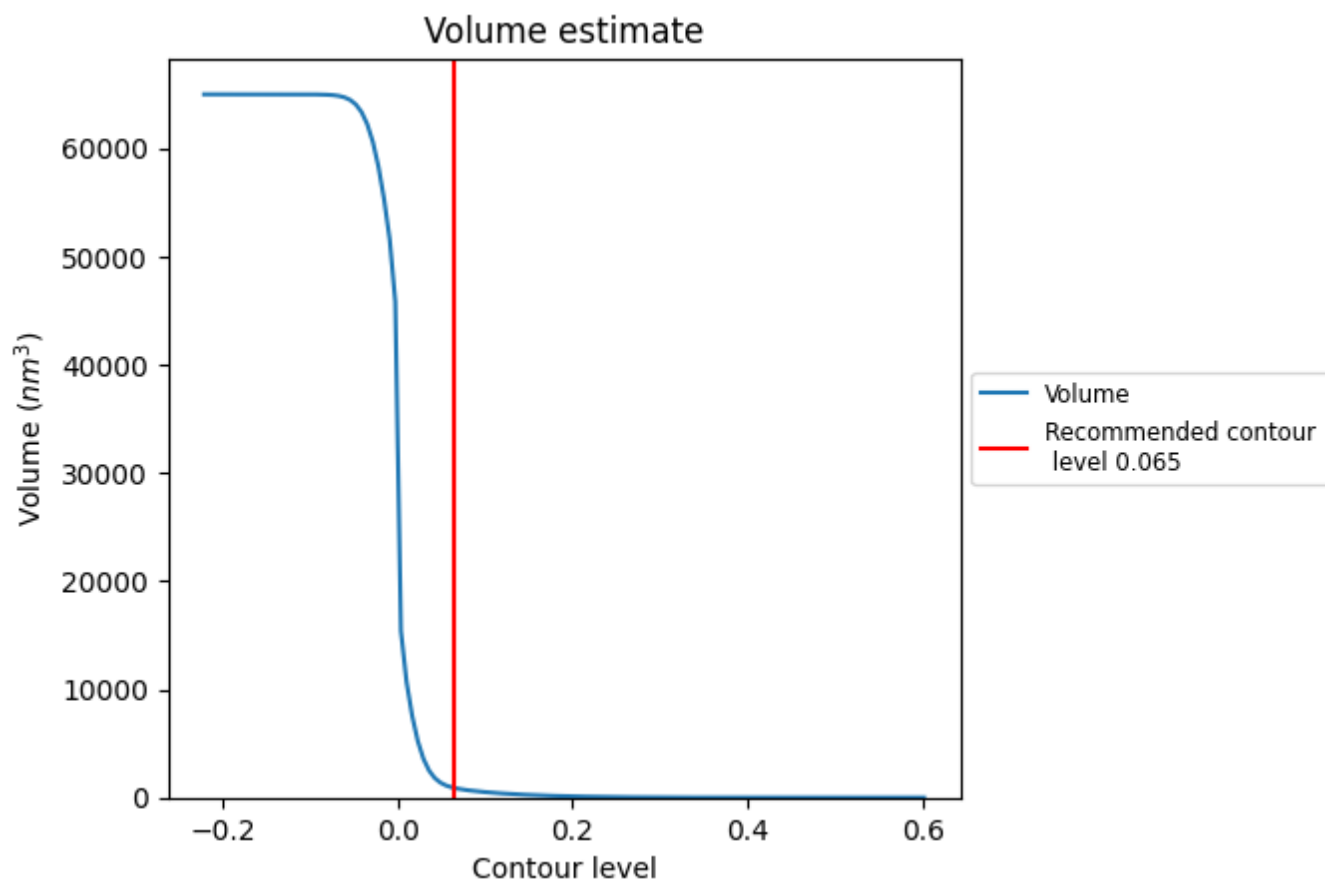
This section contains the results of statistical analysis of the map.

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.

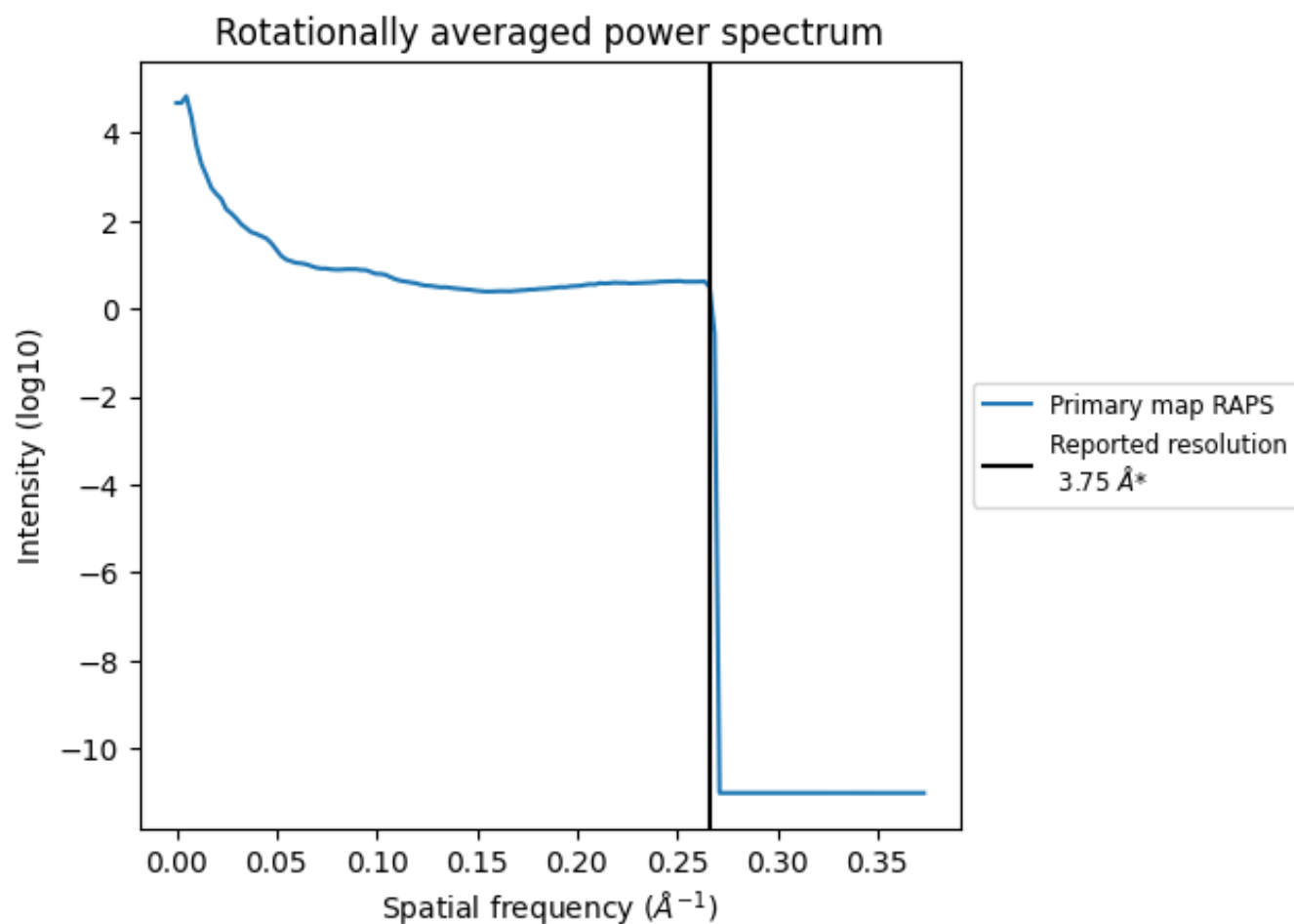
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 888 nm³; this corresponds to an approximate mass of 802 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 ⓘ

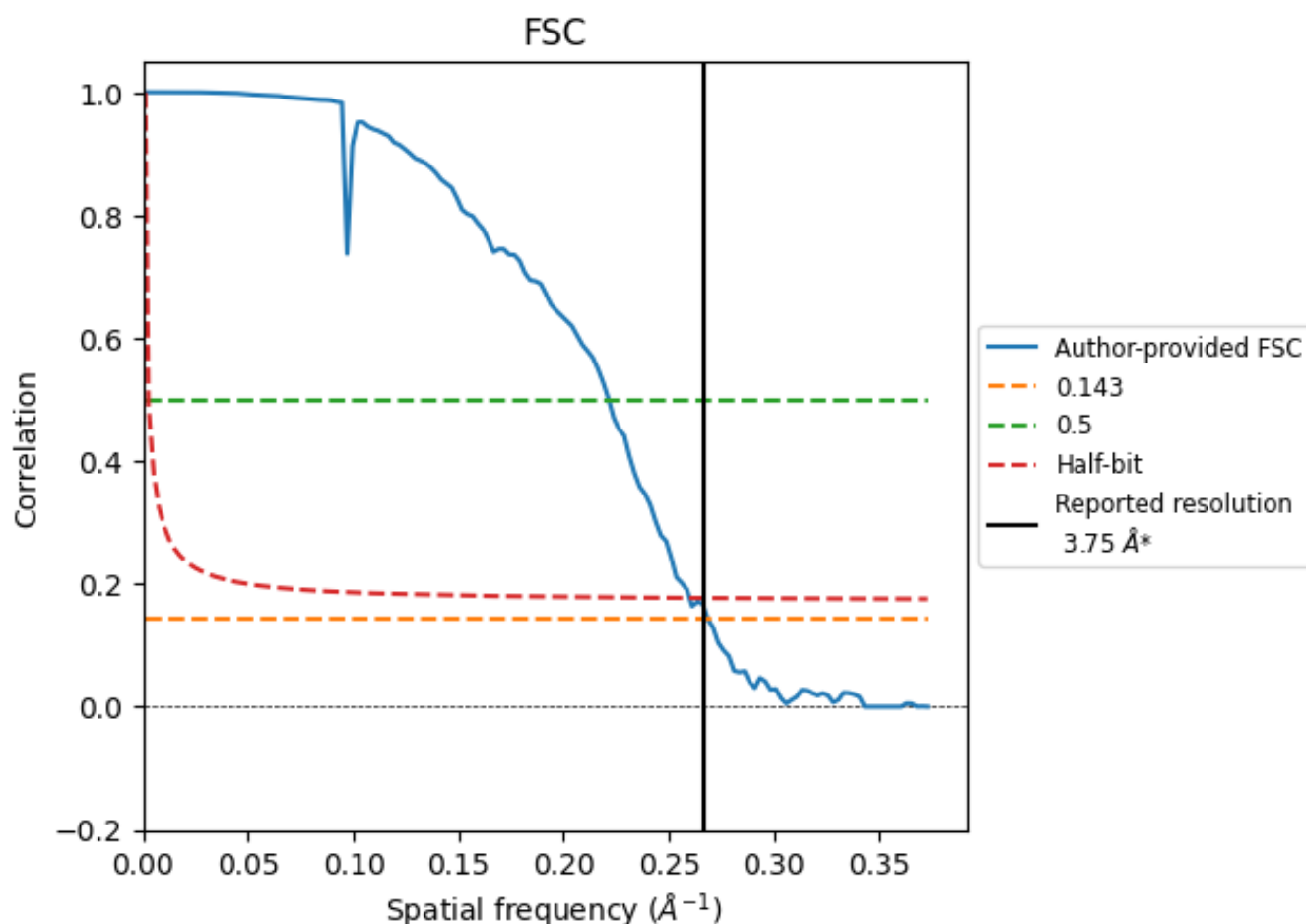


*Reported resolution corresponds to spatial frequency of 0.267 Å⁻¹

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 0.267 Å⁻¹

8.2 Resolution estimates [i](#)

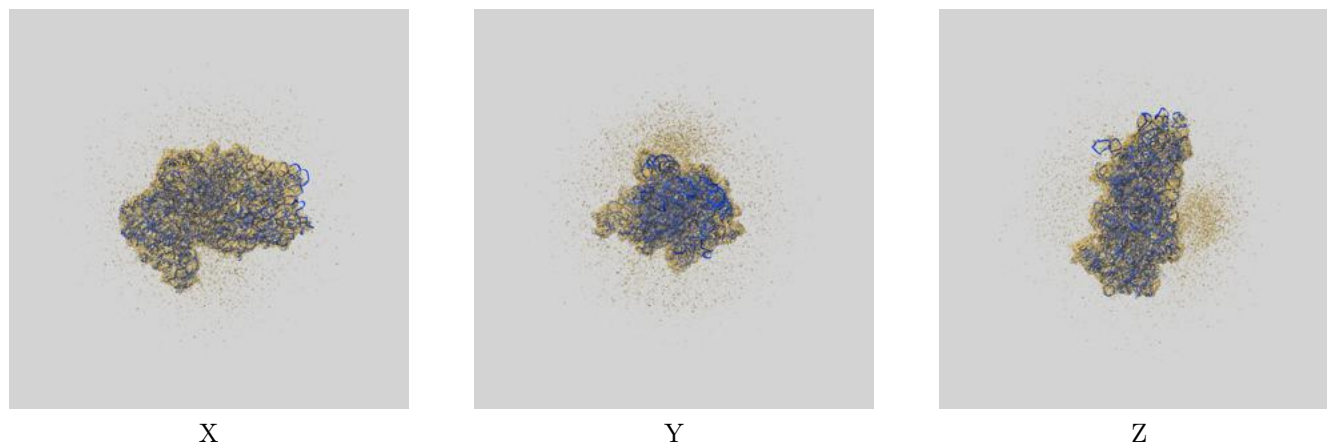
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.75	-	-
Author-provided FSC curve	3.72	4.51	3.85
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

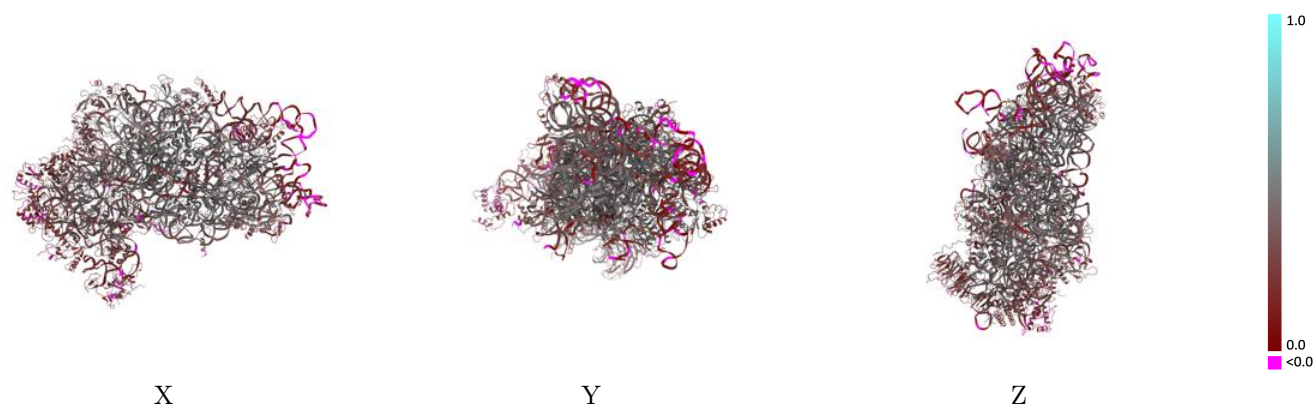
This section contains information regarding the fit between EMDB map EMD-2764 and PDB model 3J80. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

9.1 Map-model overlay [i](#)



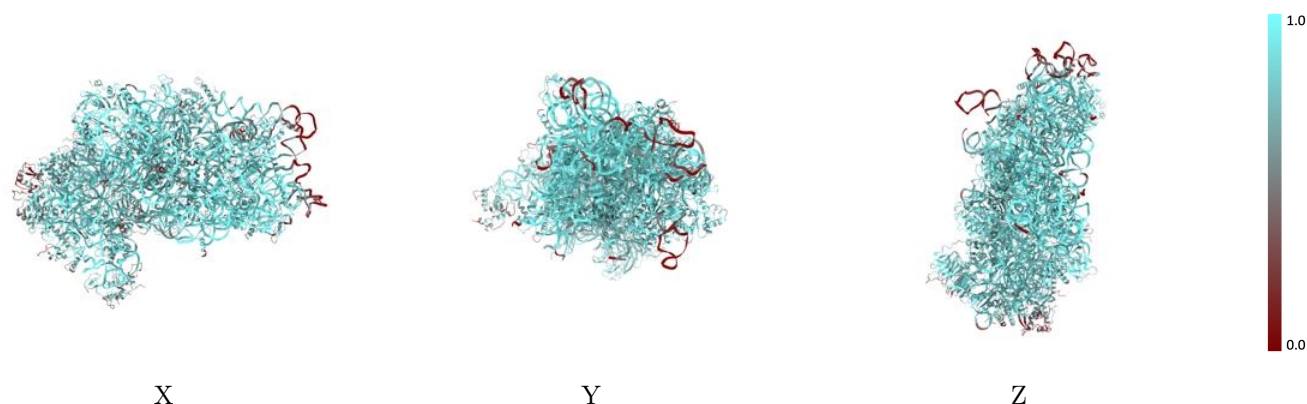
The images above show the 3D surface view of the map at the recommended contour level 0.065 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



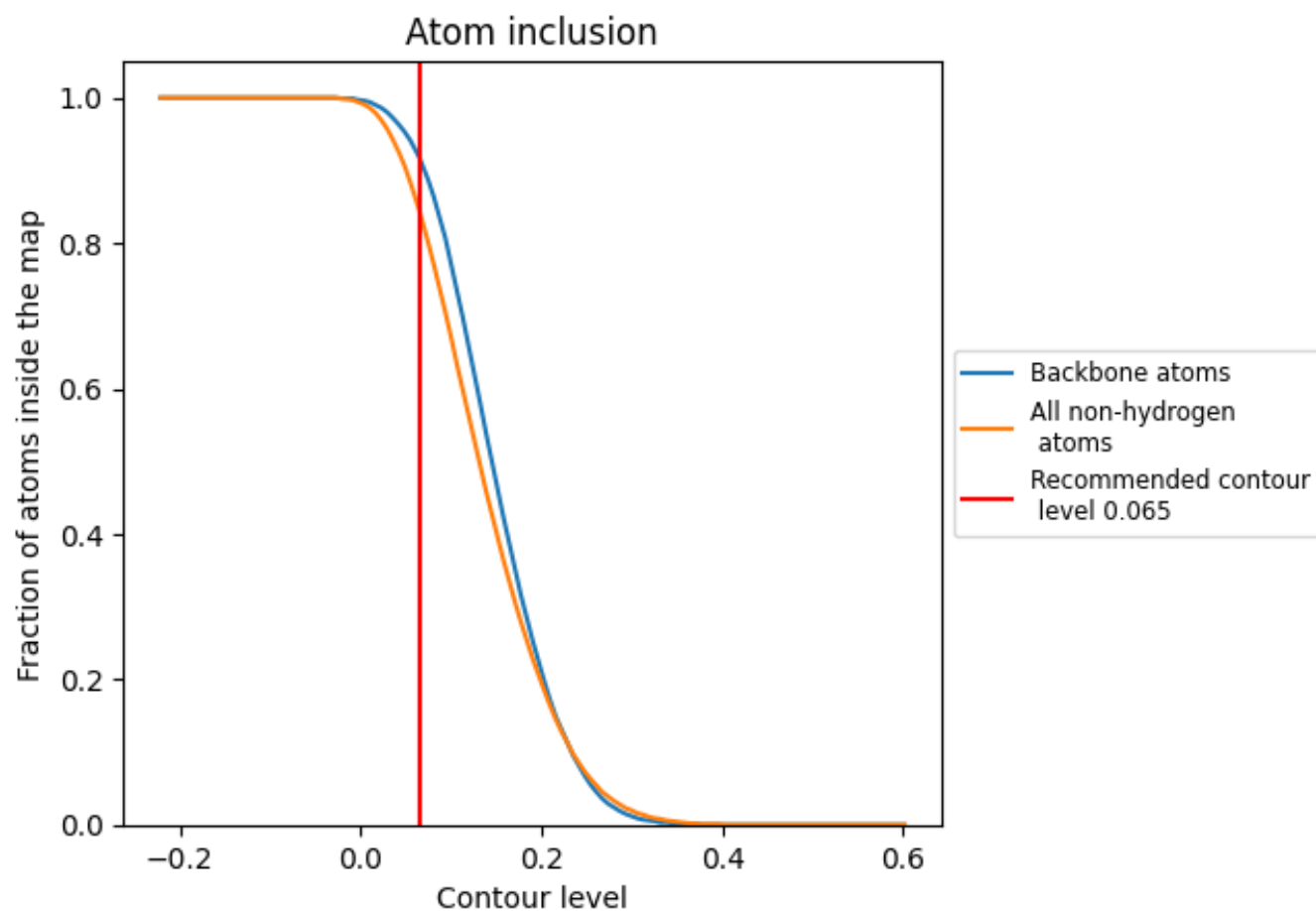
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.065).

9.4 Atom inclusion ⓘ



At the recommended contour level, 92% of all backbone atoms, 84% 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 (0.065) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8450	 0.3520
2	 0.9050	 0.3540
A	 0.8570	 0.3850
B	 0.8540	 0.3740
C	 0.8300	 0.4160
D	 0.7950	 0.3480
E	 0.8200	 0.4300
F	 0.7520	 0.3020
G	 0.8220	 0.3550
H	 0.8350	 0.3620
I	 0.8140	 0.3700
J	 0.8500	 0.4050
K	 0.7700	 0.3070
L	 0.7970	 0.4240
M	 0.5660	 0.1740
N	 0.8310	 0.3940
O	 0.8300	 0.3670
P	 0.7000	 0.2230
Q	 0.8010	 0.3550
R	 0.8100	 0.3420
S	 0.6330	 0.1820
T	 0.7560	 0.2730
U	 0.7690	 0.3710
V	 0.8280	 0.3890
W	 0.8720	 0.4450
X	 0.8880	 0.4490
Y	 0.8470	 0.3980
Z	 0.2820	 0.1170
a	 0.8660	 0.4390
b	 0.8610	 0.4120
c	 0.7720	 0.3420
d	 0.8690	 0.4280
e	 0.8070	 0.3920
f	 0.6930	 0.1990
g	 0.7810	 0.2890



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
h	 0.5420	 0.3260
i	 0.5330	 0.2640
j	 0.6930	 0.3040