



wwPDB EM Validation Summary Report ⓘ

Dec 12, 2022 – 09:15 am GMT

PDB ID : 6YAN
EMDB ID : EMD-10762
Title : Mammalian 48S late-stage translation initiation complex with histone 4 mRNA
Authors : Bochler, A.; Simonetti, A.; Guca, E.; Hashem, Y.
Deposited on : 2020-03-12
Resolution : 3.48 Å (reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

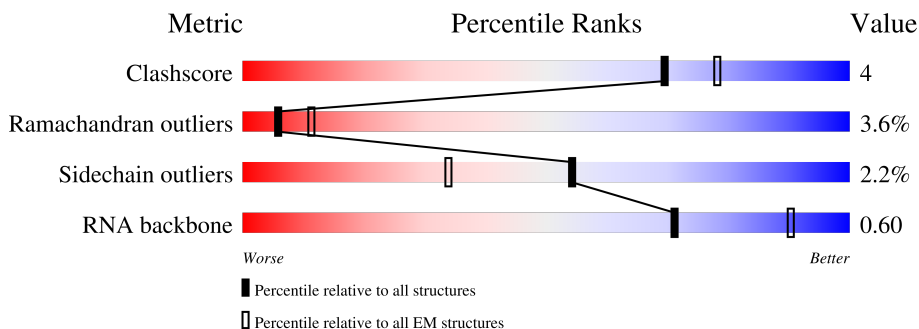
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

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 3.48 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	l	25	
2	C	208	
3	D	215	
4	E	226	
5	F	227	
6	G	263	
7	H	191	

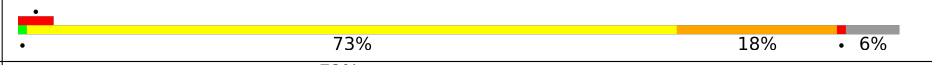



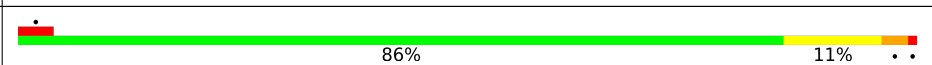

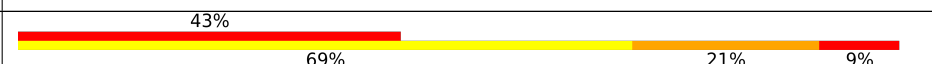
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Mol	Chain	Length	Quality of chain
8	I	237	8% 93% 7%
9	J	190	17% 89% 10%
10	K	206	7% 95% ..
11	L	182	. 94% 6%
12	M	98	12% 87% 12%
13	N	158	15% 92% 6%
14	O	124	44% 95% 5%
15	P	150	5% 98% .
16	Q	136	. 93% 7%
17	S	141	. 90% 10%
18	T	126	8% 98% .
19	V	141	. 94% 5%
20	W	104	5% 93% 7%
21	X	82	. 98% .
22	Y	129	. 98% .
23	Z	142	. 96% .
24	a	126	5% 96% ..
25	b	99	. 96% ..
26	c	84	10% 94% 5%
27	d	64	6% 94% 5%
28	e	53	. 87% 13%
29	f	71	45% 82% 17%
30	g	313	7% 96% .
31	h	75	12% 96% .
32	i	59	22% 86% 12%

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Mol	Chain	Length	Quality of chain
33	2	1863	
34	3	36	
35	A	266	
36	B	422	
37	U	142	
38	R	135	
39	1	75	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
33	C4J	2	1244	X	-	-	-

2 Entry composition [i](#)

There are 39 unique types of molecules in this entry. The entry contains 84251 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 60s ribosomal protein l41.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	208	1643	1045	289	301	8	0	0

- Molecule 3 is a protein called ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	D	215	1742	1107	309	311	15	0	0

- Molecule 4 is a protein called 40S ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	226	1743	1127	300	307	9	0	0

- Molecule 5 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	227	1765	1124	317	316	8	0	0

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

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

- Molecule 7 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	H	191	1509	943	286	273	7	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	I	237	1924	1200	387	330	7	0	0

- Molecule 9 is a protein called ribosomal protein eS7.

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

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

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

- Molecule 11 is a protein called Ribosomal protein S9 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	L	182	1499	952	300	245	2	0	0

- Molecule 12 is a protein called 40S ribosomal protein eS10.

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

- Molecule 13 is a protein called Ribosomal protein S11.

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

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

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

- Molecule 15 is a protein called ribosomal protein uS15.

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

- Molecule 16 is a protein called 40S ribosomal protein uS11.

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

- Molecule 17 is a protein called ribosomal protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	S	141	Total	C	N	O	S	0	0
			1123	715	212	193	3		

- Molecule 18 is a protein called ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	126	Total	C	N	O	S	0	0
			1020	639	188	188	5		

- Molecule 19 is a protein called 40S ribosomal protein eS19.

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

- Molecule 20 is a protein called Ribosomal_S10 domain-containing protein.

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

- Molecule 21 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	X	82	Total	C	N	O	S	0	0
			620	378	117	120	5		

- Molecule 22 is a protein called Ribosomal protein S15a.

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

- Molecule 23 is a protein called 40S ribosomal protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Z	142	Total	C	N	O	S	0	0
			1107	698	220	185	4		

- Molecule 24 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	a	126	Total	C	N	O	S	0	0
			1022	645	198	174	5		

- Molecule 25 is a protein called 40S ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	99	Total	C	N	O	S	0	0
			790	491	162	131	6		

- Molecule 26 is a protein called 40S ribosomal protein S27.

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

- Molecule 27 is a protein called ribosomal protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	d	64	Total	C	N	O	S	0	0
			507	308	102	95	2		

- Molecule 28 is a protein called ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	e	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 29 is a protein called ribosomal protein eS31.

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

- Molecule 30 is a protein called ribosomal protein RACK1.

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

- Molecule 31 is a protein called ribosomal protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	h	75	Total	C	N	O	S	0	0
			599	382	111	105	1		

- Molecule 32 is a protein called 40S ribosomal protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	i	59	Total	C	N	O	S	0	0
			473	293	104	75	1		

- Molecule 33 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	2	1744	Total	C	N	O	P	0	0
			37202	16613	6663	12186	1740		

- Molecule 34 is a RNA chain called histone 4 (H4) mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	3	36	Total	C	N	O	P	0	0
			774	346	144	249	35		

- Molecule 35 is a protein called Eukaryotic translation initiation factor 2 subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	A	266	2147	1354	376	406	11	0	0

- Molecule 36 is a protein called eukaryotic translation initiation factor 2 subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	B	422	3214	2044	561	592	17	0	0

- Molecule 37 is a protein called 40S ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	U	142	1172	733	239	199	1	0	0

- Molecule 38 is a protein called Ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	R	135	1111	704	211	189	7	0	0

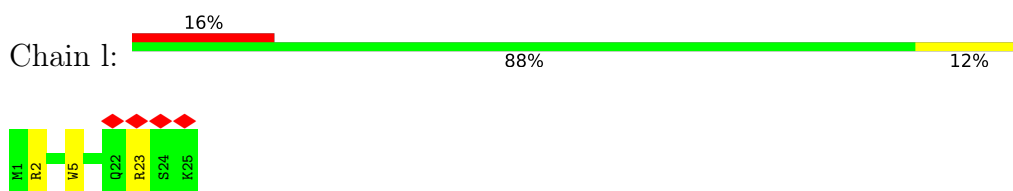
- Molecule 39 is a RNA chain called initiator methionylated tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
39	1	75	1614	722	299	519	74	0	0

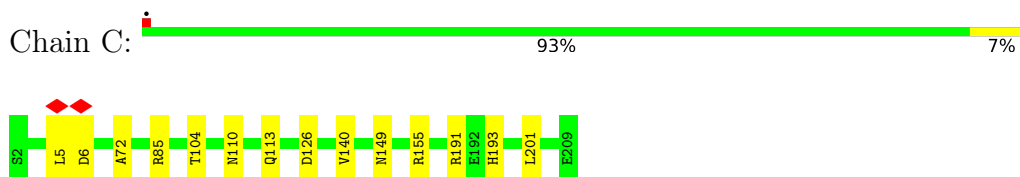
3 Residue-property plots [i](#)

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

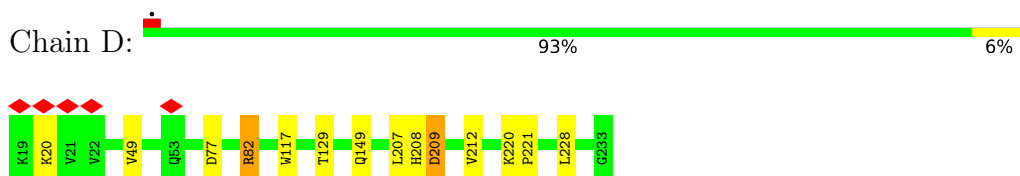
- Molecule 1: 60s ribosomal protein l41



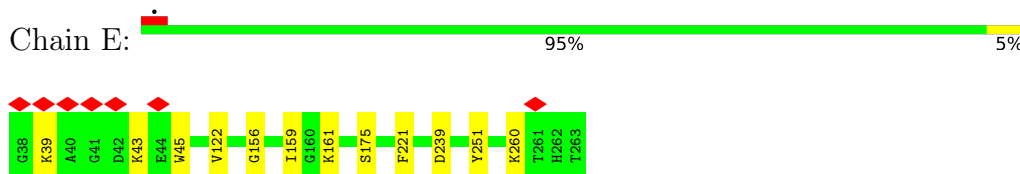
- Molecule 2: 40S ribosomal protein SA



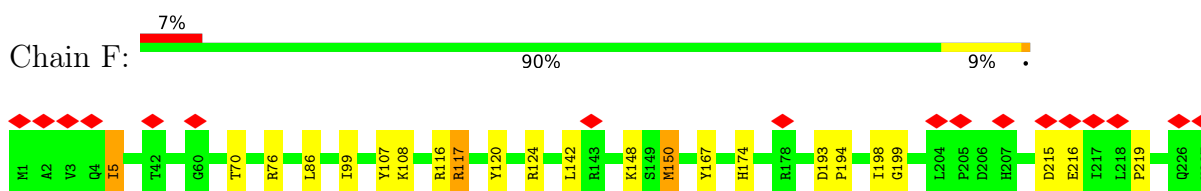
- Molecule 3: ribosomal protein eS1



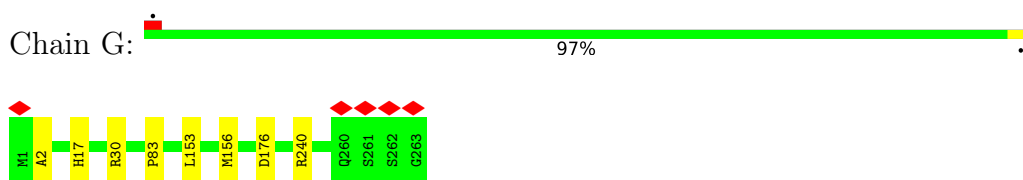
- Molecule 4: 40S ribosomal protein uS5



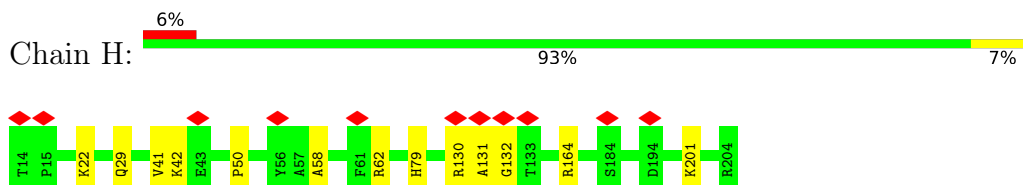
- Molecule 5: Ribosomal protein S3



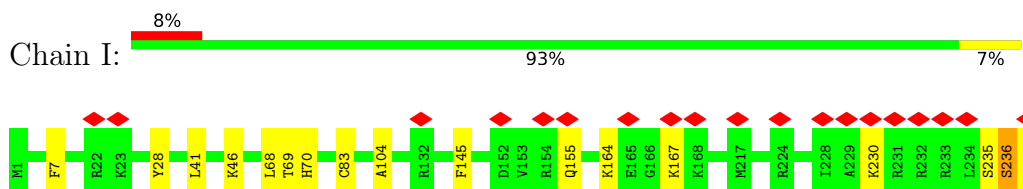
- Molecule 6: 40S ribosomal protein S4



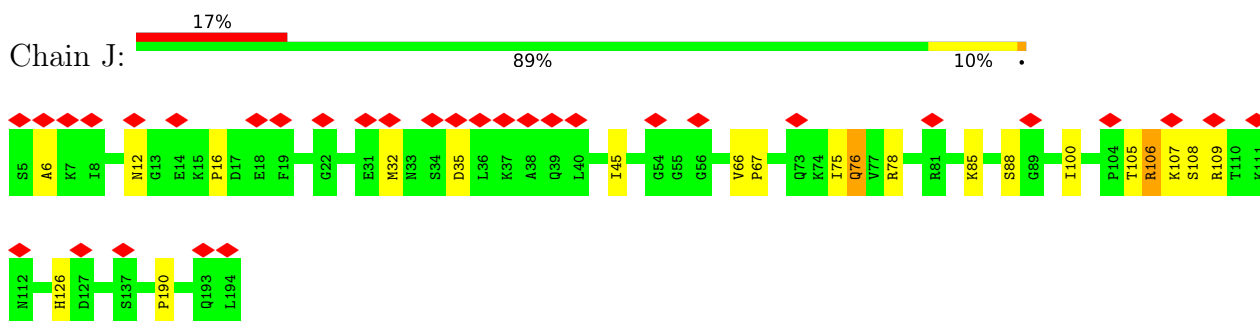
- Molecule 7: Ribosomal protein S5



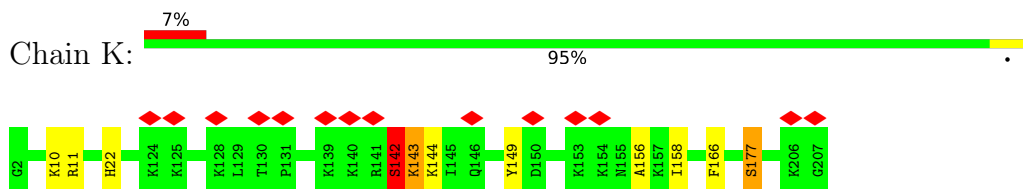
- Molecule 8: 40S ribosomal protein S6



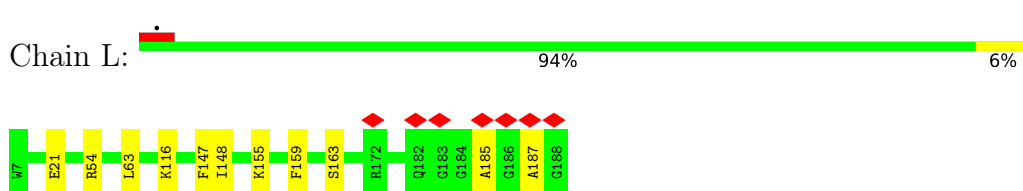
- Molecule 9: ribosomal protein eS7



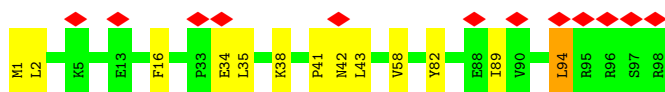
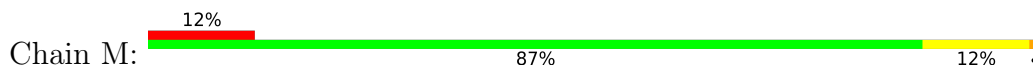
- Molecule 10: 40S ribosomal protein S8



- Molecule 11: Ribosomal protein S9 (Predicted)



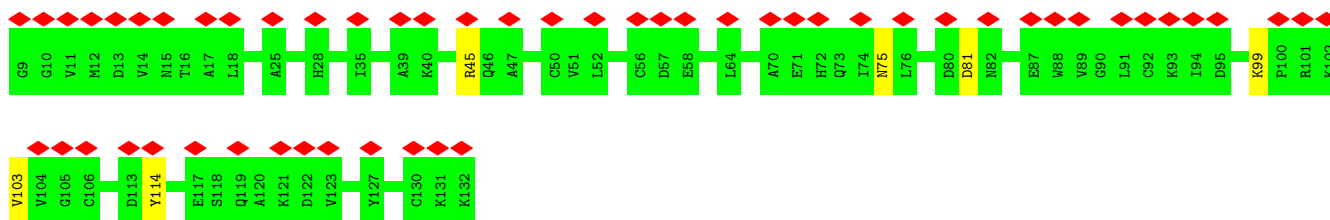
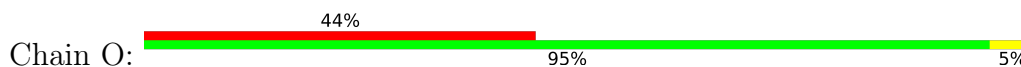
- Molecule 12: 40S ribosomal protein eS10



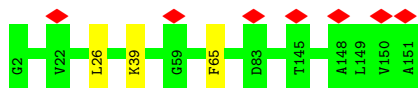
- Molecule 13: Ribosomal protein S11



- Molecule 14: 40S ribosomal protein S12



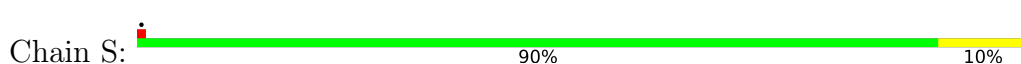
- Molecule 15: ribosomal protein uS15



- Molecule 16: 40S ribosomal protein uS11

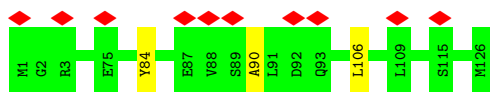


- Molecule 17: ribosomal protein uS9



- Molecule 18: ribosomal protein eS17

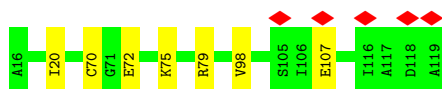
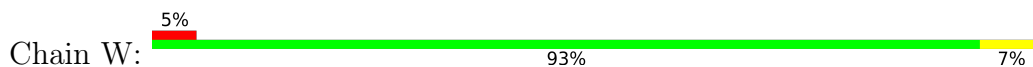




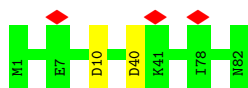
- Molecule 19: 40S ribosomal protein eS19



- Molecule 20: Ribosomal_S10 domain-containing protein



- Molecule 21: 40S ribosomal protein S21



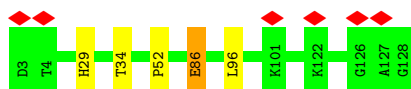
- Molecule 22: Ribosomal protein S15a



- Molecule 23: 40S ribosomal protein uS12

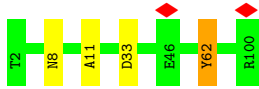


- Molecule 24: 40S ribosomal protein S24

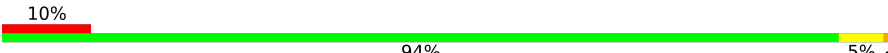


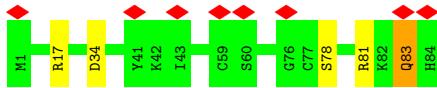
- Molecule 25: 40S ribosomal protein eS26

Chain b:  96%



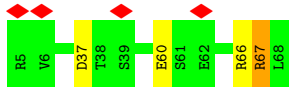
- Molecule 26: 40S ribosomal protein S27

Chain c:  10% 94% 5%




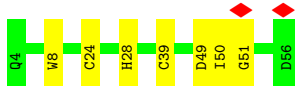
- Molecule 27: ribosomal protein eS28

Chain d:  6% 94% 5%




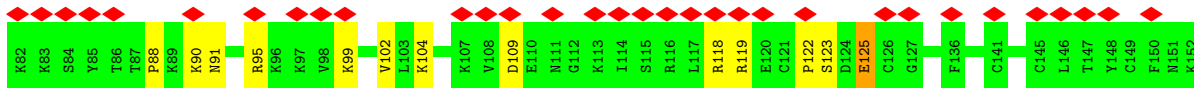
- Molecule 28: ribosomal protein uS14

Chain e:  87% 13%



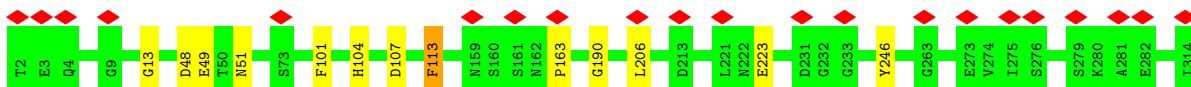
- Molecule 29: ribosomal protein eS31

Chain f:  45% 82% 17%



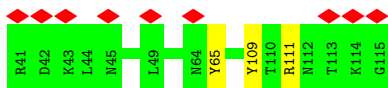
- Molecule 30: ribosomal protein RACK1

Chain g:  7% 96%

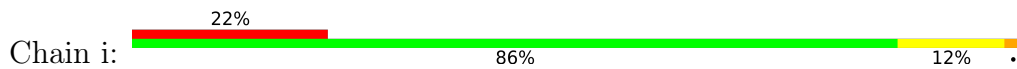


- Molecule 31: ribosomal protein eS25

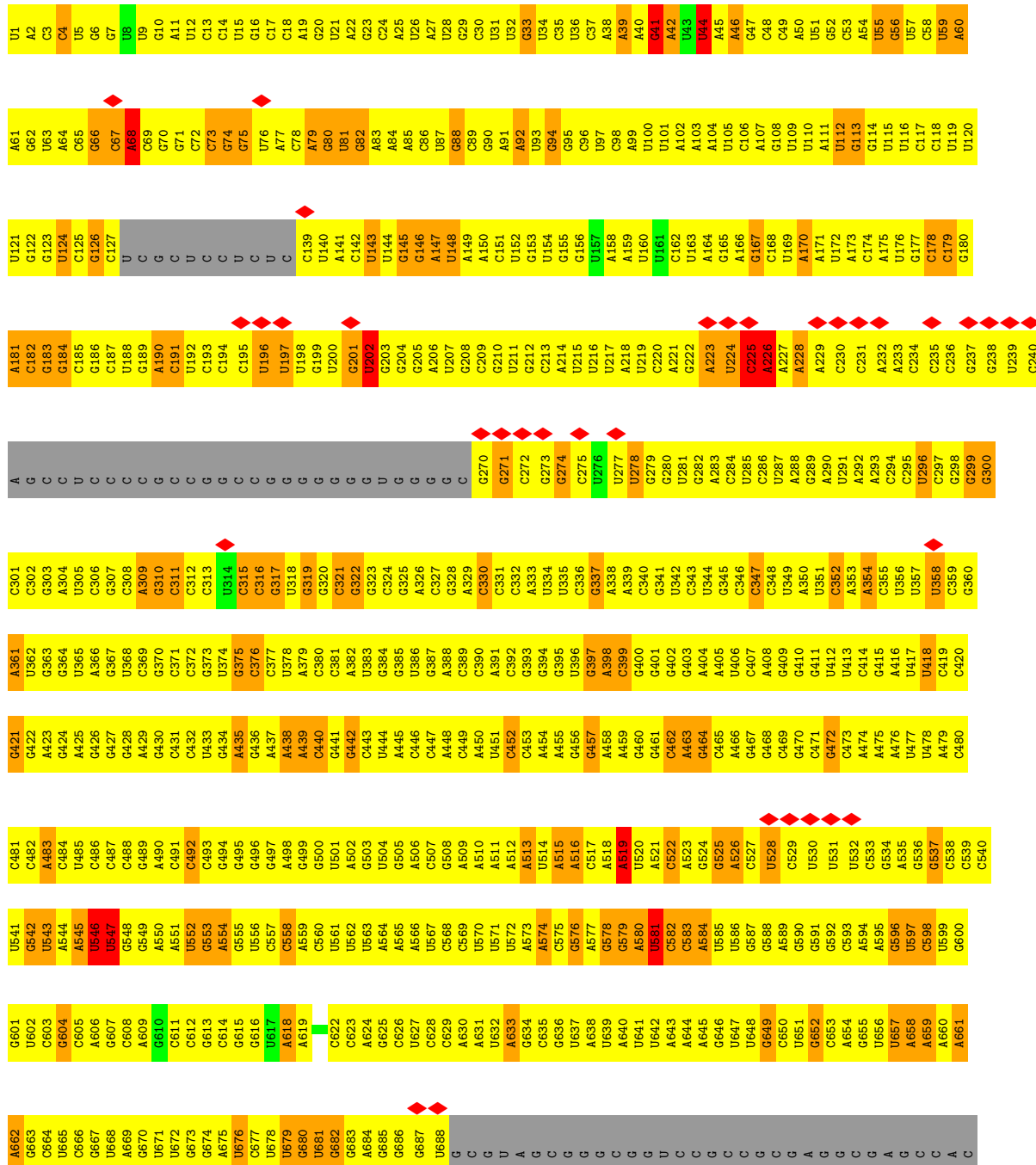
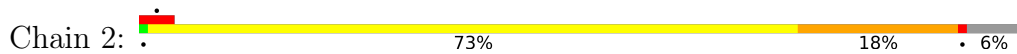
Chain h:  12% 96%



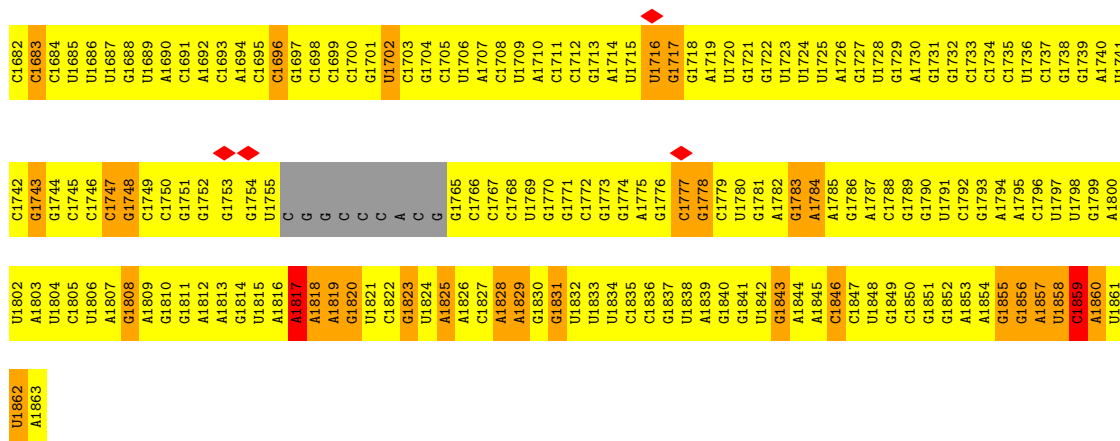
• Molecule 32: 40S ribosomal protein eS30



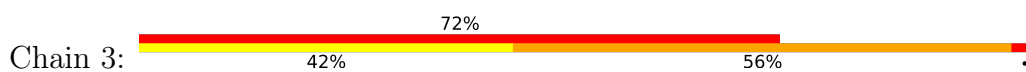
• Molecule 33: 18S ribosomal RNA



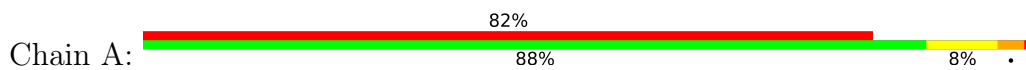
G842	G843	G844	G845	G846	G847	G848	G849	G850	G851	G852	G853	G854	G855	G856	G857	G858	G859	G860	G861	G862	G863	G864	G865	G866	G867	G868	G869	G870	G871	G872	G873	G874	G875	G876	G877	G878	G879	G880	G881	G882	G883	G884	G885	G886	G887	G888	G889	G890	G891	G892	G893	G894	G895	G896	G897	G898	G899	G900																																																												
G903	G904	G905	G906	G907	G908	G909	G910	G911	G912	G913	G914	G915	G916	G917	G918	G919	G920	G921	G922	G923	G924	G925	G926	G927	G928	G929	G930	G931	G932	G933	G934	G935	G936	G937	G938	G939	G940	G941	G942	G943	G944	G945	G946	G947	G948	G949	G950	G951	G952	G953	G954	G955	G956	G957	G958	G959	G960	G961	G962	G963	G964	G965	G966	G967	G968	G969	G970	G971	G972	G973	G974	G975	G976	G977	G978	G979	G980	G981	G982	G983	G984	G985	G986	G987	G988	G989	G990	G991	G992	G993	G994	G995	G996	G997	G998	G999	G1000	G1001	G1002	G1003	G1004	G1005	G1006	G1007	G1008	G1009	G1010	G1011	G1012	G1013	G1014	G1015	G1016	G1017	G1018	G1019	G1020	G1021
U982	C963	U964	U965	U966	U967	U968	U969	U970	U971	U972	U973	U974	U975	U976	U977	U978	U979	U980	U981	U982	U983	U984	U985	U986	U987	U988	U989	U990	U991	U992	U993	U994	U995	U996	U997	U998	U999	U1000	U1001	U1002	U1003	U1004	U1005	U1006	U1007	U1008	U1009	U1010	U1011	U1012	U1013	U1014	U1015	U1016	U1017	U1018	U1019	U1020	U1021																																																											
C1022	C1023	C1024	C1025	C1026	C1027	C1028	C1029	C1030	C1031	C1032	C1033	C1034	C1035	C1036	C1037	C1038	C1039	C1040	C1041	C1042	C1043	C1044	C1045	C1046	C1047	C1048	C1049	C1050	C1051	C1052	C1053	C1054	C1055	C1056	C1057	C1058	C1059	C1060	C1061	C1062	C1063	C1064	C1065	C1066	C1067	C1068	C1069	C1070	C1071	C1072	C1073	C1074	C1075	C1076	C1077	C1078	C1079	C1080	C1081																																																											
G1082	A1083	U1084	C1085	C1086	C1087	C1088	C1089	C1090	C1091	C1092	C1093	C1094	C1095	C1096	C1097	C1098	C1099	C1100	C1101	C1102	C1103	C1104	C1105	C1106	C1107	C1108	C1109	C1110	C1111	C1112	C1113	C1114	C1115	C1116	C1117	C1118	C1119	C1120	C1121	C1122	C1123	C1124	C1125	C1126	C1127	C1128	C1129	C1130	C1131	C1132	C1133	C1134	C1135	C1136	C1137	C1138	C1139	C1140	C1141																																																											
C1142	C1143	A1144	C1145	C1146	C1147	C1148	C1149	C1150	C1151	C1152	C1153	C1154	C1155	C1156	C1157	C1158	C1159	C1160	C1161	C1162	C1163	C1164	C1165	C1166	C1167	C1168	C1169	C1170	C1171	C1172	C1173	C1174	C1175	C1176	C1177	C1178	C1179	C1180	C1181	C1182	C1183	C1184	C1185	C1186	C1187	C1188	C1189	C1190	C1191	C1192	C1193	C1194	C1195	C1196	C1197	C1198	C1199	C1200	C1201																																																											
G1202	G1203	A1204	C1205	C1206	C1207	C1208	C1209	C1210	C1211	C1212	C1213	C1214	C1215	C1216	C1217	C1218	C1219	C1220	C1221	C1222	C1223	C1224	C1225	C1226	C1227	C1228	C1229	C1230	C1231	C1232	C1233	C1234	C1235	C1236	C1237	C1238	C1239	C1240	C1241	C1242	C1243	C1244	C4J1244	C1245	C1246	C1247	C1248	C1249	C1250	C1251	C1252	C1253	C1254	C1255	C1256	C1257	C1258	C1259	C1260	C1261																																																										
C1262	C1263	C1264	C1265	C1266	C1267	C1268	C1269	C1270	C1271	C1272	C1273	C1274	C1275	C1276	C1277	C1278	C1279	C1280	C1281	C1282	C1283	C1284	C1285	C1286	C1287	C1288	C1289	C1290	C1291	C1292	C1293	C1294	C1295	C1296	C1297	C1298	C1299	C1300	C1301	C1302	C1303	C1304	C1305	C1306	C1307	C1308	C1309	C1310	C1311	C1312	C1313	C1314	C1315	C1316	C1317	C1318	C1319	C1320	C1321																																																											
U1322	G1323	U1324	U1325	U1326	U1327	U1328	U1329	U1330	U1331	U1332	U1333	U1334	U1335	U1336	U1337	U1338	U1339	U1340	U1341	U1342	U1343	U1344	U1345	U1346	U1347	U1348	U1349	U1350	U1351	U1352	U1353	U1354	U1355	U1356	U1357	U1358	U1359	U1360	U1361	U1362	U1363	U1364	U1365	U1366	U1367	U1368	U1369	U1370	U1371	U1372	U1373	U1374	U1375	U1376	U1377	U1378	U1379	U1380	U1381																																																											
A1382	G1383	A1384	C1385	C1386	C1387	U1388	G1389	G1390	C1391	A1392	U1393	C1394	C1395	U1396	A1397	A1398	C1399	U1400	A1401	G1402	U1403	U1404	U1405	C1406	G1407	C1408	U1409	U1410	C1411	C1412	C1413	C1414	C1415	C1416	A1417	G1418	C1419	G1420	U1421	U1422	C1423	G1424	G1425	C1426	G1427	U1428	C1429	C1430	C1431	C1432	C1433	A1434	U1435	C1436	U1437	U1438	C1439	U1440	U1441																																																											
A1442	G1443	A1444	C1445	U1446	C1447	U1448	C1449	A1450	C1451	G1452	U1453	C1454	C1455	C1456	C1457	U1458	U1459	C1460	A1461	G1462	C1463	C1464	U1465	C1466	C1467	C1468	C1469	U1470	C1471	A1472	U1473	U1474	C1475	C1476	C1477	C1478	A1479	U1480	U1481	U1482	C1483	C1484	A1485	C1486	C1487	C1488	C1489	U1490	C1491	C1492	C1493	C1494	U1495	C1496	C1497	C1498	U1499	U1500	U1501																																																											
A1502	G1503	U1504	U1505	U1506	U1507	C1508	C1509	G1510	C1511	G1512	C1513	U1514	C1515	C1516	C1517	C1518	G1519	C1520	C1521	C1522	C1523	C1524	U1525	C1526	C1527	C1528	C1529	U1530	C1531	C1532	C1533	U1534	C1535	C1536	C1537	C1538	C1539	U1540	C1541	C1542	C1543	C1544	C1545	C1546	C1547	C1548	C1549	C1550	C1551	C1552	C1553	C1554	C1555	C1556	C1557	C1558	C1559	U1560	C1561																																																											
G1562	C1563	A1564	C1565	U1566	C1567	U1568	C1569	G1570	C1571	G1572	U1573	A1574	C1575	C1576	C1577	C1578	C1579	U1580	U1581	C1582	C1583	U1584	C1585	C1586	C1587	C1588	C1589	U1590	C1591	C1592	C1593	U1594	C1595	C1596	C1597	C1598	C1599	G1600	C1601	C1602	U1603	C1604	C1605	C1606	C1607	C1608	C1609	U1610	U1611	C1612	C1613	C1614	C1615	C1616	U1617	C1618	U1619	U1620	C1621																																																											
C1622	C1623	C1624	C1625	C1626	C1627	C1628	C1629	C1630	C1631	C1632	C1633	C1634	C1635	C1636	C1637	C1638	C1639	C1640	C1641	C1642	C1643	C1644	C1645	C1646	C1647	C1648	C1649	C1650	C1651	C1652	C1653	C1654	C1655	C1656	C1657	C1658	C1659	C1660	C1661	C1662	C1663	C1664	C1665	C1666	C1667	C1668	C1669	C1670	C1671	C1672	C1673	C1674	C1675	C1676	C1677	C1678	C1679	C1680	C1681																																																											



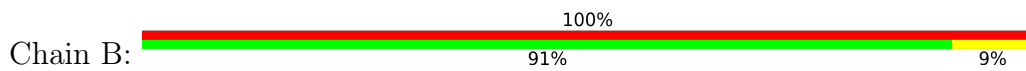
• Molecule 34: histone 4 (H4) mRNA

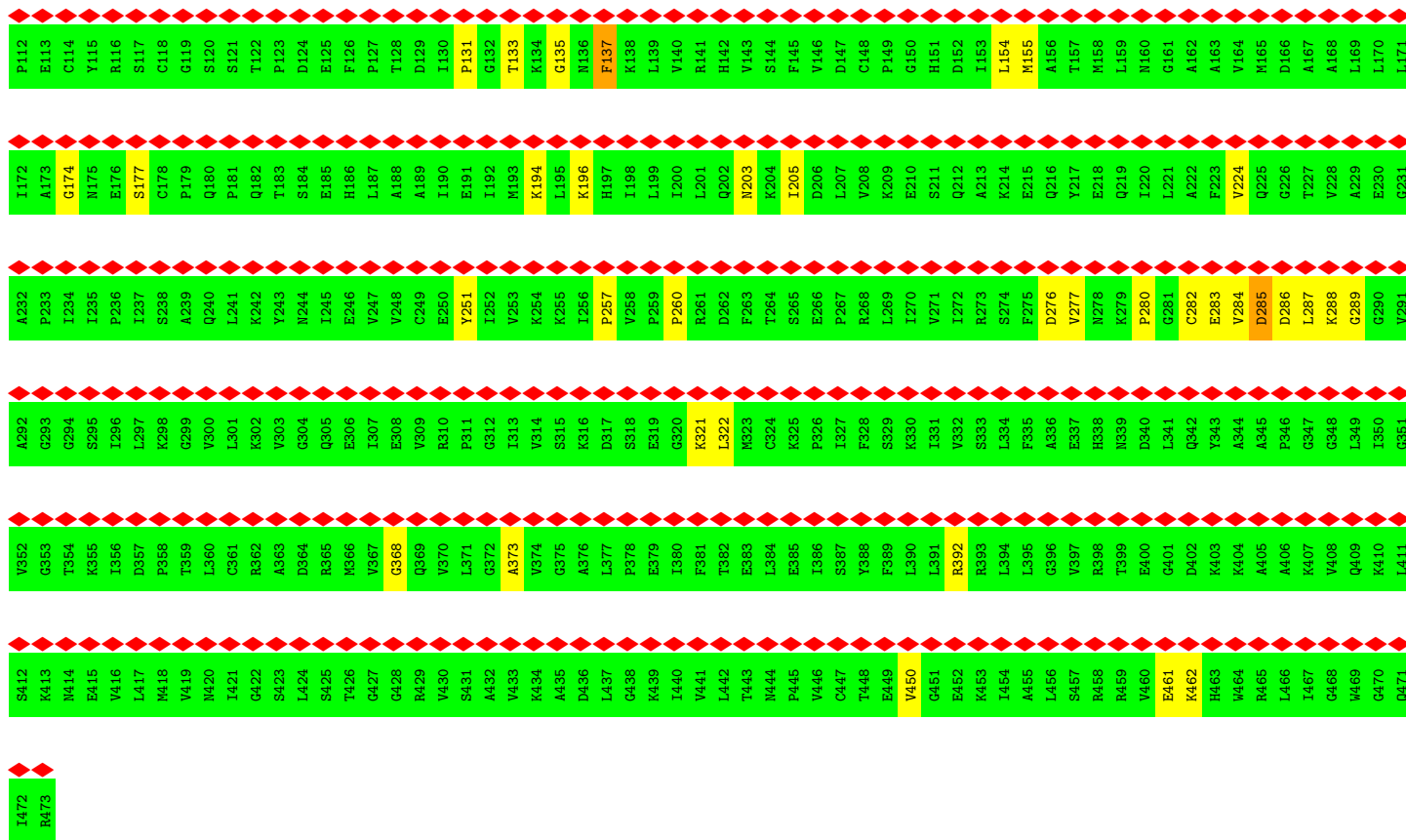


• Molecule 35: Eukaryotic translation initiation factor 2 subunit 1

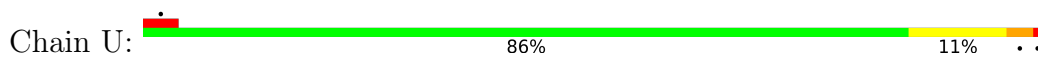


• Molecule 36: eukaryotic translation initiation factor 2 subunit gamma

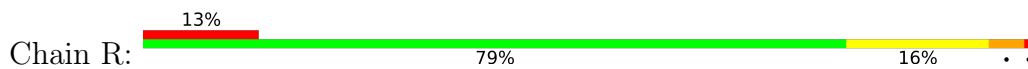




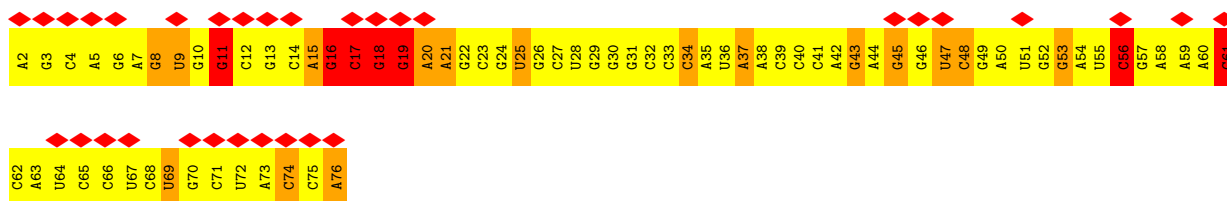
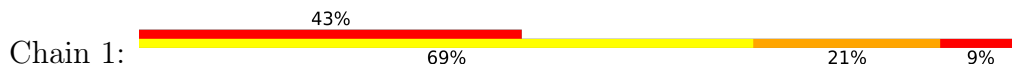
• Molecule 37: 40S ribosomal protein uS13



• Molecule 38: Ribosomal protein S15



• Molecule 39: initiator methionylated tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	372000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	26	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.110	Depositor
Minimum map value	-0.065	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0109	Depositor
Map size (\AA)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1, 1.1, 1.1	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: C4J, T6A

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	I	1.35	0/241	0.96	0/305
2	C	0.97	0/1680	0.99	0/2283
3	D	0.90	0/1770	1.02	2/2367 (0.1%)
4	E	0.91	0/1779	0.99	5/2399 (0.2%)
5	F	0.97	0/1793	1.03	1/2412 (0.0%)
6	G	0.97	0/2125	1.00	0/2856
7	H	0.99	0/1531	0.97	0/2059
8	I	1.07	0/1946	1.03	6/2587 (0.2%)
9	J	0.96	0/1553	1.00	0/2079
10	K	1.03	0/1709	1.05	5/2278 (0.2%)
11	L	1.07	0/1523	0.98	2/2031 (0.1%)
12	M	0.96	0/852	1.01	0/1147
13	N	1.00	0/1319	1.01	0/1761
14	O	0.90	0/968	1.04	2/1296 (0.2%)
15	P	0.97	0/1232	0.92	2/1656 (0.1%)
16	Q	1.02	0/1029	1.05	2/1380 (0.1%)
17	S	1.01	0/1141	1.01	0/1528
18	T	0.99	0/1032	0.99	0/1383
19	V	0.98	0/1133	0.99	3/1517 (0.2%)
20	W	0.96	0/832	1.02	0/1117
21	X	0.99	0/627	1.01	0/839
22	Y	0.99	0/1051	0.98	0/1406
23	Z	0.99	0/1125	0.99	2/1500 (0.1%)
24	a	1.01	0/1038	1.04	1/1377 (0.1%)
25	b	1.06	0/803	1.03	1/1076 (0.1%)
26	c	0.94	0/673	1.00	0/902
27	d	1.13	0/509	1.02	0/680
28	e	1.10	0/455	1.05	0/603
29	f	0.98	0/594	1.07	0/786
30	g	0.92	0/2494	1.10	4/3394 (0.1%)
31	h	0.97	0/605	1.08	2/810 (0.2%)
32	i	1.09	0/478	1.06	1/628 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	2	1.61	115/41562 (0.3%)	2.42	4485/64770 (6.9%)
34	3	1.22	0/867	1.89	54/1352 (4.0%)
35	A	1.00	0/2178	1.08	9/2935 (0.3%)
36	B	0.92	0/3267	1.07	4/4415 (0.1%)
37	U	1.01	0/1190	0.92	0/1592
38	R	0.99	0/1132	0.99	3/1510 (0.2%)
39	1	2.46	8/1770 (0.5%)	2.77	221/2759 (8.0%)
All	All	1.35	123/89606 (0.1%)	1.90	4817/129775 (3.7%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	C	0	1
3	D	0	1
5	F	0	2
8	I	0	2
9	J	0	2
11	L	0	2
12	M	0	5
17	S	0	2
26	c	0	1
28	e	0	2
29	f	0	1
31	h	0	1
32	i	0	2
33	2	1	64
34	3	1	0
35	A	0	8
36	B	0	11
37	U	0	3
39	1	3	3
All	All	5	113

The worst 5 of 123 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	1	19	G	O3'-P	43.51	2.13	1.61
39	1	16	G	O3'-P	-39.18	1.14	1.61
39	1	17	C	O3'-P	32.10	1.99	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	2	1815	U	O3'-P	-29.22	1.26	1.61
39	1	17	C	C2'-O2'	-26.05	1.07	1.41

The worst 5 of 4817 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	1	19	G	O3'-P-O5'	31.90	164.60	104.00
39	1	16	G	P-O3'-C3'	23.25	147.60	119.70
33	2	351	U	P-O3'-C3'	18.59	142.01	119.70
33	2	797	U	O3'-P-O5'	-17.82	70.15	104.00
33	2	676	U	O3'-P-O5'	-17.57	70.62	104.00

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
33	2	1244	C4J	C4'
34	3	65	G	C3'
39	1	17	C	C2',C3'
39	1	18	G	C3'

5 of 113 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	193	HIS	Peptide
3	D	208	HIS	Peptide
5	F	107	TYR	Sidechain
5	F	167	TYR	Sidechain
8	I	68	LEU	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	I	240	0	289	0	0
2	C	1643	0	1646	1	0
3	D	1742	0	1815	0	0
4	E	1743	0	1836	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	F	1765	0	1863	23	0
6	G	2083	0	2189	0	0
7	H	1509	0	1563	8	0
8	I	1924	0	2086	12	0
9	J	1530	0	1623	27	0
10	K	1680	0	1762	1	0
11	L	1499	0	1608	0	0
12	M	828	0	854	0	0
13	N	1296	0	1374	0	0
14	O	958	0	993	0	0
15	P	1208	0	1294	1	0
16	Q	1016	0	1039	0	0
17	S	1123	0	1193	2	0
18	T	1020	0	1075	0	0
19	V	1113	0	1149	5	0
20	W	822	0	887	1	0
21	X	620	0	622	0	0
22	Y	1034	0	1080	0	0
23	Z	1107	0	1179	2	0
24	a	1022	0	1084	0	0
25	b	790	0	839	0	0
26	c	659	0	683	0	0
27	d	507	0	536	0	0
28	e	445	0	442	0	0
29	f	582	0	599	0	0
30	g	2437	0	2393	0	0
31	h	599	0	655	0	0
32	i	473	0	524	0	0
33	2	37202	0	18777	310	0
34	3	774	0	390	81	0
35	A	2147	0	2187	26	0
36	B	3214	0	3354	0	0
37	U	1172	0	1226	50	0
38	R	1111	0	1166	58	0
39	1	1614	0	824	60	0
All	All	84251	0	66698	517	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 4.

The worst 5 of 517 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)
37:U:147:GLY:CA	38:R:131:PRO:HG3	1.22	1.68
37:U:147:GLY:HA3	38:R:131:PRO:CG	1.34	1.55
39:1:16:G:O3'	39:1:17:C:P	1.14	1.52
33:2:1817:A:C2'	33:2:1818:A:H5'	1.47	1.42
5:F:117:ARG:HH12	34:3:67:A:N6	1.14	1.41

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	I	23/25 (92%)	23 (100%)	0	0	100	100
2	C	206/208 (99%)	176 (85%)	21 (10%)	9 (4%)	2	20
3	D	213/215 (99%)	185 (87%)	19 (9%)	9 (4%)	3	22
4	E	224/226 (99%)	203 (91%)	16 (7%)	5 (2%)	6	35
5	F	225/227 (99%)	205 (91%)	13 (6%)	7 (3%)	4	28
6	G	261/263 (99%)	229 (88%)	26 (10%)	6 (2%)	6	34
7	H	189/191 (99%)	165 (87%)	16 (8%)	8 (4%)	3	22
8	I	233/237 (98%)	206 (88%)	20 (9%)	7 (3%)	4	28
9	J	188/190 (99%)	162 (86%)	18 (10%)	8 (4%)	2	21
10	K	204/206 (99%)	180 (88%)	18 (9%)	6 (3%)	4	29
11	L	180/182 (99%)	167 (93%)	6 (3%)	7 (4%)	3	23
12	M	96/98 (98%)	78 (81%)	12 (12%)	6 (6%)	1	13
13	N	156/158 (99%)	130 (83%)	19 (12%)	7 (4%)	2	20
14	O	122/124 (98%)	103 (84%)	15 (12%)	4 (3%)	4	27
15	P	148/150 (99%)	143 (97%)	5 (3%)	0	100	100
16	Q	134/136 (98%)	116 (87%)	11 (8%)	7 (5%)	2	16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	S	139/141 (99%)	123 (88%)	12 (9%)	4 (3%)	4	29
18	T	124/126 (98%)	114 (92%)	8 (6%)	2 (2%)	9	41
19	V	139/141 (99%)	124 (89%)	10 (7%)	5 (4%)	3	25
20	W	102/104 (98%)	95 (93%)	4 (4%)	3 (3%)	4	29
21	X	80/82 (98%)	66 (82%)	13 (16%)	1 (1%)	12	45
22	Y	127/129 (98%)	119 (94%)	6 (5%)	2 (2%)	9	41
23	Z	140/142 (99%)	127 (91%)	11 (8%)	2 (1%)	11	43
24	a	122/126 (97%)	106 (87%)	12 (10%)	4 (3%)	4	27
25	b	97/99 (98%)	81 (84%)	13 (13%)	3 (3%)	4	28
26	c	82/84 (98%)	72 (88%)	8 (10%)	2 (2%)	6	33
27	d	62/64 (97%)	54 (87%)	5 (8%)	3 (5%)	2	18
28	e	51/53 (96%)	39 (76%)	8 (16%)	4 (8%)	1	9
29	f	69/71 (97%)	56 (81%)	6 (9%)	7 (10%)	0	6
30	g	311/313 (99%)	273 (88%)	31 (10%)	7 (2%)	6	34
31	h	73/75 (97%)	70 (96%)	2 (3%)	1 (1%)	11	43
32	i	57/59 (97%)	45 (79%)	7 (12%)	5 (9%)	1	7
35	A	264/266 (99%)	225 (85%)	29 (11%)	10 (4%)	3	24
36	B	420/422 (100%)	350 (83%)	48 (11%)	22 (5%)	2	16
37	U	140/142 (99%)	121 (86%)	14 (10%)	5 (4%)	3	25
38	R	133/135 (98%)	105 (79%)	18 (14%)	10 (8%)	1	9
All	All	5534/5610 (99%)	4836 (87%)	500 (9%)	198 (4%)	6	25

5 of 198 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	209	ASP
3	D	221	PRO
5	F	193	ASP
5	F	219	PRO
6	G	2	ALA

5.3.2 Protein sidechains [i](#)

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	I	24/24 (100%)	21 (88%)	3 (12%)	4	21
2	C	174/174 (100%)	171 (98%)	3 (2%)	60	82
3	D	196/196 (100%)	192 (98%)	4 (2%)	55	79
4	E	187/187 (100%)	183 (98%)	4 (2%)	53	78
5	F	190/190 (100%)	182 (96%)	8 (4%)	30	61
6	G	225/225 (100%)	223 (99%)	2 (1%)	78	91
7	H	161/161 (100%)	159 (99%)	2 (1%)	71	87
8	I	207/207 (100%)	205 (99%)	2 (1%)	76	89
9	J	170/170 (100%)	164 (96%)	6 (4%)	36	66
10	K	177/177 (100%)	174 (98%)	3 (2%)	60	82
11	L	157/157 (100%)	156 (99%)	1 (1%)	86	94
12	M	89/89 (100%)	86 (97%)	3 (3%)	37	67
13	N	142/142 (100%)	135 (95%)	7 (5%)	25	57
14	O	104/104 (100%)	103 (99%)	1 (1%)	76	89
15	P	130/130 (100%)	129 (99%)	1 (1%)	81	92
16	Q	106/106 (100%)	103 (97%)	3 (3%)	43	72
17	S	117/117 (100%)	112 (96%)	5 (4%)	29	61
18	T	114/114 (100%)	113 (99%)	1 (1%)	78	91
19	V	113/113 (100%)	113 (100%)	0	100	100
20	W	94/94 (100%)	92 (98%)	2 (2%)	53	78
21	X	67/67 (100%)	66 (98%)	1 (2%)	65	84
22	Y	112/112 (100%)	111 (99%)	1 (1%)	78	91
23	Z	114/114 (100%)	112 (98%)	2 (2%)	59	81
24	a	108/108 (100%)	107 (99%)	1 (1%)	78	91
25	b	87/87 (100%)	86 (99%)	1 (1%)	73	88
26	c	76/76 (100%)	73 (96%)	3 (4%)	32	63
27	d	57/57 (100%)	55 (96%)	2 (4%)	36	66
28	e	47/47 (100%)	46 (98%)	1 (2%)	53	78
29	f	64/64 (100%)	58 (91%)	6 (9%)	8	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	g	272/272 (100%)	267 (98%)	5 (2%)	59	81
31	h	66/66 (100%)	66 (100%)	0	100	100
32	i	49/49 (100%)	48 (98%)	1 (2%)	55	79
35	A	238/238 (100%)	230 (97%)	8 (3%)	37	67
36	B	354/354 (100%)	350 (99%)	4 (1%)	73	88
37	U	122/122 (100%)	118 (97%)	4 (3%)	38	68
38	R	121/121 (100%)	114 (94%)	7 (6%)	20	52
All	All	4831/4831 (100%)	4723 (98%)	108 (2%)	54	77

5 of 108 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	S	131	LYS
27	d	67	ARG
37	U	141	ARG
20	W	75	LYS
24	a	29	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
36	B	160	ASN
36	B	305	GLN
36	B	203	ASN
25	b	17	HIS
36	B	65	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
33	2	1732/1863 (92%)	263 (15%)	11 (0%)
34	3	35/36 (97%)	20 (57%)	5 (14%)
39	1	74/75 (98%)	15 (20%)	5 (6%)
All	All	1841/1974 (93%)	298 (16%)	21 (1%)

5 of 298 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
33	2	4	C
33	2	33	G
33	2	41	G
33	2	42	A
33	2	44	U

5 of 21 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	3	58	G
39	1	16	G
39	1	74	C
39	1	17	C
39	1	8	G

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
33	C4J	2	1244	33	24,29,30	0.79	1 (4%)	29,42,45	1.03	1 (3%)
39	T6A	1	37	39	27,34,35	1.04	2 (7%)	29,49,52	2.64	9 (31%)

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
33	C4J	2	1244	33	1/1/7/7	9/16/34/35	0/2/2/2
39	T6A	1	37	39	-	6/19/41/42	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	1	37	T6A	C5-C4	2.51	1.47	1.40
39	1	37	T6A	O4'-C1'	2.21	1.44	1.41
33	2	1244	C4J	C1'-C5	-2.07	1.45	1.50

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	1	37	T6A	C12-N11-C10	8.56	136.20	121.94
39	1	37	T6A	C2-N1-C6	7.01	122.61	116.59
39	1	37	T6A	C14-C12-C13	3.68	116.47	110.19
39	1	37	T6A	N3-C2-N1	-3.57	123.09	128.68
33	2	1244	C4J	C4-N3-C2	-3.41	121.15	125.46

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
33	2	1244	C4J	C4'

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
33	2	1244	C4J	C31-C3-N3-C2
33	2	1244	C4J	C31-C3-N3-C4
33	2	1244	C4J	C3-C31-C32-C34
33	2	1244	C4J	C3-C31-C32-N33
33	2	1244	C4J	N33-C32-C34-O36

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
33	2	1244	C4J	3	0
39	1	37	T6A	5	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
33	2	6
39	1	5
8	I	1
24	a	1

The worst 5 of 13 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	730:C	O3'	731:C	P	8.58
1	I	217:MET	C	218:LYS	N	3.94
1	a	9:THR	C	10:ARG	N	3.27
1	1	19:G	O3'	20:A	P	2.13
1	1	17:C	O3'	18:G	P	1.99

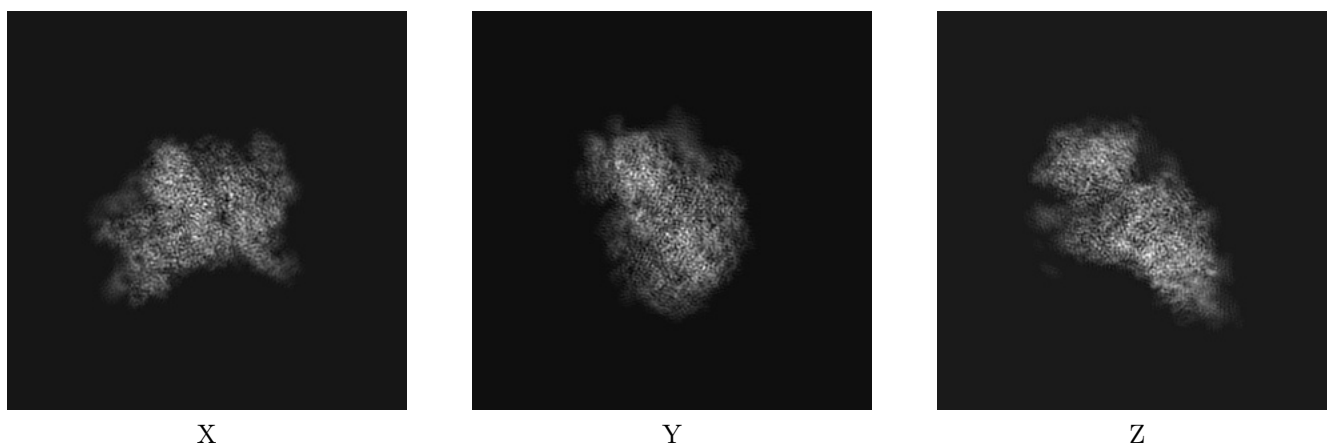
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10762. 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](#)

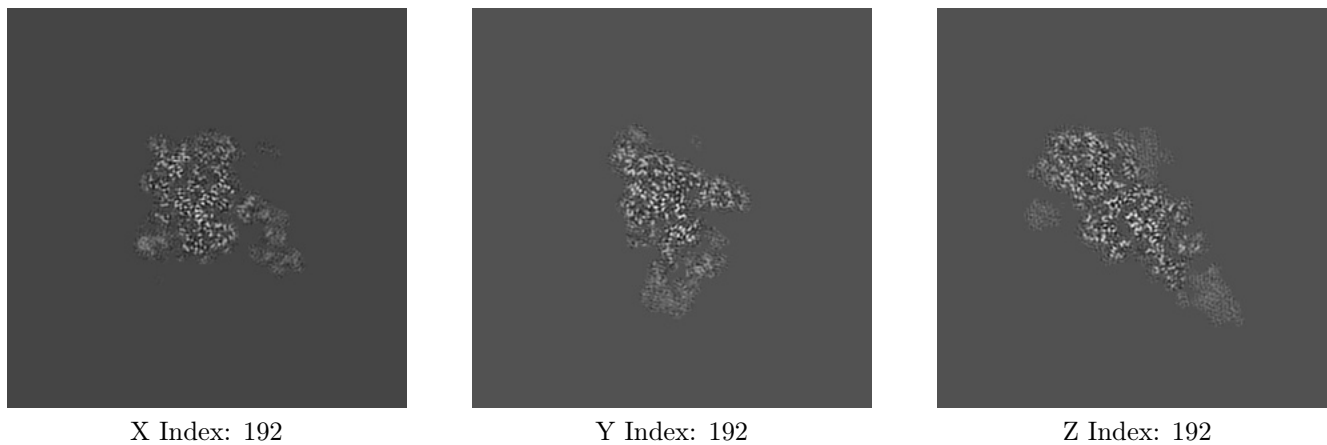
6.1.1 Primary map



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

6.2 Central slices [i](#)

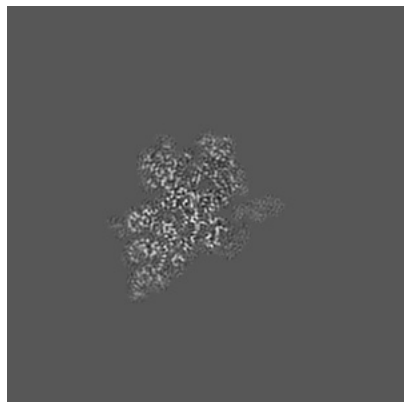
6.2.1 Primary map



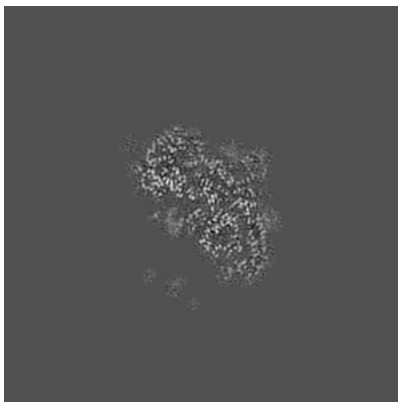
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

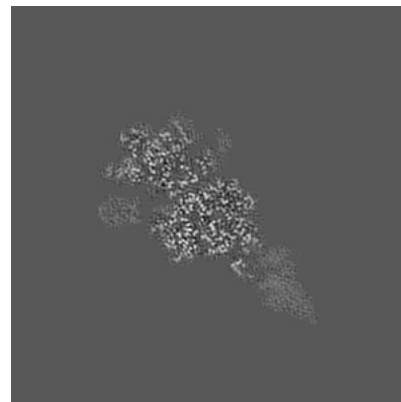
6.3.1 Primary map



X Index: 208



Y Index: 160

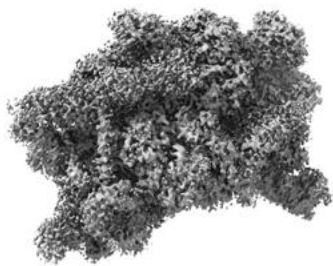


Z Index: 199

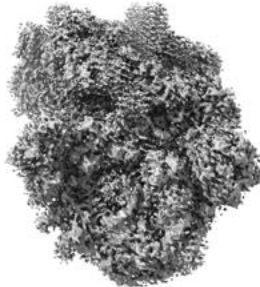
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0109. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

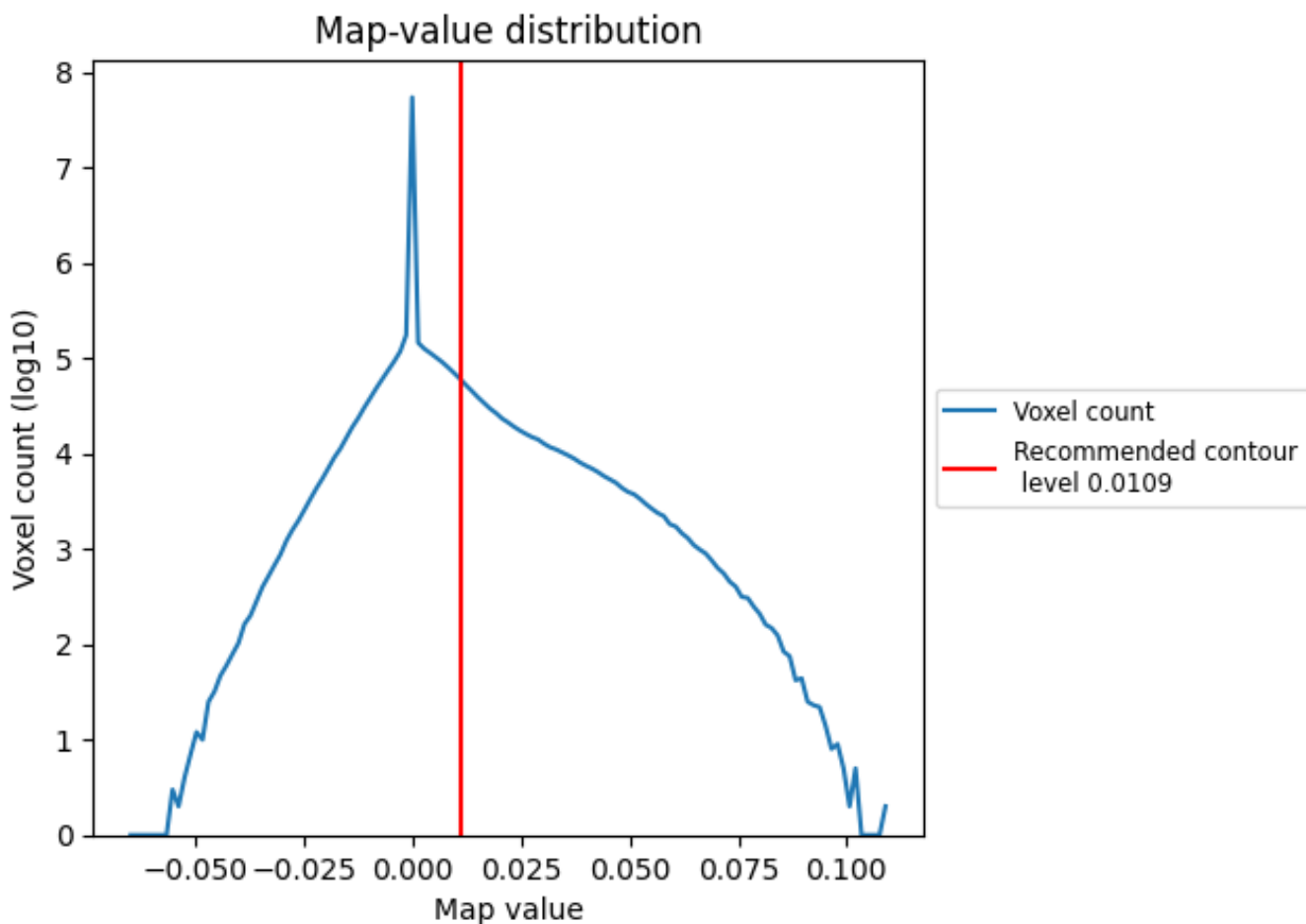
6.5 Mask visualisation

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

7 Map analysis [i](#)

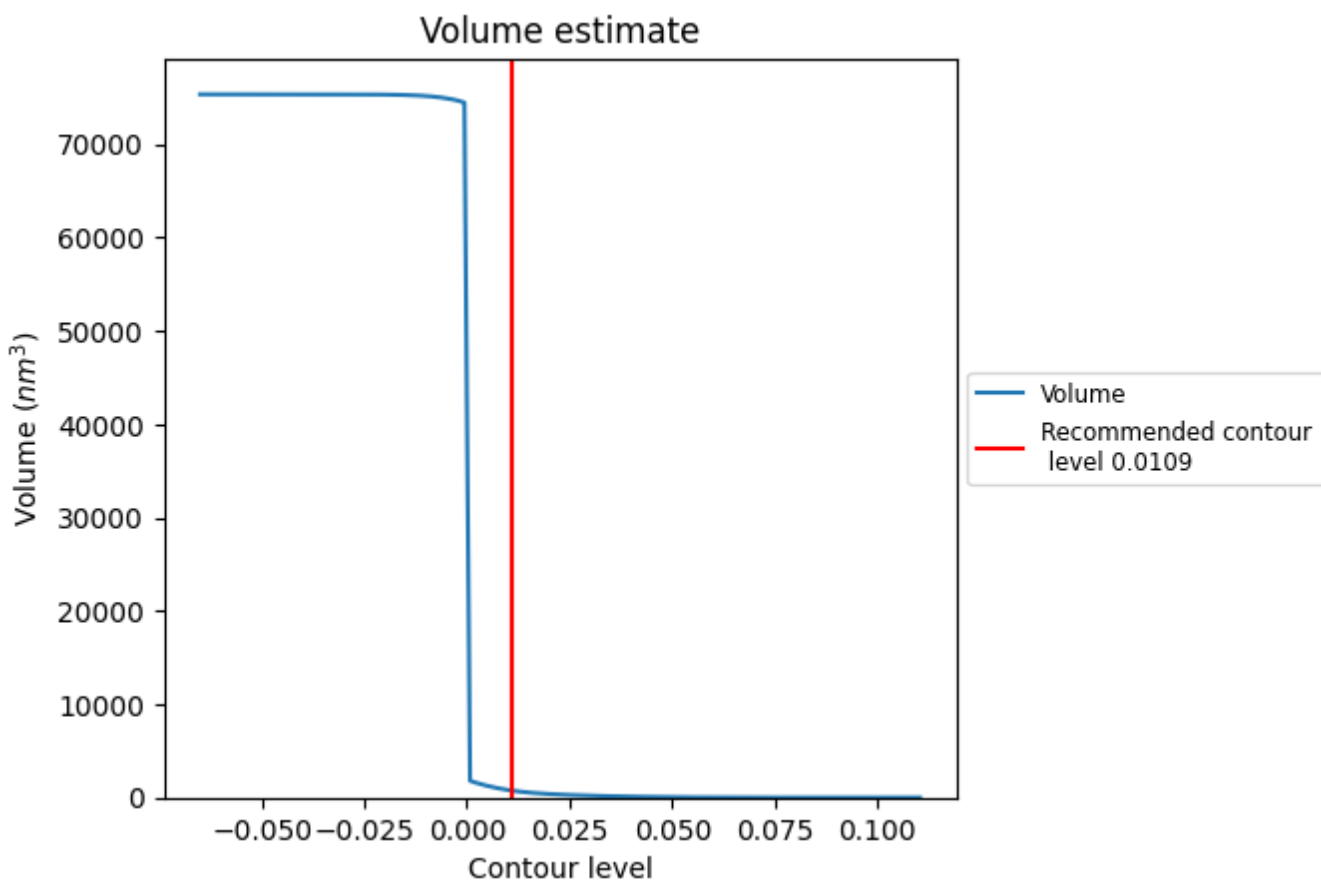
This section contains the results of statistical analysis of the map.

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.

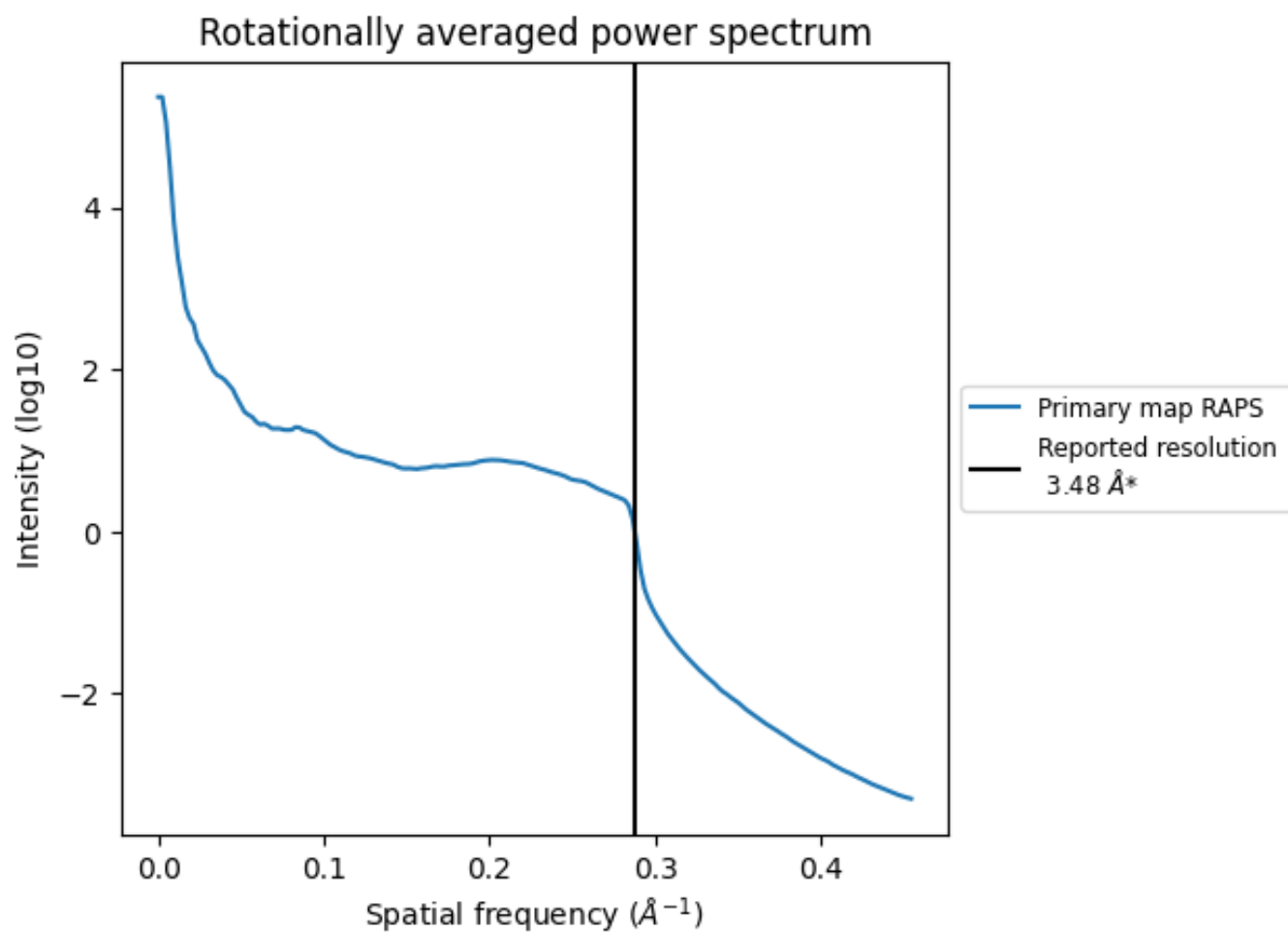
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 753 nm³; this corresponds to an approximate mass of 680 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.287\AA^{-1}

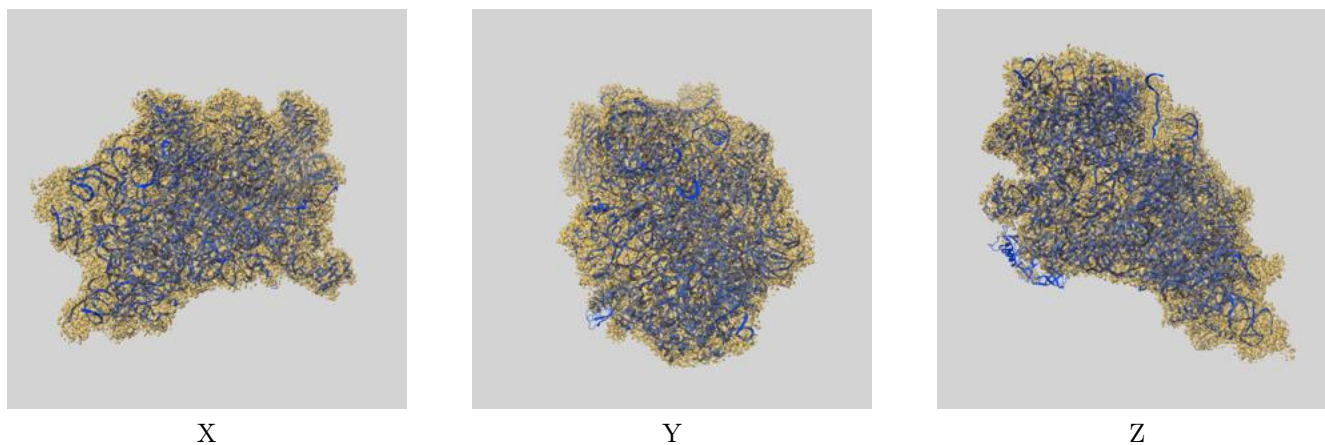
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

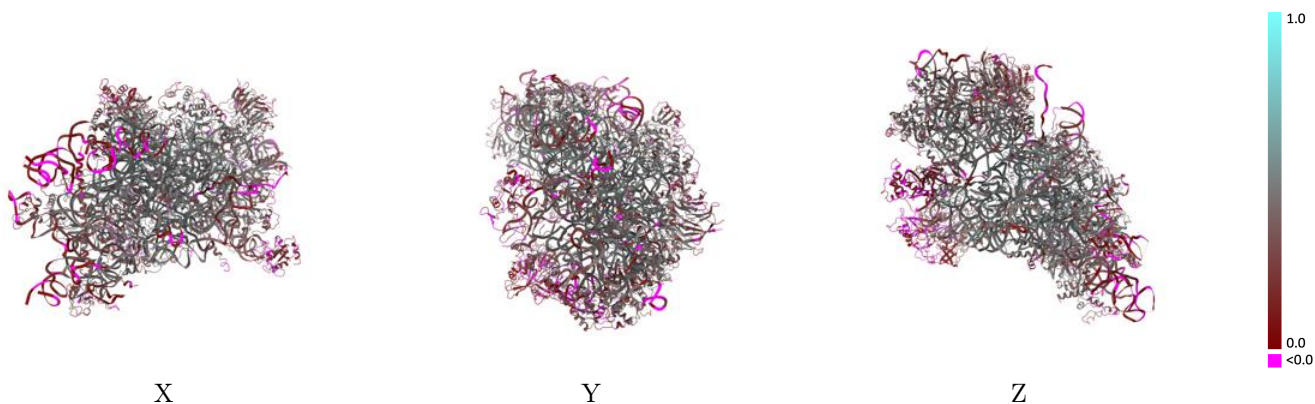
This section contains information regarding the fit between EMDB map EMD-10762 and PDB model 6YAN. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



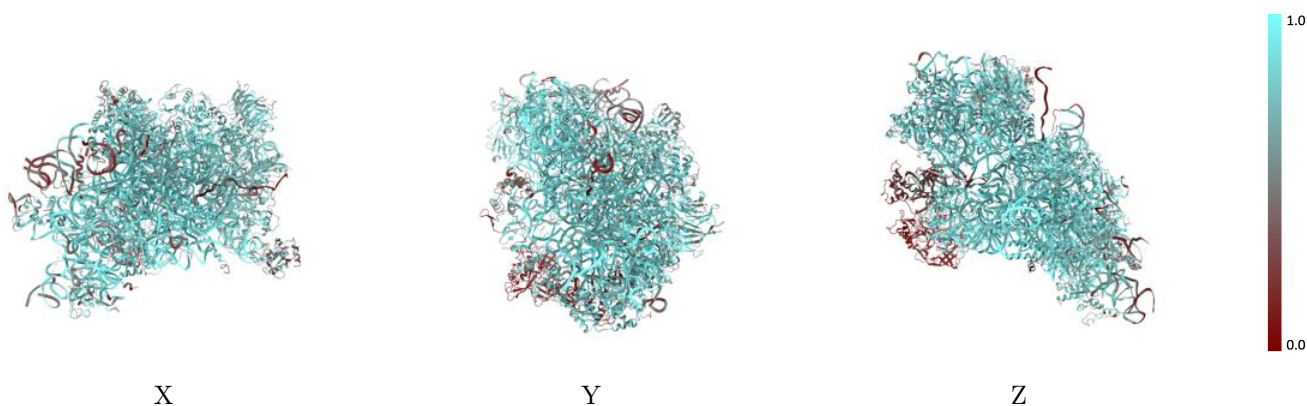
The images above show the 3D surface view of the map at the recommended contour level 0.0109 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



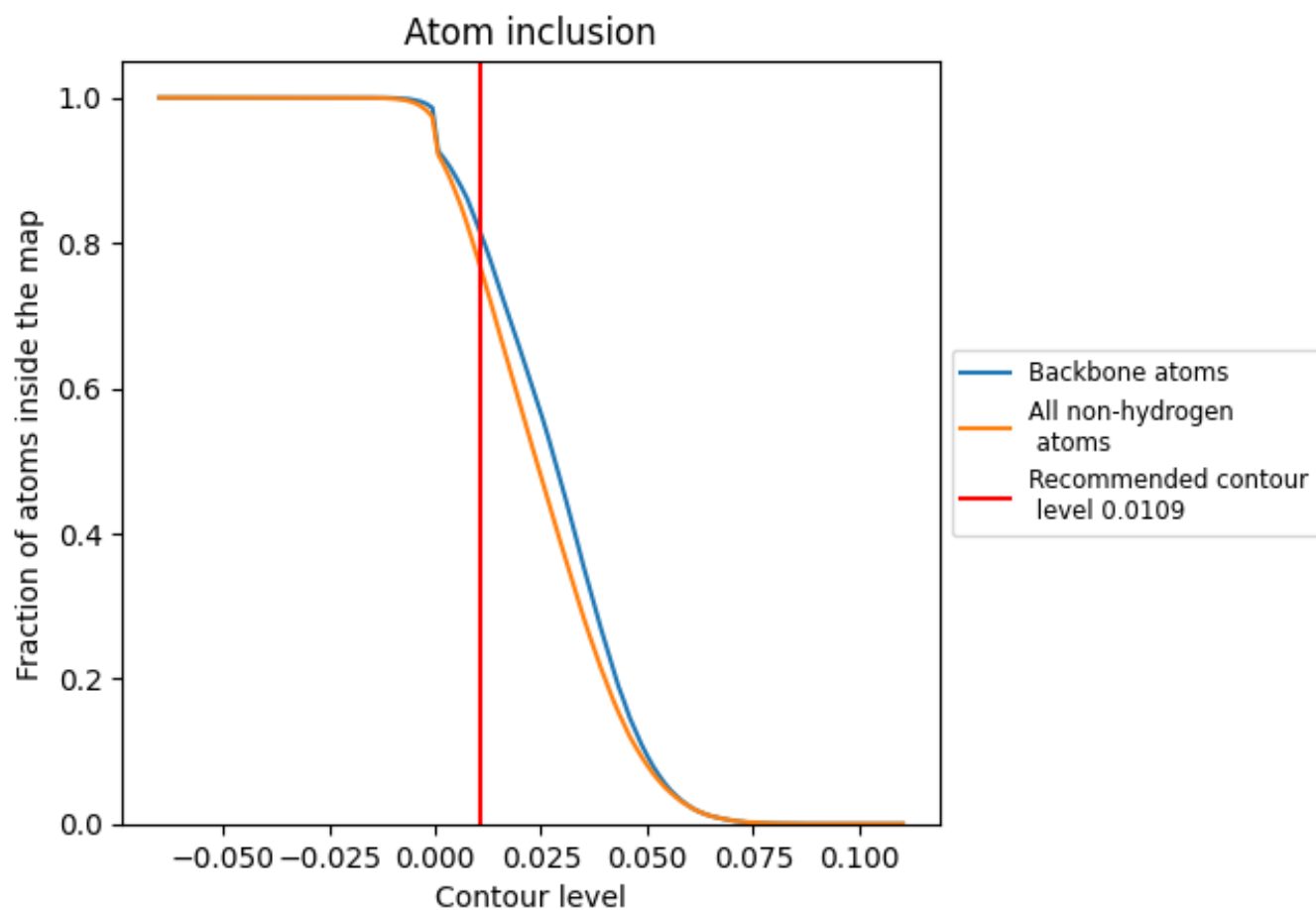
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0109).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 76% 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 (0.0109) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7631	 0.3510
1	 0.5062	 0.1520
2	 0.8838	 0.4010
3	 0.3269	 0.1390
A	 0.1818	 0.0510
B	 0.0079	 -0.0120
C	 0.8302	 0.4210
D	 0.7890	 0.4010
E	 0.8249	 0.4440
F	 0.7364	 0.3530
G	 0.8137	 0.4160
H	 0.7841	 0.3830
I	 0.7258	 0.2980
J	 0.6342	 0.2810
K	 0.7708	 0.3630
L	 0.8230	 0.4160
M	 0.7419	 0.3150
N	 0.7486	 0.3830
O	 0.4364	 0.1240
P	 0.8055	 0.3960
Q	 0.8065	 0.4090
R	 0.7001	 0.3020
S	 0.8142	 0.4180
T	 0.7288	 0.3300
U	 0.7693	 0.3430
V	 0.7773	 0.3790
W	 0.7503	 0.3450
X	 0.7921	 0.3780
Y	 0.8683	 0.4780
Z	 0.8509	 0.4510
a	 0.7968	 0.3730
b	 0.8331	 0.4320
c	 0.7403	 0.3230
d	 0.7536	 0.3660
e	 0.8103	 0.3800



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Chain	Atom inclusion	Q-score
f	 0.4427	 0.0750
g	 0.7391	 0.3250
h	 0.7055	 0.3110
i	 0.6228	 0.2840
l	 0.7671	 0.3910