



wwPDB EM Validation Summary Report ⓘ

Oct 13, 2024 – 12:43 am BST

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.dev113
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

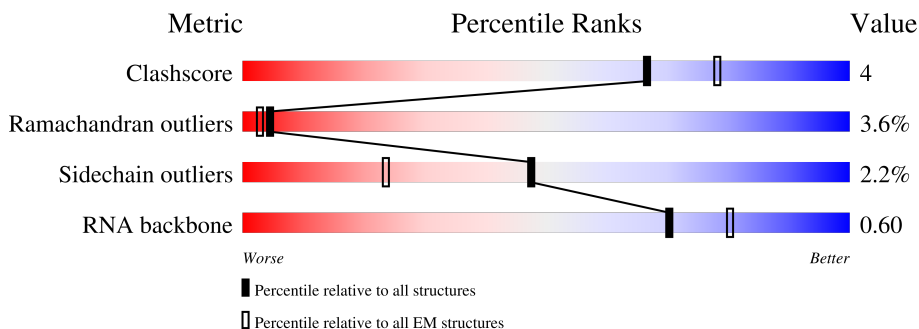
1 Overall quality at a glance

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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	<div> <div>16%</div> <div>88%</div> <div>12%</div> </div>
2	C	208	<div> <div>93%</div> <div>7%</div> </div>
3	D	215	<div> <div>93%</div> <div>6%</div> </div>
4	E	226	<div> <div>95%</div> <div>5%</div> </div>
5	F	227	<div> <div>7%</div> <div>90%</div> <div>9%</div> </div>
6	G	263	<div> <div>97%</div> </div>
7	H	191	<div> <div>6%</div> <div>93%</div> <div>7%</div> </div>





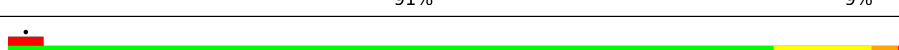
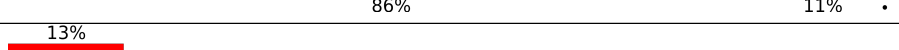
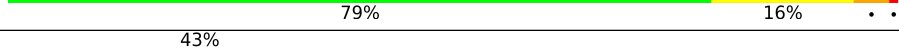
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Mol	Chain	Length	Quality of chain
8	I	237	
9	J	190	
10	K	206	
11	L	182	
12	M	98	
13	N	158	
14	O	124	
15	P	150	
16	Q	136	
17	S	141	
18	T	126	
19	V	141	
20	W	104	
21	X	82	
22	Y	129	
23	Z	142	
24	a	126	
25	b	99	
26	c	84	
27	d	64	
28	e	53	
29	f	71	
30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

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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

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
1	l	25	Total	C	N	O	S	0	0
			240	145	64	28	3		

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

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

- Molecule 3 is a protein called ribosomal protein eS1.

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

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

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

- Molecule 5 is a protein called Ribosomal protein S3.

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

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

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

- Molecule 7 is a protein called Ribosomal protein S5.

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

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

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

- Molecule 9 is a protein called ribosomal protein eS7.

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

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

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

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

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

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

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

- Molecule 13 is a protein called Ribosomal protein S11.

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

- 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
35	A	266	Total	C	N	O	S	0	0
			2147	1354	376	406	11		

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

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

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

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

- Molecule 38 is a protein called Ribosomal protein S15.

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

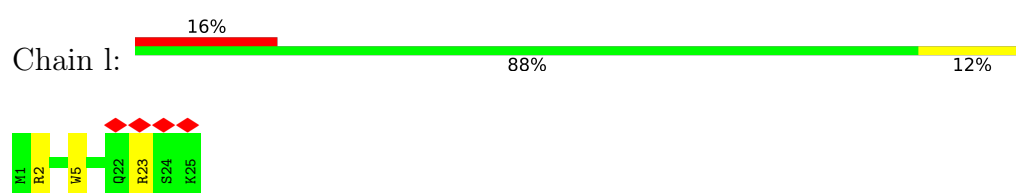
- Molecule 39 is a RNA chain called initiator methionylated tRNA.

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

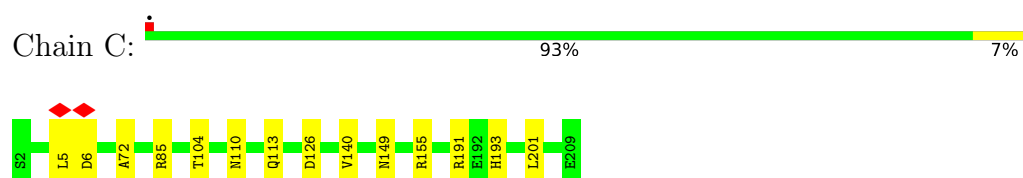
3 Residue-property plots

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.

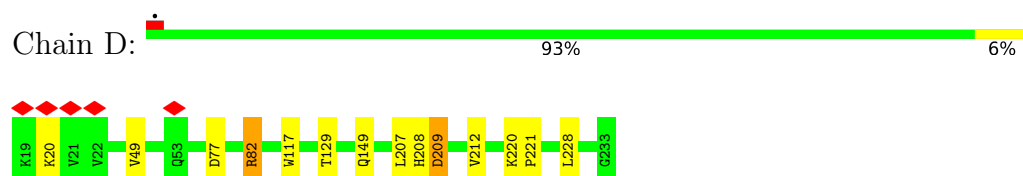
- Molecule 1: 60s ribosomal protein l41



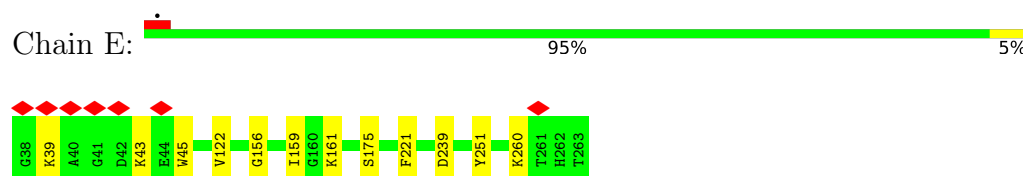
- Molecule 2: 40S ribosomal protein SA



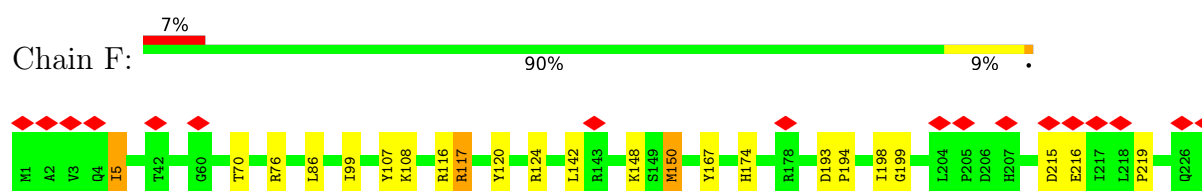
- Molecule 3: ribosomal protein eS1



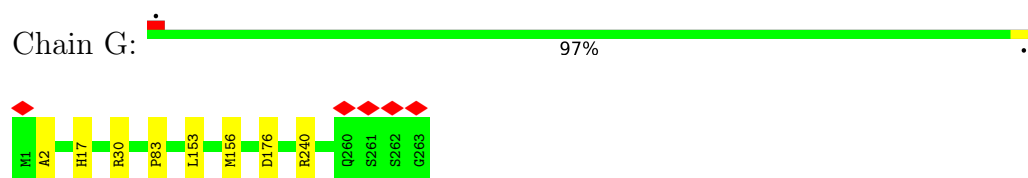
- Molecule 4: 40S ribosomal protein uS5



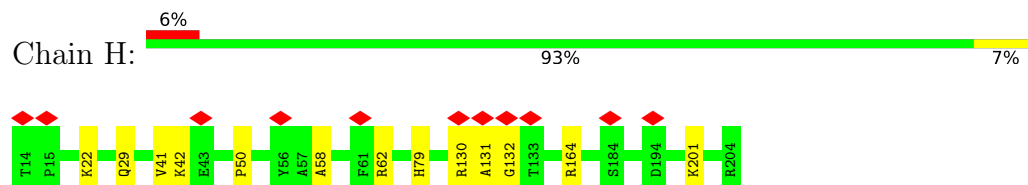
- Molecule 5: Ribosomal protein S3



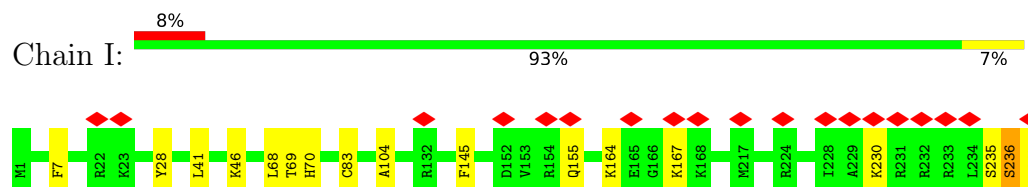
- Molecule 6: 40S ribosomal protein S4



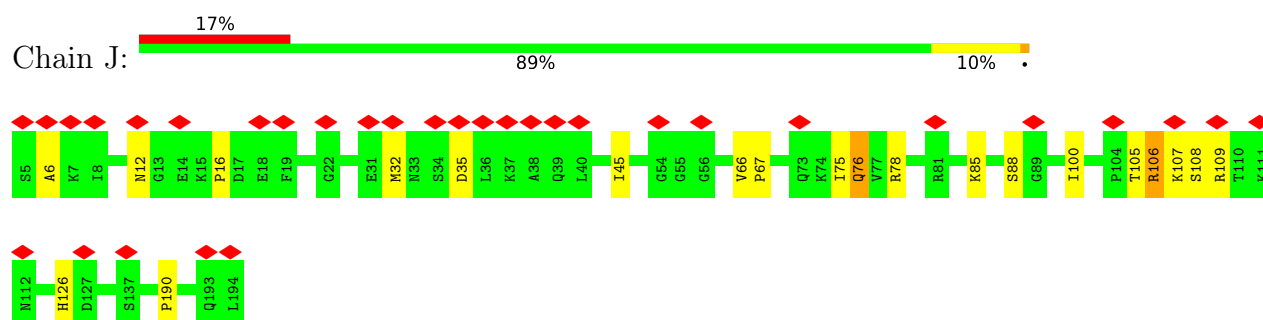
- Molecule 7: Ribosomal protein S5



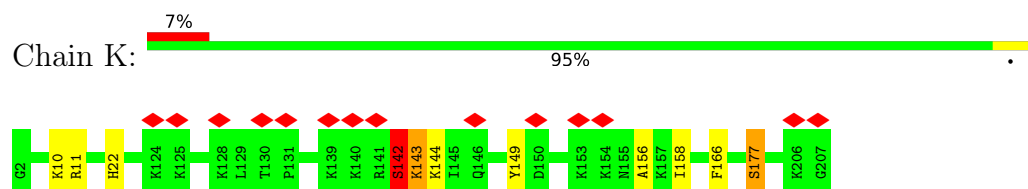
- Molecule 8: 40S ribosomal protein S6



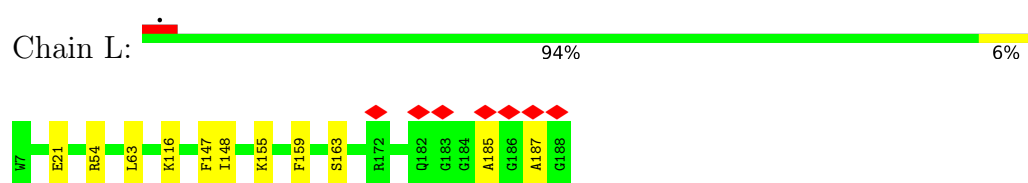
- Molecule 9: ribosomal protein eS7



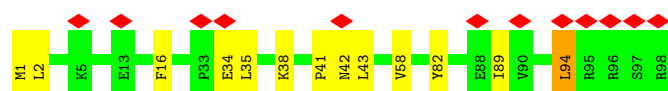
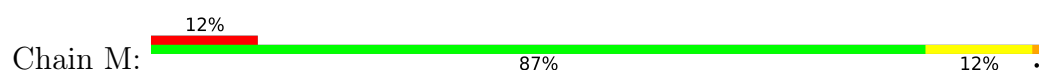
- Molecule 10: 40S ribosomal protein S8



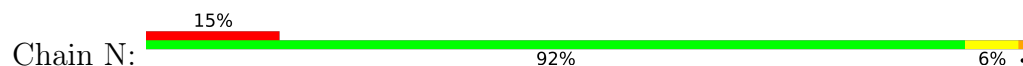
- Molecule 11: Ribosomal protein S9 (Predicted)



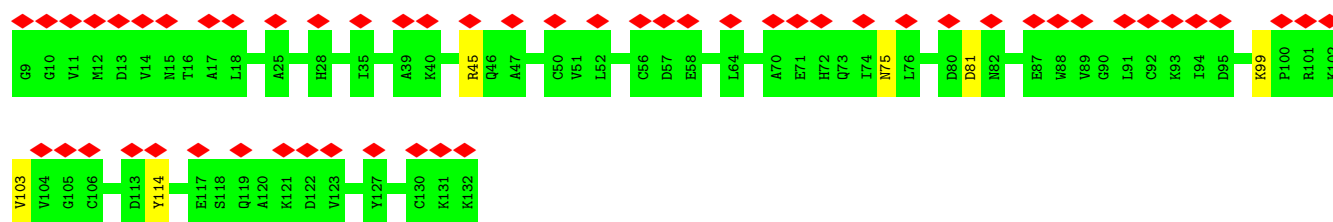
- Molecule 12: 40S ribosomal protein eS10



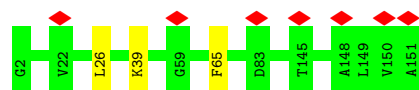
• Molecule 13: Ribosomal protein S11



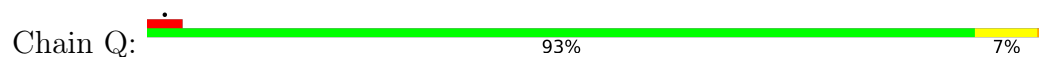
• Molecule 14: 40S ribosomal protein S12



• Molecule 15: ribosomal protein uS15



• Molecule 16: 40S ribosomal protein uS11

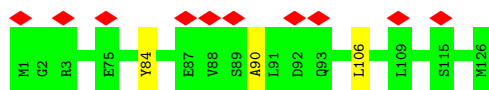


• Molecule 17: ribosomal protein uS9



• Molecule 18: ribosomal protein eS17

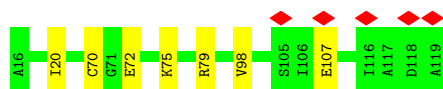




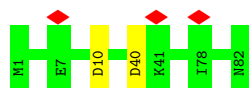
- Molecule 19: 40S ribosomal protein eS19



- Molecule 20: Ribosomal_S10 domain-containing protein



- Molecule 21: 40S ribosomal protein S21



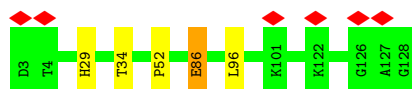
- Molecule 22: Ribosomal protein S15a



- Molecule 23: 40S ribosomal protein uS12

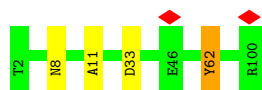


- Molecule 24: 40S ribosomal protein S24




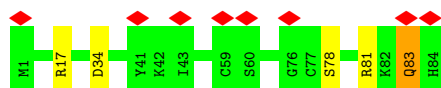
- Molecule 25: 40S ribosomal protein eS26

Chain b:  96% . .



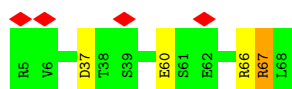
- Molecule 26: 40S ribosomal protein S27

Chain c:  10% 94% 5% .




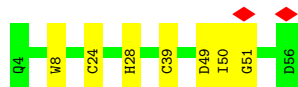
- Molecule 27: ribosomal protein eS28

Chain d:  6% 94% 5% .




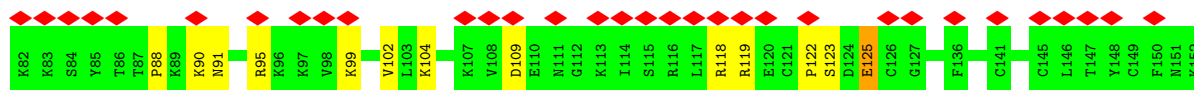
- Molecule 28: ribosomal protein uS14

Chain e:  87% 13%



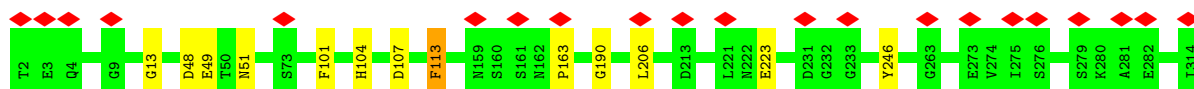
- Molecule 29: ribosomal protein eS31

Chain f:  45% 82% 17% .



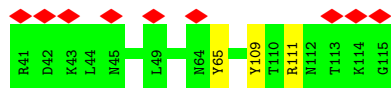
- Molecule 30: ribosomal protein RACK1

Chain g:  7% 96% .

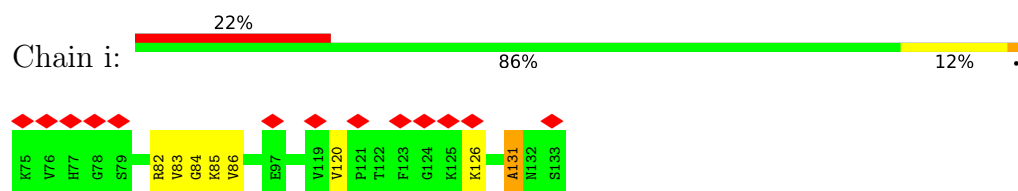


- Molecule 31: ribosomal protein eS25

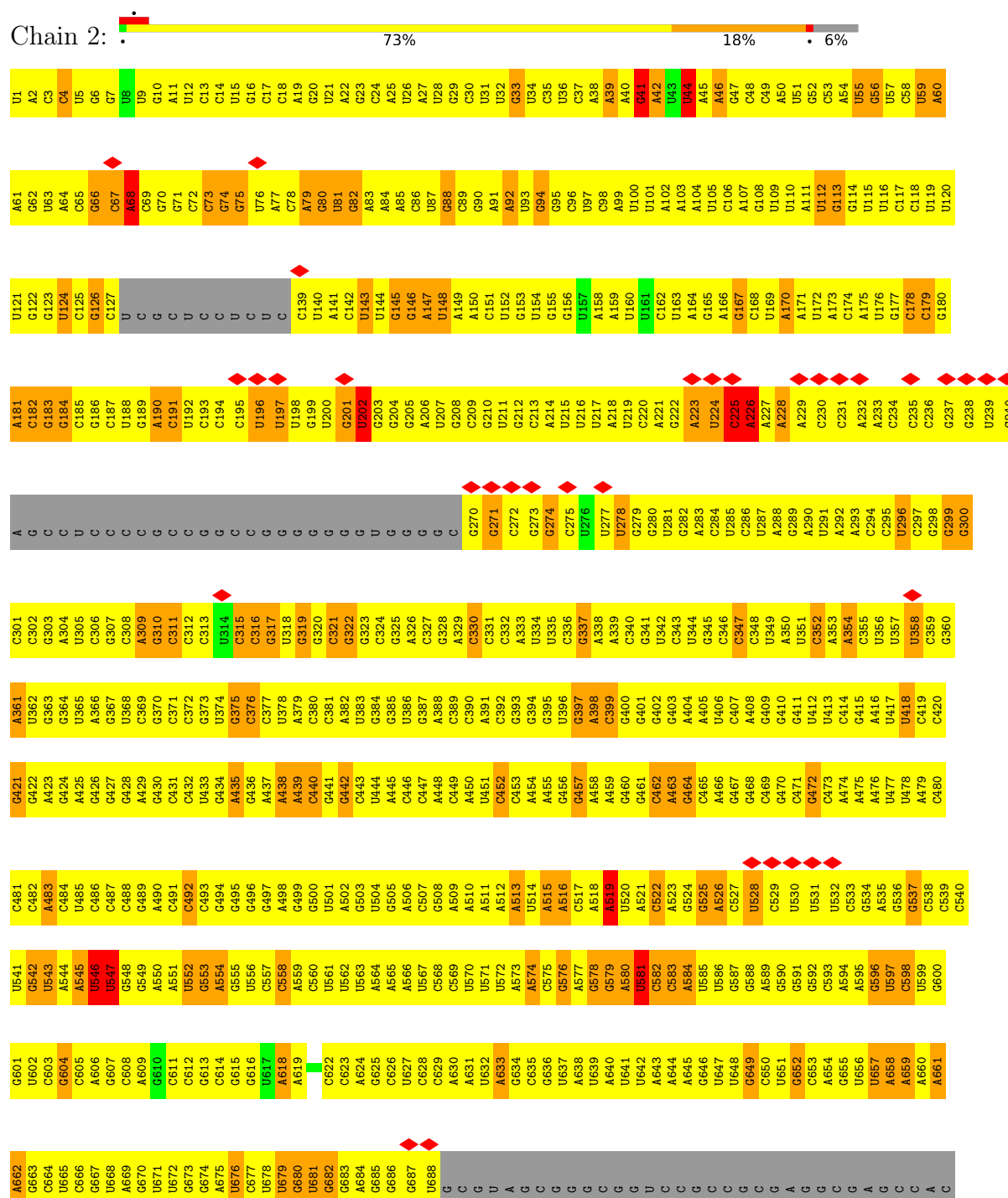
Chain h:  12% 96% .



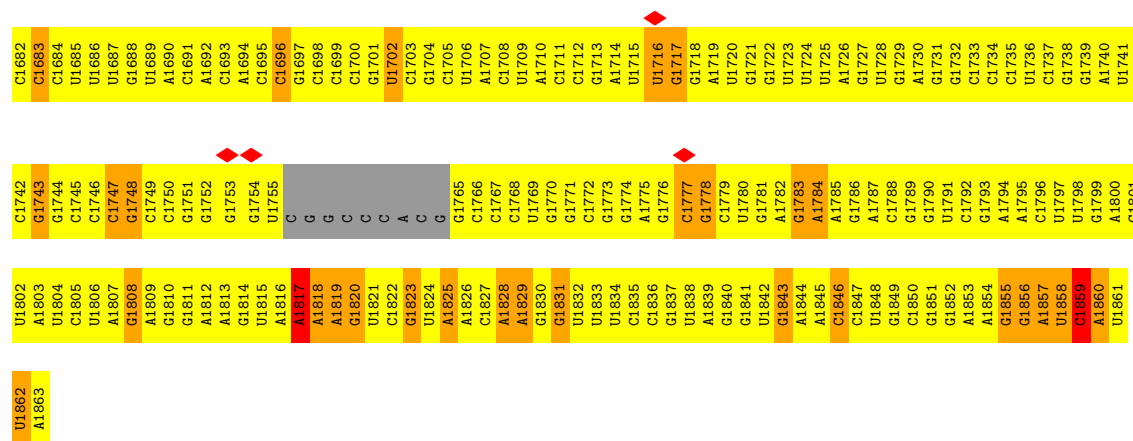
• Molecule 32: 40S ribosomal protein eS30



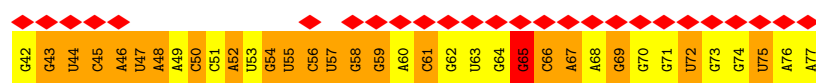
• Molecule 33: 18S ribosomal RNA



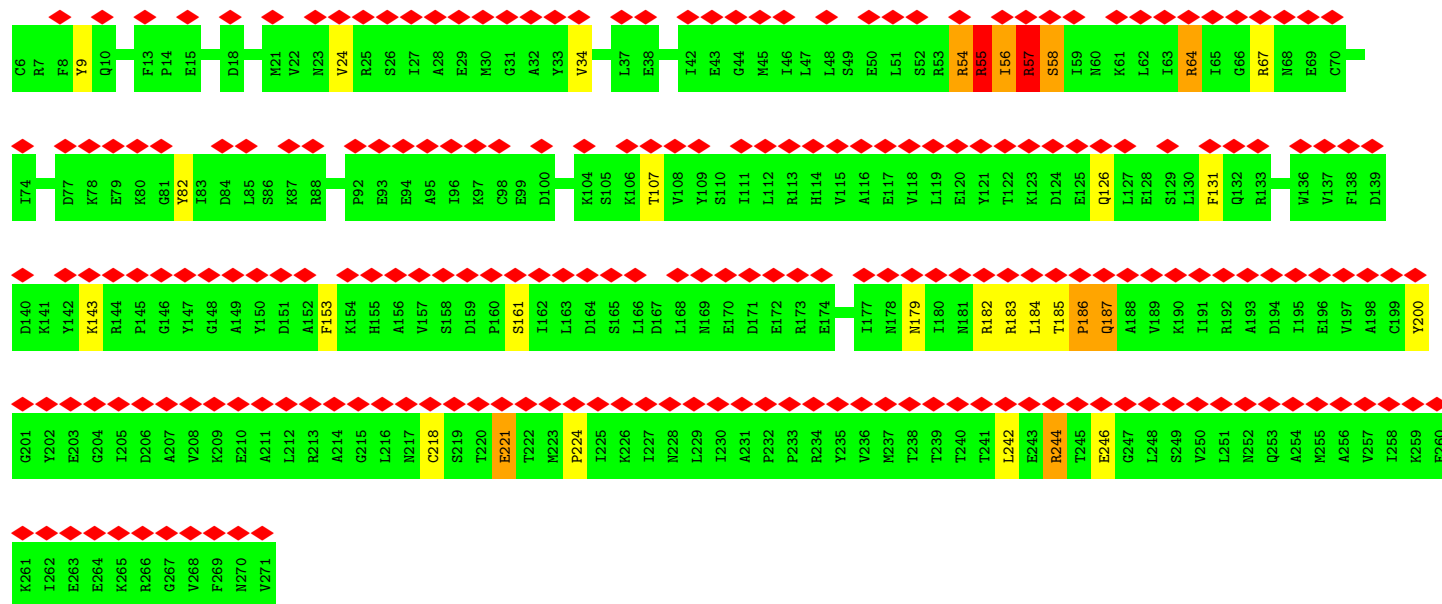
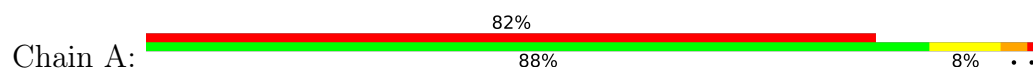
C1622	C1623	C1663	C1664	A1502	A1503	A1442	A1382	U1322	C1262	G1202	C1142	G1082	C1022	U982	U902	G842	C
G1563	G1564	A1564	A1565	G1505	G1506	G1443	G1383	G1323	C1263	G1203	C1143	A1083	A1023	C963	G903	A843	G
A1624	A1625	A1566	A1567	U1505	U1506	A1444	A1384	G1324	C1264	A1204	A1144	U1084	A1024	U964	A904	A844	C
A1626	A1627	G1566	G1567	G1507	G1508	G1445	U1386	G1326	G1266	G1206	A1145	C1086	A1026	G966	G906	A845	C
G1627	G1628	G1567	G1568	U1509	C1508	G1447	C1387	G1327	C1267	G1207	G1146	C1087	A1027	G967	C907	C947	G
A1628	A1629	C1568	C1569	G1509	G1508	A1448	U1388	A1328	C1268	G1208	U1148	G1088	G1028	A968	C908	G848	U728
A1630	A1631	G1570	G1571	G1510	G1509	A1449	G1389	U1329	C1269	C1209	C1149	A1089	G1029	C969	A909	C849	C729
G1631	G1632	G1572	G1573	G1511	G1510	A1450	C1391	G1331	G1270	A1210	U1150	A1090	A1030	C970	U910	A850	C730
A1632	A1633	A1574	A1575	G1512	G1511	A1451	A1392	C1332	A1272	C1212	U1152	G1092	A1032	G972	A912	G851	C731
A1634	A1635	A1576	A1577	C1513	C1512	G1453	U1393	G1333	C1273	A1213	G1153	G1093	G1033	C973	U913	A791	C732
A1636	A1637	A1578	A1579	U1514	U1513	G1454	G1394	G1334	A1274	C1214	G1154	C1094	U1034	G974	A914	G792	G733
A1638	A1639	C1576	C1577	G1515	G1514	G1455	C1395	U1335	C1275	C1215	U1155	G1095	C1035	C975	A915	G855	C734
U1637	U1637	U1577	U1577	A1517	A1516	G1456	U1396	U1336	G1276	A1216	U1156	A1096	G1036	A976	A916	G856	C735
U1638	U1638	U1577	U1577	A1517	A1516	G1457	A1397	C1337	G1277	G1217	U1157	U1097	G1037	A977	G917	A857	C736
U1638	U1638	U1578	U1578	C1518	C1517	U1458	A1398	U1338	A1278	G1218	C1158	G1098	A1038	A978	A918	U796	C737
U1639	U1639	C1579	C1579	G1519	G1518	U1459	C1399	U1339	C1279	A1219	C1159	G1099	G1039	A979	G919	A797	U738
U1640	U1640	A1581	A1581	G1520	G1519	A1460	U1400	A1340	A1280	G1220	G1160	G1100	G1040	C980	G920	A798	U739
U1642	U1642	A1582	A1582	C1522	C1521	A1461	A1401	G1341	G1281	U1221	G1161	G1101	U1041	G981	G921	A861	U740
U1643	U1643	A1583	A1583	G1523	G1522	G1462	G1402	U1342	G1282	G1222	G1162	G1102	A1042	G982	A922	U862	C741
U1644	U1644	A1584	A1584	C1524	C1523	C1463	A1403	G1343	A1283	G1223	G1163	G1103	C1043	A983	C923	U801	C742
U1645	U1645	A1585	A1585	U1524	U1523	C1464	U1404	G1344	U1284	A1224	G1164	G1104	G1044	C984	G924	U802	U743
U1646	U1646	C1586	C1586	U1525	U1524	A1465	A1405	U1345	U1285	G1225	G1165	C1105	A1045	C985	G925	A865	C744
U1647	U1647	A1586	A1586	A1526	A1525	C1466	C1406	U1346	G1286	C1226	A1166	G1106	A1046	A986	C926	A804	U745
U1648	U1648	C1587	C1587	C1527	C1526	G1467	G1407	G1347	A1287	C1227	G1167	U1107	G1047	G987	C927	A805	C746
U1649	U1649	A1588	A1588	A1528	A1527	C1468	C1408	G1348	G1288	G1228	U1168	U1108	A1048	A988	G928	A806	C747
U1650	U1650	A1589	A1589	C1529	C1528	G1469	G1409	A1349	A1289	G1229	A1169	A1109	C1049	G989	G929	A807	U748
U1651	U1651	U1590	U1590	U1530	U1529	A1470	A1410	G1350	G1290	G1230	U1170	U1110	G1050	C990	G930	A808	C749
U1652	U1652	C1591	C1591	G1531	G1530	G1471	C1411	C1351	A1291	G1231	G1171	U1111	A1051	C991	G931	A809	C750
U1653	U1653	A1592	A1592	A1532	A1531	A1472	C1412	G1352	U1292	G1232	G1172	C1112	C1052	A992	G932	U810	C751
U1654	U1654	C1593	C1593	C1533	C1532	U1473	C1413	A1353	U1293	C1233	U1173	C1113	C1053	A993	G933	U811	C752
U1654	U1654	A1594	A1594	U1534	U1533	U1474	A1414	U1354	G1294	U1234	U1174	C1114	A1054	A994	A934	G812	C753
U1655	U1655	G1595	G1595	G1535	G1534	G1475	C1415	U1355	A1295	U1235	G1175	U1115	G1055	C995	U935	G813	C754
U1656	U1656	C1596	C1596	A1536	A1535	A1476	G1416	U1356	U1296	A1236	C1176	U1116	A1056	C996	C936	A814	C755
U1657	U1657	U1597	U1597	C1537	C1536	G1477	A1417	G1357	A1297	G1237	G1177	U1117	U1057	A997	C937	G876	C756
U1658	U1658	A1598	A1598	U1538	U1537	C1478	G1418	U1358	G1298	U1238	A1178	A1118	A1058	U998	G938	U816	C
U1659	U1659	G1599	G1599	C1539	C1538	A1479	G1419	U1359	G1299	U1239	A1179	C1119	C1059	U999	U939	U817	C
U1660	U1660	A1600	A1600	U1540	U1539	U1480	G1420	U1360	U1300	U1240	G1180	C1120	C1060	U1000	A940	U818	C
U1661	U1661	A1601	A1601	G1541	G1540	U1481	A1421	G1361	C1301	G1241	C1181	C1121	G1061	G1001	U941	C880	C
U1662	U1662	C1602	C1602	A1542	A1541	A1482	G1422	G1362	U1302	A1242	U1182	C1122	U1062	C1002	U942	A881	C
U1663	U1663	A1603	A1603	G1543	G1542	A1483	U1423	U1363	G1303	C1243	G1183	C1123	C1063	C1003	G943	A821	C
U1664	U1664	C1604	C1604	U1544	U1543	C1484	G1424	U1364	U1304	C4J1244	A1184	C1124	G1064	A1004	G944	A822	C
U1665	U1665	G1605	G1605	U1545	U1544	A1485	G1425	A1365	C1305	C1245	A1185	G1125	U1065	A1005	G945	A823	C
U1666	U1666	A1606	A1606	U1546	U1545	G1486	G1426	A1366	U1306	A1246	A1186	G1126	A1066	G1006	C946	A824	C
U1667	U1667	C1607	C1607	C1547	C1546	G1487	G1427	U1367	C1307	A1247	C1187	G1127	G1067	A1007	C947	A825	C
U1668	U1668	A1608	A1608	U1549	U1548	U1488	G1428	U1368	G1308	C1248	U1188	C1128	U1068	A1008	G948	A826	C
U1669	U1669	C1609	C1609	U1550	U1549	A1489	U1429	C1369	A1309	A1249	U1189	A1129	U1069	U1009	C949	G827	C
U1670	U1670	U1610	U1610	U1550	U1549	U1490	C1429	C1370	U1310	C1250	A1190	G1130	C1070	U1010	U950	U889	C
U1671	U1671	U1611	U1611	A1551	A1550	G1491	C1430	G1371	U1311	G1251	A1191	C1131	C1071	U1011	A951	C829	C
U1672	U1672	C1612	C1612	U1552	U1551	U1492	C1431	A1372	C1312	G1252	A1192	U1132	G1072	U1012	A952	C830	C
U1673	U1673	G1613	G1613	C1553	C1552	G1493	C1432	U1373	U1313	G1253	G1193	U1133	A1073	U1013	A953	C831	C
U1674	U1674	A1614	A1614	U1554	U1553	A1494	A1433	A1374	G1314	A1254	U1194	C1134	C1074	U1014	G954	A832	C
U1675	U1675	A1615	A1615	U1555	U1554	A1495	A1434	A1375	U1315	A1255	G1195	C1135	C1075	U1015	G955	A833	C
U1676	U1676	C1616	C1616	A1556	A1555	G1496	A1435	C1376	G1316	A1256	A1196	G1136	A1076	A1016	U956	A834	C
U1677	U1677	U1617	U1617	C1557	C1556	G1497	A1436	G1377	G1317	C1257	U1197	G1137	U1077	U1017	G957	C835	C
C1678	C1678	A1618	A1618	U1558	U1557	C1498	U1437	A1378	G1318	C1258	U1198	G1138	A1078	U1018	A958	C836	C
U1679	U1679	C1619	C1619	C1559	C1558	U1620	U1438	A1379	U1319	U1259	G1199	A1139	A1079	A1019	A959	G837	C
U1680	U1680	U1620	U1620	U1560	U1559	U1600	U1439	C1380	G1320	A1260	A1200	A1140	A1080	A1019	A960	C838	C
U1681	U1681	G1621	G1621	U1561	U1560	U1601	U1440	G1381	G1321	A1261	C1201	A1141	C1081	U1021	U961	A900	C
																C901	C
																U940	C
																G941	C
																	G



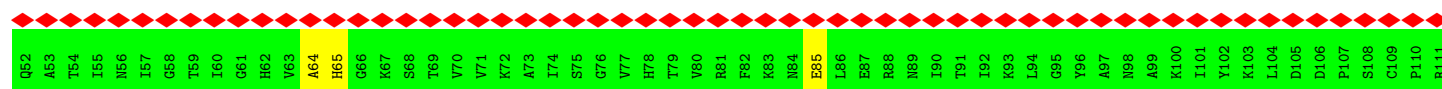
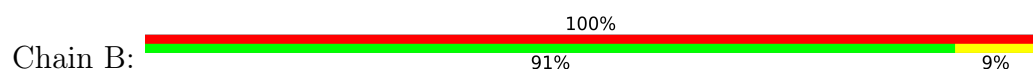
• Molecule 34: histone 4 (H4) mRNA

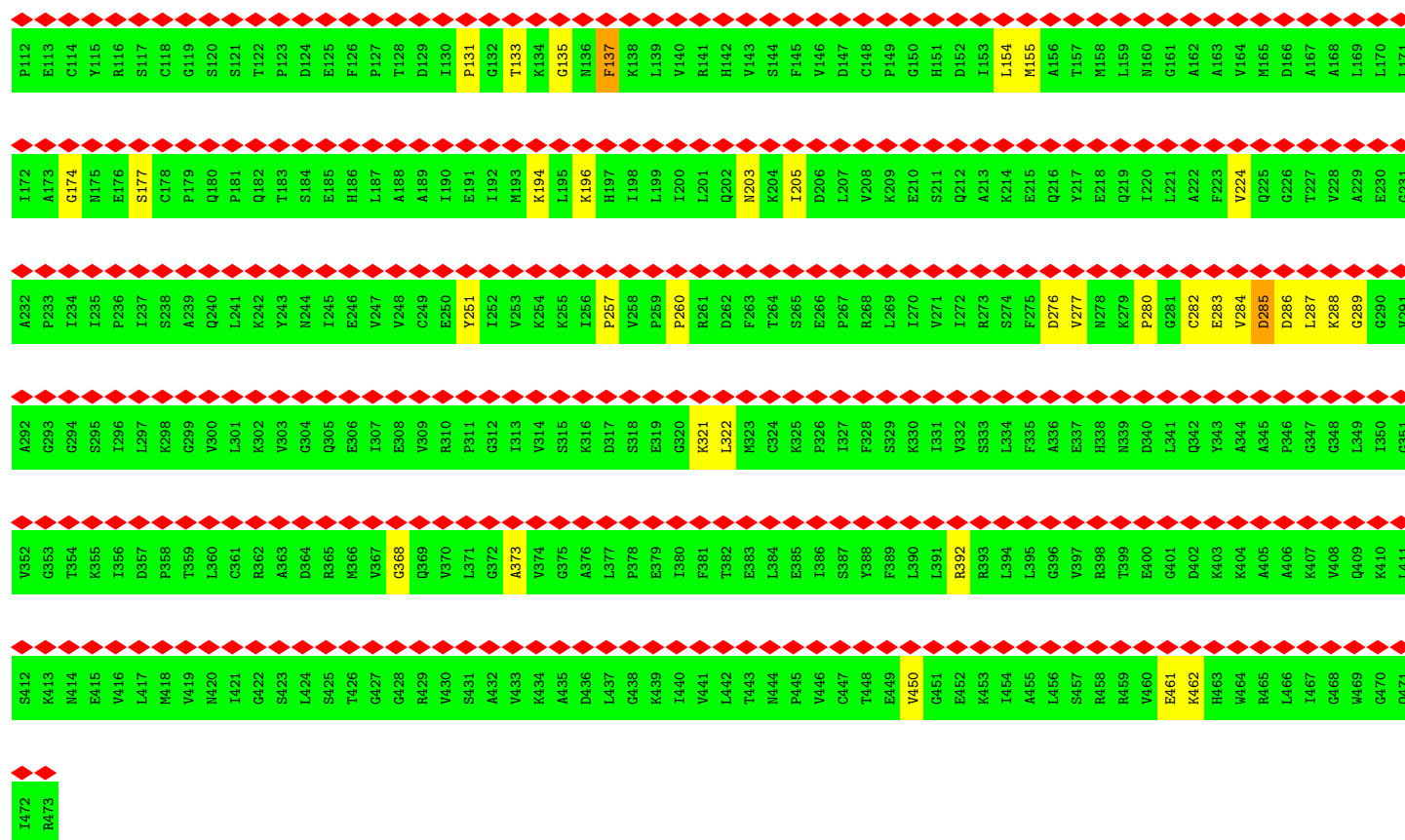


• Molecule 35: Eukaryotic translation initiation factor 2 subunit 1

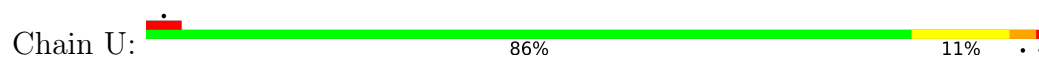


• Molecule 36: eukaryotic translation initiation factor 2 subunit gamma

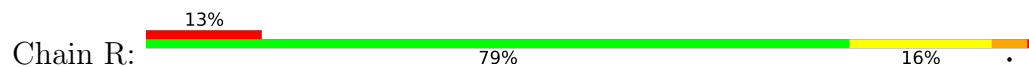




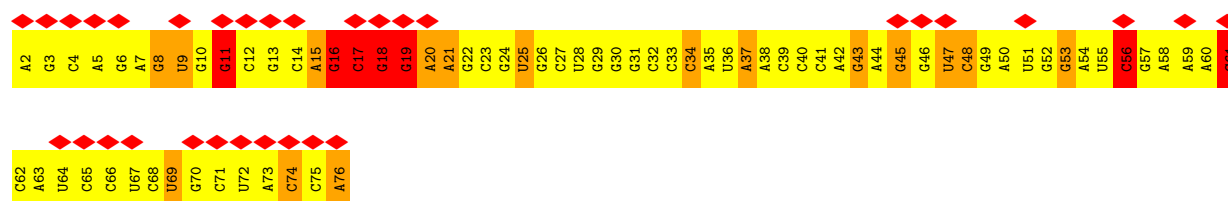
• Molecule 37: 40S ribosomal protein uS13



• 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 ⓘ

5.1 Standard geometry ⓘ

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

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	C3',C2'
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	18
3	D	213/215 (99%)	185 (87%)	19 (9%)	9 (4%)	2	19
4	E	224/226 (99%)	203 (91%)	16 (7%)	5 (2%)	5	31
5	F	225/227 (99%)	205 (91%)	13 (6%)	7 (3%)	3	26
6	G	261/263 (99%)	229 (88%)	26 (10%)	6 (2%)	5	31
7	H	189/191 (99%)	165 (87%)	16 (8%)	8 (4%)	2	19
8	I	233/237 (98%)	206 (88%)	20 (9%)	7 (3%)	3	26
9	J	188/190 (99%)	162 (86%)	18 (10%)	8 (4%)	2	19
10	K	204/206 (99%)	180 (88%)	18 (9%)	6 (3%)	3	27
11	L	180/182 (99%)	167 (93%)	6 (3%)	7 (4%)	2	21
12	M	96/98 (98%)	78 (81%)	12 (12%)	6 (6%)	1	12
13	N	156/158 (99%)	130 (83%)	19 (12%)	7 (4%)	2	18
14	O	122/124 (98%)	103 (84%)	15 (12%)	4 (3%)	3	24
15	P	148/150 (99%)	143 (97%)	5 (3%)	0	100	100
16	Q	134/136 (98%)	116 (87%)	11 (8%)	7 (5%)	1	15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	S	139/141 (99%)	123 (88%)	12 (9%)	4 (3%)	3	27
18	T	124/126 (98%)	114 (92%)	8 (6%)	2 (2%)	8	37
19	V	139/141 (99%)	124 (89%)	10 (7%)	5 (4%)	3	22
20	W	102/104 (98%)	95 (93%)	4 (4%)	3 (3%)	3	27
21	X	80/82 (98%)	66 (82%)	13 (16%)	1 (1%)	10	41
22	Y	127/129 (98%)	119 (94%)	6 (5%)	2 (2%)	8	37
23	Z	140/142 (99%)	127 (91%)	11 (8%)	2 (1%)	9	40
24	a	122/126 (97%)	106 (87%)	12 (10%)	4 (3%)	3	24
25	b	97/99 (98%)	81 (84%)	13 (13%)	3 (3%)	3	26
26	c	82/84 (98%)	72 (88%)	8 (10%)	2 (2%)	5	30
27	d	62/64 (97%)	54 (87%)	5 (8%)	3 (5%)	2	17
28	e	51/53 (96%)	39 (76%)	8 (16%)	4 (8%)	1	8
29	f	69/71 (97%)	56 (81%)	6 (9%)	7 (10%)	0	6
30	g	311/313 (99%)	273 (88%)	31 (10%)	7 (2%)	5	31
31	h	73/75 (97%)	70 (96%)	2 (3%)	1 (1%)	9	40
32	i	57/59 (97%)	45 (79%)	7 (12%)	5 (9%)	0	7
35	A	264/266 (99%)	225 (85%)	29 (11%)	10 (4%)	2	21
36	B	420/422 (100%)	350 (83%)	48 (11%)	22 (5%)	1	15
37	U	140/142 (99%)	121 (86%)	14 (10%)	5 (4%)	3	22
38	R	133/135 (98%)	105 (79%)	18 (14%)	10 (8%)	1	9
All	All	5534/5610 (99%)	4836 (87%)	500 (9%)	198 (4%)	4	22

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 ⓘ

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%)	3	19
2	C	174/174 (100%)	171 (98%)	3 (2%)	56	75
3	D	196/196 (100%)	192 (98%)	4 (2%)	50	72
4	E	187/187 (100%)	183 (98%)	4 (2%)	48	71
5	F	190/190 (100%)	182 (96%)	8 (4%)	25	54
6	G	225/225 (100%)	223 (99%)	2 (1%)	75	85
7	H	161/161 (100%)	159 (99%)	2 (1%)	67	81
8	I	207/207 (100%)	205 (99%)	2 (1%)	73	84
9	J	170/170 (100%)	164 (96%)	6 (4%)	31	60
10	K	177/177 (100%)	174 (98%)	3 (2%)	56	75
11	L	157/157 (100%)	156 (99%)	1 (1%)	84	91
12	M	89/89 (100%)	86 (97%)	3 (3%)	32	60
13	N	142/142 (100%)	135 (95%)	7 (5%)	21	50
14	O	104/104 (100%)	103 (99%)	1 (1%)	73	84
15	P	130/130 (100%)	129 (99%)	1 (1%)	79	87
16	Q	106/106 (100%)	103 (97%)	3 (3%)	38	65
17	S	117/117 (100%)	112 (96%)	5 (4%)	25	54
18	T	114/114 (100%)	113 (99%)	1 (1%)	75	85
19	V	113/113 (100%)	113 (100%)	0	100	100
20	W	94/94 (100%)	92 (98%)	2 (2%)	48	71
21	X	67/67 (100%)	66 (98%)	1 (2%)	60	77
22	Y	112/112 (100%)	111 (99%)	1 (1%)	75	85
23	Z	114/114 (100%)	112 (98%)	2 (2%)	54	74
24	a	108/108 (100%)	107 (99%)	1 (1%)	75	85
25	b	87/87 (100%)	86 (99%)	1 (1%)	70	82
26	c	76/76 (100%)	73 (96%)	3 (4%)	27	57
27	d	57/57 (100%)	55 (96%)	2 (4%)	31	60
28	e	47/47 (100%)	46 (98%)	1 (2%)	48	71
29	f	64/64 (100%)	58 (91%)	6 (9%)	7	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	g	272/272 (100%)	267 (98%)	5 (2%)	54	74
31	h	66/66 (100%)	66 (100%)	0	100	100
32	i	49/49 (100%)	48 (98%)	1 (2%)	50	72
35	A	238/238 (100%)	230 (97%)	8 (3%)	32	60
36	B	354/354 (100%)	350 (99%)	4 (1%)	70	82
37	U	122/122 (100%)	118 (97%)	4 (3%)	33	61
38	R	121/121 (100%)	114 (94%)	7 (6%)	17	44
All	All	4831/4831 (100%)	4723 (98%)	108 (2%)	47	70

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	$\# Z > 2$
39	T6A	1	37	39	27,34,35	1.04	2 (7%)	29,49,52	2.64	9 (31%)
33	C4J	2	1244	33	24,29,30	0.79	1 (4%)	29,42,45	1.03	1 (3%)

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

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
39	1	37	T6A	5	0
33	2	1244	C4J	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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

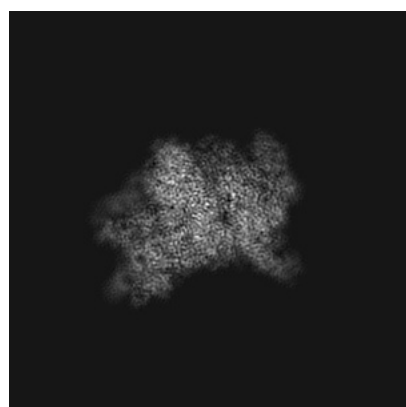
6 Map visualisation [i](#)

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.

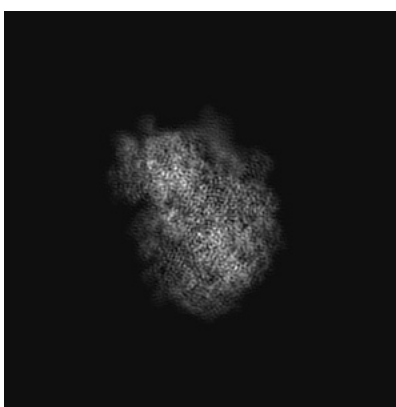
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

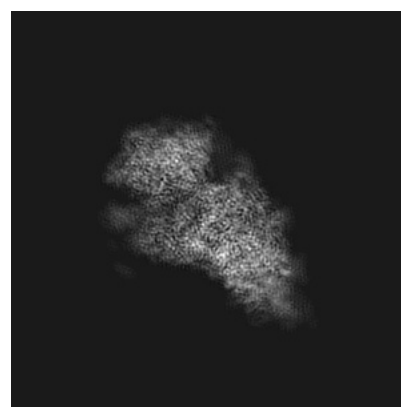
6.1.1 Primary map



X



Y

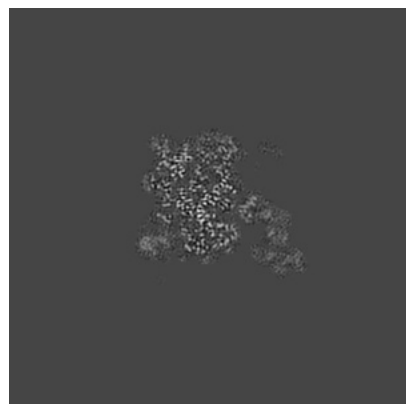


Z

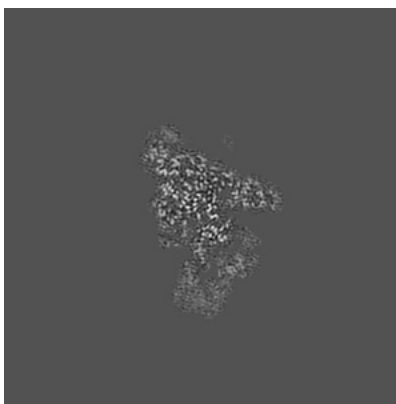
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

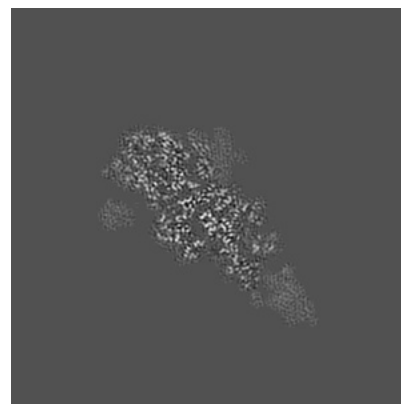
6.2.1 Primary map



X Index: 192



Y Index: 192

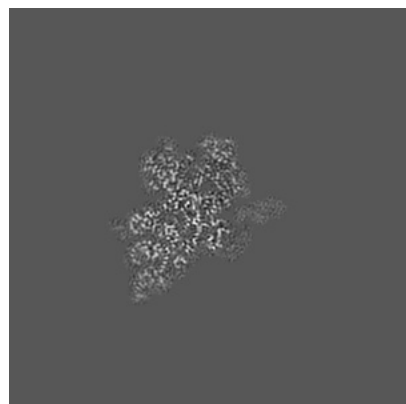


Z Index: 192

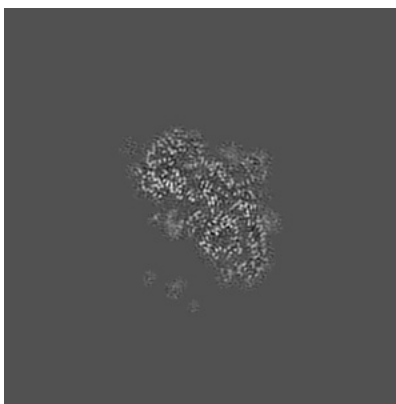
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

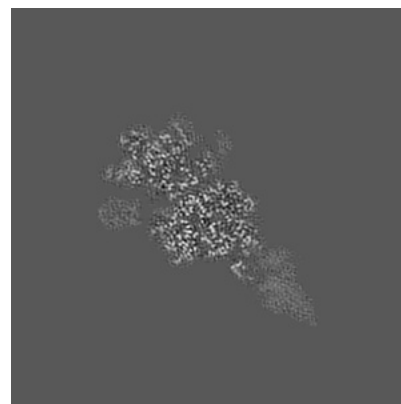
6.3.1 Primary map



X Index: 208



Y Index: 160

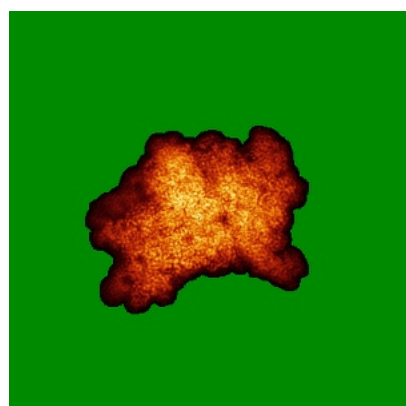


Z Index: 199

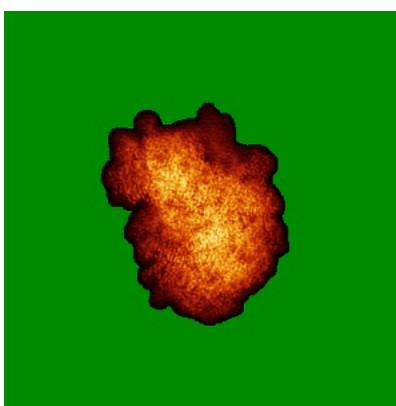
The images above show the largest variance slices of the map in three orthogonal directions.

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

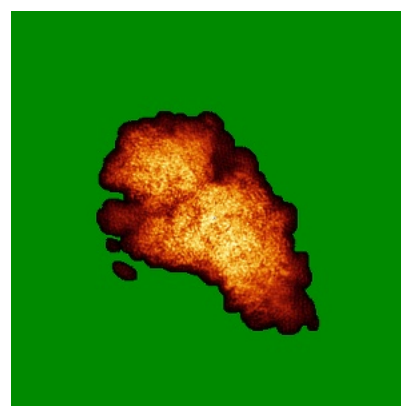
6.4.1 Primary map



X



Y

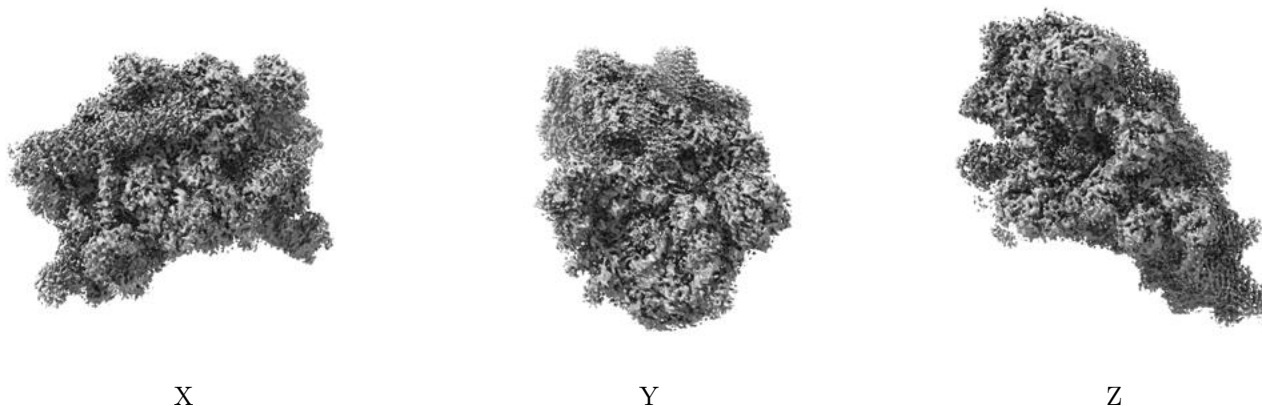


Z

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 0.0109. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

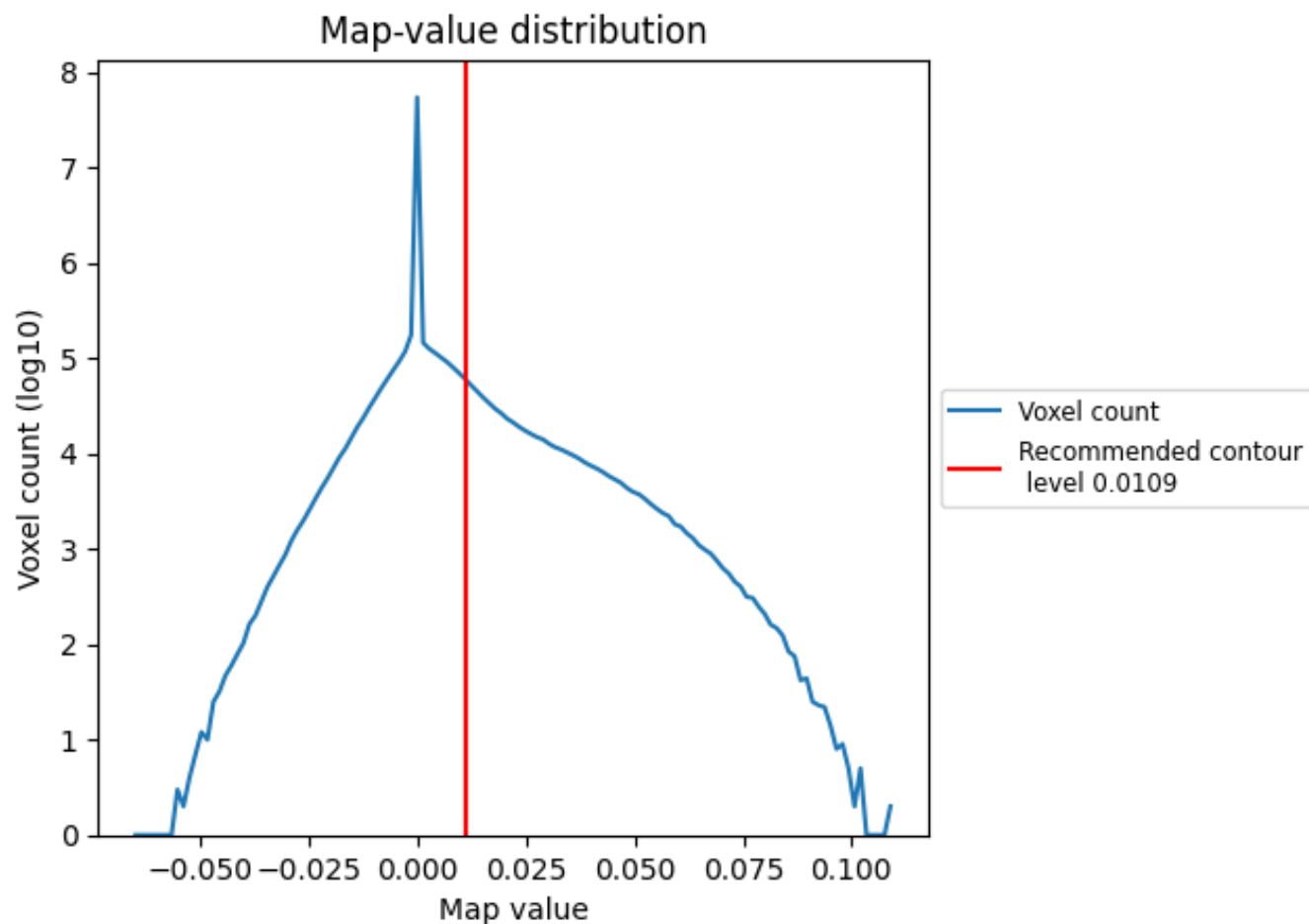
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

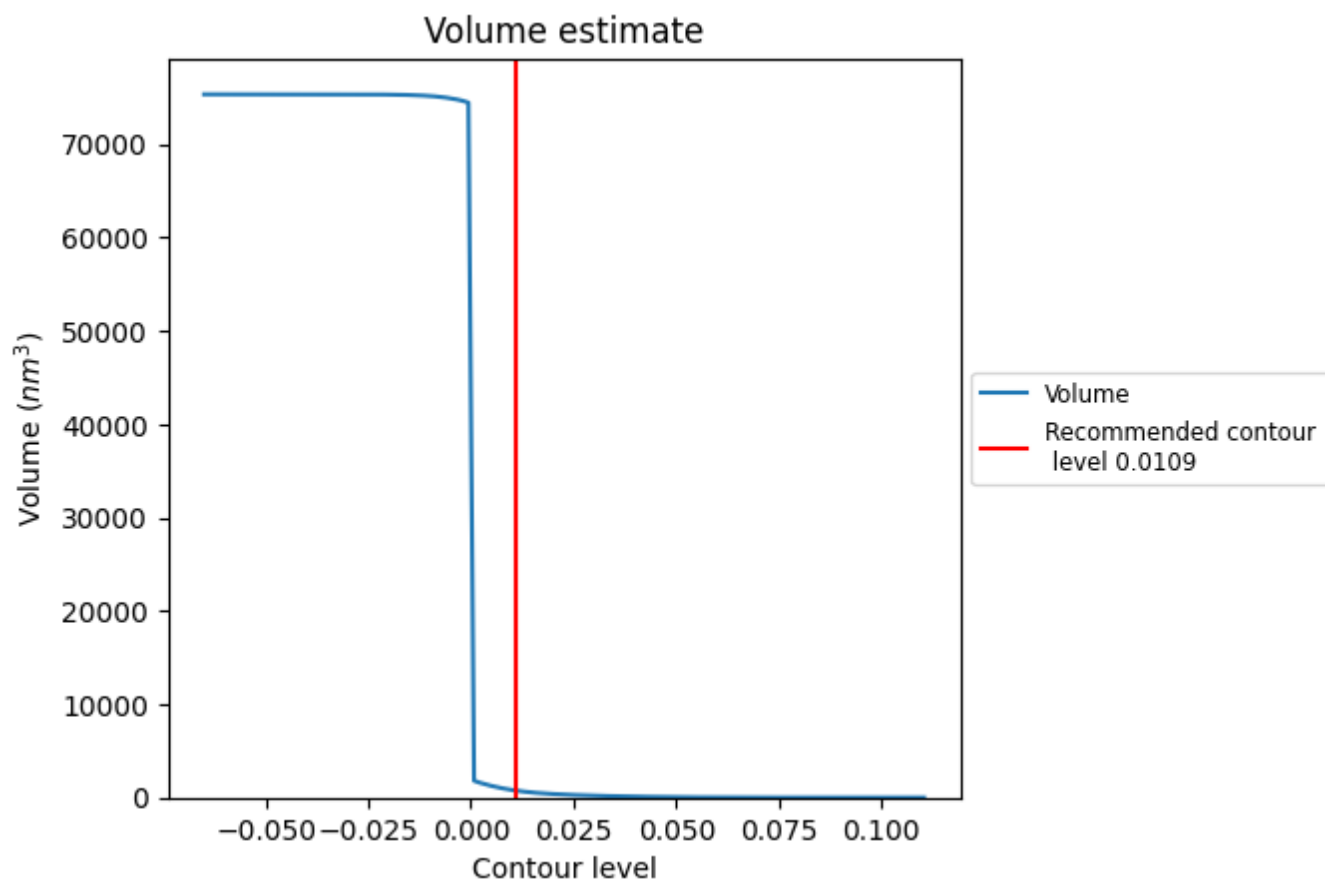
This section contains the results of statistical analysis of the map.

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.

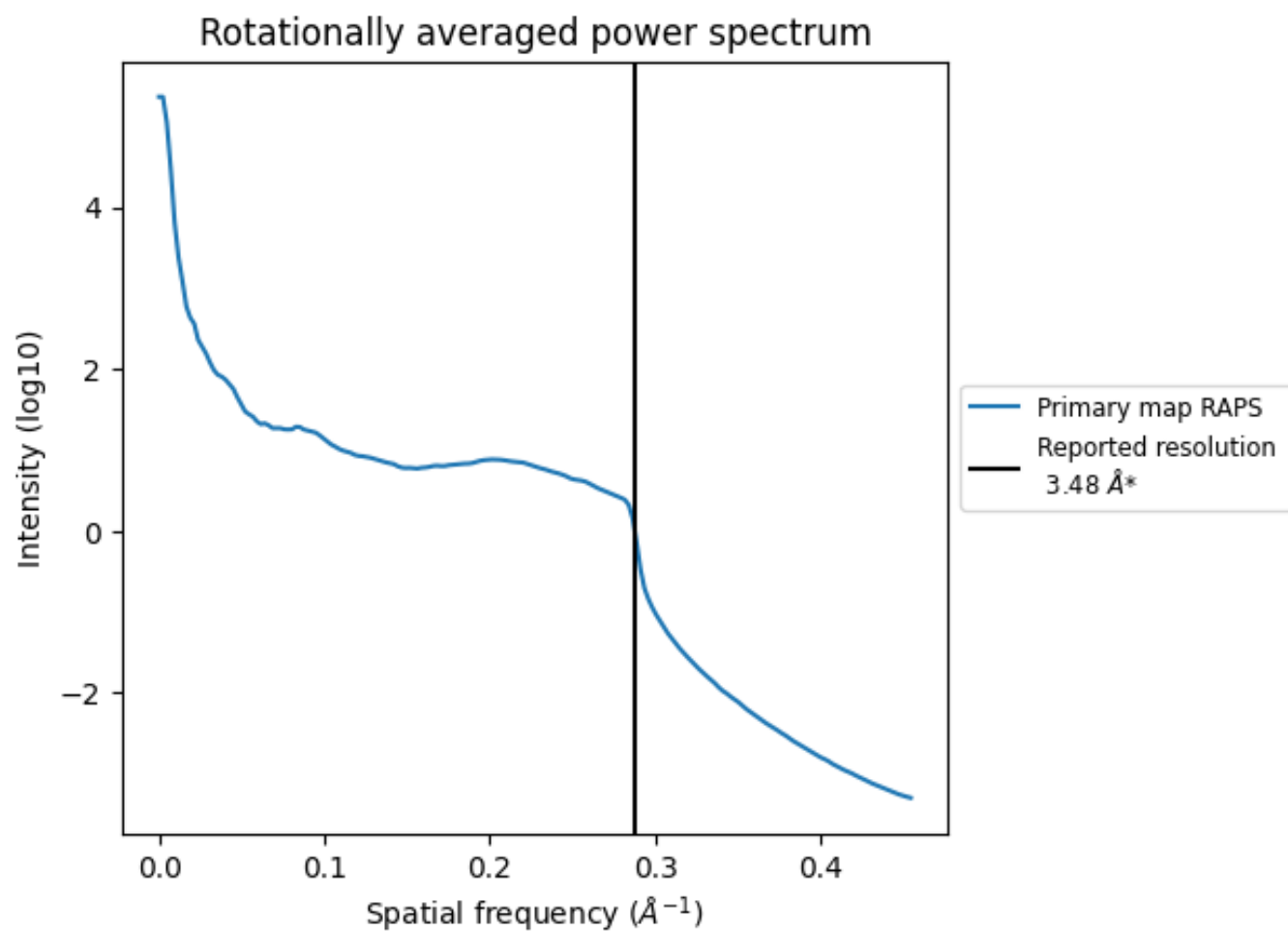
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.287 Å⁻¹

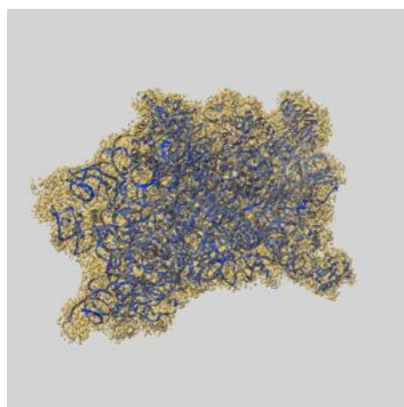
8 Fourier-Shell correlation

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

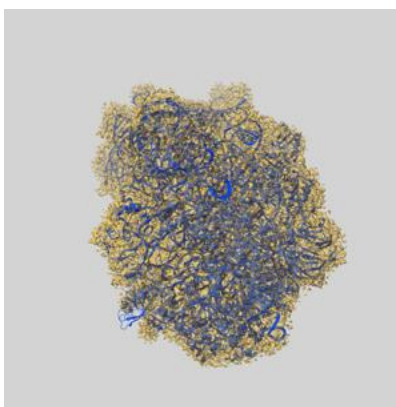
9 Map-model fit [i](#)

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.

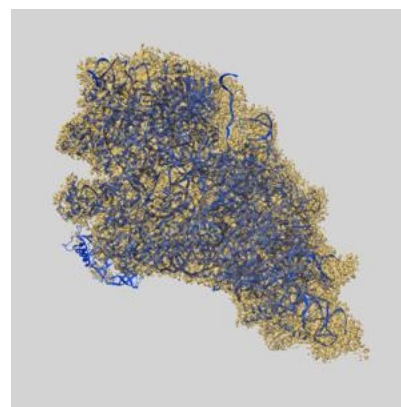
9.1 Map-model overlay [i](#)



X



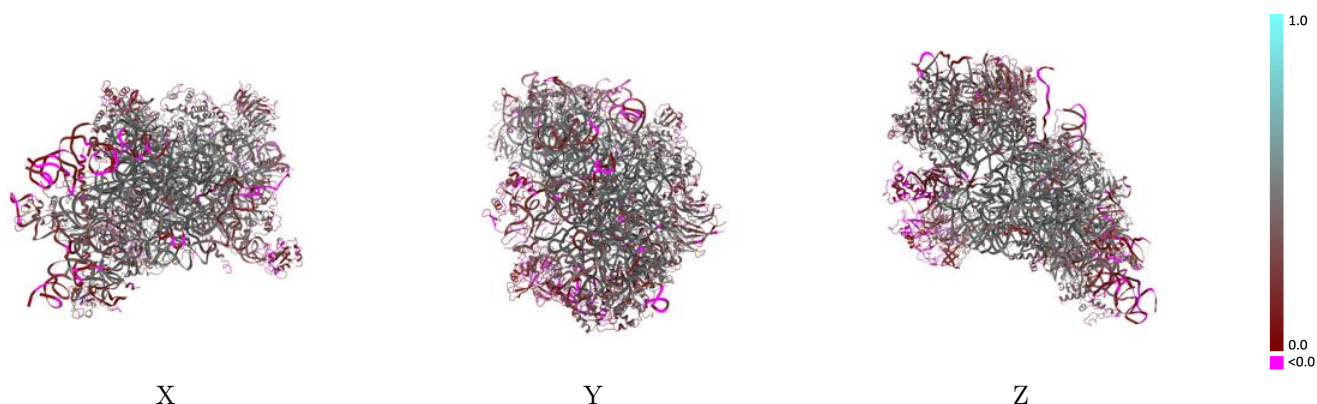
Y



Z

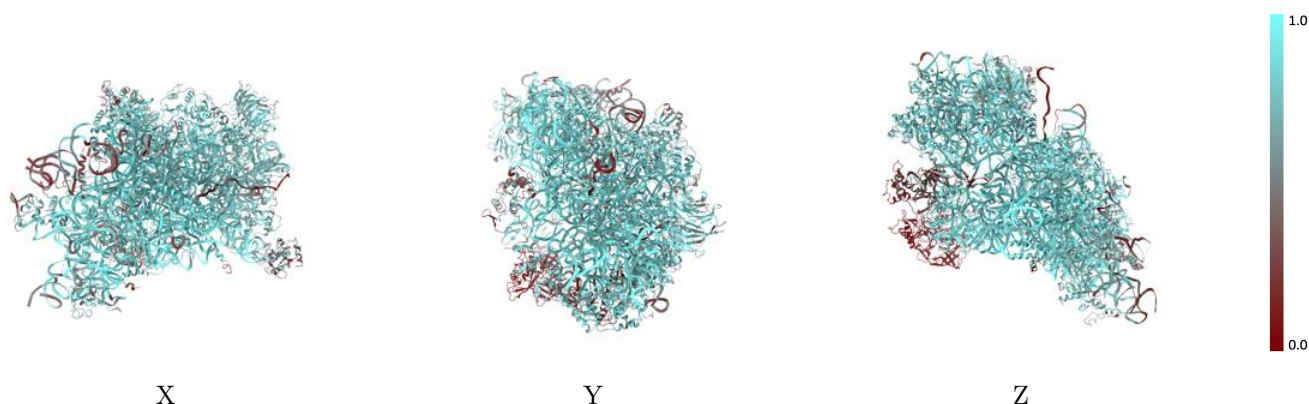
The images above show the 3D surface view of the map at the recommended contour level 0.0109 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



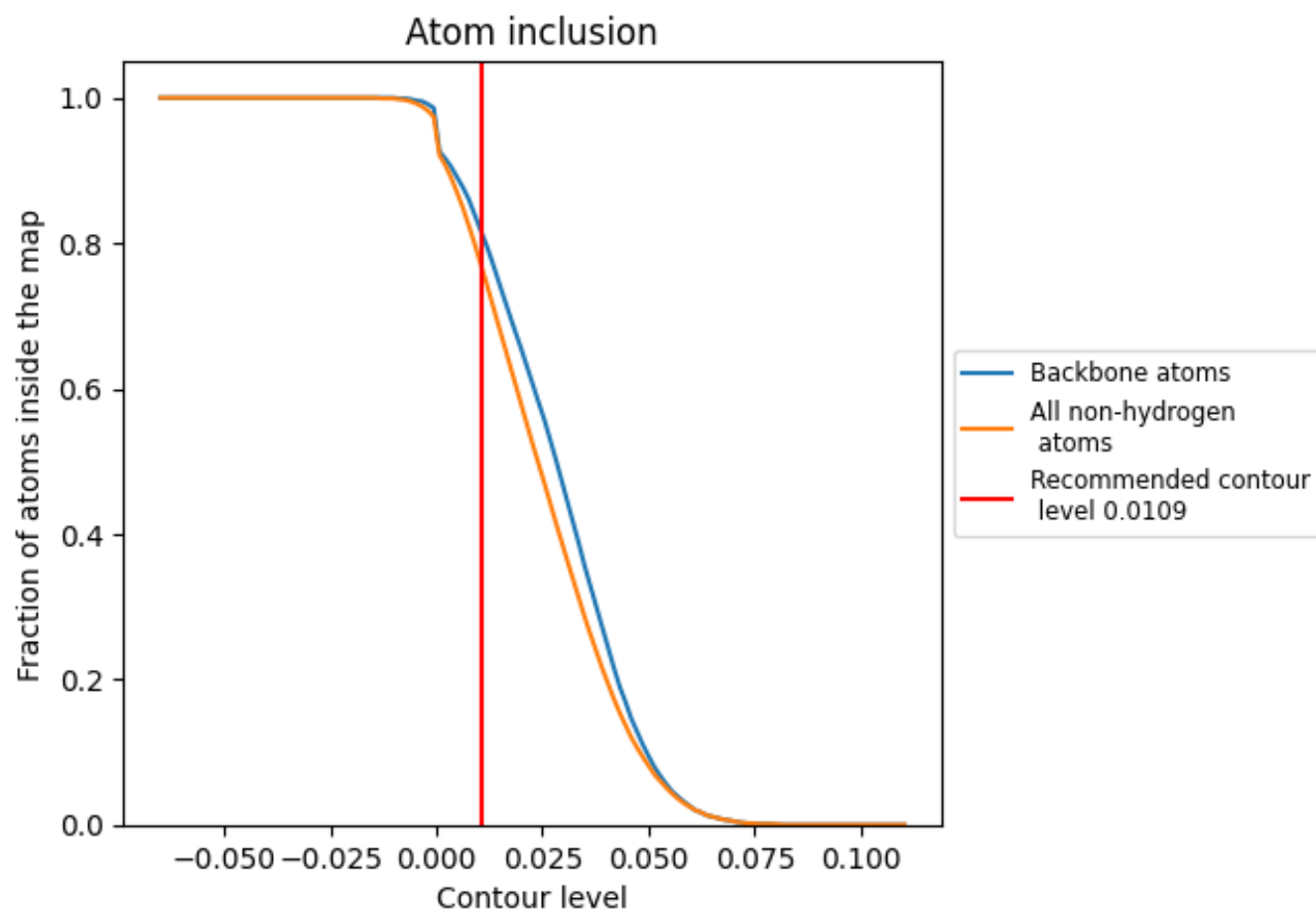
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.7630	 0.3510
1	 0.5060	 0.1520
2	 0.8840	 0.4010
3	 0.3270	 0.1390
A	 0.1820	 0.0510
B	 0.0080	 -0.0120
C	 0.8300	 0.4210
D	 0.7890	 0.4010
E	 0.8250	 0.4440
F	 0.7360	 0.3530
G	 0.8140	 0.4160
H	 0.7840	 0.3830
I	 0.7260	 0.2980
J	 0.6340	 0.2810
K	 0.7710	 0.3630
L	 0.8230	 0.4160
M	 0.7420	 0.3150
N	 0.7490	 0.3830
O	 0.4360	 0.1240
P	 0.8050	 0.3960
Q	 0.8060	 0.4090
R	 0.7000	 0.3020
S	 0.8140	 0.4180
T	 0.7290	 0.3300
U	 0.7690	 0.3430
V	 0.7770	 0.3790
W	 0.7500	 0.3450
X	 0.7920	 0.3780
Y	 0.8680	 0.4780
Z	 0.8510	 0.4510
a	 0.7970	 0.3730
b	 0.8330	 0.4320
c	 0.7400	 0.3230
d	 0.7540	 0.3660
e	 0.8100	 0.3800



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Chain	Atom inclusion	Q-score
f	 0.4430	 0.0750
g	 0.7390	 0.3250
h	 0.7060	 0.3110
i	 0.6230	 0.2840
l	 0.7670	 0.3910