



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 09:29 AM UTC

PDB ID : 4D5L / pdb_00004d5l
EMDB ID : EMD-2810
Title : Cryo-EM structures of ribosomal 80S complexes with termination factors and cricket paralysis virus IRES reveal the IRES in the translocated state
Authors : Muhs, M.; Hilal, T.; Mielke, T.; Skabkin, M.A.; Sanbonmatsu, K.Y.; Pestova, T.V.; Spahn, C.M.T.
Deposited on : 2014-11-05
Resolution : 9.00 Å (reported)
Based on initial model : 4CXC

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

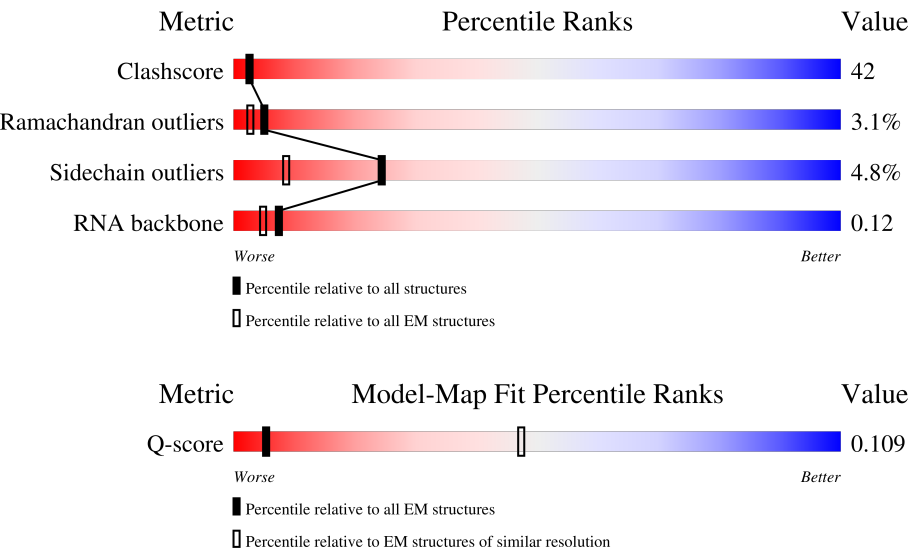
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 9.00 Å.

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



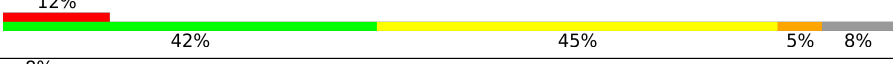
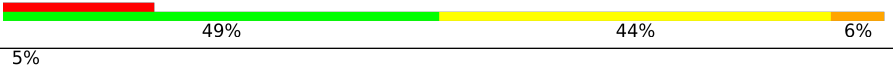
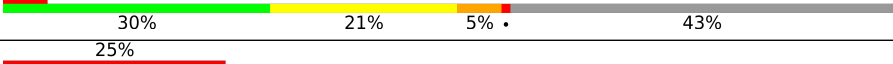
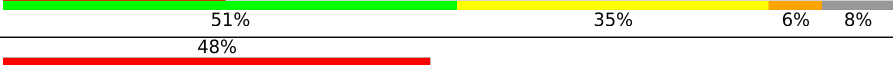
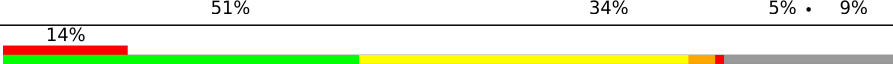
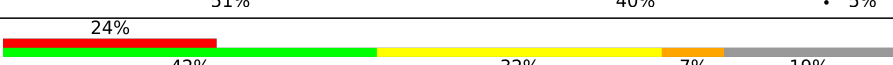
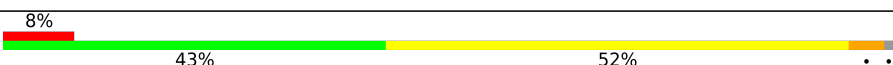
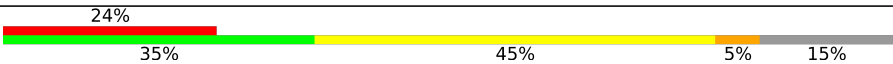
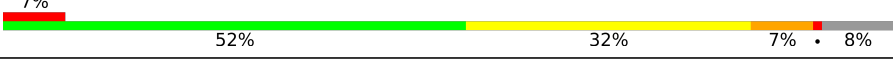
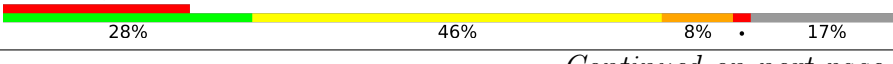
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	282 (8.20 - 9.20)

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

Mol	Chain	Length	Quality of chain
1	1	1869	6% 38% 47% 7%
2	A	295	38% 40% 31% 26%
3	B	264	11% 31% 40% 8% 19%

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Mol	Chain	Length	Quality of chain
4	C	293	
5	D	243	
6	E	263	
7	F	204	
8	G	249	
9	H	194	
10	I	208	
11	J	194	
12	K	165	
13	L	158	
14	M	132	
15	N	151	
16	O	151	
17	P	145	
18	Q	146	
19	R	135	
20	S	152	
21	T	145	
22	U	119	
23	V	83	
24	W	130	
25	X	142	
26	Y	133	
27	Z	125	
28	a	115	

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Mol	Chain	Length	Quality of chain
29	b	84	29%54%38%5%
30	c	69	19%41%42%7%10%
31	d	56	5%36%54%5%
32	e	59	31%56%29%14%
33	f	156	14%20%18%61%
34	g	317	30%58%38%

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 75320 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S RRNA 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	1742	Total	C	N	O	P	0	0
			37159	16589	6665	12164	1741		

- Molecule 2 is a protein called 40S RIBOSOMAL PROTEIN ES26.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	218	Total	C	N	O	S	0	0
			1719	1091	301	319	8		

- Molecule 3 is a protein called 40S RIBOSOMAL PROTEIN ES27.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 4 is a protein called 40S RIBOSOMAL PROTEIN ES28.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	222	Total	C	N	O	S	0	0
			1724	1114	296	304	10		

- Molecule 5 is a protein called 40S RIBOSOMAL PROTEIN US14.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	212	Total	C	N	O	S	0	0
			1646	1050	299	290	7		

- Molecule 6 is a protein called 40S RIBOSOMAL PROTEIN ES30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	257	Total	C	N	O	S	0	0
			2031	1298	381	344	8		

- Molecule 7 is a protein called 40S RIBOSOMAL PROTEIN ES31.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	188	Total	C	N	O	S	0	0
			1486	930	283	266	7		

- Molecule 8 is a protein called 40S RIBOSOMAL PROTEIN RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	232	Total	C	N	O	S	0	0
			1884	1176	379	322	7		

- Molecule 9 is a protein called 40S RIBOSOMAL PROTEIN ES7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	191	Total	C	N	O	S	0	0
			1535	978	282	274	1		

- Molecule 10 is a protein called 40S RIBOSOMAL PROTEIN ES8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	207	Total	C	N	O	S	0	0
			1695	1064	334	292	5		

- Molecule 11 is a protein called 40S RIBOSOMAL PROTEIN US4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	179	Total	C	N	O	S	0	0
			1495	953	299	241	2		

- Molecule 12 is a protein called 40S RIBOSOMAL PROTEIN ES10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	94	Total	C	N	O	S	0	0
			791	519	138	129	5		

- Molecule 13 is a protein called 40S RIBOSOMAL PROTEIN US17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	146	Total	C	N	O	S	0	0
			1199	764	224	205	6		

- Molecule 14 is a protein called 40S RIBOSOMAL PROTEIN ES12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	120	Total	C	N	O	S	0	0
			931	584	164	174	9		

- Molecule 15 is a protein called 40S RIBOSOMAL PROTEIN US15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	150	Total	C	N	O	S	0	0
			1207	773	229	204	1		

- Molecule 16 is a protein called 40S RIBOSOMAL PROTEIN US11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	137	Total	C	N	O	S	0	0
			1023	627	200	190	6		

- Molecule 17 is a protein called 40S RIBOSOMAL PROTEIN US19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	118	Total	C	N	O	S	0	0
			981	625	183	166	7		

- Molecule 18 is a protein called 40S RIBOSOMAL PROTEIN US9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	139	Total	C	N	O	S	0	0
			1108	704	210	191	3		

- Molecule 19 is a protein called 40S RIBOSOMAL PROTEIN ES17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	109	Total	C	N	O	S	0	0
			893	561	170	159	3		

- Molecule 20 is a protein called 40S RIBOSOMAL PROTEIN US13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	142	Total	C	N	O	S	0	0
			1172	736	236	199	1		

- Molecule 21 is a protein called 40S RIBOSOMAL PROTEIN ES19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 22 is a protein called 40S RIBOSOMAL PROTEIN US10.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	101	Total	C	N	O	S	0	0
			803	502	153	144	4		

- Molecule 23 is a protein called 40S RIBOSOMAL PROTEIN ES21.

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

- Molecule 24 is a protein called 40S RIBOSOMAL PROTEIN US8.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	129	Total	C	N	O	S	0	0
			1033	659	193	175	6		

- Molecule 25 is a protein called 40S RIBOSOMAL PROTEIN US12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	134	Total	C	N	O	S	0	0
			1046	663	205	176	2		

- Molecule 26 is a protein called 40S RIBOSOMAL PROTEIN ES24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	122	Total	C	N	O	S	0	0
			1002	635	196	166	5		

- Molecule 27 is a protein called 40S RIBOSOMAL PROTEIN ES25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	76	Total	C	N	O	S	0	0
			605	387	112	105	1		

- Molecule 28 is a protein called 40S RIBOSOMAL PROTEIN US2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	96	Total	C	N	O	S	0	0
			767	476	159	127	5		

- Molecule 29 is a protein called 40S RIBOSOMAL PROTEIN ES1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	80	Total	C	N	O	S	0	0
			625	391	116	111	7		

- Molecule 30 is a protein called 40S RIBOSOMAL PROTEIN US5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	62	Total	C	N	O	S	0	0
			490	298	99	91	2		

- Molecule 31 is a protein called 40S RIBOSOMAL PROTEIN US3.

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

- Molecule 32 is a protein called 40S RIBOSOMAL PROTEIN ES4.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	51	Total	C	N	O	S	0	0
			412	258	90	63	1		

- Molecule 33 is a protein called 40S RIBOSOMAL PROTEIN US7.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	61	Total	C	N	O	S	0	0
			497	312	94	84	7		

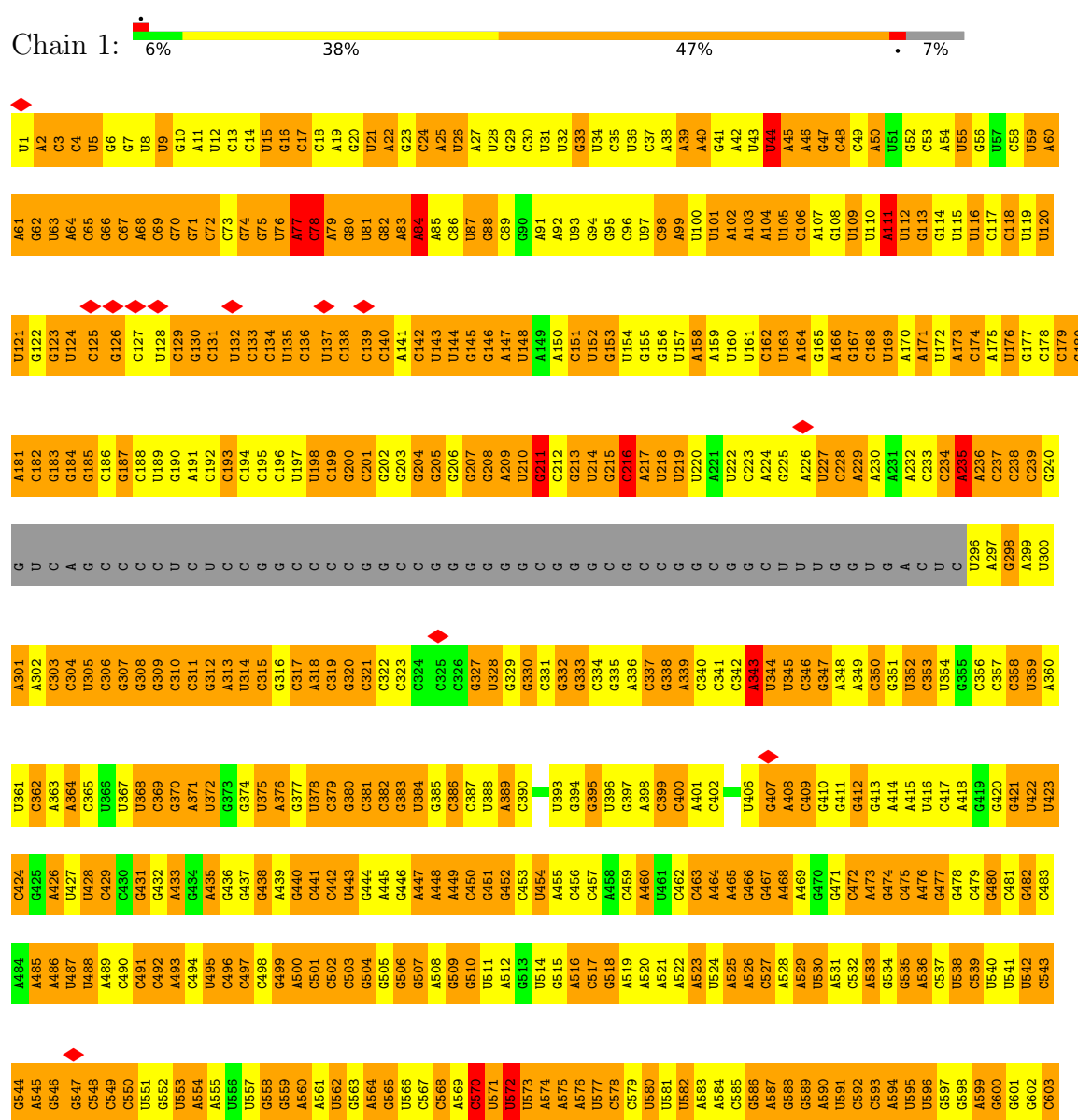
- Molecule 34 is a protein called 40S RIBOSOMAL PROTEIN ES6.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	314	Total	C	N	O	S	0	0
			2440	1537	425	466	12		

3 Residue-property plots

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

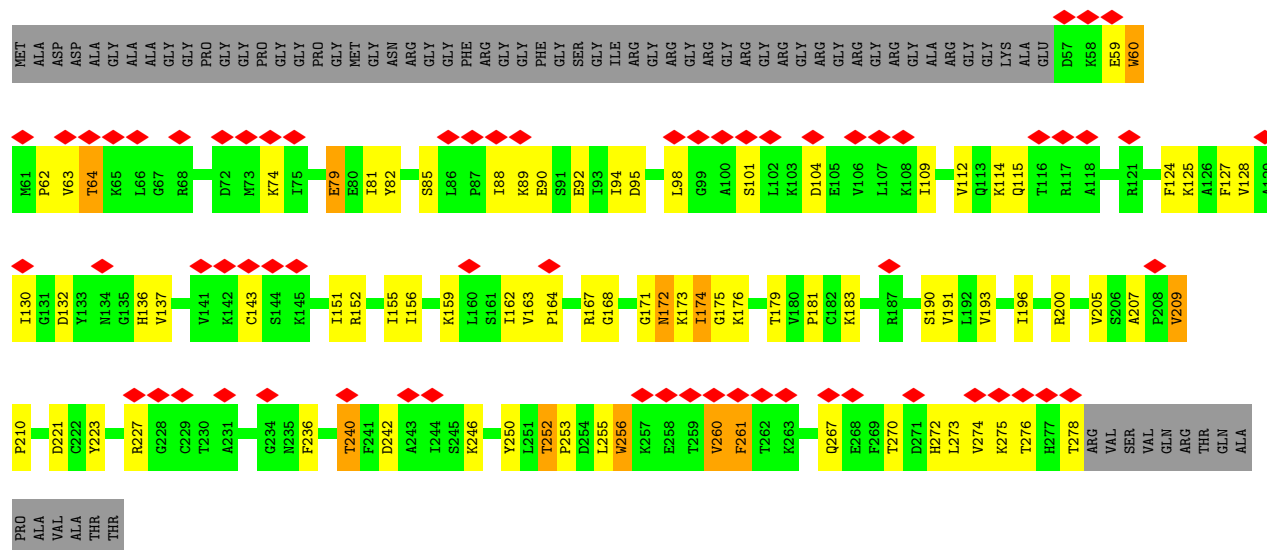
• Molecule 1: 18S RRNA 2



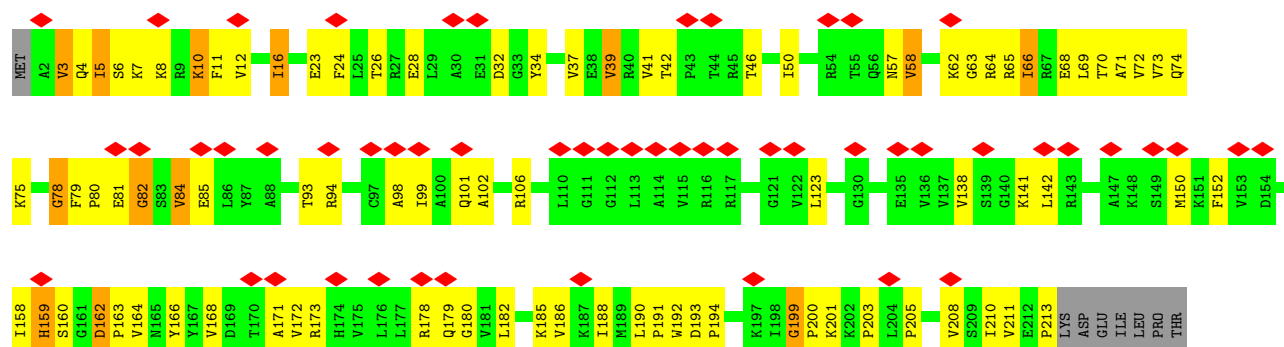
G1394	A1392	G1270	G1210	A1150	C1090	A1028	U966	C905	U844	G	A	A664	A604
A1395	U1333	C1271	G1211	G1151	C1091	G1029	U967	U906	G845	C	C	G665	A605
C1396	G1334	C1272	G1212	U1152	G1092	A1030	U968	A908	G846	G	C	U666	G606
G1397	G1335	G1273	C1213	C1153	A1093	A1031	U969	A908	A847	G	C	U667	U607
G1398	C1336	C1274	A1214	U1154	C1094	C1032	G970	C911	U848	G	C	A668	C608
C1399	C1337	G1275	C1215	U1155	C1095	G1033	G971	C911	A849	G	C	A669	U609
U1400	G1338	A1276	A1216	U1156	G1096	A1034	A972	C912	C850	C	C	A670	G610
A1401	U1339	C1277	G1217	G1157	G1097	A1035	C973	A913	C851	C	C	A671	G611
A1402	U1340	A1278	C1218	G1158	C1098	A1036	C974	U914	G852	U	U	A672	U612
C1403	C1341	G1279	C1219	G1159	G1099	G1037	G975	G915	C853	C	C	G673	G613
U1404	U1342	C1280	A1220	U1160	A1100	U1038	G976	A916	A854	C	C	C674	C614
A1405	U1343	G1281	G1221	U1161	U1101	C1039	C977	U917	G855	C	C	U675	C615
G1406	A1344	A1282	G1222	C1162	G1102	G1040	G978	U918	C736	C	C	G676	A616
U1407	G1345	C1283	A1223	C1163	C1103	G1041	C979	A919	G737	C	C	U677	C617
U1408	U1346	A1284	G1224	G1164	G1104	A1042	A980	U914	G738	C	C	U678	C618
A1409	U1347	G1285	U1225	G1165	G1105	G1043	A981	G921	G859	U799	C	A679	A619
C1410	G1348	A1287	G1226	G1166	C1106	G1044	G982	A922	C860	U800	C	G680	G620
G1411	G1349	U1287	G1227	G1167	G1107	U1045	A983	G923	A861	U801	C	U681	C621
U1288	U1288	U1288	A1228	G1168	G1108	U1046	C984	G924	A862	A802	C	U682	C622
U1289	U1289	U1289	G1229	G1169	C1109	U1047	G985	G925	U863	C803	C	G683	G623
A1414	G1352	C1230	C1230	A1170	G1110	U1048	G986	C927	A864	U804	C	G684	C624
C1415	A1353	C1231	C1231	G1171	G1111	A1049	A987	C927	A865	U805	C	A685	G625
C1416	G1354	A1291	U1232	U1172	U1112	A1050	C988	G928	U866	U806	C	U686	G626
C1417	C1355	C1292	G1233	A1173	U1113	A1051	C989	G929	G867	G807	C	U687	U627
C1418	G1356	U1296	G1234	A1174	A1113	G1052	A990	C930	G868	A808	C	U688	A628
A1419	A1357	U1297	G1235	G1175	U1114	C1053	G991	G932	A870	A810	C	U689	A629
G1420	U1358	C1298	G1236	G1176	U1115	G1054	A992	G933	U871	A811	C	G690	U630
A1421	U1359	U1299	C1237	U1177	C1116	U1055	G993	G934	A872	A812	C	G691	U631
U1360	U1360	A1299	U1238	U1178	C1117	U1056	C994	G934	G873	U813	C	G692	C632
A1301	G1361	U1300	U1239	G1179	A1119	U1057	C995	G935	A874	U814	C	A693	C633
C1423	C1362	A1301	U1240	C1180	U1120	A1058	C999	C936	G875	U815	C	G694	G634
G1424	C1363	G1302	A1241	A1181	A1120	G1059	C1000	U939	C876	A816	C	C695	C635
C1303	U1364	C1303	U1242	A1182	G1121	A1060	C1001	U939	C877	G817	C	G696	C636
U1425	U1365	U1304	U1243	A1183	A1122	U1061	U1002	U940	G878	A818	C	G	U637
U1426	U1366	C1305	U1244	G1184	C1123	A1062	U1003	C941	C879	G819	C	G	C638
G1428	A1369	U1306	G1245	C1185	C1124	U1063	U1004	G942	U880	U820	C	C	C639
G1429	U1370	U1307	A1246	U1186	G1125	C1064	U1004	G942	U880	U820	C	C	A640
U1308	U1371	U1308	C1247	G1187	G1126	G1065	G1005	U943	U883	U822	U	G	A641
C1309	U1372	C1309	U1249	A1188	C1127	U1066	C1006	U945	U883	U822	U	G	U642
U1430	C1373	U1310	C1249	A1189	G1128	C1067	C1007	U945	C884	U823	C	C	A643
U1432	C1374	C1311	A1250	C1191	C1129	U1068	A1008	U946	C884	C824	C	C	G644
C1433	G1375	G1312	A1251	U1192	G1130	U1069	A1009	G947	A886	A825	U	G	C645
C1434	A1376	A1313	C1252	U1193	G1131	A1070	G1010	C948	U887	A826	U	G	U646
C1435	C1377	C1315	A1253	U1194	A1133	G1071	A1011	G949	A827	A827	C	C	U647
C1436	U1378	C1316	C1254	A1194	G1134	C1074	A1012	C950	U888	G828	C	C	A648
C1437	A1379	C1317	G1255	A1195	C1135	U1075	U1013	C951	U889	G829	C	C	U649
A1438	C1380	G1318	G1256	A1196	C1136	C1076	G1014	G891	U890	A830	U	G	A650
A1439	G1381	C1319	G1257	U1197	U1136	U1015	U1015	C953	G891	G831	C	C	U651
G1440	A1382	U1319	G1258	G1198	U1137	G1076	U1016	U954	U892	G832	U	C	U652
U1441	C1383	G1320	A1259	G1199	C1138	C1079	U1017	A955	U893	C833	C	C	A653
U1442	A1384	C1321	A1260	A1200	C1139	U1080	U1017	G956	G894	C834	C	C	G654
C1443	G1385	G1322	C1261	U1201	G1140	U1081	C1019	A957	G895	C835	U	C	A655
U1444	U1386	U1323	C1262	U1202	G1141	A1082	C1019	G958	U896	G836	A	G	G656
A1445	G1387	G1324	U1263	G1203	G1142	A1083	U1021	G959	U897	G837	G	G	U657
U1446	A1388	G1325	U1264	A1204	A1143	U1084	U1021	U960	U898	A837	A	C	G658
G1447	C1389	U1326	A1265	C1205	A1144	C1085	U1022	G961	U899	G838	G	C	U659
A1448	U1390	G1327	C1266	G1206	A1145	G1086	A1023	A962	C900	C839	U	C	C660
G1449	C1391	G1328	C1267	G1207	G1146	U1087	A1024	A963	G901	C840	U	C	U661
G1450	U1392	G1330	C1268	A1208	C1147	U1088	U1025	A964	G902	G841	U	C	G662
A1451	G1393	C1331	G1269	A1209	A1148	G1089	C1026	U965	A904	C943	C	C	C663
A1452													
A1453													



- Molecule 4: 40S RIBOSOMAL PROTEIN ES28



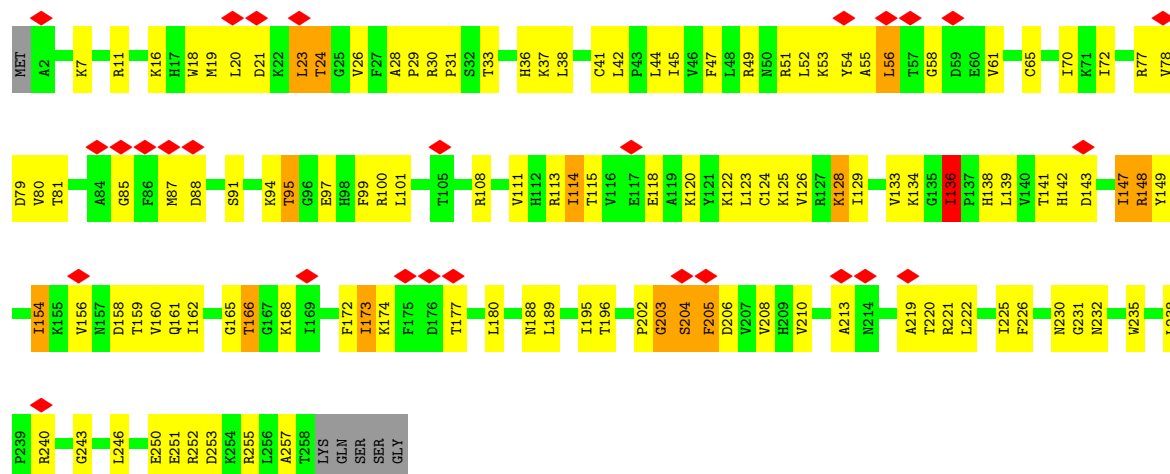
- Molecule 5: 40S RIBOSOMAL PROTEIN US14



THR
PRO
ILE
SER
GLU
GLN
LYS
GLY
GLY
LYS
PRO
GLU
PRO
PRO
ALA
MET
PRO
GLN
PRO
VAL
THR
ALA

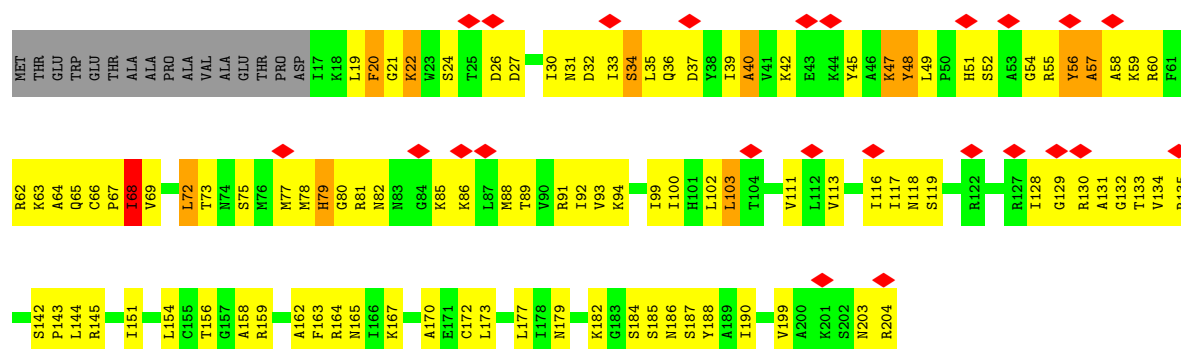
• Molecule 6: 40S RIBOSOMAL PROTEIN ES30

Chain E: 11% 51% 41% 5%



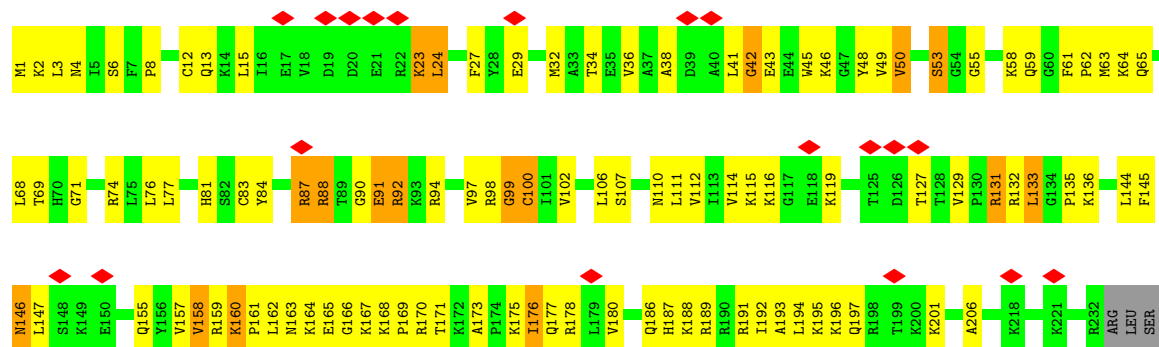
• Molecule 7: 40S RIBOSOMAL PROTEIN ES31

Chain F: 12% 42% 45% 5% 8%



• Molecule 8: 40S RIBOSOMAL PROTEIN RACK1

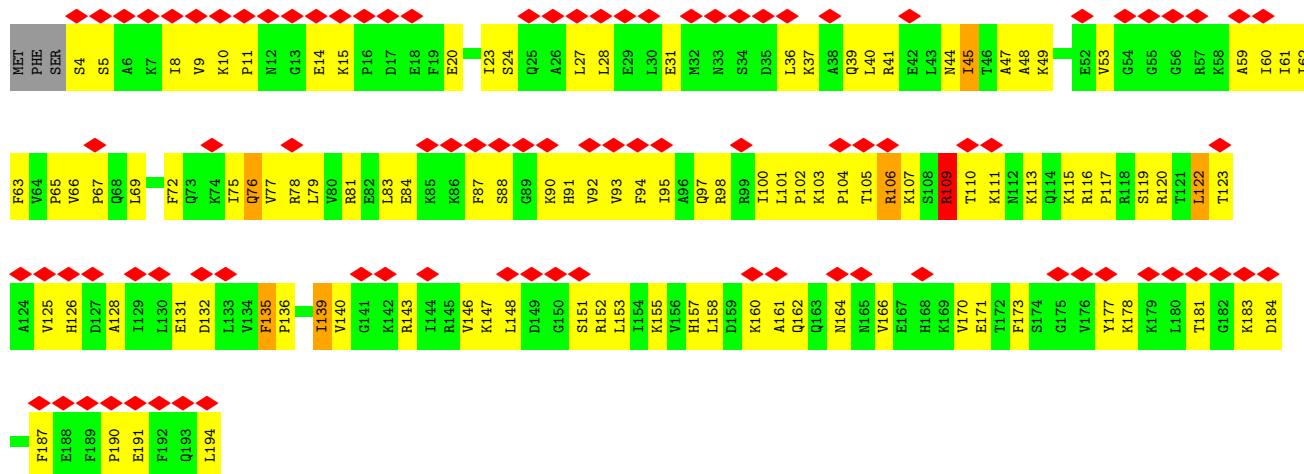
Chain G: 8% 49% 37% 7% 7%



SER
LEU
ARG
ALA
SER
THR
SER
LYS
GLU
SER
GLN
LYS

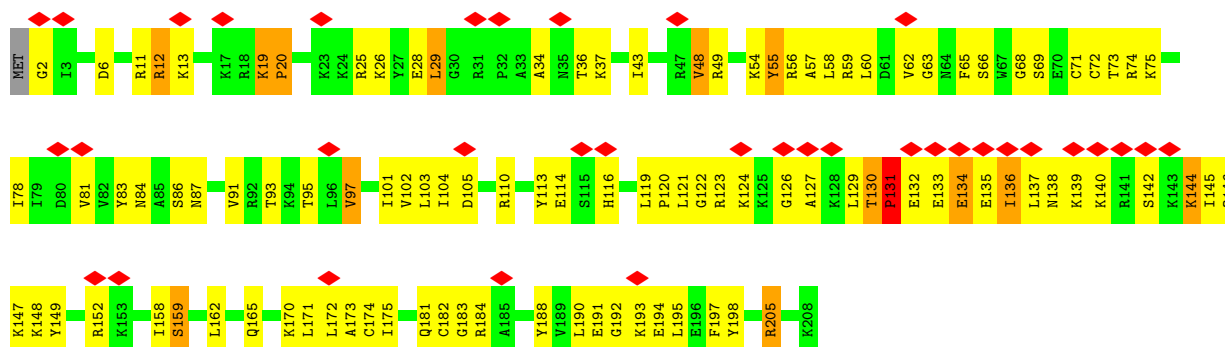
• Molecule 9: 40S RIBOSOMAL PROTEIN ES7

Chain H: 47% 43% 52%



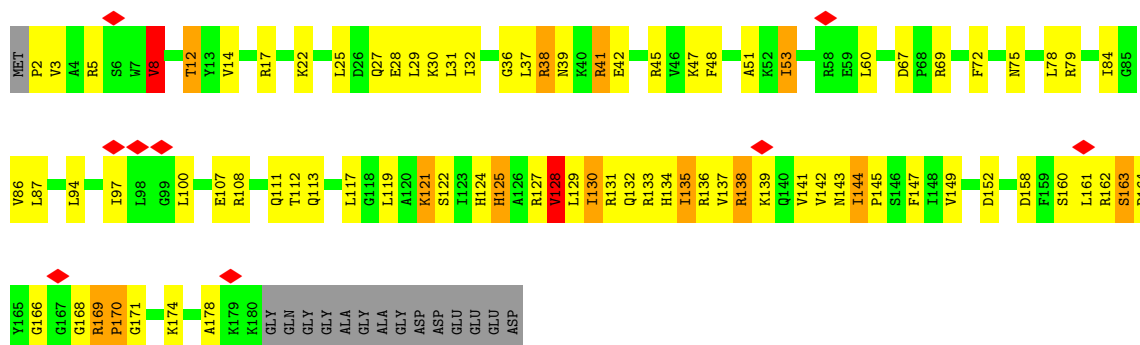
• Molecule 10: 40S RIBOSOMAL PROTEIN ES8

Chain I: 17% 49% 44% 6%

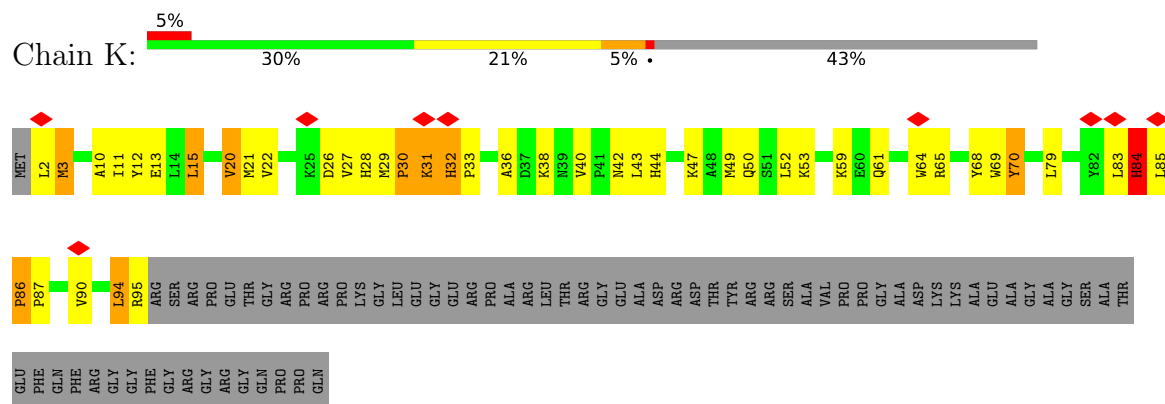


• Molecule 11: 40S RIBOSOMAL PROTEIN US4

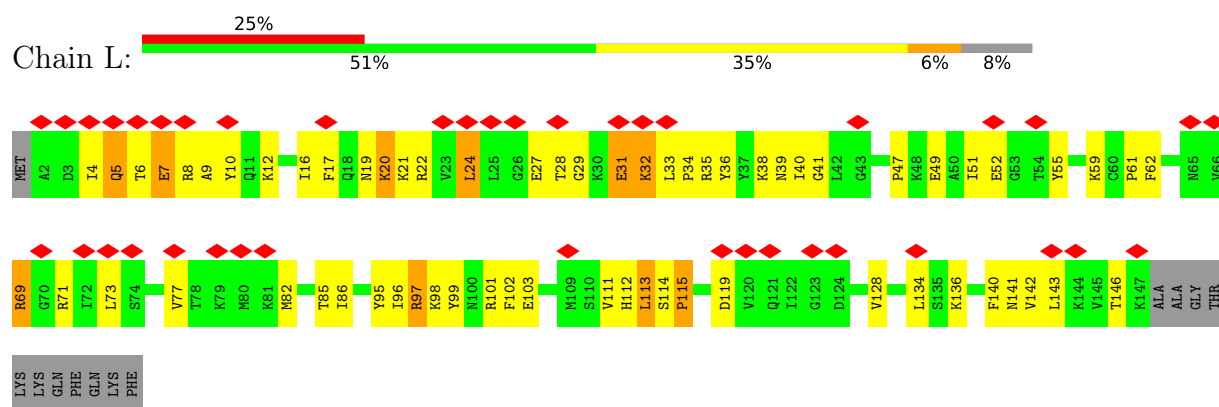
Chain J: 5% 49% 36% 7% 8%



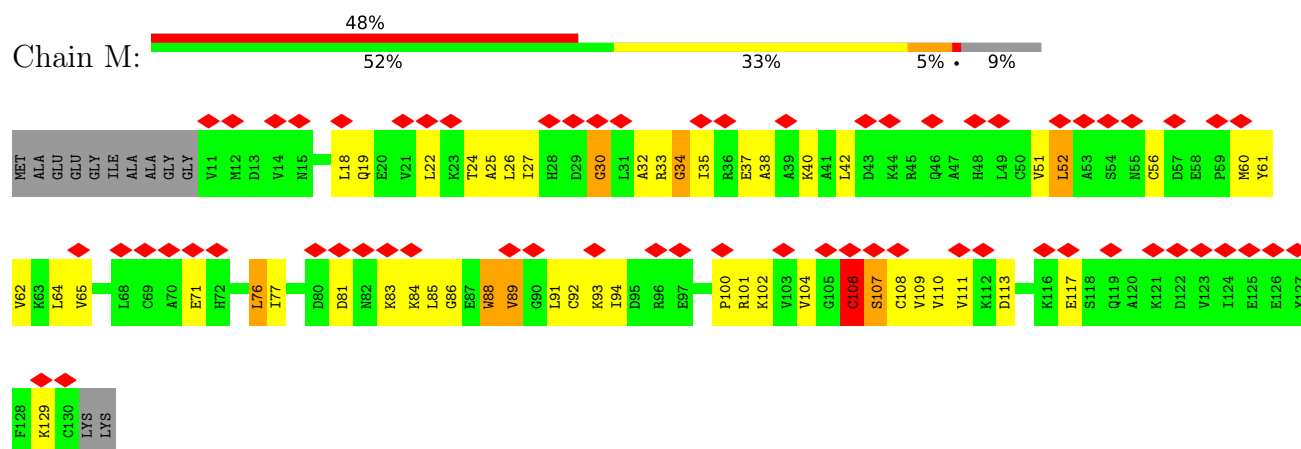
• Molecule 12: 40S RIBOSOMAL PROTEIN ES10



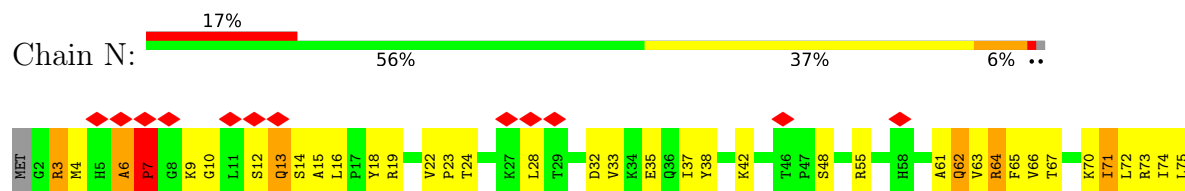
• Molecule 13: 40S RIBOSOMAL PROTEIN US17



• Molecule 14: 40S RIBOSOMAL PROTEIN ES12



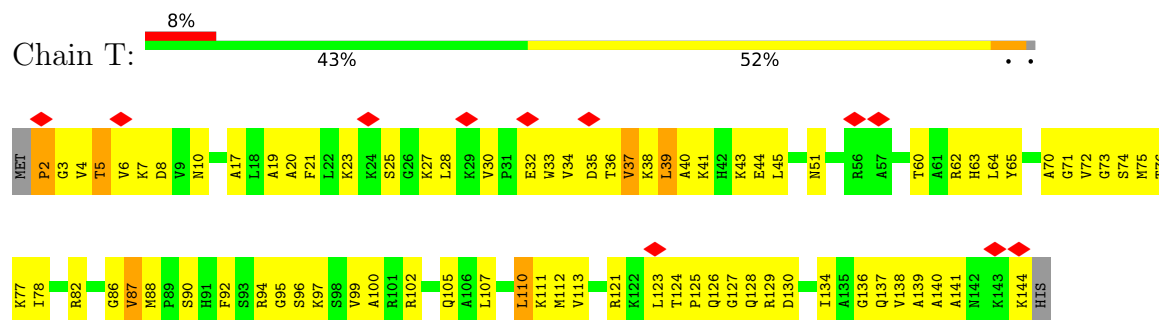
• Molecule 15: 40S RIBOSOMAL PROTEIN US15



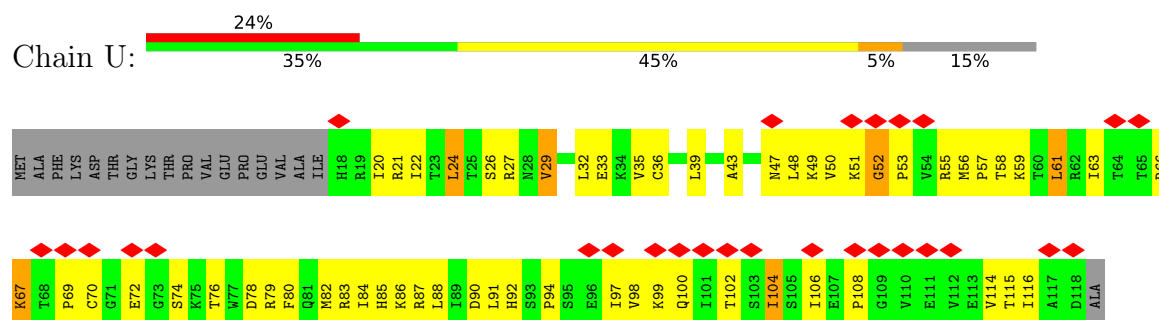
- Molecule 20: 40S RIBOSOMAL PROTEIN US13



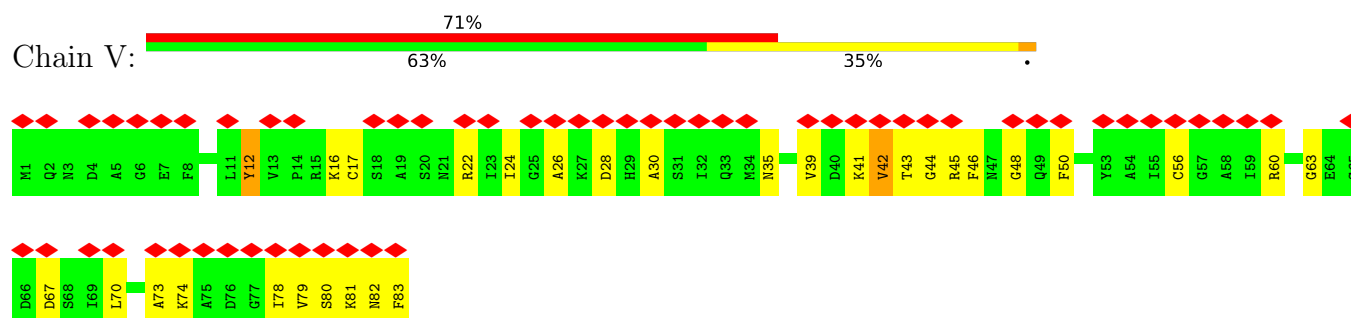
- Molecule 21: 40S RIBOSOMAL PROTEIN ES19



- Molecule 22: 40S RIBOSOMAL PROTEIN US10



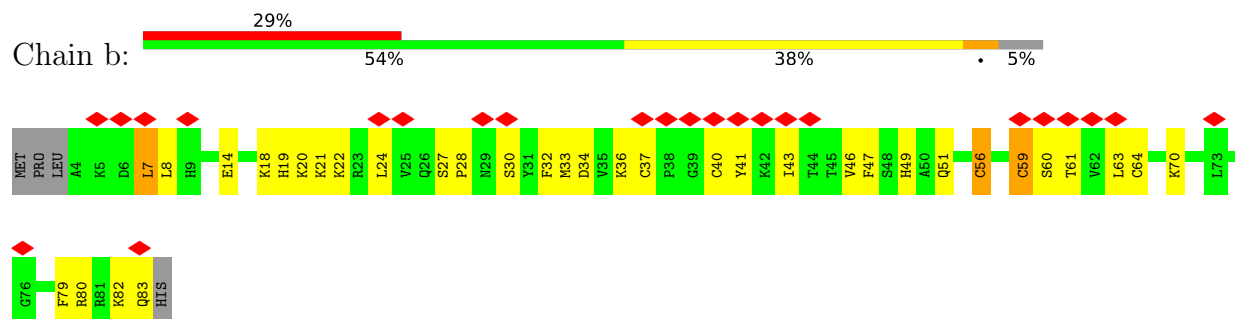
- Molecule 23: 40S RIBOSOMAL PROTEIN ES21



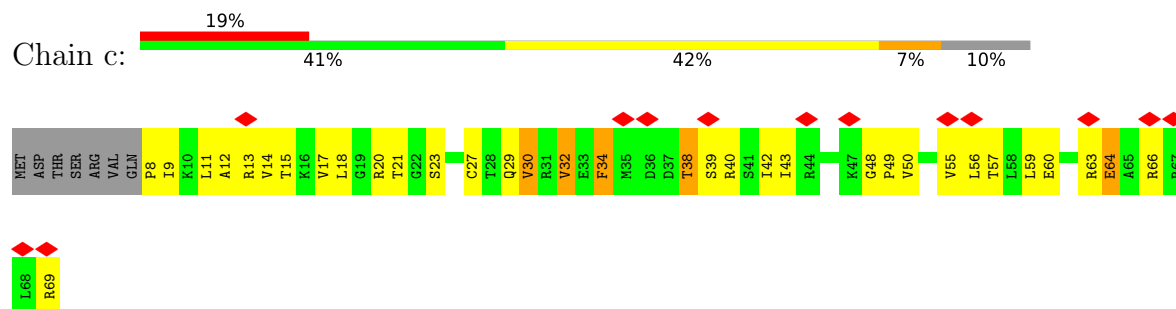
- Molecule 24: 40S RIBOSOMAL PROTEIN US8



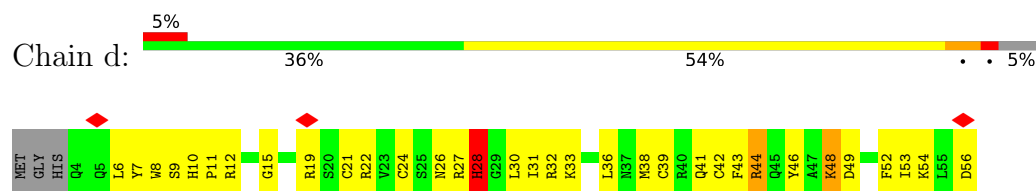
- Molecule 29: 40S RIBOSOMAL PROTEIN ES1



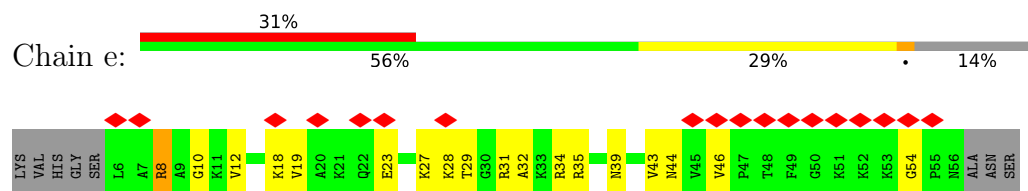
- Molecule 30: 40S RIBOSOMAL PROTEIN US5



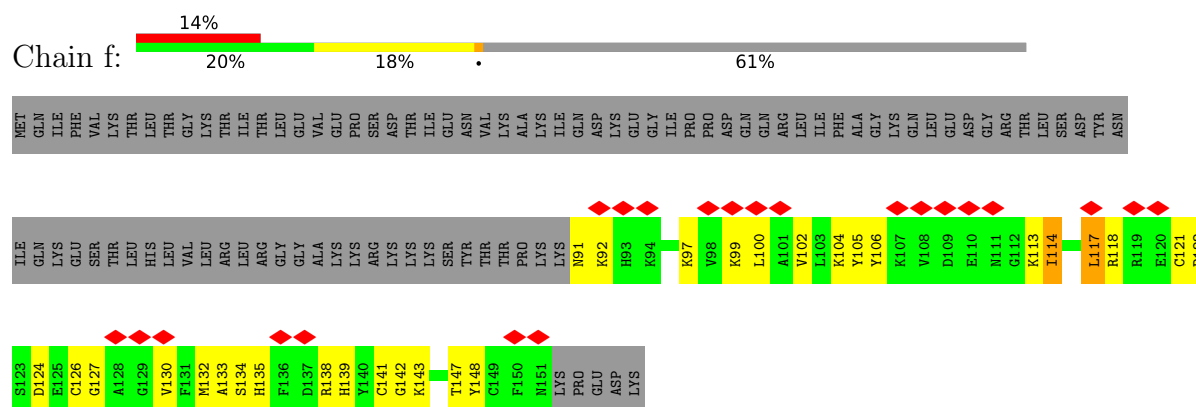
- Molecule 31: 40S RIBOSOMAL PROTEIN US3



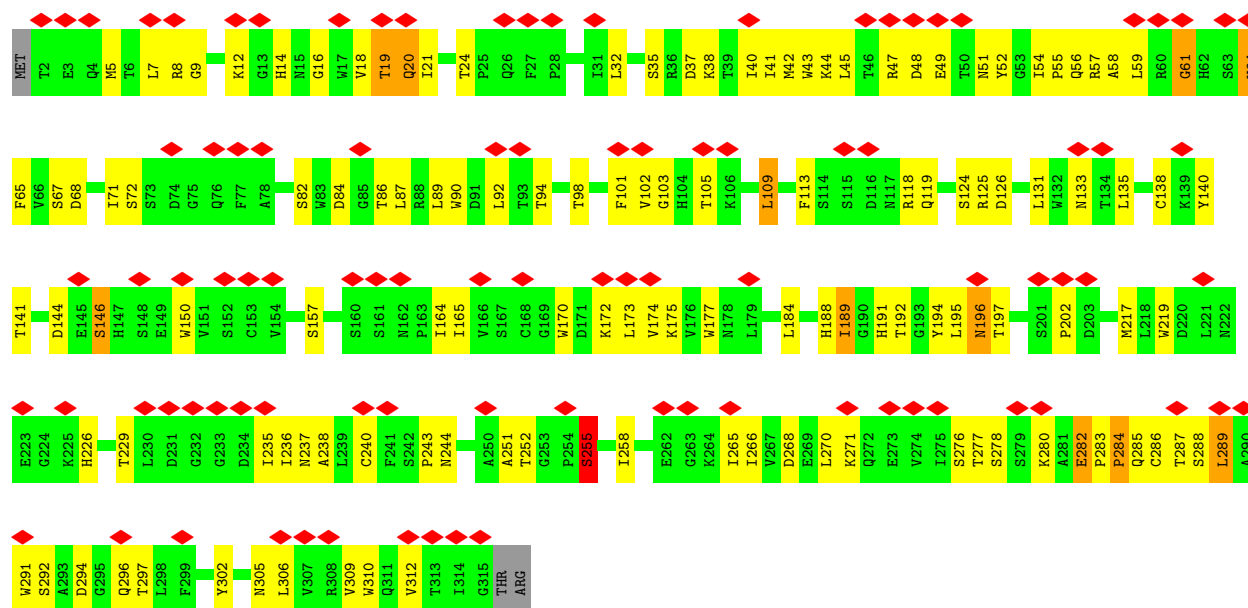
- Molecule 32: 40S RIBOSOMAL PROTEIN ES4



- Molecule 33: 40S RIBOSOMAL PROTEIN US7



● Molecule 34: 40S RIBOSOMAL PROTEIN ES6



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	109596	Depositor
Resolution determination method	Not provided	
CTF correction method	DEFOCUS GROUP	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	65520	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	12.036	Depositor
Minimum map value	-3.841	Depositor
Average map value	0.203	Depositor
Map value standard deviation	0.880	Depositor
Recommended contour level	2.5	Depositor
Map size ($\text{\AA}$)	467.99997, 467.99997, 467.99997	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.56, 1.56, 1.56	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	1	0.31	0/41550	0.66	11/64763 (0.0%)
2	A	0.89	4/1756 (0.2%)	1.16	11/2386 (0.5%)
3	B	0.83	0/1756	1.20	13/2350 (0.6%)
4	C	0.69	0/1761	1.10	5/2379 (0.2%)
5	D	0.63	0/1672	1.15	9/2250 (0.4%)
6	E	0.72	0/2072	1.16	10/2793 (0.4%)
7	F	0.68	0/1507	1.15	10/2026 (0.5%)
8	G	0.77	1/1907 (0.1%)	1.23	10/2538 (0.4%)
9	H	0.75	0/1558	1.26	12/2087 (0.6%)
10	I	0.75	0/1724	1.12	6/2298 (0.3%)
11	J	0.74	0/1520	1.25	13/2030 (0.6%)
12	K	0.77	0/815	1.10	5/1101 (0.5%)
13	L	0.69	0/1220	1.16	8/1633 (0.5%)
14	M	0.74	0/941	1.19	3/1264 (0.2%)
15	N	0.69	0/1231	1.21	12/1656 (0.7%)
16	O	0.73	0/1036	1.16	6/1391 (0.4%)
17	P	0.66	0/1000	1.07	2/1335 (0.1%)
18	Q	0.69	0/1125	1.10	3/1506 (0.2%)
19	R	0.69	0/904	1.11	6/1208 (0.5%)
20	S	0.69	0/1190	1.14	5/1594 (0.3%)
21	T	0.68	0/1131	1.10	3/1515 (0.2%)
22	U	0.76	0/813	1.17	3/1092 (0.3%)
23	V	0.70	0/643	1.16	2/860 (0.2%)
24	W	0.69	0/1050	1.12	6/1406 (0.4%)
25	X	0.76	0/1063	1.11	1/1421 (0.1%)
26	Y	0.71	0/1019	1.12	5/1354 (0.4%)
27	Z	0.68	0/611	1.14	3/820 (0.4%)
28	a	0.78	0/778	1.19	7/1041 (0.7%)
29	b	0.70	0/637	1.09	2/854 (0.2%)
30	c	0.71	0/492	1.15	5/657 (0.8%)
31	d	0.73	0/454	1.10	1/603 (0.2%)
32	e	0.70	0/417	1.09	0/548
33	f	0.76	0/507	1.33	5/673 (0.7%)
34	g	0.69	0/2497	1.06	7/3399 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.55	5/80357 (0.0%)	0.91	210/116831 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1	0	24

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	203	PHE	CA-C	6.94	1.60	1.52
2	A	203	PHE	C-N	5.73	1.40	1.33
2	A	204	TYR	N-CA	5.64	1.53	1.46
8	G	131	ARG	C-N	-5.24	1.27	1.33
2	A	202	TYR	CA-C	5.06	1.59	1.53

The worst 5 of 210 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	37	ALA	N-CA-C	11.17	123.46	111.28
33	f	124	ASP	N-CA-C	-10.45	97.14	111.56
5	D	58	VAL	N-CA-C	10.33	120.34	110.42
15	N	24	THR	N-CA-C	9.81	121.73	111.14
4	C	60	TRP	N-CA-C	9.67	121.42	111.07

There are no chirality outliers.

5 of 24 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	111	A	Sidechain
1	1	44	U	Sidechain
1	1	77	A	Sidechain
1	1	84	A	Sidechain
1	1	88	G	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	37159	0	18780	3755	0
2	A	1719	0	1717	132	0
3	B	1729	0	1803	143	0
4	C	1724	0	1808	65	0
5	D	1646	0	1737	87	0
6	E	2031	0	2138	118	0
7	F	1486	0	1545	109	0
8	G	1884	0	2044	156	0
9	H	1535	0	1632	133	0
10	I	1695	0	1785	116	0
11	J	1495	0	1615	94	0
12	K	791	0	811	53	0
13	L	1199	0	1269	74	0
14	M	931	0	961	44	0
15	N	1207	0	1294	67	0
16	O	1023	0	1050	61	0
17	P	981	0	1026	56	0
18	Q	1108	0	1174	78	0
19	R	893	0	946	65	0
20	S	1172	0	1229	77	0
21	T	1112	0	1146	117	0
22	U	803	0	866	80	0
23	V	636	0	637	43	0
24	W	1033	0	1080	65	0
25	X	1046	0	1110	69	0
26	Y	1002	0	1075	66	0
27	Z	605	0	665	57	0
28	a	767	0	816	101	0
29	b	625	0	642	38	0
30	c	490	0	520	35	0
31	d	444	0	442	53	0
32	e	412	0	463	36	0
33	f	497	0	497	36	0
34	g	2440	0	2396	120	0
All	All	75320	0	58719	5599	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 42.

The worst 5 of 5599 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1431:G:H2'	1:1:1432:U:C6	1.77	1.18
1:1:377:G:H4'	10:I:97:VAL:HG13	1.24	1.18
1:1:571:U:H3'	1:1:572:U:C5'	1.77	1.15
1:1:569:A:H2'	1:1:570:C:H5''	1.24	1.14
1:1:1547:C:H3'	1:1:1548:G:H5''	1.29	1.14

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	216/295 (73%)	209 (97%)	5 (2%)	2 (1%)	14	51
3	B	211/264 (80%)	176 (83%)	18 (8%)	17 (8%)	1	9
4	C	220/293 (75%)	213 (97%)	2 (1%)	5 (2%)	5	28
5	D	210/243 (86%)	201 (96%)	4 (2%)	5 (2%)	4	27
6	E	255/263 (97%)	237 (93%)	13 (5%)	5 (2%)	6	31
7	F	186/204 (91%)	163 (88%)	13 (7%)	10 (5%)	1	15
8	G	230/249 (92%)	216 (94%)	5 (2%)	9 (4%)	2	19
9	H	189/194 (97%)	178 (94%)	7 (4%)	4 (2%)	5	30
10	I	205/208 (99%)	184 (90%)	14 (7%)	7 (3%)	3	21
11	J	177/194 (91%)	168 (95%)	6 (3%)	3 (2%)	7	36
12	K	92/165 (56%)	84 (91%)	1 (1%)	7 (8%)	1	10
13	L	144/158 (91%)	133 (92%)	5 (4%)	6 (4%)	2	17
14	M	118/132 (89%)	111 (94%)	1 (1%)	6 (5%)	1	15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	N	148/151 (98%)	138 (93%)	5 (3%)	5 (3%)	3	21
16	O	135/151 (89%)	129 (96%)	3 (2%)	3 (2%)	5	29
17	P	116/145 (80%)	106 (91%)	5 (4%)	5 (4%)	2	17
18	Q	137/146 (94%)	129 (94%)	6 (4%)	2 (2%)	8	40
19	R	105/135 (78%)	99 (94%)	4 (4%)	2 (2%)	6	32
20	S	140/152 (92%)	125 (89%)	7 (5%)	8 (6%)	1	14
21	T	141/145 (97%)	135 (96%)	4 (3%)	2 (1%)	9	40
22	U	99/119 (83%)	95 (96%)	3 (3%)	1 (1%)	12	49
23	V	81/83 (98%)	78 (96%)	1 (1%)	2 (2%)	4	26
24	W	127/130 (98%)	118 (93%)	7 (6%)	2 (2%)	7	38
25	X	132/142 (93%)	120 (91%)	5 (4%)	7 (5%)	1	15
26	Y	120/133 (90%)	114 (95%)	2 (2%)	4 (3%)	3	21
27	Z	74/125 (59%)	71 (96%)	0	3 (4%)	2	18
28	a	94/115 (82%)	85 (90%)	5 (5%)	4 (4%)	2	17
29	b	78/84 (93%)	70 (90%)	8 (10%)	0	100	100
30	c	60/69 (87%)	57 (95%)	1 (2%)	2 (3%)	3	21
31	d	51/56 (91%)	44 (86%)	7 (14%)	0	100	100
32	e	49/59 (83%)	43 (88%)	5 (10%)	1 (2%)	6	31
33	f	59/156 (38%)	53 (90%)	6 (10%)	0	100	100
34	g	312/317 (98%)	291 (93%)	14 (4%)	7 (2%)	5	29
All	All	4711/5475 (86%)	4373 (93%)	192 (4%)	146 (3%)	5	22

5 of 146 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	76	ASN
3	B	132	GLY
3	B	148	ASN
3	B	154	SER
3	B	176	VAL

5.3.2 Protein sidechains ⓘ

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	181/243 (74%)	177 (98%)	4 (2%)	45	64
3	B	194/231 (84%)	182 (94%)	12 (6%)	16	38
4	C	188/225 (84%)	179 (95%)	9 (5%)	23	44
5	D	175/202 (87%)	164 (94%)	11 (6%)	16	37
6	E	220/225 (98%)	207 (94%)	13 (6%)	18	39
7	F	158/170 (93%)	152 (96%)	6 (4%)	29	50
8	G	202/218 (93%)	196 (97%)	6 (3%)	36	57
9	H	171/174 (98%)	170 (99%)	1 (1%)	78	83
10	I	179/180 (99%)	167 (93%)	12 (7%)	15	36
11	J	160/168 (95%)	152 (95%)	8 (5%)	22	43
12	K	85/136 (62%)	81 (95%)	4 (5%)	23	45
13	L	133/142 (94%)	130 (98%)	3 (2%)	44	64
14	M	102/108 (94%)	96 (94%)	6 (6%)	18	39
15	N	130/131 (99%)	128 (98%)	2 (2%)	57	72
16	O	107/119 (90%)	99 (92%)	8 (8%)	12	33
17	P	107/130 (82%)	103 (96%)	4 (4%)	30	51
18	Q	115/121 (95%)	111 (96%)	4 (4%)	32	53
19	R	99/122 (81%)	92 (93%)	7 (7%)	13	35
20	S	123/132 (93%)	115 (94%)	8 (6%)	15	37
21	T	113/115 (98%)	106 (94%)	7 (6%)	16	38
22	U	93/107 (87%)	87 (94%)	6 (6%)	15	37
23	V	67/67 (100%)	67 (100%)	0	100	100
24	W	112/113 (99%)	108 (96%)	4 (4%)	31	52
25	X	108/114 (95%)	104 (96%)	4 (4%)	30	51
26	Y	107/115 (93%)	100 (94%)	7 (6%)	15	37
27	Z	67/103 (65%)	62 (92%)	5 (8%)	12	33
28	a	83/98 (85%)	76 (92%)	7 (8%)	10	30
29	b	72/76 (95%)	68 (94%)	4 (6%)	19	40
30	c	55/62 (89%)	52 (94%)	3 (6%)	19	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	d	47/49 (96%)	44 (94%)	3 (6%)	16	37
32	e	42/48 (88%)	39 (93%)	3 (7%)	13	35
33	f	54/140 (39%)	51 (94%)	3 (6%)	19	40
34	g	272/275 (99%)	260 (96%)	12 (4%)	25	47
All	All	4121/4659 (88%)	3925 (95%)	196 (5%)	24	44

5 of 196 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	R	58	MET
24	W	20	ARG
19	R	118	GLN
21	T	33	TRP
26	Y	21	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 101 such sidechains are listed below:

Mol	Chain	Res	Type
17	P	35	GLN
23	V	2	GLN
34	g	196	ASN
18	Q	86	GLN
21	T	51	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1738/1869 (92%)	1041 (59%)	152 (8%)

5 of 1041 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	A
1	1	3	C
1	1	4	C
1	1	5	U
1	1	6	G

5 of 152 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1494	U
1	1	1824	A
1	1	1534	C
1	1	1637	A
1	1	1862	G

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

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

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](#)

There are no chain breaks in this entry.

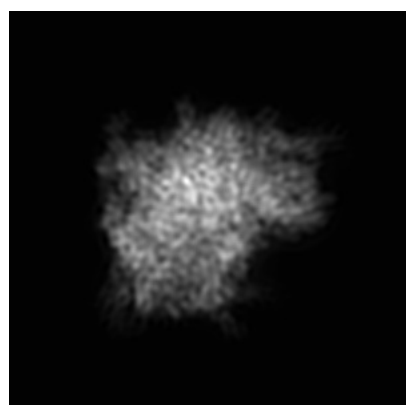
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2810. These allow visual inspection of the internal detail of the map and identification of artifacts.

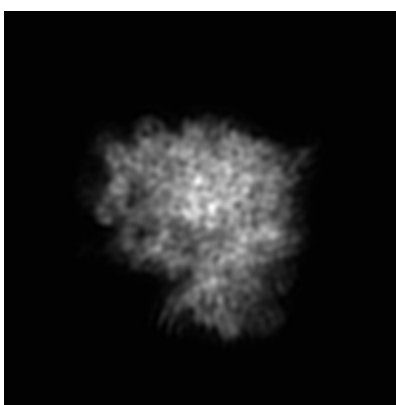
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

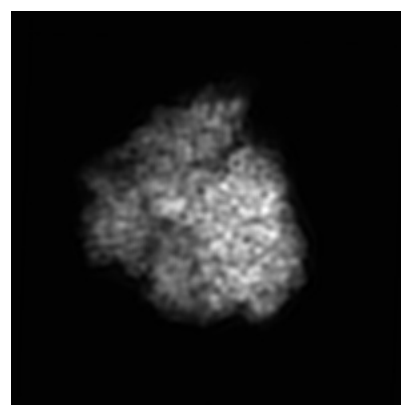
6.1.1 Primary map



X



Y

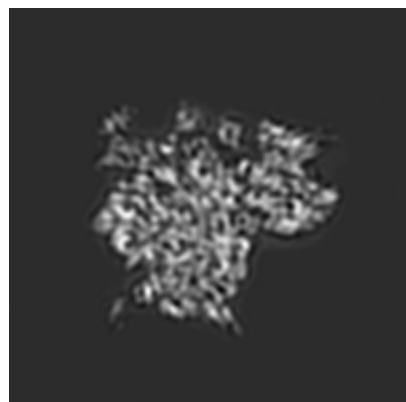


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 150



Y Index: 150



Z Index: 150

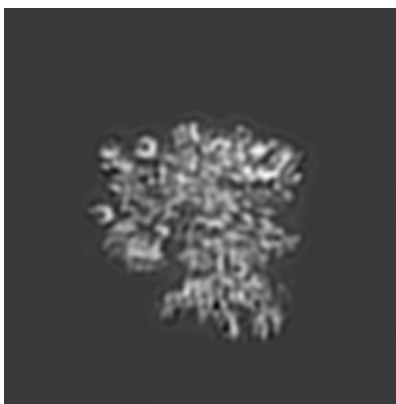
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 173



Y Index: 149

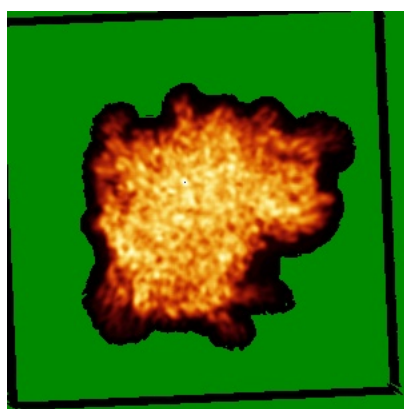


Z Index: 154

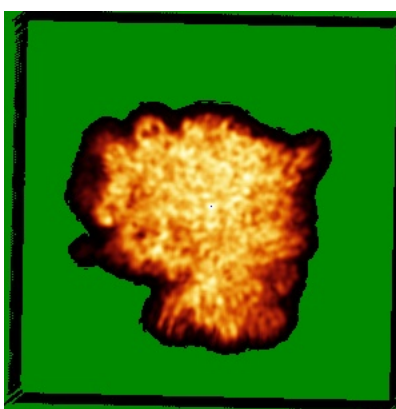
The images above show the largest variance slices of the map in three orthogonal directions.

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

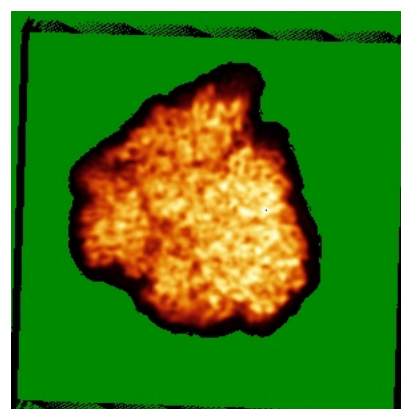
6.4.1 Primary map



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

This section was not generated.

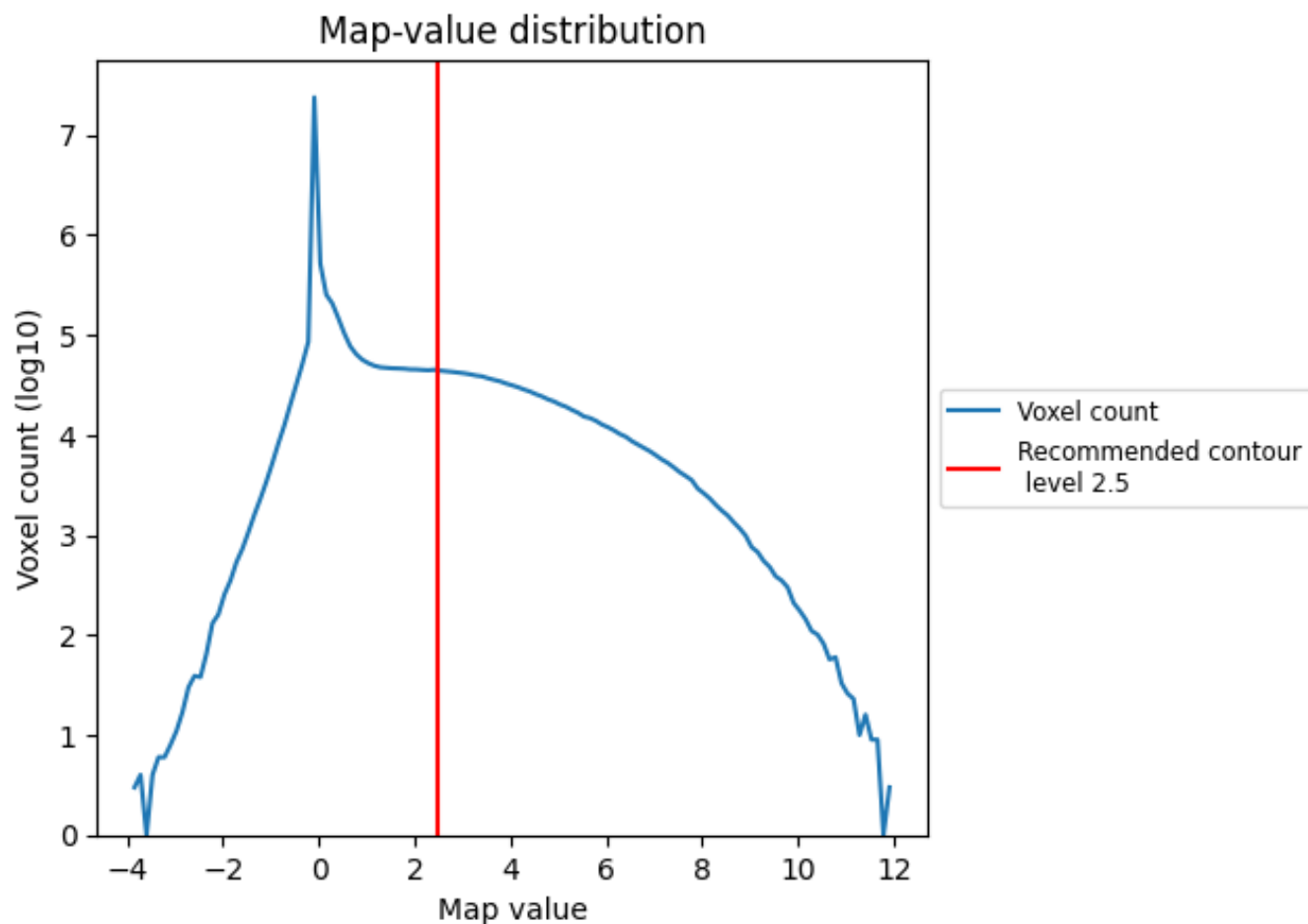
6.6 Mask visualisation

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

7 Map analysis [i](#)

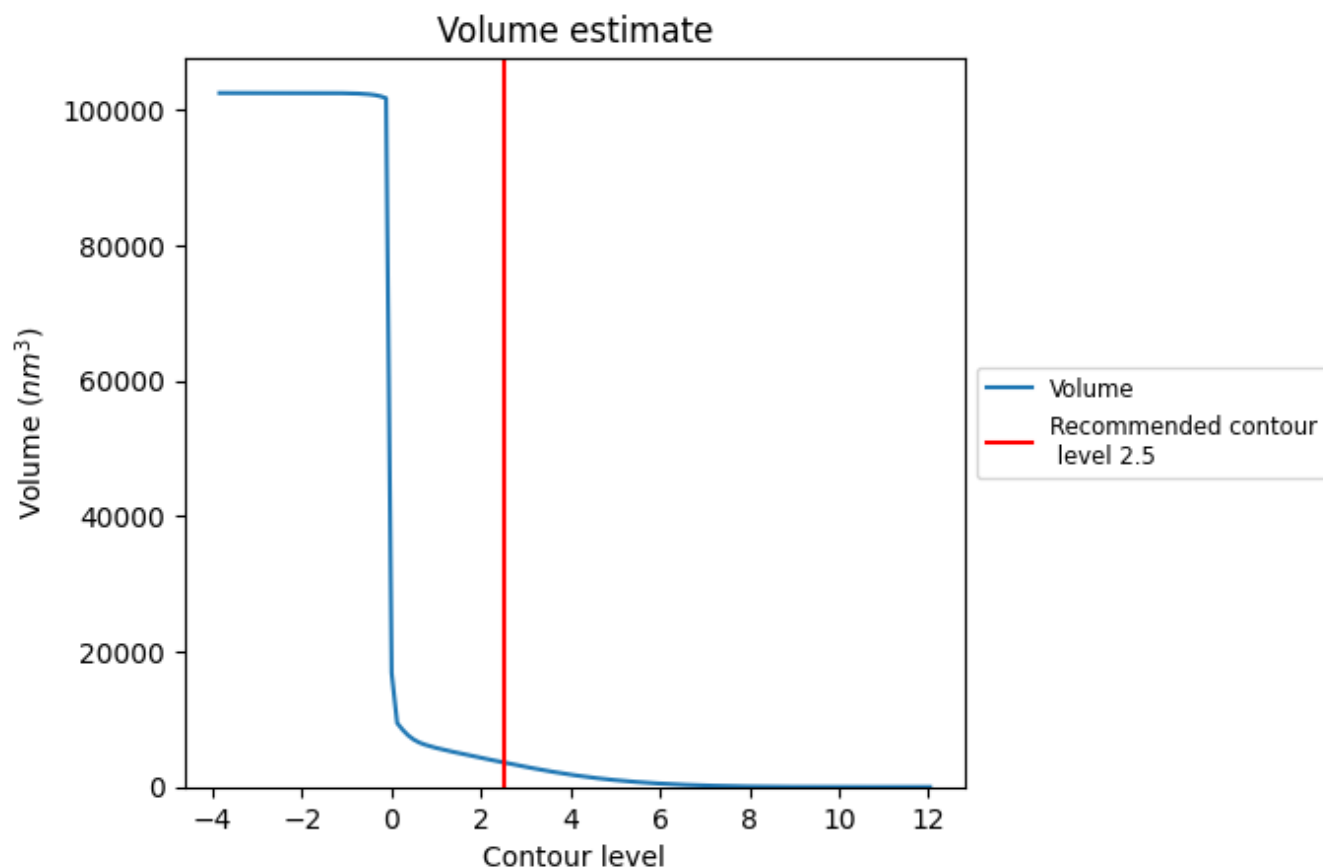
This section contains the results of statistical analysis of the map.

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.

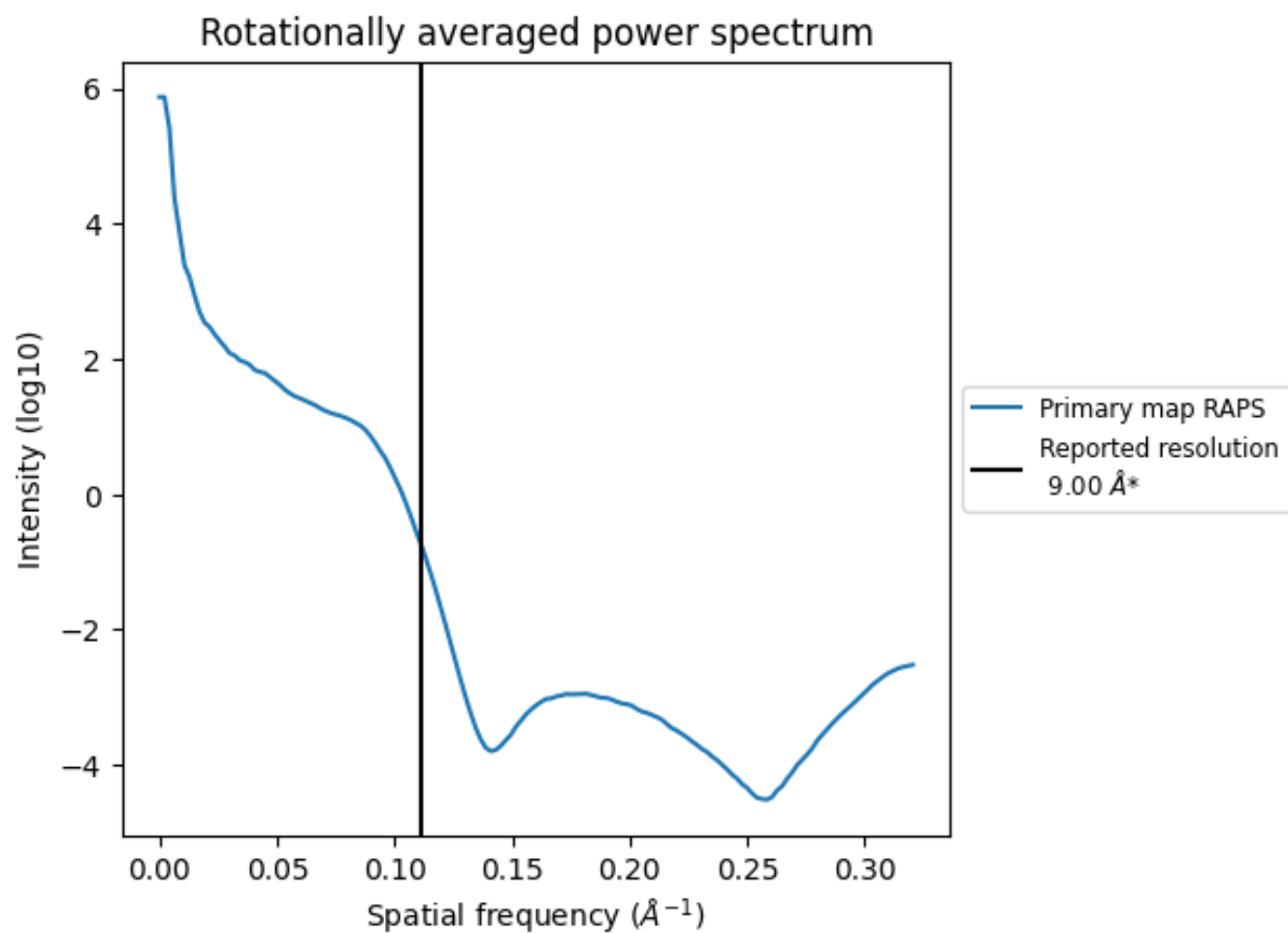
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3628 nm^3 ; this corresponds to an approximate mass of 3277 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 0.111 Å⁻¹

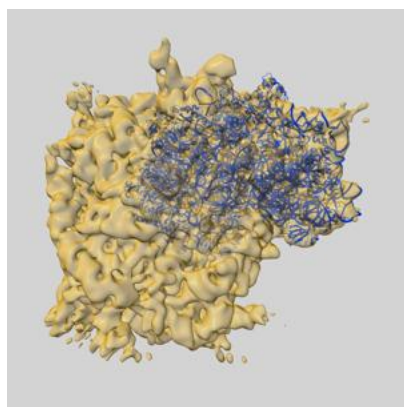
8 Fourier-Shell correlation

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

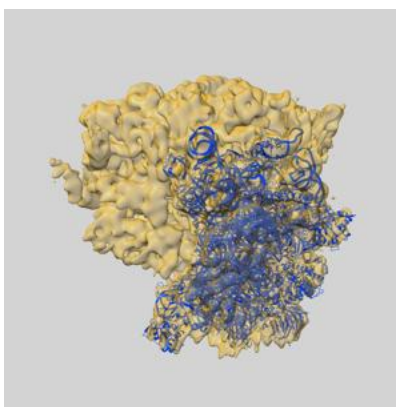
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2810 and PDB model 4D5L. Per-residue inclusion information can be found in section [3](#) on page [10](#).

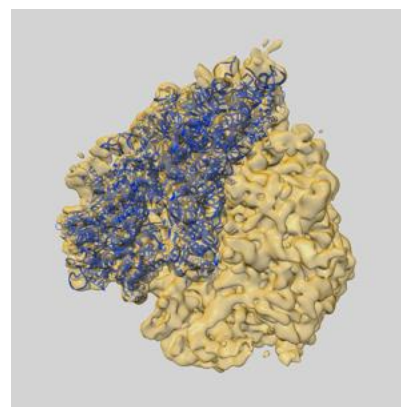
9.1 Map-model overlay [i](#)



X



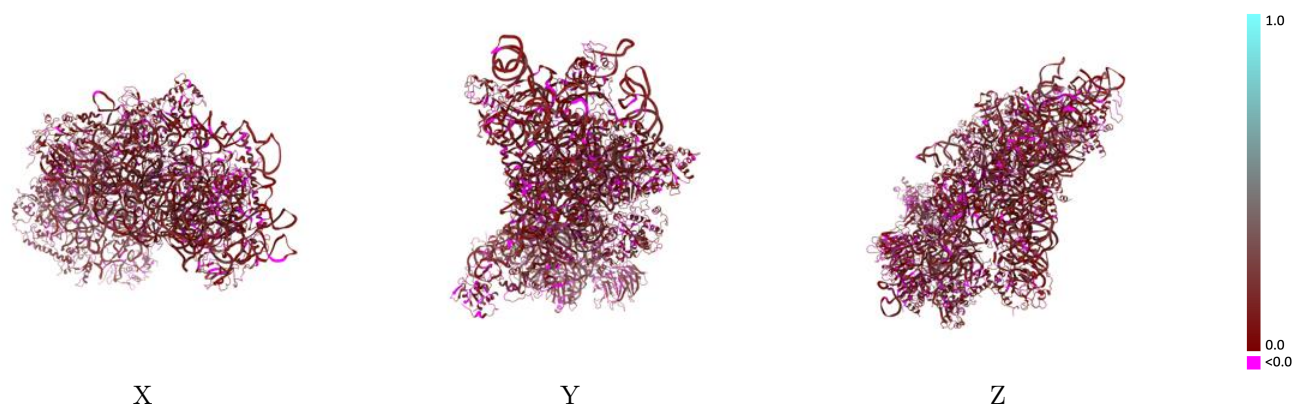
Y



Z

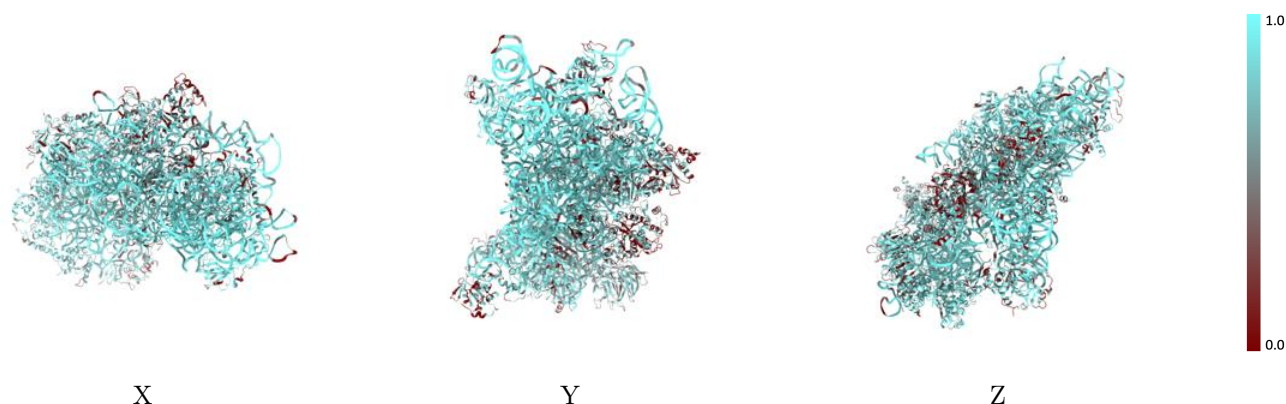
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



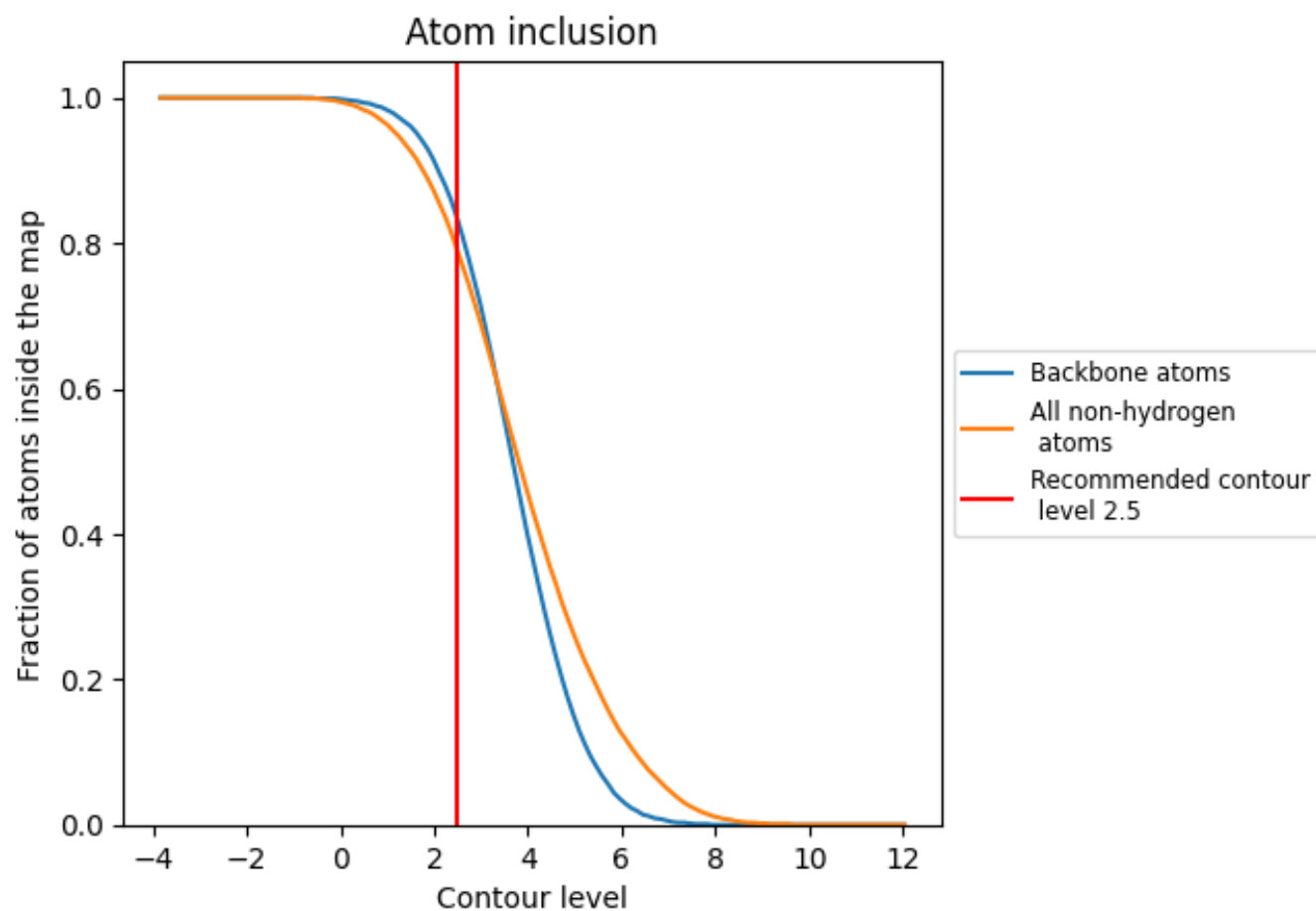
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 79% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7890	 0.1090
1	 0.9130	 0.1300
A	 0.4630	 0.0870
B	 0.7130	 0.1180
C	 0.5850	 0.1000
D	 0.6490	 0.0960
E	 0.7460	 0.0850
F	 0.7590	 0.1020
G	 0.8000	 0.0860
H	 0.4120	 0.0890
I	 0.6990	 0.0840
J	 0.7900	 0.0940
K	 0.7740	 0.0990
L	 0.6190	 0.0850
M	 0.4350	 0.0490
N	 0.6890	 0.1010
O	 0.6840	 0.0880
P	 0.7300	 0.1050
Q	 0.7810	 0.0790
R	 0.5800	 0.0950
S	 0.7630	 0.0980
T	 0.7910	 0.0900
U	 0.6140	 0.0550
V	 0.3070	 0.0670
W	 0.6500	 0.0720
X	 0.6990	 0.0900
Y	 0.8120	 0.0920
Z	 0.8360	 0.1260
a	 0.6580	 0.0570
b	 0.6180	 0.0960
c	 0.6850	 0.0880
d	 0.8100	 0.0640
e	 0.5950	 0.0640
f	 0.5510	 0.0420
g	 0.6050	 0.0890

