



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 02:03 PM UTC

PDB ID : 7PAI / pdb_00007pai
EMDB ID : EMD-13273
Title : 70S ribosome with P-site tRNA in Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-07-30
Resolution : 6.70 Å(reported)
Based on initial models : 4V7C, 7OOD, 7OOC

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

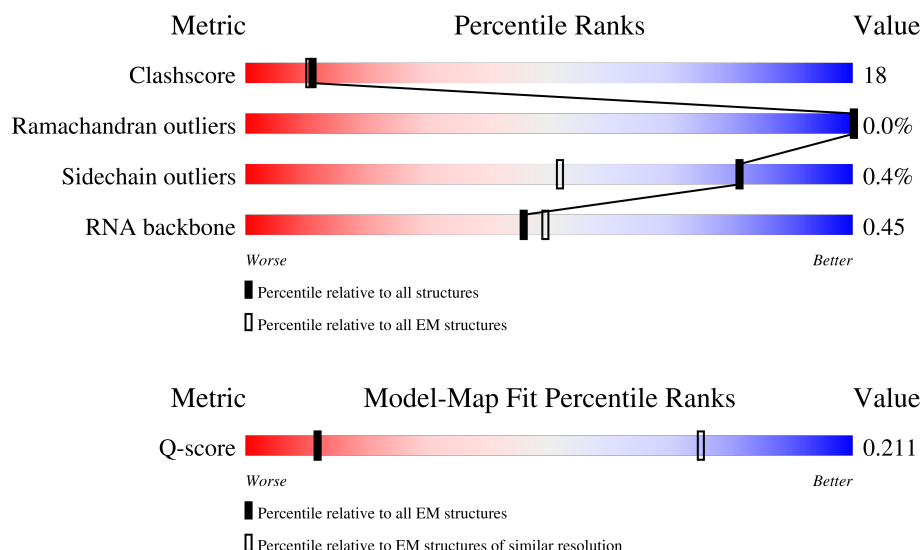
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 6.70 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	523 (6.20 - 7.20)

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	0	48	 73% 25%
2	1	59	 71% 29%
3	2	37	 5% 41% 59%

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Mol	Chain	Length	Quality of chain
4	A	294	
5	B	273	
6	C	205	
7	D	219	
8	E	215	
9	F	155	
10	G	142	
11	H	132	
12	I	108	
13	J	121	
14	K	139	
15	L	124	
16	M	61	
17	N	86	
18	O	94	
19	P	85	
20	Q	104	
21	R	87	
22	S	87	
23	T	60	
24	a	287	
25	b	287	
26	c	212	
27	d	180	
28	e	184	

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Mol	Chain	Length	Quality of chain
29	f	149	
30	g	161	
31	h	137	
32	i	146	
33	j	122	
34	k	151	
35	l	139	
36	m	124	
37	n	116	
38	o	119	
39	p	127	
40	q	100	
41	r	159	
42	s	237	
43	t	111	
44	u	104	
45	v	65	
46	w	111	
47	x	97	
48	y	57	
49	z	53	
50	3	2907	
51	4	108	
52	5	1520	
53	7	76	

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 144502 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 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	47	Total	C	N	O	S	0	0
			380	236	81	61	2		

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	59	Total	C	N	O	S	0	0
			477	300	99	77	1		

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	37	Total	C	N	O	S	0	0
			304	189	65	46	4		

- Molecule 4 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	240	Total	C	N	O	S	0	0
			1921	1226	334	352	9		

- Molecule 5 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	215	Total	C	N	O	S	0	0
			1698	1073	313	307	5		

- Molecule 6 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	203	Total	C	N	O	S	0	0
			1660	1051	314	290	5		

- Molecule 7 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	153	Total	C	N	O	S	0	0
			1173	742	226	202	3		

- Molecule 8 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	167	Total	C	N	O	S	0	0
			1362	857	240	263	2		

- Molecule 9 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	154	Total	C	N	O	S	0	0
			1246	785	239	216	6		

- Molecule 10 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	141	Total	C	N	O	S	0	0
			1110	723	193	192	2		

- Molecule 11 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	128	Total	C	N	O	S	0	0
			1028	655	191	181	1		

- Molecule 12 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	101	Total	C	N	O	S	0	0
			809	523	142	143	1		

- Molecule 13 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	114	Total	C	N	O	S	0	0
			829	514	153	156	6		

- Molecule 14 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	136	Total	C	N	O	S	0	0
			1076	680	213	181	2		

- Molecule 15 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	118	Total	C	N	O		0	0
			951	594	191	166			

- Molecule 16 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	60	Total	C	N	O	S	0	0
			474	302	96	72	4		

- Molecule 17 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	83	Total	C	N	O		0	0
			673	428	125	120			

- Molecule 18 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	80	Total	C	N	O	S	0	0
			646	414	119	111	2		

- Molecule 19 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	P	83	Total	C	N	O		0	0
			675	425	135	115			

- Molecule 20 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Q	65	Total	C	N	O	S	0	0
			535	342	103	86	4		

- Molecule 21 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	R	84	Total	C	N	O	S	0	0
			682	435	127	118	2		

- Molecule 22 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	S	77	Total	C	N	O		0	0
			629	383	135	111			

- Molecule 23 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	T	53	Total	C	N	O	S	0	0
			471	295	103	72	1		

- Molecule 24 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	a	285	Total	C	N	O	S	0	0
			2225	1385	437	397	6		

- Molecule 25 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	229	Total	C	N	O	S	0	0
			1762	1119	318	318	7		

- Molecule 26 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	c	210	Total	C	N	O	S	0	0
			1644	1047	297	297	3		

- Molecule 27 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	d	175	Total	C	N	O	S	0	0
			1388	893	245	246	4		

- Molecule 28 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	e	176	Total	C	N	O	0	0
			1396	899	247	250		

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	f	145	Total	C	N	O	S	0
			1160	746	204	207	3	0

- Molecule 30 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	g	126	Total	C	N	O	S	0
			960	612	167	178	3	0

- Molecule 31 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	h	128	Total	C	N	O	S	0
			959	616	160	177	6	0

- Molecule 32 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	i	144	Total	C	N	O	S	0
			1164	737	213	209	5	0

- Molecule 33 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	j	122	Total	C	N	O	S	0
			944	595	178	167	4	0

- Molecule 34 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	k	148	Total	C	N	O	0	0
			1153	731	226	196		

- Molecule 35 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	l	136	Total	C	N	O	S	0	0
			1079	694	196	182	7		

- Molecule 36 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	m	119	Total	C	N	O	S	0	0
			958	609	175	171	3		

- Molecule 37 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	n	112	Total	C	N	O	S	0	0
			889	557	175	155	2		

- Molecule 38 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	o	115	Total	C	N	O	S	0	0
			938	592	180	165	1		

- Molecule 39 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	p	114	Total	C	N	O	S	0	0
			947	603	188	154	2		

- Molecule 40 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	q	99	Total	C	N	O	S	0	0
			811	525	148	134	4		

- Molecule 41 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	r	139	Total	C	N	O	S	0	0
			1068	663	207	191	7		

- Molecule 42 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	s	92	Total	C	N	O	S	0	0
			720	475	122	122	1		

- Molecule 43 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	t	111	Total	C	N	O	S	0	0
			872	550	166	153	3		

- Molecule 44 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	u	86	Total	C	N	O	S	0	0
			657	409	130	117	1		

- Molecule 45 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	v	63	Total	C	N	O	S	0	0
			513	317	108	87	1		

- Molecule 46 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	w	100	Total	C	N	O	0	0
			818	517	153	148		

- Molecule 47 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	x	44	Total	C	N	O	S	0	0
			344	221	55	64	4		

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	y	56	Total	C	N	O	S	0	0
			452	274	98	75	5		

- Molecule 49 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

- Molecule 50 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 51 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

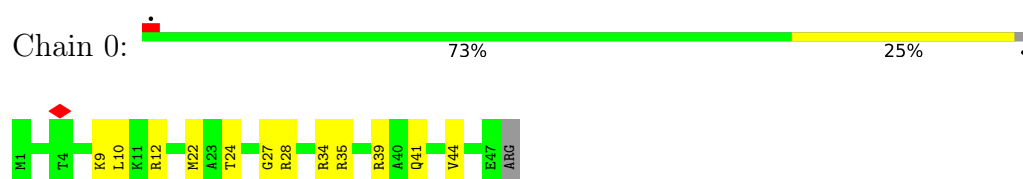
- Molecule 53 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

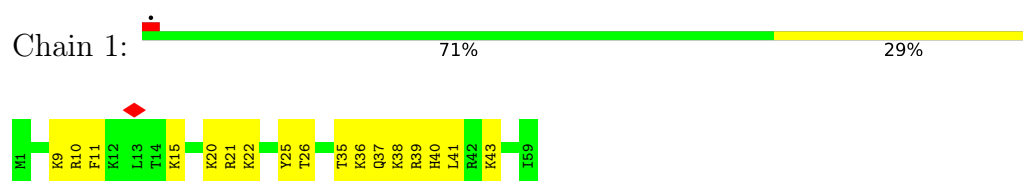
3 Residue-property plots

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.

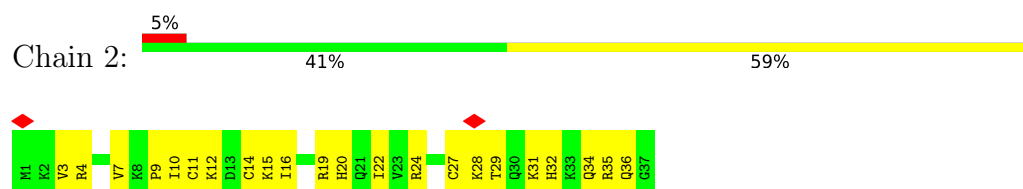
- Molecule 1: 50S ribosomal protein L34



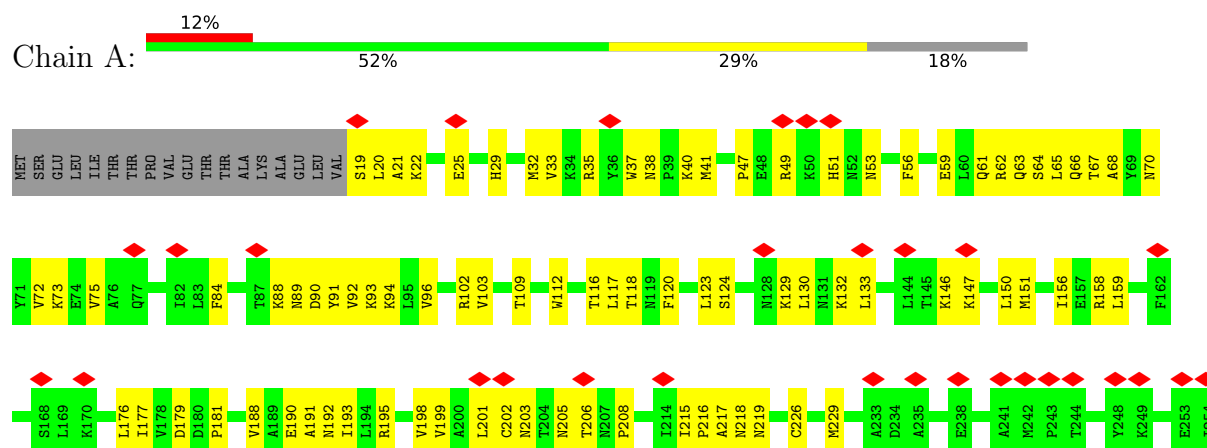
- Molecule 2: 50S ribosomal protein L35

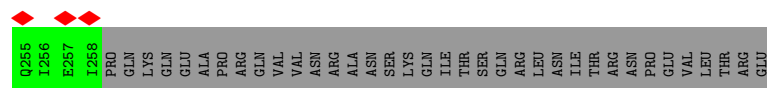


- Molecule 3: 50S ribosomal protein L36

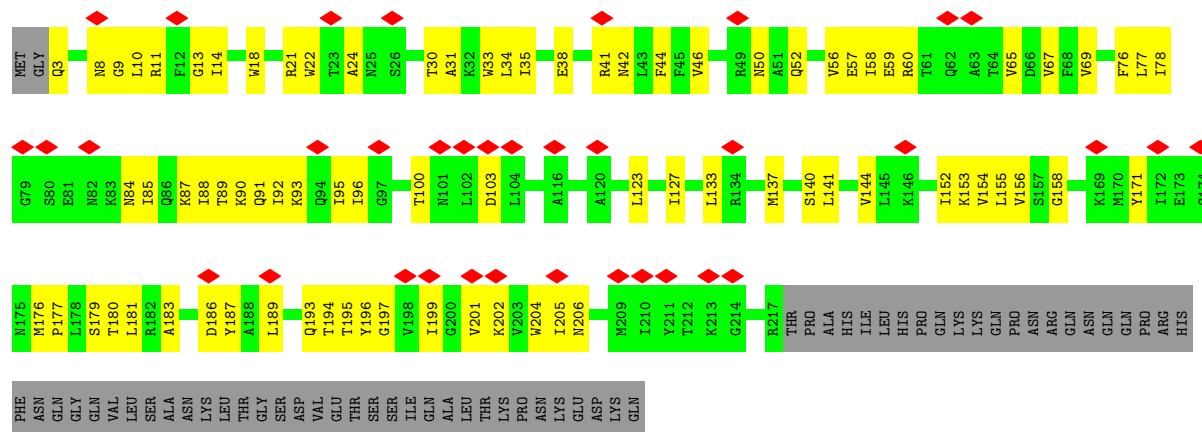


- Molecule 4: 30S ribosomal protein S2

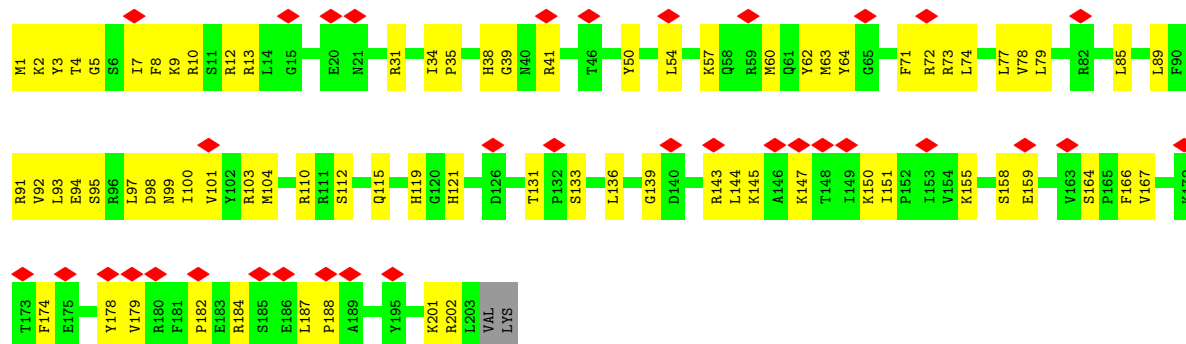




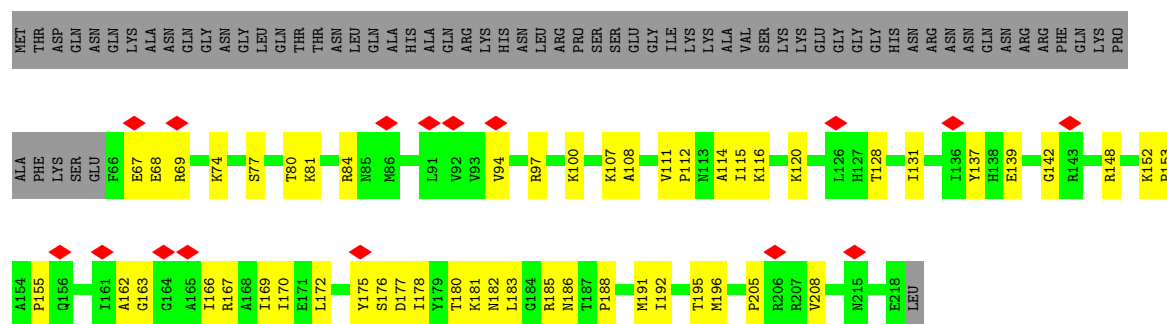
• Molecule 5: 30S ribosomal protein S3



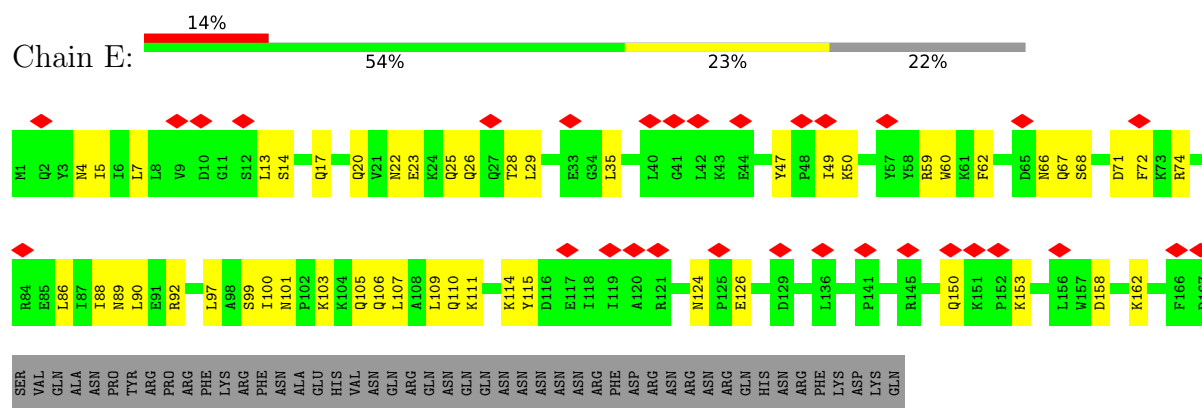
• Molecule 6: 30S ribosomal protein S4



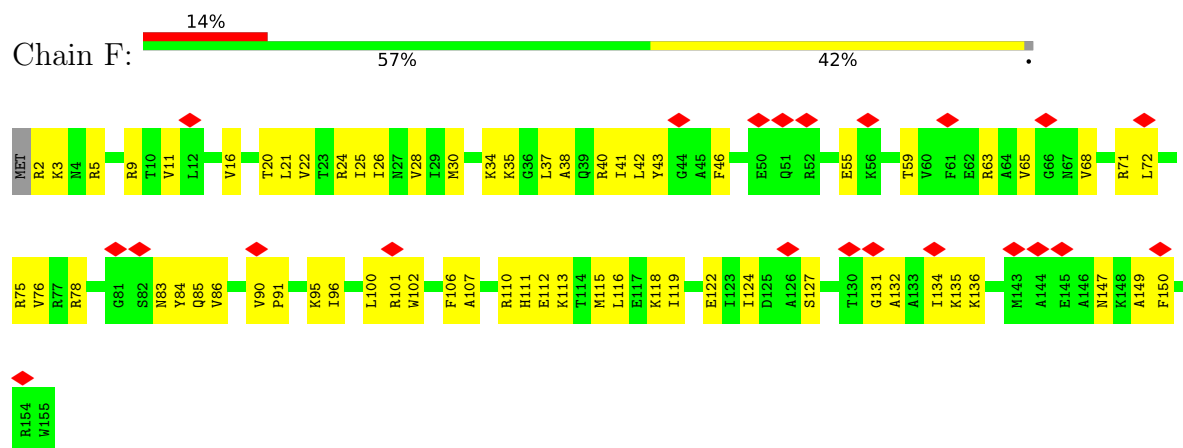
• Molecule 7: 30S ribosomal protein S5



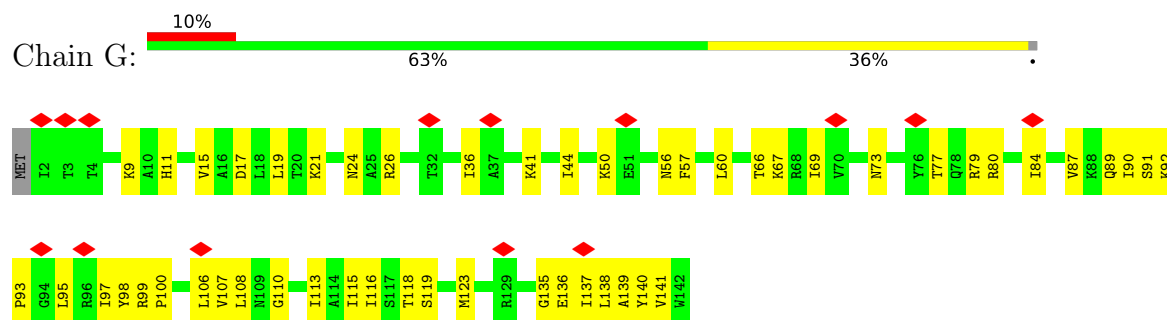
• Molecule 8: 30S ribosomal protein S6



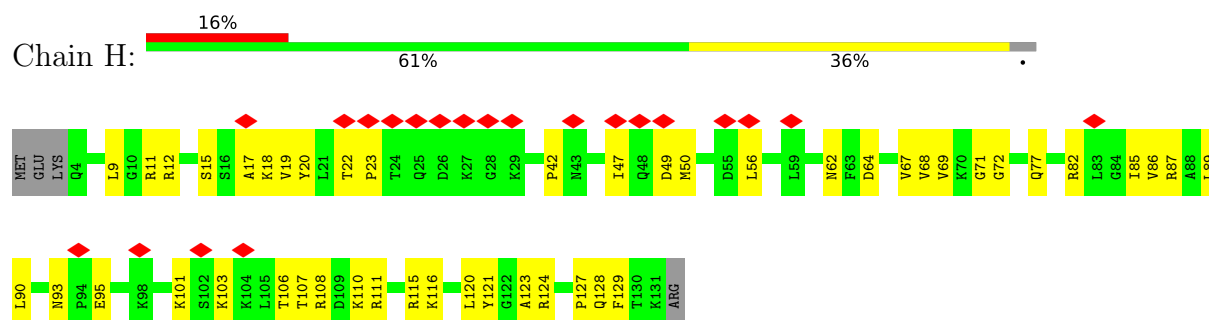
- Molecule 9: 30S ribosomal protein S7



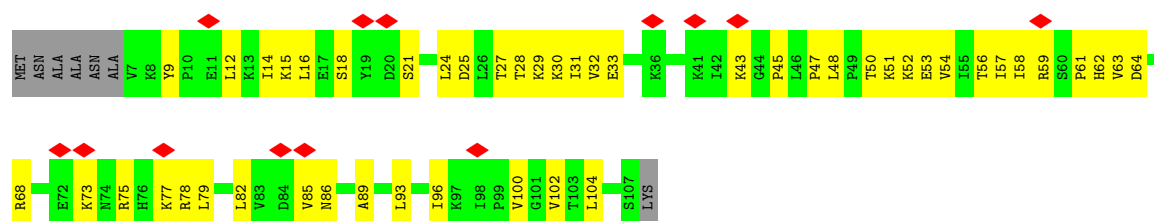
- Molecule 10: 30S ribosomal protein S8



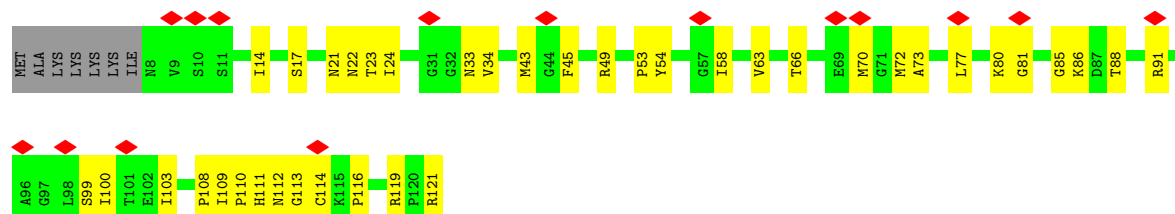
- Molecule 11: 30S ribosomal protein S9



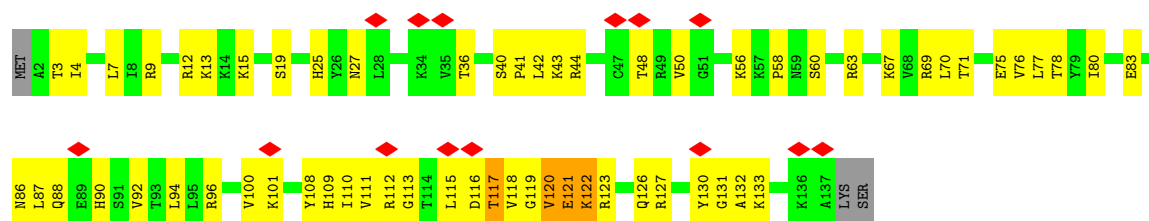
- Molecule 12: 30S ribosomal protein S10



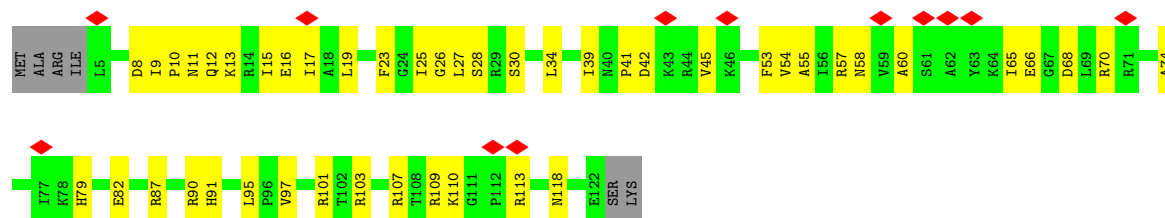
- Molecule 13: 30S ribosomal protein S11



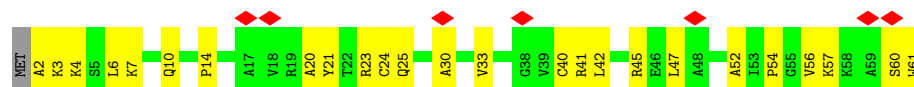
- Molecule 14: 30S ribosomal protein S12



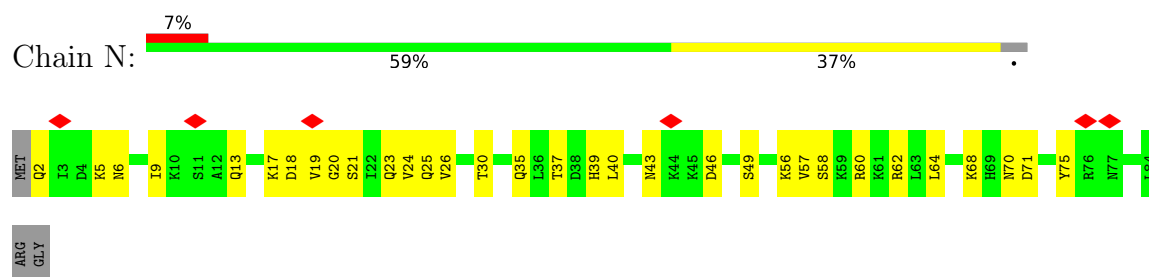
- Molecule 15: 30S ribosomal protein S13



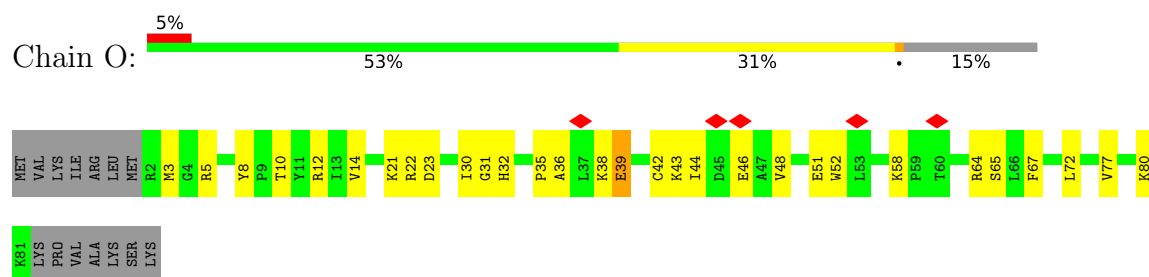
- Molecule 16: 30S ribosomal protein S14 type Z



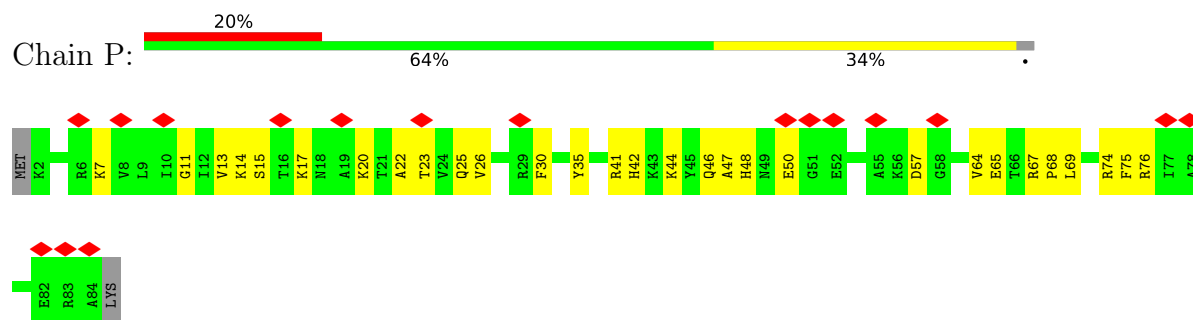
- Molecule 17: 30S ribosomal protein S15



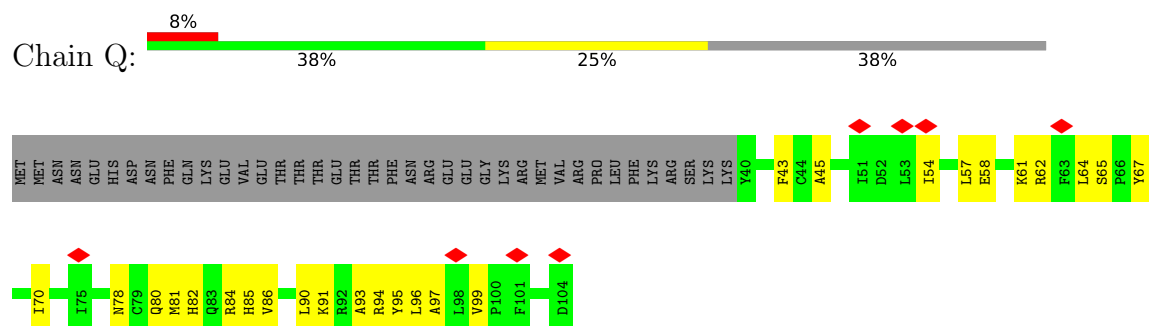
- Molecule 18: 30S ribosomal protein S16



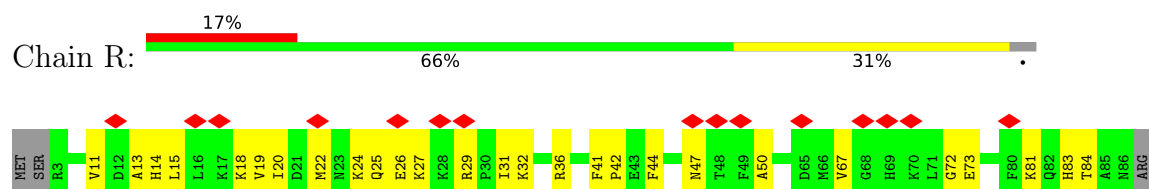
- Molecule 19: 30S ribosomal protein S17

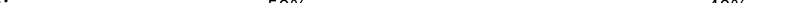


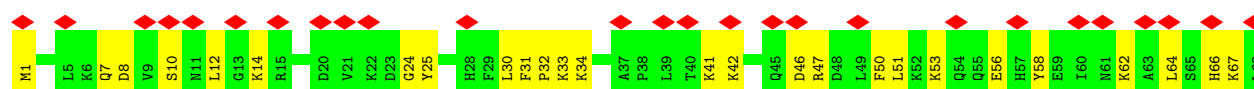
- Molecule 20: 30S ribosomal protein S18

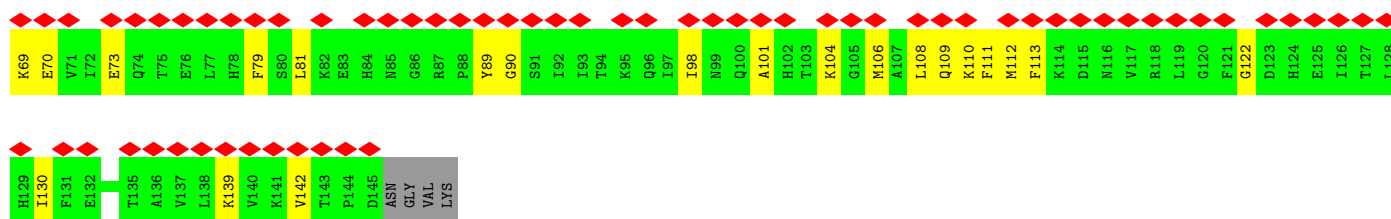


- Molecule 21: 30S ribosomal protein S19

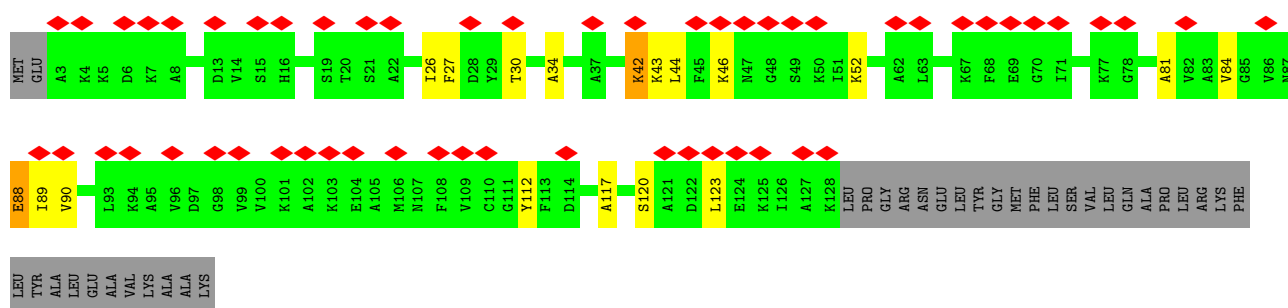


Chain c: 

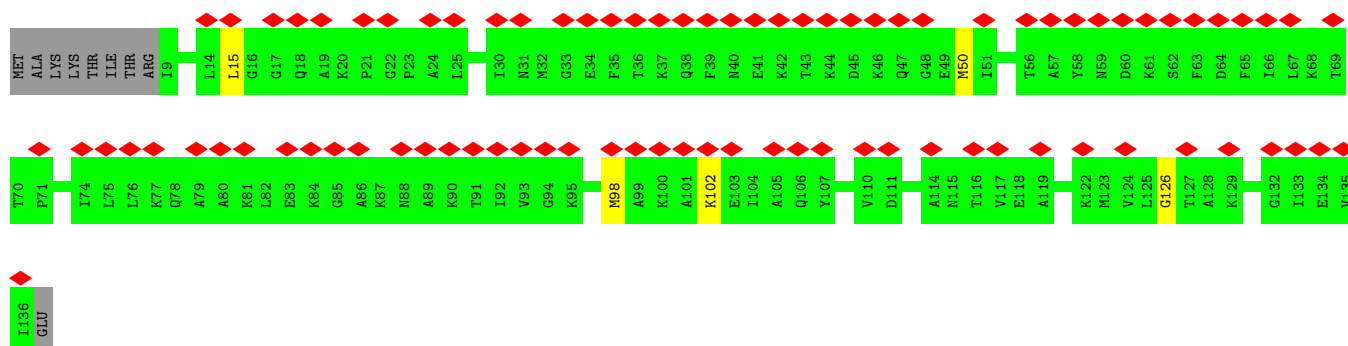
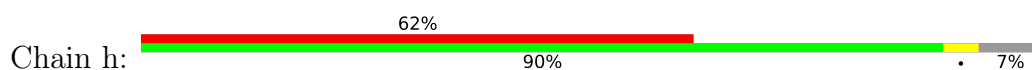




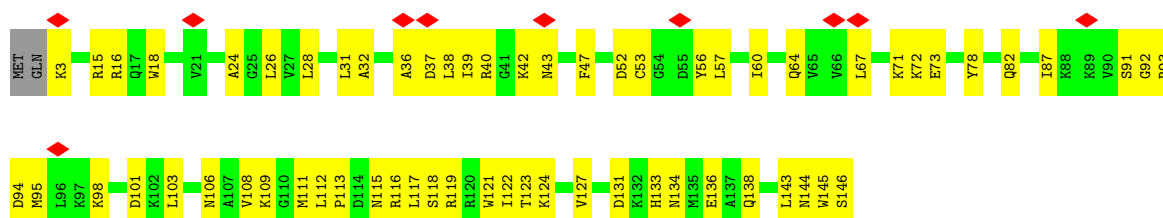
• Molecule 30: 50S ribosomal protein L10



• Molecule 31: 50S ribosomal protein L11

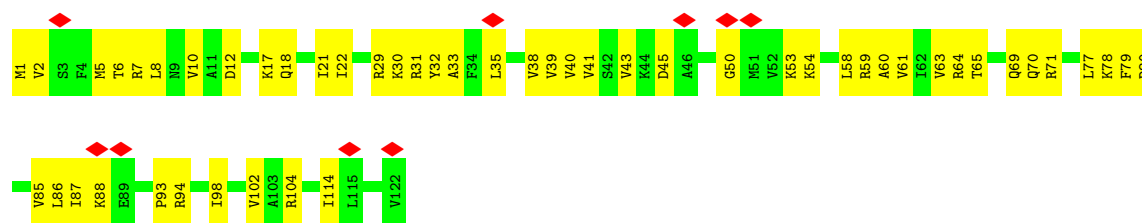


• Molecule 32: 50S ribosomal protein L13

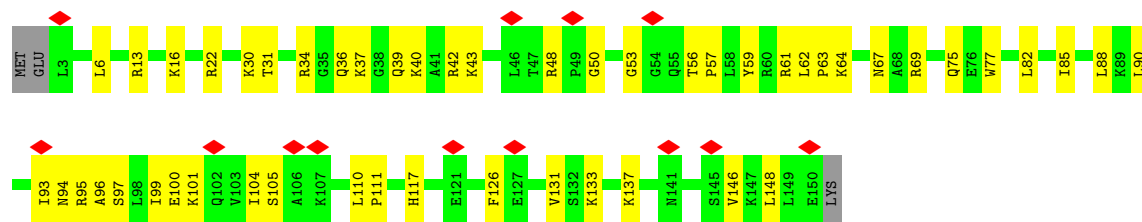


• Molecule 33: 50S ribosomal protein L14

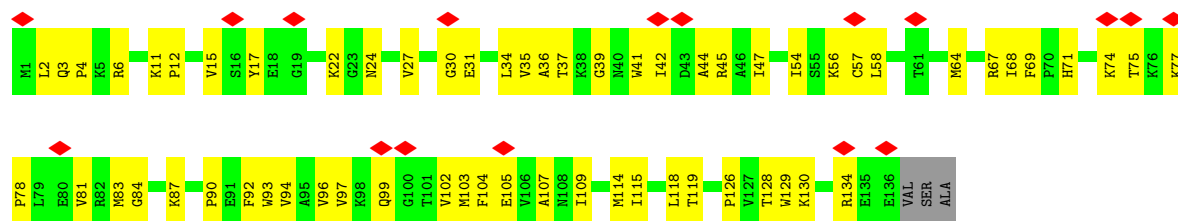




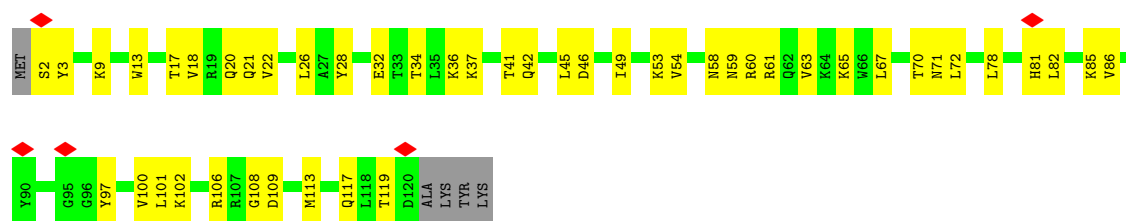
• Molecule 34: 50S ribosomal protein L15



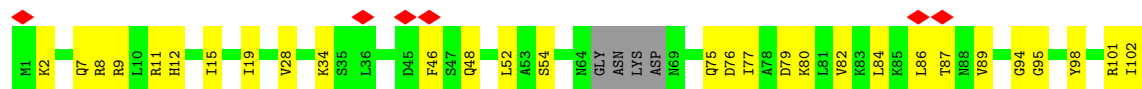
• Molecule 35: 50S ribosomal protein L16

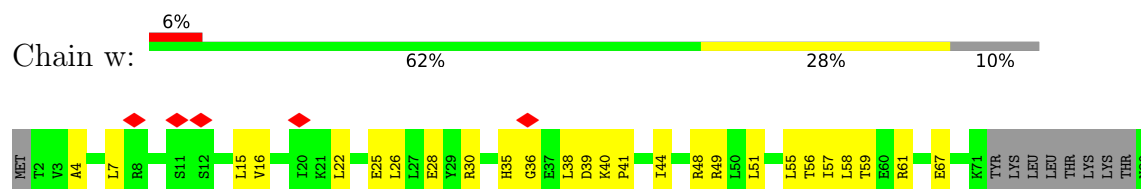


• Molecule 36: 50S ribosomal protein L17



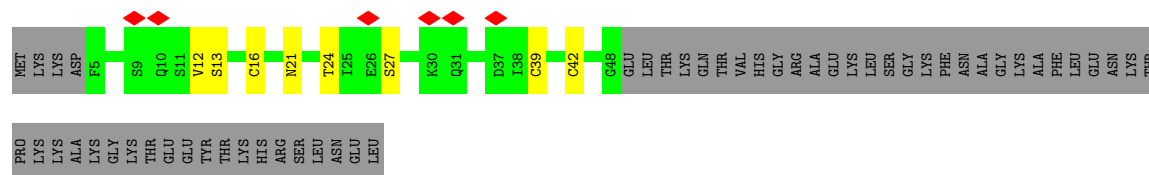
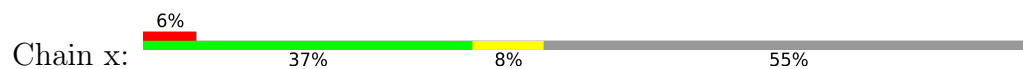
• Molecule 37: 50S ribosomal protein L18



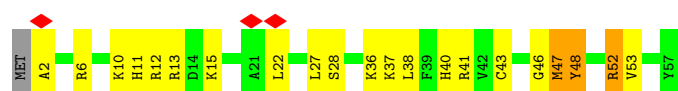




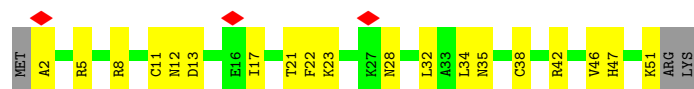
- Molecule 47: 50S ribosomal protein L31



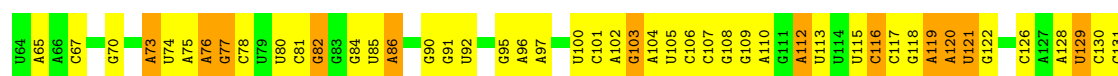
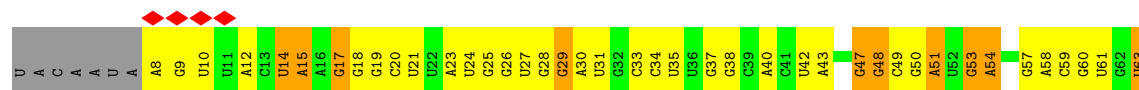
- Molecule 48: 50S ribosomal protein L32



- Molecule 49: 50S ribosomal protein L33 1



- Molecule 50: 23S ribosomal RNA

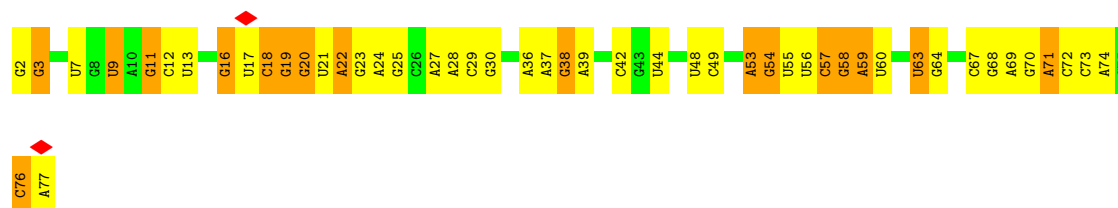
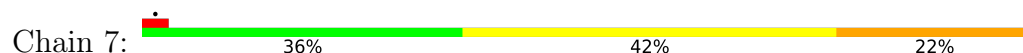


U1279	G1280	G1281	G1282	A1283	A1284	U1285	G1286	G1287	G1288	G1289	G1290	G1291	A1292	U1293	G1294	A1295	A1298	A1299	C1300	G1301	C1302	U1303	U1304	G1305	G1306	G1307	A1308	G1309	U1310	G1311	U1312	G1313	A1314	A1315	U1316	G1317	U1318	C1319	C1320	C1321	A1322	A1323	A1324	C1325	C1326	G1327	U1328	U1329	A1332	A1336	G1337	G1338	U1341	C1342	C1343																
G1145	A1146	G1147	U1148	G1149	U1150	U1151	U1154	G1155	A1156	G1157	C1158	G1159	A1160	U1161	G1162	G1163	U1164	U1165	G1166	U1167	A1168	A1169	C1170	G1171	G1172	G1173	G1174	G1175	U1176	A1177	A1178	G1179	U1180	A1181	U1182	A1183	U1184	U1185	A1186	C1187	G1188	G1189	A1190	A1191	U1196	G1197	G1198	A1201	A1202	G1203	A1204	U1207	A1208	U1209	A1210																
U1211	C1212	U1213	U1214	G1215	U1216	G1217	G1218	U1219	A1220	G1221	A1222	C1223	G1224	A1225	G1226	C1227	G1228	U1229	U1230	U1231	U1232	A1233	U1234	U1235	G1236	U1240	A1243	A1244	G1245	U1246	A1247	A1248	A1249	A1250	G1251	C1252	U1253	U1254	G1255	A1256	G1257	C1258	A1259	U1260	U1261	G1262	G1263	U1264	G1265	G1266	U1267	U1268	C1269	C1270	A1271	G1278															
G1145	A1146	G1147	U1148	G1149	U1150	U1151	U1154	G1155	A1156	G1157	C1158	G1159	A1160	U1161	G1162	G1163	U1164	U1165	G1166	U1167	A1168	A1169	C1170	G1171	G1172	G1173	G1174	G1175	U1176	A1177	A1178	G1179	U1180	A1181	U1182	A1183	U1184	U1185	A1186	C1187	G1188	G1189	A1190	A1191	U1196	G1197	G1198	A1201	A1202	G1203	A1204	U1207	A1208	U1209	A1210																
U1006	A1009	G1010	A1011	G1012	G1013	A1016	A1017	A1018	A1019	U1020	C1021	C1022	C1023	A1024	G1025	U1026	U1027	C1028	A1029	U1030	U1031	A1032	A1033	A1034	U1035	A1036	A1037	G1038	G1039	U1040	C1041	C1042	C1043	C1044	A1045	A1046	A1047	A1048	U1049	A1050	U1054	A1055	A1056	G1057	A1061	A1062	G1065	G1066	A1067	U1068	G1069	U1070	G1071	A1072																	
U939	A940	C941	A942	A943	U944	U945	A946	A947	A948	C949	U950	C951	U952	G953	A954	A955	C958	C959	A960	U961	U962	U963	A964	U965	U966	G967	C974	G975	C976	U977	G978	U979	A981	A982	G982	A983	C984	A985	U986	U987	G988	G989	G990	C991	G992	A993	U994	A995	A996	G997	C998	U999	U1000	C1001	A1002	G1005															
A1073	A1074	G1075	U1076	G1077	C1078	U1079	A1080	U1081	A1082	A1083	C1084	A1085	G1086	A1092	U1093	G1094	U1095	U1096	U1097	C1098	C1099	U1100	U1101	A1102	G1103	A1104	A1105	G1106	C1107	A1108	G1109	U1113	U1114	G1115	U1116	U1117	U1118	U1119	G1124	U1125	G1126	C1127	G1128	U1129	A1130	A1131	G1134	A1138	C1139	U1140	U1141	U1142	U1143	C1144																	
G1145	A1146	G1147	U1148	G1149	U1150	U1151	U1154	G1155	A1156	G1157	C1158	G1159	A1160	U1161	G1162	G1163	U1164	U1165	G1166	U1167	A1168	A1169	C1170	G1171	G1172	G1173	G1174	G1175	U1176	A1177	A1178	G1179	U1180	A1181	U1182	A1183	U1184	U1185	A1186	C1187	G1188	G1189	A1190	A1191	U1196	G1197	G1198	A1201	A1202	G1203	A1204	U1207	A1208	U1209	A1210																
U1211	C1212	U1213	U1214	G1215	U1216	G1217	G1218	U1219	A1220	G1221	A1222	C1223	G1224	A1225	G1226	C1227	G1228	U1229	U1230	U1231	U1232	A1233	U1234	U1235	G1236	U1240	A1243	A1244	G1245	U1246	A1247	A1248	A1249	A1250	G1251	C1252	U1253	U1254	G1255	A1256	G1257	C1258	A1259	U1260	U1261	G1262	G1263	U1264	G1265	G1266	U1267	U1268	C1269	C1270	A1271	G1278															
A333	A334	C335	C336	U337	G338	G341	G342	A343	A344	A345	G346	C347	A348	U403	C404	C405	C406	U407	G408	A409	G410	A411	A412	G413	G418	A419	A420	A421	A422	C423	C424	U425	U426	A427	U428	U429	U430	G431	G432	G433	G363	A364	G367	C368	C369	C370	C371	G372	U373	A374	U377	G378	A379	A380	A381	U382	U383	U452	U453	U385	U386	U387	U388	C389	A390	G461	C462	U463	A464	A465	A466





- Molecule 53: tRNA-Phe



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	6223	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.902	Depositor
Minimum map value	-0.783	Depositor
Average map value	0.025	Depositor
Map value standard deviation	0.128	Depositor
Recommended contour level	0.47	Depositor
Map size (Å)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7005, 1.7005, 1.7005	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	0	0.13	0/383	0.38	0/504
2	1	0.18	0/484	0.54	0/637
3	2	0.16	0/306	0.46	0/401
4	A	0.14	0/1954	0.43	0/2642
5	B	0.17	0/1721	0.49	0/2323
6	C	0.16	0/1691	0.49	0/2267
7	D	0.18	0/1188	0.52	1/1593 (0.1%)
8	E	0.16	0/1384	0.48	2/1867 (0.1%)
9	F	0.19	0/1266	0.56	1/1700 (0.1%)
10	G	0.17	0/1126	0.53	0/1517
11	H	0.17	0/1044	0.46	0/1395
12	I	0.20	0/820	0.58	1/1103 (0.1%)
13	J	0.15	0/844	0.44	0/1136
14	K	0.28	0/1094	0.60	2/1468 (0.1%)
15	L	0.18	0/962	0.50	0/1289
16	M	0.18	0/483	0.51	0/643
17	N	0.14	0/679	0.49	1/907 (0.1%)
18	O	0.18	0/659	0.57	1/885 (0.1%)
19	P	0.14	0/684	0.42	0/913
20	Q	0.19	0/545	0.60	0/730
21	R	0.15	0/698	0.49	0/936
22	S	0.17	0/631	0.46	0/838
23	T	0.19	0/475	0.55	0/621
24	a	0.15	0/2267	0.43	0/3044
25	b	0.17	0/1795	0.51	0/2412
26	c	0.18	0/1671	0.51	1/2246 (0.0%)
27	d	0.15	0/1409	0.44	0/1894
28	e	0.14	0/1420	0.42	0/1912
29	f	0.19	0/1183	0.56	2/1587 (0.1%)
30	g	0.41	0/969	0.73	0/1295
31	h	0.16	0/968	0.43	0/1298
32	i	0.15	0/1186	0.46	0/1592
33	j	0.16	0/953	0.47	0/1275
34	k	0.17	0/1170	0.46	0/1559

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	l	0.17	0/1104	0.47	0/1481
36	m	0.22	0/973	0.58	0/1309
37	n	0.18	0/897	0.53	0/1198
38	o	0.17	0/948	0.49	0/1262
39	p	0.19	0/961	0.48	0/1278
40	q	0.18	0/828	0.56	0/1111
41	r	0.17	0/1077	0.52	0/1441
42	s	0.16	0/732	0.52	1/988 (0.1%)
43	t	0.14	0/879	0.44	0/1165
44	u	0.15	0/665	0.43	0/884
45	v	0.22	0/519	0.53	0/695
46	w	0.18	0/826	0.47	0/1104
47	x	0.17	0/353	0.40	0/474
48	y	0.31	0/457	0.67	0/601
49	z	0.14	0/412	0.48	0/547
50	3	0.09	0/69073	0.23	0/107710
51	4	0.10	0/2505	0.28	0/3902
52	5	0.09	0/35768	0.22	0/55764
53	7	0.10	0/1808	0.28	0/2817
All	All	0.13	0/156897	0.33	13/234160 (0.0%)

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
10	G	0	1
13	J	0	1
18	O	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	F	16	VAL	N-CA-C	-6.73	107.32	113.71
8	E	162	LYS	CA-C-N	6.26	133.51	121.54
8	E	162	LYS	C-N-CA	6.26	133.51	121.54
14	K	122	LYS	N-CA-C	-6.25	105.23	112.86
7	D	155	PRO	CA-N-CD	-6.21	103.31	112.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	G	108	LEU	Peptide
13	J	111	HIS	Peptide
18	O	39	GLU	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	0	380	0	429	8	0
2	1	477	0	530	24	0
3	2	304	0	350	16	0
4	A	1921	0	1973	60	0
5	B	1698	0	1768	64	0
6	C	1660	0	1719	62	0
7	D	1173	0	1267	34	0
8	E	1362	0	1377	42	0
9	F	1246	0	1308	55	0
10	G	1110	0	1226	41	0
11	H	1028	0	1094	37	0
12	I	809	0	894	41	0
13	J	829	0	855	35	0
14	K	1076	0	1170	49	0
15	L	951	0	1014	32	0
16	M	474	0	509	22	0
17	N	673	0	730	28	0
18	O	646	0	677	26	0
19	P	675	0	728	24	0
20	Q	535	0	562	23	0
21	R	682	0	691	25	0
22	S	629	0	681	33	0
23	T	471	0	522	18	0
24	a	2225	0	2301	101	0
25	b	1762	0	1808	91	0
26	c	1644	0	1731	69	0
27	d	1388	0	1469	47	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	e	1396	0	1481	33	0
29	f	1160	0	1172	34	0
30	g	960	0	1014	5	0
31	h	959	0	1039	3	0
32	i	1164	0	1192	56	0
33	j	944	0	1019	44	0
34	k	1153	0	1256	46	0
35	l	1079	0	1134	52	0
36	m	958	0	1011	38	0
37	n	889	0	952	26	0
38	o	938	0	1008	48	0
39	p	947	0	1028	64	0
40	q	811	0	858	38	0
41	r	1068	0	1150	52	0
42	s	720	0	803	19	0
43	t	872	0	972	18	0
44	u	657	0	695	23	0
45	v	513	0	560	28	0
46	w	818	0	870	21	0
47	x	344	0	333	4	0
48	y	452	0	472	23	0
49	z	408	0	440	14	0
50	3	61664	0	30954	1830	0
51	4	2239	0	1137	67	0
52	5	31943	0	16058	925	0
53	7	1618	0	821	47	0
All	All	144502	0	98812	4165	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 18.

The worst 5 of 4165 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)
52:5:1331:A:N6	52:5:1340:G:H1	1.44	1.13
52:5:1136:G:H1	52:5:1151:A:N6	1.53	1.07
50:3:1807:C:H42	50:3:1824:G:N2	1.51	1.06
52:5:684:A:H62	52:5:700:G:N2	1.55	1.03
52:5:69:G:H1	52:5:86:A:H61	1.06	1.01

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	0	45/48 (94%)	44 (98%)	1 (2%)	0	100	100
2	1	57/59 (97%)	54 (95%)	3 (5%)	0	100	100
3	2	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
4	A	238/294 (81%)	222 (93%)	16 (7%)	0	100	100
5	B	213/273 (78%)	196 (92%)	17 (8%)	0	100	100
6	C	201/205 (98%)	191 (95%)	10 (5%)	0	100	100
7	D	151/219 (69%)	145 (96%)	6 (4%)	0	100	100
8	E	165/215 (77%)	147 (89%)	18 (11%)	0	100	100
9	F	152/155 (98%)	135 (89%)	17 (11%)	0	100	100
10	G	139/142 (98%)	125 (90%)	14 (10%)	0	100	100
11	H	126/132 (96%)	115 (91%)	11 (9%)	0	100	100
12	I	99/108 (92%)	87 (88%)	12 (12%)	0	100	100
13	J	112/121 (93%)	105 (94%)	7 (6%)	0	100	100
14	K	134/139 (96%)	125 (93%)	9 (7%)	0	100	100
15	L	116/124 (94%)	104 (90%)	12 (10%)	0	100	100
16	M	58/61 (95%)	56 (97%)	2 (3%)	0	100	100
17	N	81/86 (94%)	81 (100%)	0	0	100	100
18	O	78/94 (83%)	70 (90%)	8 (10%)	0	100	100
19	P	81/85 (95%)	78 (96%)	3 (4%)	0	100	100
20	Q	63/104 (61%)	51 (81%)	12 (19%)	0	100	100
21	R	82/87 (94%)	73 (89%)	9 (11%)	0	100	100
22	S	75/87 (86%)	74 (99%)	1 (1%)	0	100	100
23	T	51/60 (85%)	50 (98%)	1 (2%)	0	100	100
24	a	283/287 (99%)	265 (94%)	18 (6%)	0	100	100
25	b	227/287 (79%)	214 (94%)	13 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	c	208/212 (98%)	197 (95%)	11 (5%)	0	100	100
27	d	173/180 (96%)	160 (92%)	13 (8%)	0	100	100
28	e	174/184 (95%)	166 (95%)	8 (5%)	0	100	100
29	f	143/149 (96%)	125 (87%)	18 (13%)	0	100	100
30	g	124/161 (77%)	109 (88%)	13 (10%)	2 (2%)	7	38
31	h	126/137 (92%)	114 (90%)	12 (10%)	0	100	100
32	i	142/146 (97%)	136 (96%)	6 (4%)	0	100	100
33	j	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
34	k	146/151 (97%)	139 (95%)	7 (5%)	0	100	100
35	l	134/139 (96%)	124 (92%)	10 (8%)	0	100	100
36	m	117/124 (94%)	108 (92%)	9 (8%)	0	100	100
37	n	108/116 (93%)	99 (92%)	9 (8%)	0	100	100
38	o	113/119 (95%)	101 (89%)	12 (11%)	0	100	100
39	p	112/127 (88%)	108 (96%)	4 (4%)	0	100	100
40	q	97/100 (97%)	90 (93%)	7 (7%)	0	100	100
41	r	137/159 (86%)	134 (98%)	3 (2%)	0	100	100
42	s	90/237 (38%)	88 (98%)	2 (2%)	0	100	100
43	t	109/111 (98%)	104 (95%)	5 (5%)	0	100	100
44	u	84/104 (81%)	81 (96%)	3 (4%)	0	100	100
45	v	61/65 (94%)	59 (97%)	2 (3%)	0	100	100
46	w	96/111 (86%)	89 (93%)	7 (7%)	0	100	100
47	x	42/97 (43%)	35 (83%)	7 (17%)	0	100	100
48	y	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
49	z	48/53 (91%)	47 (98%)	1 (2%)	0	100	100
All	All	5820/6670 (87%)	5418 (93%)	400 (7%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
30	g	88	GLU
30	g	42	LYS

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	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
4	A	212/262 (81%)	211 (100%)	1 (0%)	81	83
5	B	180/232 (78%)	180 (100%)	0	100	100
6	C	181/183 (99%)	181 (100%)	0	100	100
7	D	123/178 (69%)	123 (100%)	0	100	100
8	E	150/196 (76%)	150 (100%)	0	100	100
9	F	131/132 (99%)	131 (100%)	0	100	100
10	G	123/124 (99%)	123 (100%)	0	100	100
11	H	111/115 (96%)	111 (100%)	0	100	100
12	I	95/99 (96%)	95 (100%)	0	100	100
13	J	91/97 (94%)	91 (100%)	0	100	100
14	K	117/120 (98%)	114 (97%)	3 (3%)	40	62
15	L	100/105 (95%)	99 (99%)	1 (1%)	68	78
16	M	47/48 (98%)	47 (100%)	0	100	100
17	N	76/78 (97%)	76 (100%)	0	100	100
18	O	69/82 (84%)	69 (100%)	0	100	100
19	P	73/75 (97%)	73 (100%)	0	100	100
20	Q	56/94 (60%)	56 (100%)	0	100	100
21	R	74/77 (96%)	74 (100%)	0	100	100
22	S	70/77 (91%)	70 (100%)	0	100	100
23	T	49/56 (88%)	49 (100%)	0	100	100
24	a	241/243 (99%)	241 (100%)	0	100	100
25	b	186/233 (80%)	186 (100%)	0	100	100
26	c	182/184 (99%)	182 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	d	150/154 (97%)	150 (100%)	0	100	100
28	e	153/159 (96%)	153 (100%)	0	100	100
29	f	123/134 (92%)	123 (100%)	0	100	100
30	g	101/129 (78%)	91 (90%)	10 (10%)	7	24
31	h	102/110 (93%)	102 (100%)	0	100	100
32	i	126/128 (98%)	126 (100%)	0	100	100
33	j	103/103 (100%)	103 (100%)	0	100	100
34	k	123/126 (98%)	123 (100%)	0	100	100
35	l	113/115 (98%)	113 (100%)	0	100	100
36	m	105/109 (96%)	105 (100%)	0	100	100
37	n	96/99 (97%)	96 (100%)	0	100	100
38	o	101/105 (96%)	101 (100%)	0	100	100
39	p	100/108 (93%)	100 (100%)	0	100	100
40	q	90/91 (99%)	90 (100%)	0	100	100
41	r	116/132 (88%)	116 (100%)	0	100	100
42	s	82/208 (39%)	82 (100%)	0	100	100
43	t	96/96 (100%)	96 (100%)	0	100	100
44	u	69/85 (81%)	69 (100%)	0	100	100
45	v	58/60 (97%)	58 (100%)	0	100	100
46	w	87/98 (89%)	87 (100%)	0	100	100
47	x	41/86 (48%)	41 (100%)	0	100	100
48	y	48/49 (98%)	45 (94%)	3 (6%)	16	37
49	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5093/5751 (89%)	5075 (100%)	18 (0%)	81	84

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	g	90	VAL
48	y	52	ARG
48	y	48	TYR
30	g	43	LYS
30	g	89	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 70 such sidechains are listed below:

Mol	Chain	Res	Type
39	p	85	HIS
41	r	52	ASN
44	u	64	ASN
14	K	88	GLN
14	K	86	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	2875/2907 (98%)	733 (25%)	25 (0%)
51	4	103/108 (95%)	34 (33%)	5 (4%)
52	5	1490/1520 (98%)	349 (23%)	6 (0%)
53	7	75/76 (98%)	25 (33%)	2 (2%)
All	All	4543/4611 (98%)	1141 (25%)	38 (0%)

5 of 1141 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	12	A
50	3	14	U
50	3	15	A
50	3	17	G
50	3	29	G

5 of 38 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	4	59	A
52	5	1373	A
51	4	70	G
52	5	448	A
53	7	19	G

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

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

5.5 Carbohydrates [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.

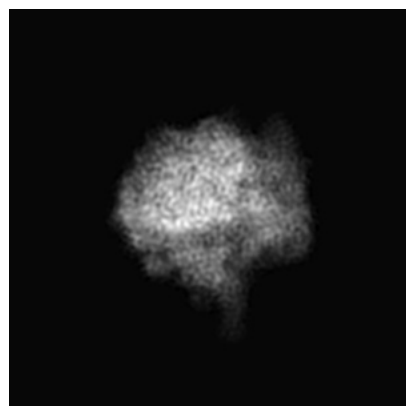
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13273. These allow visual inspection of the internal detail of the map and identification of artifacts.

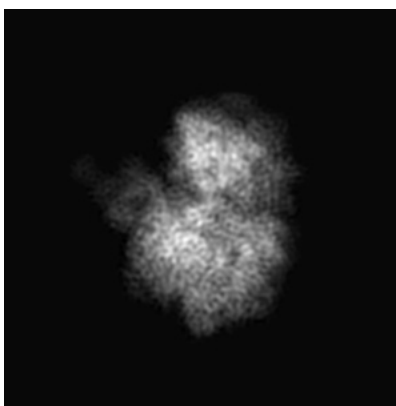
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

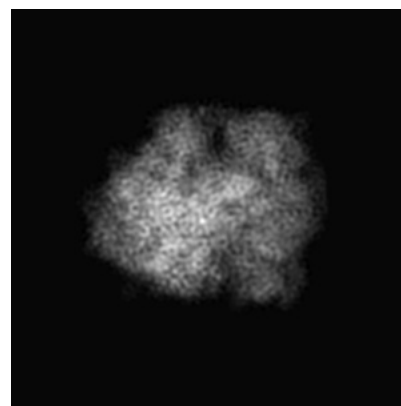
6.1.1 Primary map



X

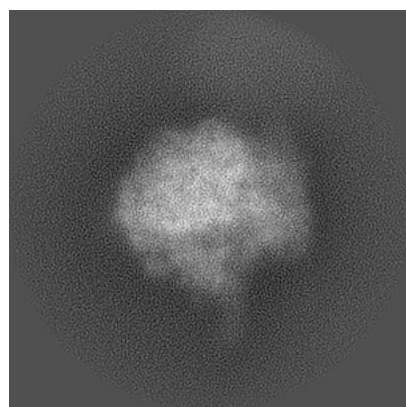


Y

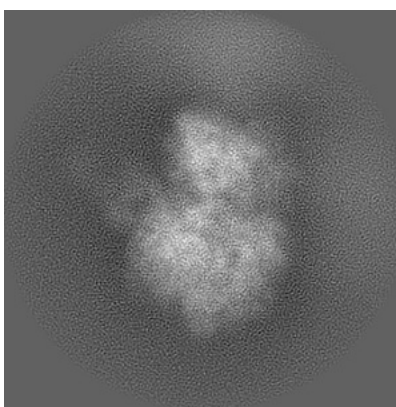


Z

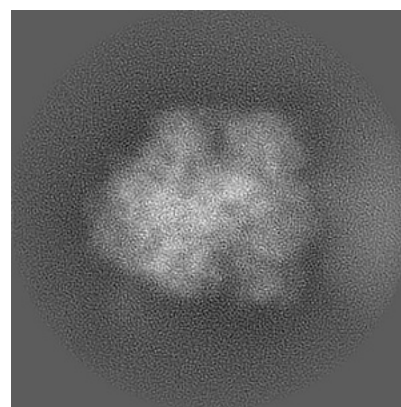
6.1.2 Raw map



X



Y

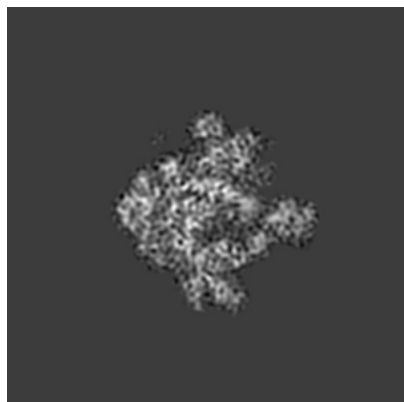


Z

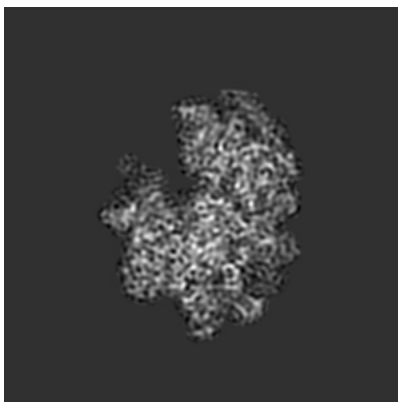
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

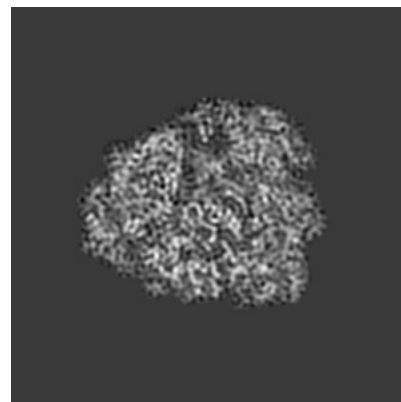
6.2.1 Primary map



X Index: 128

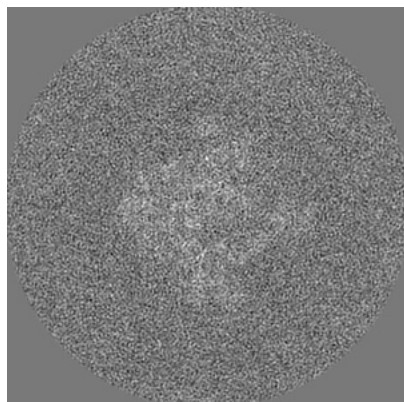


Y Index: 128

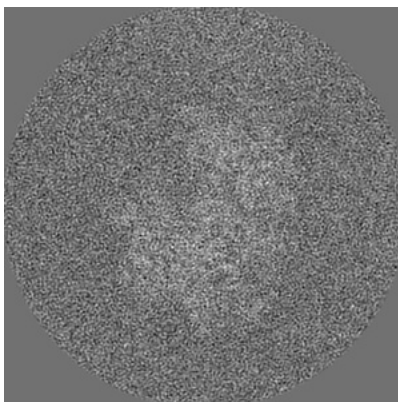


Z Index: 128

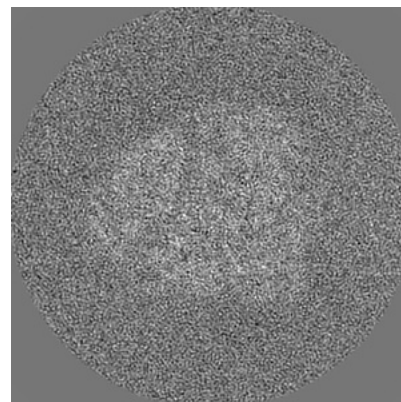
6.2.2 Raw map



X Index: 128



Y Index: 128

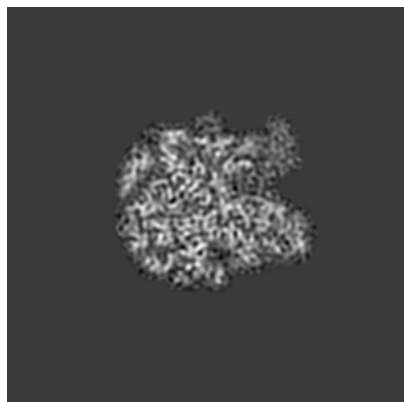


Z Index: 128

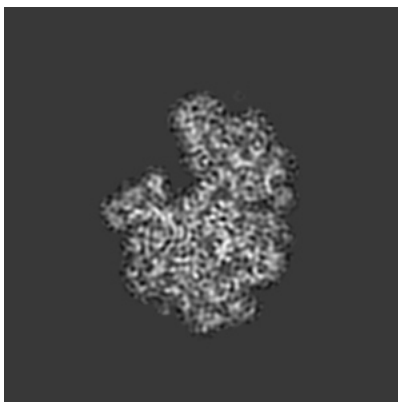
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

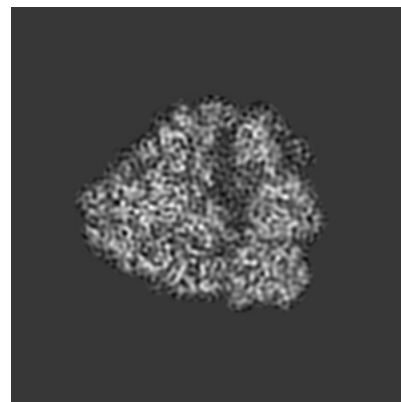
6.3.1 Primary map



X Index: 104

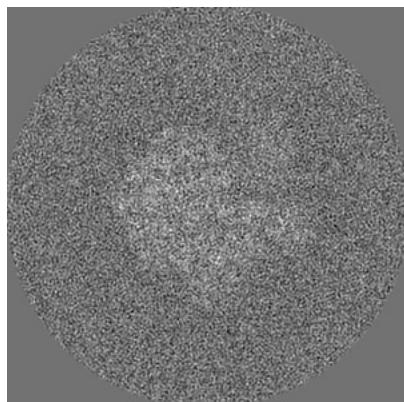


Y Index: 120

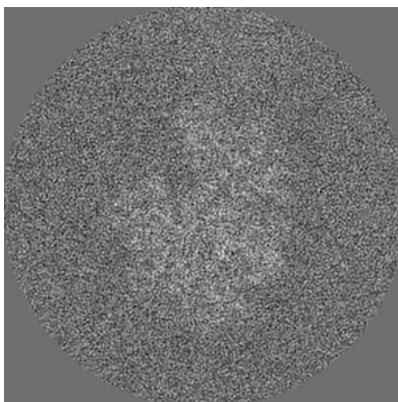


Z Index: 122

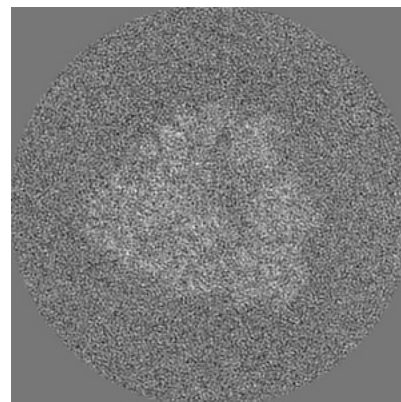
6.3.2 Raw map



X Index: 119



Y Index: 120

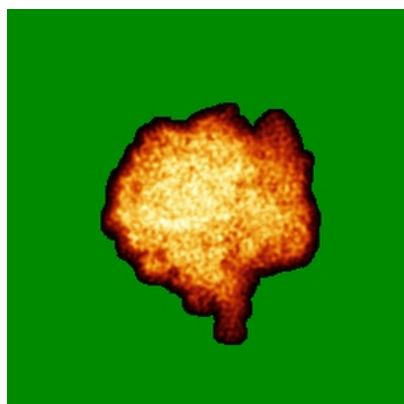


Z Index: 122

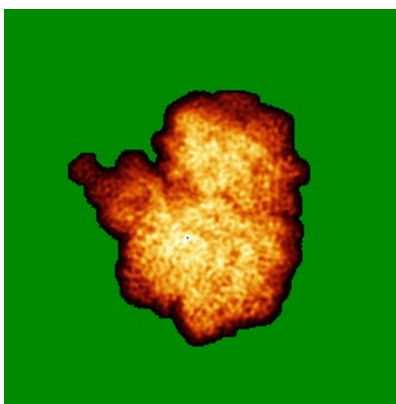
The images above show the largest variance slices of the map in three orthogonal directions.

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

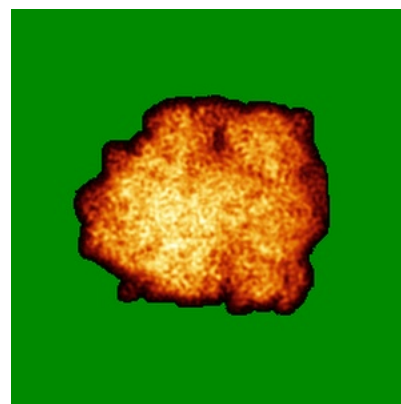
6.4.1 Primary map



X

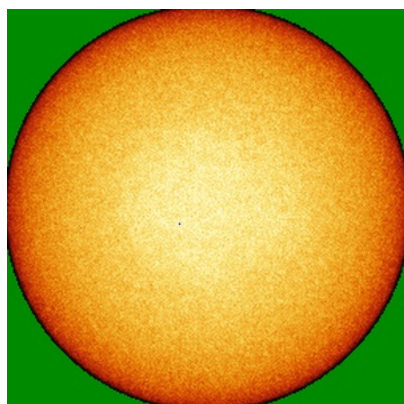


Y

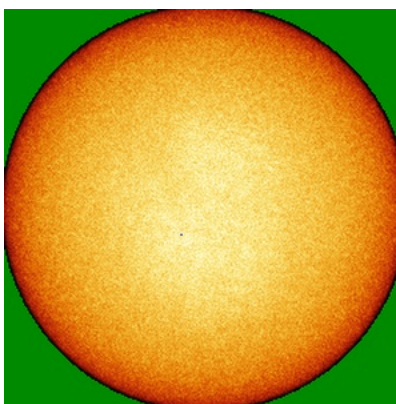


Z

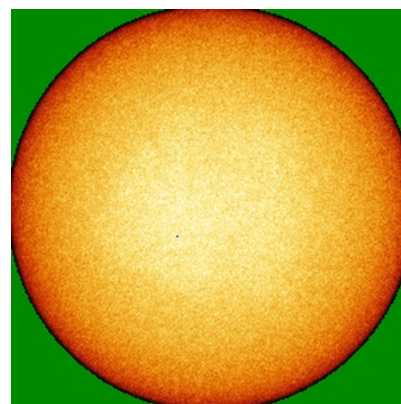
6.4.2 Raw map



X



Y

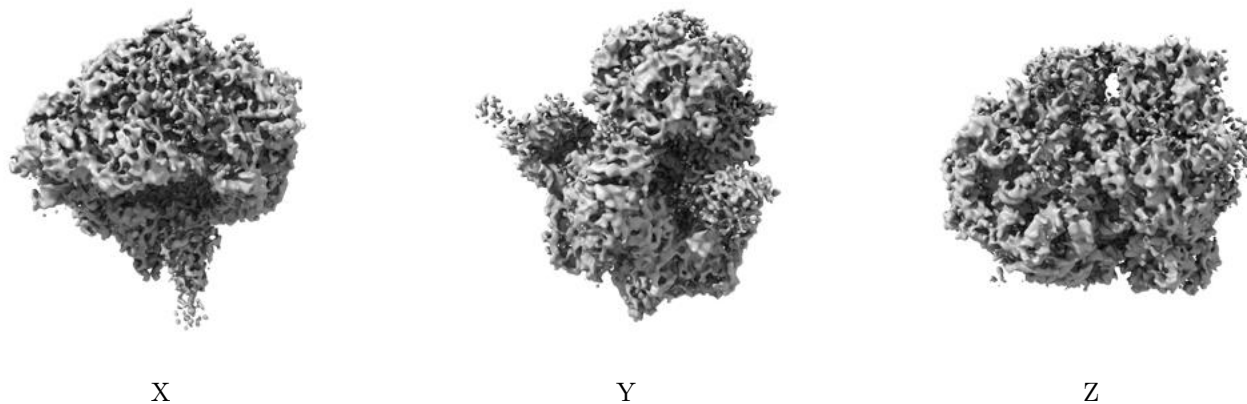


Z

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

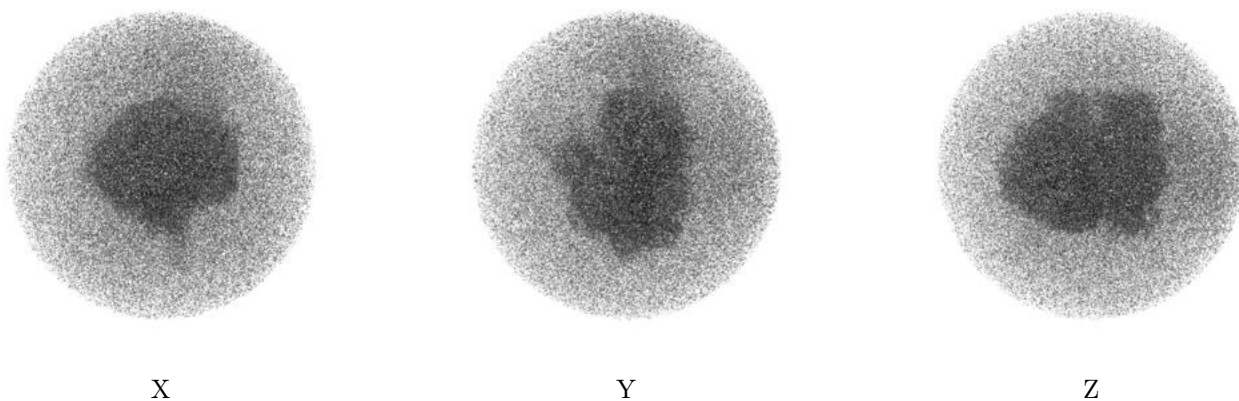
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.47. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

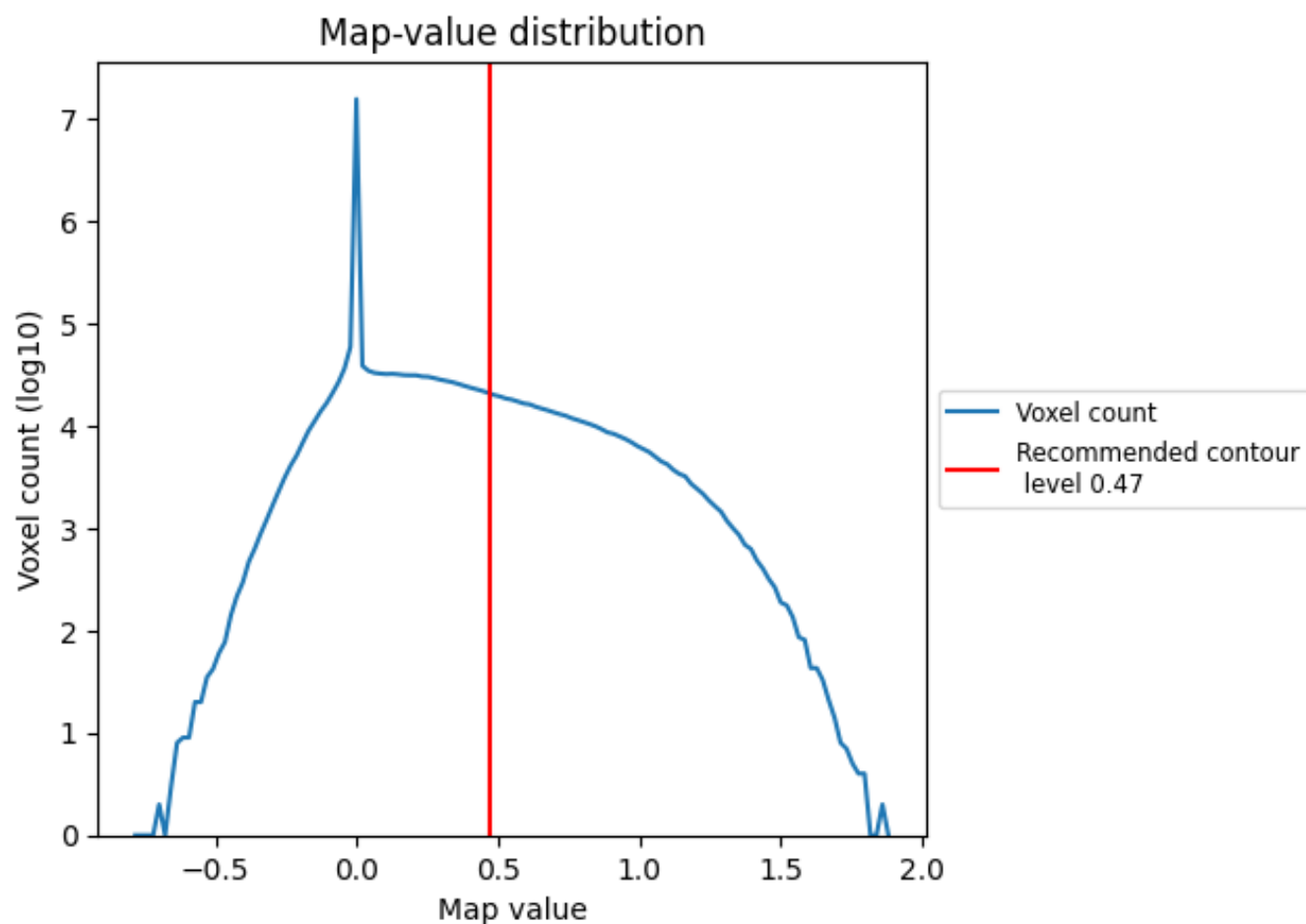
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

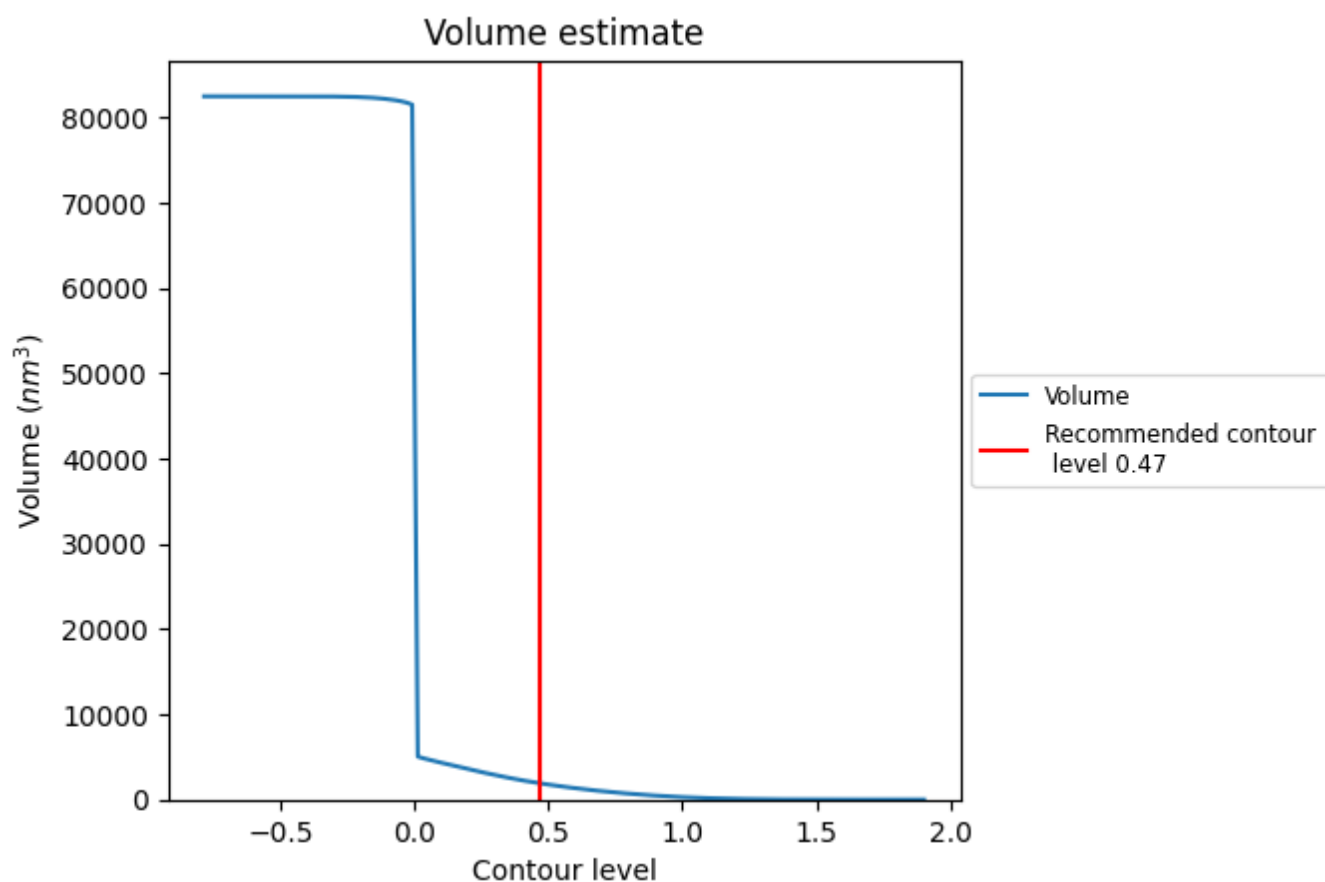
This section contains the results of statistical analysis of the map.

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.

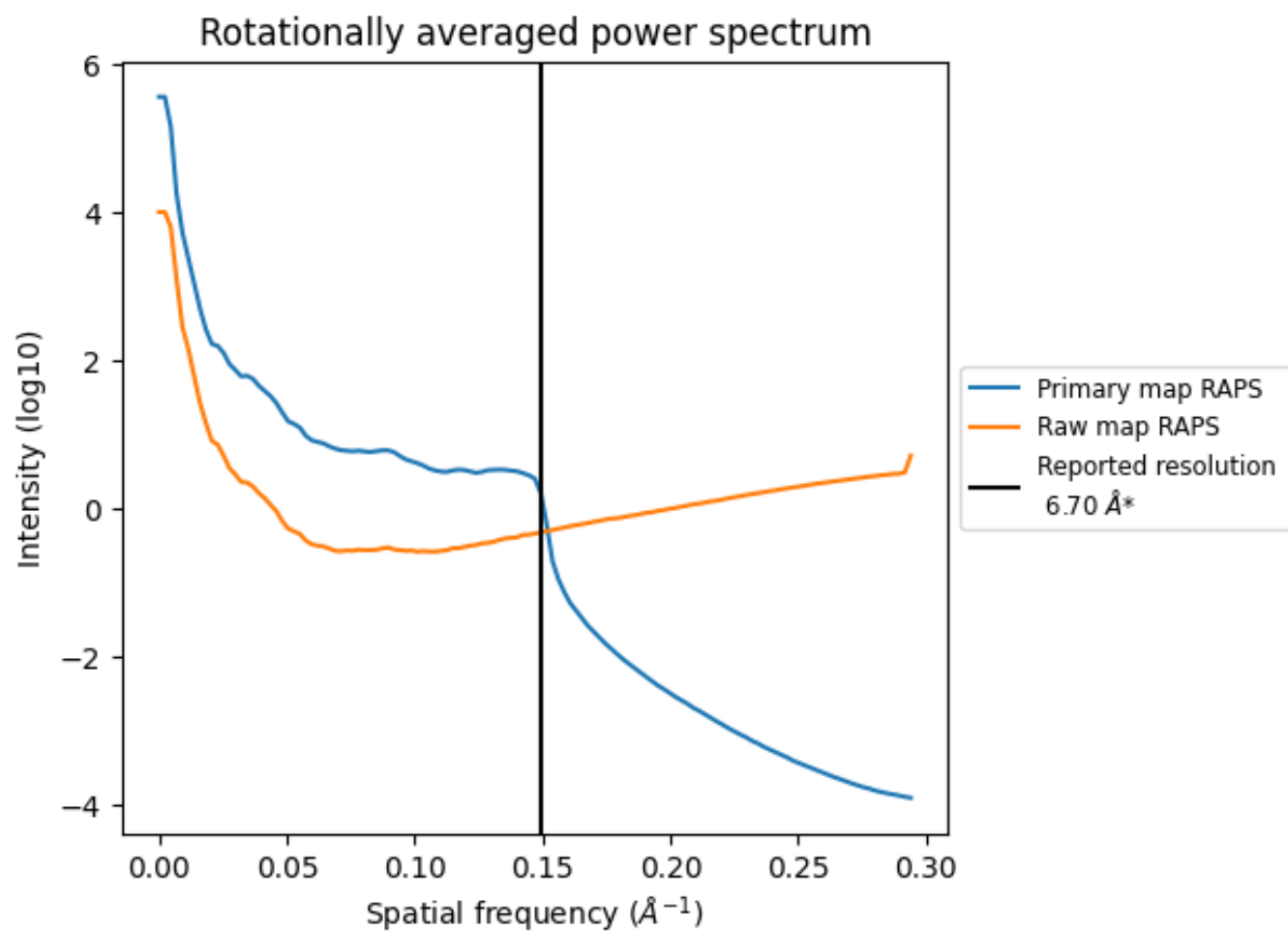
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1908 nm^3 ; this corresponds to an approximate mass of 1723 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 ⓘ

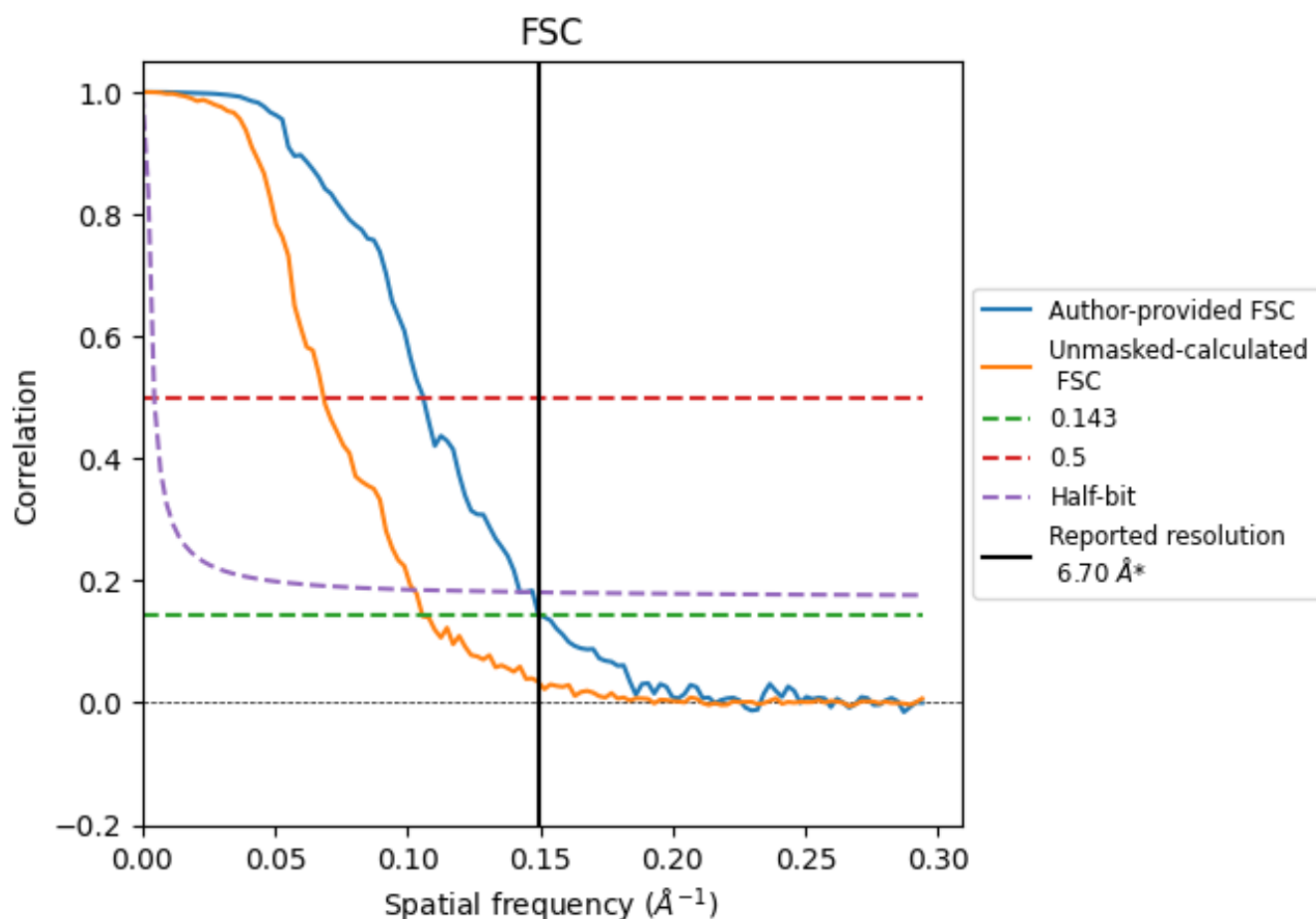


*Reported resolution corresponds to spatial frequency of 0.149 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.149 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

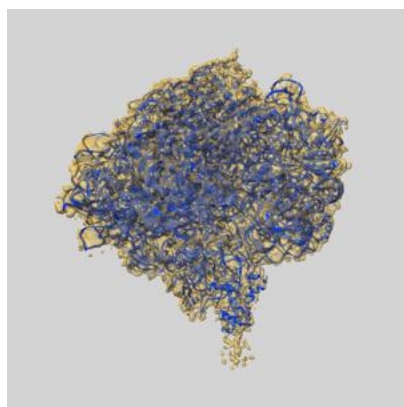
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.70	-	-
Author-provided FSC curve	6.65	9.44	7.02
Unmasked-calculated*	9.47	14.62	9.77

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 9.47 differs from the reported value 6.7 by more than 10 %

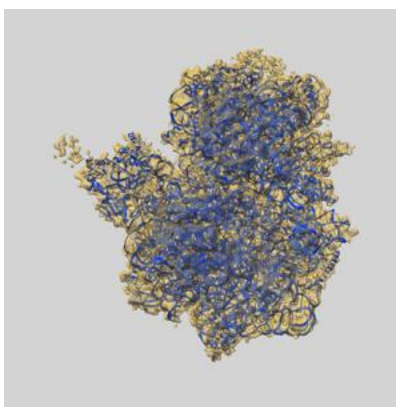
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13273 and PDB model 7PAI. Per-residue inclusion information can be found in section [3](#) on page [13](#).

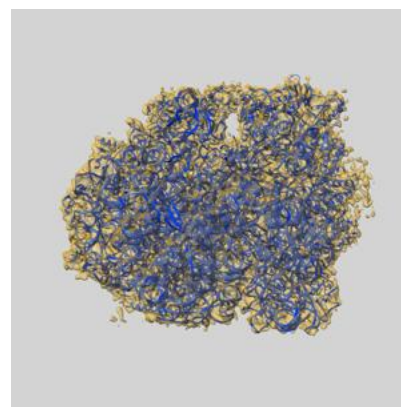
9.1 Map-model overlay [i](#)



X



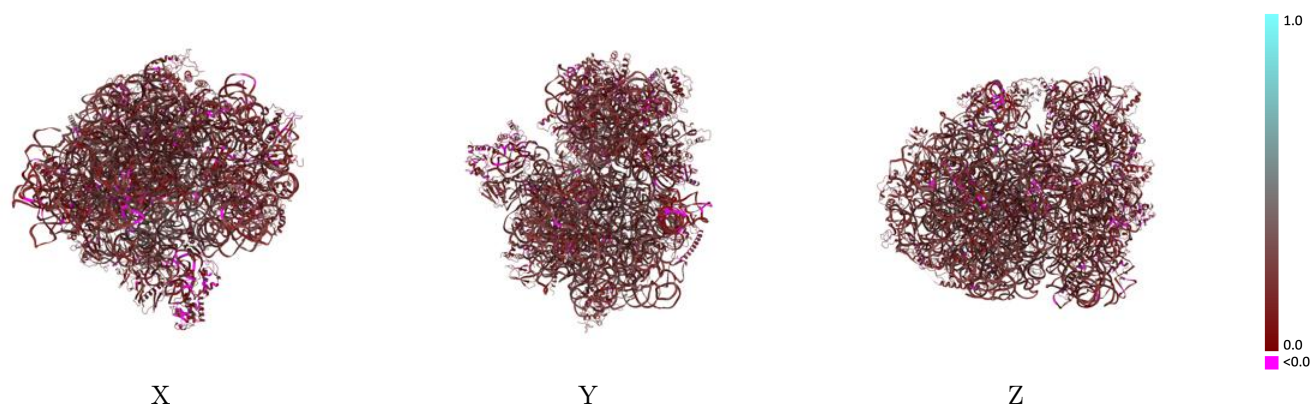
Y



Z

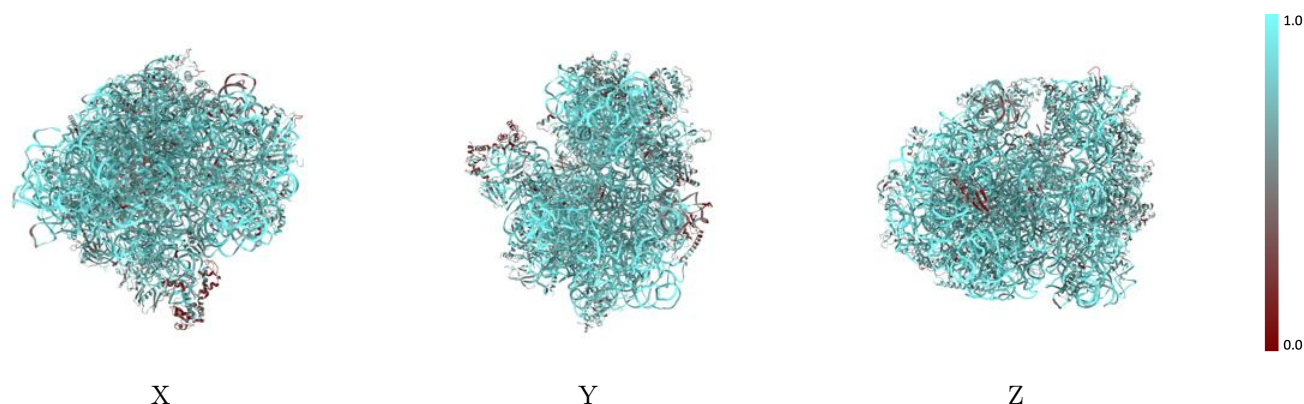
The images above show the 3D surface view of the map at the recommended contour level 0.47 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



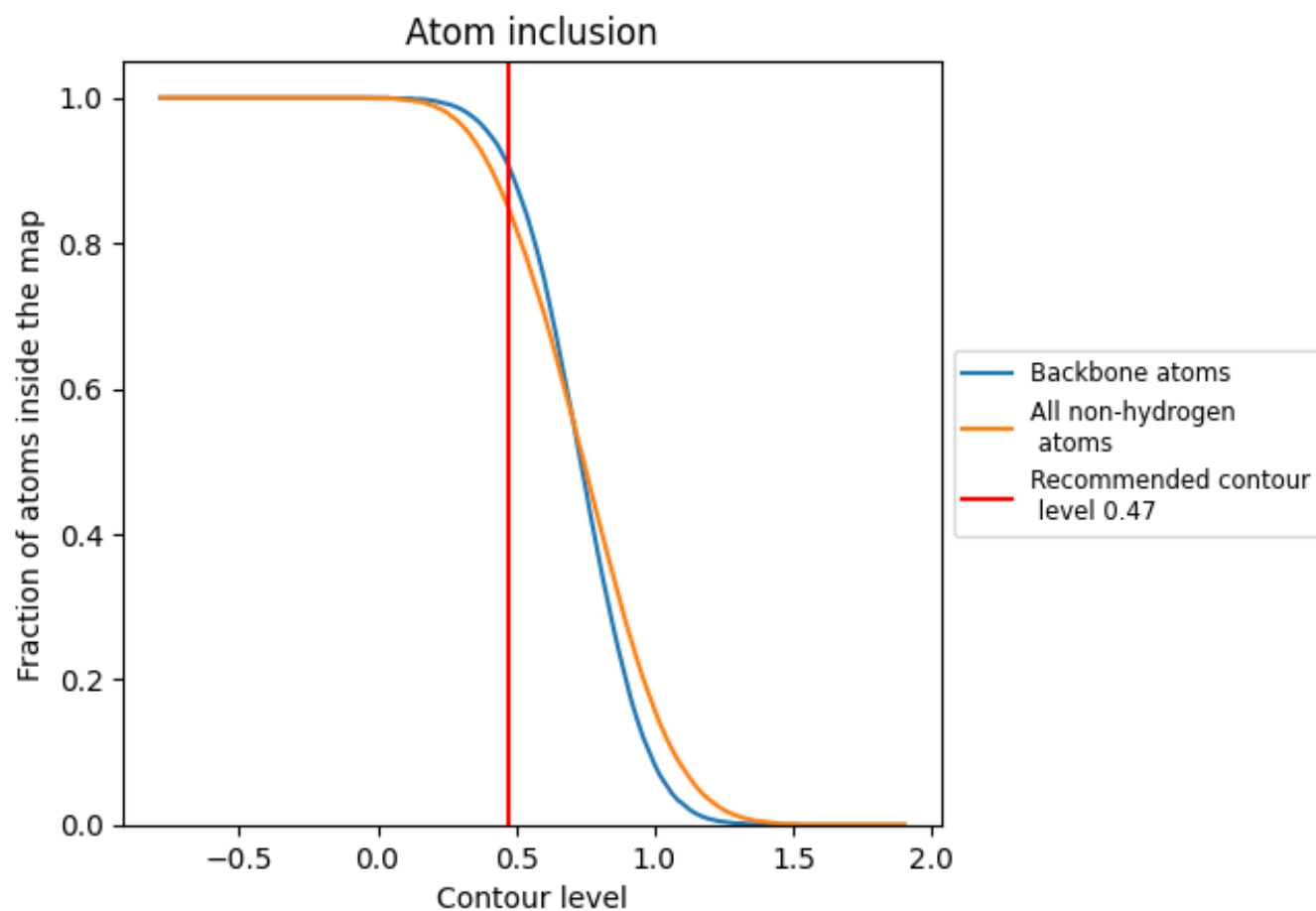
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.47).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 85% 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 (0.47) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8510	 0.2110
0	 0.7840	 0.1880
1	 0.7770	 0.2000
2	 0.7630	 0.1700
3	 0.9360	 0.2240
4	 0.9290	 0.2270
5	 0.9370	 0.2140
7	 0.8860	 0.2070
A	 0.6430	 0.1980
B	 0.6500	 0.1880
C	 0.6510	 0.1760
D	 0.6610	 0.1840
E	 0.6170	 0.2090
F	 0.6550	 0.1850
G	 0.6700	 0.1770
H	 0.6790	 0.1690
I	 0.6460	 0.1810
J	 0.6890	 0.1930
K	 0.7160	 0.2000
L	 0.6850	 0.2000
M	 0.7360	 0.1620
N	 0.6840	 0.1980
O	 0.7280	 0.1710
P	 0.6590	 0.1890
Q	 0.6960	 0.1780
R	 0.6400	 0.1800
S	 0.7390	 0.1850
T	 0.6900	 0.1980
a	 0.7540	 0.1940
b	 0.7200	 0.1870
c	 0.7240	 0.2140
d	 0.6880	 0.1920
e	 0.6460	 0.2040
f	 0.3310	 0.1710
g	 0.4420	 0.1380



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Chain	Atom inclusion	Q-score
h	 0.3080	 0.1460
i	 0.7390	 0.1980
j	 0.6880	 0.2040
k	 0.7240	 0.2010
l	 0.7200	 0.2110
m	 0.7310	 0.2010
n	 0.7220	 0.1960
o	 0.6710	 0.1970
p	 0.7530	 0.1730
q	 0.6820	 0.1940
r	 0.7460	 0.1950
s	 0.7550	 0.2250
t	 0.6210	 0.1950
u	 0.7480	 0.1990
v	 0.7480	 0.1930
w	 0.6840	 0.1920
x	 0.6710	 0.2290
y	 0.7560	 0.2130
z	 0.7930	 0.2150