



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 09:00 PM UTC

PDB ID : 5H1S / pdb_00005h1s
EMDB ID : EMD-9572
Title : Structure of the large subunit of the chloro-ribosome
Authors : Ahmed, T.; Yin, Z.; Bhushan, S.
Deposited on : 2016-10-11
Resolution : 3.50 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:

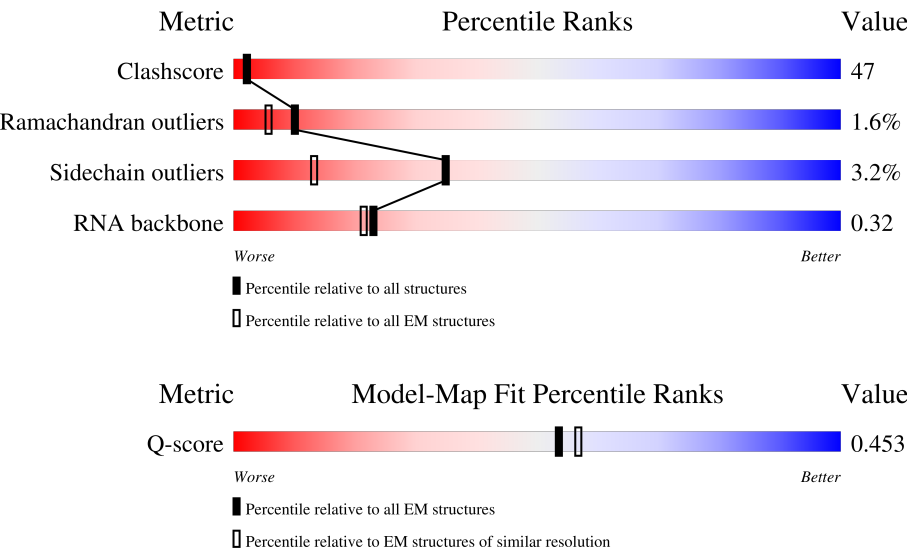
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.50 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.



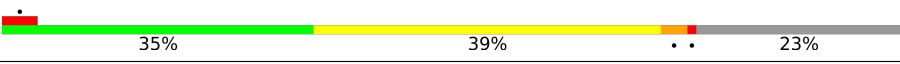
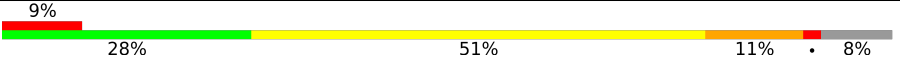
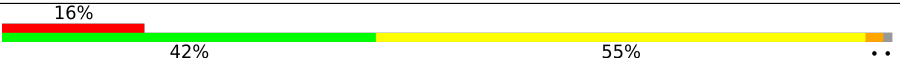
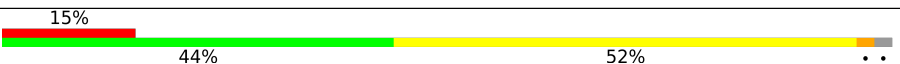
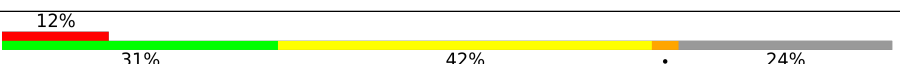
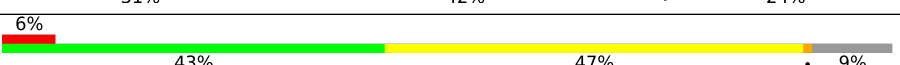
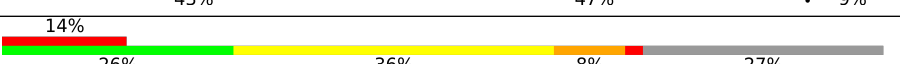
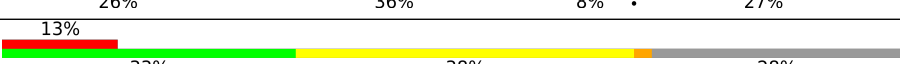
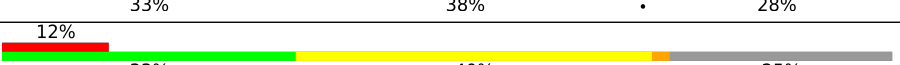
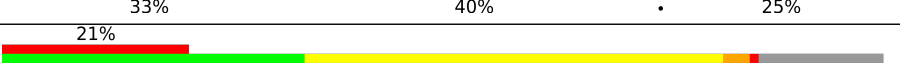
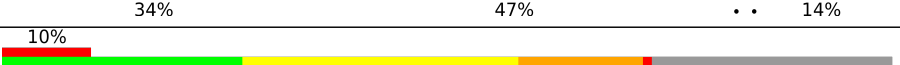
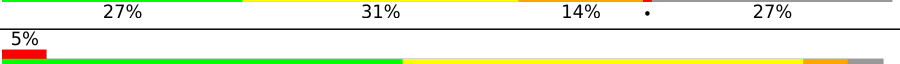
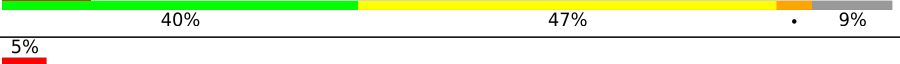
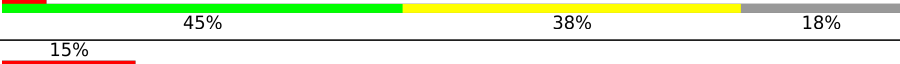
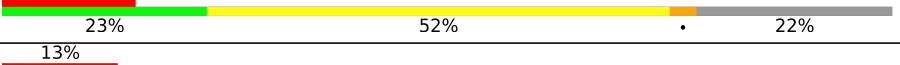
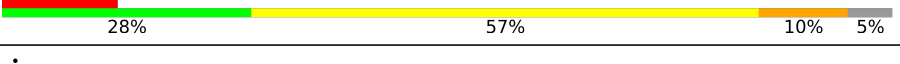
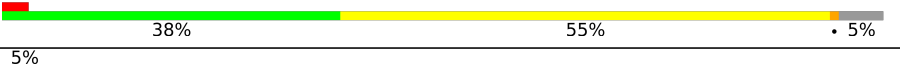
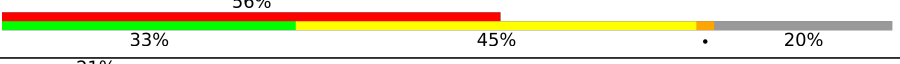
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	A	2810	11% 29%44%27%
2	C	106	6% 9%48%38% ••
3	B	121	12% 43%41% •

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Mol	Chain	Length	Quality of chain
4	L	191	
5	M	121	
6	N	192	
7	O	135	
8	P	116	
9	Q	123	
10	R	156	
11	S	127	
12	T	201	
13	U	199	
14	V	122	
15	W	145	
16	X	137	
17	Y	77	
18	Z	109	
19	E	271	
20	b	56	
21	c	65	
22	d	60	
23	e	73	
24	f	37	
25	F	221	
26	G	243	
27	H	220	
28	I	182	

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Mol	Chain	Length	Quality of chain
29	J	155	26%18%14%66%
30	g	142	8%18%13%70%
31	a	94	39%12%26%60%
32	h	116	18%17%60%

2 Entry composition

There are 32 unique types of molecules in this entry. The entry contains 90825 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 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2799	Total	C	N	O	P	0	0
			60117	26819	11134	19365	2799		

- Molecule 2 is a RNA chain called Spinach chloroplast 4.5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	102	Total	C	N	O	P	0	0
			2187	977	403	705	102		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	117	Total	C	N	O	P	0	0
			2500	1116	452	815	117		

- Molecule 4 is a protein called 50S ribosomal protein L13, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	147	Total	C	N	O	S	0	0
			1184	754	225	202	3		

- Molecule 5 is a protein called 50S ribosomal protein L14, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	121	Total	C	N	O	S	0	0
			942	588	179	170	5		

- Molecule 6 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	177	Total	C	N	O	S	0	0
			1342	836	264	236	6		

- Molecule 7 is a protein called 50S ribosomal protein L16, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	O	134	Total	C	N	O	S	0	0
			1067	672	217	173	5		

- Molecule 8 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	P	116	Total	C	N	O	S	0	0
			944	592	193	155	4		

- Molecule 9 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Q	120	Total	C	N	O	S	0	0
			947	589	183	170	5		

- Molecule 10 is a protein called 50S ribosomal protein L19, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	R	118	Total	C	N	O	S	0	0
			953	610	186	156	1		

- Molecule 11 is a protein called 50S ribosomal protein L20, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	S	115	Total	C	N	O	S	0	0
			996	633	208	153	2		

- Molecule 12 is a protein called 50S ribosomal protein L21, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	T	147	Total	C	N	O	0	0
			1171	759	202	210		

- Molecule 13 is a protein called 50S ribosomal protein L22, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	U	144	Total	C	N	O	S	0	0
			1149	731	210	200	8		

- Molecule 14 is a protein called 50S ribosomal protein L23, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	V	92	Total	C	N	O	S	0	0
			740	477	129	132	2		

- Molecule 15 is a protein called 50S ribosomal protein L24, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	W	124	Total	C	N	O	S	0	0
			993	624	187	180	2		

- Molecule 16 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	X	100	Total	C	N	O	S	0	0
			810	511	159	140			

- Molecule 17 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Y	74	Total	C	N	O	S	0	0
			605	385	121	98	1		

- Molecule 18 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Z	90	Total	C	N	O	S	0	0
			754	470	150	131	3		

- Molecule 19 is a protein called 50S ribosomal protein L2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	E	247	Total	C	N	O	S	0	0
			1904	1181	390	327	6		

- Molecule 20 is a protein called 50S ribosomal protein L32, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	b	46	Total	C	N	O	S	0	0
			378	250	70	58			

- Molecule 21 is a protein called 50S ribosomal protein L33, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	c	51	Total	C	N	O	S	0	0
			415	258	83	70	4		

- Molecule 22 is a protein called 50S ribosomal protein L34, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	d	57	Total	C	N	O	S	0	0
			445	268	103	71	3		

- Molecule 23 is a protein called 50S ribosomal protein L35, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	e	69	Total	C	N	O	S	0	0
			563	353	119	90	1		

- Molecule 24 is a protein called 50S ribosomal protein L36, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	f	37	Total	C	N	O	S	0	0
			304	186	70	44	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	F	212	Total	C	N	O	S	0	0
			1620	1025	295	289	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	G	210	Total	C	N	O	S	0	0
			1655	1052	308	292	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	H	175	Total	C	N	O	S	0	0
			1351	862	233	248	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	I	173	Total	C	N	O	S	0	0
			1353	855	249	245	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	J	53	Total	C	N	O	S	0	0
			423	280	74	68	1		

- Molecule 30 is a protein called 50S ribosomal protein 5 alpha, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	g	43	Total	C	N	O	S	0	0
			345	218	65	59	3		

- Molecule 31 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	38	Total	C	N	O	S	0	0
			300	187	49	62	2		

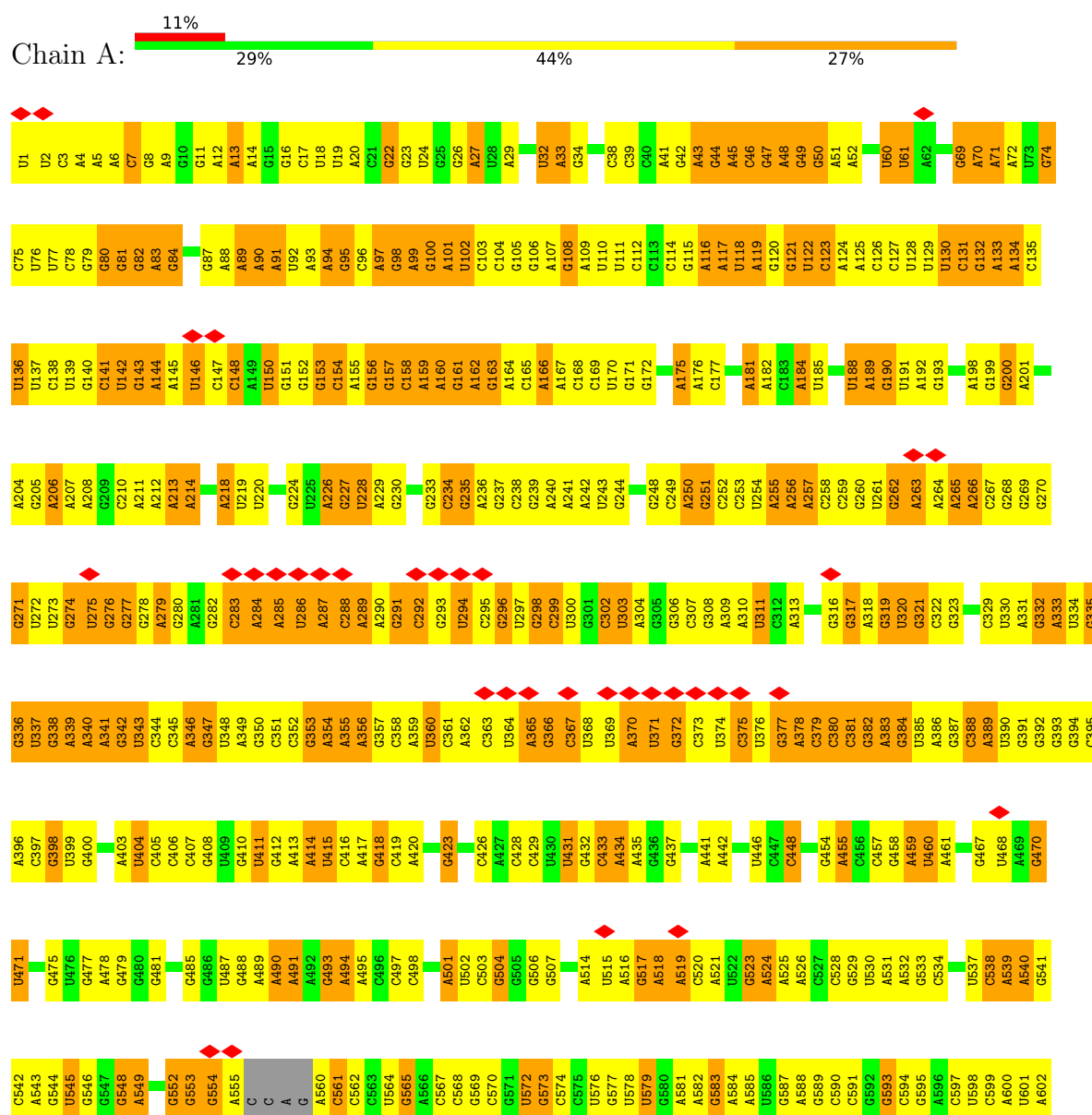
- Molecule 32 is a protein called 50S ribosomal protein 6, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	h	46	Total	C	N	O	S	0	0
			368	237	71	59	1		

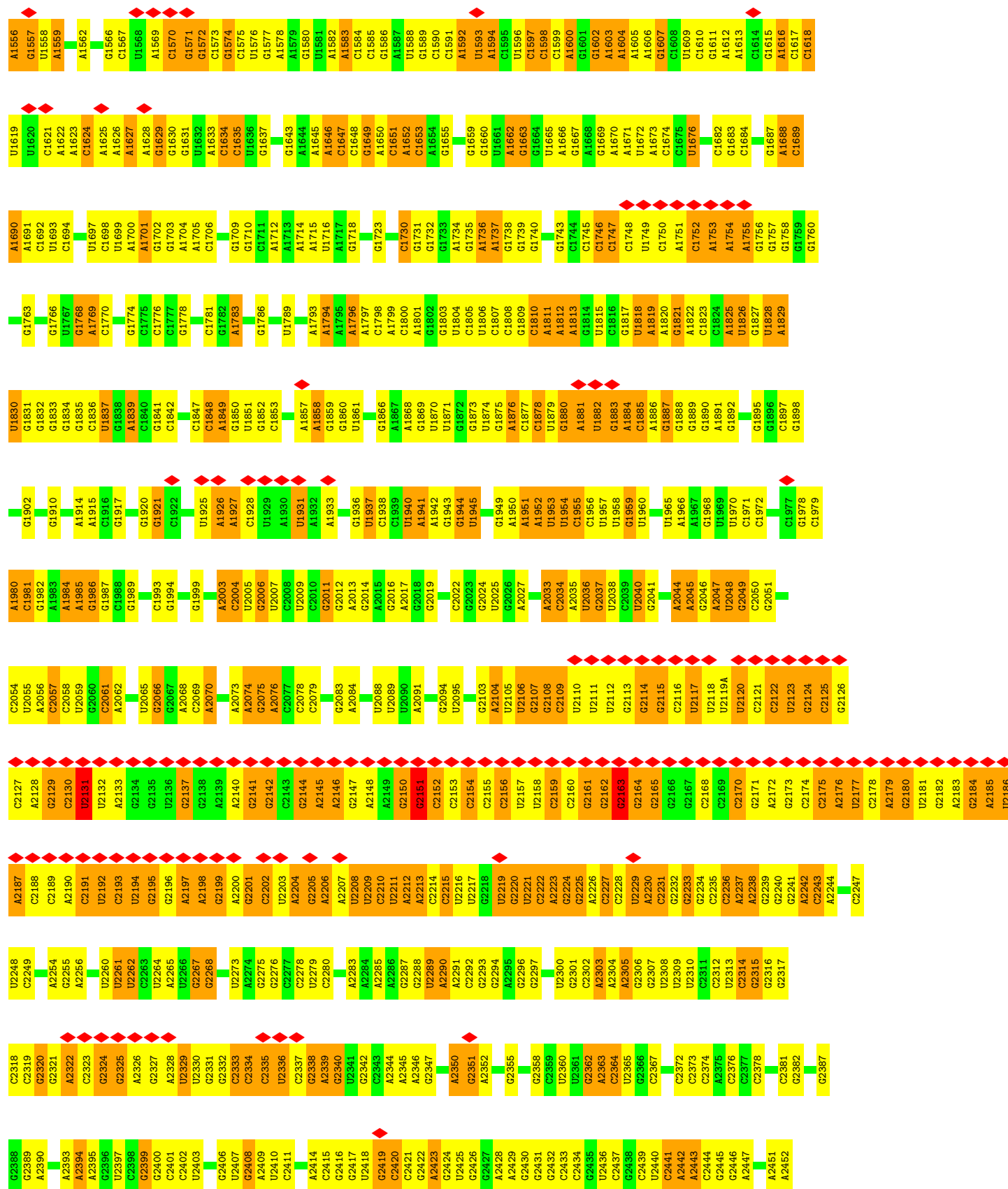
3 Residue-property plots

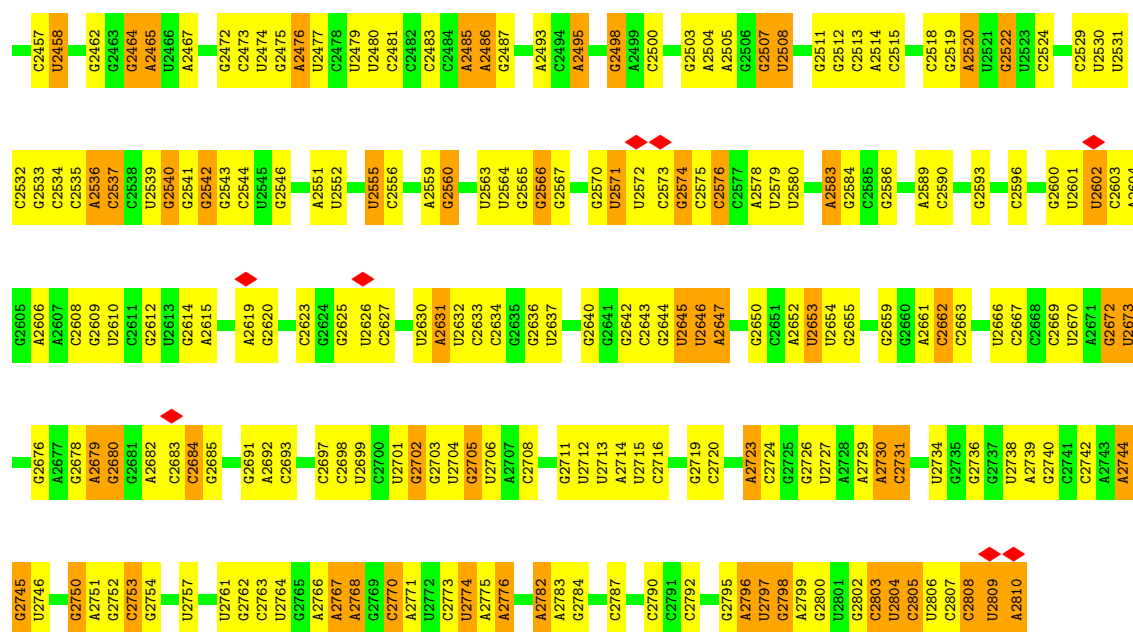
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 23S rRNA

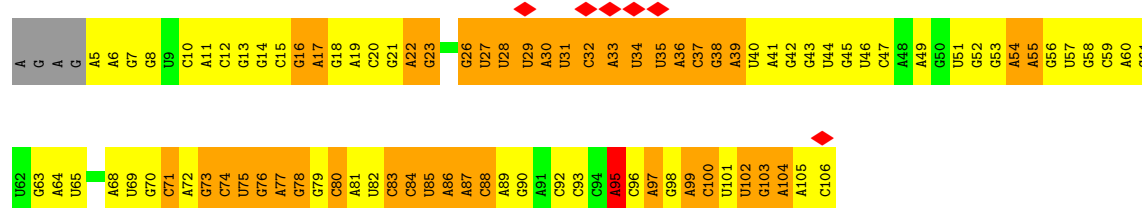


A1496	G1428	C1338	A1267	U1193	C1130	G1070	A1007	U942	U880	U814	G734	U865	G603
A1497	C1429	C1341	A1268	G1194	A1131	C1071	A1008	C943	U881	A815	U735	U666	G604
G1498	C1430	C1342	G1269	U1195	C1132	A1072	A1009	C944	C882	G816	G736	G667	C805
G1499	C1431	A1196	G1270	A1196	U1133	G1073	C1010	A945	C883	C817	G737	U668	A606
U1500	U1432	A1343	G1271	A1197	U1134	A1074	C1011	A946	G884	G820	A738	C669	G607
G1501	U1433	G1344	A1272	A1198	U1135	G1075	G1012	A947	G885	U821	G739	U670	U608
A1502	G1434	G1345	G1273	A1199	A1136	A1076	G1013	U948	U886	U822	G740	C671	G609
C1503	U1435	U1346	A1274	A1200	C1137	A1078	G1016	U949	G887	U823	U741	U672	G610
C1504	U1436	U1347	A1275	A1201	G1138	G1079	G1017	A950	C888	U824	C747	G679	G611
C1505	G1437	G1349	U1276	A1202	A1139	C1080	A1018	A951	G889	C825	G748	A681	U612
U1506	G1438	U1350	G1277	C1203	C1141	A1082	C1020	A952	G890	G829	G749	A682	G614
U1507	G1443	C1351	U1278	A1204	G1142	G1083	U1019	G953	G891	A830	A750	C683	G615
U	A1444	G1352	G1281	G1207	C1143	A1084	A1022	G954	C892	A831	U758	G685	U617
U	A1448	A1353	U1282	U1208	U1144	G1085	C1023	G955	C893	A832	G759	A686	A618
U	C1449	U1361	U1283	U1209	C1145	A1086	A1024	U956	G894	A833	A760	A687	A619
U	G1450	G1362	U1284	A1210	U1146	G1087	G1025	U957	C895	G836	G762	C688	G620
U	G1451	C1366	G1287	G1211	U1147	U1088	A1028	A959	G896	U837	A763	C689	G621
C	G1452	U1288	U1220	U1219	G1150	U1089	A1029	A960	A897	U838	A764	U690	A622
A	G1454	A1289	U1221	U1220	G1153	U1090	G1030	G961	G898	A840	G765	G691	A623
G1515	G1457	A1290	U1224	U1224	A1154	G1091	C1031	G962	A899	G841	G766	G692	A624
G1516	C1458	C1291	G1225	U1226	A1155	C1092	C1032	U963	G900	G842	G767	G693	C625
G1517	U1459	G1292	U1226	U1227	G1156	C1093	C1033	G964	C901	G843	G768	G694	C626
U1518	A1460	C1293	U1227	U1227	A1157	C1094	C1034	G965	G902	G844	G769	G695	C627
A1519	G1461	A1294	G1231	G1231	U1158	U1094	U1035	G966	G903	G845	G770	U696	A628
A1520	U1462	A1295	A1232	A1232	G1159	G1095	A1036	G967	G904	G846	G771	C697	C629
A1522	U1463	C1296	G1233	G1233	A1160	U1096	A1037	G968	U904	G850	G772	C698	C630
A1523	U1464	A1298	A1234	A1234	A1161	G1097	A1038	G969	A905	U851	A773	A700	G631
A1524	A1465	U1299	A1235	A1235	C1162	A1098	A1039	G970	C906	U852	A774	A701	G632
G1524	G1466	U1306	A1236	A1236	G1163	A1099	U1040	G971	C907	G853	G781	C702	A633
G1525	C1467	G1307	G1237	G1237	U1164	A1098	G1041	G972	C907	G854	G782	C703	G634
G1526	C1468	A1308	G1238	G1238	G1165	G1099	A1042	G973	A908	A854	G783	A704	C635
G1527	G1469	U1309	G1239	G1239	U1166	C1100	C1043	A975	A909	C855	A785	A705	C636
U1528	A1470	A1308	G1240	G1240	C1167	A1101	G1044	G976	A910	U856	G786	G706	U637
A1529	C1397	C1310	U1241	U1241	U1168	A1102	G1045	G977	U911	G857	G787	G712	A639
G1530	G1398	A1169	A1242	G1242	U1170	C1103	U1047	A978	C912	G858	G788	G713	G640
A1531	U1399	G1171	U1245	U1245	C1172	C1104	C1048	U979	G913	A859	G789	G714	C641
G1532	U1400	C1172	G1246	G1246	U1173	A1105	A1049	G980	A914	C860	G790	G715	G642
A1533	G1401	G1174	A1247	A1247	G1175	C1106	U1051	G981	G915	A861	G791	A716	A643
A1534	U1404	U1175	G1248	G1248	U1176	C1107	G1052	G982	C917	U862	A792	A717	A644
A1535	C1404	C1317	G1251	G1251	U1177	C1108	A1053	G983	A918	C863	G793	G718	A645
U1536	A1405	C1318	C1252	C1252	U1178	C1109	U1054	G984	A919	U864	A794	G719	G648
U1537	C1406	G1319	G1253	G1253	U1179	U1109	A1055	U986	A920	A865	U795	C719	A649
C1540	A1408	A1321	U1254	U1254	G1181	U1110	A1056	A987	C921	G866	G721	U720	G650
U1541	A1413	A1323	U1255	U1255	G1182	G1111	A1057	A988	U922	G867	G722	G721	U651
C1542	A1414	G1331	G1256	G1256	A1182	C1112	U1060	G989	C923	U870	G723	G724	C652
G1543	U1417	G1332	A1258	A1258	U1183	A1113	G1061	C993	U924	A871	G724	G725	U653
G1544	U1418	U1333	G1259	G1259	C1184	A1114	G1062	A994	A927	G803	G726	U725	U654
C1547	U1418	U1334	G1260	G1260	U1185	A1115	U1063	G997	U928	A804	A727	G726	A658
U1548	C1425	U1335	A1261	A1261	G1187	A1116	G1065	U998	A929	G805	G727	G727	G659
G1545	U1426	C1336	A1262	A1262	U1188	G1117	G1066	G1000	A932	C806	A728	A728	G660
U1549	G1493	U1337	C1264	C1264	U1189	U1118	U1069	G999	G933	C807	G729	G729	G661
G1551	C1494	U1337	C1264	C1264	G1189	U1119	U1069	G1001	A934	A811	A730	A730	C662
U1552	G1495	U1337	C1264	C1264	A1192	C1120	U1069	G1002	U935	G812	C731	C731	A664
C1554						G1121		G1003	A936	C813	A732	A732	
G1555						U1122		G1004	C941		A733	A733	

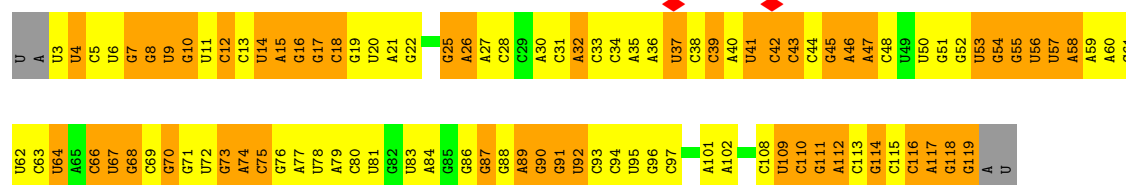




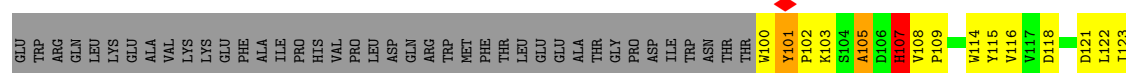
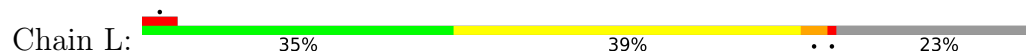
- Molecule 2: Spinach chloroplast 4.5S rRNA

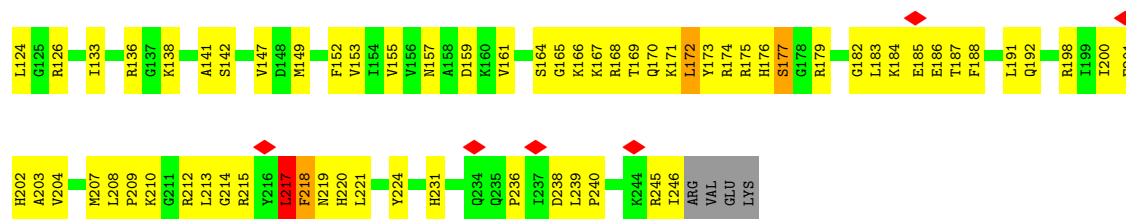


- Molecule 3: 5S rRNA

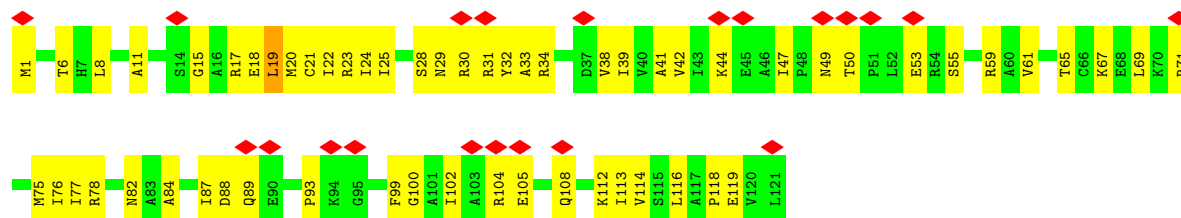


- Molecule 4: 50S ribosomal protein L13, chloroplastic

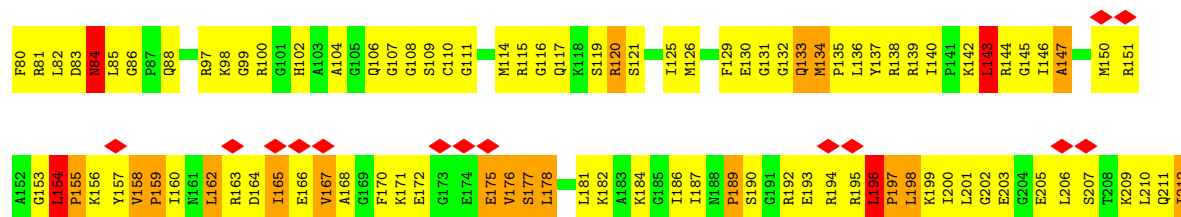




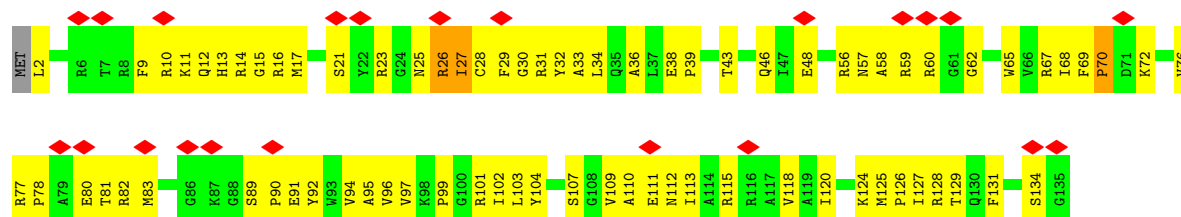
• Molecule 5: 50S ribosomal protein L14, chloroplastic



• Molecule 6: 50S ribosomal protein L15

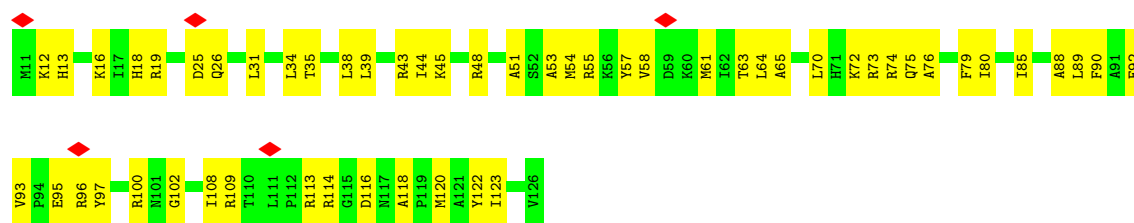


• Molecule 7: 50S ribosomal protein L16, chloroplastic

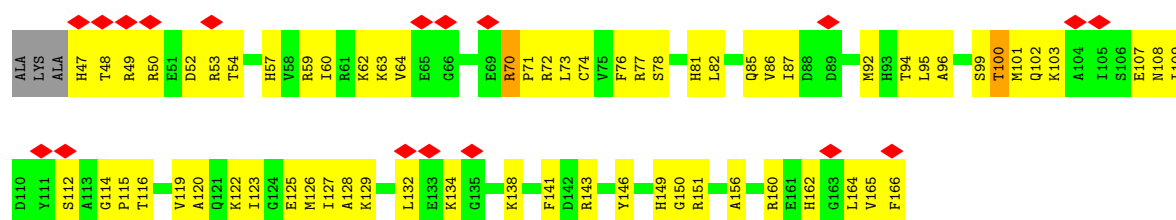
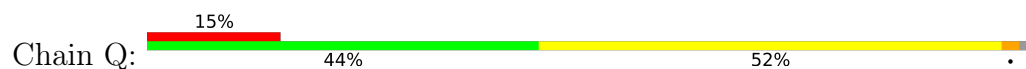


• Molecule 8: 50S ribosomal protein L17

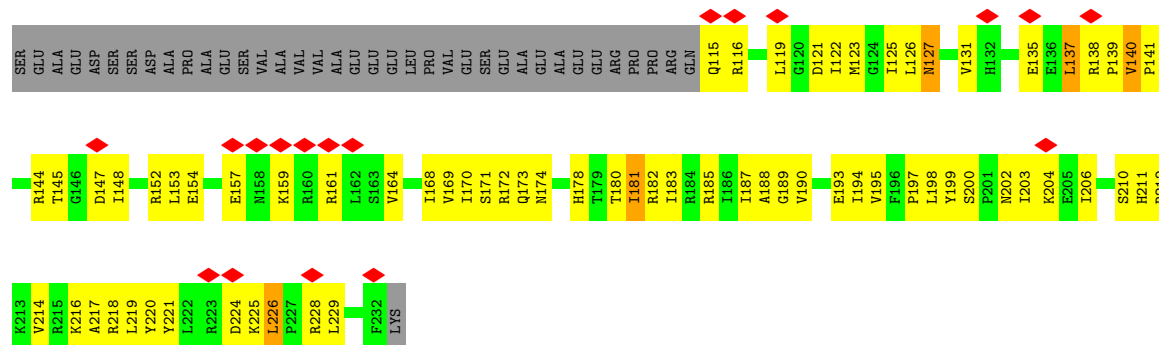




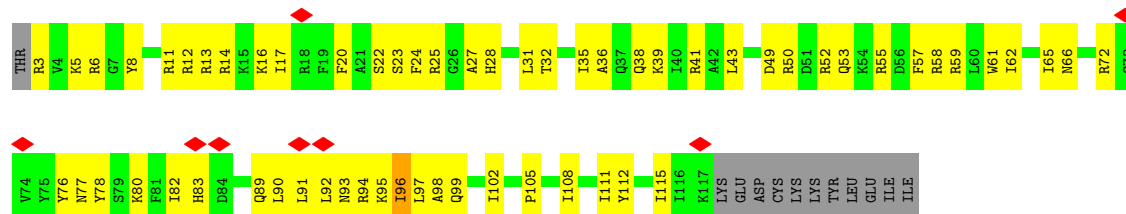
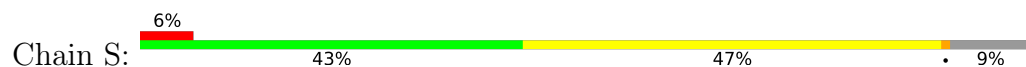
- Molecule 9: 50S ribosomal protein L18



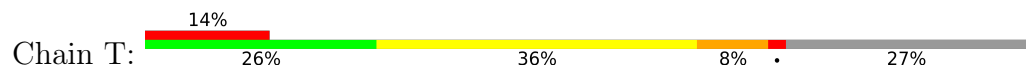
- Molecule 10: 50S ribosomal protein L19, chloroplastic

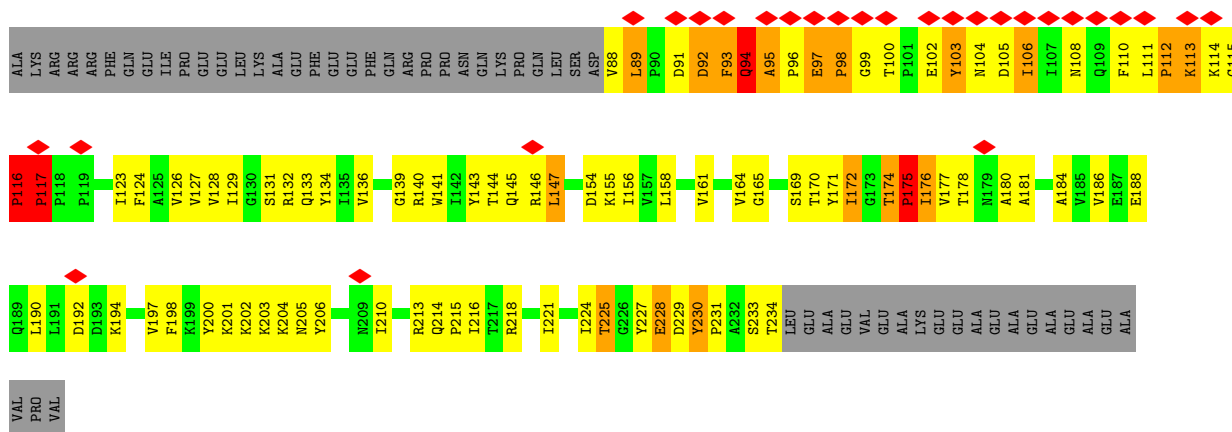


- Molecule 11: 50S ribosomal protein L20, chloroplastic

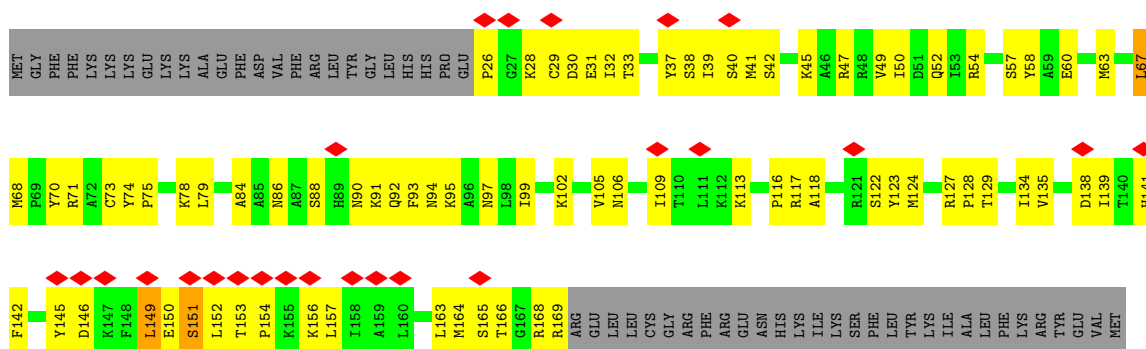


- Molecule 12: 50S ribosomal protein L21, chloroplastic

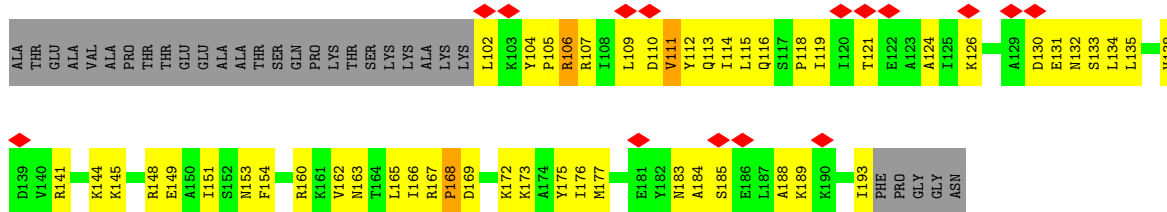




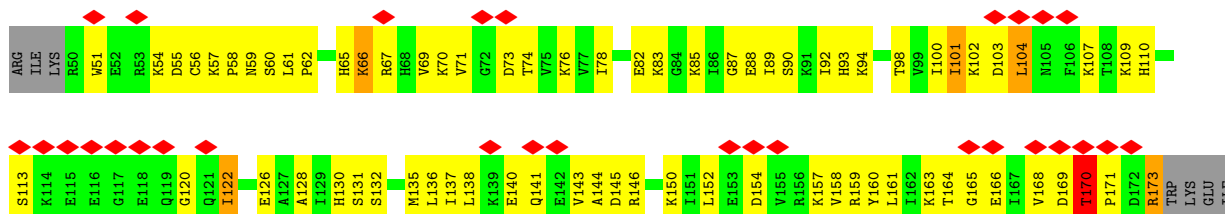
- Molecule 13: 50S ribosomal protein L22, chloroplastic



- Molecule 14: 50S ribosomal protein L23, chloroplastic



- Molecule 15: 50S ribosomal protein L24, chloroplastic



GLN
ASN
LYS
LYS
GLU
SER
GLU
THR
ALA
VAL
ALA
VAL
ALA
ALA

• Molecule 16: 50S ribosomal protein L27

Chain X: 10% 27% 31% 14% 27%

ALA HIS LYS LYS GLY ALA GLY SER
T66 K67 N68 G69 R70 D71 S72
G73 G74 G75 R76 L77 G78
V79 K80 K81 Q82 Y82
Q85 V86 A87 LYS
I93 I94
R97 G98 F101 H102
K111 D112
D120 G121 L122 V123 K124 F125
E126 K127 Y128 G129 P130
D131 K132 K133 K134 V135 S136 V137

Y138 P139 R140 I141 I142 Q143 P144 E145 N146 P147 N148
A152 P153 K154 R155 E156 N157 F158 R159 L160 Q161 R162 E163 K164
K165 LYS
ALA ARG ARG GLU TYR PHE GLN PRO
GLN LEU ILE LEU
ALA SER ALA ALA THR ASP
ASN ALA ASP GLU SER VAL CYS

• Molecule 17: 50S ribosomal protein L28

Chain Y: 5% 45% 45% 5%

R72 R73 I74 C75 T78 G79 K80 K81 S82 N83 R87
N92 R93 K94 T95 R97 L98 Q99 F100 V101 L102 E103
K106 R107 R115 F116 V117
R120 L121 S122 T123 K124 A125 L126 K127
T128 I129 E130 K131 N132 G133
V137 A138 G142 I143 D144 L145 ARG LYS GLU

R72 R73 I74 C75 T78 G79 K80 K81 S82 N83 R87
N92 R93 K94 T95 R97 L98 Q99 F100 V101 L102 E103
K106 R107 R115 F116 V117
R120 L121 S122 T123 K124 A125 L126 K127
T128 I129 E130 K131 N132 G133
V137 A138 G142 I143 D144 L145 ARG LYS GLU

• Molecule 18: 50S ribosomal protein L29

Chain Z: 15% 36% 40% 6% 17%

LYS LYS D63 E64 L65 L68 T72 W73 E74 Q75 L76 W77 E78 E79 L83
E86 L87 F88 M89 L90 R91 L92 Q93 S95 A96 R97 E98 N99 F100 K101 P102
S103 D104 F105 G106 M107 M108 R109 K110 R111 M115 L116 T117 V118
R119 R120 R121 R122 E123 I124 E125 Q126 G127

LYS LYS D63 E64 L65 L68 T72 W73 E74 Q75 L76 W77 E78 E79 L83
E86 L87 F88 M89 L90 R91 L92 Q93 S95 A96 R97 E98 N99 F100 K101 P102
S103 D104 F105 G106 M107 M108 R109 K110 R111 M115 L116 T117 V118
R119 R120 R121 R122 E123 I124 E125 Q126 G127

• Molecule 19: 50S ribosomal protein L2, chloroplastic

Chain E: 10% 40% 47% 9%

ALA ILE HIS LEU TYR LYS THR SER THR SER SER THR ARG ASN GLY VAL GLN VAL LYS SER
N23 P24 R25 N26 T29 S30 G31 Q32 C35 G36 K37 G38 R39 N40 A41 R42 G43 I44 T45 T46 A47
R48 H49 R50 K55 R56 L57 Y58 R59 K60 I61 D62 F63 R64 R65 N66

ALA ILE HIS LEU TYR LYS THR SER THR SER SER THR ARG ASN GLY VAL GLN VAL LYS SER
N23 P24 R25 N26 T29 S30 G31 Q32 C35 G36 K37 G38 R39 N40 A41 R42 G43 I44 T45 T46 A47
R48 H49 R50 K55 R56 L57 Y58 R59 K60 I61 D62 F63 R64 R65 N66

E67 K68 D69 V75 T76 I77 D80 R83 N84 A85 Y86 I87 C88 L89 I90 H91 G95 E96 R97 R98
H102 P103 A106 V113 S114 G115 T116 E117 K121 M122 G123 N124 A125 L126 P127 T129
T129 M130 M131 P132 L133 G134 T135 A136 I137 H138 M139 I140 F141 E141 I142 T143 L144

E67 K68 D69 V75 T76 I77 D80 R83 N84 A85 Y86 I87 C88 L89 I90 H91 G95 E96 R97 R98
H102 P103 A106 V113 S114 G115 T116 E117 K121 M122 G123 N124 A125 L126 P127 T129
T129 M130 M131 P132 L133 G134 T135 A136 I137 H138 M139 I140 F141 E141 I142 T143 L144

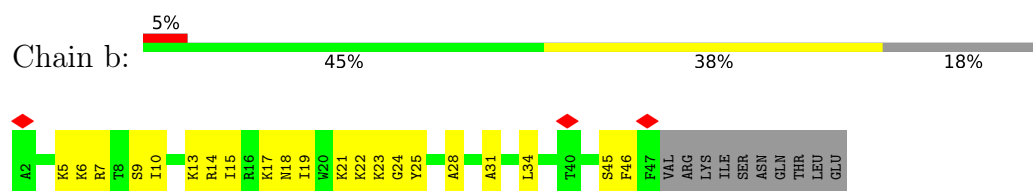
G145 R146 G147 G148 Q149 A151 R152 A153 P154 G155 A156 V157 L160 I161 A162 K166 T169
L172 P173 S174 G175 E176 L179 I180 S181 K182 M183 C184 T187 Q190 V191 M197 Q198
K199 R200 L201 G202 R203 A204 G205 S206 W209 L210 G211 R212 K213 P214 V215 V216 T217

G145 R146 G147 G148 Q149 A151 R152 A153 P154 G155 A156 V157 L160 I161 A162 K166 T169
L172 P173 S174 G175 E176 L179 I180 S181 K182 M183 C184 T187 Q190 V191 M197 Q198
K199 R200 L201 G202 R203 A204 G205 S206 W209 L210 G211 R212 K213 P214 V215 V216 T217

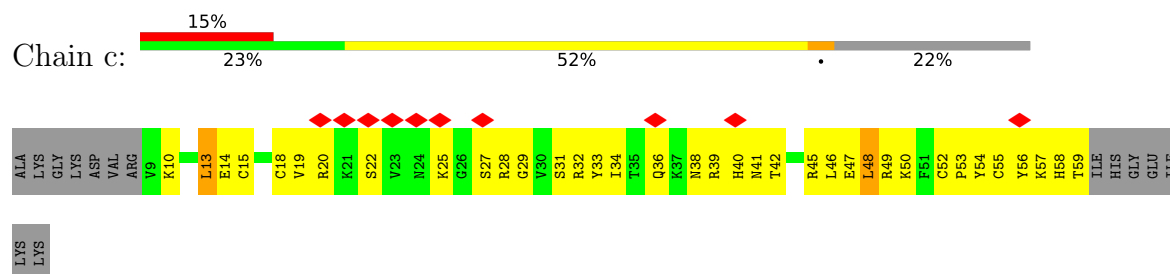
G218 V219 M220 M221 N222 P223 V224 H226 H228 G229 E232 P236 G238 R239 T243 T244
W246 G247 Y248 R253 R256 K257 R258 M259 K260 Y261 S262 D263 N264 F265 I266 I267
R268 R269 ARG SER LYS

G218 V219 M220 M221 N222 P223 V224 H226 H228 G229 E232 P236 G238 R239 T243 T244
W246 G247 Y248 R253 R256 K257 R258 M259 K260 Y261 S262 D263 N264 F265 I266 I267
R268 R269 ARG SER LYS

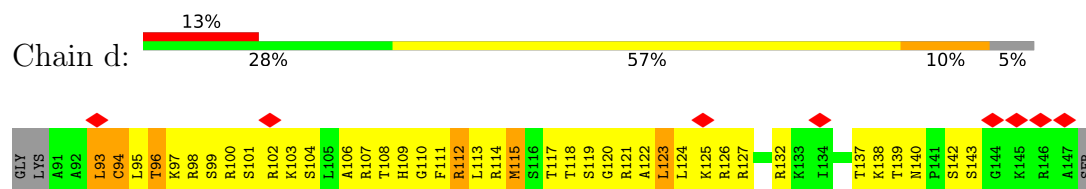
- Molecule 20: 50S ribosomal protein L32, chloroplastic



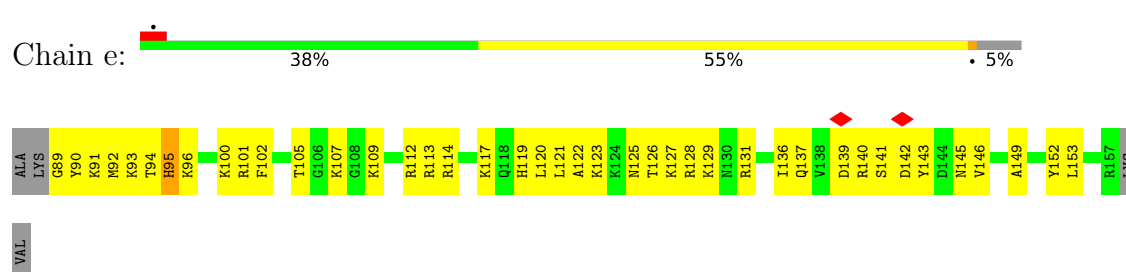
- Molecule 21: 50S ribosomal protein L33, chloroplastic



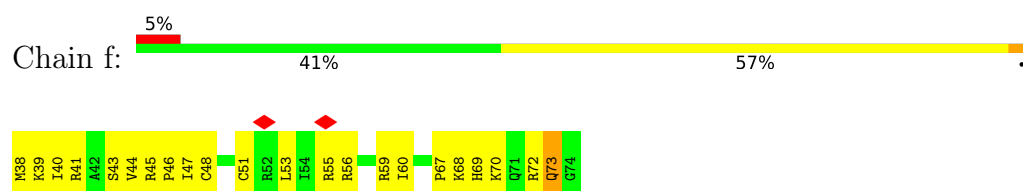
- Molecule 22: 50S ribosomal protein L34, chloroplastic



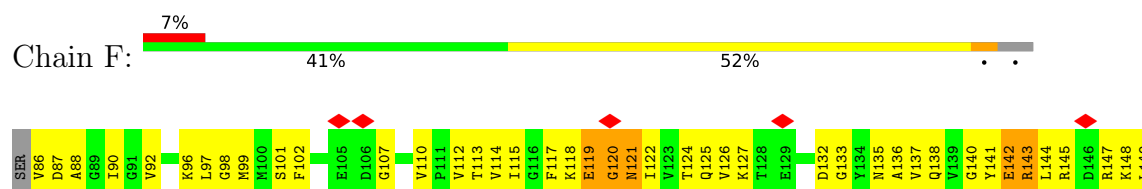
- Molecule 23: 50S ribosomal protein L35, chloroplastic

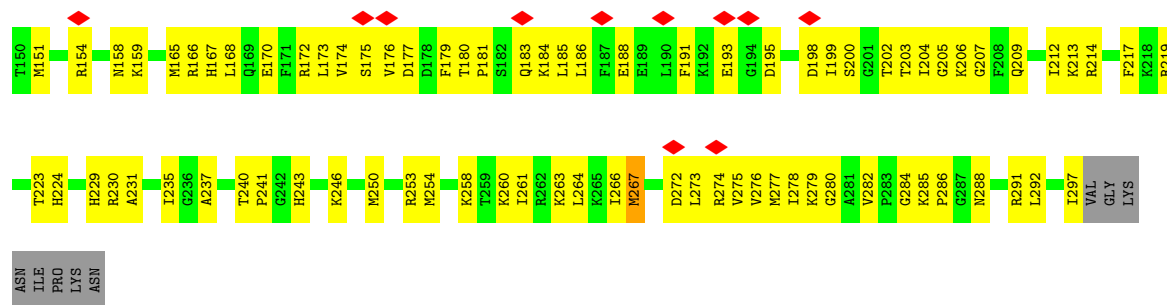


- Molecule 24: 50S ribosomal protein L36, chloroplastic

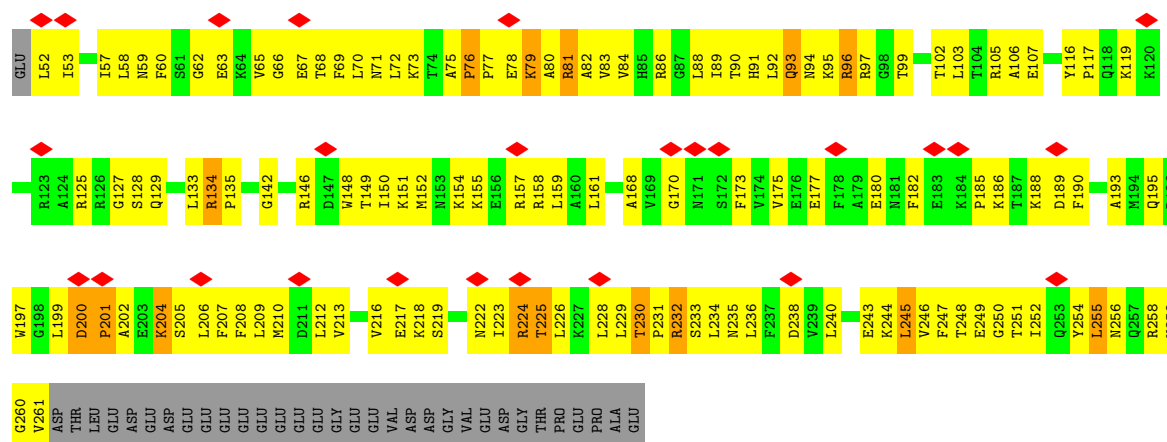


- Molecule 25: 50S ribosomal protein L3

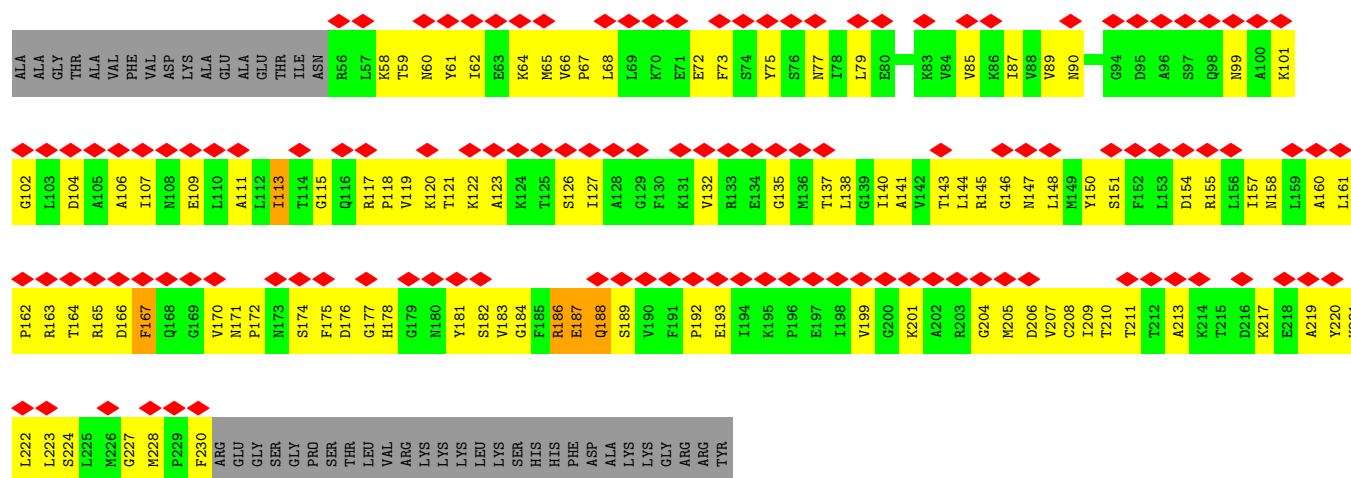




- Molecule 26: 50S ribosomal protein L4, chloroplastic

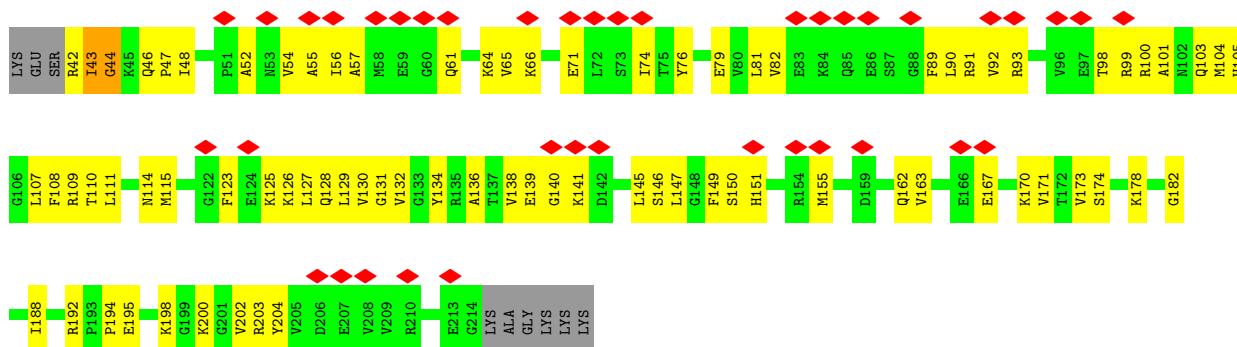


- Molecule 27: 50S ribosomal protein L5, chloroplastic

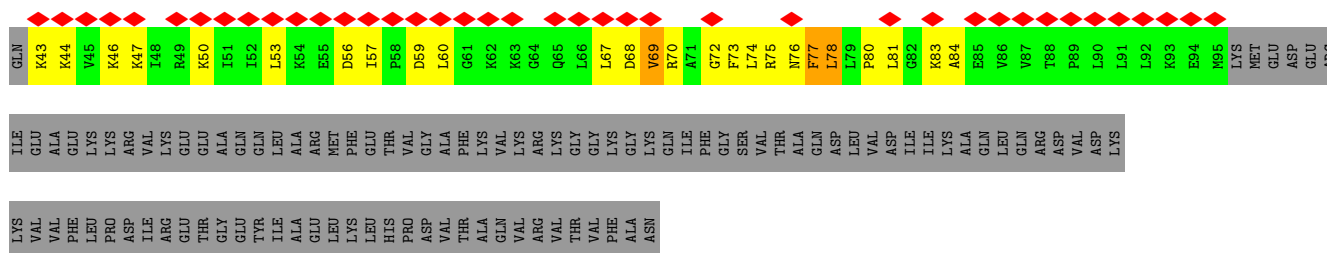


- Molecule 28: 50S ribosomal protein L6

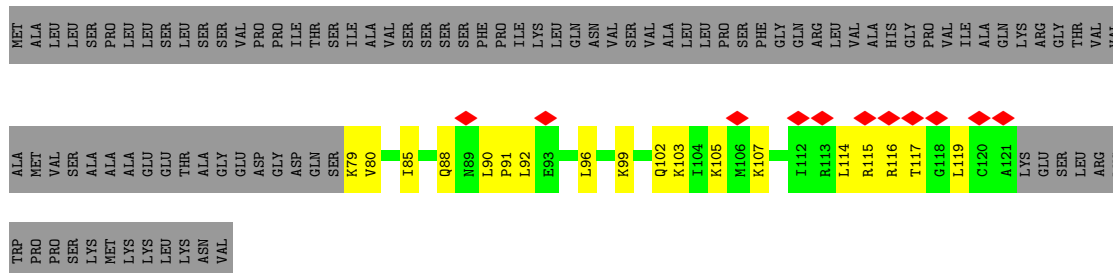




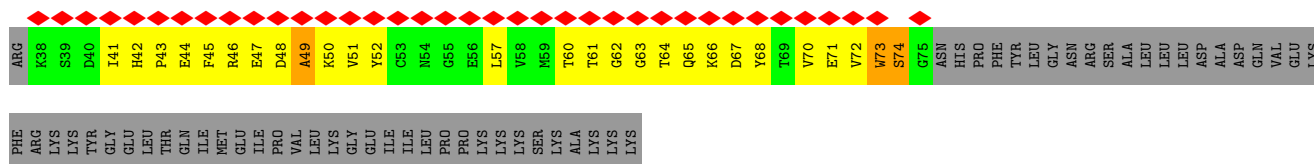
- Molecule 29: 50S ribosomal protein L9



- Molecule 30: 50S ribosomal protein 5 alpha, chloroplastic

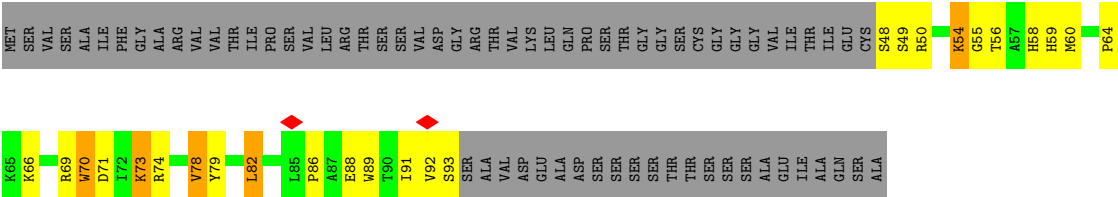


- Molecule 31: 50S ribosomal protein L31



- Molecule 32: 50S ribosomal protein 6, chloroplastic





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	174949	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	26	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	109375	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.928	Depositor
Minimum map value	-0.585	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.132	Depositor
Map size ($\text{\AA}$)	399.36, 399.36, 399.36	wwPDB
Map dimensions	312, 312, 312	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.28, 1.28, 1.28	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	A	0.41	19/67340 (0.0%)	0.49	1/105056 (0.0%)
2	C	1.19	6/2449 (0.2%)	0.60	0/3817
3	B	0.43	0/2796	0.58	0/4357
4	L	0.64	0/1212	0.78	4/1634 (0.2%)
5	M	0.56	0/951	0.68	2/1282 (0.2%)
6	N	0.51	0/1361	1.12	16/1806 (0.9%)
7	O	0.59	1/1089 (0.1%)	0.74	0/1461
8	P	0.62	0/959	0.75	0/1280
9	Q	0.48	0/963	0.70	1/1293 (0.1%)
10	R	0.59	0/967	0.93	2/1300 (0.2%)
11	S	0.72	0/1013	0.91	0/1351
12	T	0.73	0/1199	1.07	14/1633 (0.9%)
13	U	0.60	0/1168	0.88	2/1566 (0.1%)
14	V	0.51	0/749	0.72	0/1006
15	W	0.50	1/1006 (0.1%)	0.87	3/1343 (0.2%)
16	X	0.71	0/825	1.20	12/1099 (1.1%)
17	Y	0.64	0/615	0.83	0/819
18	Z	0.65	1/762 (0.1%)	1.08	8/1012 (0.8%)
19	E	0.61	0/1938	0.89	6/2603 (0.2%)
20	b	0.66	0/387	0.67	0/513
21	c	0.51	0/422	0.89	1/564 (0.2%)
22	d	0.57	0/447	0.91	2/588 (0.3%)
23	e	0.68	0/569	0.87	0/752
24	f	0.63	0/306	0.84	0/403
25	F	0.65	0/1646	0.78	2/2201 (0.1%)
26	G	0.63	0/1687	0.93	8/2271 (0.4%)
27	H	0.32	0/1372	0.61	0/1848
28	I	0.41	0/1374	0.64	1/1849 (0.1%)
29	J	0.29	0/427	0.71	1/568 (0.2%)
30	g	0.47	0/345	0.92	0/455
31	a	0.31	0/306	0.83	1/413 (0.2%)
32	h	0.67	0/382	1.03	6/520 (1.2%)
All	All	0.50	28/99032 (0.0%)	0.60	93/148663 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
9	Q	0	1
10	R	0	1
11	S	0	3
13	U	0	1
19	E	0	3
24	f	0	1
25	F	0	1
26	G	0	2
27	H	0	1
32	h	0	2
All	All	0	16

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	95	A	C6-N1	24.88	1.85	1.35
2	C	95	A	N3-C4	23.03	1.80	1.34
2	C	95	A	C2-N3	21.28	1.76	1.33
2	C	95	A	N1-C2	21.17	1.76	1.34
2	C	95	A	C5-C6	19.24	1.79	1.41

The worst 5 of 93 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	X	131	ASP	N-CA-C	9.62	121.85	111.36
6	N	196	LEU	C-N-CD	-8.82	88.83	125.00
16	X	132	LYS	N-CA-C	8.08	122.97	110.20
16	X	129	GLY	N-CA-C	-8.06	95.90	112.34
16	X	73	LYS	N-CA-C	7.98	120.06	111.36

There are no chirality outliers.

5 of 16 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	Q	70	ARG	Peptide
10	R	190	VAL	Peptide
11	S	24	PHE	Peptide
11	S	82	ILE	Peptide

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Mol	Chain	Res	Type	Group
11	S	96	ILE	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	A	60117	0	30254	4123	0
2	C	2187	0	1099	307	0
3	B	2500	0	1263	332	0
4	L	1184	0	1221	141	0
5	M	942	0	996	53	0
6	N	1342	0	1413	419	0
7	O	1067	0	1121	106	0
8	P	944	0	1004	74	0
9	Q	947	0	966	85	0
10	R	953	0	1044	84	0
11	S	996	0	1060	127	0
12	T	1171	0	1216	230	0
13	U	1149	0	1220	106	0
14	V	740	0	795	103	0
15	W	993	0	1054	133	0
16	X	810	0	847	188	0
17	Y	605	0	652	53	0
18	Z	754	0	804	100	0
19	E	1904	0	1982	224	0
20	b	378	0	413	32	0
21	c	415	0	434	55	0
22	d	445	0	501	72	0
23	e	563	0	621	68	0
24	f	304	0	342	45	0
25	F	1620	0	1699	182	0
26	G	1655	0	1723	244	0
27	H	1351	0	1407	165	0
28	I	1353	0	1416	91	0
29	J	423	0	488	40	0
30	g	345	0	395	30	0
31	a	300	0	279	114	0
32	h	368	0	386	55	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	90825	0	60115	6942	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 47.

The worst 5 of 6942 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:A:2351:G:C4	9:Q:64:VAL:HG21	1.27	1.61
2:C:95:A:C5	2:C:95:A:C6	1.79	1.59
16:X:128:TYR:CB	16:X:134:LYS:CD	1.78	1.58
11:S:91:LEU:CD1	12:T:175:PRO:HB3	1.30	1.55
1:A:274:G:C6	1:A:433:C:C6	1.94	1.54

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	
4	L	145/191 (76%)	120 (83%)	21 (14%)	4 (3%)	4	26
5	M	119/121 (98%)	97 (82%)	22 (18%)	0	100	100
6	N	175/192 (91%)	156 (89%)	6 (3%)	13 (7%)	1	9
7	O	132/135 (98%)	107 (81%)	23 (17%)	2 (2%)	8	37
8	P	114/116 (98%)	96 (84%)	18 (16%)	0	100	100
9	Q	118/123 (96%)	99 (84%)	19 (16%)	0	100	100
10	R	116/156 (74%)	89 (77%)	26 (22%)	1 (1%)	14	47
11	S	113/127 (89%)	91 (80%)	22 (20%)	0	100	100
12	T	145/201 (72%)	108 (74%)	28 (19%)	9 (6%)	1	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	U	142/199 (71%)	117 (82%)	24 (17%)	1 (1%)	18	51
14	V	90/122 (74%)	79 (88%)	9 (10%)	2 (2%)	5	30
15	W	122/145 (84%)	95 (78%)	25 (20%)	2 (2%)	7	36
16	X	98/137 (72%)	87 (89%)	7 (7%)	4 (4%)	2	19
17	Y	72/77 (94%)	61 (85%)	11 (15%)	0	100	100
18	Z	88/109 (81%)	85 (97%)	3 (3%)	0	100	100
19	E	245/271 (90%)	187 (76%)	57 (23%)	1 (0%)	30	62
20	b	44/56 (79%)	35 (80%)	9 (20%)	0	100	100
21	c	49/65 (75%)	34 (69%)	15 (31%)	0	100	100
22	d	55/60 (92%)	47 (86%)	6 (11%)	2 (4%)	2	22
23	e	67/73 (92%)	50 (75%)	16 (24%)	1 (2%)	8	37
24	f	35/37 (95%)	30 (86%)	5 (14%)	0	100	100
25	F	210/221 (95%)	173 (82%)	37 (18%)	0	100	100
26	G	208/243 (86%)	166 (80%)	40 (19%)	2 (1%)	12	44
27	H	173/220 (79%)	145 (84%)	27 (16%)	1 (1%)	21	54
28	I	171/182 (94%)	142 (83%)	27 (16%)	2 (1%)	10	41
29	J	51/155 (33%)	41 (80%)	9 (18%)	1 (2%)	6	32
30	g	41/142 (29%)	36 (88%)	5 (12%)	0	100	100
31	a	36/94 (38%)	26 (72%)	9 (25%)	1 (3%)	4	26
32	h	44/116 (38%)	31 (70%)	12 (27%)	1 (2%)	5	30
All	All	3218/4086 (79%)	2630 (82%)	538 (17%)	50 (2%)	10	36

5 of 50 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	L	107	HIS
6	N	143	LEU
6	N	147	ALA
6	N	154	LEU
6	N	155	PRO

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	
4	L	125/165 (76%)	122 (98%)	3 (2%)	43	64
5	M	101/101 (100%)	98 (97%)	3 (3%)	36	60
6	N	135/144 (94%)	125 (93%)	10 (7%)	13	37
7	O	107/108 (99%)	105 (98%)	2 (2%)	50	68
8	P	96/96 (100%)	96 (100%)	0	100	100
9	Q	99/100 (99%)	99 (100%)	0	100	100
10	R	104/135 (77%)	100 (96%)	4 (4%)	29	55
11	S	102/114 (90%)	102 (100%)	0	100	100
12	T	129/174 (74%)	119 (92%)	10 (8%)	11	36
13	U	126/176 (72%)	124 (98%)	2 (2%)	55	70
14	V	81/103 (79%)	80 (99%)	1 (1%)	63	73
15	W	112/129 (87%)	108 (96%)	4 (4%)	31	57
16	X	85/111 (77%)	72 (85%)	13 (15%)	3	16
17	Y	64/67 (96%)	60 (94%)	4 (6%)	16	42
18	Z	83/97 (86%)	80 (96%)	3 (4%)	31	57
19	E	195/216 (90%)	187 (96%)	8 (4%)	27	53
20	b	39/49 (80%)	39 (100%)	0	100	100
21	c	48/59 (81%)	47 (98%)	1 (2%)	47	66
22	d	47/49 (96%)	44 (94%)	3 (6%)	16	42
23	e	59/62 (95%)	58 (98%)	1 (2%)	53	70
24	f	34/34 (100%)	34 (100%)	0	100	100
25	F	174/182 (96%)	170 (98%)	4 (2%)	44	64
26	G	176/205 (86%)	169 (96%)	7 (4%)	28	54
27	H	148/183 (81%)	145 (98%)	3 (2%)	48	67
28	I	147/154 (96%)	147 (100%)	0	100	100
29	J	47/134 (35%)	46 (98%)	1 (2%)	47	66
30	g	39/121 (32%)	39 (100%)	0	100	100
31	a	33/83 (40%)	32 (97%)	1 (3%)	36	60
32	h	40/96 (42%)	39 (98%)	1 (2%)	42	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2775/3447 (80%)	2686 (97%)	89 (3%)	35 59

5 of 89 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	Z	120	ARG
23	e	153	LEU
19	E	44	ILE
19	E	259	ASN
25	F	186	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 73 such sidechains are listed below:

Mol	Chain	Res	Type
23	e	145	ASN
28	I	105	HIS
25	F	135	ASN
26	G	71	ASN
12	T	94	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2796/2810 (99%)	962 (34%)	106 (3%)
2	C	101/106 (95%)	45 (44%)	4 (3%)
3	B	116/121 (95%)	54 (46%)	5 (4%)
All	All	3013/3037 (99%)	1061 (35%)	115 (3%)

5 of 1061 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	C
1	A	13	A
1	A	22	G
1	A	27	A
1	A	32	U

5 of 115 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1334	U
3	B	7	G
1	A	1828	U
2	C	35	U
1	A	2536	A

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.

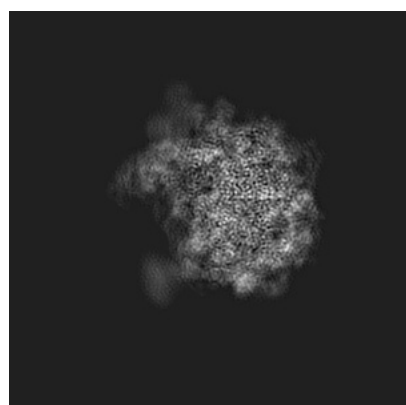
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9572. These allow visual inspection of the internal detail of the map and identification of artifacts.

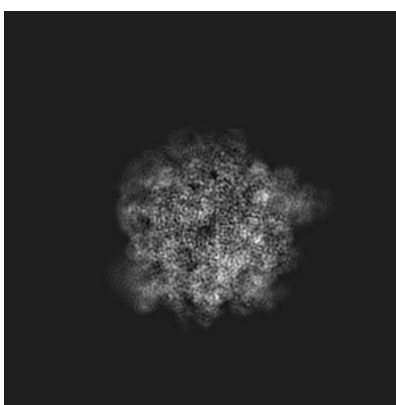
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

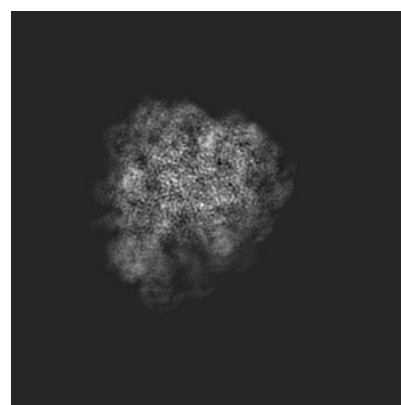
6.1.1 Primary map



X



Y

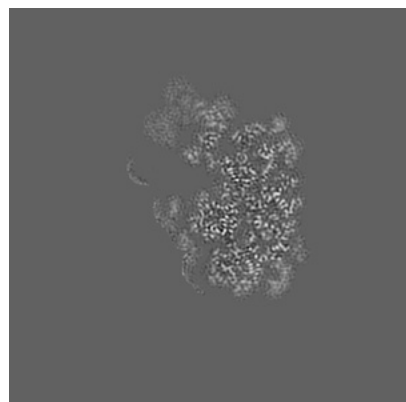


Z

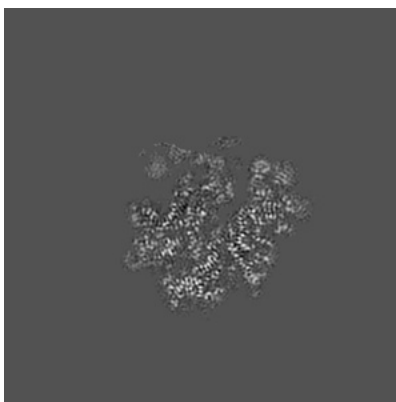
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

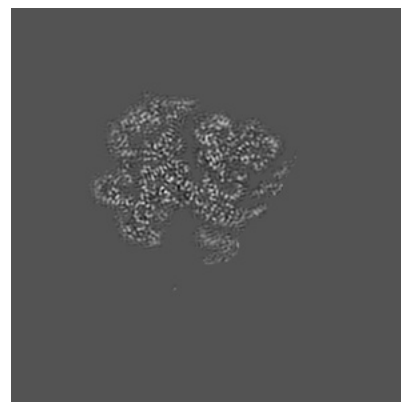
6.2.1 Primary map



X Index: 156



Y Index: 156

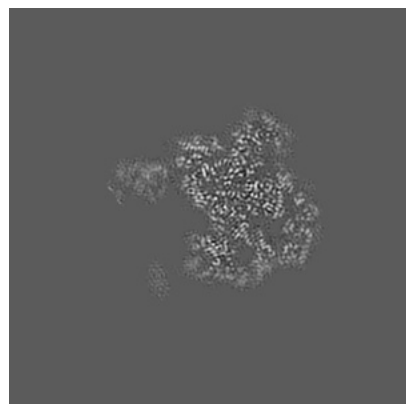


Z Index: 156

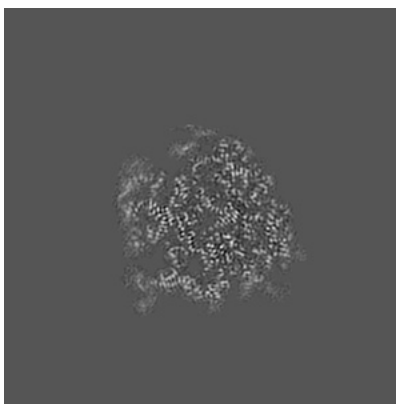
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

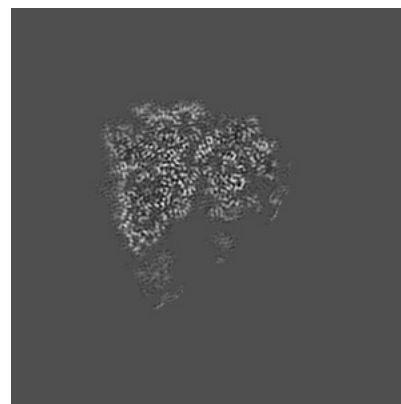
6.3.1 Primary map



X Index: 120



Y Index: 186

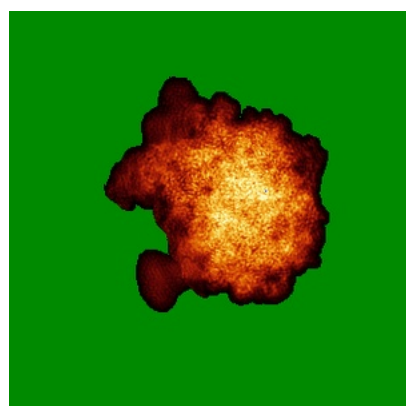


Z Index: 166

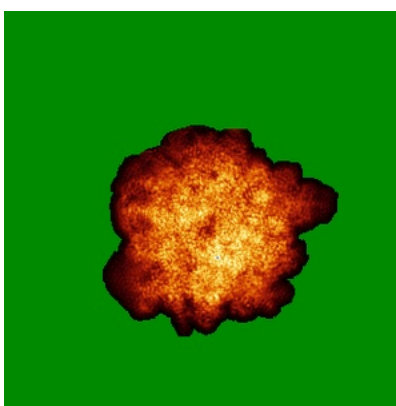
The images above show the largest variance slices of the map in three orthogonal directions.

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

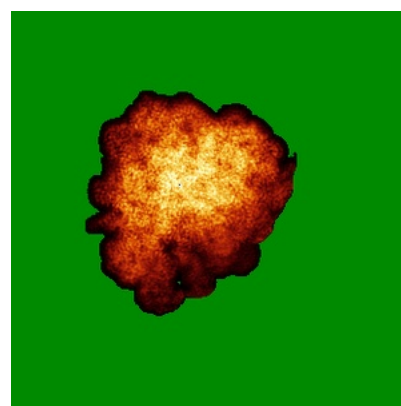
6.4.1 Primary map



X



Y

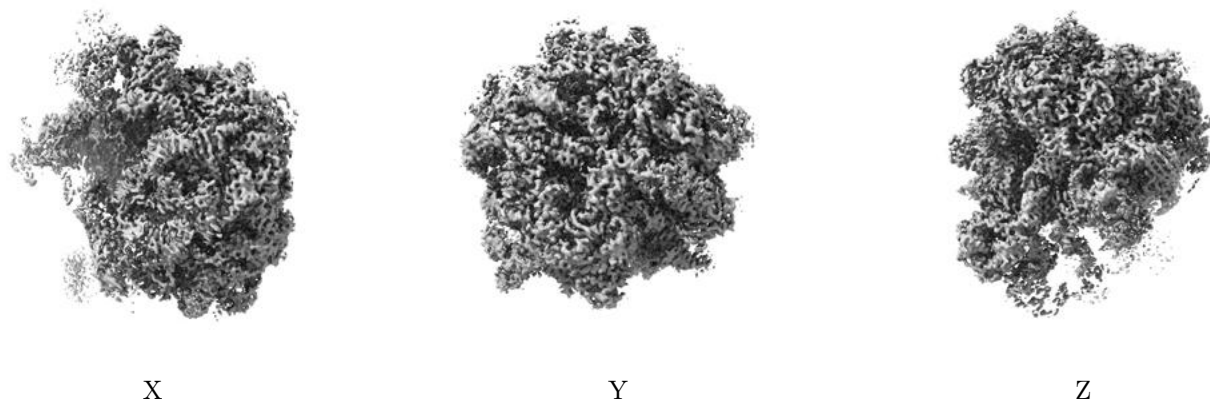


Z

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

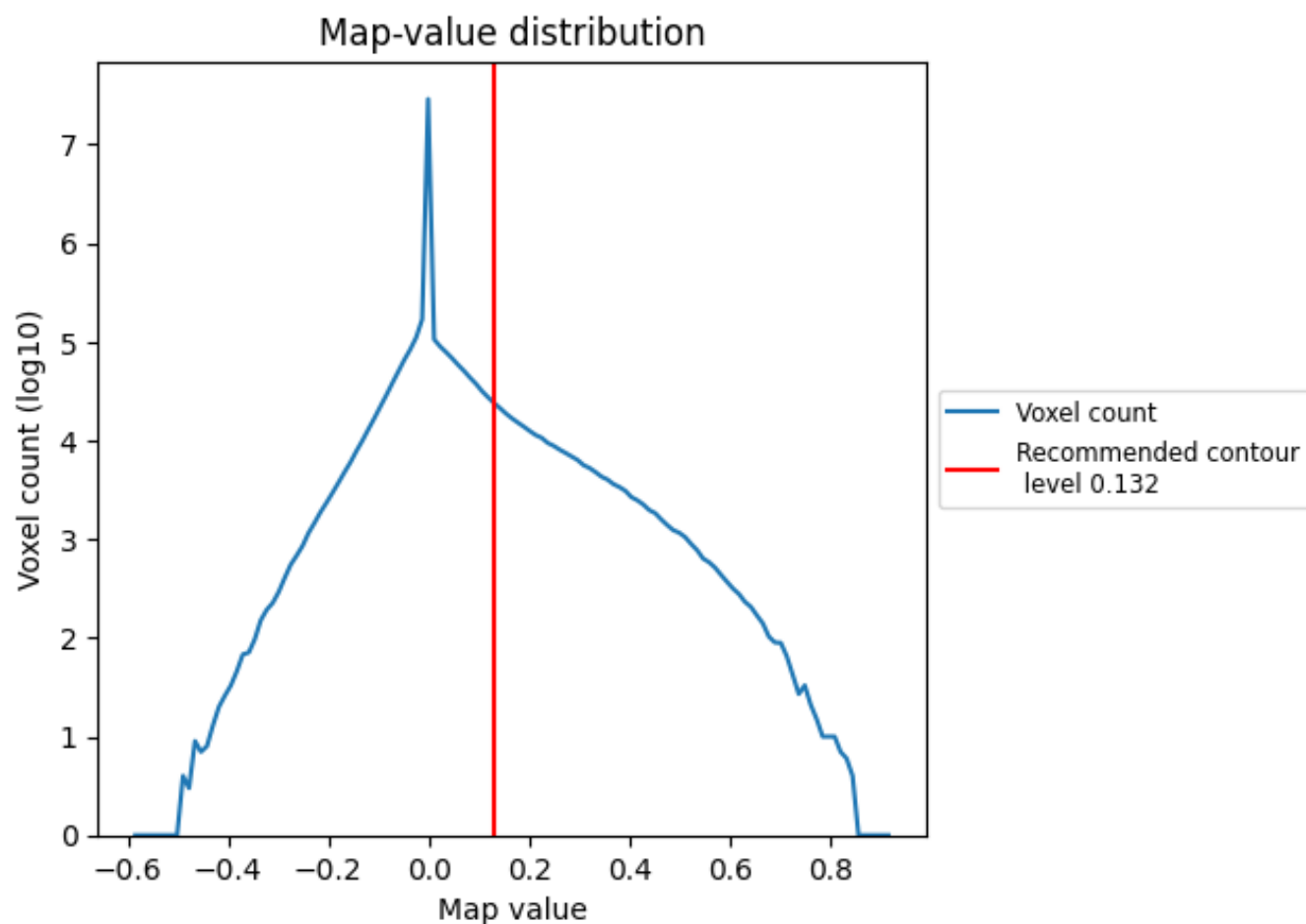
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

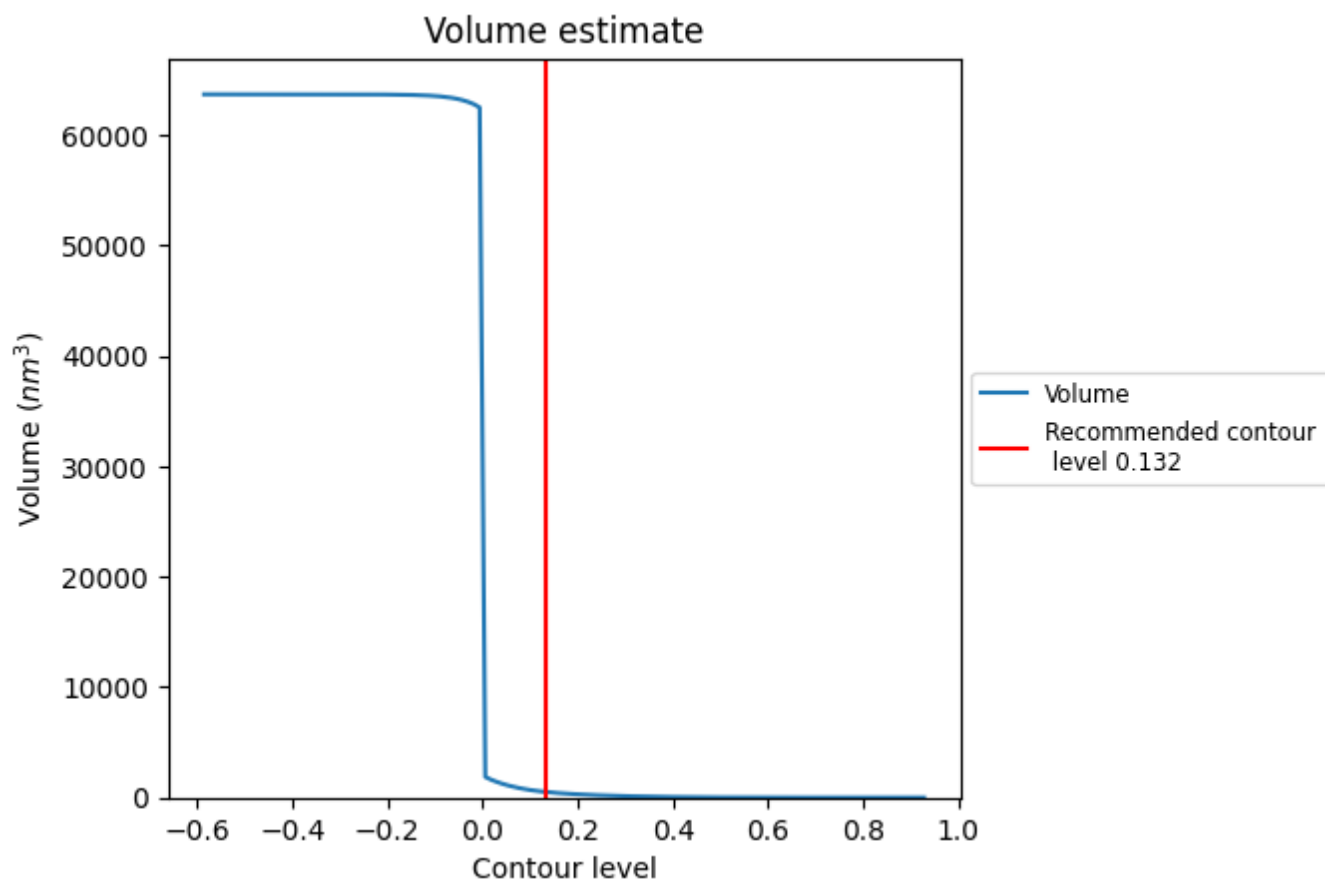
This section contains the results of statistical analysis of the map.

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.

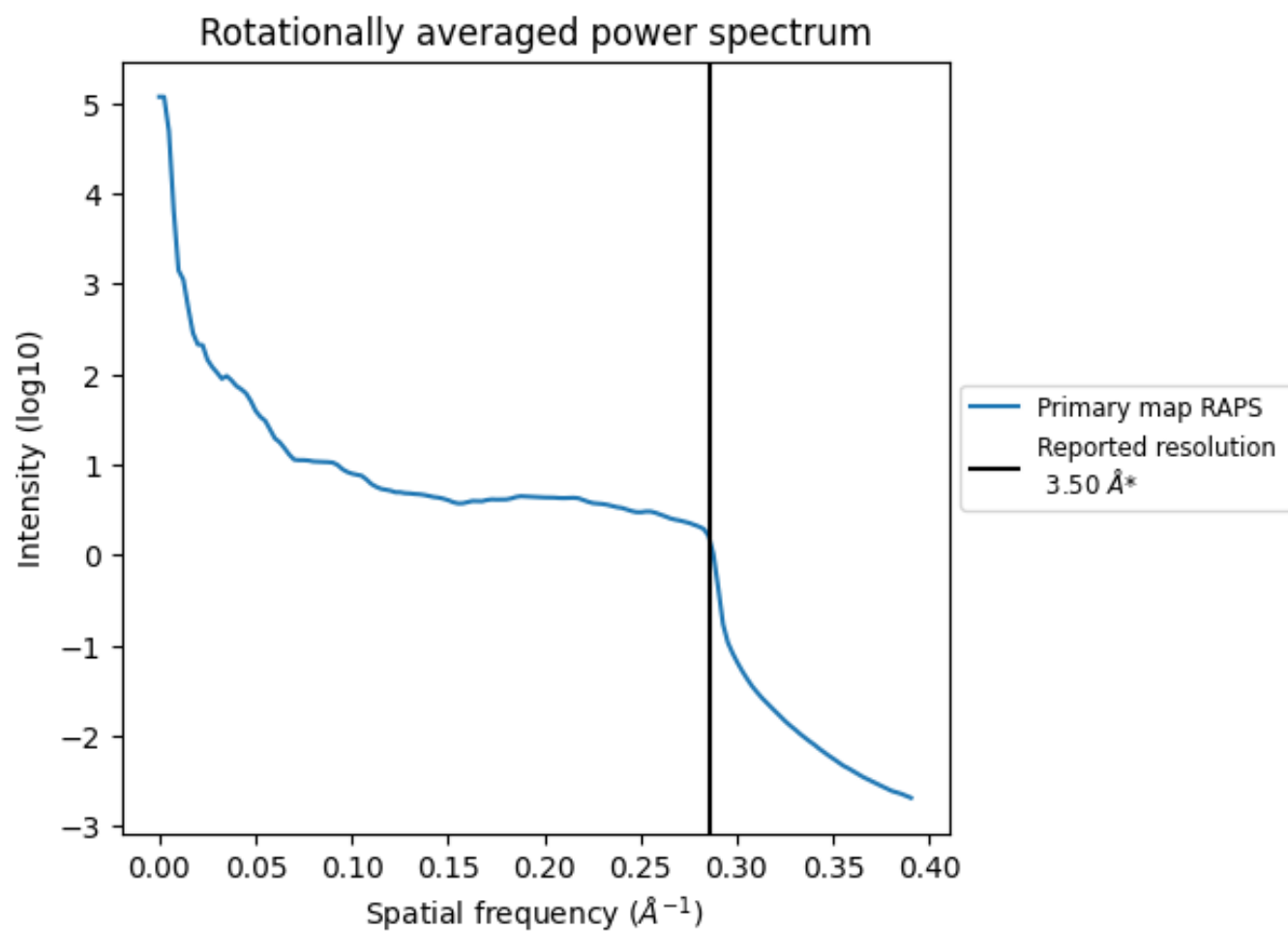
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 516 nm^3 ; this corresponds to an approximate mass of 466 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 0.286 Å⁻¹

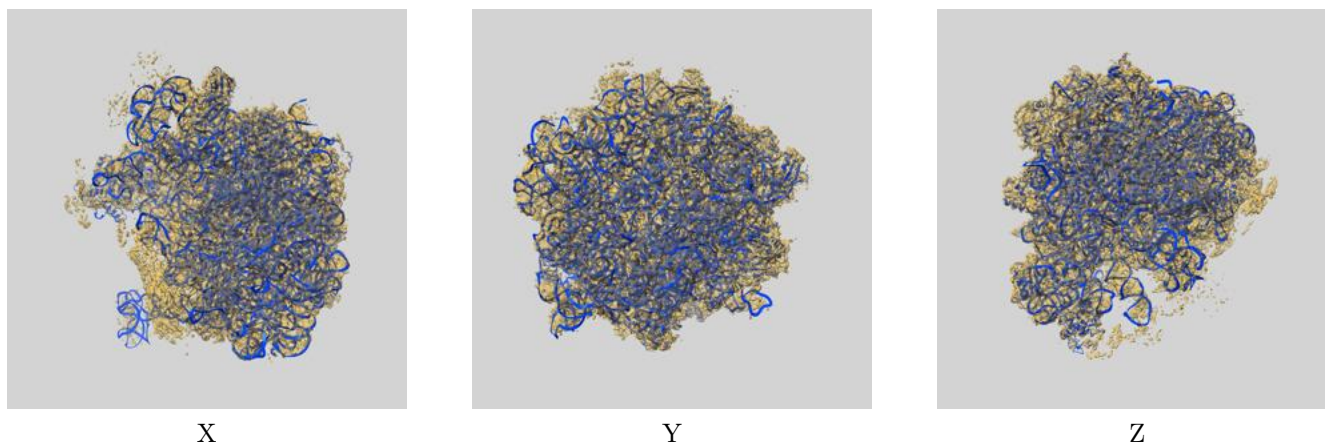
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

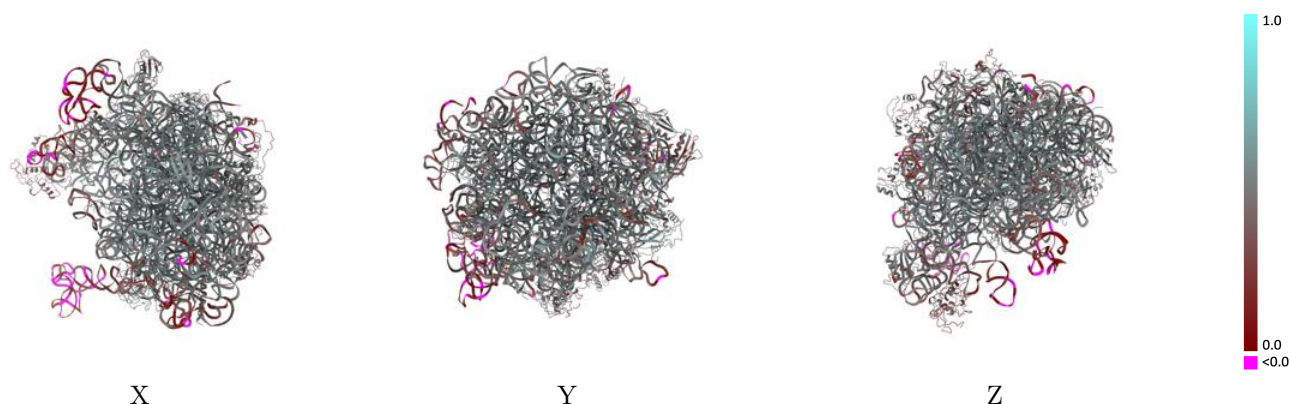
This section contains information regarding the fit between EMDB map EMD-9572 and PDB model 5H1S. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

9.1 Map-model overlay [i](#)



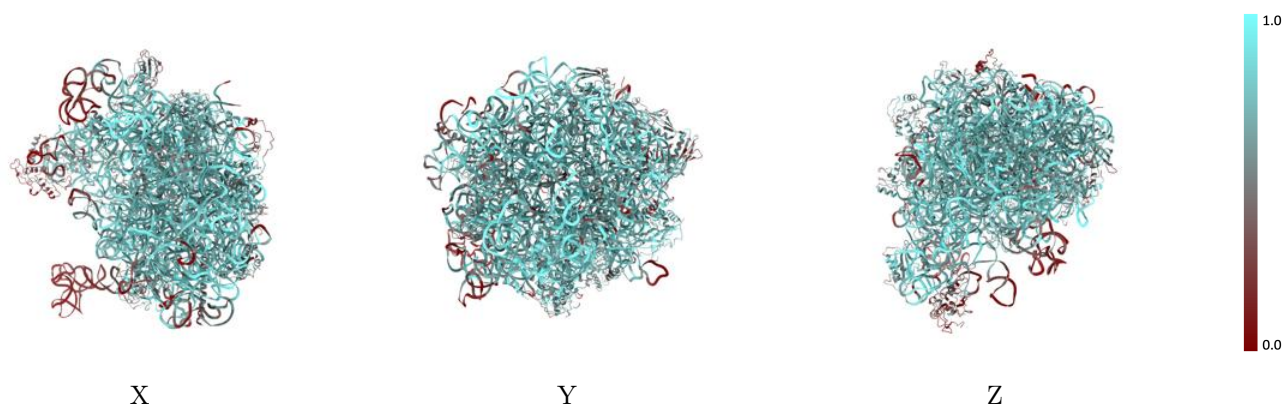
The images above show the 3D surface view of the map at the recommended contour level 0.132 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



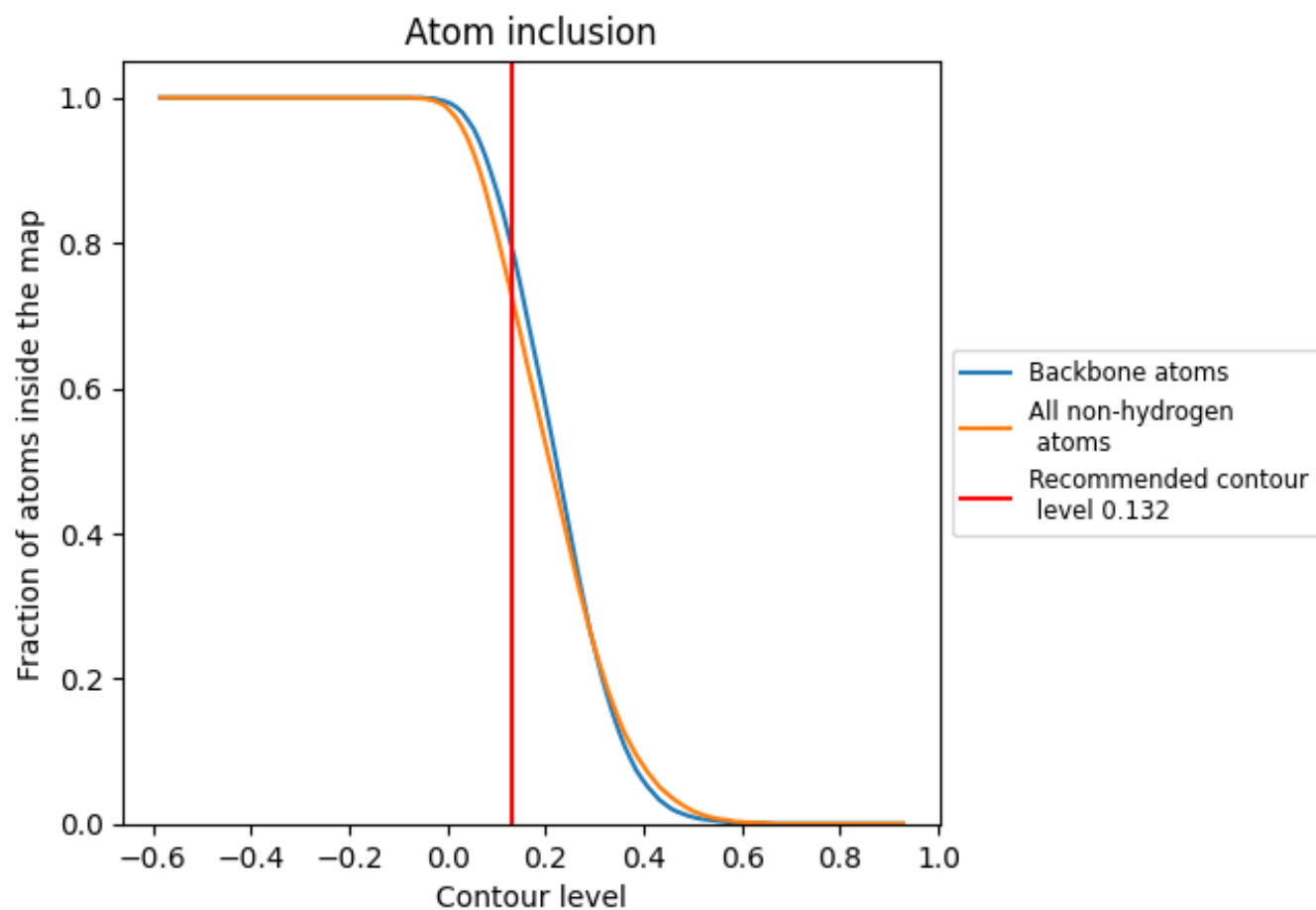
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.132).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 72% 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 (0.132) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7240	 0.4530
A	 0.7630	 0.4510
B	 0.8060	 0.4300
C	 0.8050	 0.4520
E	 0.6720	 0.4930
F	 0.6860	 0.4970
G	 0.6490	 0.4640
H	 0.2820	 0.3440
I	 0.5670	 0.4240
J	 0.2110	 0.3920
L	 0.7250	 0.5060
M	 0.5960	 0.4760
N	 0.6780	 0.4590
O	 0.6460	 0.4630
P	 0.7130	 0.5020
Q	 0.6240	 0.4310
R	 0.6100	 0.4800
S	 0.7360	 0.4770
T	 0.6270	 0.4750
U	 0.6060	 0.4530
V	 0.5720	 0.4870
W	 0.5730	 0.4400
X	 0.6440	 0.4660
Y	 0.6960	 0.4980
Z	 0.6040	 0.4490
a	 0.1020	 0.2240
b	 0.6790	 0.4930
c	 0.6150	 0.4100
d	 0.6820	 0.5020
e	 0.7360	 0.5200
f	 0.6840	 0.4880
g	 0.5570	 0.4140
h	 0.7260	 0.4920

