



wwPDB EM Validation Summary Report ⓘ

Mar 31, 2025 – 04:20 PM JST

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:

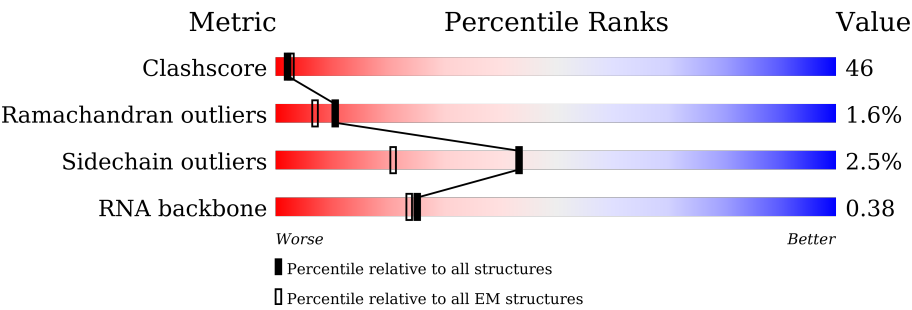
EMDB validation analysis : 0.0.1.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

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.





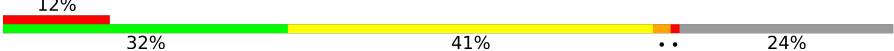
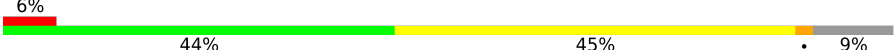
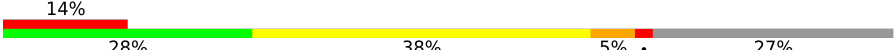
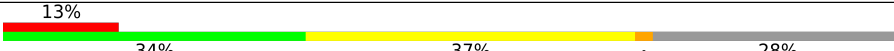
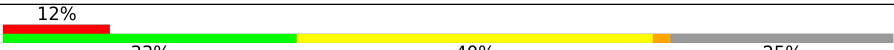
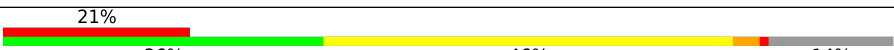
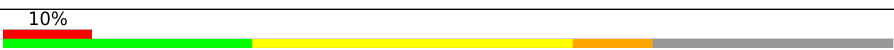
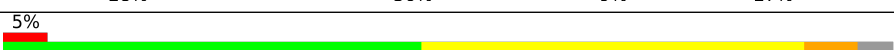
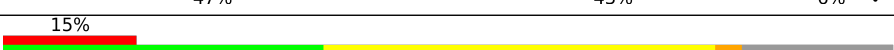
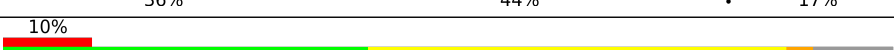

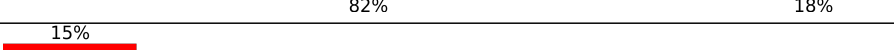
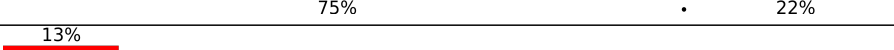
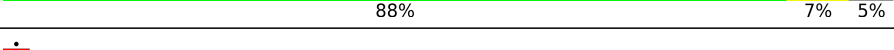
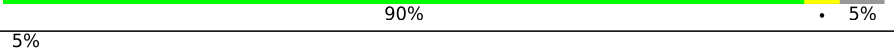
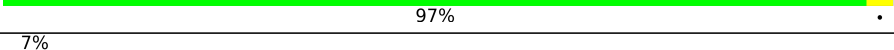
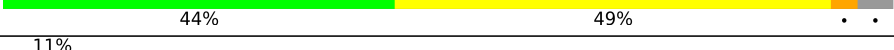


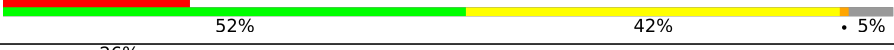



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	A	2810	<div><div>11%</div><div>29%43%27%</div><div>.</div></div>
2	C	106	<div><div>6%</div><div>9%46%37%</div><div>. .</div></div>
3	B	121	<div><div>12%</div><div>43%40%</div><div>. .</div></div>
4	L	191	<div><div>36%39%</div><div>. .23%</div></div>
5	M	121	<div><div>17%</div><div>54%46%</div></div>
6	N	192	<div><div>9%</div><div>31%51%9%8%</div><div>. .</div></div>
7	O	135	<div><div>16%</div><div>44%54%</div><div>. .</div></div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
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	
29	J	155	
30	g	142	
31	a	94	
32	h	116	

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		

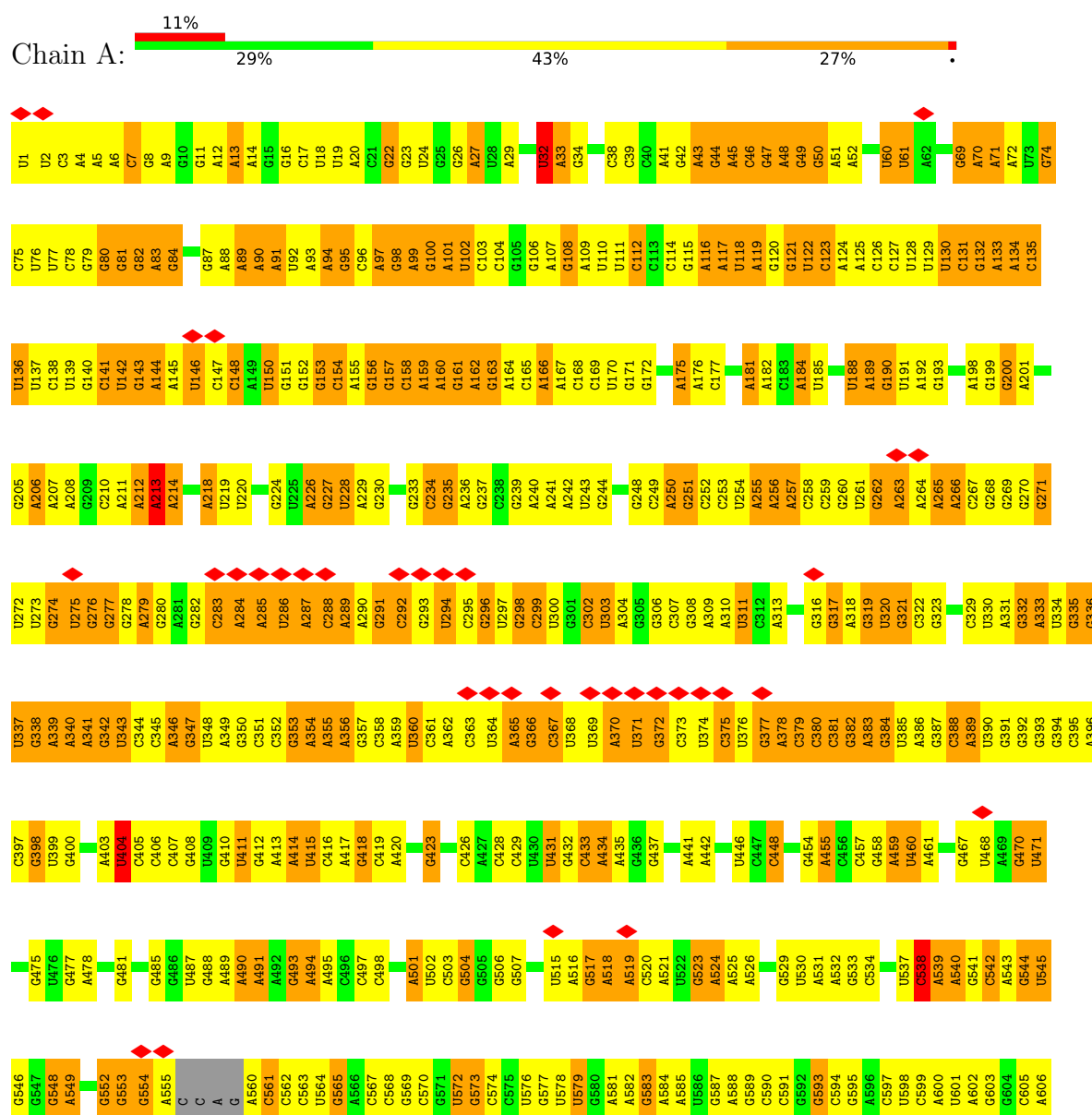
- Molecule 32 is a protein called 50S ribosomal protein 6, chloroplastic.

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

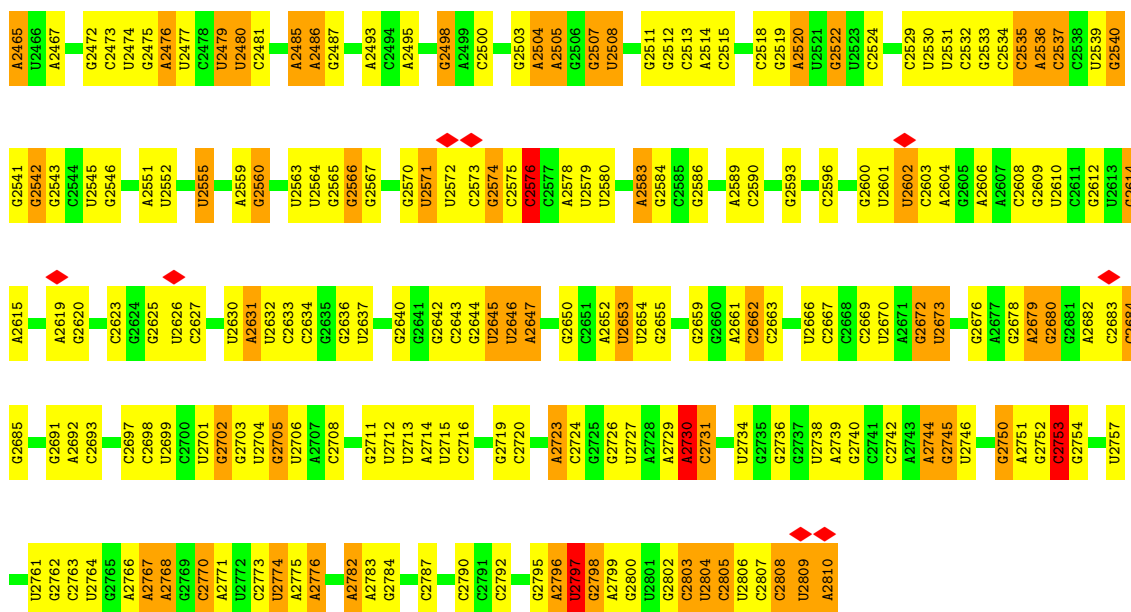
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

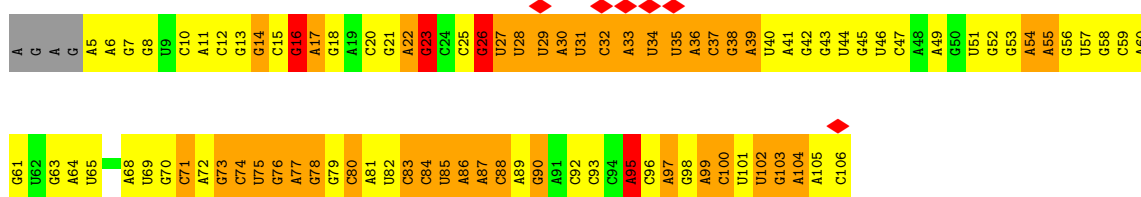


G1494	G1495	A1496	A1497	G1498	G1499	U1500	G1501	A1502	C1503	C1504	U1505	U1506	G1507	U	U	U	U	U	C	A	G1515	G1516	G1517	G1518	G1519	A1520	G1521	A1522	A1523	G1524	G1525	G1526	G1527	U1528	A1529	G1530	A1531	G1532	A1533	A1534	A1535	A1536	U1537	G1538	C1539	C1540	U1541	G1542	G1543	A1544	G1545	C1546	C1547	A1548	A1549	U1550	G1551	U1552	U1553
U1426	A1427	C1428	C1429	C1430	C1431	U1432	U1433	G1434	U1435	U1436	G1437	G1438	G1443	A1444	U1448	C1449	G1450	G1451	A1452	C1453	G1454	G1457	C1458	U1459	A1460	G1461	G1462	U1463	A1464	A1465	G1466	C1467	G1468	G1469	A1470	A1471	A1472	G1473	A1474	U1475	G1476	G1477	U1478	U1479	A1480	C1481	C1482	G1483	U1484	U1485	U1486	C1487	U1488	A1489	C1493				
C1336	U1337	C1338	C1341	A1342	A1343	G1344	G1345	U1346	U1347	C1348	G1349	U1350	C1351	C1352	A1353	U1361	G1362	A1363	C1366	U1373	A1374	A1375	G1376	C1379	G1385	A1386	A1387	A1388	G1389	G1390	C1391	G1392	U1393	A1394	C1397	G1398	A1399	U1400	G1401	A1406	C1407	A1408	A1413	A1414	U1415	A1416	U1417	U1418	C1425										
C1264	G1265	G1266	A1267	A1268	G1269	C1270	G1271	A1272	G1273	A1274	U1275	G1276	G1277	U1278	G1281	C1282	U1283	U1284	G1285	A1286	C1287	U1288	A1289	A1290	C1291	G1292	C1293	A1294	A1295	A1296	C1297	A1298	U1299	A1305	G1306	A1307	A1308	U1309	C1310	C1311	A1312	A1313	G1314	G1315	C1316	C1317	C1318	C1319	G1320	A1321	A1322	A1323	G1332	U1333	U1334	C1335			
A1192	U1193	U1194	U1195	A1196	A1197	A1198	A1199	A1200	A1201	A1202	C1203	A1204	G1207	G1208	U1209	A1210	G1211	U1219	U1220	U1224	G1225	U1226	U1227	G1231	A1232	G1233	A1234	A1235	A1236	C1237	G1238	C1239	G1240	U1241	G1242	U1245	G1246	A1247	G1248	G1251	C1252	G1253	U1254	U1255	G1256	G1257	A1258	C1259	G1260	A1261	A1262	G1263							
C1128	U1129	C1130	A1131	C1132	U1133	A1134	A1135	U1136	C1137	G1138	A1139	G1140	C1141	G1142	C1143	U1144	C1145	U1146	U1147	G1150	G1153	A1154	A1155	G1156	A1157	U1158	G1159	A1160	A1161	C1162	G1163	G1164	G1165	C1166	C1167	U1168	A1169	G1170	A1171	C1172	G1173	G1174	U1175	C1176	U1177	U1178	C1179	G1180	U1181	A1182	A1183	G1184	C1185	U1186	G1187	U1188	G1189		
U1069	G1070	C1071	A1072	G1073	U1074	G1075	C1076	U1077	A1078	G1079	C1080	C1081	A1082	G1083	C1084	A1085	G1086	G1087	U1088	U1089	U1090	G1091	C1092	C1093	U1094	A1095	G1096	A1097	U1098	A1099	C1100	A1101	G1102	C1103	C1104	A1105	C1106	C1107	C1108	U1109	U1110	G1111	A1112	A1113	A1114	G1115	U1116	G1117	U1118	G1119	C1120	G1121	U1122	A1123	A1124	U1125	A1126	G1127	
G1004	G1005	A1006	A1007	A1008	A1009	C1010	A1011	G1012	C1013	G1016	G1017	A1018	U1019	C1020	A1021	G1022	C1023	A1024	G1025	A1028	A1029	G1030	G1031	C1032	C1033	C1034	C1035	U1036	A1037	A1038	A1039	U1040	A1041	A1042	C1043	C1044	G1045	U1046	U1047	C1048	A1049	G1050	U1051	G1052	A1053	U1054	A1055	A1056	A1057	A1060	G1061	G1062	U1063	A1064	G1065	U1066			
C941	U942	C943	C944	A945	A946	A947	U948	A949	A950	C951	A952	G953	G954	G955	G956	U957	C958	A959	G960	G961	G962	U963	C964	G965	G966	C967	C968	A969	G970	U971	G972	A973	G974	A975	C976	G977	A978	U979	G980	G981	G982	G983	G984	A985	U986	A987	A988	G989	C993	A994	G997	U998	G1000	A1001	C1002	A1003			
U879	U880	U881	U882	G883	G884	U885	U886	U887	C888	G889	G890	G891	C892	C893	G894	C895	G896	A897	G898	A899	G899	G900	C901	G902	G903	U904	A905	C906	C907	A908	A909	A910	U911	C912	G913	A914	G915	G916	C917	A918	A919	A920	C921	U922	C923	U924	A927	U928	A929	A932	G933	A934	U935	A936	U937	G938	A939	C940	
U814	A815	C816	C817	U818	G819	G820	U821	U822	C823	U824	C825	C828	G829	A830	A831	A832	G836	U837	U838	A839	A840	G841	C842	C843	G844	C845	A846	G850	U851	U852	G853	A854	C855	U856	G857	G858	A859	C860	A861	C862	U863	U864	A865	G866	G867	G868	G869	U870	A871	A872	A873	C875	A876	C877	U878				
G735	G737	U738	U739	U740	U741	C747	C748	C749	A750	U751	U755	U758	G759	C760	A761	G762	A764	A767	G768	C769	G770	U773	U774	A775	G782	U783	U784	G785	A786	G787	G788	G789	U790	G791	A792	A793	A794	U795	G796	C800	U801	C802	G803	A804	A805	C806	C807	A811	G812	C813									
U668	C669	A670	C671	U672	U675	G679	G680	U681	U682	A683	C684	G685	A686	C687	C688	C689	U690	G691	U694	G695	A696	U697	C698	U699	A700	U701	C702	C703	A704	U705	G706	G712	A713	U714	G715	A716	A717	G718	C719	U720	U721	G722	G723	G724	G726	A727	A728	A729	C730	U731	A732	U733	G734	U735					
G607	U608	G609	G610	C611	U612	U613	G614	G615	U616	U617	A618	A619	G621	G622	A623	A624	C625	C626	C627	A628	C629	C630	G631	G632	A633	G634	C635	C636	G637	U638	A639	G640	C641	A643	A644	A645	G648	A649	G650	U651	C652	U653	U654	C655	A656	U657	A658	G659	G660	C661	A662	A663	A664	U665	U666	G667			

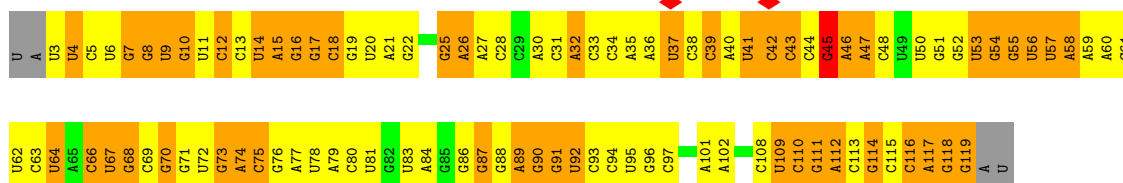
A2395	G2396	A2397	G2398	G2399	G2400	G2401	G2402	G2403	G2406	G2407	G2408	A2409	G2410	G2411	A2414	G2415	G2416	G2417	G2418	G2419	G2420	G2421	G2422	G2423	G2424	G2425	G2426	G2427	A2428	A2429	G2430	G2431	G2432	G2433	G2434	G2437	G2438	G2439	G2440	G2441	G2442	G2443	G2444	G2445	G2446	A2447	A2451	A2452	G2457	G2458	G2462	G2463	G2464																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
A2392	C2393	G2394	G2395	G2396	G2397	G2398	G2399	G2400	G2401	G2402	G2403	G2404	G2405	G2406	G2407	G2408	G2409	G2410	G2411	G2412	G2413	G2414	G2415	G2416	G2417	G2418	G2419	G2420	G2421	G2422	G2423	G2424	G2425	G2426	G2427	G2428	G2429	G2430	G2431	G2432	G2433	G2434	G2435	G2436	G2437	G2438	G2439	G2440	G2441	G2442	G2443	G2444	G2445	G2446	G2447	G2448	G2449	G2450	G2451	G2452	G2453	G2454	G2455	G2456	G2457	G2458	G2459	G2460	G2461	G2462	G2463	G2464																																																																																																																																																																																																																																																																																																																																																																																																																																																
C2191	U2192	C2193	U2194	G2195	G2196	G2197	G2198	G2199	G2200	G2201	G2202	G2203	G2204	G2205	G2206	G2207	G2208	G2209	G2210	G2211	G2212	G2213	G2214	G2215	G2216	G2217	G2218	G2219	G2220	G2221	G2222	G2223	G2224	G2225	G2226	G2227	G2228	G2229	G2230	G2231	G2232	G2233	G2234	G2235	G2236	G2237	G2238	G2239	G2240	G2241	G2242	G2243	G2244	G2245	G2246	G2247	G2248	G2249	G2250	G2251	G2252	G2253	G2254	G2255	G2256	G2257	G2258	G2259	G2260	G2261	G2262	G2263	G2264	G2265	G2266	G2267	G2268	G2269	G2270	G2271	G2272	G2273	G2274	G2275	G2276	G2277	G2278	G2279	G2280	G2281	G2282	G2283	G2284	G2285	G2286	G2287	G2288	G2289	G2290	G2291	G2292	G2293	G2294	G2295	G2296	G2297	G2298	G2299	G2300	G2301	G2302	G2303	G2304	G2305	G2306	G2307	G2308	G2309	G2310	G2311	G2312	G2313	G2314	G2315	G2316	G2317	G2318	G2319	G2320	G2321	G2322	G2323	G2324	G2325	G2326	G2327	G2328	G2329	G2330	G2331	G2332	G2333	G2334	G2335	G2336	G2337	G2338	G2339	G2340	G2341	G2342	G2343	G2344	G2345	G2346	G2347	G2348	G2349	G2350	G2351	G2352	G2353	G2354	G2355	G2356	G2357	G2358	G2359	G2360	G2361	G2362	G2363	G2364	G2365	G2366	G2367	G2368	G2369	G2370	G2371	G2372	G2373	G2374	G2375	G2376	G2377	G2378	G2379	G2380	G2381	G2382	G2383	G2384	G2385	G2386	G2387	G2388	G2389	G2390	G2391	G2392	G2393	G2394	G2395	G2396	G2397	G2398	G2399	G2400	G2401	G2402	G2403	G2404	G2405	G2406	G2407	G2408	G2409	G2410	G2411	G2412	G2413	G2414	G2415	G2416	G2417	G2418	G2419	G2420	G2421	G2422	G2423	G2424	G2425	G2426	G2427	G2428	G2429	G2430	G2431	G2432	G2433	G2434	G2435	G2436	G2437	G2438	G2439	G2440	G2441	G2442	G2443	G2444	G2445	G2446	G2447	G2448	G2449	G2450	G2451	G2452	G2453	G2454	G2455	G2456	G2457	G2458	G2459	G2460	G2461	G2462	G2463	G2464																																																																																																																																																																																																																																							
U2131	U2132	A2133	G2134	G2135	U2136	G2137	G2138	G2139	A2140	G2141	G2142	G2143	G2144	A2145	A2146	G2147	G2148	G2149	G2150	G2151	G2152	G2153	G2154	G2155	G2156	U2157	U2158	G2159	G2160	G2161	G2162	G2163	G2164	G2165	G2166	G2167	G2168	G2169	G2170	G2171	G2172	G2173	G2174	G2175	G2176	G2177	G2178	G2179	G2180	G2181	G2182	G2183	G2184	G2185	G2186	G2187	G2188	G2189	G2190	G2191	G2192	G2193	G2194	G2195	G2196	G2197	G2198	G2199	G2200	G2201	G2202	G2203	G2204	G2205	G2206	G2207	G2208	G2209	G2210	G2211	G2212	G2213	G2214	G2215	G2216	G2217	G2218	G2219	G2220	G2221	G2222	G2223	G2224	G2225	G2226	G2227	G2228	G2229	G2230	G2231	G2232	G2233	G2234	G2235	G2236	G2237	G2238	G2239	G2240	G2241	G2242	G2243	G2244	G2245	G2246	G2247	G2248	G2249	G2250	G2251	G2252	G2253	G2254	G2255	G2256	G2257	G2258	G2259	G2260	G2261	G2262	G2263	G2264	G2265	G2266	G2267	G2268	G2269	G2270	G2271	G2272	G2273	G2274	G2275	G2276	G2277	G2278	G2279	G2280	G2281	G2282	G2283	G2284	G2285	G2286	G2287	G2288	G2289	G2290	G2291	G2292	G2293	G2294	G2295	G2296	G2297	G2298	G2299	G2300	G2301	G2302	G2303	G2304	G2305	G2306	G2307	G2308	G2309	G2310	G2311	G2312	G2313	G2314	G2315	G2316	G2317	G2318	G2319	G2320	G2321	G2322	G2323	G2324	G2325	G2326	G2327	G2328	G2329	G2330	G2331	G2332	G2333	G2334	G2335	G2336	G2337	G2338	G2339	G2340	G2341	G2342	G2343	G2344	G2345	G2346	G2347	G2348	G2349	G2350	G2351	G2352	G2353	G2354	G2355	G2356	G2357	G2358	G2359	G2360	G2361	G2362	G2363	G2364	G2365	G2366	G2367	G2368	G2369	G2370	G2371	G2372	G2373	G2374	G2375	G2376	G2377	G2378	G2379	G2380	G2381	G2382	G2383	G2384	G2385	G2386	G2387	G2388	G2389	G2390	G2391	G2392	G2393	G2394	G2395	G2396	G2397	G2398	G2399	G2400	G2401	G2402	G2403	G2404	G2405	G2406	G2407	G2408	G2409	G2410	G2411	G2412	G2413	G2414	G2415	G2416	G2417	G2418	G2419	G2420	G2421	G2422	G2423	G2424	G2425	G2426	G2427	G2428	G2429	G2430	G2431	G2432	G2433	G2434	G2435	G2436	G2437	G2438	G2439	G2440	G2441	G2442	G2443	G2444	G2445	G2446	G2447	G2448	G2449	G2450	G2451	G2452	G2453	G2454	G2455	G2456	G2457	G2458	G2459	G2460	G2461	G2462	G2463	G2464																																																																																																																																																																											
G1902	G1910	A1914	A1915	G1916	G1917	G1920	G1921	G1922	U1925	A1926	A1927	U1928	U1929	A1930	U1931	A1932	A1933	G1936	U1937	G1938	G1939	U1940	A1941	A1942	G1943	G1944	U1945	G1949	A1950	A1951	A1952	U1953	U1954	U1955	U1956	U1957	U1958	G1959	U1960	U1965	A1966	A1967	G1968	U1969	U1970	C1971	C1972	G1977	G1978	A1980	G1981	G1982	G1983	A1984	G1985	G1986	G1987	G1988	G1989	A1990	G1991	G1992	G1993	G1994	G1995	G1996	G1997	G1998	G1999	G2000	G2001	G2002	G2003	G2004	G2005	G2006	G2007	G2008	G2009	G2010	G2011	G2012	A2013	G2014	A2015	G2016	A2017	G2018	G2019	G2020	G2021	G2022	G2023	G2024	G2025	G2026	A2027	A2033	G2034	U2035	U2036	G2037	U2038	G2039	G2040	G2041	A2044	A2045	G2046	A2047	U2048	G2049	G2050	G2051	G2054	U2055	A2056	G2057	G2058	U2059	G2060	G2061	A2062	U2065	G2066	G2069	A2070	G2073	A2074	G2075	A2076	G2077	G2078	G2079	G2083	A2084	U2088	U2089	G2090	A2091	G2094	U2095	G2103	A2104	U2105	G2106	G2107	G2108	U2109	G2110	U2111	U2112	G2113	G2114	G2115	G2116	U2117	U2118	U2119	U2120	U2121	G2122	U2123	G2124	G2125	G2126	G2127	A2128	G2129	G2130	G2131	G2132	G2133	G2134	G2135	G2136	G2137	G2138	G2139	G2140	G2141	G2142	G2143	G2144	G2145	G2146	G2147	G2148	G2149	G2150	G2151	G2152	G2153	G2154	G2155	G2156	G2157	G2158	G2159	G2160	G2161	G2162	G2163	G2164	G2165	G2166	G2167	G2168	G2169	G2170	G2171	G2172	G2173	G2174	G2175	G2176	G2177	G2178	G2179	G2180	G2181	G2182	G2183	G2184	G2185	G2186	G2187	G2188	G2189	G2190	G2191	G2192	G2193	G2194	G2195	G2196	G2197	G2198	G2199	G2200	G2201	G2202	G2203	G2204	G2205	G2206	G2207	G2208	G2209	G2210	G2211	G2212	G2213	G2214	G2215	G2216	G2217	G2218	G2219	G2220	G2221	G2222	G2223	G2224	G2225	G2226	G2227	G2228	G2229	G2230	G2231	G2232	G2233	G2234	G2235	G2236	G2237	G2238	G2239	G2240	G2241	G2242	G2243	G2244	G2245	G2246	G2247	G2248	G2249	G2250	G2251	G2252	G2253	G2254	G2255	G2256	G2257	G2258	G2259	G2260	G2261	G2262	G2263	G2264	G2265	G2266	G2267	G2268	G2269	G2270	G2271	G2272	G2273	G2274	G2275	G2276	G2277	G2278	G2279	G2280	G2281	G2282	G2283	G2284	G2285	G2286	G2287	G2288	G2289	G2290	G2291	G2292	G2293	G2294	G2295	G2296	G2297	G2298	G2299	G2300	G2301	G2302	G2303	G2304	G2305	G2306	G2307	G2308	G2309	G2310	G2311	G2312	G2313	G2314	G2315	G2316	G2317	G2318	G2319	G2320	G2321	G2322	G2323	G2324	G2325	G2326	G2327	G2328	G2329	G2330	G2331	G2332	G2333	G2334	G2335	G2336	G2337	G2338	G2339	G2340	G2341	G2342	G2343	G2344	G2345	G2346	G2347	G2348	G2349	G2350	G2351	G2352	G2353	G2354	G2355	G2356	G2357	G2358	G2359	G2360	G2361	G2362	G2363	G2364	G2365	G2366	G2367	G2368	G2369	G2370	G2371	G2372	G2373	G2374	G2375	G2376	G2377	G2378	G2379	G2380	G2381	G2382	G2383	G2384	G2385	G2386	G2387	G2388	G2389	G2390	G2391	G2392	G2393	G2394	G2395	G2396	G2397	G2398	G2399	G2400	G2401	G2402	G2403	G2404	G2405	G2406	G2407	G2408	G2409	G2410	G2411	G2412	G2413	G2414	G2415	G2416	G2417	G2418	G2419	G2420	G2421	G2422	G2423	G2424	G2425	G2426	G2427	G2428	G2429	G2430	G2431	G2432	G2433	G2434	G2435	G2436	G2437	G2438	G2439	G2440	G2441	G2442	G2443	G2444	G2445	G2446	G2447	G2448	G2449	G2450	G2451	G2452	G2453	G2454	G2455	G2456	G2457	G2458	G2459	G2460	G2461	G2462	G2463	G2464
G1763	G1766	G1767	G1768	G1769	G1770	G1774	G1775	G1776	G1777	G1778	G1781	G1782	G1783	G1786	U1789	A1793	A1794	A1795	A1796	A1797	A1799	C1800	G1801	G1803	G1804	G1805	G1806	G1807	G1808	G1809	G1810	A1811	A1812	A1813	G1814	U1815	G1816	G1817	A1819	A1820	G1821	G1822	G1823	G1824	A1825	U1826	G1827	U1828	G1829	U1830	G1831	G1832	G1833	G1834	G1835	U1836	G1837	G1838	G1839	G1840	G1841	G1842	C1847	C1848	A1849	G1850	U1851	G1852	C1853	A1857	A1858	G1859	G1860	U1861	G1866	A1867	G1868	U1869	U1870	G1871	G1872	G1873	G1874	G1875	A1876	C1877	G1878	A1879	G1880	G1881	U1882	G1883	A1884	C1885	A1886	G1887	G1888	G1889	G1890	A1891	G1892	G1895	G1896	G1897	G1898	G1902	G1910	A1914	A1915	G1916	G1917	G1																																																																																																																																																																																																																																																																																																																																																																																																								



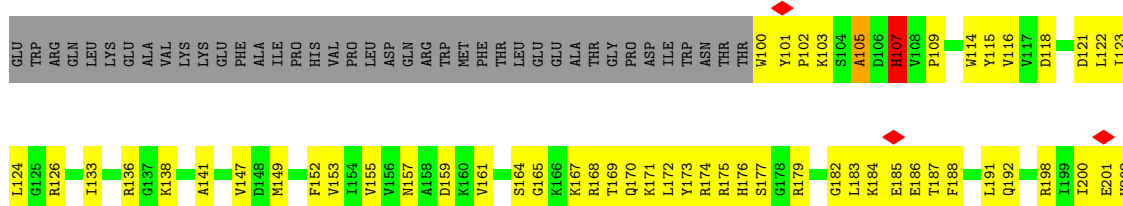
• Molecule 2: Spinach chloroplast 4.5S rRNA



• Molecule 3: 5S rRNA

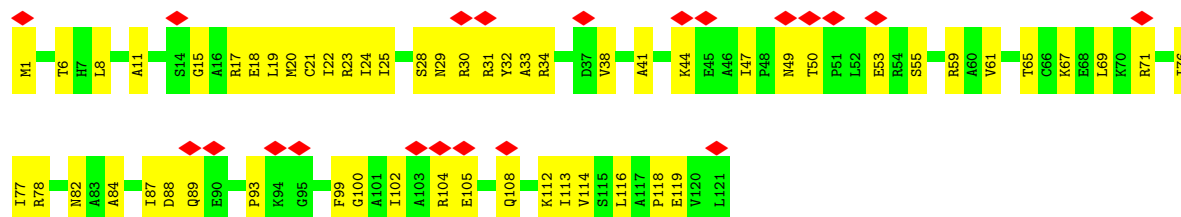


• Molecule 4: 50S ribosomal protein L13, chloroplastic

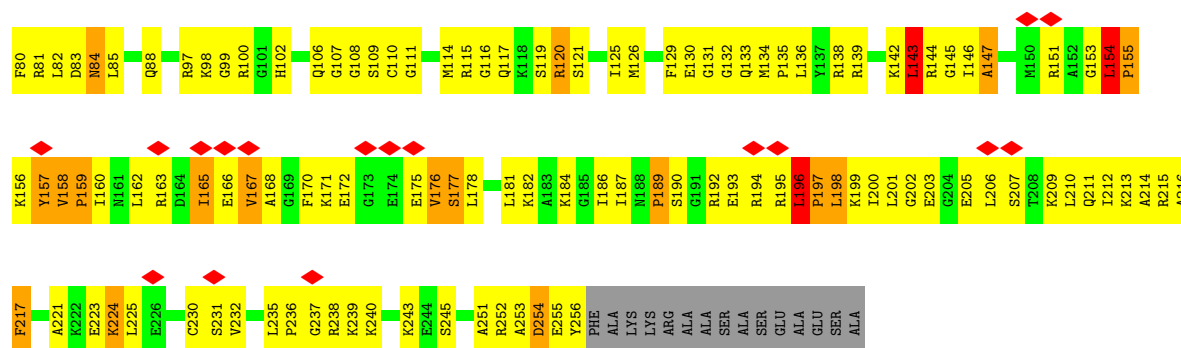




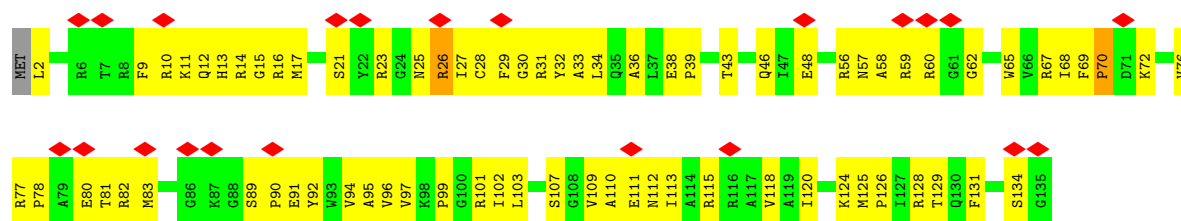
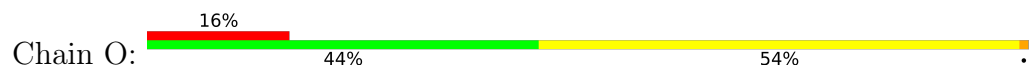
- Molecule 5: 50S ribosomal protein L14, chloroplastic



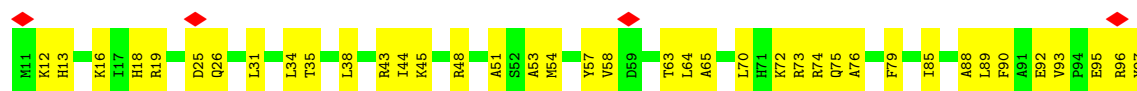
- Molecule 6: 50S ribosomal protein L15

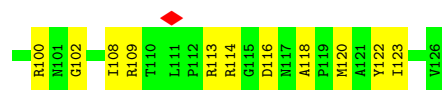


- Molecule 7: 50S ribosomal protein L16, chloroplastic

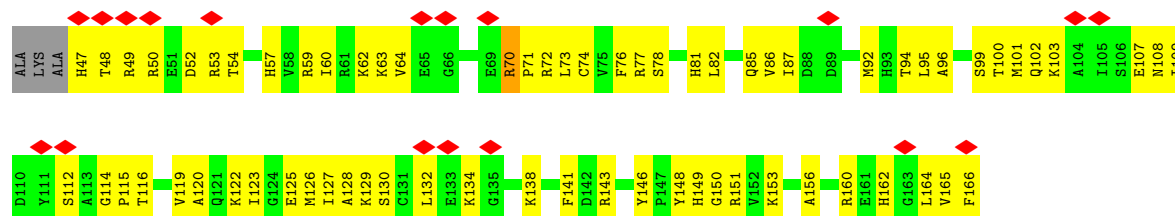
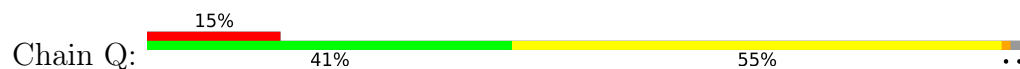


- Molecule 8: 50S ribosomal protein L17

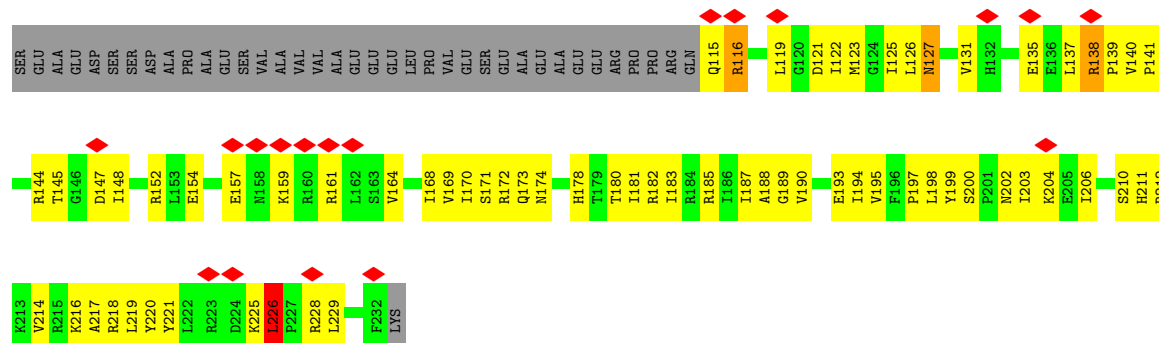




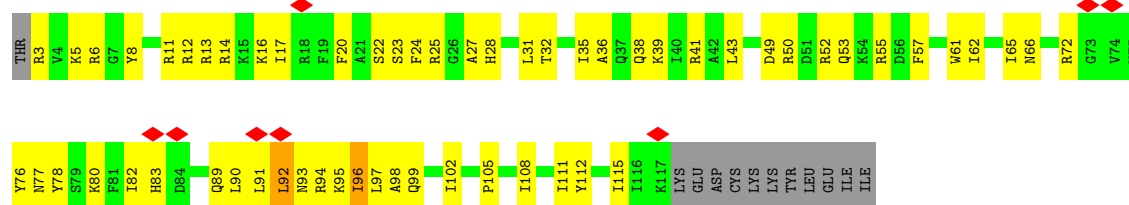
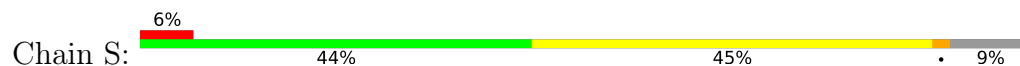
• Molecule 9: 50S ribosomal protein L18



• Molecule 10: 50S ribosomal protein L19, chloroplastic

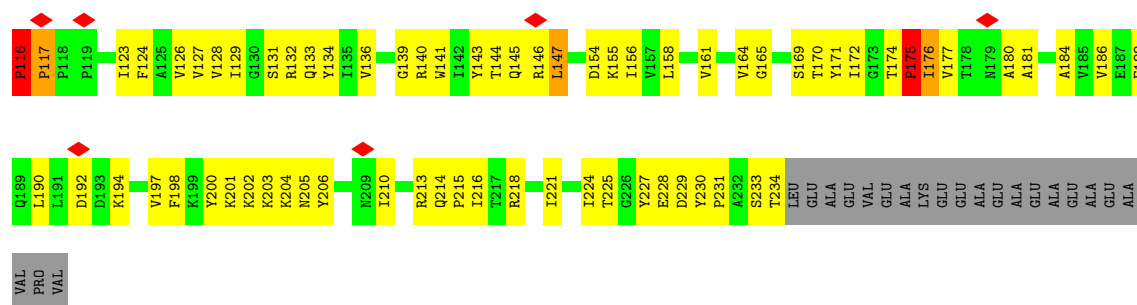


• Molecule 11: 50S ribosomal protein L20, chloroplastic

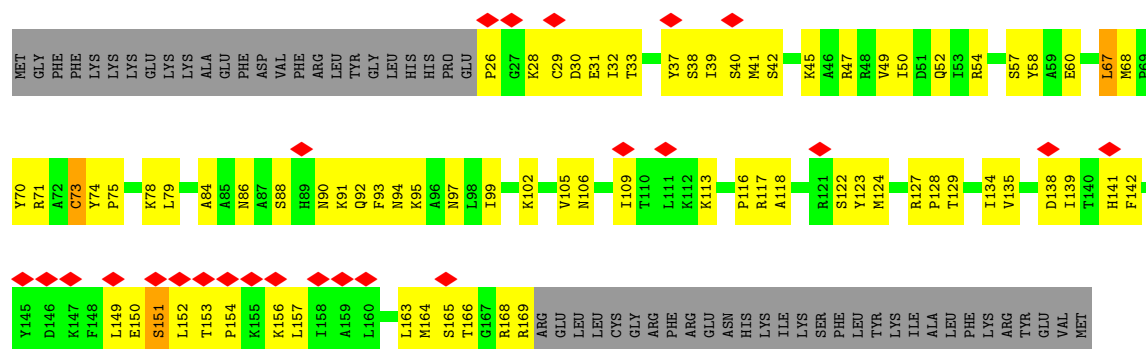


• Molecule 12: 50S ribosomal protein L21, chloroplastic

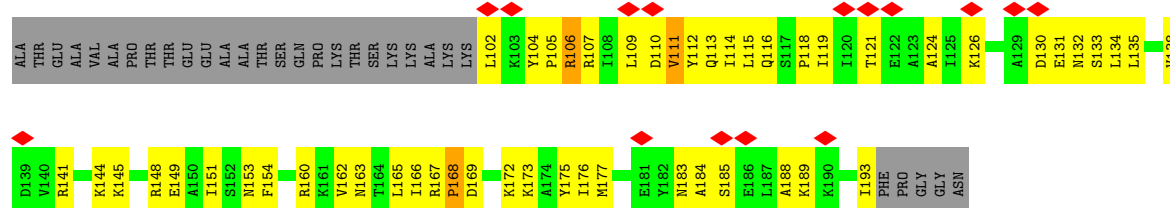




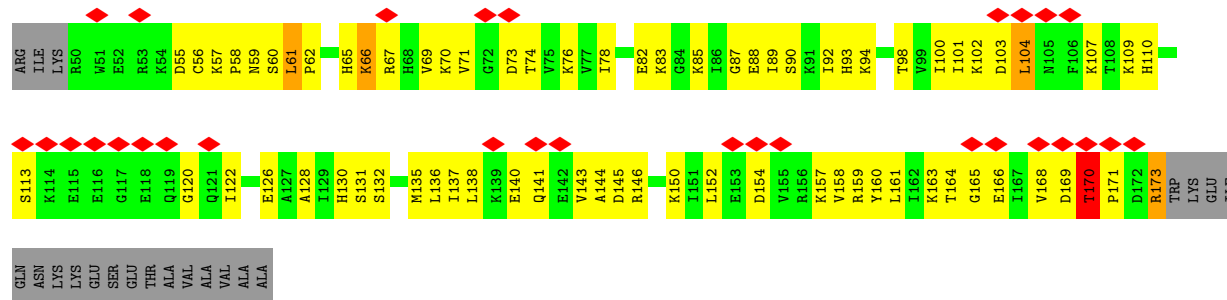
- Molecule 13: 50S ribosomal protein L22, chloroplastic



- Molecule 14: 50S ribosomal protein L23, chloroplastic



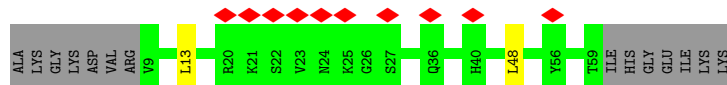
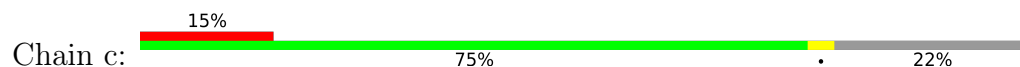
- Molecule 15: 50S ribosomal protein L24, chloroplastic



- Molecule 16: 50S ribosomal protein L27



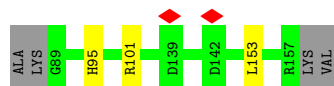
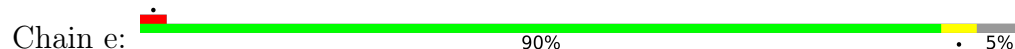
- Molecule 21: 50S ribosomal protein L33, chloroplastic



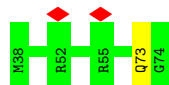
- Molecule 22: 50S ribosomal protein L34, chloroplastic



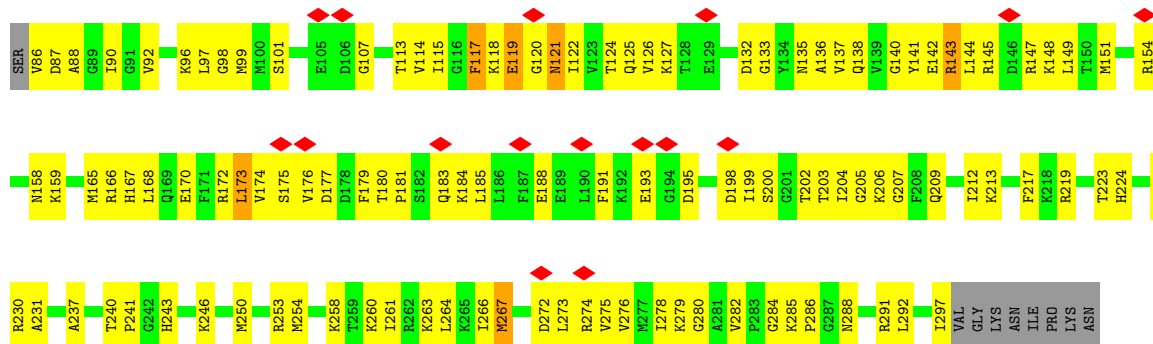
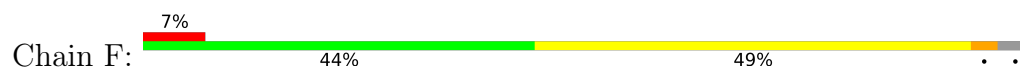
- Molecule 23: 50S ribosomal protein L35, chloroplastic



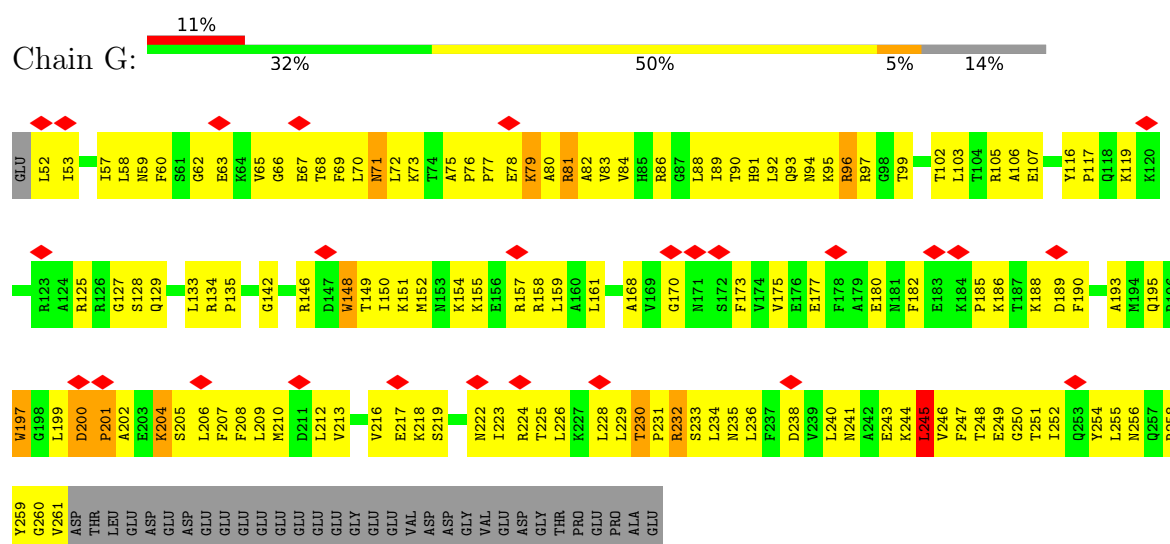
- Molecule 24: 50S ribosomal protein L36, chloroplastic



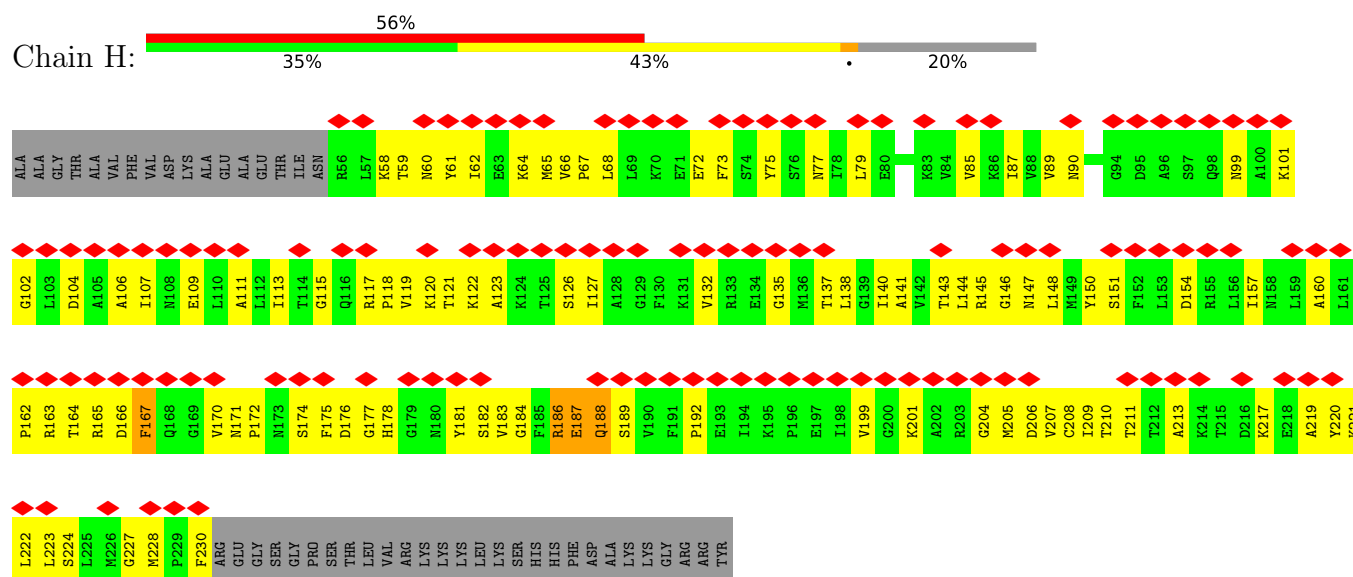
- Molecule 25: 50S ribosomal protein L3



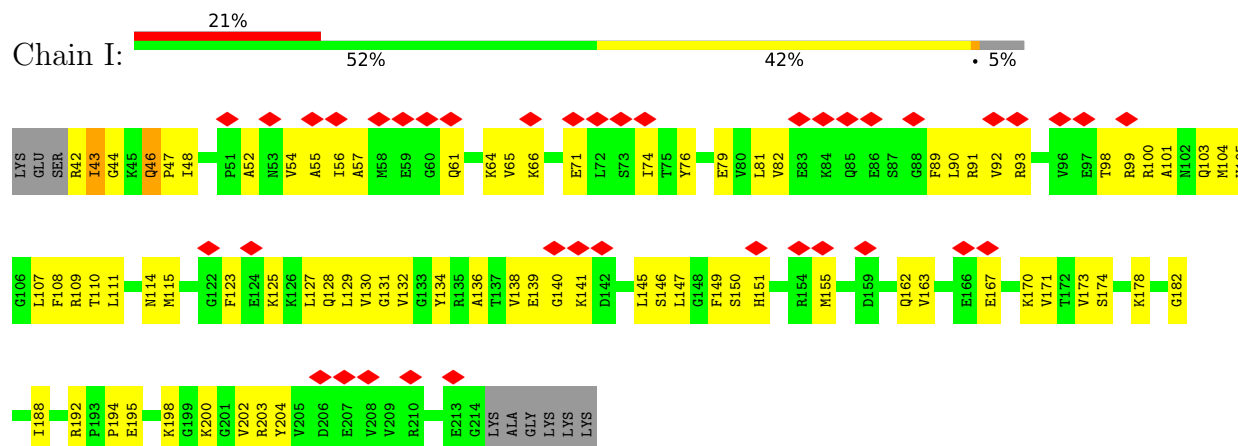
- Molecule 26: 50S ribosomal protein L4, chloroplastic



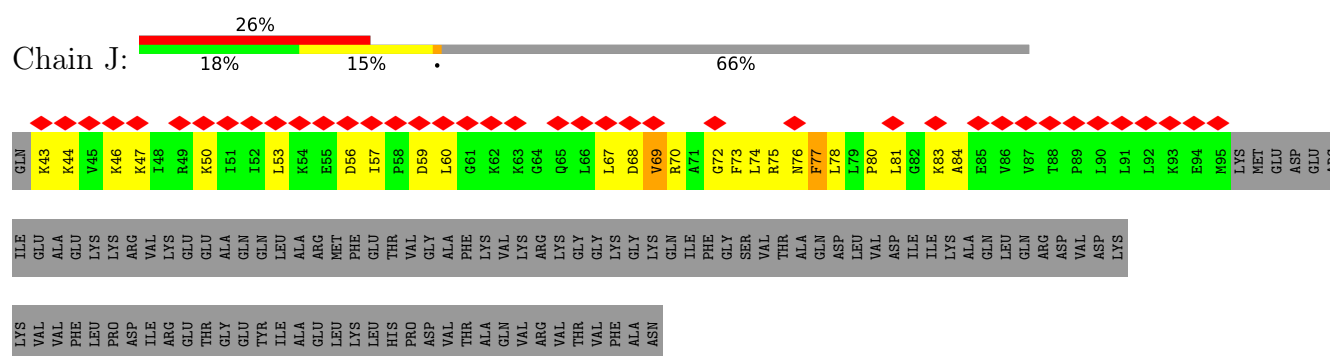
- Molecule 27: 50S ribosomal protein L5, chloroplastic



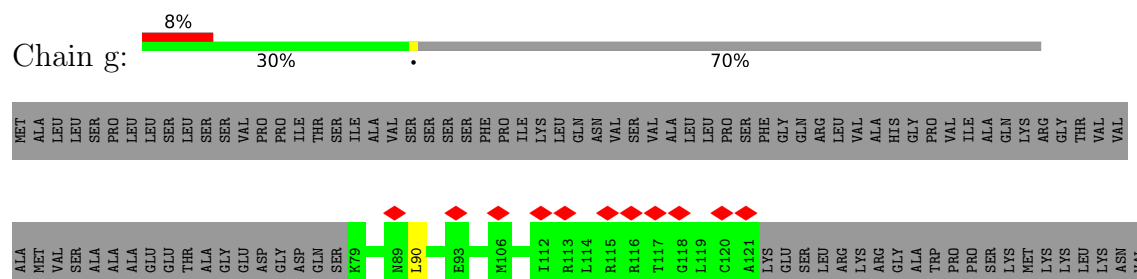
- Molecule 28: 50S ribosomal protein L6



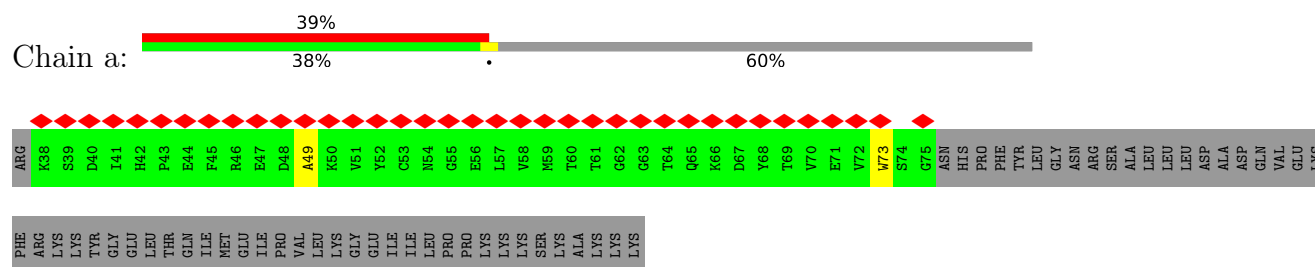
- Molecule 29: 50S ribosomal protein L9



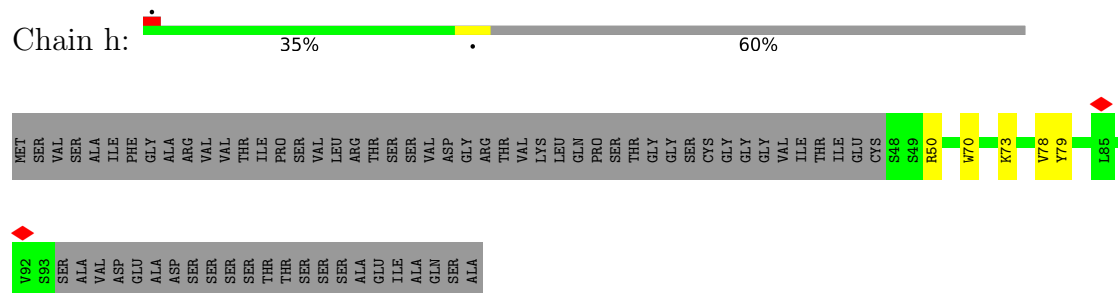
- Molecule 30: 50S ribosomal protein 5 alpha, chloroplastic



- 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 (\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 (\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	0.80	18/67340 (0.0%)	0.94	109/105056 (0.1%)
2	C	3.05	9/2449 (0.4%)	1.30	26/3817 (0.7%)
3	B	0.78	0/2796	0.87	2/4357 (0.0%)
4	L	0.67	0/1212	0.68	1/1634 (0.1%)
5	M	0.60	0/951	0.69	1/1282 (0.1%)
6	N	0.40	0/1361	0.77	3/1806 (0.2%)
7	O	0.63	1/1089 (0.1%)	0.71	1/1461 (0.1%)
8	P	0.63	0/959	0.76	0/1280
9	Q	0.52	0/963	0.67	0/1293
10	R	0.61	0/967	0.79	2/1300 (0.2%)
11	S	0.77	0/1013	0.82	1/1351 (0.1%)
12	T	0.73	0/1199	0.88	3/1633 (0.2%)
13	U	0.60	1/1168 (0.1%)	0.69	0/1566
14	V	0.53	0/749	0.65	0/1006
15	W	0.49	0/1006	0.67	2/1343 (0.1%)
16	X	0.66	0/825	0.80	2/1099 (0.2%)
17	Y	0.65	0/615	0.78	2/819 (0.2%)
18	Z	0.52	0/762	0.71	0/1012
19	E	0.60	0/1938	0.78	1/2603 (0.0%)
20	b	0.72	0/387	0.65	0/513
21	c	0.55	0/422	0.85	1/564 (0.2%)
22	d	0.45	0/447	0.63	0/588
23	e	0.72	0/569	0.82	1/752 (0.1%)
24	f	0.57	0/306	0.78	0/403
25	F	0.66	0/1646	0.74	1/2201 (0.0%)
26	G	0.65	2/1687 (0.1%)	0.78	1/2271 (0.0%)
27	H	0.37	0/1372	0.60	0/1848
28	I	0.49	0/1374	0.63	1/1849 (0.1%)
29	J	0.33	0/427	0.65	0/568
30	g	0.44	0/345	0.85	1/455 (0.2%)
31	a	0.29	0/306	0.60	0/413
32	h	0.70	1/382 (0.3%)	0.81	2/520 (0.4%)
All	All	0.88	32/99032 (0.0%)	0.90	164/148663 (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 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	95	A	N3-C4	76.76	1.80	1.34
2	C	95	A	C6-N1	71.09	1.85	1.35
2	C	95	A	C5-C4	50.90	1.74	1.38
2	C	95	A	C2-N3	47.29	1.76	1.33
2	C	95	A	N1-C2	47.04	1.76	1.34

The worst 5 of 164 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	95	A	N1-C2-N3	-28.24	115.18	129.30
2	C	95	A	C2-N3-C4	24.30	122.75	110.60
2	C	95	A	N7-C8-N9	14.45	121.03	113.80
6	N	196	LEU	C-N-CD	-14.44	88.83	120.60
2	C	95	A	C4-C5-N7	-13.30	104.05	110.70

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

Continued on next page...

Continued from previous page...

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	3962	0
2	C	2187	0	1099	306	0
3	B	2500	0	1263	331	0
4	L	1184	0	1221	135	0
5	M	942	0	996	51	0
6	N	1342	0	1413	392	0
7	O	1067	0	1120	103	0
8	P	944	0	1004	68	0
9	Q	947	0	966	87	0
10	R	953	0	1044	80	0
11	S	996	0	1060	122	0
12	T	1171	0	1216	216	0
13	U	1149	0	1220	98	0
14	V	740	0	795	103	0
15	W	993	0	1054	127	0
16	X	810	0	847	185	0
17	Y	605	0	652	51	0
18	Z	754	0	804	99	0
19	E	1904	0	1982	219	0
20	b	378	0	413	0	0
21	c	415	0	434	0	0
22	d	445	0	501	0	0
23	e	563	0	621	0	0
24	f	304	0	342	0	0
25	F	1620	0	1699	174	0
26	G	1655	0	1723	238	0
27	H	1351	0	1407	136	0
28	I	1353	0	1416	90	0
29	J	423	0	488	39	0
30	g	345	0	395	0	0
31	a	300	0	279	0	0
32	h	368	0	386	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	90825	0	60114	6418	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 46.

The worst 5 of 6418 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	27
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	39
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	49
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

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	U	142/199 (71%)	117 (82%)	24 (17%)	1 (1%)	19	53
14	V	90/122 (74%)	79 (88%)	9 (10%)	2 (2%)	5	31
15	W	122/145 (84%)	95 (78%)	25 (20%)	2 (2%)	8	38
16	X	98/137 (72%)	87 (89%)	7 (7%)	4 (4%)	2	20
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	64
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%)	3	22
23	e	67/73 (92%)	50 (75%)	16 (24%)	1 (2%)	8	39
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%)	13	46
27	H	173/220 (79%)	145 (84%)	27 (16%)	1 (1%)	22	56
28	I	171/182 (94%)	142 (83%)	27 (16%)	2 (1%)	11	43
29	J	51/155 (33%)	41 (80%)	9 (18%)	1 (2%)	6	33
30	g	41/142 (29%)	36 (88%)	5 (12%)	0	100	100
31	a	36/94 (38%)	26 (72%)	9 (25%)	1 (3%)	4	27
32	h	44/116 (38%)	31 (70%)	12 (27%)	1 (2%)	5	31
All	All	3218/4086 (79%)	2630 (82%)	538 (17%)	50 (2%)	10	38

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%)	124 (99%)	1 (1%)	79	88
5	M	101/101 (100%)	101 (100%)	0	100	100
6	N	135/144 (94%)	126 (93%)	9 (7%)	13	40
7	O	107/108 (99%)	107 (100%)	0	100	100
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%)	101 (97%)	3 (3%)	37	64
11	S	102/114 (90%)	102 (100%)	0	100	100
12	T	129/174 (74%)	122 (95%)	7 (5%)	18	46
13	U	126/176 (72%)	125 (99%)	1 (1%)	79	88
14	V	81/103 (79%)	80 (99%)	1 (1%)	67	82
15	W	112/129 (87%)	109 (97%)	3 (3%)	40	65
16	X	85/111 (77%)	74 (87%)	11 (13%)	3	18
17	Y	64/67 (96%)	61 (95%)	3 (5%)	22	51
18	Z	83/97 (86%)	79 (95%)	4 (5%)	21	50
19	E	195/216 (90%)	189 (97%)	6 (3%)	35	63
20	b	39/49 (80%)	39 (100%)	0	100	100
21	c	48/59 (81%)	47 (98%)	1 (2%)	48	71
22	d	47/49 (96%)	45 (96%)	2 (4%)	25	54
23	e	59/62 (95%)	58 (98%)	1 (2%)	56	75
24	f	34/34 (100%)	34 (100%)	0	100	100
25	F	174/182 (96%)	170 (98%)	4 (2%)	45	69
26	G	176/205 (86%)	169 (96%)	7 (4%)	27	56
27	H	148/183 (81%)	146 (99%)	2 (1%)	62	79
28	I	147/154 (96%)	147 (100%)	0	100	100
29	J	47/134 (35%)	46 (98%)	1 (2%)	48	71
30	g	39/121 (32%)	39 (100%)	0	100	100
31	a	33/83 (40%)	32 (97%)	1 (3%)	36	63
32	h	40/96 (42%)	40 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2775/3447 (80%)	2707 (98%)	68 (2%)	43 67

5 of 68 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
26	G	71	ASN
26	G	81	ARG
27	H	188	GLN
15	W	173	ARG
15	W	170	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
15	W	68	HIS
26	G	93	GLN
18	Z	77	ASN
26	G	71	ASN
27	H	90	ASN

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.

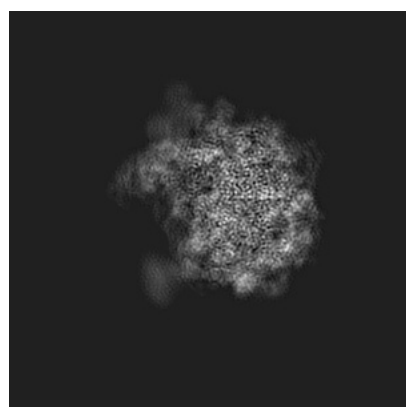
6 Map visualisation [i](#)

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.

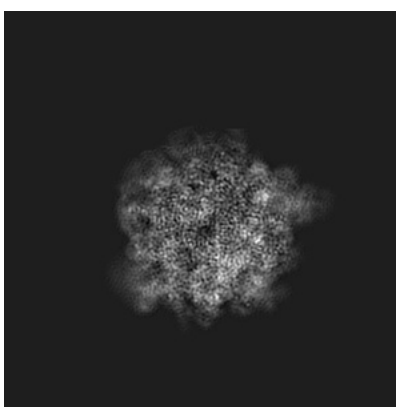
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

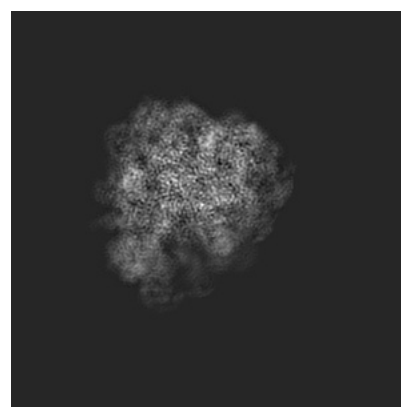
6.1.1 Primary map



X



Y

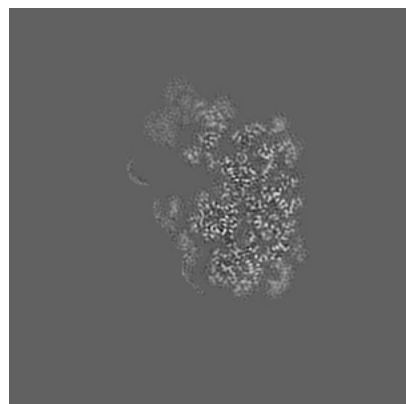


Z

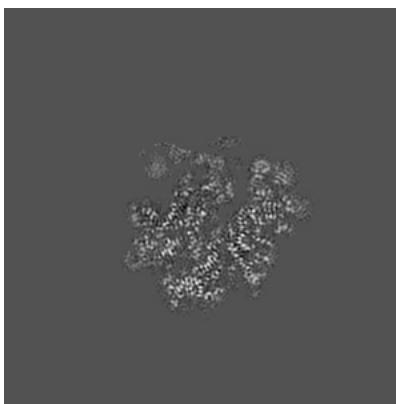
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

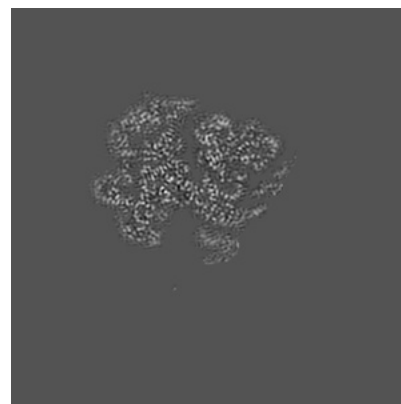
6.2.1 Primary map



X Index: 156



Y Index: 156

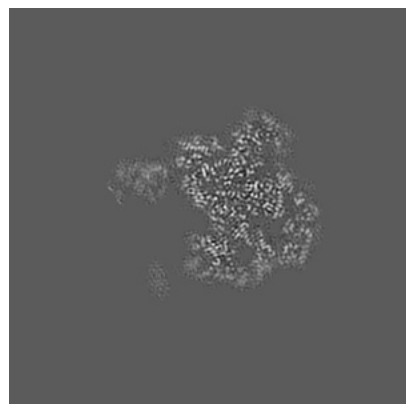


Z Index: 156

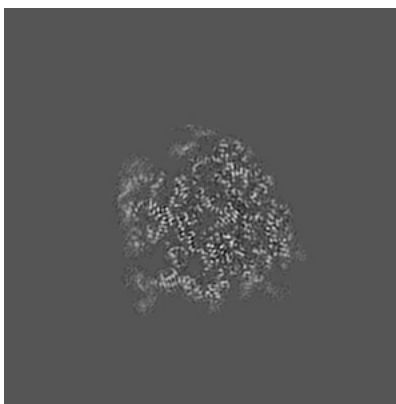
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

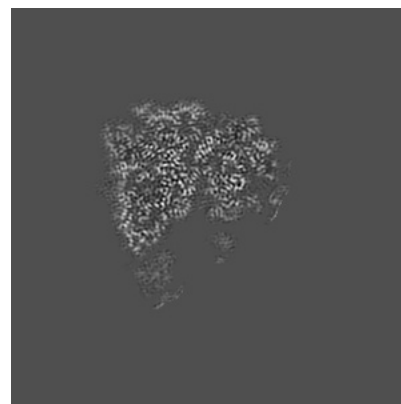
6.3.1 Primary map



X Index: 120



Y Index: 186

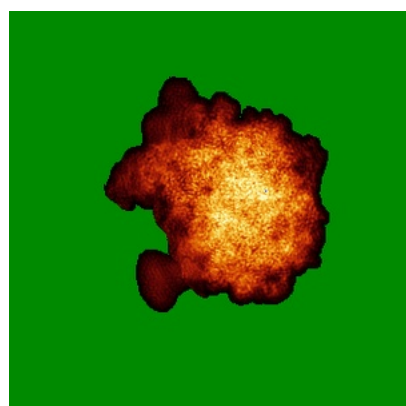


Z Index: 166

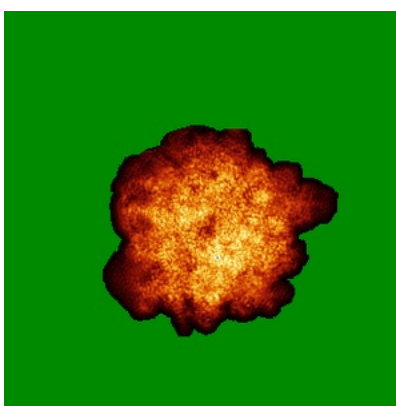
The images above show the largest variance slices of the map in three orthogonal directions.

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

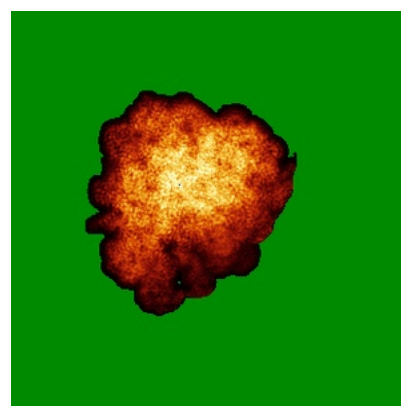
6.4.1 Primary map



X



Y

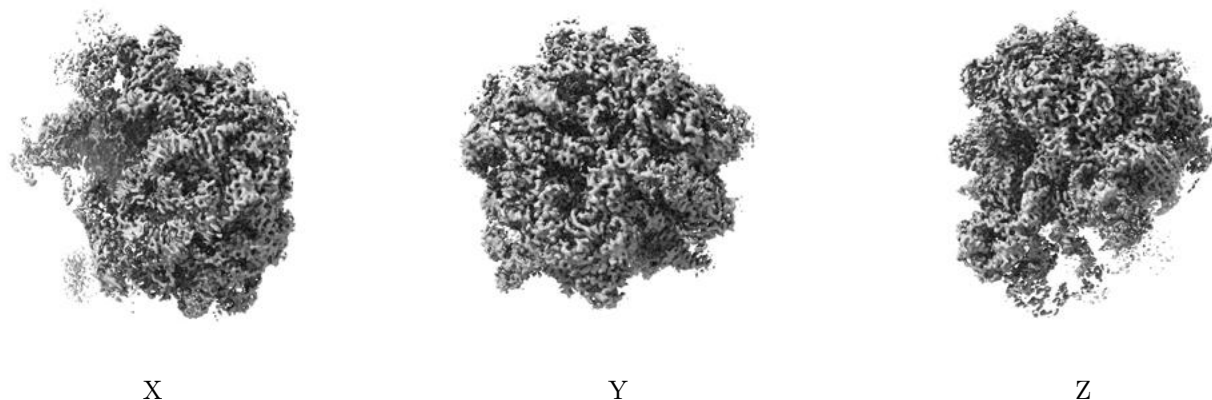


Z

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.

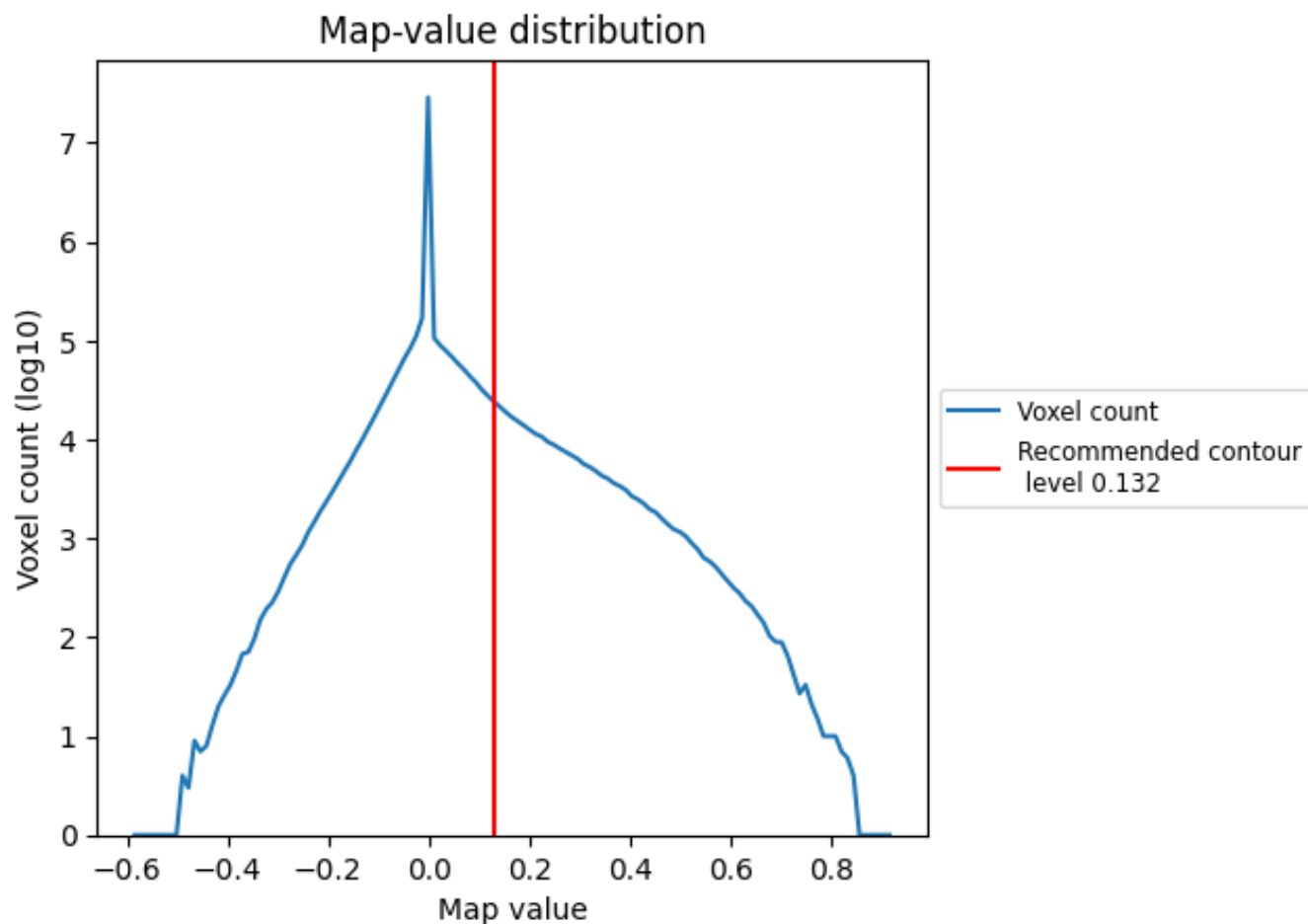
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

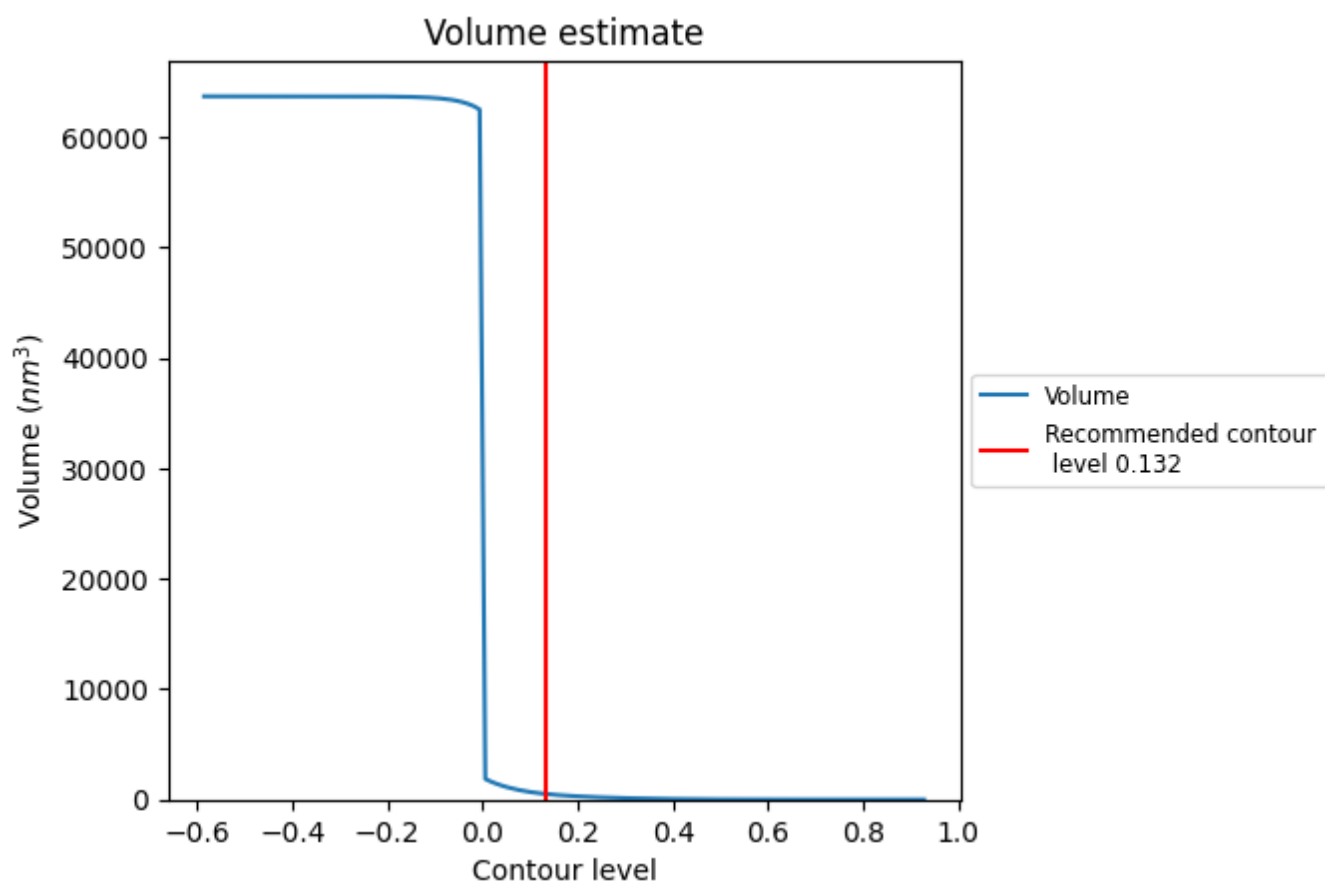
This section contains the results of statistical analysis of the map.

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.

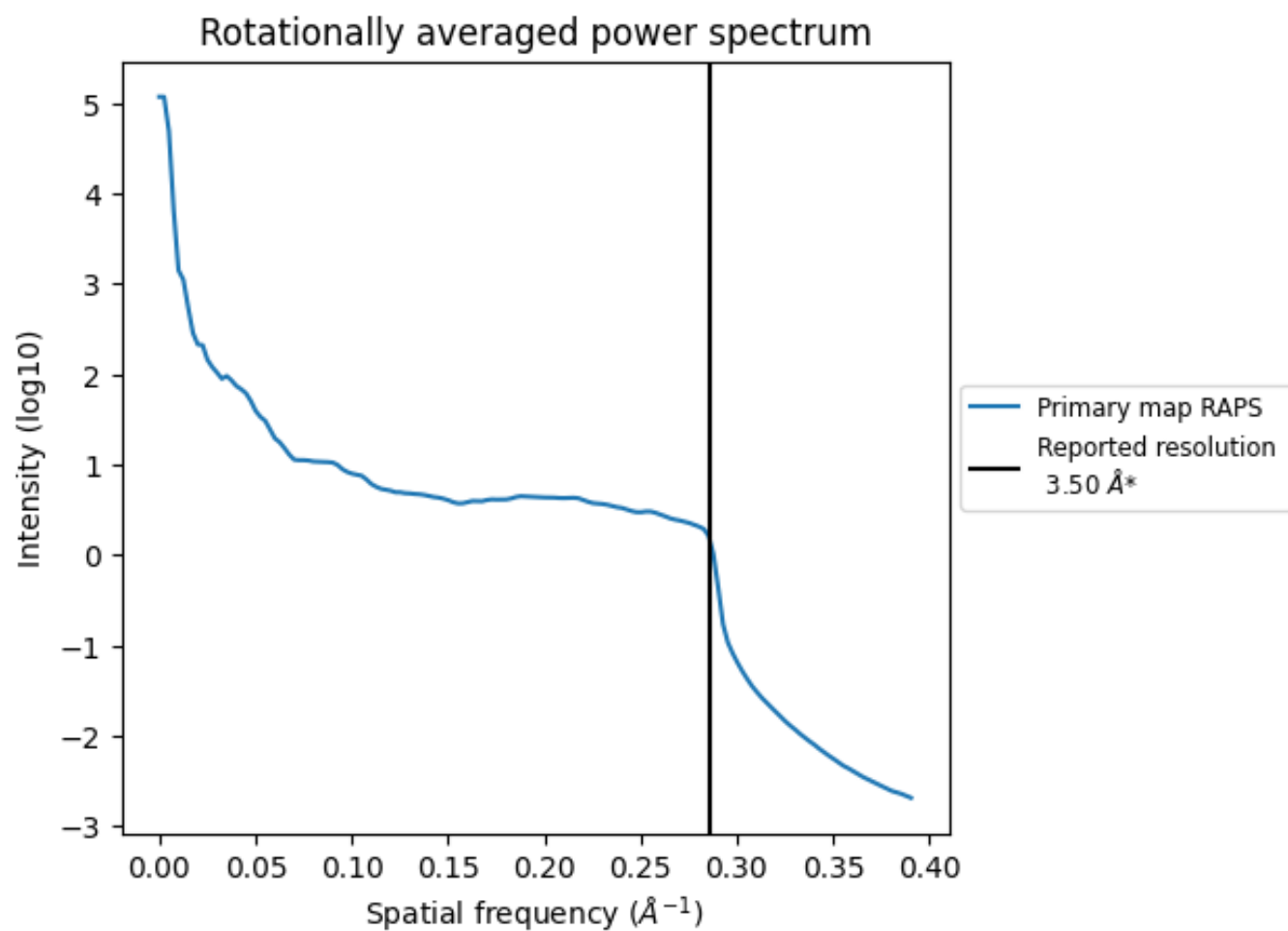
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 516 nm³; 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

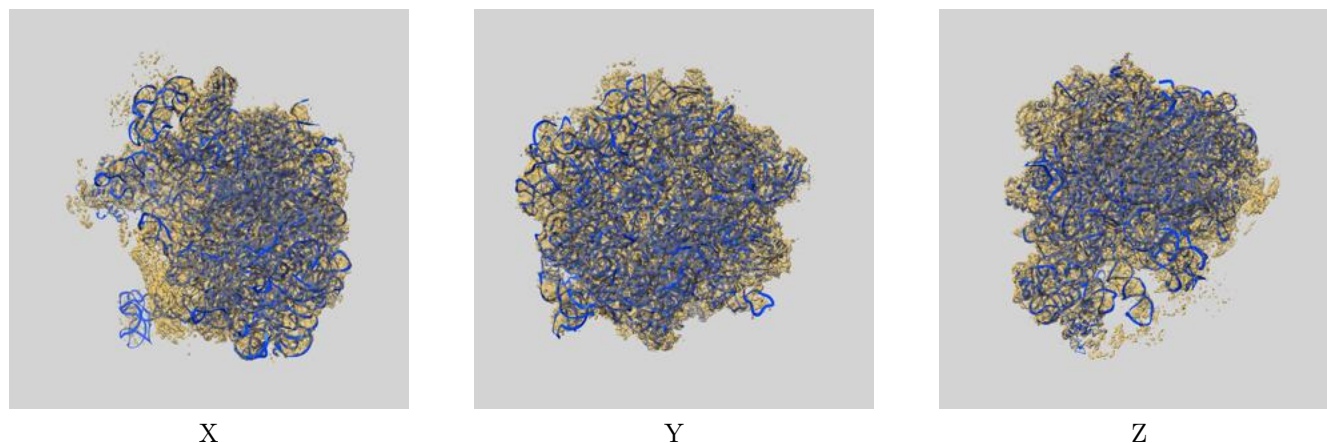
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

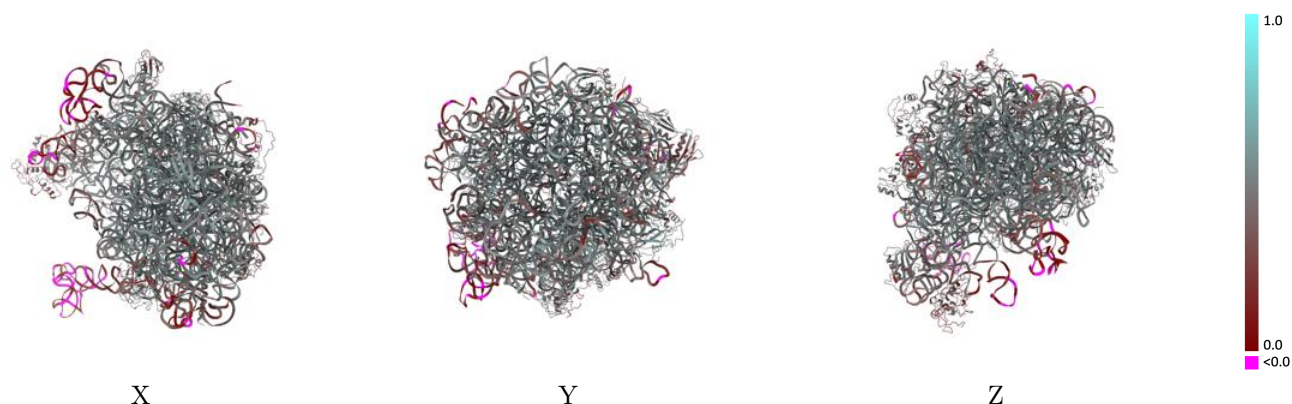
This section contains information regarding the fit between EMDB map EMD-9572 and PDB model 5H1S. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)



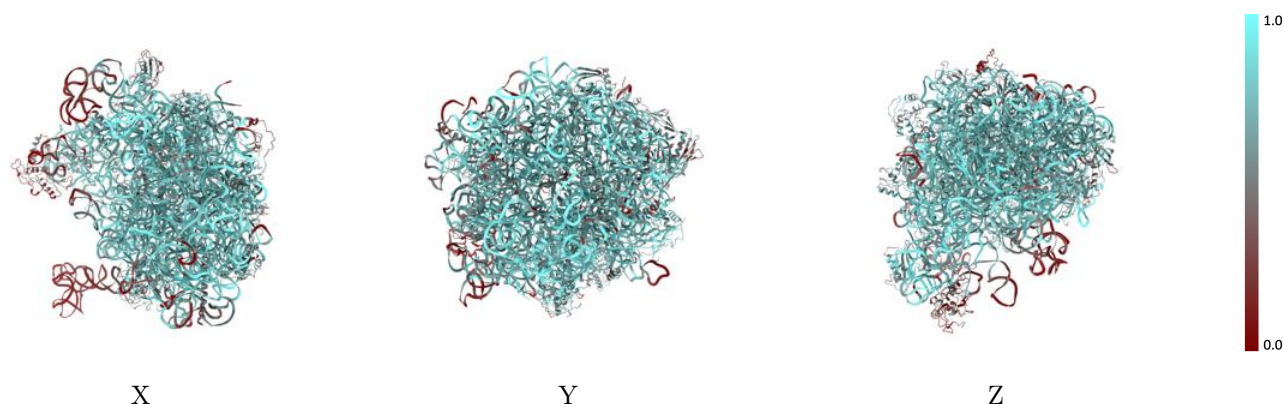
The images above show the 3D surface view of the map at the recommended contour level 0.132 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



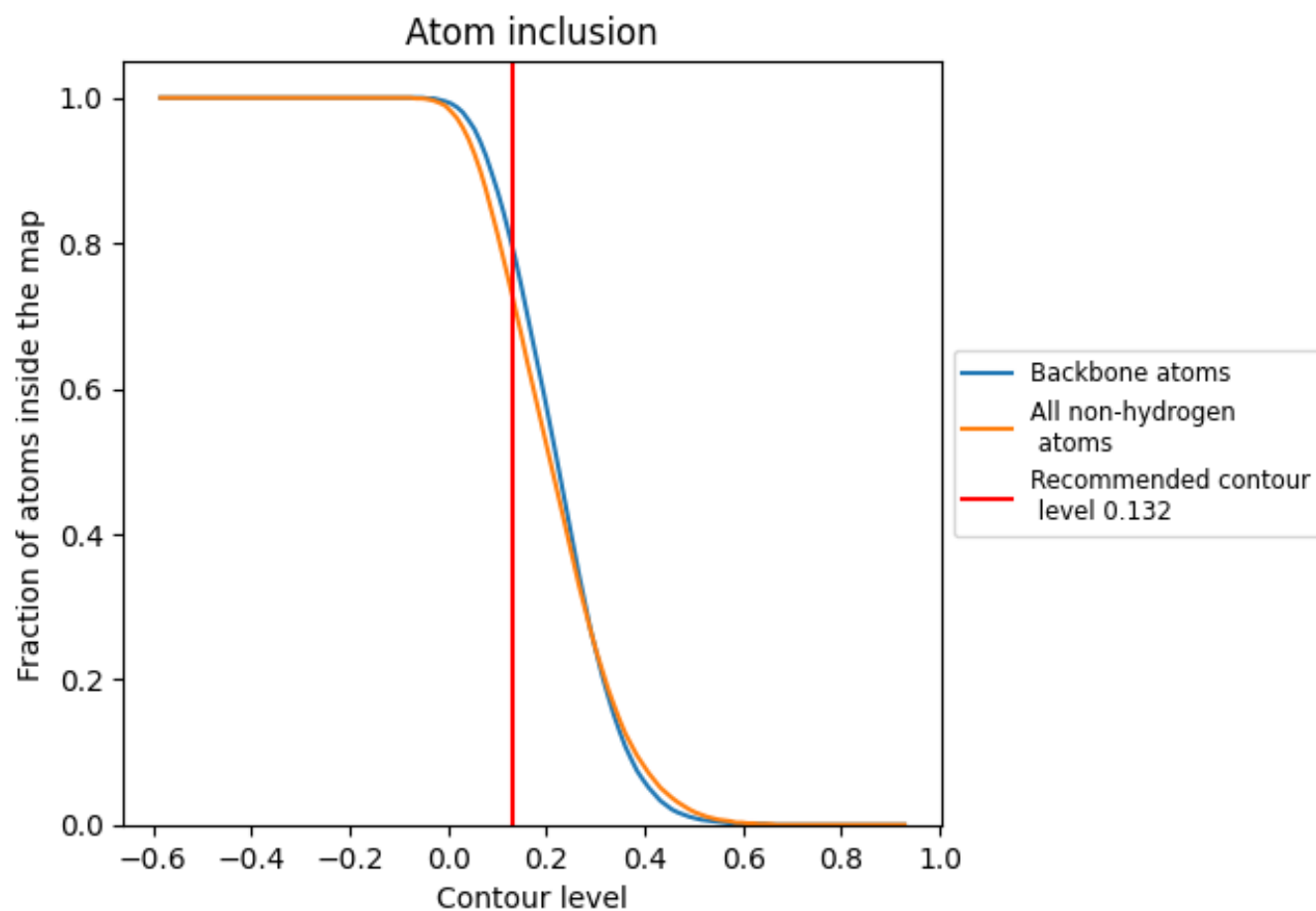
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

