



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 10:40 AM UTC

PDB ID : 5MMM / pdb_00005mmm
EMDB ID : EMD-3533
Title : Structure of the 70S chloroplast ribosome
Authors : Bieri, P.; Leibundgut, M.; Saurer, M.; Boehringer, D.; Ban, N.
Deposited on : 2016-12-11
Resolution : 3.40 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:

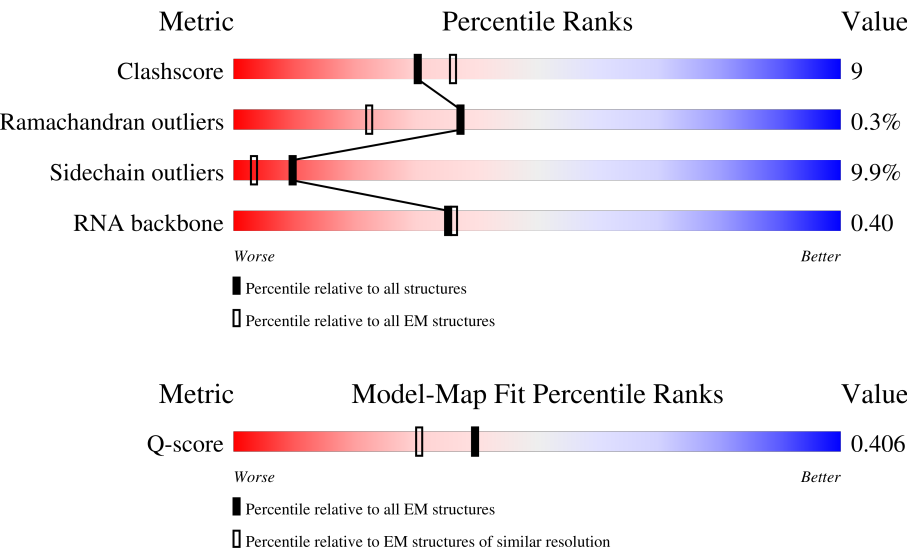
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.40 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.



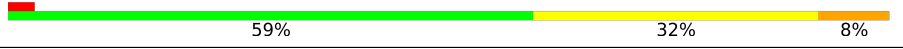
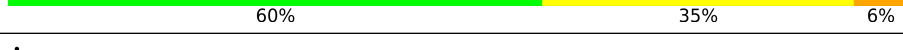
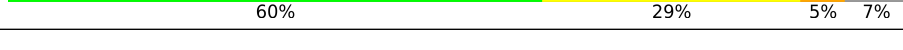
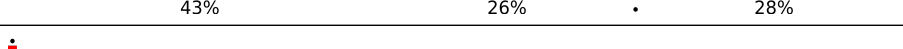
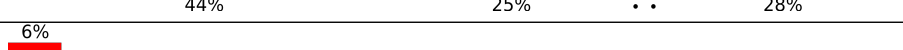
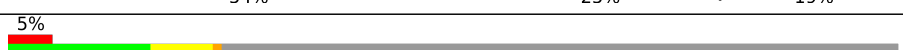
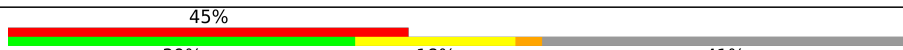
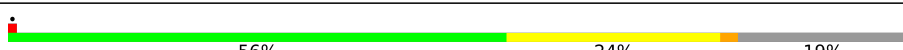
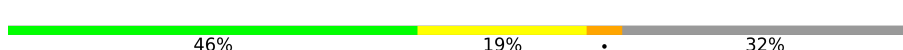
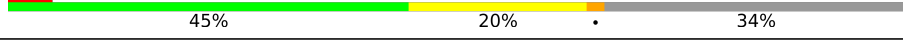
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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

Mol	Chain	Length	Quality of chain
1	0	130	
2	1	57	
3	2	66	

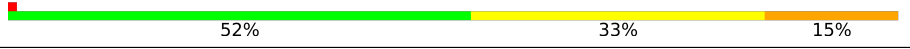
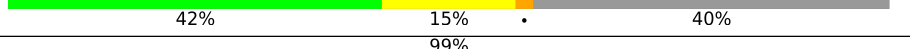
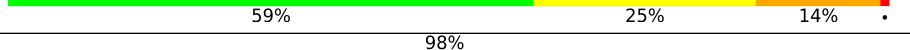
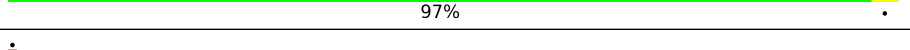
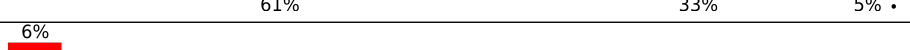
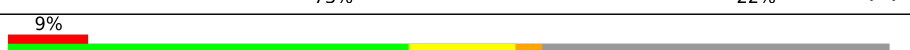
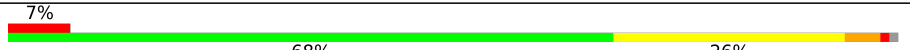
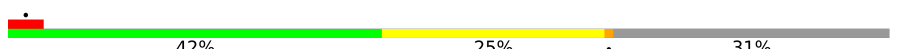
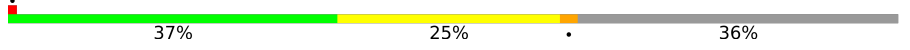
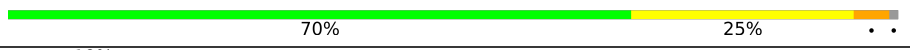
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Mol	Chain	Length	Quality of chain
4	3	152	
5	4	159	
6	5	37	
7	6	142	
8	7	116	
9	A	2810	
10	B	121	
11	C	272	
12	D	305	
13	E	293	
14	F	258	
15	G	220	
16	H	196	
17	I	232	
18	J	224	
19	K	250	
20	L	121	
21	M	271	
22	N	135	
23	O	126	
24	P	166	
25	Q	233	
26	R	128	
27	S	256	
28	T	199	

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Mol	Chain	Length	Quality of chain
29	U	198	
30	V	192	
31	W	106	
32	X	194	
33	Y	148	
34	Z	168	
35	z	76	
36	8	174	
37	a	1491	
38	b	236	
39	c	218	
40	d	201	
41	e	308	
42	f	211	
43	g	155	
44	h	134	
45	i	208	
46	j	195	
47	k	138	
48	l	123	
49	m	172	
50	n	100	
51	o	90	
52	p	88	
53	q	165	

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Mol	Chain	Length	Quality of chain
54	r	101	
55	s	92	
56	t	183	
57	u	180	
58	v	260	
59	w	179	
60	x	101	
61	y	302	

2 Entry composition

There are 63 unique types of molecules in this entry. The entry contains 152465 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	66	Total	C	N	O	S	0	0
			536	338	94	102	2		

- Molecule 2 is a protein called 50S ribosomal protein L32, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	48	Total	C	N	O		0	0
			396	261	75	60			

- Molecule 3 is a protein called 50S ribosomal protein L33, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	60	Total	C	N	O	S	0	0
			489	304	98	83	4		

- Molecule 4 is a protein called 50S ribosomal protein L34, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	60	Total	C	N	O	S	0	0
			467	282	107	75	3		

- Molecule 5 is a protein called 50S ribosomal protein L35, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	72	Total	C	N	O	S	0	0
			588	370	124	93	1		

- Molecule 6 is a protein called 50S ribosomal protein L36, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	37	Total	C	N	O	S	0	0
			305	186	70	45	4		

- Molecule 7 is a protein called plastid ribosomal protein cL37, PSRP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	49	Total	C	N	O	S	0	0
			422	268	92	57	5		

- Molecule 8 is a protein called 50S ribosomal protein 6, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	46	Total	C	N	O	S	0	0
			368	237	71	59	1		

- Molecule 9 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	2798	Total	C	N	O	P	0	0
			60083	26804	11116	19365	2798		

- Molecule 10 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	121	Total	C	N	O	P	0	0
			2584	1154	466	843	121		

- Molecule 11 is a protein called 50S ribosomal protein L2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	253	Total	C	N	O	S	0	0
			1952	1209	401	336	6		

- Molecule 12 is a protein called plastid ribosomal protein uL3c.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D	221	Total	C	N	O	S	0	0
			1686	1066	308	301	11		

- Molecule 13 is a protein called plastid ribosomal protein uL4c.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	E	212	Total	C	N	O	S	0	0
			1676	1061	312	300	3		

- Molecule 14 is a protein called plastid ribosomal protein uL5c.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	193	Total	C	N	O	S	0	0
			1454	923	255	268	8		

- Molecule 15 is a protein called plastid ribosomal protein uL6c.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	178	Total	C	N	O	S	0	0
			1391	878	256	253	4		

- Molecule 16 is a protein called plastid ribosomal protein bL9c.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	H	48	Total	C	N	O	0	0
			382	251	69	62		

- Molecule 17 is a protein called plastid ribosomal protein uL10c.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	137	Total	C	N	O	S	0	0
			1106	711	186	203	6		

- Molecule 18 is a protein called 50S ribosomal protein L11, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	133	Total	C	N	O	S	0	0
			977	624	161	186	6		

- Molecule 19 is a protein called 50S ribosomal protein L13, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	203	Total	C	N	O	S	0	0
			1648	1047	307	289	5		

- Molecule 20 is a protein called 50S ribosomal protein L14, chloroplastic.

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

- Molecule 21 is a protein called plastid ribosomal protein uL15c.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	185	Total	C	N	O	S	0	0
			1410	879	280	245	6		

- Molecule 22 is a protein called 50S ribosomal protein L16, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	135	Total	C	N	O	S	0	0
			1075	677	218	174	6		

- Molecule 23 is a protein called plastid ribosomal protein uL14c.

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

- Molecule 24 is a protein called plastid ribosomal protein uL18c.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	122	Total	C	N	O	S	0	0
			962	598	186	173	5		

- Molecule 25 is a protein called 50S ribosomal protein L19, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	118	Total	C	N	O	S	0	0
			953	611	186	155	1		

- Molecule 26 is a protein called 50S ribosomal protein L20, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	119	Total	C	N	O	S	0	0
			1029	652	213	162	2		

- Molecule 27 is a protein called 50S ribosomal protein L21, chloroplastic.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	S	170	Total	C	N	O	0	0
			1310	844	227	239		

- Molecule 28 is a protein called 50S ribosomal protein L22, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	172	Total	C	N	O	S	0	0
			1395	892	257	237	9		

- Molecule 29 is a protein called 50S ribosomal protein L23, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	96	Total	C	N	O	S	0	0
			776	503	135	136	2		

- Molecule 30 is a protein called plastid ribosomal protein uL24c.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	V	134	Total	C	N	O	S	0	0
			1078	677	203	195	3		

- Molecule 31 is a RNA chain called 4.5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	W	106	Total	C	N	O	P	0	0
			2277	1017	423	731	106		

- Molecule 32 is a protein called plastid ribosomal protein bL27c.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	X	109	Total	C	N	O	0	0
			888	560	175	153		

- Molecule 33 is a protein called plastid ribosomal protein bL28c.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Y	77	Total	C	N	O	S	0	0
			634	402	128	103	1		

- Molecule 34 is a protein called plastid ribosomal protein uL29c.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z	101	Total	C	N	O	S	0	0
			846	529	167	147	3		

- Molecule 35 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	z	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

- Molecule 36 is a protein called plastid ribosomal protein bS1c.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	8	174	Total	C	N	O		0	0
			870	522	174	174			

- Molecule 37 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	a	1484	Total	C	N	O	P	0	0
			31868	14208	5881	10295	1484		

- Molecule 38 is a protein called 30S ribosomal protein S2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	b	233	Total	C	N	O	S	0	0
			1844	1163	339	329	13		

- Molecule 39 is a protein called 30S ribosomal protein S3, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	c	216	Total	C	N	O	S	0	0
			1736	1108	313	309	6		

- Molecule 40 is a protein called 30S ribosomal protein S4, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	d	199	Total	C	N	O	S	0	0
			1633	1032	319	278	4		

- Molecule 41 is a protein called 30S ribosomal protein S5, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	e	187	Total	C	N	O	S	0	0
			1331	826	259	240	6		

- Molecule 42 is a protein called plastid ribosomal protein bS6c.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	f	113	Total	C	N	O	S	0	0
			911	583	152	172	4		

- Molecule 43 is a protein called 30S ribosomal protein S7, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	g	154	Total	C	N	O	S	0	0
			1210	753	244	210	3		

- Molecule 44 is a protein called 30S ribosomal protein S8, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	h	133	Total	C	N	O	S	0	0
			1079	679	210	185	5		

- Molecule 45 is a protein called plastid ribosomal protein uS9c.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	i	144	Total	C	N	O	S	0	0
			1119	712	211	195	1		

- Molecule 46 is a protein called plastid ribosomal protein uS10c.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	j	99	Total	C	N	O	S	0	0
			805	517	144	139	5		

- Molecule 47 is a protein called 30S ribosomal protein S11, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	k	117	Total	C	N	O	S	0	0
			882	546	181	150	5		

- Molecule 48 is a protein called 30S ribosomal protein S12, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	l	122	Total	C	N	O	S	0	0
			959	599	197	161	2		

- Molecule 49 is a protein called plastid ribosomal protein uS13c.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	m	110	Total	C	N	O	S	0	0
			904	556	182	161	5		

- Molecule 50 is a protein called 30S ribosomal protein S14, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	n	99	Total	C	N	O	S	0	0
			820	507	174	136	3		

- Molecule 51 is a protein called 30S ribosomal protein S15, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	o	75	Total	C	N	O	S	0	0
			635	404	123	107	1		

- Molecule 52 is a protein called 30S ribosomal protein S16, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	p	80	Total	C	N	O	S	0	0
			664	425	123	114	2		

- Molecule 53 is a protein called plastid ribosomal protein uS17c.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	q	86	Total	C	N	O	S	0	0
			693	434	136	119	4		

- Molecule 54 is a protein called 30S ribosomal protein S18, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	r	60	Total	C	N	O	S	0	0
			490	308	96	85	1		

- Molecule 55 is a protein called 30S ribosomal protein S19 alpha, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	s	78	Total	C	N	O	S	0	0
			631	406	119	104	2		

- Molecule 56 is a protein called plastid ribosomal protein bS20c.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	t	107	Total	C	N	O	S	0	0
			853	528	173	151	1		

- Molecule 57 is a protein called plastid ribosomal protein bS21c.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	u	65	Total	C	N	O	S	0	0
			568	339	127	100	2		

- Molecule 58 is a protein called 30S ribosomal protein 2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	v	80	Total	C	N	O	S	0	0
			613	388	104	121			

- Molecule 59 is a protein called 30S ribosomal protein 3, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	w	82	Total	C	N	O	S	0	0
			686	454	113	116	3		

- Molecule 60 is a protein called 30S ribosomal protein S31, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	x	40	Total	C	N	O	S	0	0
			309	192	69	48			

- Molecule 61 is a protein called Ribosome-binding factor PSRP1, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	y	116	Total	C	N	O	S	0	0
			919	567	181	169	2		

- Molecule 62 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
62	2	1	Total	Zn	0
			1	1	
62	5	1	Total	Zn	0
			1	1	

- Molecule 63 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
63	4	1	Total 1	Mg 1	0
63	6	1	Total 1	Mg 1	0
63	7	1	Total 1	Mg 1	0
63	A	511	Total 511	Mg 511	0
63	B	15	Total 15	Mg 15	0
63	C	1	Total 1	Mg 1	0
63	D	1	Total 1	Mg 1	0
63	E	1	Total 1	Mg 1	0
63	F	1	Total 1	Mg 1	0
63	H	1	Total 1	Mg 1	0
63	M	2	Total 2	Mg 2	0
63	P	1	Total 1	Mg 1	0
63	R	1	Total 1	Mg 1	0
63	S	1	Total 1	Mg 1	0
63	T	1	Total 1	Mg 1	0
63	U	1	Total 1	Mg 1	0
63	V	1	Total 1	Mg 1	0
63	W	14	Total 14	Mg 14	0
63	a	219	Total 219	Mg 219	0
63	k	1	Total 1	Mg 1	0
63	l	1	Total 1	Mg 1	0
63	n	1	Total 1	Mg 1	0

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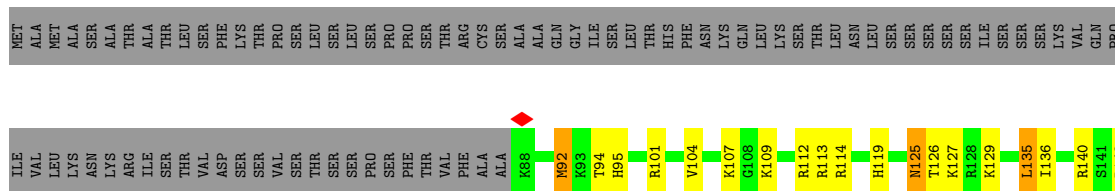
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Mol	Chain	Residues	Atoms		AltConf
63	x	1	Total	Mg	0
			1	1	



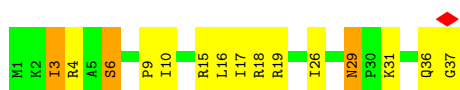
- Molecule 5: 50S ribosomal protein L35, chloroplastic

Chain 4: 31% 12% 55%



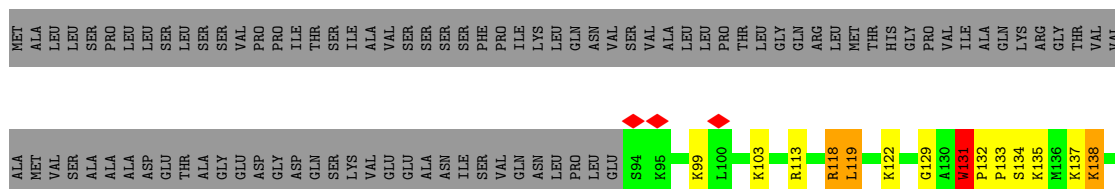
- Molecule 6: 50S ribosomal protein L36, chloroplastic

Chain 5: 59% 32% 8%



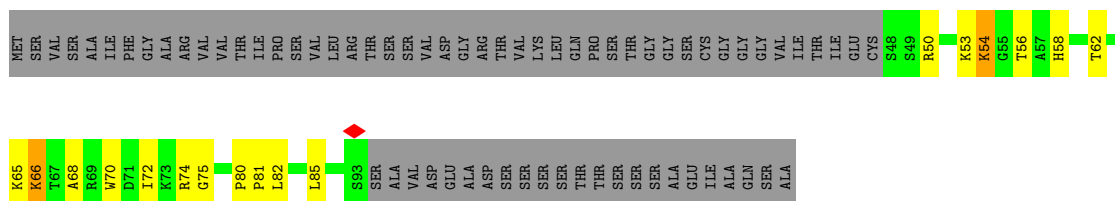
- Molecule 7: plastid ribosomal protein cL37, PSRP5

Chain 6: 25% 7% 65%



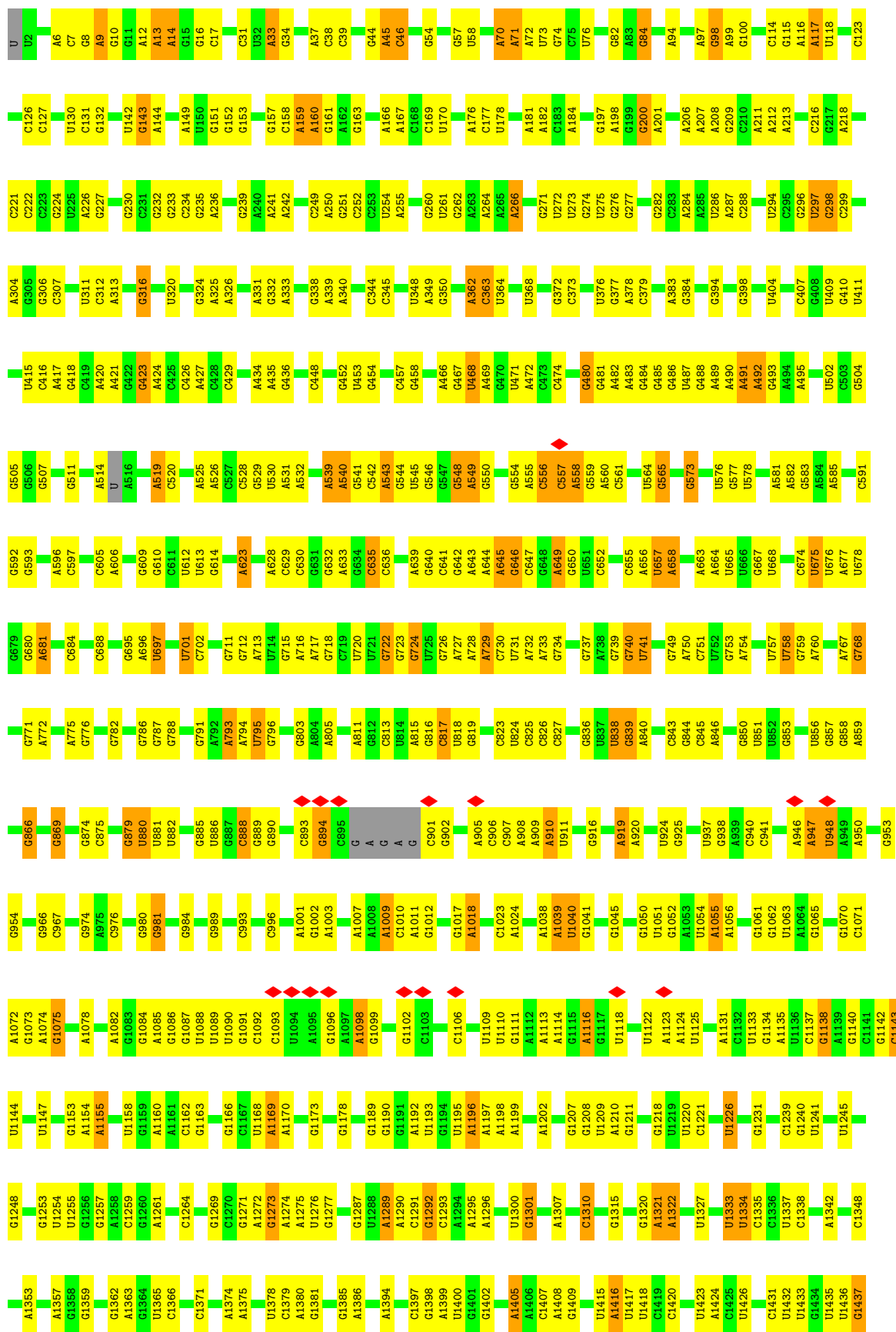
- Molecule 8: 50S ribosomal protein 6, chloroplastic

Chain 7: 25% 13% 60%

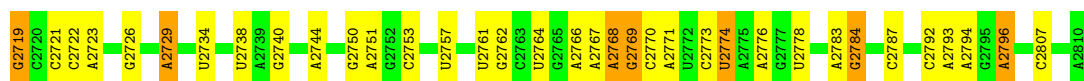


- Molecule 9: 23S ribosomal RNA

Chain A: 56% 36% 8%

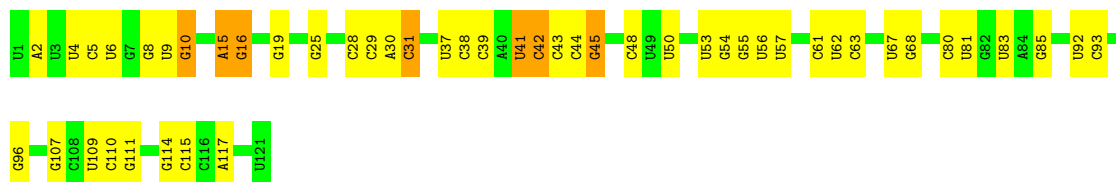


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G2620	C2515	G2427	U2264	U2194	A2133	G2051	G1944	C1854	C1750	A1616	A1522	A1444
U2621	G2518	A2428	U2266	G2195	G2194	A2053	A1950	A1857	A	U1620	G1524	G1445
G2624	G2519	A2429	G2268	A2198	G2135	C2054	A1951	A1858	C	C1621	G1526	G1446
G2625	A2520	G2430	G2269	G2199	G2136	A2055	A1952	U1861	A	G1629	U1527	G1447
G2626	U2521	G2431	G2270	A2200	G2137	A2056	U1953	C1861	A	U1630	U1528	A1448
G2627	U2522	G2432	C2271	G2201	G2138	C2057	U1959	C1862	G1756	G1631	A1529	C1449
G2628	U2523	C2439	C2278	U2203	A2140	A2062	U1974	A1863	G1760	U1632	G1530	G1450
G2629	G2524	A2442	C2281	A2204	G2141	C2063	A1974	A1864	U1760	U1633	G1531	G1454
U2630	G2525	G2443	G2281	G2205	G2142	C2064	C1975	A1865	U1761	A1634	G1532	A1531
G2636	G2526	C2444	G2281	A2206	G2143	U2065	C1976	G1865	U1762	C1635	G1533	G1455
U2637	G2527	G2445	G2281	A2207	G2144	G2066	C1977	A1867	G1763	U1636	A1534	G1457
C2637	U2528	A2446	A2285	U2208	G2145	C2069	C1978	U1870	A1764	A1535	C1458	
G2640	C2529	A2447	A2285	U2209	A2146	A2070	C1979	U1874	G1774	A1536	A1465	
U2646	U2530	U2448	G2288	A2212	A2147	A2071	A1980	U1875	G1774	G1543	G1468	
A2649	C2535	A2452	U2288	A2213	G2148	A2074	C1981	C1875	G1778	G1544	C1469	
A2652	G2542	A2456	A2290	A2217	A2149	G2075	A1984	A1877	A1783	G1546		
A2656	G2546	C2457	C2292	G2218	G2150	C2076	A1985	C1877	U1790	U1550	A1472	
A2657	U2547	U2458	G2296	U2219	C2152	C2078	U2005	U1882	C1791	G1557	U1475	
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A2661	U2555	C2463	G2302	G2225	U2157	A2091	G2014	U1887	G1888			
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U2706	G2592	A2495	A2250	A2250	C2174	U2118	G2037	U1927	A1701	A1592		
A2707	G2593	G2498	G2251	G2251	A2175	U2119	U2036	C1928	G1702	U1593		
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			U2262	U2262	A2185	U2131	G2049	C1939				
					U2186			U1940				
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					C2189							
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					C2191							
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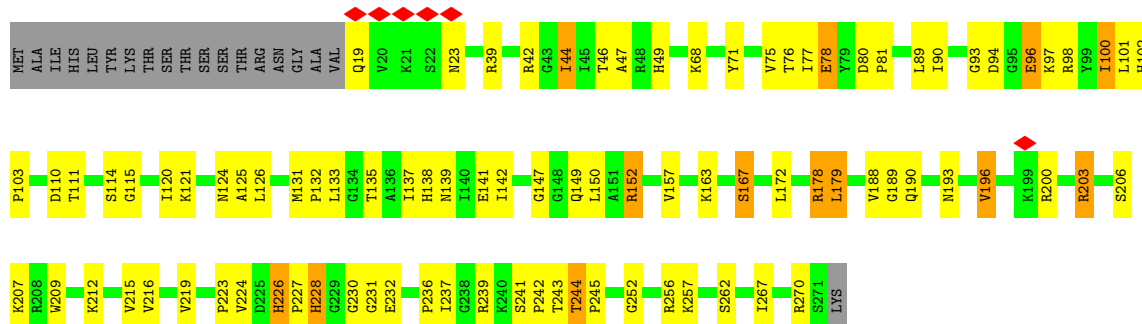
• Molecule 10: 5S ribosomal RNA

Chain B: 60% 35% 6%



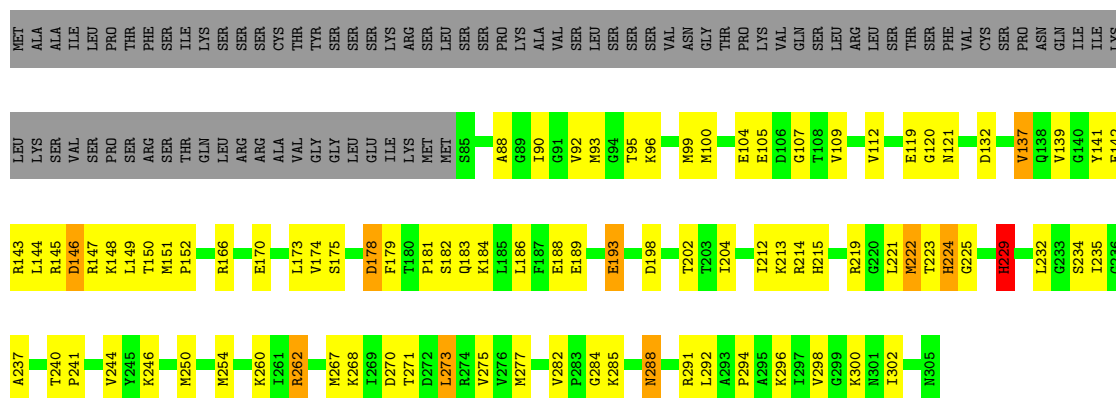
• Molecule 11: 50S ribosomal protein L2, chloroplastic

Chain C: 60% 29% 5% 7%



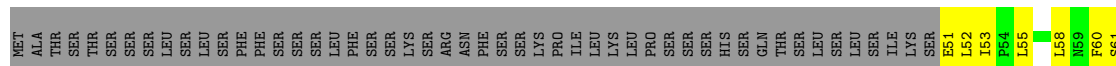
• Molecule 12: plastid ribosomal protein uL3c

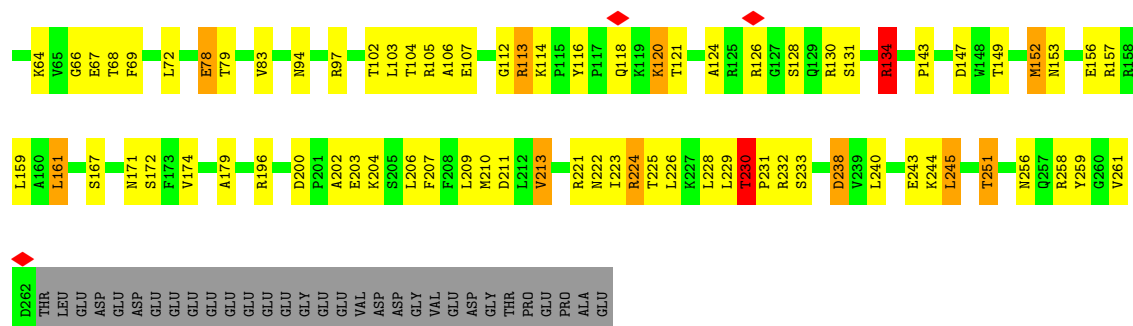
Chain D: 43% 26% 28%



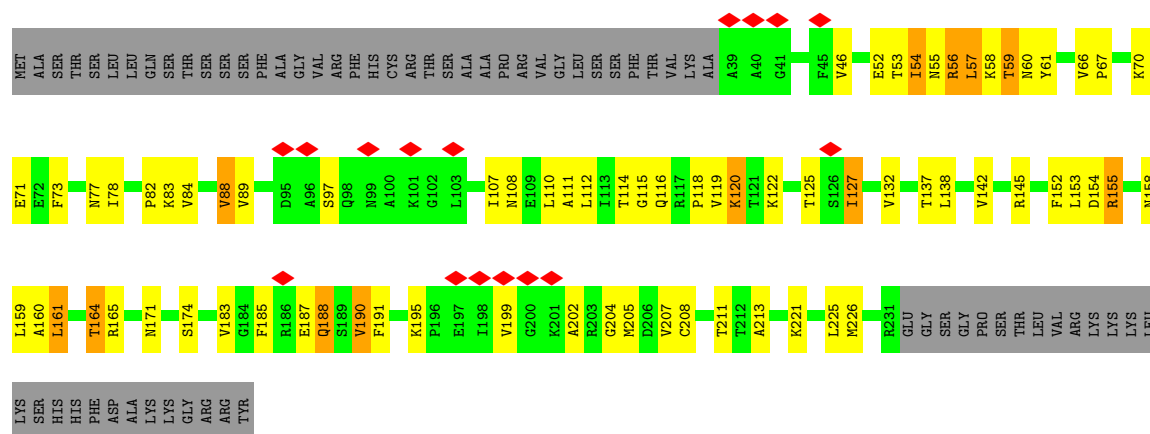
• Molecule 13: plastid ribosomal protein uL4c

Chain E: 44% 25% 28%

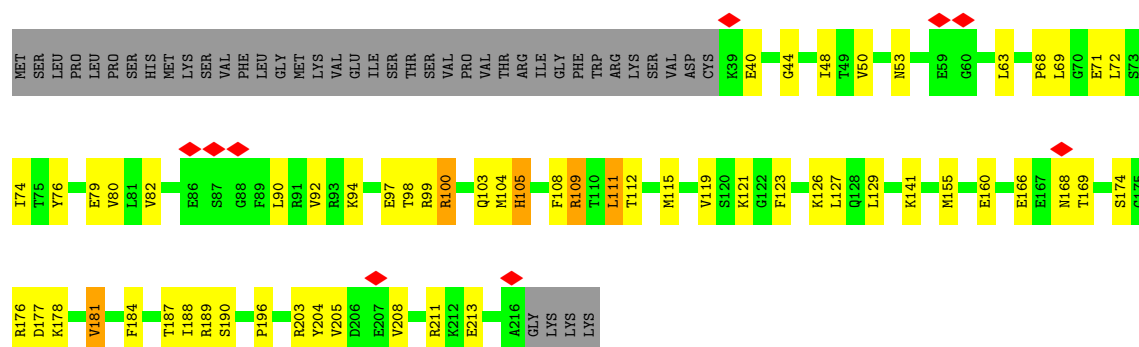




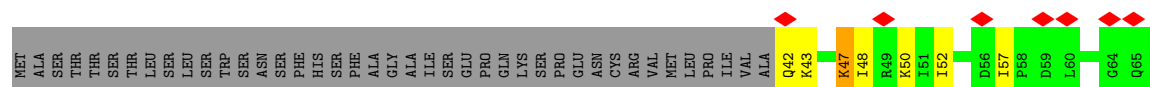
• Molecule 14: plastid ribosomal protein uL5c

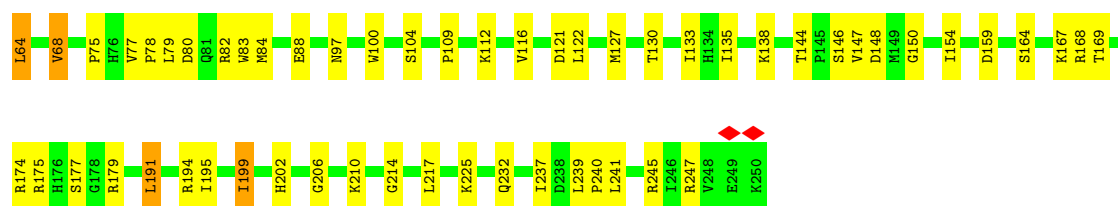


• Molecule 15: plastid ribosomal protein uL6c

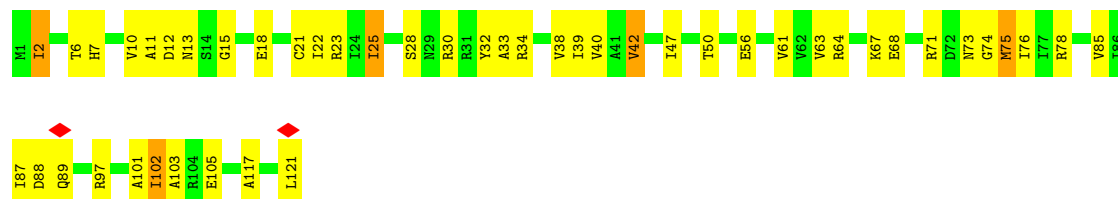


• Molecule 16: plastid ribosomal protein bL9c

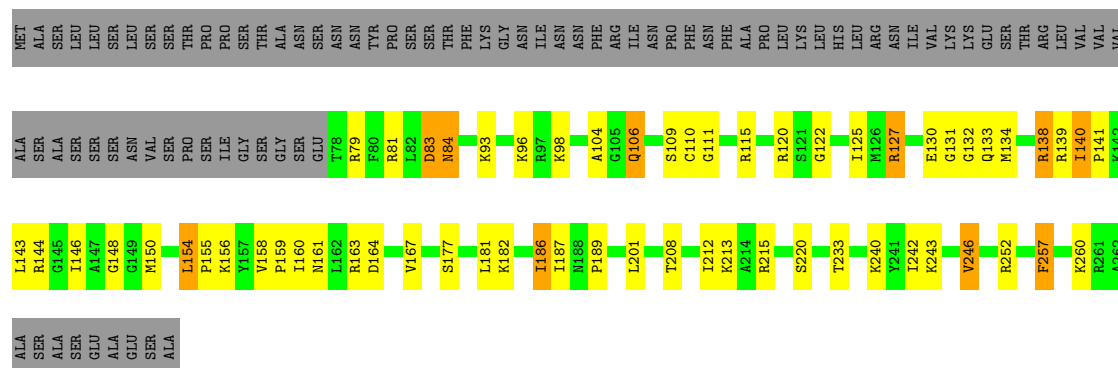




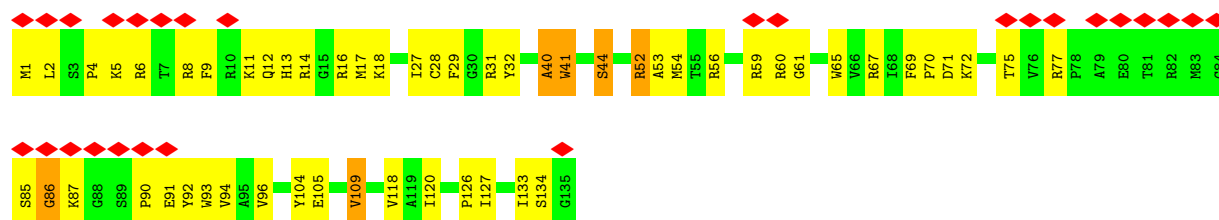
- Molecule 20: 50S ribosomal protein L14, chloroplastic



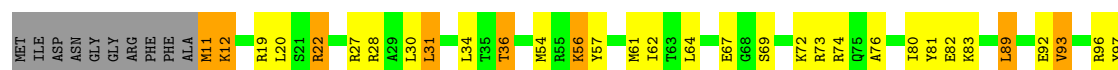
- Molecule 21: plastid ribosomal protein uL15c



- Molecule 22: 50S ribosomal protein L16, chloroplastic

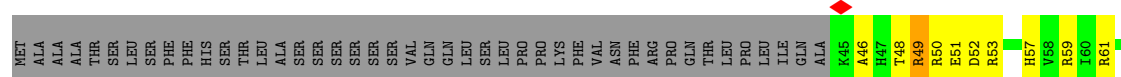


- Molecule 23: plastid ribosomal protein uL14c

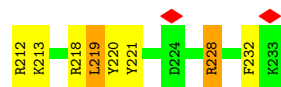
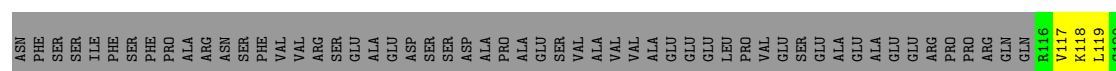
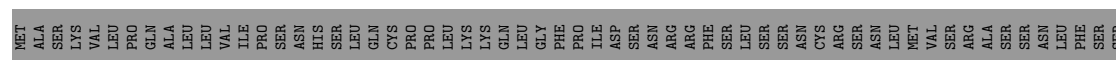
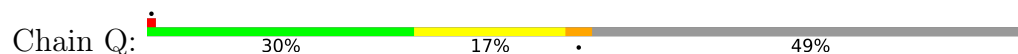




- Molecule 24: plastid ribosomal protein uL18c



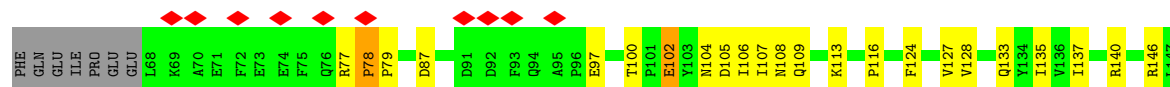
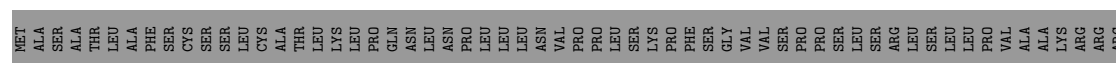
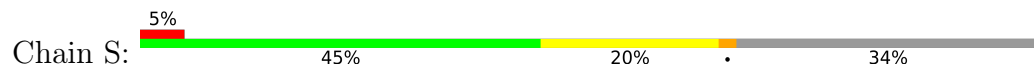
- Molecule 25: 50S ribosomal protein L19, chloroplastic



- Molecule 26: 50S ribosomal protein L20, chloroplastic

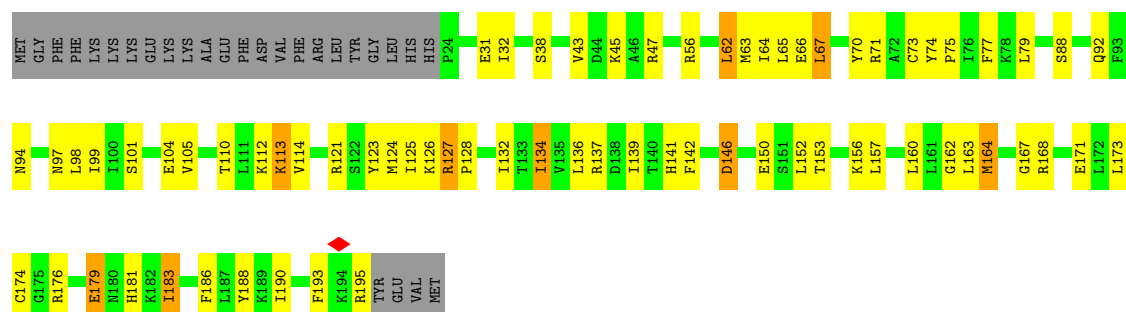


- Molecule 27: 50S ribosomal protein L21, chloroplastic

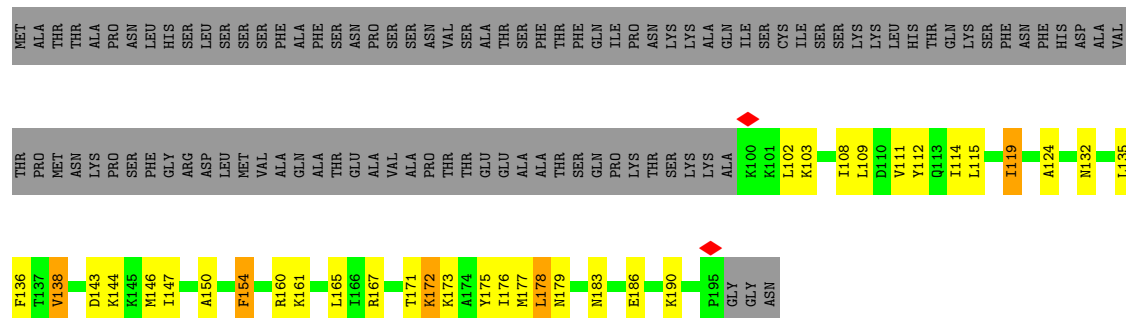
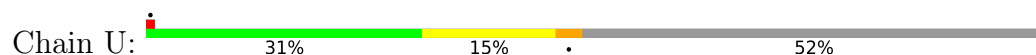




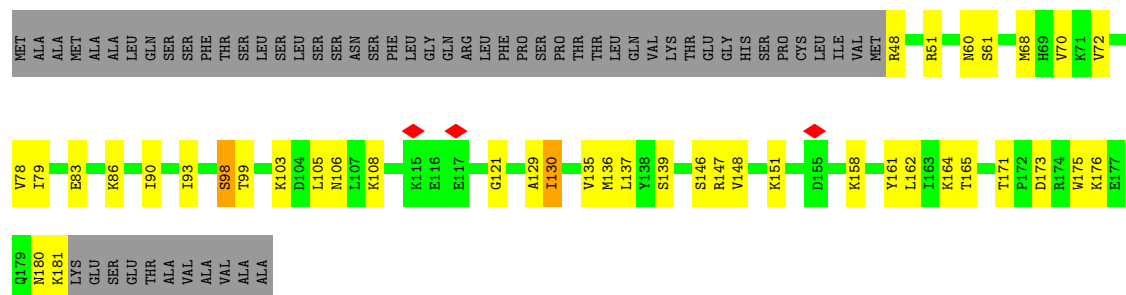
- Molecule 28: 50S ribosomal protein L22, chloroplastic



- Molecule 29: 50S ribosomal protein L23, chloroplastic

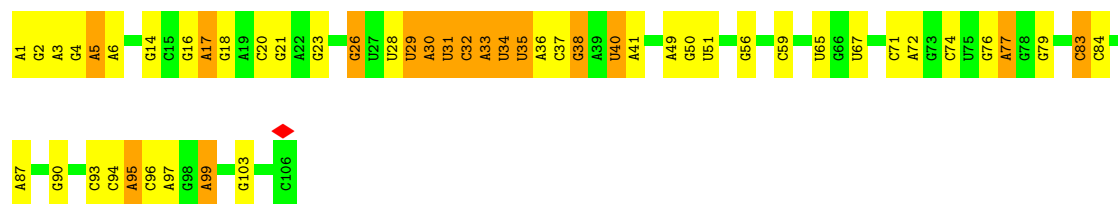


- Molecule 30: plastid ribosomal protein uL24c

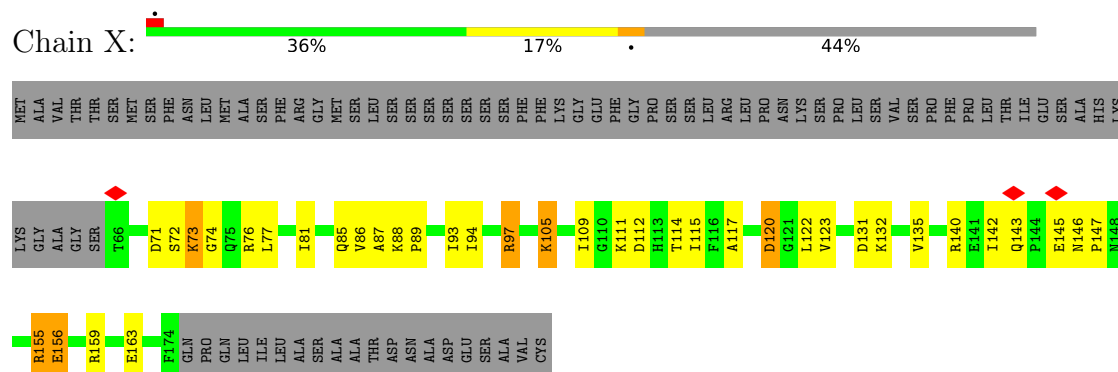


- Molecule 31: 4.5S ribosomal RNA

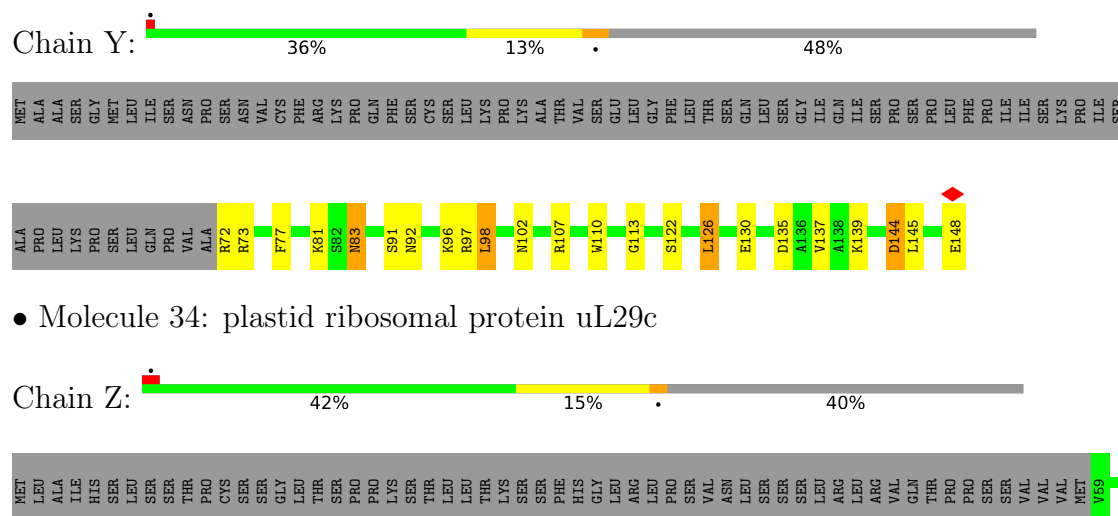




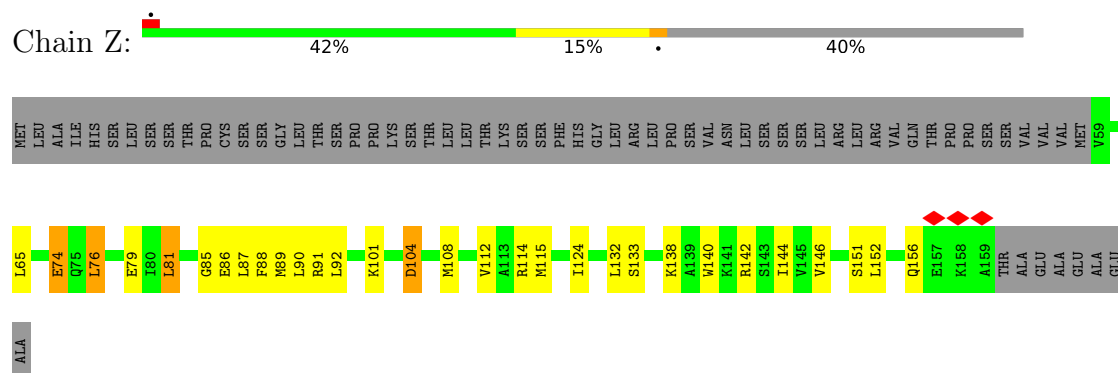
• Molecule 32: plastid ribosomal protein bL27c



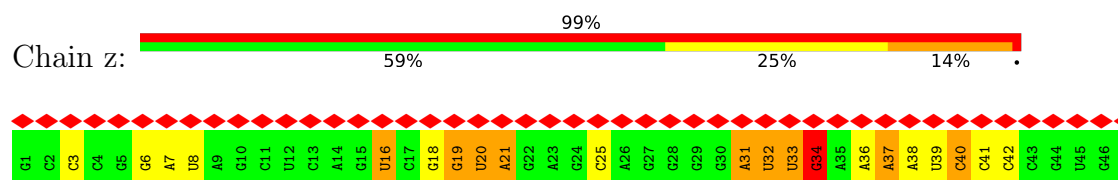
• Molecule 33: plastid ribosomal protein bL28c



• Molecule 34: plastid ribosomal protein uL29c

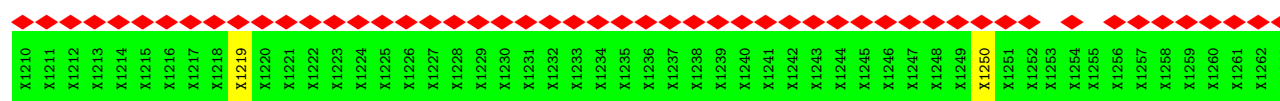
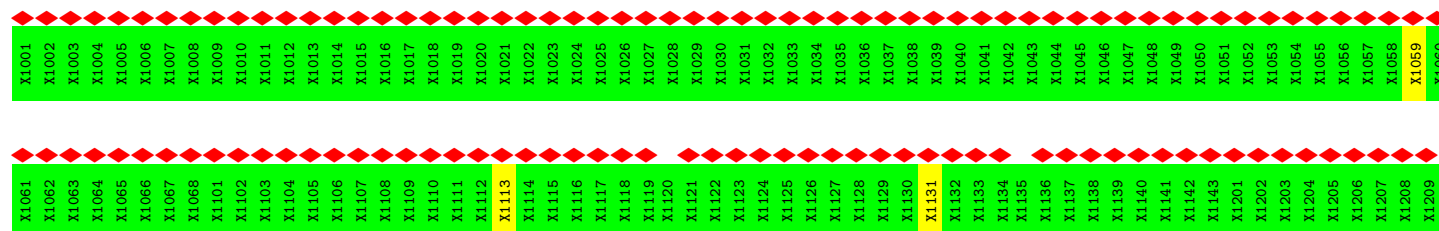


• Molecule 35: tRNA-Phe

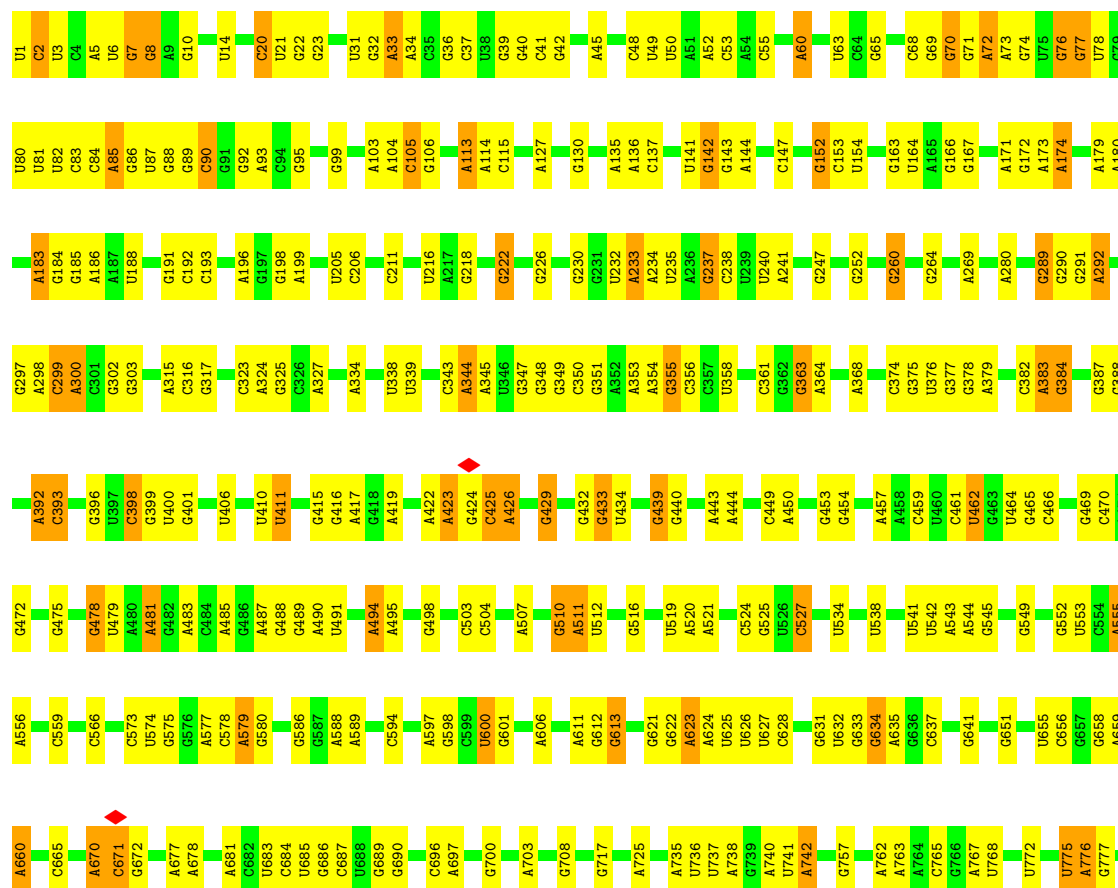


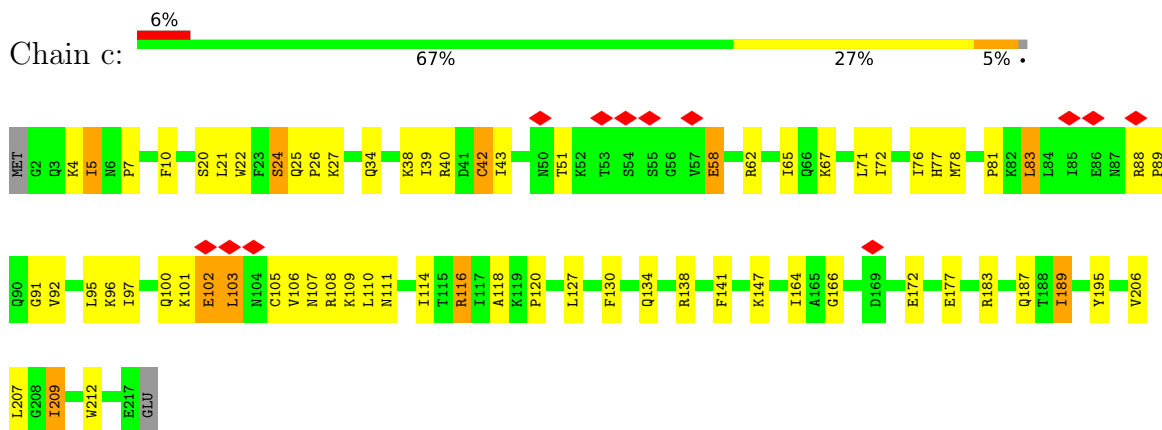


- Molecule 36: plastid ribosomal protein bS1c

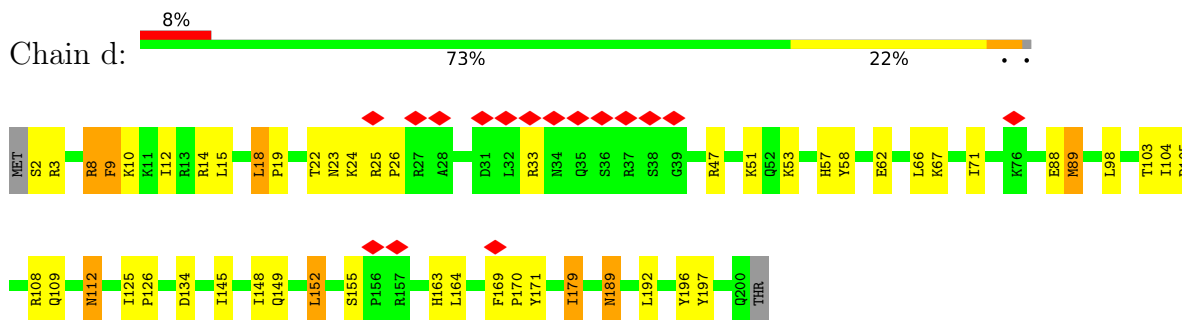


- Molecule 37: 16S ribosomal RNA

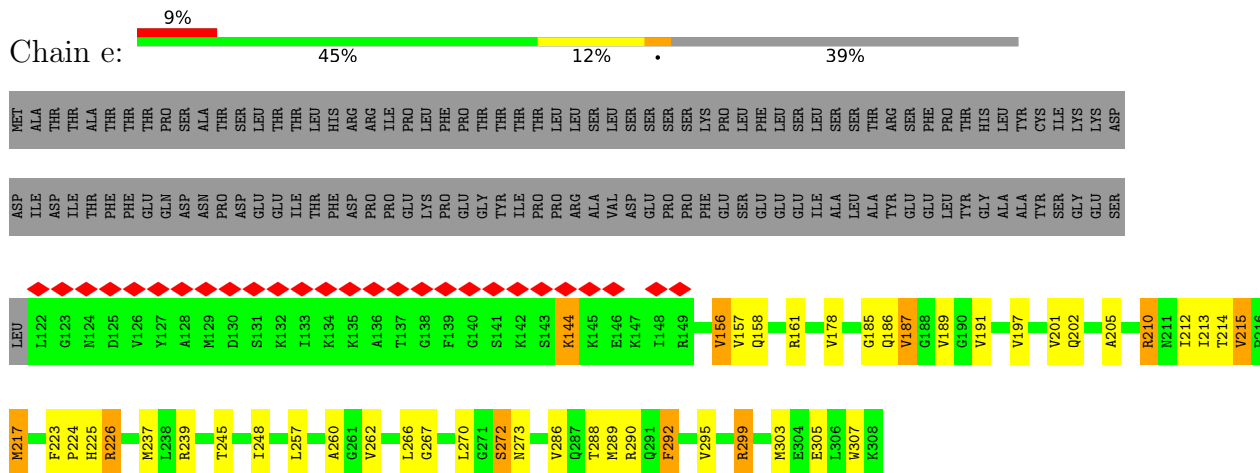




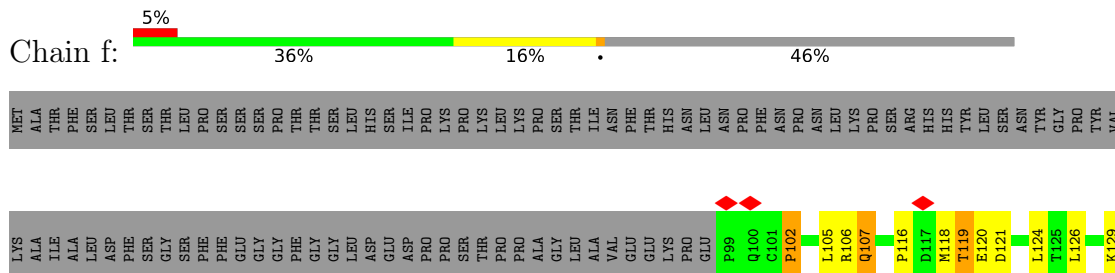
- Molecule 40: 30S ribosomal protein S4, chloroplastic



- Molecule 41: 30S ribosomal protein S5, chloroplastic

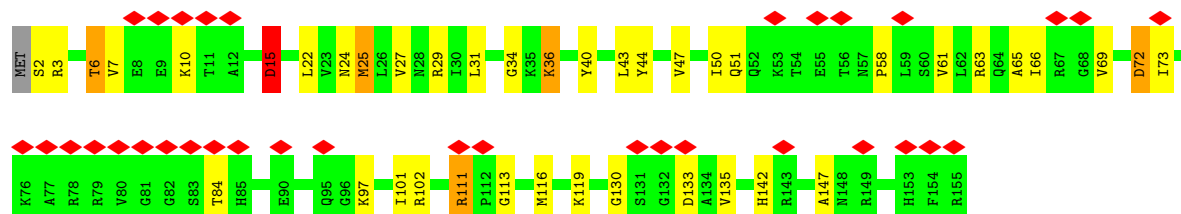
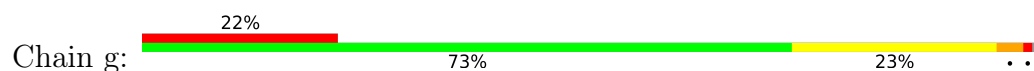


- Molecule 42: plastid ribosomal protein bS6c

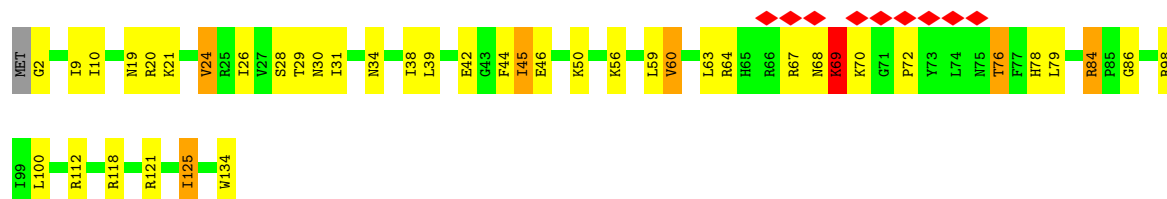




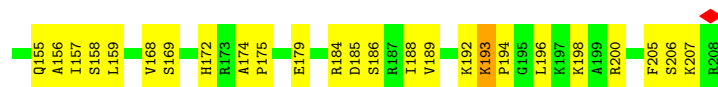
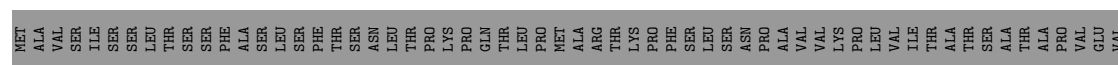
- Molecule 43: 30S ribosomal protein S7, chloroplastic



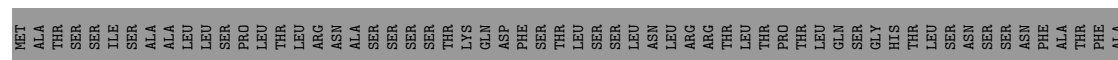
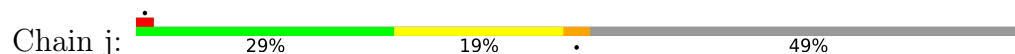
- Molecule 44: 30S ribosomal protein S8, chloroplastic

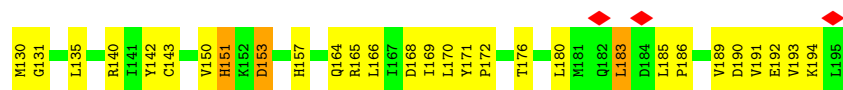


- Molecule 45: plastid ribosomal protein uS9c

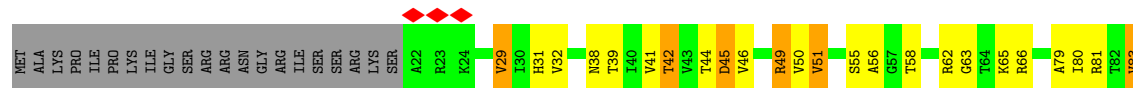


- Molecule 46: plastid ribosomal protein uS10c





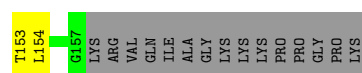
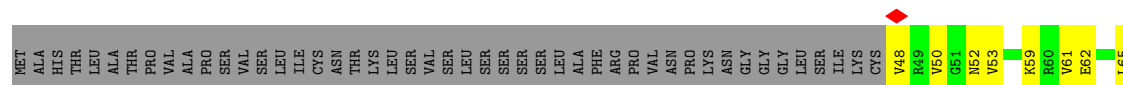
- Molecule 47: 30S ribosomal protein S11, chloroplastic



- Molecule 48: 30S ribosomal protein S12, chloroplastic



- Molecule 49: plastid ribosomal protein uS13c

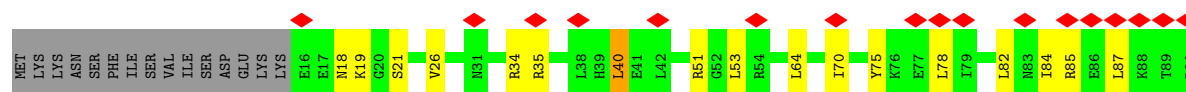


- Molecule 50: 30S ribosomal protein S14, chloroplastic

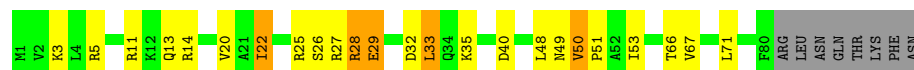


- Molecule 51: 30S ribosomal protein S15, chloroplastic

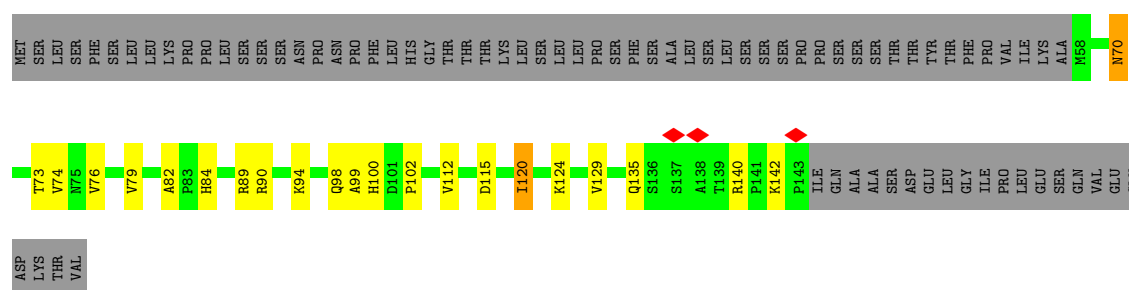
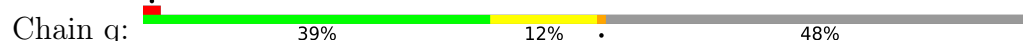




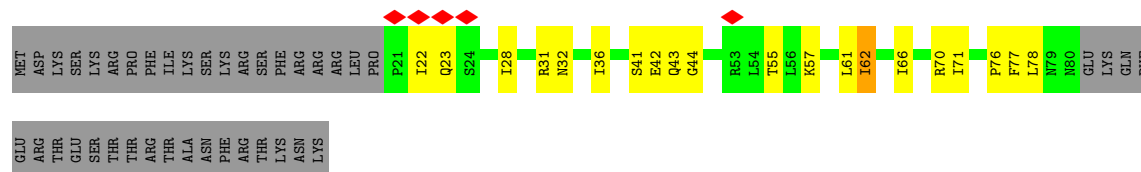
- Molecule 52: 30S ribosomal protein S16, chloroplastic



- Molecule 53: plastid ribosomal protein uS17c



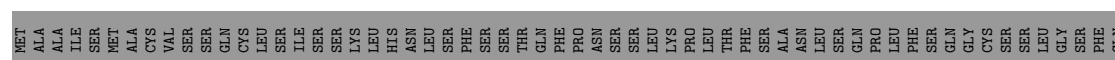
- Molecule 54: 30S ribosomal protein S18, chloroplastic



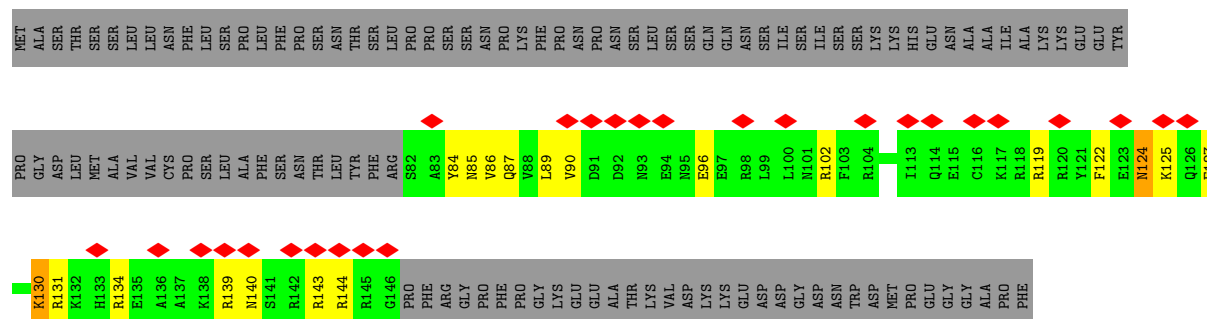
- Molecule 55: 30S ribosomal protein S19 alpha, chloroplastic



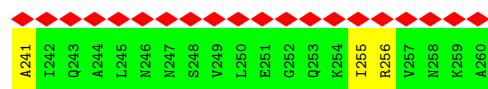
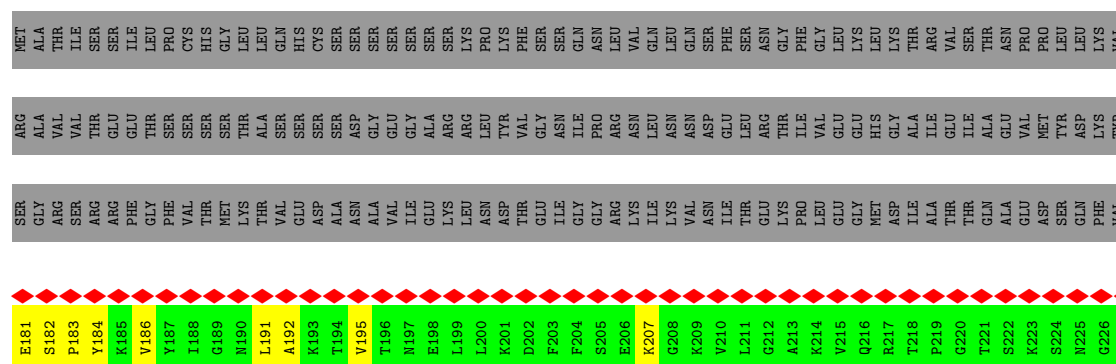
- Molecule 56: plastid ribosomal protein bS20c



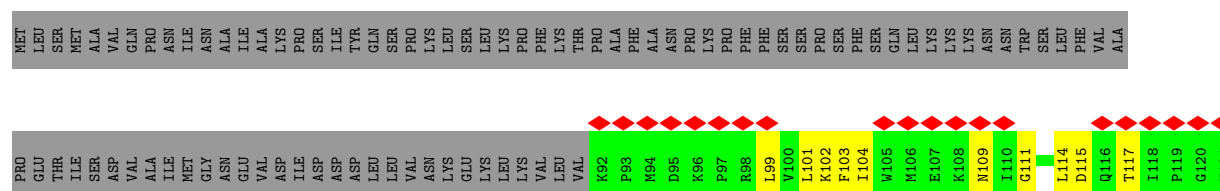
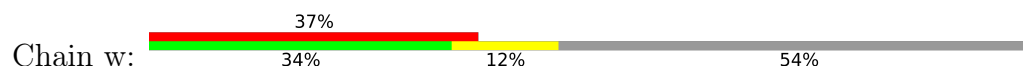
- Molecule 57: plastid ribosomal protein bS21c



- Molecule 58: 30S ribosomal protein 2, chloroplastic

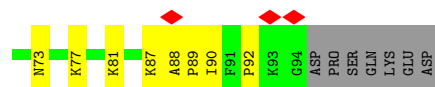
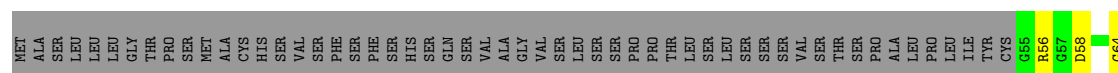


- Molecule 59: 30S ribosomal protein 3, chloroplastic

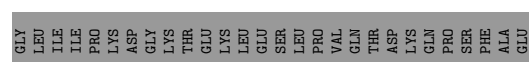
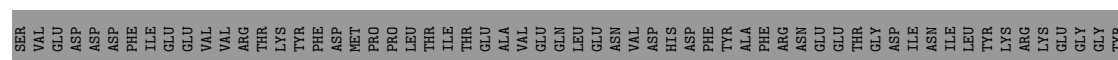
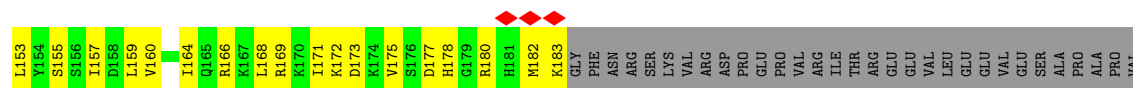




- Molecule 60: 30S ribosomal protein S31, chloroplastic



- Molecule 61: Ribosome-binding factor PSRP1, chloroplastic



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	140583	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.481	Depositor
Minimum map value	-0.179	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	444.8, 444.8, 444.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.39, 1.39, 1.39	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	0	0.85	0/548	1.23	5/737 (0.7%)
2	1	0.69	0/405	1.03	2/537 (0.4%)
3	2	0.58	0/497	1.06	3/664 (0.5%)
4	3	0.69	0/470	1.02	2/619 (0.3%)
5	4	0.68	0/594	1.03	0/784
6	5	0.49	0/307	0.91	0/403
7	6	0.57	0/425	1.23	4/551 (0.7%)
8	7	0.56	0/382	0.92	2/520 (0.4%)
9	A	0.39	0/67297	0.49	0/104984
10	B	0.28	0/2890	0.40	0/4503
11	C	0.62	0/1986	1.06	4/2666 (0.2%)
12	D	0.68	0/1713	1.06	5/2291 (0.2%)
13	E	0.68	0/1707	1.12	10/2298 (0.4%)
14	F	0.52	0/1475	0.98	6/1990 (0.3%)
15	G	0.51	0/1412	0.97	0/1898
16	H	0.55	0/386	0.90	1/514 (0.2%)
17	I	0.85	0/1129	0.89	1/1521 (0.1%)
18	J	0.96	3/992 (0.3%)	1.01	3/1343 (0.2%)
19	K	0.64	0/1688	0.95	2/2279 (0.1%)
20	L	0.64	0/951	1.07	5/1282 (0.4%)
21	M	0.63	0/1430	1.06	1/1896 (0.1%)
22	N	0.58	0/1097	0.99	2/1471 (0.1%)
23	O	0.71	0/959	1.02	1/1280 (0.1%)
24	P	0.48	0/978	0.91	1/1311 (0.1%)
25	Q	0.71	0/967	1.14	8/1299 (0.6%)
26	R	0.75	0/1046	1.01	0/1395
27	S	0.62	0/1339	1.08	7/1826 (0.4%)
28	T	0.64	0/1420	0.98	3/1900 (0.2%)
29	U	0.63	0/787	0.99	0/1056
30	V	0.53	0/1093	1.00	1/1457 (0.1%)
31	W	0.36	0/2551	0.49	0/3977
32	X	0.55	0/905	0.93	2/1204 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Y	0.57	0/644	0.90	0/856
34	Z	0.48	0/854	0.84	0/1131
35	z	0.74	0/1813	0.93	1/2823 (0.0%)
37	a	0.28	0/35687	0.39	0/55680
38	b	0.57	0/1878	0.88	2/2538 (0.1%)
39	c	0.51	0/1763	0.98	1/2370 (0.0%)
40	d	0.46	0/1661	0.95	4/2230 (0.2%)
41	e	0.60	0/1345	1.00	4/1817 (0.2%)
42	f	0.44	0/929	0.90	2/1255 (0.2%)
43	g	0.52	0/1226	0.89	5/1641 (0.3%)
44	h	0.47	0/1094	0.91	0/1467
45	i	0.47	0/1138	0.99	5/1526 (0.3%)
46	j	0.55	0/822	0.88	0/1111
47	k	0.46	0/896	1.04	4/1206 (0.3%)
48	l	0.55	0/975	0.94	1/1312 (0.1%)
49	m	0.50	0/912	0.95	0/1219
50	n	0.55	0/836	0.91	0/1116
51	o	0.46	0/642	0.83	1/852 (0.1%)
52	p	0.48	0/674	0.96	2/902 (0.2%)
53	q	0.47	0/707	0.97	4/949 (0.4%)
54	r	0.48	0/494	0.84	0/660
55	s	0.53	0/646	0.92	0/870
56	t	0.52	0/862	0.95	3/1151 (0.3%)
57	u	0.43	0/572	0.79	0/754
58	v	0.87	0/621	0.87	0/833
59	w	0.91	0/707	0.91	0/962
60	x	0.63	0/317	1.13	3/418 (0.7%)
61	y	0.52	0/930	1.01	3/1243 (0.2%)
All	All	0.46	3/163471 (0.0%)	0.66	126/243348 (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
13	E	0	1
21	M	0	1
38	b	0	1
41	e	0	1
56	t	0	2
All	All	0	6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	J	93	PRO	CA-C	6.57	1.58	1.52
18	J	125	ILE	CA-CB	5.94	1.59	1.54
18	J	90	THR	CA-CB	5.18	1.57	1.52

The worst 5 of 126 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	6	131	TRP	CA-C-N	-10.00	110.08	120.38
7	6	131	TRP	C-N-CA	-10.00	110.08	120.38
47	k	97	GLY	CA-C-N	9.71	129.97	119.87
47	k	97	GLY	C-N-CA	9.71	129.97	119.87
11	C	231	GLY	N-CA-C	-8.73	99.25	112.60

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	E	134	ARG	Peptide
21	M	104	ALA	Peptide
38	b	74	VAL	Peptide
41	e	144	LYS	Peptide
56	t	75	LYS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	536	0	515	30	0
2	1	396	0	437	11	0
3	2	489	0	507	9	0
4	3	467	0	526	12	0
5	4	588	0	658	15	0
6	5	305	0	344	14	0
7	6	422	0	508	9	0
8	7	368	0	386	7	0
9	A	60083	0	30259	642	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	B	2584	0	1305	36	0
11	C	1952	0	2038	61	0
12	D	1686	0	1772	59	0
13	E	1676	0	1737	49	0
14	F	1454	0	1488	46	0
15	G	1391	0	1458	39	0
16	H	382	0	437	10	0
17	I	1106	0	1122	40	0
18	J	977	0	1027	33	0
19	K	1648	0	1684	44	0
20	L	942	0	996	27	0
21	M	1410	0	1495	46	0
22	N	1075	0	1134	43	0
23	O	944	0	1004	30	0
24	P	962	0	984	31	0
25	Q	953	0	1050	35	0
26	R	1029	0	1092	42	0
27	S	1310	0	1315	33	0
28	T	1395	0	1482	47	0
29	U	776	0	837	24	0
30	V	1078	0	1144	21	0
31	W	2277	0	1146	27	0
32	X	888	0	923	21	0
33	Y	634	0	684	14	0
34	Z	846	0	918	19	0
35	z	1623	0	821	26	0
36	8	870	0	184	4	0
37	a	31868	0	16050	400	0
38	b	1844	0	1887	62	0
39	c	1736	0	1819	54	0
40	d	1633	0	1730	36	0
41	e	1331	0	1312	29	0
42	f	911	0	923	20	0
43	g	1210	0	1284	27	0
44	h	1079	0	1137	31	0
45	i	1119	0	1181	32	0
46	j	805	0	849	37	0
47	k	882	0	928	39	0
48	l	959	0	1035	22	0
49	m	904	0	943	31	0
50	n	820	0	858	26	0
51	o	635	0	686	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	p	664	0	703	18	0
53	q	693	0	729	13	0
54	r	490	0	532	11	0
55	s	631	0	661	21	0
56	t	853	0	915	17	0
57	u	568	0	576	15	0
58	v	613	0	621	9	0
59	w	686	0	706	15	0
60	x	309	0	323	11	0
61	y	919	0	958	45	0
62	2	1	0	0	0	0
62	5	1	0	0	0	0
63	4	1	0	0	0	0
63	6	1	0	0	0	0
63	7	1	0	0	0	0
63	A	511	0	0	0	0
63	B	15	0	0	0	0
63	C	1	0	0	0	0
63	D	1	0	0	0	0
63	E	1	0	0	0	0
63	F	1	0	0	0	0
63	H	1	0	0	0	0
63	M	2	0	0	0	0
63	P	1	0	0	0	0
63	R	1	0	0	0	0
63	S	1	0	0	0	0
63	T	1	0	0	0	0
63	U	1	0	0	0	0
63	V	1	0	0	0	0
63	W	14	0	0	0	0
63	a	219	0	0	0	0
63	k	1	0	0	0	0
63	l	1	0	0	0	0
63	n	1	0	0	0	0
63	x	1	0	0	0	0
All	All	152465	0	104763	2278	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 9.

The worst 5 of 2278 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:a:1288:A:OP1	61:y:140:ARG:NH2	1.93	1.02
17:I:122:ILE:HD12	17:I:165:CYS:HB2	1.50	0.94
9:A:652:C:N4	9:A:657:U:O4	2.01	0.94
10:B:54:G:HO2'	10:B:55:G:H8	1.00	0.93
9:A:817:C:OP2	21:M:120:ARG:NH1	2.03	0.92

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	64/130 (49%)	56 (88%)	5 (8%)	3 (5%)	2	12
2	1	46/57 (81%)	45 (98%)	1 (2%)	0	100	100
3	2	58/66 (88%)	53 (91%)	5 (9%)	0	100	100
4	3	58/152 (38%)	54 (93%)	4 (7%)	0	100	100
5	4	70/159 (44%)	66 (94%)	4 (6%)	0	100	100
6	5	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
7	6	47/142 (33%)	46 (98%)	0	1 (2%)	5	24
8	7	44/116 (38%)	41 (93%)	3 (7%)	0	100	100
11	C	251/272 (92%)	235 (94%)	15 (6%)	1 (0%)	30	59
12	D	219/305 (72%)	206 (94%)	12 (6%)	1 (0%)	24	54
13	E	210/293 (72%)	196 (93%)	14 (7%)	0	100	100
14	F	191/258 (74%)	178 (93%)	13 (7%)	0	100	100
15	G	176/220 (80%)	165 (94%)	11 (6%)	0	100	100
16	H	46/196 (24%)	43 (94%)	3 (6%)	0	100	100
17	I	135/232 (58%)	132 (98%)	3 (2%)	0	100	100
18	J	131/224 (58%)	126 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	K	201/250 (80%)	193 (96%)	8 (4%)	0	100	100
20	L	119/121 (98%)	113 (95%)	6 (5%)	0	100	100
21	M	183/271 (68%)	168 (92%)	13 (7%)	2 (1%)	11	38
22	N	133/135 (98%)	121 (91%)	12 (9%)	0	100	100
23	O	114/126 (90%)	108 (95%)	6 (5%)	0	100	100
24	P	120/166 (72%)	113 (94%)	7 (6%)	0	100	100
25	Q	116/233 (50%)	114 (98%)	2 (2%)	0	100	100
26	R	117/128 (91%)	110 (94%)	7 (6%)	0	100	100
27	S	168/256 (66%)	158 (94%)	8 (5%)	2 (1%)	10	35
28	T	170/199 (85%)	162 (95%)	7 (4%)	1 (1%)	21	50
29	U	94/198 (48%)	89 (95%)	5 (5%)	0	100	100
30	V	132/192 (69%)	123 (93%)	9 (7%)	0	100	100
32	X	107/194 (55%)	96 (90%)	11 (10%)	0	100	100
33	Y	75/148 (51%)	73 (97%)	2 (3%)	0	100	100
34	Z	99/168 (59%)	95 (96%)	3 (3%)	1 (1%)	12	40
38	b	231/236 (98%)	221 (96%)	10 (4%)	0	100	100
39	c	214/218 (98%)	201 (94%)	13 (6%)	0	100	100
40	d	197/201 (98%)	186 (94%)	11 (6%)	0	100	100
41	e	185/308 (60%)	182 (98%)	3 (2%)	0	100	100
42	f	111/211 (53%)	106 (96%)	4 (4%)	1 (1%)	14	42
43	g	152/155 (98%)	146 (96%)	6 (4%)	0	100	100
44	h	131/134 (98%)	127 (97%)	2 (2%)	2 (2%)	8	30
45	i	142/208 (68%)	136 (96%)	6 (4%)	0	100	100
46	j	97/195 (50%)	93 (96%)	3 (3%)	1 (1%)	12	40
47	k	115/138 (83%)	108 (94%)	7 (6%)	0	100	100
48	l	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
49	m	108/172 (63%)	101 (94%)	6 (6%)	1 (1%)	14	42
50	n	97/100 (97%)	92 (95%)	5 (5%)	0	100	100
51	o	73/90 (81%)	72 (99%)	1 (1%)	0	100	100
52	p	78/88 (89%)	74 (95%)	4 (5%)	0	100	100
53	q	84/165 (51%)	78 (93%)	6 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	r	58/101 (57%)	55 (95%)	3 (5%)	0	100	100
55	s	76/92 (83%)	75 (99%)	1 (1%)	0	100	100
56	t	105/183 (57%)	100 (95%)	3 (3%)	2 (2%)	6	26
57	u	63/180 (35%)	62 (98%)	1 (2%)	0	100	100
58	v	78/260 (30%)	76 (97%)	2 (3%)	0	100	100
59	w	80/179 (45%)	78 (98%)	2 (2%)	0	100	100
60	x	38/101 (38%)	37 (97%)	1 (3%)	0	100	100
61	y	114/302 (38%)	106 (93%)	8 (7%)	0	100	100
All	All	6476/9784 (66%)	6138 (95%)	319 (5%)	19 (0%)	37	65

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	92	ASP
27	S	78	PRO
49	m	53	VAL
56	t	174	TYR
11	C	232	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	57/117 (49%)	54 (95%)	3 (5%)	20	47
2	1	41/50 (82%)	37 (90%)	4 (10%)	7	27
3	2	56/60 (93%)	50 (89%)	6 (11%)	6	23
4	3	50/125 (40%)	41 (82%)	9 (18%)	2	7
5	4	62/140 (44%)	54 (87%)	8 (13%)	4	16
6	5	34/34 (100%)	29 (85%)	5 (15%)	3	12
7	6	46/124 (37%)	40 (87%)	6 (13%)	4	16
8	7	40/96 (42%)	33 (82%)	7 (18%)	2	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	C	201/217 (93%)	178 (89%)	23 (11%)	5	21
12	D	182/259 (70%)	160 (88%)	22 (12%)	5	19
13	E	179/255 (70%)	155 (87%)	24 (13%)	4	15
14	F	152/214 (71%)	134 (88%)	18 (12%)	5	20
15	G	151/190 (80%)	137 (91%)	14 (9%)	8	29
16	H	42/170 (25%)	36 (86%)	6 (14%)	3	13
17	I	119/204 (58%)	109 (92%)	10 (8%)	10	34
18	J	106/189 (56%)	100 (94%)	6 (6%)	18	45
19	K	176/213 (83%)	160 (91%)	16 (9%)	9	30
20	L	101/101 (100%)	90 (89%)	11 (11%)	6	22
21	M	141/215 (66%)	124 (88%)	17 (12%)	5	19
22	N	108/108 (100%)	97 (90%)	11 (10%)	7	25
23	O	96/103 (93%)	81 (84%)	15 (16%)	2	10
24	P	100/139 (72%)	92 (92%)	8 (8%)	11	36
25	Q	104/207 (50%)	91 (88%)	13 (12%)	4	18
26	R	106/115 (92%)	95 (90%)	11 (10%)	7	24
27	S	137/223 (61%)	129 (94%)	8 (6%)	18	45
28	T	152/176 (86%)	133 (88%)	19 (12%)	4	18
29	U	85/171 (50%)	75 (88%)	10 (12%)	5	20
30	V	121/169 (72%)	107 (88%)	14 (12%)	5	20
32	X	92/163 (56%)	75 (82%)	17 (18%)	1	7
33	Y	67/130 (52%)	58 (87%)	9 (13%)	4	15
34	Z	93/153 (61%)	82 (88%)	11 (12%)	5	20
38	b	198/201 (98%)	181 (91%)	17 (9%)	10	33
39	c	186/188 (99%)	171 (92%)	15 (8%)	11	36
40	d	178/180 (99%)	165 (93%)	13 (7%)	13	39
41	e	121/255 (48%)	105 (87%)	16 (13%)	4	16
42	f	100/186 (54%)	92 (92%)	8 (8%)	11	36
43	g	125/126 (99%)	117 (94%)	8 (6%)	16	42
44	h	116/117 (99%)	106 (91%)	10 (9%)	10	33
45	i	114/169 (68%)	100 (88%)	14 (12%)	4	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	j	91/173 (53%)	84 (92%)	7 (8%)	12	37
47	k	91/109 (84%)	81 (89%)	10 (11%)	6	22
48	l	105/106 (99%)	95 (90%)	10 (10%)	8	29
49	m	99/151 (66%)	91 (92%)	8 (8%)	11	36
50	n	89/90 (99%)	79 (89%)	10 (11%)	6	21
51	o	70/85 (82%)	68 (97%)	2 (3%)	37	60
52	p	71/79 (90%)	61 (86%)	10 (14%)	3	13
53	q	77/149 (52%)	72 (94%)	5 (6%)	15	42
54	r	56/96 (58%)	49 (88%)	7 (12%)	4	18
55	s	68/81 (84%)	63 (93%)	5 (7%)	13	38
56	t	89/156 (57%)	83 (93%)	6 (7%)	15	41
57	u	59/160 (37%)	53 (90%)	6 (10%)	7	25
58	v	67/225 (30%)	67 (100%)	0	100	100
59	w	76/162 (47%)	75 (99%)	1 (1%)	61	71
60	x	30/85 (35%)	30 (100%)	0	100	100
61	y	104/275 (38%)	99 (95%)	5 (5%)	23	50
All	All	5577/8434 (66%)	5023 (90%)	554 (10%)	10	26

5 of 554 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	j	104	ARG
47	k	102	ARG
46	j	101	ILE
53	q	76	VAL
20	L	42	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 93 such sidechains are listed below:

Mol	Chain	Res	Type
40	d	149	GLN
49	m	87	ASN
42	f	160	ASN
46	j	151	HIS
50	n	48	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	120/121 (99%)	20 (16%)	0
31	W	105/106 (99%)	34 (32%)	1 (0%)
35	z	75/76 (98%)	22 (29%)	0
37	a	1483/1491 (99%)	349 (23%)	0
9	A	2794/2810 (99%)	658 (23%)	8 (0%)
All	All	4577/4604 (99%)	1083 (23%)	9 (0%)

5 of 1083 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	8	G
9	A	9	A
9	A	10	G
9	A	12	A
9	A	13	A

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	2602	U
31	W	77	A
9	A	795	U
9	A	1520	A
9	A	2035	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](#)

Of 781 ligands modelled in this entry, 781 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
36	8	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	8	1068:UNK	C	1101:UNK	N	66.30
1	8	1143:UNK	C	1201:UNK	N	11.98

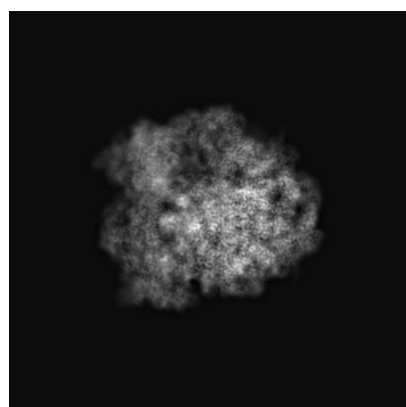
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3533. These allow visual inspection of the internal detail of the map and identification of artifacts.

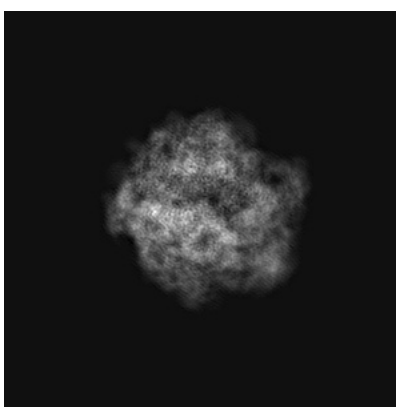
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

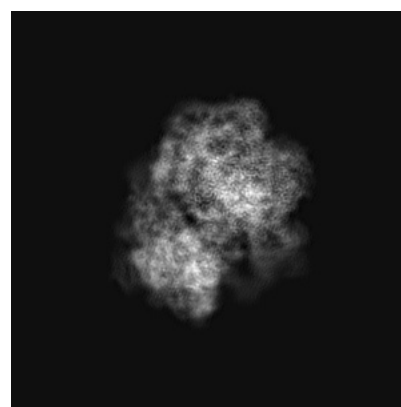
6.1.1 Primary map



X



Y

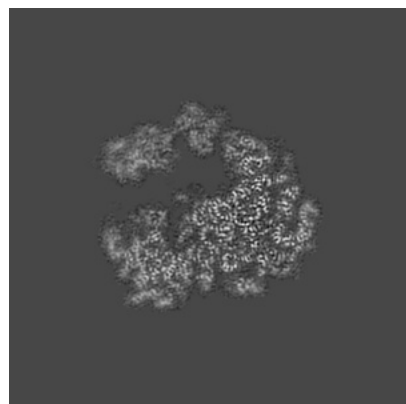


Z

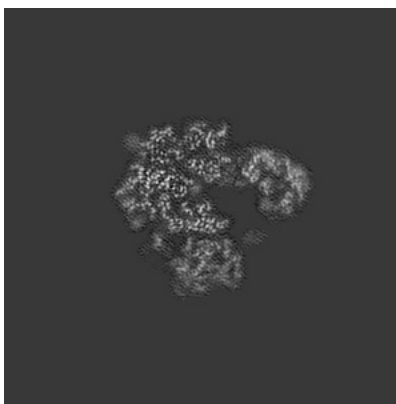
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

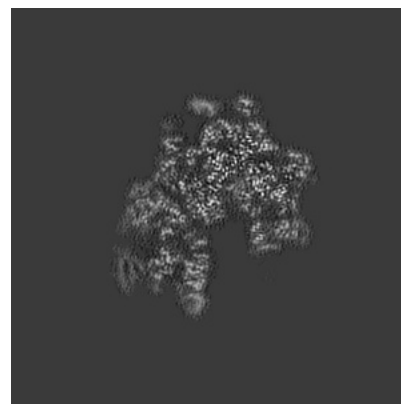
6.2.1 Primary map



X Index: 160



Y Index: 160

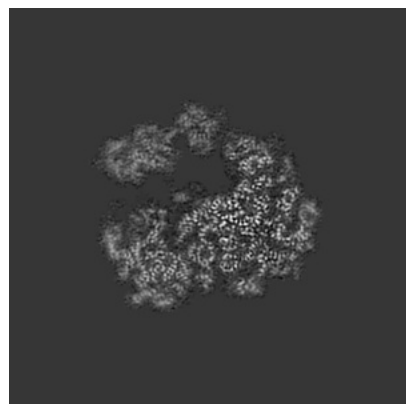


Z Index: 160

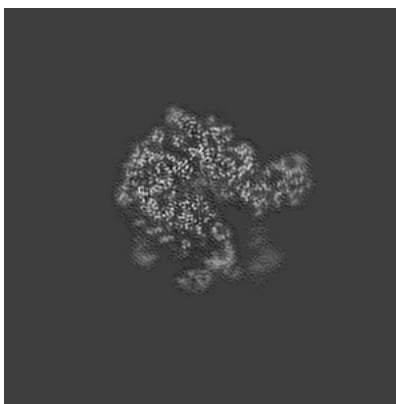
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

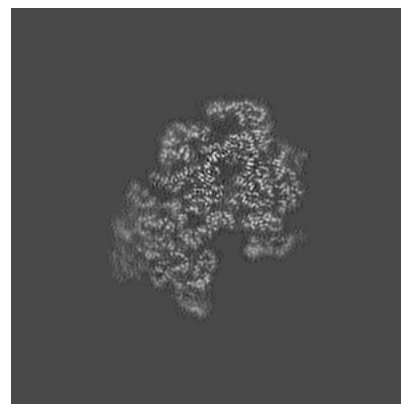
6.3.1 Primary map



X Index: 159



Y Index: 173

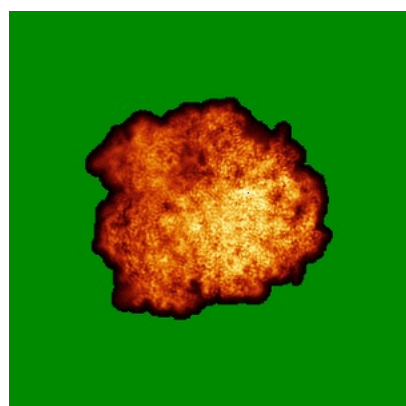


Z Index: 148

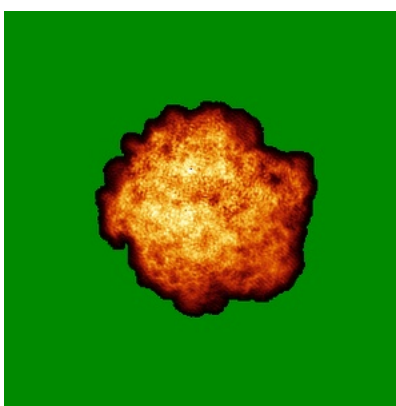
The images above show the largest variance slices of the map in three orthogonal directions.

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

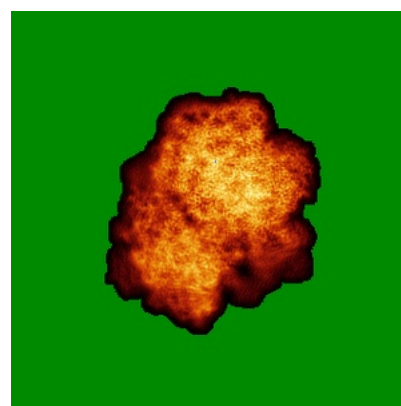
6.4.1 Primary map



X



Y

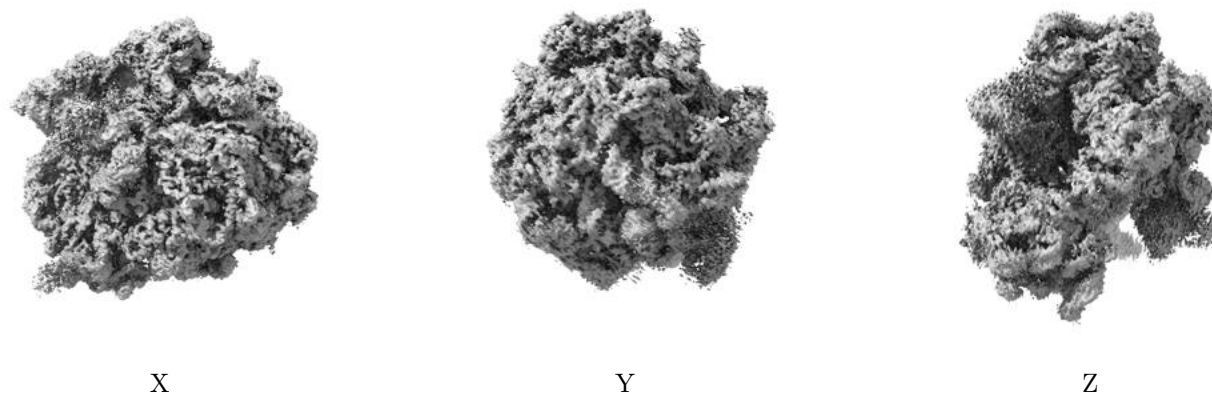


Z

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

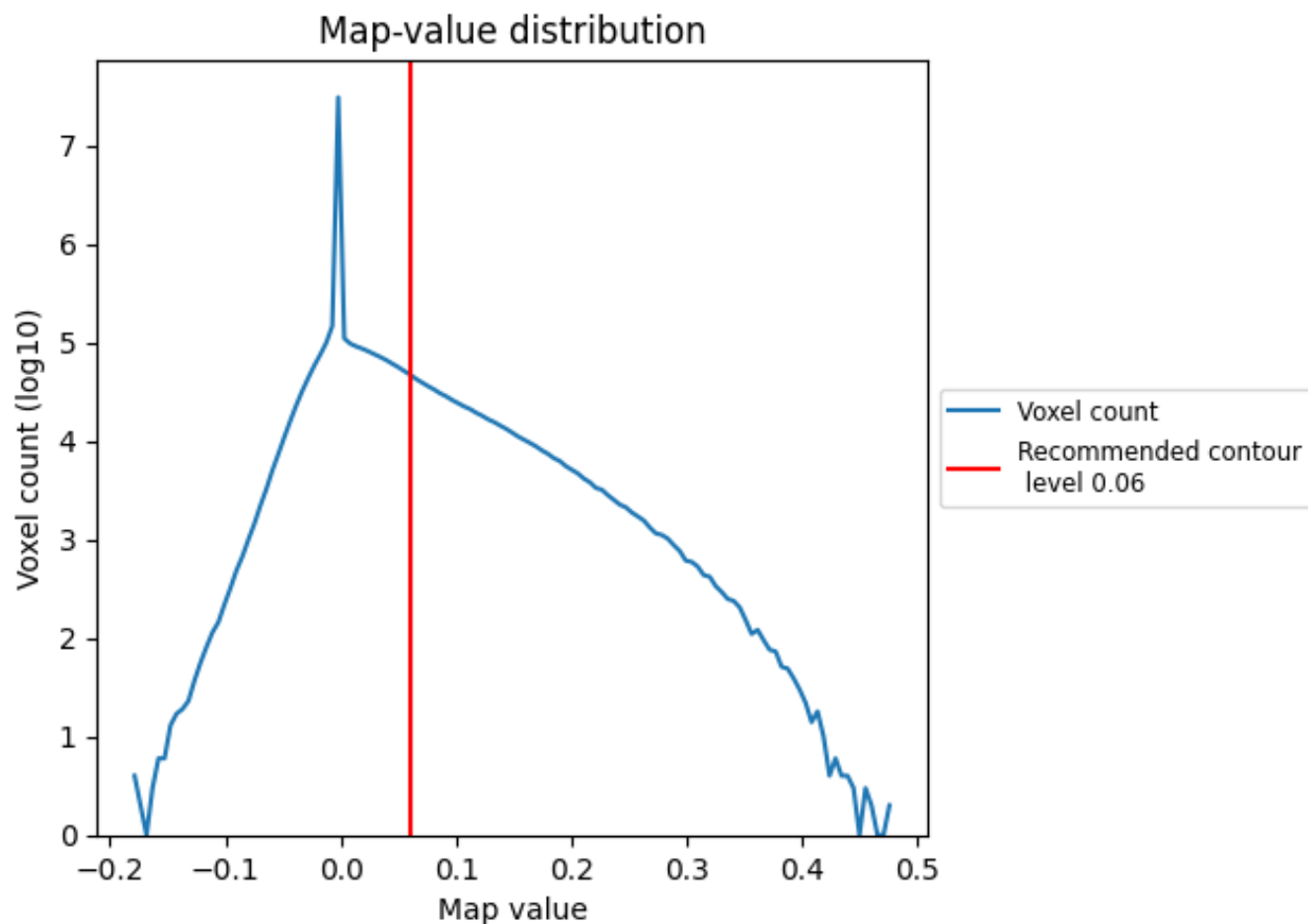
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

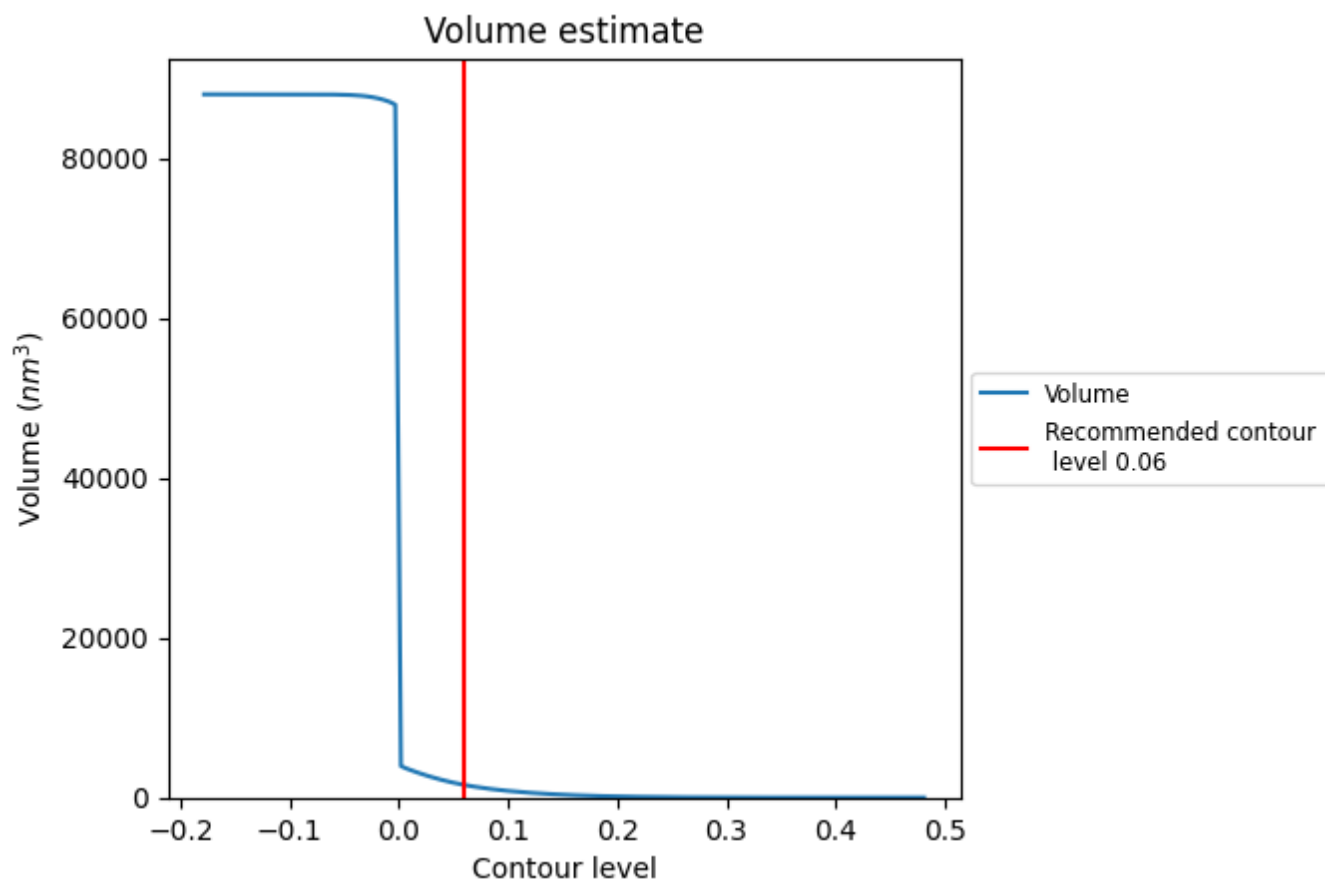
This section contains the results of statistical analysis of the map.

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.

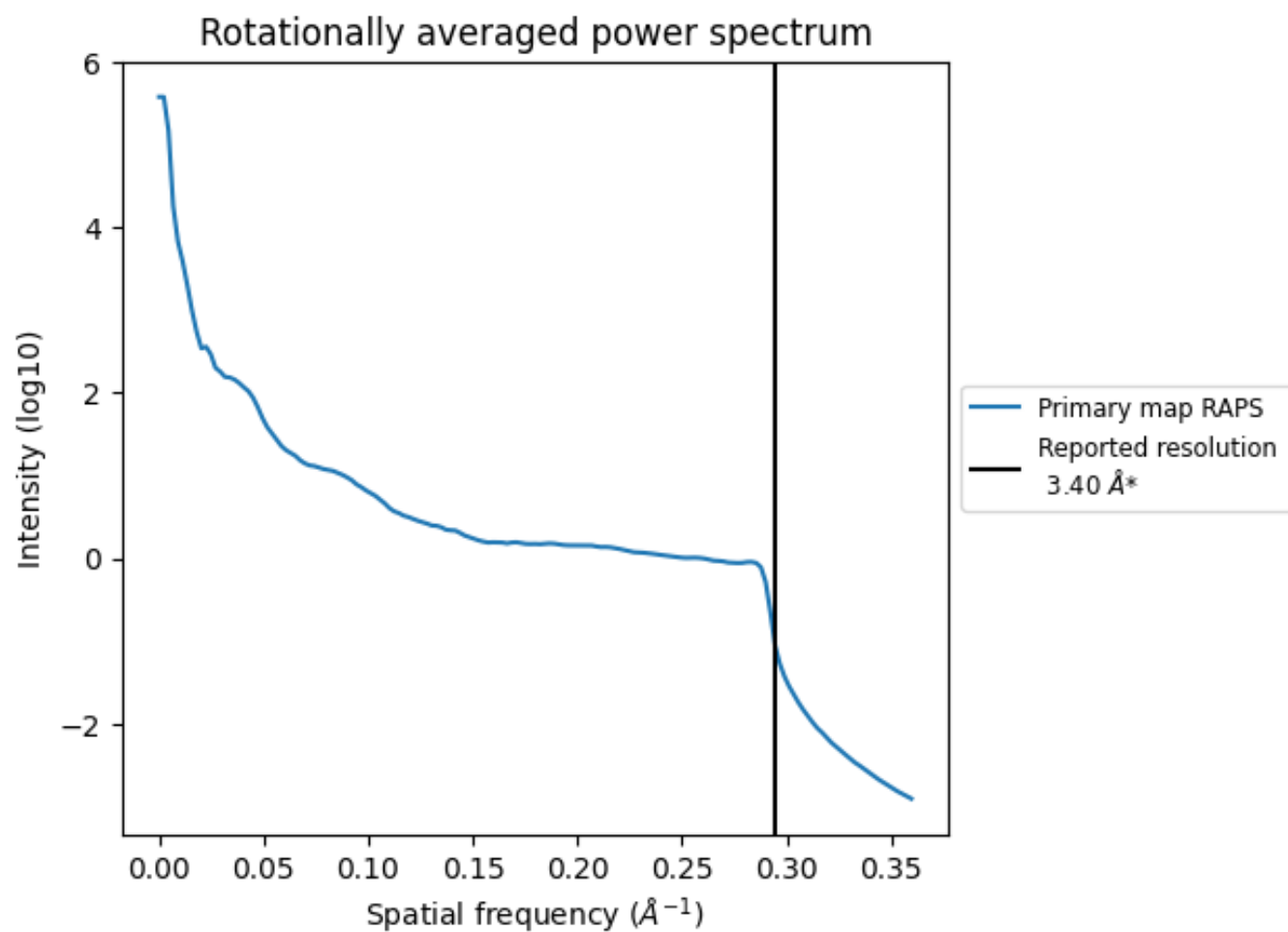
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1578 nm³; this corresponds to an approximate mass of 1425 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 ⓘ

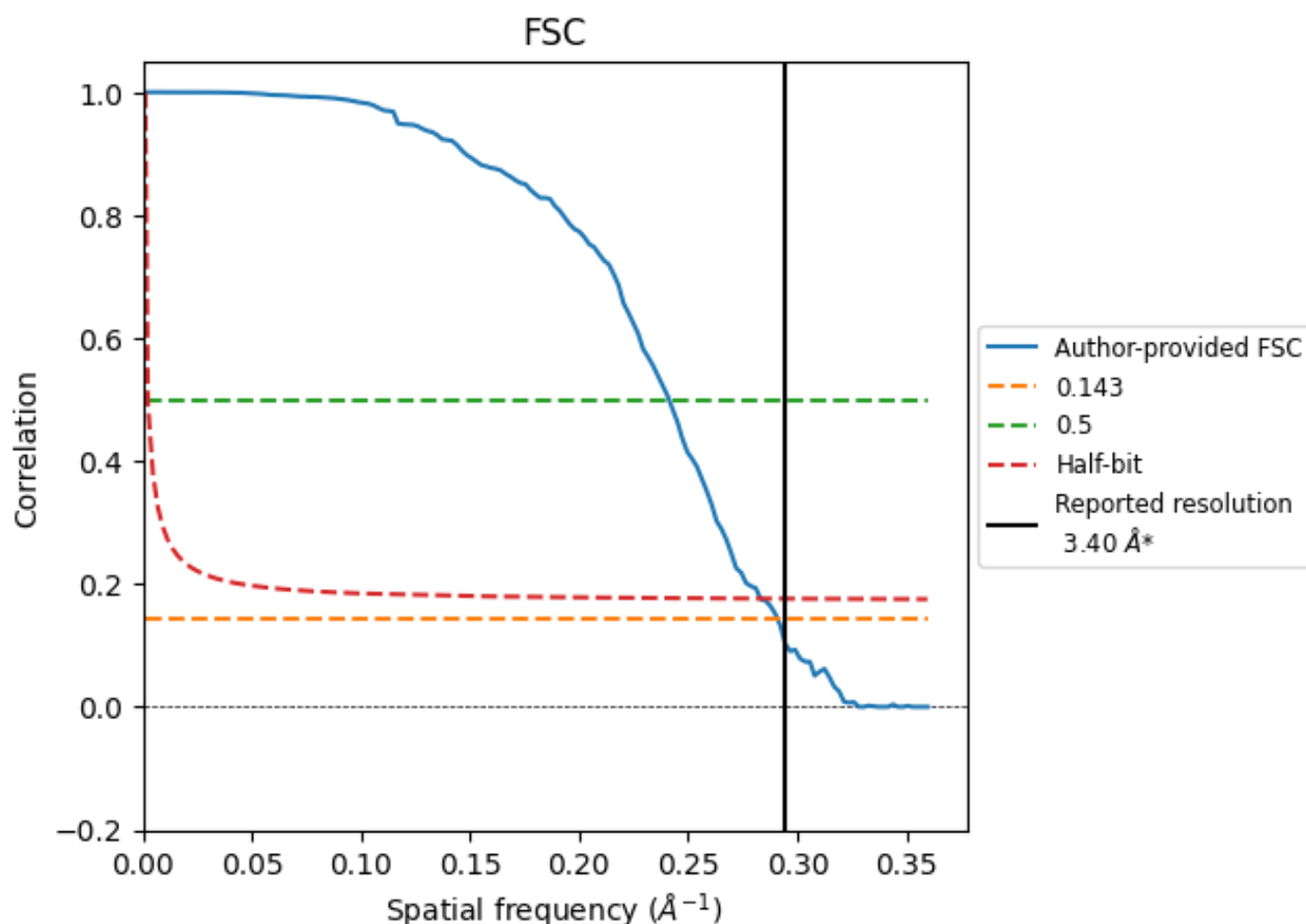


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

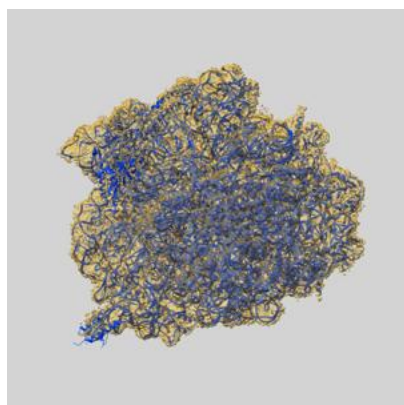
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.44	4.15	3.53
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

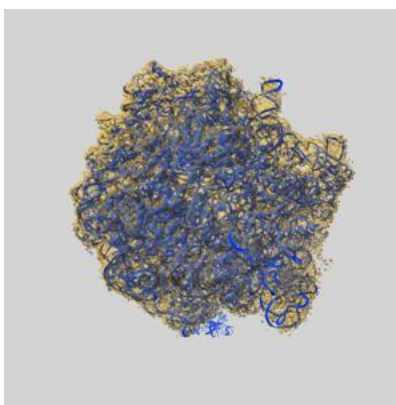
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3533 and PDB model 5MMM. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

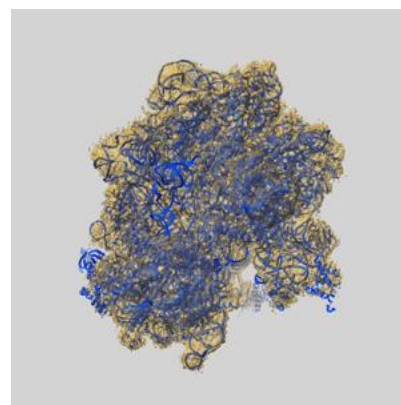
9.1 Map-model overlay [i](#)



X



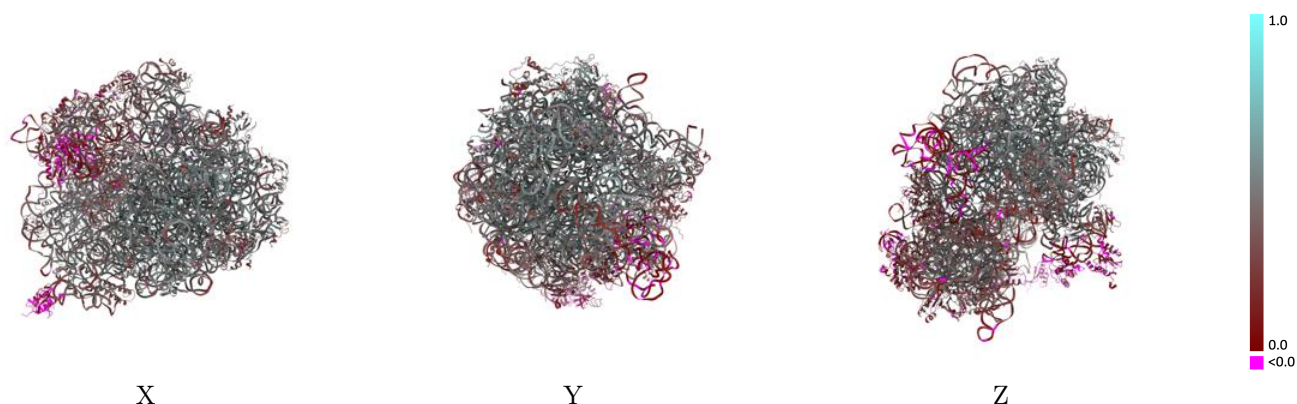
Y



Z

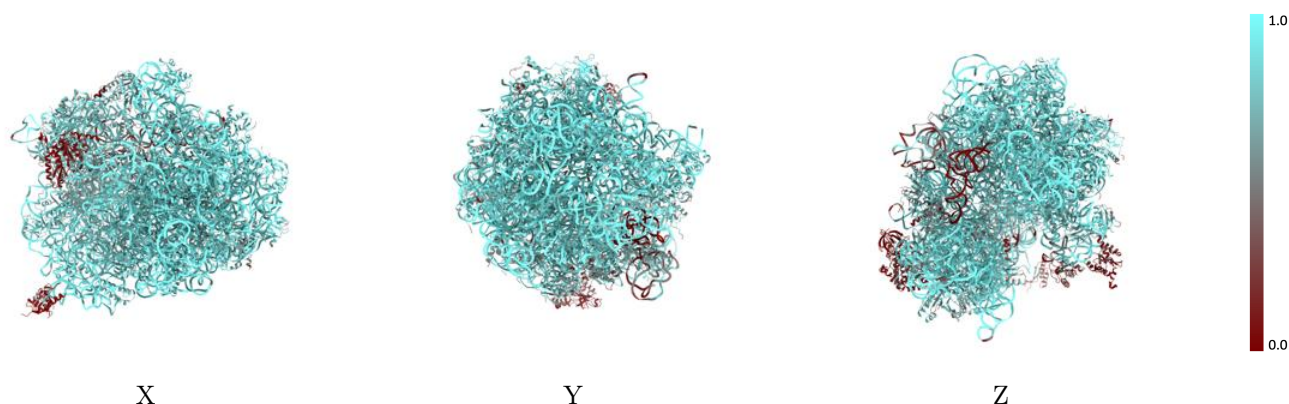
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



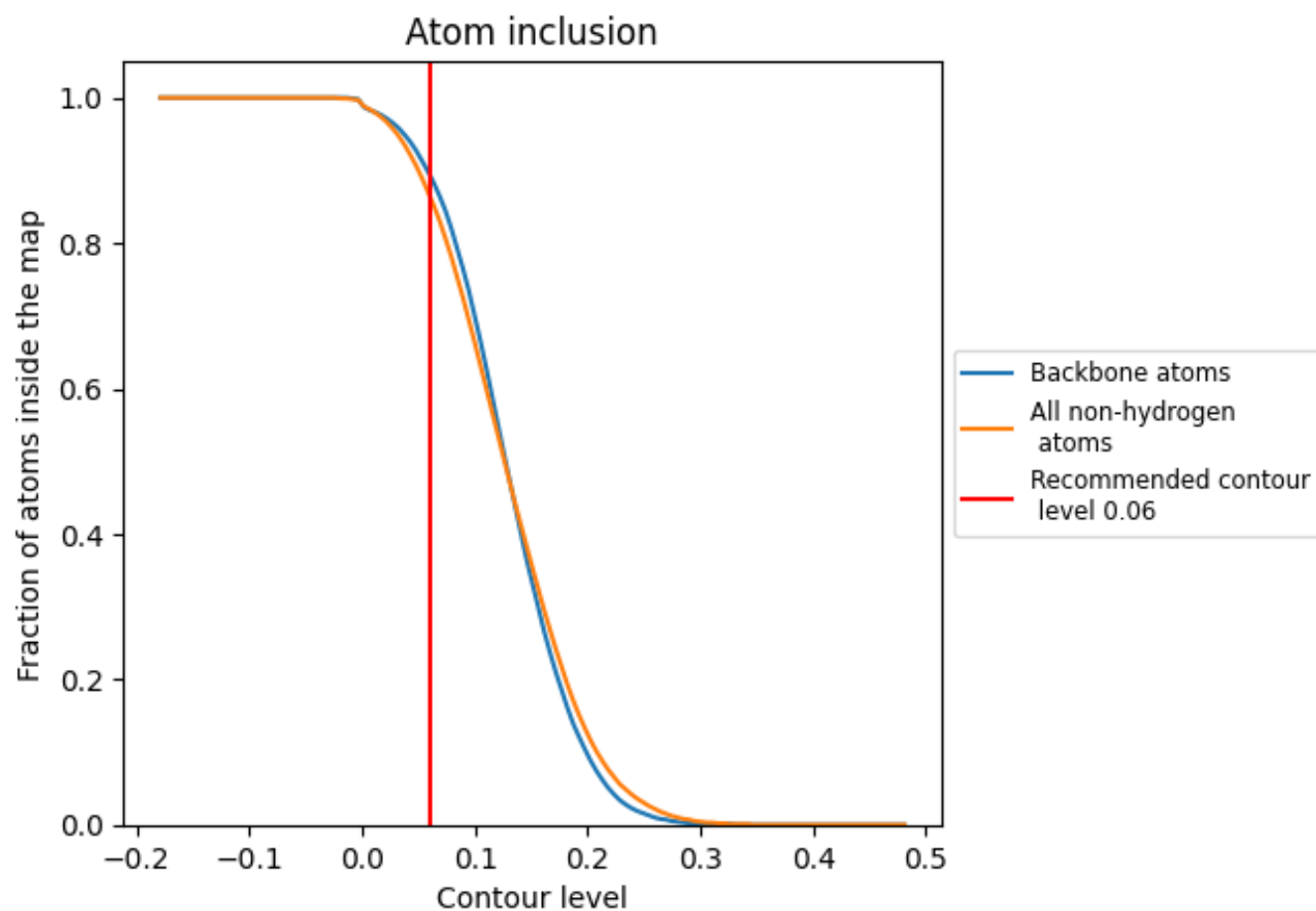
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 86% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8650	 0.4060
0	 0.5680	 0.1880
1	 0.8880	 0.4900
2	 0.8350	 0.4440
3	 0.8740	 0.5230
4	 0.8820	 0.5190
5	 0.8410	 0.4480
6	 0.7960	 0.4120
7	 0.8940	 0.4790
8	 0.0620	 0.0540
A	 0.9470	 0.4530
B	 0.9780	 0.4150
C	 0.8450	 0.4740
D	 0.8890	 0.4860
E	 0.8680	 0.4720
F	 0.7500	 0.3180
G	 0.7990	 0.3340
H	 0.5700	 0.3640
I	 0.1380	 0.0550
J	 0.2470	 0.0420
K	 0.8780	 0.4710
L	 0.8160	 0.4730
M	 0.8820	 0.4570
N	 0.6390	 0.3880
O	 0.9050	 0.4980
P	 0.8780	 0.4120
Q	 0.8480	 0.4600
R	 0.8990	 0.4970
S	 0.8360	 0.4410
T	 0.8380	 0.4460
U	 0.8200	 0.4390
V	 0.8270	 0.4310
W	 0.9750	 0.4680
X	 0.8790	 0.4610
Y	 0.8550	 0.4770



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Chain	Atom inclusion	Q-score
Z	 0.7990	 0.3890
a	 0.9670	 0.4080
b	 0.2830	 0.1970
c	 0.7350	 0.3250
d	 0.7810	 0.3520
e	 0.7450	 0.3810
f	 0.7000	 0.2920
g	 0.5710	 0.2520
h	 0.7480	 0.3400
i	 0.7890	 0.3030
j	 0.7800	 0.3140
k	 0.7790	 0.3370
l	 0.7980	 0.4510
m	 0.7590	 0.2780
n	 0.8300	 0.3360
o	 0.5640	 0.3050
p	 0.8550	 0.3850
q	 0.8030	 0.3690
r	 0.7610	 0.3150
s	 0.7530	 0.3000
t	 0.8080	 0.3470
u	 0.4500	 0.2220
v	 0.0030	 -0.0100
w	 0.1540	 0.0220
x	 0.8470	 0.3380
y	 0.6370	 0.3190
z	 0.0430	 0.0540