



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 08:33 PM UTC

PDB ID : 7PAN / pdb_00007pan
EMDB ID : EMD-13278
Title : 70S ribosome with A/P- and P/E-site tRNAs in Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-07-30
Resolution : 9.70 Å(reported)
Based on initial models : 4V7C, 7OOD, 7OOC

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

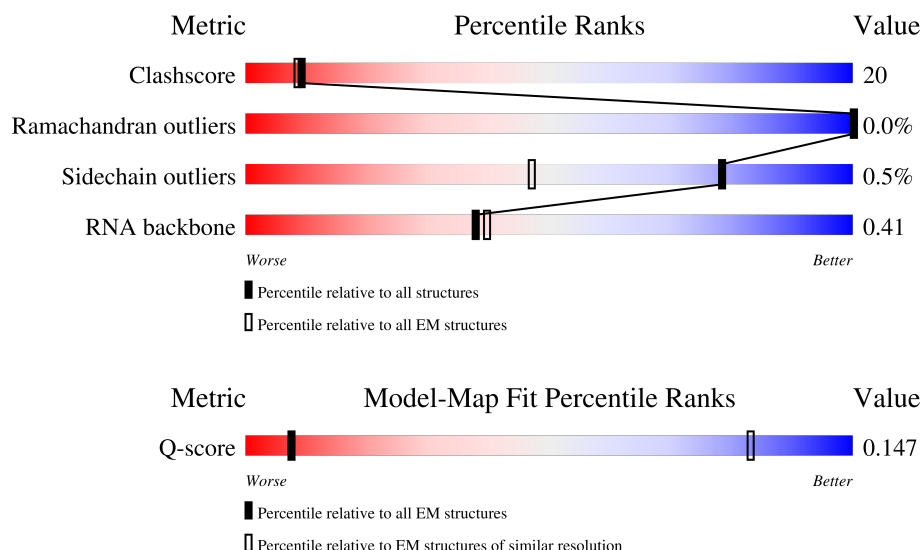
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 9.70 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	165 (9.20 - 10.20)

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

Mol	Chain	Length	Quality of chain
1	0	48	
2	1	59	
3	2	37	

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

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

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Mol	Chain	Length	Quality of chain
53	8	76	 A horizontal bar chart showing the quality of chain 8. The bar is divided into three segments: green (42%), yellow (41%), and orange (17%). A small red square is at the beginning of the green segment. 42%41%17%

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 146120 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L34.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

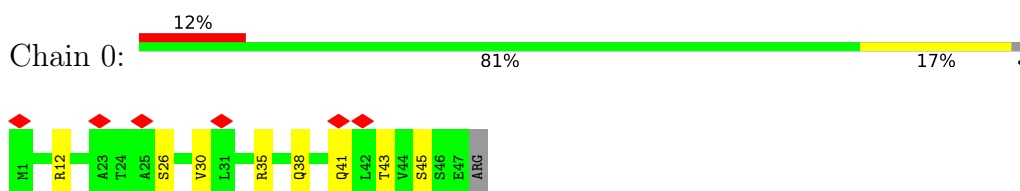
- Molecule 53 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
53	8	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

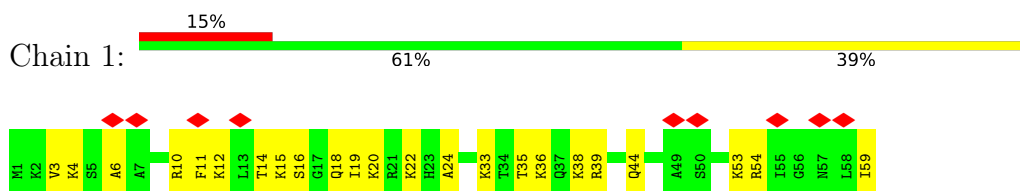
3 Residue-property plots

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

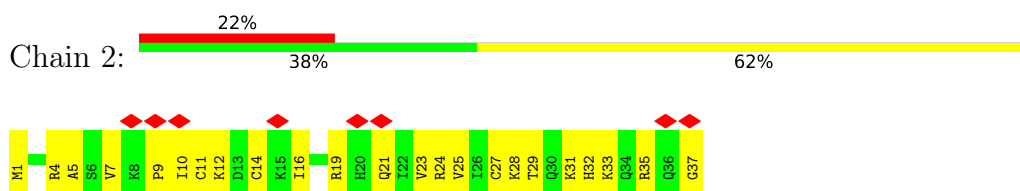
- Molecule 1: 50S ribosomal protein L34



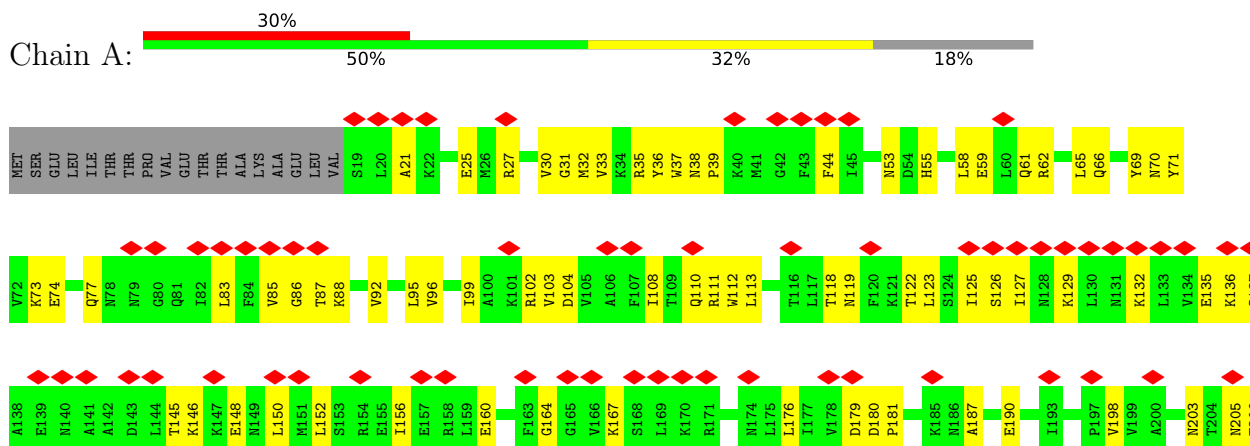
- Molecule 2: 50S ribosomal protein L35

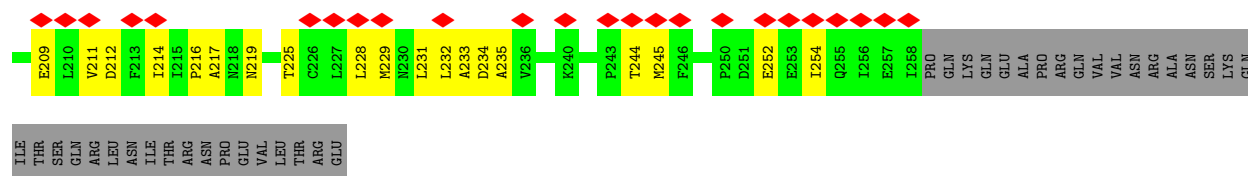


- Molecule 3: 50S ribosomal protein L36

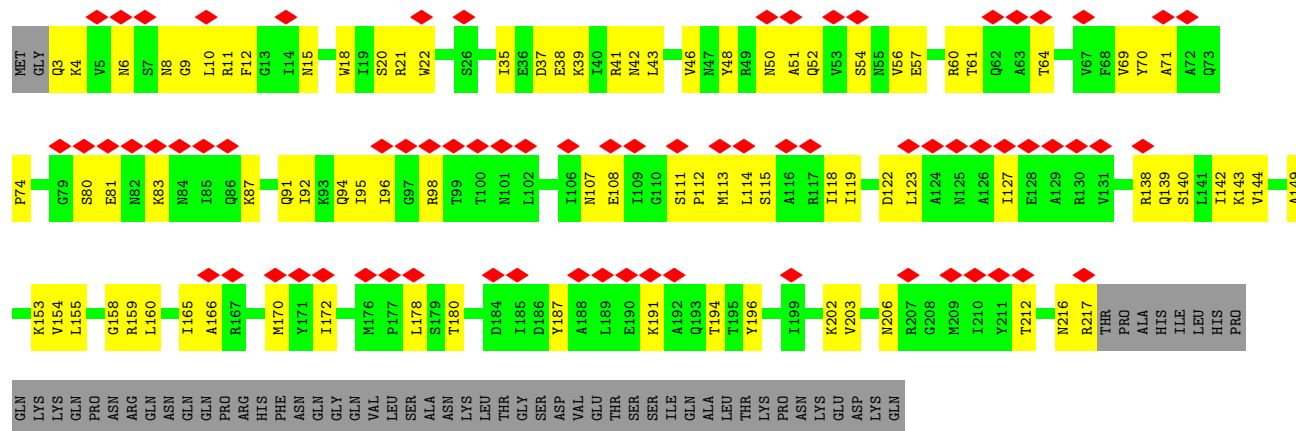


- Molecule 4: 30S ribosomal protein S2

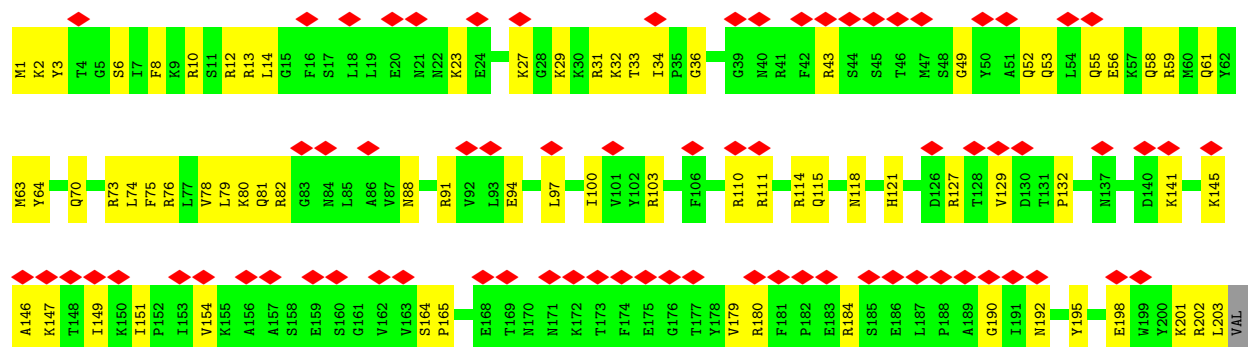




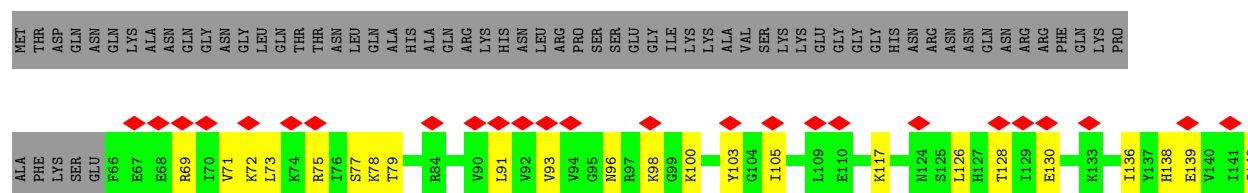
• Molecule 5: 30S ribosomal protein S3

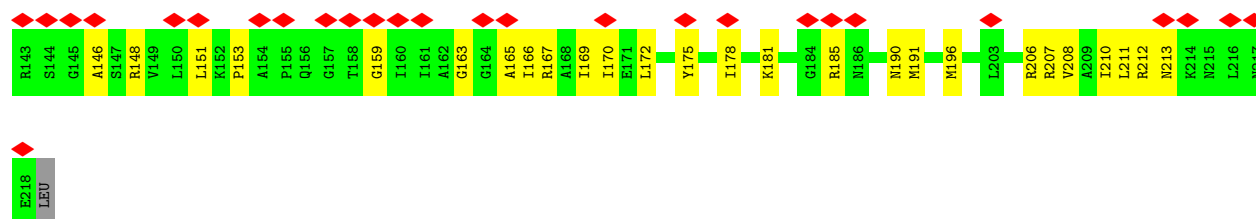


• Molecule 6: 30S ribosomal protein S4

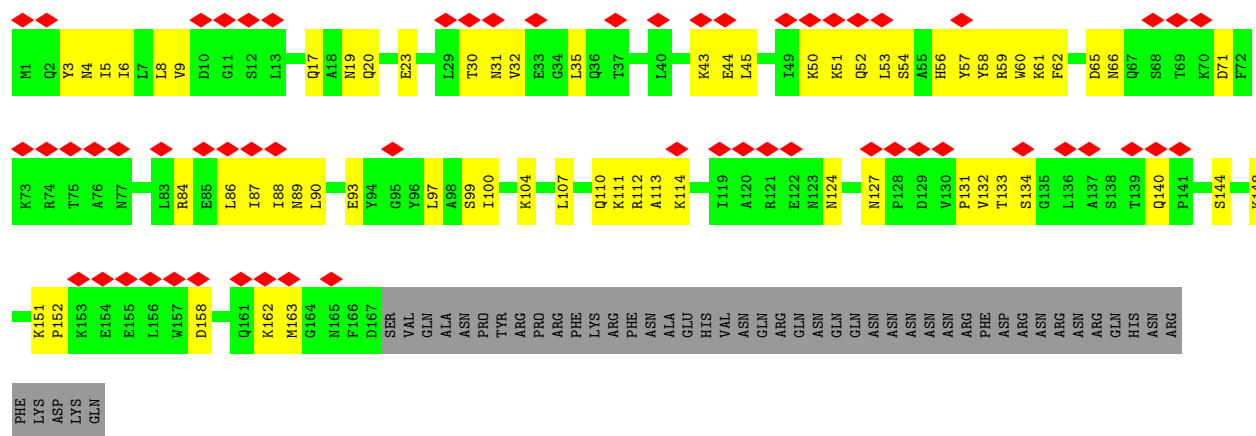


• Molecule 7: 30S ribosomal protein S5

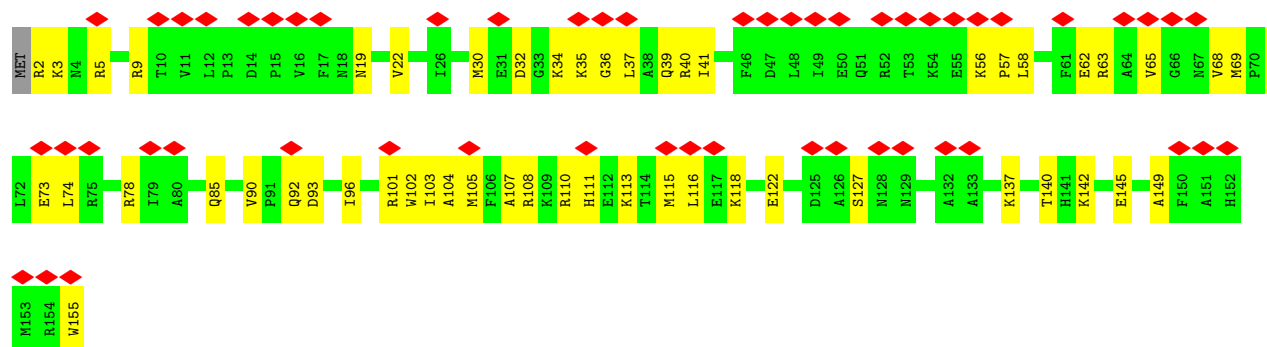




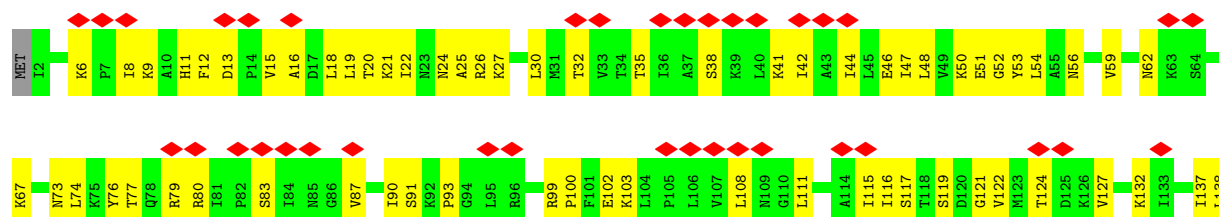
• Molecule 8: 30S ribosomal protein S6



• Molecule 9: 30S ribosomal protein S7

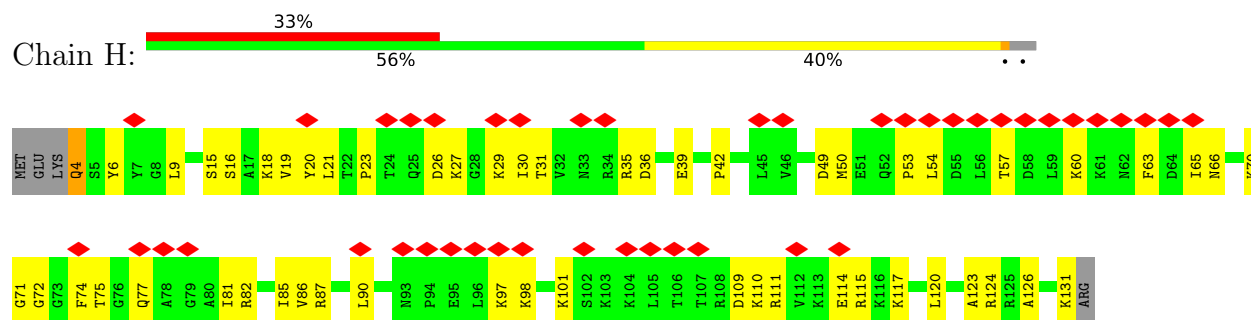


• Molecule 10: 30S ribosomal protein S8

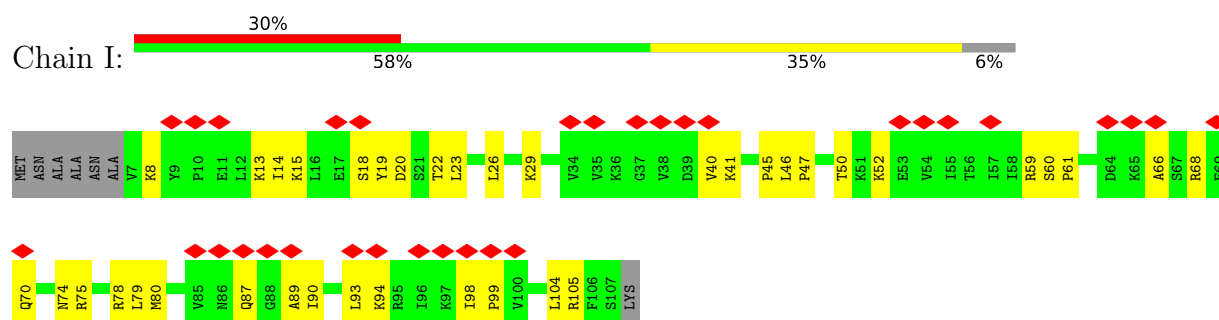


A139
Y140
V141
W142

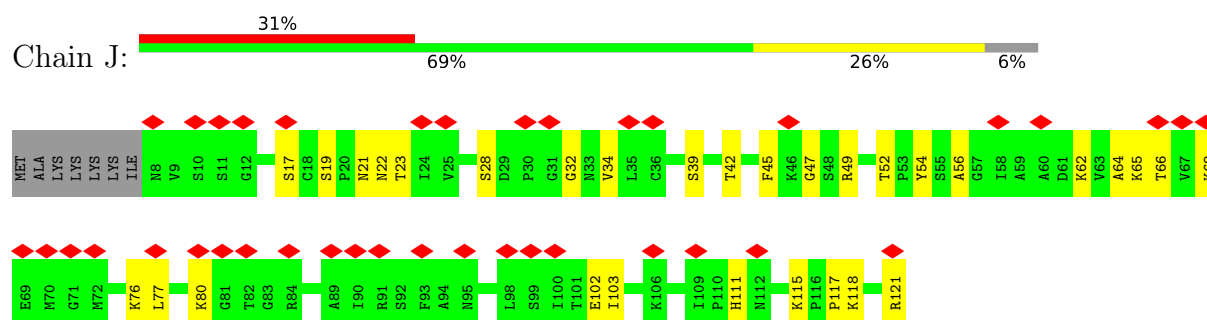
• Molecule 11: 30S ribosomal protein S9



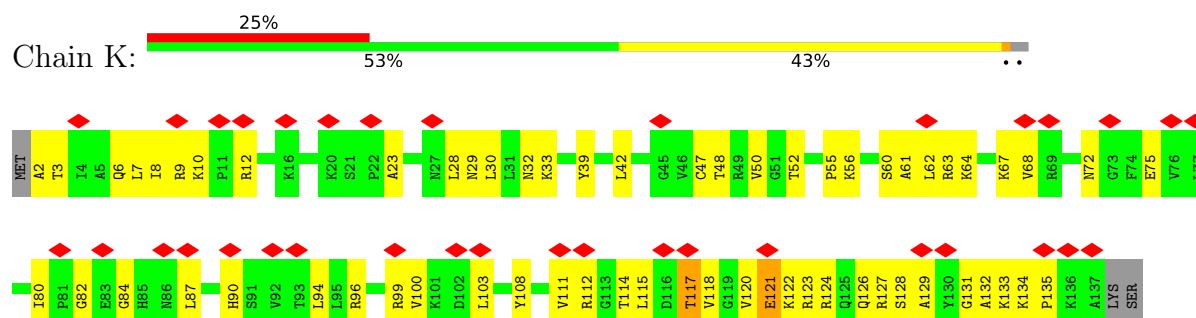
• Molecule 12: 30S ribosomal protein S10



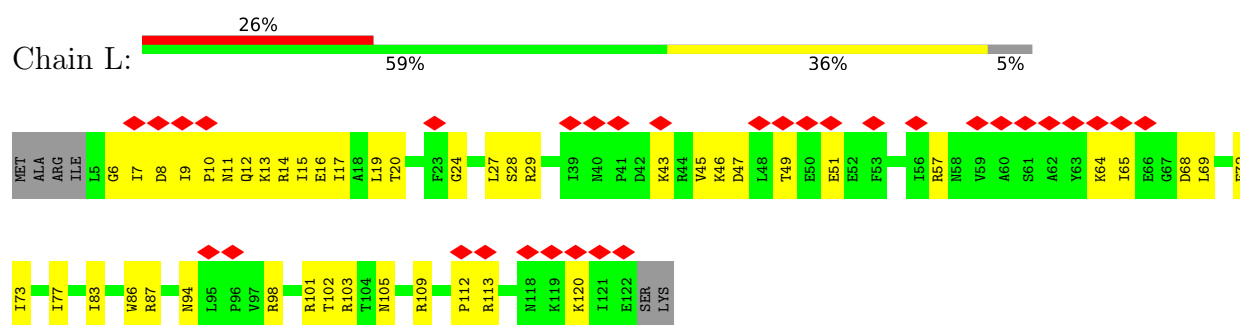
• Molecule 13: 30S ribosomal protein S11



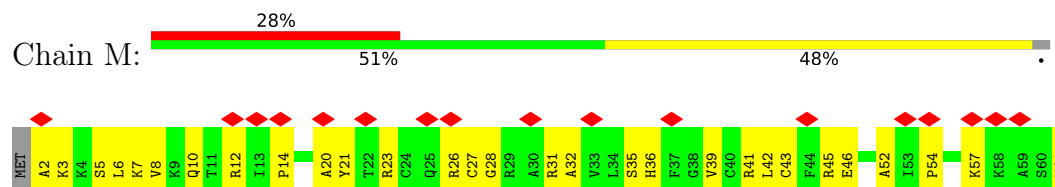
• Molecule 14: 30S ribosomal protein S12



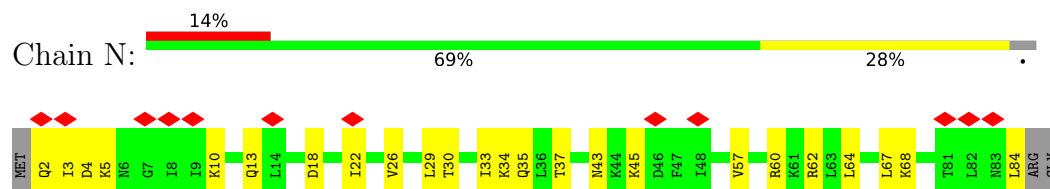
• Molecule 15: 30S ribosomal protein S13



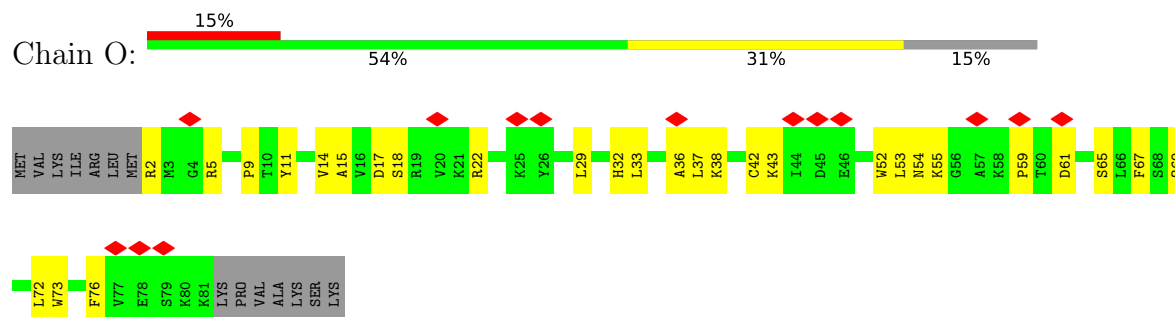
- Molecule 16: 30S ribosomal protein S14 type Z



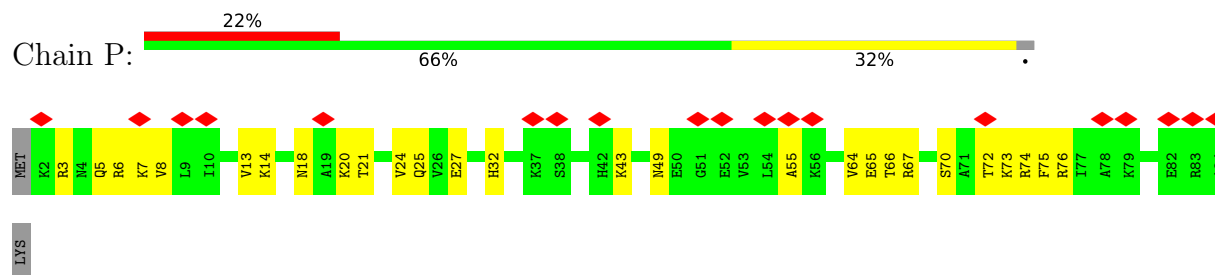
- Molecule 17: 30S ribosomal protein S15



- Molecule 18: 30S ribosomal protein S16

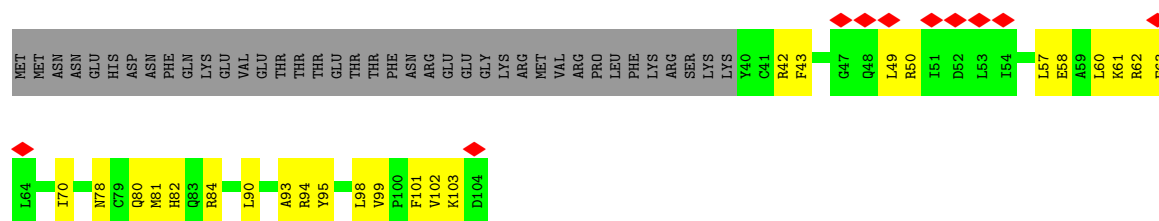


- Molecule 19: 30S ribosomal protein S17

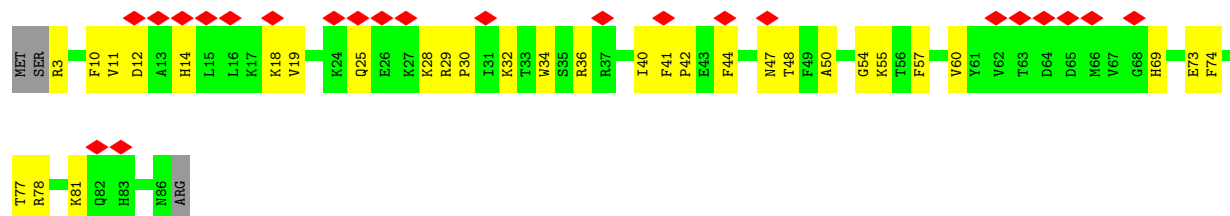


- Molecule 20: 30S ribosomal protein S18

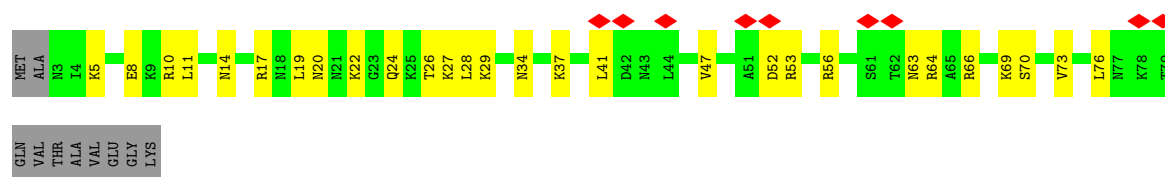




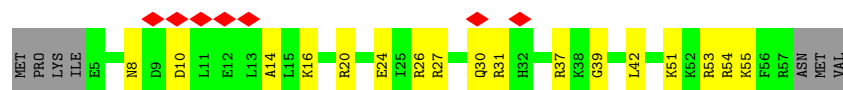
• Molecule 21: 30S ribosomal protein S19



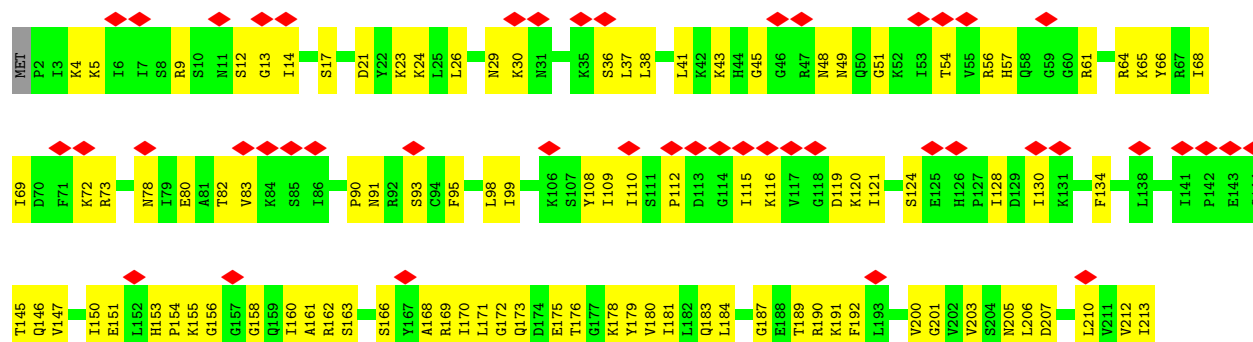
• Molecule 22: 30S ribosomal protein S20



• Molecule 23: 30S ribosomal protein S21

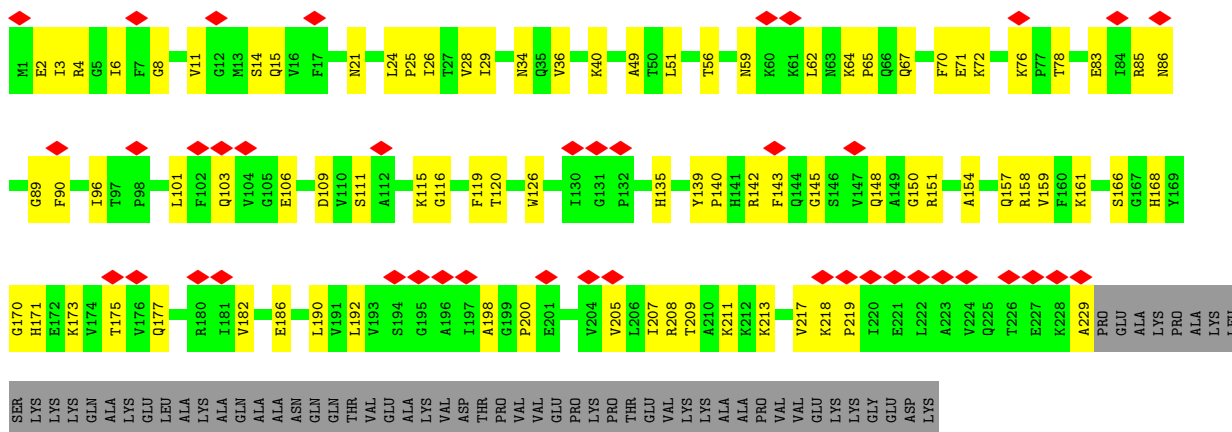


• Molecule 24: 50S ribosomal protein L2

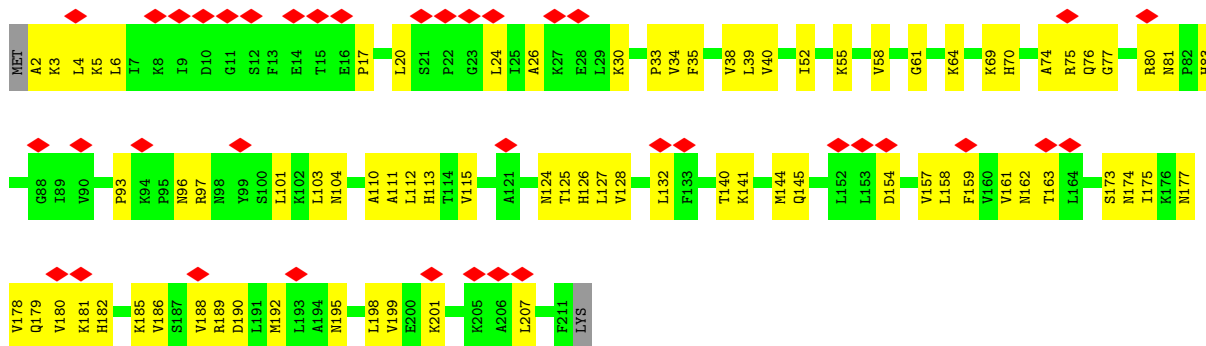




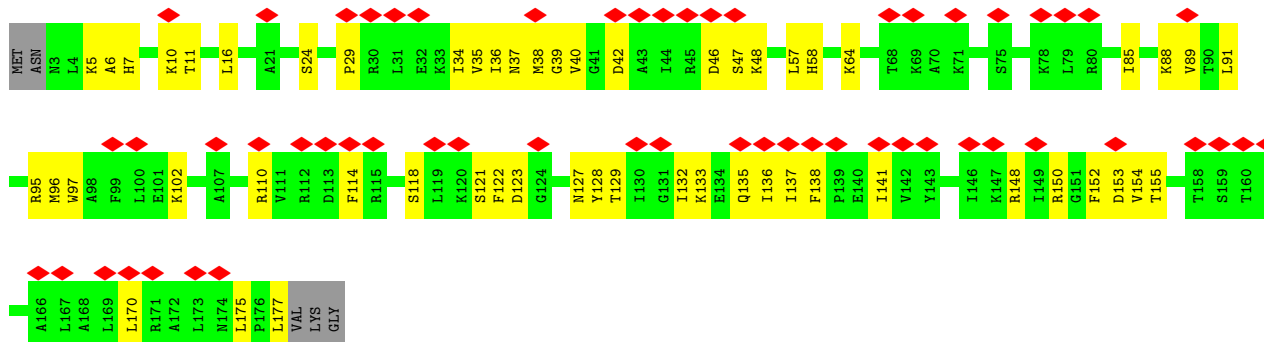
• Molecule 25: 50S ribosomal protein L3



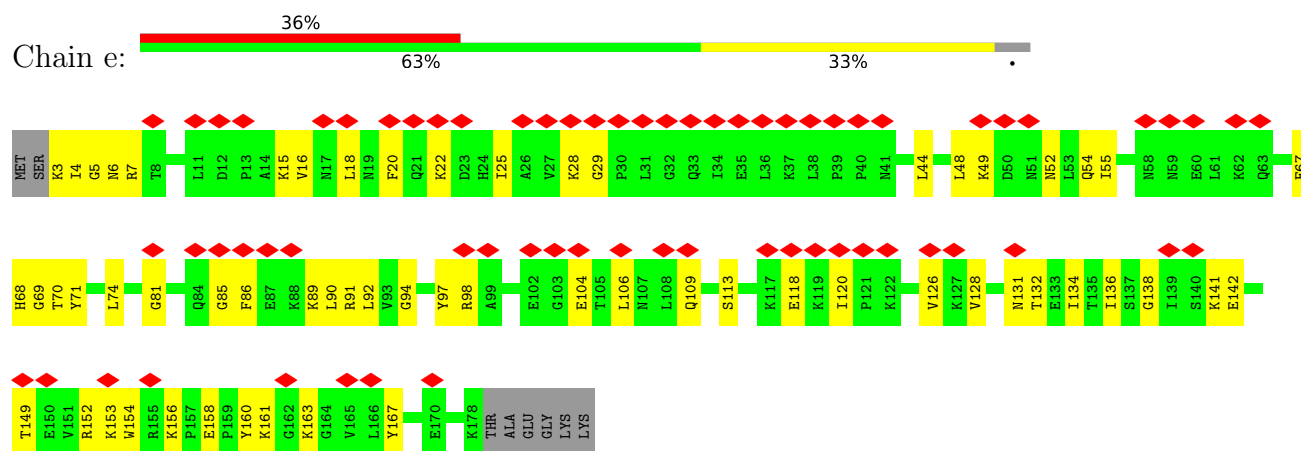
• Molecule 26: 50S ribosomal protein L4



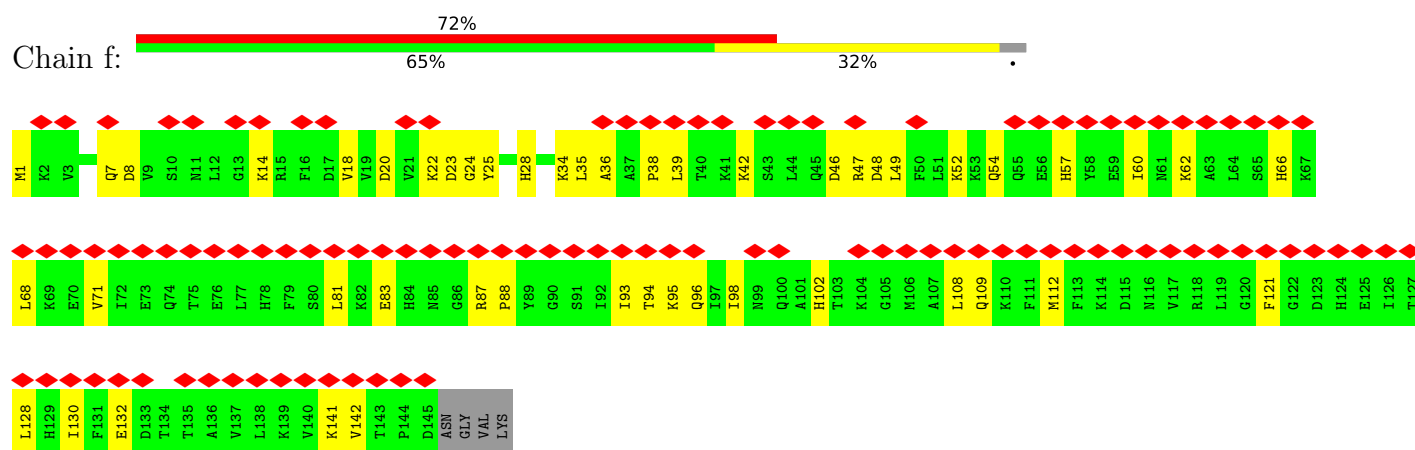
• Molecule 27: 50S ribosomal protein L5



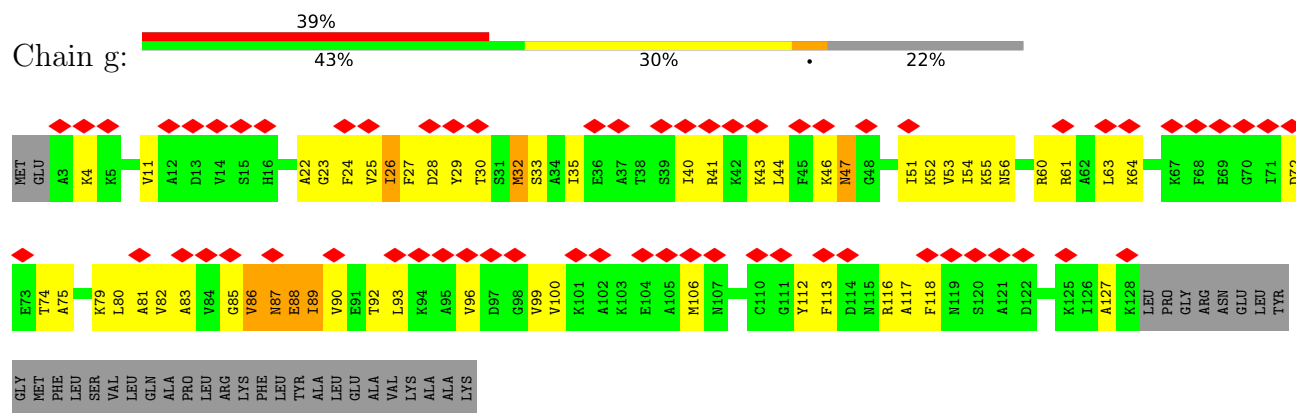
• Molecule 28: 50S ribosomal protein L6



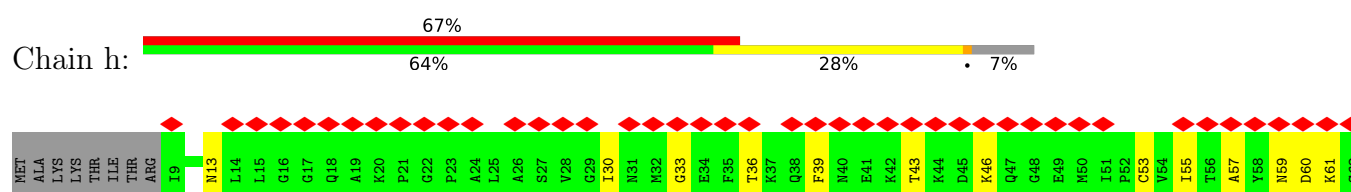
• Molecule 29: 50S ribosomal protein L9

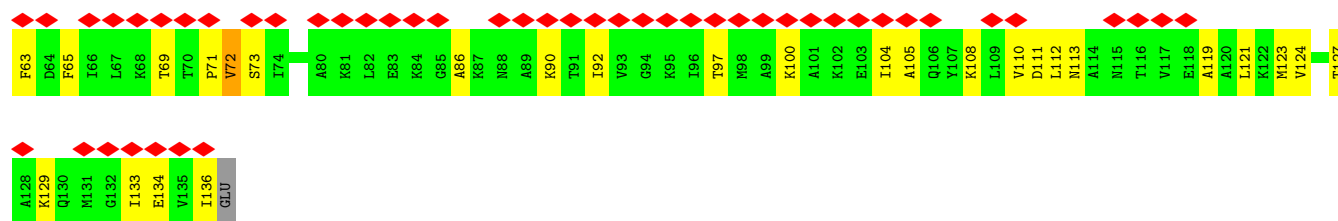


• Molecule 30: 50S ribosomal protein L10

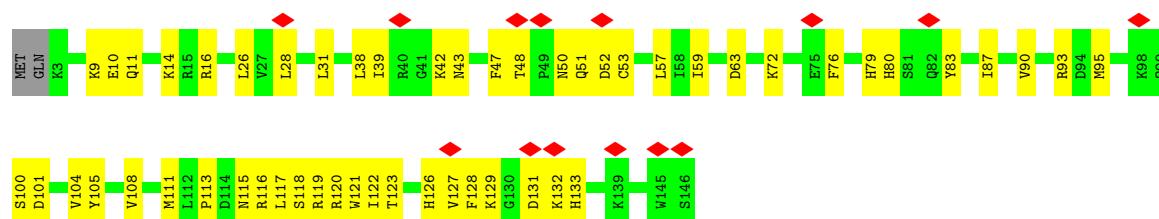


• Molecule 31: 50S ribosomal protein L11

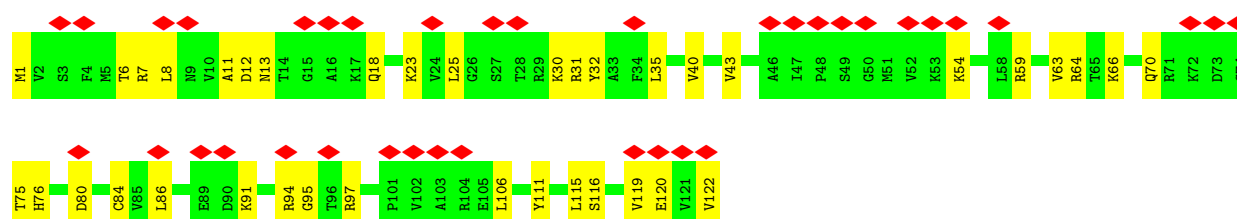




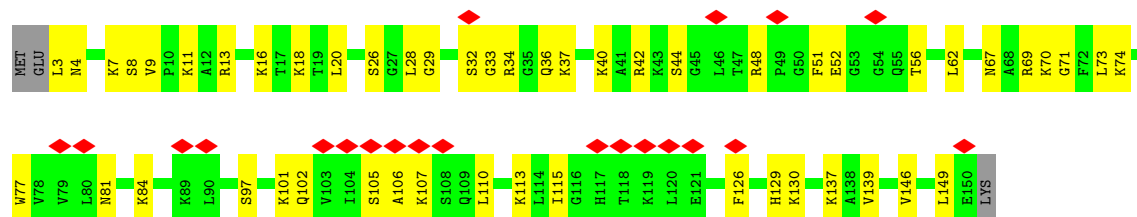
• Molecule 32: 50S ribosomal protein L13



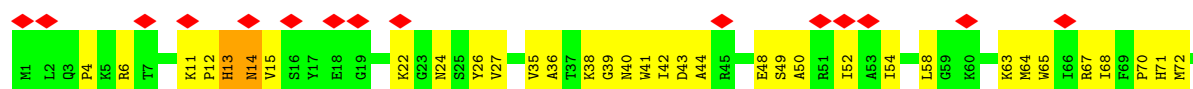
• Molecule 33: 50S ribosomal protein L14

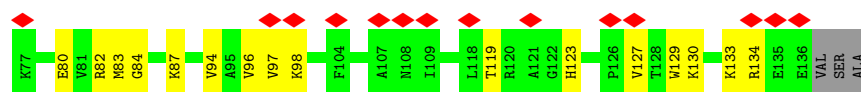


• Molecule 34: 50S ribosomal protein L15

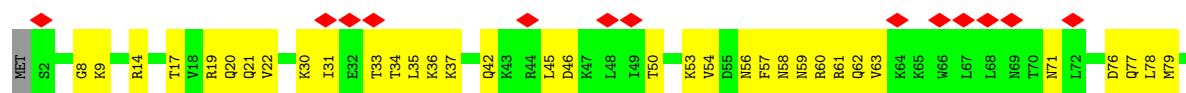


• Molecule 35: 50S ribosomal protein L16

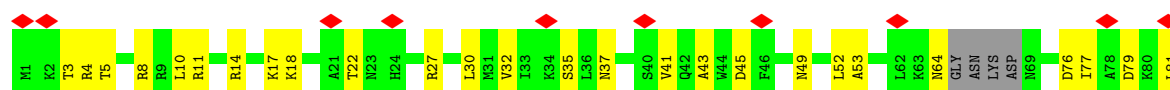




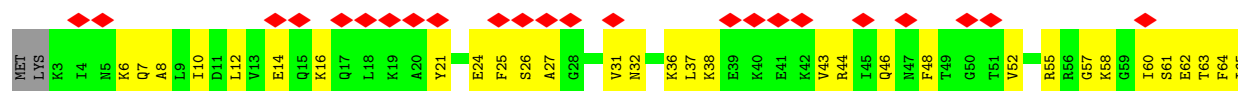
• Molecule 36: 50S ribosomal protein L17



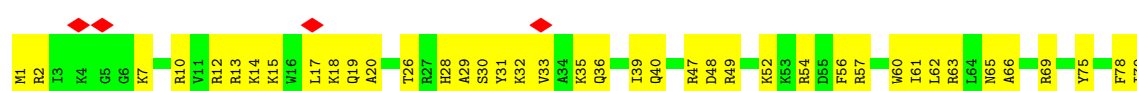
• Molecule 37: 50S ribosomal protein L18



• Molecule 38: 50S ribosomal protein L19

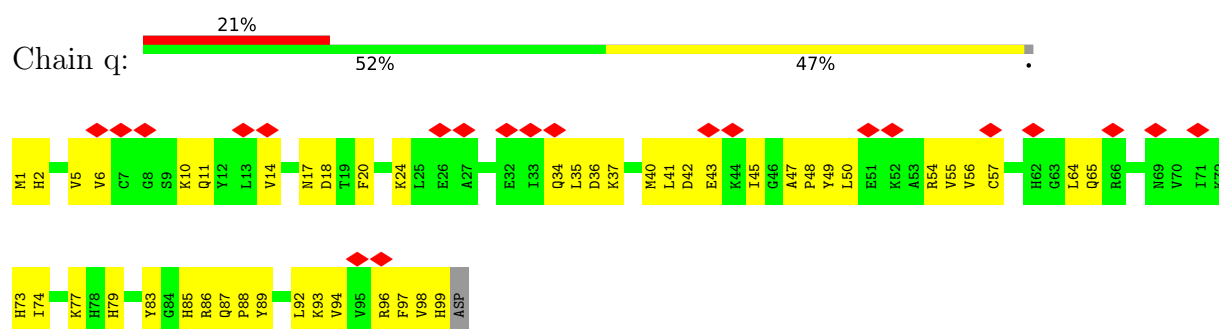


• Molecule 39: 50S ribosomal protein L20

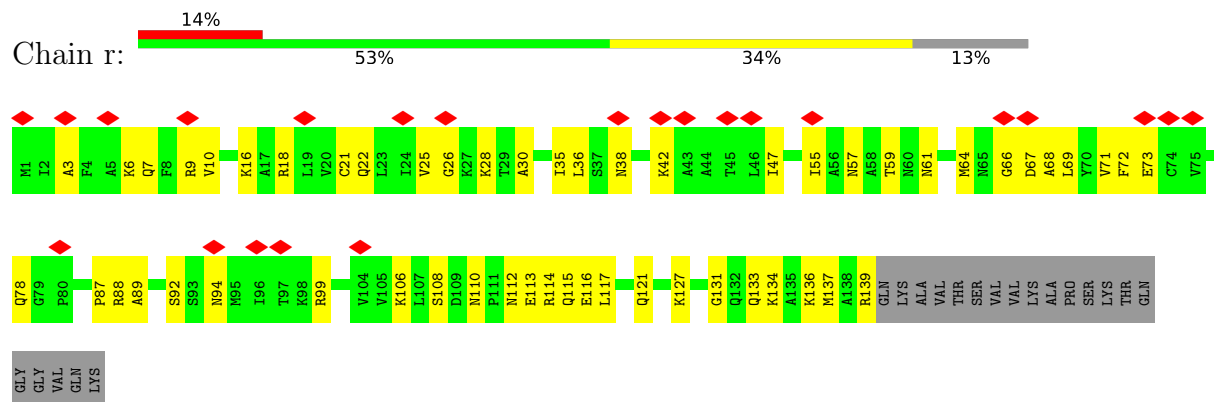


• Molecule 40: 50S ribosomal protein L21

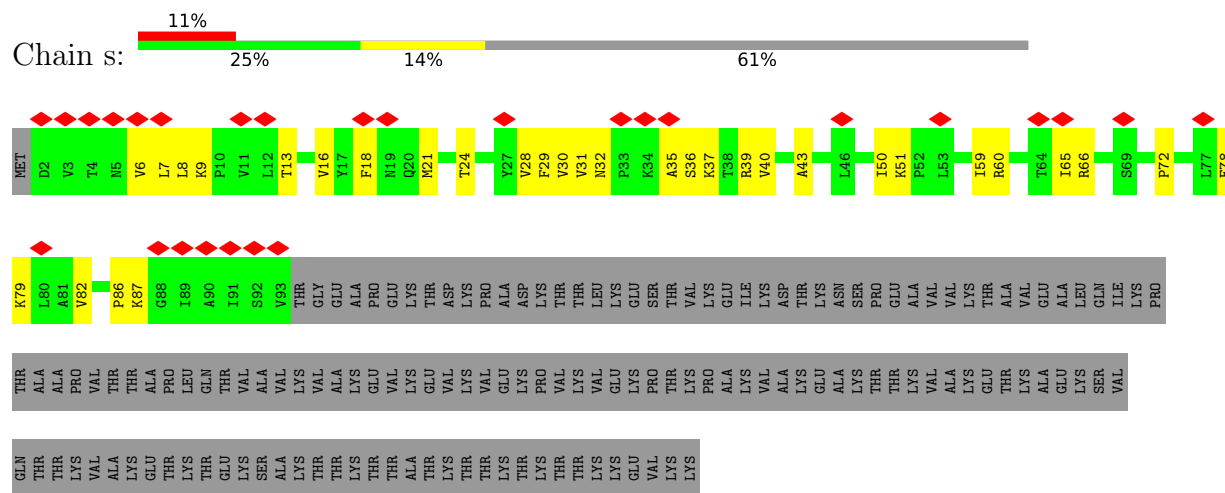




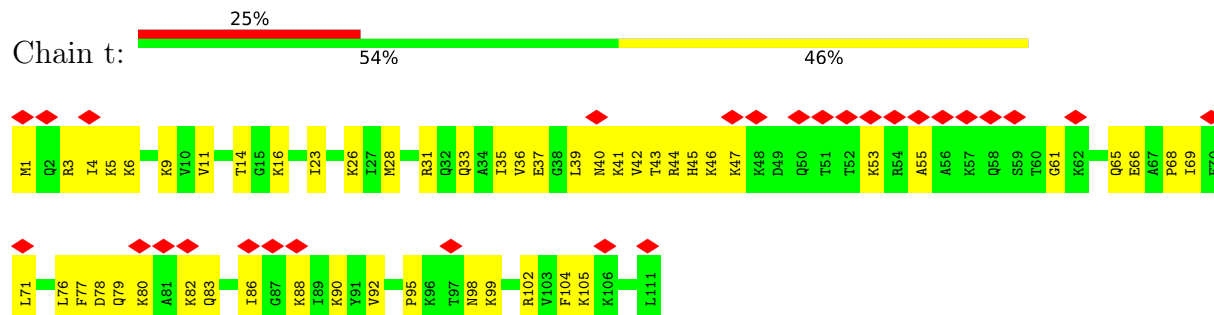
• Molecule 41: 50S ribosomal protein L22



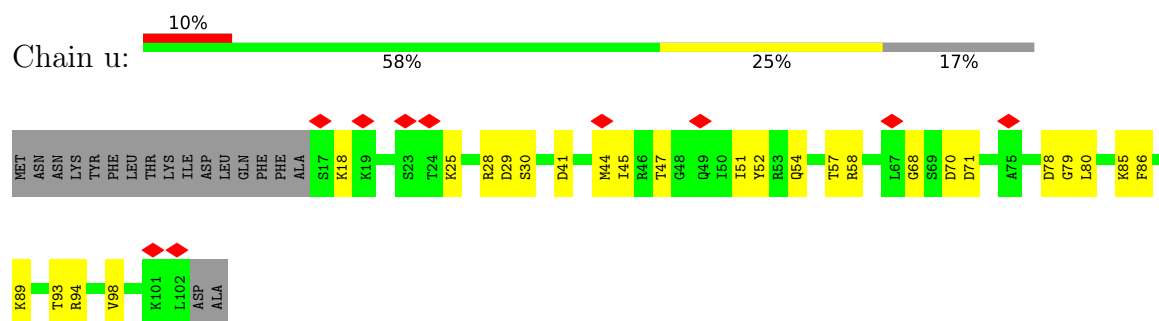
• Molecule 42: 50S ribosomal protein L23



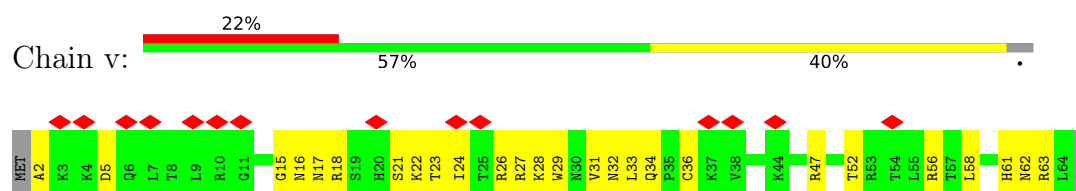
• Molecule 43: 50S ribosomal protein L24



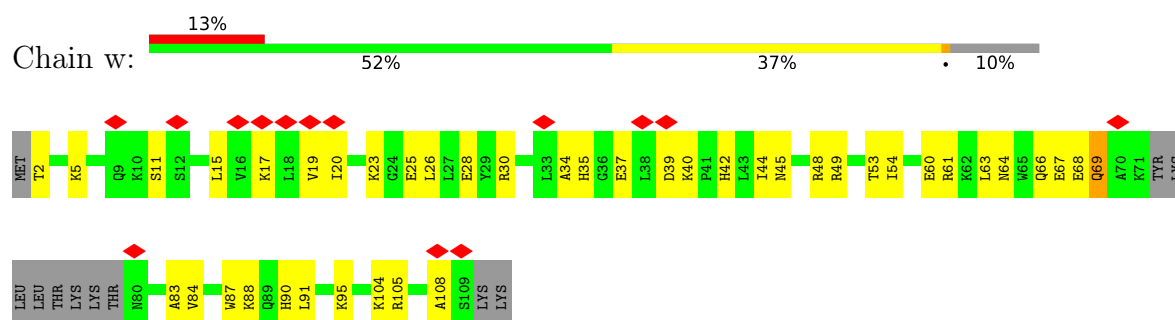
- Molecule 44: 50S ribosomal protein L27



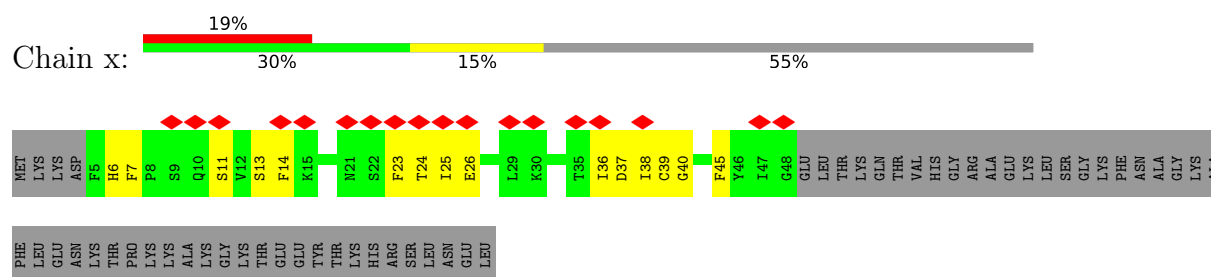
- Molecule 45: 50S ribosomal protein L28



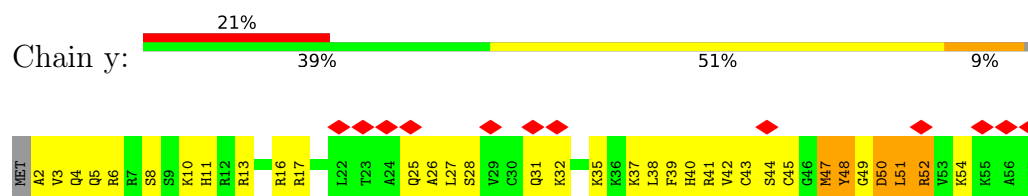
- Molecule 46: 50S ribosomal protein L29



- Molecule 47: 50S ribosomal protein L31



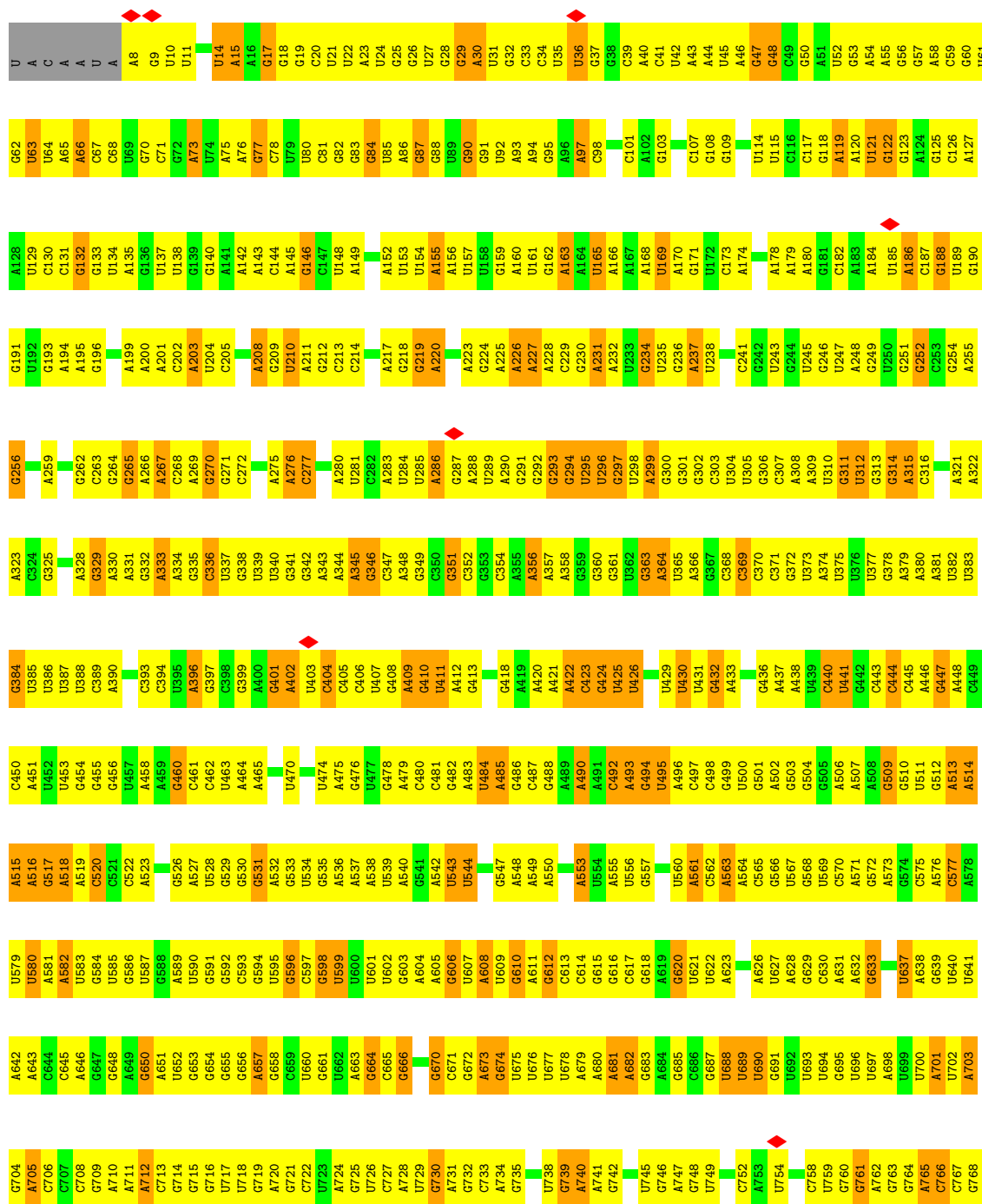
- Molecule 48: 50S ribosomal protein L32



- Molecule 49: 50S ribosomal protein L33 1

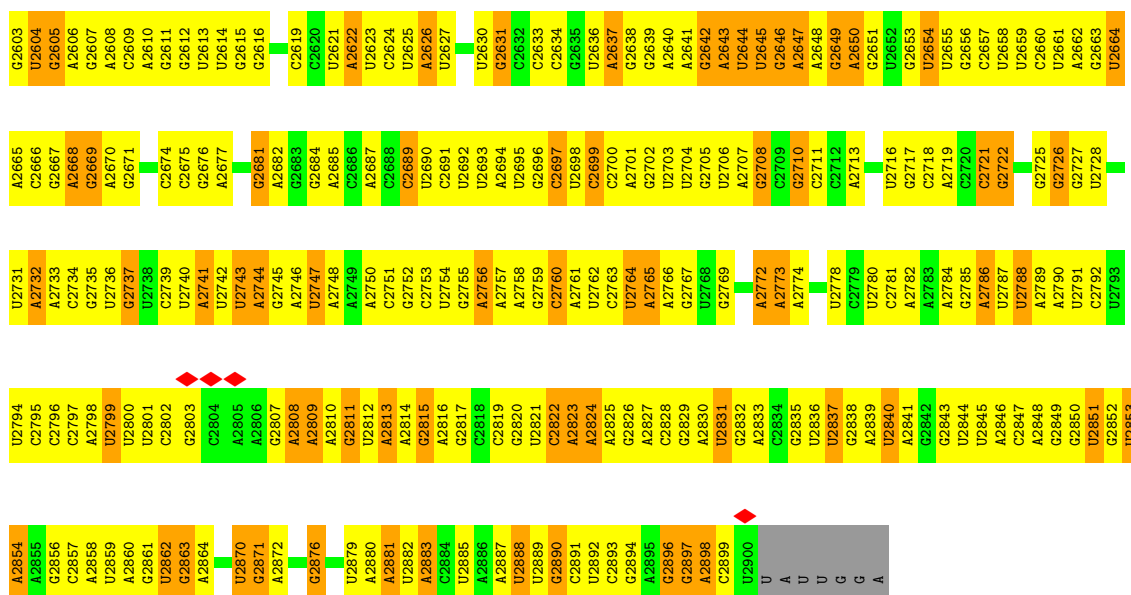


• Molecule 50: 23S ribosomal RNA

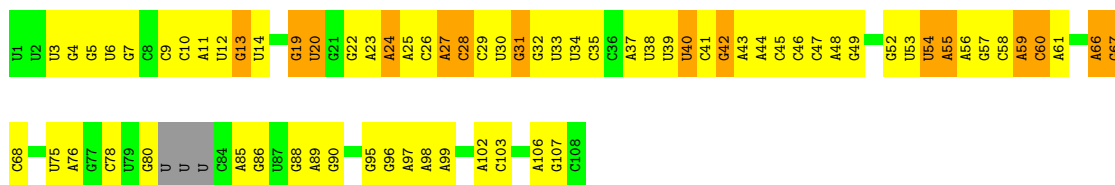


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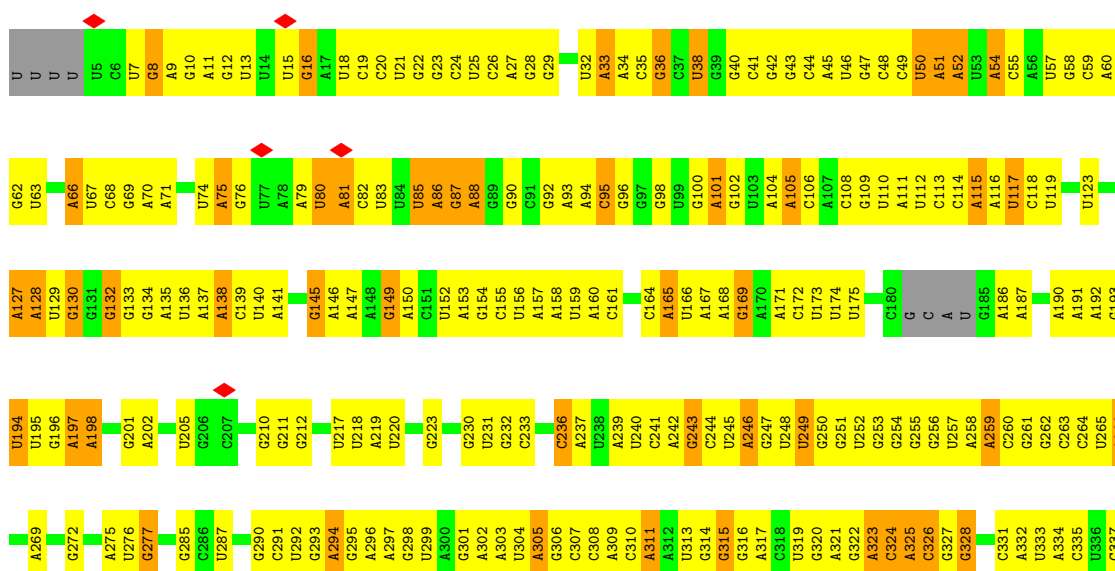
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C2460	G2525	C2460	G2399	A2335	U2273	U2206	A2144		A2022	U1959	U1887	A1822	C1757
A2461	U2526	A2461	A2400	U2337	A2274	U2207	G2145		C2023	A1960	U1888	G1823	G1759
G2462	U2527	G2462	U2401	G2338	A2275	U2208	A2146		C2024	U1889	U1889	G1824	G1760
G2463	C2528	G2463	C2402	G2339	A2276	U2209	G2147		C2025	A1961	U1890	U1825	C1761
C2464	C2529	C2464	G2403	U2340	A2277	G2210			A2026	U1891	U1891	G1826	G1762
U2465	U2530	U2465	G2404	G2341	G2278	U2211	C2150		G2027	U1892	U1892	U1827	A1763
G2466	C2531	G2466	G2405	U2342	G2279	U2212	G2151		G2028	U1961	U1893	U1828	G1764
A2467	G2532	A2467	U2406	U2343	U2280	A2213	C2152		C2029	U1963	A1891	U1829	U1765
U2468	A2533	U2468	G2407	A2344	U2281	A2214	U2153		U2029	G1966	A1892	G1830	A1766
A2469	G2534	A2469	G2408	G2345	A2282	G2217	A2154		A2030	U1967	A1893	G1831	A1767
U2470	C2535	U2470	U2409	G2346	C2283	U2218	G2155		C2031	A1968	G1894	G1832	U1768
U2536	U2536	U2471	C2410	G2347	G2286	U2219	G2156		A2032	A1969	A1895	G1833	A1769
G2537		G2472	A2211	A2286	A2286	A2220	G2157		G2033				
							G2158						



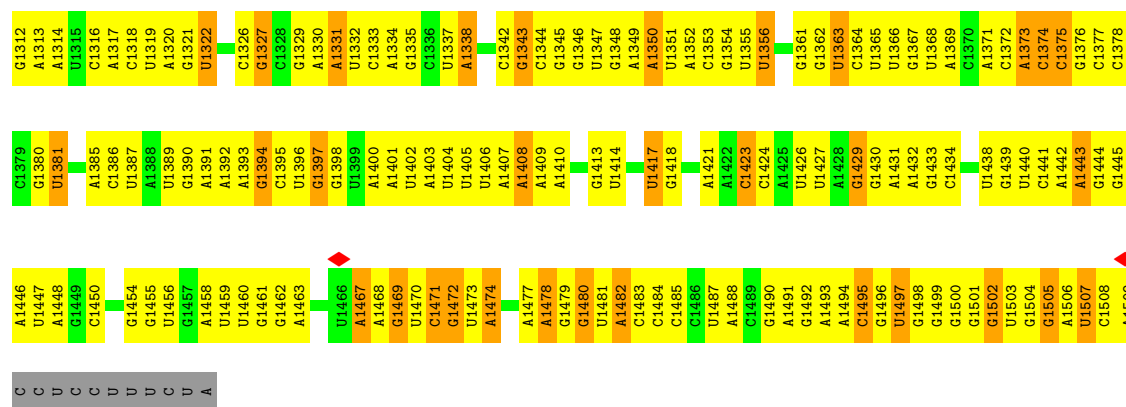
• Molecule 51: 5S ribosomal RNA



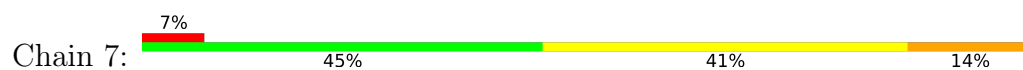
• Molecule 52: 16S ribosomal RNA



A1250	G1251	U1191	U1124	C1057	U987	G923	U856	U795	A734	U669	G599	A535	C469	G402	C338
A1254	A1255	U1193	C1125	A1058	G988	A924	A859	A796	C735	G670	G600	U536	U470	A403	U339
G1195	G1196	U1194	A1127	U1061	A989	C926	C860	G797	U736	G671	U601	A537	A471	A404	A340
G1197	G1198	G1063	G1128	C1062	C990	C929	A861	G798	U737	G672	U603	G539	A473	A405	C341
G1199	G1199	U1064	G1130	U1064	G998	A930	U864	G800	A738	A673	A806	U540	G474	A406	G342
A1261	A1261	G1065	A1131	G1065	C999	C931	U865	C802	C741	U674	A607	C541	U475	U408	G344
A1262	A1262	A932	A1132	A932	C999	A932	A866	C803	C742	U675	G608	G542	U476	A409	A346
A1263	A1263	A1001	A1133	A1001	A1001	A933	A867	A804	A743	C677	G609	G544	U477	A410	G346
A1264	A1264	G1068	C1134	G1068	A1002	G934	G868	C805	A744	A678	G610	A545	G478	A411	C348
A1202	A1202	U1069	U1135	U1069	G1003	C934	U869	A806	U745	U679	A611	G546	U481	C412	A349
A1203	A1203	G1070	G1136	G1070	U1004	U838	A870	C807	A746	U680	G612	C547	U482	A350	G350
A1204	A1204	A1071	C1137	A1071	U1007	G939	U871	C808	C747	U681	U483	G548	U483	C351	A352
G1205	G1205	G1072	U1138	G1072	U1008	G940	C872	G809	U748	G682	C616	U549	U484	A418	A352
G1206	G1206	A1073	A1139	A1073	G1008	A941	U873	U810	U749	G683	U617	U550	U485	A419	A353
U1207	U1207	U1074	G1140	U1074	G1009	G942	C876	A811	A750	A684	U618	A551	A487	A420	U354
G1208	G1208	G1075	A1141	G1075	A1010	C943	C877	A812	C751	G685	A619	U552	U488	G421	A355
G1209	G1209	U1076	A1142	U1076	A1011	U945	C878	A813	G752	C686	A620	C553	U489	A422	G356
U1210	U1210	U1077	G1142	U1077	A1012	U946	U878	C814	C753	G688	C621	C554	U490	G357	G358
A1211	A1211	C1013	G1149	G1078	G1013	G946	U879	G815	U754	G688	A622	G556	U491	A359	A360
A1212	A1212	A1014	A1150	U947	A1014	U947	G880	U816	U755	G688	G623	G557	U492	A425	A360
A1213	A1213	G1019	A1151	G881	G1019	U948	G881	U817	A756	G688	U624	A557	G491	A426	A360
A1214	A1214	U1018	A1152	U882	G1018	G949	U882	A818	G757	G688	U625	U558	G492	A427	U361
U1215	U1215	G1083	A1154	U883	U951	C950	U883	G819	U760	U694	U627	U559	A493	A428	U362
G1216	G1216	A1084	A1155	U885	U952	U952	U885	A820	G761	U694	A628	U560	A494	A429	U363
G1217	G1217	G1085	A1156	A886	A953	A953	A886	A821	G762	U694	A628	A561	U499	A430	U364
G1218	G1218	U1086	A1157	A887	A954	A954	A887	A822	G763	U694	C631	U562	G500	G430	U365
G1219	G1219	G1091	A1158	U888	U955	U955	A888	C923	A763	U694	A632	U563	U499	U431	U366
A1220	A1220	U1092	A1159	U889	U956	U956	U889	A825	A765	U694	U633	G565	U503	A432	A367
A1221	A1221	A1093	A1160	U890	C957	C957	U890	G826	G766	U694	U634	G565	A504	U434	C368
A1222	A1222	G1094	A1161	U891	A958	A958	C991	G829	G767	U694	G635	G568	U505	U435	A369
A1223	A1223	A1095	A1162	U892	A959	A959	G892	U830	G768	U694	G636	U569	U506	A370	A370
A1224	A1224	G1096	A1163	U893	G961	G961	A896	G831	U769	U694	G637	A570	A507	U440	U371
A1225	A1225	U1097	U1164	U894	G962	G962	A897	G832	G770	U694	A638	A571	A508	U441	A372
A1226	A1226	G1098	G1165	U895	G963	G963	A898	G833	G771	U694	U639	A572	A509	G442	A373
A1227	A1227	U1099	A1166	U896	A964	A964	A899	G834	G772	U694	U640	G573	C509	G443	G374
A1228	A1228	C1100	C1167	U897	C965	C965	U899	G835	G773	U694	U641	C574	A511	G444	C375
A1229	A1229	A1101	G1168	U898	A966	A966	G900	G836	A774	U694	U642	A575	A446	A445	A376
A1290	A1290	U1102	U1169	U899	G967	G967	U905	G837	C775	U694	U643	A576	A447	A446	A379
A1291	A1291	C1103	C1170	U900	G968	G968	U906	U838	C776	U694	U644	C580	A448	A448	G380
A1292	A1292	G1104	A1171	U901	G969	G969	C906	U839	A777	U694	U645	A581	A449	A449	C381
A1293	A1293	U1105	A1172	U902	A970	A970	A907	C840	A778	U694	U646	G582	A450	A450	G382
A1294	A1294	U1106	A1173	U903	G1041	G1041	A908	C841	A779	U694	U647	G583	A451	A451	U383
U1295	U1295	G1110	U1174	U904	U1042	U1042	A909	C842	U780	U694	U648	G584	A452	A452	A384
G1296	G1296	U1111	C1175	A971	G1043	G1043	C910	C843	A781	U694	U649	G585	A453	A453	G385
G1297	G1297	U1112	A1176	A972	C1044	C1044	C911	C844	U782	U694	U650	G586	A454	A454	U386
U1298	U1298	U1113	C1177	C974	C1045	C1045	G912	U845	G783	U694	U651	G587	A455	A455	G387
C1300	C1300	U1114	C1178	C975	A1046	A1046	G913	C846	A784	U694	U652	G588	A456	A456	G388
U1301	U1301	U1115	A1179	U976	U1047	U1047	A914	C847	U785	U694	U653	A587	A457	A457	U389
A1302	A1302	G1116	U1180	U977	G1048	G1048	U915	G847	U786	U694	U654	U588	A458	A458	A393
U1303	U1303	U1117	G1181	A978	U1049	U1049	U916	U848	A787	U694	U655	U589	A459	A459	U394
A1304	A1304	U1118	C1182	C979	G1050	G1050	U917	A849	A788	U694	U656	G590	G527	G527	G395
A1305	A1305	U1119	C1183	C980	U1051	U1051	G918	U851	G789	U694	U657	A591	G528	G528	C396
A1306	A1306	A1118	C1184	U1119	U1052	U1052	C919	U852	A790	U694	U658	A592	U529	U529	U463
A1307	A1307	U1120	C1185	A882	U1053	U1053	G920	G853	A791	U694	U659	A593	A531	A531	C397
A1245	A1245	U1121	U1186	G933	G1054	G1054	G921	A854	A792	U694	U660	A594	A465	A465	G388
A1246	A1246	U1122	U1187	U986	U1055	U1055	G922	A855	C793	U694	U661	G595	U532	U532	C399
U1247	U1247	U1123	U1188	U986	U1056	U1056	G923	A856	C794	U694	U662	A596	A466	A466	G400
U1248	U1248	G1123	U1189	U986	U1056	U1056	G924	A857	C795	U694	U663	A597	U533	U533	U401



- Molecule 53: tRNA-Phe



- Molecule 53: tRNA-Phe



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	1449	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.387	Depositor
Minimum map value	-0.395	Depositor
Average map value	0.026	Depositor
Map value standard deviation	0.118	Depositor
Recommended contour level	0.47	Depositor
Map size (Å)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7005, 1.7005, 1.7005	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.15	0/383	0.42	0/504
2	1	0.16	0/484	0.44	0/637
3	2	0.14	0/306	0.35	0/401
4	A	0.16	0/1954	0.42	0/2642
5	B	0.16	0/1721	0.46	0/2323
6	C	0.16	0/1691	0.43	0/2267
7	D	0.16	0/1188	0.40	0/1593
8	E	0.17	0/1384	0.41	0/1867
9	F	0.17	0/1266	0.42	0/1700
10	G	0.17	0/1126	0.48	0/1517
11	H	0.16	0/1044	0.44	0/1395
12	I	0.17	0/820	0.40	0/1103
13	J	0.15	0/844	0.40	0/1136
14	K	0.29	0/1094	0.60	0/1468
15	L	0.17	0/962	0.42	0/1289
16	M	0.19	0/483	0.52	0/643
17	N	0.14	0/679	0.38	0/907
18	O	0.15	0/659	0.43	0/885
19	P	0.16	0/684	0.47	0/913
20	Q	0.16	0/545	0.42	0/730
21	R	0.17	0/698	0.49	0/936
22	S	0.14	0/631	0.38	0/838
23	T	0.13	0/475	0.34	0/621
24	a	0.17	0/2267	0.45	0/3044
25	b	0.16	0/1795	0.43	0/2412
26	c	0.14	0/1671	0.38	0/2246
27	d	0.16	0/1409	0.42	0/1894
28	e	0.16	0/1420	0.43	0/1912
29	f	0.19	0/1183	0.43	0/1587
30	g	0.42	0/969	0.75	0/1295
31	h	0.16	0/968	0.47	1/1298 (0.1%)
32	i	0.16	0/1186	0.41	0/1592
33	j	0.17	0/953	0.45	0/1275
34	k	0.16	0/1170	0.44	0/1559

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	l	0.16	0/1104	0.40	0/1481
36	m	0.17	0/973	0.47	0/1309
37	n	0.15	0/897	0.42	0/1198
38	o	0.16	0/948	0.43	0/1262
39	p	0.15	0/961	0.40	0/1278
40	q	0.19	0/828	0.49	0/1111
41	r	0.16	0/1077	0.38	0/1441
42	s	0.16	0/732	0.46	0/988
43	t	0.15	0/879	0.41	0/1165
44	u	0.17	0/665	0.47	0/884
45	v	0.23	0/519	0.52	0/695
46	w	0.15	0/826	0.38	0/1104
47	x	0.15	0/353	0.37	0/474
48	y	0.32	0/457	0.65	1/601 (0.2%)
49	z	0.17	0/412	0.47	0/547
50	3	0.11	0/69073	0.27	0/107710
51	4	0.10	0/2505	0.26	0/3902
52	5	0.11	0/35768	0.25	0/55764
53	7	0.12	0/1808	0.30	0/2817
53	8	0.12	0/1808	0.30	0/2817
All	All	0.13	0/158705	0.32	2/236977 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
21	R	0	1
35	l	0	1
41	r	0	1
42	s	0	1
All	All	0	4

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	h	72	VAL	N-CA-C	-7.66	105.09	111.91
48	y	48	TYR	N-CA-C	-6.39	101.92	110.55

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	R	25	GLN	Peptide
35	l	13	HIS	Peptide
41	r	9	ARG	Peptide
42	s	65	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	0	380	0	429	8	0
2	1	477	0	530	22	0
3	2	304	0	350	17	0
4	A	1921	0	1973	62	0
5	B	1698	0	1768	57	0
6	C	1660	0	1719	68	0
7	D	1173	0	1267	40	0
8	E	1362	0	1377	62	0
9	F	1246	0	1308	43	0
10	G	1110	0	1226	54	0
11	H	1028	0	1094	46	0
12	I	809	0	894	30	0
13	J	829	0	855	31	0
14	K	1076	0	1170	55	0
15	L	951	0	1014	42	0
16	M	474	0	509	35	0
17	N	673	0	730	19	0
18	O	646	0	677	22	0
19	P	675	0	728	23	0
20	Q	535	0	562	24	0
21	R	682	0	691	32	0
22	S	629	0	681	25	0
23	T	471	0	522	10	0
24	a	2225	0	2301	105	0
25	b	1762	0	1808	74	0
26	c	1644	0	1731	54	0
27	d	1388	0	1469	52	0
28	e	1396	0	1481	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	f	1160	0	1172	35	0
30	g	960	0	1014	49	0
31	h	959	0	1039	32	0
32	i	1164	0	1192	42	0
33	j	944	0	1019	33	0
34	k	1153	0	1256	52	0
35	l	1079	0	1134	47	0
36	m	958	0	1011	46	0
37	n	889	0	952	39	0
38	o	938	0	1008	40	0
39	p	947	0	1028	49	0
40	q	811	0	858	33	0
41	r	1068	0	1150	50	0
42	s	720	0	803	26	0
43	t	872	0	972	45	0
44	u	657	0	695	25	0
45	v	513	0	560	43	0
46	w	818	0	870	35	0
47	x	344	0	333	14	0
48	y	452	0	472	35	0
49	z	408	0	440	19	0
50	3	61664	0	30954	2207	0
51	4	2239	0	1137	54	0
52	5	31943	0	16058	1145	0
53	7	1618	0	821	25	0
53	8	1618	0	821	41	0
All	All	146120	0	99633	4756	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 20.

The worst 5 of 4756 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)
50:3:711:A:N6	50:3:837:A:H2	1.48	1.12
50:3:711:A:N6	50:3:837:A:C2	2.18	1.10
50:3:2400:A:N6	50:3:2430:C:H42	1.53	1.06
50:3:1803:U:H3	50:3:1830:G:H1	1.06	1.02
50:3:2122:G:N2	50:3:2179:A:H61	1.58	1.00

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	45/48 (94%)	44 (98%)	1 (2%)	0	100	100
2	1	57/59 (97%)	52 (91%)	5 (9%)	0	100	100
3	2	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
4	A	238/294 (81%)	213 (90%)	25 (10%)	0	100	100
5	B	213/273 (78%)	197 (92%)	16 (8%)	0	100	100
6	C	201/205 (98%)	189 (94%)	12 (6%)	0	100	100
7	D	151/219 (69%)	145 (96%)	6 (4%)	0	100	100
8	E	165/215 (77%)	143 (87%)	22 (13%)	0	100	100
9	F	152/155 (98%)	140 (92%)	12 (8%)	0	100	100
10	G	139/142 (98%)	123 (88%)	16 (12%)	0	100	100
11	H	126/132 (96%)	113 (90%)	13 (10%)	0	100	100
12	I	99/108 (92%)	94 (95%)	5 (5%)	0	100	100
13	J	112/121 (93%)	102 (91%)	10 (9%)	0	100	100
14	K	134/139 (96%)	121 (90%)	13 (10%)	0	100	100
15	L	116/124 (94%)	103 (89%)	13 (11%)	0	100	100
16	M	58/61 (95%)	49 (84%)	9 (16%)	0	100	100
17	N	81/86 (94%)	80 (99%)	1 (1%)	0	100	100
18	O	78/94 (83%)	72 (92%)	6 (8%)	0	100	100
19	P	81/85 (95%)	78 (96%)	3 (4%)	0	100	100
20	Q	63/104 (61%)	53 (84%)	10 (16%)	0	100	100
21	R	82/87 (94%)	67 (82%)	15 (18%)	0	100	100
22	S	75/87 (86%)	75 (100%)	0	0	100	100
23	T	51/60 (85%)	50 (98%)	1 (2%)	0	100	100
24	a	283/287 (99%)	247 (87%)	36 (13%)	0	100	100
25	b	227/287 (79%)	207 (91%)	20 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	c	208/212 (98%)	202 (97%)	6 (3%)	0	100	100
27	d	173/180 (96%)	168 (97%)	5 (3%)	0	100	100
28	e	174/184 (95%)	163 (94%)	11 (6%)	0	100	100
29	f	143/149 (96%)	131 (92%)	12 (8%)	0	100	100
30	g	124/161 (77%)	113 (91%)	11 (9%)	0	100	100
31	h	126/137 (92%)	117 (93%)	9 (7%)	0	100	100
32	i	142/146 (97%)	134 (94%)	8 (6%)	0	100	100
33	j	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
34	k	146/151 (97%)	133 (91%)	13 (9%)	0	100	100
35	l	134/139 (96%)	131 (98%)	2 (2%)	1 (1%)	18	56
36	m	117/124 (94%)	112 (96%)	5 (4%)	0	100	100
37	n	108/116 (93%)	101 (94%)	7 (6%)	0	100	100
38	o	113/119 (95%)	101 (89%)	12 (11%)	0	100	100
39	p	112/127 (88%)	107 (96%)	5 (4%)	0	100	100
40	q	97/100 (97%)	87 (90%)	10 (10%)	0	100	100
41	r	137/159 (86%)	130 (95%)	7 (5%)	0	100	100
42	s	90/237 (38%)	84 (93%)	6 (7%)	0	100	100
43	t	109/111 (98%)	98 (90%)	11 (10%)	0	100	100
44	u	84/104 (81%)	80 (95%)	4 (5%)	0	100	100
45	v	61/65 (94%)	56 (92%)	5 (8%)	0	100	100
46	w	96/111 (86%)	93 (97%)	3 (3%)	0	100	100
47	x	42/97 (43%)	37 (88%)	5 (12%)	0	100	100
48	y	54/57 (95%)	49 (91%)	4 (7%)	1 (2%)	6	32
49	z	48/53 (91%)	46 (96%)	2 (4%)	0	100	100
All	All	5820/6670 (87%)	5378 (92%)	440 (8%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
48	y	52	ARG
35	l	14	ASN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
4	A	212/262 (81%)	212 (100%)	0	100	100
5	B	180/232 (78%)	180 (100%)	0	100	100
6	C	181/183 (99%)	181 (100%)	0	100	100
7	D	123/178 (69%)	123 (100%)	0	100	100
8	E	150/196 (76%)	150 (100%)	0	100	100
9	F	131/132 (99%)	131 (100%)	0	100	100
10	G	123/124 (99%)	123 (100%)	0	100	100
11	H	111/115 (96%)	110 (99%)	1 (1%)	70	79
12	I	95/99 (96%)	95 (100%)	0	100	100
13	J	91/97 (94%)	91 (100%)	0	100	100
14	K	117/120 (98%)	112 (96%)	5 (4%)	26	47
15	L	100/105 (95%)	100 (100%)	0	100	100
16	M	47/48 (98%)	47 (100%)	0	100	100
17	N	76/78 (97%)	76 (100%)	0	100	100
18	O	69/82 (84%)	69 (100%)	0	100	100
19	P	73/75 (97%)	73 (100%)	0	100	100
20	Q	56/94 (60%)	56 (100%)	0	100	100
21	R	74/77 (96%)	74 (100%)	0	100	100
22	S	70/77 (91%)	70 (100%)	0	100	100
23	T	49/56 (88%)	49 (100%)	0	100	100
24	a	241/243 (99%)	241 (100%)	0	100	100
25	b	186/233 (80%)	186 (100%)	0	100	100
26	c	182/184 (99%)	182 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	d	150/154 (97%)	150 (100%)	0	100	100
28	e	153/159 (96%)	153 (100%)	0	100	100
29	f	123/134 (92%)	123 (100%)	0	100	100
30	g	101/129 (78%)	90 (89%)	11 (11%)	6	21
31	h	102/110 (93%)	102 (100%)	0	100	100
32	i	126/128 (98%)	126 (100%)	0	100	100
33	j	103/103 (100%)	103 (100%)	0	100	100
34	k	123/126 (98%)	123 (100%)	0	100	100
35	l	113/115 (98%)	113 (100%)	0	100	100
36	m	105/109 (96%)	105 (100%)	0	100	100
37	n	96/99 (97%)	96 (100%)	0	100	100
38	o	101/105 (96%)	101 (100%)	0	100	100
39	p	100/108 (93%)	100 (100%)	0	100	100
40	q	90/91 (99%)	90 (100%)	0	100	100
41	r	116/132 (88%)	116 (100%)	0	100	100
42	s	82/208 (39%)	82 (100%)	0	100	100
43	t	96/96 (100%)	96 (100%)	0	100	100
44	u	69/85 (81%)	69 (100%)	0	100	100
45	v	58/60 (97%)	58 (100%)	0	100	100
46	w	87/98 (89%)	86 (99%)	1 (1%)	65	76
47	x	41/86 (48%)	41 (100%)	0	100	100
48	y	48/49 (98%)	43 (90%)	5 (10%)	7	22
49	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5093/5751 (89%)	5070 (100%)	23 (0%)	78	83

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	g	88	GLU
46	w	69	GLN
30	g	90	VAL
48	y	47	MET
30	g	26	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 75 such sidechains are listed below:

Mol	Chain	Res	Type
33	j	69	GLN
43	t	2	GLN
34	k	55	GLN
40	q	34	GLN
11	H	62	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	2875/2907 (98%)	829 (28%)	31 (1%)
51	4	103/108 (95%)	33 (32%)	2 (1%)
52	5	1490/1520 (98%)	393 (26%)	6 (0%)
53	7	75/76 (98%)	25 (33%)	1 (1%)
53	8	75/76 (98%)	25 (33%)	1 (1%)
All	All	4618/4687 (98%)	1305 (28%)	41 (0%)

5 of 1305 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	14	U
50	3	15	A
50	3	17	G
50	3	29	G
50	3	30	A

5 of 41 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	3	2823	A
52	5	425	G
50	3	2862	U
51	4	59	A
52	5	1133	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

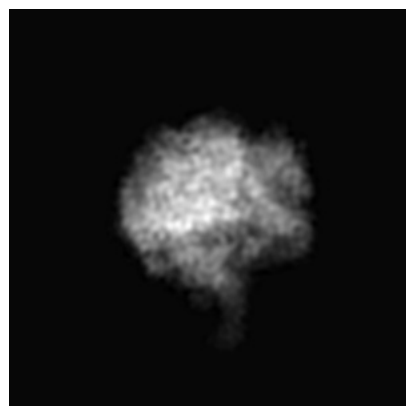
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13278. These allow visual inspection of the internal detail of the map and identification of artifacts.

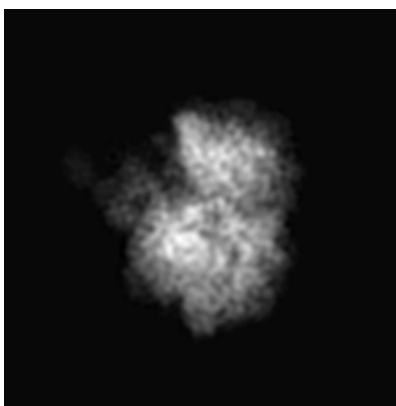
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

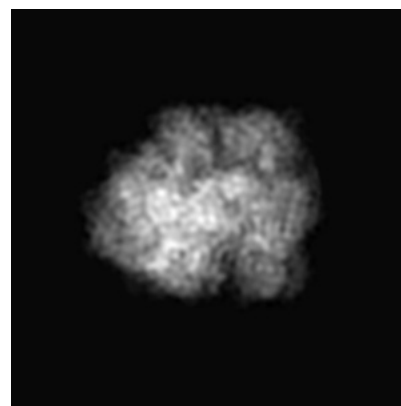
6.1.1 Primary map



X

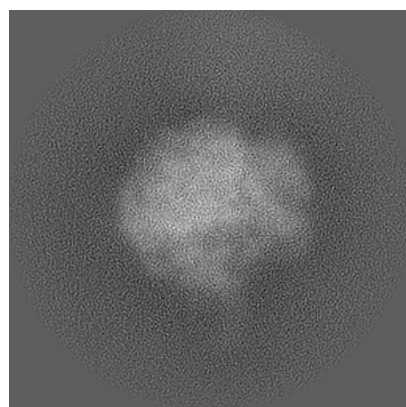


Y

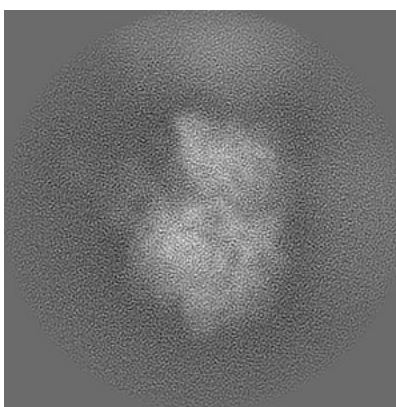


Z

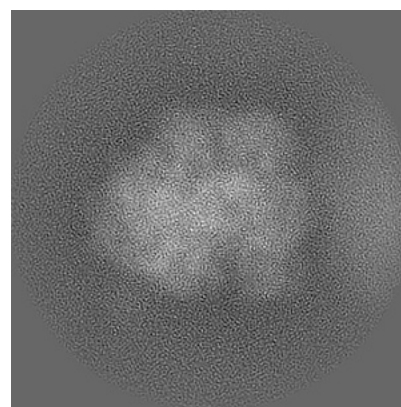
6.1.2 Raw map



X



Y

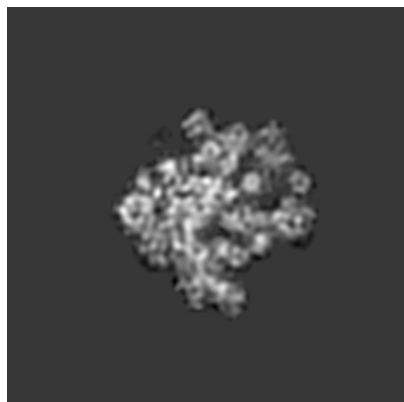


Z

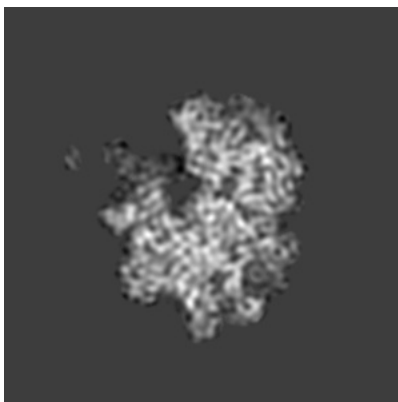
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

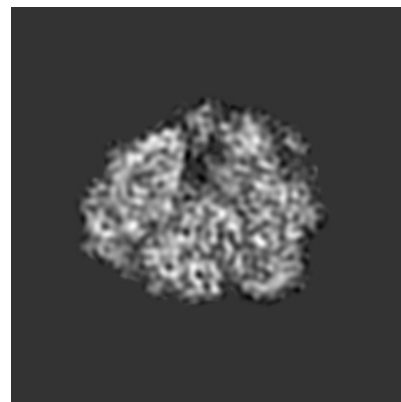
6.2.1 Primary map



X Index: 128

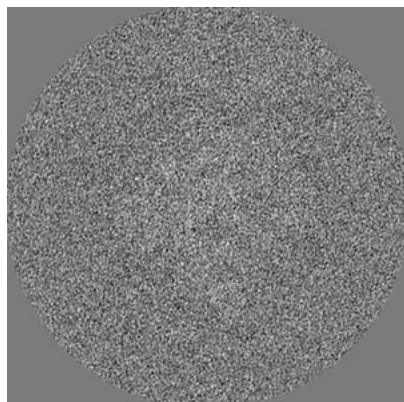


Y Index: 128

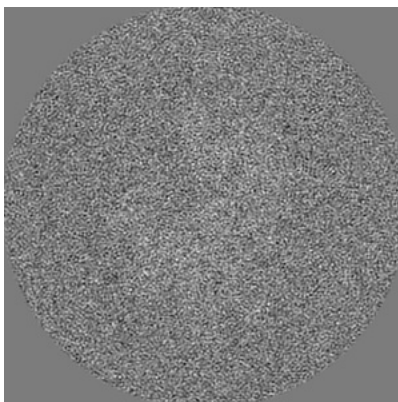


Z Index: 128

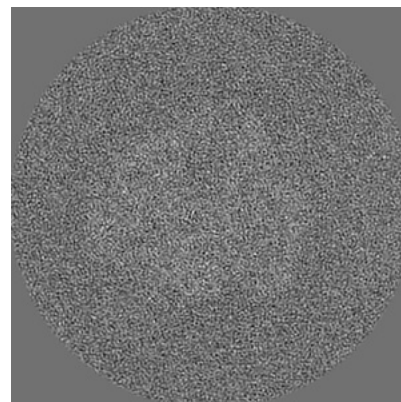
6.2.2 Raw map



X Index: 128



Y Index: 128

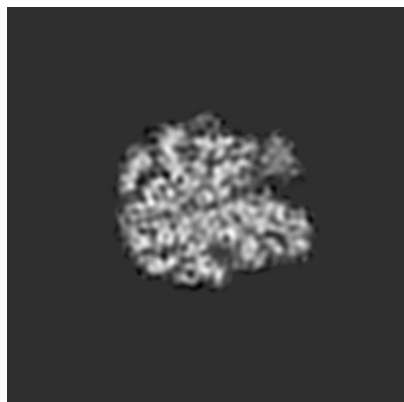


Z Index: 128

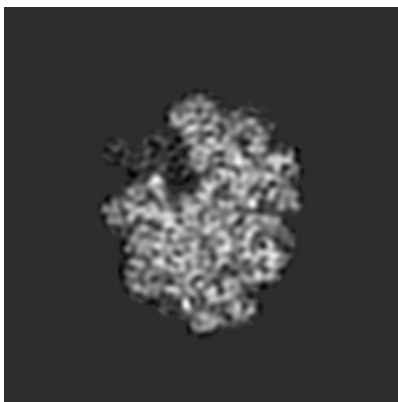
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

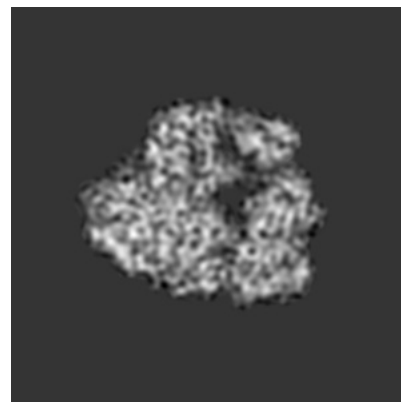
6.3.1 Primary map



X Index: 105

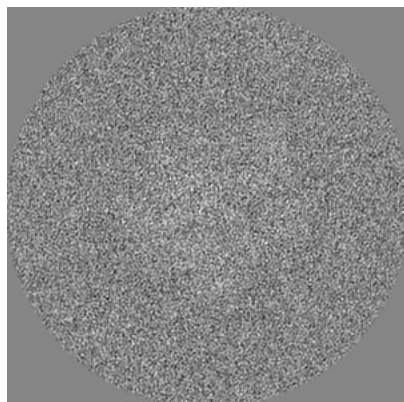


Y Index: 121

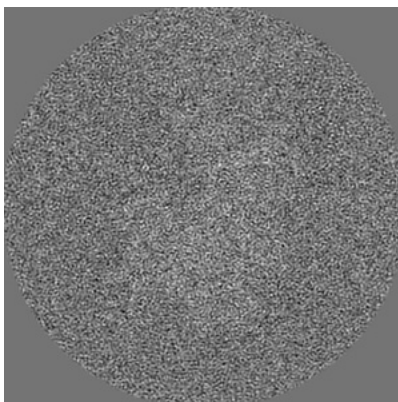


Z Index: 120

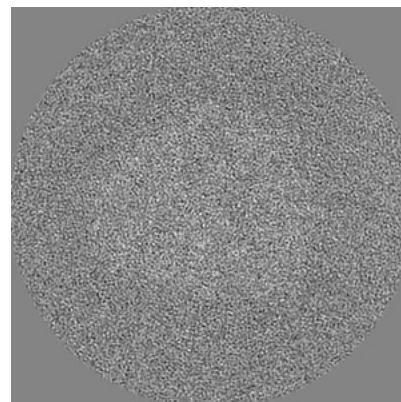
6.3.2 Raw map



X Index: 121



Y Index: 129



Z Index: 125

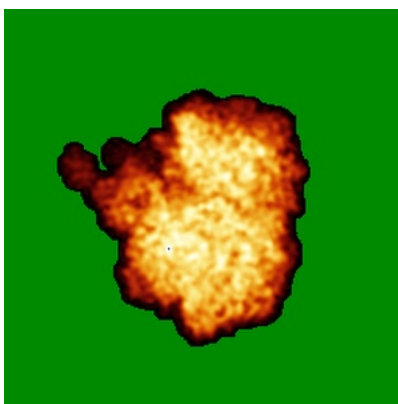
The images above show the largest variance slices of the map in three orthogonal directions.

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

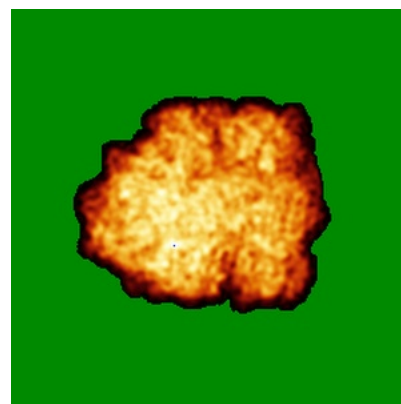
6.4.1 Primary map



X

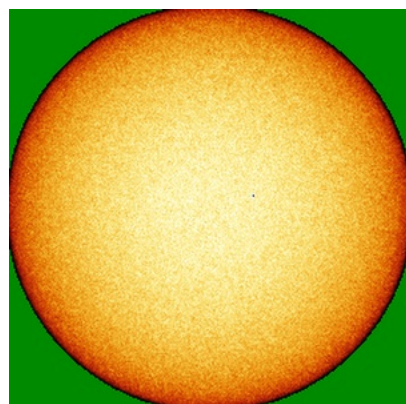


Y

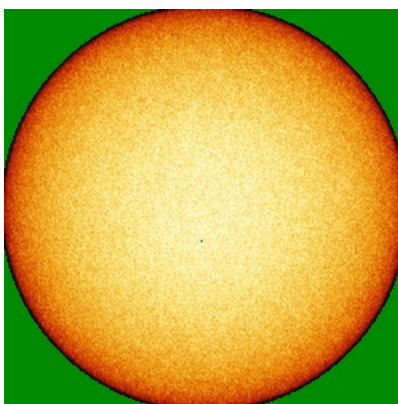


Z

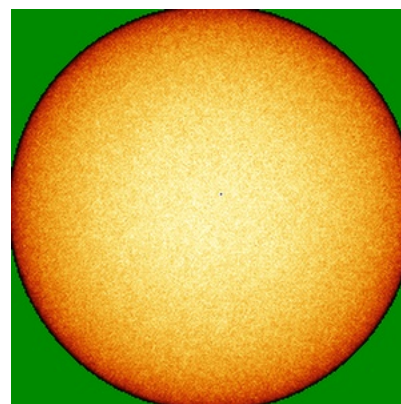
6.4.2 Raw map



X



Y



Z

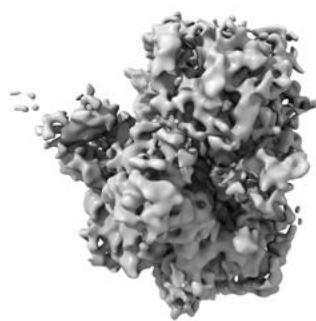
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

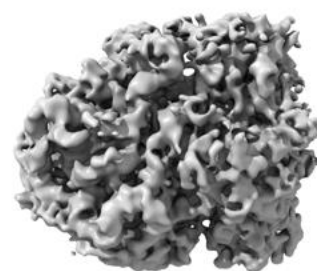
6.5.1 Primary map



X



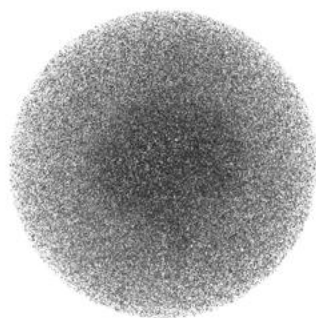
Y



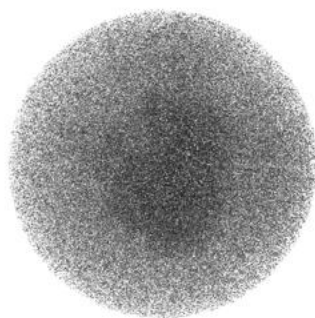
Z

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

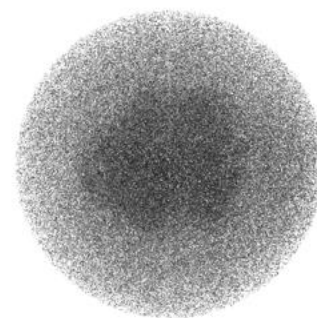
6.5.2 Raw map



X



Y



Z

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

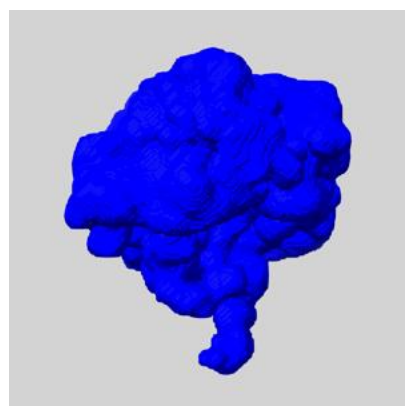
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

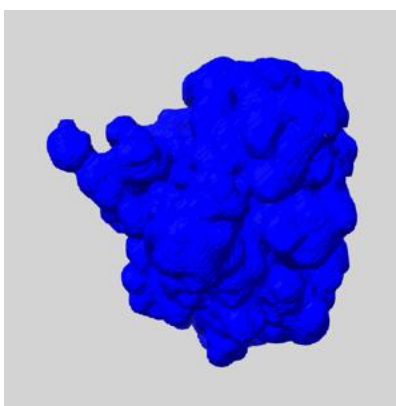
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

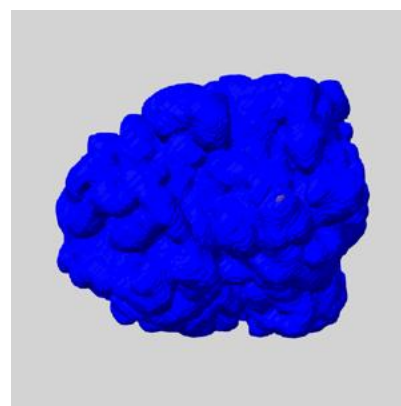
6.6.1 emd_13278_msk_1.map [i](#)



X



Y

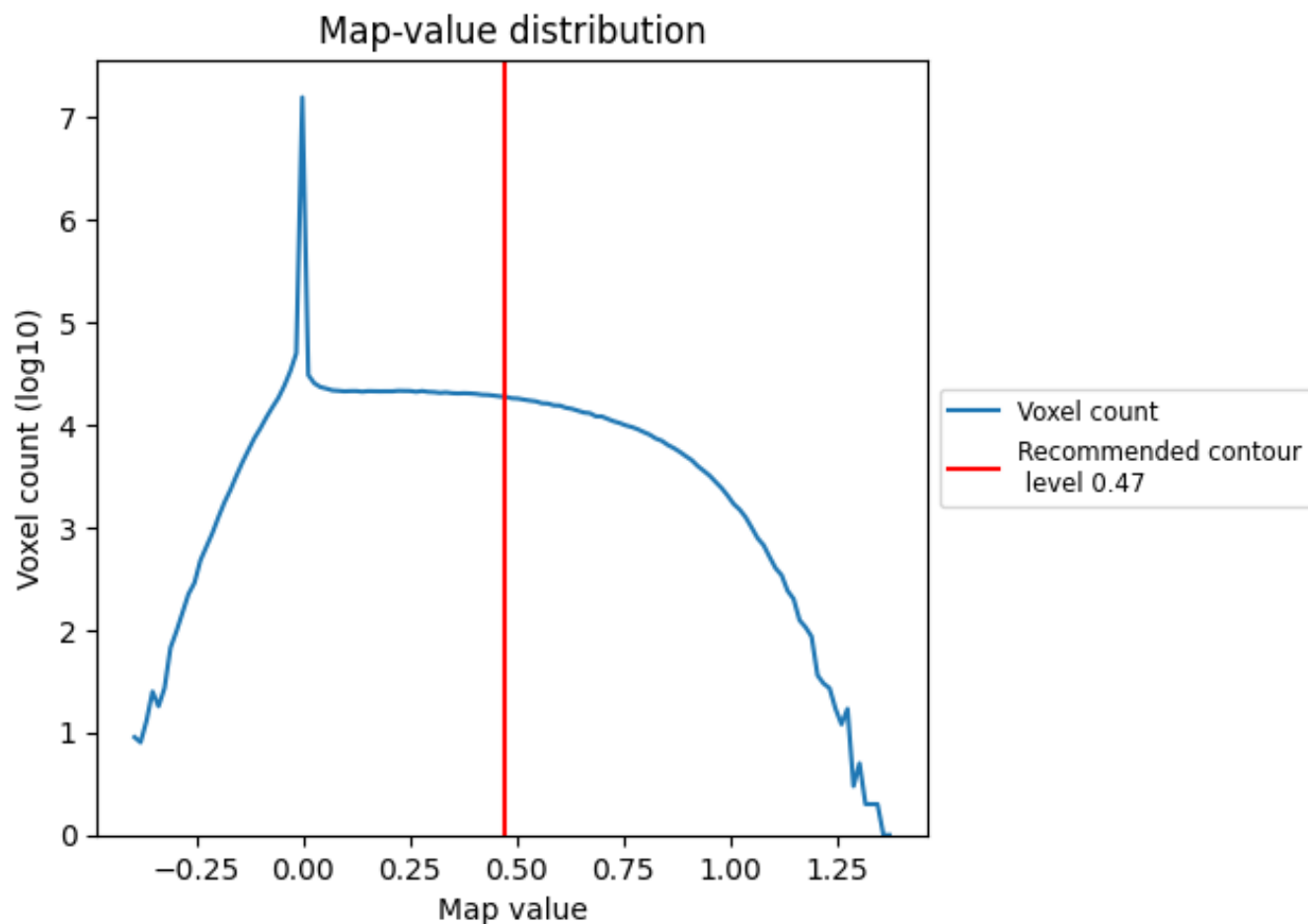


Z

7 Map analysis [i](#)

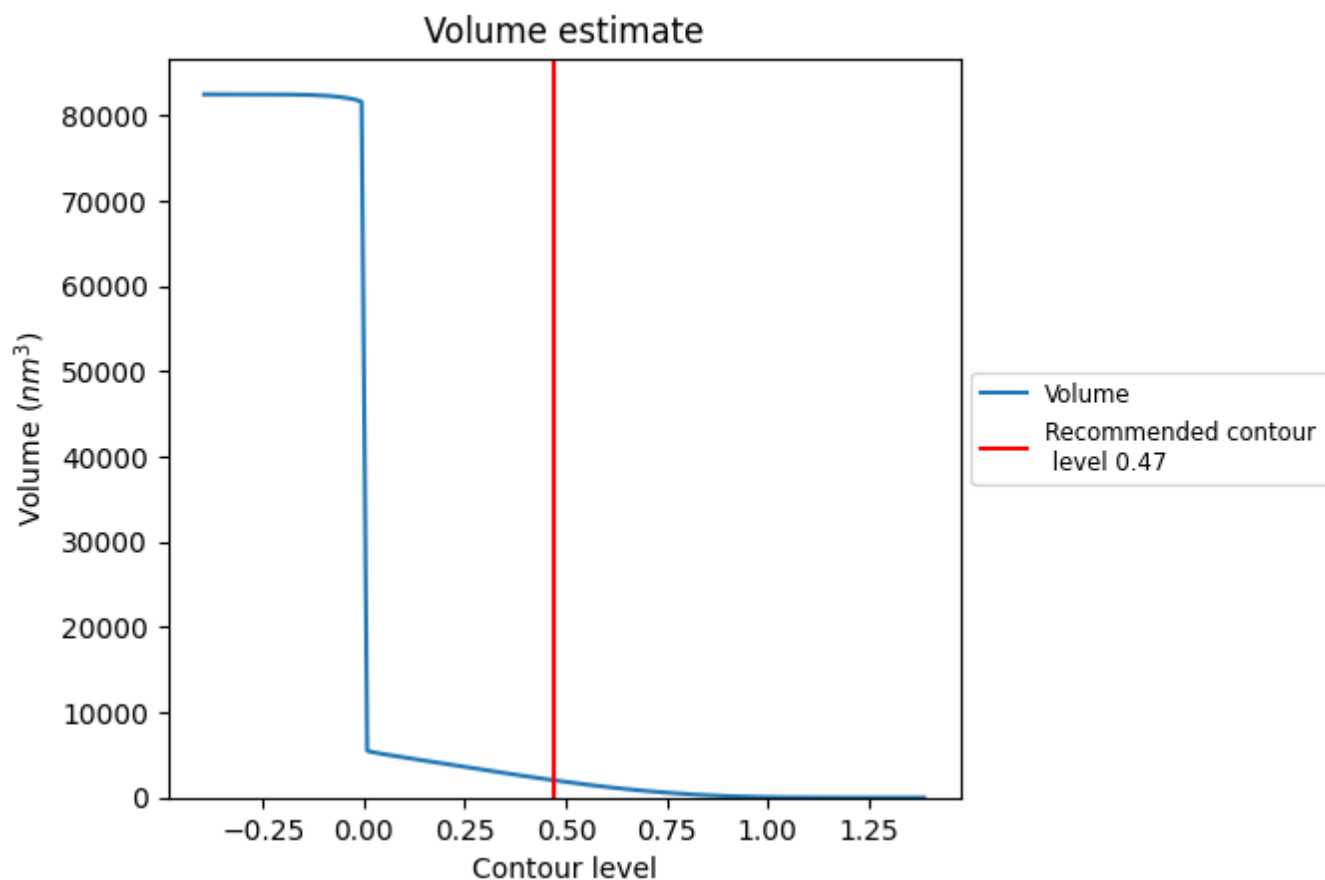
This section contains the results of statistical analysis of the map.

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.

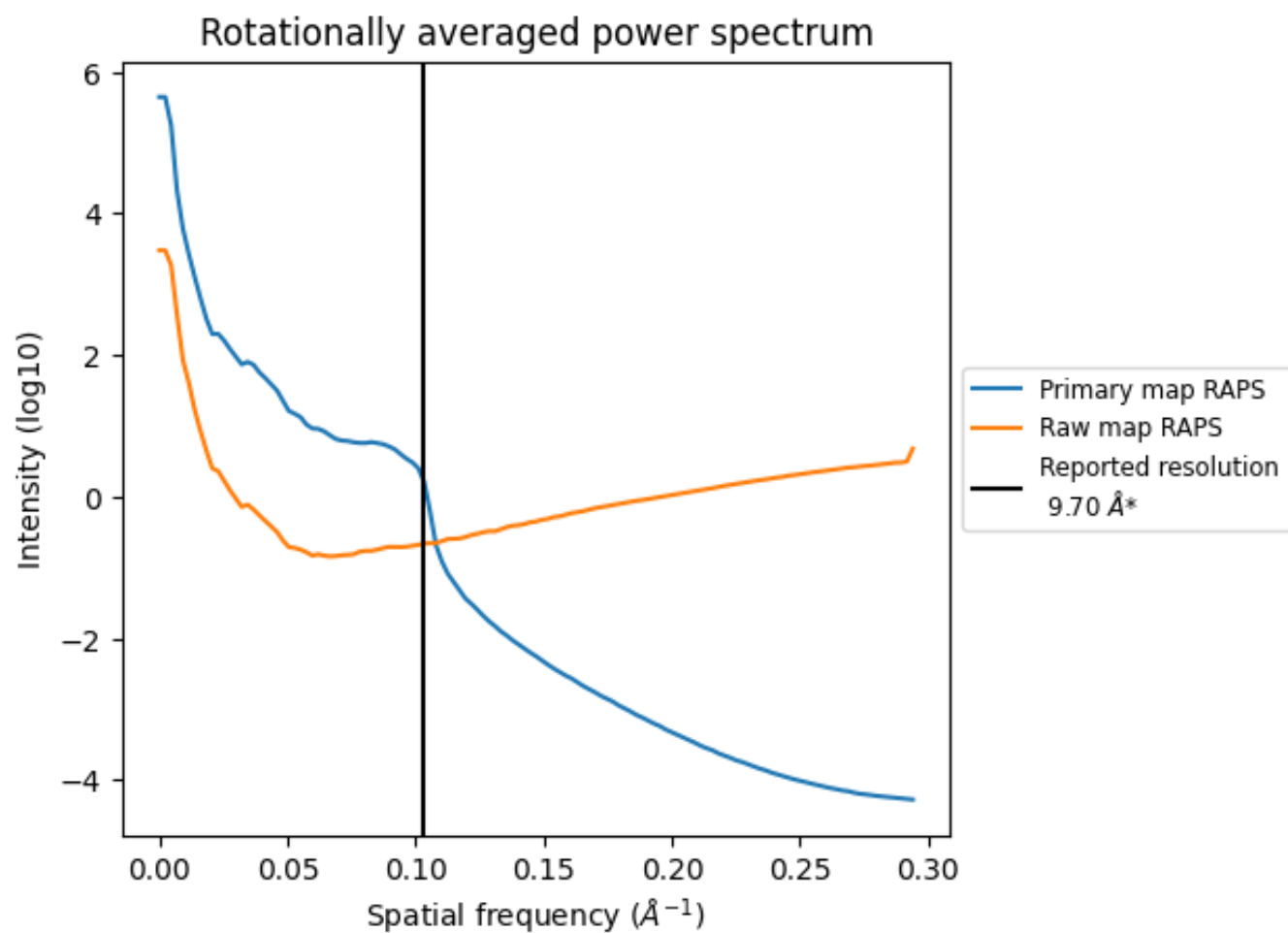
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2033 nm³; this corresponds to an approximate mass of 1837 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 ⓘ

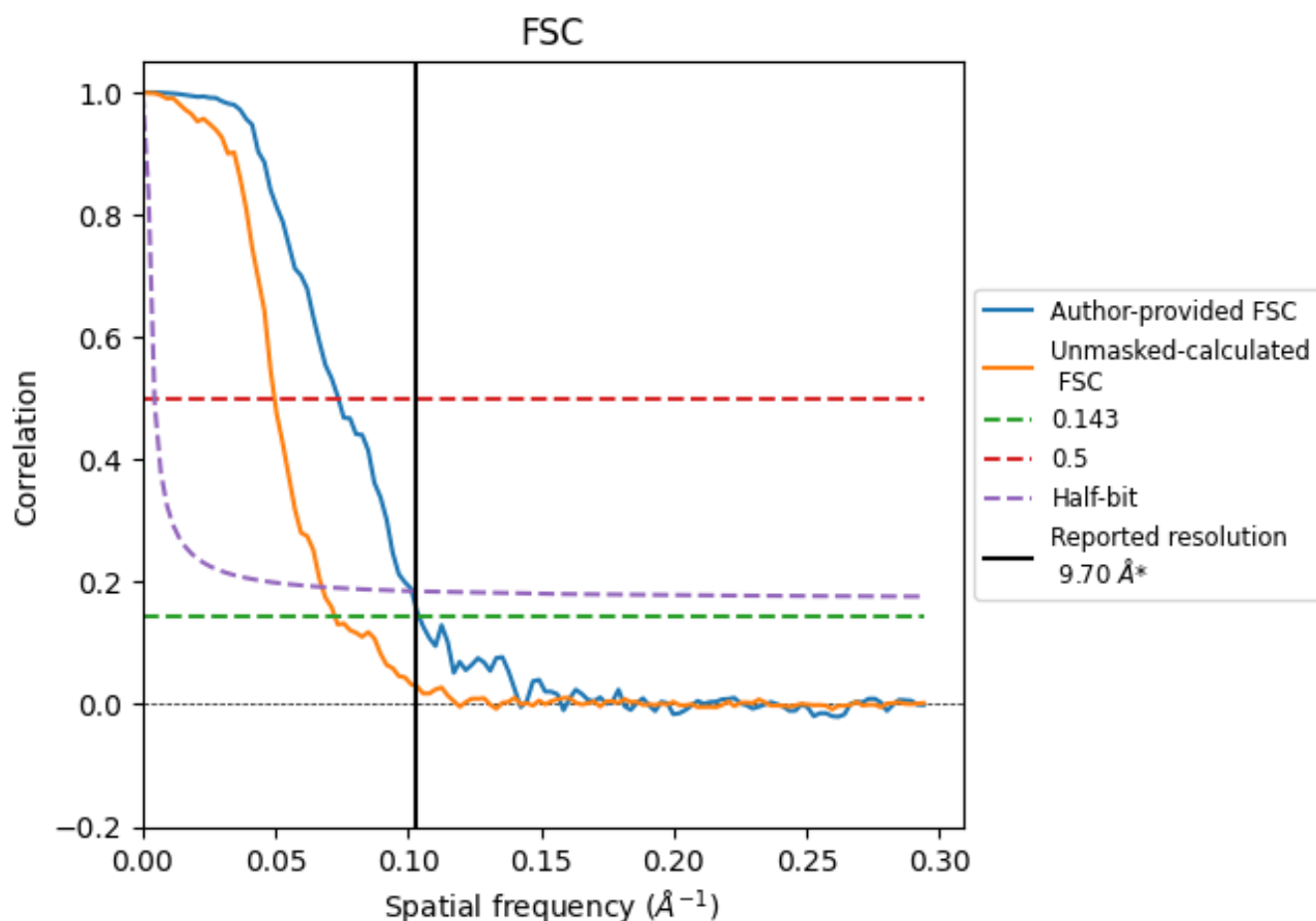


*Reported resolution corresponds to spatial frequency of 0.103 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.103 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

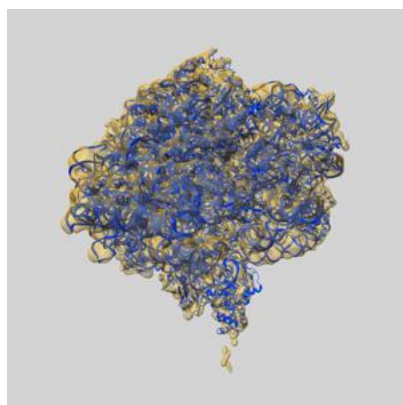
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.70	-	-
Author-provided FSC curve	9.61	13.57	9.87
Unmasked-calculated*	13.79	20.12	14.79

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 13.79 differs from the reported value 9.7 by more than 10 %

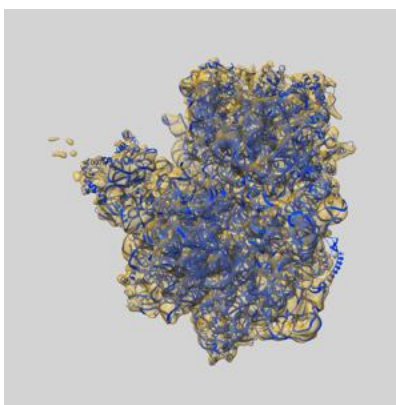
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13278 and PDB model 7PAN. Per-residue inclusion information can be found in section [3](#) on page [14](#).

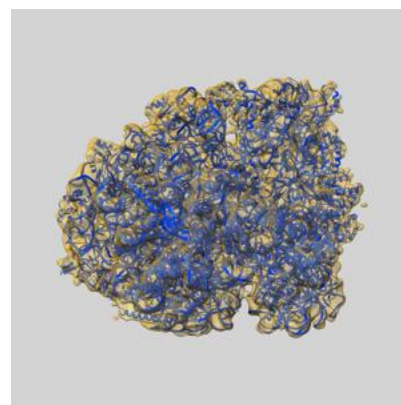
9.1 Map-model overlay [i](#)



X



Y



Z

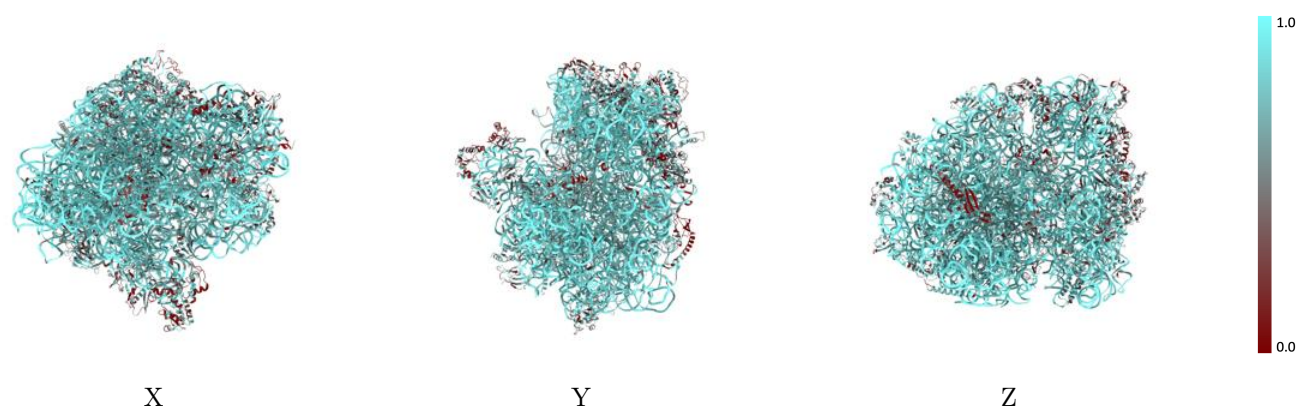
The images above show the 3D surface view of the map at the recommended contour level 0.47 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



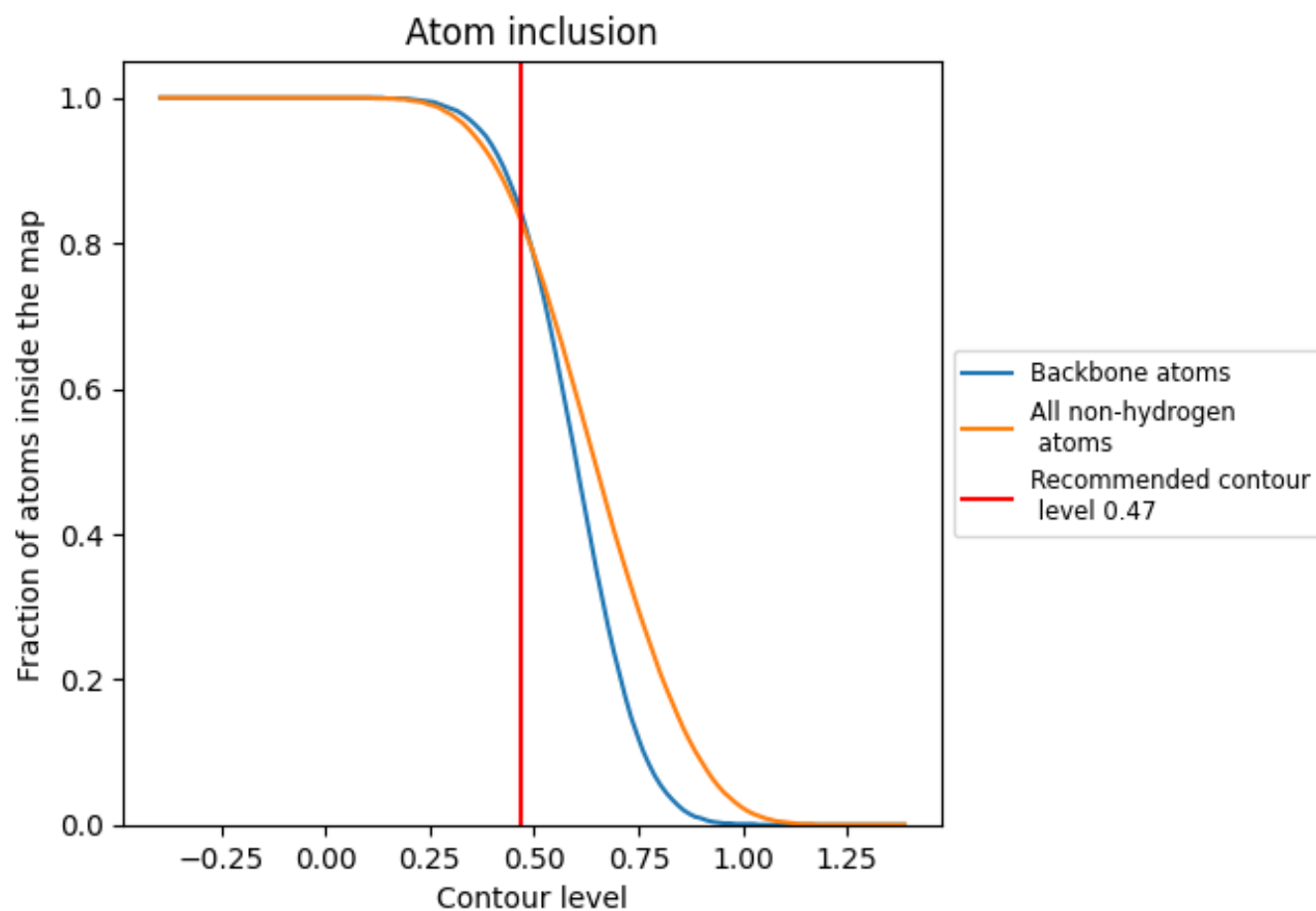
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.47).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 83% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.47) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8290	 0.1470
0	 0.7530	 0.1220
1	 0.7060	 0.1230
2	 0.6450	 0.0820
3	 0.9400	 0.1570
4	 0.9440	 0.1640
5	 0.9350	 0.1570
7	 0.7490	 0.1370
8	 0.8830	 0.1570
A	 0.5060	 0.1420
B	 0.5400	 0.1360
C	 0.5640	 0.1210
D	 0.5660	 0.1190
E	 0.5190	 0.1510
F	 0.5090	 0.1280
G	 0.6040	 0.1200
H	 0.5600	 0.1100
I	 0.5380	 0.1290
J	 0.5920	 0.1180
K	 0.6300	 0.1150
L	 0.5990	 0.1220
M	 0.6370	 0.0800
N	 0.6600	 0.1710
O	 0.6690	 0.1390
P	 0.6710	 0.1360
Q	 0.6670	 0.1260
R	 0.6280	 0.0970
S	 0.7120	 0.1280
T	 0.6500	 0.1670
a	 0.6750	 0.0960
b	 0.6580	 0.1160
c	 0.6790	 0.1350
d	 0.5600	 0.1310
e	 0.5200	 0.1290
f	 0.2320	 0.1430



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Chain	Atom inclusion	Q-score
g	 0.4320	 0.1160
h	 0.2510	 0.0830
i	 0.7380	 0.1360
j	 0.5920	 0.1140
k	 0.7110	 0.1120
l	 0.6760	 0.1180
m	 0.6840	 0.1210
n	 0.7110	 0.1370
o	 0.5720	 0.1390
p	 0.7570	 0.1250
q	 0.6470	 0.1450
r	 0.6760	 0.1330
s	 0.6160	 0.1360
t	 0.5920	 0.1150
u	 0.7530	 0.1110
v	 0.6790	 0.1040
w	 0.7040	 0.1740
x	 0.5040	 0.1390
y	 0.7010	 0.1110
z	 0.7510	 0.1370