



wwPDB EM Validation Summary Report ⓘ

Mar 4, 2026 – 06:19 PM UTC

PDB ID : 7PAQ / pdb_00007paq
EMDB ID : EMD-13280
Title : 70S ribosome with EF-G, 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 : 8.90 Å (reported)
Based on initial models : 4V7D, 7OOC, 4V7C, 7OOD

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:

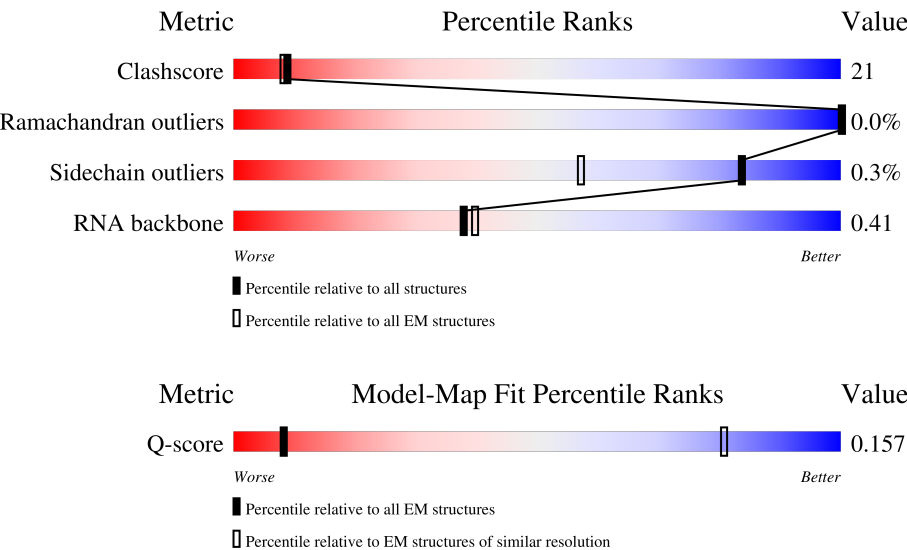
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 8.90 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	258 (8.40 - 9.40)

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	10% 50% 48% .
2	1	59	7% 66% 34%
3	2	37	14% 43% 57%

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Mol	Chain	Length	Quality of chain
4	9	688	
5	A	294	
6	B	273	
7	C	205	
8	D	219	
9	E	215	
10	F	155	
11	G	142	
12	H	132	
13	I	108	
14	J	121	
15	K	139	
16	L	124	
17	M	61	
18	N	86	
19	O	94	
20	P	85	
21	Q	104	
22	R	87	
23	S	87	
24	T	60	
25	W	122	
26	a	287	
27	b	287	
28	c	212	

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Mol	Chain	Length	Quality of chain
29	d	180	
30	e	184	
31	f	149	
32	g	161	
33	h	137	
34	i	146	
35	j	122	
36	k	151	
37	l	139	
38	m	124	
39	n	116	
40	o	119	
41	p	127	
42	q	100	
43	r	159	
44	s	237	
45	t	111	
46	u	104	
47	v	65	
48	w	111	
49	x	97	
50	y	57	
51	z	53	
52	3	2907	
53	4	108	

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Mol	Chain	Length	Quality of chain
54	5	1520	20%61%17%
55	7	76	14%30%50%20%
55	8	76	33%49%18%

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 151980 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 Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	9	682	Total	C	N	O	S	0	0
			5326	3369	911	1021	25		

- Molecule 5 is a protein called 30S ribosomal protein S2.

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

- Molecule 6 is a protein called 30S ribosomal protein S3.

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

- Molecule 7 is a protein called 30S ribosomal protein S4.

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

- Molecule 8 is a protein called 30S ribosomal protein S5.

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

- Molecule 9 is a protein called 30S ribosomal protein S6.

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

- Molecule 10 is a protein called 30S ribosomal protein S7.

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

- Molecule 11 is a protein called 30S ribosomal protein S8.

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

- Molecule 12 is a protein called 30S ribosomal protein S9.

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

- Molecule 13 is a protein called 30S ribosomal protein S10.

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

- Molecule 14 is a protein called 30S ribosomal protein S11.

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

- Molecule 15 is a protein called 30S ribosomal protein S12.

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

- Molecule 16 is a protein called 30S ribosomal protein S13.

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

- Molecule 17 is a protein called 30S ribosomal protein S14 type Z.

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

- Molecule 18 is a protein called 30S ribosomal protein S15.

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

- Molecule 19 is a protein called 30S ribosomal protein S16.

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

- Molecule 20 is a protein called 30S ribosomal protein S17.

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

- Molecule 21 is a protein called 30S ribosomal protein S18.

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

- Molecule 22 is a protein called 30S ribosomal protein S19.

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

- Molecule 23 is a protein called 30S ribosomal protein S20.

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

- Molecule 24 is a protein called 30S ribosomal protein S21.

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

- Molecule 25 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	69	Total	C	N	O	S	0	0
			534	342	87	103	2		

- Molecule 26 is a protein called 50S ribosomal protein L2.

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

- Molecule 27 is a protein called 50S ribosomal protein L3.

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

- Molecule 28 is a protein called 50S ribosomal protein L4.

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

- Molecule 29 is a protein called 50S ribosomal protein L5.

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

- Molecule 30 is a protein called 50S ribosomal protein L6.

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

- Molecule 31 is a protein called 50S ribosomal protein L9.

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

- Molecule 32 is a protein called 50S ribosomal protein L10.

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

- Molecule 33 is a protein called 50S ribosomal protein L11.

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

- Molecule 34 is a protein called 50S ribosomal protein L13.

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

- Molecule 35 is a protein called 50S ribosomal protein L14.

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

- Molecule 36 is a protein called 50S ribosomal protein L15.

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

- Molecule 37 is a protein called 50S ribosomal protein L16.

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

- Molecule 38 is a protein called 50S ribosomal protein L17.

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

- Molecule 39 is a protein called 50S ribosomal protein L18.

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

- Molecule 40 is a protein called 50S ribosomal protein L19.

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

- Molecule 41 is a protein called 50S ribosomal protein L20.

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

- Molecule 42 is a protein called 50S ribosomal protein L21.

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

- Molecule 43 is a protein called 50S ribosomal protein L22.

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

- Molecule 44 is a protein called 50S ribosomal protein L23.

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

- Molecule 45 is a protein called 50S ribosomal protein L24.

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

- Molecule 46 is a protein called 50S ribosomal protein L27.

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

- Molecule 47 is a protein called 50S ribosomal protein L28.

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

- Molecule 48 is a protein called 50S ribosomal protein L29.

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

- Molecule 49 is a protein called 50S ribosomal protein L31.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L33 1.

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

- Molecule 52 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 53 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 54 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

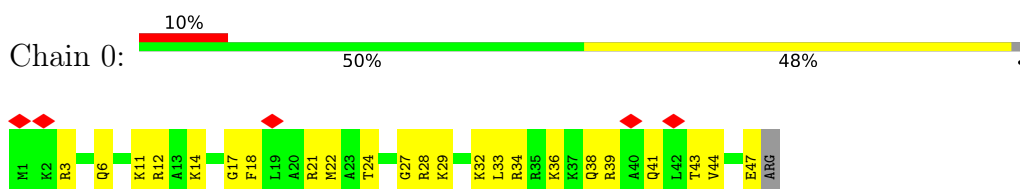
- Molecule 55 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
55	8	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

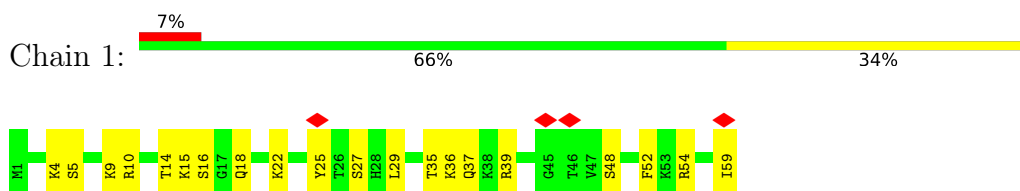
3 Residue-property plots

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.

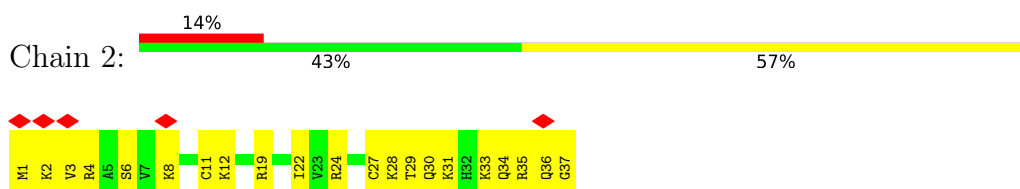
- Molecule 1: 50S ribosomal protein L34



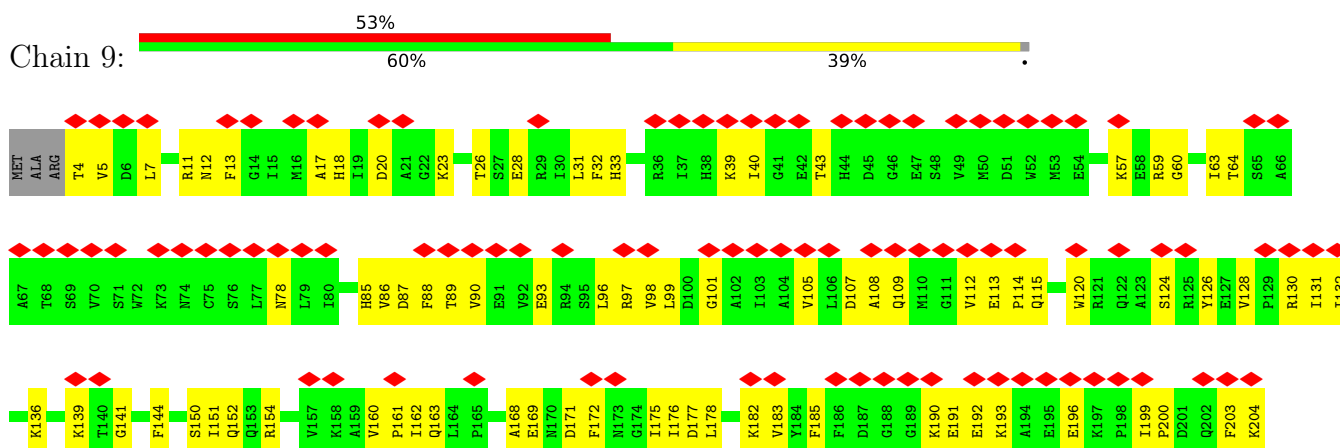
- Molecule 2: 50S ribosomal protein L35

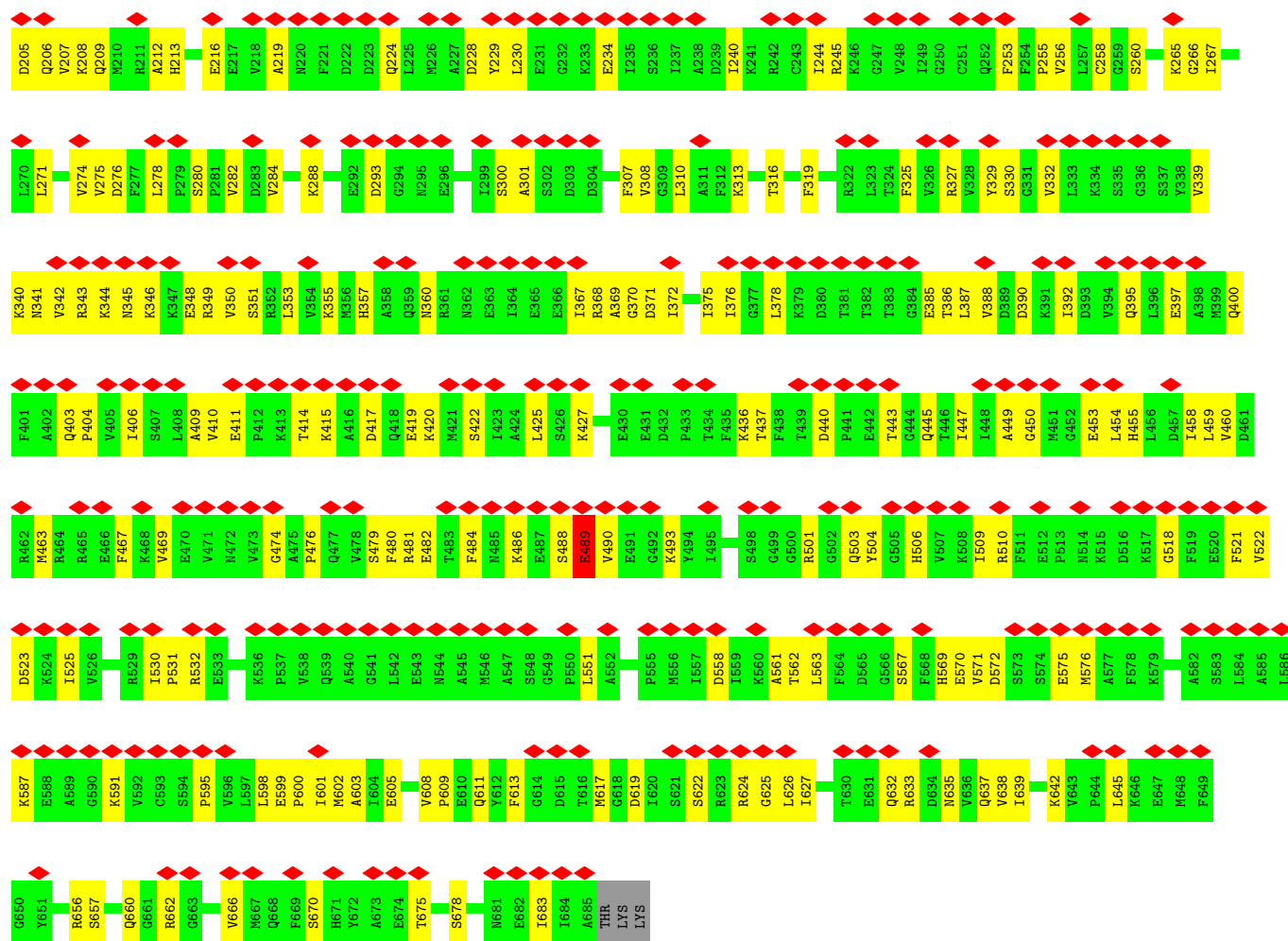


- Molecule 3: 50S ribosomal protein L36

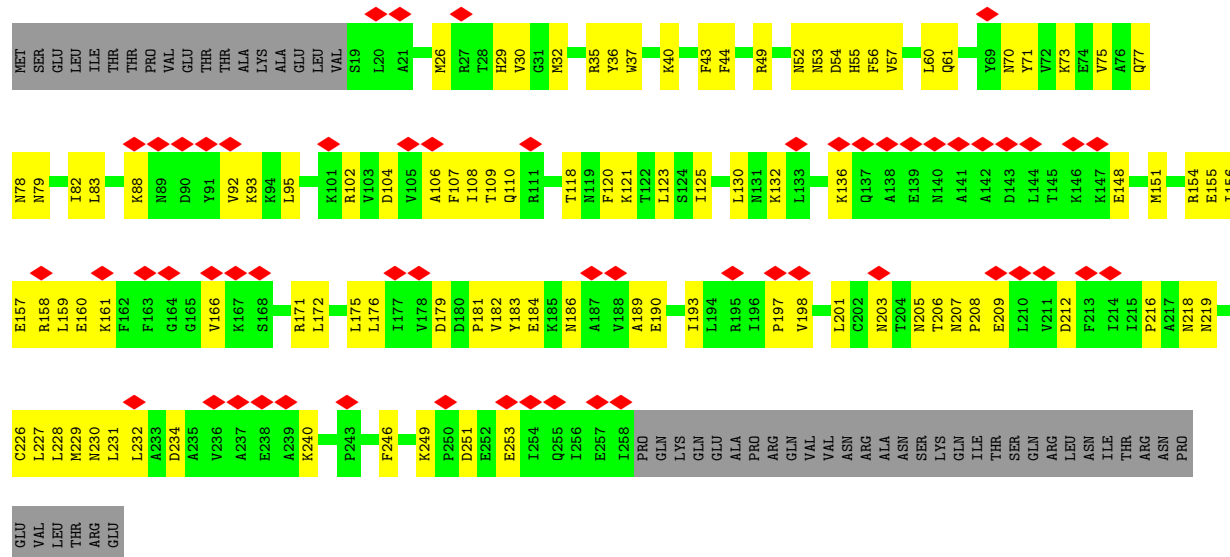


- Molecule 4: Elongation factor G

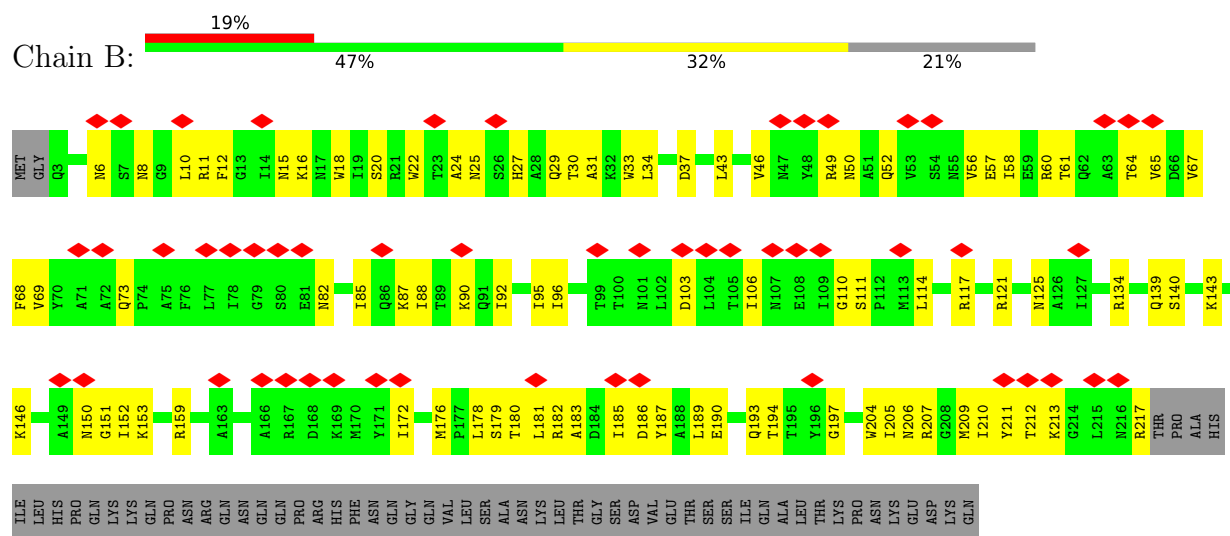




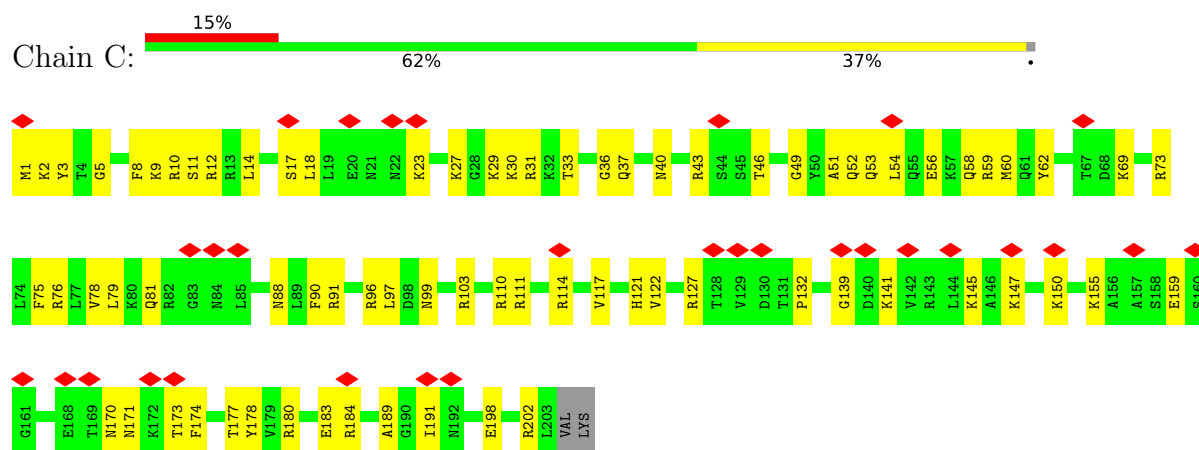
• Molecule 5: 30S ribosomal protein S2



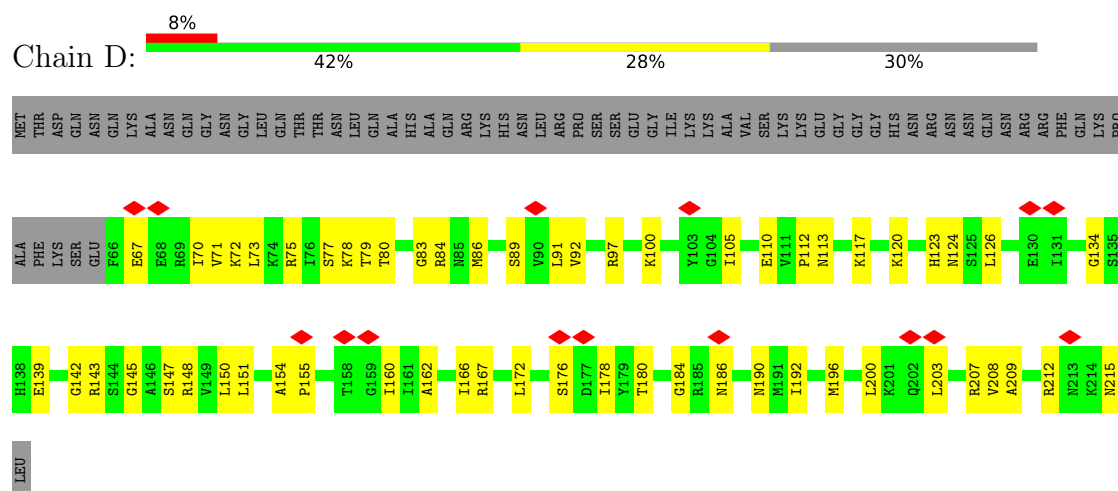
- Molecule 6: 30S ribosomal protein S3



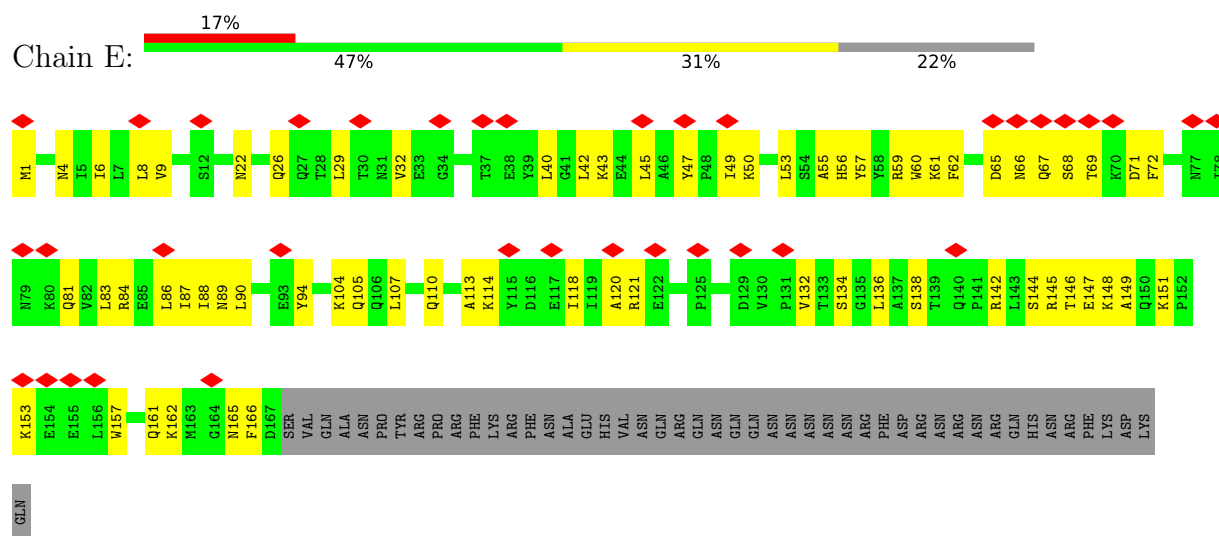
- Molecule 7: 30S ribosomal protein S4



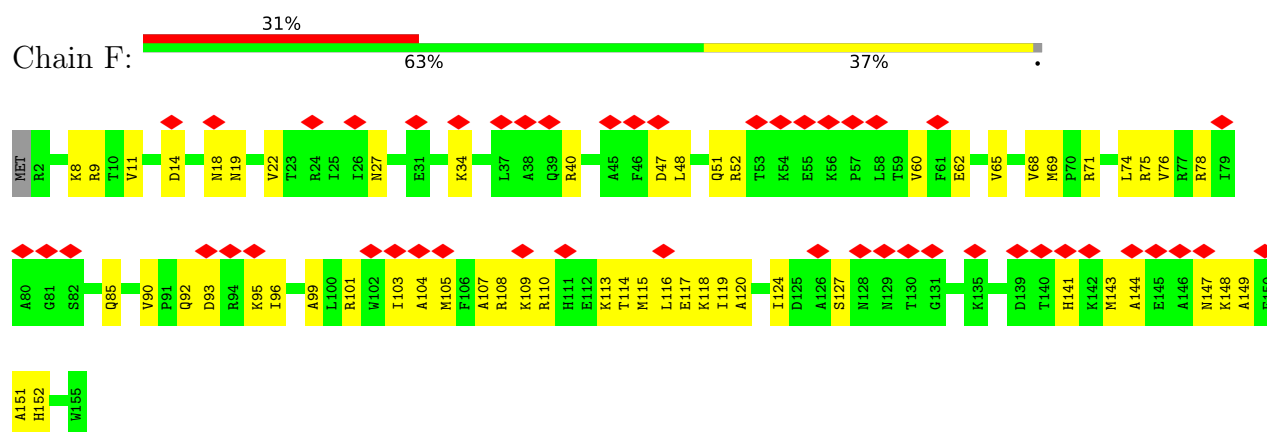
- Molecule 8: 30S ribosomal protein S5



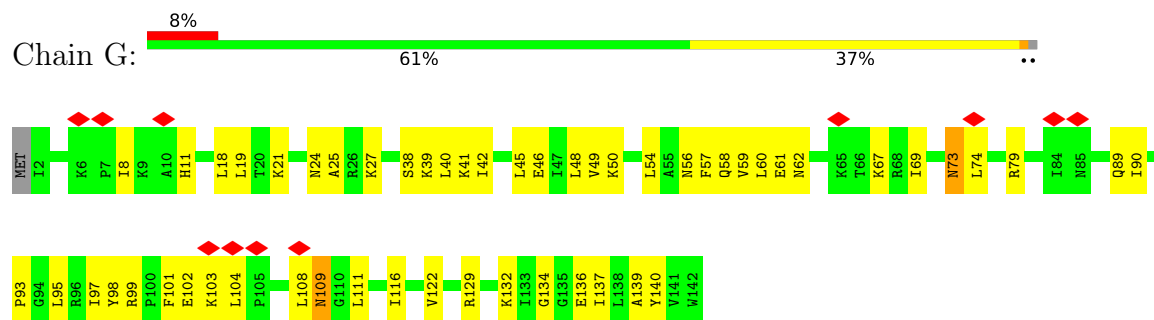
- Molecule 9: 30S ribosomal protein S6



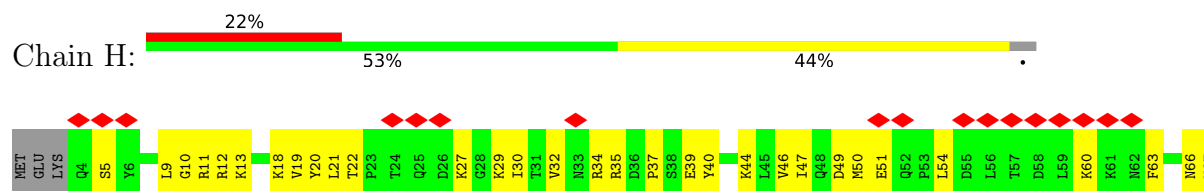
- Molecule 10: 30S ribosomal protein S7

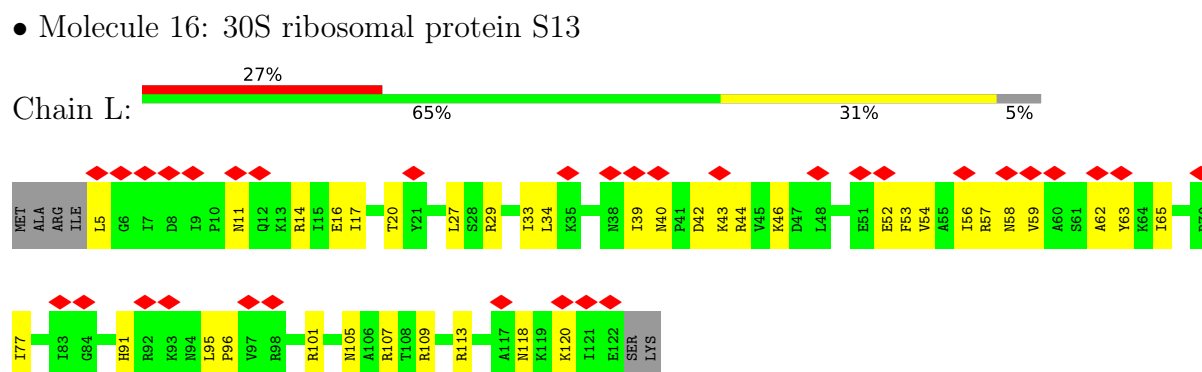
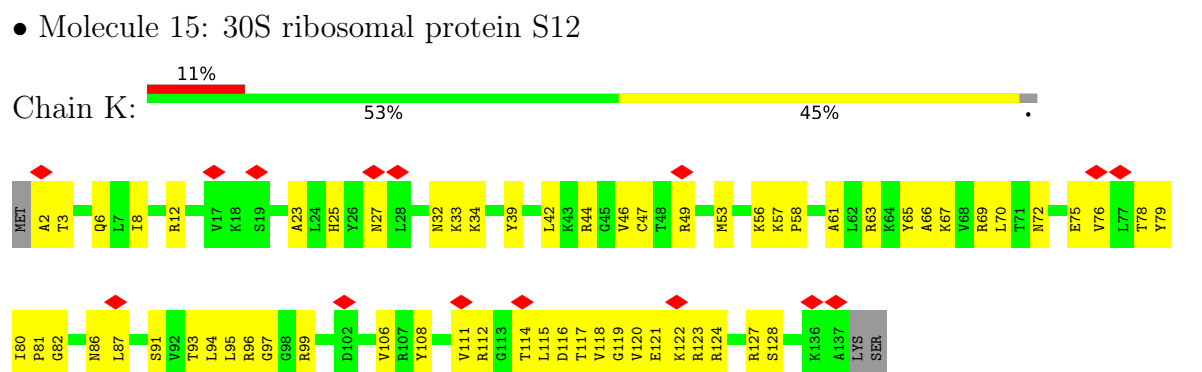
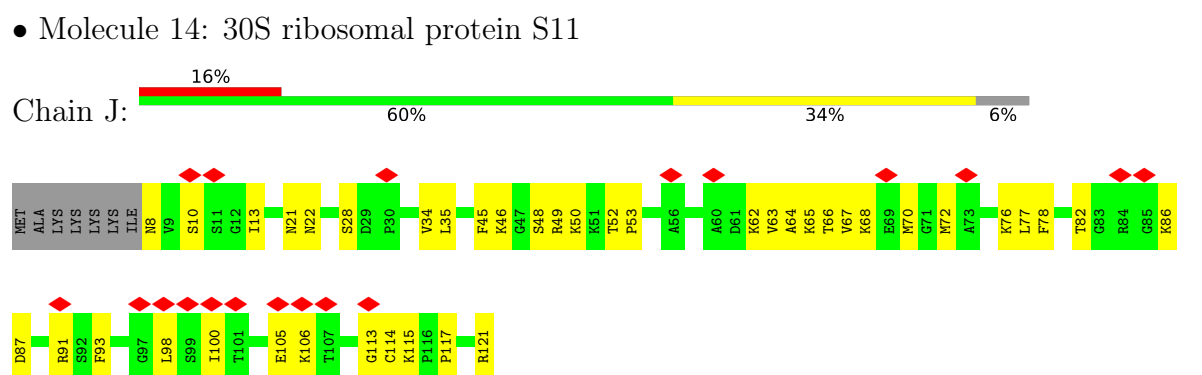
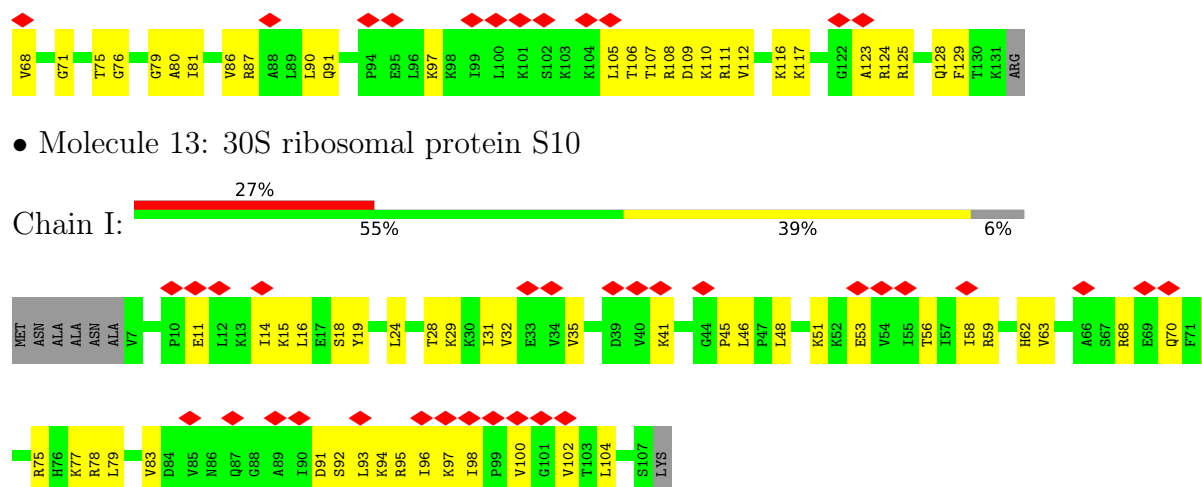


- Molecule 11: 30S ribosomal protein S8

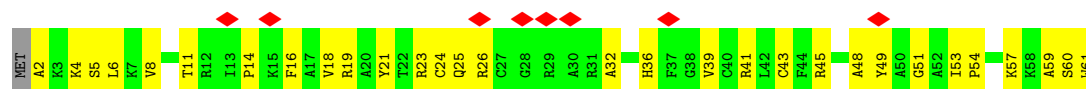


- Molecule 12: 30S ribosomal protein S9





- Molecule 17: 30S ribosomal protein S14 type Z



- Molecule 18: 30S ribosomal protein S15



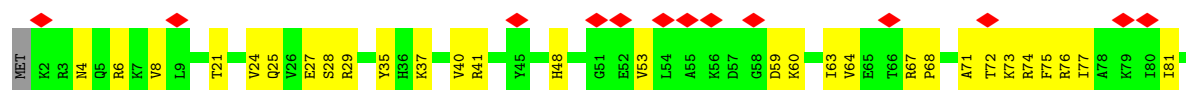
GLY

- Molecule 19: 30S ribosomal protein S16



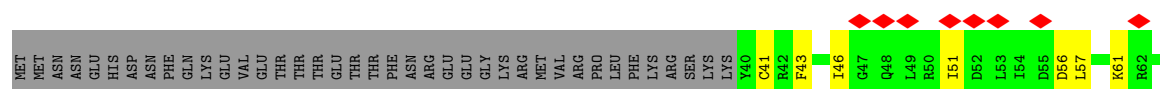
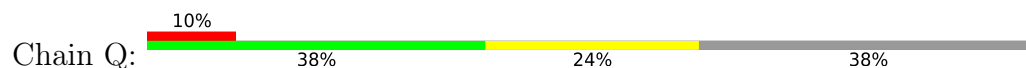
LYS
PRO
VAL
ALA
LYS
SER
LYS

- Molecule 20: 30S ribosomal protein S17



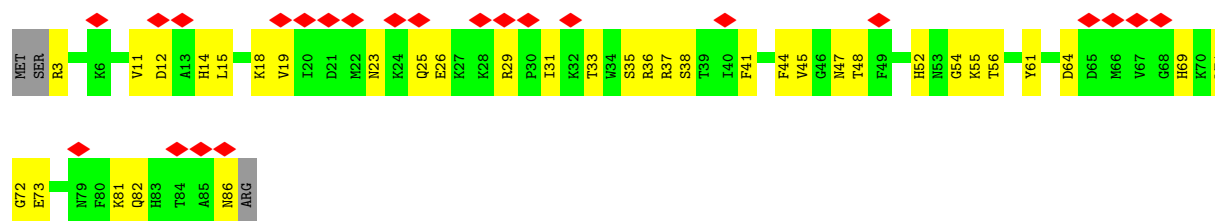
ASP
LYS

- Molecule 21: 30S ribosomal protein S18

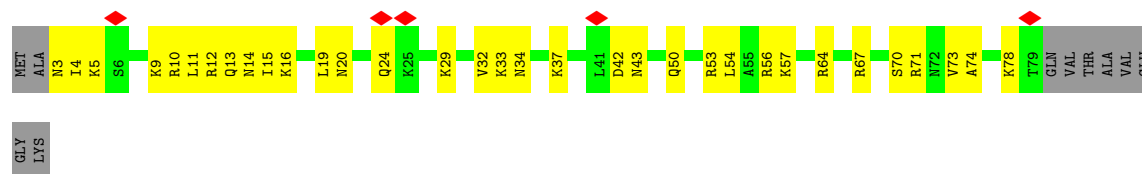


- Molecule 22: 30S ribosomal protein S19





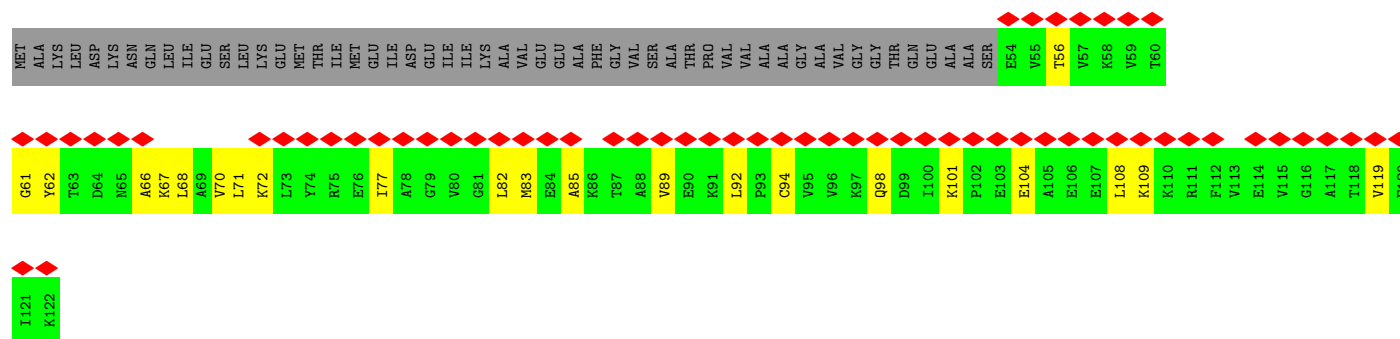
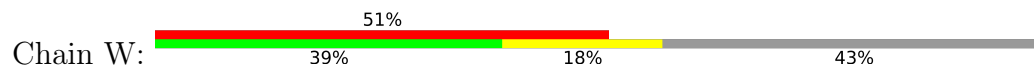
- Molecule 23: 30S ribosomal protein S20



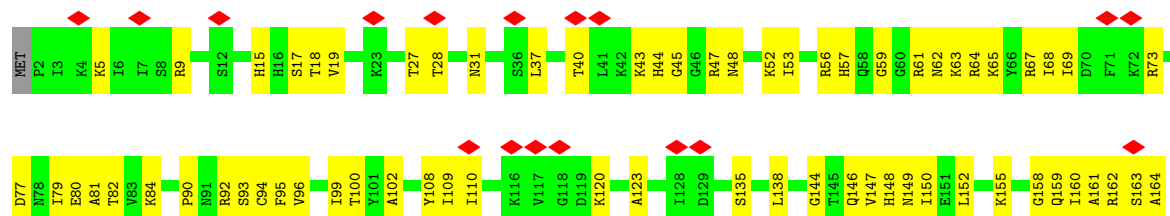
- Molecule 24: 30S ribosomal protein S21

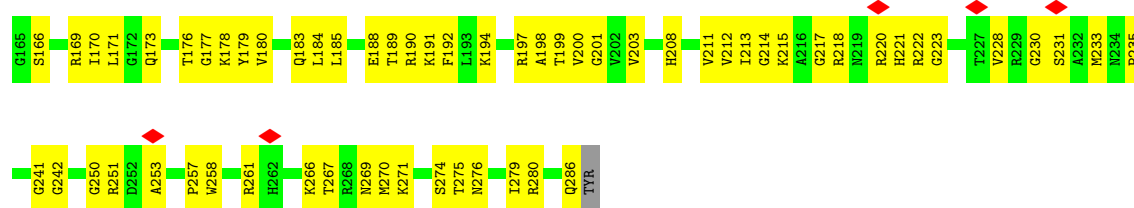


- Molecule 25: 50S ribosomal protein L7/L12

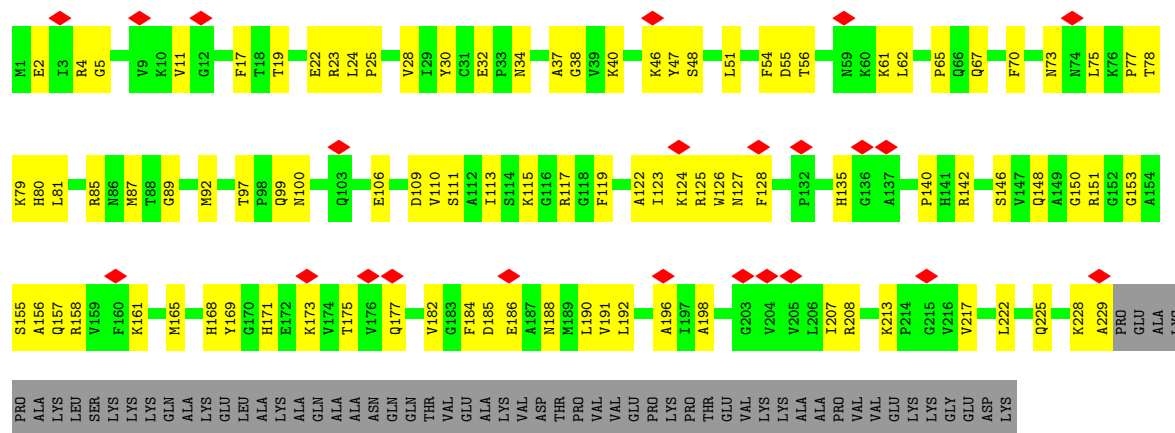


- Molecule 26: 50S ribosomal protein L2

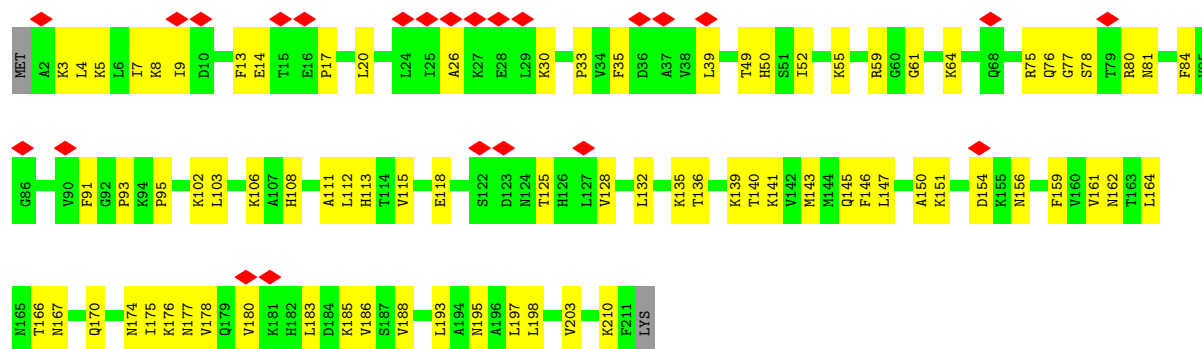




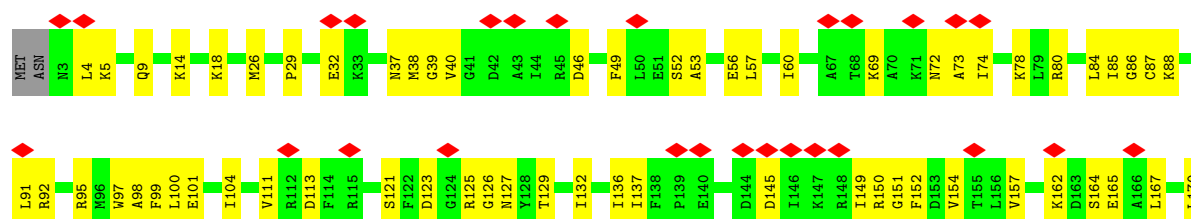
• Molecule 27: 50S ribosomal protein L3



• Molecule 28: 50S ribosomal protein L4

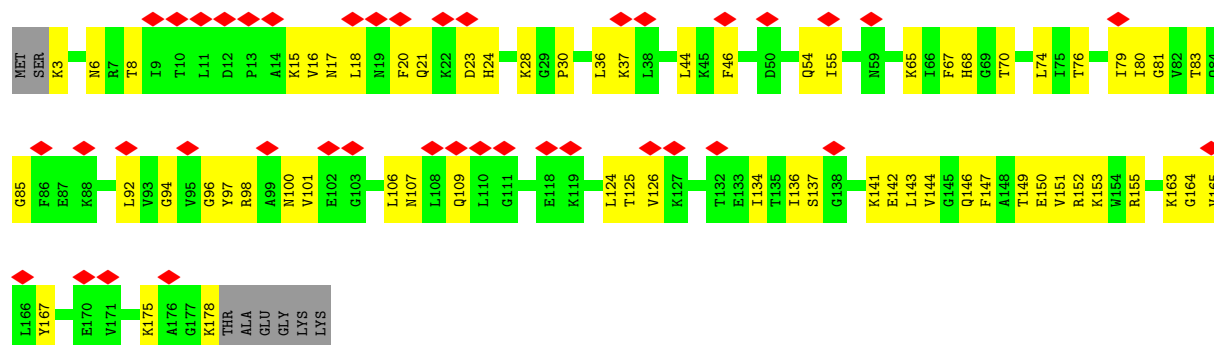


• Molecule 29: 50S ribosomal protein L5

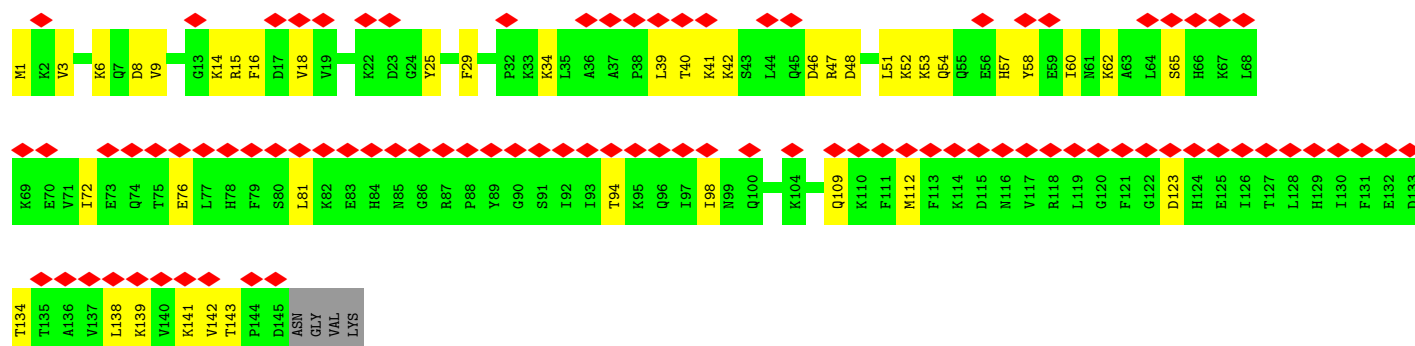




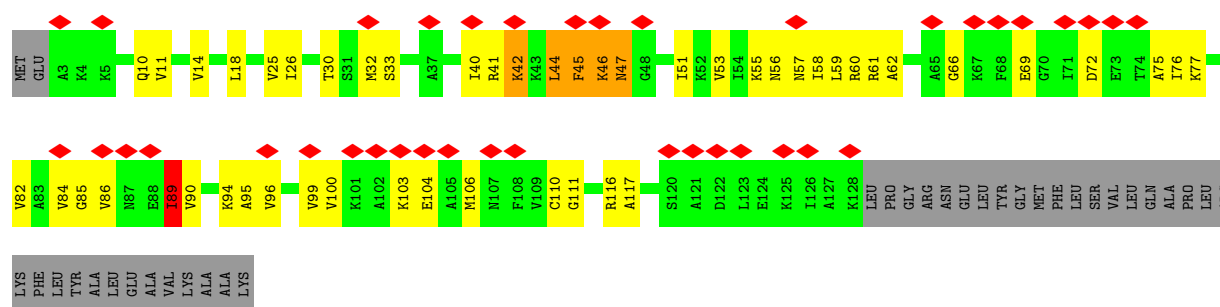
• Molecule 30: 50S ribosomal protein L6



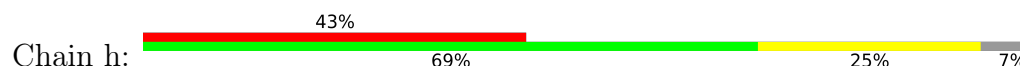
• Molecule 31: 50S ribosomal protein L9

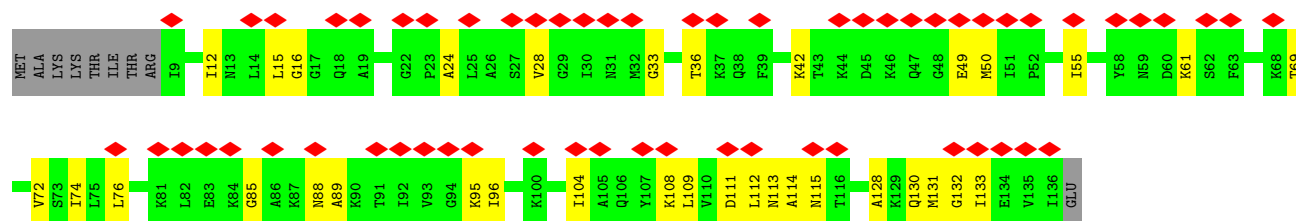


• Molecule 32: 50S ribosomal protein L10

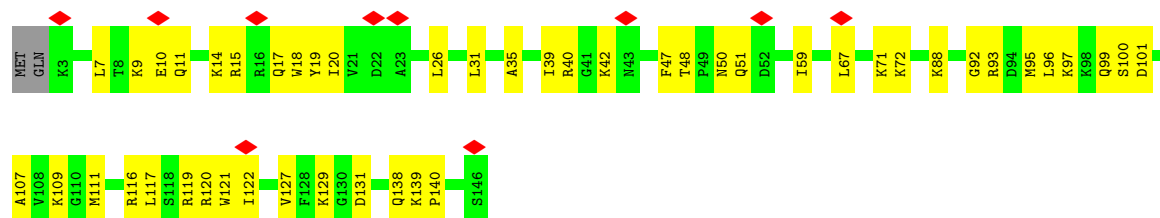


• Molecule 33: 50S ribosomal protein L11

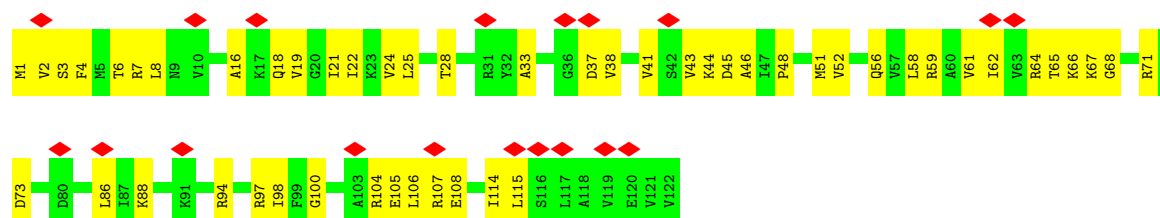




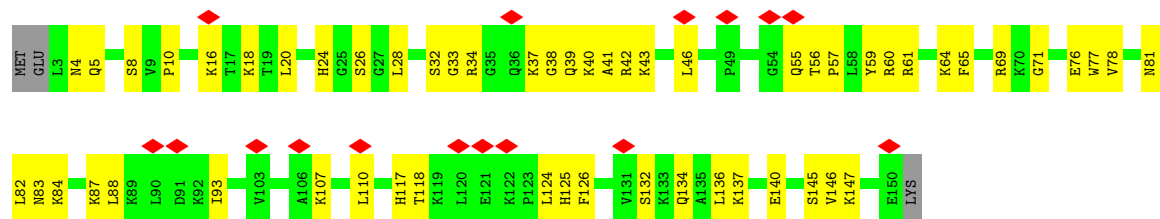
• Molecule 34: 50S ribosomal protein L13



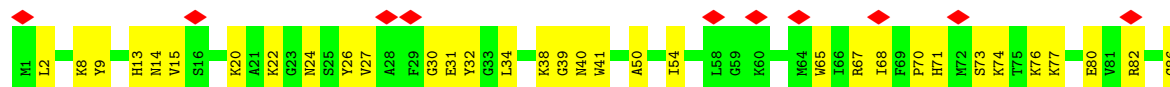
• Molecule 35: 50S ribosomal protein L14



• Molecule 36: 50S ribosomal protein L15

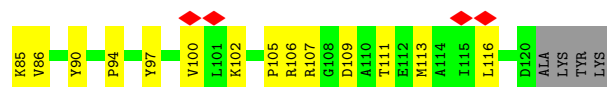


• Molecule 37: 50S ribosomal protein L16





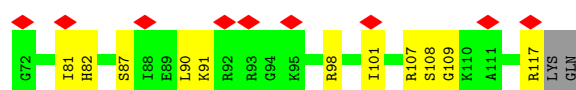
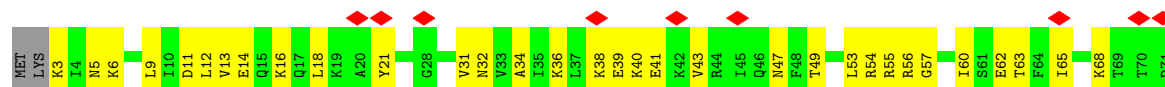
- Molecule 38: 50S ribosomal protein L17



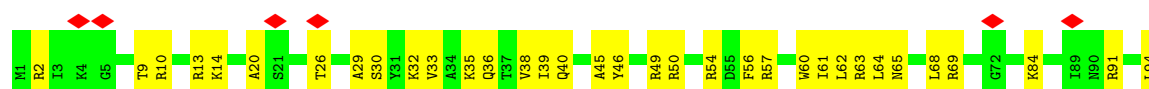
- Molecule 39: 50S ribosomal protein L18



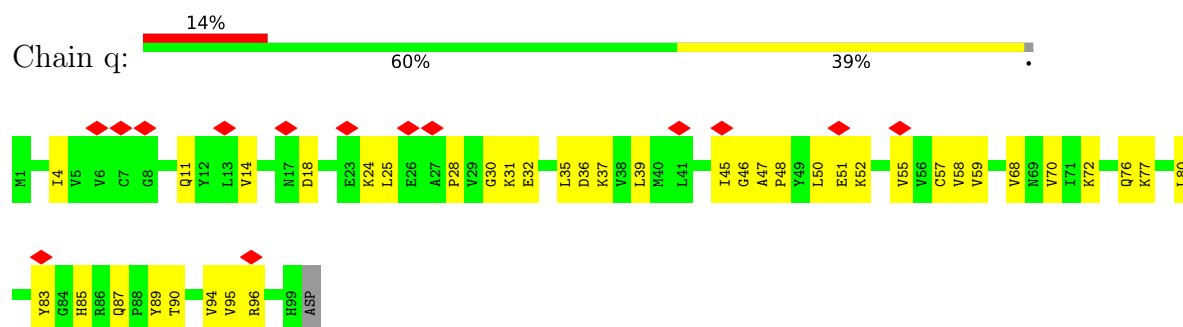
- Molecule 40: 50S ribosomal protein L19



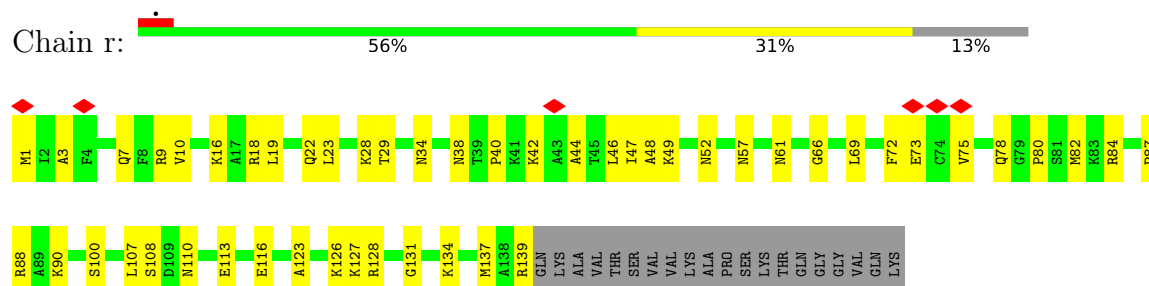
- Molecule 41: 50S ribosomal protein L20



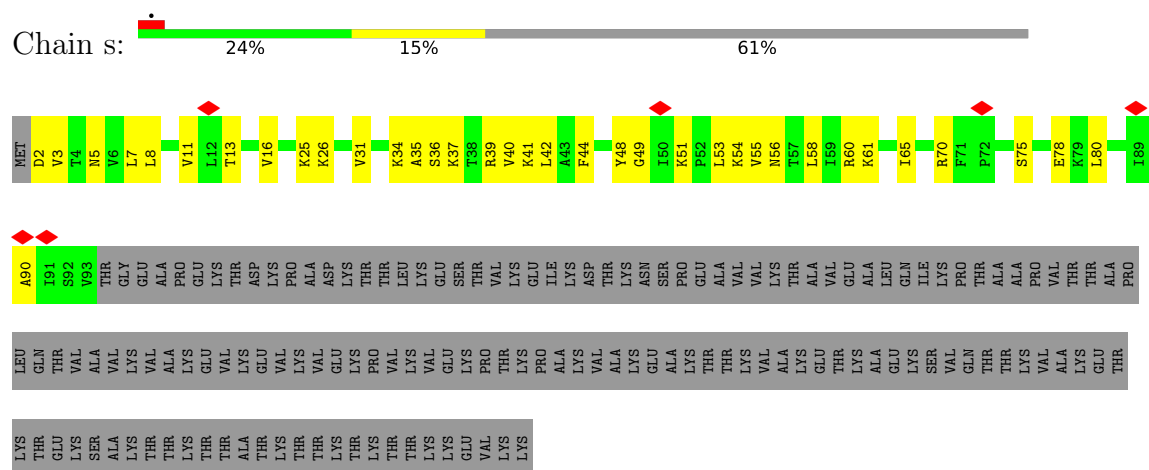
- Molecule 42: 50S ribosomal protein L21



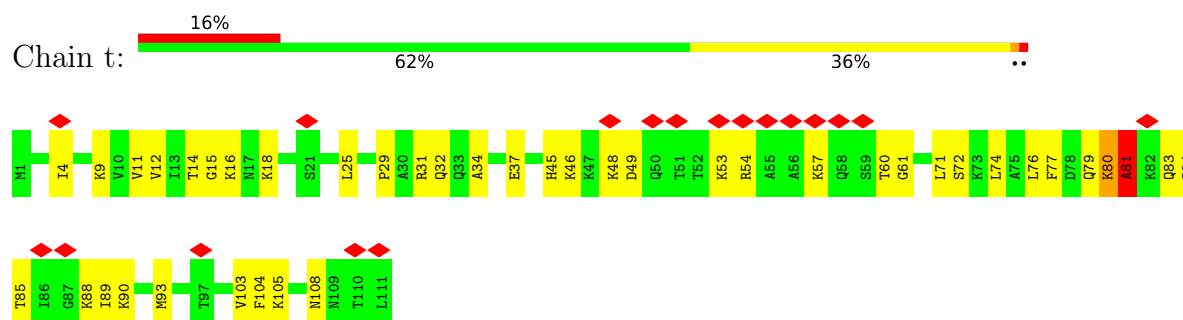
- Molecule 43: 50S ribosomal protein L22



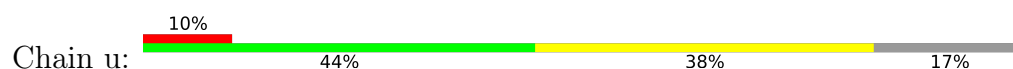
- Molecule 44: 50S ribosomal protein L23

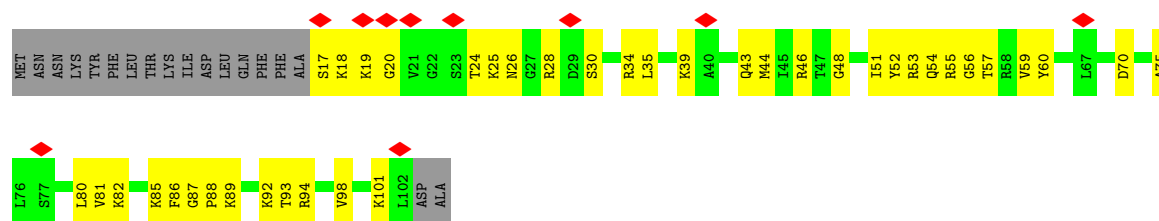


- Molecule 45: 50S ribosomal protein L24



- Molecule 46: 50S ribosomal protein L27

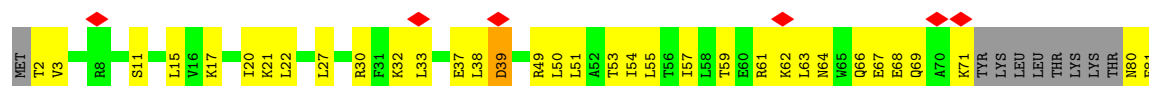




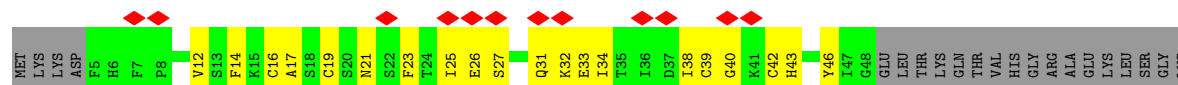
- Molecule 47: 50S ribosomal protein L28



- Molecule 48: 50S ribosomal protein L29



- Molecule 49: 50S ribosomal protein L31



- Molecule 50: 50S ribosomal protein L32

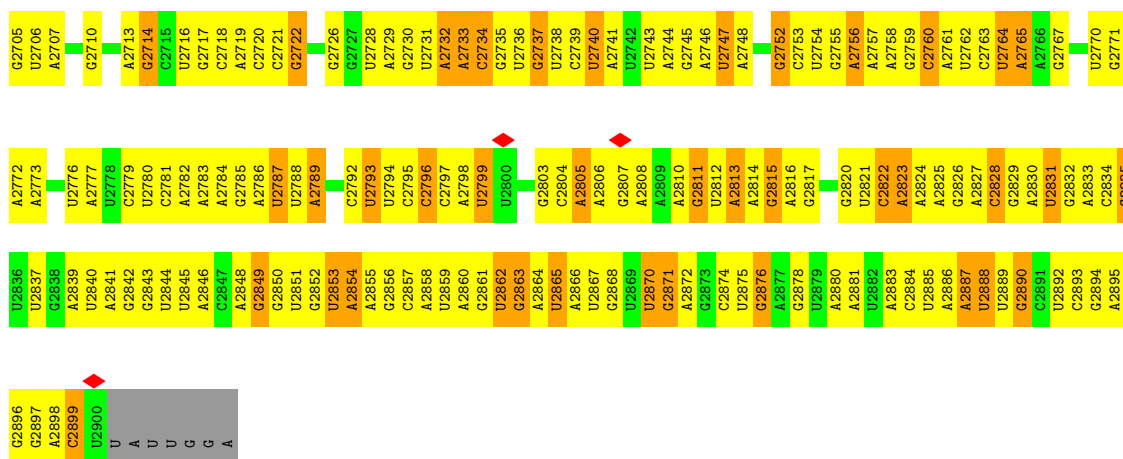


- Molecule 51: 50S ribosomal protein L33 1



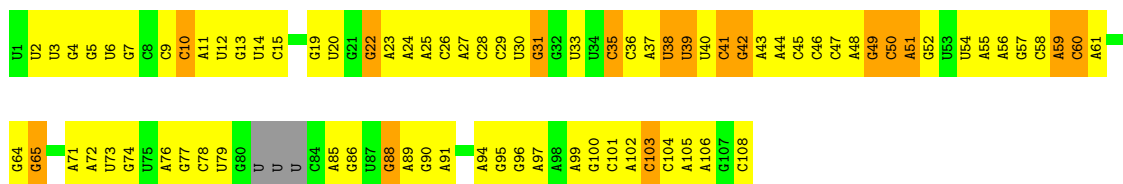
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U091	U092	C093	C094	U095	G096	A097	A098	G0914	G0915	U0916	G0917	G0918	C0919	G0920	C0921	C0922	A0923	C0924	C0925	C0926	C0927	C0928	C0929	C0930	G0931	U0932	A0933	G0934	A0935	A0936	A0937	A0938	U0939	A0943	U0944	U0945	A0946	A0947	A0948	C0949	U0952	G0953	A0954	A0955	C0959	A0960	U0961	U0962	U0963	A0964	U0965	U0966	U0967	U0968	A0969	U0970	U0971	C0972	U0973	C0974	C0975	C0976	A0977	G0978	G0979	A0981	C0982	A0983	A0987	A0988	G0989	U0990	G0991	G0992	A0993	A0994	A0995	G0996	A0997	A0998</																																																																																																																																																																																																																																																																																																											





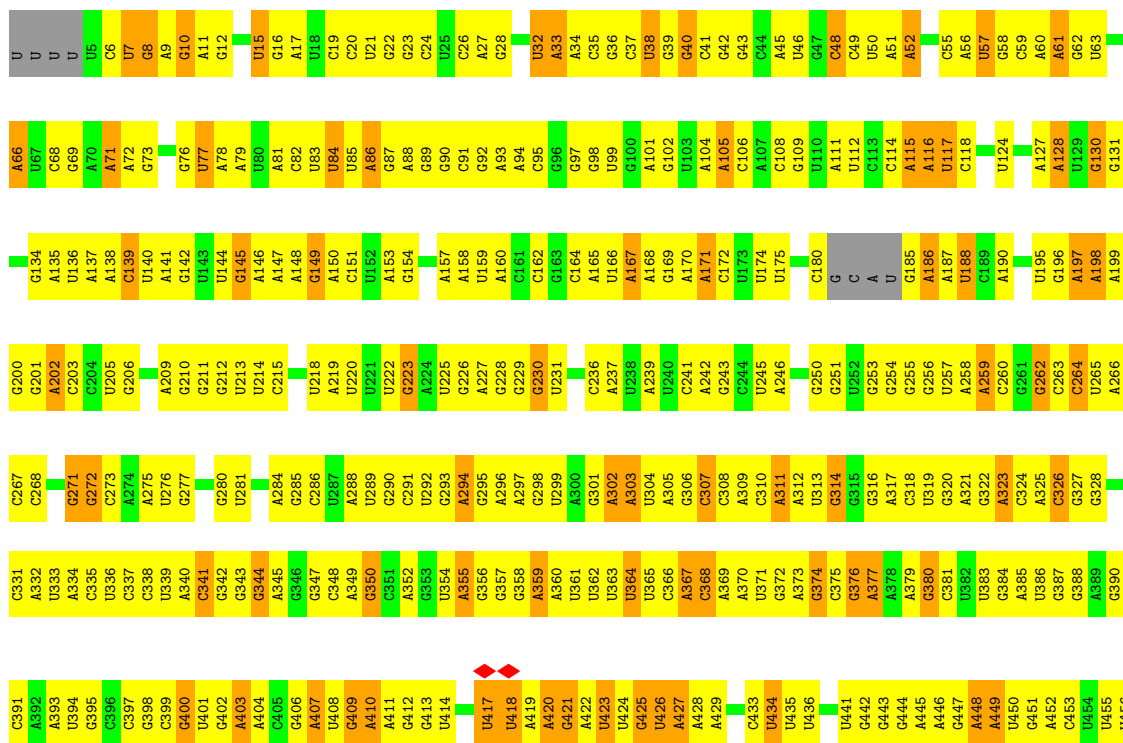
• Molecule 53: 5S ribosomal RNA

Chain 4: 22% 60% 15%



• Molecule 54: 16S ribosomal RNA

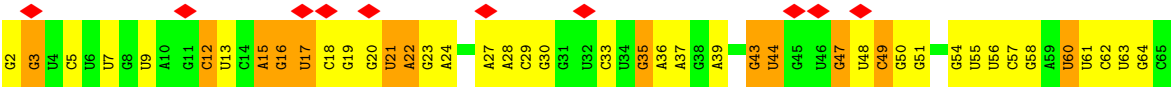
Chain 5: 20% 61% 17%



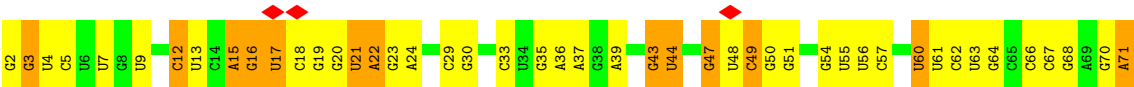
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A1349	A1227	G1165	C1104	G1039	A972	C906	A838	G771	G707	A642	A581	G519	G488
A1350	A1228	A1166	C1105	U1040	A973	A907	U844	A774	A708	U643	G582	C520	C459
U1351	A1229	C1167	U1106	G1041	C974	A908	G845	G775	A709	U644	U589	C521	A460
A1352	U1230	G1168	U1107	G1042	C975	A909	G846	A776	G710	A645	G586	G525	G461
C1353	U1231	A1169	A1108	U1043	U976	G910	G847	A777	A711	U646	A587	C526	G462
A1293	C1232	C1170	U1109	G1044	U977	G911	U848	A778	A712	U647	U588	C527	U463
U1294	U1233	A1171	C1110	C1045	A978	G912	A849	U760	A713	C848	U589	G528	A464
U1295	C1234	A1172	G1111	U1047	C979	A914	G850	A761	C714	U649	U589	G529	A465
G1297	C1235	A1173	U1112	G1048	C980	U915	G851	G782	A715	A650	A591	A530	U466
U1298	G1237	U1174	U1113	U1049	U981	U916	U852	G783	C716		A592	G468	C468
C1358	C1238	C1175	A1114	G1049	A982	G917	U785	A784	C717	G853	A593	A531	C469
U1359	U1239	A1176	U1115	U1050	G983	G917	U786	U785	A718	U654	A594	C468	U470
G1360	U1240	U1177	U1116	U1051	A984	A918	U857		G719	G855	A594	A532	
G1361	G1241	C1178	U1117	G1052		C919	A858		U720	U656	A595	A533	A471
U1362	U1242	A1179	C1118		U987	G920	A859	A789	G721	U657	U596	C534	A472
U1363	A1243	U1180	C1119	G1055	G988	G921	A860	U790	G722	G858	C597	A535	A473
C1364	A1244	G1181	A1120	U1056	A989	G922	A861	A791	G723	U598	C597	A536	G474
U1365	U1245	C1182	U1121	C1057	C990		A862		G724	U599	G599	G538	U475
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G1367	G1247	U1184	G1123		C994	C929	U864	U795	A726	G661	U601	G599	U477
U1368	U1248	C1185	U1124	C1062	U995	A930	U865	A796	G662	G662	G602	C541	G478
C1369	G1249	U1187	C1125	G1063	U996	C931	A866	G797	A664	A664	U603	G542	A479
U1370	A1250	U1188	A1126	U1064	G997	A932	A867		G665	G665	A605	C543	C480
C1371	G1251	C1189	G1127	G1065		A933	U868	G800	A731		A605	C544	U481
A1313	C1252	U1190	U1128	U1066	A1000	G934	U869	U861	A732	U668	A606	A544	G482
U1314	A1253	U1191	C1129	C1067	A1001	U935	A870	C802	A733	U669	A607	A545	U483
C1372	U1254	C1192	G1130	G1068	U1002	G936	U871	C803	G608	G670	G608	C547	A484
U1373	U1255	G1193	U1131	U1069	G1003	U938	C872	A811	G609	G671	G609	C548	C485
C1374	G1256	U1194	G1132	G1070	U1004	G939	C874	A812	U549	A672	C610	U549	C486
U1380	G1257	A1195	A1133	A1071		G940	C875	A813	A738	A673	A611	U550	U487
C1381	U1258		C1134	G1072	G1009	G941	C876	C807	G612	U674	G612	A551	U488
U1382	U1259	U1199	U1135	A1073	A1010	G942	C877	C808	G740	U675	U552	U552	U489
A1383	U1260	G1200	G1136	U1074	A1011	C943	U878	G815	U676	C553	C553	C553	U490
C1384	A1261	C1201	C1137	G1075	U1012	G944	G879	A816	C742	C554	C541	C541	U491
U1385	U1262	A1202	U1138	U1076	A1013	U945	G880	U817	A743	G555	G555	G555	G492
A1324	G1263	C1203	A1140	U1077	A1014	G946	G881	A818	U744	A678	U617	G556	C493
U1325	U1264	U1204	U1141		U1015	U947	U882	G819	U745	U679	U618	A557	A494
C1326	U1265	C1205	G1142	U1082	A1016	U948	U883	A820	A746	U681	A619	U558	U495
U1388	U1266	A1211	A1143	A1083	U1017	G949	G884	A821	C747	G682	A620	U559	A496
C1389	G1267	C1212	C1144	A1084	U1018	C950	U885	U817	U748	G683	C621	U560	A497
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A1391	C1269	C1208	A1145	U1086	G1019	U952	C887	G819	A750	G685	G623	U562	U499
C1392	U1270	U1210	A1146	C1087	G	A953	A888	A820	C752	C686	U624	U563	G500
A1393	U1271	A1211	G1149	C1088	A	A954	U889	A821	G753	G687	U625	G564	A501
G1394	C1272	C1212	G1150	C1089	G	U955	U890	A822	C754	G688	G626	G565	C502
C1395	A1273	A1213	A1151	G1090	U	U956	C891	C823	U754	U689	U627	G566	G503
U1396	G1274	U1214	G1152	C1091	U	G957	G892	U824	U755	G690	A628	C567	U498
C1397	U1275	A1215	G1153	A1092	A	G958	C893	A825	A756	A691	U629	G568	U499
U1398	U1276	G1216	A1154	A1093	A		U894	G826		A692	G630	U569	A504
C1399	G1277	C1217	C1155	C1094	C1028	G961	A895		C759	A693	C631	A570	A507
A1400	U1278	U1218	G1156	G1095	C1029	A964	G896	G829	U760	A571	A632	A571	C509
U1401	C1279	C1219	U1157	A1096	G1030	U965	U899	U830	U761	A572	U634	A572	U510
C1402		A1220	G1158	G1097	A1031	C966	A966	C831	G762	U698	U634	G573	A511
A1403	U1282	A1221	A1159	C1098	G1032	C967	A901	G832	A763	A699	G635	C574	U512
U1404	A1283	U1222	G1160	G1099	U1033	G968	A902	G833		G700	G636	A575	G513
C1344	G1285	A1223	G1161	A1101	G1034	U969	A903	G834	G766	A701	A637	A576	U514
U1406	U1286	C1224	G1162	C1101	G1034	G968	A903	G835	G767	U704	A638	G577	G515
A1407	G1287	A1225	A1163	A1102	A1037	A970	C904	C836	U768	A705	A639	C516	C517



• Molecule 55: tRNA-Phe



• Molecule 55: tRNA-Phe



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	1479	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	1.530	Depositor
Minimum map value	-0.551	Depositor
Average map value	0.027	Depositor
Map value standard deviation	0.125	Depositor
Recommended contour level	0.45	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	0.16	0/383	0.42	0/504
2	1	0.18	0/484	0.45	0/637
3	2	0.13	0/306	0.37	0/401
4	9	0.16	0/5419	0.47	2/7307 (0.0%)
5	A	0.15	0/1954	0.40	0/2642
6	B	0.14	0/1721	0.41	0/2323
7	C	0.14	0/1691	0.40	0/2267
8	D	0.13	0/1188	0.37	0/1593
9	E	0.15	0/1384	0.40	0/1867
10	F	0.16	0/1266	0.41	0/1700
11	G	0.15	0/1126	0.42	0/1517
12	H	0.14	0/1044	0.44	0/1395
13	I	0.15	0/820	0.44	0/1103
14	J	0.15	0/844	0.43	0/1136
15	K	0.27	0/1094	0.59	1/1468 (0.1%)
16	L	0.16	0/962	0.43	0/1289
17	M	0.14	0/483	0.40	0/643
18	N	0.13	0/679	0.39	0/907
19	O	0.14	0/659	0.37	0/885
20	P	0.15	0/684	0.41	0/913
21	Q	0.13	0/545	0.42	0/730
22	R	0.18	0/698	0.49	0/936
23	S	0.14	0/631	0.39	0/838
24	T	0.13	0/475	0.40	0/621
25	W	0.12	0/538	0.33	0/722
26	a	0.16	0/2267	0.44	0/3044
27	b	0.14	0/1795	0.38	0/2412
28	c	0.14	0/1671	0.40	0/2246
29	d	0.14	0/1409	0.40	0/1894
30	e	0.16	0/1420	0.40	0/1912
31	f	0.15	0/1183	0.46	1/1587 (0.1%)
32	g	0.42	0/969	0.71	2/1295 (0.2%)
33	h	0.16	0/968	0.43	0/1298
34	i	0.14	0/1186	0.41	0/1592

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	j	0.15	0/953	0.40	0/1275
36	k	0.14	0/1170	0.43	0/1559
37	l	0.15	0/1104	0.45	0/1481
38	m	0.14	0/973	0.36	0/1309
39	n	0.15	0/897	0.45	0/1198
40	o	0.15	0/948	0.45	0/1262
41	p	0.14	0/961	0.38	0/1278
42	q	0.18	0/828	0.45	0/1111
43	r	0.14	0/1077	0.42	0/1441
44	s	0.15	0/732	0.48	0/988
45	t	0.18	0/879	0.49	1/1165 (0.1%)
46	u	0.15	0/665	0.42	0/884
47	v	0.23	0/519	0.54	0/695
48	w	0.16	0/826	0.46	0/1104
49	x	0.13	0/353	0.39	0/474
50	y	0.38	0/457	0.65	0/601
51	z	0.15	0/412	0.38	0/547
52	3	0.11	0/69073	0.28	5/107710 (0.0%)
53	4	0.10	0/2505	0.27	0/3902
54	5	0.10	0/35768	0.24	0/55764
55	7	0.12	0/1808	0.31	0/2817
55	8	0.12	0/1808	0.31	0/2817
All	All	0.13	0/164662	0.33	12/245006 (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
4	9	0	2
11	G	0	1
45	t	0	2
All	All	0	5

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	3	1033	A	OP1-P-OP2	-13.39	79.43	119.60
52	3	1033	A	O5'-P-OP2	-11.35	73.95	108.00
52	3	1032	A	OP1-P-O3'	-10.94	75.18	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	3	1032	A	OP2-P-O3'	9.07	135.22	108.00
52	3	1033	A	O5'-P-OP1	7.92	131.76	108.00

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	9	488	SER	Peptide
4	9	489	GLU	Peptide
11	G	109	ASN	Peptide
45	t	80	LYS	Peptide
45	t	81	ALA	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	21	0
2	1	477	0	530	19	0
3	2	304	0	350	20	0
4	9	5326	0	5343	214	0
5	A	1921	0	1973	71	0
6	B	1698	0	1768	77	0
7	C	1660	0	1719	59	0
8	D	1173	0	1267	45	0
9	E	1362	0	1377	63	0
10	F	1246	0	1308	51	0
11	G	1110	0	1226	50	0
12	H	1028	0	1094	54	0
13	I	809	0	894	35	0
14	J	829	0	855	33	0
15	K	1076	0	1170	52	0
16	L	951	0	1014	29	0
17	M	474	0	509	27	0
18	N	673	0	730	22	0
19	O	646	0	677	23	0
20	P	675	0	728	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	Q	535	0	562	24	0
22	R	682	0	691	33	0
23	S	629	0	681	32	0
24	T	471	0	522	15	0
25	W	534	0	572	14	0
26	a	2225	0	2301	107	0
27	b	1762	0	1808	88	0
28	c	1644	0	1731	68	0
29	d	1388	0	1469	49	0
30	e	1396	0	1481	48	0
31	f	1160	0	1172	27	0
32	g	960	0	1014	39	0
33	h	959	0	1039	23	0
34	i	1164	0	1192	38	0
35	j	944	0	1019	49	0
36	k	1153	0	1256	56	0
37	l	1079	0	1134	50	0
38	m	958	0	1011	40	0
39	n	889	0	952	42	0
40	o	938	0	1008	34	0
41	p	947	0	1028	41	0
42	q	811	0	858	28	0
43	r	1068	0	1150	50	0
44	s	720	0	803	29	0
45	t	872	0	972	43	0
46	u	657	0	695	33	0
47	v	513	0	560	49	0
48	w	818	0	870	28	0
49	x	344	0	333	17	0
50	y	452	0	472	25	0
51	z	408	0	440	21	0
52	3	61664	0	30954	2184	0
53	4	2239	0	1137	66	0
54	5	31943	0	16058	1208	0
55	7	1618	0	821	46	0
55	8	1618	0	821	45	0
All	All	151980	0	105548	5122	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 21.

The worst 5 of 5122 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)
54:5:627:U:N3	54:5:628:A:N6	1.89	1.21
38:m:2:SER:N	52:3:1692:A:HO2'	1.47	1.13
52:3:341:G:N2	52:3:364:A:H61	1.44	1.13
54:5:1001:A:H62	54:5:1019:G:N2	1.47	1.11
52:3:2483:C:H42	52:3:2537:G:N2	1.51	1.07

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	45/48 (94%)	42 (93%)	3 (7%)	0	100	100
2	1	57/59 (97%)	48 (84%)	9 (16%)	0	100	100
3	2	35/37 (95%)	32 (91%)	3 (9%)	0	100	100
4	9	680/688 (99%)	630 (93%)	50 (7%)	0	100	100
5	A	238/294 (81%)	218 (92%)	20 (8%)	0	100	100
6	B	213/273 (78%)	193 (91%)	20 (9%)	0	100	100
7	C	201/205 (98%)	190 (94%)	11 (6%)	0	100	100
8	D	151/219 (69%)	145 (96%)	6 (4%)	0	100	100
9	E	165/215 (77%)	147 (89%)	18 (11%)	0	100	100
10	F	152/155 (98%)	147 (97%)	5 (3%)	0	100	100
11	G	139/142 (98%)	124 (89%)	15 (11%)	0	100	100
12	H	126/132 (96%)	111 (88%)	15 (12%)	0	100	100
13	I	99/108 (92%)	92 (93%)	7 (7%)	0	100	100
14	J	112/121 (93%)	107 (96%)	5 (4%)	0	100	100
15	K	134/139 (96%)	113 (84%)	21 (16%)	0	100	100
16	L	116/124 (94%)	106 (91%)	10 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	M	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
18	N	81/86 (94%)	80 (99%)	1 (1%)	0	100	100
19	O	78/94 (83%)	74 (95%)	4 (5%)	0	100	100
20	P	81/85 (95%)	78 (96%)	3 (4%)	0	100	100
21	Q	63/104 (61%)	57 (90%)	6 (10%)	0	100	100
22	R	82/87 (94%)	71 (87%)	11 (13%)	0	100	100
23	S	75/87 (86%)	74 (99%)	1 (1%)	0	100	100
24	T	51/60 (85%)	50 (98%)	1 (2%)	0	100	100
25	W	67/122 (55%)	65 (97%)	2 (3%)	0	100	100
26	a	283/287 (99%)	245 (87%)	38 (13%)	0	100	100
27	b	227/287 (79%)	211 (93%)	16 (7%)	0	100	100
28	c	208/212 (98%)	199 (96%)	9 (4%)	0	100	100
29	d	173/180 (96%)	159 (92%)	14 (8%)	0	100	100
30	e	174/184 (95%)	163 (94%)	11 (6%)	0	100	100
31	f	143/149 (96%)	134 (94%)	9 (6%)	0	100	100
32	g	124/161 (77%)	115 (93%)	9 (7%)	0	100	100
33	h	126/137 (92%)	116 (92%)	10 (8%)	0	100	100
34	i	142/146 (97%)	135 (95%)	7 (5%)	0	100	100
35	j	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
36	k	146/151 (97%)	135 (92%)	11 (8%)	0	100	100
37	l	134/139 (96%)	129 (96%)	5 (4%)	0	100	100
38	m	117/124 (94%)	112 (96%)	5 (4%)	0	100	100
39	n	108/116 (93%)	99 (92%)	9 (8%)	0	100	100
40	o	113/119 (95%)	107 (95%)	6 (5%)	0	100	100
41	p	112/127 (88%)	110 (98%)	2 (2%)	0	100	100
42	q	97/100 (97%)	83 (86%)	14 (14%)	0	100	100
43	r	137/159 (86%)	125 (91%)	12 (9%)	0	100	100
44	s	90/237 (38%)	79 (88%)	11 (12%)	0	100	100
45	t	109/111 (98%)	95 (87%)	13 (12%)	1 (1%)	14	51
46	u	84/104 (81%)	81 (96%)	3 (4%)	0	100	100
47	v	61/65 (94%)	55 (90%)	6 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	w	96/111 (86%)	87 (91%)	8 (8%)	1 (1%)	12	49
49	x	42/97 (43%)	40 (95%)	2 (5%)	0	100	100
50	y	54/57 (95%)	48 (89%)	5 (9%)	1 (2%)	6	32
51	z	48/53 (91%)	45 (94%)	3 (6%)	0	100	100
All	All	6567/7480 (88%)	6073 (92%)	491 (8%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
45	t	81	ALA
50	y	53	VAL
48	w	39	ASP

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	9	579/584 (99%)	579 (100%)	0	100	100
5	A	212/262 (81%)	212 (100%)	0	100	100
6	B	180/232 (78%)	180 (100%)	0	100	100
7	C	181/183 (99%)	181 (100%)	0	100	100
8	D	123/178 (69%)	123 (100%)	0	100	100
9	E	150/196 (76%)	150 (100%)	0	100	100
10	F	131/132 (99%)	131 (100%)	0	100	100
11	G	123/124 (99%)	122 (99%)	1 (1%)	73	80
12	H	111/115 (96%)	111 (100%)	0	100	100
13	I	95/99 (96%)	95 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	J	91/97 (94%)	91 (100%)	0	100	100
15	K	117/120 (98%)	115 (98%)	2 (2%)	53	69
16	L	100/105 (95%)	100 (100%)	0	100	100
17	M	47/48 (98%)	47 (100%)	0	100	100
18	N	76/78 (97%)	76 (100%)	0	100	100
19	O	69/82 (84%)	69 (100%)	0	100	100
20	P	73/75 (97%)	73 (100%)	0	100	100
21	Q	56/94 (60%)	56 (100%)	0	100	100
22	R	74/77 (96%)	74 (100%)	0	100	100
23	S	70/77 (91%)	70 (100%)	0	100	100
24	T	49/56 (88%)	49 (100%)	0	100	100
25	W	58/98 (59%)	58 (100%)	0	100	100
26	a	241/243 (99%)	241 (100%)	0	100	100
27	b	186/233 (80%)	186 (100%)	0	100	100
28	c	182/184 (99%)	182 (100%)	0	100	100
29	d	150/154 (97%)	150 (100%)	0	100	100
30	e	153/159 (96%)	153 (100%)	0	100	100
31	f	123/134 (92%)	123 (100%)	0	100	100
32	g	101/129 (78%)	90 (89%)	11 (11%)	6	21
33	h	102/110 (93%)	102 (100%)	0	100	100
34	i	126/128 (98%)	126 (100%)	0	100	100
35	j	103/103 (100%)	103 (100%)	0	100	100
36	k	123/126 (98%)	123 (100%)	0	100	100
37	l	113/115 (98%)	113 (100%)	0	100	100
38	m	105/109 (96%)	105 (100%)	0	100	100
39	n	96/99 (97%)	96 (100%)	0	100	100
40	o	101/105 (96%)	101 (100%)	0	100	100
41	p	100/108 (93%)	100 (100%)	0	100	100
42	q	90/91 (99%)	90 (100%)	0	100	100
43	r	116/132 (88%)	116 (100%)	0	100	100
44	s	82/208 (39%)	82 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	t	96/96 (100%)	96 (100%)	0	100	100
46	u	69/85 (81%)	69 (100%)	0	100	100
47	v	58/60 (97%)	58 (100%)	0	100	100
48	w	87/98 (89%)	87 (100%)	0	100	100
49	x	41/86 (48%)	41 (100%)	0	100	100
50	y	48/49 (98%)	44 (92%)	4 (8%)	10	30
51	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5730/6433 (89%)	5712 (100%)	18 (0%)	84	86

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

Mol	Chain	Res	Type
50	y	47	MET
50	y	53	VAL
50	y	52	ARG
32	g	46	LYS
32	g	90	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 81 such sidechains are listed below:

Mol	Chain	Res	Type
32	g	119	ASN
40	o	47	ASN
34	i	43	ASN
35	j	112	ASN
43	r	22	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	2875/2907 (98%)	826 (28%)	28 (0%)
53	4	103/108 (95%)	31 (30%)	2 (1%)
54	5	1490/1520 (98%)	387 (25%)	1 (0%)
55	7	75/76 (98%)	25 (33%)	1 (1%)
55	8	75/76 (98%)	25 (33%)	1 (1%)
All	All	4618/4687 (98%)	1294 (28%)	33 (0%)

5 of 1294 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	14	U
52	3	15	A
52	3	27	U
52	3	28	G
52	3	29	G

5 of 33 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	4	54	U
53	4	59	A
55	8	16	G
52	3	1209	U
52	3	1104	A

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

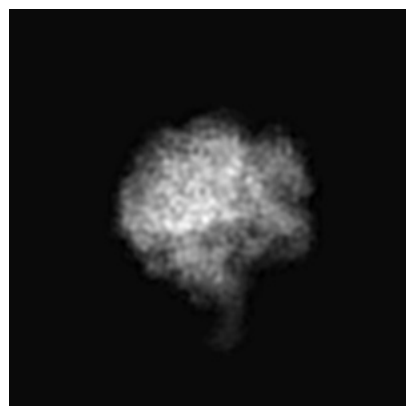
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13280. These allow visual inspection of the internal detail of the map and identification of artifacts.

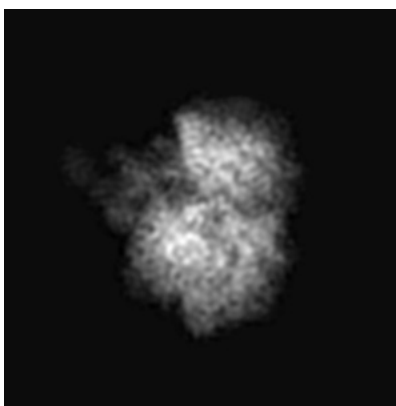
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

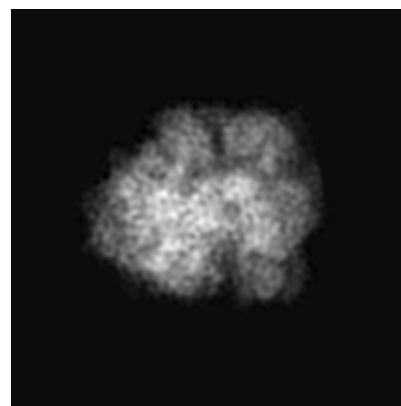
6.1.1 Primary map



X

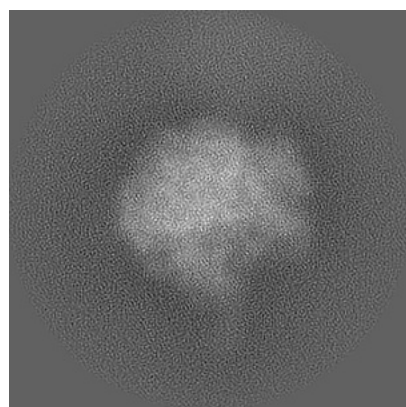


Y

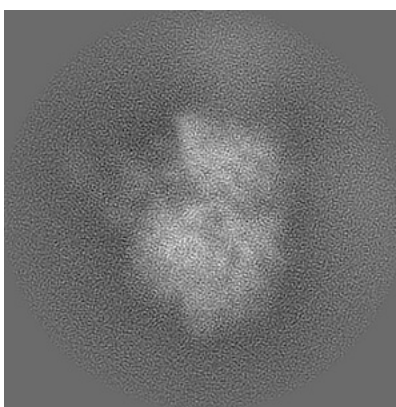


Z

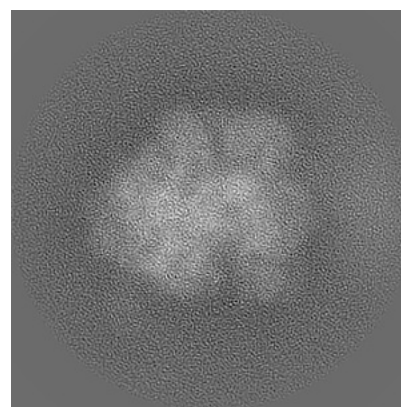
6.1.2 Raw map



X



Y

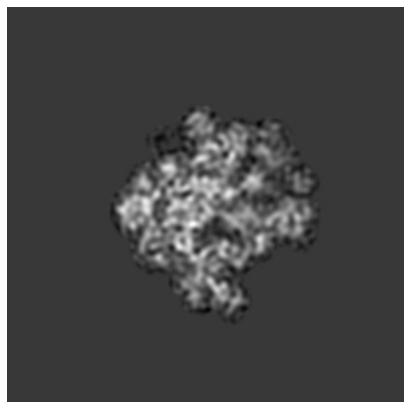


Z

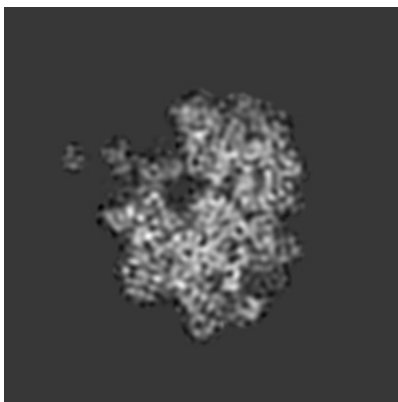
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

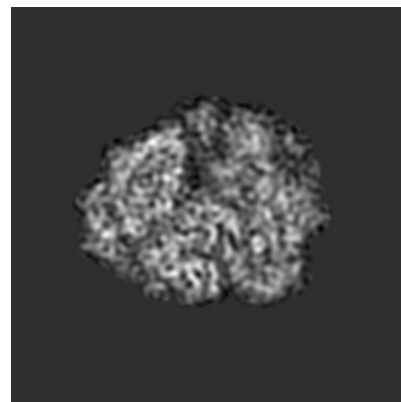
6.2.1 Primary map



X Index: 128

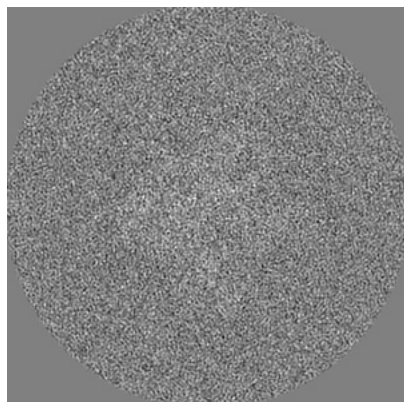


Y Index: 128

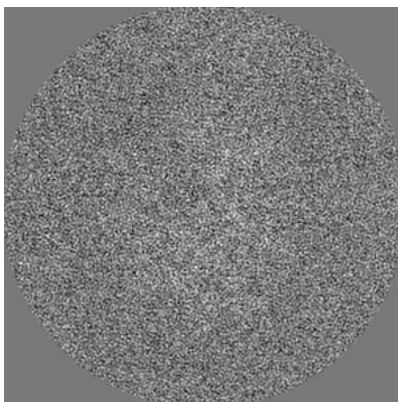


Z Index: 128

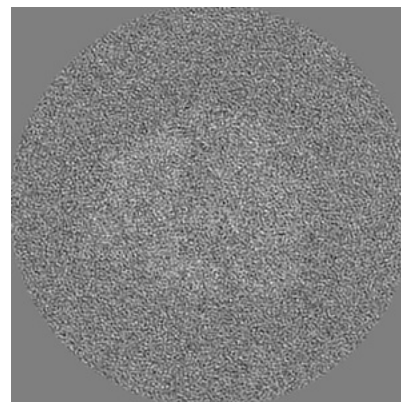
6.2.2 Raw map



X Index: 128



Y Index: 128

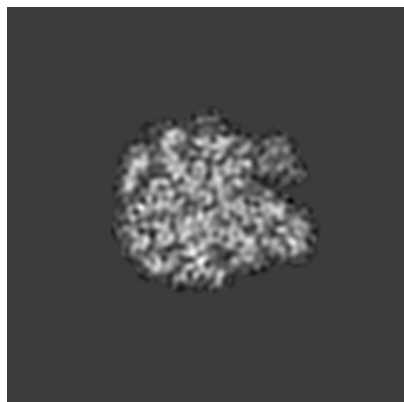


Z Index: 128

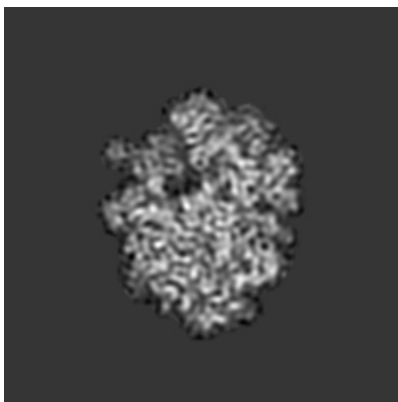
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 104

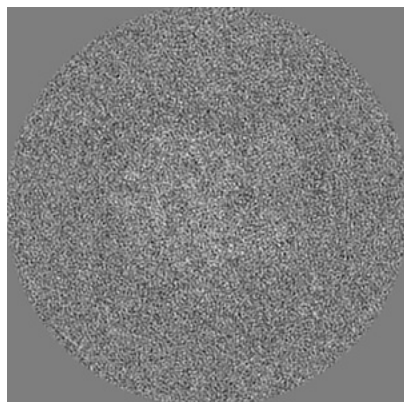


Y Index: 119

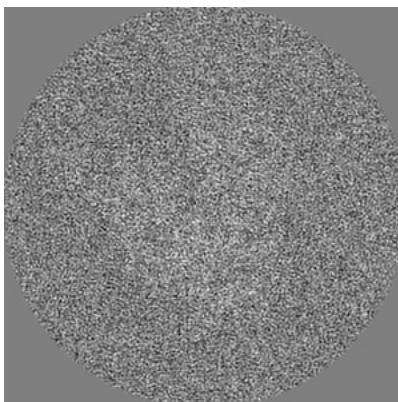


Z Index: 121

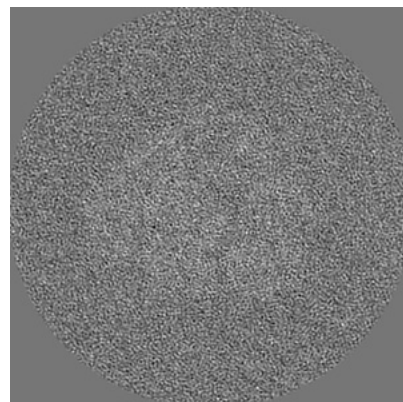
6.3.2 Raw map



X Index: 118



Y Index: 136



Z Index: 125

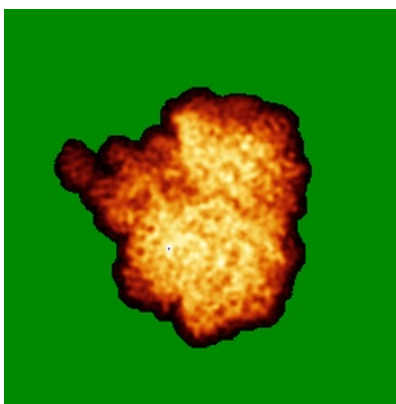
The images above show the largest variance slices of the map in three orthogonal directions.

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

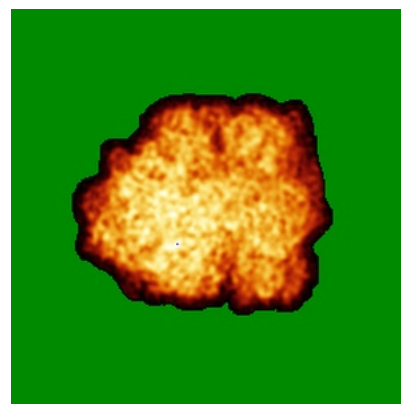
6.4.1 Primary map



X

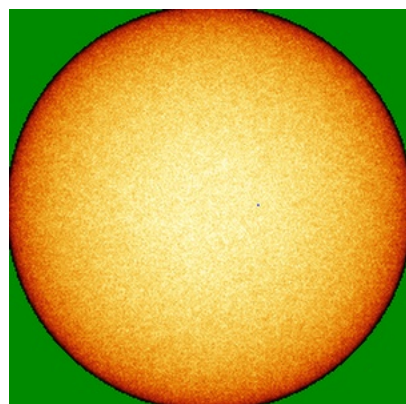


Y

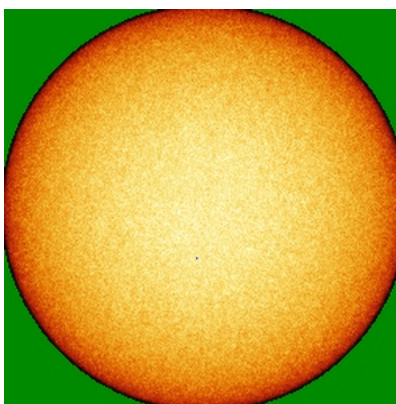


Z

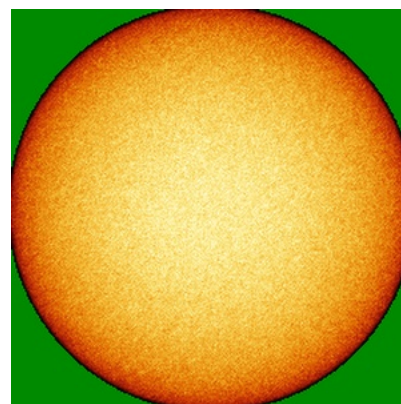
6.4.2 Raw map



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](#)

This section was not generated.

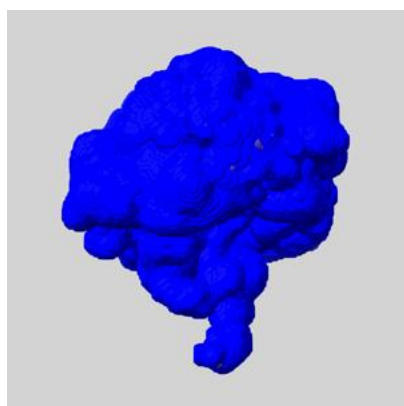
6.6 Mask visualisation [i](#)

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

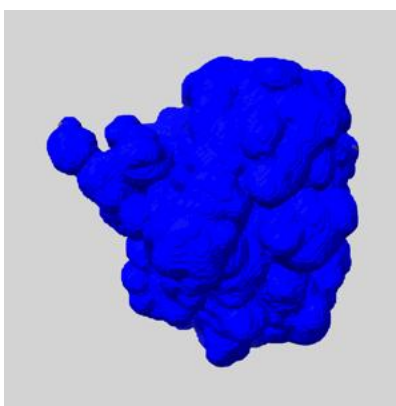
A mask typically either:

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

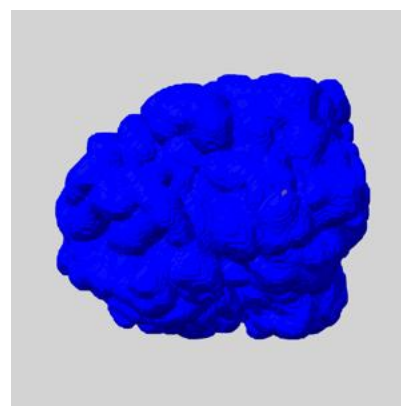
6.6.1 emd_13280_msk_1.map [i](#)



X



Y

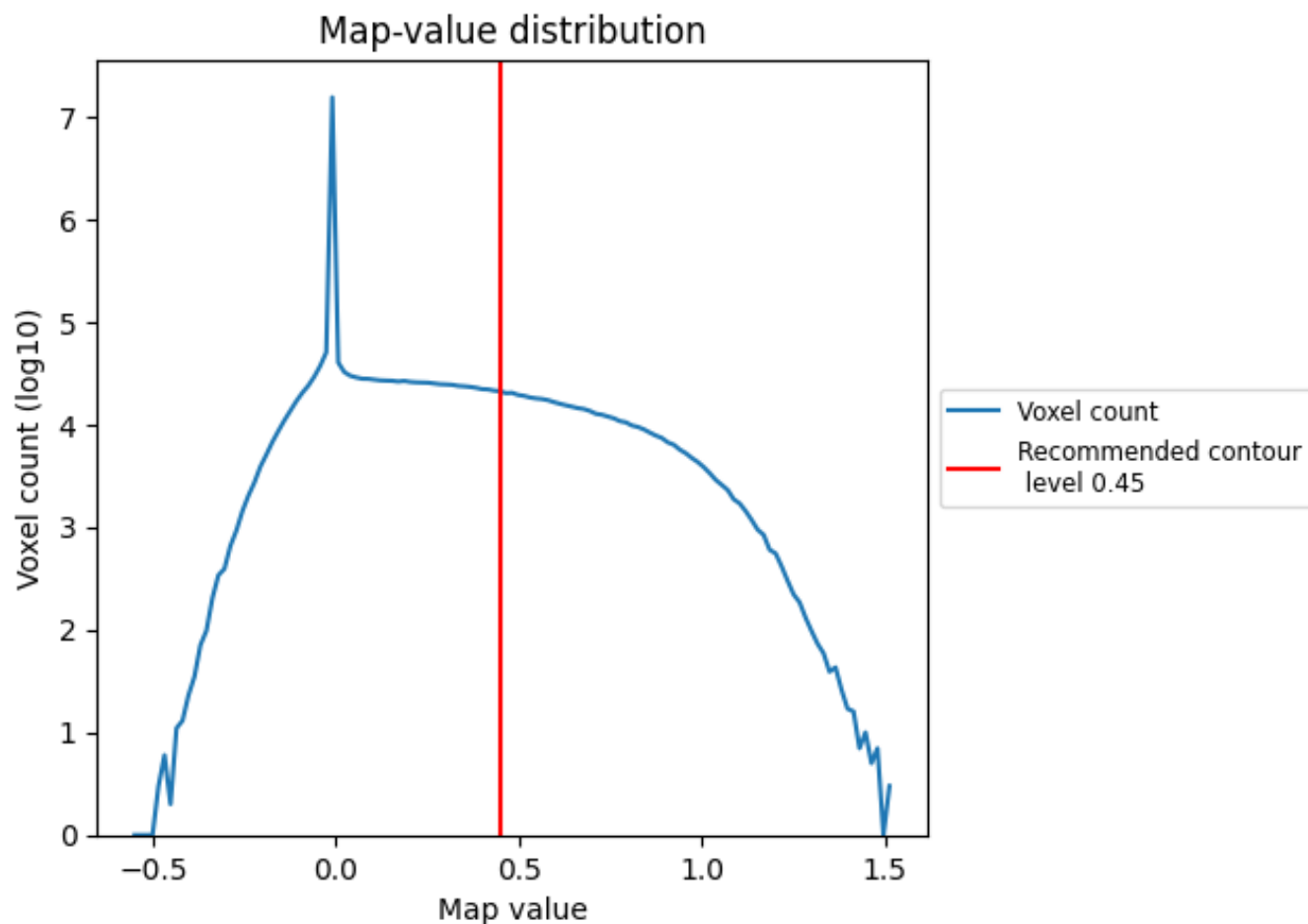


Z

7 Map analysis [i](#)

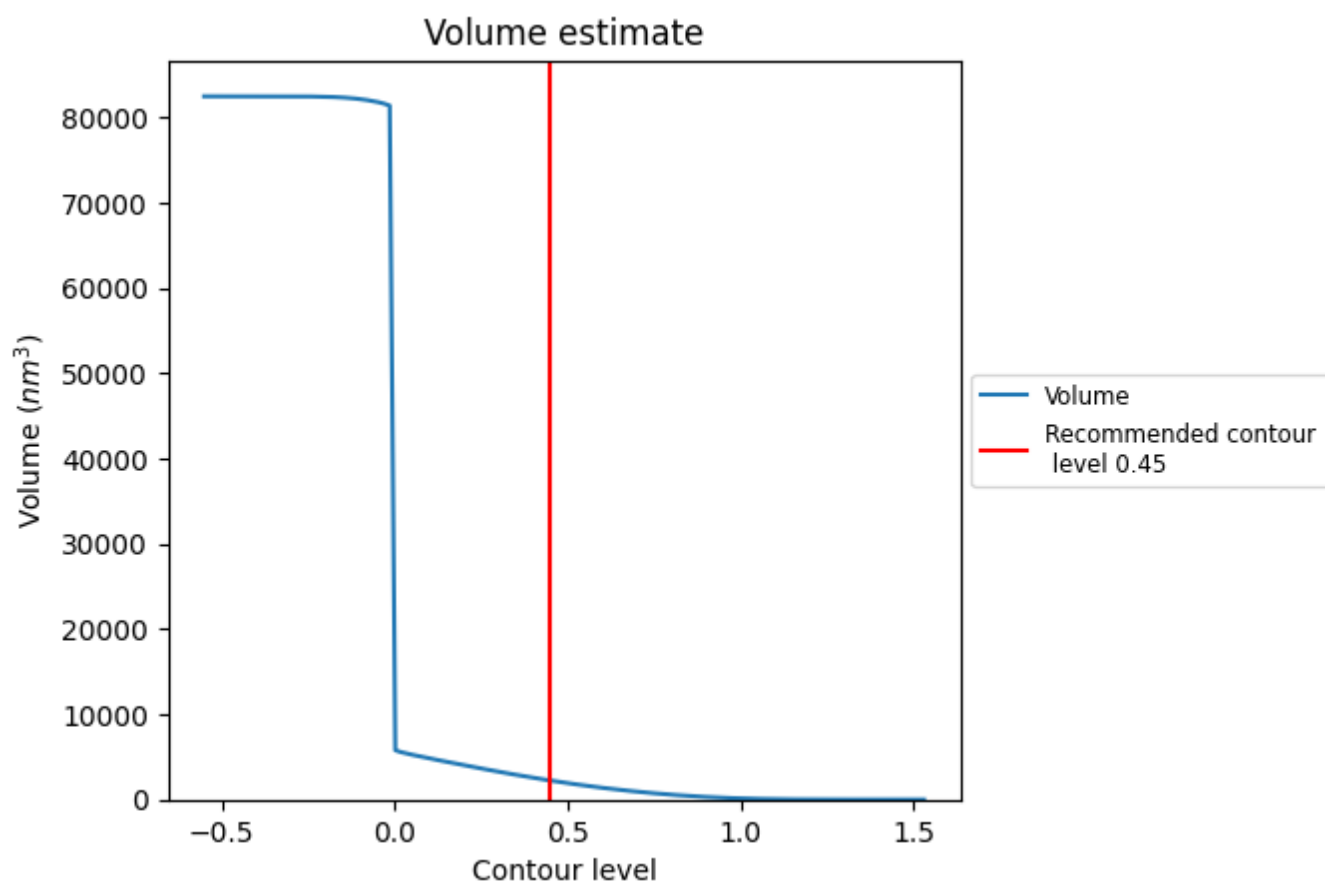
This section contains the results of statistical analysis of the map.

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.

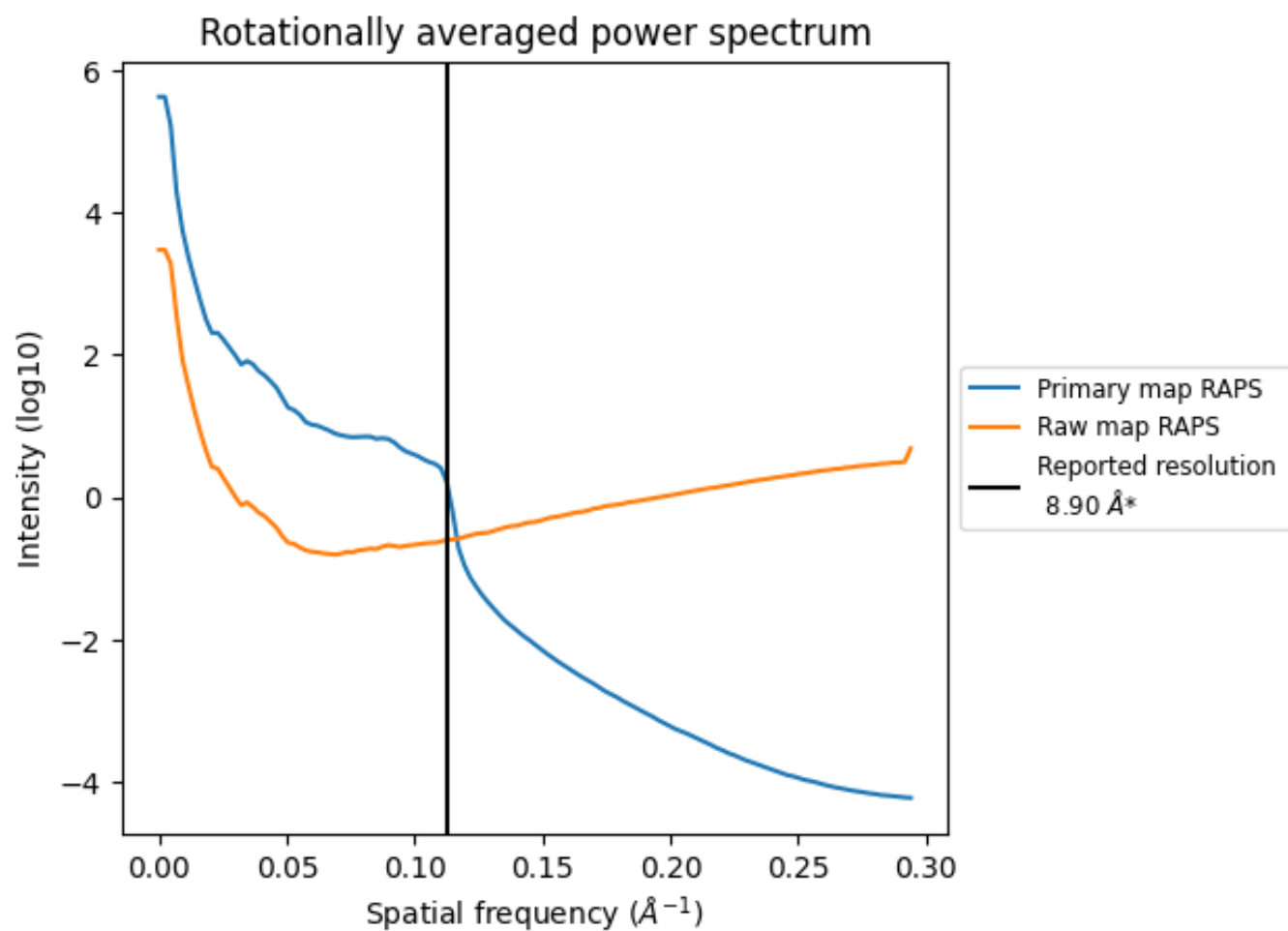
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2232 nm³; this corresponds to an approximate mass of 2016 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 ⓘ

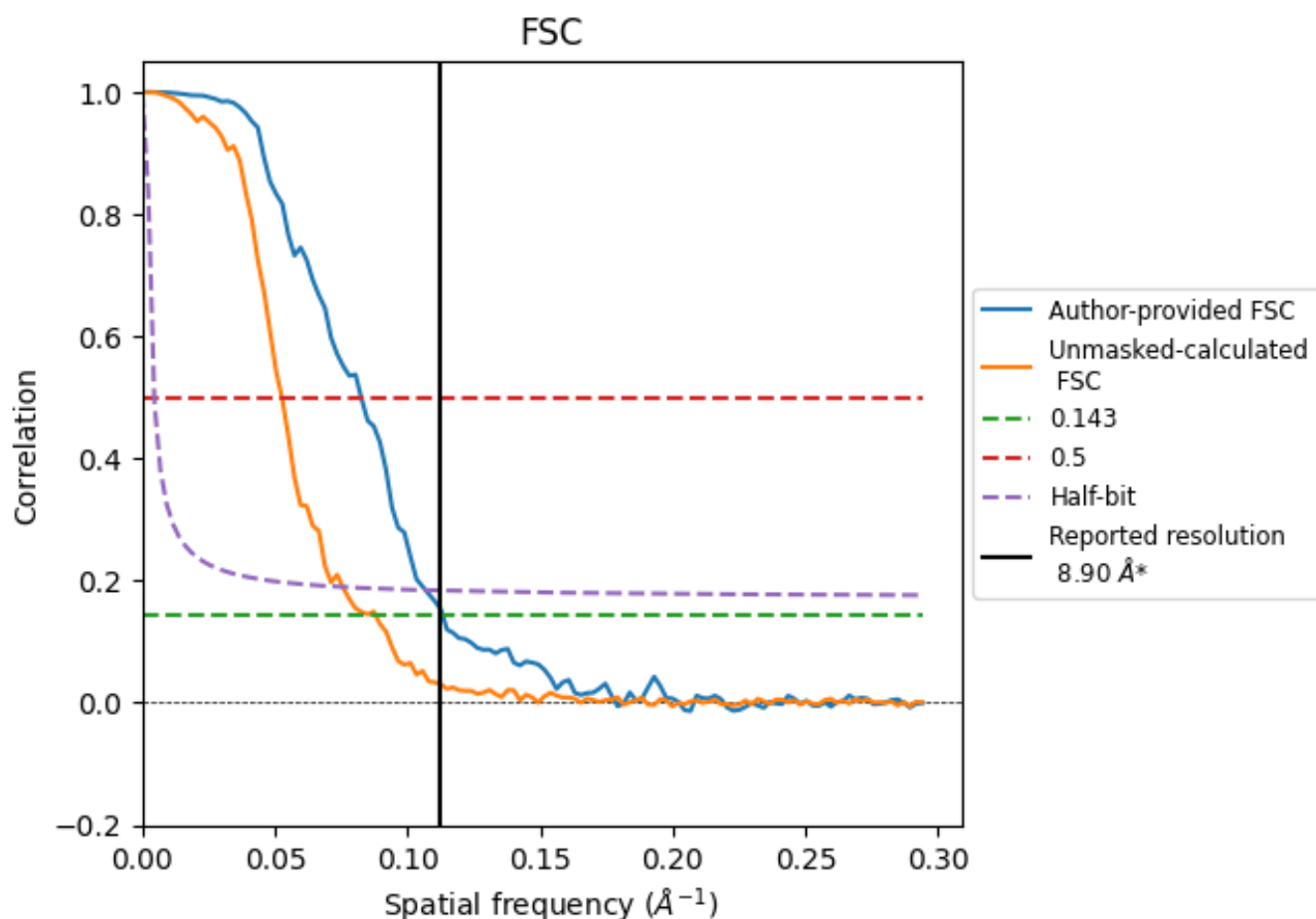


*Reported resolution corresponds to spatial frequency of 0.112 $\text{\AA}^{-1}$

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 0.112 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

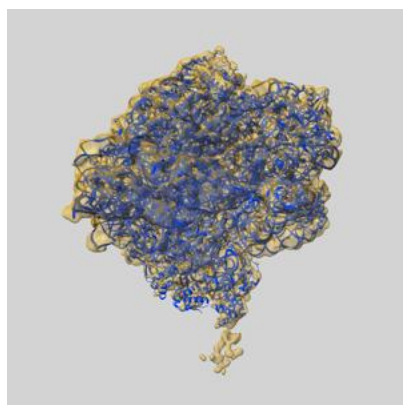
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.90	-	-
Author-provided FSC curve	8.83	12.12	9.36
Unmasked-calculated*	11.36	18.98	13.23

*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 11.36 differs from the reported value 8.9 by more than 10 %

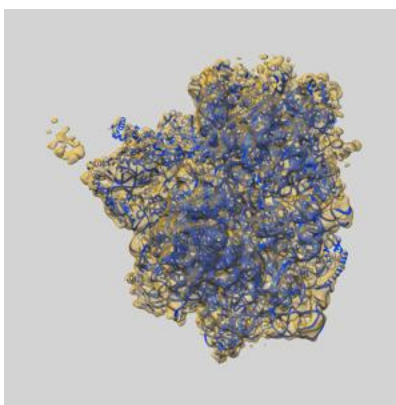
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13280 and PDB model 7PAQ. Per-residue inclusion information can be found in section [3](#) on page [14](#).

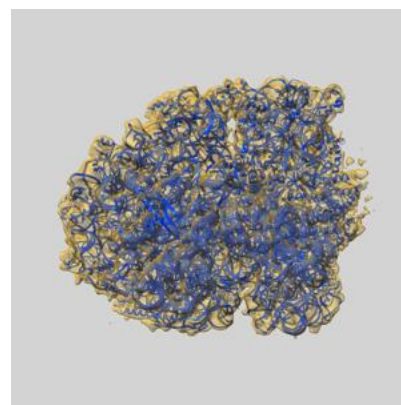
9.1 Map-model overlay [i](#)



X



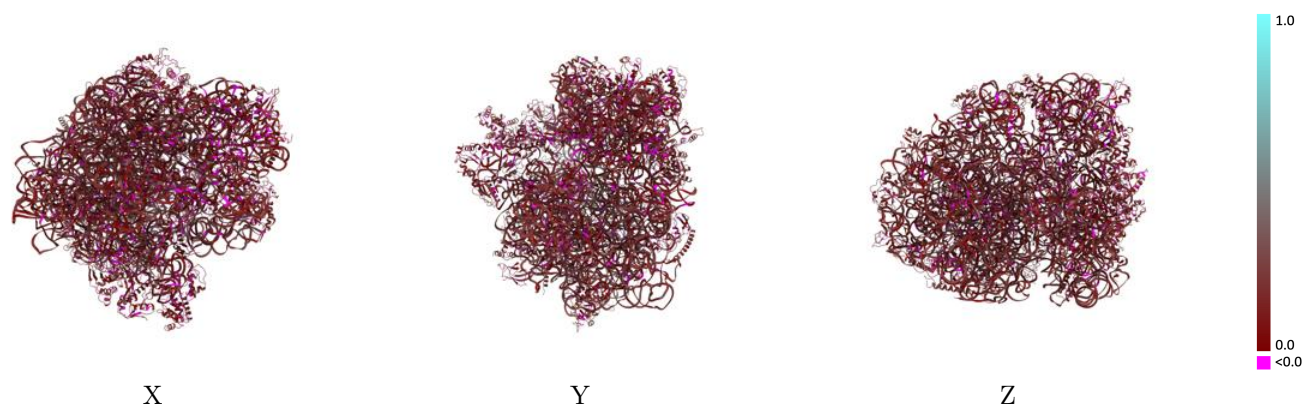
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.45 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](#)

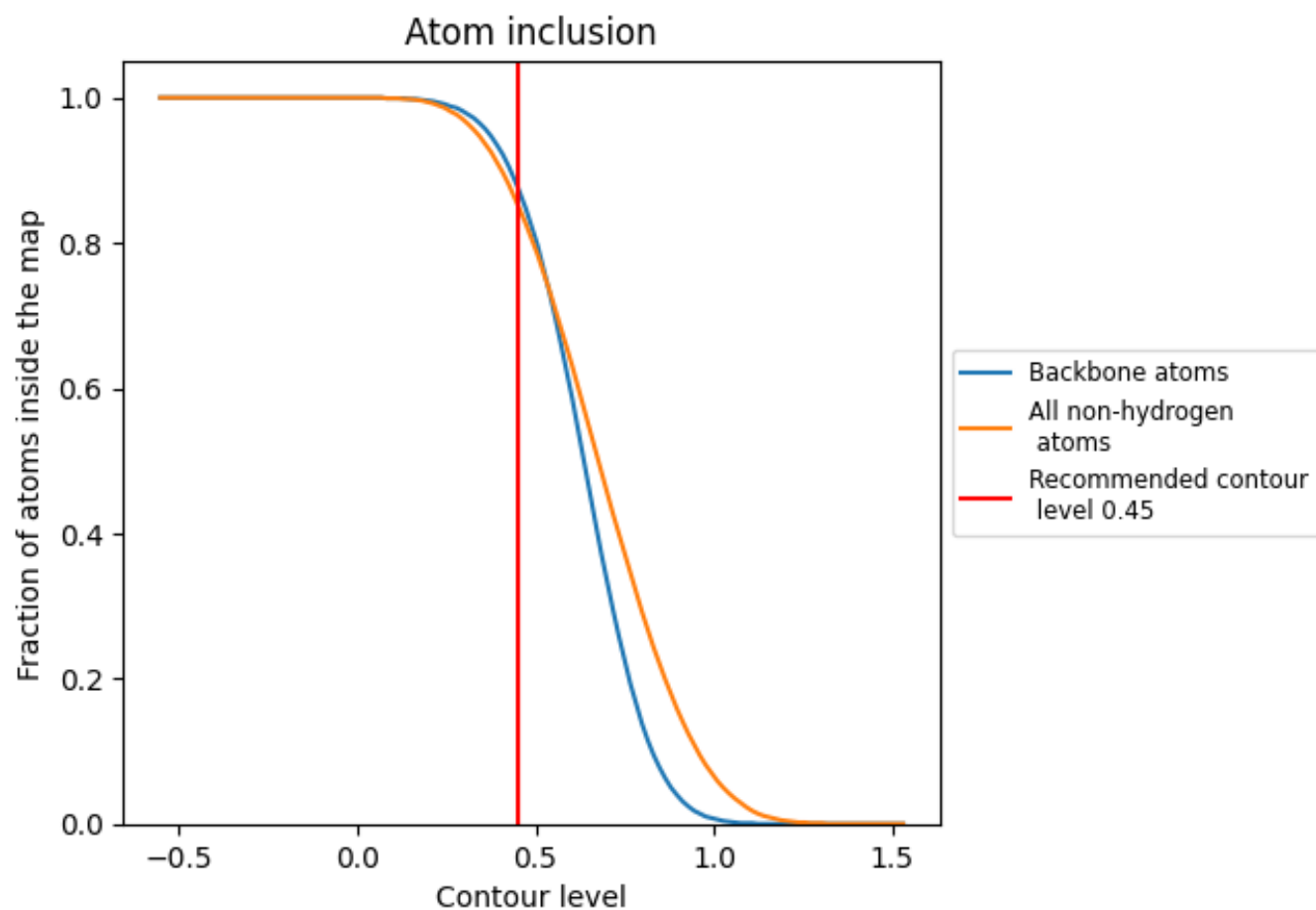


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 85% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8530	 0.1570
0	 0.7780	 0.1250
1	 0.7720	 0.1190
2	 0.7670	 0.1010
3	 0.9620	 0.1720
4	 0.9740	 0.1830
5	 0.9560	 0.1660
7	 0.7210	 0.1000
8	 0.9180	 0.1630
9	 0.3870	 0.1310
A	 0.6140	 0.1520
B	 0.6360	 0.1370
C	 0.7230	 0.1250
D	 0.7090	 0.1260
E	 0.6450	 0.1560
F	 0.5860	 0.1220
G	 0.7160	 0.1490
H	 0.6650	 0.1120
I	 0.6150	 0.1030
J	 0.6660	 0.1340
K	 0.7260	 0.1480
L	 0.5900	 0.1010
M	 0.7060	 0.0620
N	 0.7190	 0.1570
O	 0.7960	 0.1540
P	 0.7090	 0.1360
Q	 0.7040	 0.1270
R	 0.6630	 0.0920
S	 0.7740	 0.1490
T	 0.7080	 0.1570
W	 0.1140	 0.1060
a	 0.7850	 0.1190
b	 0.7240	 0.1210
c	 0.7270	 0.1530
d	 0.6920	 0.1440



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Chain	Atom inclusion	Q-score
e	 0.6580	 0.1410
f	 0.3120	 0.1430
g	 0.5850	 0.1270
h	 0.4740	 0.1320
i	 0.7550	 0.1460
j	 0.6730	 0.1370
k	 0.7550	 0.1270
l	 0.7510	 0.1220
m	 0.7640	 0.1380
n	 0.7830	 0.1490
o	 0.7100	 0.1490
p	 0.7990	 0.1320
q	 0.7560	 0.1500
r	 0.8050	 0.1560
s	 0.7690	 0.1490
t	 0.6500	 0.1390
u	 0.7770	 0.1090
v	 0.7250	 0.1080
w	 0.7640	 0.1860
x	 0.6120	 0.1390
y	 0.8300	 0.1250
z	 0.8620	 0.1350