



wwPDB EM Validation Summary Report ⓘ

Mar 14, 2026 – 12:27 AM UTC

PDB ID : 7PAR / pdb_00007par
EMDB ID : EMD-13281
Title : 70S ribosome with EF-G, ap/P- and pe/E-site tRNAs in Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-07-30
Resolution : 8.20 Å (reported)
Based on initial models : 4V7C, 7OOD, 7OOC, 4V7D

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

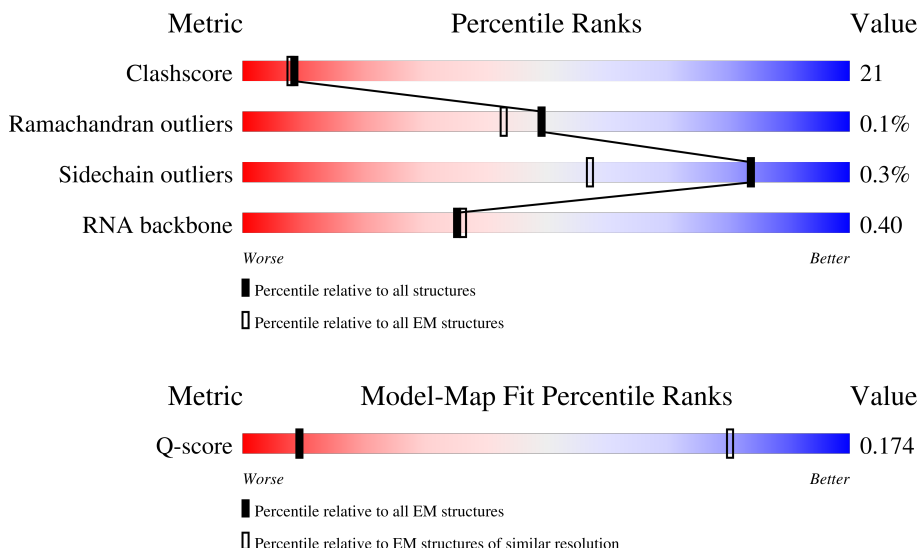
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.20 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	337 (7.70 - 8.70)

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	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	 21% 61% 17%
55	7	76	 29% 53% 18%
55	8	76	 18% 30% 53% 17%

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		

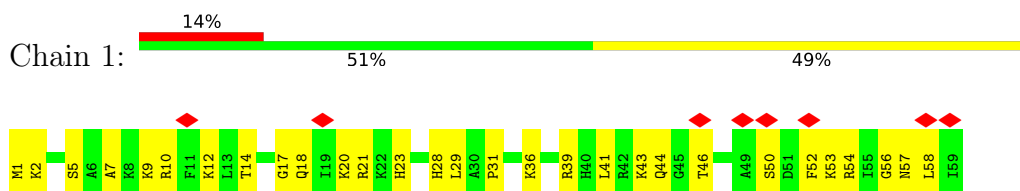
3 Residue-property plots [i](#)

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.

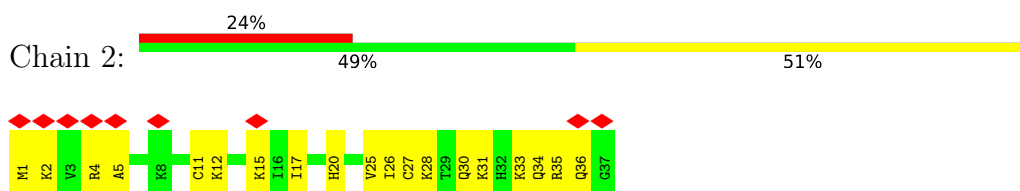
- Molecule 1: 50S ribosomal protein L34



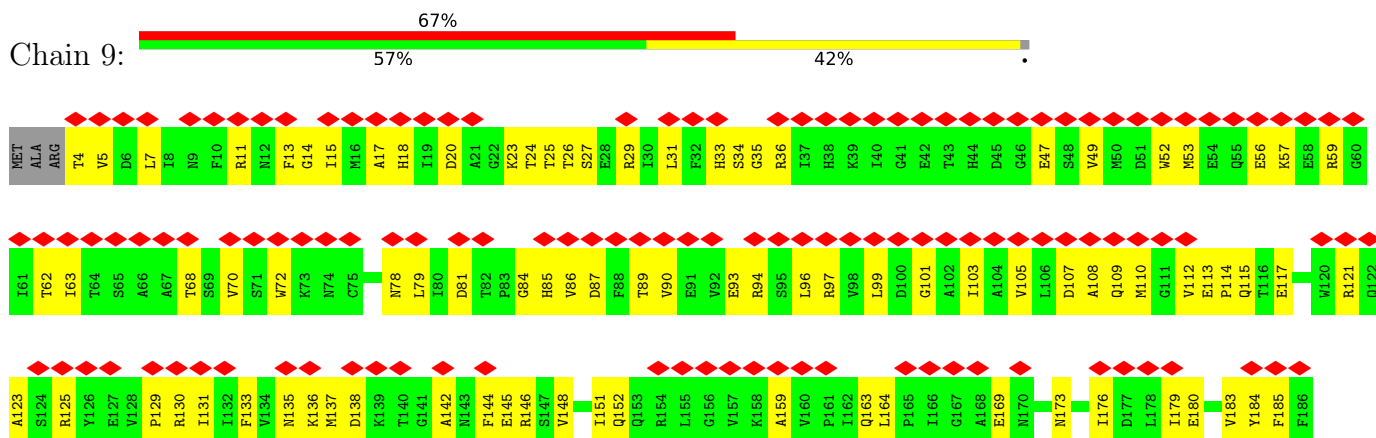
- Molecule 2: 50S ribosomal protein L35



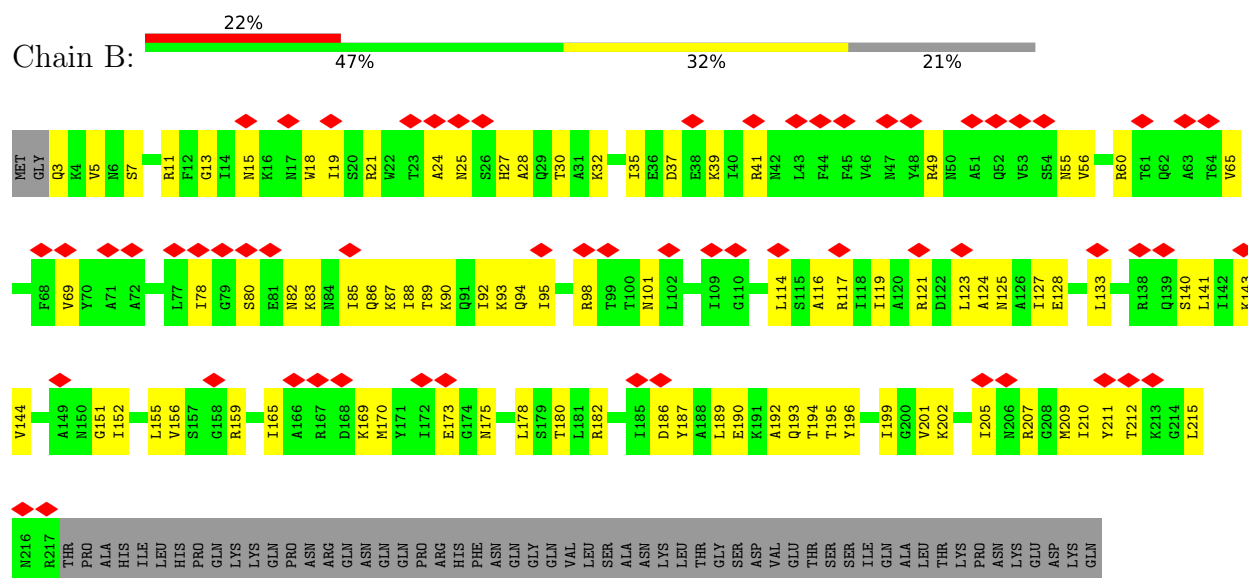
- Molecule 3: 50S ribosomal protein L36



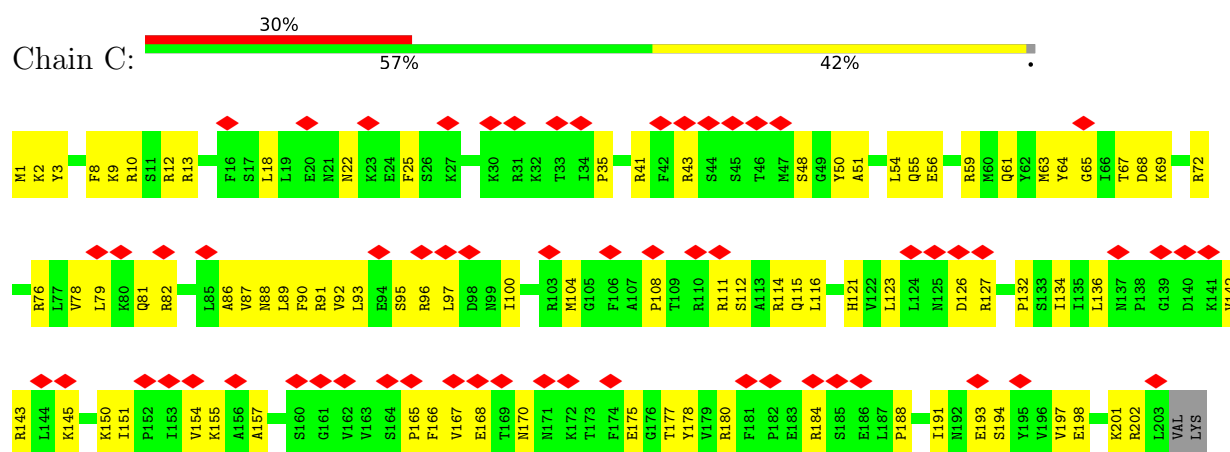
- Molecule 4: Elongation factor G



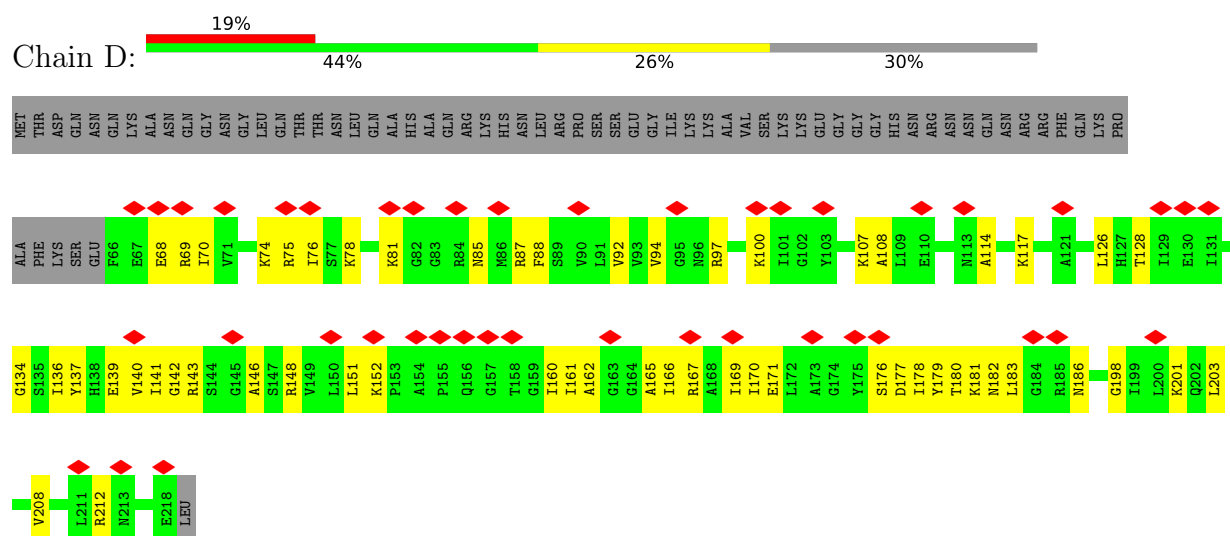
• Molecule 6: 30S ribosomal protein S3



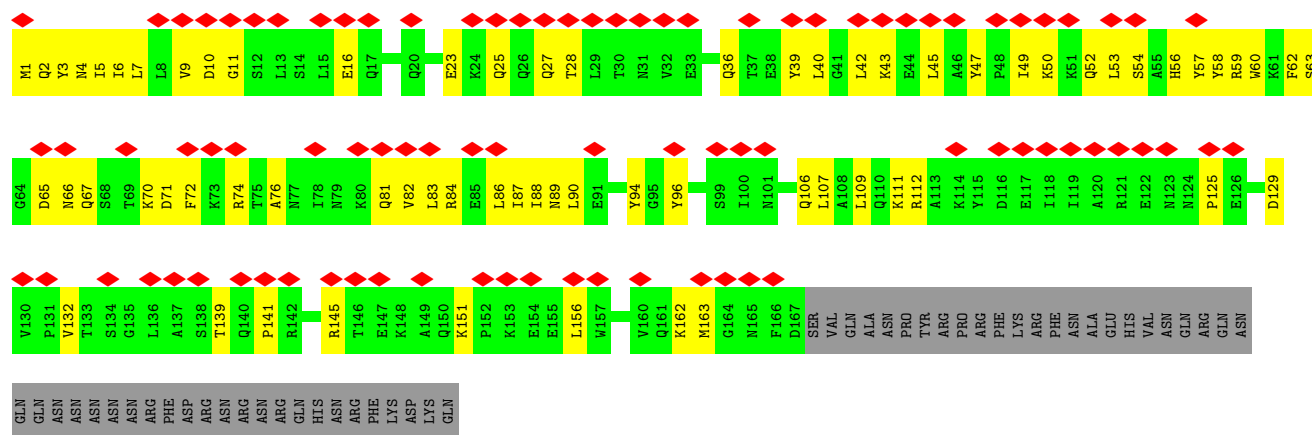
• Molecule 7: 30S ribosomal protein S4



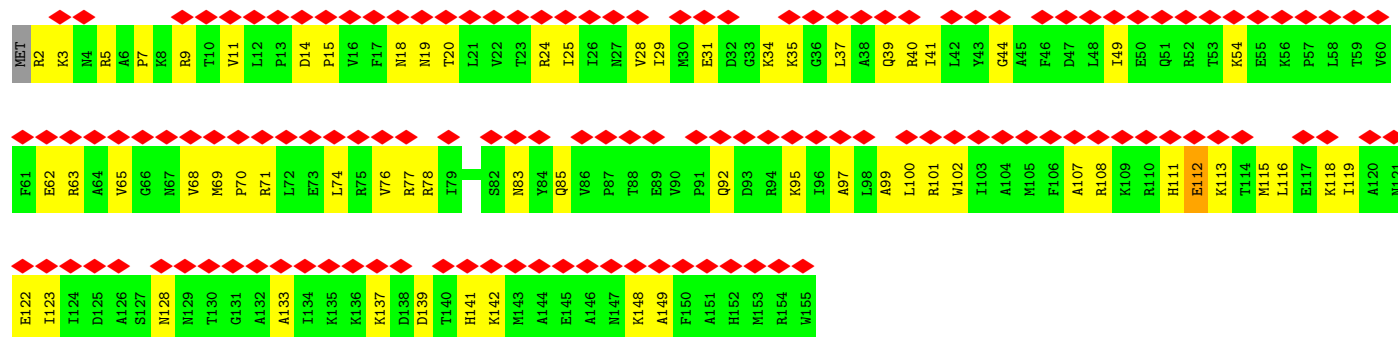
• Molecule 8: 30S ribosomal protein S5



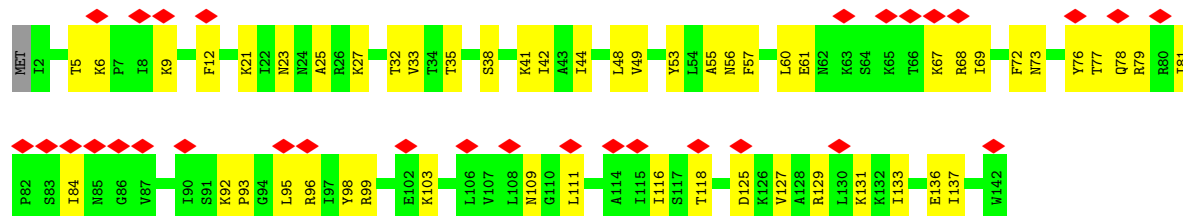
Chain E:



Chain F: 86% 58% 41%

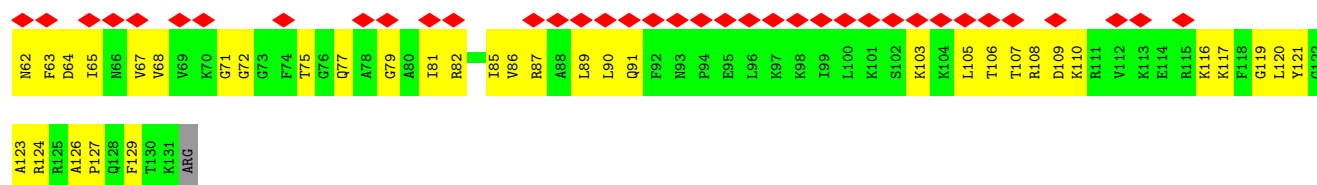


Chain G:

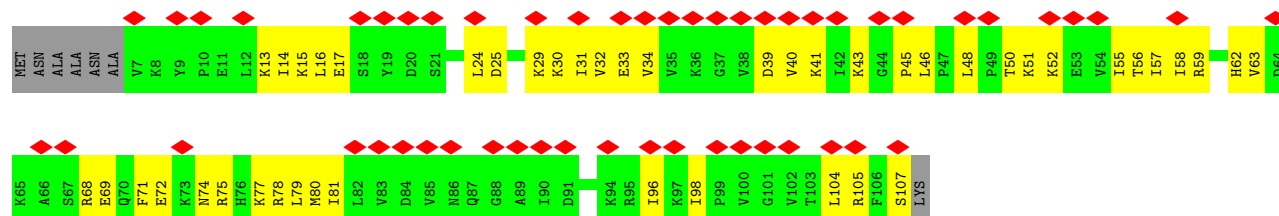


Chain H: 64% 44% 53%

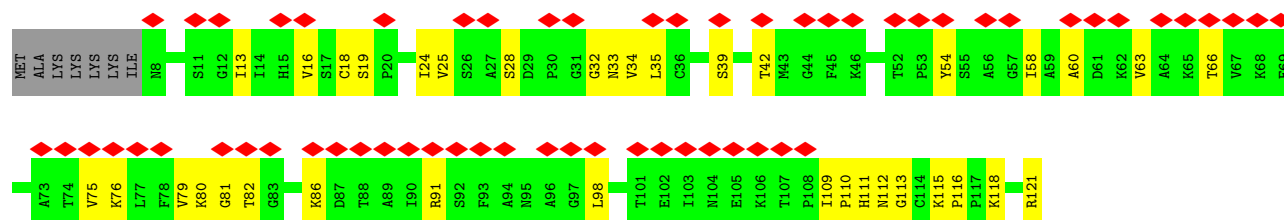




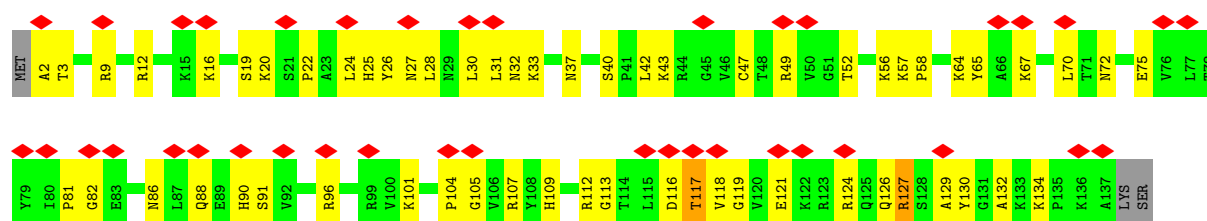
• Molecule 13: 30S ribosomal protein S10



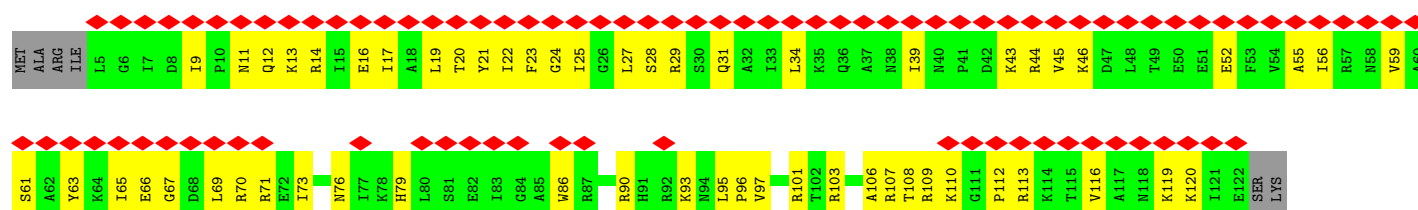
• Molecule 14: 30S ribosomal protein S11



• Molecule 15: 30S ribosomal protein S12



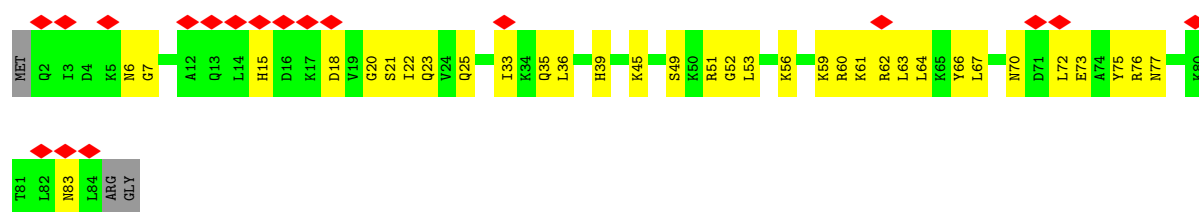
• Molecule 16: 30S ribosomal protein S13



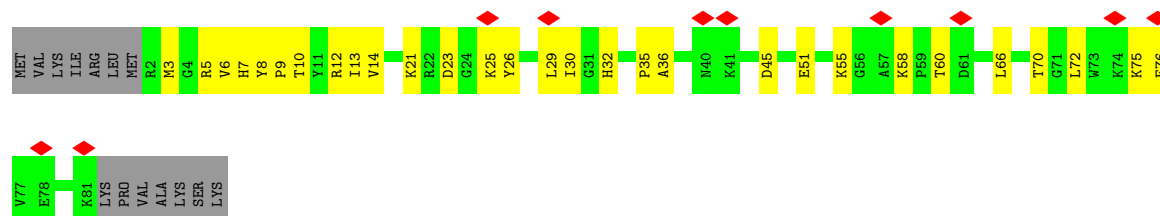
- Molecule 17: 30S ribosomal protein S14 type Z



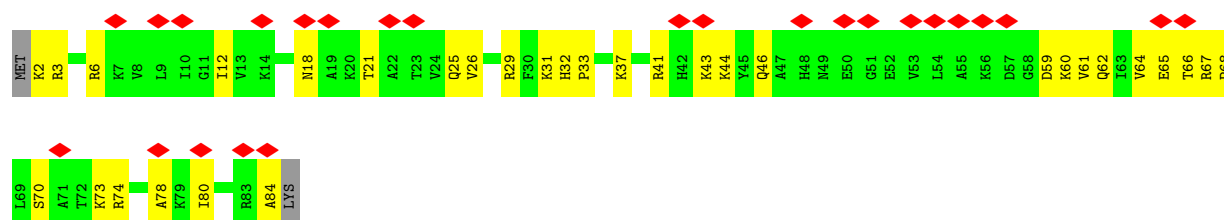
- Molecule 18: 30S ribosomal protein S15



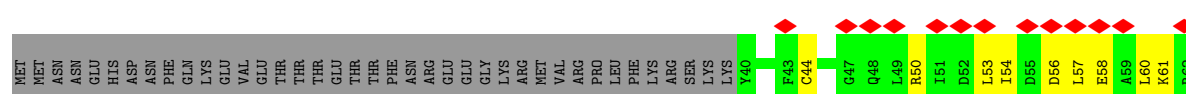
- Molecule 19: 30S ribosomal protein S16

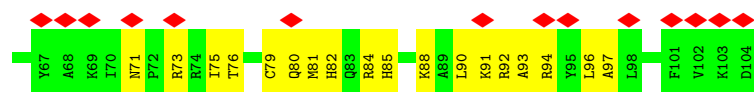


- Molecule 20: 30S ribosomal protein S17

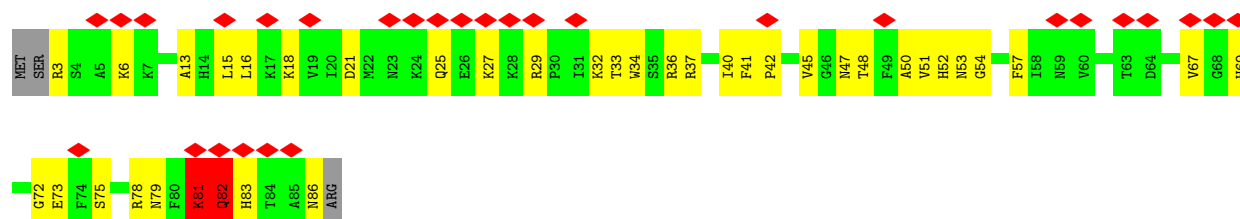


- Molecule 21: 30S ribosomal protein S18

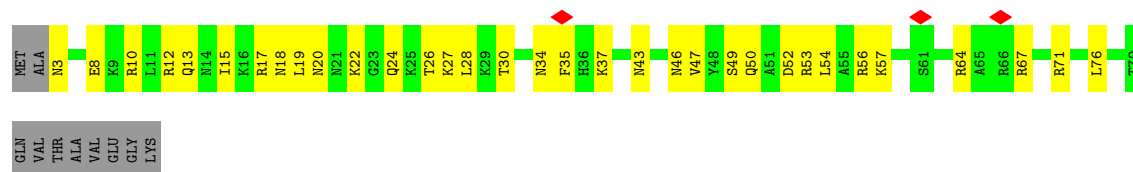




- Molecule 22: 30S ribosomal protein S19



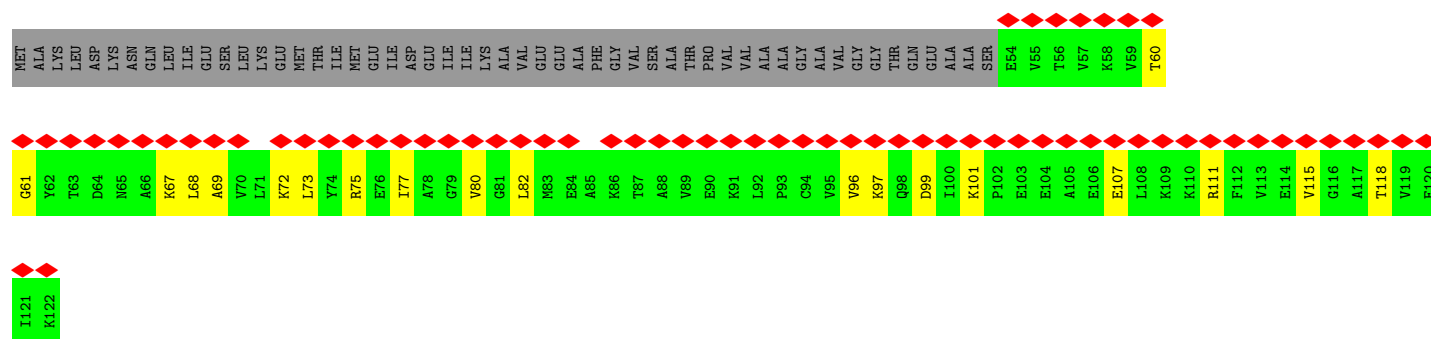
- Molecule 23: 30S ribosomal protein S20



- Molecule 24: 30S ribosomal protein S21

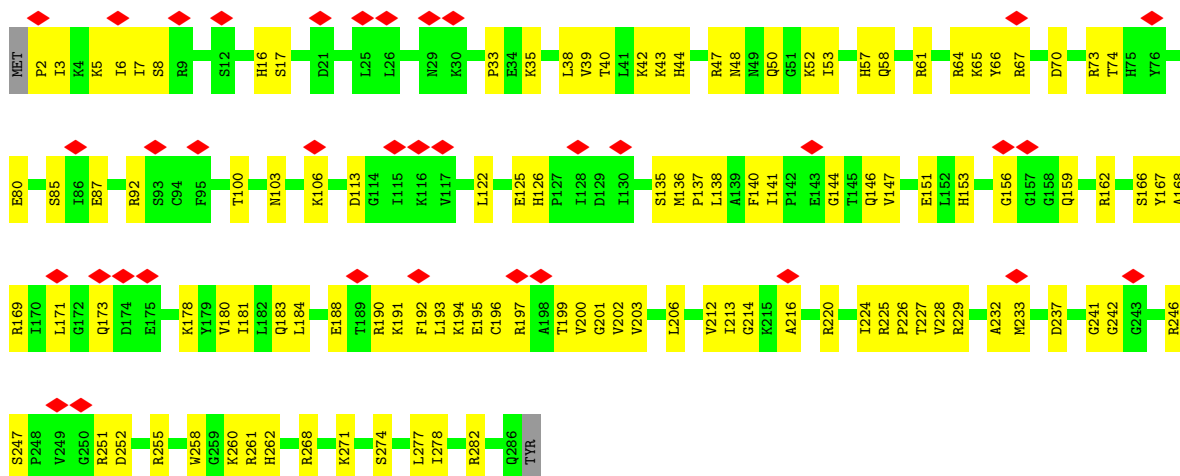


- Molecule 25: 50S ribosomal protein L7/L12

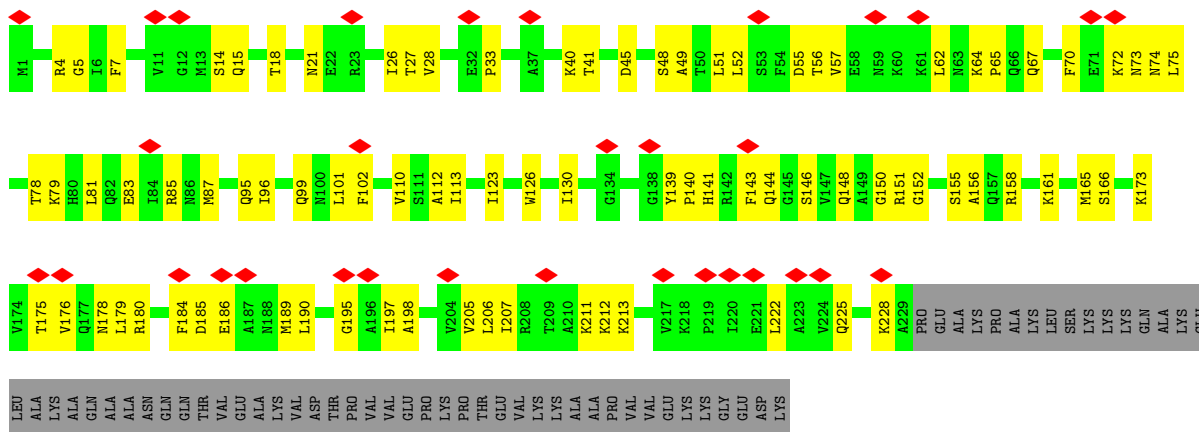


- Molecule 26: 50S ribosomal protein L2

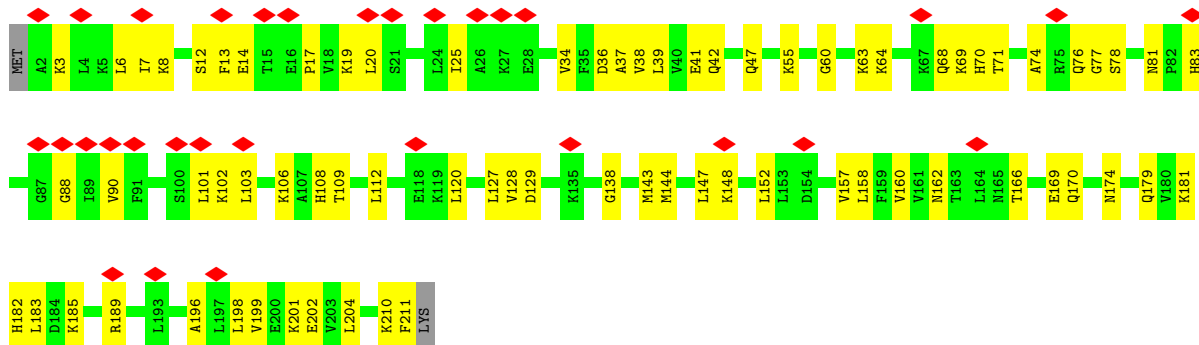




• Molecule 27: 50S ribosomal protein L3

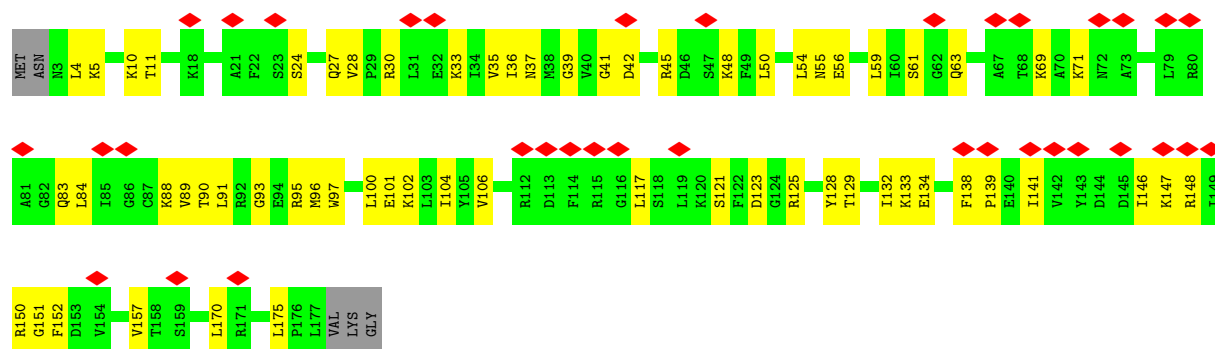


• Molecule 28: 50S ribosomal protein L4

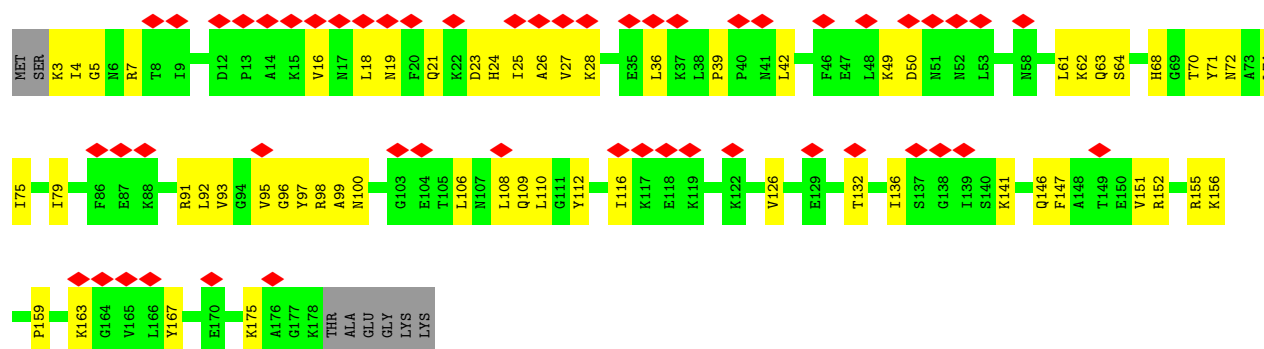


• Molecule 29: 50S ribosomal protein L5

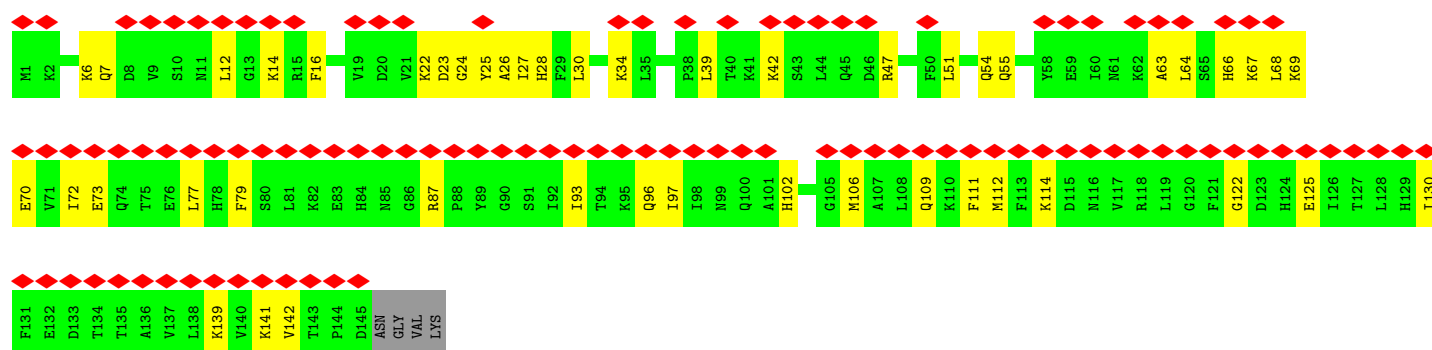




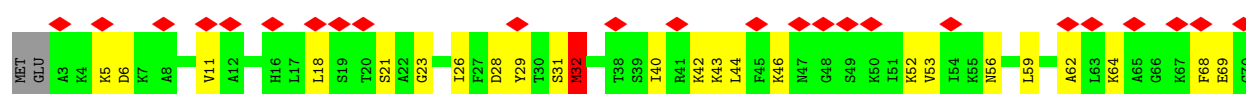
• Molecule 30: 50S ribosomal protein L6

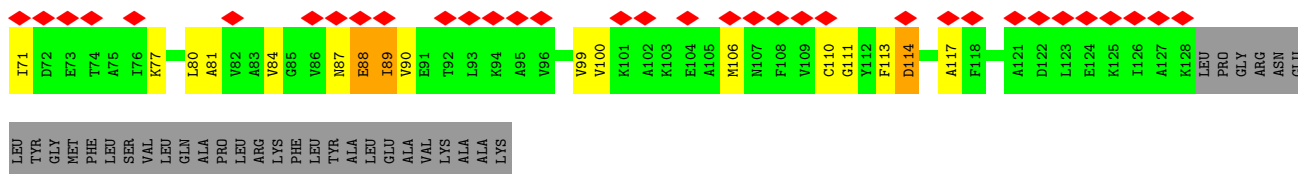


• Molecule 31: 50S ribosomal protein L9

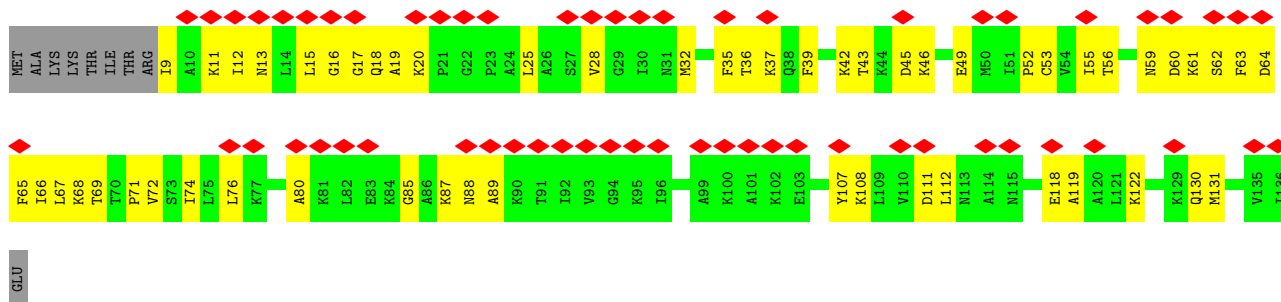
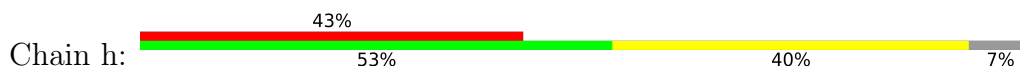


• Molecule 32: 50S ribosomal protein L10

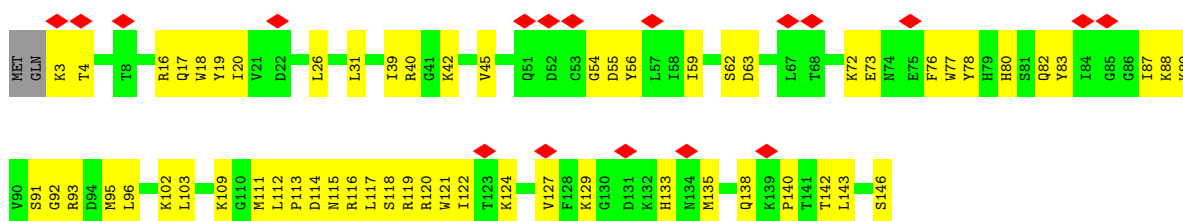




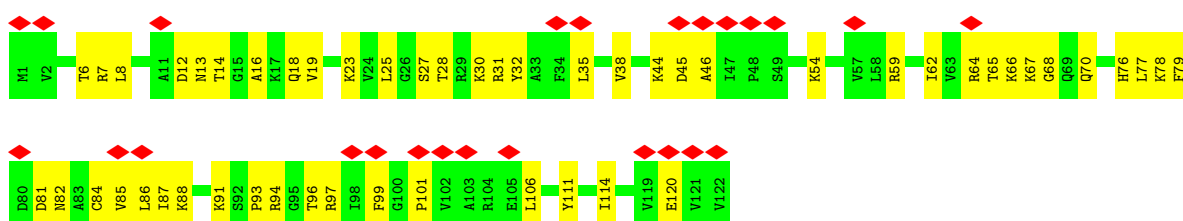
• Molecule 33: 50S ribosomal protein L11



• Molecule 34: 50S ribosomal protein L13

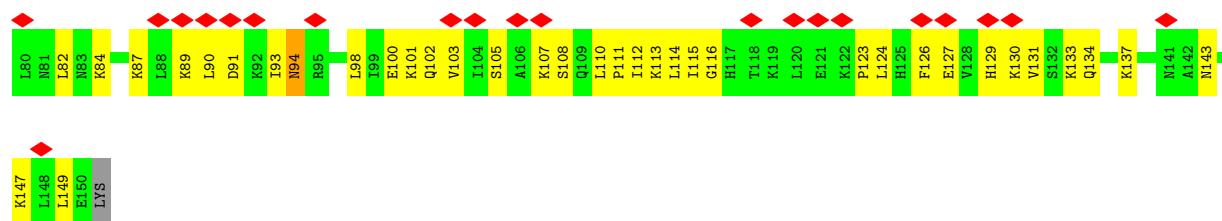


• Molecule 35: 50S ribosomal protein L14

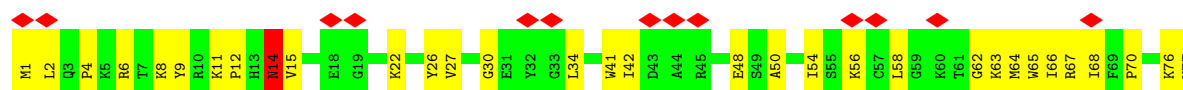


• Molecule 36: 50S ribosomal protein L15





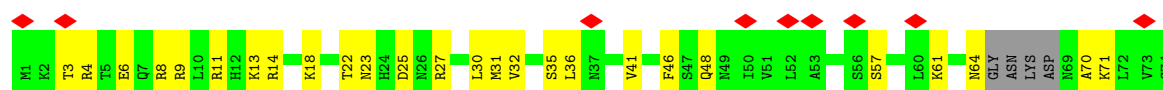
• Molecule 37: 50S ribosomal protein L16



• Molecule 38: 50S ribosomal protein L17



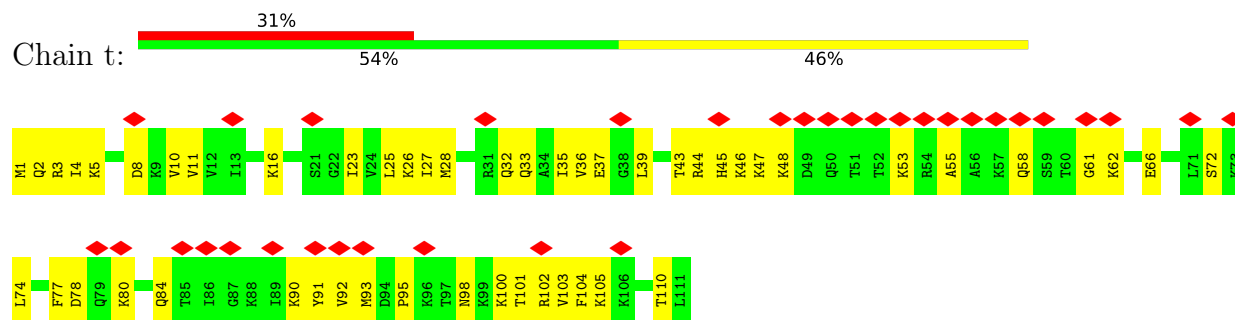
• Molecule 39: 50S ribosomal protein L18



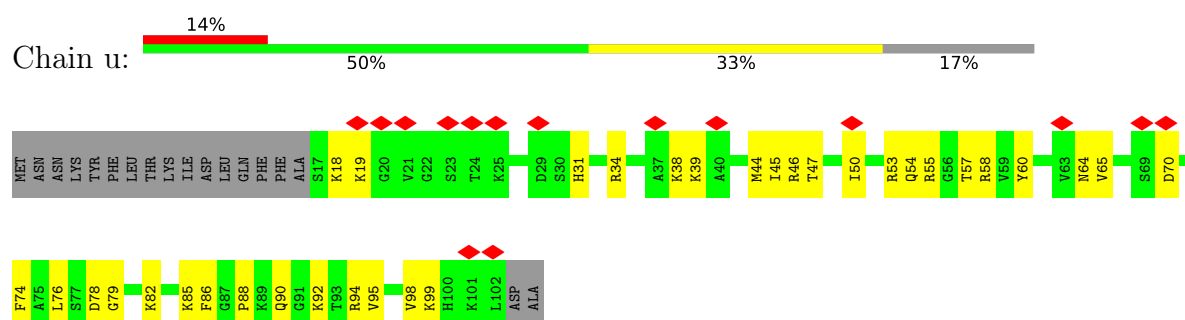
• Molecule 40: 50S ribosomal protein L19



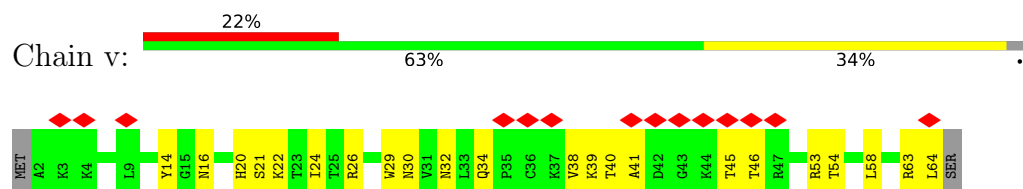
- Molecule 45: 50S ribosomal protein L24



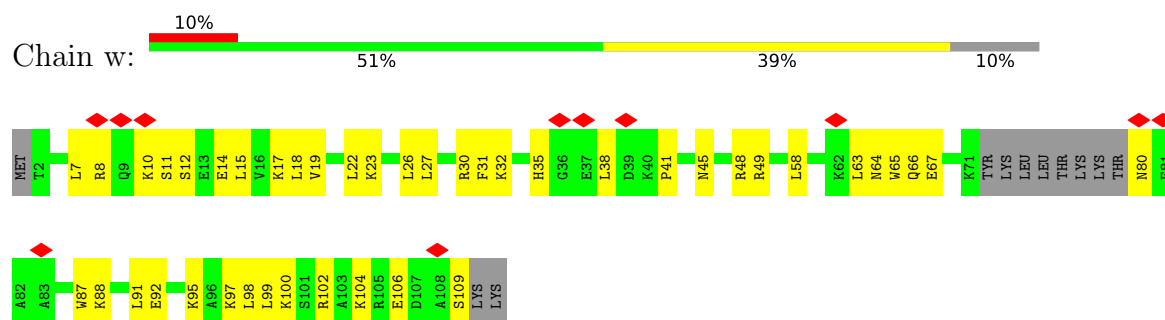
- Molecule 46: 50S ribosomal protein L27



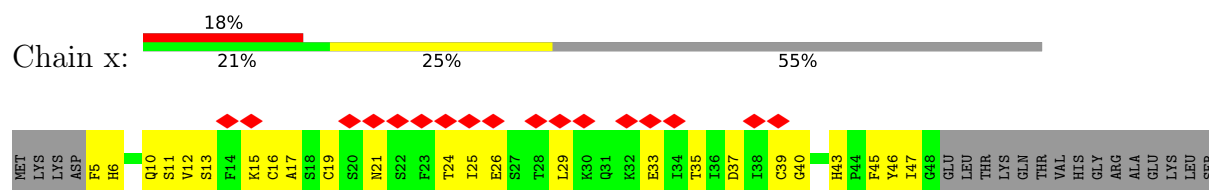
- Molecule 47: 50S ribosomal protein L28



- Molecule 48: 50S ribosomal protein L29

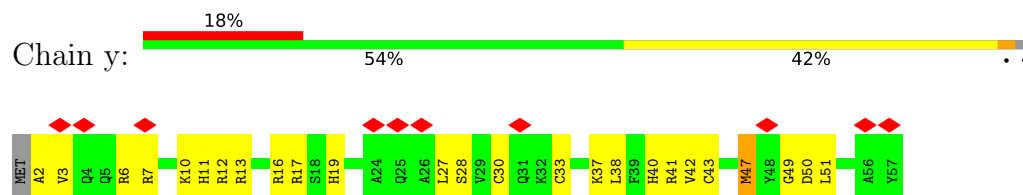


- Molecule 49: 50S ribosomal protein L31

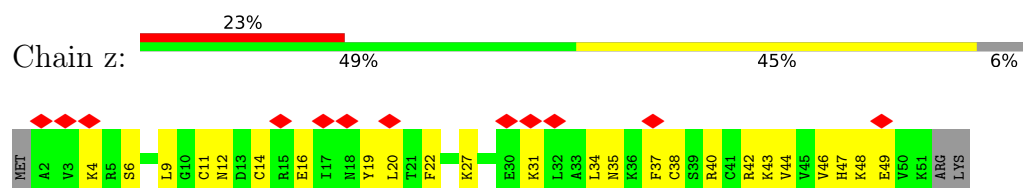


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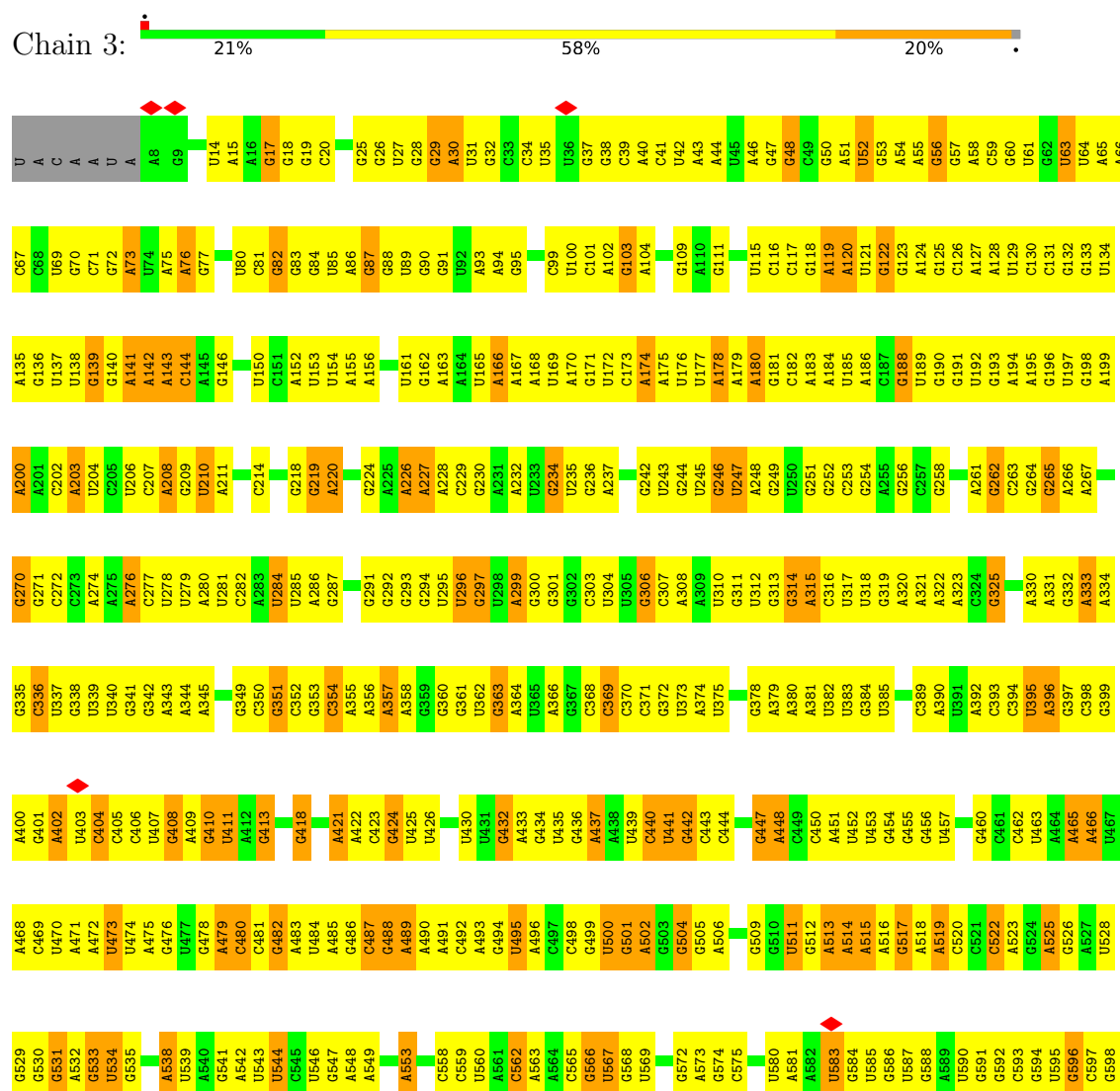
• Molecule 50: 50S ribosomal protein L32



• Molecule 51: 50S ribosomal protein L33 1

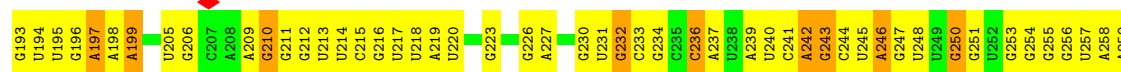


• Molecule 52: 23S ribosomal RNA

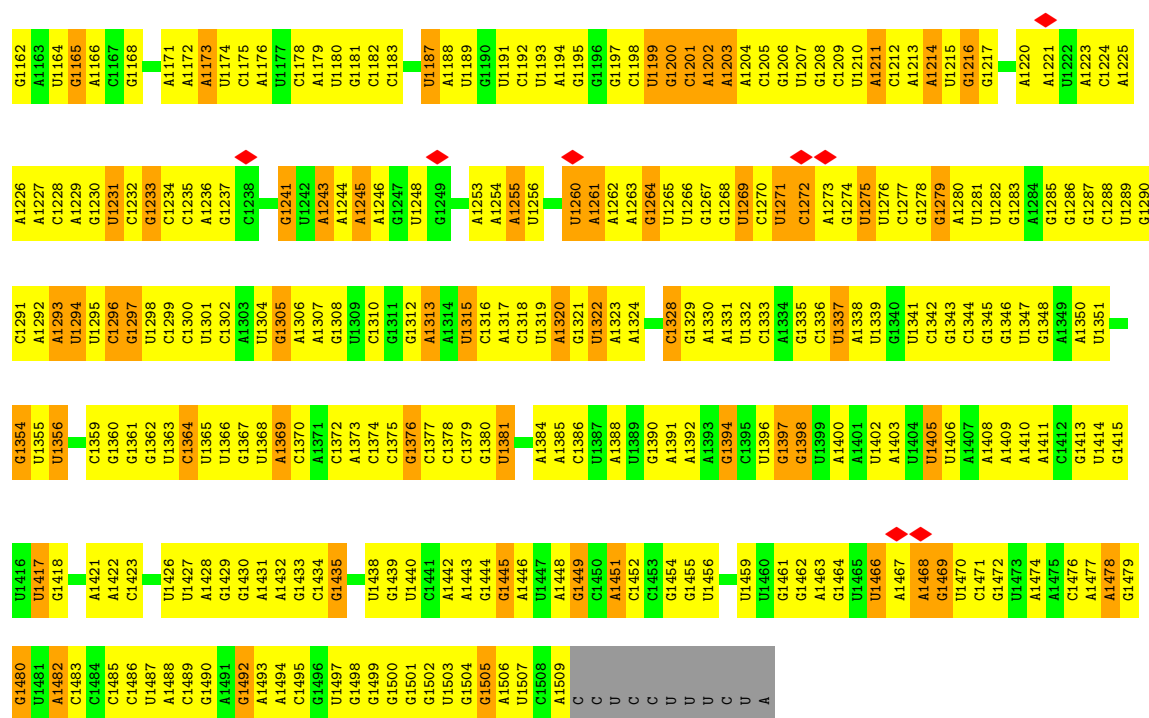


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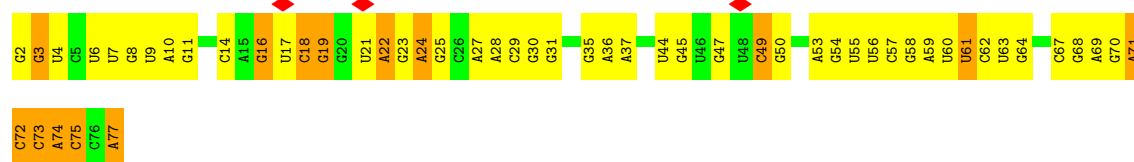
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U2462	U2396	U2332	G2265	G2139	A2073	U2018	U1891	U1823	G1760	G1695	C1632
G2463	A2397	G2333	G2266	U2140	A2074	G2019	U1892	G1824	C1761	C1696	C1633
A2464	U2398	U2334	C2267	G2141	A2075	A2020	U1893	U1825	A1762	C1697	A1634
C2465	G2399	U2335	G2268	U2142	U2081	A2021	A1894				
U2466	U2400	A2336	C2269	G2143							
G2467	C2403	U2337	C2272								



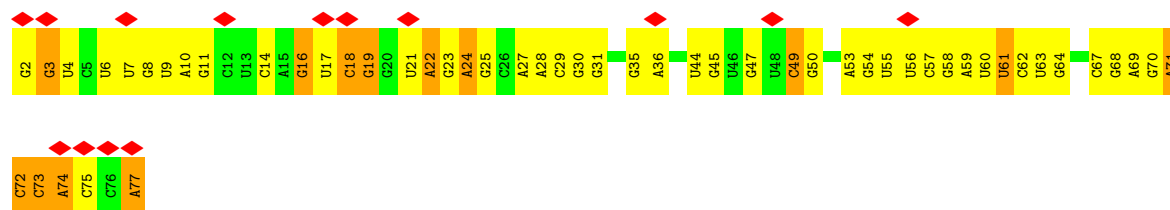
G1097	C1036	A972	G911	U844	C776	G651	G582	G519	G458	A393	G328	C280
C1098	A1037	A973	G912	U847	A777	A852	G583	C520	G461	A394	C329	G261
G1099	G1038	C974	A913	G848	A778	U654	G584	A521	G462	G395	C330	G262
A1102	G1039	C975	A914	U849	A779	G655	G585	G522	C463	C396	C331	C263
G1103	U1040	U976	U915	G850	G780	G656	G586	U523	U464	C397	U332	A332
C1104	G1042	A978	U916	U851	A781	G657	G587	C524	A465	G398	U333	U265
C1105	U1043	C979	A918	U852	G782	G658	G588	G525	A466	G399	A334	A266
U1106	G1044	C980	G919	A854	G783	A859	G589	C526	U467	C400	A335	C267
U1107	C1045	U981	G920	G855	A784	G661	A591	G527	U468	G401	C287	C288
A1108	A1046	A982	G921	U856	A787	G662	A592	G528	C469	U401	C289	C289
C1109	U1047	G983	G922	A858	U790	G663	A593	A531	U470	A402	A270	A270
U1110	G1048	A984	G923	A859	A791	G664	G594	A532	U471	A403	G271	G271
G1111	U1050	G985	G924	C860	A792	G665	G595	A533	G472	A404	G272	G272
U1112	U1051	U986	C926	A861	C792	U666	U596	A534	A473	C405	C273	C273
U1113	G1052	U987	C927	C862	G793	U667	C597	C534	A474	G406	A274	A274
A1114	G1053	G988	G928	A863	C794	U668	C598	A535	U475	A407	A275	A275
G1115	U1054	A989	C929	U864	U795	G670	G599	U536	U476	U408	U276	U276
U1116	C1055	C990	A930	U865	A796	G671	G600	A537	U477	G409	G277	G277
U1117	G1056	A991	C931	A866	G797	A672	G601	A538	U478	A410	A278	A278
U1118	U1057	U995	A932	A867	U798	A673	A605	G539	G479	C347	G285	G285
U1119	C1058	U996	G933	U870	G799	A674	A606	U540	A479	C348	C286	C286
G1120	G1059	G997	G934	C871	U800	U675	A607	C541	C480	A349	U287	U287
U1121	C1062	G998	G935	U872	C802	U676	G608	G542	U481	C351	A288	A288
U1122	G1063	C999	G936	U873	A804	C677	G609	C543	G482	C352	U289	U289
G1123	U1064	A1000	G937	U874	C805	A678	A611	A544	U483	A419	A352	A352
U1124	U1065	U1001	U938	C875	A806	U679	A612	A545	A484	A420	G290	G290
C1125	C1066	A1002	G939	G876	G809	U681	G616	G546	C485	G421	C291	C291
U1126	U1067	G1003	G940	C877	U812	G682	U617	C547	C486	A422	U292	U292
A1127	C1068	U1004	G942	U878	A813	G683	U618	G548	A487	U423	G293	G293
G1128	U1069	U1005	C943	G879	A814	G684	A519	U550	U488	U424	A294	A294
U1133	G1070	U1006	A944	G880	G815	G685	A620	A551	U489	G425	A297	A297
C1134	U1071	A1007	U945	G881	G816	G686	C621	U552	A490	A426	G298	G298
U1135	G1072	G1008	G946	U882	U845	C886	G622	C553	U491	U361	U299	U299
G1136	U1073	U1009	U948	U883	A819	G688	G623	C554	A492	A428	A300	A300
U1137	U1074	A1010	G949	U885	A820	U689	G624	G555	U493	U362	G301	G301
U1138	G1075	A1011	C950	U886	G821	G690	U625	A557	U495	U363	A302	A302
A1139	U1076	C1013	U951	C887	A822	A691	G626	U558	A496	U364	A303	A303
U1140	U1077	U1014	U952	U888	G823	A692	U627	U559	A497	U365	U304	U304
U1141	G1078	A1015	A953	U889	U824	U694	A628	U560	G498	C367	A305	A305
G1142	U1079	U1016	A954	C891	A825	U695	U629	A561	U499	C368	G306	G306
C1143	G1080	A1016	U955	G892	G826	G896	G630	U562	G500	A369	C307	C307
U1144	U1081	G1019	U956	A895	C827	U697	A632	U563	A501	U370	C308	C308
A1145	U1082	G	C957	G896	U828	U698	U633	G564	C502	U371	A309	A309
A1146	A1083	A	G958	U829	G829	A699	U634	G568	G503	G372	C310	C310
U1147	U1084	C	A959	A897	U830	A700	G638	U569	A504	G443	A311	A311
U1148	G1085	G	C960	U897	C831	U701	A639	A570	C505	G374	A312	A312
U1149	C1087	U	G961	G900	G832	A702	A639	A571	U506	G375	G316	G316
C1088	U1088	U	A901	A901	G833	U703	C640	A572	A507	G376	A317	A317
A1151	G1089	A	A902	A902	G834	U704	U641	G573	A508	G447	C318	C318
G1152	U1090	A	A964	C904	G835	A705	A642	C574	C509	A448	U319	U319
C1091	G1091	G	C965	G837	C836	U706	U643	A575	U510	G380	G320	G320
U1092	G1092	G1028	A966	U905	G837	G707	U644	A576	A511	U450	A321	A321
A1093	G1093	G1029	A967	C906	A838	U708	U645	A577	U512	G384	G322	G322
C1094	U1094	U1030	A908	U839	G840	A709	A646	G577	G513	A452	A323	A323
A1158	G1095	U1031	A909	C841	U772	A710	U649	C578	U514	U453	C324	C324
G1159	U1096	U1033	C910	U773	A774	G711	A650	G580	G515	G387	A325	A325
G1160				G775				A581	C517	U456	G388	G388
G1161									A518	A457	A389	A389



• 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	3324	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	1.470	Depositor
Minimum map value	-0.452	Depositor
Average map value	0.026	Depositor
Map value standard deviation	0.123	Depositor
Recommended contour level	0.5	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	0.14	0/383	0.45	0/504
2	1	0.16	0/484	0.49	0/637
3	2	0.14	0/306	0.39	0/401
4	9	0.17	0/5419	0.48	1/7307 (0.0%)
5	A	0.14	0/1954	0.39	0/2642
6	B	0.15	0/1721	0.45	0/2323
7	C	0.17	0/1691	0.45	0/2267
8	D	0.15	0/1188	0.44	0/1593
9	E	0.16	0/1384	0.42	0/1867
10	F	0.21	0/1266	0.51	0/1700
11	G	0.17	0/1126	0.49	0/1517
12	H	0.15	0/1044	0.49	0/1395
13	I	0.14	0/820	0.44	0/1103
14	J	0.14	0/844	0.42	0/1136
15	K	0.29	0/1094	0.60	1/1468 (0.1%)
16	L	0.16	0/962	0.41	0/1289
17	M	0.17	0/483	0.48	0/643
18	N	0.14	0/679	0.41	0/907
19	O	0.15	0/659	0.47	0/885
20	P	0.15	0/684	0.44	0/913
21	Q	0.15	0/545	0.52	0/730
22	R	0.16	0/698	0.53	0/936
23	S	0.16	0/631	0.43	0/838
24	T	0.13	0/475	0.38	0/621
25	W	0.14	0/538	0.42	0/722
26	a	0.15	0/2267	0.44	0/3044
27	b	0.16	0/1795	0.46	0/2412
28	c	0.14	0/1671	0.44	0/2246
29	d	0.15	0/1409	0.43	0/1894
30	e	0.17	0/1420	0.44	0/1912
31	f	0.15	0/1183	0.44	0/1587
32	g	0.41	0/969	0.68	0/1295
33	h	0.13	0/968	0.38	0/1298
34	i	0.14	0/1186	0.45	0/1592

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	j	0.16	0/953	0.45	0/1275
36	k	0.15	0/1170	0.41	0/1559
37	l	0.18	0/1104	0.53	0/1481
38	m	0.16	0/973	0.48	0/1309
39	n	0.16	0/897	0.43	0/1198
40	o	0.15	0/948	0.45	0/1262
41	p	0.17	0/961	0.47	0/1278
42	q	0.17	0/828	0.46	0/1111
43	r	0.15	0/1077	0.46	0/1441
44	s	0.18	0/732	0.53	0/988
45	t	0.15	0/879	0.40	0/1165
46	u	0.15	0/665	0.45	0/884
47	v	0.19	0/519	0.53	0/695
48	w	0.13	0/826	0.41	0/1104
49	x	0.15	0/353	0.44	0/474
50	y	0.35	0/457	0.64	0/601
51	z	0.15	0/412	0.40	0/547
52	3	0.11	0/69073	0.27	0/107710
53	4	0.11	0/2505	0.28	0/3902
54	5	0.10	0/35768	0.25	0/55764
55	7	0.12	0/1808	0.35	0/2817
55	8	0.12	0/1808	0.35	0/2817
All	All	0.13	0/164662	0.34	2/245006 (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
10	F	0	1
12	H	0	1
15	K	0	2
22	R	0	2
32	g	0	1
37	l	0	1
All	All	0	10

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	9	480	PHE	N-CA-C	5.90	115.64	107.73
15	K	119	GLY	CA-C-O	-5.07	117.83	122.24

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	9	295	ASN	Peptide
4	9	297	VAL	Peptide
10	F	112	GLU	Peptide
12	H	62	ASN	Peptide
15	K	126	GLN	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	26	0
2	1	477	0	530	32	0
3	2	304	0	350	17	0
4	9	5326	0	5343	233	0
5	A	1921	0	1973	71	0
6	B	1698	0	1768	65	0
7	C	1660	0	1719	73	0
8	D	1173	0	1267	52	0
9	E	1362	0	1377	68	0
10	F	1246	0	1308	59	0
11	G	1110	0	1226	42	0
12	H	1028	0	1094	62	0
13	I	809	0	894	44	0
14	J	829	0	855	34	0
15	K	1076	0	1170	46	0
16	L	951	0	1014	47	0
17	M	474	0	509	36	0
18	N	673	0	730	27	0
19	O	646	0	677	24	0
20	P	675	0	728	28	0
21	Q	535	0	562	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	R	682	0	691	34	0
23	S	629	0	681	30	0
24	T	471	0	522	22	0
25	W	534	0	572	19	0
26	a	2225	0	2301	96	0
27	b	1762	0	1808	76	0
28	c	1644	0	1731	63	0
29	d	1388	0	1469	51	0
30	e	1396	0	1481	41	0
31	f	1160	0	1172	39	0
32	g	960	0	1014	23	0
33	h	959	0	1039	40	0
34	i	1164	0	1192	59	0
35	j	944	0	1019	45	0
36	k	1153	0	1256	63	0
37	l	1079	0	1134	50	0
38	m	958	0	1011	35	0
39	n	889	0	952	33	0
40	o	938	0	1008	49	0
41	p	947	0	1028	46	0
42	q	811	0	858	44	0
43	r	1068	0	1150	54	0
44	s	720	0	803	33	0
45	t	872	0	972	48	0
46	u	657	0	695	34	0
47	v	513	0	560	20	0
48	w	818	0	870	32	0
49	x	344	0	333	20	0
50	y	452	0	472	26	0
51	z	408	0	440	17	0
52	3	61664	0	30954	2216	0
53	4	2239	0	1137	69	0
54	5	31943	0	16058	1209	0
55	7	1618	0	821	43	0
55	8	1618	0	821	41	0
All	All	151980	0	105548	5230	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 5230 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)
52:3:1243:A:N6	52:3:1265:G:H21	1.29	1.28
52:3:1243:A:H62	52:3:1265:G:N2	1.38	1.22
4:9:500:GLY:H	54:5:1469:G:H5"	1.02	1.10
30:e:16:VAL:HA	30:e:28:LYS:O	1.52	1.07
52:3:1807:C:H42	52:3:1824:G:N2	1.55	1.04

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%)	49 (86%)	8 (14%)	0	100	100
3	2	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
4	9	680/688 (99%)	628 (92%)	52 (8%)	0	100	100
5	A	238/294 (81%)	222 (93%)	16 (7%)	0	100	100
6	B	213/273 (78%)	196 (92%)	17 (8%)	0	100	100
7	C	201/205 (98%)	185 (92%)	16 (8%)	0	100	100
8	D	151/219 (69%)	137 (91%)	14 (9%)	0	100	100
9	E	165/215 (77%)	145 (88%)	20 (12%)	0	100	100
10	F	152/155 (98%)	140 (92%)	12 (8%)	0	100	100
11	G	139/142 (98%)	121 (87%)	18 (13%)	0	100	100
12	H	126/132 (96%)	113 (90%)	13 (10%)	0	100	100
13	I	99/108 (92%)	91 (92%)	8 (8%)	0	100	100
14	J	112/121 (93%)	106 (95%)	6 (5%)	0	100	100
15	K	134/139 (96%)	114 (85%)	20 (15%)	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%)	54 (93%)	4 (7%)	0	100	100
18	N	81/86 (94%)	79 (98%)	2 (2%)	0	100	100
19	O	78/94 (83%)	72 (92%)	6 (8%)	0	100	100
20	P	81/85 (95%)	76 (94%)	5 (6%)	0	100	100
21	Q	63/104 (61%)	54 (86%)	9 (14%)	0	100	100
22	R	82/87 (94%)	74 (90%)	6 (7%)	2 (2%)	4	27
23	S	75/87 (86%)	74 (99%)	1 (1%)	0	100	100
24	T	51/60 (85%)	49 (96%)	2 (4%)	0	100	100
25	W	67/122 (55%)	63 (94%)	4 (6%)	0	100	100
26	a	283/287 (99%)	268 (95%)	15 (5%)	0	100	100
27	b	227/287 (79%)	215 (95%)	12 (5%)	0	100	100
28	c	208/212 (98%)	193 (93%)	15 (7%)	0	100	100
29	d	173/180 (96%)	160 (92%)	13 (8%)	0	100	100
30	e	174/184 (95%)	162 (93%)	12 (7%)	0	100	100
31	f	143/149 (96%)	129 (90%)	14 (10%)	0	100	100
32	g	124/161 (77%)	111 (90%)	12 (10%)	1 (1%)	16	54
33	h	126/137 (92%)	118 (94%)	8 (6%)	0	100	100
34	i	142/146 (97%)	134 (94%)	8 (6%)	0	100	100
35	j	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
36	k	146/151 (97%)	136 (93%)	10 (7%)	0	100	100
37	l	134/139 (96%)	120 (90%)	12 (9%)	2 (2%)	8	40
38	m	117/124 (94%)	112 (96%)	5 (4%)	0	100	100
39	n	108/116 (93%)	96 (89%)	12 (11%)	0	100	100
40	o	113/119 (95%)	104 (92%)	9 (8%)	0	100	100
41	p	112/127 (88%)	111 (99%)	1 (1%)	0	100	100
42	q	97/100 (97%)	89 (92%)	8 (8%)	0	100	100
43	r	137/159 (86%)	128 (93%)	9 (7%)	0	100	100
44	s	90/237 (38%)	76 (84%)	14 (16%)	0	100	100
45	t	109/111 (98%)	101 (93%)	8 (7%)	0	100	100
46	u	84/104 (81%)	82 (98%)	2 (2%)	0	100	100
47	v	61/65 (94%)	59 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	w	96/111 (86%)	91 (95%)	5 (5%)	0	100	100
49	x	42/97 (43%)	31 (74%)	11 (26%)	0	100	100
50	y	54/57 (95%)	52 (96%)	1 (2%)	1 (2%)	6	32
51	z	48/53 (91%)	45 (94%)	3 (6%)	0	100	100
All	All	6567/7480 (88%)	6062 (92%)	499 (8%)	6 (0%)	49	83

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
22	R	81	LYS
22	R	82	GLN
32	g	32	MET
50	y	49	GLY
37	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	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%)	123 (100%)	0	100	100
12	H	111/115 (96%)	111 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	I	95/99 (96%)	95 (100%)	0	100	100
14	J	91/97 (94%)	91 (100%)	0	100	100
15	K	117/120 (98%)	113 (97%)	4 (3%)	32	54
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%)	122 (99%)	1 (1%)	73	80
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	s	82/208 (39%)	82 (100%)	0	100	100
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%)	45 (94%)	3 (6%)	16	37
51	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5730/6433 (89%)	5711 (100%)	19 (0%)	84	86

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	g	90	VAL
50	y	50	ASP
50	y	51	LEU
50	y	47	MET
32	g	43	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 99 such sidechains are listed below:

Mol	Chain	Res	Type
27	b	80	HIS
31	f	84	HIS
27	b	95	GLN
28	c	177	ASN
35	j	9	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	2875/2907 (98%)	844 (29%)	36 (1%)
53	4	103/108 (95%)	38 (36%)	3 (2%)
54	5	1490/1520 (98%)	392 (26%)	4 (0%)
55	7	75/76 (98%)	23 (30%)	3 (4%)
55	8	75/76 (98%)	23 (30%)	3 (4%)
All	All	4618/4687 (98%)	1320 (28%)	49 (1%)

5 of 1320 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	14	U
52	3	15	A
52	3	17	G
52	3	29	G
52	3	30	A

5 of 49 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	3	2668	A
52	3	2897	G
52	3	2764	U
52	3	2823	A
53	4	54	U

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

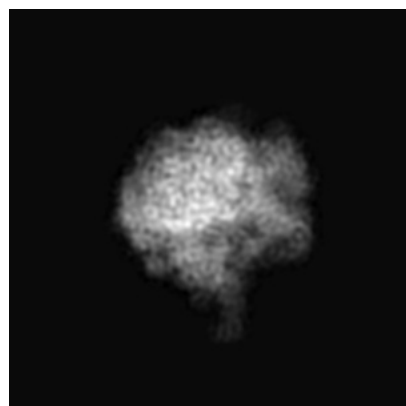
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13281. These allow visual inspection of the internal detail of the map and identification of artifacts.

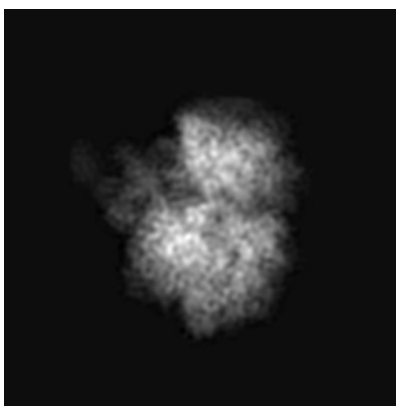
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

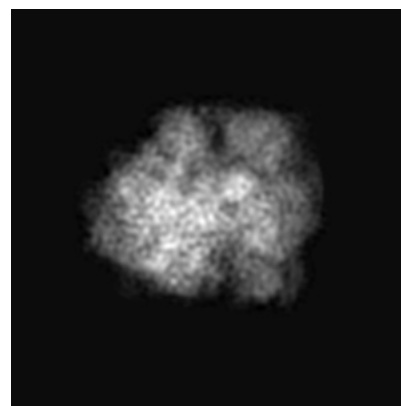
6.1.1 Primary map



X

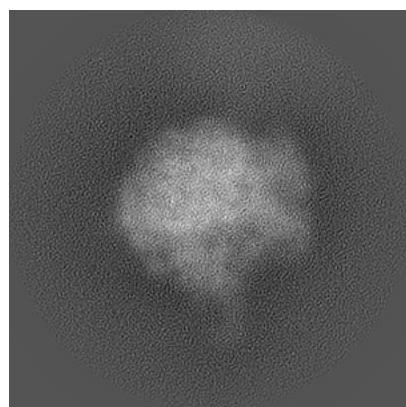


Y

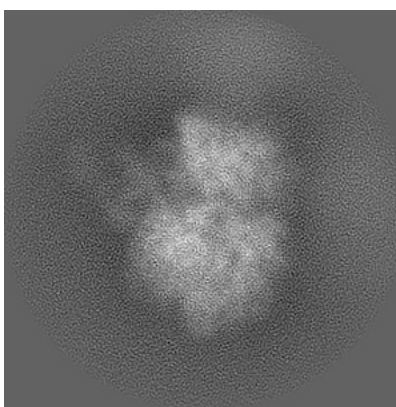


Z

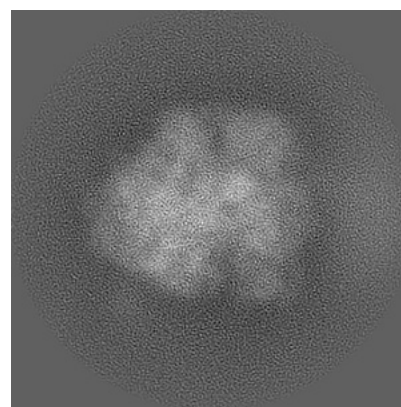
6.1.2 Raw map



X



Y

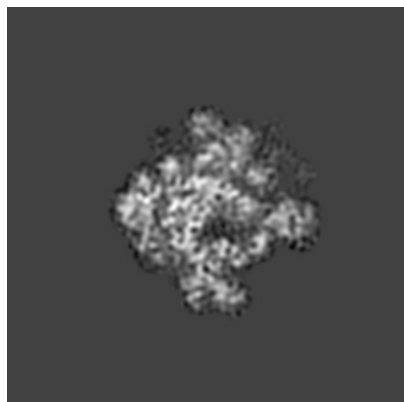


Z

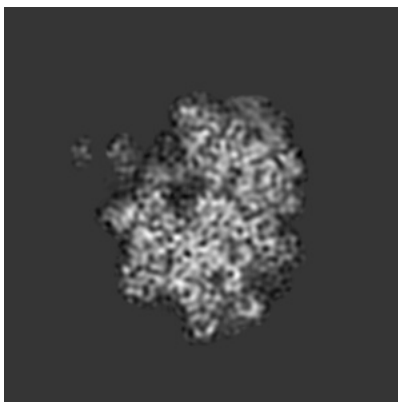
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

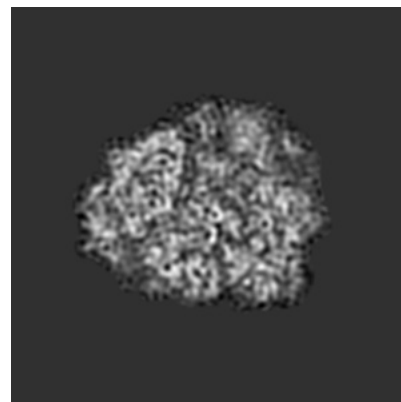
6.2.1 Primary map



X Index: 128

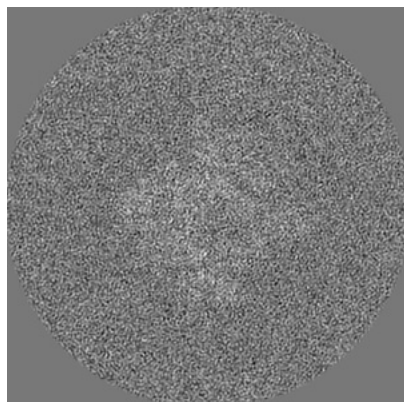


Y Index: 128

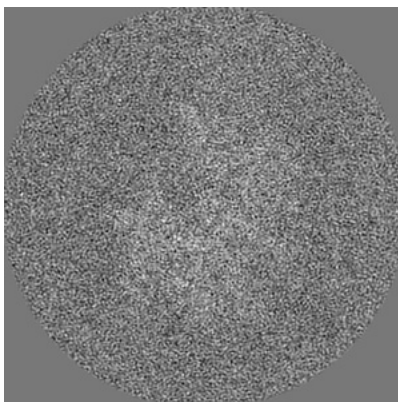


Z Index: 128

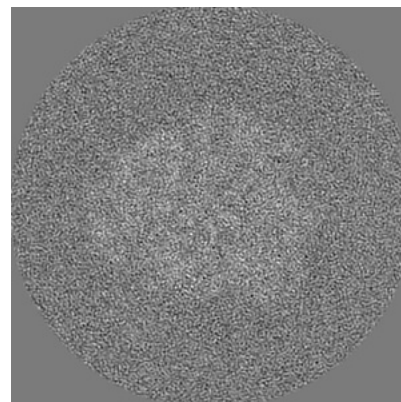
6.2.2 Raw map



X Index: 128



Y Index: 128

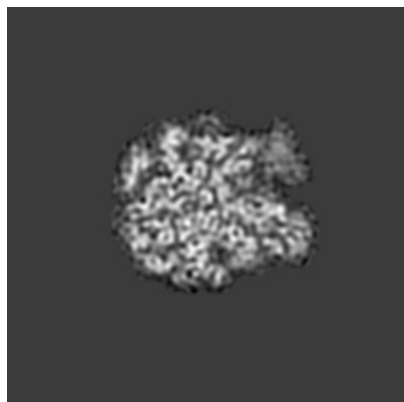


Z Index: 128

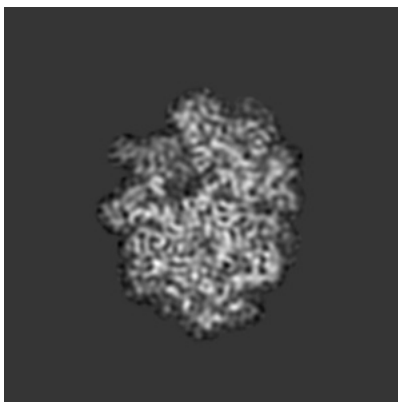
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

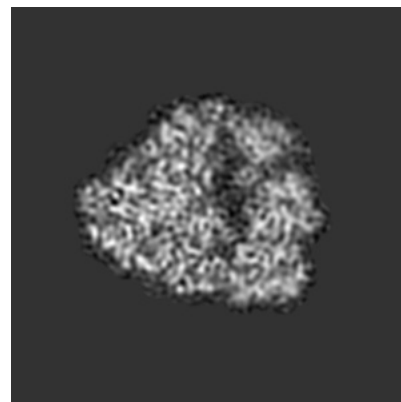
6.3.1 Primary map



X Index: 104

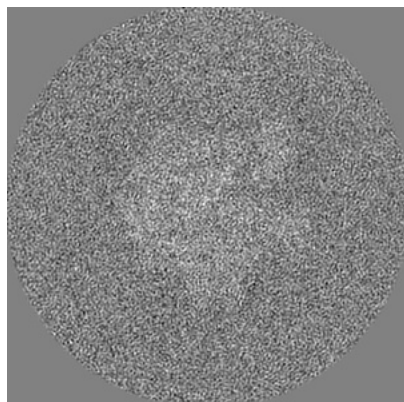


Y Index: 120

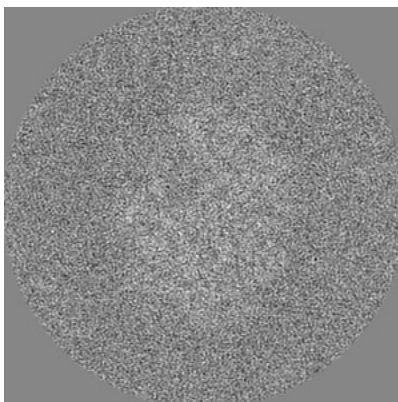


Z Index: 122

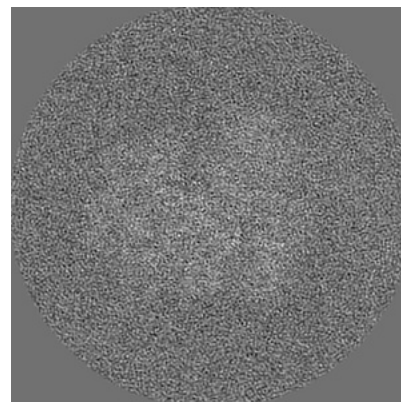
6.3.2 Raw map



X Index: 120



Y Index: 122

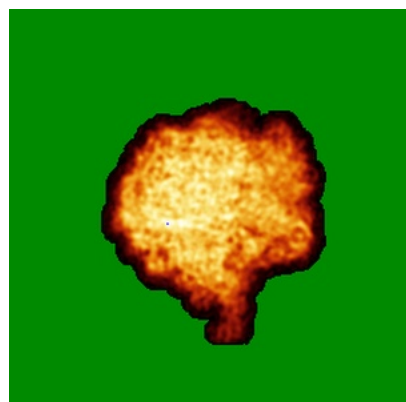


Z Index: 133

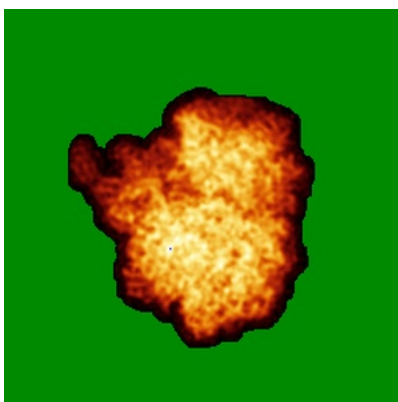
The images above show the largest variance slices of the map in three orthogonal directions.

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

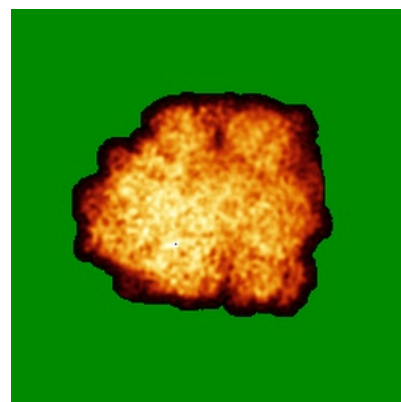
6.4.1 Primary map



X

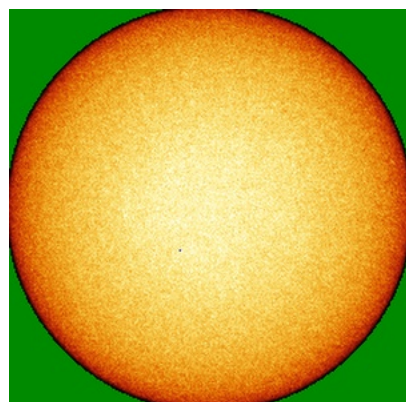


Y

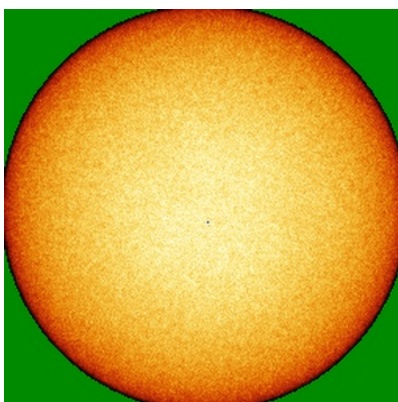


Z

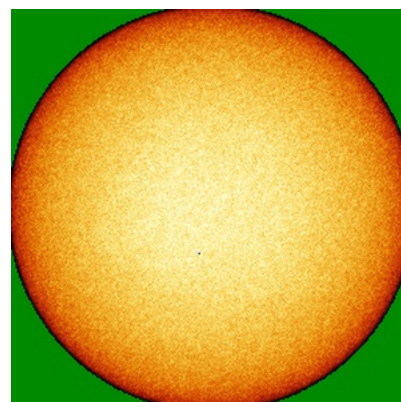
6.4.2 Raw map



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.

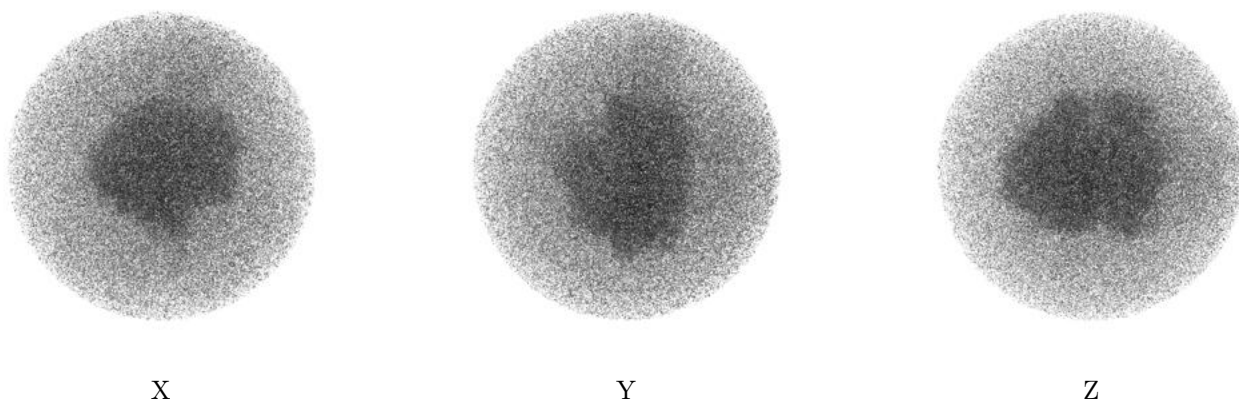
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. 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



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.

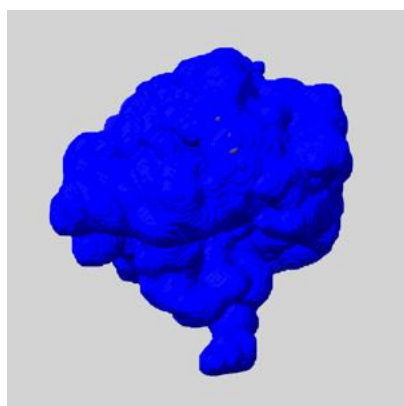
6.6 Mask visualisation [i](#)

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

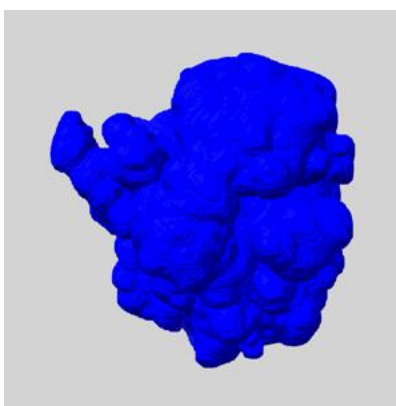
A mask typically either:

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

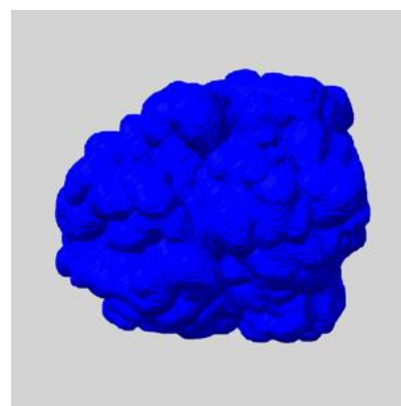
6.6.1 emd_13281_msk_1.map [i](#)



X



Y

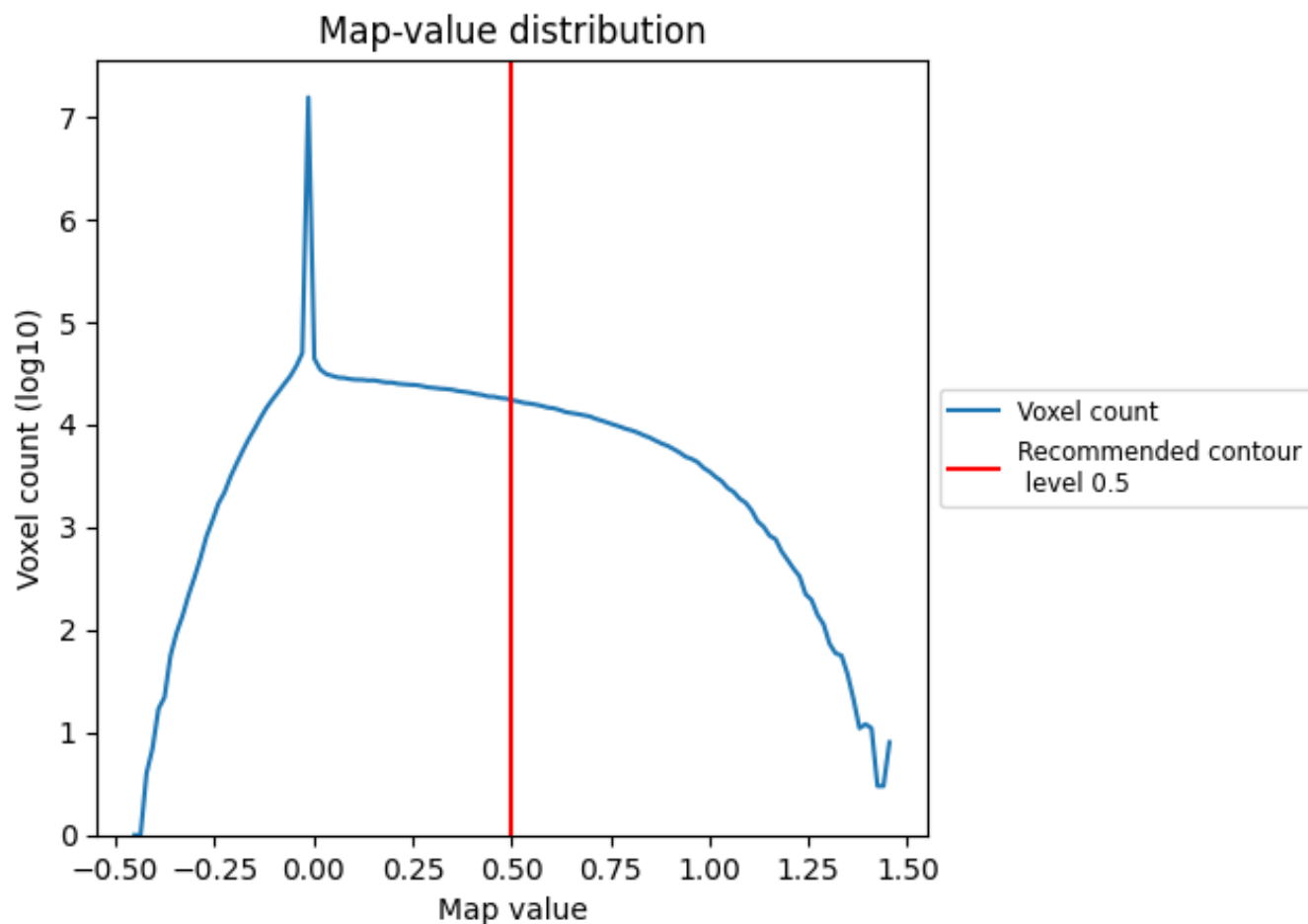


Z

7 Map analysis [i](#)

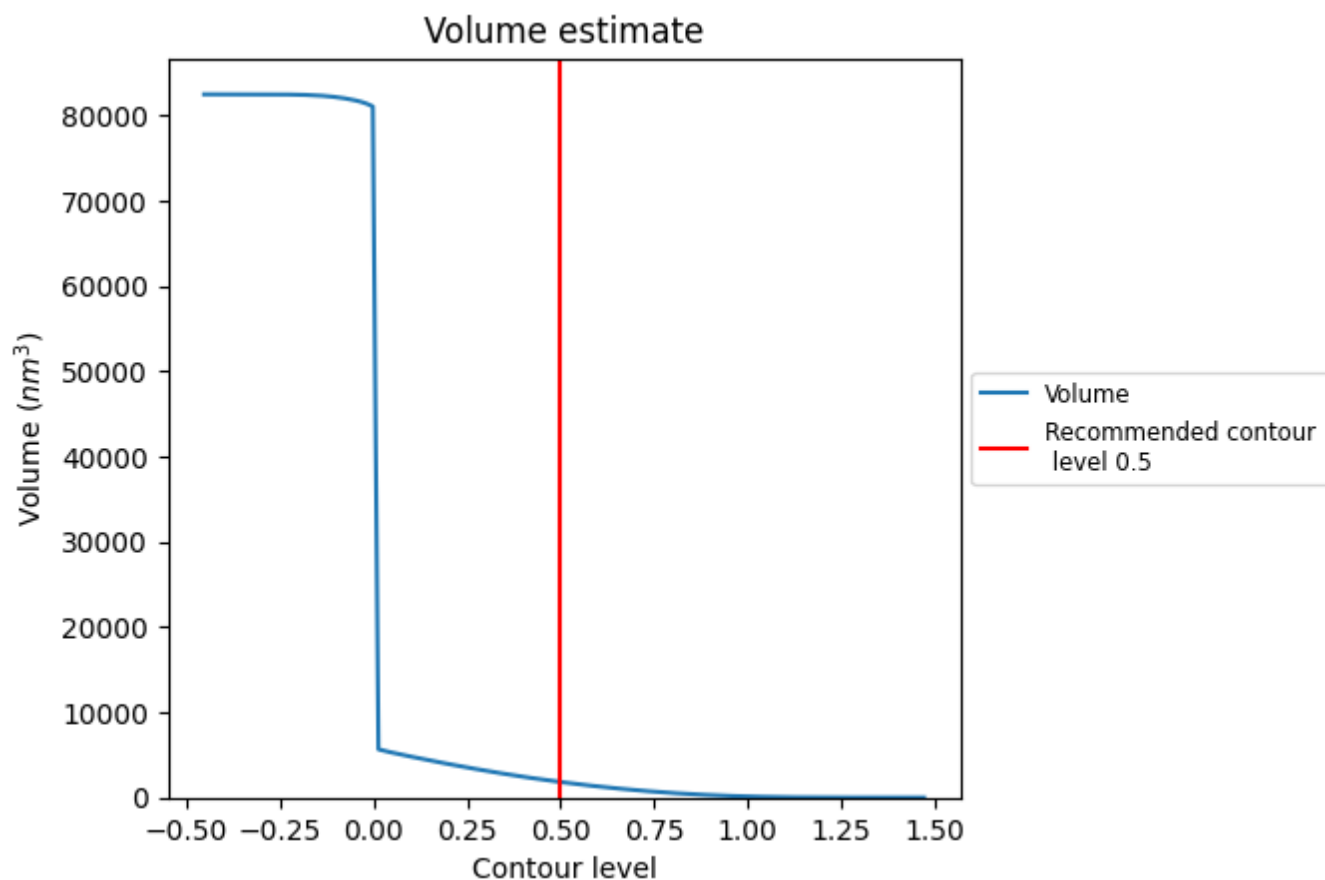
This section contains the results of statistical analysis of the map.

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.

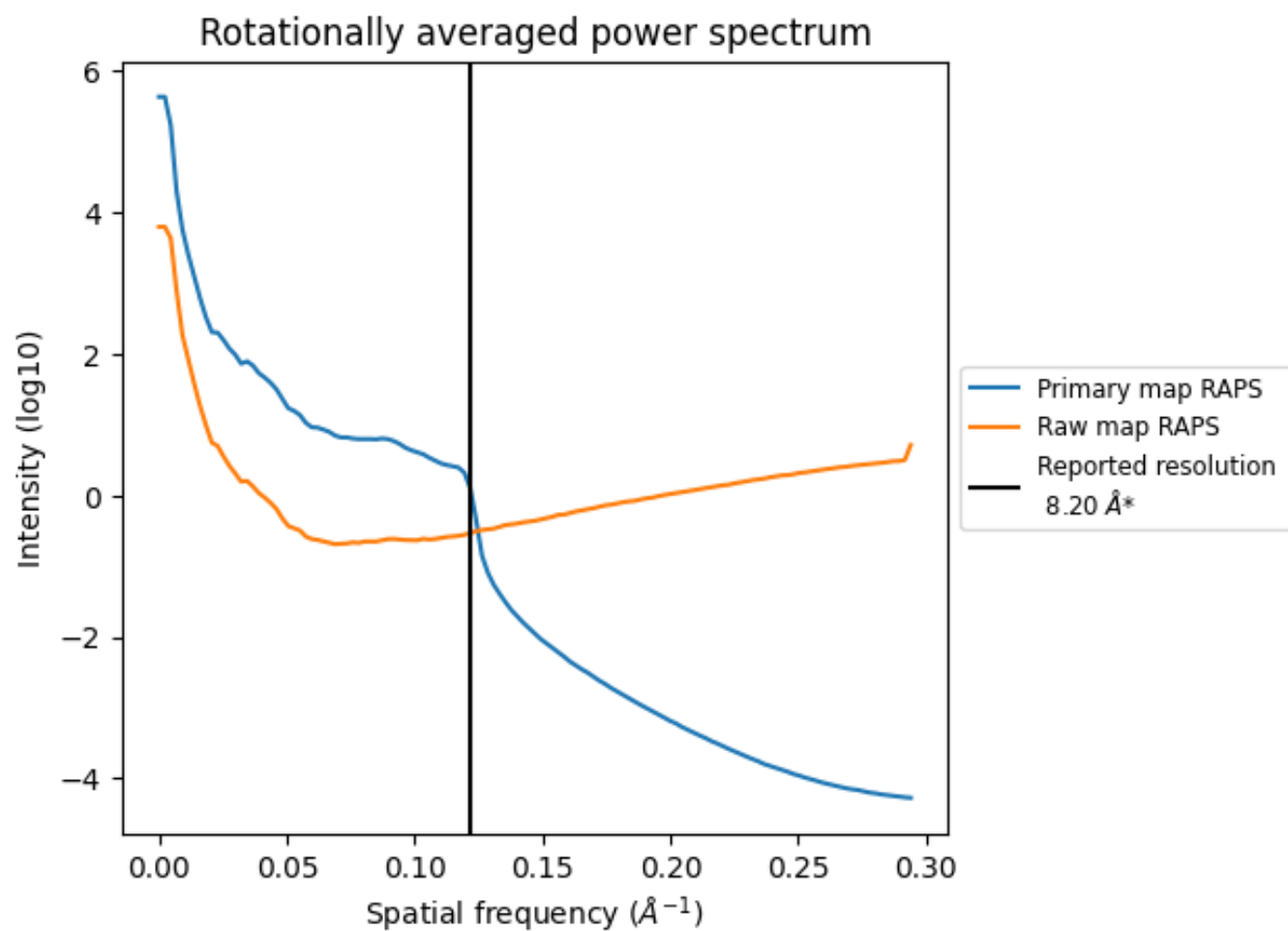
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1826 nm³; this corresponds to an approximate mass of 1649 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 ⓘ

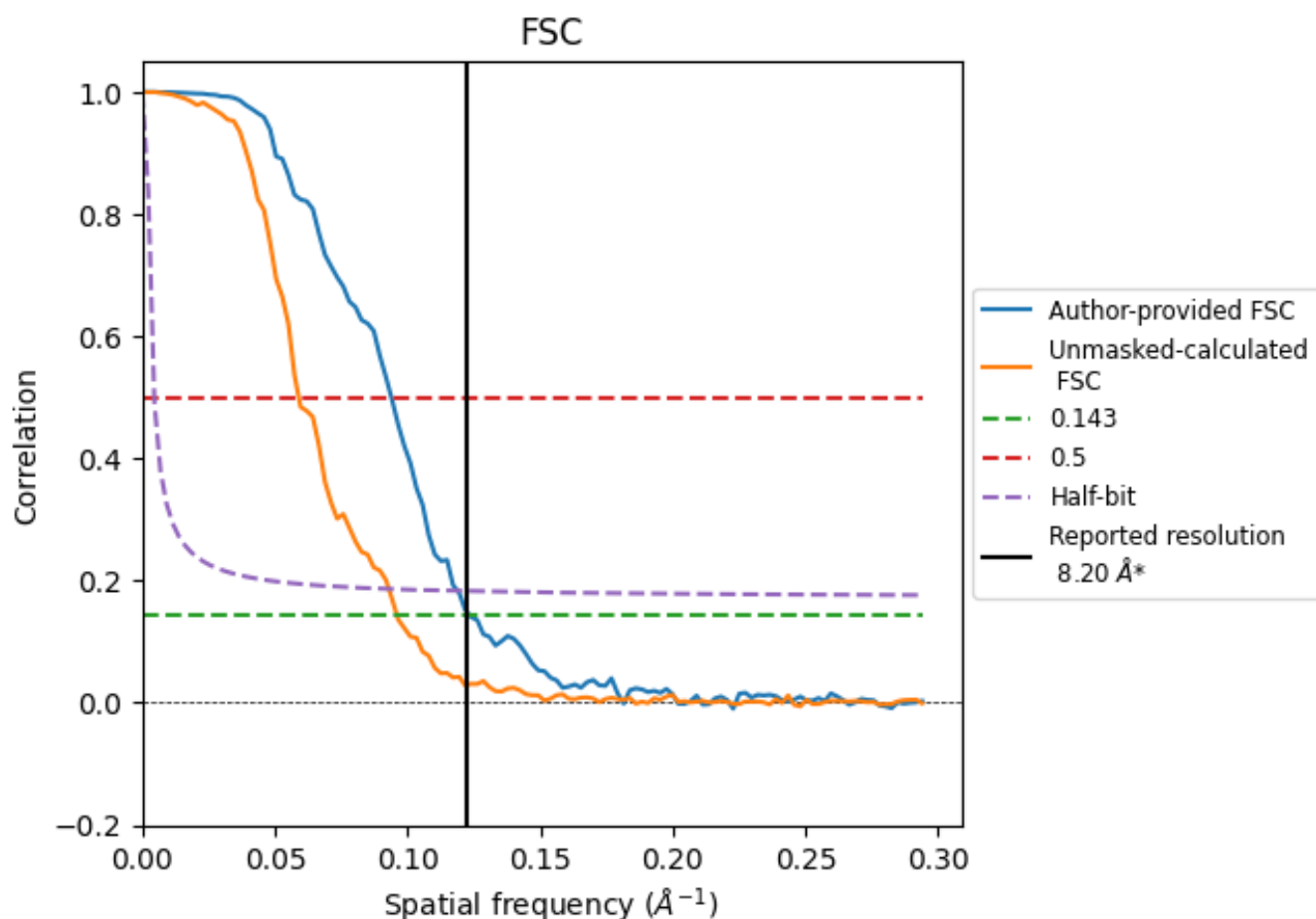


*Reported resolution corresponds to spatial frequency of 0.122 $\text{\AA}^{-1}$

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 0.122 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

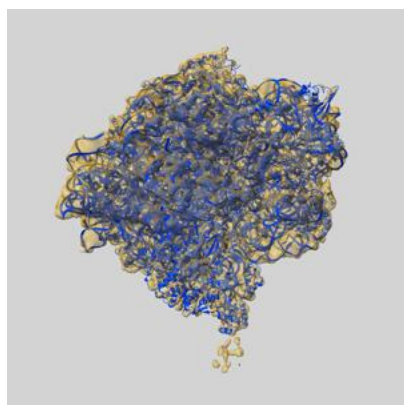
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.20	-	-
Author-provided FSC curve	8.10	10.65	8.40
Unmasked-calculated*	10.42	16.95	10.75

*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 10.42 differs from the reported value 8.2 by more than 10 %

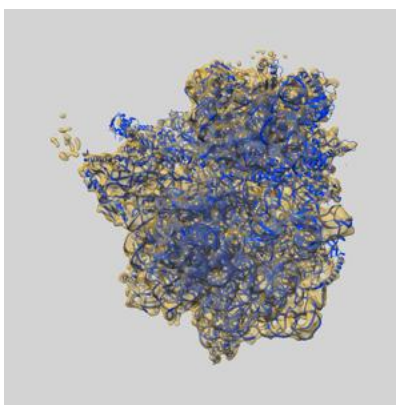
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13281 and PDB model 7PAR. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

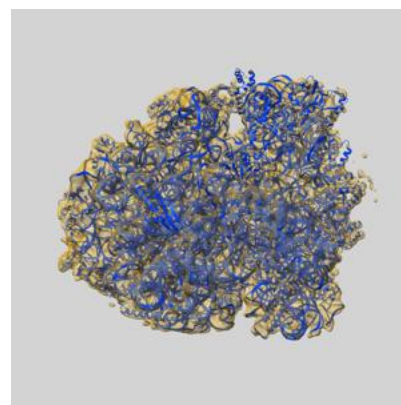
9.1 Map-model overlay [i](#)



X



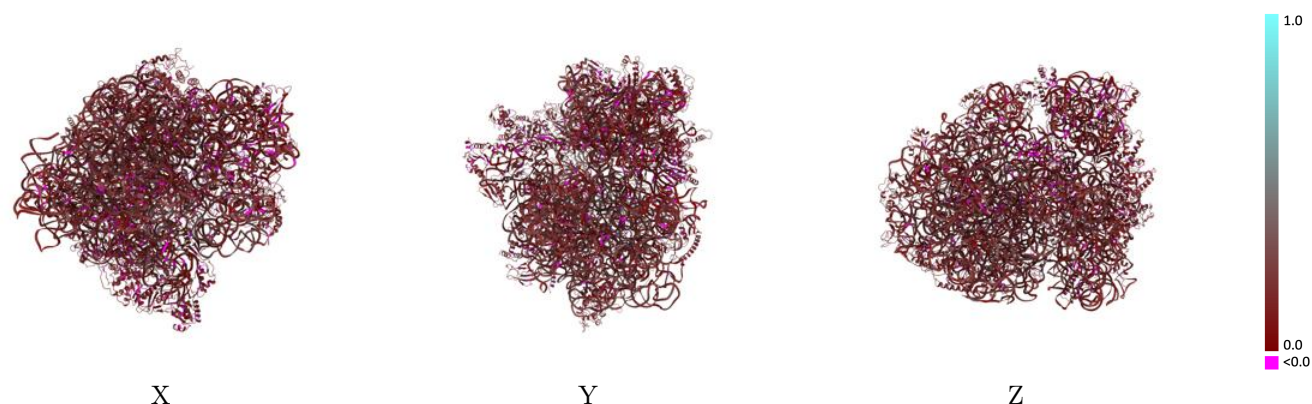
Y



Z

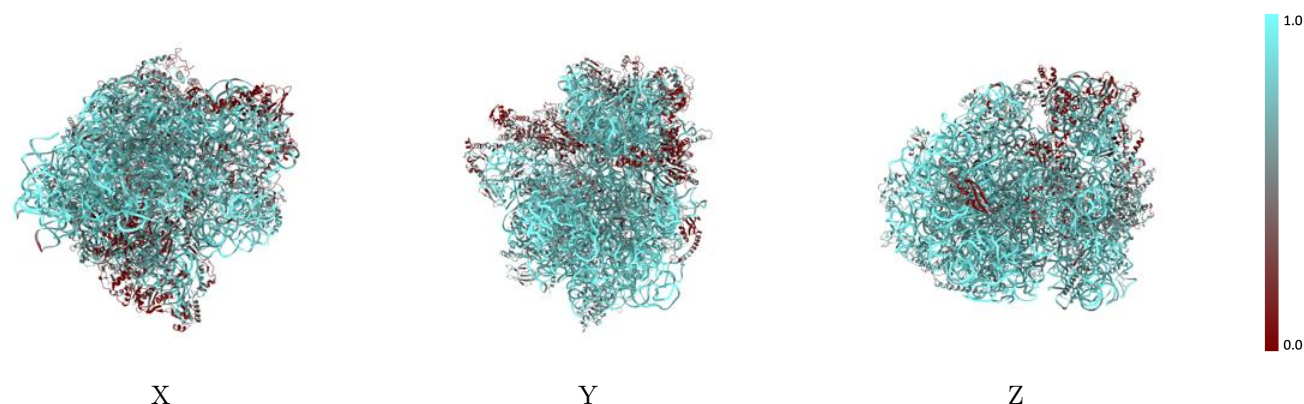
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



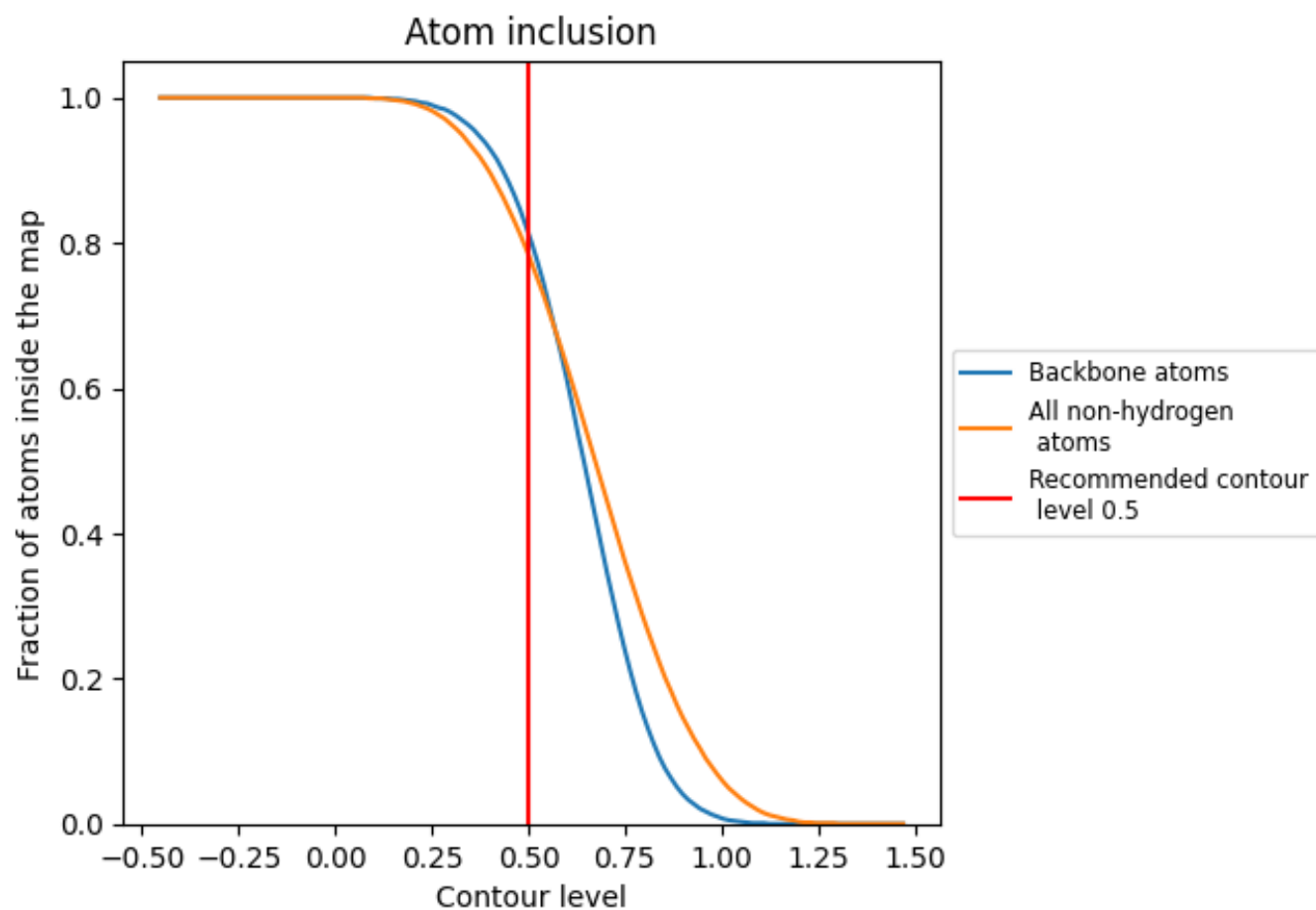
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 78% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7850	 0.1740
0	 0.7510	 0.1490
1	 0.7100	 0.1560
2	 0.6150	 0.1280
3	 0.9390	 0.1920
4	 0.9390	 0.1940
5	 0.8980	 0.1750
7	 0.8500	 0.1720
8	 0.6720	 0.1280
9	 0.2760	 0.1460
A	 0.4860	 0.1740
B	 0.5510	 0.1620
C	 0.5660	 0.1500
D	 0.5660	 0.1560
E	 0.3950	 0.1580
F	 0.1320	 0.1380
G	 0.5630	 0.1500
H	 0.3030	 0.1210
I	 0.4390	 0.1390
J	 0.4030	 0.1040
K	 0.5730	 0.1570
L	 0.2310	 0.1350
M	 0.7470	 0.1130
N	 0.6060	 0.1710
O	 0.7080	 0.1660
P	 0.5950	 0.1440
Q	 0.5250	 0.1320
R	 0.5400	 0.1240
S	 0.6850	 0.1650
T	 0.5360	 0.1690
W	 0.0470	 0.1360
a	 0.6830	 0.1460
b	 0.6330	 0.1510
c	 0.6540	 0.1660
d	 0.6130	 0.1600



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Chain	Atom inclusion	Q-score
e	 0.5420	 0.1710
f	 0.2320	 0.1580
g	 0.4480	 0.1460
h	 0.4330	 0.1560
i	 0.6660	 0.1640
j	 0.5510	 0.1670
k	 0.6910	 0.1610
l	 0.6730	 0.1550
m	 0.6740	 0.1570
n	 0.6600	 0.1590
o	 0.6320	 0.1850
p	 0.7000	 0.1420
q	 0.6470	 0.1610
r	 0.6900	 0.1610
s	 0.6330	 0.1670
t	 0.5490	 0.1470
u	 0.6580	 0.1380
v	 0.6480	 0.1260
w	 0.6450	 0.1860
x	 0.5160	 0.1510
y	 0.6570	 0.1430
z	 0.6120	 0.1600