



wwPDB EM Validation Summary Report ⓘ

Sep 16, 2026 – 03:07 pm BST

PDB ID : 9SL7 / pdb_00009sl7
EMDB ID : EMD-53676
Title : Model of M. pneumoniae 70S transertion-like (stable RNAP)
Authors : Dobbs, J.M.; Mahamid, J.
Deposited on : 2025-09-03
Resolution : 26.70 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

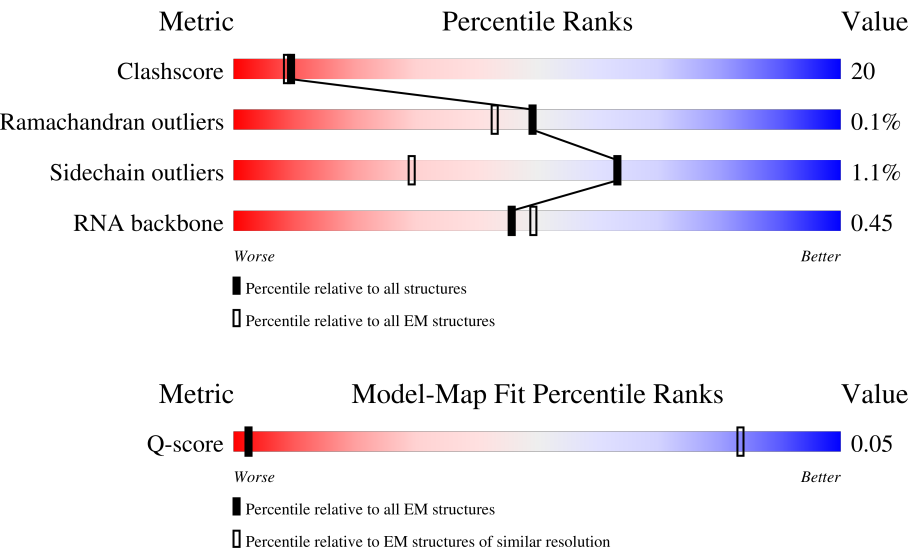
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 26.70 Å.

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



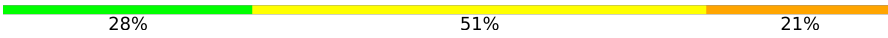
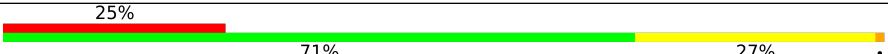
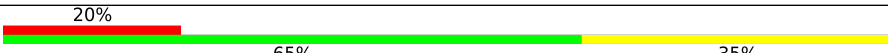
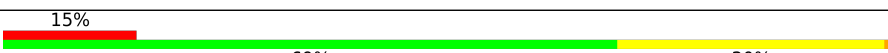
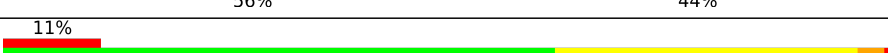
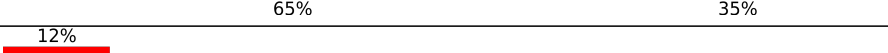
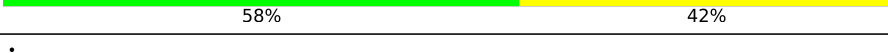
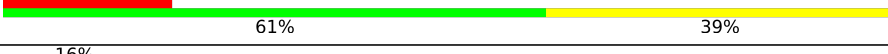
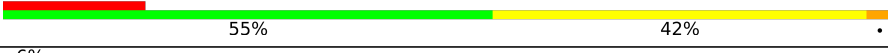
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	6 (26.50 - 27.20)

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

Mol	Chain	Length	Quality of chain
1	0	47	
2	1	59	
3	2	37	

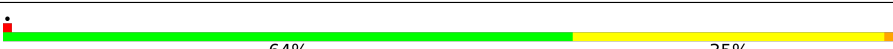
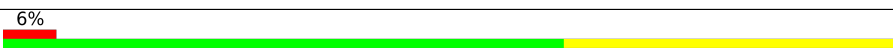
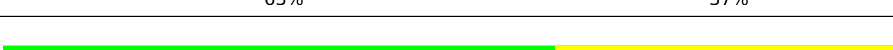
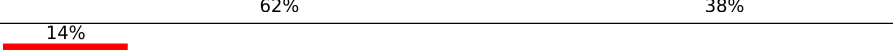
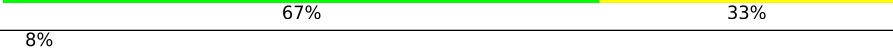
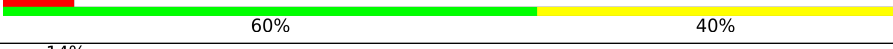
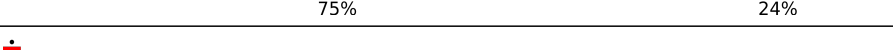
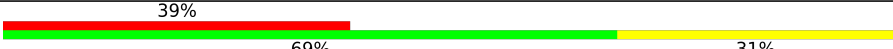
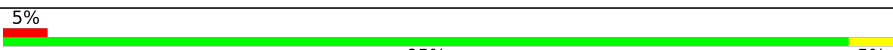
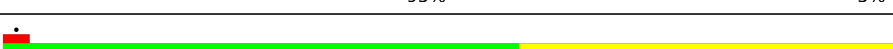
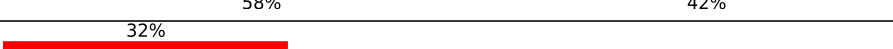
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Mol	Chain	Length	Quality of chain
4	3	2878	
5	4	105	
6	5	1493	
7	6	327	
7	AB	327	
8	7	76	
9	8	944	
10	9	1391	
11	A	240	
12	AA	89	
13	AC	366	
14	AD	32	
15	AE	32	
16	AF	160	
17	B	215	
18	C	203	
19	D	153	
20	E	167	
21	F	154	
22	G	141	
23	H	128	
24	I	101	
25	J	114	
26	K	136	
27	L	118	

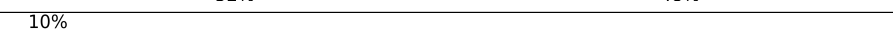
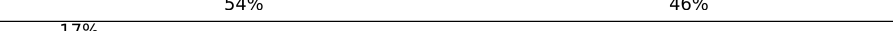
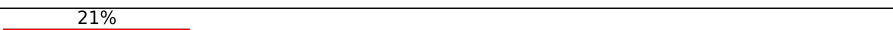
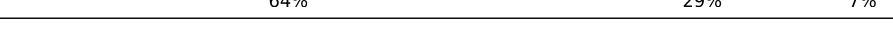
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Mol	Chain	Length	Quality of chain
28	M	60	
29	N	83	
30	O	80	
31	P	83	
32	Q	65	
33	R	84	
34	S	77	
35	T	53	
36	U	161	
37	V	29	
37	W	29	
37	X	29	
37	Y	29	
38	Z	1276	
39	a	285	
40	b	229	
41	c	210	
42	d	175	
43	e	176	
44	f	145	
45	h	128	
46	i	144	
47	j	122	
48	k	148	
49	l	136	

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Mol	Chain	Length	Quality of chain
50	m	119	 58% 42%
51	n	116	 69% 28%
52	o	115	 54% 46%
53	p	114	 52% 48%
54	q	99	 54% 46%
55	r	139	 53% 47%
56	s	92	 65% 35%
57	t	111	 71% 29%
58	u	86	 69% 31%
59	v	63	 46% 54%
60	w	108	 64% 29% 7%
61	x	44	 82% 18%
62	y	56	 64% 30% 5%
63	z	50	 62% 38%

2 Entry composition

There are 63 unique types of molecules in this entry. The entry contains 184921 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 Large ribosomal subunit protein bL34.

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 RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 6 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

- Molecule 7 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	308	Total	C	N	O	S	0	0
			2421	1550	407	454	10		
7	AB	312	Total	C	N	O	S	0	0
			2452	1571	412	459	10		

- Molecule 8 is a RNA chain called tRNA-Phe.

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

- Molecule 9 is a protein called SecDF.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	8	899	Total	C	N	O	S	0	0
			7063	4595	1165	1293	10		

- Molecule 10 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	9	1391	Total	C	N	O	S	0	0
			10948	6905	1892	2114	37		

- Molecule 11 is a protein called Small ribosomal subunit protein uS2.

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

- Molecule 12 is a protein called Probable DNA-directed RNA polymerase subunit delta.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AA	89	Total	C	N	O	S	0	0
			770	505	122	140	3		

- Molecule 13 is a protein called Transcription termination/antitermination protein NusA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AC	366	Total	C	N	O	S	0	0
			2884	1834	479	562	9		

- Molecule 14 is a DNA chain called DNA chain A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AD	32	Total	C	N	O	P	0	0
			663	317	124	190	32		

- Molecule 15 is a DNA chain called DNA chain B.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AE	32	Total	C	N	O	P	0	0
			649	313	110	194	32		

- Molecule 16 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AF	160	Total	C	N	O	S	0	0
			1277	821	220	233	3		

- Molecule 17 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 18 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 19 is a protein called Small ribosomal subunit protein uS5.

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

- Molecule 20 is a protein called Small ribosomal subunit protein bS6.

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

- Molecule 21 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 22 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 23 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 24 is a protein called Small ribosomal subunit protein uS10.

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

- Molecule 25 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 26 is a protein called Small ribosomal subunit protein uS12.

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

- Molecule 27 is a protein called Small ribosomal subunit protein uS13.

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

- Molecule 28 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 29 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 30 is a protein called Small ribosomal subunit protein bS16.

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

- Molecule 31 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 32 is a protein called Small ribosomal subunit protein bS18.

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

- Molecule 33 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 34 is a protein called Small ribosomal subunit protein bS20.

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

- Molecule 35 is a protein called Small ribosomal subunit protein bS21.

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

- Molecule 36 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	U	161	Total	C	N	O	S	0	0
			1239	796	213	225	5		

- Molecule 37 is a protein called Large ribosomal subunit protein bL12.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	V	29	Total	C	N	O	S	0	0
			232	146	34	50	2		
37	W	29	Total	C	N	O	S	0	0
			232	146	34	50	2		
37	X	29	Total	C	N	O	S	0	0
			232	146	34	50	2		
37	Y	29	Total	C	N	O	S	0	0
			232	146	34	50	2		

- Molecule 38 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Z	1276	Total	C	N	O	S	0	0
			10085	6431	1752	1872	30		

- Molecule 39 is a protein called Large ribosomal subunit protein uL2.

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

- Molecule 40 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 41 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 42 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 43 is a protein called Large ribosomal subunit protein uL6.

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

- Molecule 44 is a protein called Large ribosomal subunit protein bL9.

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

- Molecule 45 is a protein called Large ribosomal subunit protein uL11.

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

- Molecule 46 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 47 is a protein called 50S ribosomal protein L14.

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

- Molecule 48 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 49 is a protein called Large ribosomal subunit protein uL16.

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

- Molecule 50 is a protein called Large ribosomal subunit protein bL17.

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

- Molecule 51 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 52 is a protein called Large ribosomal subunit protein bL19.

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

- Molecule 53 is a protein called Large ribosomal subunit protein bL20.

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

- Molecule 54 is a protein called Large ribosomal subunit protein bL21.

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

- Molecule 55 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 56 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 57 is a protein called 50S ribosomal protein L24.

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

- Molecule 58 is a protein called Large ribosomal subunit protein bL27.

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

- Molecule 59 is a protein called Large ribosomal subunit protein bL28.

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

- Molecule 60 is a protein called Large ribosomal subunit protein uL29.

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

- Molecule 61 is a protein called Large ribosomal subunit protein bL31.

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

- Molecule 62 is a protein called Large ribosomal subunit protein bL32.

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

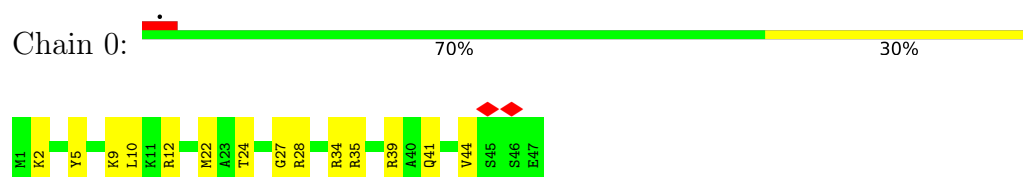
- Molecule 63 is a protein called Large ribosomal subunit protein bL33A.

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

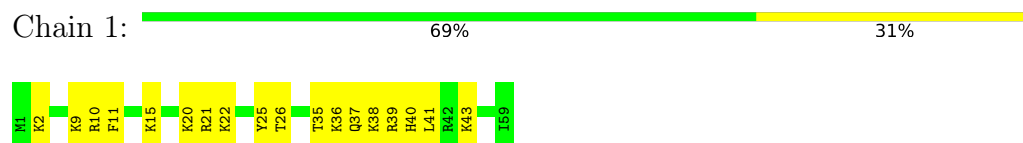
3 Residue-property plots

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.

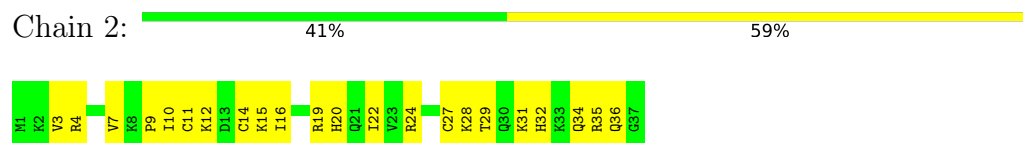
- Molecule 1: Large ribosomal subunit protein bL34



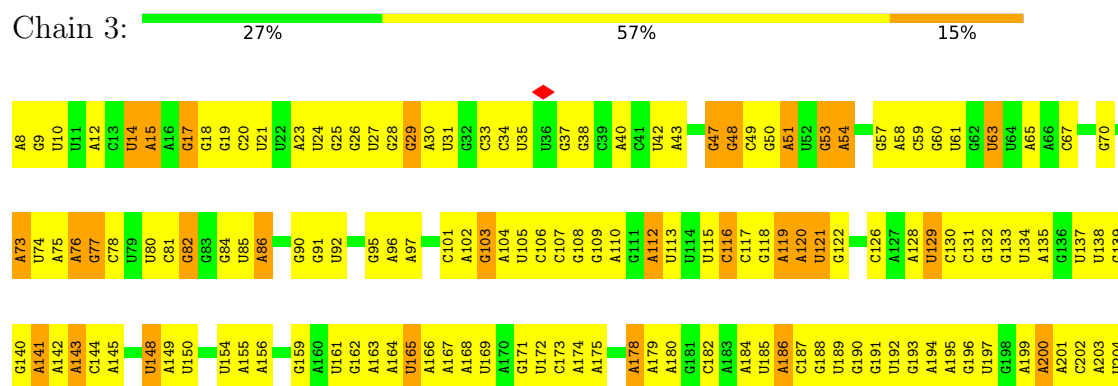
- Molecule 2: 50S ribosomal protein L35



- Molecule 3: 50S ribosomal protein L36

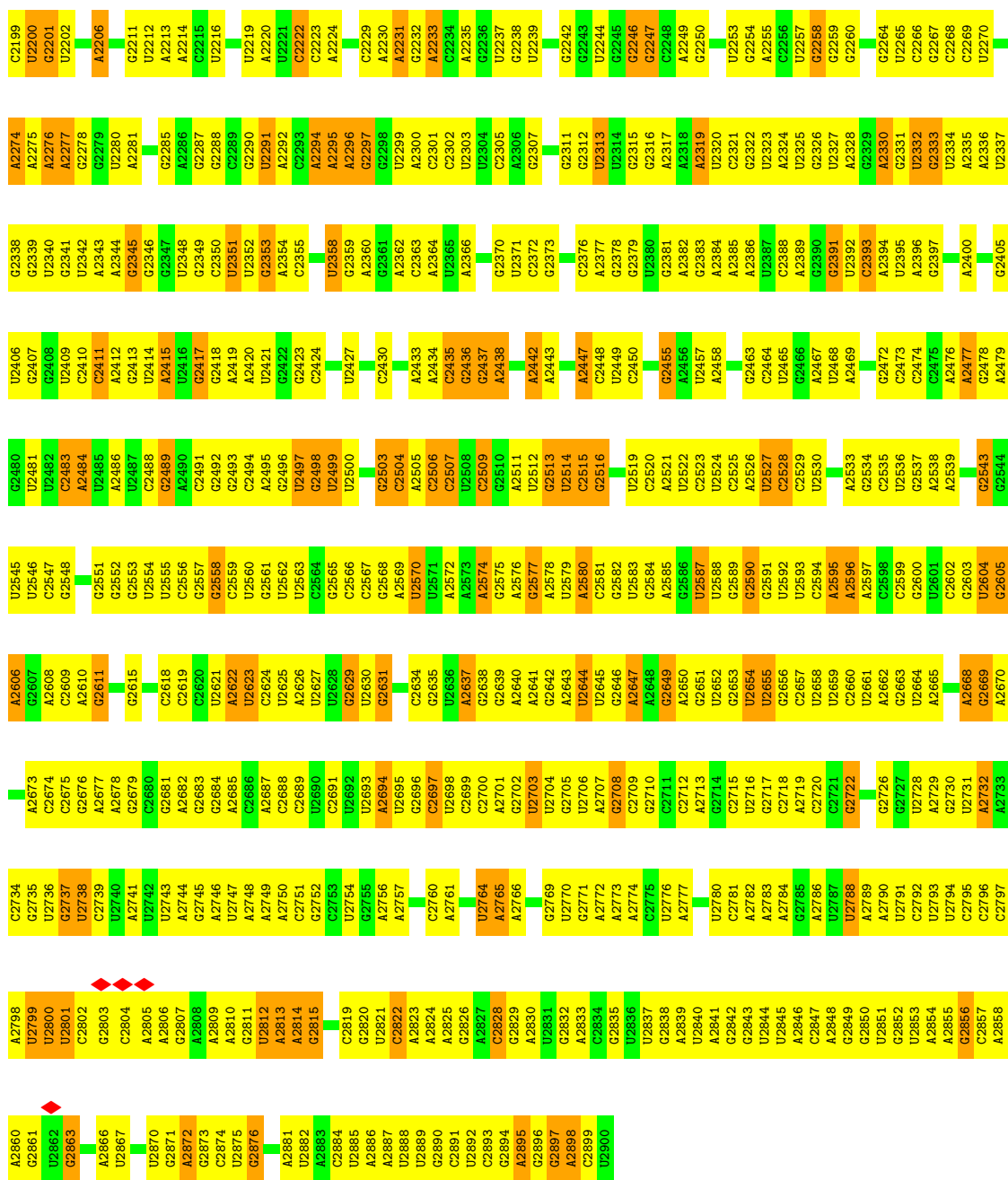


- Molecule 4: 23S ribosomal RNA



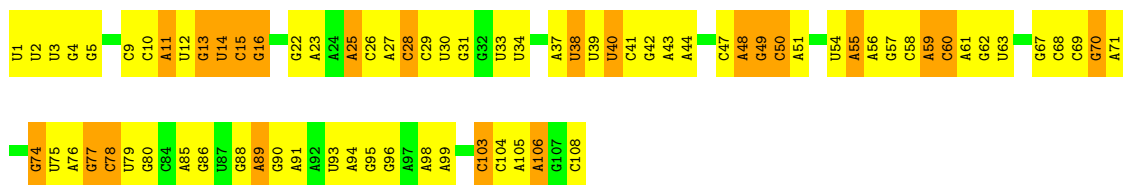
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G1155	C1086	C1021	U952	A877	G816	U744	A680	U546	G482	G413	A345	A276	G209
C1156	C1087	C1022	G953	A878	A816	U745	A681	A547	A483		G346	G347	U210
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C1176	U1108	C1043	C980	G904	A839	G768	U700	C570	A299	G437	C369	A299	C229
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A1208	G1142	G1075	A1009	A940	A864	A799	G730	G530	C394	A464	A394	G329	G254
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G1215	C1149	A1082	A1017	A948	C872	U808	U739	U539	G476		U407	G338	A269
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											G410	G342	G272

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		C1342	A1412	A1480	G1553	C1633	C1706	A1769	A1836	G1913	C1990	A2061	G2122	
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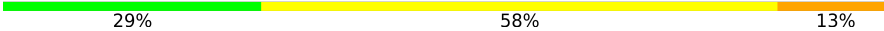


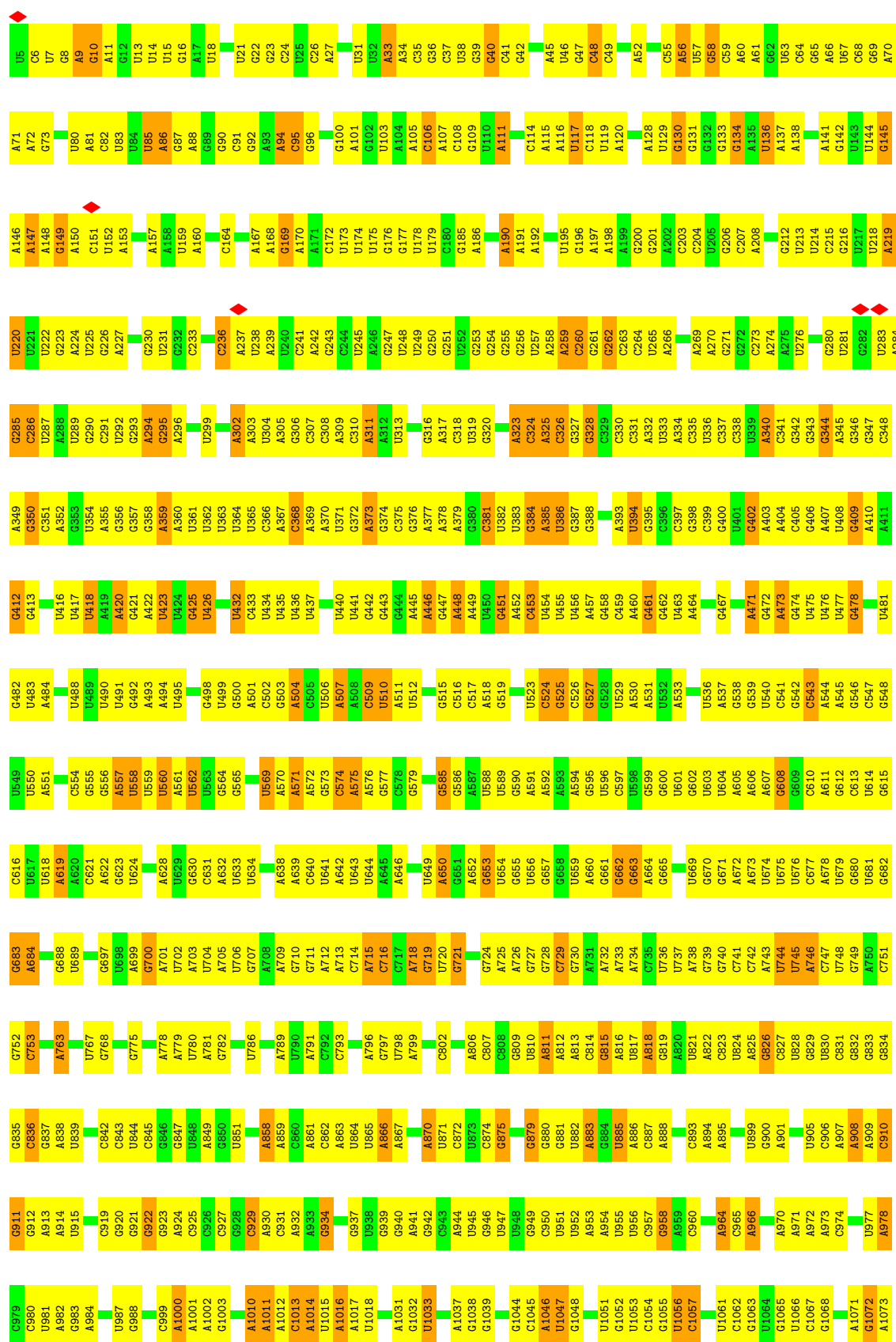
• Molecule 5: 5S ribosomal RNA

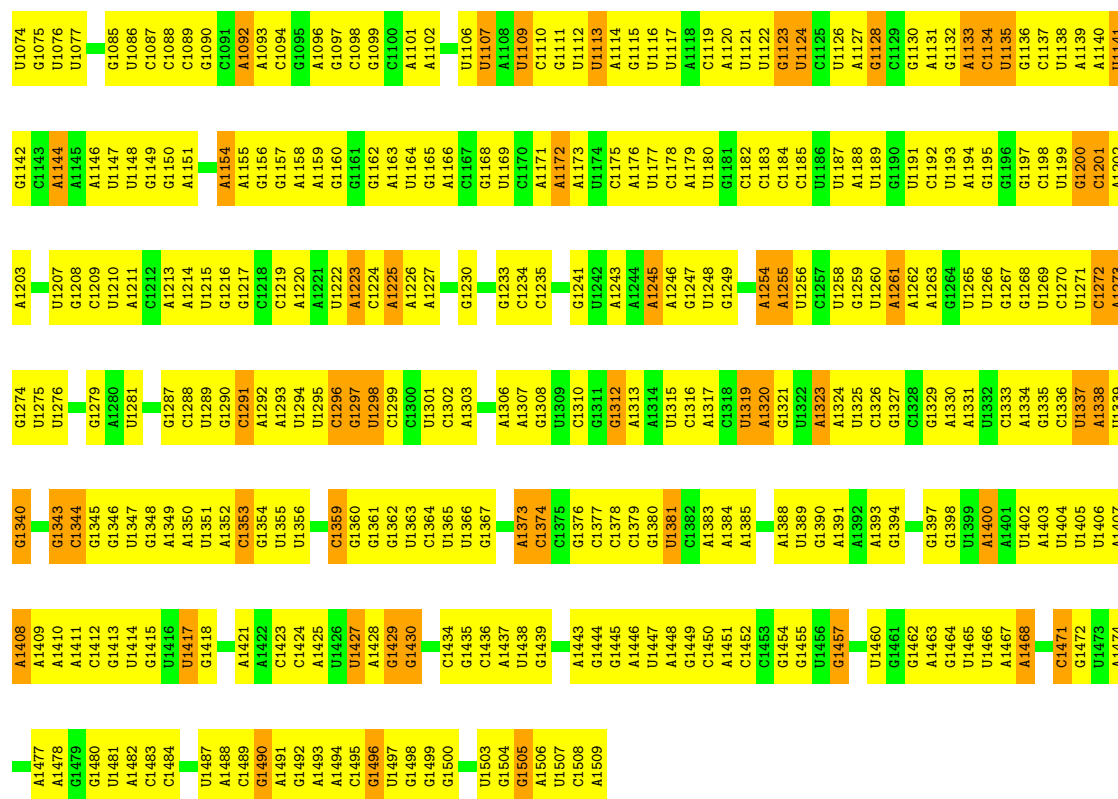
Chain 4: 28% 51% 21%



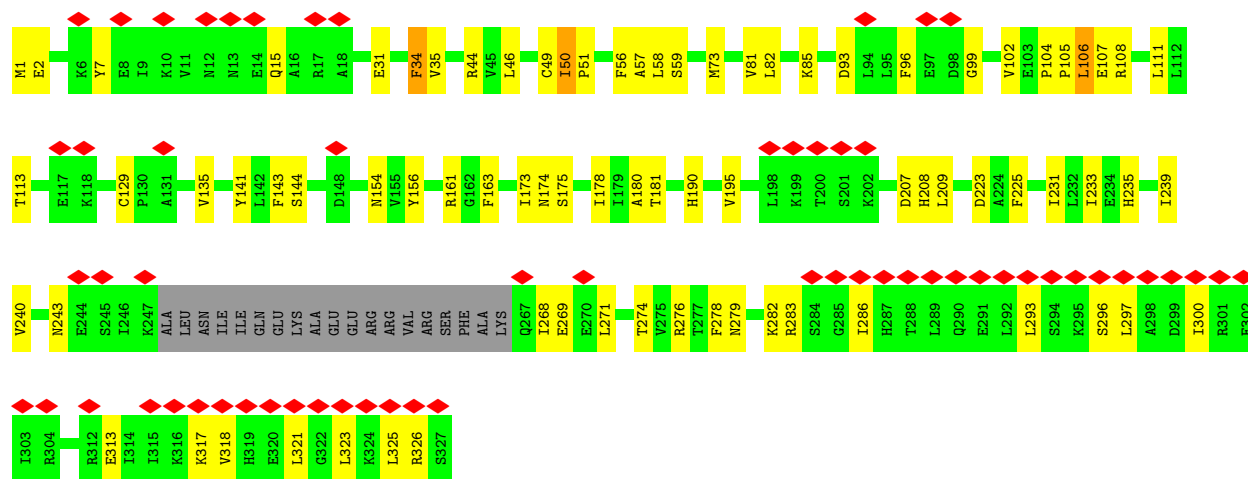
• Molecule 6: 16S ribosomal RNA

Chain 5:  29% 58% 13%



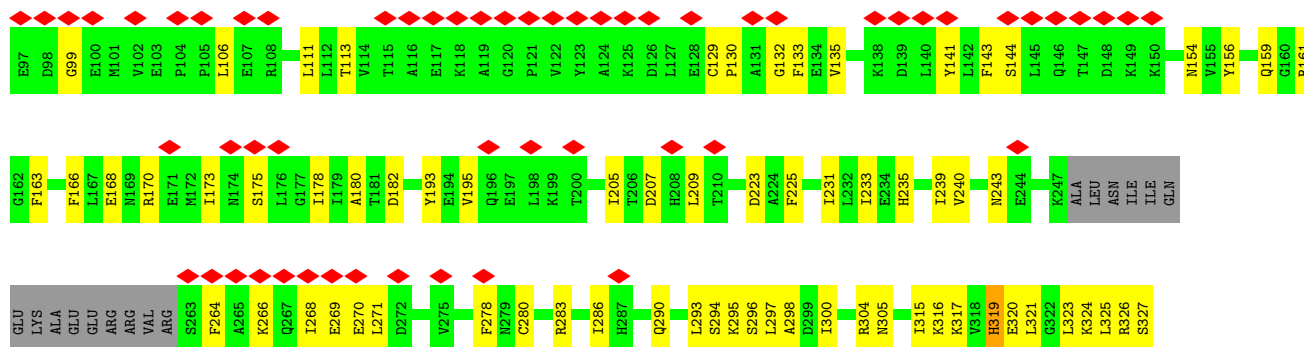


• Molecule 7: DNA-directed RNA polymerase subunit alpha

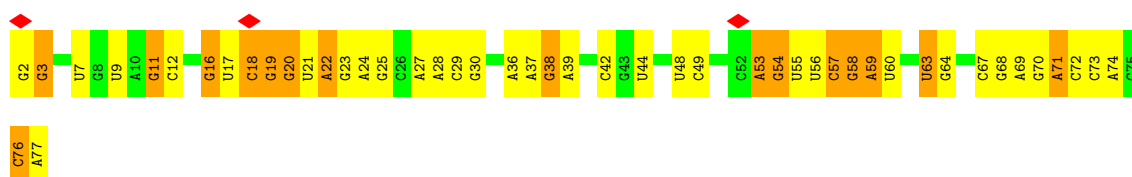


• Molecule 7: DNA-directed RNA polymerase subunit alpha

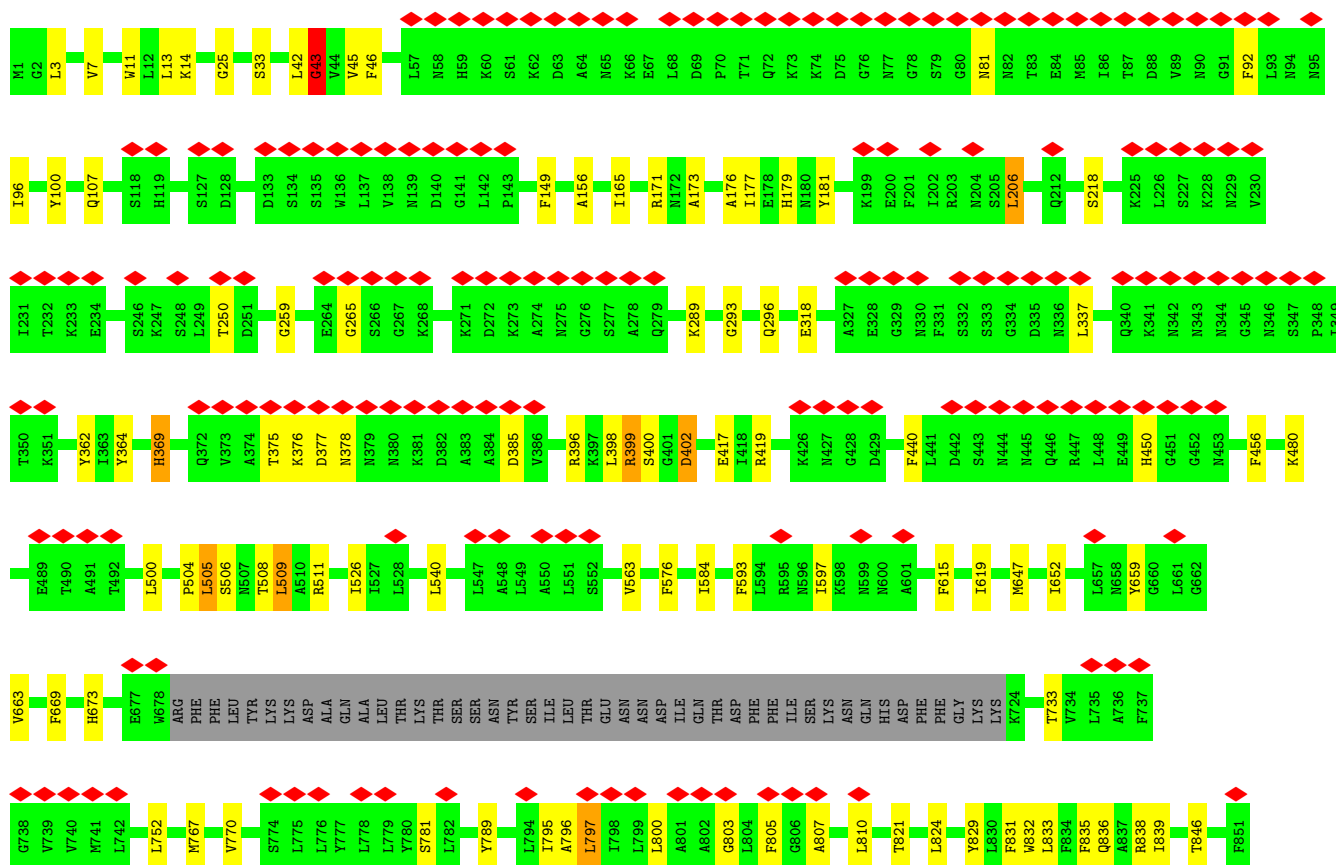
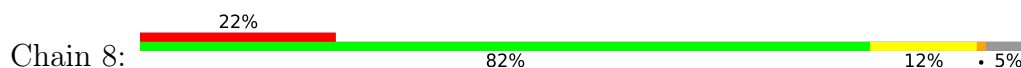


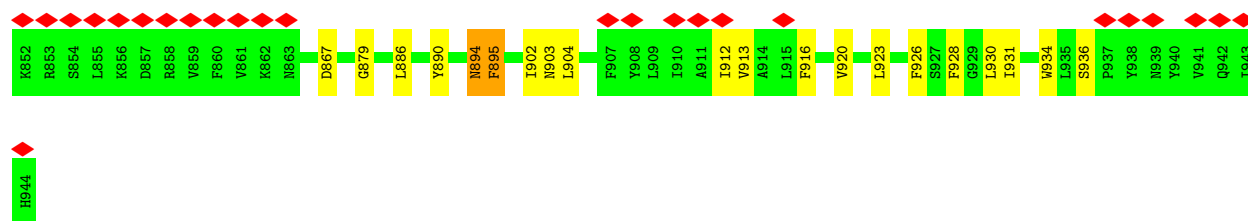


• Molecule 8: tRNA-Phe

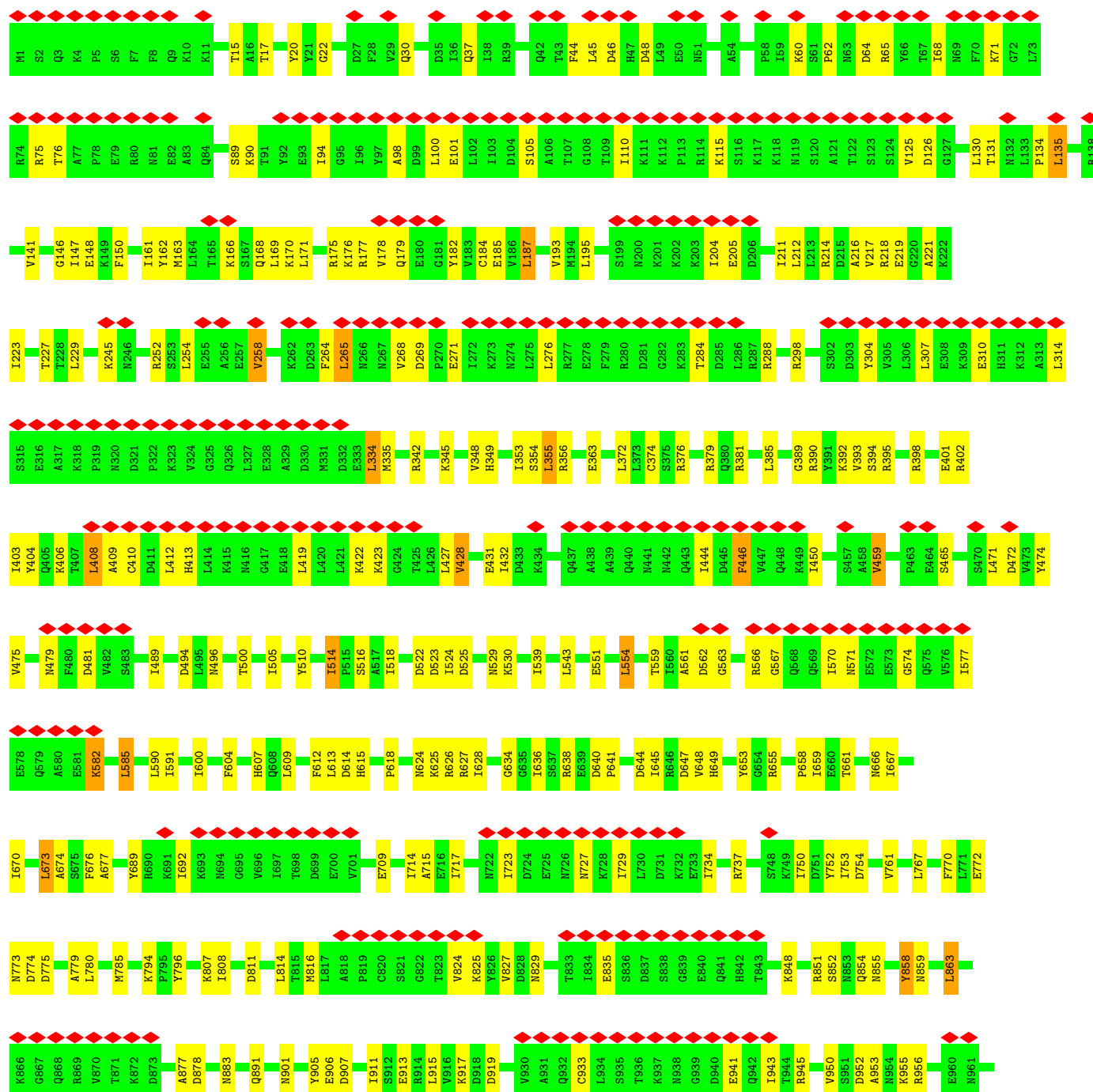
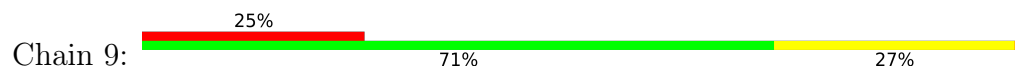


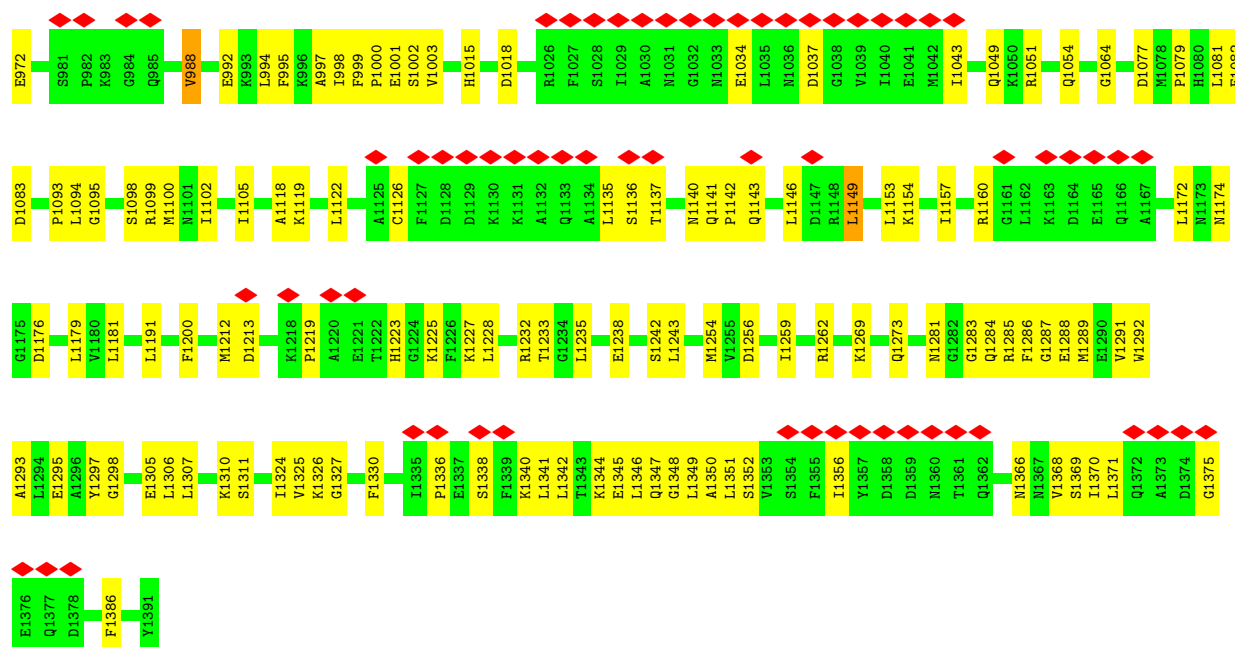
• Molecule 9: SecDF



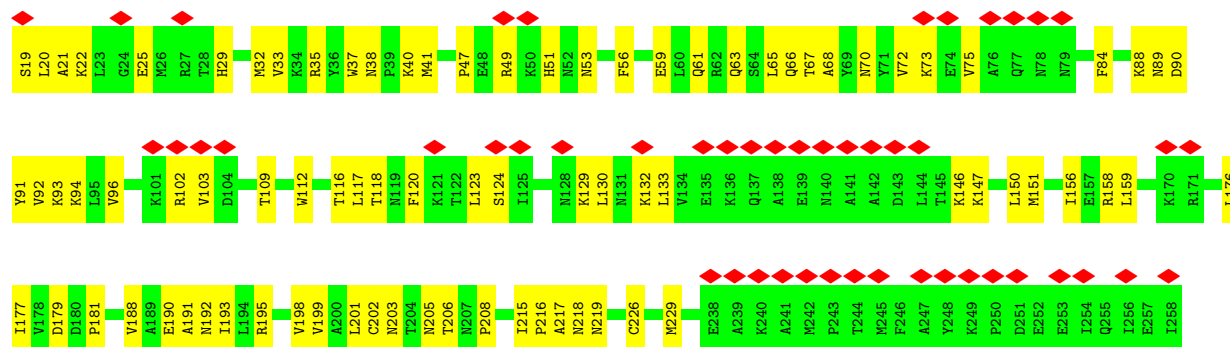


• Molecule 10: DNA-directed RNA polymerase subunit beta

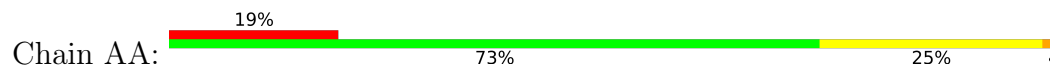




• Molecule 11: Small ribosomal subunit protein uS2

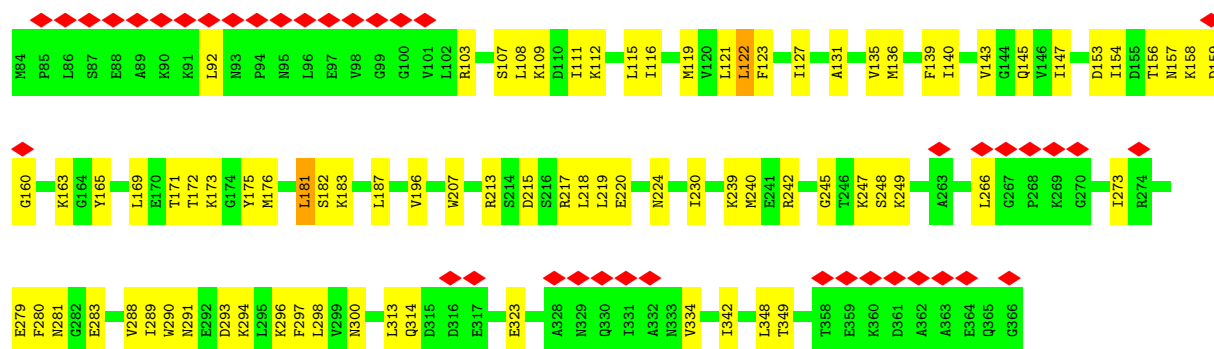


• Molecule 12: Probable DNA-directed RNA polymerase subunit delta



• Molecule 13: Transcription termination/antitermination protein NusA

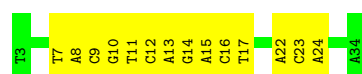




- Molecule 14: DNA chain A



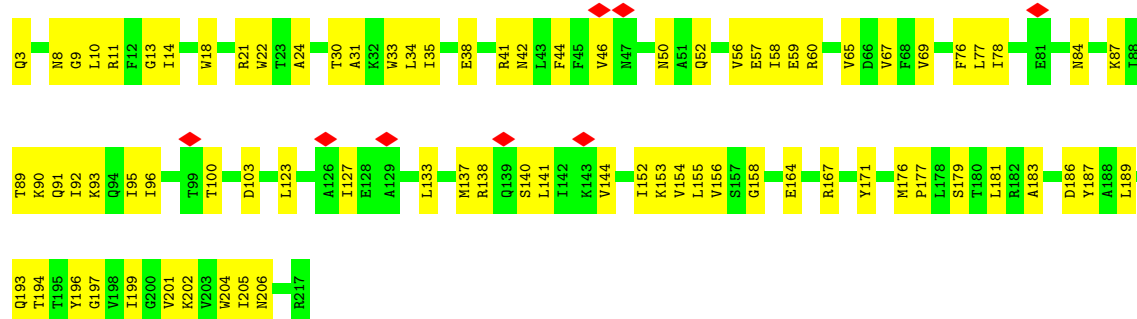
- Molecule 15: DNA chain B



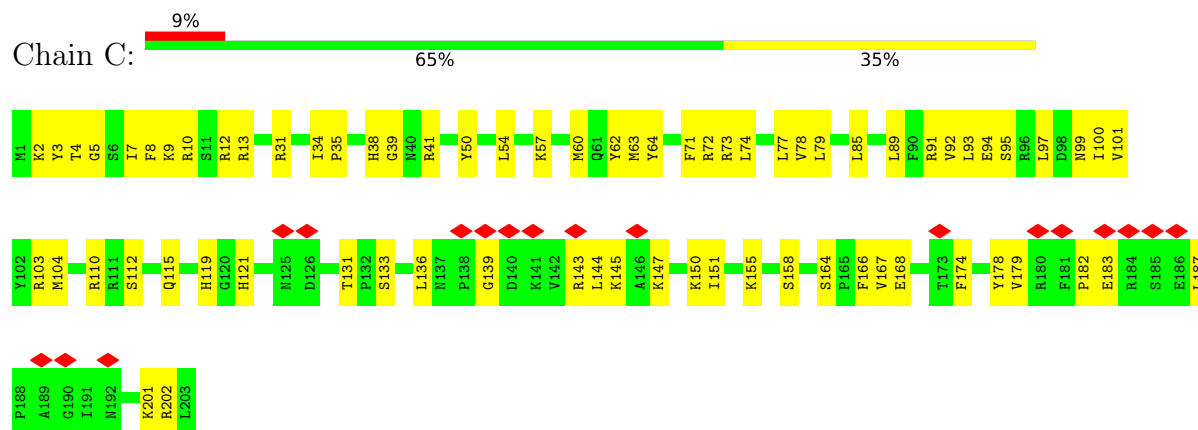
- Molecule 16: Transcription termination/antitermination protein NusG



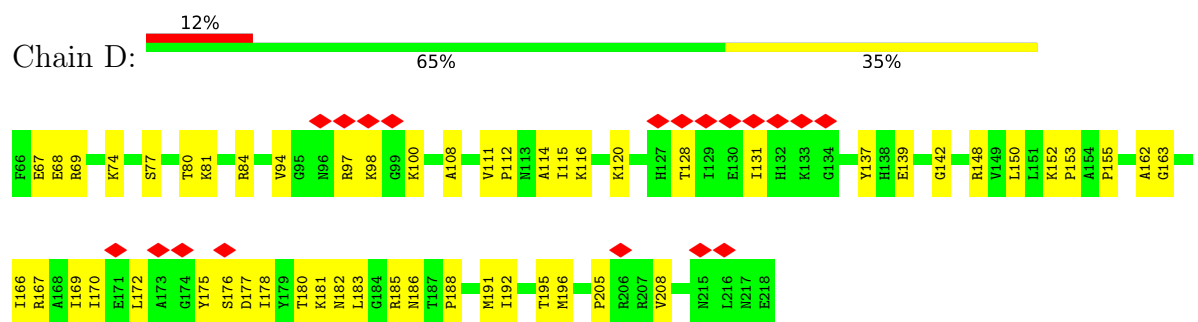
- Molecule 17: Small ribosomal subunit protein uS3



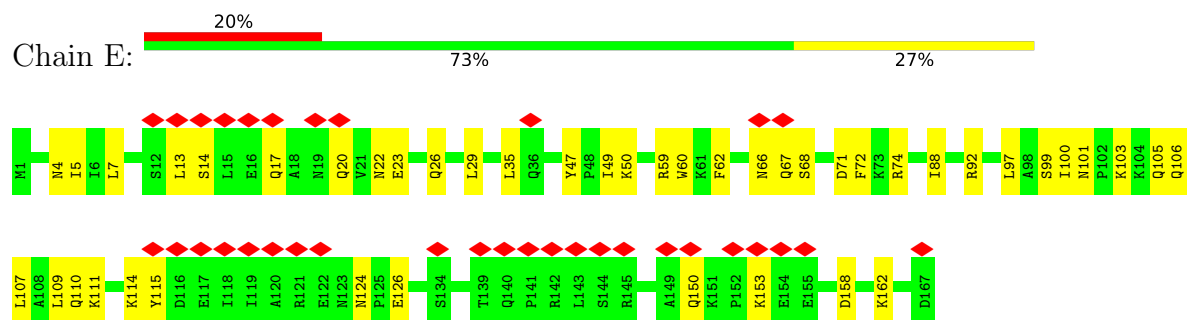
- Molecule 18: Small ribosomal subunit protein uS4



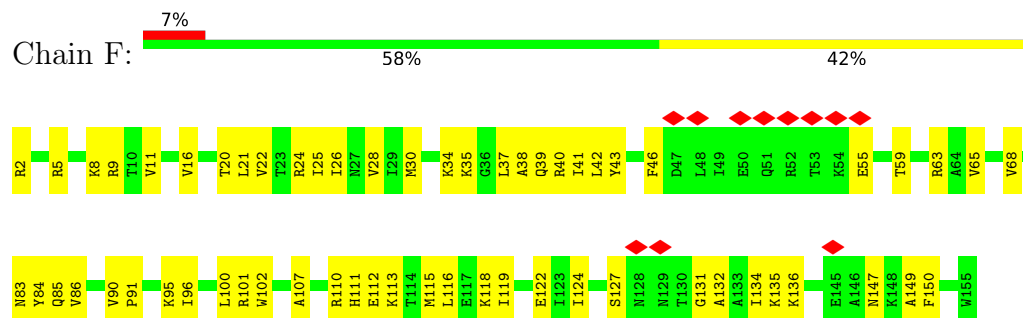
- Molecule 19: Small ribosomal subunit protein uS5



- Molecule 20: Small ribosomal subunit protein bS6

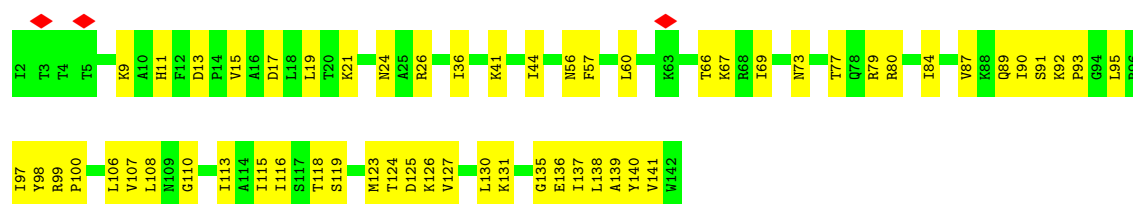


- Molecule 21: Small ribosomal subunit protein uS7



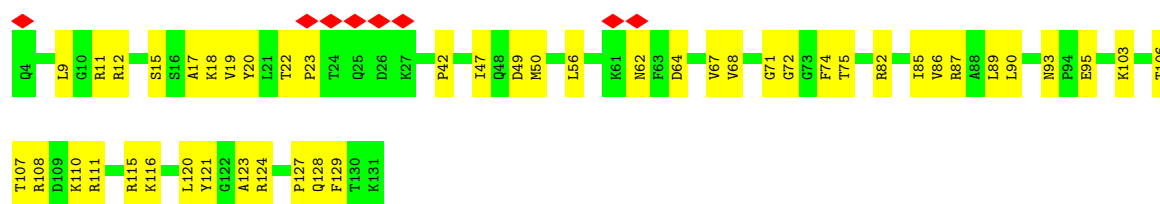
- Molecule 22: Small ribosomal subunit protein uS8

Chain G: 



- Molecule 23: Small ribosomal subunit protein uS9

Chain H: 



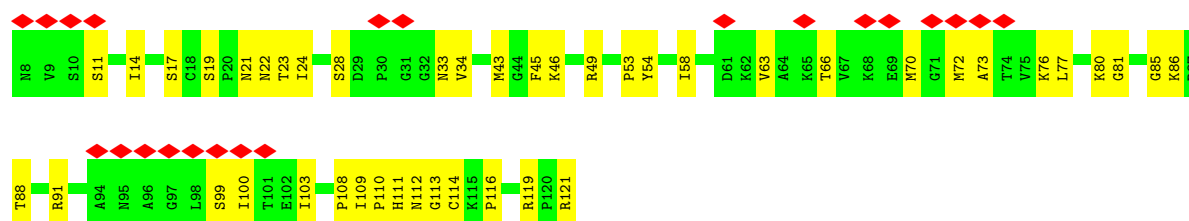
- Molecule 24: Small ribosomal subunit protein uS10

Chain I: 



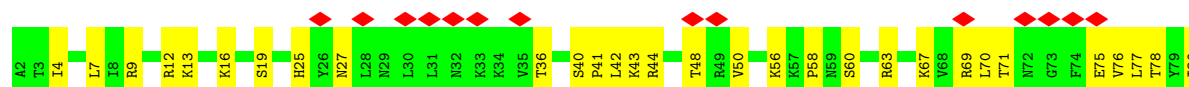
- Molecule 25: Small ribosomal subunit protein uS11

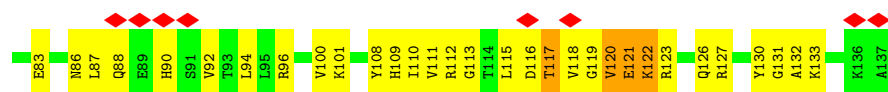
Chain J: 



- Molecule 26: Small ribosomal subunit protein uS12

Chain K: 





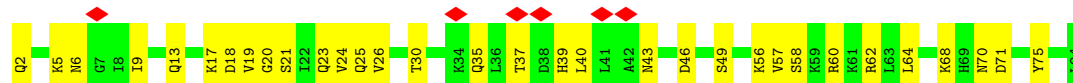
- Molecule 27: Small ribosomal subunit protein uS13



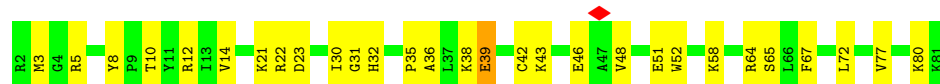
- Molecule 28: Small ribosomal subunit protein uS14



- Molecule 29: Small ribosomal subunit protein uS15



- Molecule 30: Small ribosomal subunit protein bS16



- Molecule 31: Small ribosomal subunit protein uS17

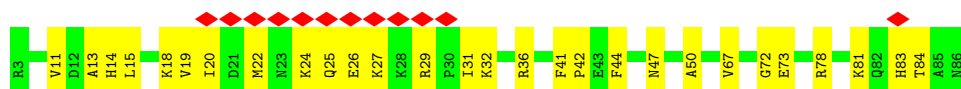


- Molecule 32: Small ribosomal subunit protein bS18

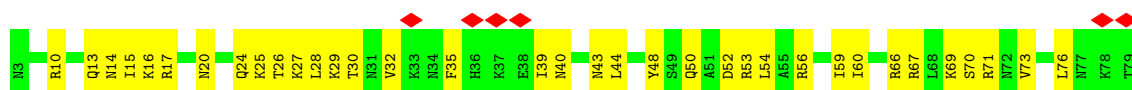




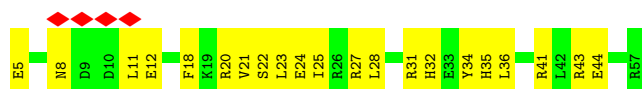
- Molecule 33: Small ribosomal subunit protein uS19



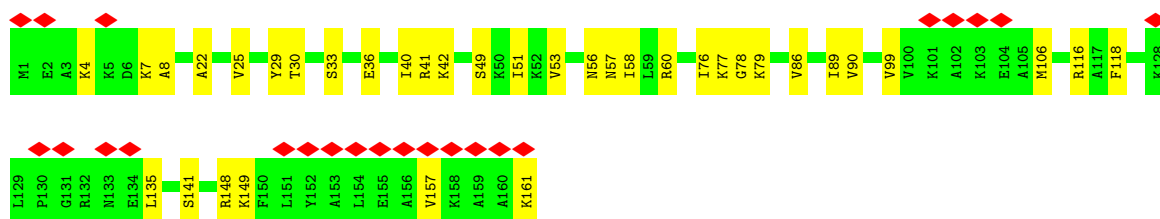
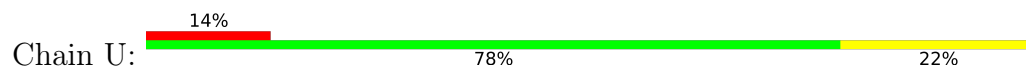
- Molecule 34: Small ribosomal subunit protein bS20



- Molecule 35: Small ribosomal subunit protein bS21



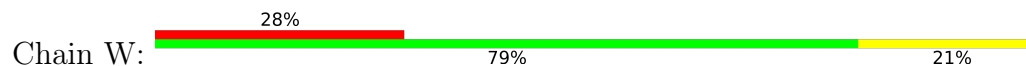
- Molecule 36: 50S ribosomal protein L10

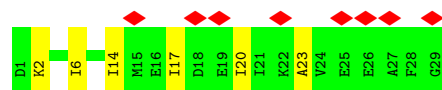


- Molecule 37: Large ribosomal subunit protein bL12

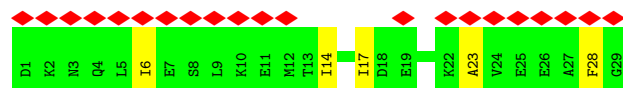
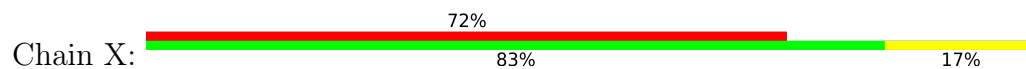


- Molecule 37: Large ribosomal subunit protein bL12

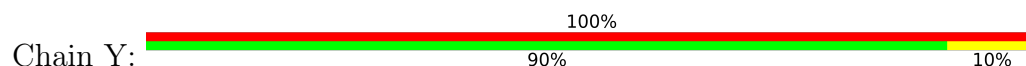




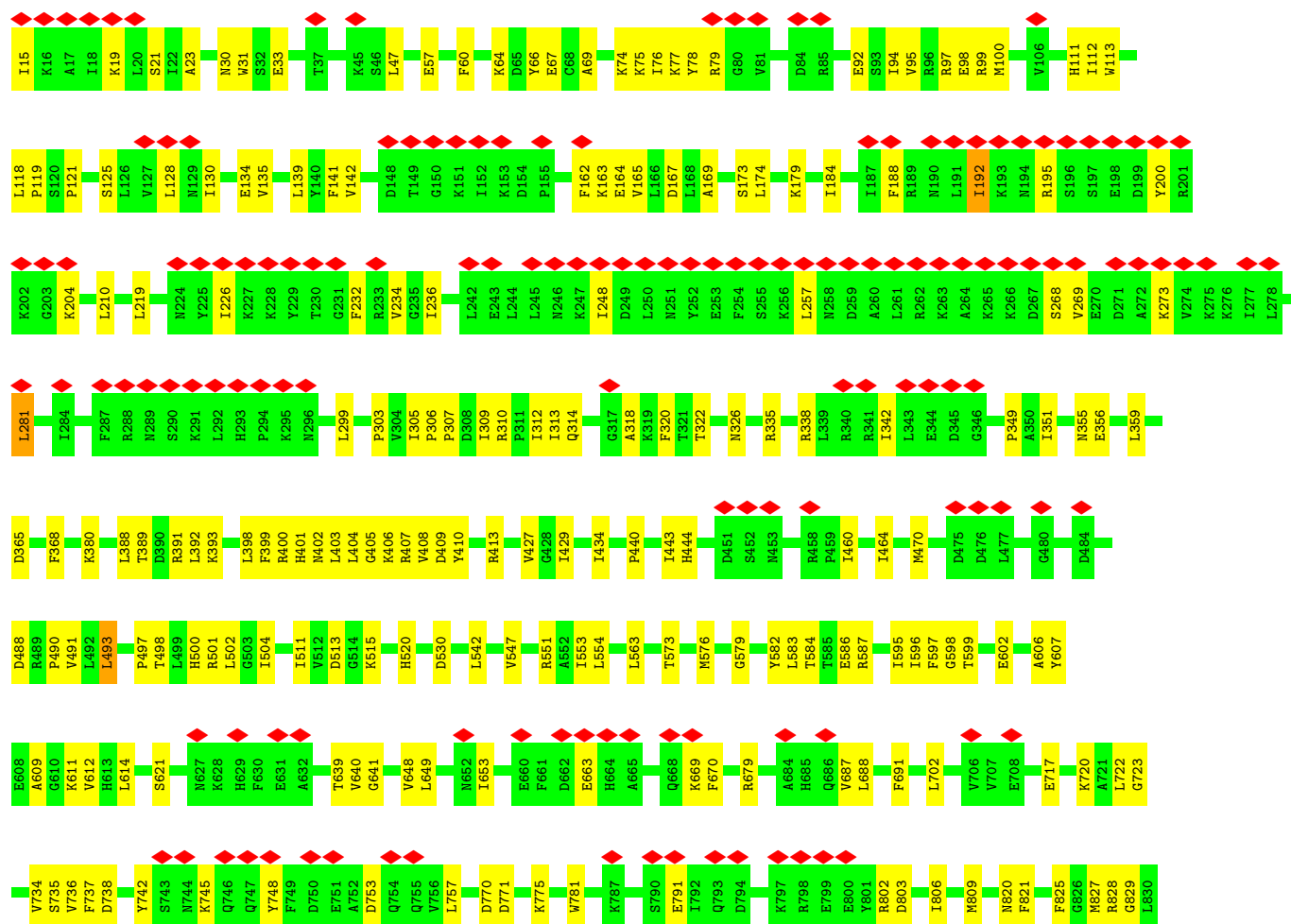
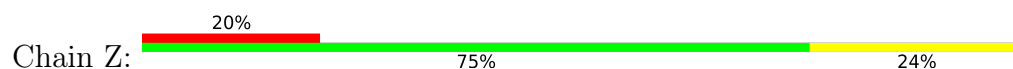
- Molecule 37: Large ribosomal subunit protein bL12

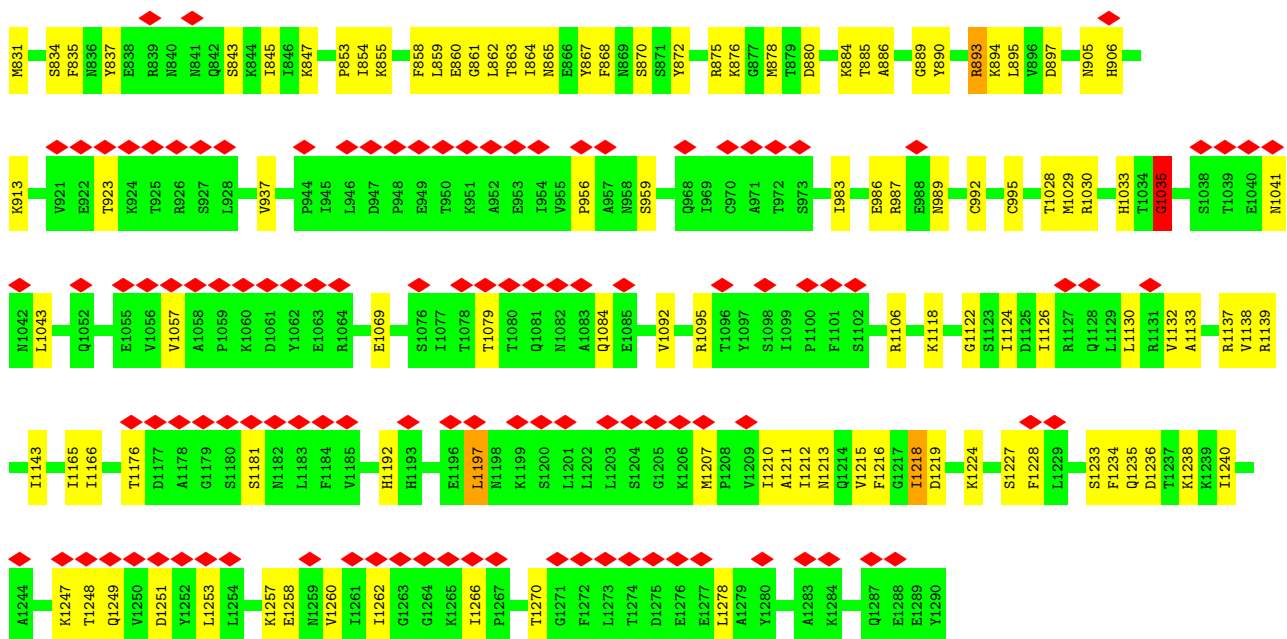


- Molecule 37: Large ribosomal subunit protein bL12

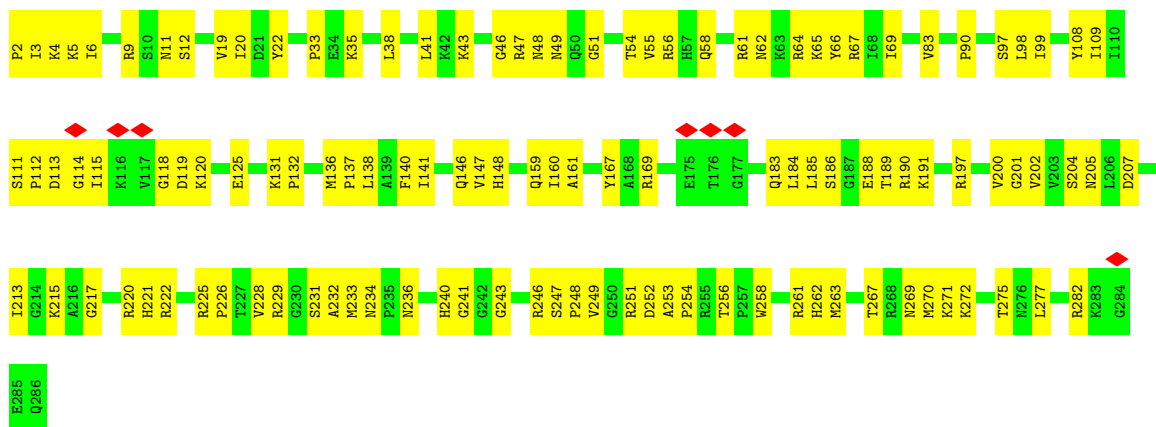


- Molecule 38: DNA-directed RNA polymerase subunit beta'

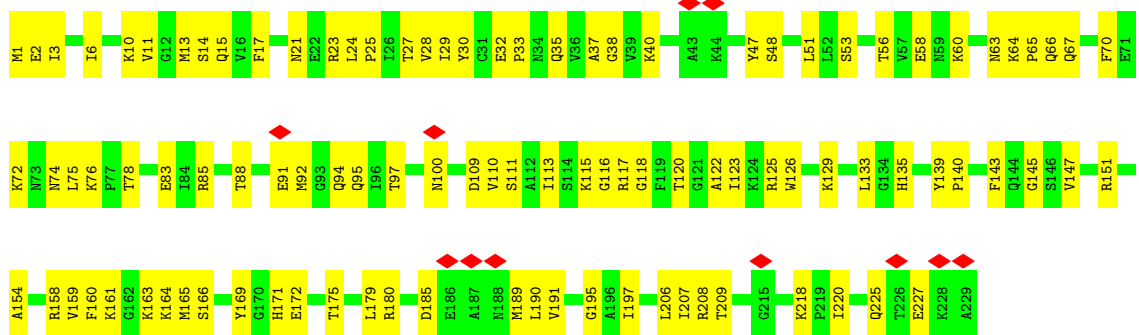




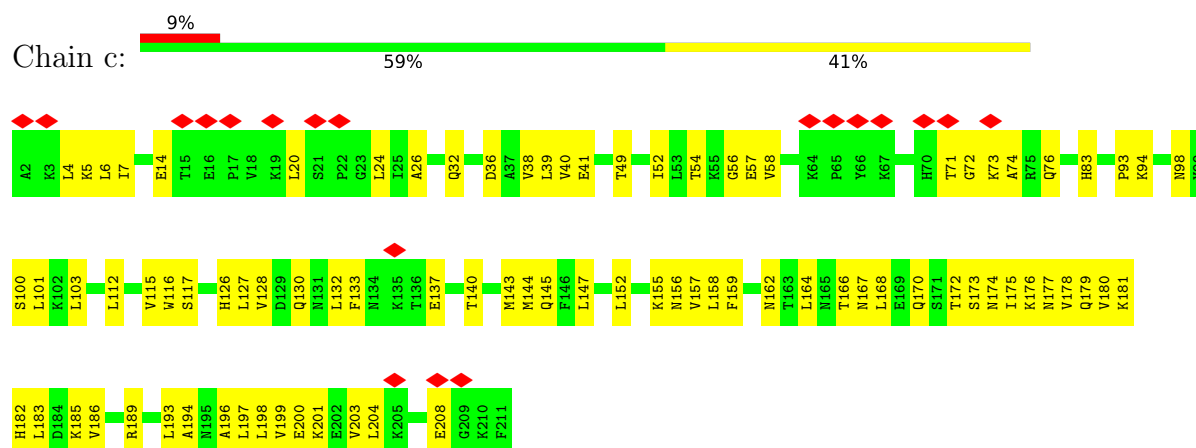
• Molecule 39: Large ribosomal subunit protein uL2



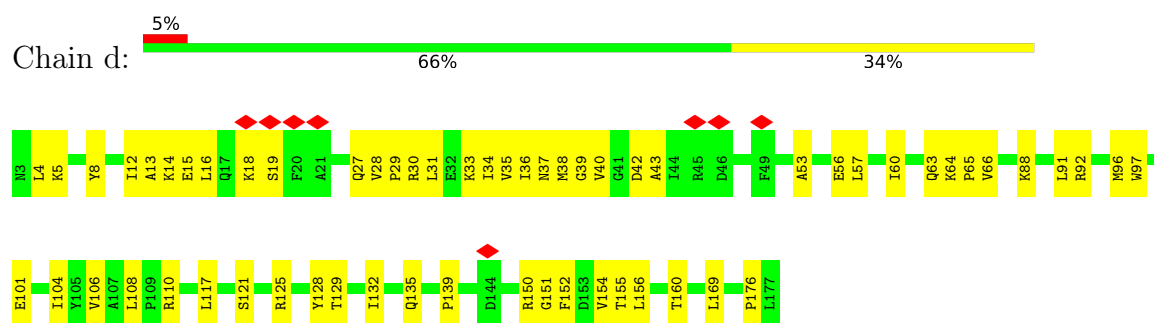
• Molecule 40: Large ribosomal subunit protein uL3



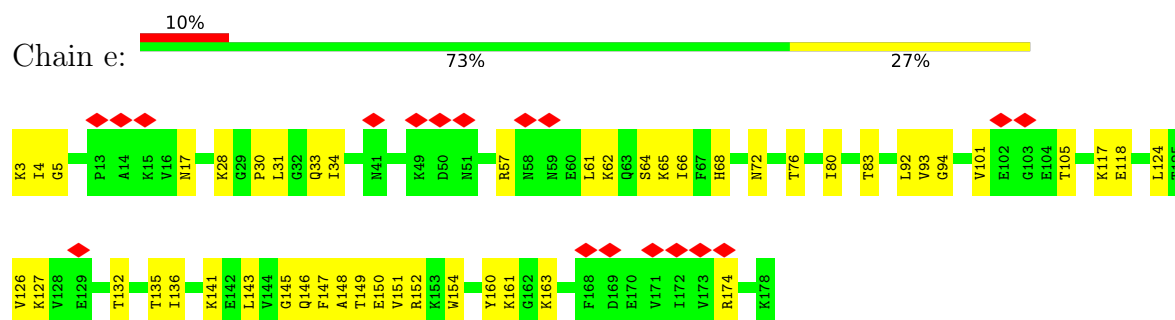
- Molecule 41: Large ribosomal subunit protein uL4



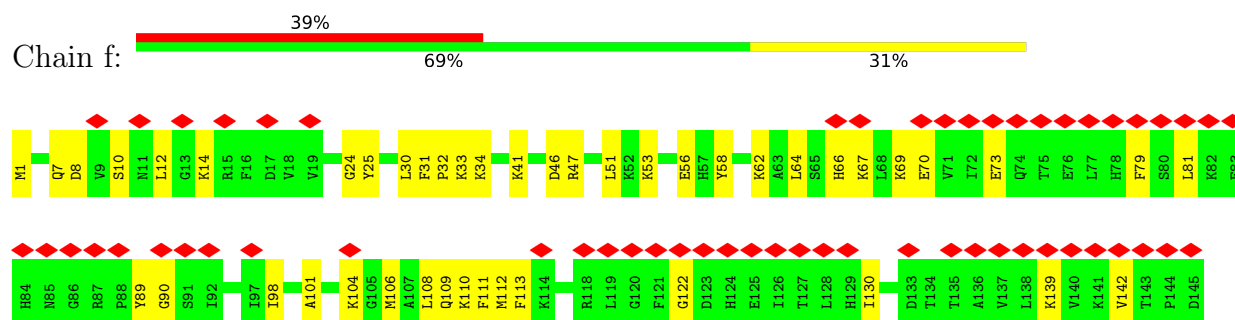
- Molecule 42: Large ribosomal subunit protein uL5



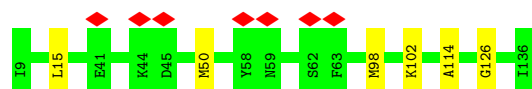
- Molecule 43: Large ribosomal subunit protein uL6



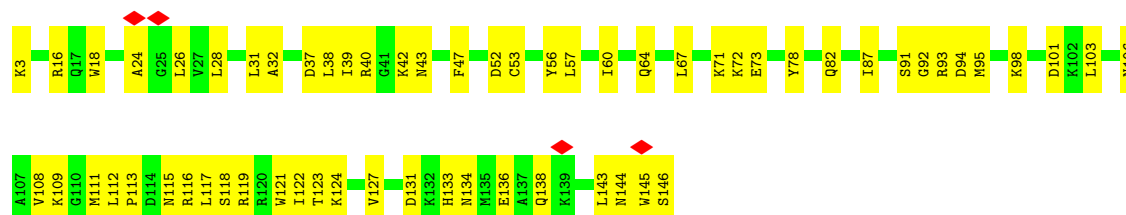
- Molecule 44: Large ribosomal subunit protein bL9



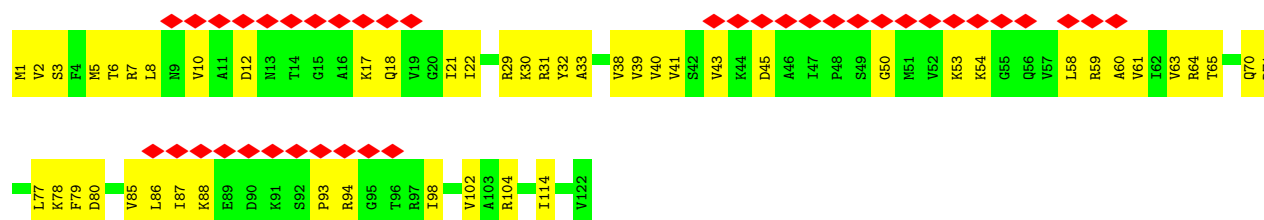
- Molecule 45: Large ribosomal subunit protein uL11



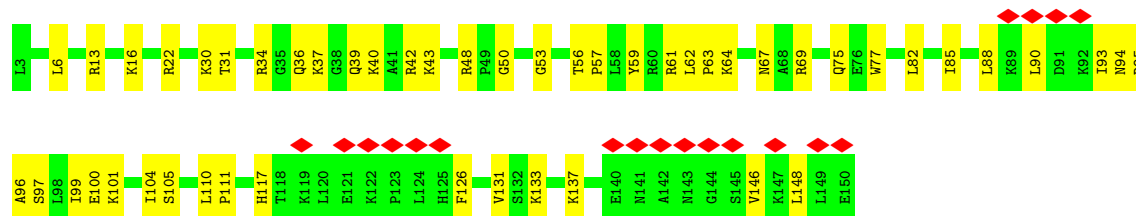
- Molecule 46: Large ribosomal subunit protein uL13



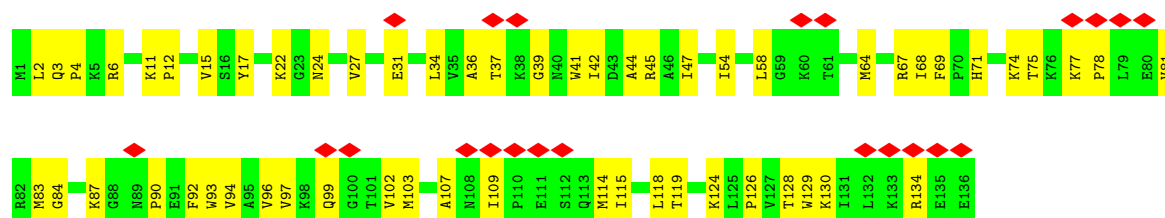
- Molecule 47: 50S ribosomal protein L14



- Molecule 48: Large ribosomal subunit protein uL15

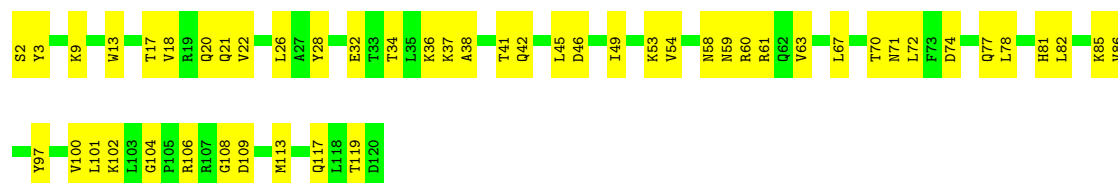


- Molecule 49: Large ribosomal subunit protein uL16



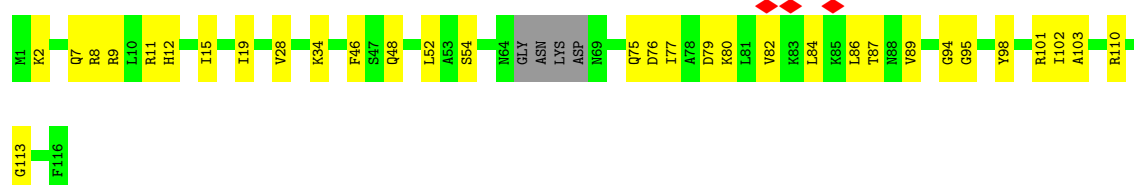
- Molecule 50: Large ribosomal subunit protein bL17

Chain m:  58% 42%



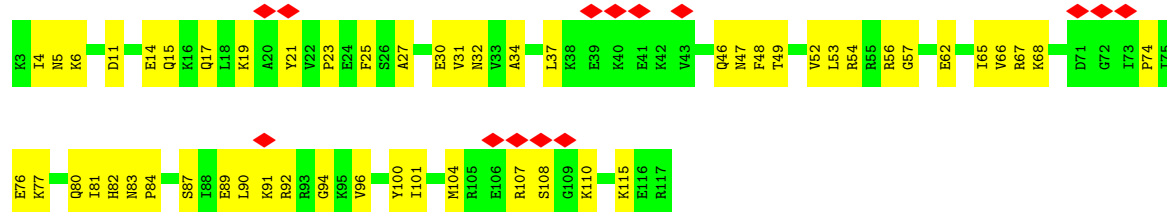
- Molecule 51: Large ribosomal subunit protein uL18

Chain n:  69% 28%



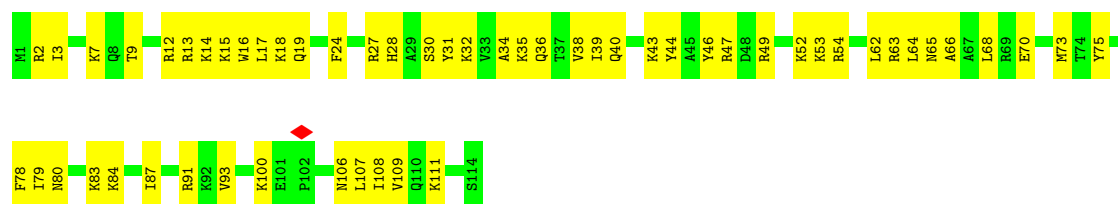
- Molecule 52: Large ribosomal subunit protein bL19

Chain o:  12% 54% 46%



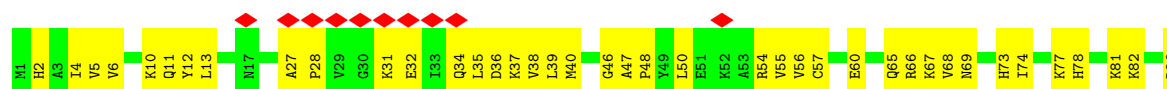
- Molecule 53: Large ribosomal subunit protein bL20

Chain p:  52% 48%



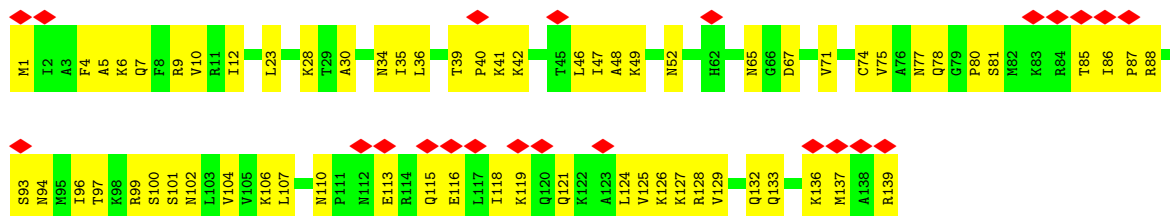
- Molecule 54: Large ribosomal subunit protein bL21

Chain q:  10% 54% 46%





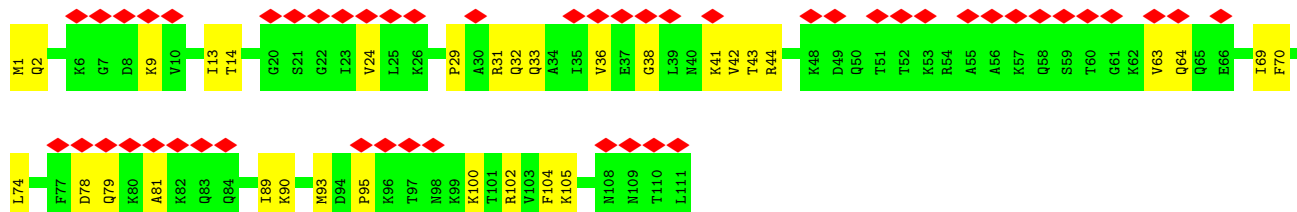
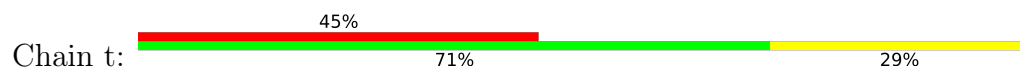
- Molecule 55: Large ribosomal subunit protein uL22



- Molecule 56: Large ribosomal subunit protein uL23



- Molecule 57: 50S ribosomal protein L24



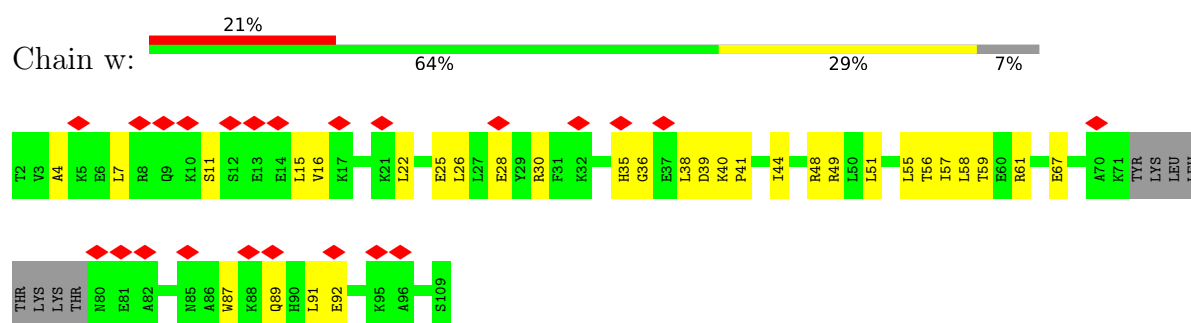
- Molecule 58: Large ribosomal subunit protein bL27



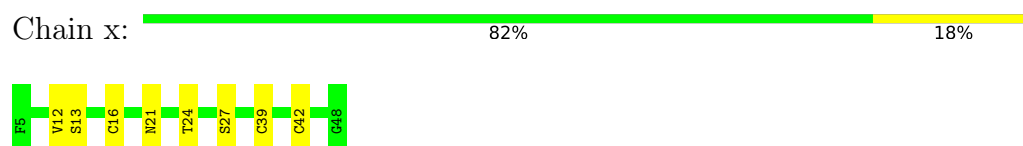
- Molecule 59: Large ribosomal subunit protein bL28



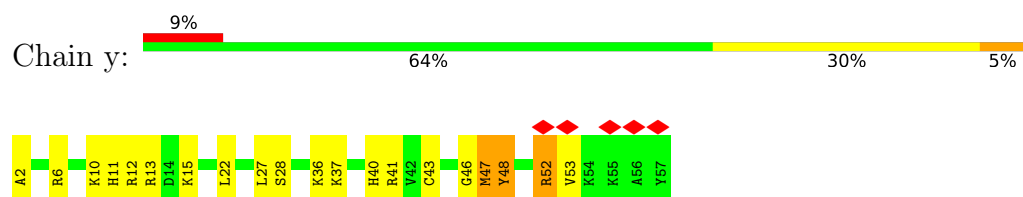
- Molecule 60: Large ribosomal subunit protein uL29



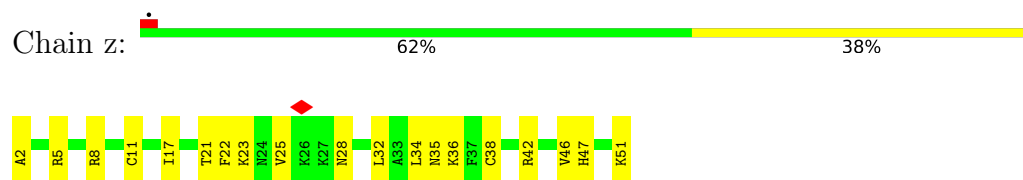
- Molecule 61: Large ribosomal subunit protein bL31



- Molecule 62: Large ribosomal subunit protein bL32



- Molecule 63: Large ribosomal subunit protein bL33A



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	119	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	120	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.526	Depositor
Minimum map value	-0.717	Depositor
Average map value	0.018	Depositor
Map value standard deviation	0.134	Depositor
Recommended contour level	0.162	Depositor
Map size (Å)	500.0, 500.0, 500.0	wwPDB
Map dimensions	100, 100, 100	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	5.0, 5.0, 5.0	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	0.38	0/504
2	1	0.19	0/484	0.54	0/637
3	2	0.17	0/306	0.45	0/401
4	3	0.10	0/69073	0.23	0/107710
5	4	0.11	0/2505	0.28	0/3902
6	5	0.10	0/35768	0.23	0/55764
7	6	0.68	0/2458	1.00	0/3313
7	AB	0.69	0/2490	1.00	0/3355
8	7	0.11	0/1808	0.28	0/2817
9	8	0.75	0/7216	1.28	12/9795 (0.1%)
10	9	0.70	0/11124	1.06	0/15014
11	A	0.15	0/1954	0.44	0/2642
12	AA	0.69	0/792	1.05	0/1065
13	AC	0.70	0/2922	1.01	0/3944
14	AD	0.47	0/745	0.61	1/1149 (0.1%)
15	AE	0.65	1/725 (0.1%)	0.75	2/1115 (0.2%)
16	AF	0.71	0/1298	1.00	0/1752
17	B	0.18	0/1721	0.49	0/2323
18	C	0.17	0/1691	0.49	0/2267
19	D	0.19	0/1188	0.52	1/1593 (0.1%)
20	E	0.17	0/1384	0.48	2/1867 (0.1%)
21	F	0.19	0/1266	0.56	1/1700 (0.1%)
22	G	0.18	0/1126	0.53	0/1517
23	H	0.17	0/1044	0.47	0/1395
24	I	0.20	0/820	0.58	1/1103 (0.1%)
25	J	0.16	0/844	0.44	0/1136
26	K	0.28	0/1094	0.60	2/1468 (0.1%)
27	L	0.19	0/962	0.50	0/1289
28	M	0.19	0/483	0.51	0/643
29	N	0.15	0/679	0.49	1/907 (0.1%)
30	O	0.18	0/659	0.57	1/885 (0.1%)
31	P	0.15	0/684	0.42	0/913
32	Q	0.20	0/545	0.60	0/730
33	R	0.16	0/698	0.49	0/936

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	S	0.18	0/631	0.46	0/838
35	T	0.20	0/475	0.56	0/621
36	U	0.68	0/1254	1.10	0/1677
37	V	0.65	0/232	1.16	2/307 (0.7%)
37	W	0.60	0/232	1.10	0/307
37	X	0.65	0/232	1.04	0/307
37	Y	0.64	0/232	1.07	0/307
38	Z	0.71	0/10259	1.06	2/13846 (0.0%)
39	a	0.16	0/2267	0.43	0/3044
40	b	0.17	0/1795	0.51	0/2412
41	c	0.19	0/1671	0.51	1/2246 (0.0%)
42	d	0.16	0/1409	0.44	0/1894
43	e	0.15	0/1420	0.43	0/1912
44	f	0.20	0/1183	0.56	2/1587 (0.1%)
45	h	0.16	0/968	0.43	0/1298
46	i	0.16	0/1186	0.46	0/1592
47	j	0.17	0/953	0.47	0/1275
48	k	0.17	0/1170	0.46	0/1559
49	l	0.18	0/1104	0.48	0/1481
50	m	0.22	0/973	0.58	0/1309
51	n	0.19	0/897	0.53	0/1198
52	o	0.17	0/948	0.50	0/1262
53	p	0.20	0/961	0.48	0/1278
54	q	0.18	0/828	0.56	0/1111
55	r	0.18	0/1077	0.52	0/1441
56	s	0.17	0/732	0.52	1/988 (0.1%)
57	t	0.15	0/879	0.45	0/1165
58	u	0.16	0/665	0.43	0/884
59	v	0.23	0/519	0.53	0/695
60	w	0.18	0/826	0.48	0/1104
61	x	0.17	0/353	0.40	0/474
62	y	0.32	0/457	0.67	0/601
63	z	0.15	0/412	0.48	0/547
All	All	0.34	1/198139 (0.0%)	0.56	32/290118 (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
9	8	0	4

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
10	9	0	1
22	G	0	1
25	J	0	1
30	O	0	1
38	Z	0	1
All	All	0	9

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	AE	22	DA	O3'-P	-15.35	1.38	1.61

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	AE	22	DA	P-O3'-C3'	14.71	142.26	120.20
14	AD	17	DT	P-O3'-C3'	8.52	132.99	120.20
9	8	42	LEU	CA-C-N	8.34	137.76	121.41
9	8	42	LEU	C-N-CA	8.34	137.76	121.41
15	AE	22	DA	O3'-P-O5'	-8.26	91.62	104.00

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	8	362	TYR	Sidechain
9	8	399	ARG	Peptide
9	8	419	ARG	Sidechain
9	8	450	HIS	Peptide
10	9	858	TYR	Sidechain

5.2 Too-close contacts [i](#)

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	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	1	477	0	530	23	0
3	2	304	0	350	16	0
4	3	61664	0	30953	1930	0
5	4	2239	0	1137	65	0
6	5	31943	0	16058	910	0
7	6	2421	0	2495	139	0
7	AB	2452	0	2522	223	0
8	7	1618	0	821	44	0
9	8	7063	0	7119	60	0
10	9	10948	0	11063	1047	0
11	A	1921	0	1973	60	0
12	AA	770	0	739	52	0
13	AC	2884	0	2938	436	0
14	AD	663	0	361	82	0
15	AE	649	0	364	102	0
16	AF	1277	0	1328	92	0
17	B	1698	0	1765	63	0
18	C	1660	0	1719	67	0
19	D	1173	0	1267	34	0
20	E	1362	0	1377	41	0
21	F	1246	0	1308	53	0
22	G	1110	0	1221	60	0
23	H	1028	0	1094	35	0
24	I	809	0	894	37	0
25	J	829	0	855	39	0
26	K	1076	0	1170	48	0
27	L	951	0	1014	35	0
28	M	474	0	509	24	0
29	N	673	0	730	29	0
30	O	646	0	677	24	0
31	P	675	0	728	25	0
32	Q	535	0	562	22	0
33	R	682	0	691	25	0
34	S	629	0	681	34	0
35	T	471	0	522	18	0
36	U	1239	0	1301	127	0
37	V	232	0	237	9	0
37	W	232	0	237	8	0
37	X	232	0	237	10	0
37	Y	232	0	237	7	0
38	Z	10085	0	10375	841	0
39	a	2225	0	2301	104	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
40	b	1762	0	1808	90	0
41	c	1644	0	1731	70	0
42	d	1388	0	1469	46	0
43	e	1396	0	1481	33	0
44	f	1160	0	1172	34	0
45	h	959	0	1039	9	0
46	i	1164	0	1192	52	0
47	j	944	0	1019	44	0
48	k	1153	0	1256	46	0
49	l	1079	0	1134	49	0
50	m	958	0	1011	40	0
51	n	889	0	952	26	0
52	o	938	0	1008	47	0
53	p	947	0	1028	68	0
54	q	811	0	858	39	0
55	r	1068	0	1150	56	0
56	s	720	0	803	20	0
57	t	872	0	972	18	0
58	u	657	0	695	22	0
59	v	513	0	560	30	0
60	w	818	0	870	21	0
61	x	344	0	333	4	0
62	y	452	0	472	21	0
63	z	408	0	440	15	0
All	All	184921	0	139342	6242	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 20.

The worst 5 of 6242 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)
4:3:1081:A:C4	36:U:7:LYS:HD3	1.25	1.68
10:9:999:PHE:CZ	13:AC:108:LEU:HD23	1.23	1.67
7:6:107:GLU:HG3	7:AB:319:HIS:CD2	1.30	1.66
10:9:1342:LEU:CD1	38:Z:392:LEU:CD2	1.79	1.61
10:9:999:PHE:CE1	13:AC:108:LEU:HD23	1.28	1.60

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	45/47 (96%)	44 (98%)	1 (2%)	0	100	100
2	1	57/59 (97%)	54 (95%)	3 (5%)	0	100	100
3	2	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
7	6	304/327 (93%)	301 (99%)	3 (1%)	0	100	100
7	AB	308/327 (94%)	305 (99%)	3 (1%)	0	100	100
9	8	895/944 (95%)	849 (95%)	37 (4%)	9 (1%)	12	49
10	9	1389/1391 (100%)	1355 (98%)	33 (2%)	1 (0%)	48	83
11	A	238/240 (99%)	222 (93%)	16 (7%)	0	100	100
12	AA	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
13	AC	358/366 (98%)	350 (98%)	6 (2%)	2 (1%)	21	59
16	AF	158/160 (99%)	155 (98%)	1 (1%)	2 (1%)	9	42
17	B	213/215 (99%)	196 (92%)	17 (8%)	0	100	100
18	C	201/203 (99%)	191 (95%)	10 (5%)	0	100	100
19	D	151/153 (99%)	145 (96%)	6 (4%)	0	100	100
20	E	165/167 (99%)	147 (89%)	18 (11%)	0	100	100
21	F	152/154 (99%)	135 (89%)	17 (11%)	0	100	100
22	G	139/141 (99%)	125 (90%)	14 (10%)	0	100	100
23	H	126/128 (98%)	115 (91%)	11 (9%)	0	100	100
24	I	99/101 (98%)	87 (88%)	12 (12%)	0	100	100
25	J	112/114 (98%)	105 (94%)	7 (6%)	0	100	100
26	K	134/136 (98%)	125 (93%)	9 (7%)	0	100	100
27	L	116/118 (98%)	104 (90%)	12 (10%)	0	100	100
28	M	58/60 (97%)	56 (97%)	2 (3%)	0	100	100
29	N	81/83 (98%)	81 (100%)	0	0	100	100
30	O	78/80 (98%)	70 (90%)	8 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	P	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
32	Q	63/65 (97%)	51 (81%)	12 (19%)	0	100	100
33	R	82/84 (98%)	73 (89%)	9 (11%)	0	100	100
34	S	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
35	T	51/53 (96%)	50 (98%)	1 (2%)	0	100	100
36	U	159/161 (99%)	154 (97%)	4 (2%)	1 (1%)	21	59
37	V	27/29 (93%)	27 (100%)	0	0	100	100
37	W	27/29 (93%)	27 (100%)	0	0	100	100
37	X	27/29 (93%)	27 (100%)	0	0	100	100
37	Y	27/29 (93%)	27 (100%)	0	0	100	100
38	Z	1274/1276 (100%)	1252 (98%)	21 (2%)	1 (0%)	48	83
39	a	283/285 (99%)	266 (94%)	17 (6%)	0	100	100
40	b	227/229 (99%)	213 (94%)	14 (6%)	0	100	100
41	c	208/210 (99%)	197 (95%)	11 (5%)	0	100	100
42	d	173/175 (99%)	160 (92%)	13 (8%)	0	100	100
43	e	174/176 (99%)	166 (95%)	8 (5%)	0	100	100
44	f	143/145 (99%)	125 (87%)	18 (13%)	0	100	100
45	h	126/128 (98%)	114 (90%)	12 (10%)	0	100	100
46	i	142/144 (99%)	136 (96%)	6 (4%)	0	100	100
47	j	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
48	k	146/148 (99%)	139 (95%)	7 (5%)	0	100	100
49	l	134/136 (98%)	124 (92%)	10 (8%)	0	100	100
50	m	117/119 (98%)	110 (94%)	7 (6%)	0	100	100
51	n	108/116 (93%)	99 (92%)	9 (8%)	0	100	100
52	o	113/115 (98%)	102 (90%)	11 (10%)	0	100	100
53	p	112/114 (98%)	108 (96%)	4 (4%)	0	100	100
54	q	97/99 (98%)	90 (93%)	7 (7%)	0	100	100
55	r	137/139 (99%)	134 (98%)	3 (2%)	0	100	100
56	s	90/92 (98%)	88 (98%)	2 (2%)	0	100	100
57	t	109/111 (98%)	104 (95%)	5 (5%)	0	100	100
58	u	84/86 (98%)	81 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
59	v	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
60	w	96/108 (89%)	89 (93%)	7 (7%)	0	100	100
61	x	42/44 (96%)	35 (83%)	7 (17%)	0	100	100
62	y	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
63	z	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
All	All	10736/10965 (98%)	10226 (95%)	494 (5%)	16 (0%)	49	83

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	8	398	LEU
16	AF	95	ARG
9	8	43	GLY
9	8	265	GLY
9	8	376	LYS

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	40/40 (100%)	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
7	6	269/285 (94%)	262 (97%)	7 (3%)	40	62
7	AB	272/285 (95%)	265 (97%)	7 (3%)	40	62
9	8	766/808 (95%)	741 (97%)	25 (3%)	33	55
10	9	1213/1213 (100%)	1188 (98%)	25 (2%)	47	65
11	A	212/212 (100%)	211 (100%)	1 (0%)	81	83
12	AA	83/83 (100%)	79 (95%)	4 (5%)	23	44
13	AC	327/327 (100%)	322 (98%)	5 (2%)	57	72
16	AF	140/140 (100%)	134 (96%)	6 (4%)	26	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	B	180/180 (100%)	180 (100%)	0	100	100
18	C	181/181 (100%)	181 (100%)	0	100	100
19	D	123/123 (100%)	123 (100%)	0	100	100
20	E	150/150 (100%)	150 (100%)	0	100	100
21	F	131/131 (100%)	131 (100%)	0	100	100
22	G	123/123 (100%)	123 (100%)	0	100	100
23	H	111/111 (100%)	111 (100%)	0	100	100
24	I	95/95 (100%)	95 (100%)	0	100	100
25	J	91/91 (100%)	91 (100%)	0	100	100
26	K	117/117 (100%)	114 (97%)	3 (3%)	40	62
27	L	100/100 (100%)	99 (99%)	1 (1%)	68	78
28	M	47/47 (100%)	47 (100%)	0	100	100
29	N	76/76 (100%)	76 (100%)	0	100	100
30	O	69/69 (100%)	69 (100%)	0	100	100
31	P	73/73 (100%)	73 (100%)	0	100	100
32	Q	56/56 (100%)	56 (100%)	0	100	100
33	R	74/74 (100%)	74 (100%)	0	100	100
34	S	70/70 (100%)	70 (100%)	0	100	100
35	T	49/49 (100%)	49 (100%)	0	100	100
36	U	129/129 (100%)	129 (100%)	0	100	100
37	V	26/26 (100%)	26 (100%)	0	100	100
37	W	26/26 (100%)	26 (100%)	0	100	100
37	X	26/26 (100%)	26 (100%)	0	100	100
37	Y	26/26 (100%)	26 (100%)	0	100	100
38	Z	1113/1113 (100%)	1100 (99%)	13 (1%)	63	75
39	a	241/241 (100%)	241 (100%)	0	100	100
40	b	186/186 (100%)	186 (100%)	0	100	100
41	c	182/182 (100%)	182 (100%)	0	100	100
42	d	150/150 (100%)	150 (100%)	0	100	100
43	e	153/153 (100%)	153 (100%)	0	100	100
44	f	123/131 (94%)	123 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	h	102/102 (100%)	102 (100%)	0	100	100
46	i	126/126 (100%)	126 (100%)	0	100	100
47	j	103/103 (100%)	103 (100%)	0	100	100
48	k	123/123 (100%)	123 (100%)	0	100	100
49	l	113/113 (100%)	113 (100%)	0	100	100
50	m	105/105 (100%)	105 (100%)	0	100	100
51	n	96/99 (97%)	96 (100%)	0	100	100
52	o	101/101 (100%)	101 (100%)	0	100	100
53	p	100/100 (100%)	100 (100%)	0	100	100
54	q	90/90 (100%)	90 (100%)	0	100	100
55	r	116/116 (100%)	116 (100%)	0	100	100
56	s	82/82 (100%)	82 (100%)	0	100	100
57	t	96/96 (100%)	96 (100%)	0	100	100
58	u	69/69 (100%)	69 (100%)	0	100	100
59	v	58/58 (100%)	58 (100%)	0	100	100
60	w	87/95 (92%)	87 (100%)	0	100	100
61	x	41/41 (100%)	41 (100%)	0	100	100
62	y	48/48 (100%)	45 (94%)	3 (6%)	16	37
63	z	47/47 (100%)	47 (100%)	0	100	100
All	All	9408/9498 (99%)	9308 (99%)	100 (1%)	63	76

5 of 100 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	A	51	HIS
13	AC	121	LEU
62	y	52	ARG
12	AA	8	LEU
7	AB	59	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 132 such sidechains are listed below:

Mol	Chain	Res	Type
49	l	113	GLN

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Mol	Chain	Res	Type
53	p	85	HIS
62	y	19	HIS
7	AB	305	ASN
7	AB	287	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	3	2875/2878 (99%)	733 (25%)	25 (0%)
5	4	103/105 (98%)	34 (33%)	5 (4%)
6	5	1490/1493 (99%)	348 (23%)	6 (0%)
8	7	75/76 (98%)	25 (33%)	2 (2%)
All	All	4543/4552 (99%)	1140 (25%)	38 (0%)

5 of 1140 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	3	12	A
4	3	14	U
4	3	15	A
4	3	17	G
4	3	29	G

5 of 38 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	4	59	A
6	5	1373	A
5	4	70	G
6	5	448	A
8	7	19	G

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 [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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
13	AC	3
15	AE	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AC	292:GLU	C	293:ASP	N	8.91
1	AC	143:VAL	C	144:GLY	N	6.10
1	AC	215:ASP	C	216:SER	N	3.12
1	AE	22:DA	O3'	23:DC	P	1.38

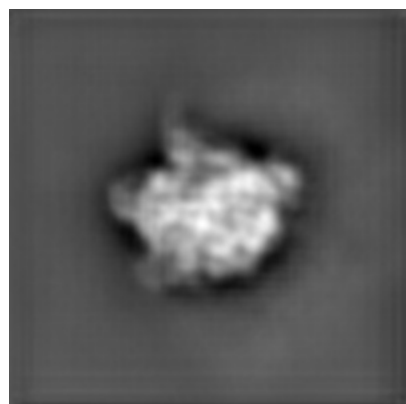
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53676. These allow visual inspection of the internal detail of the map and identification of artifacts.

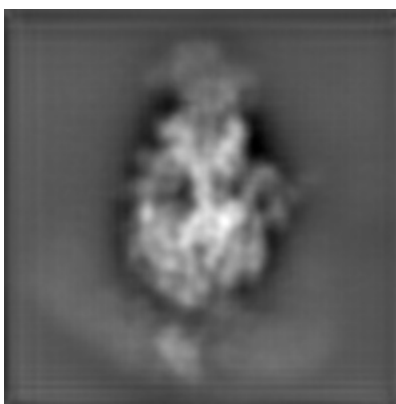
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

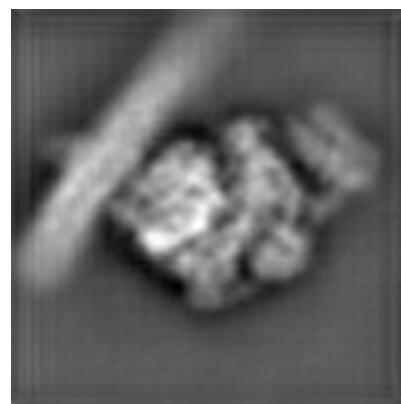
6.1.1 Primary map



X

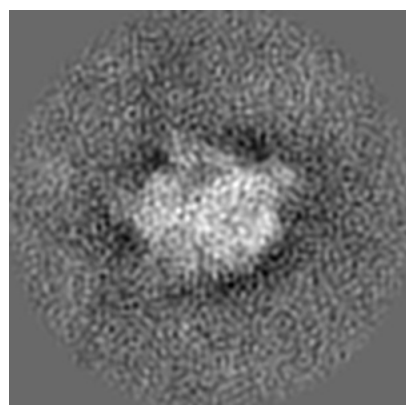


Y

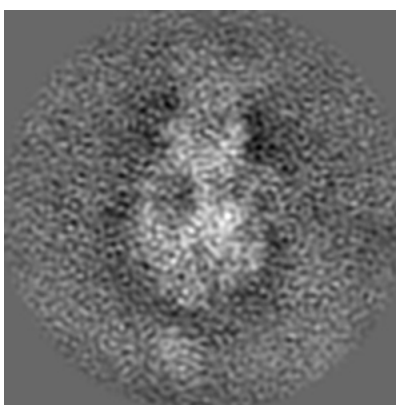


Z

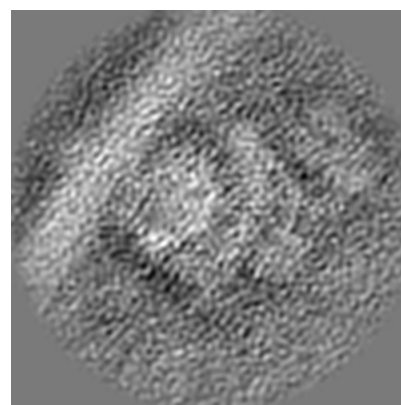
6.1.2 Raw map



X



Y

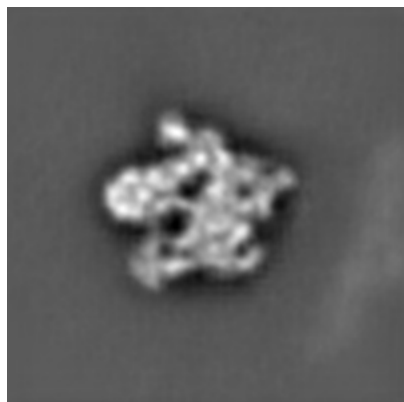


Z

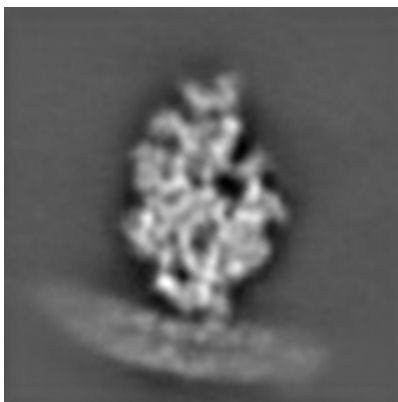
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

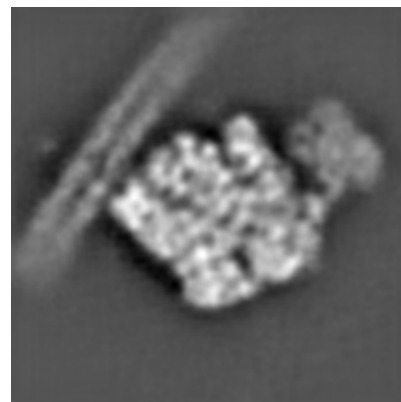
6.2.1 Primary map



X Index: 50

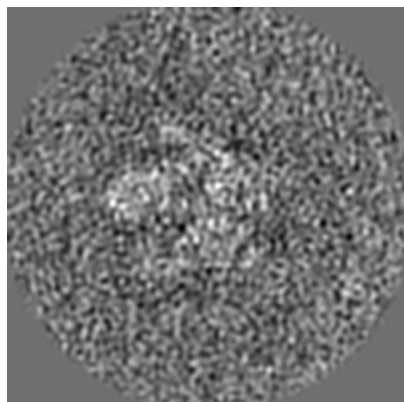


Y Index: 50

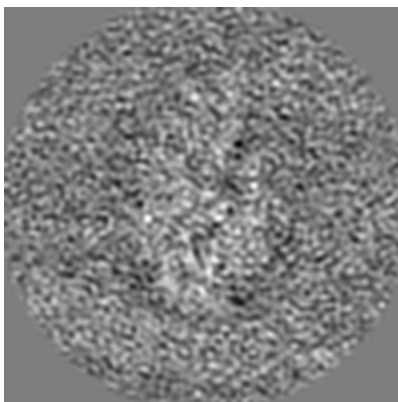


Z Index: 50

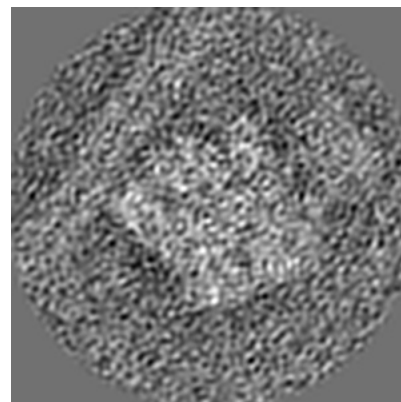
6.2.2 Raw map



X Index: 50



Y Index: 50

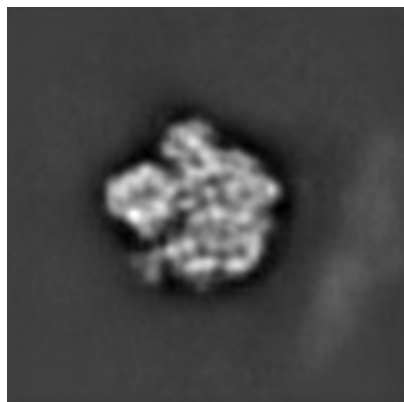


Z Index: 50

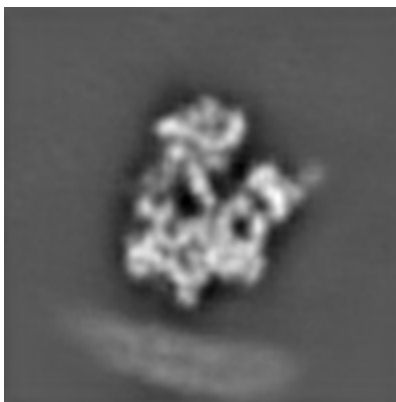
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

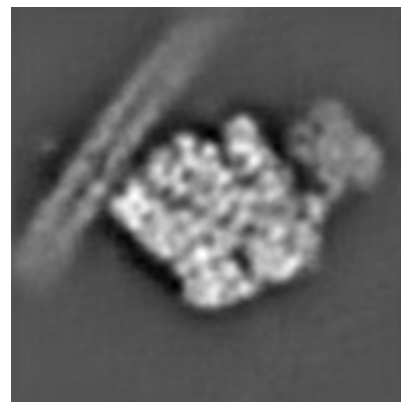
6.3.1 Primary map



X Index: 47

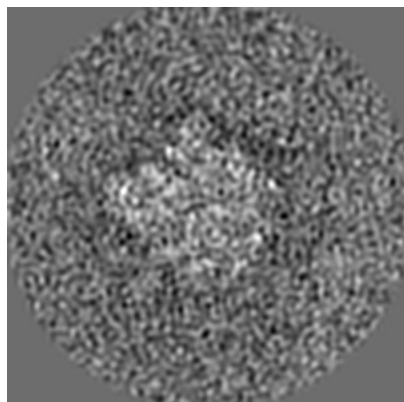


Y Index: 42

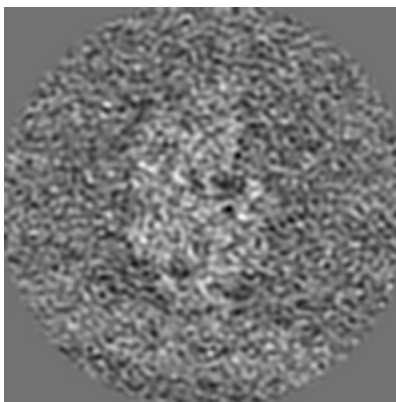


Z Index: 50

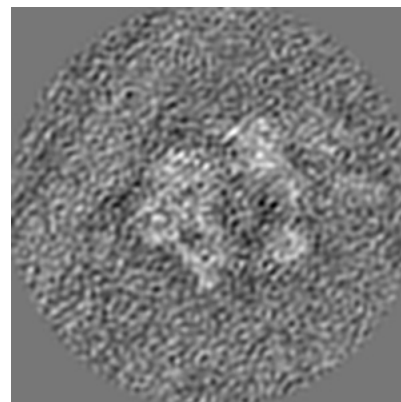
6.3.2 Raw map



X Index: 46



Y Index: 51

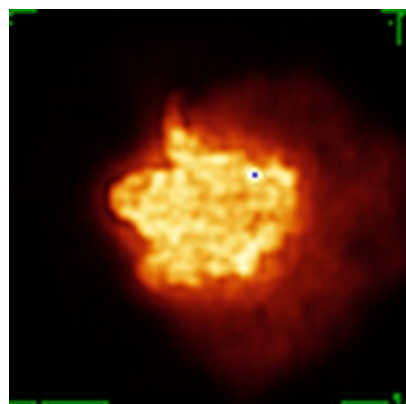


Z Index: 58

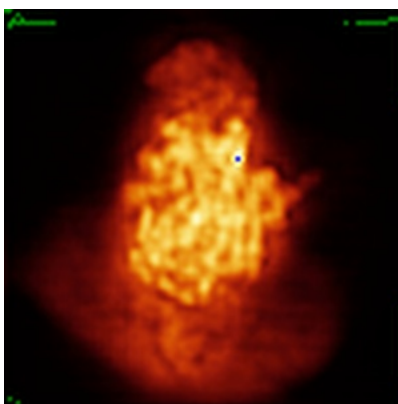
The images above show the largest variance slices of the map in three orthogonal directions.

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

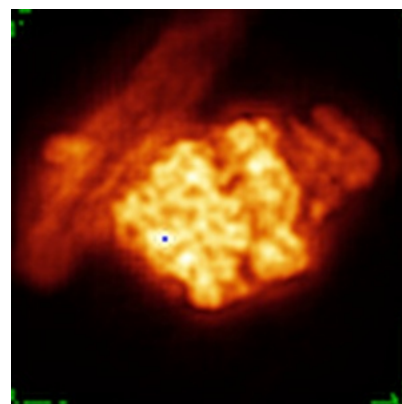
6.4.1 Primary map



X

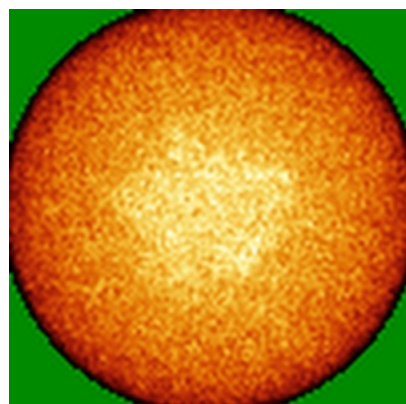


Y

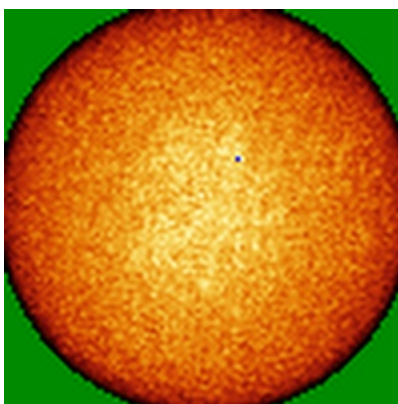


Z

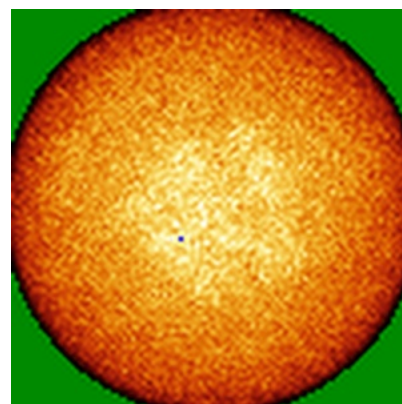
6.4.2 Raw map



X



Y

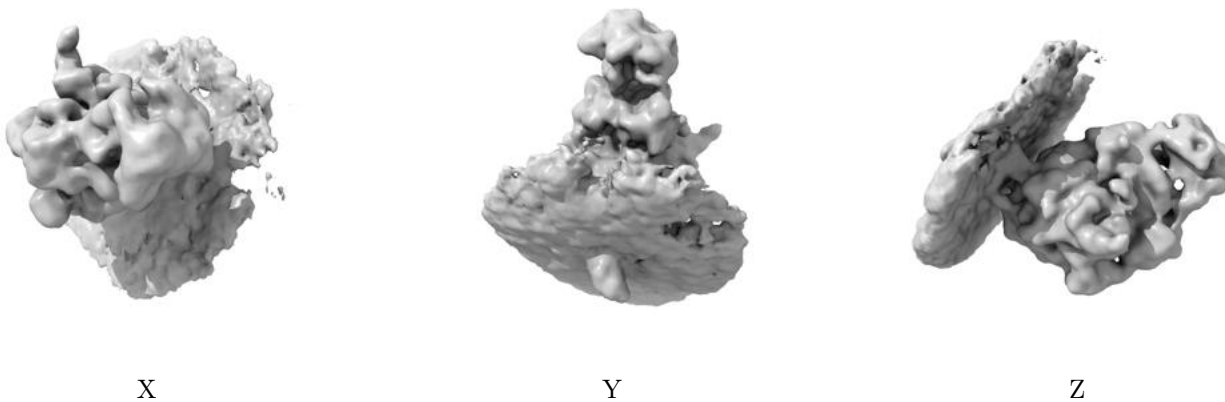


Z

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.

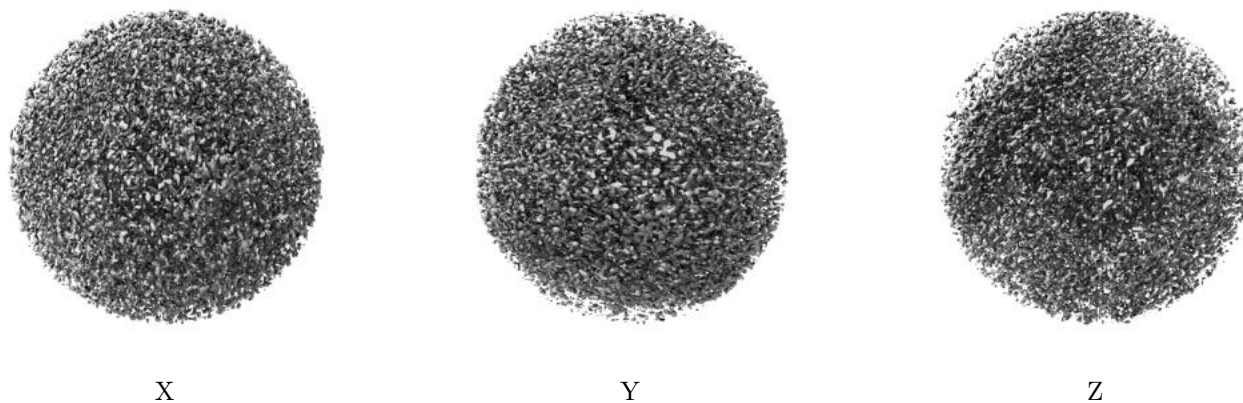
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.162. 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.

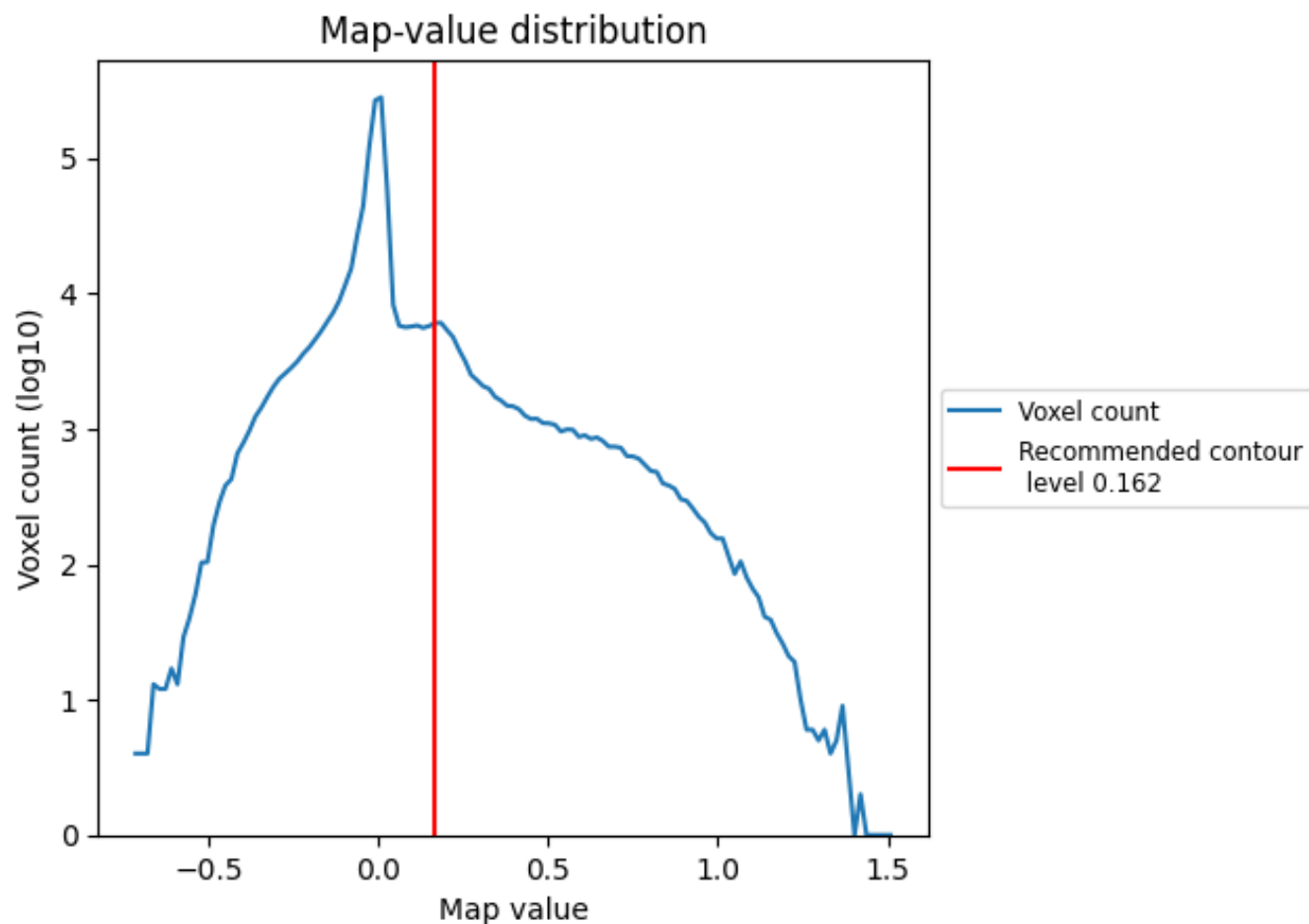
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

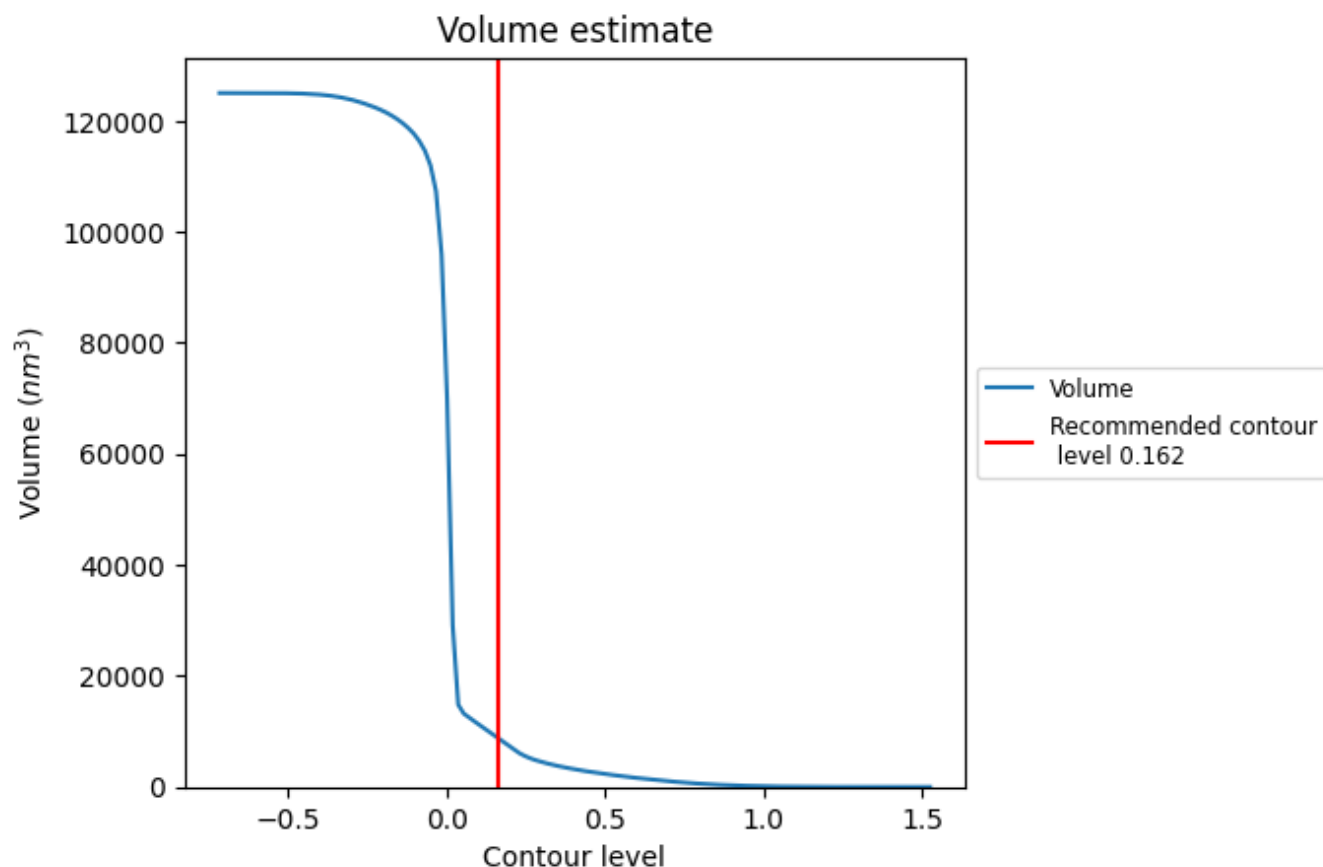
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

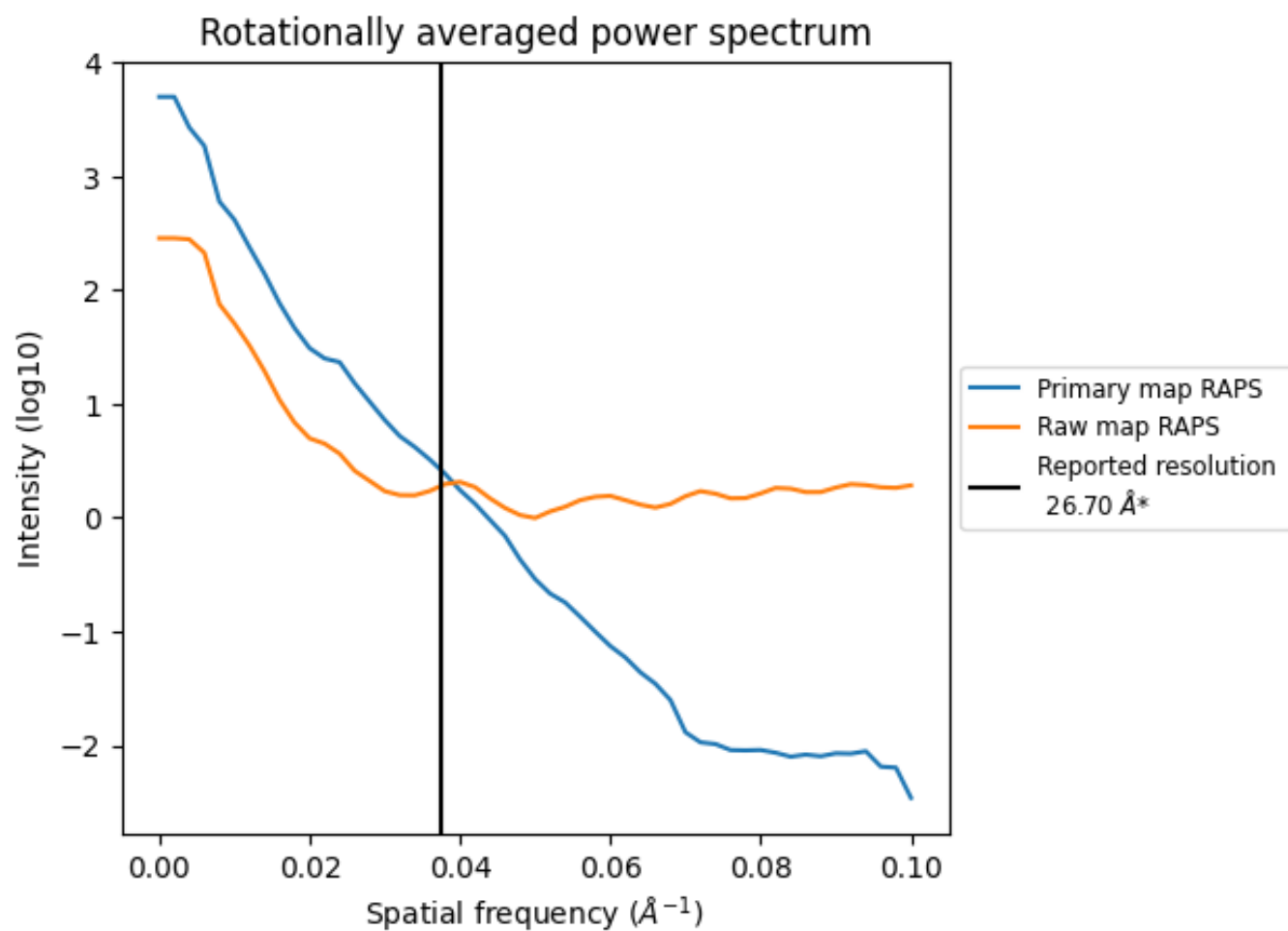
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 8809 nm³; this corresponds to an approximate mass of 7957 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 ⓘ

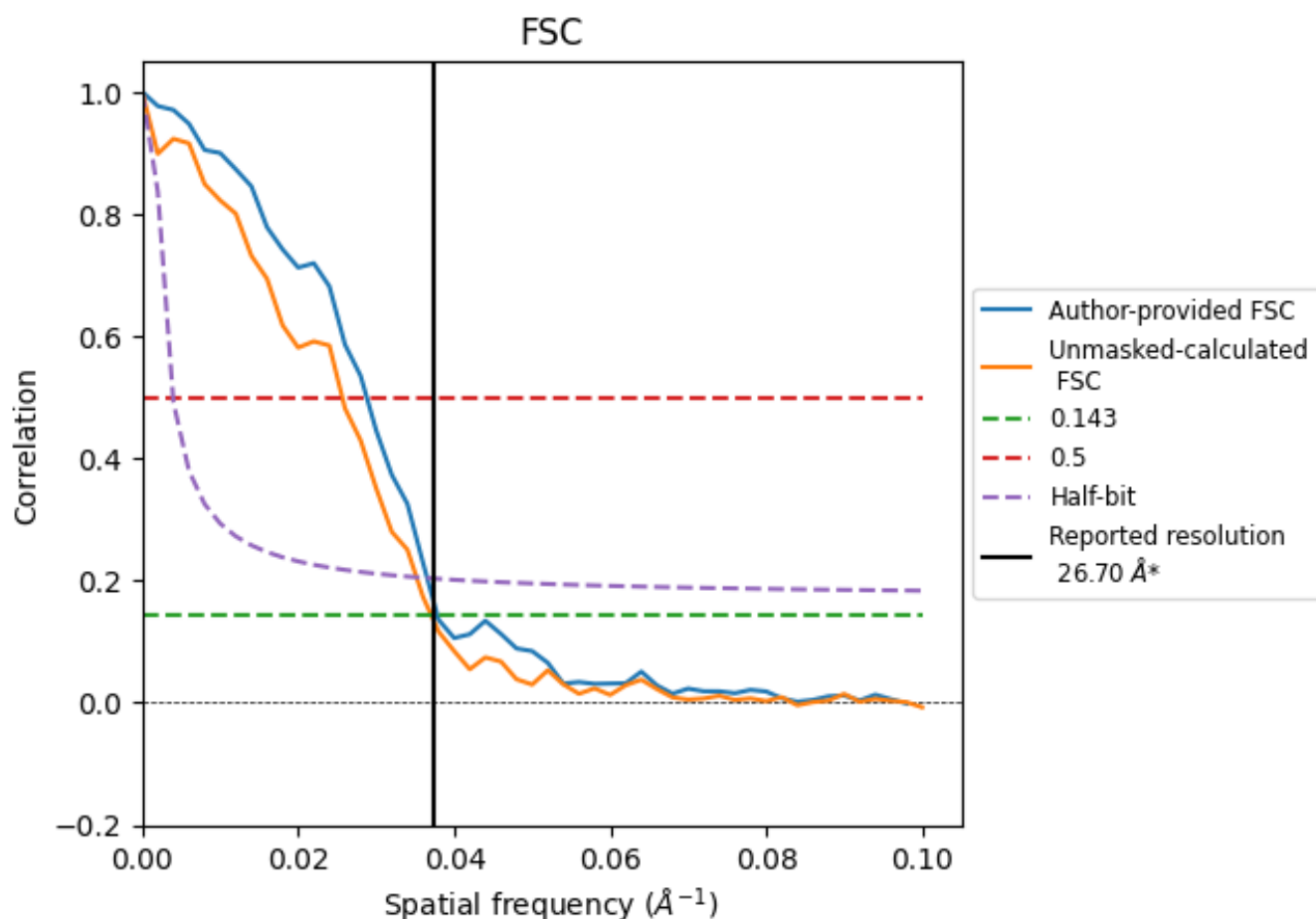


*Reported resolution corresponds to spatial frequency of $0.037 \text{ \AA}^{-1}$

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 0.037 Å⁻¹

8.2 Resolution estimates [i](#)

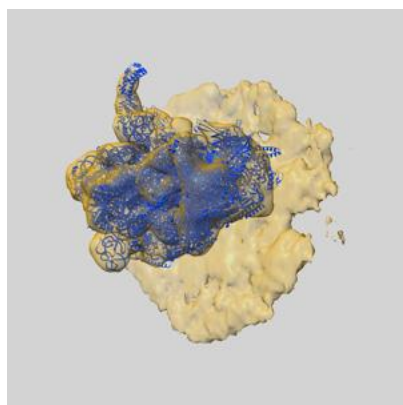
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	26.70	-	-
Author-provided FSC curve	26.46	34.72	27.32
Unmasked-calculated*	26.95	39.06	28.41

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

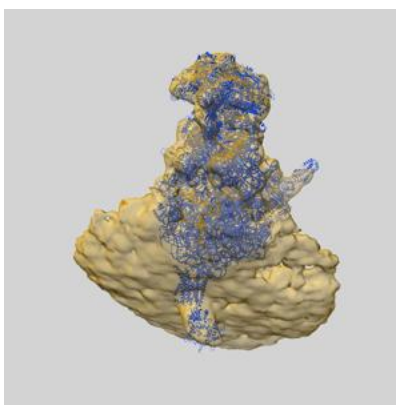
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53676 and PDB model 9SL7. Per-residue inclusion information can be found in section 3 on page 16.

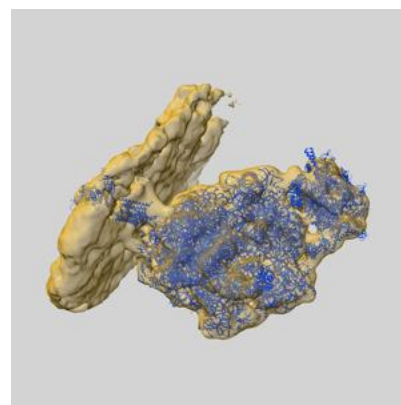
9.1 Map-model overlay [i](#)



X



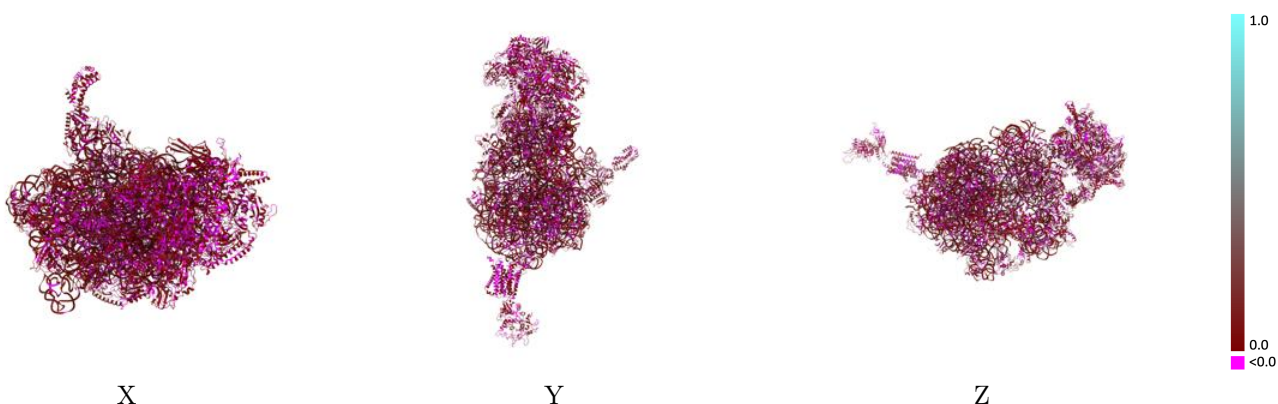
Y



Z

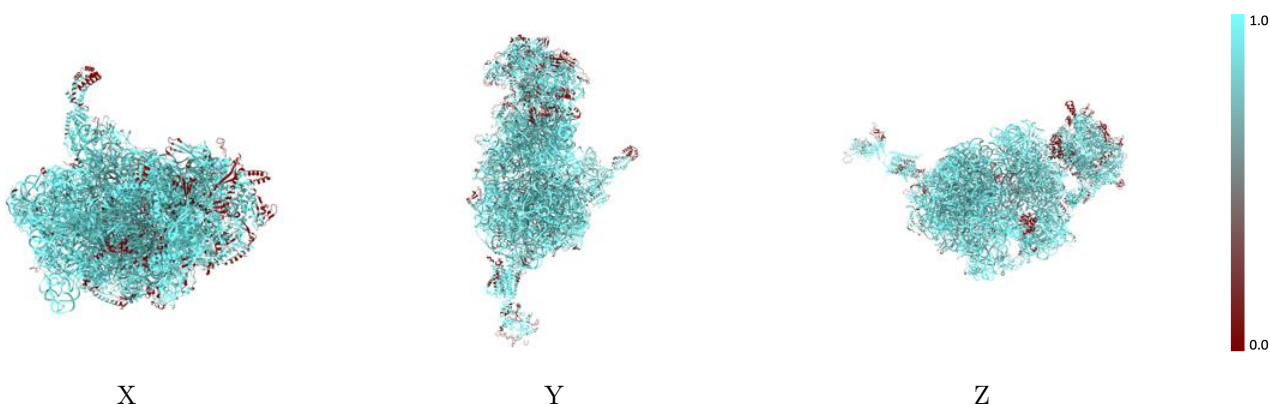
The images above show the 3D surface view of the map at the recommended contour level 0.162 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



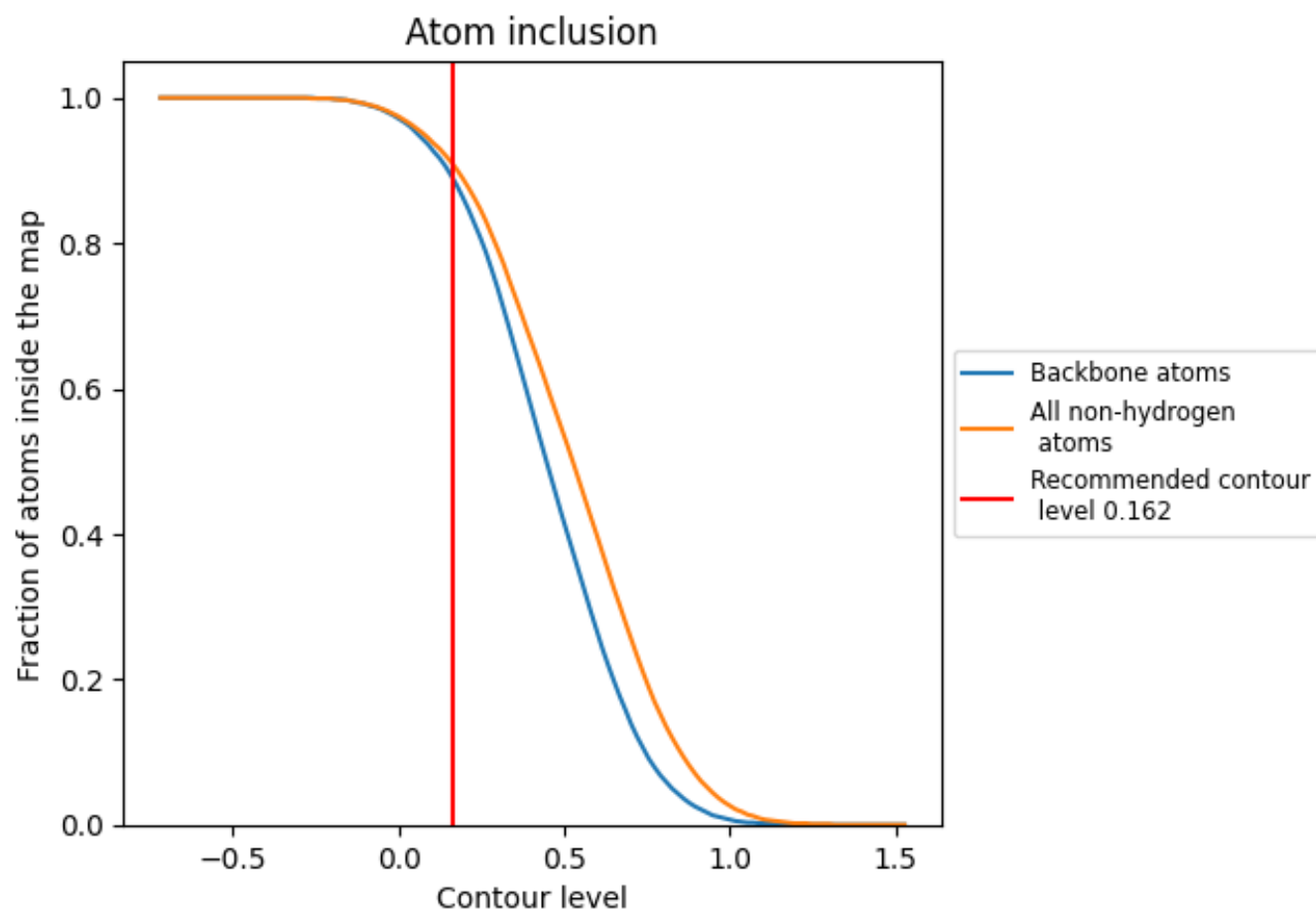
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.162).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 91% 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 (0.162) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9100	 0.0500
0	 0.9400	 -0.0500
1	 1.0000	 -0.0300
2	 0.9800	 -0.0170
3	 0.9890	 0.0680
4	 0.9990	 0.0860
5	 0.9860	 0.0700
6	 0.7820	 0.0430
7	 0.9170	 0.0820
8	 0.7540	 0.0290
9	 0.7330	 0.0270
A	 0.7880	 0.0440
AA	 0.7820	 0.0580
AB	 0.7180	 0.0420
AC	 0.8350	 0.0560
AD	 0.8900	 0.0440
AE	 0.9580	 0.0880
AF	 0.8620	 0.0600
B	 0.9430	 0.0320
C	 0.8880	 0.0030
D	 0.8380	 0.0280
E	 0.7500	 0.0400
F	 0.9120	 0.0330
G	 0.9560	 0.0320
H	 0.9200	 0.0290
I	 0.9170	 0.0340
J	 0.7940	 0.0170
K	 0.8110	 0.0290
L	 0.9220	 0.0260
M	 0.9710	 -0.0930
N	 0.9030	 0.0350
O	 0.9630	 -0.0070
P	 0.9090	 0.0160
Q	 0.9980	 0.0250
R	 0.8430	 0.0580



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Continued from previous page...

Chain	Atom inclusion	Q-score
S	 0.9290	 0.0130
T	 0.9170	 0.0230
U	 0.8220	 0.0490
V	 0.9010	 0.1110
W	 0.7280	 0.0710
X	 0.2500	 0.0370
Y	 0.0000	 0.0310
Z	 0.7660	 0.0370
a	 0.9700	 0.0100
b	 0.9320	 0.0290
c	 0.8810	 0.0290
d	 0.9310	 0.0270
e	 0.8660	 0.0370
f	 0.5810	 0.0190
h	 0.9090	 0.0640
i	 0.9550	 0.0210
j	 0.6670	 -0.0030
k	 0.8630	 0.0130
l	 0.7910	 0.0190
m	 0.9840	 0.0100
n	 0.9550	 0.0080
o	 0.8450	 0.0250
p	 0.9760	 -0.0120
q	 0.8860	 0.0300
r	 0.8200	 0.0180
s	 0.9510	 0.0180
t	 0.5210	 -0.0210
u	 0.9440	 0.0150
v	 0.9430	 -0.0310
w	 0.7420	 0.0180
x	 0.9940	 0.1000
y	 0.8920	 0.0050
z	 0.9570	 -0.0040