



wwPDB EM Validation Summary Report ⓘ

Sep 16, 2026 – 03:38 pm BST

PDB ID : 9SL5 / pdb_00009sl5
EMDB ID : EMD-53671
Title : Model of M. pneumoniae 70S eT-TC (stable)
Authors : Dobbs, J.M.; Mahamid, J.
Deposited on : 2025-09-03
Resolution : 6.50 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:

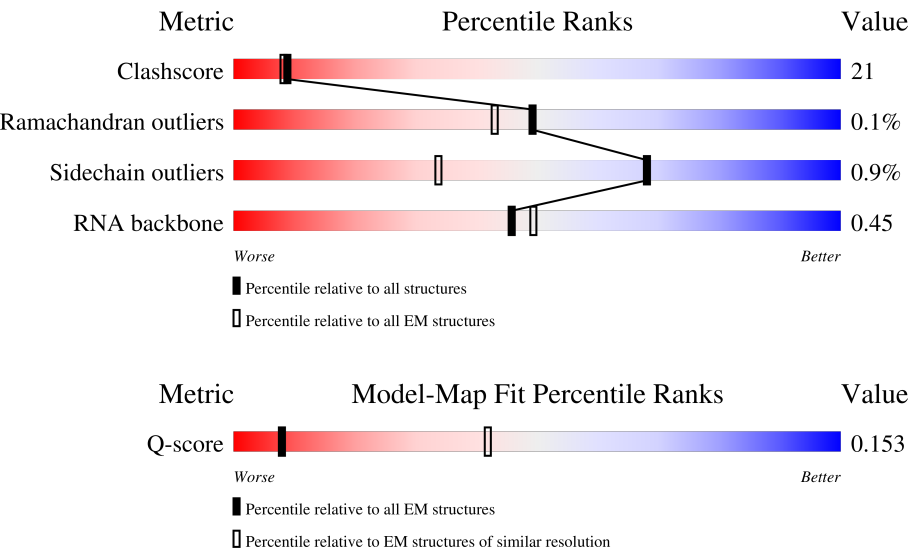
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 6.50 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.



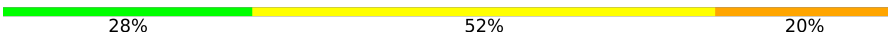
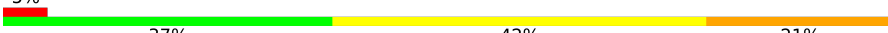
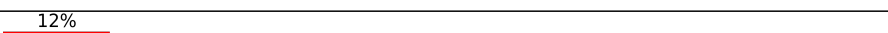
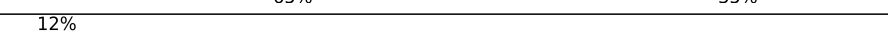
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	556 (6.00 - 7.00)

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	13% 72% 28%
2	1	59	12% 69% 31%
3	2	37	• 41% 59%

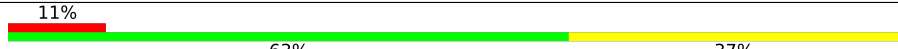
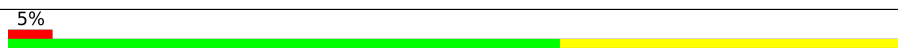
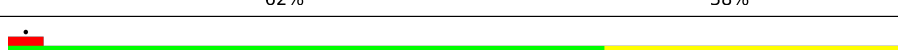
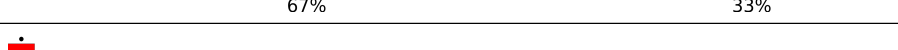
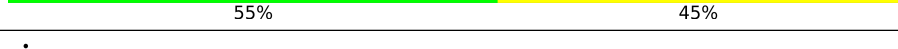
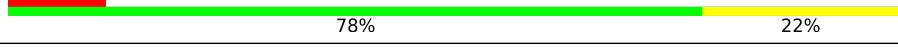
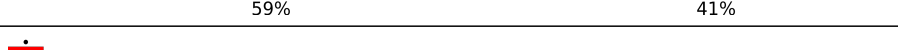
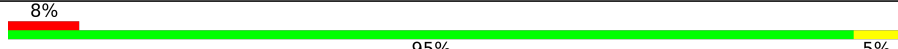
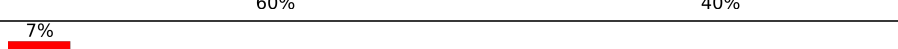
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Mol	Chain	Length	Quality of chain
4	3	2878	
5	4	105	
6	5	1493	
7	6	327	
7	AB	327	
8	7	76	
9	9	1391	
10	A	240	
11	AA	89	
12	AC	366	
13	AD	32	
14	AE	32	
15	AF	160	
16	B	215	
17	C	203	
18	D	153	
19	E	167	
20	F	154	
21	G	141	
22	H	128	
23	I	101	
24	J	114	
25	K	136	
26	L	118	
27	M	60	

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Mol	Chain	Length	Quality of chain
28	N	83	
29	O	80	
30	P	83	
31	Q	65	
32	R	84	
33	S	77	
34	T	53	
35	U	161	
36	V	29	
36	W	29	
36	X	29	
36	Y	29	
37	Z	1276	
38	a	285	
39	b	229	
40	c	210	
41	d	175	
42	e	176	
43	f	145	
44	h	128	
45	i	144	
46	j	122	
47	k	148	
48	l	136	
49	m	119	

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Mol	Chain	Length	Quality of chain
50	n	116	
51	o	115	
52	p	114	
53	q	99	
54	r	139	
55	s	92	
56	t	111	
57	u	86	
58	v	63	
59	w	108	
60	x	44	
61	y	56	
62	z	50	

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 177858 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 DNA-directed RNA polymerase subunit beta.

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

- Molecule 10 is a protein called Small ribosomal subunit protein uS2.

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

- Molecule 11 is a protein called Probable DNA-directed RNA polymerase subunit delta.

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

- Molecule 12 is a protein called Transcription termination/antitermination protein NusA.

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

- Molecule 13 is a DNA chain called DNA.

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

- Molecule 14 is a DNA chain called DNA.

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

- Molecule 15 is a protein called Transcription termination/antitermination protein NusG.

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

- Molecule 16 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 17 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 18 is a protein called Small ribosomal subunit protein uS5.

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

- Molecule 19 is a protein called Small ribosomal subunit protein bS6.

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

- Molecule 20 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 21 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 22 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 23 is a protein called Small ribosomal subunit protein uS10.

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

- Molecule 24 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 25 is a protein called Small ribosomal subunit protein uS12.

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

- Molecule 26 is a protein called Small ribosomal subunit protein uS13.

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

- Molecule 27 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 28 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 29 is a protein called Small ribosomal subunit protein bS16.

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

- Molecule 30 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 31 is a protein called Small ribosomal subunit protein bS18.

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

- Molecule 32 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 33 is a protein called Small ribosomal subunit protein bS20.

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

- Molecule 34 is a protein called Small ribosomal subunit protein bS21.

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

- Molecule 35 is a protein called 50S ribosomal protein L10.

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

- Molecule 36 is a protein called Large ribosomal subunit protein bL12.

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

- Molecule 37 is a protein called DNA-directed RNA polymerase subunit beta'.

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

- Molecule 38 is a protein called Large ribosomal subunit protein uL2.

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

- Molecule 39 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 40 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 41 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 42 is a protein called Large ribosomal subunit protein uL6.

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

- Molecule 43 is a protein called Large ribosomal subunit protein bL9.

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

- Molecule 44 is a protein called Large ribosomal subunit protein uL11.

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

- Molecule 45 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 46 is a protein called 50S ribosomal protein L14.

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

- Molecule 47 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 48 is a protein called Large ribosomal subunit protein uL16.

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

- Molecule 49 is a protein called Large ribosomal subunit protein bL17.

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

- Molecule 50 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 51 is a protein called Large ribosomal subunit protein bL19.

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

- Molecule 52 is a protein called Large ribosomal subunit protein bL20.

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

- Molecule 53 is a protein called Large ribosomal subunit protein bL21.

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

- Molecule 54 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 55 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 56 is a protein called 50S ribosomal protein L24.

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

- Molecule 57 is a protein called Large ribosomal subunit protein bL27.

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

- Molecule 58 is a protein called Large ribosomal subunit protein bL28.

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

- Molecule 59 is a protein called Large ribosomal subunit protein uL29.

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

- Molecule 60 is a protein called Large ribosomal subunit protein bL31.

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

- Molecule 61 is a protein called Large ribosomal subunit protein bL32.

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

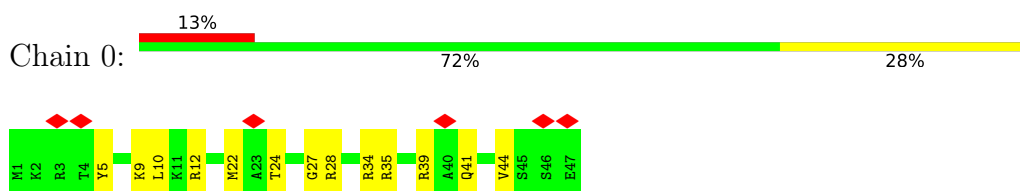
- Molecule 62 is a protein called Large ribosomal subunit protein bL33A.

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

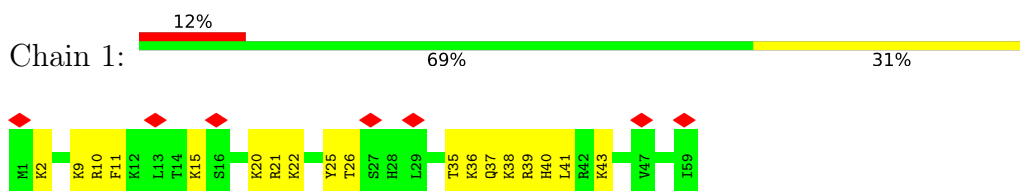
3 Residue-property plots

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.

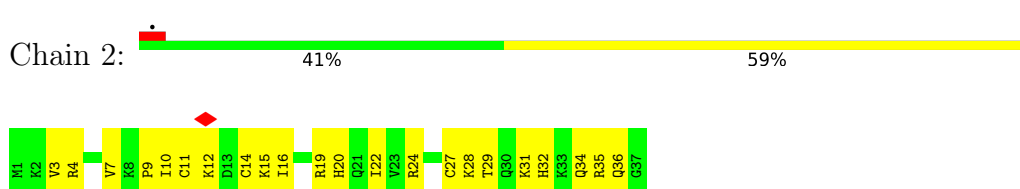
- Molecule 1: Large ribosomal subunit protein bL34



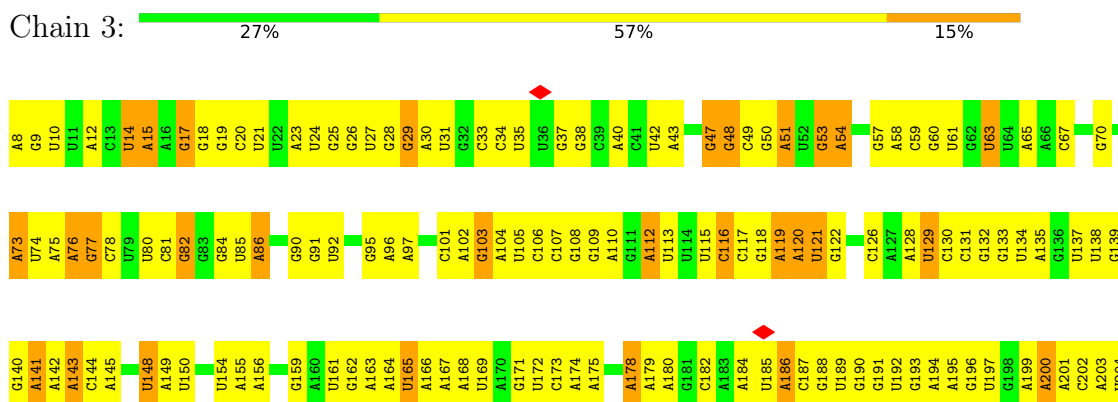
- Molecule 2: 50S ribosomal protein L35



- Molecule 3: 50S ribosomal protein L36

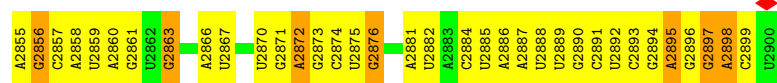


- Molecule 4: 23S ribosomal RNA



U1150	A1083	G1018	C949	G873	G811	G742	U676	G610	U544	C480	U411	A343	A274	C205
U1151	C1084	A1019	U950	U874	G812	G743	A679	A611	C545	C481	A412	A344	A275	
U1154	A1085	G1020	U951	G875	G813	U744	A680	G612	U546	G482	G413	A345	A276	A208
G1155	G1086	C1021	U952	A876	U814	U745	G680	G613	G547	A483		G346		G209
C1156	C1087	C1022	G953	G877	A816	G746	A681	C614	A548	U484	G418	A347	U279	U210
A1157	A1088	C1023	A954	A878	A817	A747	A682	G615	A549	A485	A419	A348	A280	A211
G1157	G1089	A1024	A955		A818		G683	G616	A550	A486	A420	G349	U281	G212
C1158	C1090	G1025		A881	A819	G752	A684	C617	C551	G488	A421	C350		G213
C1159	G1091	A1026	C958	C882	U819	A753	G685		C552	G489	A422	C351	U284	C214
G1160	A1092	U1027	C959	A883	U820	U754	C686	G620	A553	A490	C423	C352	U285	A215
A1161	A1093	A960	A960		C821	C755	C687	G621		A491	G424	C353	A286	C216
G1162	G1094	A1029	U961	U886	C822	A756	U688	G622	C558	A492	U425	C354	G287	A217
C1163	C1095	U1030	U962		A823	A757	U689	G623	C559	A493	U426	A355	A288	G218
A1164	A1096	U1031	U963	G891	A824	G758	U690	U624	U560	A494	A427	A356	U289	G219
U1165	G1097	A1032	A964	G892	U825		G691	U625	A561	G495	U428	A357	A290	A220
G1166	C1098	A1033	U965	A893	C826	U759	U692	G626	C562	U496	U429	A358	G291	A221
U1167	C1099	A1034	U966	G894	G827	G760	U693	G627	A563	A497	U430	G359	G292	A222
A1168	U1100	U1035	U967	G895	A828	A762	U694	G628	A564	C497	U431	G360	G293	A223
U1169	A1036	A1036		U896	A829	G763	G695	G629	C565	C498	G432		G294	G224
C1170	A1037	A1037	C974	A897	A830	G764	U696	C630	G566	C499	A433	G363	U295	A225
G1171	G1103	G1038	G975	A898	U831	A765	U697	A631	U567	U500	A434	A364	U296	A226
G1172	A1104	A1039	C976	A899	C832	C766	A698	G632	C568	G501	U435	G372	G297	A227
G1173	A1105	U1040	A977	G900	C833	C767	U699	G633	U569	A502	G436	G367	U298	A228
G1174	G1106	C1041	G978	C901		G768	U700		C570		A437	C369	A299	A229
G1175	C1042	U901	U979	U902	A837	A769	A701	U636	A571	G505	A438	C370	G300	G230
U1176	C1043	A903	C980	A903	U838	A770	U702	U637	G572		U439	C371	G301	A231
A1178	A1044	C904	A981	U905	A839	C771	A703	A638	A573	G509	U441	G372	G306	U232
G1179	G1045	U906	G982	C906	G840	C772	G704	G639	C575	U511	G442	G373	C307	A233
U1180	A1046	U907	C984	G906	C841	G773	C705	U640	C576	U512		A374	G308	G234
G1181	C1114	A1047	C984		U842	A774			C577	A513	C445		A309	U235
A1181	A1048	A1048	A985	A912	G843	C775	A711	C645		A514	A446	U377	U310	G236
U1182	U1049	U1049	G986	G914	G844		A712	A646	U580	A515	G447	G378	G311	A237
A1183	U1117	A1050	U987	G914	U845	G780	C713	G647	A581	A516	A448	A379	U312	U238
U1184	U1118		G988	A915	U846	U781	G714	G648	A582	G517	C449	A380	G313	U239
U1185	U1054	U1054	G989	U916	C847	U782	G715	A649	A583	A518	C450	A381	G314	C241
A1186	A1055	A1055	G990	G917	U848	G783	G716	G650		A519	A451	U382	A315	G242
C1187	A1056	A1056	G991	G918	C849	A784		A651	U587	C520	U452	U383	C316	U243
C1188	G1057	G1057	G992	C919	G850		G719	U652	G588	G521	U453	G384	U317	U244
G1189	A1061	A1061	A993	G920	U851	G788		G653	G589	U528	U454	U385	U318	U245
A1190	C1127	A1062	U994	G928	C852	A789	A720	G654	A589	G529	C462	A392	G319	G246
A1191	G1128		A995	G929	G853	U790	G721	G655	U590	A523	G463	U393	A328	
U1192	U1129		A996	G930	A854	A791	C722	G656	G591	G524	U464	C394	G329	U247
A1130			G997	C930	A855	G792	U723	A657	G592	A525	A465	A330		
A1131			C998	G931	A856	C793	A724	G658	C593	G526	A466		A322	U250
			U999	U932	U857	G794	G725	C659	G594	A527	G460	A390	A323	G251
			U1000		A858	G795	U726		U595	U528	C461	U391	G325	G252
			C1001		C859	A796	C727	G661	G596	G529	C462	A392	C253	
			A1002		C860	U797	A728	U662	C597	G530	U463	C393	G254	
					C861	G798	U729	A663	G598	G531	A464	C394	A255	
					U862	A799	G730		U599	A532	A465	A330	G256	
					U863	C800	A731	G666	U600	G533	A466	G401	C257	
					A864	U801	G732	A667	U601	U534	U467	A402	G258	
					A865	U802	G733	A668	U602	G535	A468	U403	A259	
					C866	C803	A734	A669	G603	A536		C404	G335	A267
					C867			G670	A604	A537	U474	C405	G336	G268
					C868	A806	U737	C671	A605	A538		C406	U337	A269
					U869	U807	U738	G672	G606	U539	G476	U407	G338	
					A870	U808	G739	A673	U607	A540	U477	G408	G270	
					C871	A809	A741	G674	A608		G478	A409	G341	
					C872	G810		U675	U609	U543	A479	G410	G342	

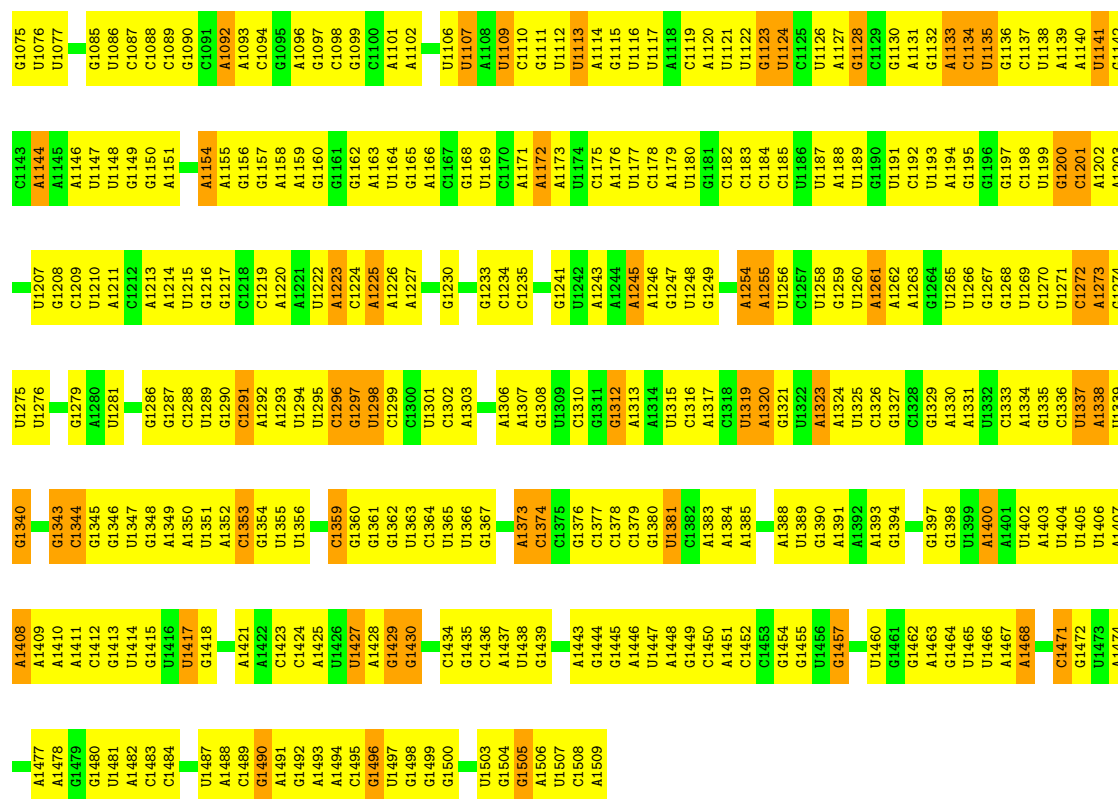




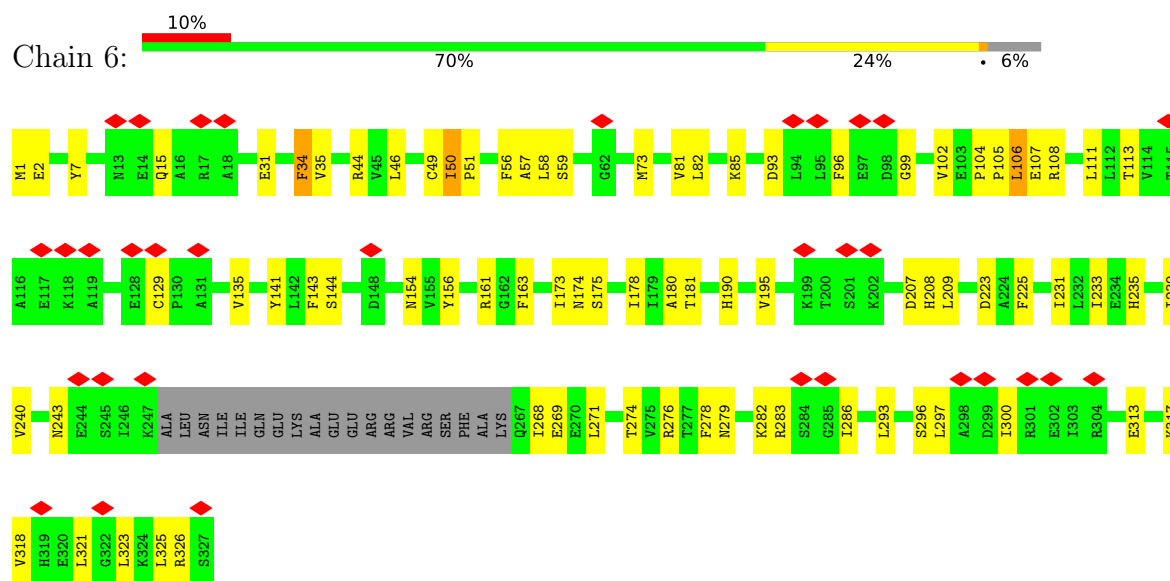
Chain 4: 28% 52% 20%

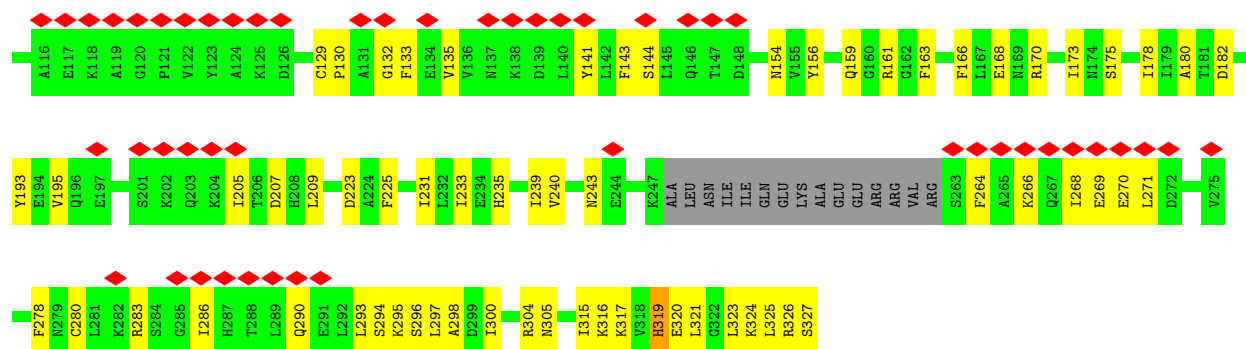




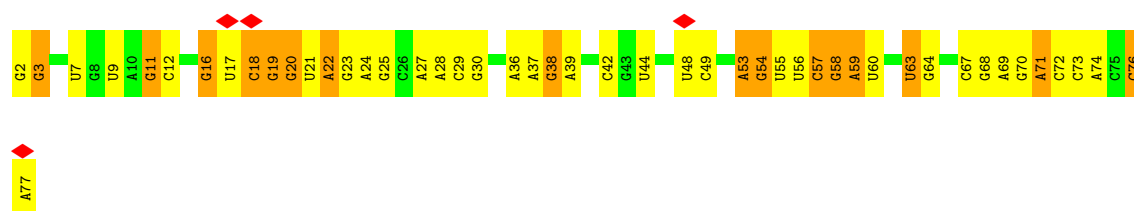


• Molecule 7: DNA-directed RNA polymerase subunit alpha

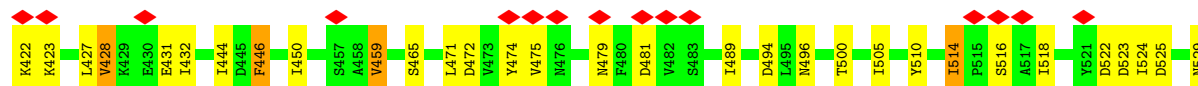
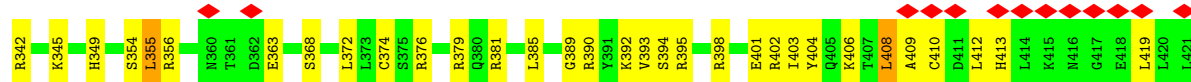
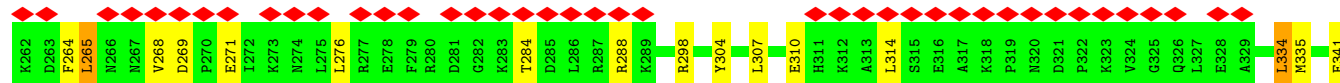
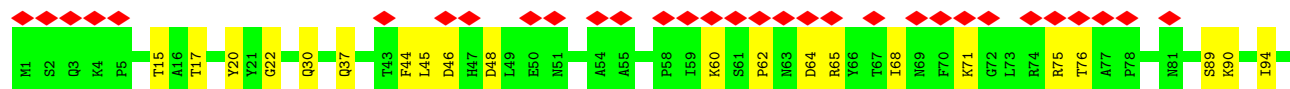


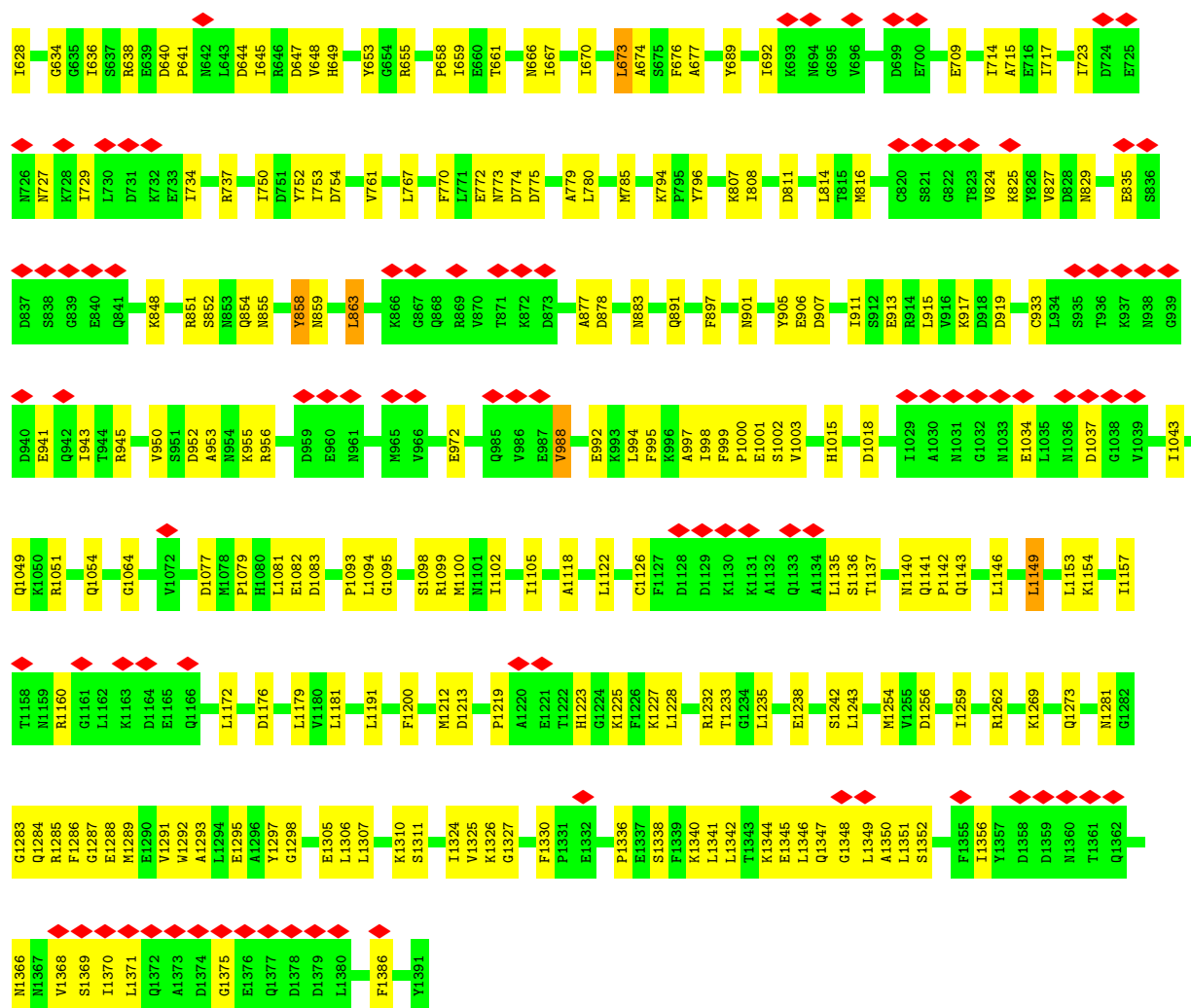


• Molecule 8: tRNA-Phe

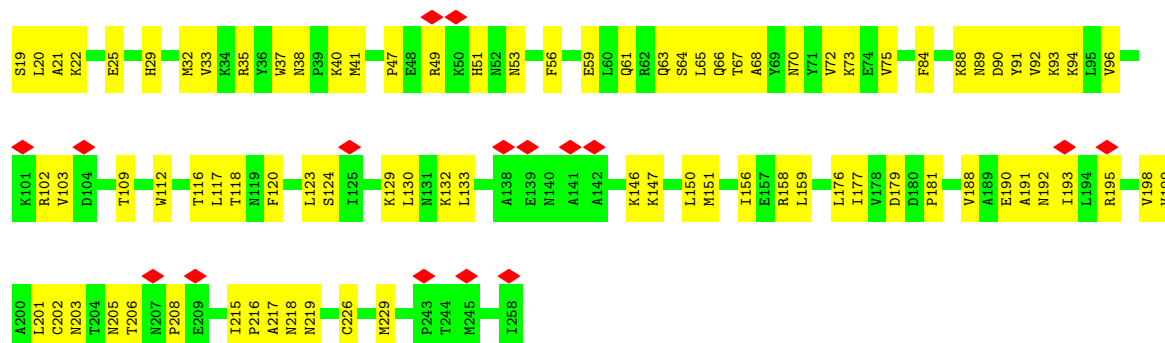


• Molecule 9: DNA-directed RNA polymerase subunit beta

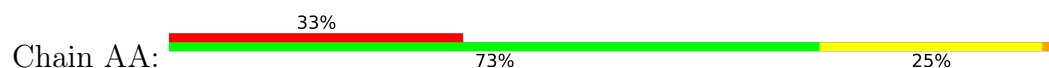


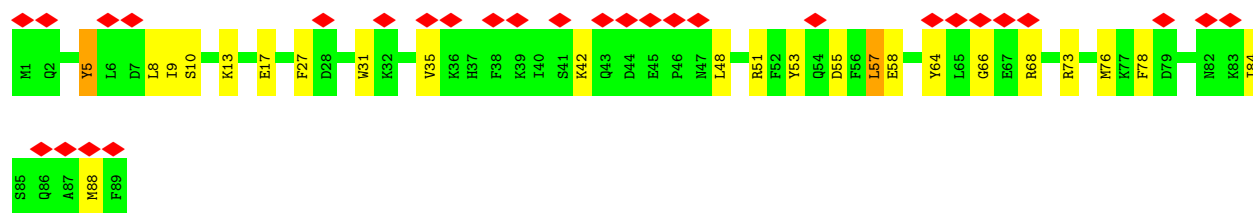


• Molecule 10: Small ribosomal subunit protein uS2

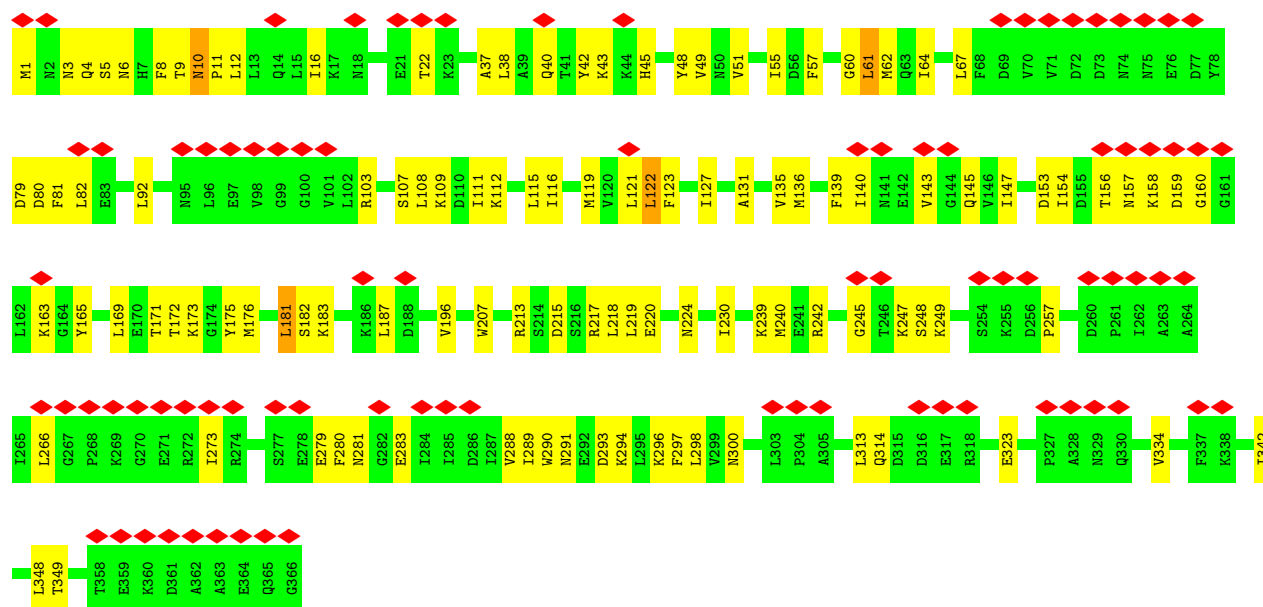


• Molecule 11: Probable DNA-directed RNA polymerase subunit delta





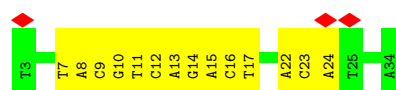
• Molecule 12: Transcription termination/antitermination protein NusA



• Molecule 13: DNA

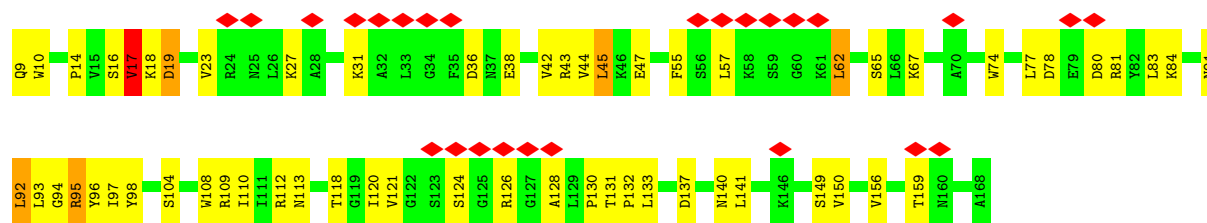


• Molecule 14: DNA

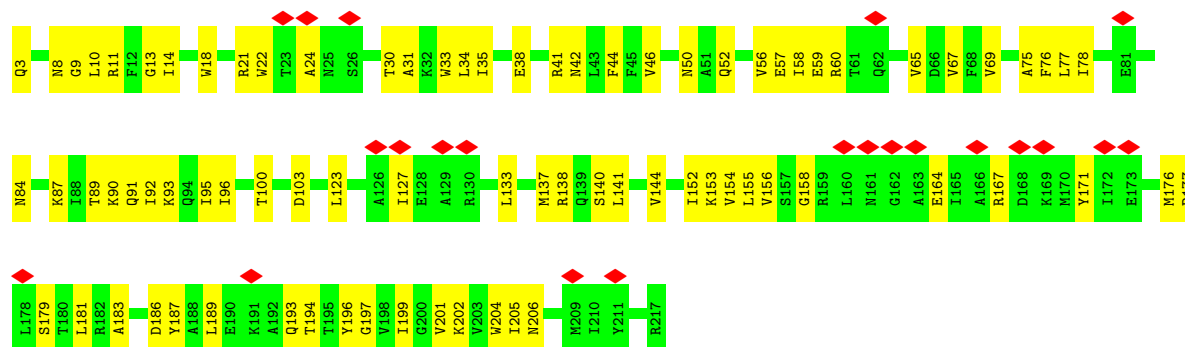


• Molecule 15: Transcription termination/antitermination protein NusG

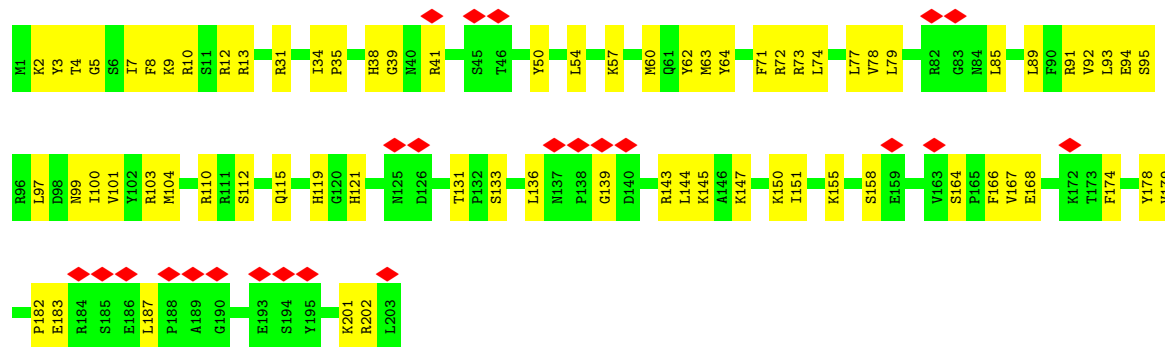




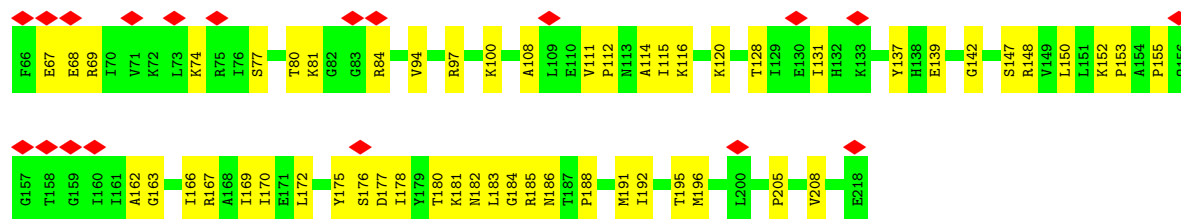
- Molecule 16: Small ribosomal subunit protein uS3



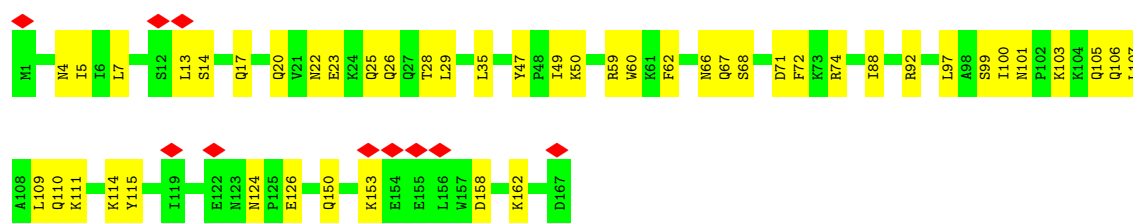
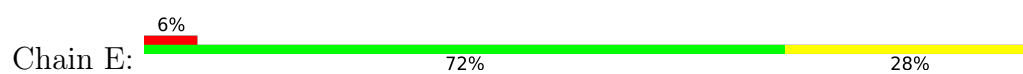
- Molecule 17: Small ribosomal subunit protein uS4



- Molecule 18: Small ribosomal subunit protein uS5



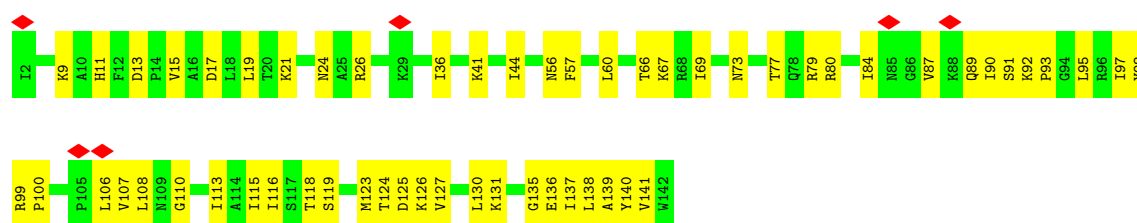
- Molecule 19: Small ribosomal subunit protein bS6



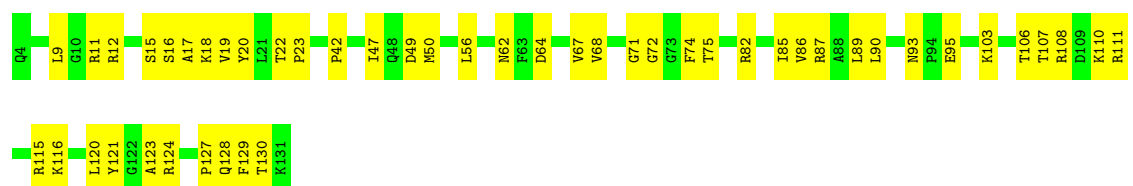
- Molecule 20: Small ribosomal subunit protein uS7



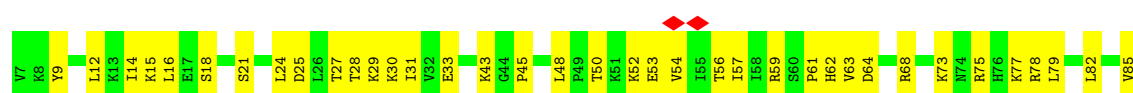
- Molecule 21: Small ribosomal subunit protein uS8



- Molecule 22: Small ribosomal subunit protein uS9



- Molecule 23: Small ribosomal subunit protein uS10

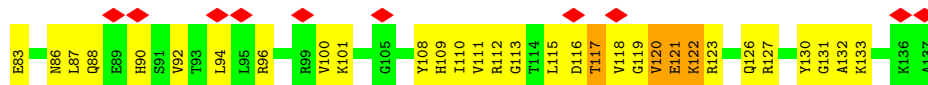
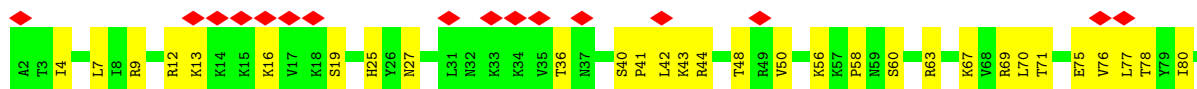




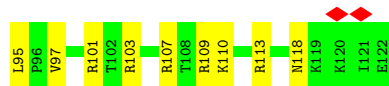
- Molecule 24: Small ribosomal subunit protein uS11



- Molecule 25: Small ribosomal subunit protein uS12



- Molecule 26: Small ribosomal subunit protein uS13

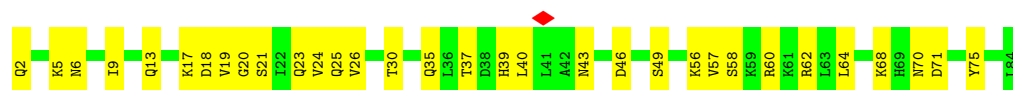


- Molecule 27: Small ribosomal subunit protein uS14

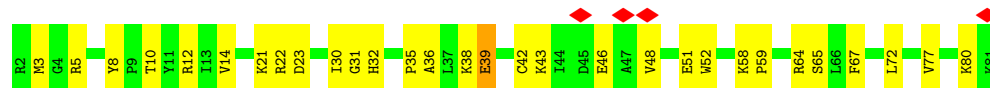


- Molecule 28: Small ribosomal subunit protein uS15





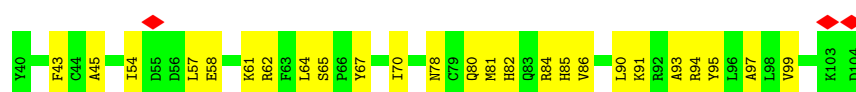
- Molecule 29: Small ribosomal subunit protein bS16



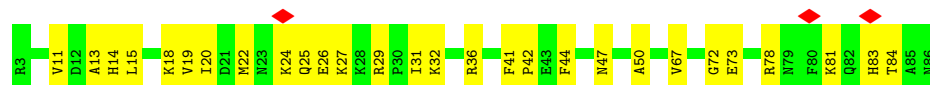
- Molecule 30: Small ribosomal subunit protein uS17



- Molecule 31: Small ribosomal subunit protein bS18



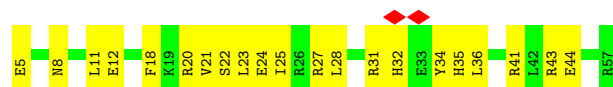
- Molecule 32: Small ribosomal subunit protein uS19



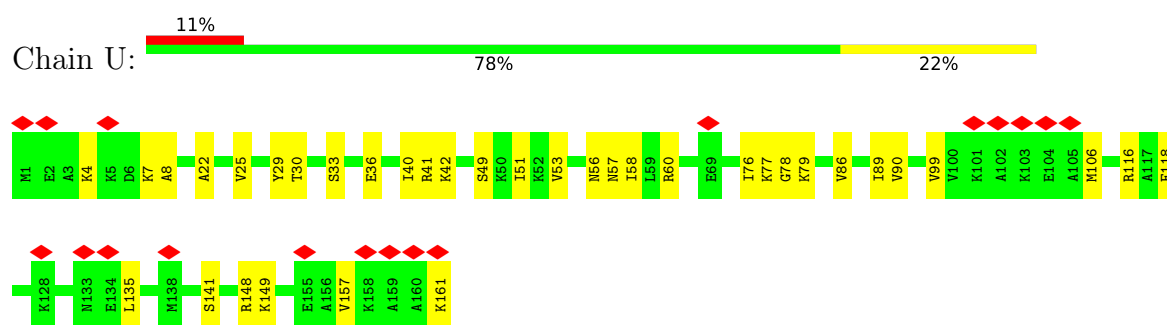
- Molecule 33: Small ribosomal subunit protein bS20



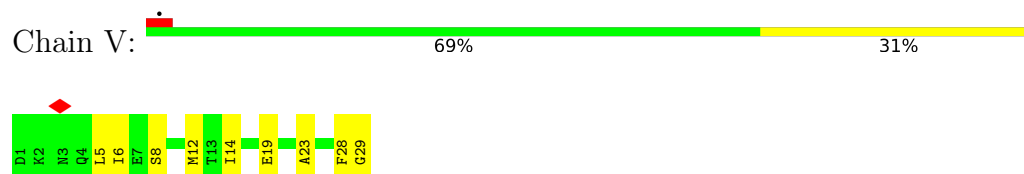
- Molecule 34: Small ribosomal subunit protein bS21



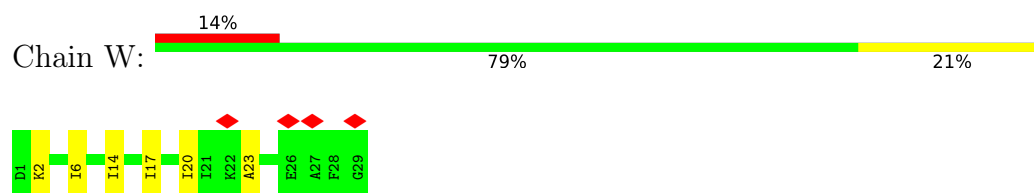
- Molecule 35: 50S ribosomal protein L10



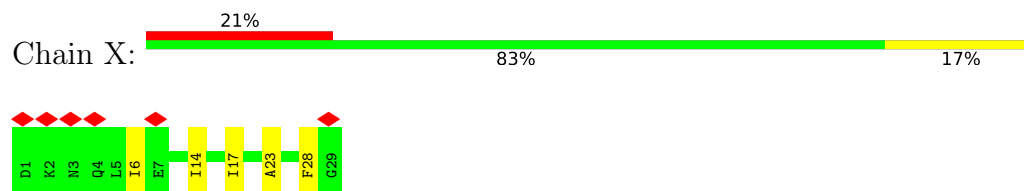
- Molecule 36: Large ribosomal subunit protein bL12



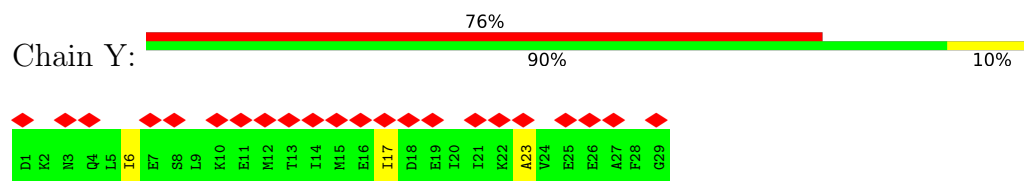
- Molecule 36: Large ribosomal subunit protein bL12



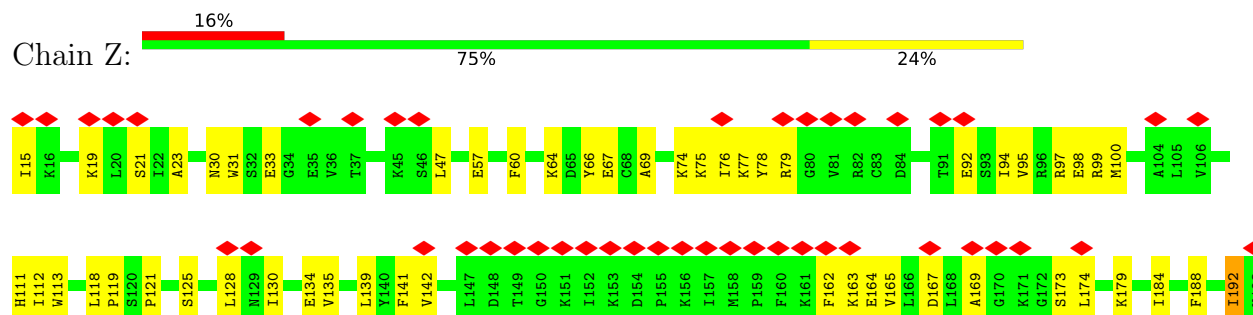
- Molecule 36: Large ribosomal subunit protein bL12

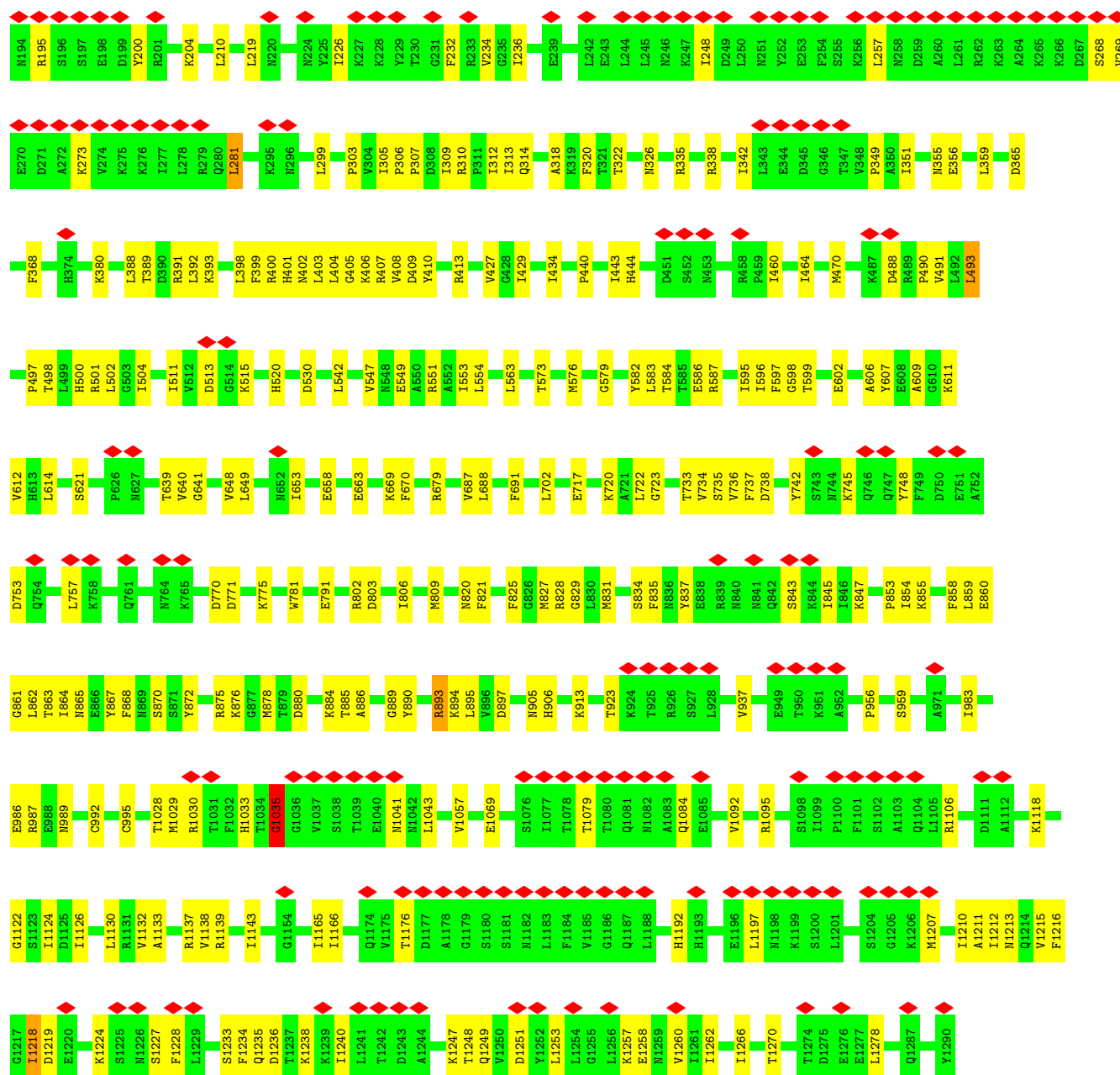


- Molecule 36: Large ribosomal subunit protein bL12

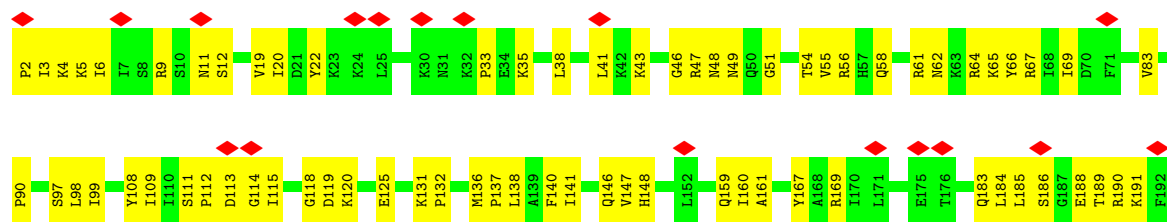


- Molecule 37: DNA-directed RNA polymerase subunit beta'





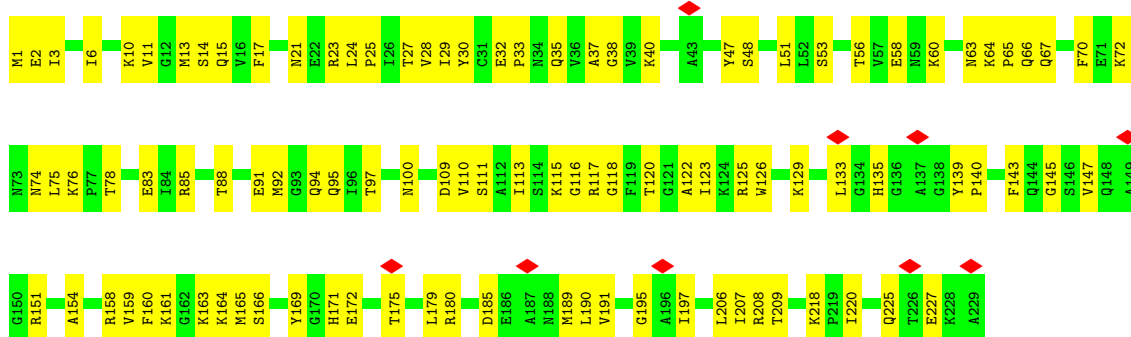
• Molecule 38: Large ribosomal subunit protein uL2





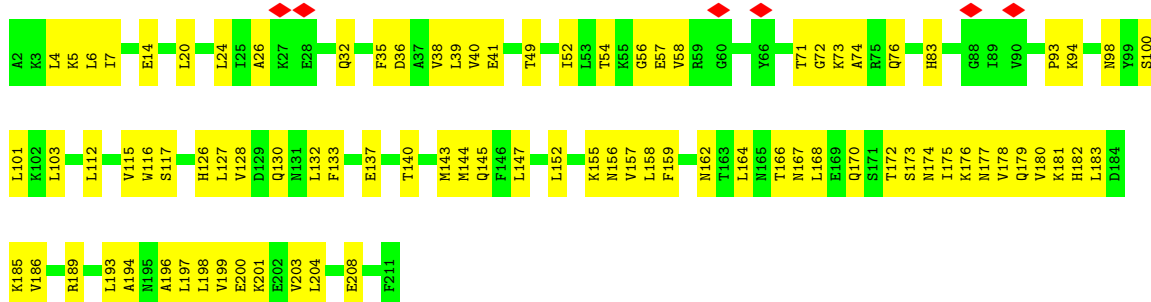
• Molecule 39: Large ribosomal subunit protein uL3

Chain b: 55% 45%



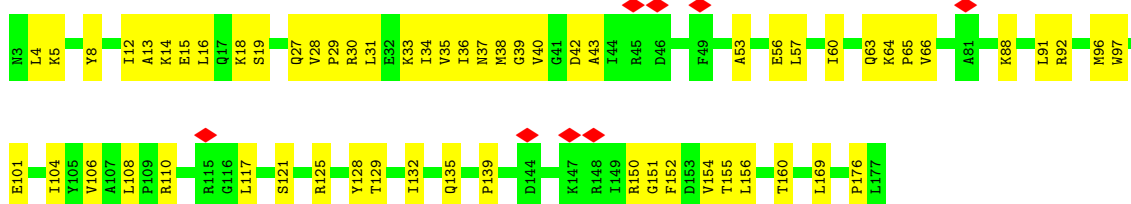
• Molecule 40: Large ribosomal subunit protein uL4

Chain c: 59% 41%



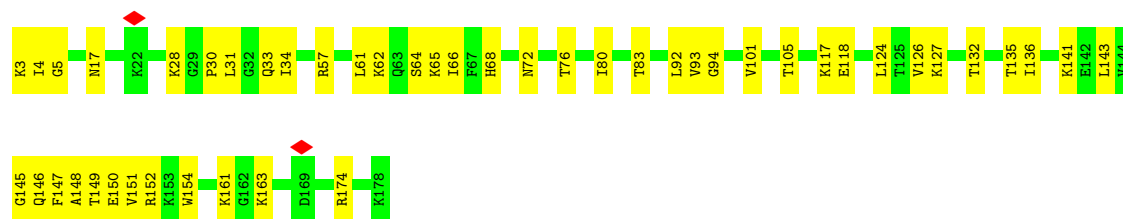
• Molecule 41: Large ribosomal subunit protein uL5

Chain d: 5% 66% 34%

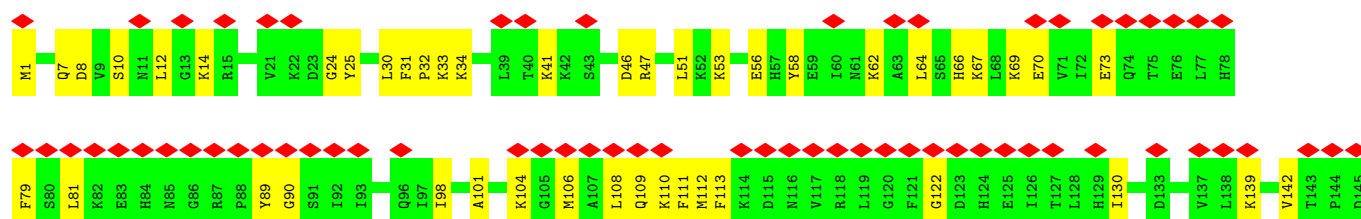


• Molecule 42: Large ribosomal subunit protein uL6

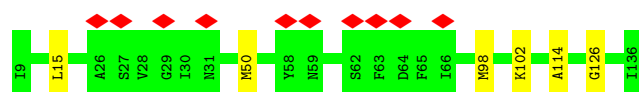
Chain e: 73% 27%



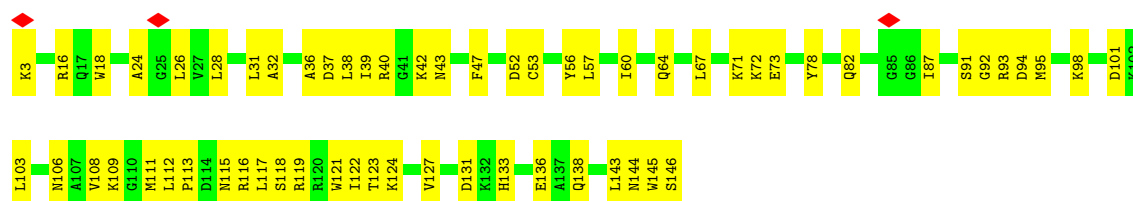
- Molecule 43: Large ribosomal subunit protein bL9



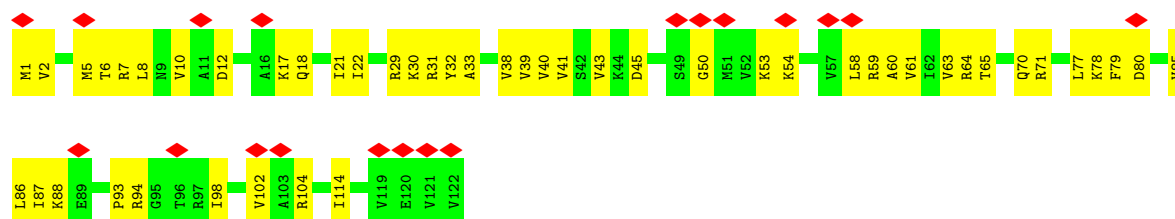
- Molecule 44: Large ribosomal subunit protein uL11



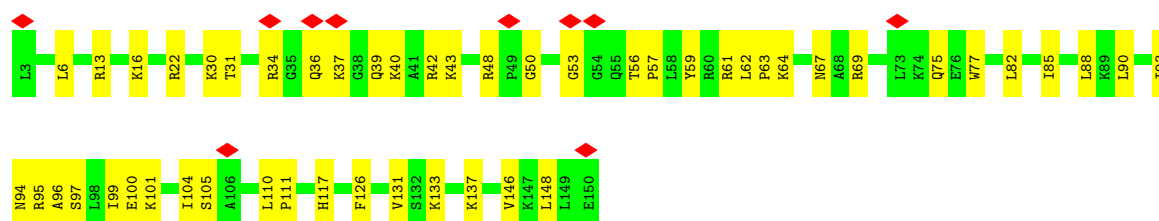
- Molecule 45: Large ribosomal subunit protein uL13



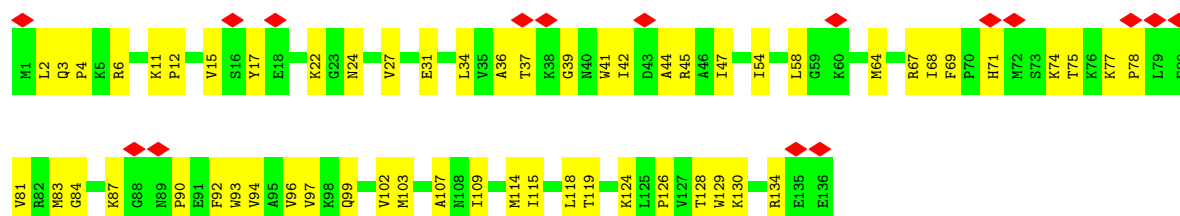
- Molecule 46: 50S ribosomal protein L14



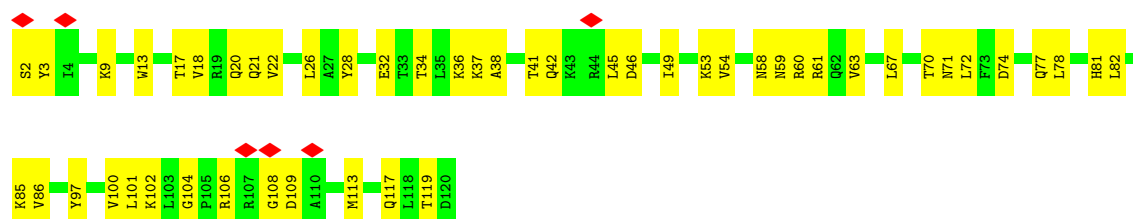
- Molecule 47: Large ribosomal subunit protein uL15



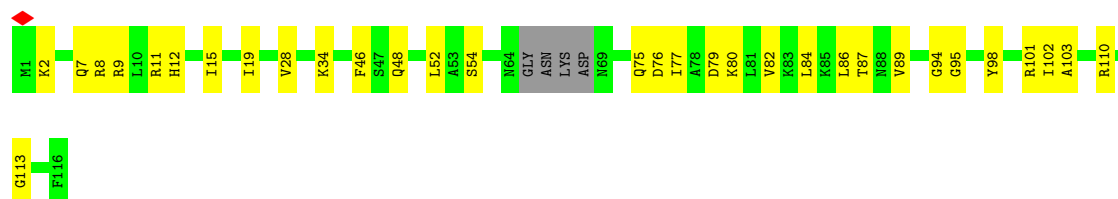
- Molecule 48: Large ribosomal subunit protein uL16



- Molecule 49: Large ribosomal subunit protein bL17



- Molecule 50: Large ribosomal subunit protein uL18

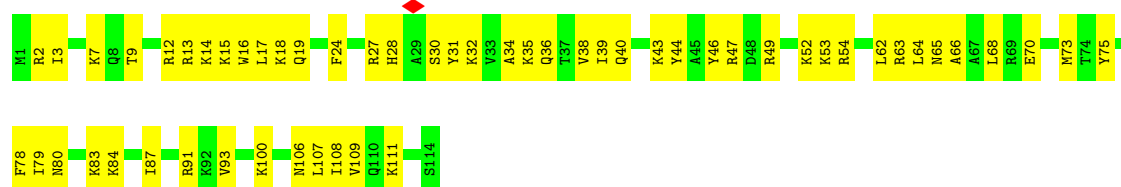


- Molecule 51: Large ribosomal subunit protein bL19

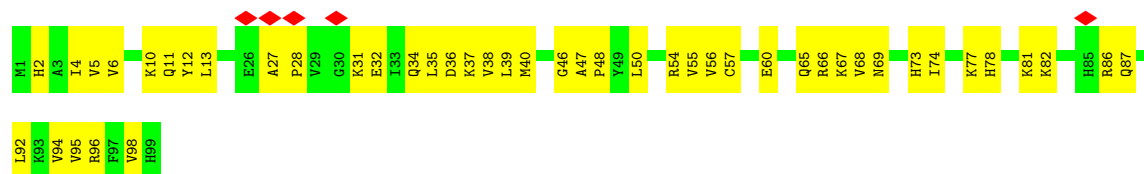




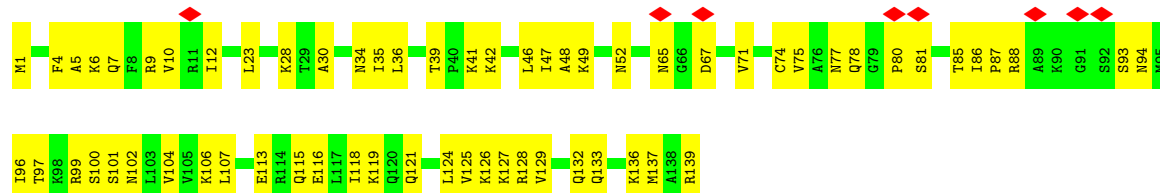
- Molecule 52: Large ribosomal subunit protein bL20



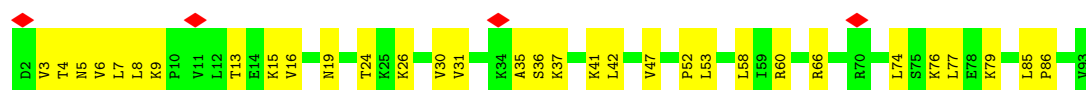
- Molecule 53: Large ribosomal subunit protein bL21



- Molecule 54: Large ribosomal subunit protein uL22

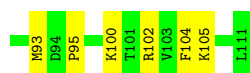


- Molecule 55: Large ribosomal subunit protein uL23

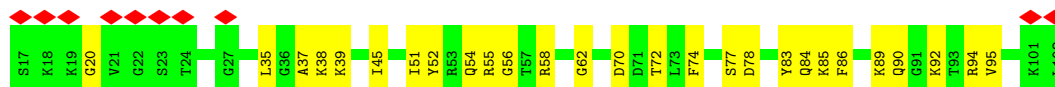


- Molecule 56: 50S ribosomal protein L24





- Molecule 57: Large ribosomal subunit protein bL27



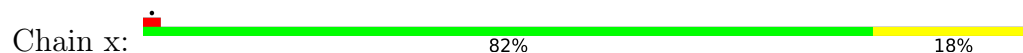
- Molecule 58: Large ribosomal subunit protein bL28



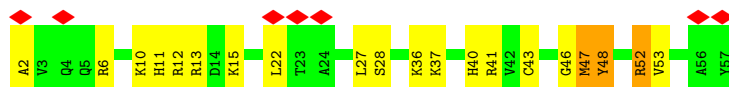
- Molecule 59: Large ribosomal subunit protein uL29



- Molecule 60: Large ribosomal subunit protein bL31

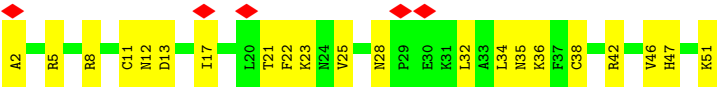


- Molecule 61: Large ribosomal subunit protein bL32



- Molecule 62: 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	3261	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	0.019	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00157	Depositor
Map size (Å)	600.0, 600.0, 600.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.0, 2.0, 2.0	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	0.18	0/484	0.54	0/637
3	2	0.16	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	0.09	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	9	0.70	0/11124	1.06	0/15014
10	A	0.15	0/1954	0.43	0/2642
11	AA	0.69	0/792	1.05	0/1065
12	AC	0.70	0/2922	1.01	0/3944
13	AD	0.47	0/745	0.61	1/1149 (0.1%)
14	AE	0.65	1/725 (0.1%)	0.75	2/1115 (0.2%)
15	AF	0.70	0/1298	1.00	0/1752
16	B	0.18	0/1721	0.49	0/2323
17	C	0.17	0/1691	0.49	0/2267
18	D	0.19	0/1188	0.52	1/1593 (0.1%)
19	E	0.17	0/1384	0.48	2/1867 (0.1%)
20	F	0.19	0/1266	0.56	1/1700 (0.1%)
21	G	0.18	0/1126	0.53	0/1517
22	H	0.17	0/1044	0.47	0/1395
23	I	0.20	0/820	0.58	1/1103 (0.1%)
24	J	0.16	0/844	0.44	0/1136
25	K	0.28	0/1094	0.60	2/1468 (0.1%)
26	L	0.19	0/962	0.50	0/1289
27	M	0.18	0/483	0.51	0/643
28	N	0.15	0/679	0.49	1/907 (0.1%)
29	O	0.18	0/659	0.57	1/885 (0.1%)
30	P	0.15	0/684	0.42	0/913
31	Q	0.20	0/545	0.60	0/730
32	R	0.16	0/698	0.49	0/936
33	S	0.18	0/631	0.46	0/838

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	T	0.20	0/475	0.56	0/621
35	U	0.68	0/1254	1.11	0/1677
36	V	0.65	0/232	1.16	2/307 (0.7%)
36	W	0.60	0/232	1.10	0/307
36	X	0.64	0/232	1.04	0/307
36	Y	0.64	0/232	1.07	0/307
37	Z	0.71	0/10259	1.06	2/13846 (0.0%)
38	a	0.16	0/2267	0.43	0/3044
39	b	0.17	0/1795	0.51	0/2412
40	c	0.19	0/1671	0.51	1/2246 (0.0%)
41	d	0.16	0/1409	0.44	0/1894
42	e	0.15	0/1420	0.43	0/1912
43	f	0.19	0/1183	0.56	2/1587 (0.1%)
44	h	0.16	0/968	0.43	0/1298
45	i	0.16	0/1186	0.46	0/1592
46	j	0.16	0/953	0.47	0/1275
47	k	0.17	0/1170	0.46	0/1559
48	l	0.18	0/1104	0.47	0/1481
49	m	0.22	0/973	0.58	0/1309
50	n	0.18	0/897	0.53	0/1198
51	o	0.17	0/948	0.50	0/1262
52	p	0.19	0/961	0.48	0/1278
53	q	0.18	0/828	0.56	0/1111
54	r	0.18	0/1077	0.52	0/1441
55	s	0.17	0/732	0.52	1/988 (0.1%)
56	t	0.15	0/879	0.44	0/1165
57	u	0.16	0/665	0.43	0/884
58	v	0.23	0/519	0.53	0/695
59	w	0.18	0/826	0.48	0/1104
60	x	0.17	0/353	0.40	0/474
61	y	0.31	0/457	0.67	0/601
62	z	0.15	0/412	0.48	0/547
All	All	0.32	1/190923 (0.0%)	0.52	20/280323 (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	9	0	1
21	G	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
24	J	0	1
29	O	0	1
37	Z	0	1
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
14	AE	22	DA	O3'-P	-15.33	1.38	1.61

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	AE	22	DA	P-O3'-C3'	14.70	142.26	120.20
13	AD	17	DT	P-O3'-C3'	8.53	132.99	120.20
14	AE	22	DA	O3'-P-O5'	-8.26	91.61	104.00
20	F	16	VAL	N-CA-C	-6.73	107.32	113.71
19	E	162	LYS	CA-C-N	6.28	133.54	121.54

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	9	858	TYR	Sidechain
21	G	108	LEU	Peptide
24	J	111	HIS	Peptide
29	O	39	GLU	Peptide
37	Z	893	ARG	Sidechain

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	9	0
2	1	477	0	530	23	0
3	2	304	0	350	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	3	61664	0	30953	1938	0
5	4	2239	0	1137	64	0
6	5	31943	0	16058	914	0
7	6	2421	0	2495	140	0
7	AB	2452	0	2522	225	0
8	7	1618	0	821	44	0
9	9	10948	0	11063	1048	0
10	A	1921	0	1973	61	0
11	AA	770	0	739	52	0
12	AC	2884	0	2938	438	0
13	AD	663	0	361	82	0
14	AE	649	0	364	102	0
15	AF	1277	0	1328	92	0
16	B	1698	0	1765	64	0
17	C	1660	0	1719	67	0
18	D	1173	0	1267	34	0
19	E	1362	0	1377	41	0
20	F	1246	0	1308	53	0
21	G	1110	0	1221	60	0
22	H	1028	0	1094	37	0
23	I	809	0	894	37	0
24	J	829	0	855	39	0
25	K	1076	0	1170	48	0
26	L	951	0	1014	34	0
27	M	474	0	509	23	0
28	N	673	0	730	29	0
29	O	646	0	677	26	0
30	P	675	0	728	25	0
31	Q	535	0	562	22	0
32	R	682	0	691	25	0
33	S	629	0	681	34	0
34	T	471	0	522	18	0
35	U	1239	0	1301	127	0
36	V	232	0	237	9	0
36	W	232	0	237	8	0
36	X	232	0	237	10	0
36	Y	232	0	237	7	0
37	Z	10085	0	10375	842	0
38	a	2225	0	2301	106	0
39	b	1762	0	1808	92	0
40	c	1644	0	1731	71	0
41	d	1388	0	1469	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	e	1396	0	1481	32	0
43	f	1160	0	1172	34	0
44	h	959	0	1039	9	0
45	i	1164	0	1192	53	0
46	j	944	0	1019	43	0
47	k	1153	0	1256	47	0
48	l	1079	0	1134	49	0
49	m	958	0	1011	40	0
50	n	889	0	952	26	0
51	o	938	0	1008	47	0
52	p	947	0	1028	66	0
53	q	811	0	858	39	0
54	r	1068	0	1150	53	0
55	s	720	0	803	20	0
56	t	872	0	972	18	0
57	u	657	0	695	22	0
58	v	513	0	560	30	0
59	w	818	0	870	21	0
60	x	344	0	333	4	0
61	y	452	0	472	21	0
62	z	408	0	440	16	0
All	All	177858	0	132223	6198	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 6198 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	35:U:7:LYS:HD3	1.25	1.69
9:9:999:PHE:CZ	12:AC:108:LEU:HD23	1.23	1.67
7:6:107:GLU:HG3	7:AB:319:HIS:CD2	1.30	1.66
9:9:1342:LEU:CD1	37:Z:392:LEU:CD2	1.79	1.61
9:9:999:PHE:CE1	12: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	9	1389/1391 (100%)	1355 (98%)	33 (2%)	1 (0%)	48	83
10	A	238/240 (99%)	222 (93%)	16 (7%)	0	100	100
11	AA	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
12	AC	358/366 (98%)	350 (98%)	6 (2%)	2 (1%)	21	59
15	AF	158/160 (99%)	155 (98%)	1 (1%)	2 (1%)	9	42
16	B	213/215 (99%)	196 (92%)	17 (8%)	0	100	100
17	C	201/203 (99%)	191 (95%)	10 (5%)	0	100	100
18	D	151/153 (99%)	145 (96%)	6 (4%)	0	100	100
19	E	165/167 (99%)	147 (89%)	18 (11%)	0	100	100
20	F	152/154 (99%)	135 (89%)	17 (11%)	0	100	100
21	G	139/141 (99%)	125 (90%)	14 (10%)	0	100	100
22	H	126/128 (98%)	115 (91%)	11 (9%)	0	100	100
23	I	99/101 (98%)	87 (88%)	12 (12%)	0	100	100
24	J	112/114 (98%)	105 (94%)	7 (6%)	0	100	100
25	K	134/136 (98%)	125 (93%)	9 (7%)	0	100	100
26	L	116/118 (98%)	104 (90%)	12 (10%)	0	100	100
27	M	58/60 (97%)	56 (97%)	2 (3%)	0	100	100
28	N	81/83 (98%)	81 (100%)	0	0	100	100
29	O	78/80 (98%)	70 (90%)	8 (10%)	0	100	100
30	P	81/83 (98%)	78 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	Q	63/65 (97%)	51 (81%)	12 (19%)	0	100	100
32	R	82/84 (98%)	72 (88%)	10 (12%)	0	100	100
33	S	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
34	T	51/53 (96%)	50 (98%)	1 (2%)	0	100	100
35	U	159/161 (99%)	154 (97%)	4 (2%)	1 (1%)	21	59
36	V	27/29 (93%)	27 (100%)	0	0	100	100
36	W	27/29 (93%)	27 (100%)	0	0	100	100
36	X	27/29 (93%)	27 (100%)	0	0	100	100
36	Y	27/29 (93%)	27 (100%)	0	0	100	100
37	Z	1274/1276 (100%)	1252 (98%)	21 (2%)	1 (0%)	48	83
38	a	283/285 (99%)	265 (94%)	18 (6%)	0	100	100
39	b	227/229 (99%)	214 (94%)	13 (6%)	0	100	100
40	c	208/210 (99%)	197 (95%)	11 (5%)	0	100	100
41	d	173/175 (99%)	161 (93%)	12 (7%)	0	100	100
42	e	174/176 (99%)	166 (95%)	8 (5%)	0	100	100
43	f	143/145 (99%)	125 (87%)	18 (13%)	0	100	100
44	h	126/128 (98%)	114 (90%)	12 (10%)	0	100	100
45	i	142/144 (99%)	136 (96%)	6 (4%)	0	100	100
46	j	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
47	k	146/148 (99%)	139 (95%)	7 (5%)	0	100	100
48	l	134/136 (98%)	124 (92%)	10 (8%)	0	100	100
49	m	117/119 (98%)	110 (94%)	7 (6%)	0	100	100
50	n	108/116 (93%)	99 (92%)	9 (8%)	0	100	100
51	o	113/115 (98%)	101 (89%)	12 (11%)	0	100	100
52	p	112/114 (98%)	108 (96%)	4 (4%)	0	100	100
53	q	97/99 (98%)	90 (93%)	7 (7%)	0	100	100
54	r	137/139 (99%)	134 (98%)	3 (2%)	0	100	100
55	s	90/92 (98%)	88 (98%)	2 (2%)	0	100	100
56	t	109/111 (98%)	104 (95%)	5 (5%)	0	100	100
57	u	84/86 (98%)	81 (96%)	3 (4%)	0	100	100
58	v	61/63 (97%)	59 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
59	w	96/108 (89%)	89 (93%)	7 (7%)	0	100	100
60	x	42/44 (96%)	35 (83%)	7 (17%)	0	100	100
61	y	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
62	z	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
All	All	9841/10021 (98%)	9376 (95%)	458 (5%)	7 (0%)	49	83

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	AF	95	ARG
9	9	582	LYS
37	Z	1035	GLY
35	U	106	MET
12	AC	3	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	40/40 (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	9	1213/1213 (100%)	1188 (98%)	25 (2%)	47	65
10	A	212/212 (100%)	211 (100%)	1 (0%)	81	83
11	AA	83/83 (100%)	79 (95%)	4 (5%)	23	44
12	AC	327/327 (100%)	322 (98%)	5 (2%)	57	72
15	AF	140/140 (100%)	134 (96%)	6 (4%)	26	47
16	B	180/180 (100%)	180 (100%)	0	100	100
17	C	181/181 (100%)	181 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	D	123/123 (100%)	123 (100%)	0	100	100
19	E	150/150 (100%)	150 (100%)	0	100	100
20	F	131/131 (100%)	131 (100%)	0	100	100
21	G	123/123 (100%)	123 (100%)	0	100	100
22	H	111/111 (100%)	111 (100%)	0	100	100
23	I	95/95 (100%)	95 (100%)	0	100	100
24	J	91/91 (100%)	91 (100%)	0	100	100
25	K	117/117 (100%)	114 (97%)	3 (3%)	40	62
26	L	100/100 (100%)	99 (99%)	1 (1%)	68	78
27	M	47/47 (100%)	47 (100%)	0	100	100
28	N	76/76 (100%)	76 (100%)	0	100	100
29	O	69/69 (100%)	69 (100%)	0	100	100
30	P	73/73 (100%)	73 (100%)	0	100	100
31	Q	56/56 (100%)	56 (100%)	0	100	100
32	R	74/74 (100%)	74 (100%)	0	100	100
33	S	70/70 (100%)	70 (100%)	0	100	100
34	T	49/49 (100%)	49 (100%)	0	100	100
35	U	129/129 (100%)	129 (100%)	0	100	100
36	V	26/26 (100%)	26 (100%)	0	100	100
36	W	26/26 (100%)	26 (100%)	0	100	100
36	X	26/26 (100%)	26 (100%)	0	100	100
36	Y	26/26 (100%)	26 (100%)	0	100	100
37	Z	1113/1113 (100%)	1100 (99%)	13 (1%)	63	75
38	a	241/241 (100%)	241 (100%)	0	100	100
39	b	186/186 (100%)	186 (100%)	0	100	100
40	c	182/182 (100%)	182 (100%)	0	100	100
41	d	150/150 (100%)	150 (100%)	0	100	100
42	e	153/153 (100%)	153 (100%)	0	100	100
43	f	123/131 (94%)	123 (100%)	0	100	100
44	h	102/102 (100%)	102 (100%)	0	100	100
45	i	126/126 (100%)	126 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	j	103/103 (100%)	103 (100%)	0	100	100
47	k	123/123 (100%)	123 (100%)	0	100	100
48	l	113/113 (100%)	113 (100%)	0	100	100
49	m	105/105 (100%)	105 (100%)	0	100	100
50	n	96/99 (97%)	96 (100%)	0	100	100
51	o	101/101 (100%)	101 (100%)	0	100	100
52	p	100/100 (100%)	100 (100%)	0	100	100
53	q	90/90 (100%)	90 (100%)	0	100	100
54	r	116/116 (100%)	116 (100%)	0	100	100
55	s	82/82 (100%)	82 (100%)	0	100	100
56	t	96/96 (100%)	96 (100%)	0	100	100
57	u	69/69 (100%)	69 (100%)	0	100	100
58	v	58/58 (100%)	58 (100%)	0	100	100
59	w	87/95 (92%)	87 (100%)	0	100	100
60	x	41/41 (100%)	41 (100%)	0	100	100
61	y	48/48 (100%)	45 (94%)	3 (6%)	16	37
62	z	47/47 (100%)	47 (100%)	0	100	100
All	All	8642/8690 (99%)	8567 (99%)	75 (1%)	68	79

5 of 75 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
25	K	122	LYS
37	Z	1278	LEU
37	Z	174	LEU
37	Z	757	LEU
9	9	673	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 121 such sidechains are listed below:

Mol	Chain	Res	Type
25	K	86	ASN
54	r	52	ASN
35	U	57	ASN
53	q	69	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
58	v	16	ASN

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%)	349 (23%)	6 (0%)
8	7	75/76 (98%)	25 (33%)	2 (2%)
All	All	4543/4552 (99%)	1141 (25%)	38 (0%)

5 of 1141 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
12	AC	3
14	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

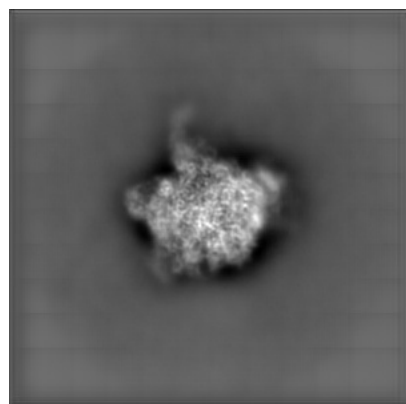
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53671. These allow visual inspection of the internal detail of the map and identification of artifacts.

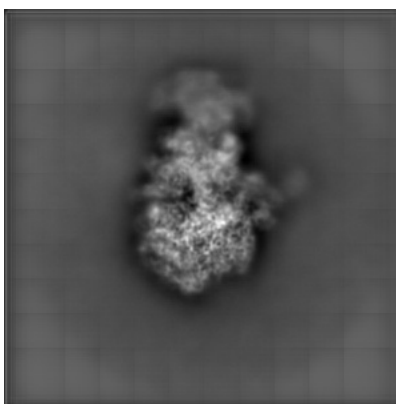
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

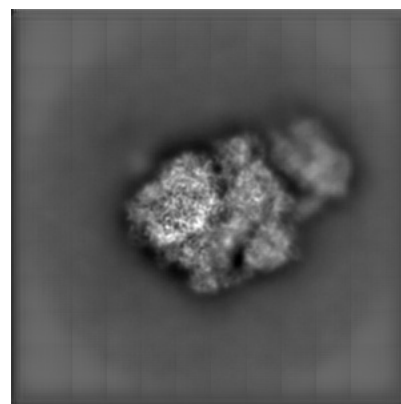
6.1.1 Primary map



X

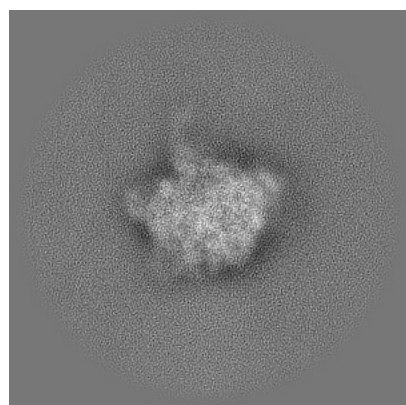


Y

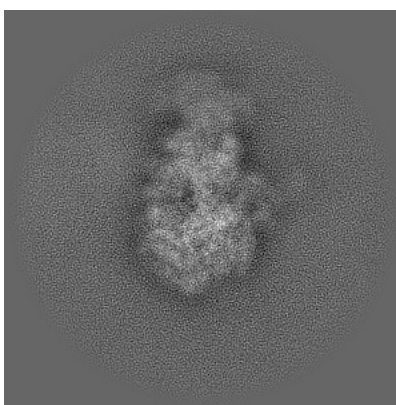


Z

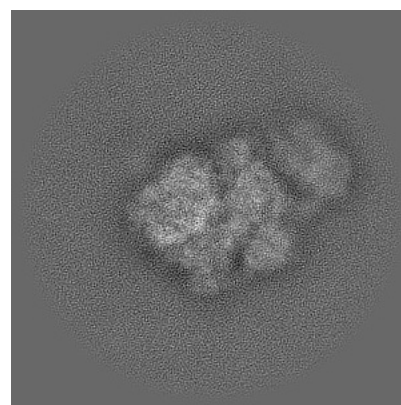
6.1.2 Raw map



X



Y

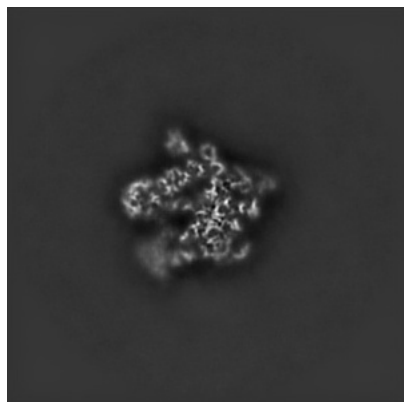


Z

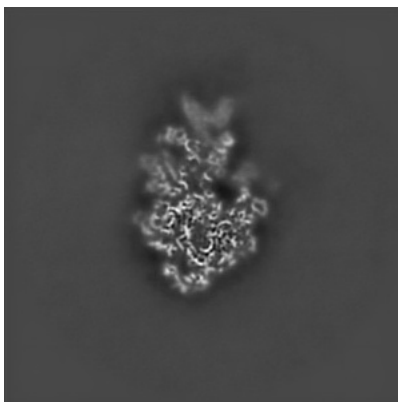
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

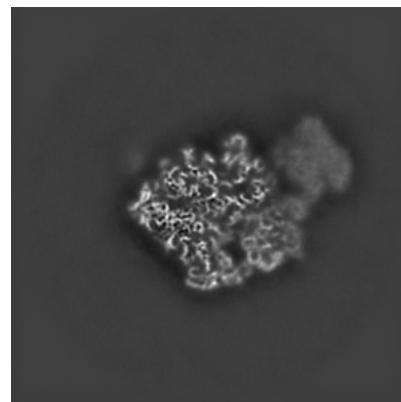
6.2.1 Primary map



X Index: 150

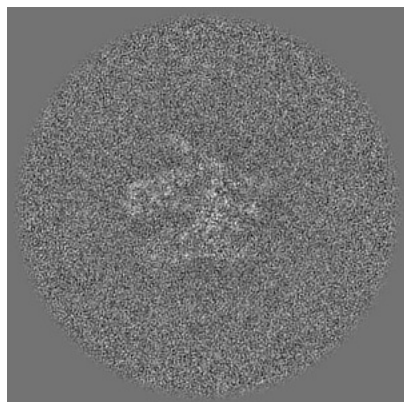


Y Index: 150

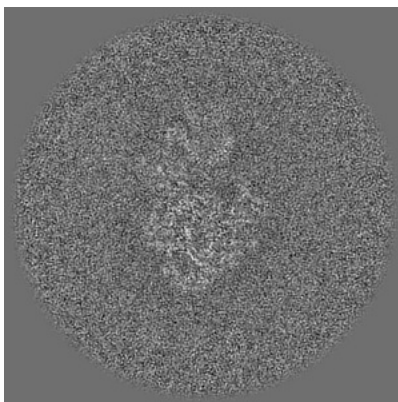


Z Index: 150

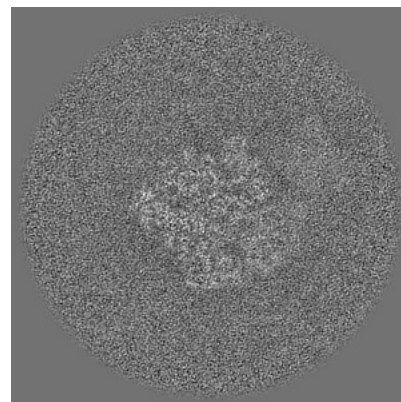
6.2.2 Raw map



X Index: 150



Y Index: 150

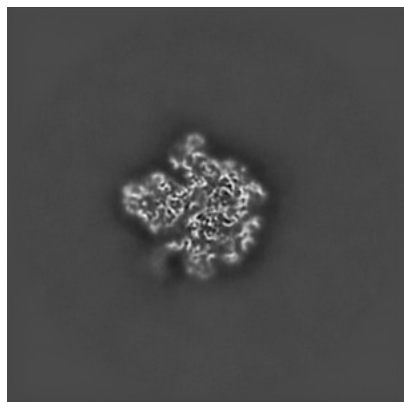


Z Index: 150

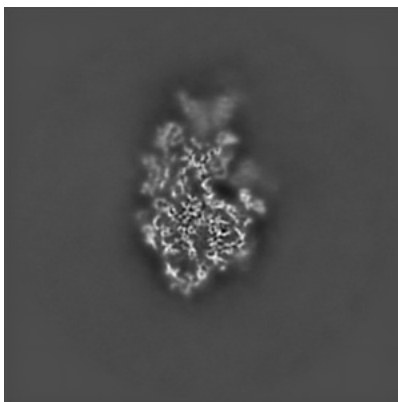
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

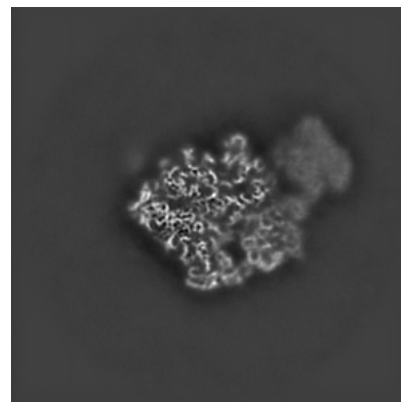
6.3.1 Primary map



X Index: 140

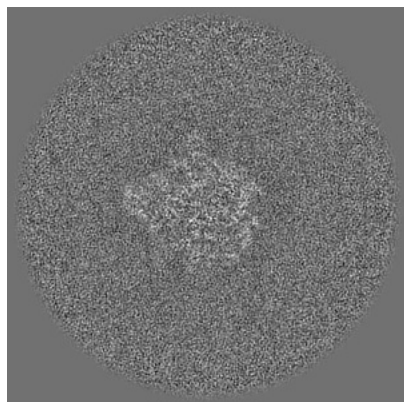


Y Index: 154

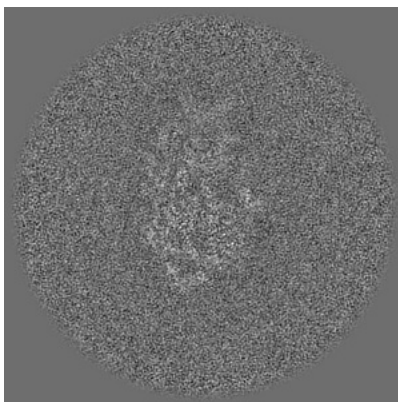


Z Index: 150

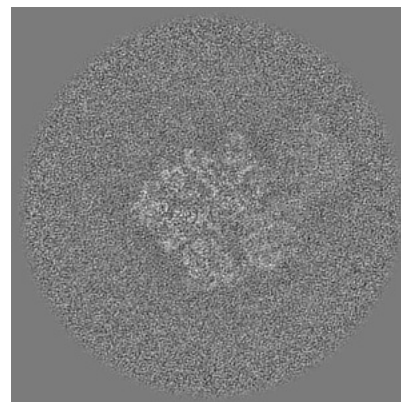
6.3.2 Raw map



X Index: 140



Y Index: 153

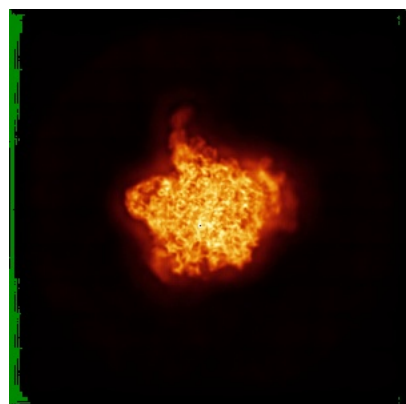


Z Index: 151

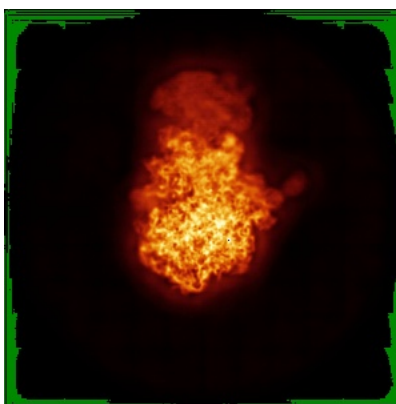
The images above show the largest variance slices of the map in three orthogonal directions.

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

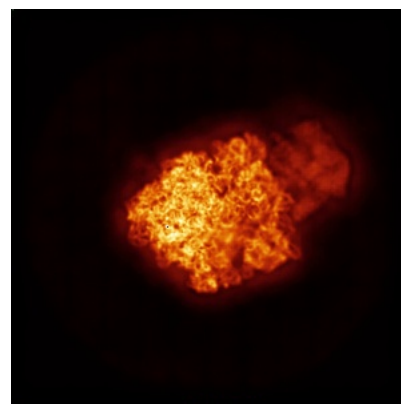
6.4.1 Primary map



X

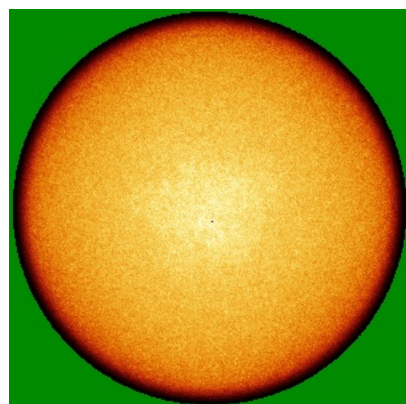


Y

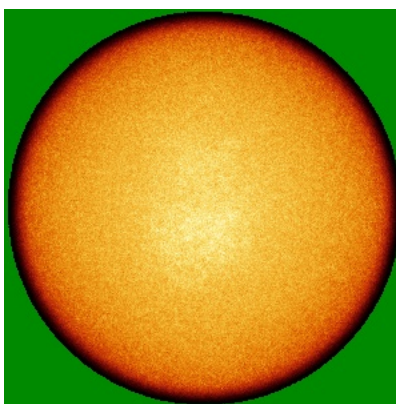


Z

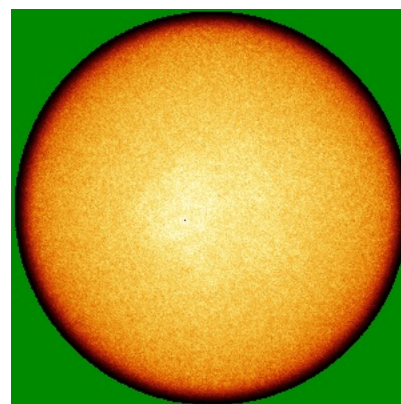
6.4.2 Raw map



X



Y

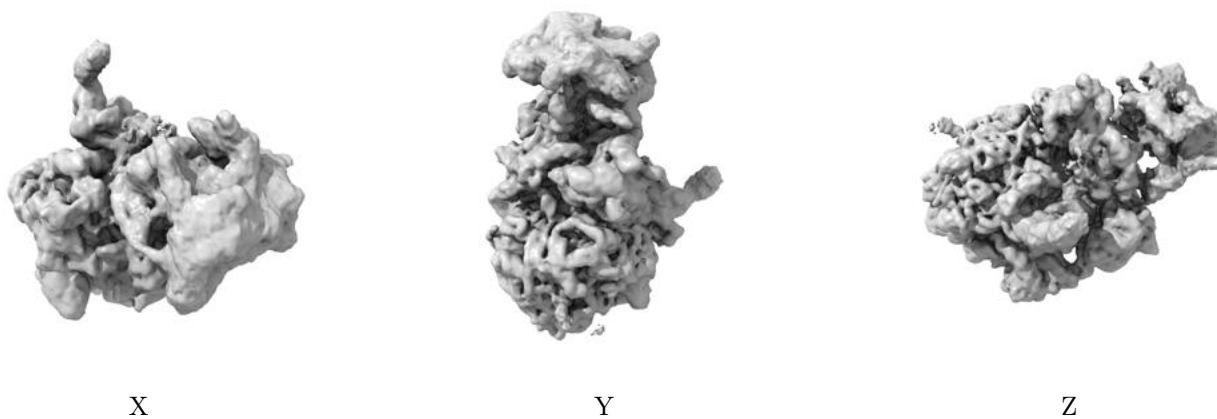


Z

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.

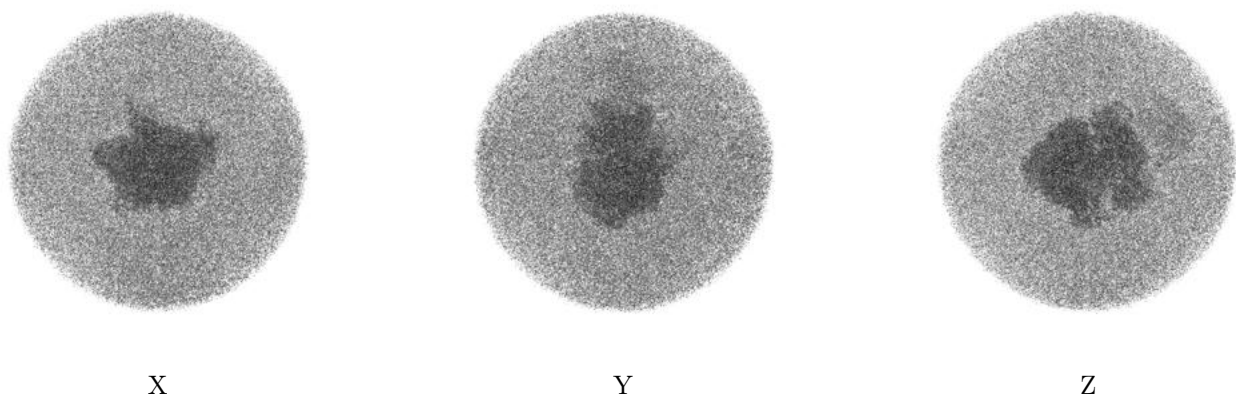
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00157. 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.

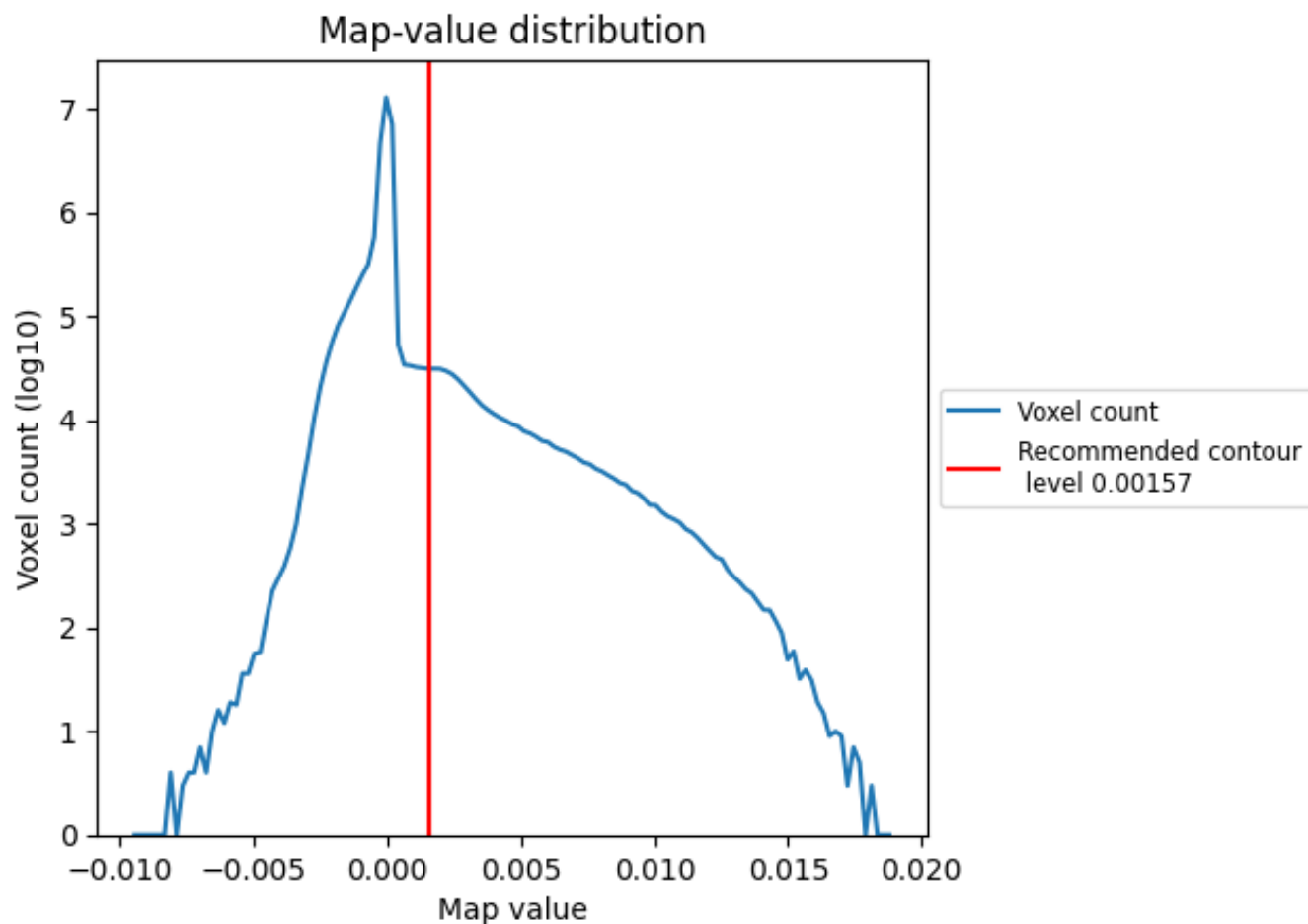
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

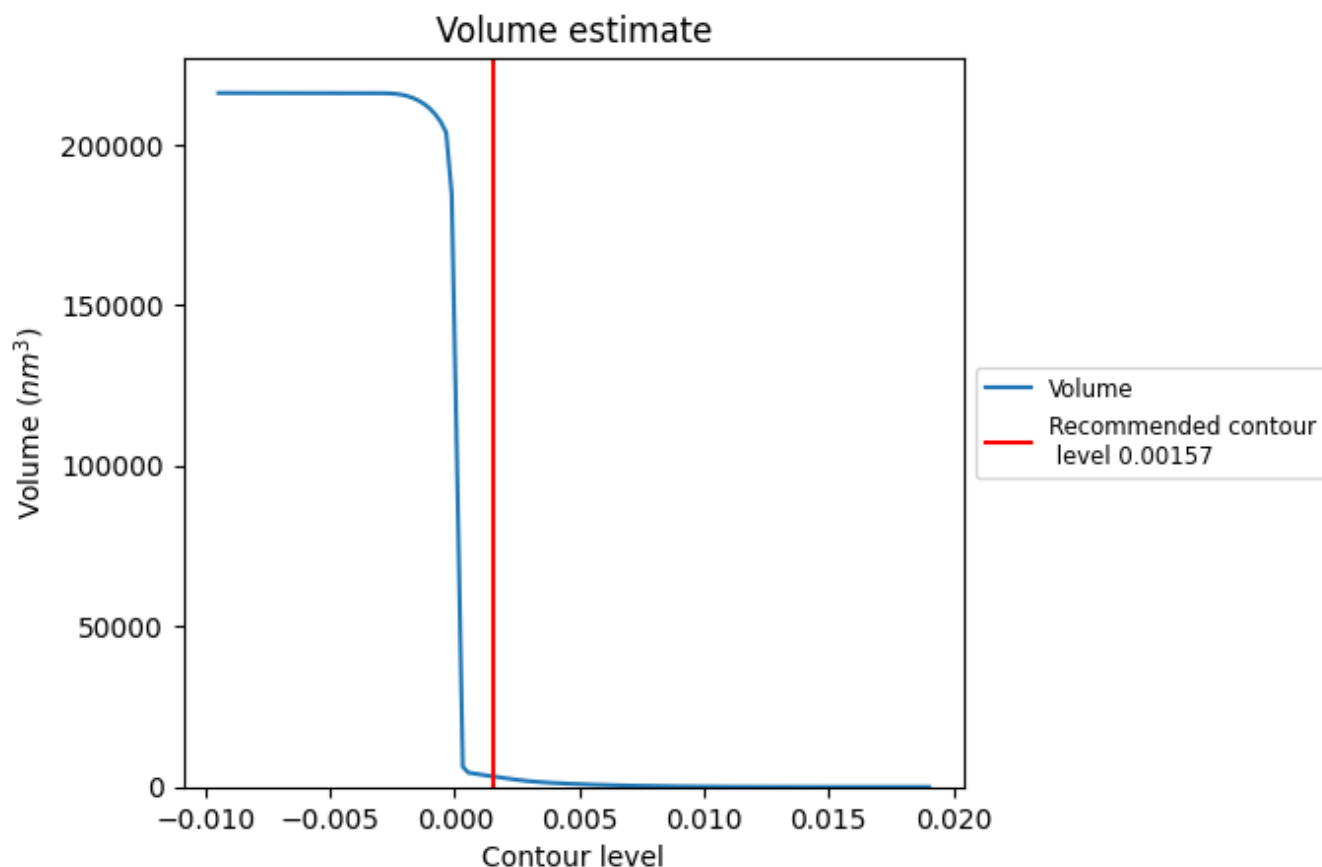
This section contains the results of statistical analysis of the map.

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.

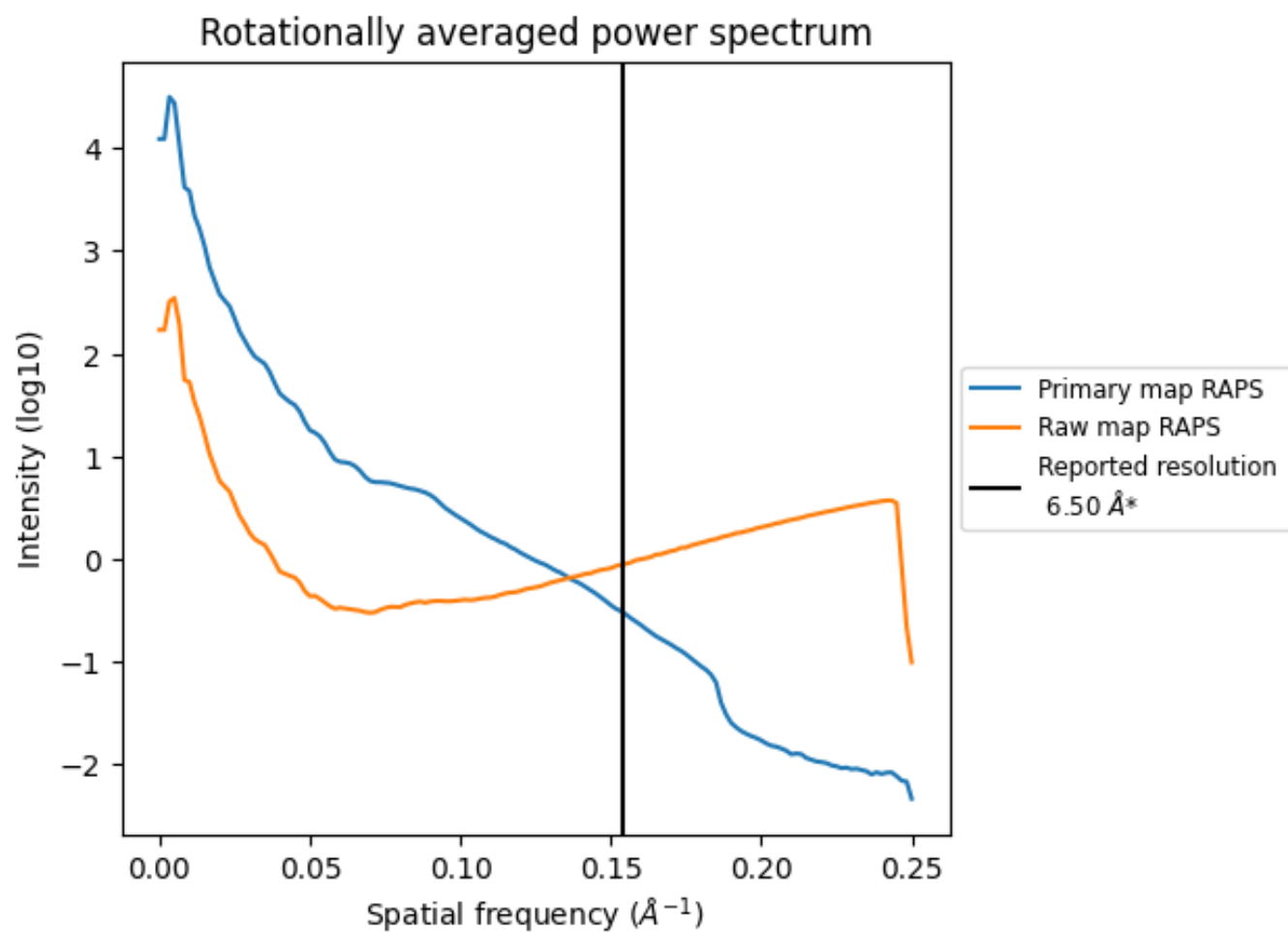
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3244 nm³; this corresponds to an approximate mass of 2931 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 ⓘ

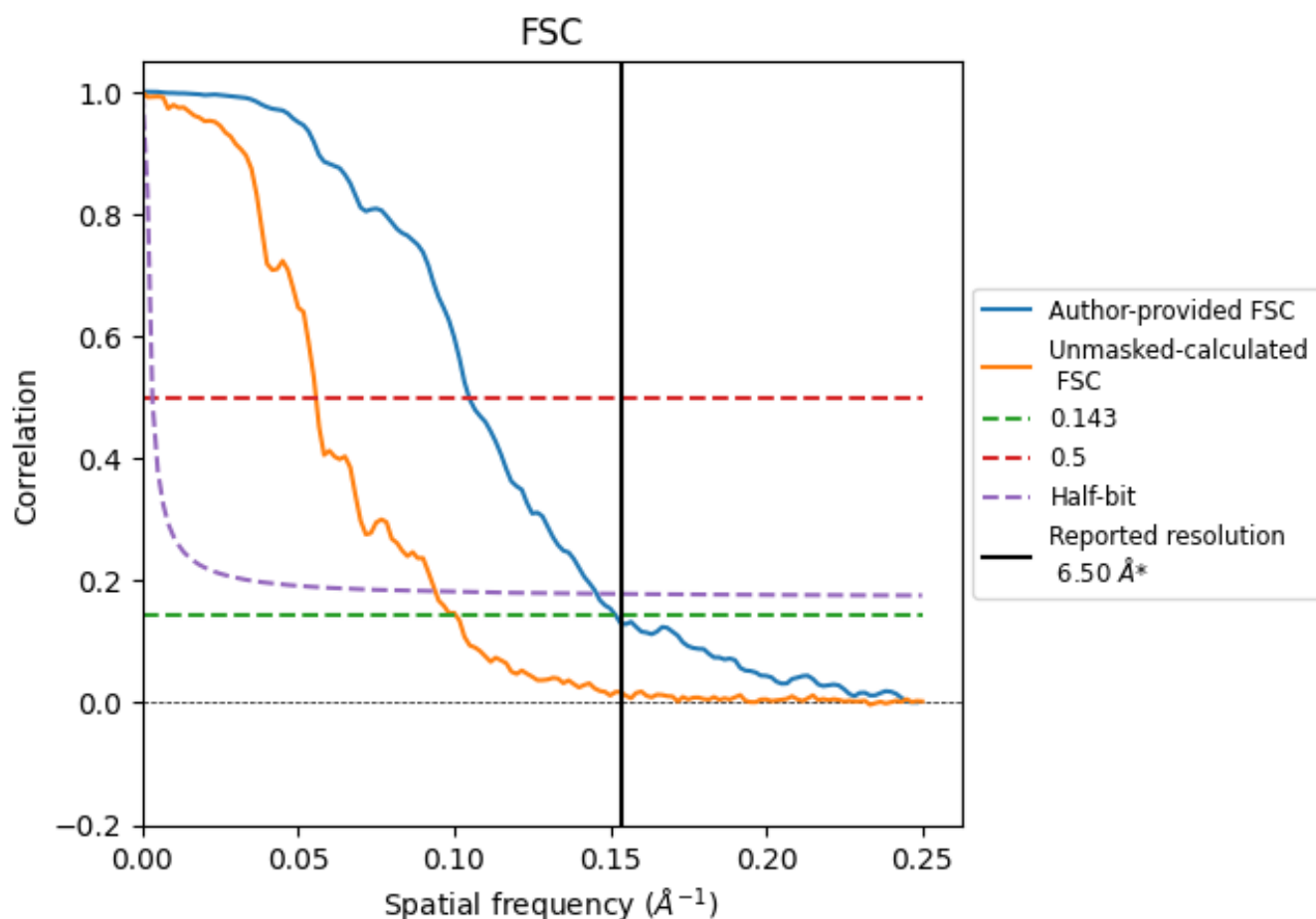


*Reported resolution corresponds to spatial frequency of 0.154 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.154 Å⁻¹

8.2 Resolution estimates [i](#)

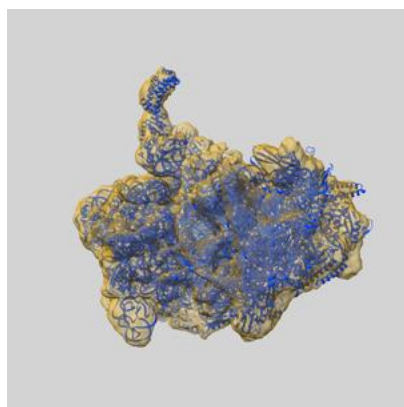
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.50	-	-
Author-provided FSC curve	6.59	9.54	6.87
Unmasked-calculated*	9.95	17.95	10.64

*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 9.95 differs from the reported value 6.5 by more than 10 %

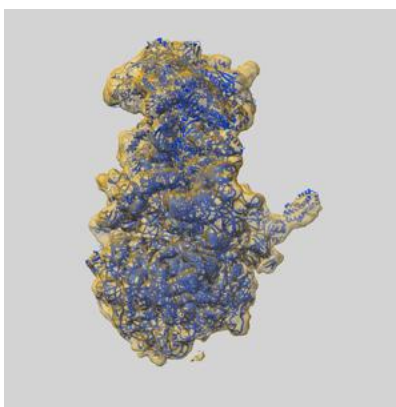
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53671 and PDB model 9SL5. Per-residue inclusion information can be found in section 3 on page 16.

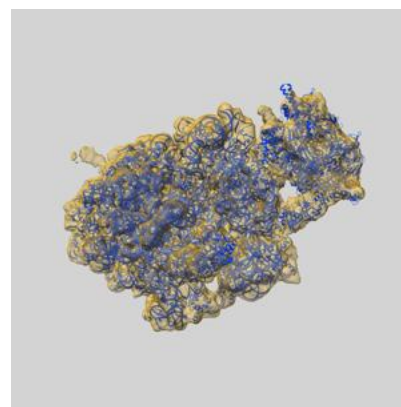
9.1 Map-model overlay [i](#)



X



Y



Z

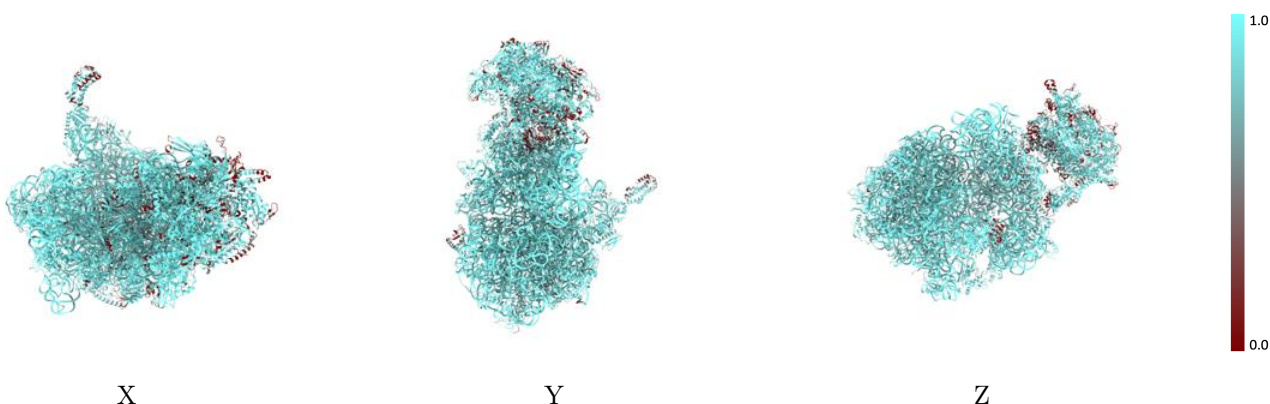
The images above show the 3D surface view of the map at the recommended contour level 0.00157 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



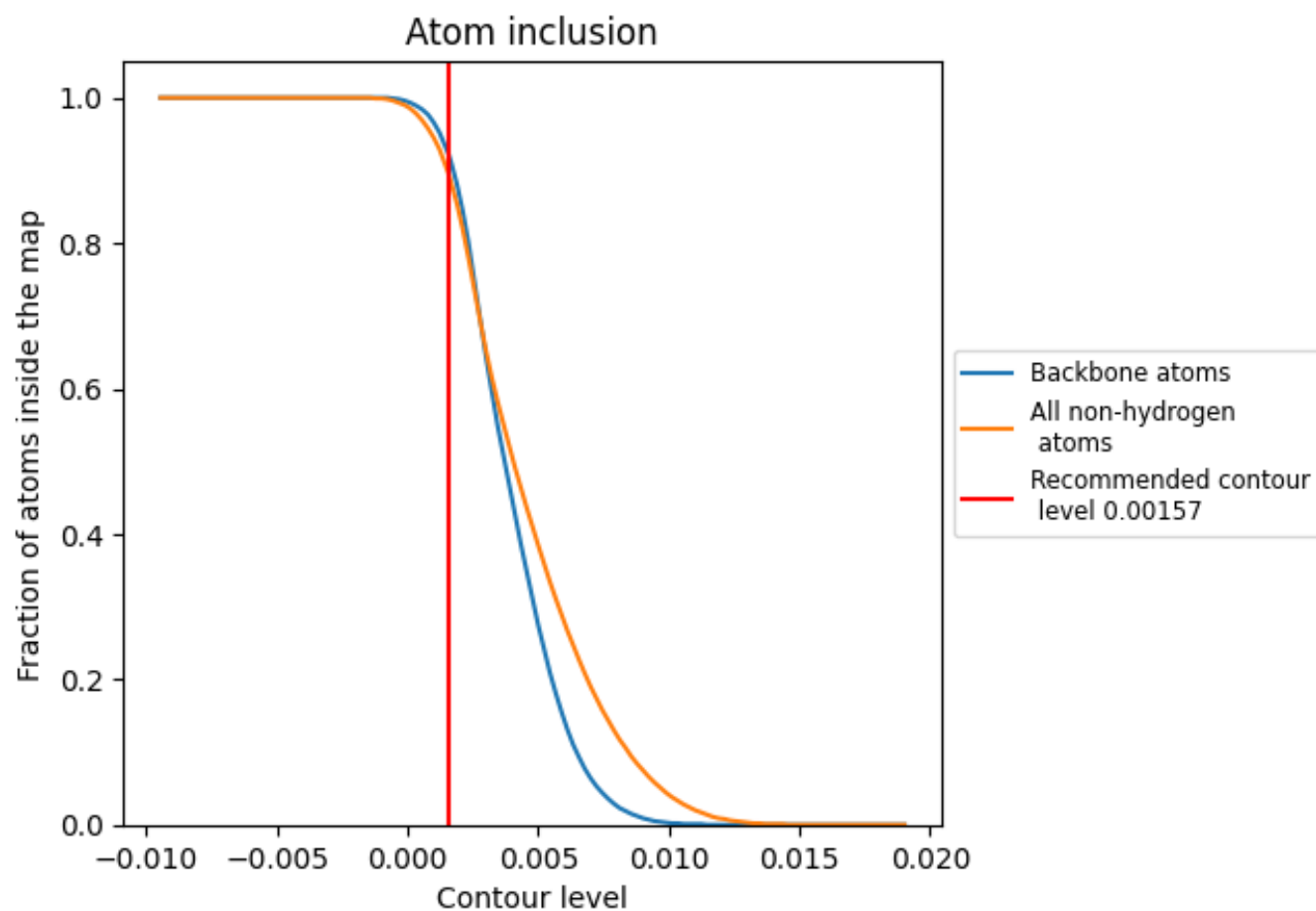
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00157).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 90% 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 (0.00157) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8950	 0.1530
0	 0.6600	 0.1260
1	 0.6820	 0.1230
2	 0.7940	 0.1270
3	 0.9690	 0.2090
4	 0.9900	 0.1930
5	 0.9800	 0.1780
6	 0.8490	 0.0460
7	 0.8790	 0.1600
9	 0.7820	 0.0440
A	 0.8640	 0.1490
AA	 0.6360	 0.0470
AB	 0.7580	 0.0600
AC	 0.7420	 0.0340
AD	 0.9120	 0.0810
AE	 0.8440	 0.0800
AF	 0.8220	 0.0600
B	 0.8020	 0.1240
C	 0.7780	 0.0990
D	 0.6930	 0.1330
E	 0.8500	 0.1430
F	 0.9120	 0.1360
G	 0.8060	 0.1310
H	 0.9550	 0.1160
I	 0.9320	 0.1320
J	 0.8290	 0.1280
K	 0.6860	 0.1000
L	 0.8670	 0.1210
M	 0.8090	 0.0630
N	 0.8870	 0.1530
O	 0.8330	 0.1040
P	 0.8160	 0.0960
Q	 0.9150	 0.1050
R	 0.9100	 0.1040
S	 0.8850	 0.1240



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Chain	Atom inclusion	Q-score
T	 0.7990	 0.1310
U	 0.8500	 0.0910
V	 0.9010	 0.0460
W	 0.8320	 0.0690
X	 0.7110	 0.0830
Y	 0.3150	 0.0320
Z	 0.7810	 0.0640
a	 0.7700	 0.1430
b	 0.8400	 0.1540
c	 0.8220	 0.1550
d	 0.8920	 0.1260
e	 0.8920	 0.1510
f	 0.5100	 0.1000
h	 0.8660	 0.0850
i	 0.8380	 0.1460
j	 0.6530	 0.1510
k	 0.8020	 0.1500
l	 0.7630	 0.1450
m	 0.7890	 0.1500
n	 0.9100	 0.1490
o	 0.7580	 0.1400
p	 0.8080	 0.1310
q	 0.8500	 0.1510
r	 0.7720	 0.1550
s	 0.7910	 0.1380
t	 0.7820	 0.1060
u	 0.7800	 0.1370
v	 0.7190	 0.1240
w	 0.8660	 0.1520
x	 0.9150	 0.1280
y	 0.7370	 0.1310
z	 0.8490	 0.1290