



wwPDB EM Validation Summary Report ⓘ

Jun 15, 2026 – 07:30 PM EDT

PDB ID : 8VOO / pdb_00008voo
EMDB ID : EMD-43387
Title : Escherichia coli transcription-translation loosely coupled complex (TTC-LC) containing mRNA with a 39 nt long spacer, ops signal, RfaH, NusA, and fMet-tRNAs in E-site and P-site
Authors : Molodtsov, V.; Wang, C.; Ebright, R.H.
Deposited on : 2024-01-15
Resolution : 3.40 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:

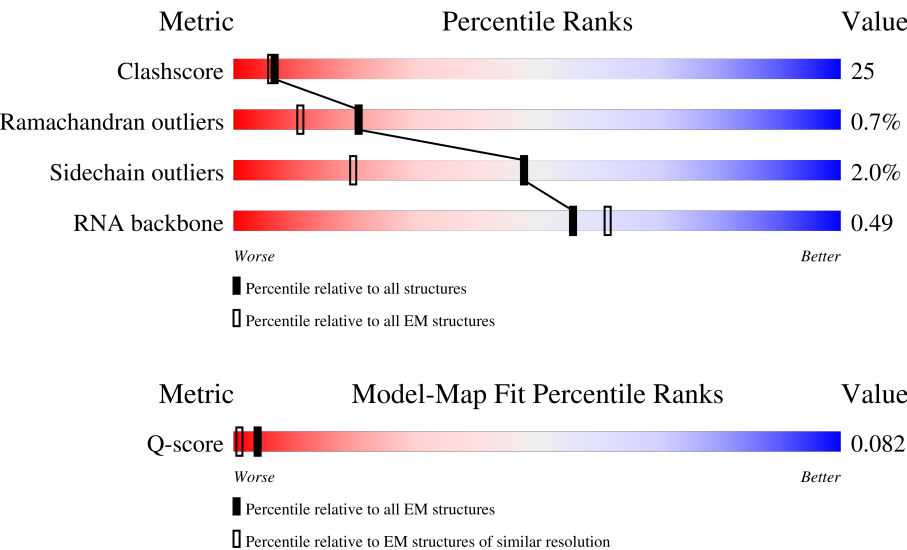
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	103	9% 60% 40%
2	1	110	58% 42%
3	2	100	6% 51% 42% 6%

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Mol	Chain	Length	Quality of chain
4	3	104	
5	4	94	
6	5	38	
7	6	38	
8	7	56	
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AB	162	
13	AC	329	
13	AD	329	
14	AE	1407	
15	AF	91	
16	AG	495	
17	C	75	
18	D	1542	
19	E	87	
20	F	71	
21	G	241	
22	H	557	
23	I	233	
24	J	206	
25	K	167	
26	L	135	

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Mol	Chain	Length	Quality of chain
27	M	179	
28	N	130	
29	O	130	
30	P	103	
31	Q	129	
32	R	124	
33	S	101	
34	T	89	
35	U	82	
36	V	84	
37	W	92	
38	X	118	
39	Y	142	
40	Z	121	
41	a	2904	
42	b	85	
43	c	78	
44	d	120	
45	e	63	
46	f	59	
47	g	70	
48	h	273	
49	i	57	
50	j	209	
51	k	55	

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Mol	Chain	Length	Quality of chain
52	l	201	
53	m	46	
54	n	179	
55	o	65	
56	p	177	
57	q	38	
58	r	149	
59	s	142	
60	t	123	
61	u	144	
62	v	136	
63	w	127	
64	x	117	
65	y	115	
66	z	118	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
68	ZN	AE	1502	-	-	X	-

2 Entry composition [i](#)

There are 68 unique types of molecules in this entry. The entry contains 280046 atoms, of which 98638 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 Ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	103	Total	C	H	N	O	0	0
			1655	516	839	153	145		

- Molecule 2 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	110	Total	C	H	N	O	0	0
			1779	532	922	166	156		

- Molecule 3 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	94	Total	C	H	N	O	0	0
			1557	470	811	140	134		

- Molecule 4 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	103	Total	C	H	N	O	0	0
			1632	498	844	148	142		

- Molecule 5 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	94	Total	C	H	N	O	0	0
			1533	479	780	137	134		

- Molecule 6 is a DNA chain called NT DNA ops.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	35	Total	C	N	O	P	0	0
			726	342	141	208	35		

- Molecule 7 is a DNA chain called T DNA ops.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	35	Total	C	N	O	P	0	0
			703	336	117	215	35		

- Molecule 8 is a RNA chain called mRNA with 39 nt long spacer.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	25	Total	C	N	O	P	0	0
			527	235	80	187	25		

- Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	9	148	Total	C	N	O	S	0	0
			1117	705	196	209	7		

- Molecule 10 is a RNA chain called E-site and P-site tRNA (fMet).

Mol	Chain	Residues	Atoms						AltConf	Trace
10	A	76	Total 2446	C 723	H 826	N 295	O 527	P 75	0	0
10	B	76	Total 2433	C 723	H 813	N 295	O 527	P 75	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AA	1316	Total	C	N	O	S	0	0
			10381	6514	1810	2014	43		

- Molecule 12 is a protein called Transcription antitermination protein RfaH.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AB	161	Total	C	N	O	S	0	0
			1286	828	222	232	4		

- Molecule 13 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AC	221	Total	C	N	O	S	0	0
			1698	1060	299	333	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	AD	299	Total	C	N	O	S	0	0
			2078	1287	378	407	6		

- Molecule 14 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AE	1337	Total	C	N	O	S	0	0
			10404	6535	1856	1963	50		

- Molecule 15 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AF	82	Total	C	N	O	S	0	0
			650	396	122	131	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AG	495	Total	C	N	O	S	0	0
			3852	2396	669	774	13		

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	C	66	Total	C	H	N	O	S	0	0
			1103	344	559	102	97	1		

- Molecule 18 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	D	1524	Total	C	H	N	O	P	0	0
			49126	14585	16423	6003	10591	1524		

- Molecule 19 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace	
19	E	86	Total	C	H	N	O	S	0	0
			1388	414	719	138	114	3		

- Molecule 20 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	F	70	Total	C	H	N	O	S	0	0
			1218	366	629	125	97	1		

- Molecule 21 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	G	225	Total	C	H	N	O	S	0	0
			3545	1113	1785	316	323	8		

- Molecule 22 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	H	259	Total	C	H	N	O	S	0	0
			3184	1073	1454	305	349	3		

- Molecule 23 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	I	208	Total	C	H	N	O	S	0	0
			3346	1036	1710	307	290	3		

- Molecule 24 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	J	205	Total	C	H	N	O	S	0	0
			3350	1026	1707	315	298	4		

- Molecule 25 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	K	156	Total	C	H	N	O	S	0	0
			2348	717	1196	217	212	6		

- Molecule 26 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	L	104	Total	C	H	N	O	S	0	0
			1694	536	846	153	152	7		

- Molecule 27 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	M	151	Total	C	H	N	O	S	0	0
			2416	735	1235	227	215	4		

- Molecule 28 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	N	129	Total	C	H	N	O	S	0	0
			2010	616	1031	173	184	6		

- Molecule 29 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	O	127	Total	C	H	N	O	S	0	0
			2092	634	1070	206	179	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
30	P	99	Total	C	H	N	O	S	0	0
			1621	495	831	151	143	1		

- Molecule 31 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	Q	117	Total	C	H	N	O	S	0	0
			1764	540	887	174	160	3		

- Molecule 32 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	R	121	Total	C	H	N	O	S	0	0
			1940	580	1001	194	161	4		

- Molecule 33 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	S	100	Total	C	H	N	O	S	0	0
			1649	499	844	164	139	3		

- Molecule 34 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	T	88	Total	C	H	N	O	S	0	0
			1448	439	734	144	130	1		

- Molecule 35 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	U	82	Total	C	H	N	O	S	0	0
			1315	406	666	128	114	1		

- Molecule 36 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	V	80	Total	C	H	N	O	S	0	0
			1339	411	691	121	113	3		

- Molecule 37 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	W	83	Total	C	H	N	O	S	0	0
			1351	424	688	126	111	2		

- Molecule 38 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	X	116	Total	C	H	N	O	S	0	0
			1864	558	964	181	158	3		

- Molecule 39 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Y	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 40 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Z	30	Total	C	N	O	S	0	0
			227	144	33	47	3		

- Molecule 41 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	a	2880	Total	C	H	N	O	P	0	0
			92918	27587	31077	11398	19976	2880		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	887	A	U	conflict	GB 937521852

- Molecule 42 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	b	76	Total	C	H	N	O	S	0	0
			1181	360	599	117	104	1		

- Molecule 43 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	c	77	Total	C	H	N	O	S	0	0
			1277	388	652	129	106	2		

- Molecule 44 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	d	120	Total	C	H	N	O	P	0	0
			3870	1144	1301	468	837	120		

- Molecule 45 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	e	62	Total	C	H	N	O	S	0	0
			1032	308	531	98	94	1		

- Molecule 46 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	f	58	Total	C	H	N	O	S	0	0
			936	281	488	87	78	2		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
47	g	66	Total	C	H	N	O	S	0	0
			1042	323	520	99	94	6		

- Molecule 48 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	h	271	Total	C	H	N	O	S	0	0
			4236	1288	2154	423	364	7		

- Molecule 49 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	i	56	Total	C	H	N	O	S	0	0
			903	269	459	94	80	1		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
50	j	209	Total	C	H	N	O	S	0	0
			3182	979	1617	288	294	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
51	k	52	Total	C	H	N	O		0	0
			890	275	464	78	73			

- Molecule 52 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	l	201	Total	C	H	N	O	S	0	0
			3171	974	1619	283	290	5		

- Molecule 53 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	m	46	Total	C	H	N	O	S	0	0
			795	228	418	90	57	2		

- Molecule 54 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	n	177	Total	C	H	N	O	S	0	0
			2853	899	1443	249	256	6		

- Molecule 55 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	o	64	Total	C	H	N	O	S	0	0
			1076	323	572	105	74	2		

- Molecule 56 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	p	175	Total	C	H	N	O	S	0	0
			2671	826	1358	241	244	2		

- Molecule 57 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	q	38	Total	C	H	N	O	S	0	0
			645	185	343	65	48	4		

- Molecule 58 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	r	149	Total	C	H	N	O	S	0	0
			2259	699	1148	197	214	1		

- Molecule 59 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	s	142	Total	C	H	N	O	S	0	0
			2291	714	1162	212	199	4		

- Molecule 60 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	t	123	Total	C	H	N	O	S	0	0
			1969	593	1023	181	166	6		

- Molecule 61 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	u	144	Total	C	H	N	O	S	0	0
			2182	654	1129	207	190	2		

- Molecule 62 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	v	136	Total	C	H	N	O	S	0	0
			2231	686	1157	205	177	6		

- Molecule 63 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms						AltConf	Trace
63	w	119	Total	C	H	N	O	S	0	0
			1945	588	994	195	163	5		

- Molecule 64 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	x	116	Total	C	H	N	O		
			1815	552	923	178	162	0	0

- Molecule 65 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms						AltConf	Trace
65	y	114	Total	C	H	N	O	S	0	0
			1879	574	962	179	163	1		

- Molecule 66 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	z	117	Total	C	H	N	O		
			1967	604	1020	192	151	0	0

- Molecule 67 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
67	AE	1	Total	Mg	0
			1	1	

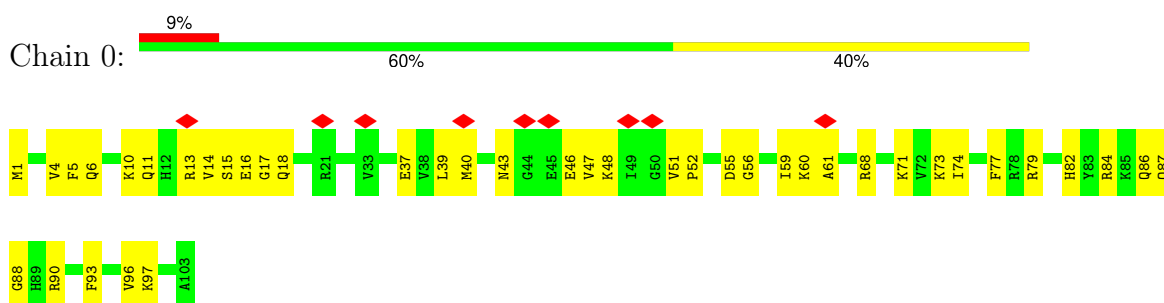
- Molecule 68 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
68	AE	2	Total	Zn	0
			2	2	

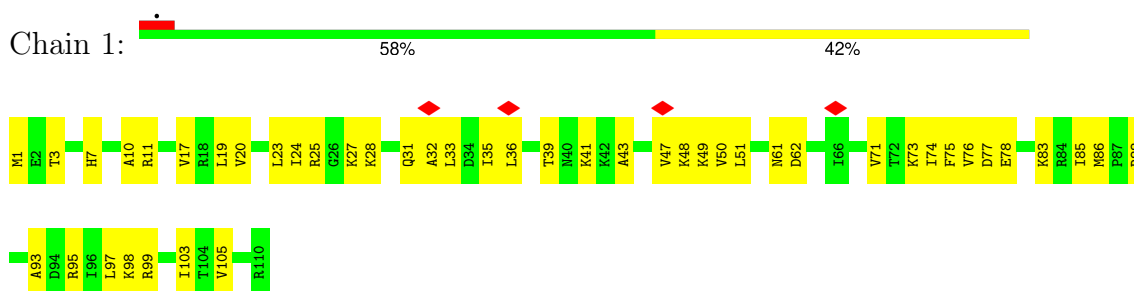
3 Residue-property plots [i](#)

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

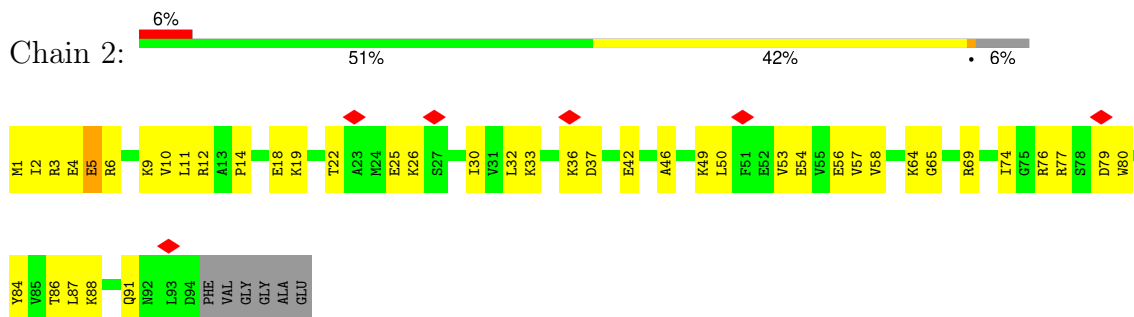
• Molecule 1: Ribosomal protein L21



• Molecule 2: 50S ribosomal protein L22

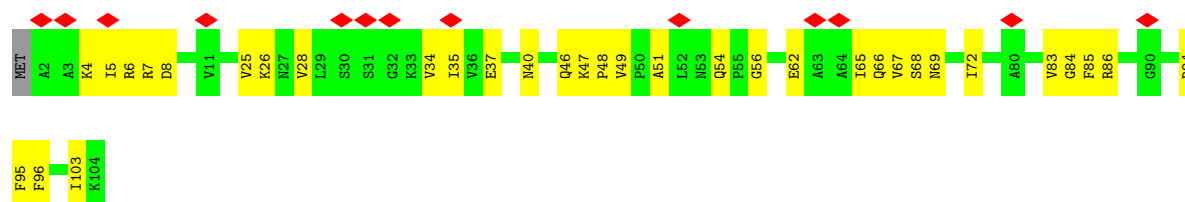


• Molecule 3: 50S ribosomal protein L23

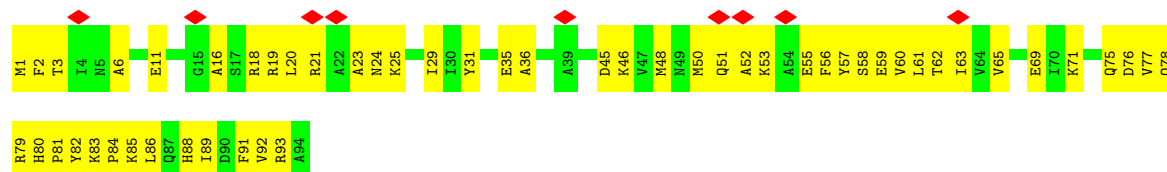
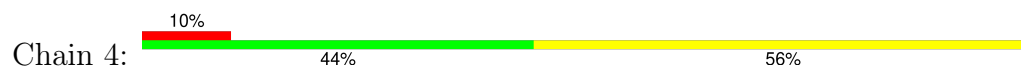


• Molecule 4: 50S ribosomal protein L24





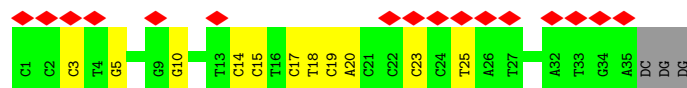
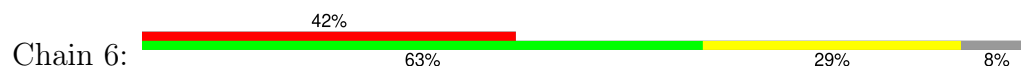
• Molecule 5: 50S ribosomal protein L25



• Molecule 6: NT DNA ops



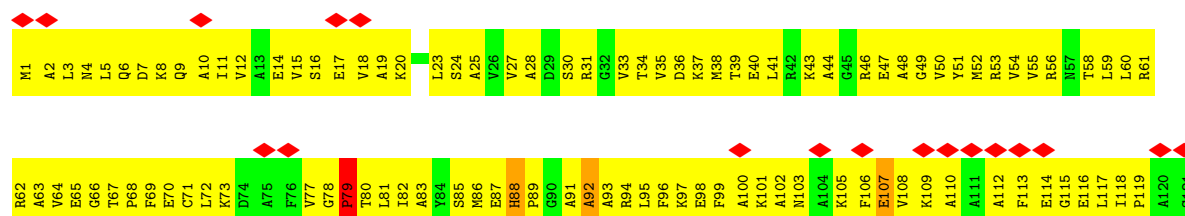
• Molecule 7: T DNA ops

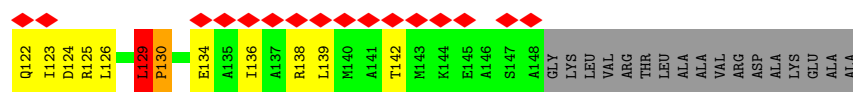


• Molecule 8: mRNA with 39 nt long spacer

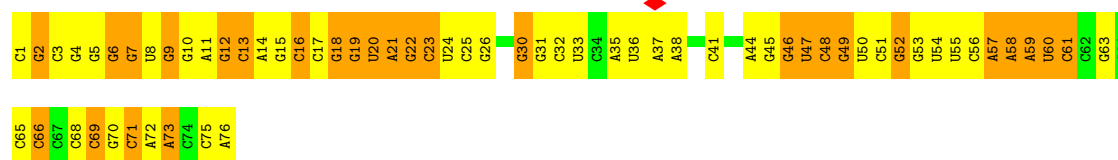
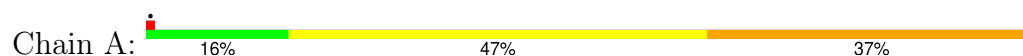


• Molecule 9: 50S ribosomal protein L10

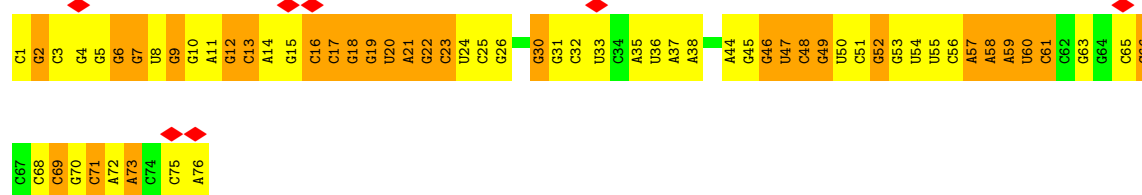
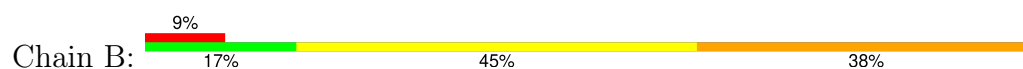




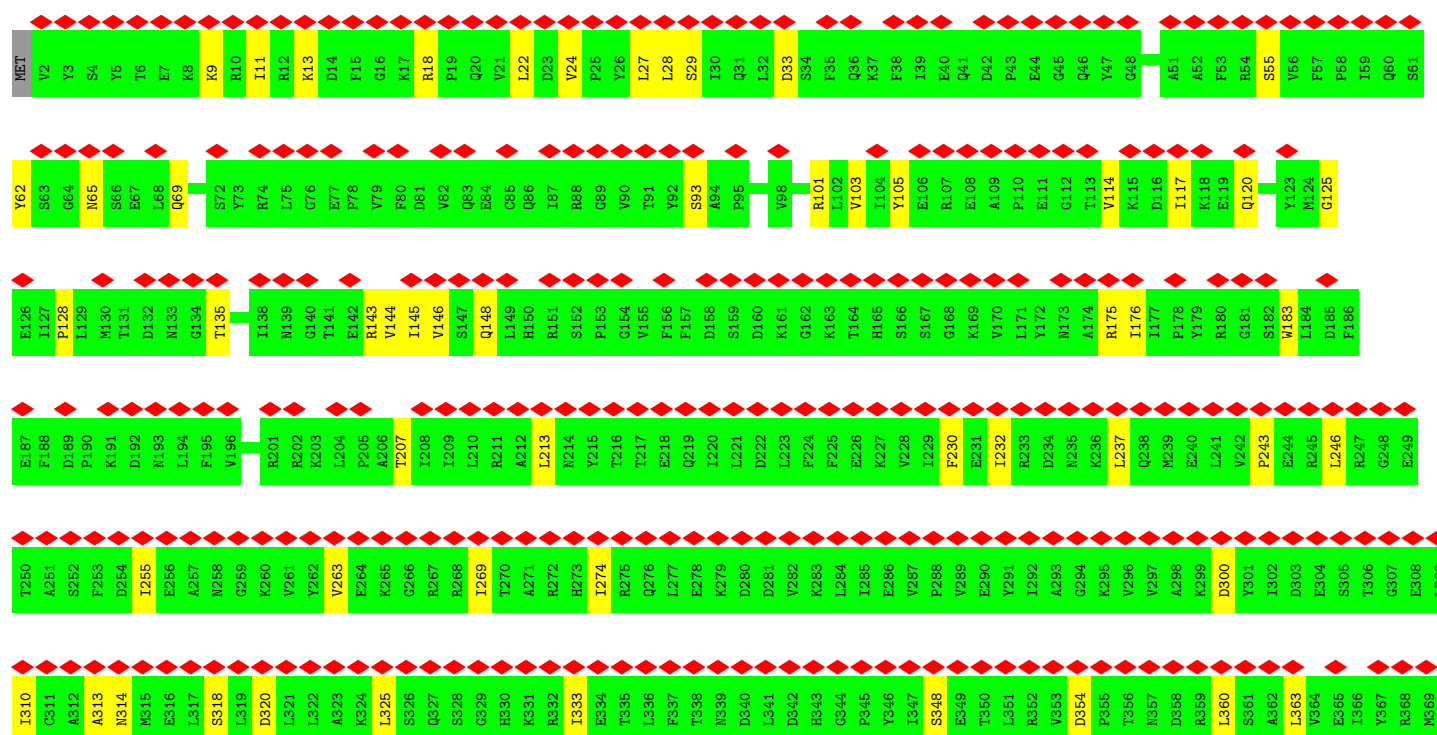
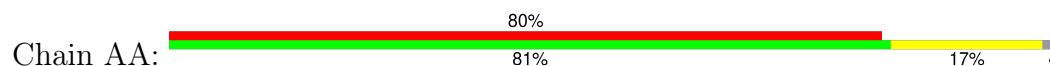
• Molecule 10: E-site and P-site tRNA (fMet)



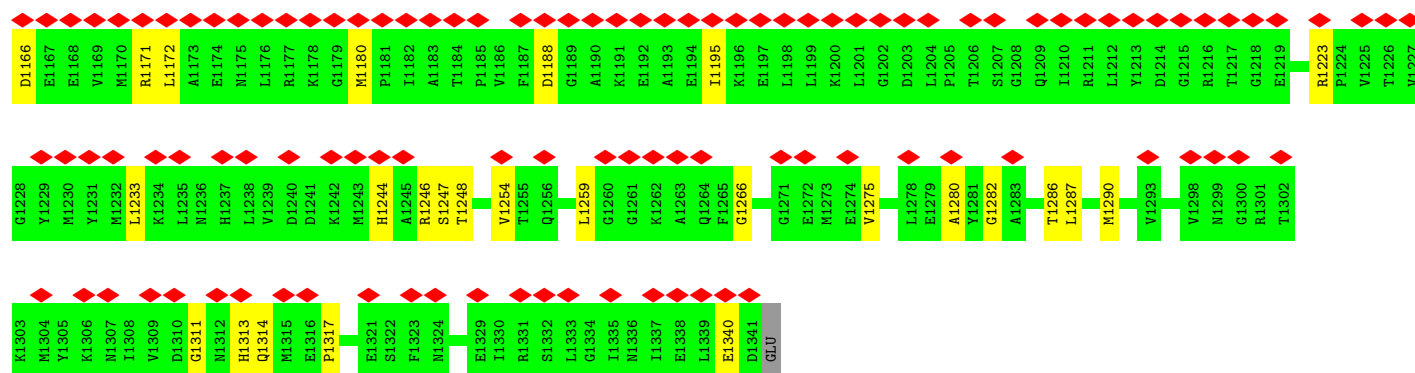
• Molecule 10: E-site and P-site tRNA (fMet)



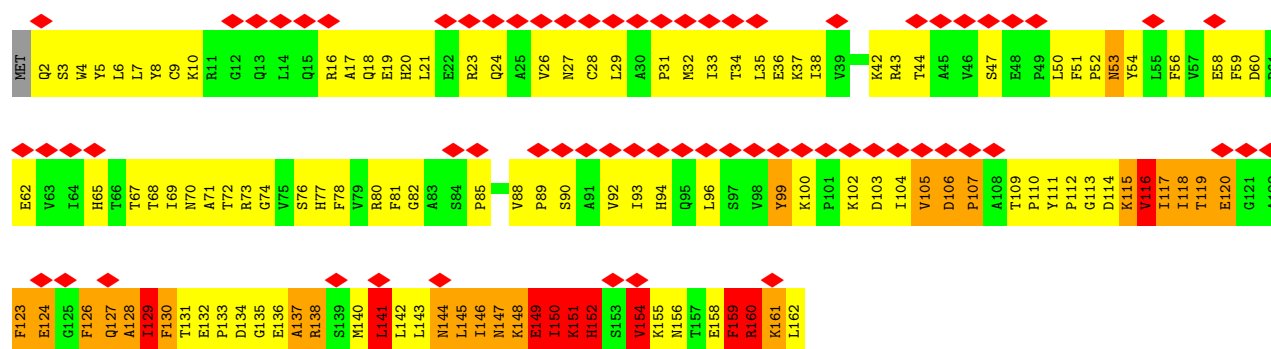
• Molecule 11: DNA-directed RNA polymerase subunit beta



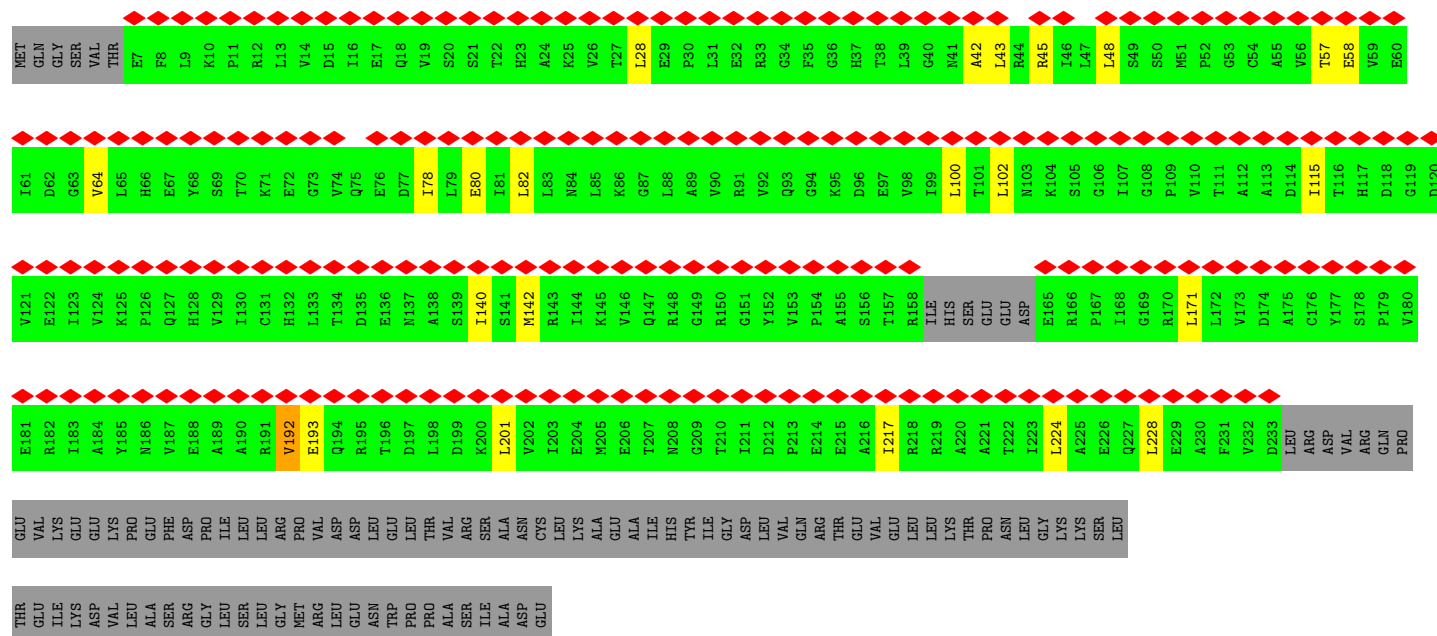
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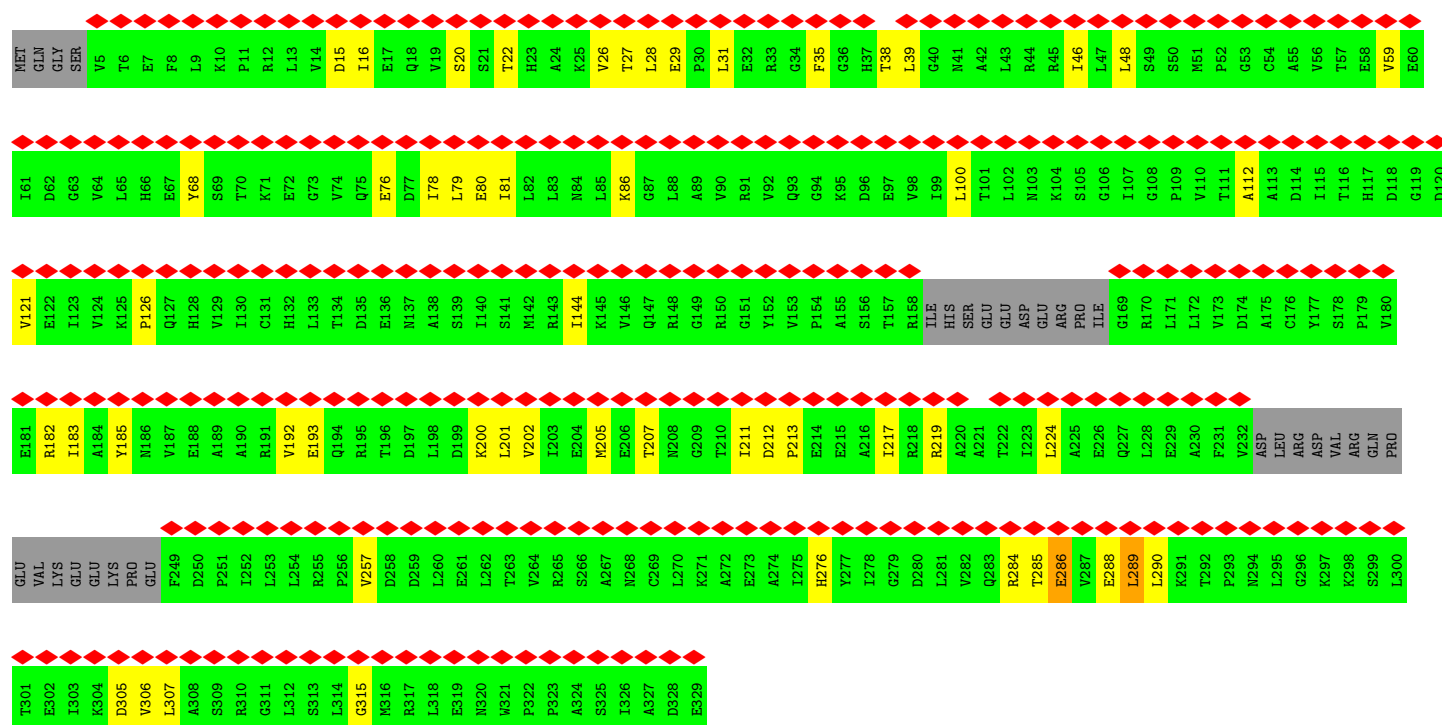
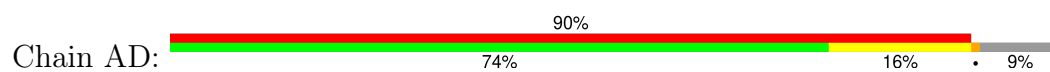
• Molecule 12: Transcription antitermination protein RfaH



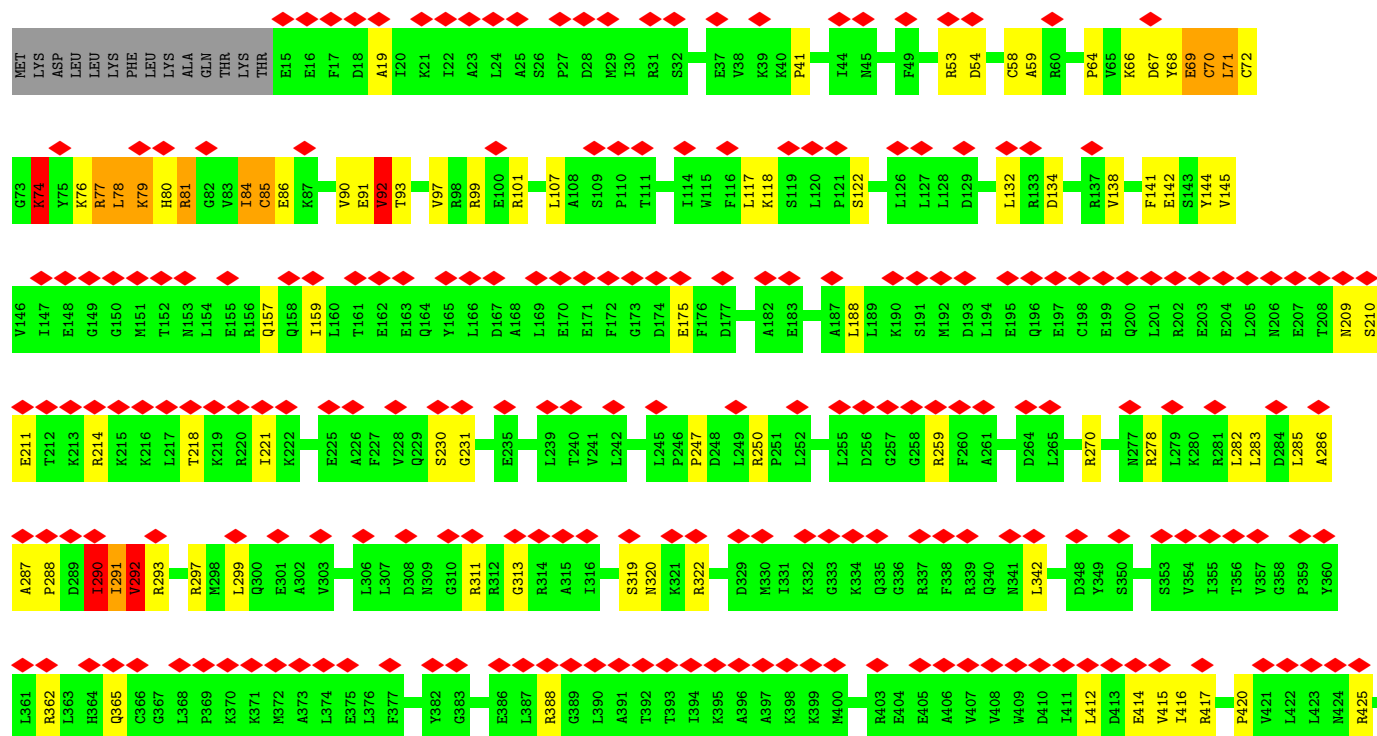
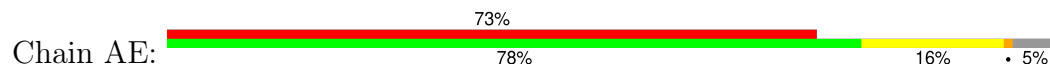
• Molecule 13: DNA-directed RNA polymerase subunit alpha



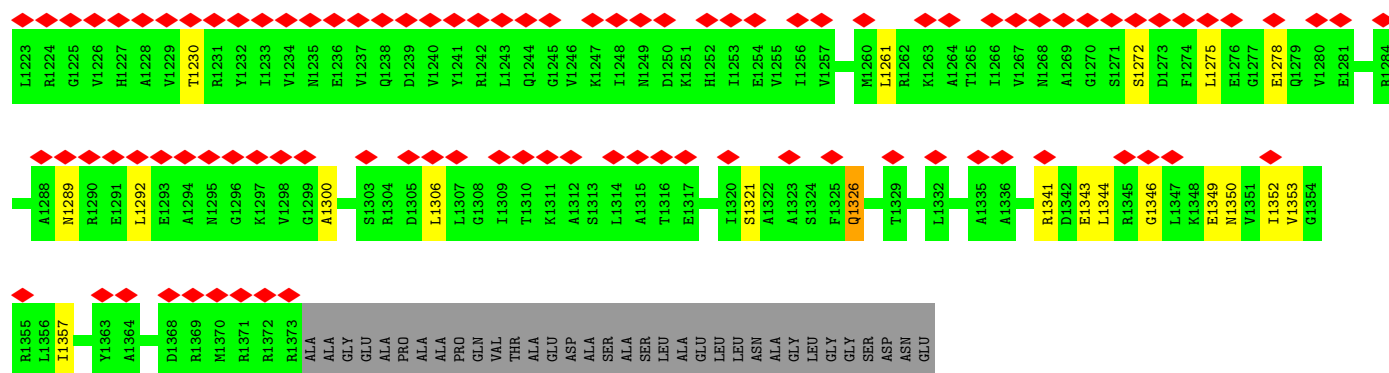
• Molecule 13: DNA-directed RNA polymerase subunit alpha



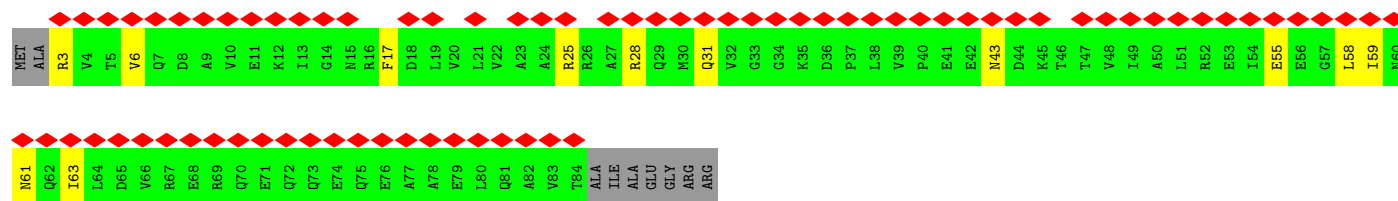
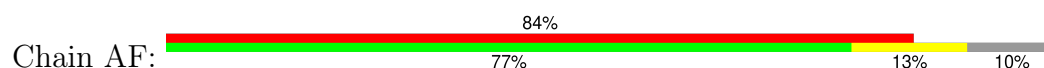
• Molecule 14: DNA-directed RNA polymerase subunit beta'



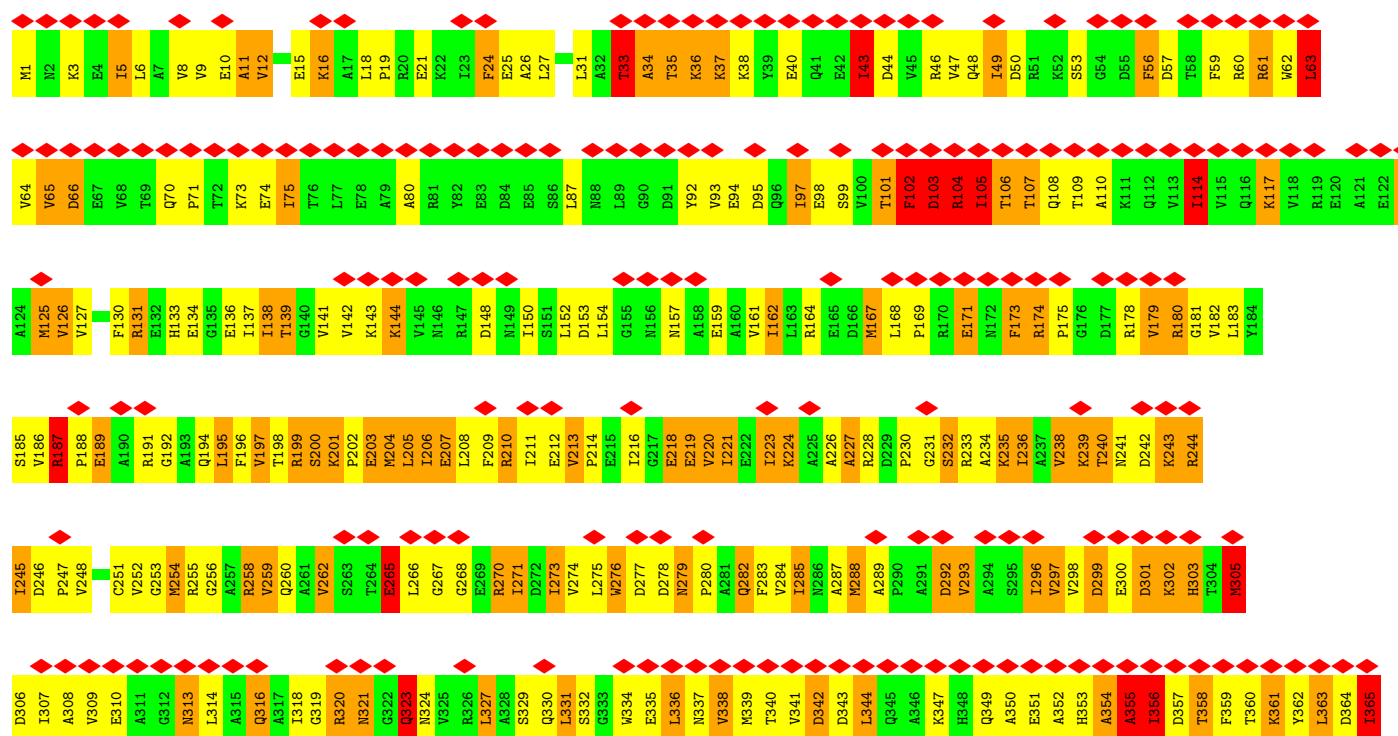
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P1179	L1059	ALA	L1059	A879	A879	I820	E756	A996	G636	R576	D516	I447
V1180	V1060	SER	V1060	V880	V880	M821	T757	M697	A637	A577	C517	Q448
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I1190	G1070	P952	I1070	D889	D889	D830	G766	V706	I646	G586	V526	Y457
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V1198	L1078	L960	V1078	C898	C898	R838	I774	E714	I654	Q594	E534	L472
F1199	K1079	S961	F1079	H899	H899	V839	T775	K715	S655	R535	R535	T473
E1200	I1080	P962	E1080	G900	G900	L840	T776	Q716	E656	L536	L536	L474
G1201	D1081	V963	G1081	R901	R901	G841	H777	V717	A657	G597	Y537	E475
E1202	P1082	K964	E1082	D902	D902	R842	G778	S718	E658	K598	R538	A476
R1203	A1083	S965	R1083	L903	L903	V843	A779	F719	A659	K599	S539	A480
V1204	Q1084	P966	V1084	A904	A904	T844	R780	N720	E660	G540	G540	R481
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R1206	N1086	N968	R1086	H907	H907	E846	G782	I722	A662	S602	A542	M484
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S1211	P1091	L973	S1091	X911	X911	P851	A787	D727	Q668	C608	V548	M488
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A1216	V1096	R978	A1096	G916	G916	T856	L796	S733	G613	G613	T553	P493
F1217	F1097	V979	F1097	V917	V917	L857	T797	V673	L614	L614	E554	P498
H1218	A1097	T980	H1097	I918	I918	V858	R798	A734	K615	K615	Y555	I499
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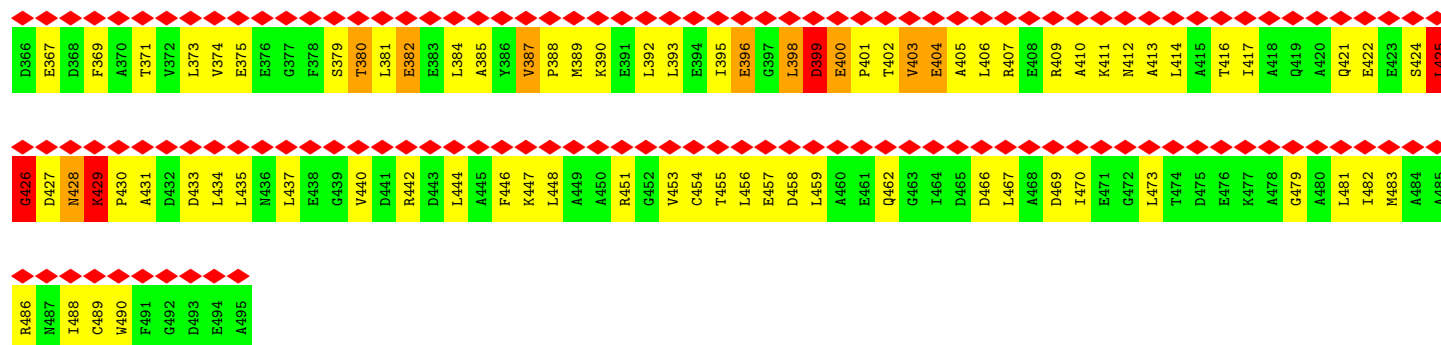


• Molecule 15: DNA-directed RNA polymerase subunit omega

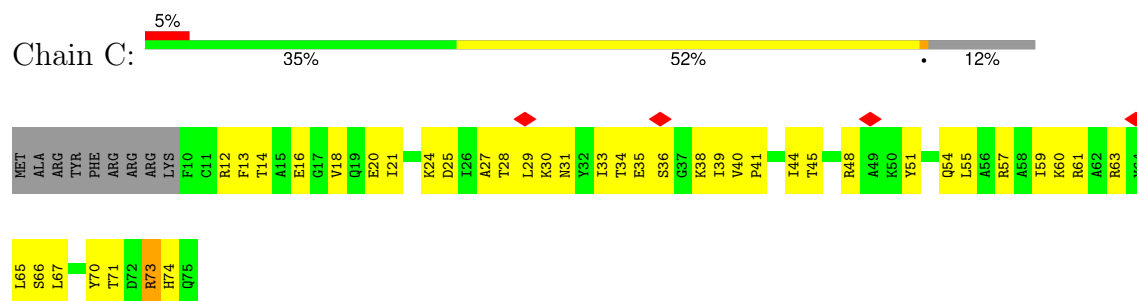


• Molecule 16: Transcription termination/antitermination protein NusA

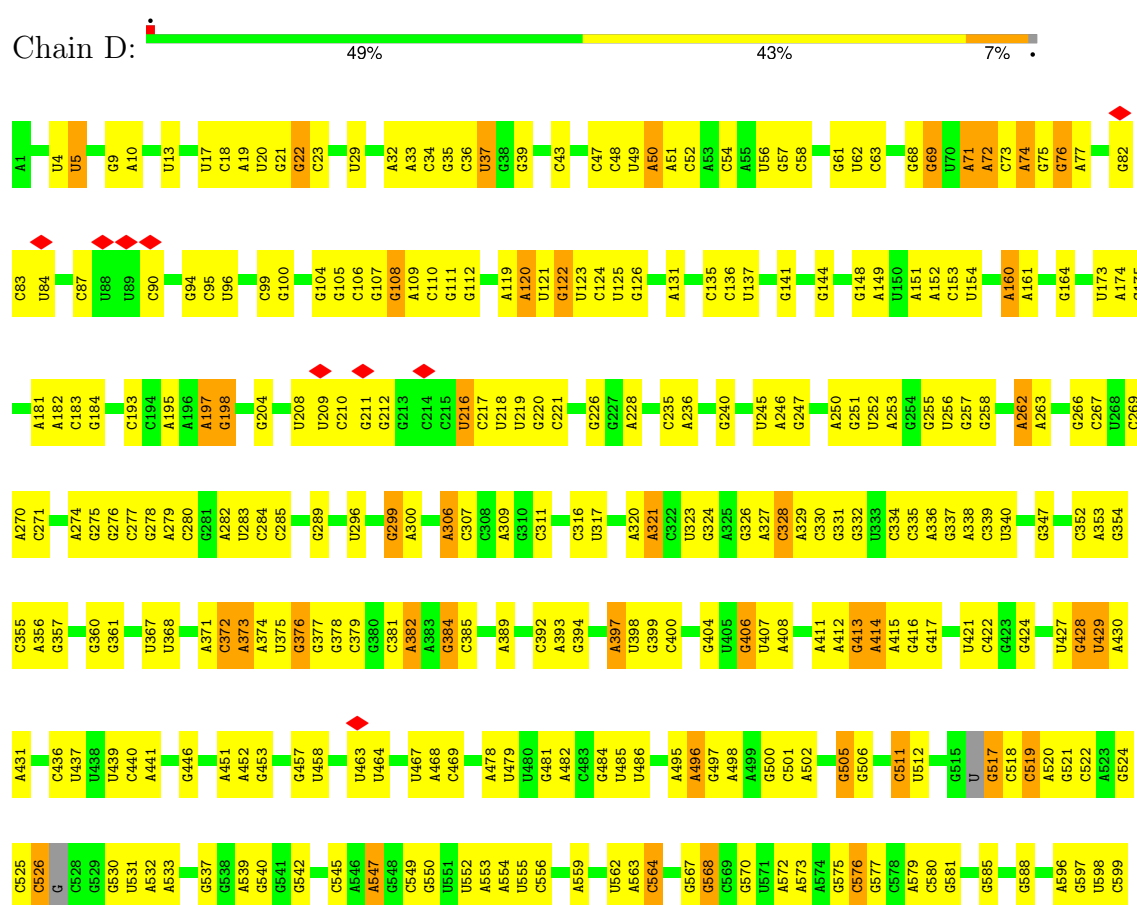




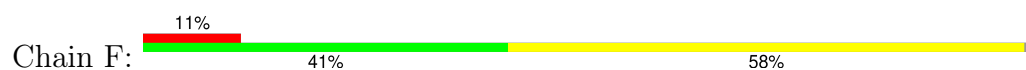
- Molecule 17: 30S ribosomal protein S18



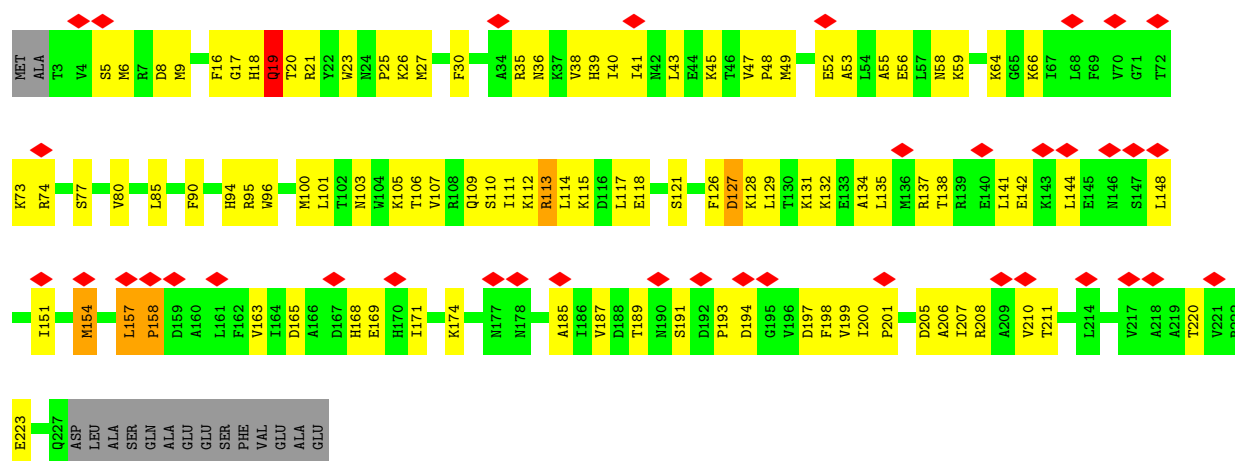
- Molecule 18: 16S rRNA



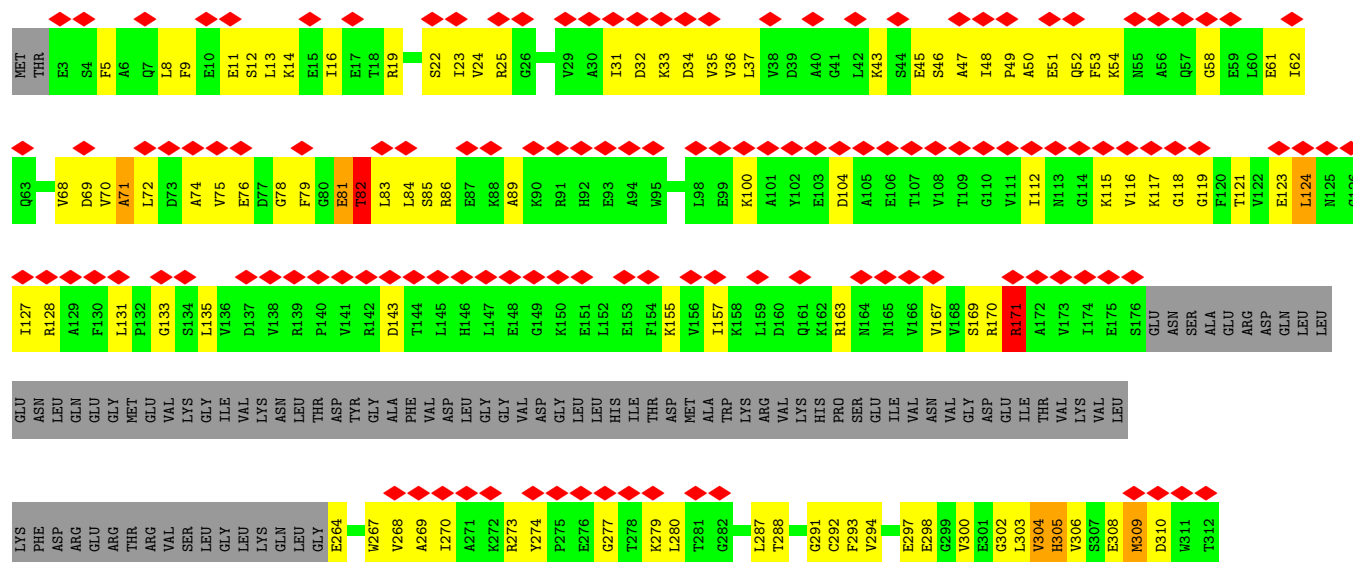


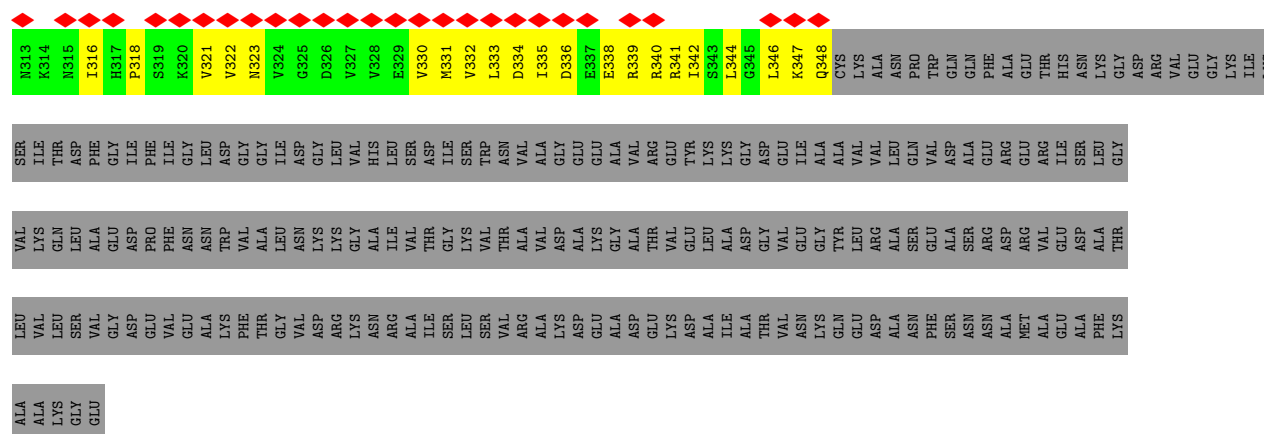


• Molecule 21: 30S ribosomal protein S2

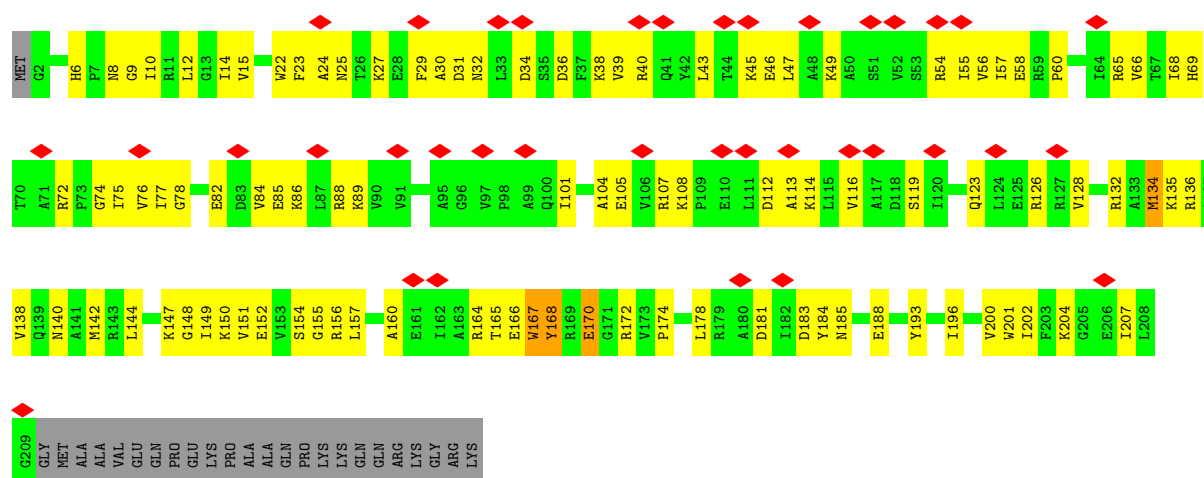
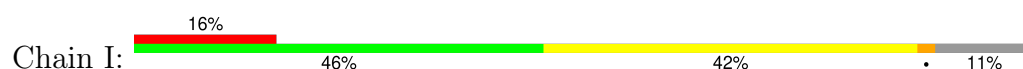


• Molecule 22: 30S ribosomal protein S1

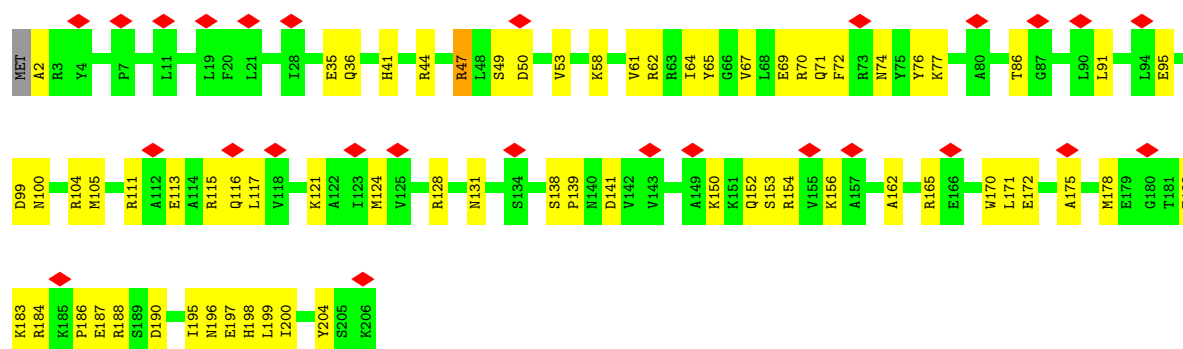




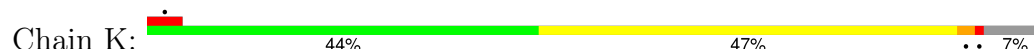
• Molecule 23: 30S ribosomal protein S3

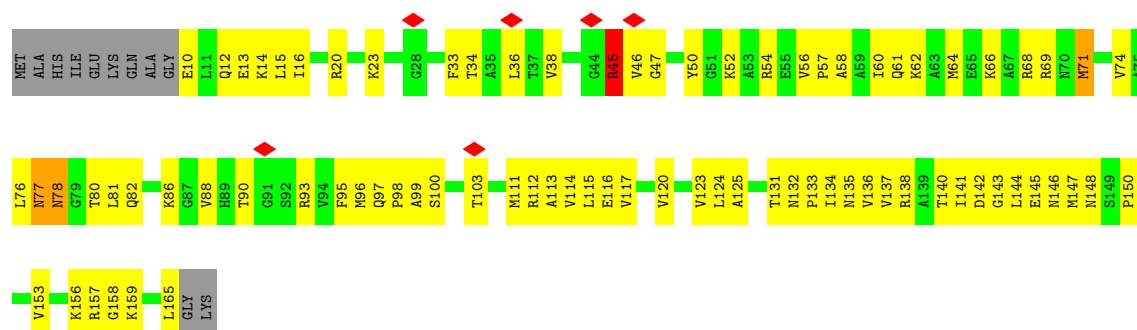


• Molecule 24: 30S ribosomal protein S4

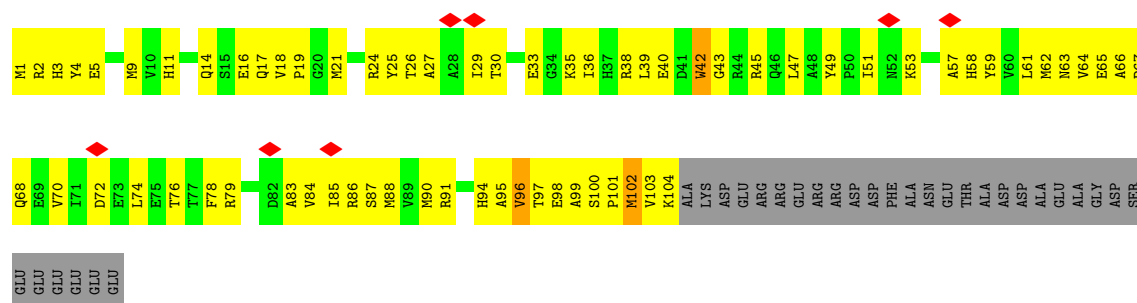


• Molecule 25: 30S ribosomal protein S5

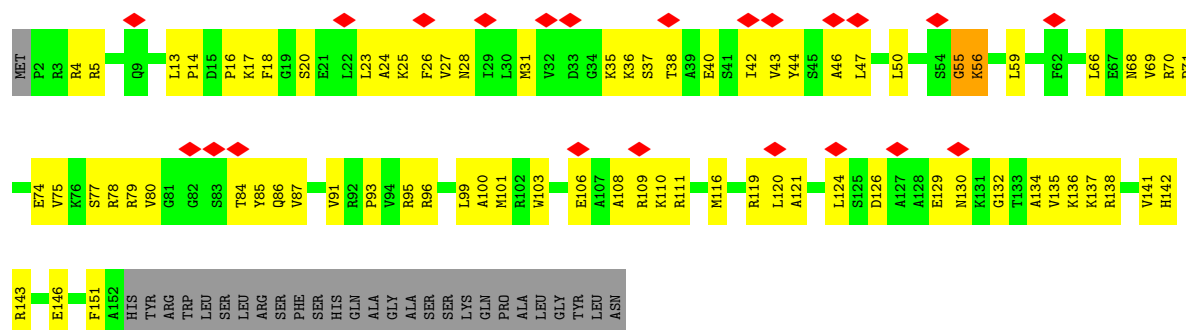




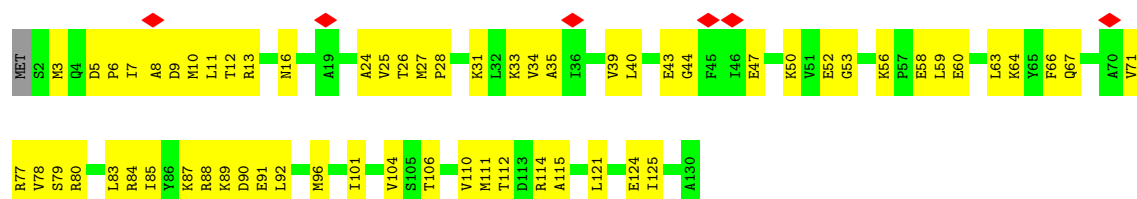
- Molecule 26: 30S ribosomal protein S6



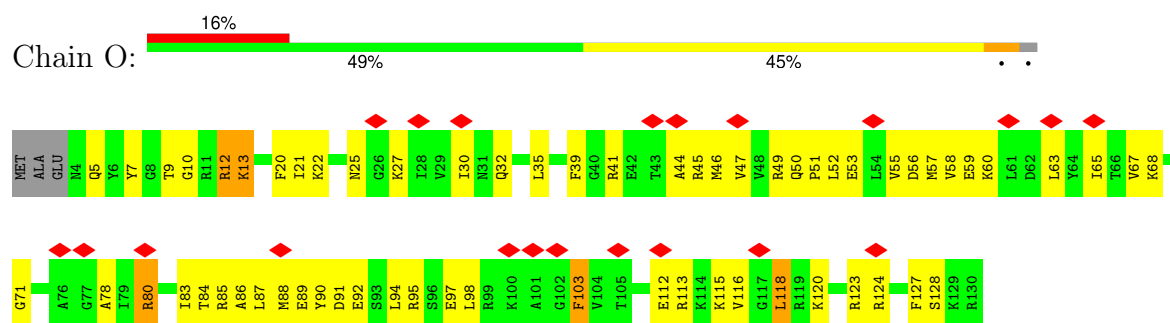
- Molecule 27: 30S ribosomal protein S7



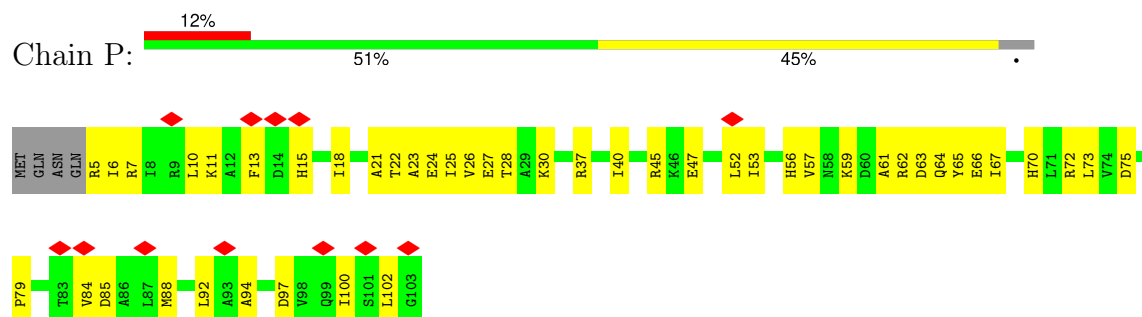
- Molecule 28: 30S ribosomal protein S8



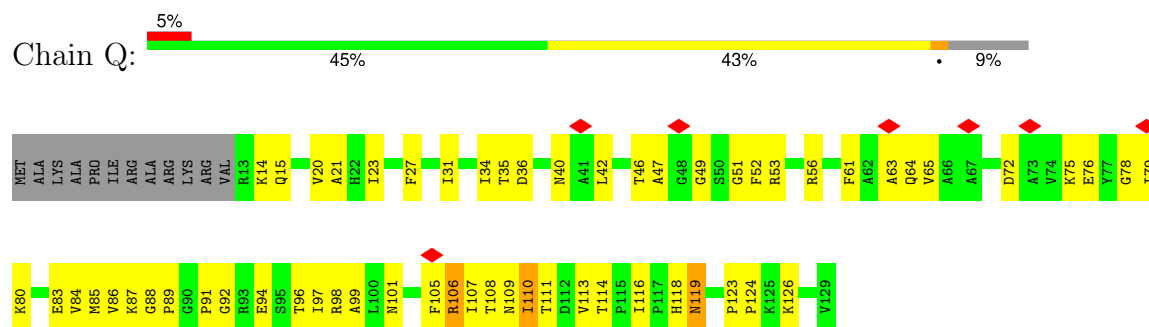
- Molecule 29: 30S ribosomal protein S9



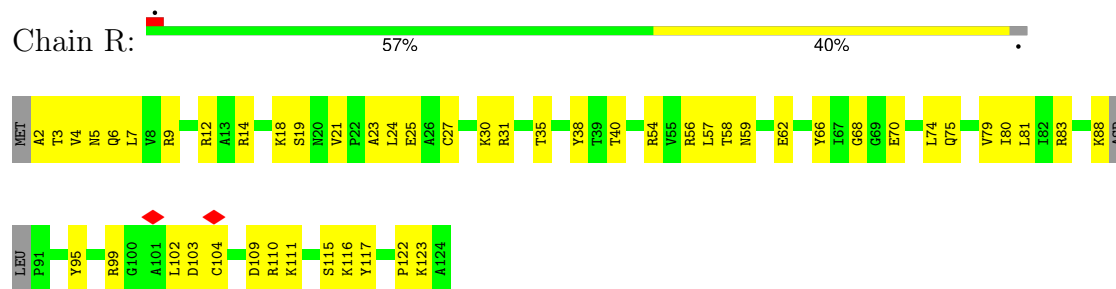
• Molecule 30: 30S ribosomal protein S10



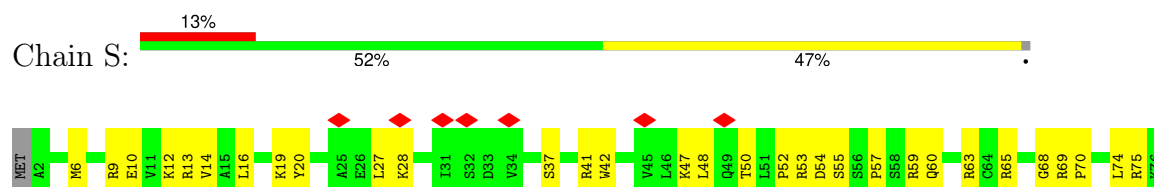
• Molecule 31: 30S ribosomal protein S11

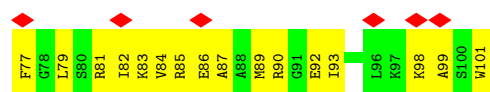


• Molecule 32: 30S ribosomal protein S12

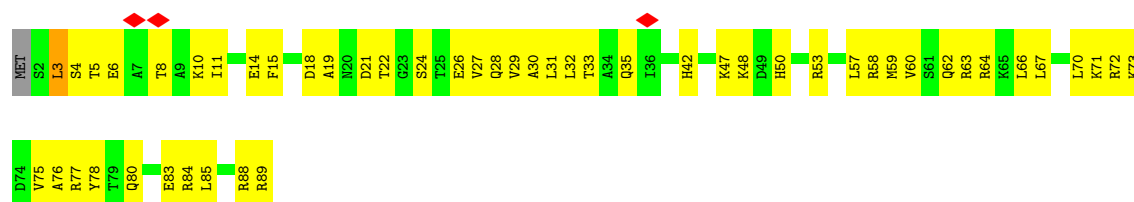


• Molecule 33: 30S ribosomal protein S14

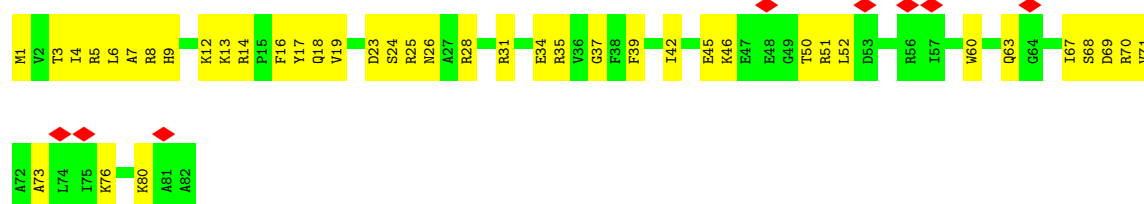




- Molecule 34: Small ribosomal subunit protein uS15



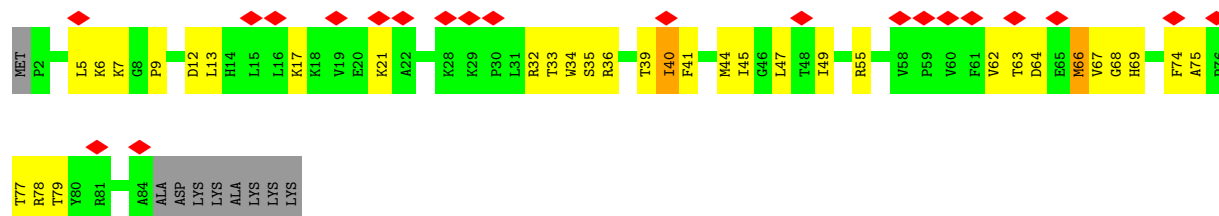
- Molecule 35: 30S ribosomal protein S16



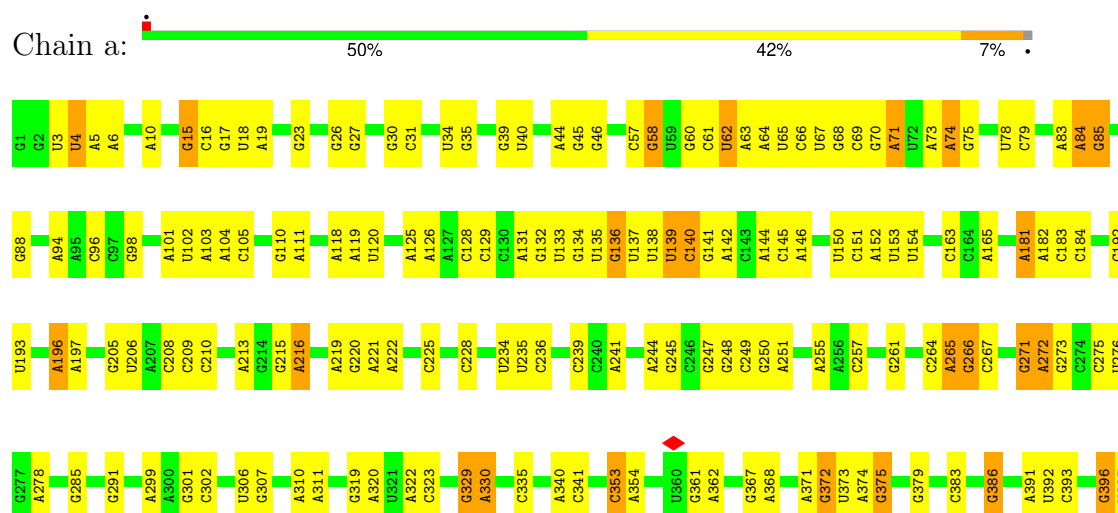
- Molecule 36: 30S ribosomal protein S17



- Molecule 37: 30S ribosomal protein S19

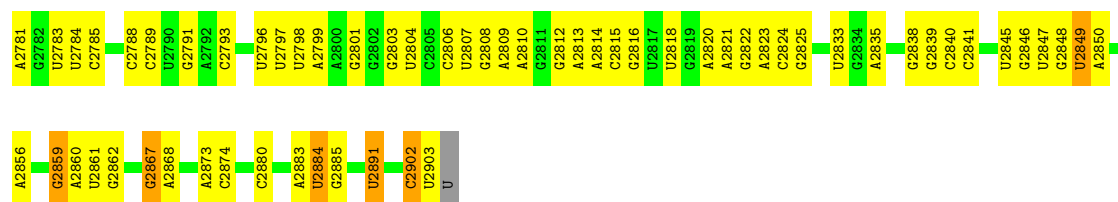


- Molecule 38: 30S ribosomal protein S13

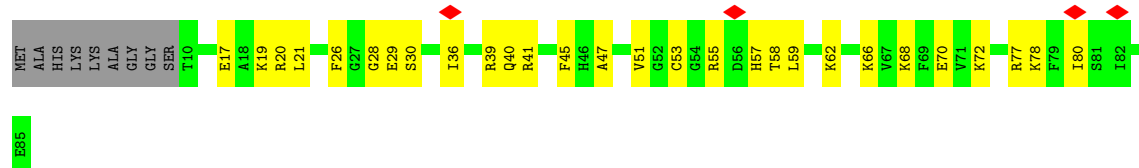


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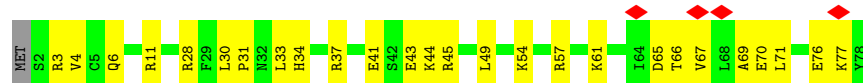
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A2052	C2055	G2056	A2060	G2061	A2062	G2063	G2064	G2065	G2066	G2067	U2068	G	A2070	A2071	C2072	G2073	U	U2075	A2082	G2083	U2086	G2087	C2091	U2092	G2093	A2095	G2096	A2097	U2098	G2099	G2100	A2108	U2109	G2110	G2111	G2112	U2113	A2114	G2115	G2116	A2117	U2118	G2121	U2122	G2123	G2124	G2125	A2126	G2127	G2128														
A1981	U1982	G1983	A1987	U1991	G1992	U1993	G1996	G1997	G1998	G1999	G2000	G2002	C2006	G2007	A2008	G2009	G2010	U2011	G2012	A2013	A2014	U2015	A2016	U2017	A2020	U2021	U2022	G2023	G2024	C2025	U1951	G1952	C1870	G1953	G1954	U1955	U1956	C1957	G1958	U1959	A1960	G2035	C2036	A2037	U1963	G2038	U2039	G1964	C2040	U2041	A2042	C2043	C2044	G2049	A2051									
G1824	U1825	G1826	U1827	G1828	A1829	U1830	G1831	G1832	G1833	U1834	G	G1835	G1836	G1839	G1840	U1841	G1842	G1843	G1844	G1845	G1846	U1847	G2010	A1848	A1853	A1854	U1855	U1856	G1857	A1858	U1859	C2021	G1862	U1796	A1871	G1872	G1873	U1798	G1874	G1875	C1800	A1801	A1802	A1803	A1808	G1811	U1708	G1894	A1885	A1889	U1817	A1890	A1900	G1906	G1907									
G1614	C1730	G1731	C1617	A	G1619	G1622	U1647	U1648	U1649	A1650	G1651	G1652	G1653	U1654	A1655	C1656	U1657	C1658	G1659	G1664	A1664	A1665	G1666	G1667	A1668	G1674	U1675	A1676	A1677	G1681	C1682	A1791	U1683	G1684	C1793	U1688	U1689	A1792	C1795	U1693	G1694	G1695	A1700	G1703	G1707	C1708	G1709	G1710	U1714	U1715	A1819	U1720	G1721	G1722	G1723									



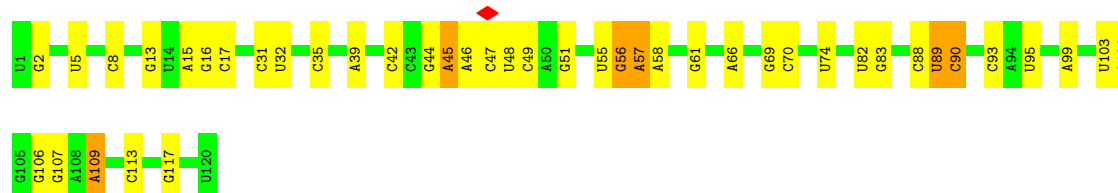
- Molecule 42: 50S ribosomal protein L27



- Molecule 43: 50S ribosomal protein L28



- Molecule 44: 5S rRNA



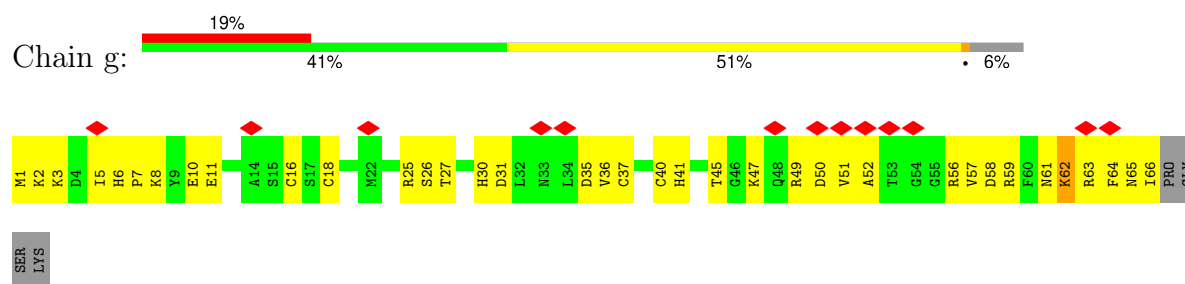
- Molecule 45: 50S ribosomal protein L29



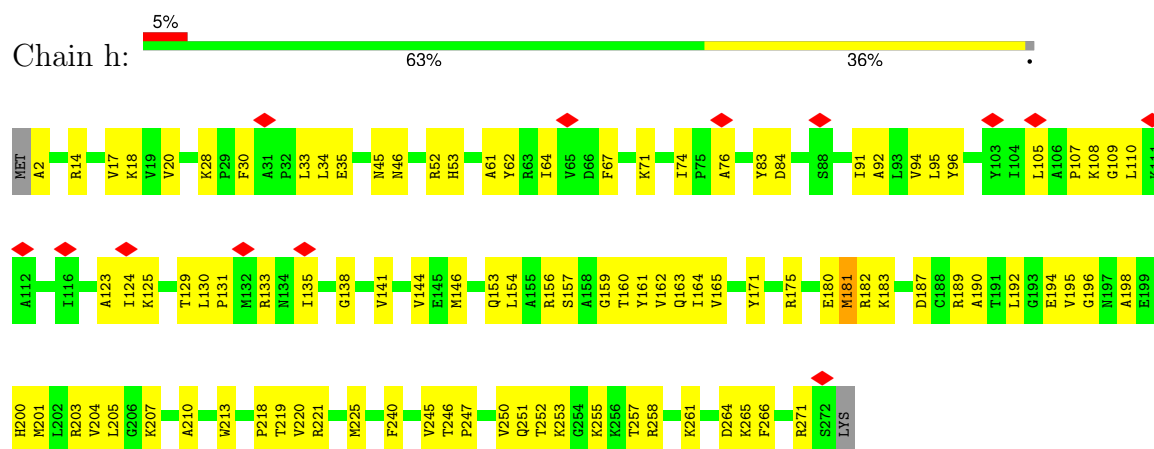
- Molecule 46: 50S ribosomal protein L30



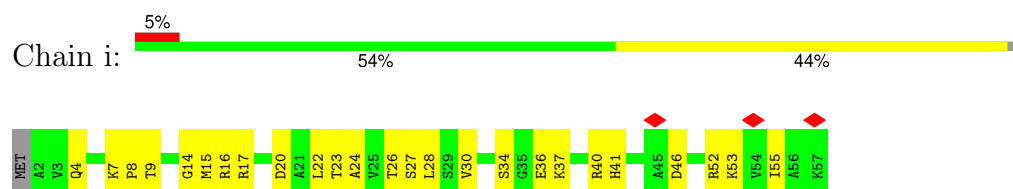
- Molecule 47: 50S ribosomal protein L31



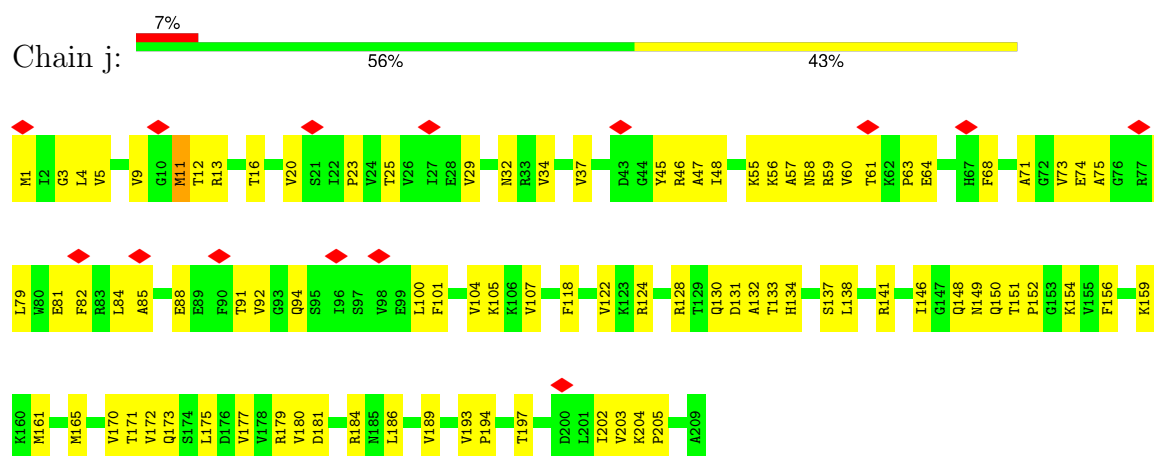
- Molecule 48: 50S ribosomal protein L2



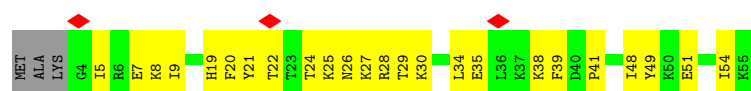
- Molecule 49: 50S ribosomal protein L32



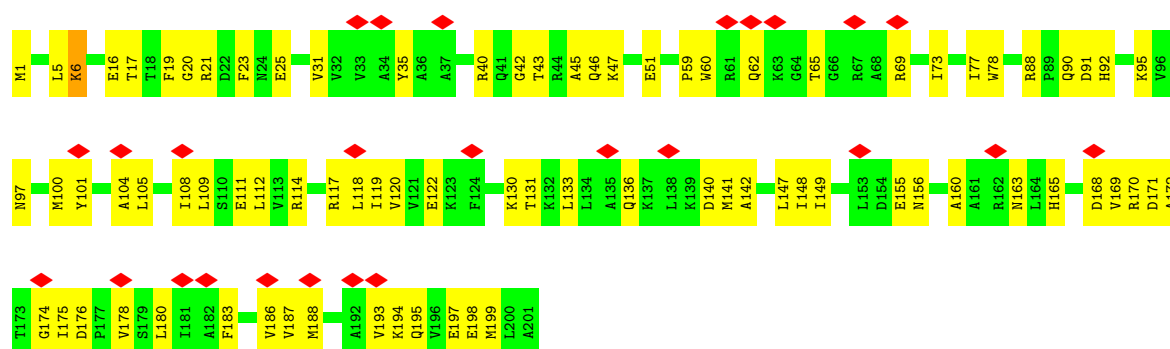
- Molecule 50: 50S ribosomal protein L3



- Molecule 51: 50S ribosomal protein L33



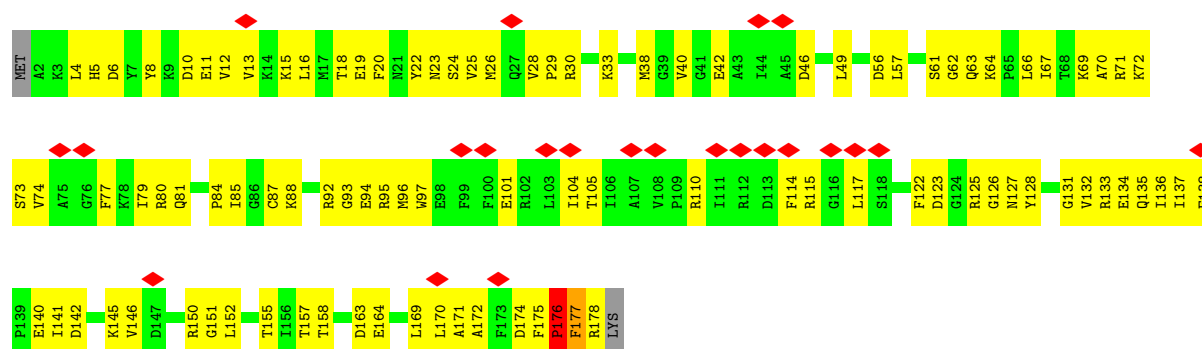
• Molecule 52: 50S ribosomal protein L4



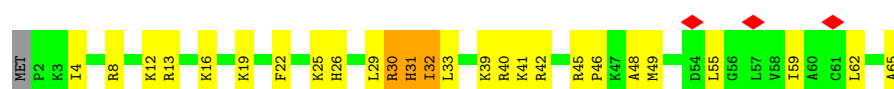
• Molecule 53: 50S ribosomal protein L34



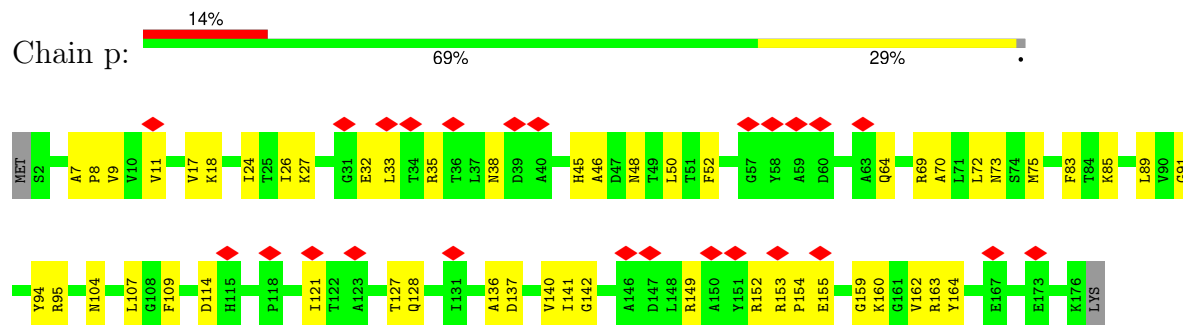
• Molecule 54: 50S ribosomal protein L5



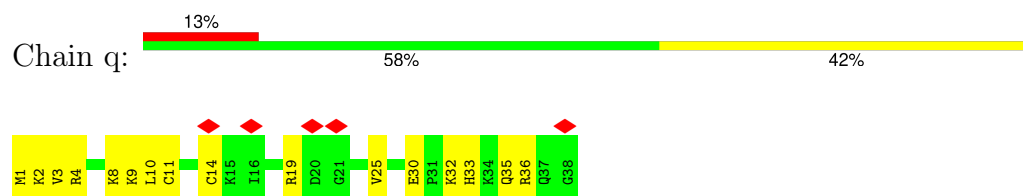
• Molecule 55: 50S ribosomal protein L35



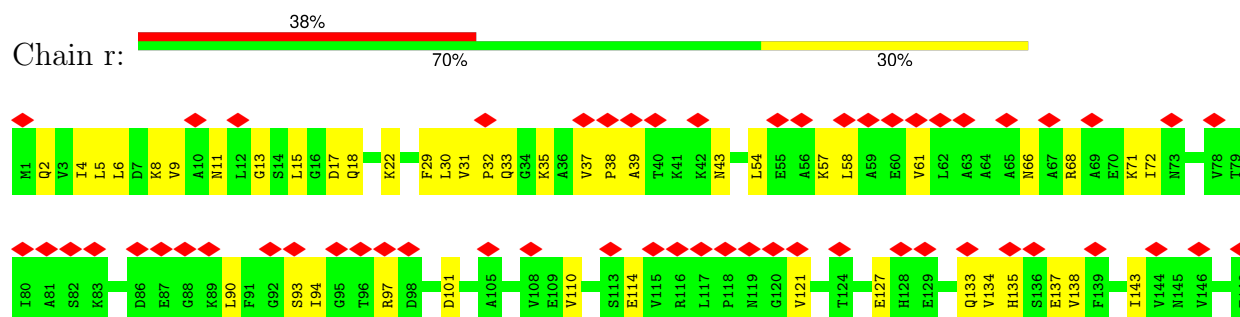
- Molecule 56: 50S ribosomal protein L6



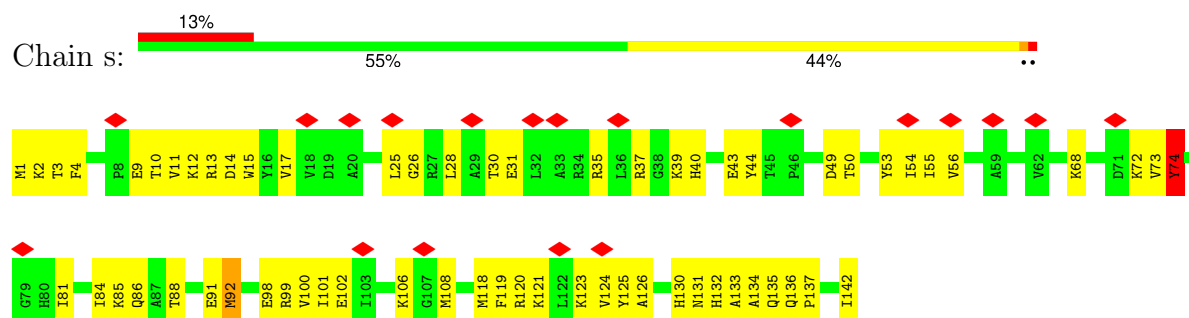
- Molecule 57: 50S ribosomal protein L36



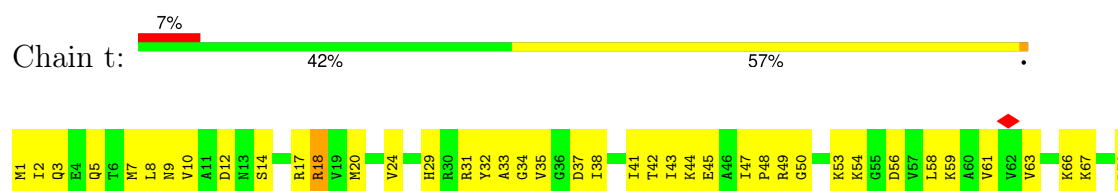
- Molecule 58: 50S ribosomal protein L9

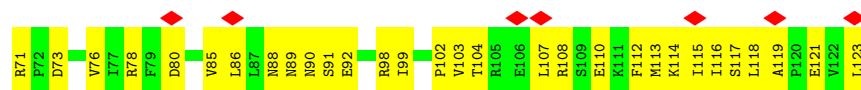


- Molecule 59: 50S ribosomal protein L13



- Molecule 60: 50S ribosomal protein L14

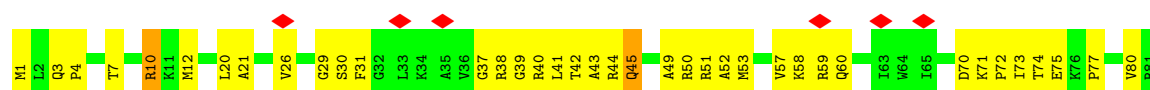




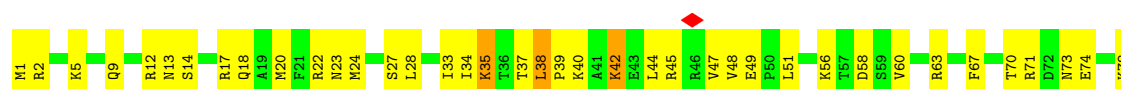
- Molecule 61: 50S ribosomal protein L15



- Molecule 62: 50S ribosomal protein L16



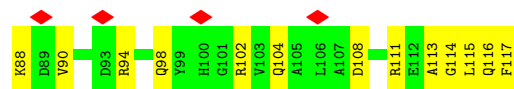
- Molecule 63: 50S ribosomal protein L17

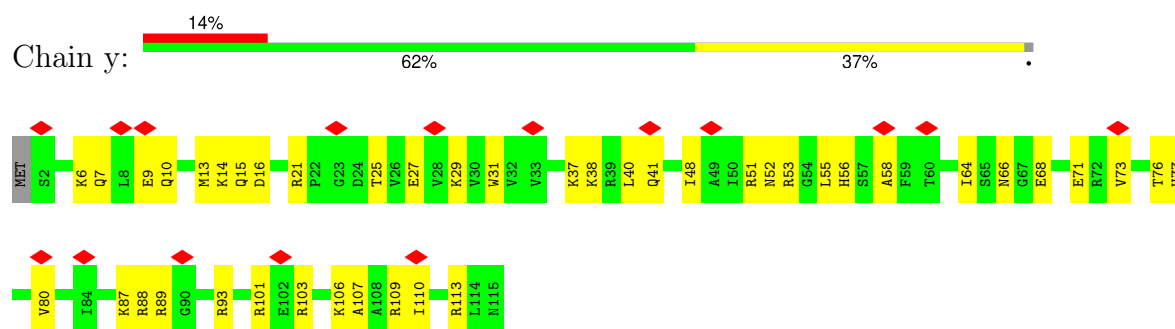


- Molecule 64: 50S ribosomal protein L18

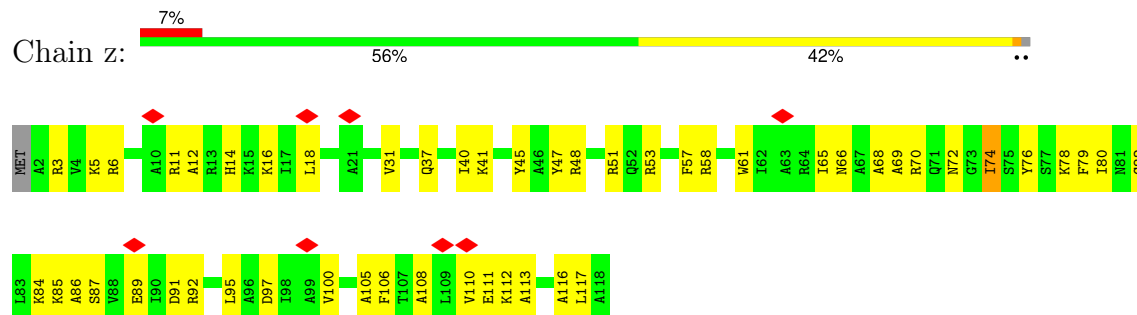


- Molecule 65: 50S ribosomal protein L19





• Molecule 66: 50S ribosomal protein L20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	15810	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1250	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.019	Depositor
Minimum map value	-0.087	Depositor
Average map value	-0.006	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.000001	Depositor
Map size (Å)	533.2, 533.2, 533.2	wwPDB
Map dimensions	620, 620, 620	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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	0.43	0/829	0.51	0/1107
2	1	0.60	0/864	0.63	0/1156
3	2	0.55	1/752 (0.1%)	0.67	0/1005
4	3	0.36	0/796	0.49	0/1062
5	4	0.57	0/766	0.63	0/1025
6	5	0.57	0/816	0.78	0/1259
7	6	0.57	0/783	0.78	0/1203
8	7	0.61	2/585 (0.3%)	0.91	3/906 (0.3%)
9	9	0.37	0/1131	0.73	2/1524 (0.1%)
10	A	0.27	0/1810	0.58	0/2821
10	B	0.27	0/1810	0.58	0/2821
11	AA	0.38	0/10547	0.62	0/14232
12	AB	0.53	0/1317	1.20	17/1786 (1.0%)
13	AC	0.38	0/1718	0.62	0/2328
13	AD	0.37	0/2096	0.69	3/2854 (0.1%)
14	AE	0.39	0/10561	0.64	5/14258 (0.0%)
15	AF	0.30	0/652	0.61	0/879
16	AG	0.97	6/3897 (0.2%)	1.40	49/5273 (0.9%)
17	C	0.67	0/553	0.81	1/743 (0.1%)
18	D	0.29	0/36610	0.41	9/57091 (0.0%)
19	E	0.61	0/675	0.72	0/895
20	F	0.53	0/597	0.61	0/792
21	G	0.68	5/1791 (0.3%)	0.79	8/2413 (0.3%)
22	H	0.38	0/1746	0.81	0/2382
23	I	0.57	1/1663 (0.1%)	0.68	4/2241 (0.2%)
24	J	0.46	0/1665	0.58	0/2227
25	K	0.72	2/1165 (0.2%)	0.86	6/1568 (0.4%)
26	L	0.68	1/867 (0.1%)	0.79	1/1171 (0.1%)
27	M	0.56	0/1195	0.69	2/1602 (0.1%)
28	N	0.50	0/989	0.58	0/1326
29	O	0.66	3/1034 (0.3%)	0.79	3/1375 (0.2%)
30	P	0.51	0/800	0.73	0/1082

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	Q	0.72	2/893 (0.2%)	0.76	2/1205 (0.2%)
32	R	0.49	0/952	0.59	0/1274
33	S	0.53	0/817	0.61	0/1088
34	T	0.57	1/722 (0.1%)	0.68	0/964
35	U	0.42	0/659	0.53	0/884
36	V	0.49	0/657	0.62	0/881
37	W	0.56	1/680 (0.1%)	0.62	1/915 (0.1%)
38	X	0.45	0/909	0.72	1/1215 (0.1%)
39	Y	0.38	2/1046 (0.2%)	0.66	2/1410 (0.1%)
40	Z	0.13	0/227	0.41	0/304
41	a	0.30	0/69247	0.43	10/107985 (0.0%)
42	b	0.42	0/589	0.55	0/779
43	c	0.51	0/635	0.61	0/848
44	d	0.25	0/2872	0.37	0/4478
45	e	0.69	2/502 (0.4%)	0.65	1/667 (0.1%)
46	f	0.52	0/452	0.57	0/605
47	g	0.45	1/531 (0.2%)	0.64	0/709
48	h	0.50	1/2121 (0.0%)	0.59	1/2852 (0.0%)
49	i	0.41	0/450	0.55	0/599
50	j	0.51	0/1586	0.57	1/2134 (0.0%)
51	k	0.46	0/433	0.63	0/576
52	l	0.51	1/1571 (0.1%)	0.62	0/2113
53	m	0.45	0/380	0.56	0/498
54	n	0.46	0/1434	0.66	1/1926 (0.1%)
55	o	0.51	0/513	0.71	1/676 (0.1%)
56	p	0.42	0/1333	0.62	2/1805 (0.1%)
57	q	0.45	0/303	0.64	0/397
58	r	0.28	0/1122	0.48	0/1515
59	s	0.70	2/1152 (0.2%)	0.74	2/1551 (0.1%)
60	t	0.53	0/955	0.75	3/1279 (0.2%)
61	u	0.43	0/1062	0.59	0/1413
62	v	0.60	1/1093 (0.1%)	0.77	3/1460 (0.2%)
63	w	0.83	2/964 (0.2%)	0.80	3/1289 (0.2%)
64	x	0.34	0/902	0.50	0/1209
65	y	0.41	0/929	0.54	0/1242
66	z	0.62	2/960 (0.2%)	0.62	0/1278
All	All	0.41	39/194733 (0.0%)	0.56	147/286430 (0.1%)

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	3
12	AB	0	1
13	AC	0	1
13	AD	0	2
14	AE	0	4
16	AG	0	6
21	G	0	1
22	H	0	5
23	I	0	1
25	K	0	2
29	O	0	1
38	X	0	1
39	Y	0	1
54	n	0	1
55	o	0	1
59	s	0	1
61	u	0	2
All	All	0	34

The worst 5 of 39 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	AG	429	LYS	C-N	13.93	1.51	1.33
63	w	35	LYS	CE-NZ	-12.76	1.11	1.49
29	O	80	ARG	CD-NE	-10.52	1.31	1.46
63	w	42	LYS	CD-CE	-9.42	1.24	1.52
25	K	45	ARG	CG-CD	7.72	1.75	1.52

The worst 5 of 147 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	AG	104	ARG	CA-C-N	17.97	154.32	121.97
16	AG	104	ARG	C-N-CA	17.97	154.32	121.97
16	AG	246	ASP	CA-C-N	14.49	137.95	119.84
16	AG	246	ASP	C-N-CA	14.49	137.95	119.84
16	AG	354	ALA	O-C-N	-13.69	107.30	122.09

There are no chirality outliers.

5 of 34 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	9	107	GLU	Peptide

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Mol	Chain	Res	Type	Group
9	9	79	PRO	Peptide
9	9	92	ALA	Peptide
12	AB	149	GLU	Mainchain
13	AC	192	VAL	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	816	839	839	53	0
2	1	857	922	922	73	0
3	2	746	811	811	60	0
4	3	788	844	844	44	0
5	4	753	780	780	87	0
6	5	726	0	392	112	0
7	6	703	0	396	35	0
8	7	527	0	262	82	0
9	9	1117	0	1155	254	0
10	A	1620	826	827	109	0
10	B	1620	813	827	111	0
11	AA	10381	0	10388	382	0
12	AB	1286	0	1302	375	0
13	AC	1698	0	1718	13	0
13	AD	2078	0	1891	37	0
14	AE	10404	0	10625	273	0
15	AF	650	0	658	10	0
16	AG	3852	0	3828	899	0
17	C	544	559	560	110	0
18	D	32703	16423	16451	744	0
19	E	669	719	719	79	0
20	F	589	629	629	60	0
21	G	1760	1785	1787	152	0
22	H	1730	1454	1455	164	0
23	I	1636	1710	1710	129	0
24	J	1643	1707	1707	88	0
25	K	1152	1196	1196	119	0
26	L	848	846	846	105	0
27	M	1181	1235	1238	123	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	N	979	1031	1031	91	0
29	O	1022	1070	1070	92	0
30	P	790	831	831	94	0
31	Q	877	887	887	96	0
32	R	939	1001	1001	94	0
33	S	805	844	844	74	0
34	T	714	734	734	93	0
35	U	649	666	666	62	0
36	V	648	691	691	71	0
37	W	663	688	688	46	0
38	X	900	964	965	111	0
39	Y	1032	0	1088	211	0
40	Z	227	0	237	30	0
41	a	61841	31077	31120	1314	0
42	b	582	599	599	48	0
43	c	625	652	652	32	0
44	d	2569	1301	1301	43	0
45	e	501	531	531	43	0
46	f	448	488	488	37	0
47	g	522	520	520	65	0
48	h	2082	2154	2154	136	0
49	i	444	459	458	47	0
50	j	1565	1617	1616	121	0
51	k	426	464	464	42	0
52	l	1552	1619	1619	126	0
53	m	377	418	418	29	0
54	n	1410	1443	1444	152	0
55	o	504	572	572	53	0
56	p	1313	1358	1358	74	0
57	q	302	343	343	27	0
58	r	1111	1148	1148	51	0
59	s	1129	1162	1162	123	0
60	t	946	1023	1023	107	0
61	u	1053	1129	1129	78	0
62	v	1074	1157	1157	124	0
63	w	951	994	994	98	0
64	x	892	923	923	48	0
65	y	917	962	962	54	0
66	z	947	1020	1019	82	0
67	AE	1	0	0	0	0
68	AE	2	0	0	3	0
All	All	181408	98638	132670	7674	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 25.

The worst 5 of 7674 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)
6:5:11:DA:C5'	12:AB:67:THR:HG22	1.20	1.62
25:K:45:ARG:CD	25:K:45:ARG:CG	1.75	1.58
66:z:74:ILE:CG1	66:z:74:ILE:CD1	1.81	1.58
16:AG:425:LEU:CD2	16:AG:429:LYS:HE2	1.21	1.57
6:5:10:DT:C7	11:AA:62:TYR:CD2	1.84	1.57

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
2	1	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
3	2	92/100 (92%)	87 (95%)	5 (5%)	0	100	100
4	3	101/104 (97%)	98 (97%)	3 (3%)	0	100	100
5	4	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
9	9	146/165 (88%)	100 (68%)	43 (30%)	3 (2%)	5	24
11	AA	1312/1342 (98%)	1198 (91%)	113 (9%)	1 (0%)	48	78
12	AB	159/162 (98%)	103 (65%)	44 (28%)	12 (8%)	1	5
13	AC	217/329 (66%)	203 (94%)	12 (6%)	2 (1%)	14	42
13	AD	293/329 (89%)	263 (90%)	27 (9%)	3 (1%)	12	40
14	AE	1331/1407 (95%)	1211 (91%)	114 (9%)	6 (0%)	24	54
15	AF	80/91 (88%)	77 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	AG	493/495 (100%)	375 (76%)	86 (17%)	32 (6%)	1	6
17	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
19	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
20	F	68/71 (96%)	68 (100%)	0	0	100	100
21	G	223/241 (92%)	212 (95%)	10 (4%)	1 (0%)	30	59
22	H	255/557 (46%)	182 (71%)	66 (26%)	7 (3%)	4	20
23	I	206/233 (88%)	193 (94%)	13 (6%)	0	100	100
24	J	203/206 (98%)	201 (99%)	2 (1%)	0	100	100
25	K	154/167 (92%)	145 (94%)	8 (5%)	1 (1%)	21	50
26	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	12	40
27	M	149/179 (83%)	140 (94%)	8 (5%)	1 (1%)	18	47
28	N	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
29	O	125/130 (96%)	116 (93%)	8 (6%)	1 (1%)	16	44
30	P	97/103 (94%)	89 (92%)	8 (8%)	0	100	100
31	Q	115/129 (89%)	107 (93%)	8 (7%)	0	100	100
32	R	117/124 (94%)	112 (96%)	5 (4%)	0	100	100
33	S	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
34	T	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
35	U	80/82 (98%)	76 (95%)	4 (5%)	0	100	100
36	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
37	W	81/92 (88%)	80 (99%)	1 (1%)	0	100	100
38	X	114/118 (97%)	103 (90%)	9 (8%)	2 (2%)	6	26
39	Y	139/142 (98%)	101 (73%)	38 (27%)	0	100	100
40	Z	28/121 (23%)	22 (79%)	6 (21%)	0	100	100
42	b	74/85 (87%)	73 (99%)	1 (1%)	0	100	100
43	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
45	e	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
46	f	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
47	g	64/70 (91%)	62 (97%)	2 (3%)	0	100	100
48	h	269/273 (98%)	255 (95%)	14 (5%)	0	100	100
49	i	54/57 (95%)	49 (91%)	5 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
51	k	50/55 (91%)	50 (100%)	0	0	100	100
52	l	199/201 (99%)	188 (94%)	11 (6%)	0	100	100
53	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
54	n	175/179 (98%)	160 (91%)	14 (8%)	1 (1%)	21	50
55	o	62/65 (95%)	57 (92%)	4 (6%)	1 (2%)	7	29
56	p	173/177 (98%)	162 (94%)	11 (6%)	0	100	100
57	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
58	r	147/149 (99%)	139 (95%)	8 (5%)	0	100	100
59	s	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
60	t	121/123 (98%)	114 (94%)	7 (6%)	0	100	100
61	u	142/144 (99%)	134 (94%)	8 (6%)	0	100	100
62	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
63	w	117/127 (92%)	112 (96%)	5 (4%)	0	100	100
64	x	114/117 (97%)	107 (94%)	7 (6%)	0	100	100
65	y	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
66	z	115/118 (98%)	111 (96%)	4 (4%)	0	100	100
All	All	10058/11053 (91%)	9172 (91%)	811 (8%)	75 (1%)	20	47

5 of 75 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	AB	107	PRO
12	AB	130	PHE
12	AB	137	ALA
12	AB	144	ASN
12	AB	160	ARG

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	84/84 (100%)	84 (100%)	0	100	100
2	1	93/93 (100%)	93 (100%)	0	100	100
3	2	81/84 (96%)	81 (100%)	0	100	100
4	3	84/85 (99%)	84 (100%)	0	100	100
5	4	78/78 (100%)	78 (100%)	0	100	100
9	9	112/123 (91%)	112 (100%)	0	100	100
11	AA	1135/1157 (98%)	1130 (100%)	5 (0%)	84	83
12	AB	141/142 (99%)	117 (83%)	24 (17%)	2	9
13	AC	186/286 (65%)	186 (100%)	0	100	100
13	AD	185/286 (65%)	185 (100%)	0	100	100
14	AE	1122/1168 (96%)	1104 (98%)	18 (2%)	55	68
15	AF	70/75 (93%)	69 (99%)	1 (1%)	59	70
16	AG	409/409 (100%)	288 (70%)	121 (30%)	0	1
17	C	57/65 (88%)	57 (100%)	0	100	100
19	E	65/66 (98%)	65 (100%)	0	100	100
20	F	60/61 (98%)	60 (100%)	0	100	100
21	G	187/199 (94%)	187 (100%)	0	100	100
22	H	137/461 (30%)	137 (100%)	0	100	100
23	I	171/190 (90%)	171 (100%)	0	100	100
24	J	172/173 (99%)	171 (99%)	1 (1%)	78	80
25	K	119/126 (94%)	119 (100%)	0	100	100
26	L	91/116 (78%)	91 (100%)	0	100	100
27	M	124/147 (84%)	124 (100%)	0	100	100
28	N	104/105 (99%)	104 (100%)	0	100	100
29	O	105/107 (98%)	105 (100%)	0	100	100
30	P	86/90 (96%)	86 (100%)	0	100	100
31	Q	90/99 (91%)	90 (100%)	0	100	100
32	R	101/104 (97%)	101 (100%)	0	100	100
33	S	83/84 (99%)	83 (100%)	0	100	100
34	T	76/77 (99%)	76 (100%)	0	100	100
35	U	65/65 (100%)	65 (100%)	0	100	100
36	V	74/78 (95%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	W	72/79 (91%)	72 (100%)	0	100	100
38	X	94/96 (98%)	94 (100%)	0	100	100
39	Y	109/110 (99%)	109 (100%)	0	100	100
40	Z	26/85 (31%)	26 (100%)	0	100	100
42	b	58/63 (92%)	58 (100%)	0	100	100
43	c	67/68 (98%)	67 (100%)	0	100	100
45	e	54/55 (98%)	54 (100%)	0	100	100
46	f	48/49 (98%)	48 (100%)	0	100	100
47	g	59/62 (95%)	59 (100%)	0	100	100
48	h	216/218 (99%)	216 (100%)	0	100	100
49	i	47/48 (98%)	47 (100%)	0	100	100
50	j	164/164 (100%)	164 (100%)	0	100	100
51	k	47/49 (96%)	47 (100%)	0	100	100
52	l	165/165 (100%)	165 (100%)	0	100	100
53	m	38/38 (100%)	38 (100%)	0	100	100
54	n	148/150 (99%)	148 (100%)	0	100	100
55	o	51/52 (98%)	51 (100%)	0	100	100
56	p	136/138 (99%)	136 (100%)	0	100	100
57	q	34/34 (100%)	34 (100%)	0	100	100
58	r	114/114 (100%)	114 (100%)	0	100	100
59	s	116/116 (100%)	116 (100%)	0	100	100
60	t	104/104 (100%)	104 (100%)	0	100	100
61	u	103/103 (100%)	103 (100%)	0	100	100
62	v	109/109 (100%)	109 (100%)	0	100	100
63	w	99/103 (96%)	99 (100%)	0	100	100
64	x	86/87 (99%)	86 (100%)	0	100	100
65	y	99/100 (99%)	99 (100%)	0	100	100
66	z	89/90 (99%)	89 (100%)	0	100	100
All	All	8299/9132 (91%)	8129 (98%)	170 (2%)	48	65

5 of 170 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	AG	258	ARG
16	AG	323	GLN
16	AG	265	GLU
16	AG	297	VAL
16	AG	340	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 116 such sidechains are listed below:

Mol	Chain	Res	Type
21	G	36	ASN
64	x	38	GLN
27	M	86	GLN
64	x	29	HIS
55	o	28	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	75/76 (98%)	29 (38%)	8 (10%)
10	B	75/76 (98%)	29 (38%)	8 (10%)
18	D	1514/1542 (98%)	289 (19%)	20 (1%)
41	a	2859/2904 (98%)	510 (17%)	0
44	d	119/120 (99%)	15 (12%)	0
8	7	23/56 (41%)	14 (60%)	3 (13%)
All	All	4665/4774 (97%)	886 (18%)	39 (0%)

5 of 886 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	3	G
8	7	4	U
8	7	5	U
8	7	7	U
8	7	8	U

5 of 39 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
18	D	992	U
18	D	1447	A
18	D	1145	A

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Mol	Chain	Res	Type
18	D	1212	U
18	D	1492	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

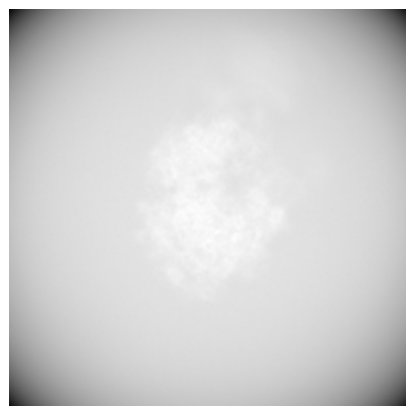
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43387. 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

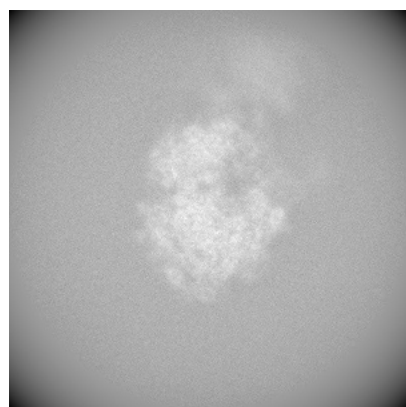


Y

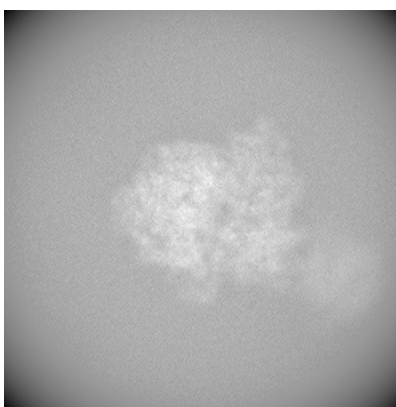


Z

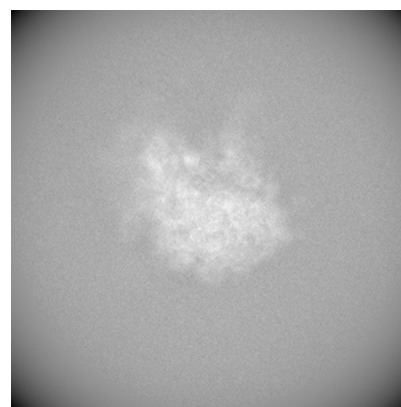
6.1.2 Raw map



X



Y

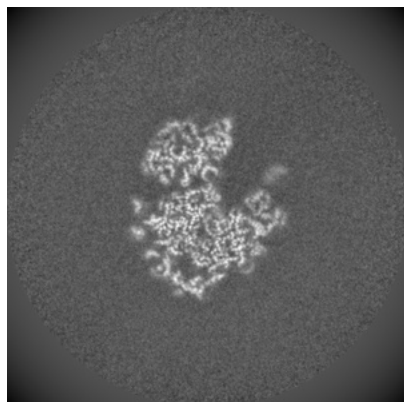


Z

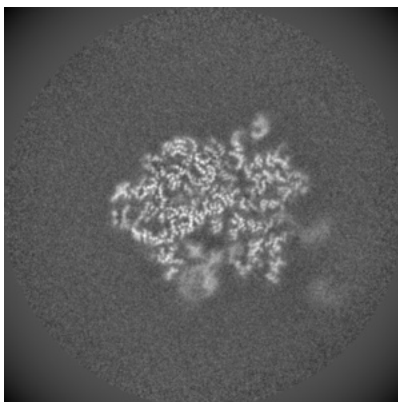
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

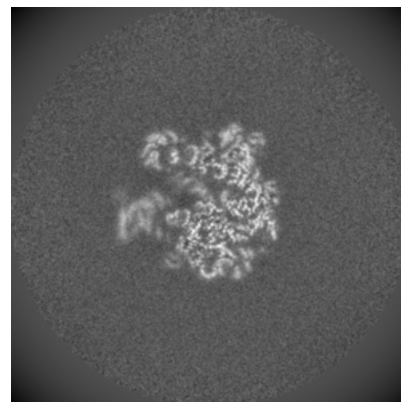
6.2.1 Primary map



X Index: 310

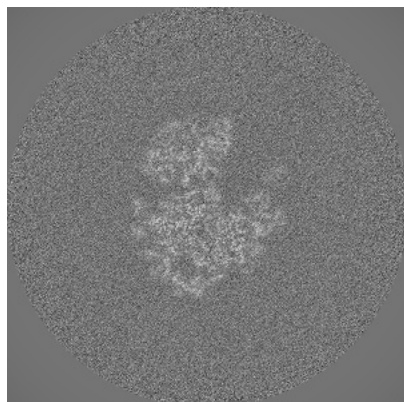


Y Index: 310

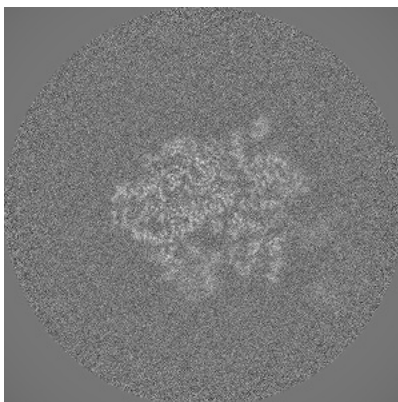


Z Index: 310

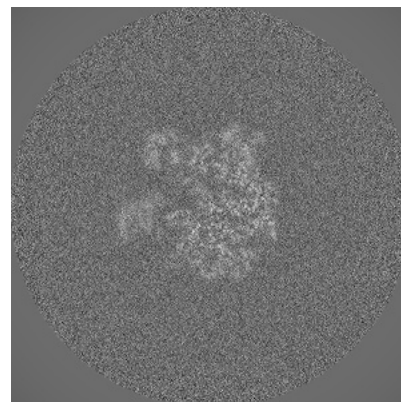
6.2.2 Raw map



X Index: 310



Y Index: 310

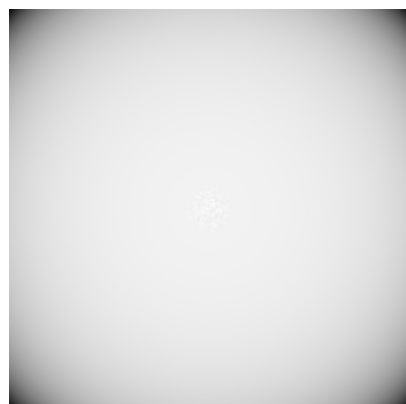


Z Index: 310

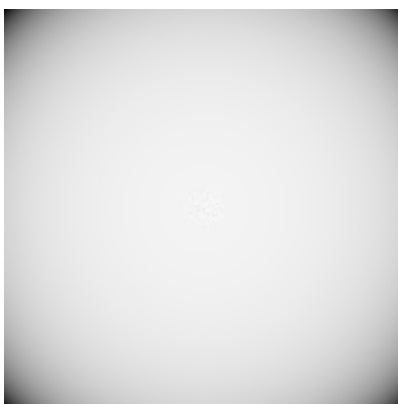
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

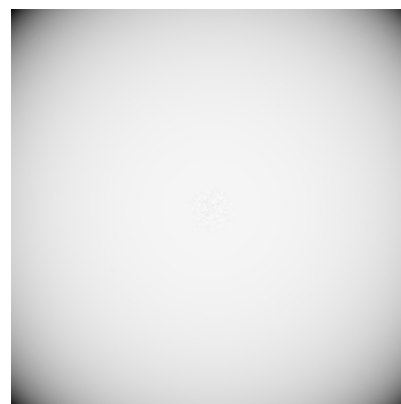
6.3.1 Primary map



X Index: 0

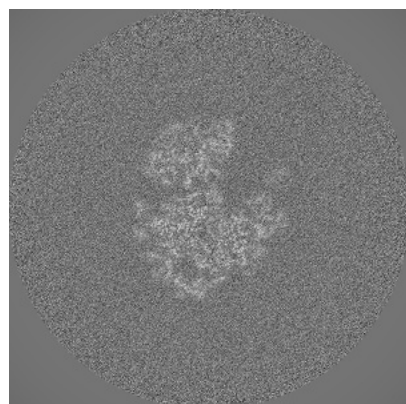


Y Index: 0

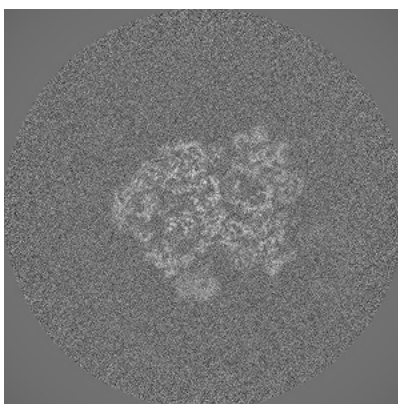


Z Index: 0

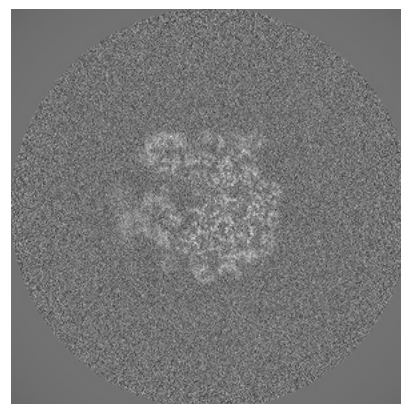
6.3.2 Raw map



X Index: 310



Y Index: 299

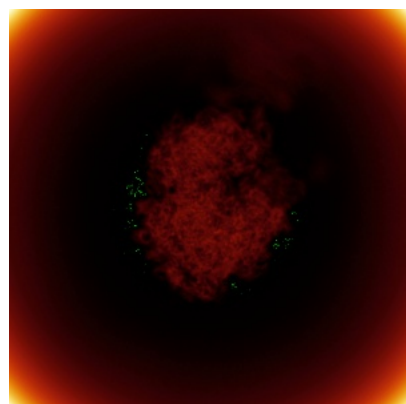


Z Index: 302

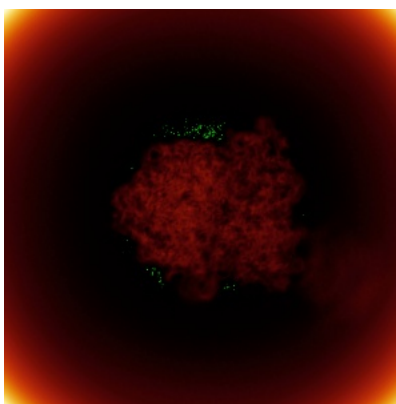
The images above show the largest variance slices of the map in three orthogonal directions.

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

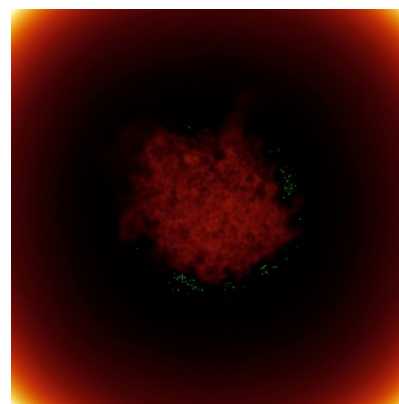
6.4.1 Primary map



X

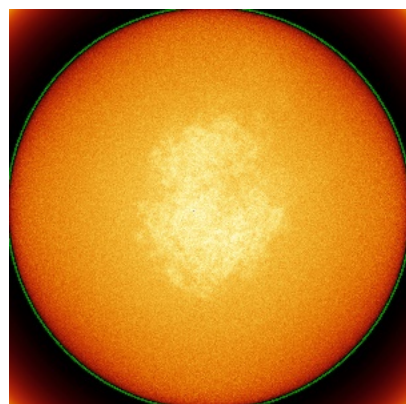


Y

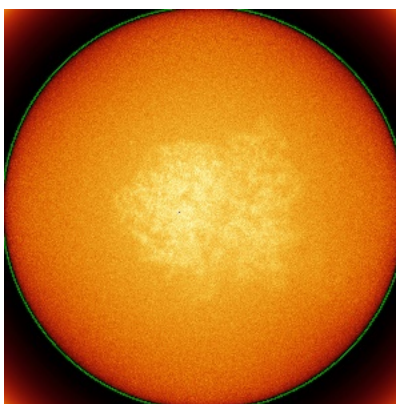


Z

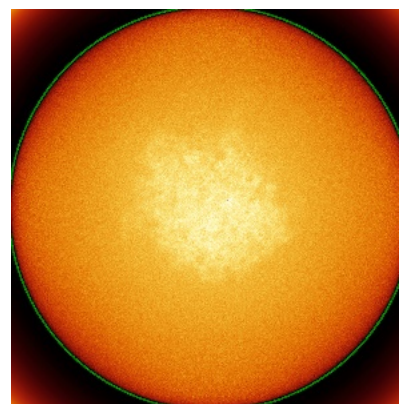
6.4.2 Raw map



X



Y

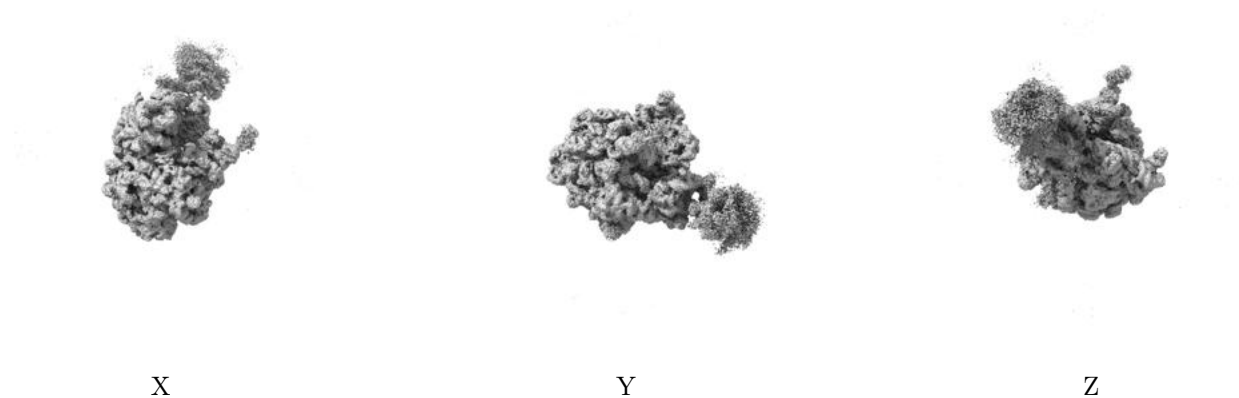


Z

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.

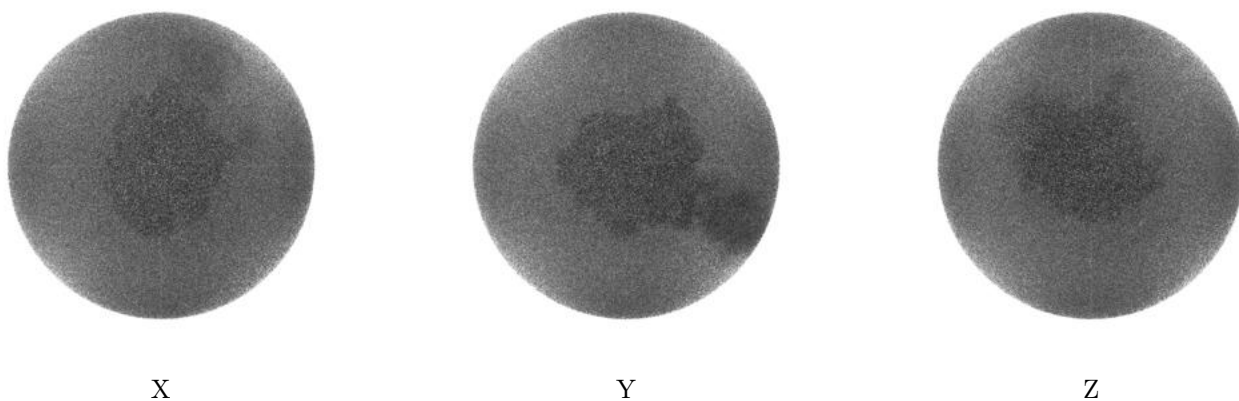
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1e-06. 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.

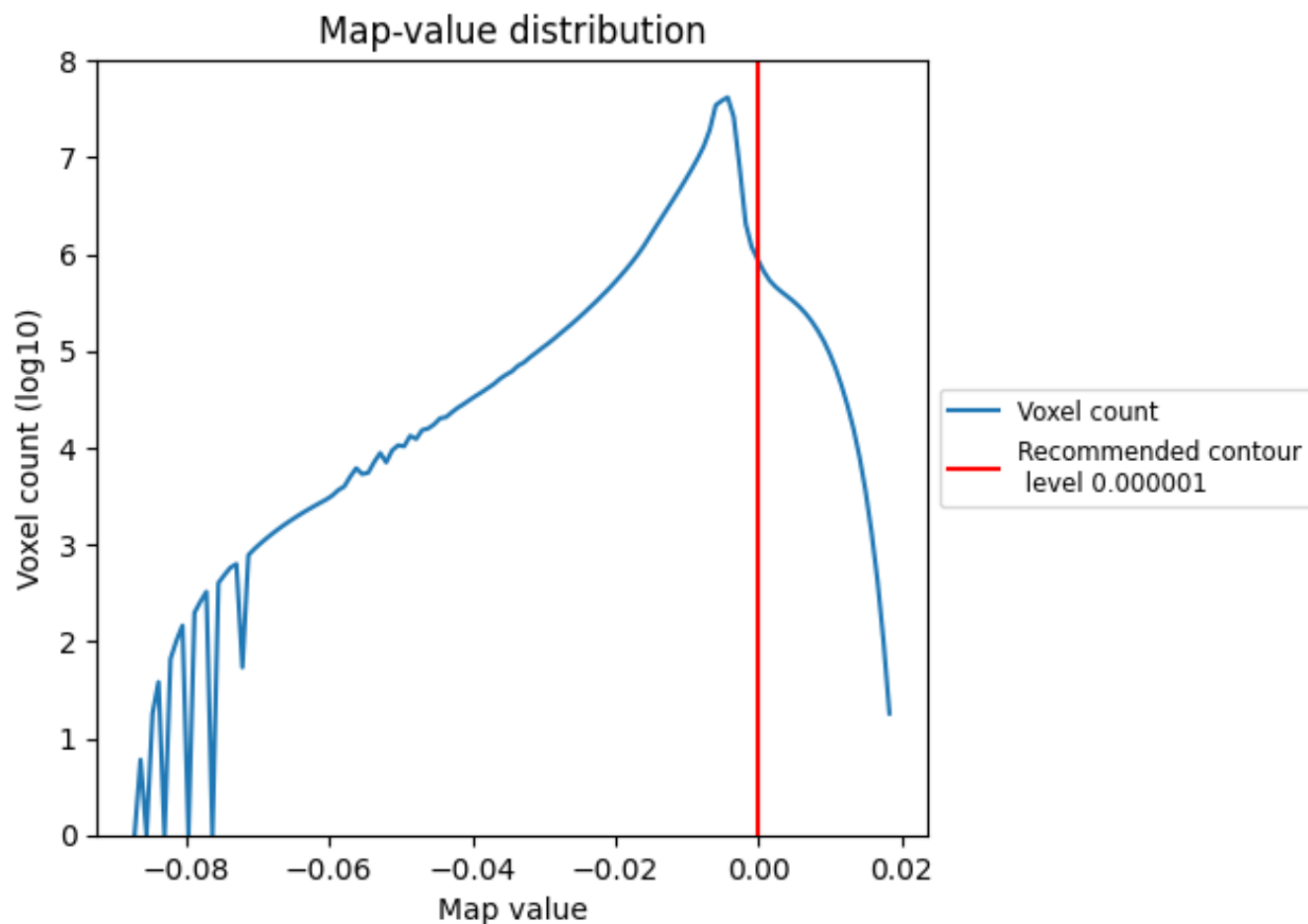
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

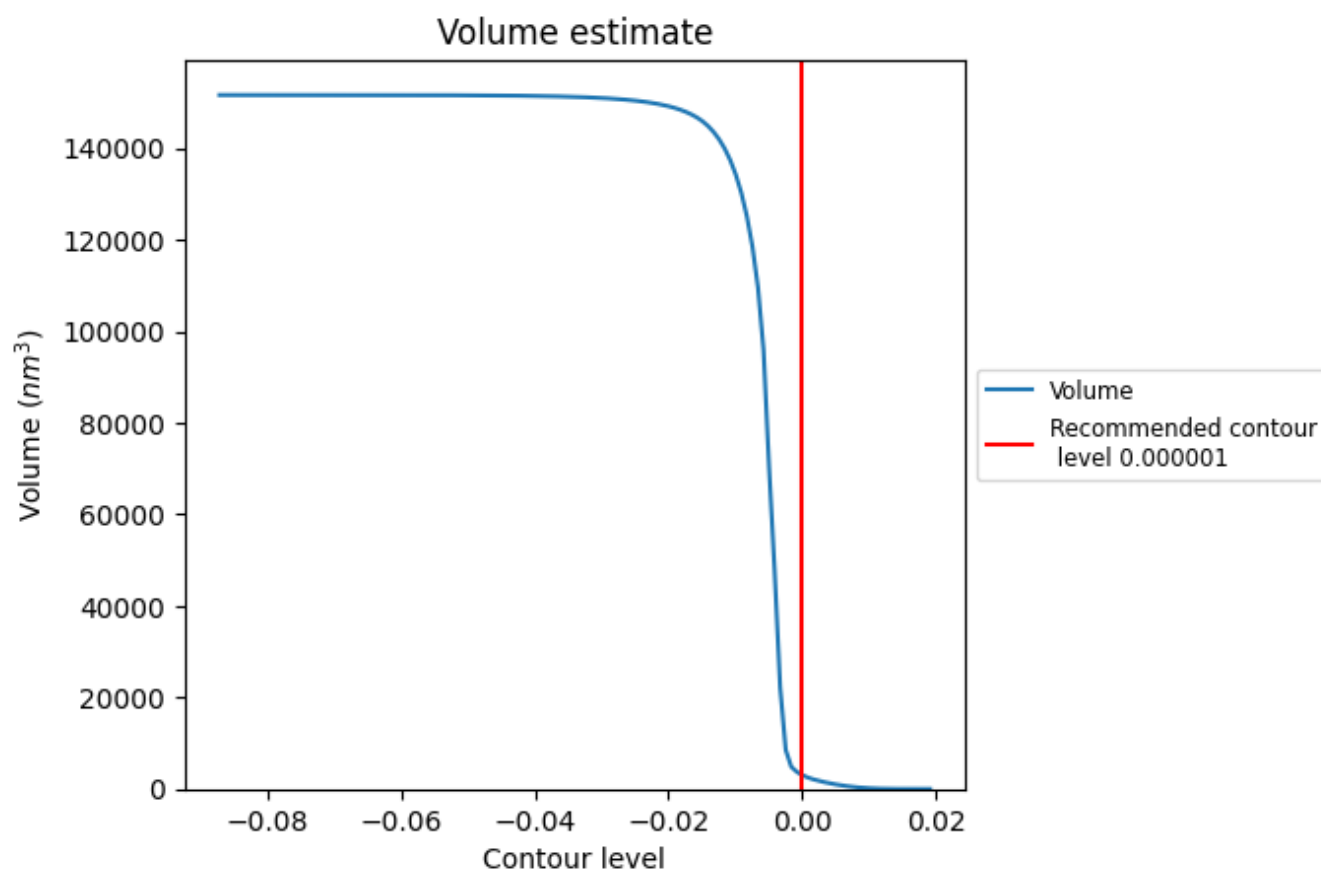
This section contains the results of statistical analysis of the map.

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.

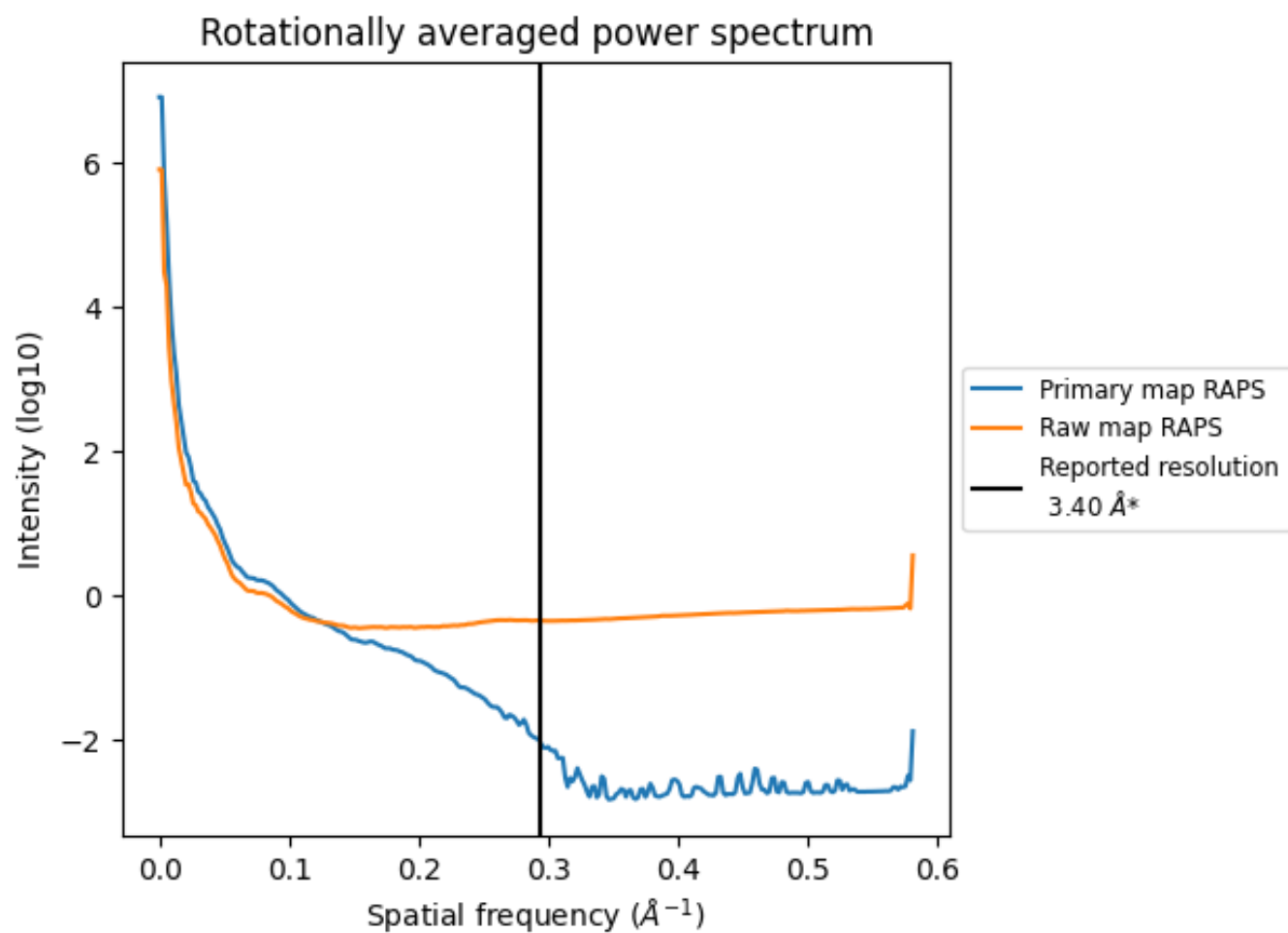
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3055 nm^3 ; this corresponds to an approximate mass of 2760 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 [i](#)

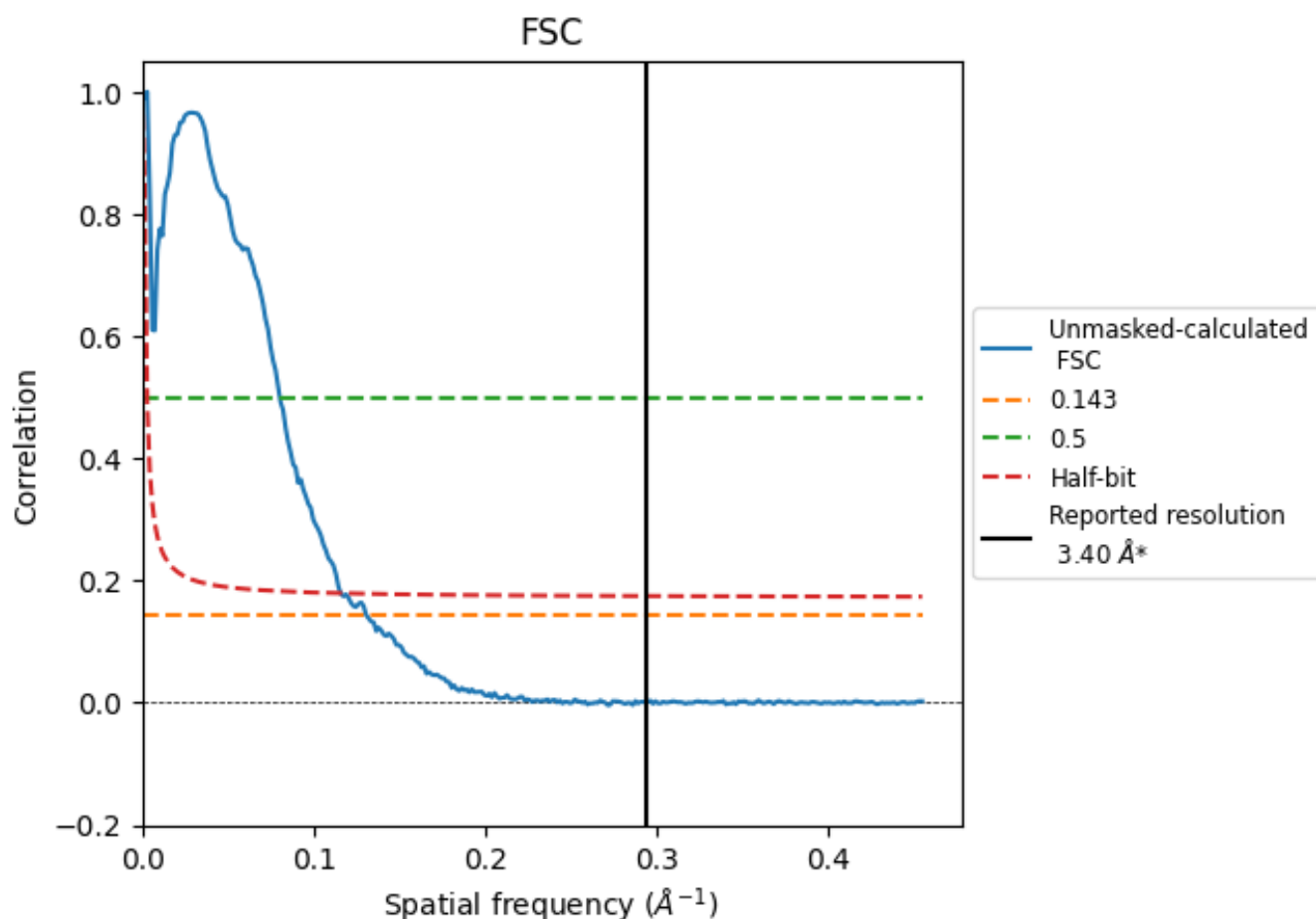


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

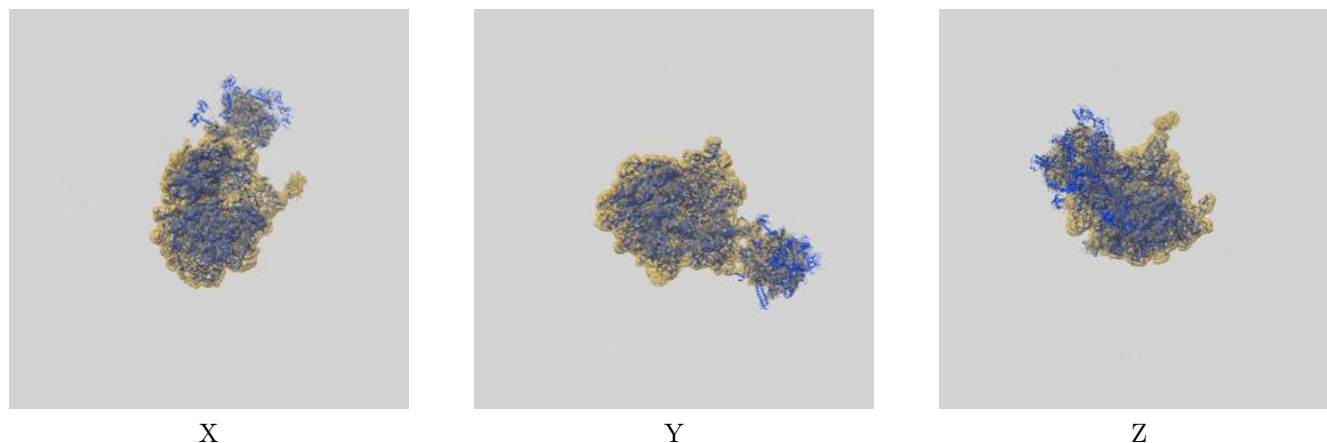
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.66	12.47	8.64

*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 7.66 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

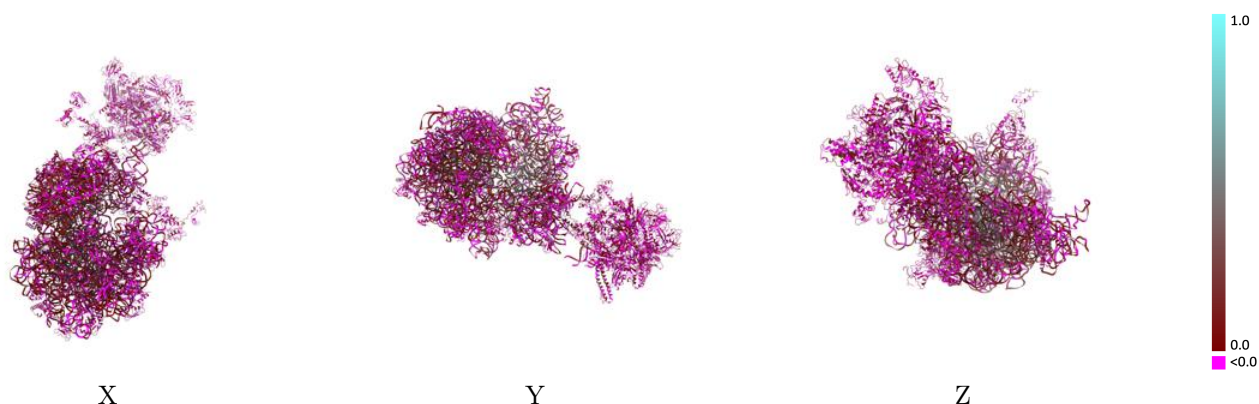
This section contains information regarding the fit between EMDB map EMD-43387 and PDB model 8VOO. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



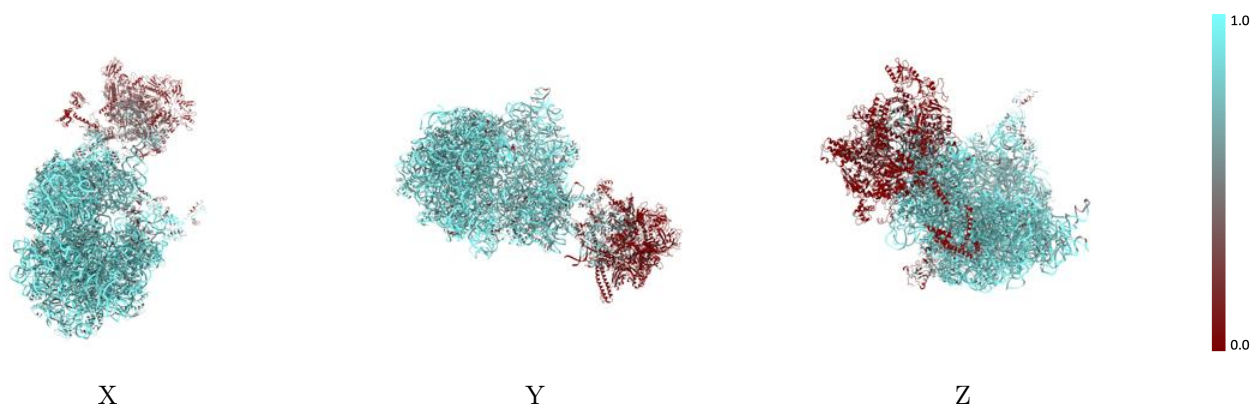
The images above show the 3D surface view of the map at the recommended contour level 1e-06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



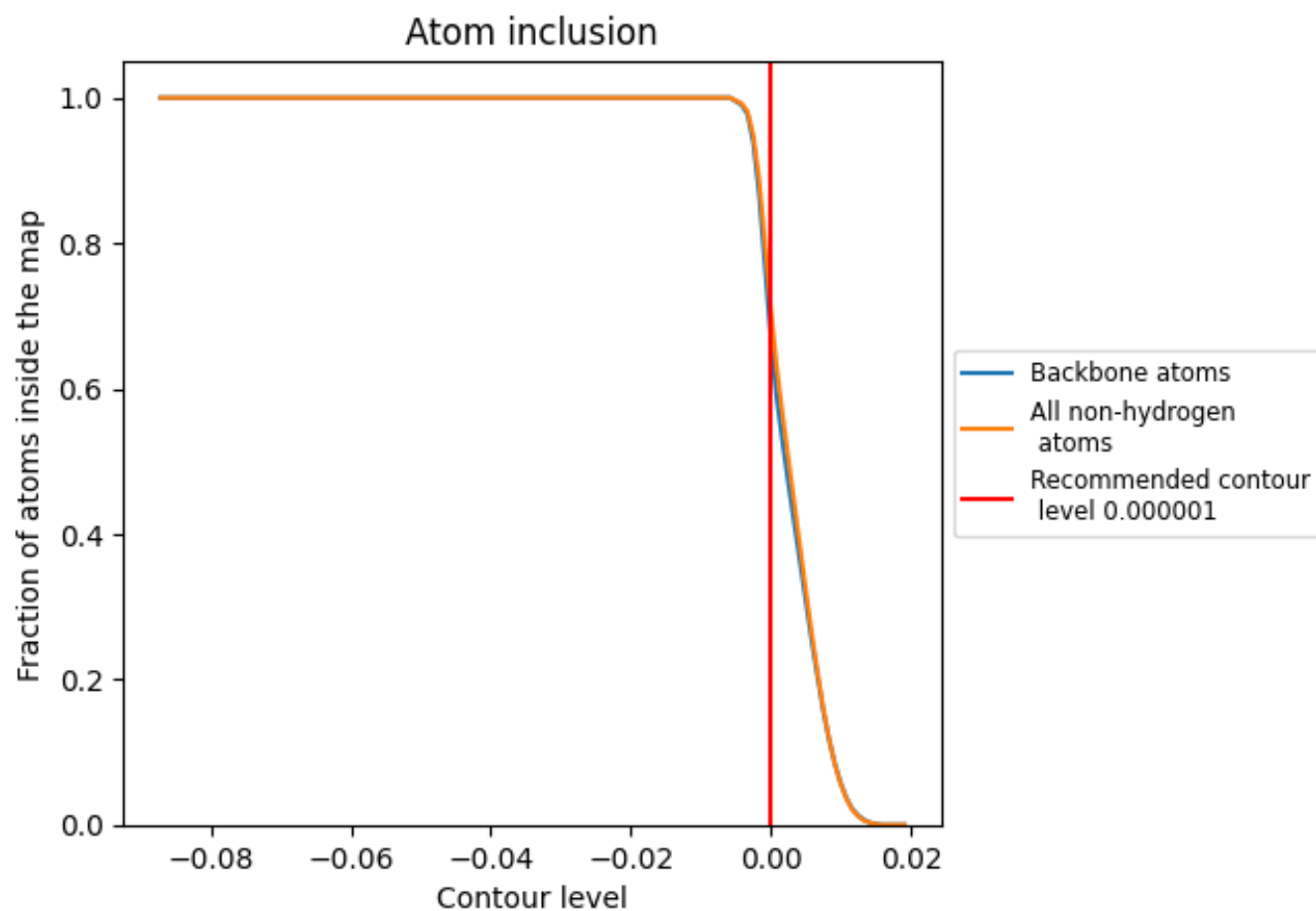
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.000001).

9.4 Atom inclusion [i](#)



At the recommended contour level, 67% of all backbone atoms, 72% 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 (0.000001) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7150	 0.0820
0	 0.8140	 0.0300
1	 0.8300	 0.1110
2	 0.8040	 0.0360
3	 0.7890	 0.0030
4	 0.8460	 0.0400
5	 0.4390	 0.0320
6	 0.3940	 0.0500
7	 0.6240	 0.0340
9	 0.7630	 0.0470
A	 0.9100	 0.1480
AA	 0.1830	 0.0160
AB	 0.5300	 0.0830
AC	 0.0480	 0.0050
AD	 0.0110	 -0.0050
AE	 0.2190	 0.0260
AF	 0.0820	 0.0210
AG	 0.2940	 0.0160
B	 0.7960	 0.0470
C	 0.8180	 0.0220
D	 0.9290	 0.1250
E	 0.8100	 0.0310
F	 0.8180	 0.1220
G	 0.7390	 0.0360
H	 0.3640	 0.0350
I	 0.7120	 0.0100
J	 0.7680	 0.0140
K	 0.8580	 0.0970
L	 0.8280	 0.0290
M	 0.7650	 0.0540
N	 0.8560	 0.0890
O	 0.7650	 0.0250
P	 0.7430	 0.0550
Q	 0.8440	 0.0920
R	 0.8880	 0.1990



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Chain	Atom inclusion	Q-score
S	 0.7890	 0.0130
T	 0.8870	 0.1380
U	 0.7800	 0.0030
V	 0.8730	 0.1410
W	 0.6860	 0.0220
X	 0.7120	 0.0150
Y	 0.7340	 0.0180
Z	 0.5150	 0.0100
a	 0.9330	 0.1160
b	 0.8290	 0.0400
c	 0.8150	 0.0890
d	 0.8920	 0.0560
e	 0.8040	 0.0220
f	 0.8780	 0.0990
g	 0.7690	 0.0300
h	 0.8340	 0.1030
i	 0.8390	 0.1070
j	 0.8140	 0.0290
k	 0.8250	 0.0300
l	 0.7980	 0.0560
m	 0.9240	 0.2220
n	 0.7950	 0.0350
o	 0.8000	 0.0480
p	 0.7680	 -0.0060
q	 0.7940	 0.0120
r	 0.5770	 0.0270
s	 0.8040	 0.0090
t	 0.8240	 0.1020
u	 0.8160	 0.0440
v	 0.8590	 0.0840
w	 0.8600	 0.0660
x	 0.7870	 0.0210
y	 0.7620	 0.0360
z	 0.8290	 0.0470