



wwPDB EM Validation Summary Report ⓘ

Jul 15, 2025 – 12:14 PM EDT

PDB ID : 8VOQ / pdb_00008voq
EMDB ID : EMD-43389
Title : Escherichia coli transcription-translation loosely coupled complex (TTC-LC) containing mRNA with a 39 nt long spacer, NusG, NusA, and fMet-tRNAs in E-site and P-site
Authors : Molodtsov, V.; Wang, C.; Ebright, R.H.
Deposited on : 2024-01-15
Resolution : 9.30 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:

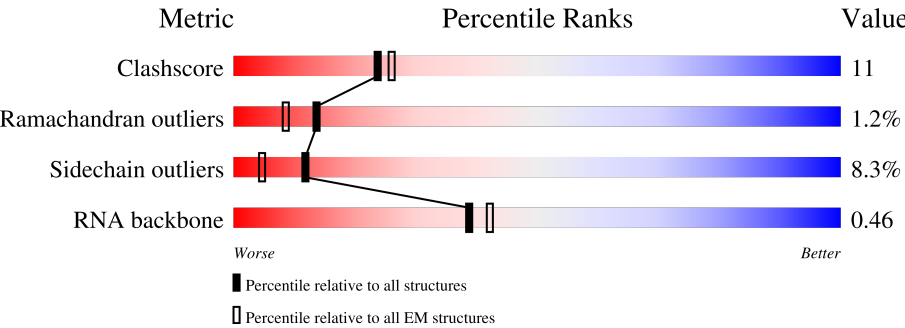
EMDB validation analysis : 0.0.1.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

1 Overall quality at a glance

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

The reported resolution of this entry is 9.30 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	<div> <div>11%</div> <div>84%</div> <div>15%</div> <div>.</div> </div>
2	1	110	<div> <div>5%</div> <div>75%</div> <div>25%</div> </div>
3	2	100	<div> <div>9%</div> <div>86%</div> <div>7%</div> <div>6%</div> <div>.</div> </div>
4	3	104	<div> <div>12%</div> <div>84%</div> <div>14%</div> <div>..</div> </div>
5	4	94	<div> <div>11%</div> <div>97%</div> <div>.</div> </div>
6	5	36	<div> <div>31%</div> <div>28%</div> <div>36%</div> <div>36%</div> </div>
7	6	36	<div> <div>25%</div> <div>36%</div> <div>39%</div> <div>25%</div> </div>

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Mol	Chain	Length	Quality of chain
8	7	56	
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AB	181	
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	
27	M	179	
28	N	130	
29	O	130	
30	P	103	

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Mol	Chain	Length	Quality of chain
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	
52	l	201	
53	m	46	
54	n	179	
55	o	65	

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Mol	Chain	Length	Quality of chain
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	

2 Entry composition

There are 68 unique types of molecules in this entry. The entry contains 291173 atoms, of which 109913 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	S	0	0
			1655	516	839	153	145	2		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
2	1	110	Total	C	H	N	O	S	0	0
			1779	532	922	166	156	3		

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

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

- 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	S	0	0
			1533	479	780	137	134	3		

- Molecule 6 is a DNA chain called NT DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	5	23	Total	C	H	N	O	P	0	0
			732	225	260	87	137	23		

- Molecule 7 is a DNA chain called T DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	6	27	Total	C	H	N	O	P	0	0
			847	259	305	89	167	27		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	31	Total	C	H	N	O	P	0	0
			744	289	97	92	235	31		

- 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	C	H	N	O	P	0	0
			2446	723	826	295	527	75		
10	B	76	Total	C	H	N	O	P	0	0
			2434	723	814	295	527	75		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AA	1340	Total	C	N	O	S	0	0
			10567	6631	1841	2052	43		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AB	161	Total	C	N	O	S	0	0
			1276	813	221	235	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AC	220	Total	C	N	O	S	0	0
			1690	1056	298	330	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	AD	298	Total	C	N	O	S	0	0
			2073	1284	377	406	6		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
14	AE	1335	Total	C	H	N	O	S	0	0
			21000	6526	10612	1854	1958	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	0	0
			1815	552	923	178	162		

- 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	0	0
			1967	604	1020	192	151		

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

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

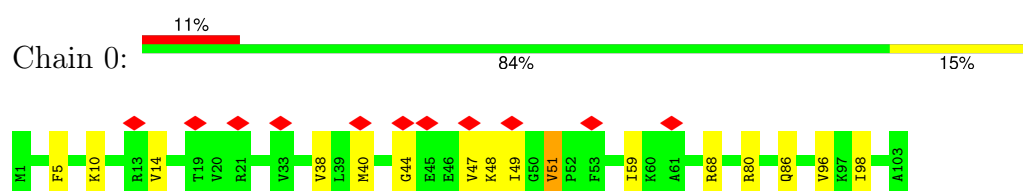
- Molecule 68 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

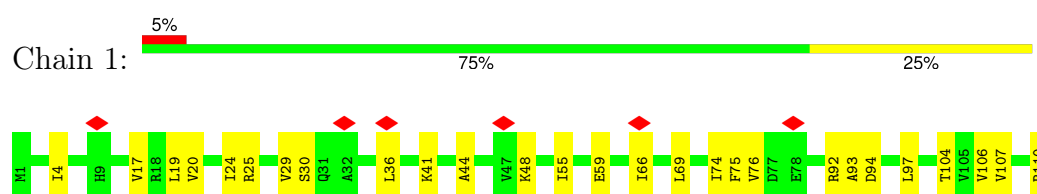
3 Residue-property plots [i](#)

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.

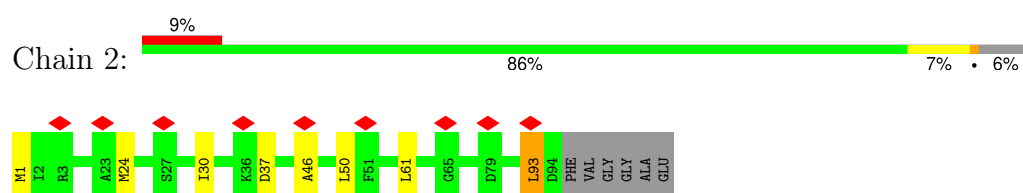
- Molecule 1: Ribosomal protein L21



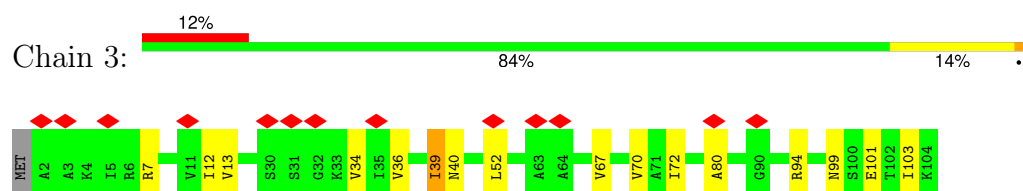
- Molecule 2: 50S ribosomal protein L22



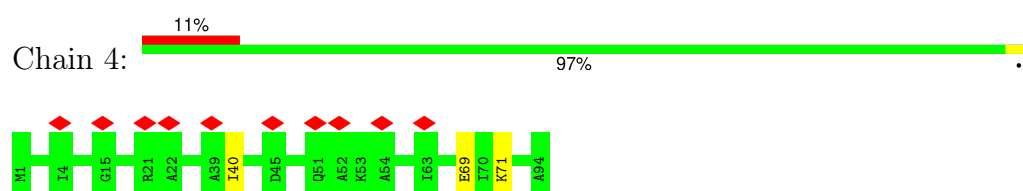
- Molecule 3: 50S ribosomal protein L23

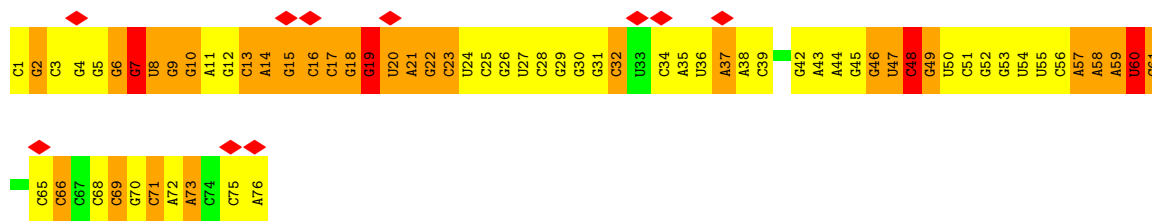


- Molecule 4: 50S ribosomal protein L24

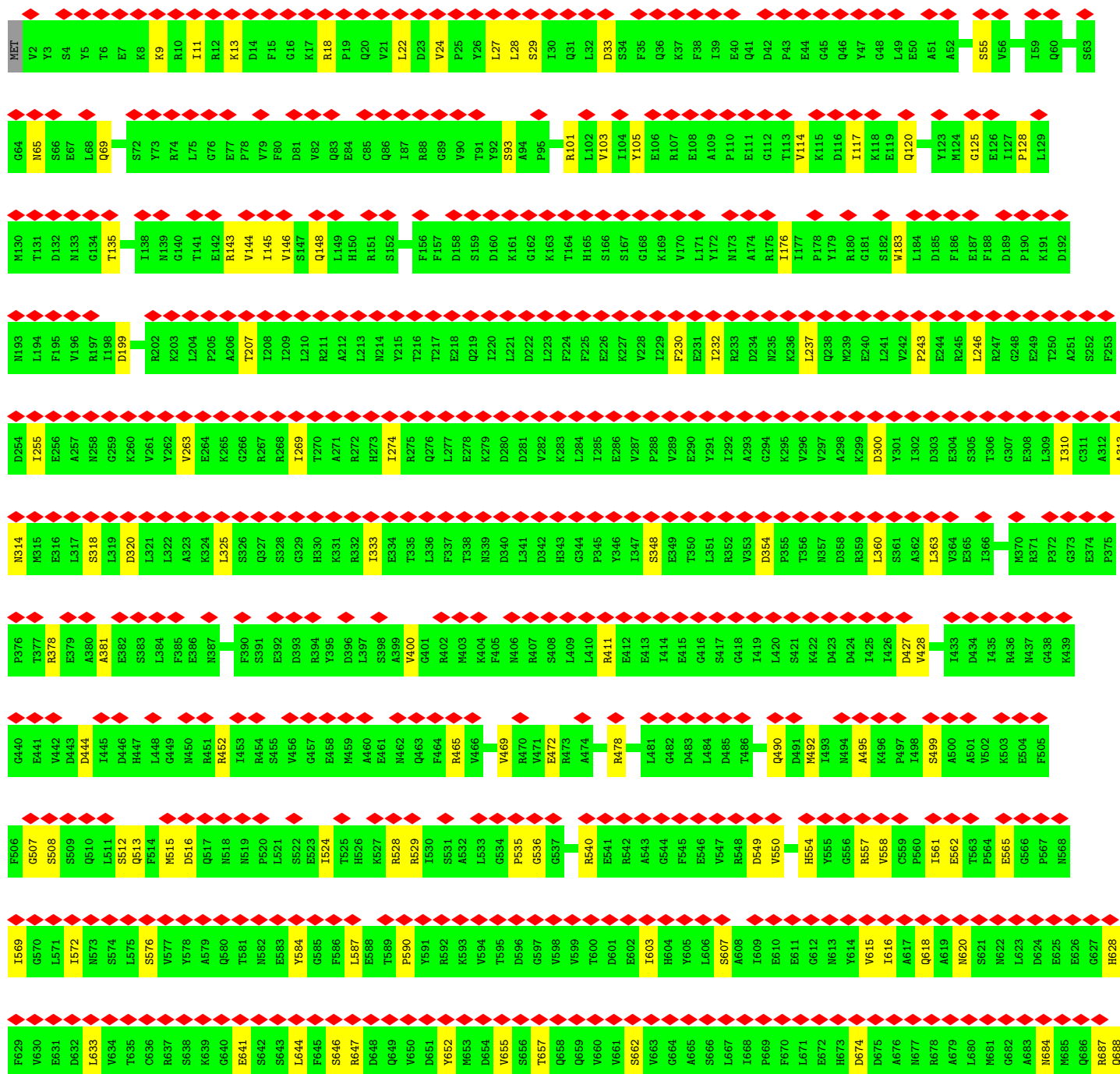
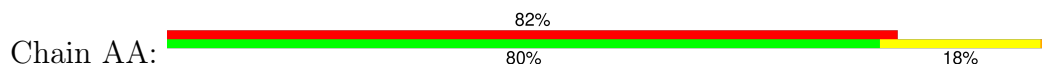


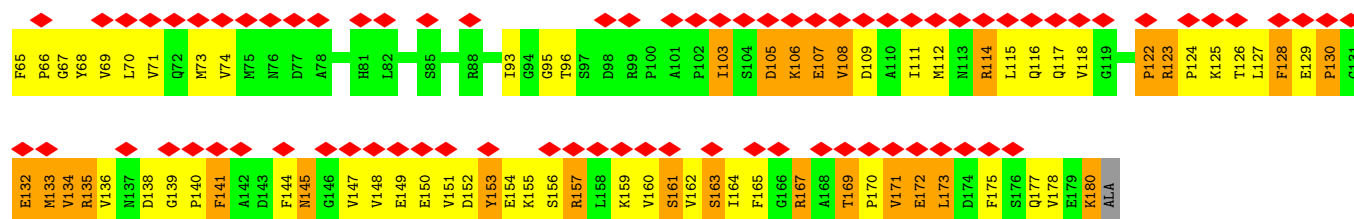
- Molecule 5: 50S ribosomal protein L25



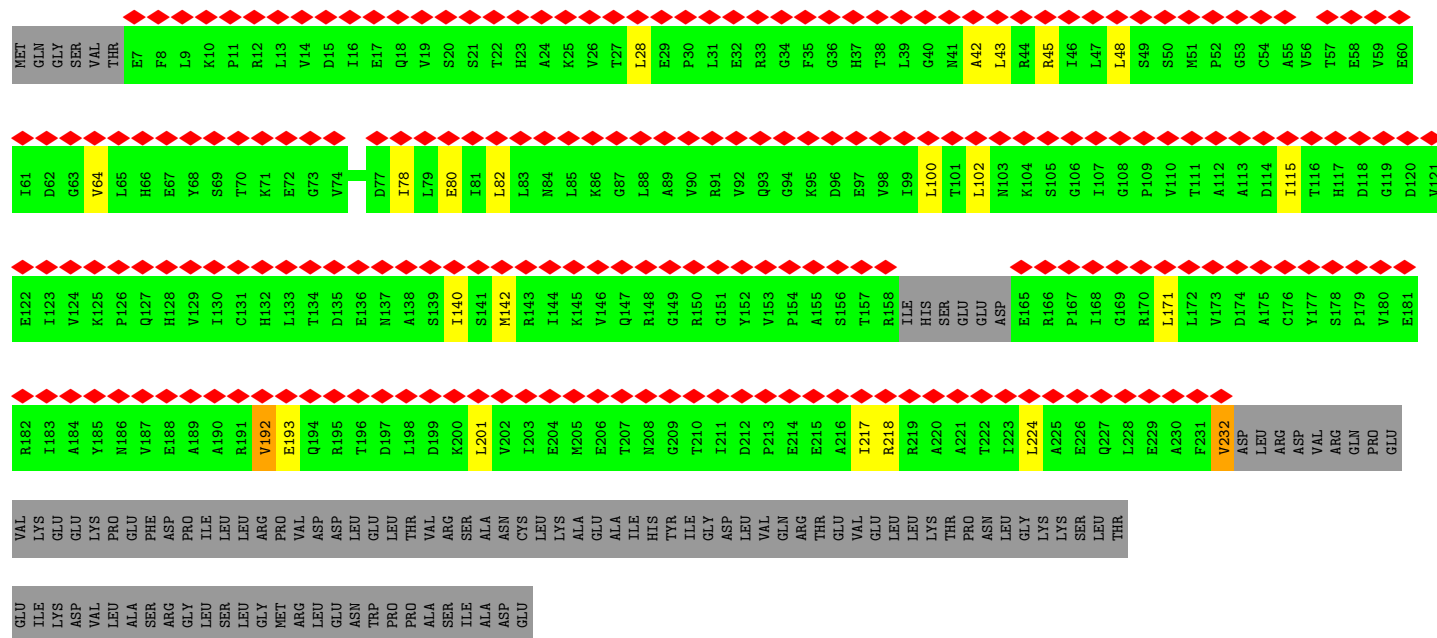


• Molecule 11: DNA-directed RNA polymerase subunit beta

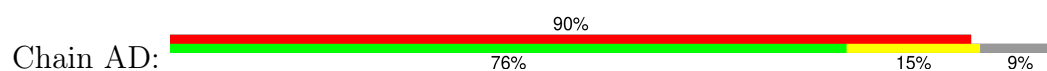


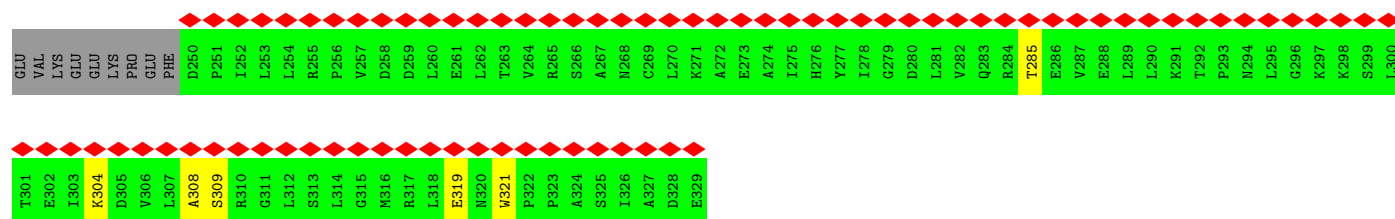


• Molecule 13: DNA-directed RNA polymerase subunit alpha

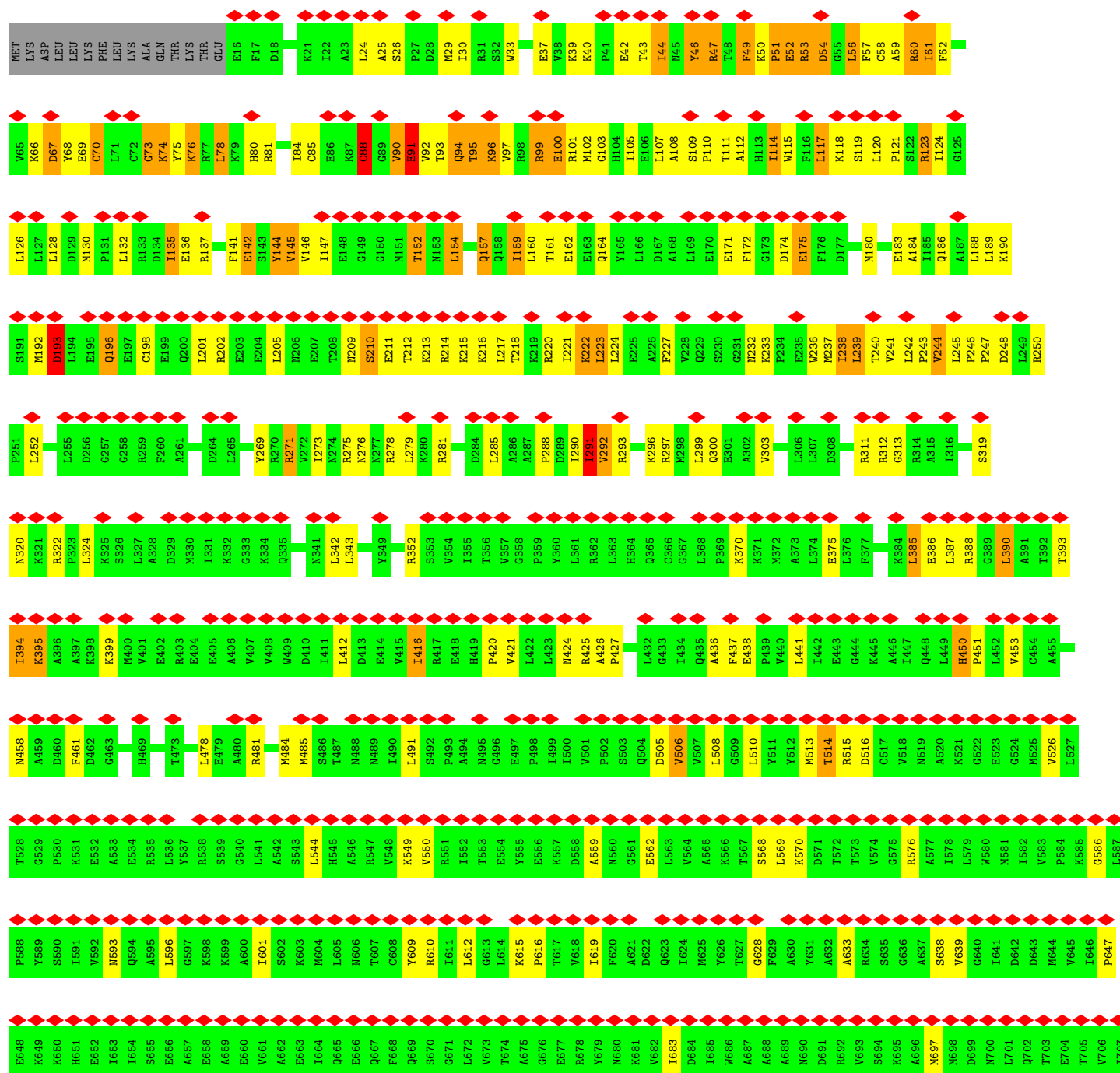
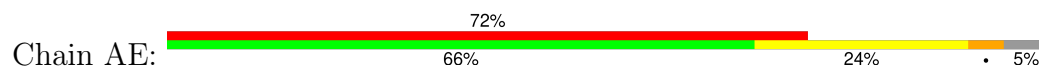


• Molecule 13: DNA-directed RNA polymerase subunit alpha

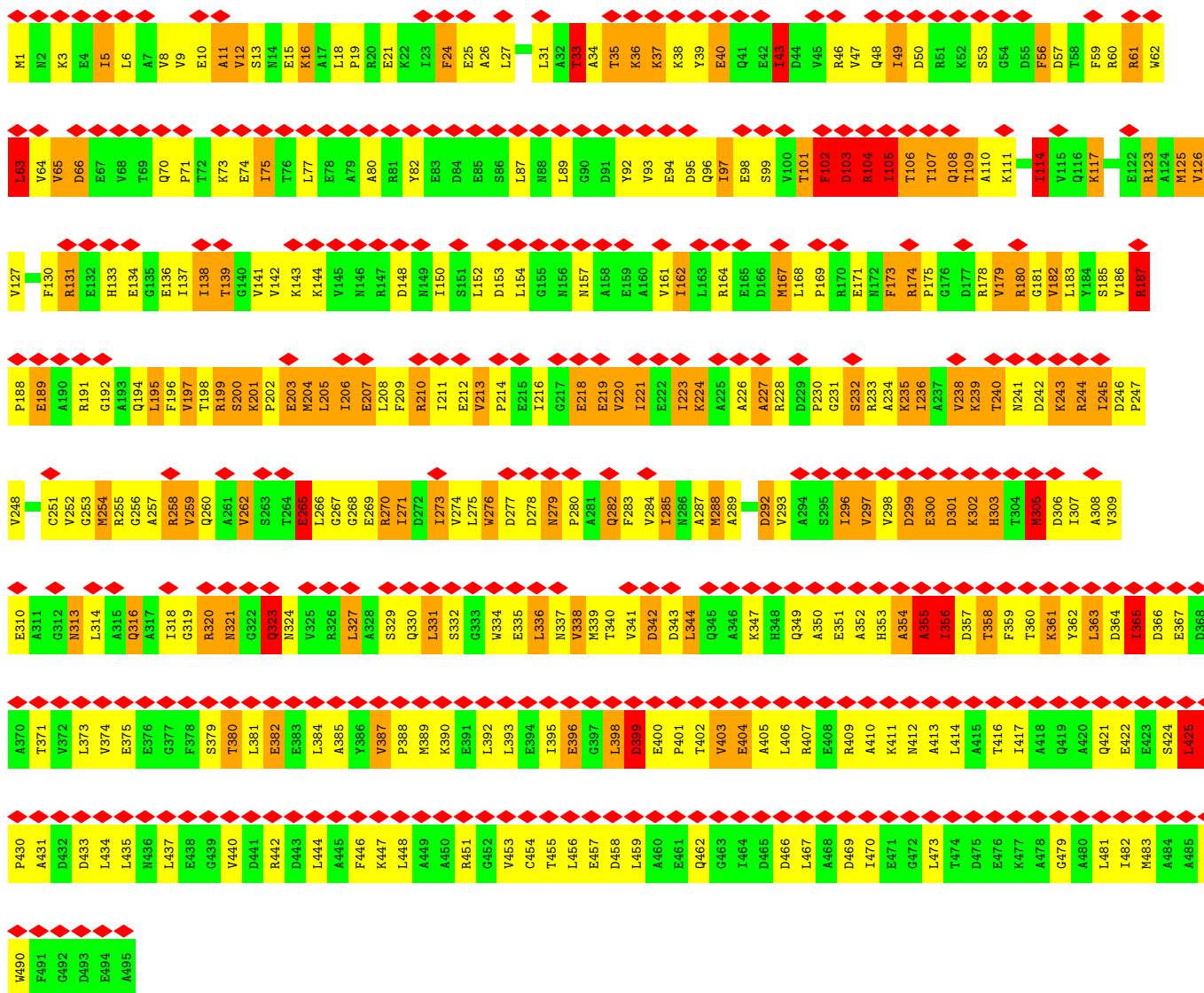




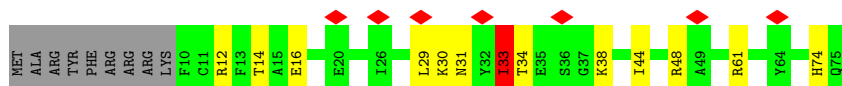
• Molecule 14: DNA-directed RNA polymerase subunit beta'



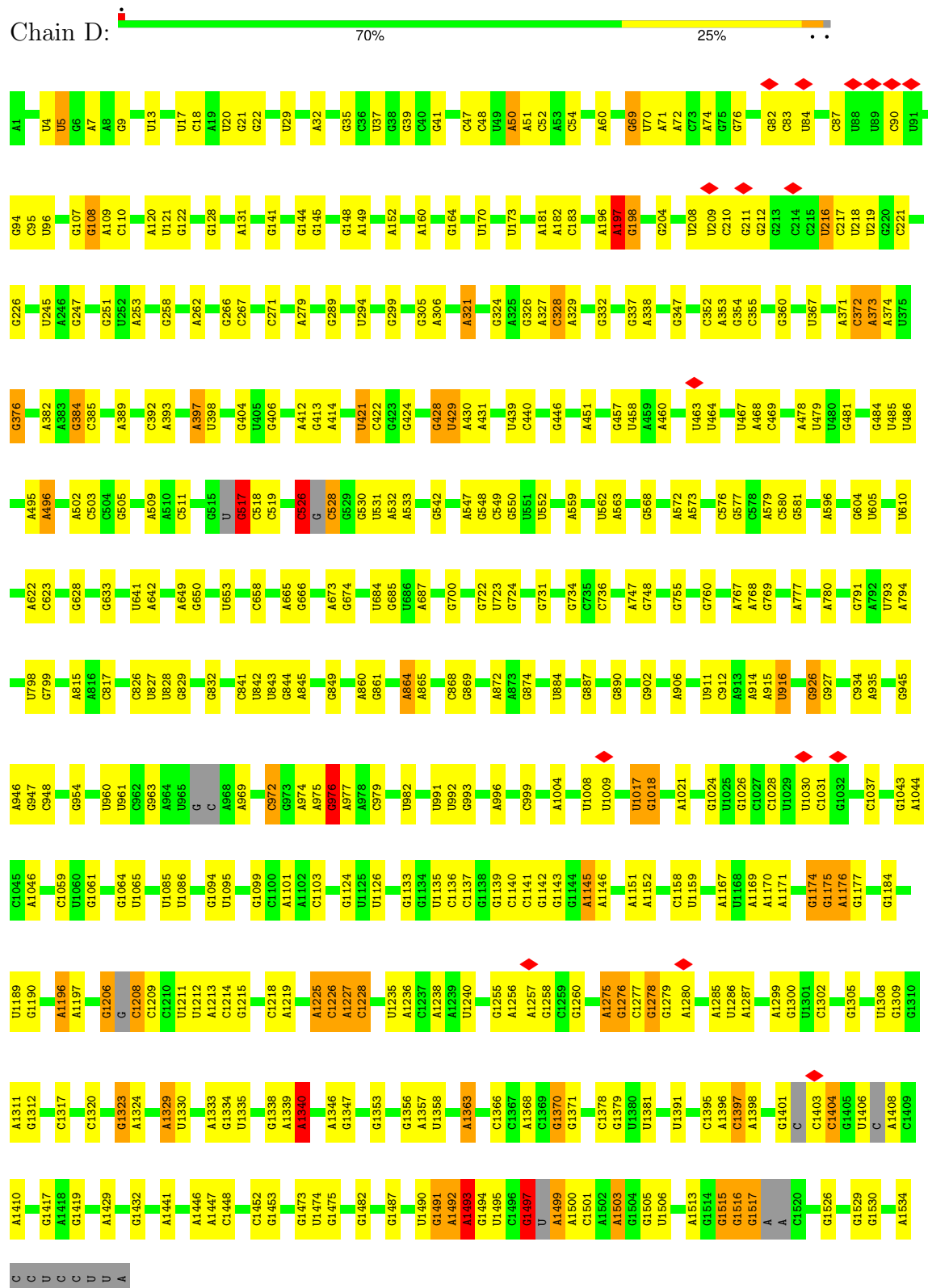


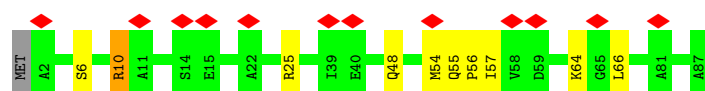
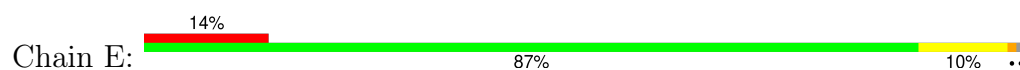


- Molecule 17: 30S ribosomal protein S18

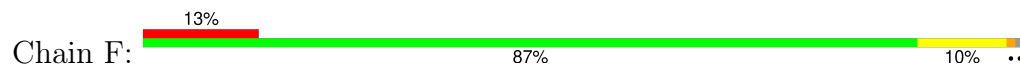


- Molecule 18: 16S rRNA

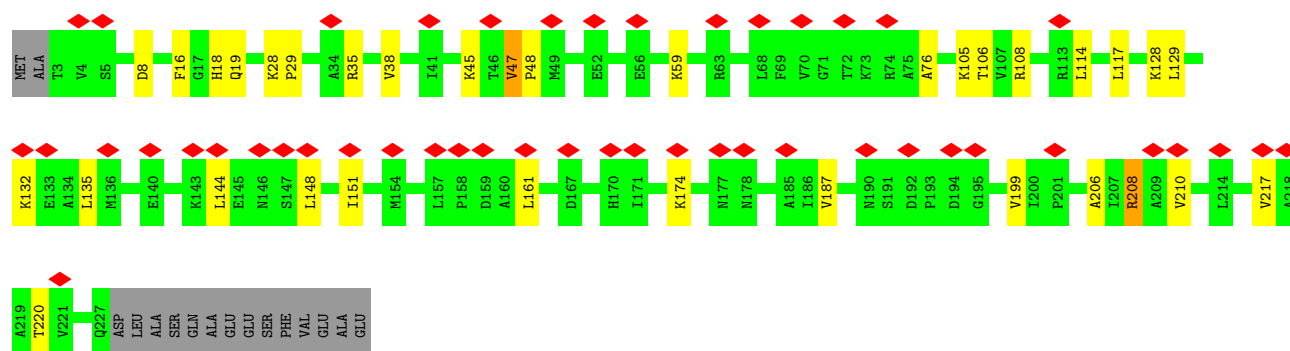
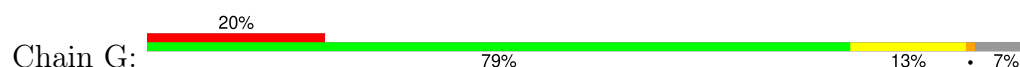




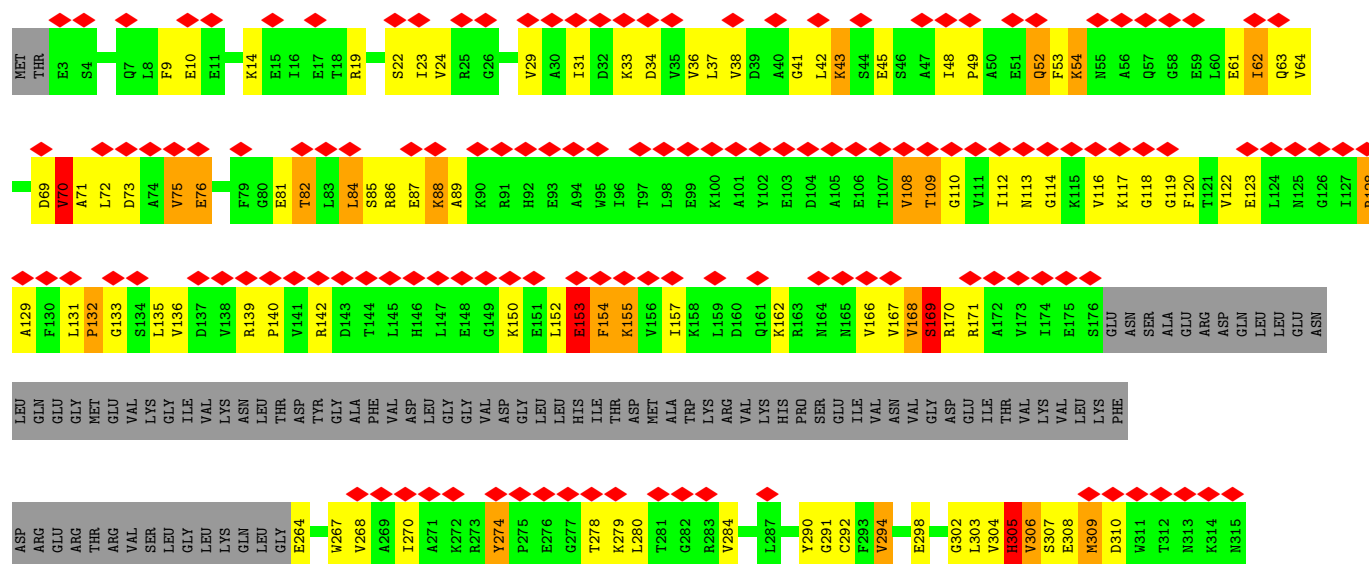
- Molecule 20: 30S ribosomal protein S21

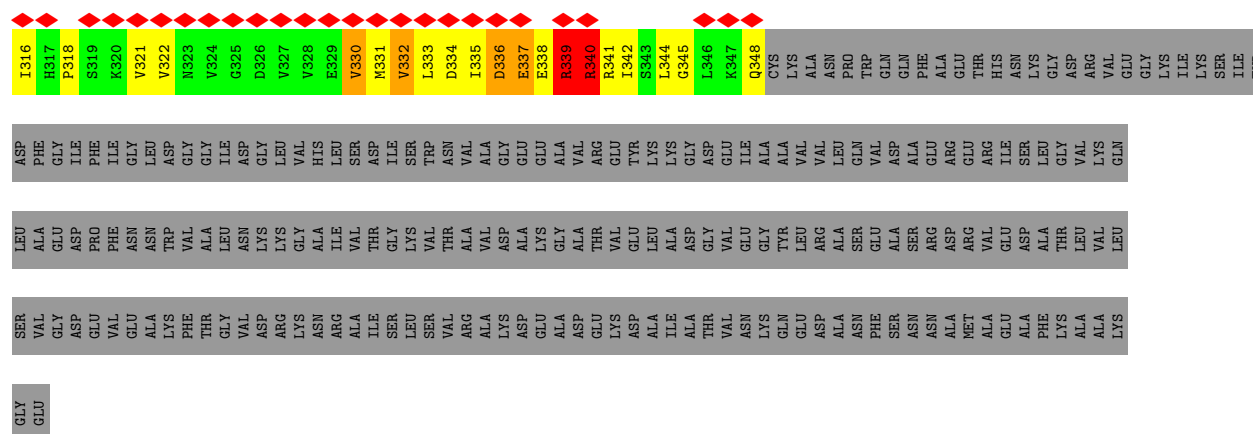


- Molecule 21: 30S ribosomal protein S2

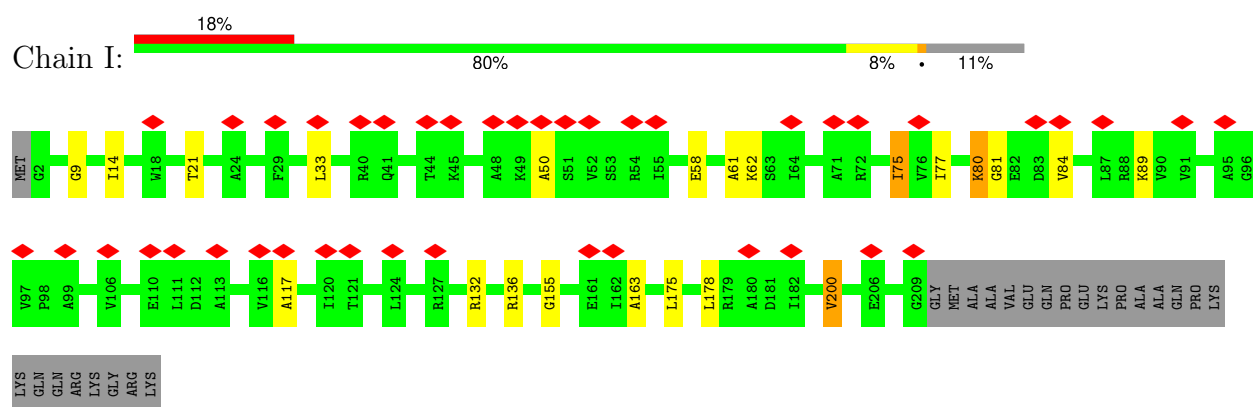


- Molecule 22: 30S ribosomal protein S1

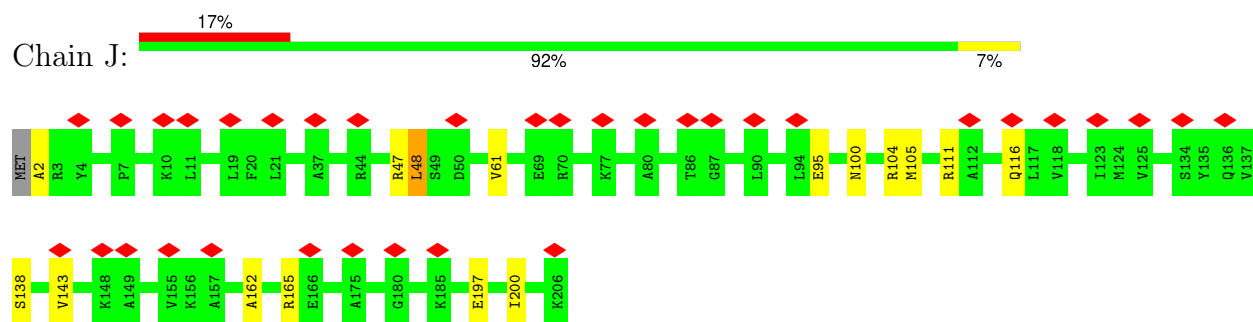




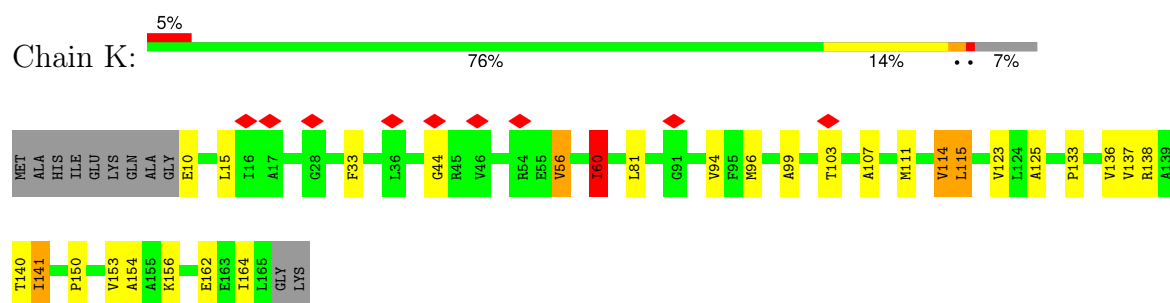
• Molecule 23: 30S ribosomal protein S3



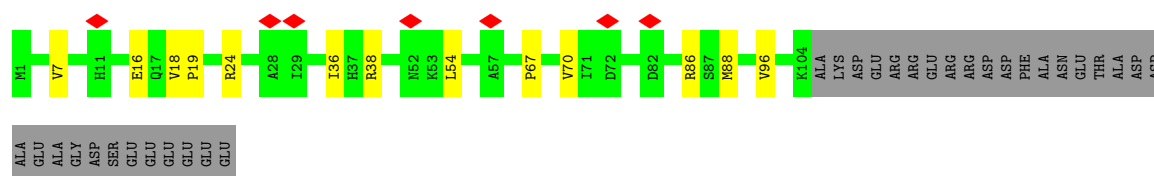
• Molecule 24: 30S ribosomal protein S4



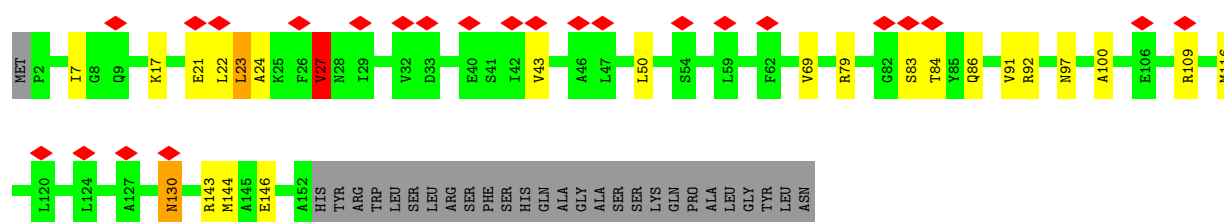
• Molecule 25: 30S ribosomal protein S5



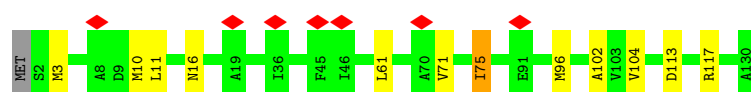
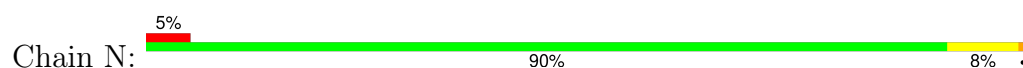
• Molecule 26: 30S ribosomal protein S6



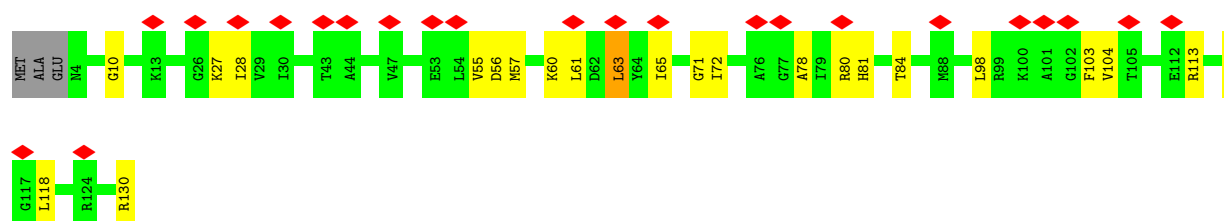
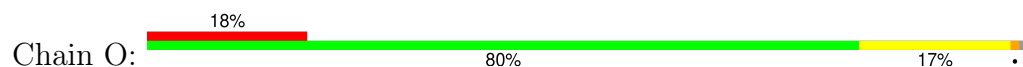
- Molecule 27: 30S ribosomal protein S7



- Molecule 28: 30S ribosomal protein S8



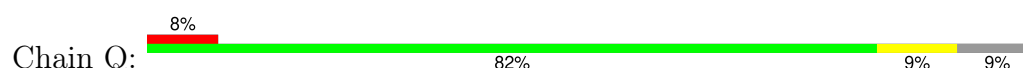
- Molecule 29: 30S ribosomal protein S9

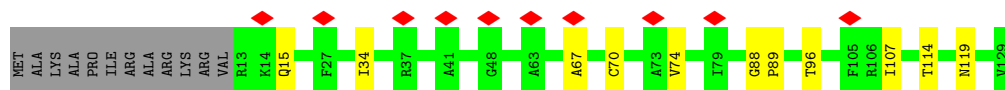


- Molecule 30: 30S ribosomal protein S10

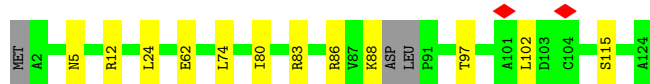
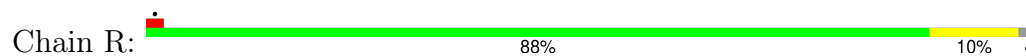


- Molecule 31: 30S ribosomal protein S11

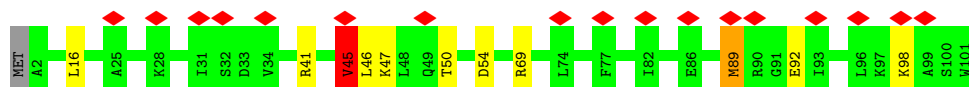
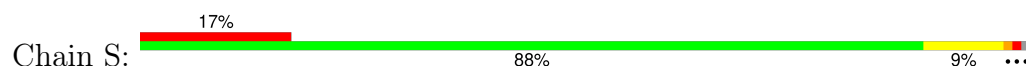




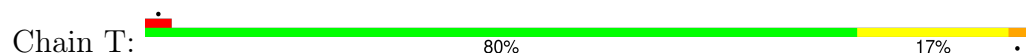
- Molecule 32: 30S ribosomal protein S12



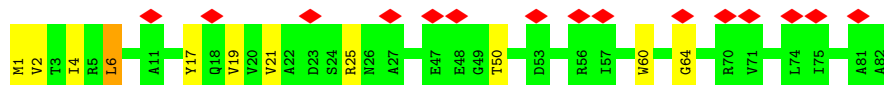
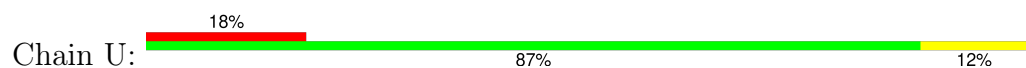
- Molecule 33: 30S ribosomal protein S14



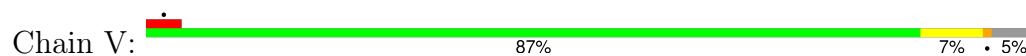
- Molecule 34: Small ribosomal subunit protein uS15



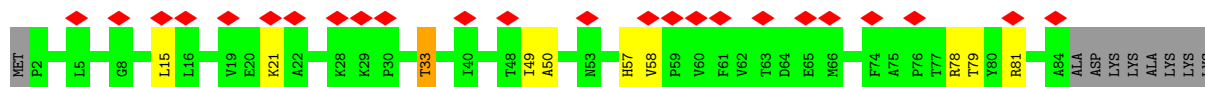
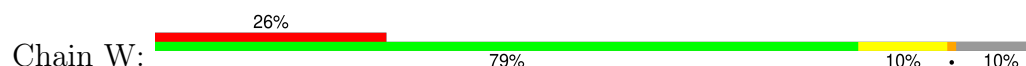
- Molecule 35: 30S ribosomal protein S16



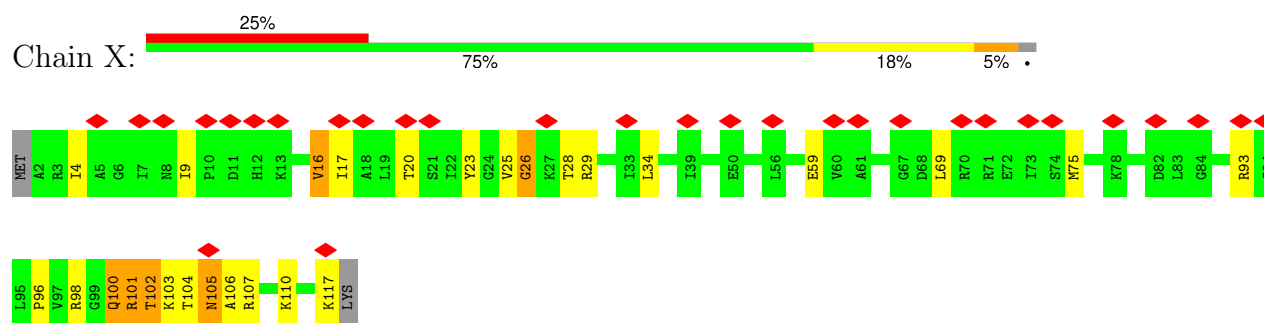
- Molecule 36: 30S ribosomal protein S17



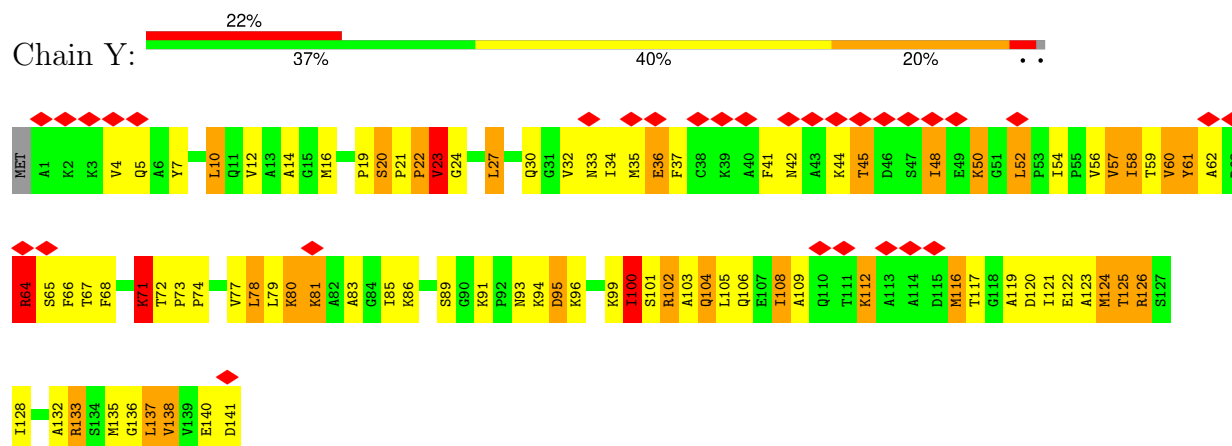
- Molecule 37: 30S ribosomal protein S19



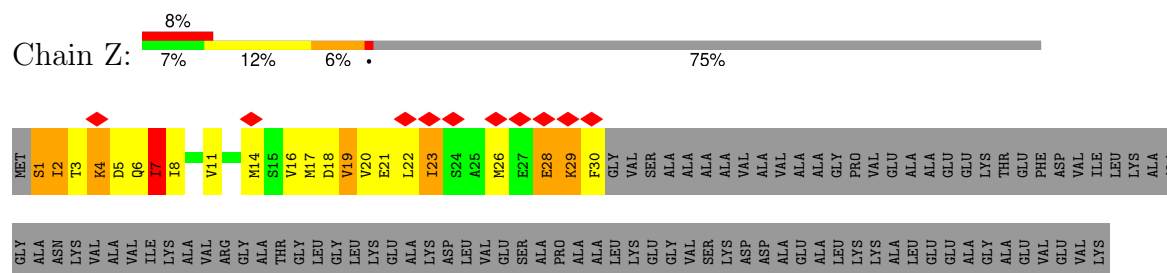
- Molecule 38: 30S ribosomal protein S13



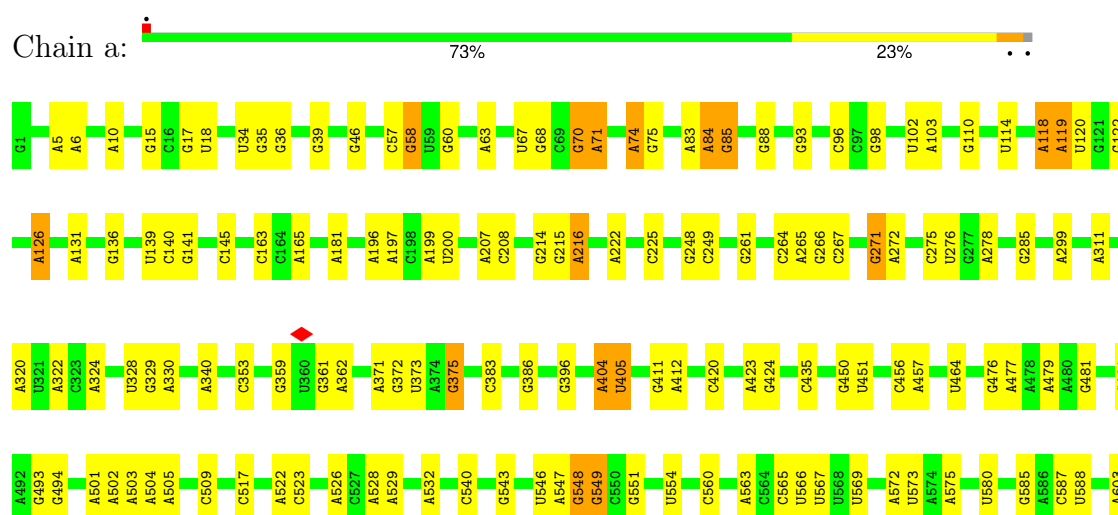
- Molecule 39: 50S ribosomal protein L11



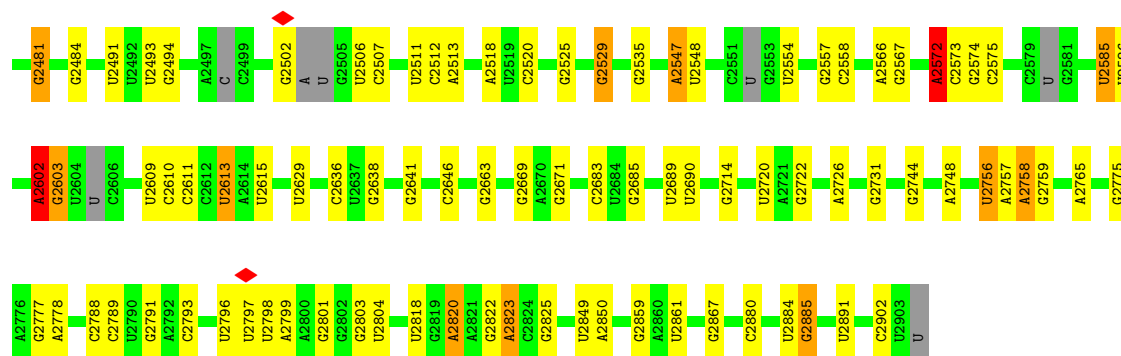
- Molecule 40: 50S ribosomal protein L7/L12



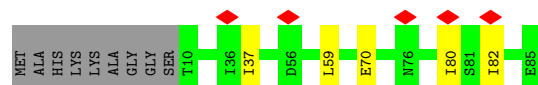
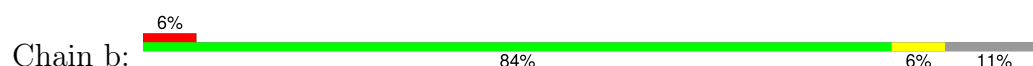
- Molecule 41: 23S rRNA



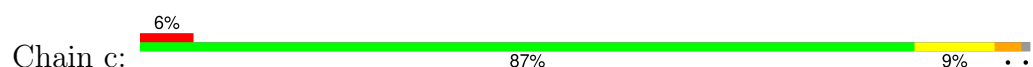
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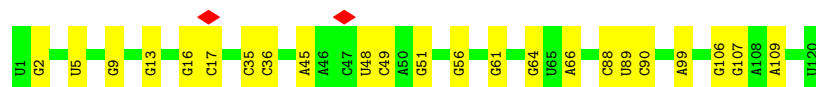
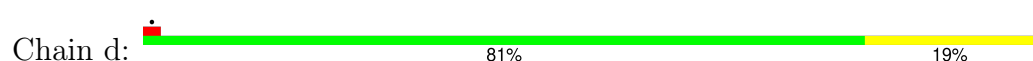
• Molecule 42: 50S ribosomal protein L27



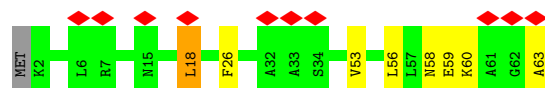
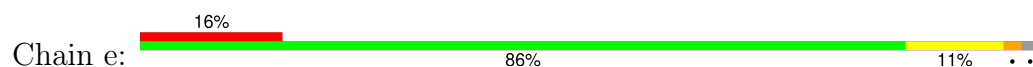
• Molecule 43: 50S ribosomal protein L28



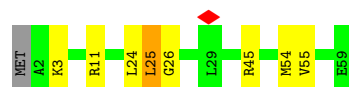
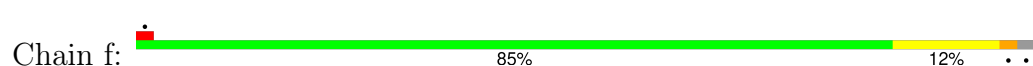
• Molecule 44: 5S rRNA




• Molecule 45: 50S ribosomal protein L29

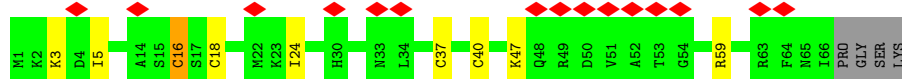


• Molecule 46: 50S ribosomal protein L30




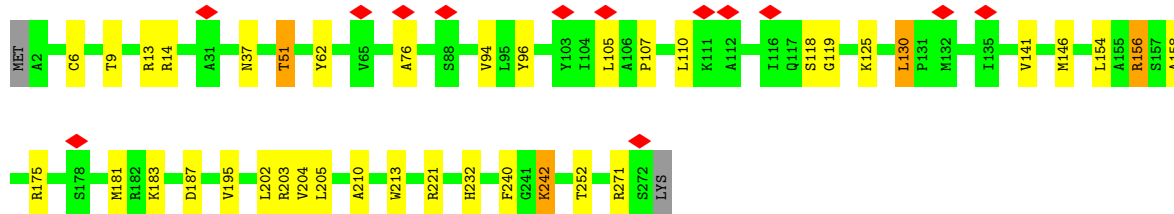
• Molecule 47: 50S ribosomal protein L31

Chain g: 




- Molecule 48: 50S ribosomal protein L2

Chain h: 




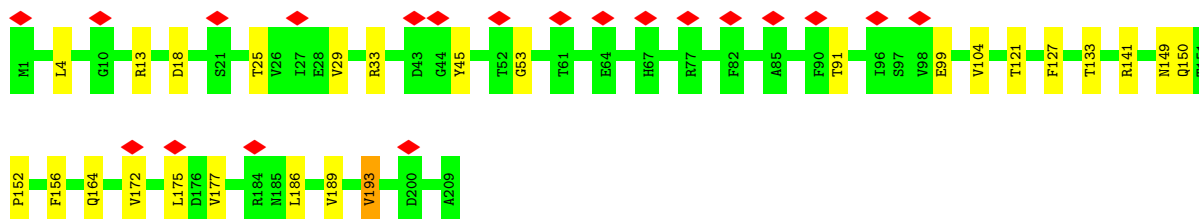
- Molecule 49: 50S ribosomal protein L32

Chain i: 




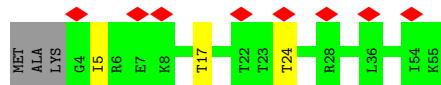
- Molecule 50: 50S ribosomal protein L3

Chain j: 




- Molecule 51: 50S ribosomal protein L33

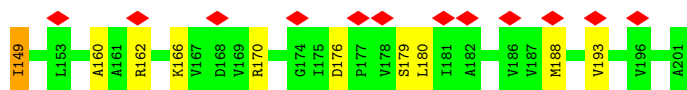
Chain k: 



- Molecule 52: 50S ribosomal protein L4

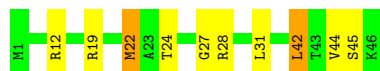
Chain l: 





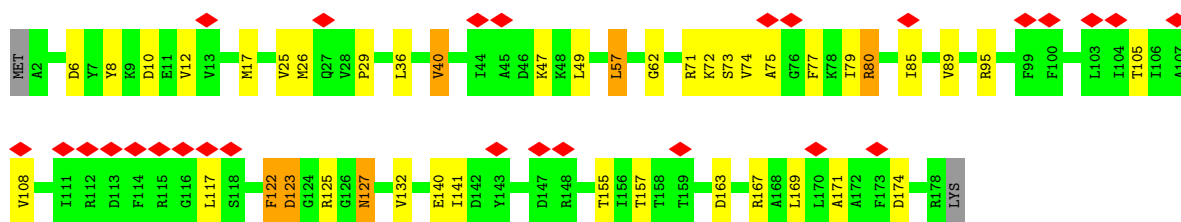
- Molecule 53: 50S ribosomal protein L34

Chain m: 78% 17%



- Molecule 54: 50S ribosomal protein L5

Chain n: 15% 75% 20%



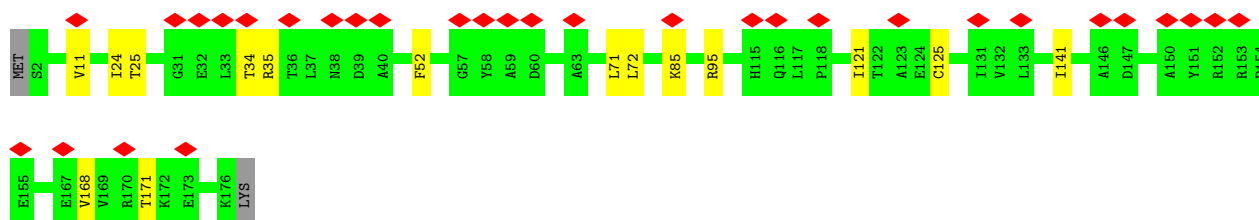
- Molecule 55: 50S ribosomal protein L35

Chain o: 9% 88% 8%



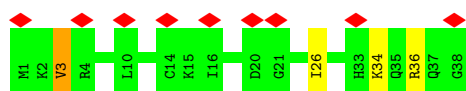
- Molecule 56: 50S ribosomal protein L6

Chain p: 18% 90% 8%

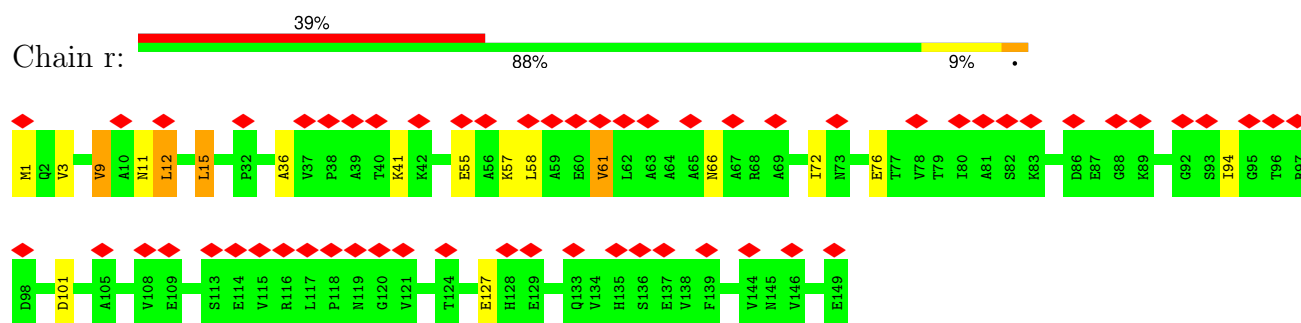


- Molecule 57: 50S ribosomal protein L36

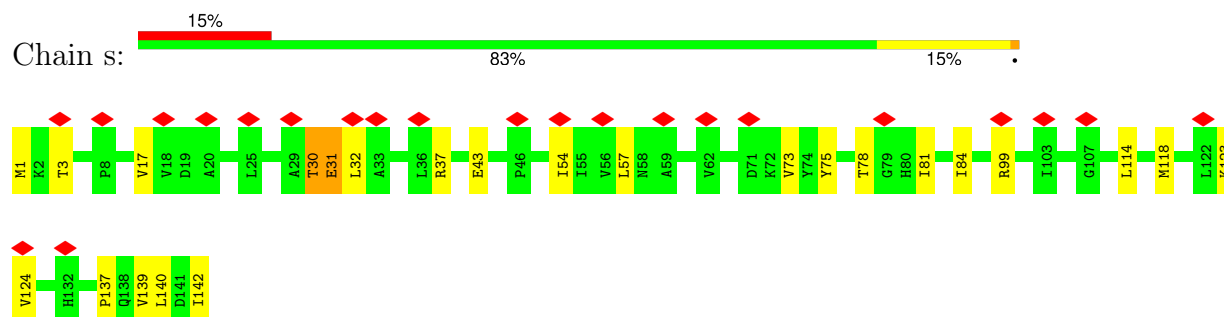
Chain q: 24% 89% 8%



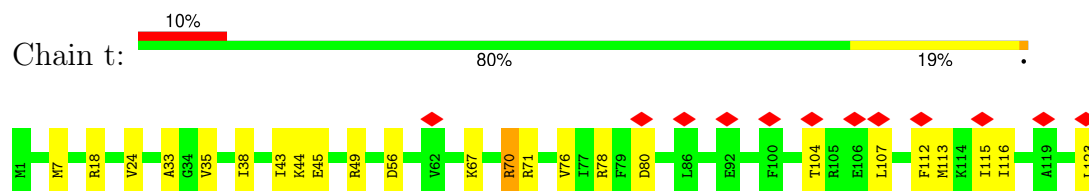
- Molecule 58: 50S ribosomal protein L9



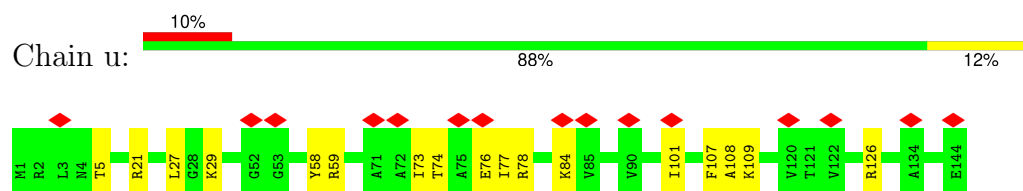
• Molecule 59: 50S ribosomal protein L13



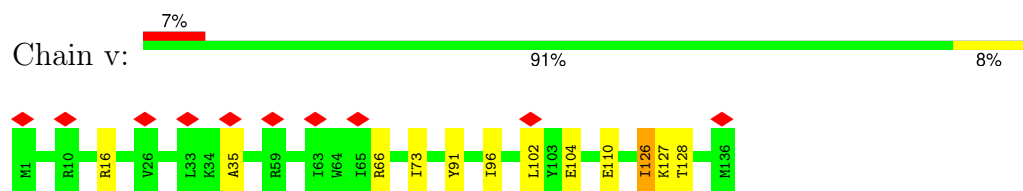
• Molecule 60: 50S ribosomal protein L14



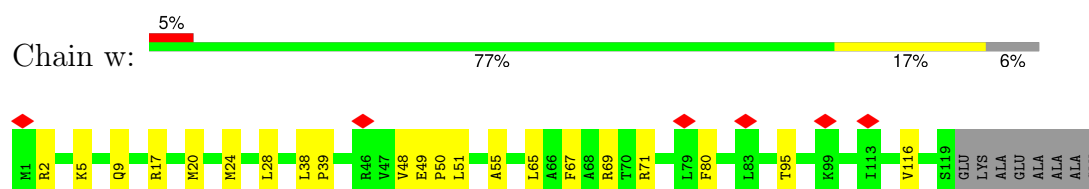
• Molecule 61: 50S ribosomal protein L15



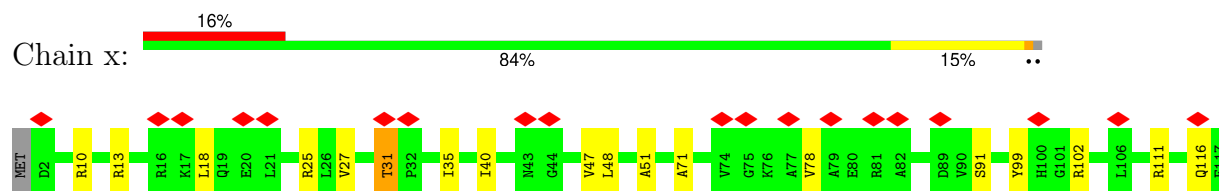
• Molecule 62: 50S ribosomal protein L16



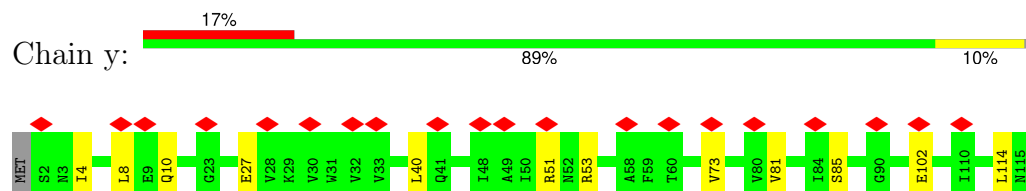
• Molecule 63: 50S ribosomal protein L17



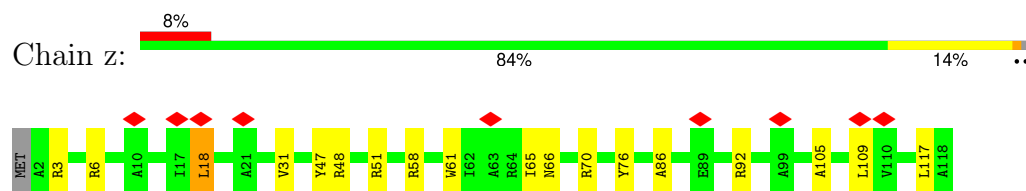
- Molecule 64: 50S ribosomal protein L18



- 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	1516	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	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	0.00000001	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: MG, ZN

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	0.50	0/829	0.74	0/1107
2	1	0.67	0/864	1.08	0/1156
3	2	0.54	0/752	0.89	0/1005
4	3	0.47	0/796	0.77	0/1062
5	4	0.52	0/766	0.88	0/1025
6	5	0.64	1/528 (0.2%)	0.55	0/810
7	6	0.56	1/603 (0.2%)	0.56	0/926
8	7	0.62	3/717 (0.4%)	0.90	4/1110 (0.4%)
9	9	1.15	3/1131 (0.3%)	1.30	3/1524 (0.2%)
10	A	0.36	0/1810	0.72	2/2821 (0.1%)
10	B	0.44	0/1810	0.87	9/2821 (0.3%)
11	AA	0.39	0/10736	0.63	0/14487
12	AB	0.55	0/1304	0.78	1/1759 (0.1%)
13	AC	0.38	0/1710	0.61	0/2317
13	AD	0.30	0/2091	0.59	0/2847
14	AE	0.56	10/10545 (0.1%)	0.79	27/14236 (0.2%)
15	AF	0.30	0/652	0.61	0/879
16	AG	0.97	5/3897 (0.1%)	1.40	49/5273 (0.9%)
17	C	0.66	0/553	1.14	1/743 (0.1%)
18	D	0.40	9/36610 (0.0%)	0.75	38/57091 (0.1%)
19	E	0.76	0/675	1.32	0/895
20	F	0.72	0/597	1.20	0/792
21	G	0.65	0/1791	1.08	1/2413 (0.0%)
22	H	0.76	4/1746 (0.2%)	1.58	34/2382 (1.4%)
23	I	0.59	0/1663	0.99	0/2241
24	J	0.63	0/1665	1.08	0/2227
25	K	0.64	1/1165 (0.1%)	1.06	2/1568 (0.1%)
26	L	0.58	0/867	0.94	0/1171
27	M	0.68	0/1195	1.19	3/1602 (0.2%)
28	N	0.56	0/989	0.91	0/1326
29	O	0.59	0/1034	1.02	1/1375 (0.1%)
30	P	0.64	0/800	1.13	4/1082 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	Q	0.55	0/893	0.91	0/1205
32	R	0.50	0/952	0.81	0/1274
33	S	0.64	0/817	1.11	1/1088 (0.1%)
34	T	0.69	0/722	1.21	0/964
35	U	0.58	0/659	0.99	0/884
36	V	0.46	0/657	0.73	0/881
37	W	0.51	0/680	0.83	0/915
38	X	0.67	0/909	1.21	3/1215 (0.2%)
39	Y	1.04	0/1046	1.09	1/1410 (0.1%)
40	Z	1.02	0/227	1.12	0/304
41	a	0.41	3/69247 (0.0%)	0.75	55/107985 (0.1%)
42	b	0.51	0/589	0.76	0/779
43	c	0.63	0/635	0.97	0/848
44	d	0.37	0/2872	0.69	0/4478
45	e	0.69	0/502	1.19	0/667
46	f	0.62	0/452	1.02	0/605
47	g	0.56	0/531	0.99	1/709 (0.1%)
48	h	0.54	0/2121	0.85	0/2852
49	i	0.53	0/450	0.94	0/599
50	j	0.60	0/1586	0.87	0/2134
51	k	0.47	0/433	0.80	0/576
52	l	0.61	0/1571	1.03	1/2113 (0.0%)
53	m	0.69	0/380	1.22	0/498
54	n	0.63	0/1434	1.18	10/1926 (0.5%)
55	o	0.64	0/513	1.11	1/676 (0.1%)
56	p	0.58	0/1333	0.89	0/1805
57	q	0.51	0/303	0.88	0/397
58	r	0.63	0/1122	0.98	1/1515 (0.1%)
59	s	0.68	0/1152	1.02	0/1551
60	t	0.57	0/955	0.88	0/1279
61	u	0.55	0/1062	0.95	1/1413 (0.1%)
62	v	0.60	0/1093	0.97	0/1460
63	w	0.68	0/964	1.13	0/1289
64	x	0.61	0/902	1.09	0/1209
65	y	0.53	0/929	0.79	0/1242
66	z	0.80	0/960	1.25	0/1278
All	All	0.50	40/194544 (0.0%)	0.84	254/286096 (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
10	A	0	2
10	B	0	2
12	AB	0	1
13	AC	0	1
13	AD	0	3
14	AE	0	5
16	AG	0	6
22	H	0	3
38	X	0	1
All	All	0	24

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	9	130	PRO	N-CA	18.14	1.70	1.47
16	AG	429	LYS	C-N	13.82	1.51	1.33
14	AE	93	THR	CA-C	12.11	1.69	1.52
22	H	169	SER	N-CA	11.81	1.61	1.46
14	AE	291	ILE	CA-C	11.52	1.67	1.52

The worst 5 of 254 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	AE	291	ILE	CA-C-N	20.29	158.49	121.97
14	AE	291	ILE	C-N-CA	20.29	158.49	121.97
16	AG	104	ARG	CA-C-N	17.90	154.19	121.97
16	AG	104	ARG	C-N-CA	17.90	154.19	121.97
18	D	1516	G	O3'-P-O5'	17.53	130.29	104.00

There are no chirality outliers.

5 of 24 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	A	19	G	Sidechain
10	A	7	G	Sidechain
12	AB	44	VAL	Mainchain
13	AC	192	VAL	Peptide
13	AD	20	SER	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	8	0
2	1	857	922	922	14	0
3	2	746	811	811	5	0
4	3	788	844	844	11	0
5	4	753	780	780	0	0
6	5	472	260	260	26	0
7	6	542	305	306	24	0
8	7	647	97	321	106	0
9	9	1117	0	1153	168	0
10	A	1620	826	826	173	0
10	B	1620	814	827	141	0
11	AA	10567	0	10584	316	0
12	AB	1276	0	1244	270	0
13	AC	1690	0	1714	15	0
13	AD	2073	0	1889	46	0
14	AE	10388	10612	10610	383	0
15	AF	650	0	658	12	0
16	AG	3852	0	3826	815	0
17	C	544	559	560	24	0
18	D	32703	16423	16459	239	0
19	E	669	719	719	4	0
20	F	589	629	629	8	0
21	G	1760	1785	1785	46	0
22	H	1730	1454	1454	212	0
23	I	1636	1710	1710	43	0
24	J	1643	1707	1707	16	0
25	K	1152	1196	1196	21	0
26	L	848	846	846	3	0
27	M	1181	1235	1235	34	0
28	N	979	1031	1031	6	0
29	O	1022	1070	1070	12	0
30	P	790	831	831	106	0
31	Q	877	887	887	4	0
32	R	939	1001	1001	6	0
33	S	805	844	844	6	0
34	T	714	734	734	7	0
35	U	649	666	666	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	V	648	691	691	4	0
37	W	663	688	688	3	0
38	X	900	964	964	58	0
39	Y	1032	0	1088	90	0
40	Z	227	0	237	19	0
41	a	61841	31077	31123	301	0
42	b	582	599	599	3	0
43	c	625	652	652	4	0
44	d	2569	1301	1301	3	0
45	e	501	531	531	5	0
46	f	448	488	488	5	0
47	g	522	520	520	11	0
48	h	2082	2154	2154	19	0
49	i	444	459	458	6	0
50	j	1565	1617	1616	16	0
51	k	426	464	464	0	0
52	l	1552	1619	1619	14	0
53	m	377	418	418	10	0
54	n	1410	1443	1444	29	0
55	o	504	572	572	3	0
56	p	1313	1358	1358	7	0
57	q	302	343	343	1	0
58	r	1111	1148	1148	6	0
59	s	1129	1162	1162	14	0
60	t	946	1023	1023	12	0
61	u	1053	1129	1129	8	0
62	v	1074	1157	1157	5	0
63	w	951	994	994	8	0
64	x	892	923	923	8	0
65	y	917	962	962	4	0
66	z	947	1020	1019	13	0
67	AE	1	0	0	0	0
68	AE	2	0	0	0	0
All	All	181260	109913	132623	3352	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 11.

The worst 5 of 3352 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)
16:AG:425:LEU:CD2	16:AG:429:LYS:HE2	1.21	1.61
16:AG:287:ALA:CA	16:AG:331:LEU:HD12	1.18	1.59
17:C:12:ARG:HG3	22:H:264:GLU:CB	1.30	1.59
22:H:131:LEU:CB	22:H:167:VAL:CA	1.78	1.58
16:AG:168:LEU:CD2	16:AG:231:GLY:HA3	1.34	1.53

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%)	3 (3%)	1 (1%)	13	49
2	1	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
3	2	92/100 (92%)	90 (98%)	2 (2%)	0	100	100
4	3	101/104 (97%)	96 (95%)	4 (4%)	1 (1%)	13	49
5	4	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
9	9	146/165 (88%)	94 (64%)	38 (26%)	14 (10%)	0	7
11	AA	1338/1342 (100%)	1206 (90%)	128 (10%)	4 (0%)	37	73
12	AB	157/181 (87%)	129 (82%)	20 (13%)	8 (5%)	1	15
13	AC	216/329 (66%)	202 (94%)	12 (6%)	2 (1%)	14	52
13	AD	292/329 (89%)	269 (92%)	23 (8%)	0	100	100
14	AE	1329/1407 (94%)	1199 (90%)	119 (9%)	11 (1%)	16	55
15	AF	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
16	AG	493/495 (100%)	375 (76%)	87 (18%)	31 (6%)	1	13
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	G	223/241 (92%)	210 (94%)	13 (6%)	0	100	100
22	H	255/557 (46%)	189 (74%)	54 (21%)	12 (5%)	2	16
23	I	206/233 (88%)	196 (95%)	9 (4%)	1 (0%)	25	64
24	J	203/206 (98%)	198 (98%)	5 (2%)	0	100	100
25	K	154/167 (92%)	146 (95%)	7 (4%)	1 (1%)	22	60
26	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	13	49
27	M	149/179 (83%)	144 (97%)	4 (3%)	1 (1%)	19	57
28	N	127/130 (98%)	121 (95%)	5 (4%)	1 (1%)	16	55
29	O	125/130 (96%)	115 (92%)	9 (7%)	1 (1%)	16	55
30	P	97/103 (94%)	87 (90%)	8 (8%)	2 (2%)	5	30
31	Q	115/129 (89%)	104 (90%)	9 (8%)	2 (2%)	7	37
32	R	117/124 (94%)	116 (99%)	1 (1%)	0	100	100
33	S	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
34	T	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
35	U	80/82 (98%)	75 (94%)	4 (5%)	1 (1%)	10	43
36	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
37	W	81/92 (88%)	78 (96%)	3 (4%)	0	100	100
38	X	114/118 (97%)	107 (94%)	5 (4%)	2 (2%)	7	35
39	Y	139/142 (98%)	102 (73%)	25 (18%)	12 (9%)	0	9
40	Z	28/121 (23%)	20 (71%)	6 (21%)	2 (7%)	1	11
42	b	74/85 (87%)	69 (93%)	5 (7%)	0	100	100
43	c	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
45	e	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
46	f	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
47	g	64/70 (91%)	63 (98%)	1 (2%)	0	100	100
48	h	269/273 (98%)	259 (96%)	9 (3%)	1 (0%)	30	68
49	i	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
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%)	190 (96%)	8 (4%)	1 (0%)	25	64
53	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	n	175/179 (98%)	162 (93%)	11 (6%)	2 (1%)	12	47
55	o	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
56	p	173/177 (98%)	161 (93%)	12 (7%)	0	100	100
57	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
58	r	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
59	s	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
60	t	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
61	u	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
62	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
63	w	117/127 (92%)	107 (92%)	10 (8%)	0	100	100
64	x	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
65	y	112/115 (97%)	104 (93%)	8 (7%)	0	100	100
66	z	115/118 (98%)	110 (96%)	4 (4%)	1 (1%)	14	52
All	All	10078/11072 (91%)	9198 (91%)	764 (8%)	116 (1%)	14	44

5 of 116 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	9	88	HIS
12	AB	118	VAL
12	AB	122	PRO
14	AE	291	ILE
16	AG	34	ALA

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%)	76 (90%)	8 (10%)	7	22
2	1	93/93 (100%)	86 (92%)	7 (8%)	11	31
3	2	81/84 (96%)	77 (95%)	4 (5%)	21	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	3	84/85 (99%)	79 (94%)	5 (6%)	16	37
5	4	78/78 (100%)	75 (96%)	3 (4%)	28	49
9	9	112/123 (91%)	63 (56%)	49 (44%)	0	0
11	AA	1155/1157 (100%)	1130 (98%)	25 (2%)	47	65
12	AB	138/158 (87%)	108 (78%)	30 (22%)	1	5
13	AC	185/286 (65%)	184 (100%)	1 (0%)	86	89
13	AD	185/286 (65%)	185 (100%)	0	100	100
14	AE	1120/1168 (96%)	1046 (93%)	74 (7%)	14	34
15	AF	70/75 (93%)	69 (99%)	1 (1%)	62	75
16	AG	409/409 (100%)	288 (70%)	121 (30%)	0	2
17	C	57/65 (88%)	55 (96%)	2 (4%)	31	51
19	E	65/66 (98%)	61 (94%)	4 (6%)	15	36
20	F	60/61 (98%)	57 (95%)	3 (5%)	20	41
21	G	187/199 (94%)	174 (93%)	13 (7%)	12	32
22	H	137/461 (30%)	124 (90%)	13 (10%)	7	22
23	I	171/190 (90%)	163 (95%)	8 (5%)	22	44
24	J	172/173 (99%)	164 (95%)	8 (5%)	22	44
25	K	119/126 (94%)	111 (93%)	8 (7%)	13	34
26	L	91/116 (78%)	84 (92%)	7 (8%)	10	30
27	M	124/147 (84%)	113 (91%)	11 (9%)	8	25
28	N	104/105 (99%)	101 (97%)	3 (3%)	37	56
29	O	105/107 (98%)	99 (94%)	6 (6%)	17	38
30	P	86/90 (96%)	73 (85%)	13 (15%)	2	11
31	Q	90/99 (91%)	88 (98%)	2 (2%)	47	65
32	R	101/104 (97%)	95 (94%)	6 (6%)	16	37
33	S	83/84 (99%)	79 (95%)	4 (5%)	21	43
34	T	76/77 (99%)	65 (86%)	11 (14%)	2	12
35	U	65/65 (100%)	60 (92%)	5 (8%)	10	30
36	V	74/78 (95%)	71 (96%)	3 (4%)	26	47
37	W	72/79 (91%)	66 (92%)	6 (8%)	9	27
38	X	94/96 (98%)	87 (93%)	7 (7%)	11	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	Y	109/110 (99%)	69 (63%)	40 (37%)	0	1
40	Z	26/85 (31%)	10 (38%)	16 (62%)	0	0
42	b	58/63 (92%)	57 (98%)	1 (2%)	56	72
43	c	67/68 (98%)	64 (96%)	3 (4%)	23	45
45	e	54/55 (98%)	51 (94%)	3 (6%)	17	38
46	f	48/49 (98%)	43 (90%)	5 (10%)	5	19
47	g	59/62 (95%)	55 (93%)	4 (7%)	13	34
48	h	216/218 (99%)	199 (92%)	17 (8%)	10	29
49	i	47/48 (98%)	41 (87%)	6 (13%)	3	14
50	j	164/164 (100%)	156 (95%)	8 (5%)	21	42
51	k	47/49 (96%)	44 (94%)	3 (6%)	14	35
52	l	165/165 (100%)	151 (92%)	14 (8%)	8	27
53	m	38/38 (100%)	36 (95%)	2 (5%)	19	40
54	n	148/150 (99%)	130 (88%)	18 (12%)	4	15
55	o	51/52 (98%)	47 (92%)	4 (8%)	10	29
56	p	136/138 (99%)	130 (96%)	6 (4%)	24	45
57	q	34/34 (100%)	31 (91%)	3 (9%)	8	25
58	r	114/114 (100%)	102 (90%)	12 (10%)	5	19
59	s	116/116 (100%)	106 (91%)	10 (9%)	8	26
60	t	104/104 (100%)	98 (94%)	6 (6%)	17	38
61	u	103/103 (100%)	96 (93%)	7 (7%)	13	34
62	v	109/109 (100%)	105 (96%)	4 (4%)	29	49
63	w	99/103 (96%)	91 (92%)	8 (8%)	9	28
64	x	86/87 (99%)	80 (93%)	6 (7%)	12	32
65	y	99/100 (99%)	91 (92%)	8 (8%)	9	28
66	z	89/90 (99%)	85 (96%)	4 (4%)	23	45
All	All	8313/9148 (91%)	7624 (92%)	689 (8%)	12	27

5 of 689 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	W	81	ARG
50	j	193	VAL

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Mol	Chain	Res	Type
39	Y	30	GLN
37	W	79	THR
40	Z	17	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 84 such sidechains are listed below:

Mol	Chain	Res	Type
26	L	11	HIS
38	X	105	ASN
26	L	94	HIS
31	Q	15	GLN
50	j	173	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	75/76 (98%)	29 (38%)	6 (8%)
10	B	75/76 (98%)	35 (46%)	6 (8%)
18	D	1514/1542 (98%)	291 (19%)	34 (2%)
41	a	2859/2904 (98%)	539 (18%)	0
44	d	119/120 (99%)	17 (14%)	0
8	7	30/56 (53%)	18 (60%)	4 (13%)
All	All	4672/4774 (97%)	929 (19%)	50 (1%)

5 of 929 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 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
18	D	531	U
18	D	992	U
18	D	1493	A
18	D	532	A

Continued on next page...

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Mol	Chain	Res	Type
18	D	722	G

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.

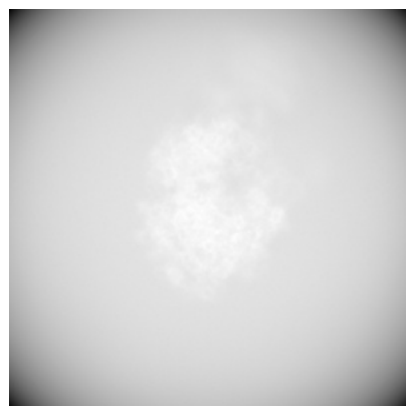
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43389. 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

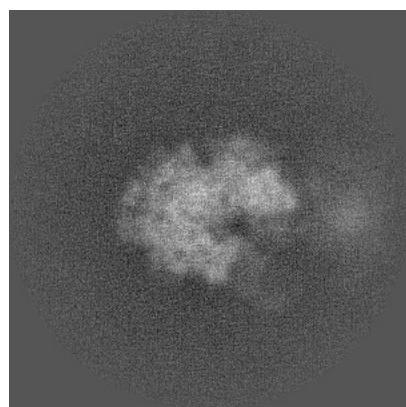


Y

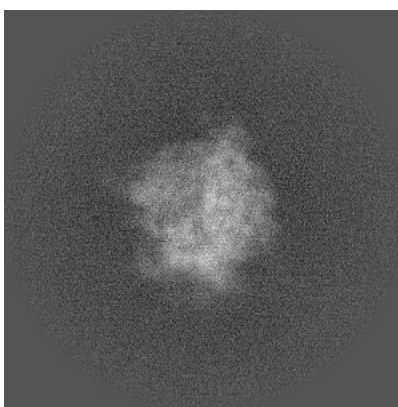


Z

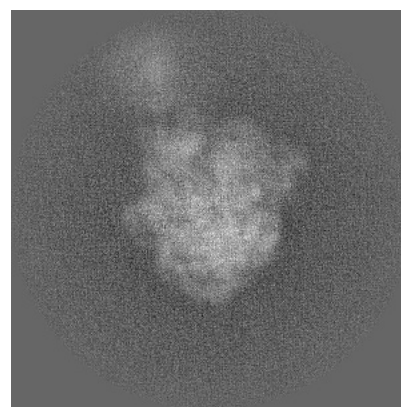
6.1.2 Raw map



X



Y

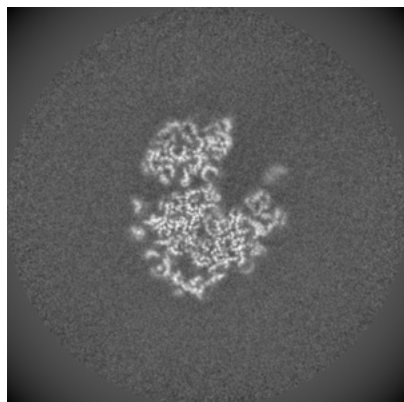


Z

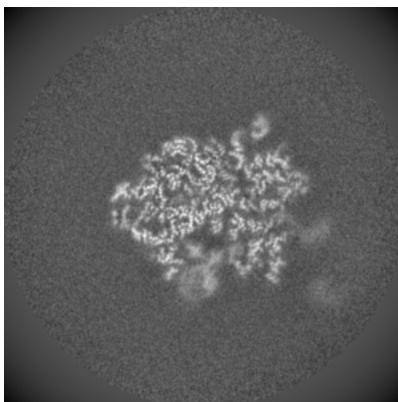
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

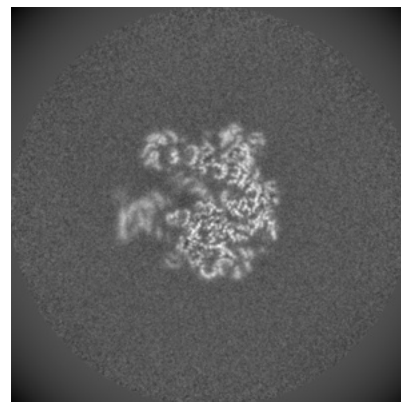
6.2.1 Primary map



X Index: 310

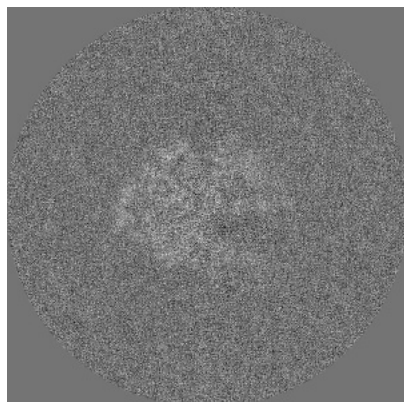


Y Index: 310

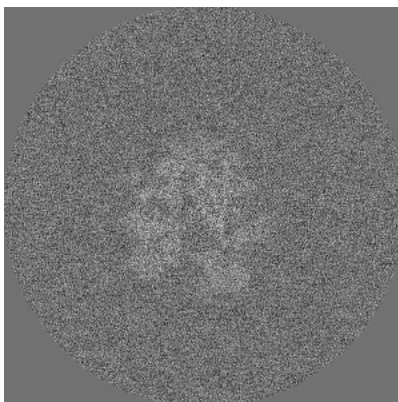


Z Index: 310

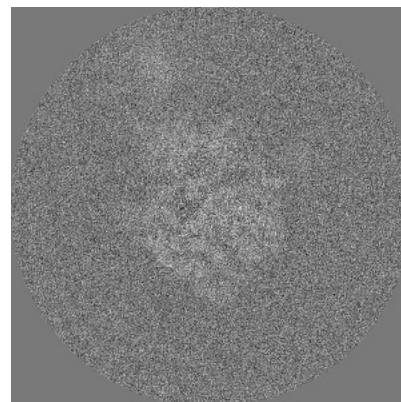
6.2.2 Raw map



X Index: 256



Y Index: 256

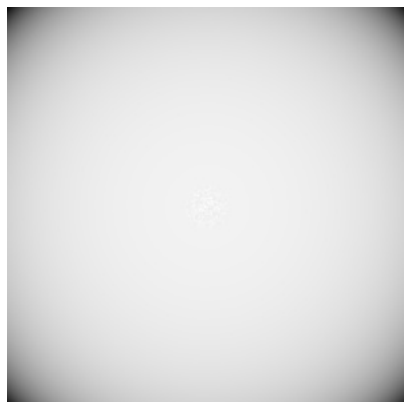


Z Index: 256

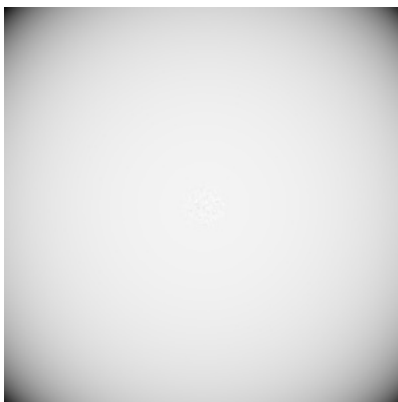
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

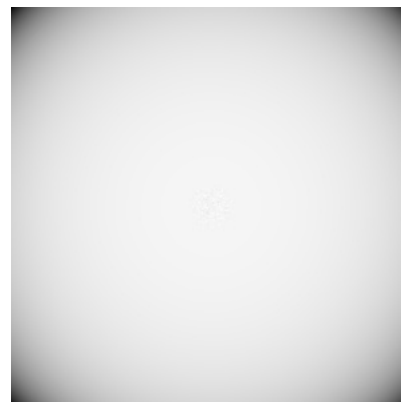
6.3.1 Primary map



X Index: 0

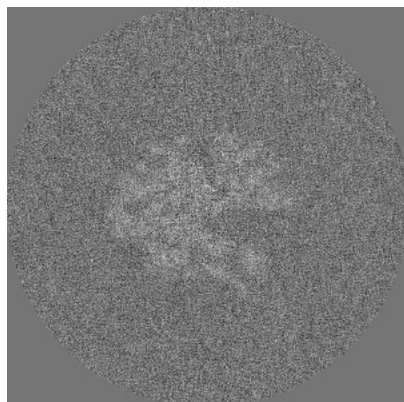


Y Index: 0

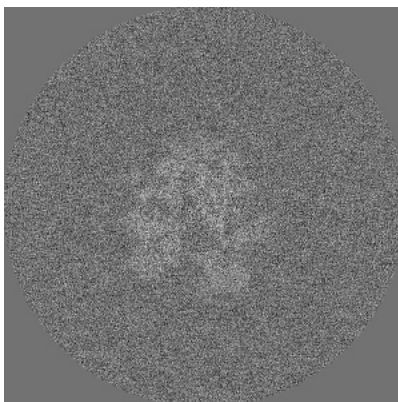


Z Index: 0

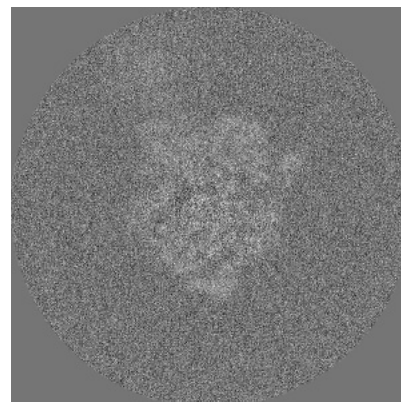
6.3.2 Raw map



X Index: 265



Y Index: 256

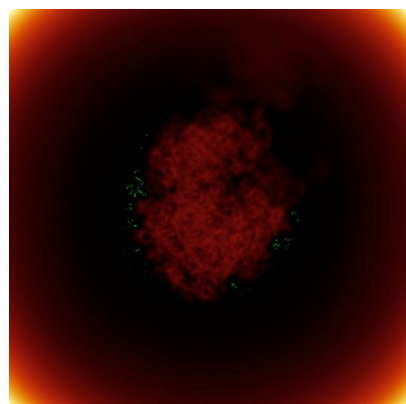


Z Index: 266

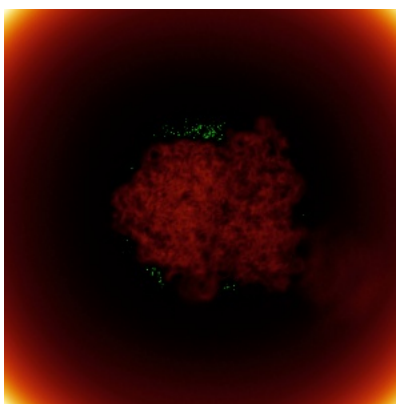
The images above show the largest variance slices of the map in three orthogonal directions.

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

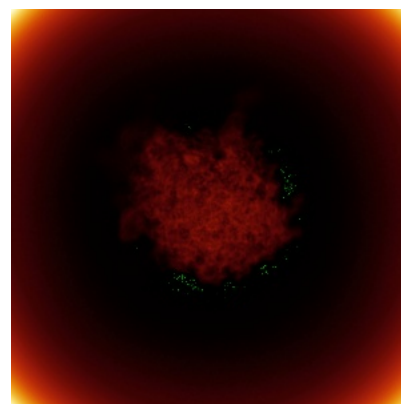
6.4.1 Primary map



X

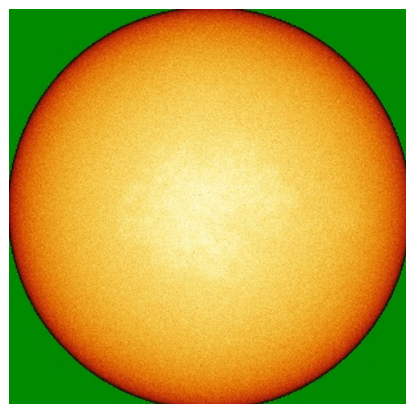


Y

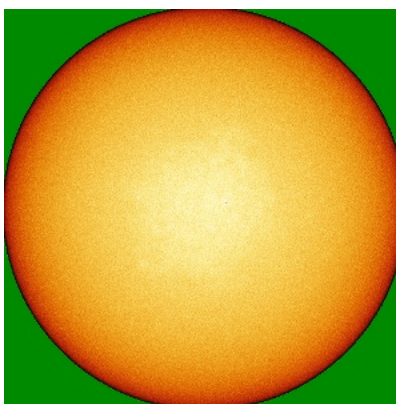


Z

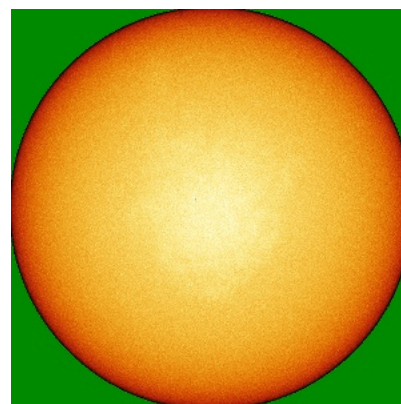
6.4.2 Raw map



X



Y

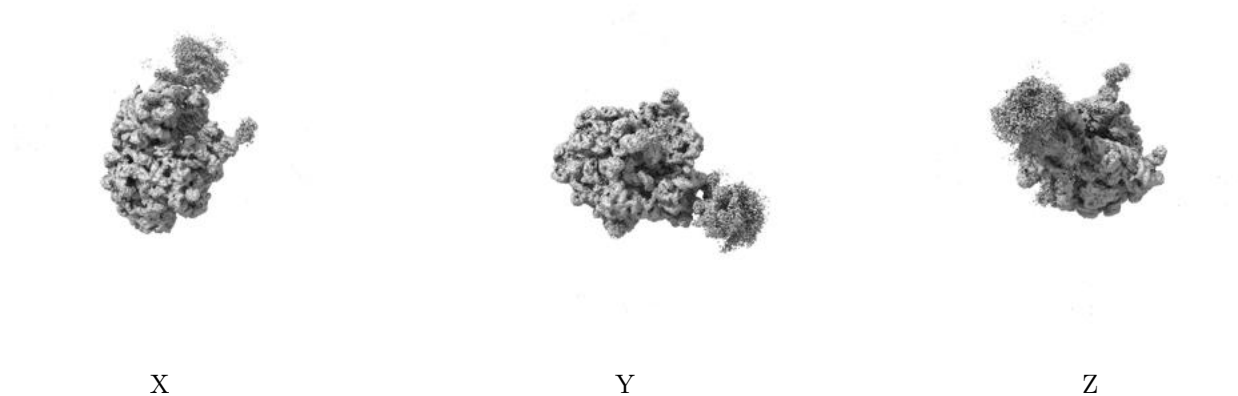


Z

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.

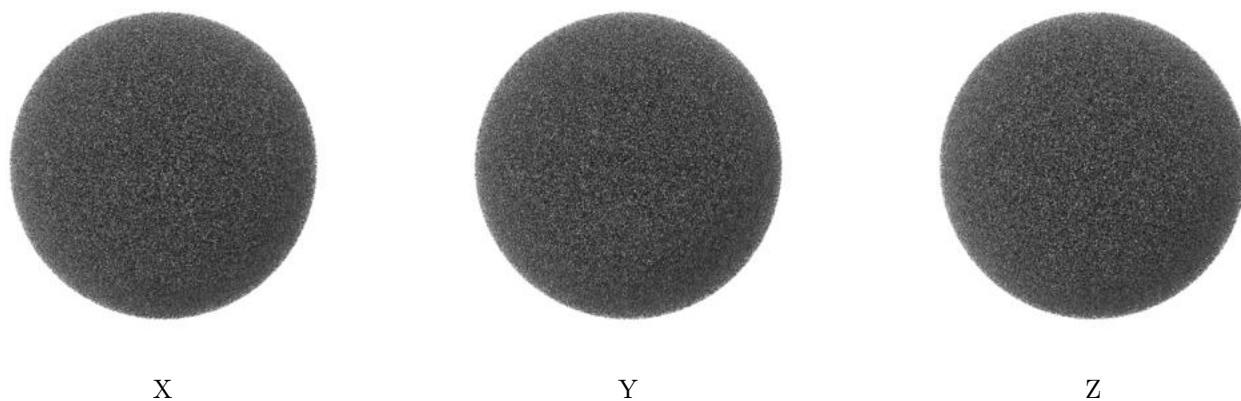
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1e-08. 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.

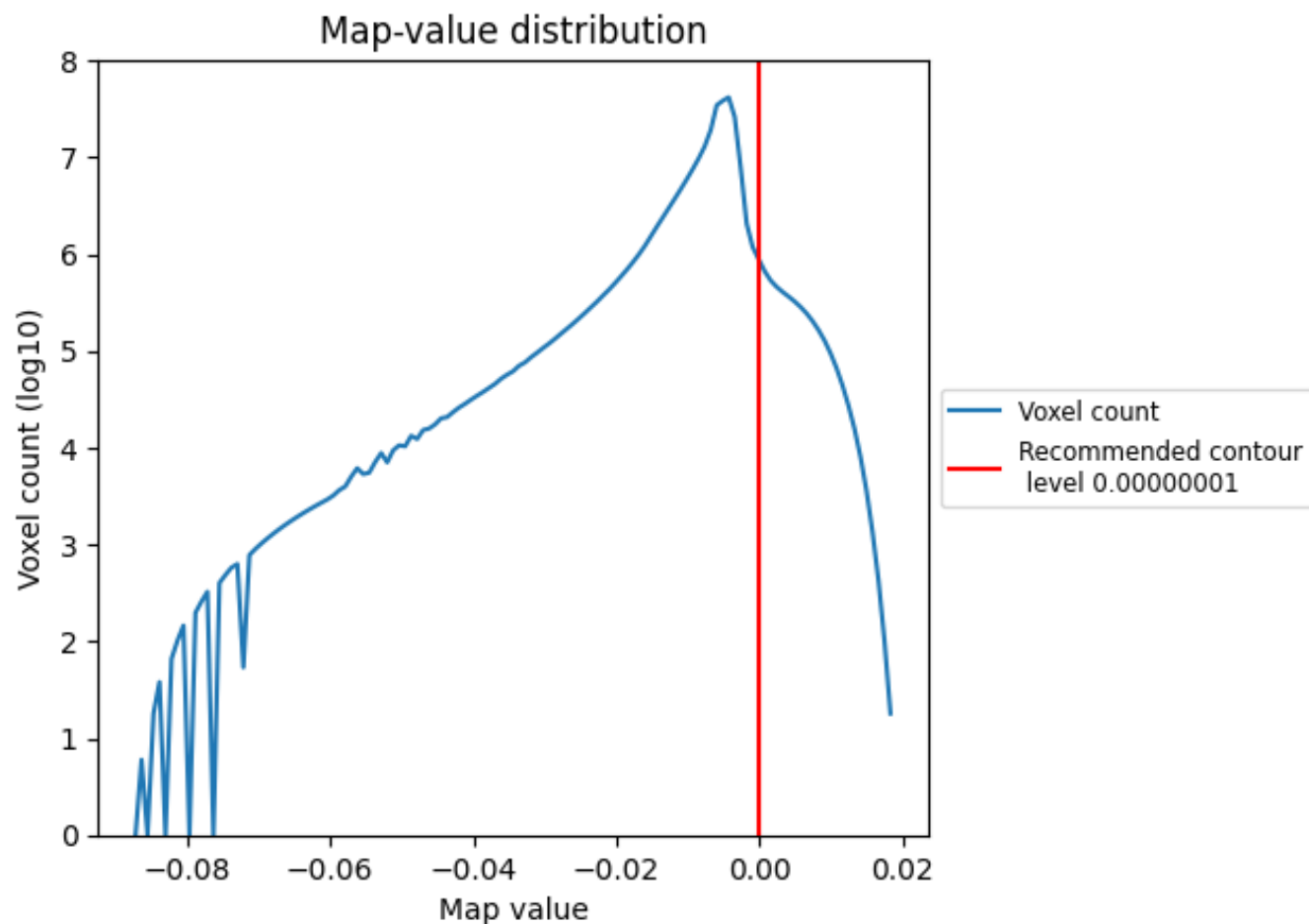
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

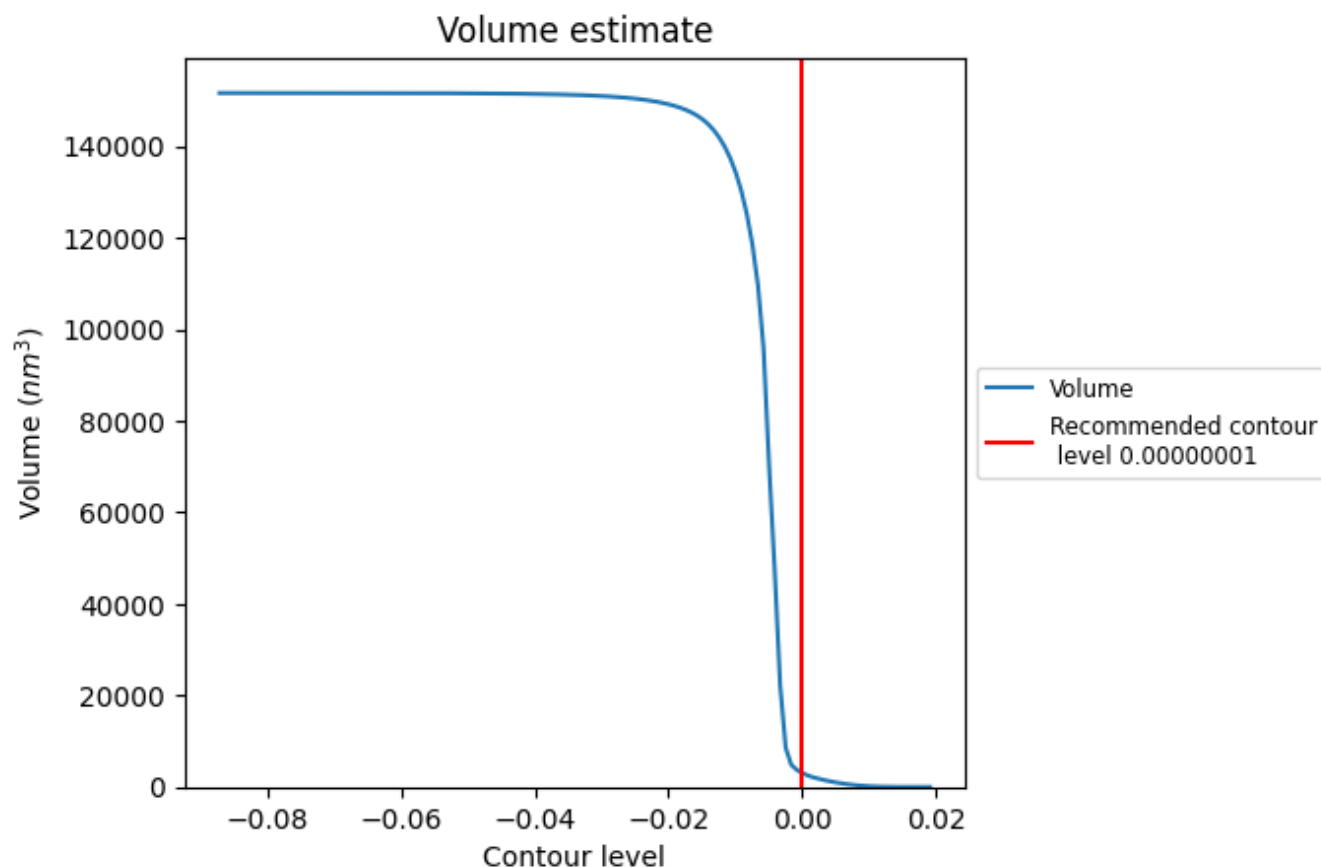
This section contains the results of statistical analysis of the map.

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.

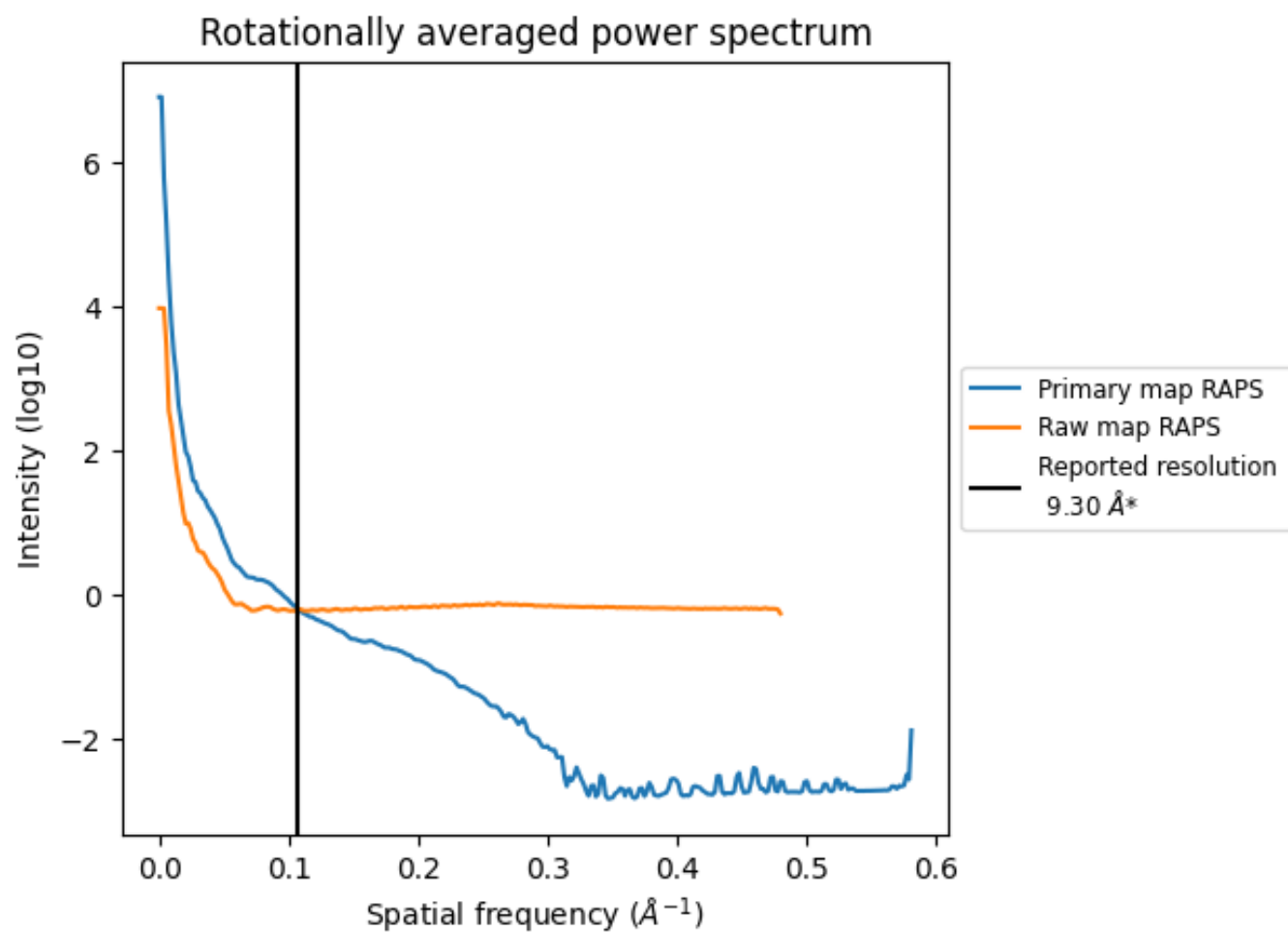
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3056 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 ⓘ

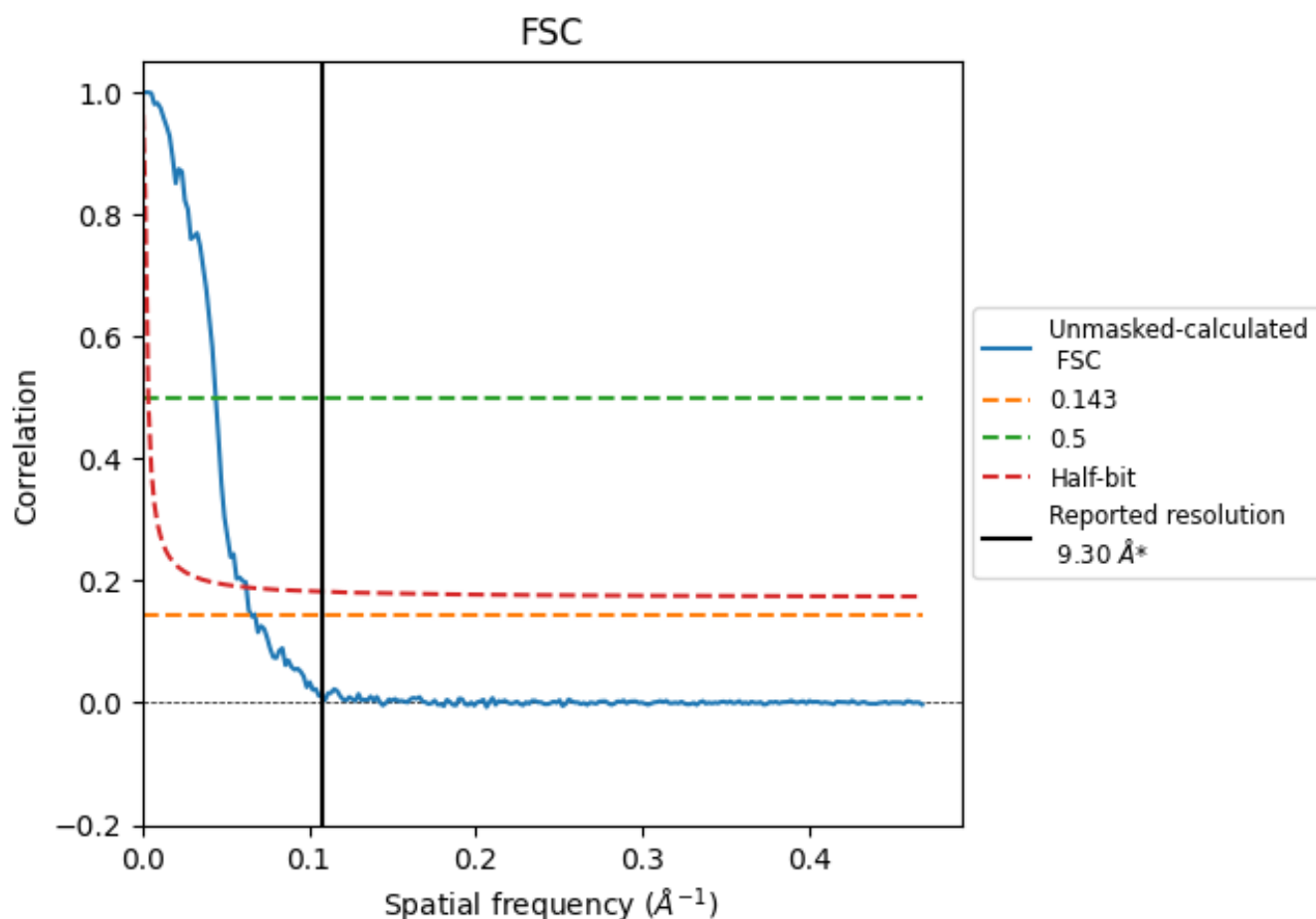


*Reported resolution corresponds to spatial frequency of 0.108 Å⁻¹

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 0.108 Å⁻¹

8.2 Resolution estimates [i](#)

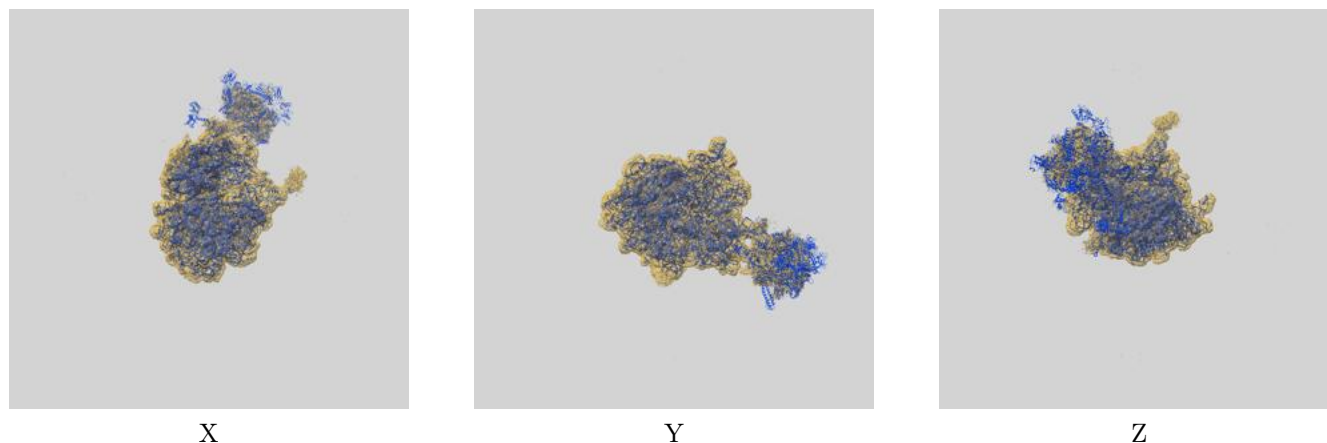
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	15.29	22.68	16.00

*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 15.29 differs from the reported value 9.3 by more than 10 %

9 Map-model fit [i](#)

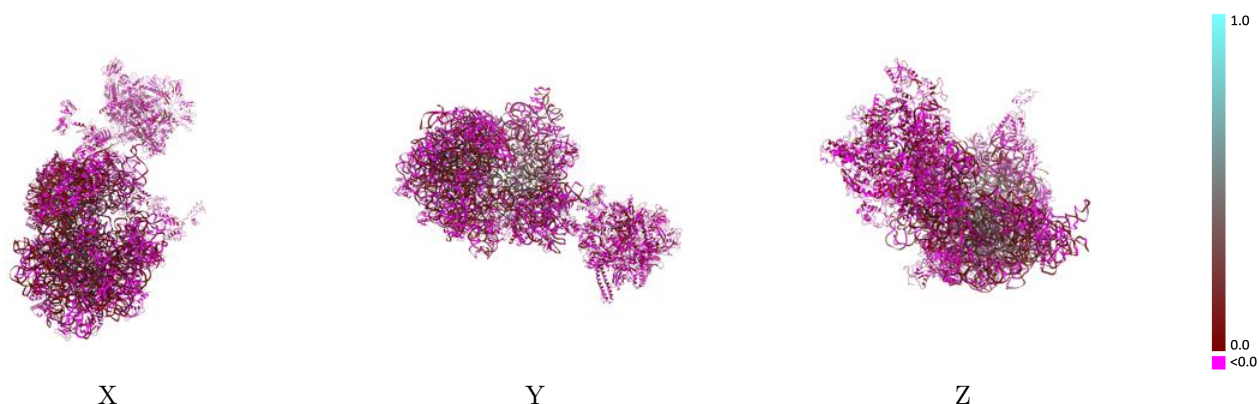
This section contains information regarding the fit between EMDB map EMD-43389 and PDB model 8VOQ. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



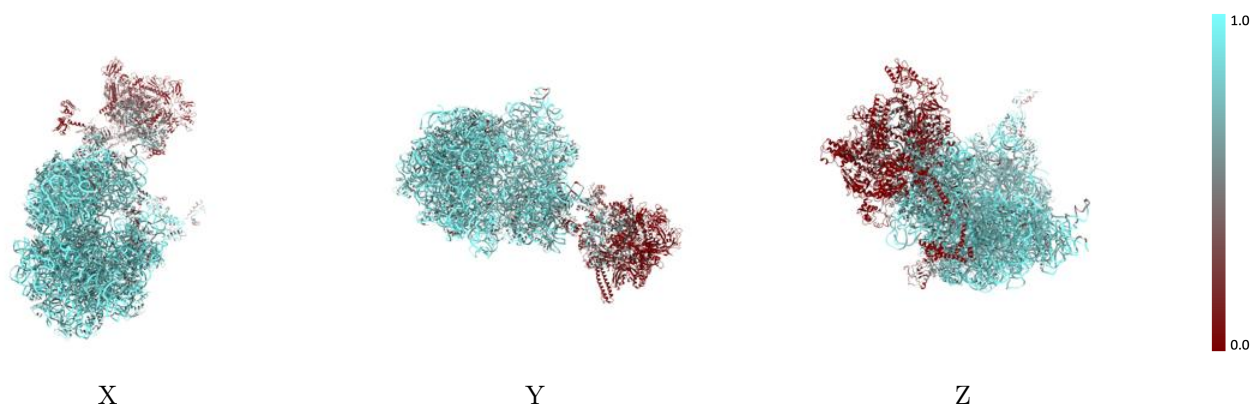
The images above show the 3D surface view of the map at the recommended contour level 1e-08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



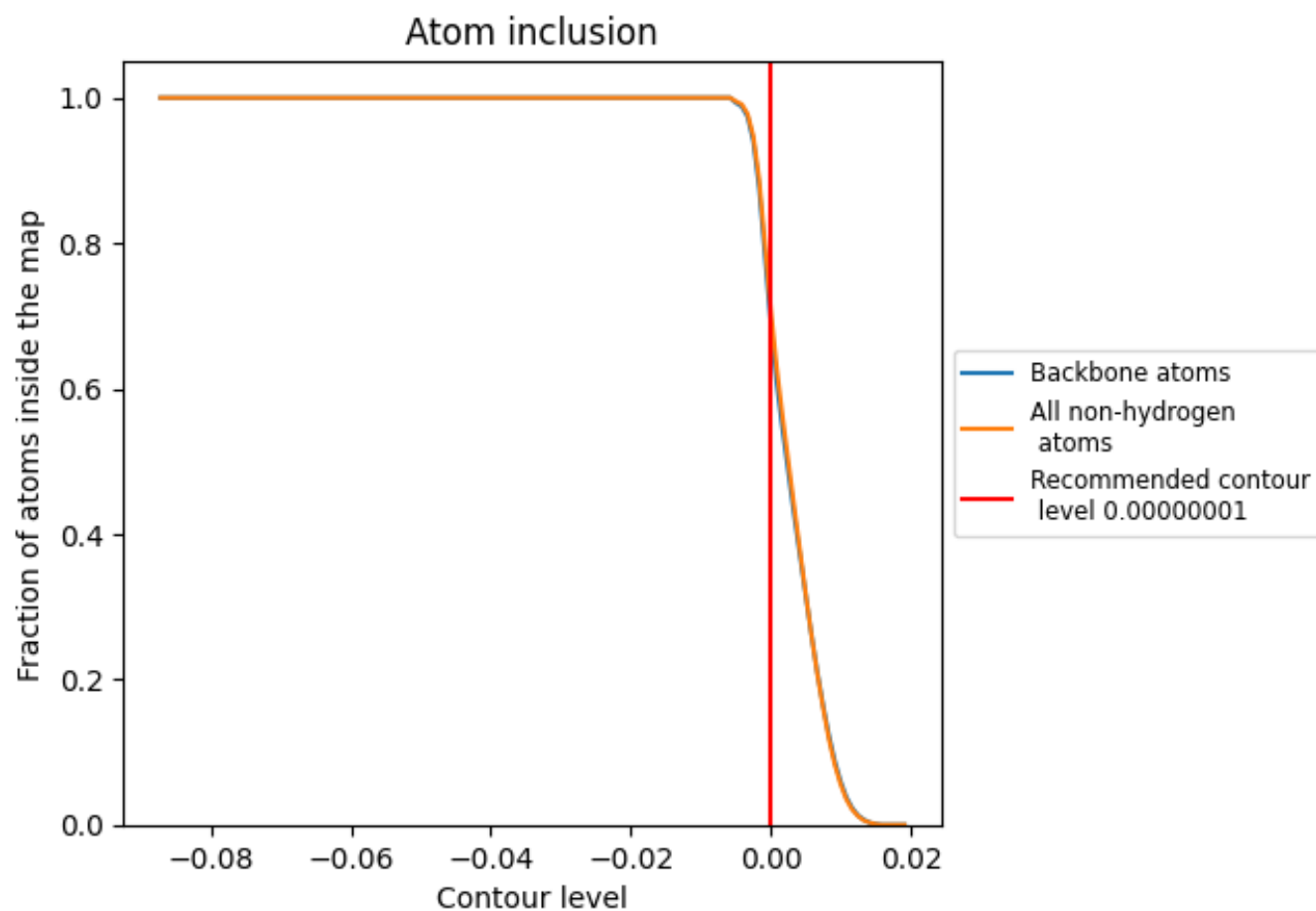
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00000001).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 71% 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 (0.00000001) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7130	 0.0660
0	 0.7800	 -0.0050
1	 0.7950	 0.0890
2	 0.7600	 0.0060
3	 0.7590	 -0.0180
4	 0.8010	 0.0100
5	 0.4810	 0.0270
6	 0.5200	 0.0900
7	 0.6290	 0.0360
9	 0.7290	 0.0280
A	 0.9080	 0.1450
AA	 0.1870	 0.0120
AB	 0.2910	 0.0040
AC	 0.0470	 0.0170
AD	 0.0180	 0.0030
AE	 0.2230	 0.0270
AF	 0.0850	 -0.0010
AG	 0.2670	 0.0110
B	 0.7860	 0.0440
C	 0.7500	 -0.0300
D	 0.9200	 0.1110
E	 0.7710	 -0.0030
F	 0.7620	 0.0940
G	 0.7050	 0.0130
H	 0.3570	 0.0270
I	 0.6560	 -0.0270
J	 0.7290	 -0.0090
K	 0.8240	 0.0540
L	 0.7740	 -0.0170
M	 0.7270	 0.0190
N	 0.8200	 0.0620
O	 0.7280	 0.0080
P	 0.6900	 0.0230
Q	 0.8080	 0.0610
R	 0.8480	 0.1640



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Chain	Atom inclusion	Q-score
S	 0.7570	 -0.0060
T	 0.8520	 0.1000
U	 0.7110	 -0.0450
V	 0.8320	 0.1160
W	 0.6520	 0.0040
X	 0.6680	 -0.0050
Y	 0.7090	 0.0130
Z	 0.5110	 0.0100
a	 0.9230	 0.1000
b	 0.7910	 -0.0090
c	 0.7600	 0.0530
d	 0.8820	 0.0440
e	 0.7440	 -0.0350
f	 0.8210	 0.0500
g	 0.7360	 0.0080
h	 0.8060	 0.0760
i	 0.8180	 0.0630
j	 0.7800	 0.0040
k	 0.7560	 0.0090
l	 0.7680	 0.0300
m	 0.8870	 0.1910
n	 0.7520	 0.0110
o	 0.7560	 -0.0020
p	 0.7250	 -0.0280
q	 0.7160	 -0.0490
r	 0.5470	 0.0070
s	 0.7500	 -0.0260
t	 0.7680	 0.0450
u	 0.7750	 0.0130
v	 0.7970	 0.0410
w	 0.8170	 0.0340
x	 0.7600	 0.0000
y	 0.7160	 0.0020
z	 0.7810	 0.0060