



wwPDB EM Validation Summary Report ⓘ

Nov 3, 2024 – 07:08 AM EST

PDB ID : 6XDR
EMDB ID : EMD-22142
Title : Escherichia coli transcription-translation complex B (TTC-B) containing an
27 nt long mRNA spacer, NusG, and fMet-tRNAs at E-site and P-site
Authors : Molodtsov, V.; Wang, C.; Su, M.; Ebright, R.H.
Deposited on : 2020-06-11
Resolution : 4.70 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

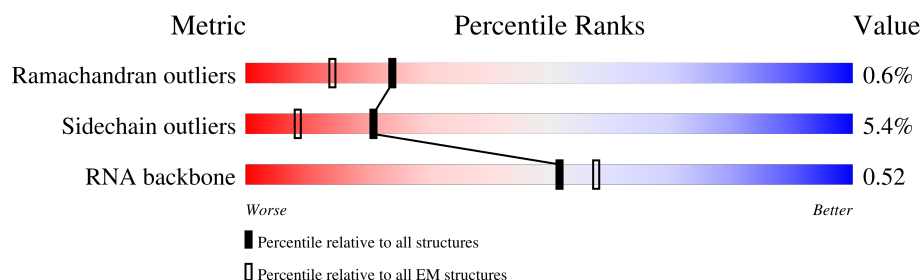
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

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 4.70 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
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	
2	1	110	
3	2	100	
4	3	104	
5	4	94	
6	5	36	
7	6	36	
8	7	44	

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Mol	Chain	Length	Quality of chain
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	C	75	
17	D	1542	
18	E	87	
19	F	71	
20	G	241	
21	H	557	
22	I	233	
23	J	206	
24	K	167	
25	L	135	
26	M	179	
27	N	130	
28	O	130	
29	P	103	
30	Q	129	
31	R	124	

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Mol	Chain	Length	Quality of chain
32	S	101	
33	T	89	
34	U	82	
35	V	84	
36	W	92	
37	X	118	
38	Y	142	
39	Z	121	
40	a	2904	
41	b	85	
42	c	78	
43	d	120	
44	e	63	
45	f	59	
46	g	70	
47	h	273	
48	i	57	
49	j	209	
50	k	55	
51	l	201	
52	m	46	
53	n	179	
54	o	65	
55	p	177	
56	q	38	

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Mol	Chain	Length	Quality of chain
57	r	149	
58	s	142	
59	t	123	
60	u	144	
61	v	136	
62	w	127	
63	x	117	
64	y	115	
65	z	118	

2 Entry composition

There are 67 unique types of molecules in this entry. The entry contains 276506 atoms, of which 99294 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein 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 27 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	34	Total	C	H	N	O	P	0	0
			804	316	97	98	259	34		

- 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
			2433	723	813	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	175	Total	C	N	O	S	0	0
			1392	881	249	255	7		

- 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	218	Total	C	N	O	S	0	0
			1677	1048	297	326	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		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	1384	VAL	MET	conflict	UNP A0A4S1NBU2

- 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 30S ribosomal protein S18.

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

- Molecule 17 is a RNA chain called 16S rRNA.

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

- Molecule 18 is a protein called 30S ribosomal protein S20.

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

- Molecule 19 is a protein called 30S ribosomal protein S21.

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

- Molecule 20 is a protein called 30S ribosomal protein S2.

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

- Molecule 21 is a protein called 30S ribosomal protein S1.

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

- Molecule 22 is a protein called 30S ribosomal protein S3.

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

- Molecule 23 is a protein called 30S ribosomal protein S4.

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

- Molecule 24 is a protein called 30S ribosomal protein S5.

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

- Molecule 25 is a protein called 30S ribosomal protein S6.

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

- Molecule 26 is a protein called 30S ribosomal protein S7.

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

- Molecule 27 is a protein called 30S ribosomal protein S8.

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

- Molecule 28 is a protein called 30S ribosomal protein S9.

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

- Molecule 29 is a protein called 30S ribosomal protein S10.

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

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

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

- Molecule 31 is a protein called 30S ribosomal protein S12.

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

- Molecule 32 is a protein called 30S ribosomal protein S14.

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

- Molecule 33 is a protein called 30S ribosomal protein S15.

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

- Molecule 34 is a protein called 30S ribosomal protein S16.

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

- Molecule 35 is a protein called 30S ribosomal protein S17.

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

- Molecule 36 is a protein called 30S ribosomal protein S19.

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

- Molecule 37 is a protein called 30S ribosomal protein S13.

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

- Molecule 38 is a protein called 50S ribosomal protein L11.

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

- Molecule 39 is a protein called 50S ribosomal protein L7/L12.

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

- Molecule 40 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	a	2880	Total	C	H	N	O	P	0	0
			92912	27587	31071	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 41 is a protein called 50S ribosomal protein L27.

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

- Molecule 42 is a protein called 50S ribosomal protein L28.

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

- Molecule 43 is a RNA chain called 5S rRNA.

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

- Molecule 44 is a protein called 50S ribosomal protein L29.

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

- Molecule 45 is a protein called 50S ribosomal protein L30.

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

- Molecule 46 is a protein called 50S ribosomal protein L31.

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

- Molecule 47 is a protein called 50S ribosomal protein L2.

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

- Molecule 48 is a protein called 50S ribosomal protein L32.

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

- Molecule 49 is a protein called 50S ribosomal protein L3.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L4.

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

- Molecule 52 is a protein called 50S ribosomal protein L34.

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

- Molecule 53 is a protein called 50S ribosomal protein L5.

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

- Molecule 54 is a protein called 50S ribosomal protein L35.

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

- Molecule 55 is a protein called 50S ribosomal protein L6.

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

- Molecule 56 is a protein called 50S ribosomal protein L36.

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

- Molecule 57 is a protein called 50S ribosomal protein L9.

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

- Molecule 58 is a protein called 50S ribosomal protein L13.

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

- Molecule 59 is a protein called 50S ribosomal protein L14.

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

- Molecule 60 is a protein called 50S ribosomal protein L15.

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

- Molecule 61 is a protein called 50S ribosomal protein L16.

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

- Molecule 62 is a protein called 50S ribosomal protein L17.

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

- Molecule 63 is a protein called 50S ribosomal protein L18.

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

- Molecule 64 is a protein called 50S ribosomal protein L19.

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

- Molecule 65 is a protein called 50S ribosomal protein L20.

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

- Molecule 66 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
66	7	1	Total	Mg	0
			1	1	

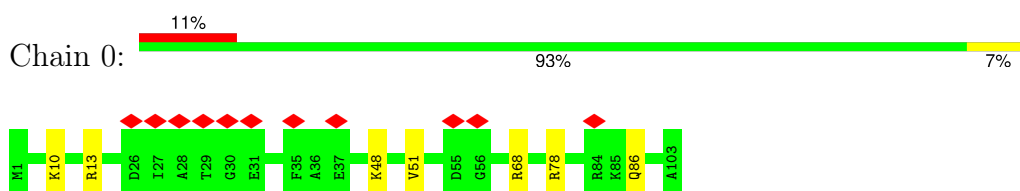
- Molecule 67 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

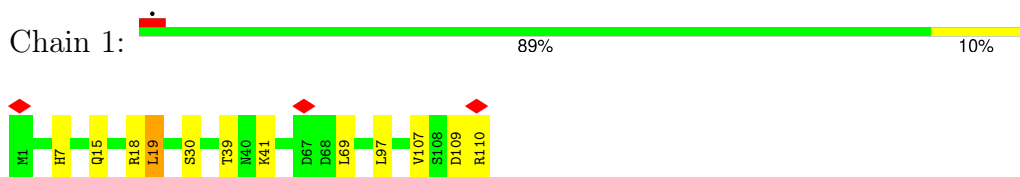
3 Residue-property plots [i](#)

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.

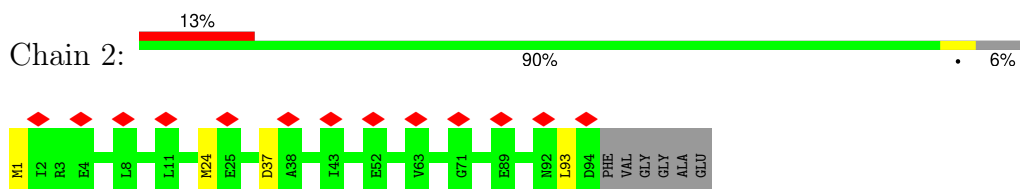
- Molecule 1: 50S ribosomal protein L21



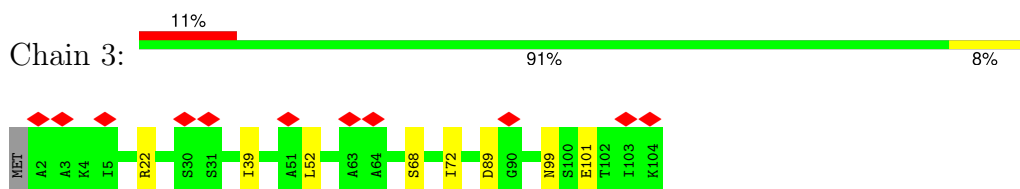
- Molecule 2: 50S ribosomal protein L22



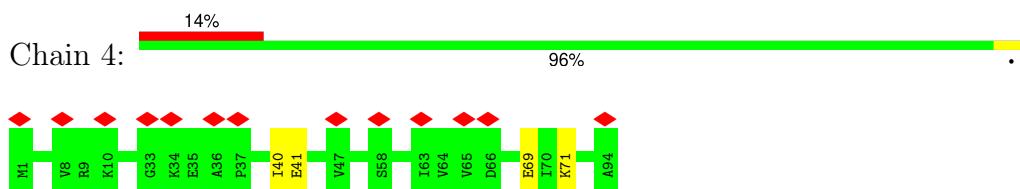
- Molecule 3: 50S ribosomal protein L23



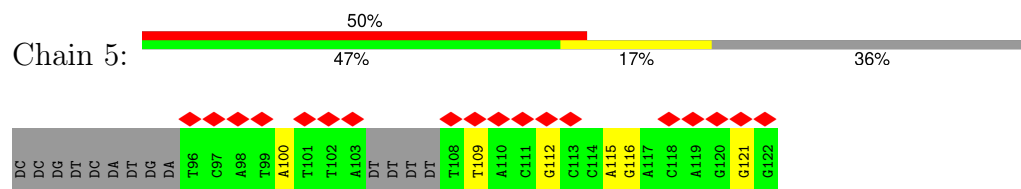
- Molecule 4: 50S ribosomal protein L24



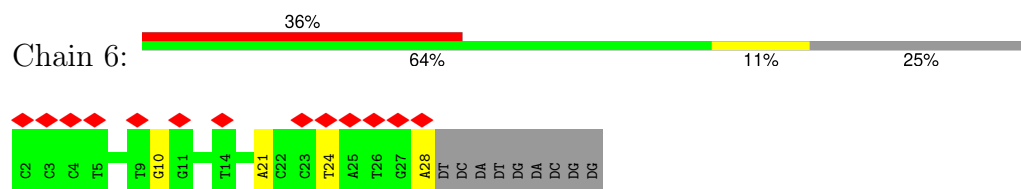
- Molecule 5: 50S ribosomal protein L25



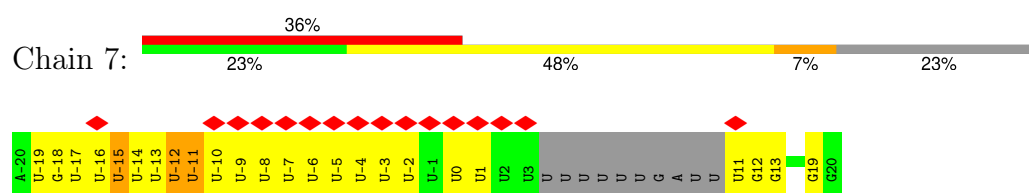
- Molecule 6: NT DNA



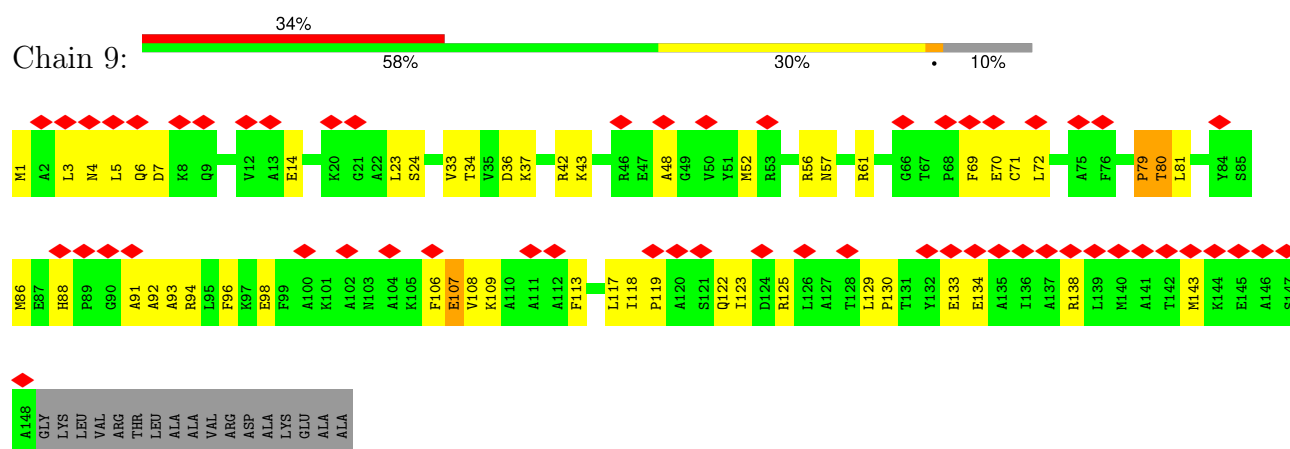
- Molecule 7: T DNA



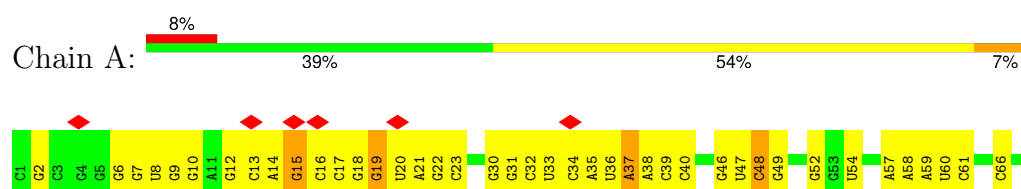
- Molecule 8: mRNA with 27 nt long spacer



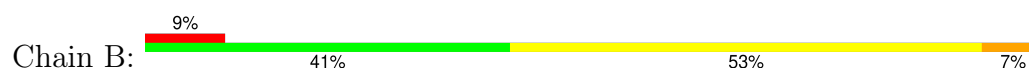
- Molecule 9: 50S ribosomal protein L10



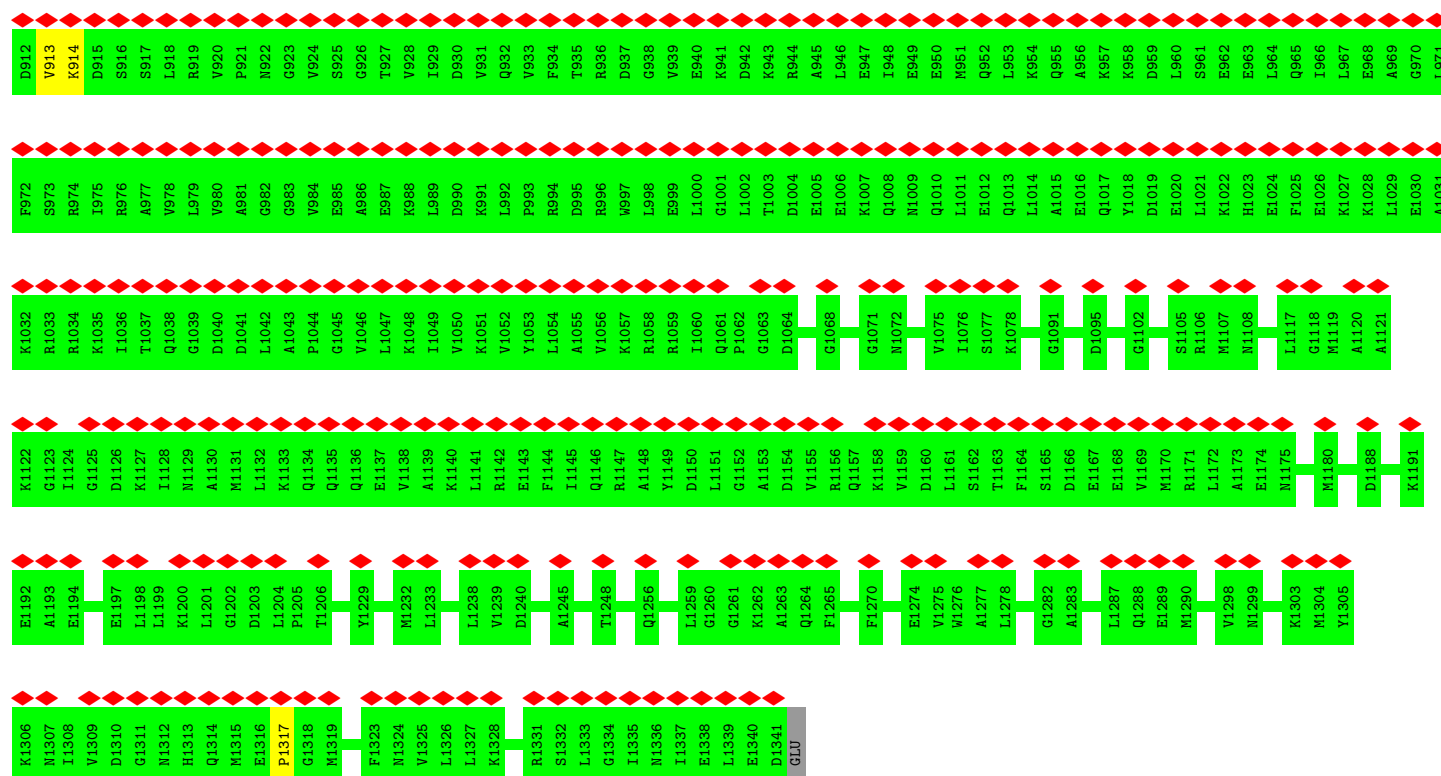
- Molecule 10: E-site and P-site tRNA (fMet)



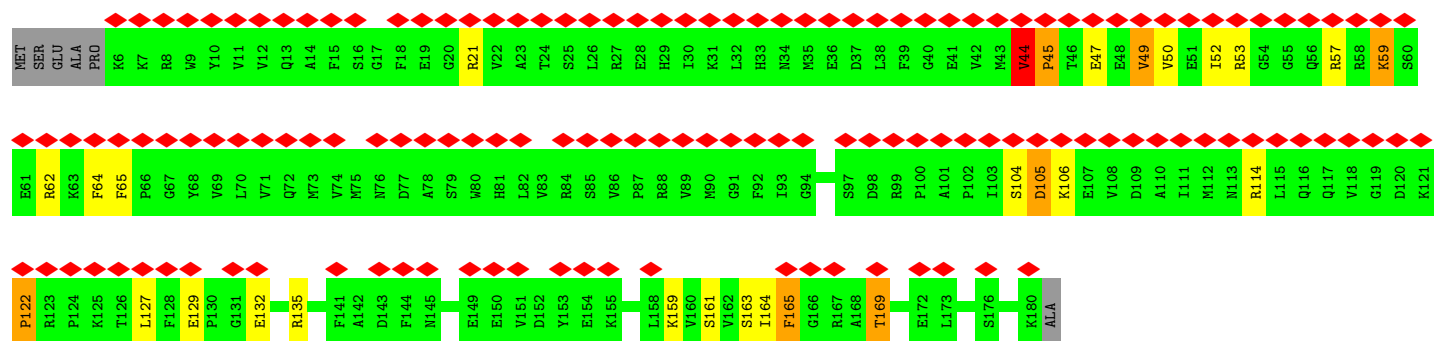
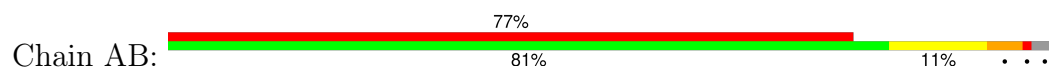
- Molecule 10: E-site and P-site tRNA (fMet)



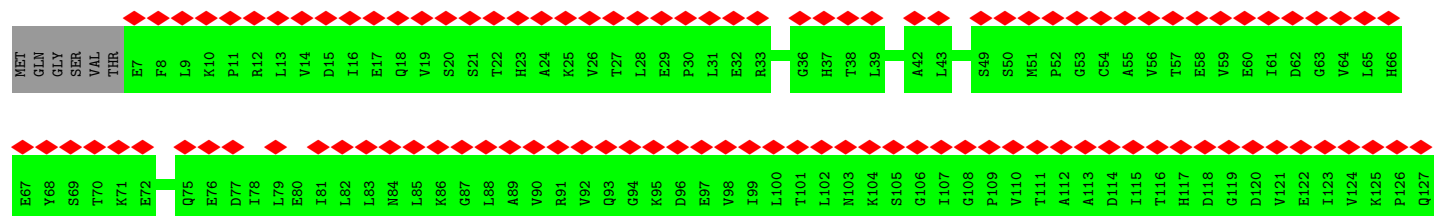


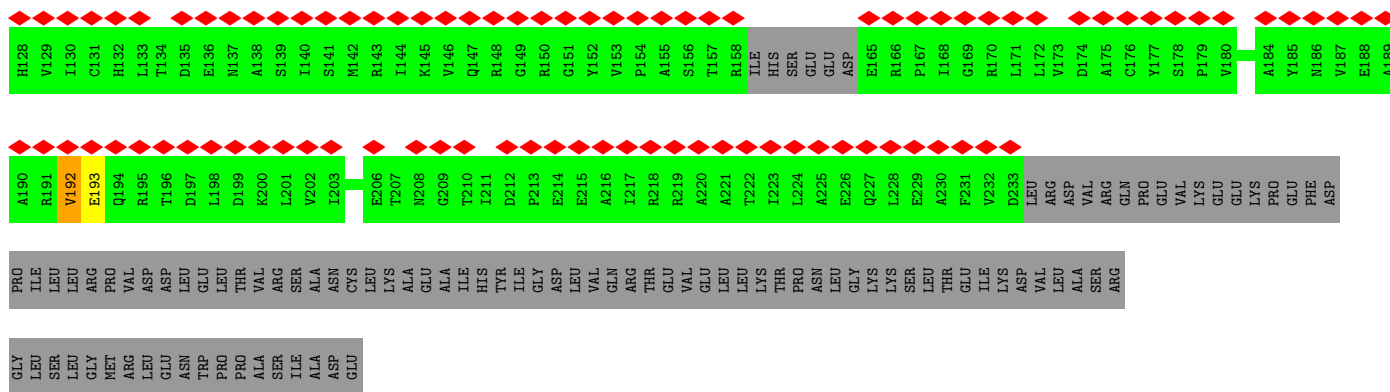


• Molecule 12: Transcription termination/antitermination protein NusG

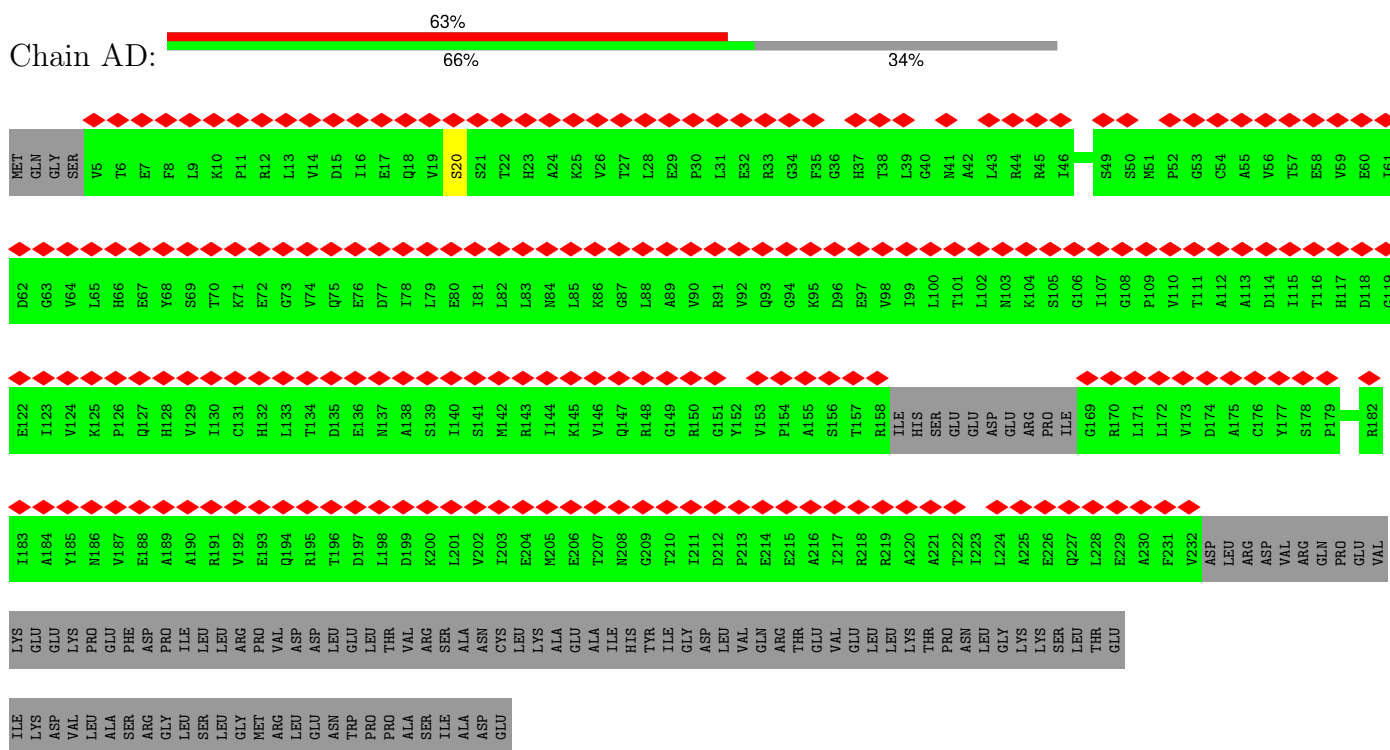


• Molecule 13: DNA-directed RNA polymerase subunit alpha

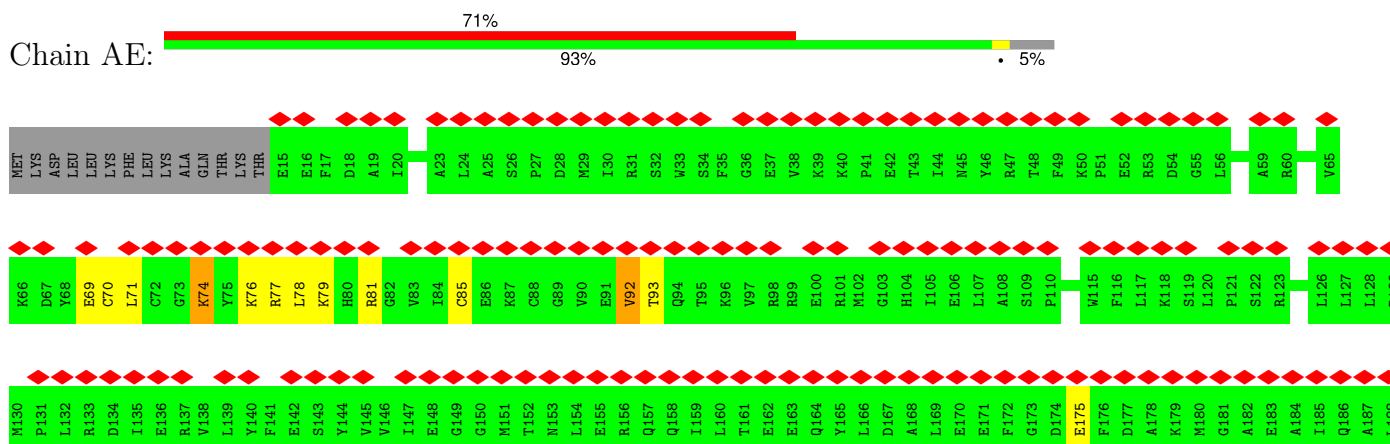




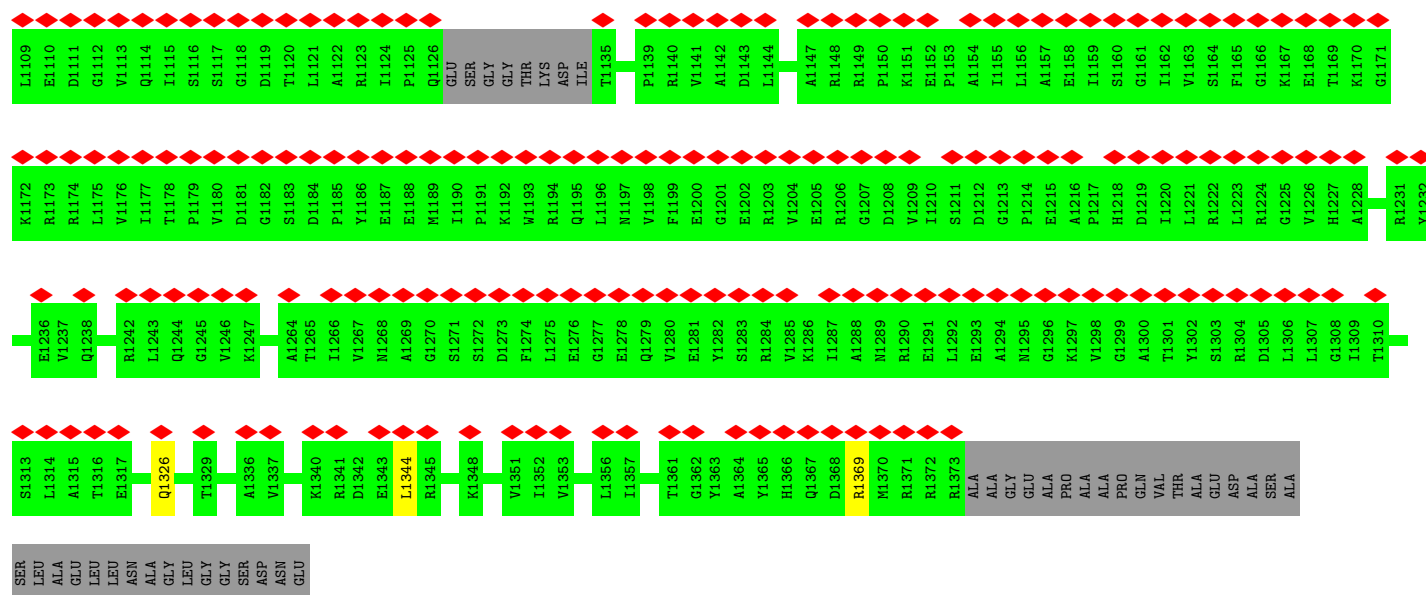
• Molecule 13: DNA-directed RNA polymerase subunit alpha



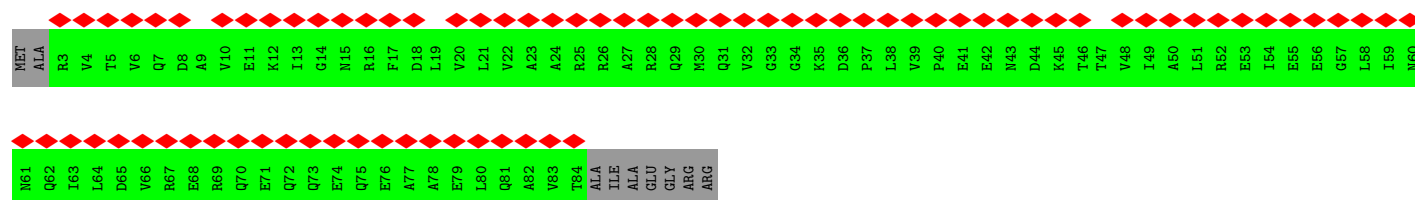
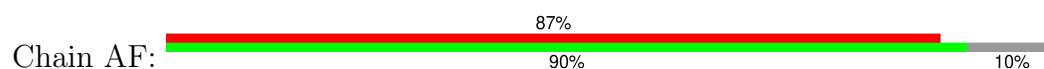
• Molecule 14: DNA-directed RNA polymerase subunit beta'



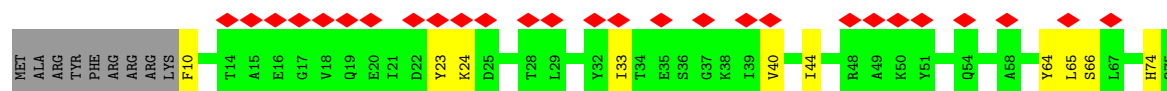
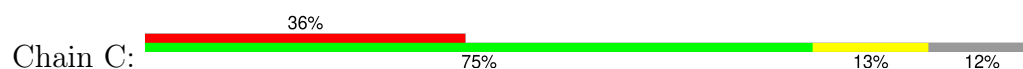
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D1051	T991	T931	W858	T786	E704	E705	D558	A482	R403	K325	L255	M192
E1052	K992	R932	P859	A787	T705	T706	A559	L483	E404	S326	D256	D193
L1053	E993	R933	R860	L788	T706	T707	N560	M484	E405	L327	G257	L194
T1054	S994	R933	N861	K789	T707	M708	G561	M485	A406	A328	G258	E195
G1055	Y995	THR	T862	A791	R708	N709	E562	A486	V407	D329	G258	E195
L1056	K996	PHE	L863	N792	R709	D710	L563	T487	V408	K330	R259	Q196
S1057	V997	ILE	L864		D710	G711	V564	N488	V409	I331	F260	E197
P998	Y999	GLY	H865	L796	G711	Q712	A565	T487	D410	K332	S263	C198
L1059	ALA	GLY	E866	T797	Q712	E713	E565	N489	I411	G333	D264	E199
V1060	SER	ALA	Q867	R798	E713	E714	K566	I490	L412	K334		Q200
A1001	ARG	ALA	W868		E714	K715	S568	L491	D413	Q335	D267	L201
V1002	ALA	ALA	C869	D802	K715	Q716	E556	S492	E414		L268	R202
L1063	ALA	GLU	D870		Q716	V717	A657	E497	V415	F338	Y269	E203
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A1065	S948		L872	V809			A577	P498	R417	G344	R271	N206
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G1006	R949		E874	E811			W580	I500	H419	S353	N274	E207
D1007	L1067		N875	D812	Y723			V501	P420	G358	R275	T208
G1008	Q951		S876	D813				P502	V421		N277	N209
E1009	V952		V877	C814	G732		V583	S503		P359		S210
Q1010	K953		D878	G815	S733		P584	Q504	R425	K280	K280	E211
V1011	N954		A879	T816	A734		K585	D505	A426	R281	R281	T212
A1012	K955		V880	H817	A735		G586	L510	P427	L282	L282	K213
G1013	Q956		V880	E818	Q736		E666	T514	T428	L383	L383	R214
G1014	S957		V880	G819	L737		Q667	R615	L429	D284	D284	K215
L1074	C888		C888	T820	R738		F668	D516	H430	L285	L285	K216
P1076	D889		D889	M821			Q669	C517	R431	K370	K370	L217
T1016	T890		T890	M822	R744		S670	V518		K371	A286	L218
V1017	S961		N891	T823	G745		G671	N519	Q435	M372	A287	K219
A1018	N962		F892	P824	L746		L672	A520	A436	A373	P288	R220
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W1020	K964		H897	I826	A748		T674	A520		E375	I290	I221
P1022	S965			E827	K749		A675	G522	V440	L376	I291	K222
H1023	V966		R901	G828	P750		G676	E523	L441	F377	V292	L223
T1024	V967		L903	G829	D751		E677	G524	I442	K377	R292	L224
Q1084	N968		A904	D830	G752		A600	M525	E443	P379	N294	E225
M1025	S969		R905	V831	G753		I601	V526	G444	F380	N294	A226
P1026	Q906		R905	K832	I754		S602	L527	K445	I381	E295	F227
V1027	S970		Q906	E833	T754		K603	L527	R446	Y382		V228
I1028	Q971		H907	P834	I755		K681	T528	Q448	G383	M298	Q229
K1029	K972		I908	L835	E756		L683	G529	L449	K384	L299	S230
E1030	L973		I909	R836	T757		L605	E529	H450	G384	A302	G231
V1031	N910		N910	D837	T758		T607	P530	P451	V303	A302	N232
S1032	K911		K911	D837	I759		C608	L536	L452	D304	A305	K233
G1033	G912		G912	R838	T760		Y609	L541	V453	L387	A305	P234
F1034	E913		E913	V839	G766		R610	A542	C454	R388	L306	E235
V1035	A914		A914	L840			I611	A542	A455	G389	G310	W236
R1036	I915		I915		F773		L612	A546	A456	L390	G310	M237
F1037	Q916		Q916	E946	I774		G613	R547	Y457	A391	R311	M237
A1097	T980		T980	D847	S775		V618	V548	M458	T392	R312	L238
T1038	E981		I918	V848	T776		L619	K549	A459	T393	G313	L239
D1039	L982		A919	L849	H777		Q623	V550	D460	I394	R314	T240
Y1099	K983				G778			R551		K395	A315	V241
M1040	L984		I923	P851	T778			I552	H469	A396		L242
L1101	L1041		Q924	G852	A779			T553	V470	A397	S319	P243
P1102	D1042		E925	G852	R780			E554	P471	N320		V244
G1103	G1043		P926	T853	K781					K321		L249
K1104	Q1044		Q927	A854	G782					R322		R250
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I1106	I1046											
V1107	R1048											



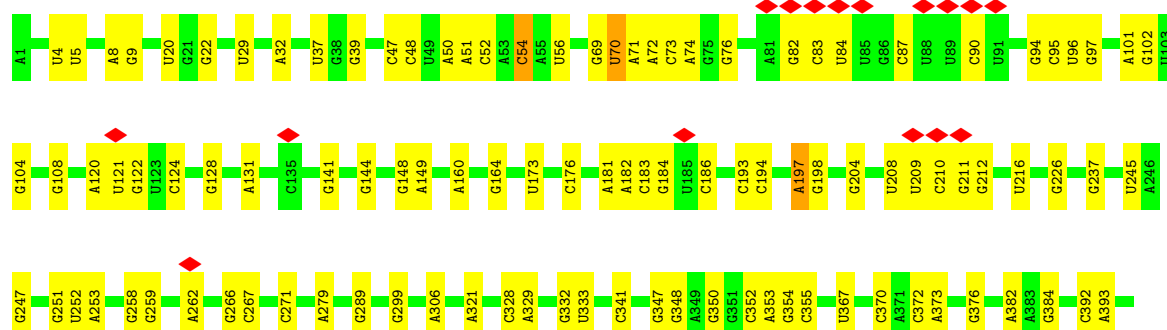
- Molecule 15: DNA-directed RNA polymerase subunit omega

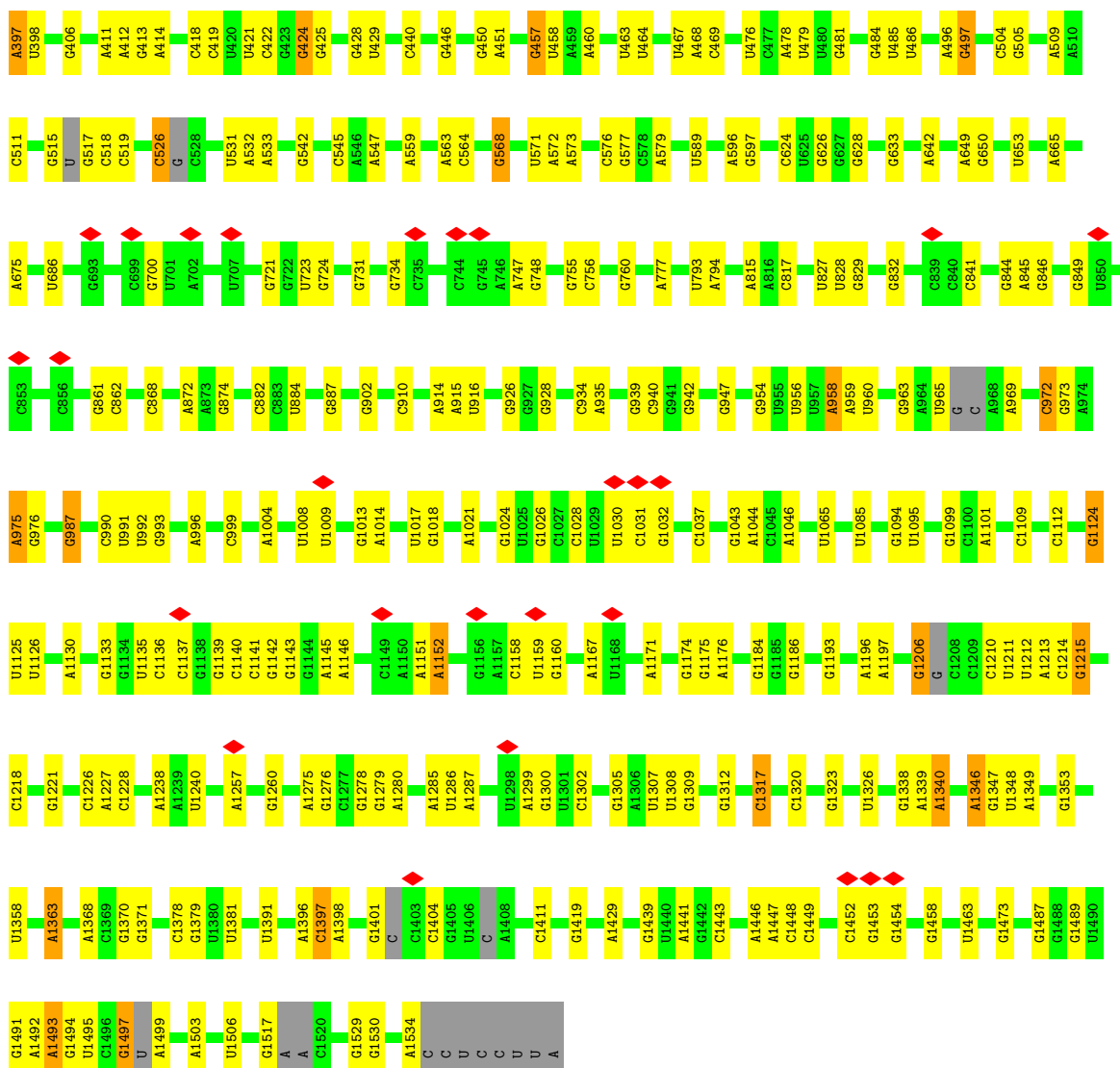


- Molecule 16: 30S ribosomal protein S18



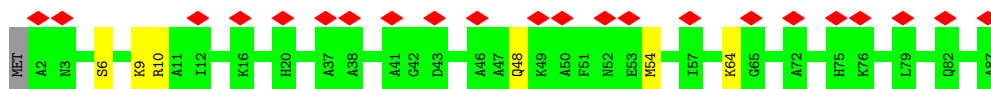
- Molecule 17: 16S rRNA





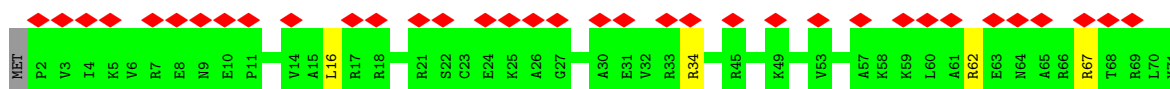
• Molecule 18: 30S ribosomal protein S20

Chain E: 25% 92% 7%

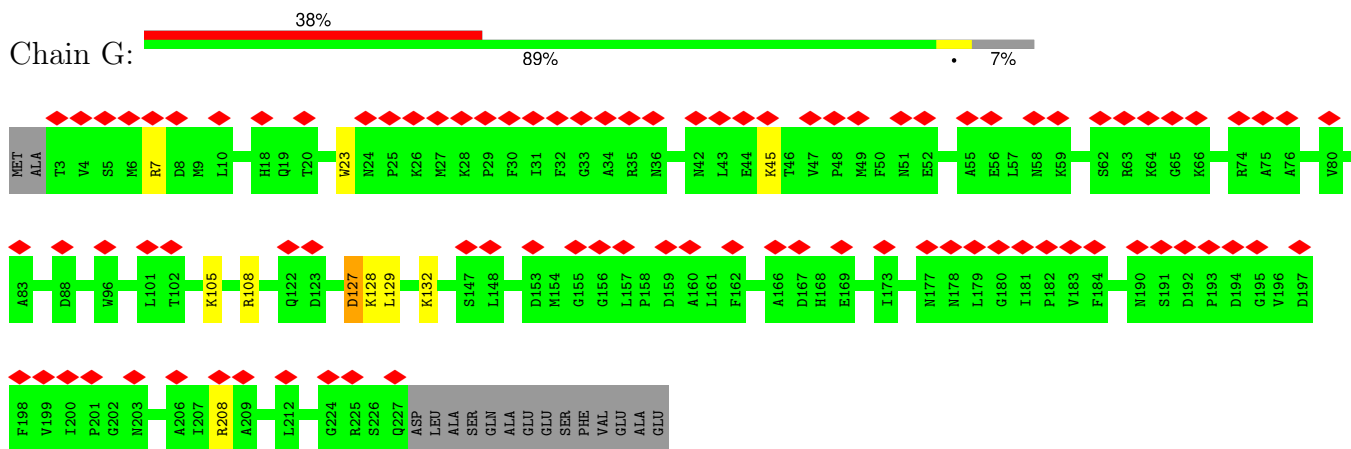


• Molecule 19: 30S ribosomal protein S21

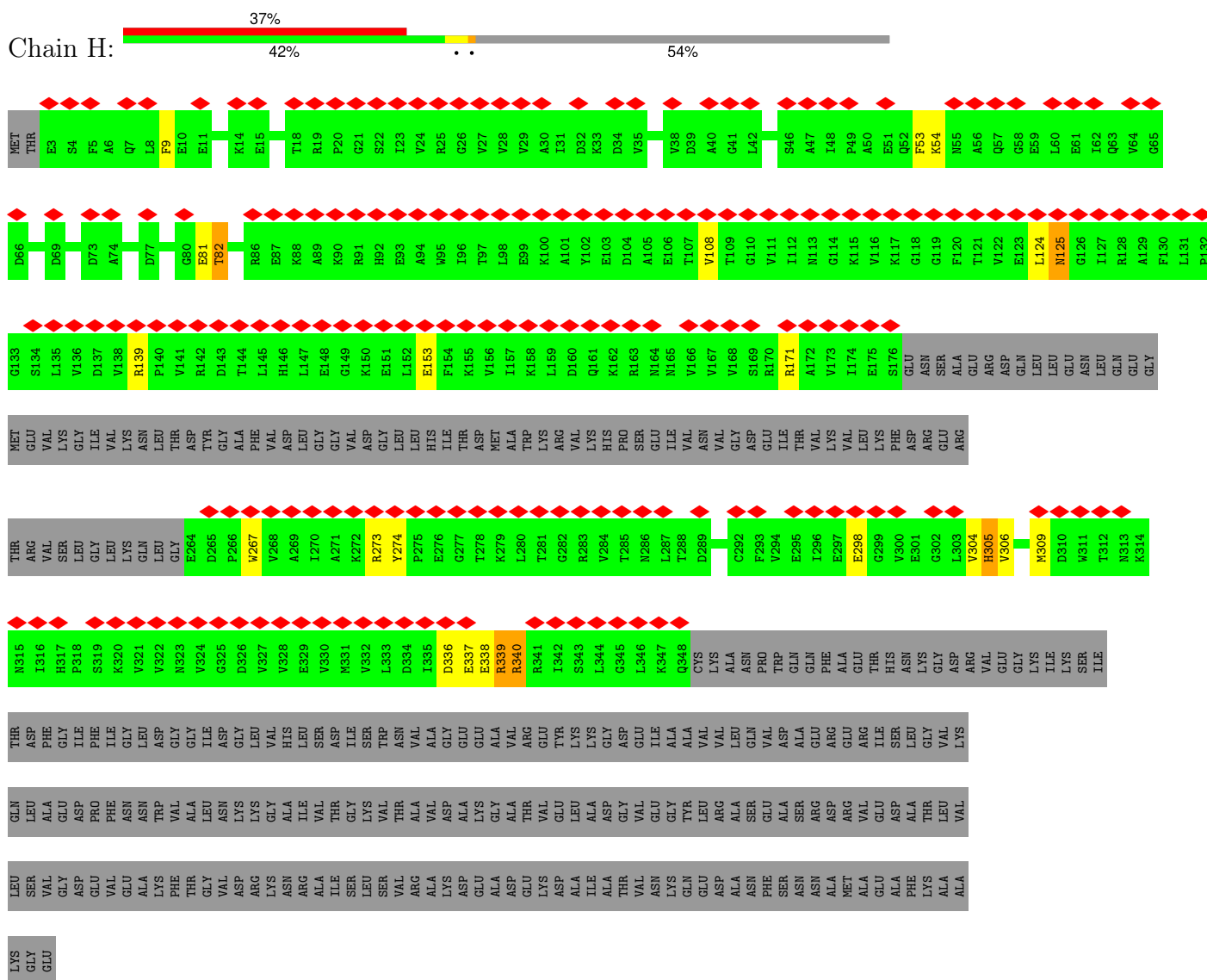
Chain F: 49% 93% 6%



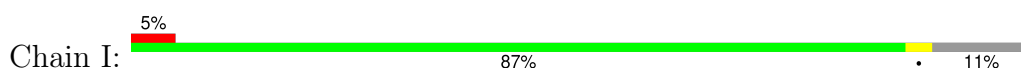
• Molecule 20: 30S ribosomal protein S2

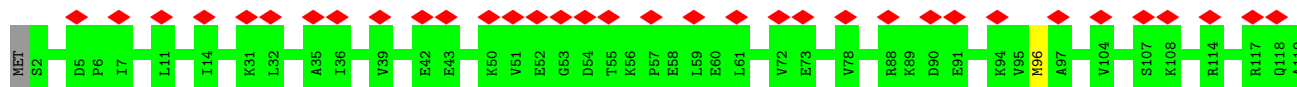


- Molecule 21: 30S ribosomal protein S1



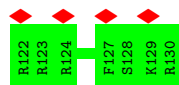
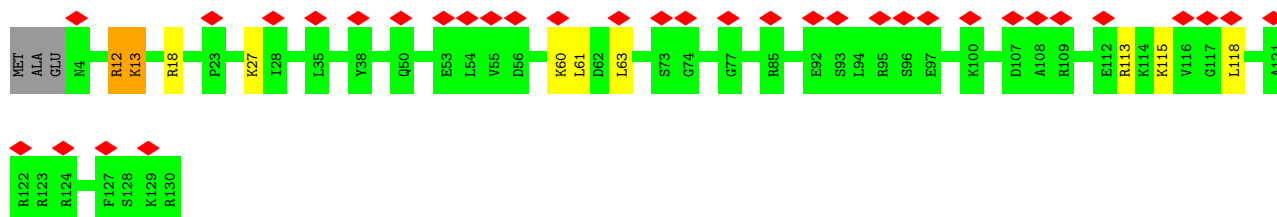
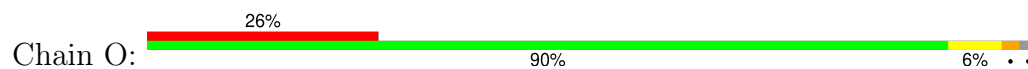
- Molecule 22: 30S ribosomal protein S3



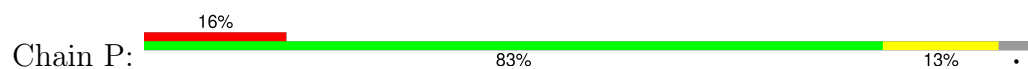




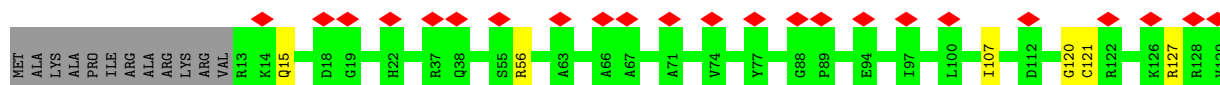
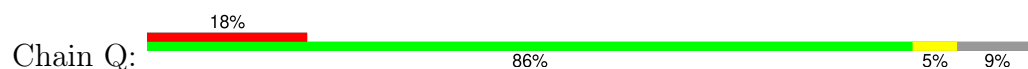
- Molecule 28: 30S ribosomal protein S9



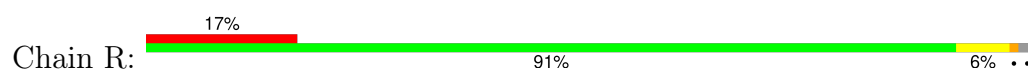
- Molecule 29: 30S ribosomal protein S10



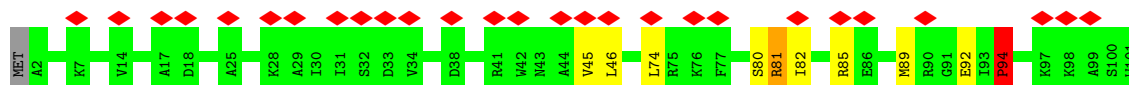
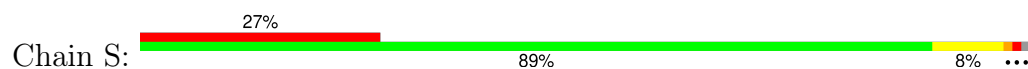
- Molecule 30: 30S ribosomal protein S11



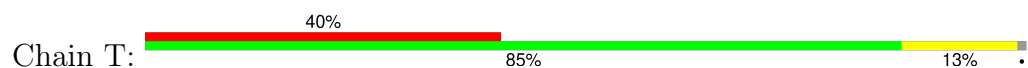
- Molecule 31: 30S ribosomal protein S12

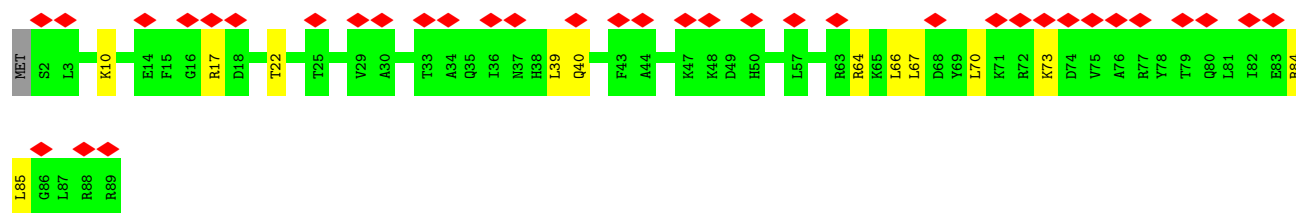


- Molecule 32: 30S ribosomal protein S14

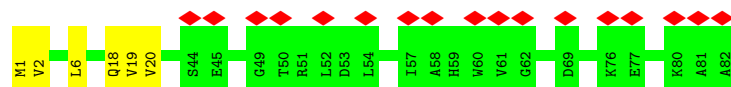
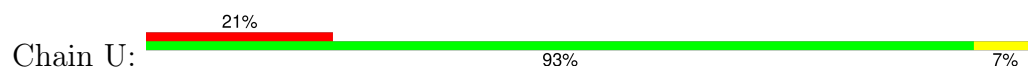


- Molecule 33: 30S ribosomal protein S15

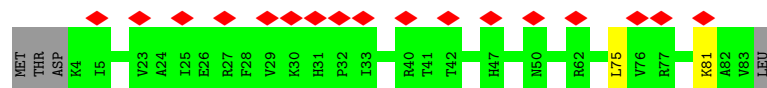




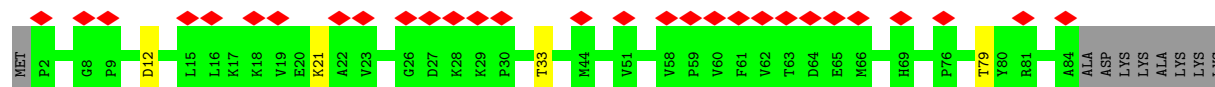
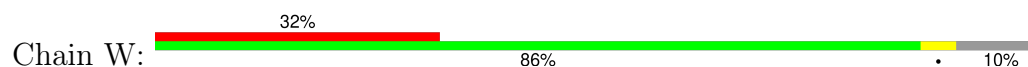
- Molecule 34: 30S ribosomal protein S16



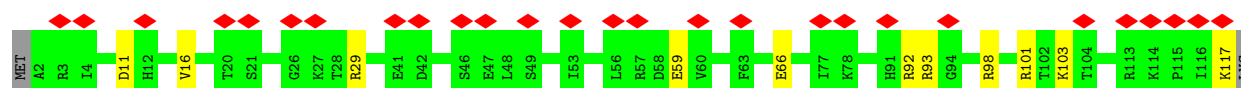
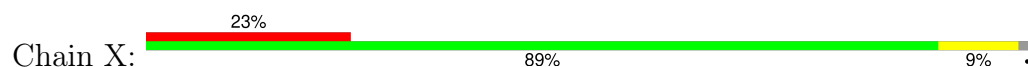
- Molecule 35: 30S ribosomal protein S17



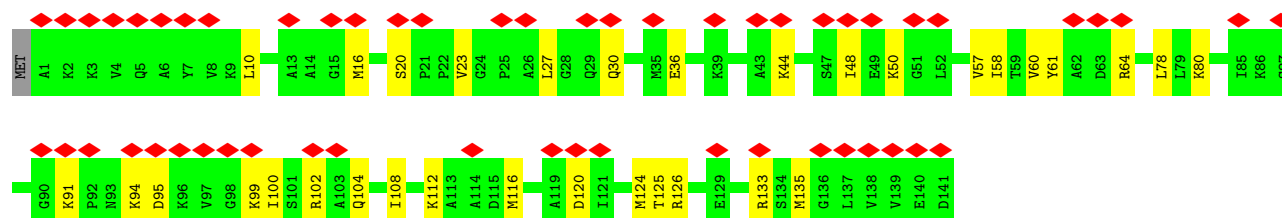
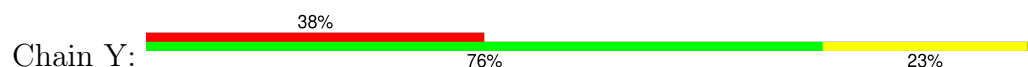
- Molecule 36: 30S ribosomal protein S19



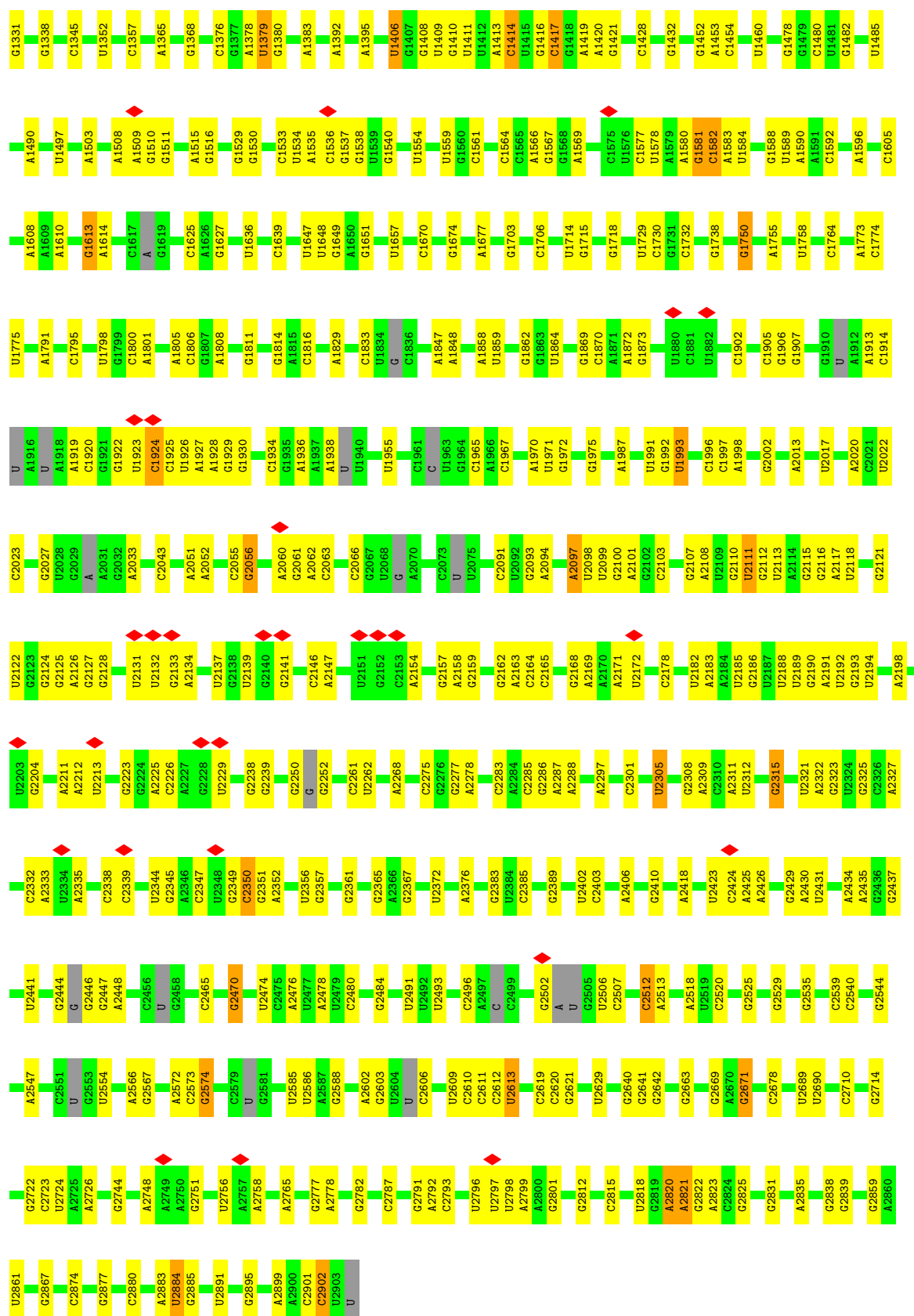
- Molecule 37: 30S ribosomal protein S13



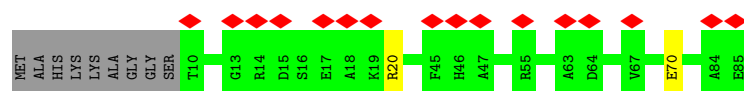
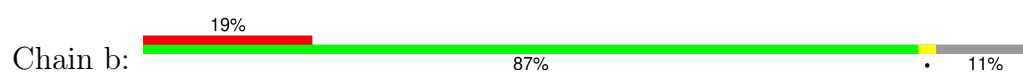
- Molecule 38: 50S ribosomal protein L11



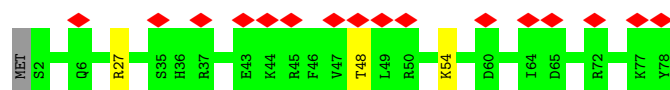
- Molecule 39: 50S ribosomal protein L7/L12



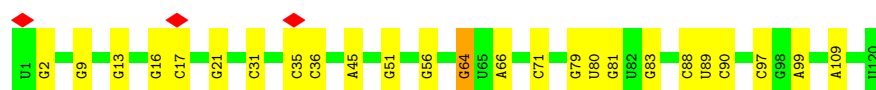
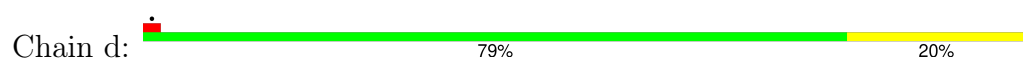
- Molecule 41: 50S ribosomal protein L27



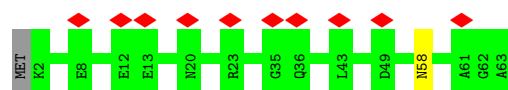
- Molecule 42: 50S ribosomal protein L28



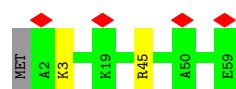
- Molecule 43: 5S rRNA



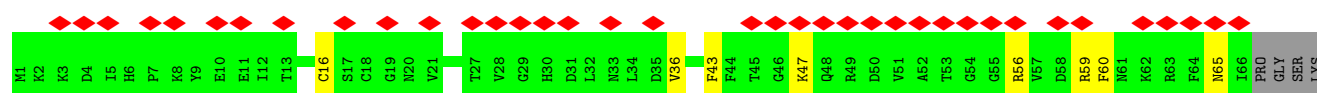
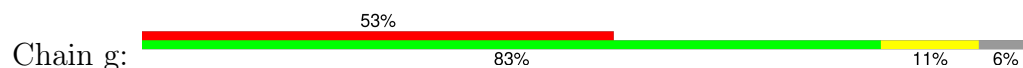
- Molecule 44: 50S ribosomal protein L29



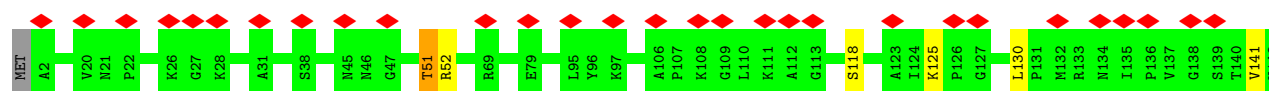
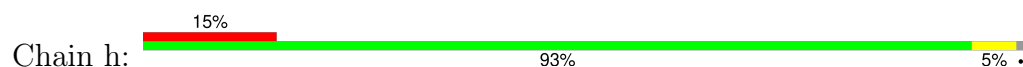
- Molecule 45: 50S ribosomal protein L30

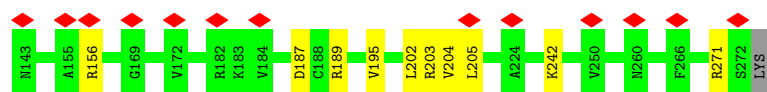


- Molecule 46: 50S ribosomal protein L31

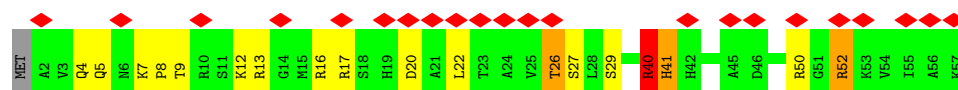
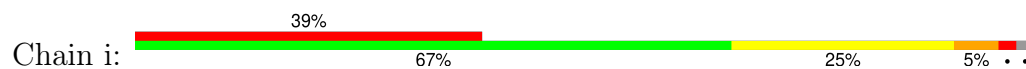


- Molecule 47: 50S ribosomal protein L2

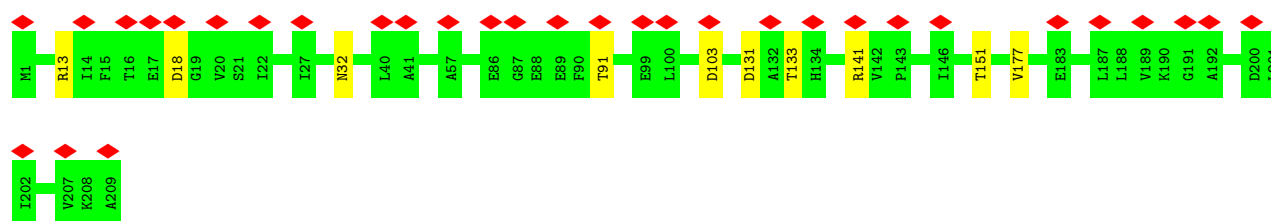




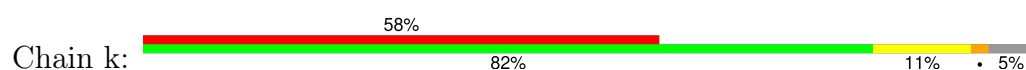
- Molecule 48: 50S ribosomal protein L32



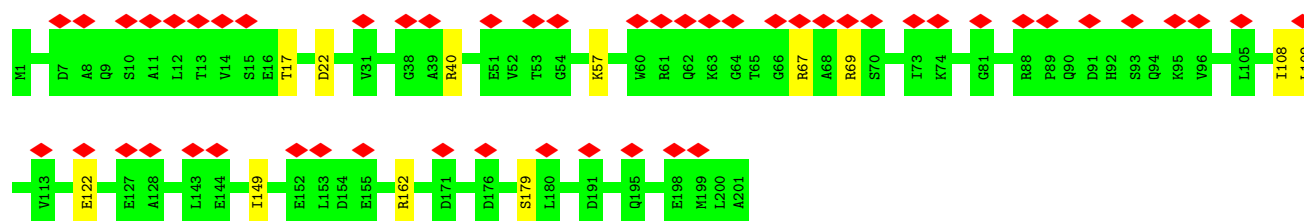
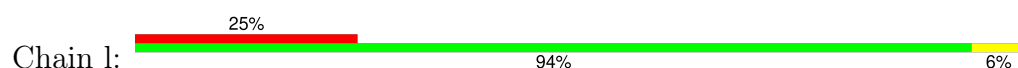
- Molecule 49: 50S ribosomal protein L3



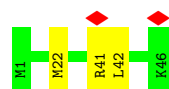
- Molecule 50: 50S ribosomal protein L33



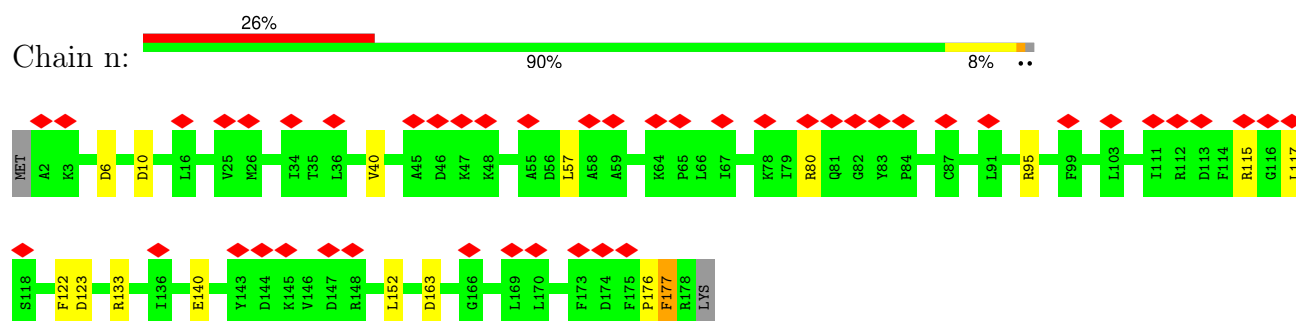
- Molecule 51: 50S ribosomal protein L4



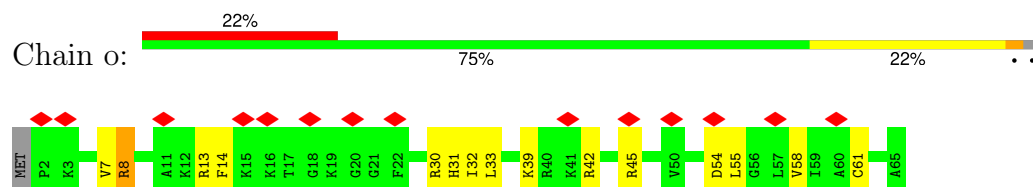
- Molecule 52: 50S ribosomal protein L34



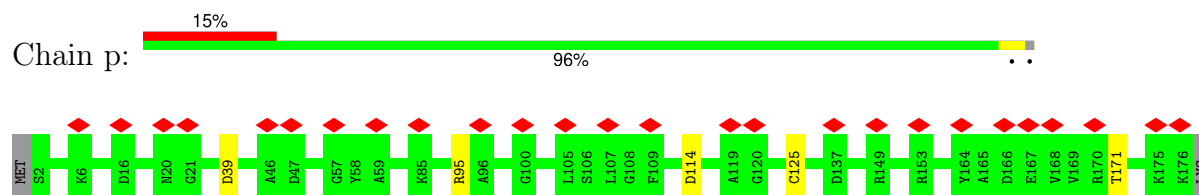
- Molecule 53: 50S ribosomal protein L5



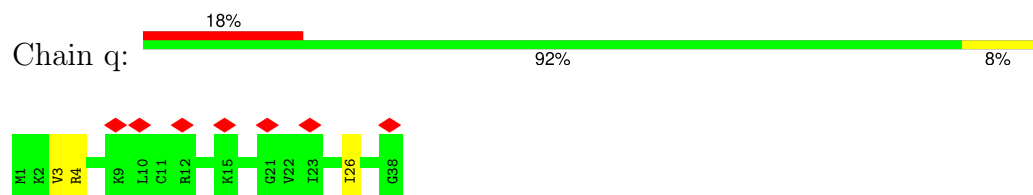
- Molecule 54: 50S ribosomal protein L35



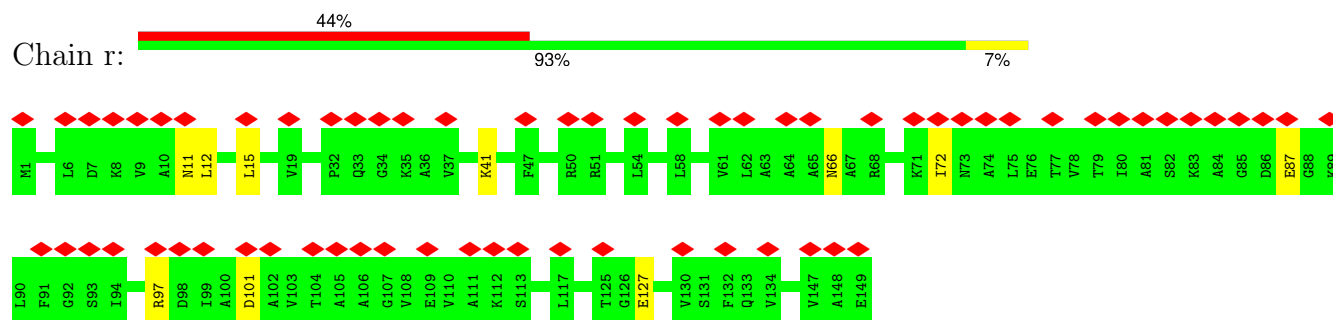
- Molecule 55: 50S ribosomal protein L6



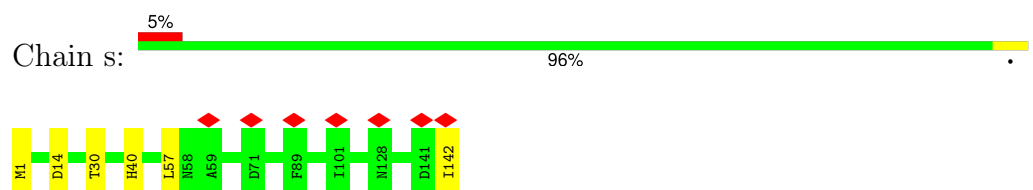
- Molecule 56: 50S ribosomal protein L36



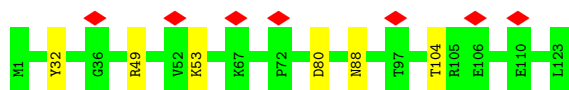
- Molecule 57: 50S ribosomal protein L9



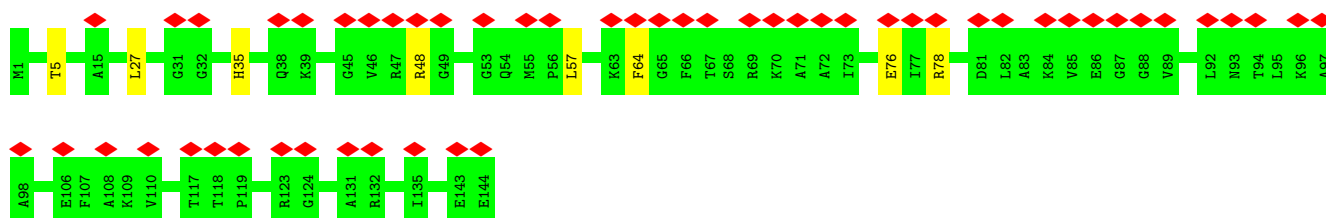
- Molecule 58: 50S ribosomal protein L13



- Molecule 59: 50S ribosomal protein L14



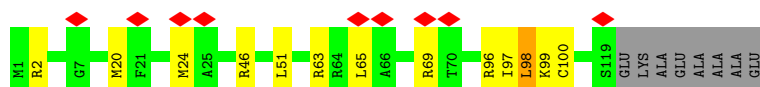
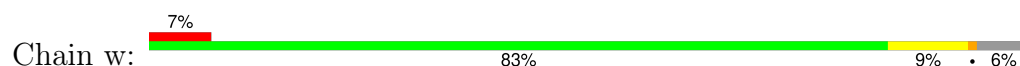
- Molecule 60: 50S ribosomal protein L15



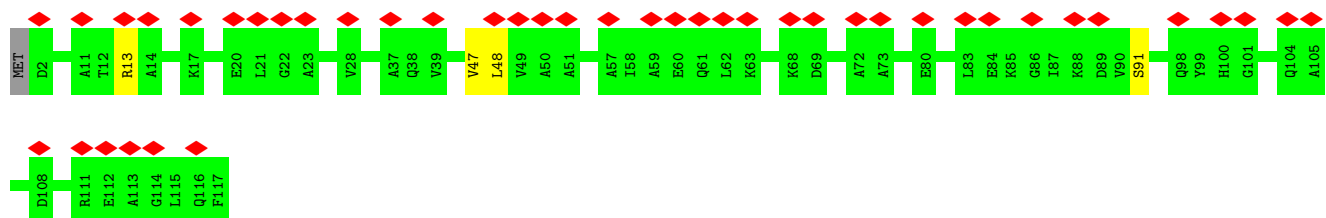
- Molecule 61: 50S ribosomal protein L16



- Molecule 62: 50S ribosomal protein L17

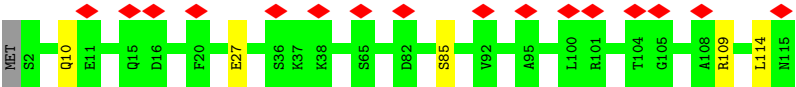


- Molecule 63: 50S ribosomal protein L18

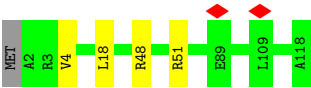


- Molecule 64: 50S ribosomal protein L19





• Molecule 65: 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	6121	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 ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.030	Depositor
Minimum map value	-0.046	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.00561	Depositor
Map size (Å)	532.48, 532.48, 532.48	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	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	0.44	0/829	0.77	1/1107 (0.1%)
2	1	0.75	2/864 (0.2%)	1.08	6/1156 (0.5%)
3	2	0.41	0/752	0.60	0/1005
4	3	0.35	0/796	0.66	2/1062 (0.2%)
5	4	0.34	0/766	0.53	0/1025
6	5	1.13	6/528 (1.1%)	0.97	1/810 (0.1%)
7	6	1.11	4/603 (0.7%)	0.97	0/926
8	7	0.66	2/783 (0.3%)	1.35	14/1212 (1.2%)
9	9	0.41	0/1131	0.72	1/1524 (0.1%)
10	A	2.15	45/1810 (2.5%)	3.07	88/2821 (3.1%)
10	B	2.15	46/1810 (2.5%)	3.07	89/2821 (3.2%)
11	AA	0.43	0/10736	0.60	1/14487 (0.0%)
12	AB	0.80	3/1421 (0.2%)	0.69	3/1914 (0.2%)
13	AC	0.41	0/1718	0.62	0/2328
13	AD	0.36	0/1696	0.62	0/2298
14	AE	0.41	0/10561	0.63	3/14258 (0.0%)
15	AF	0.33	0/652	0.57	0/879
16	C	1.66	10/553 (1.8%)	1.29	7/743 (0.9%)
17	D	0.71	47/36610 (0.1%)	1.28	300/57091 (0.5%)
18	E	0.64	1/675 (0.1%)	0.65	0/895
19	F	0.41	0/597	0.58	0/792
20	G	0.37	0/1791	0.54	0/2413
21	H	0.58	4/1746 (0.2%)	0.91	5/2382 (0.2%)
22	I	0.35	0/1663	0.54	0/2241
23	J	0.36	0/1665	0.54	1/2227 (0.0%)
24	K	0.82	6/1165 (0.5%)	0.82	7/1568 (0.4%)
25	L	0.70	2/867 (0.2%)	0.76	4/1171 (0.3%)
26	M	0.41	1/1195 (0.1%)	0.61	0/1602
27	N	0.37	0/989	0.55	0/1326
28	O	0.61	1/1034 (0.1%)	1.08	7/1375 (0.5%)
29	P	0.74	3/800 (0.4%)	0.98	8/1082 (0.7%)
30	Q	0.46	1/893 (0.1%)	0.67	4/1205 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	R	0.37	0/952	0.59	0/1274
32	S	0.56	0/817	1.00	6/1088 (0.6%)
33	T	0.42	0/722	0.60	0/964
34	U	0.36	0/659	0.61	0/884
35	V	0.35	0/657	0.54	0/881
36	W	0.38	0/680	0.63	0/915
37	X	0.49	1/909 (0.1%)	0.86	2/1215 (0.2%)
38	Y	0.30	0/1046	0.50	0/1410
39	Z	0.28	0/227	0.46	0/304
40	a	1.08	188/69247 (0.3%)	1.55	922/107985 (0.9%)
41	b	0.46	0/589	0.62	0/779
42	c	0.50	0/635	0.67	1/848 (0.1%)
43	d	0.67	4/2872 (0.1%)	1.13	21/4478 (0.5%)
44	e	0.39	0/502	0.57	0/667
45	f	0.37	0/452	0.58	0/605
46	g	0.48	0/531	0.61	1/709 (0.1%)
47	h	0.41	0/2121	0.62	1/2852 (0.0%)
48	i	1.93	18/450 (4.0%)	2.94	30/599 (5.0%)
49	j	0.53	1/1586 (0.1%)	0.67	3/2134 (0.1%)
50	k	0.59	1/433 (0.2%)	0.88	2/576 (0.3%)
51	l	0.46	0/1571	0.62	2/2113 (0.1%)
52	m	0.53	0/380	0.99	0/498
53	n	0.44	0/1434	0.70	1/1926 (0.1%)
54	o	1.11	8/513 (1.6%)	1.08	6/676 (0.9%)
55	p	0.31	0/1333	0.55	0/1805
56	q	0.46	0/303	0.76	2/397 (0.5%)
57	r	0.32	0/1122	0.55	0/1515
58	s	0.42	0/1152	0.57	0/1551
59	t	0.38	0/955	0.61	0/1279
60	u	0.52	0/1062	0.72	2/1413 (0.1%)
61	v	0.42	0/1093	0.65	0/1460
62	w	0.82	4/964 (0.4%)	1.54	15/1289 (1.2%)
63	x	0.36	0/902	0.58	0/1209
64	y	0.37	0/929	0.75	2/1242 (0.2%)
65	z	0.56	1/960 (0.1%)	0.73	2/1278 (0.2%)
All	All	0.85	410/190459 (0.2%)	1.29	1573/280564 (0.6%)

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
10	A	0	2
10	B	0	2
11	AA	0	1
12	AB	0	1
13	AC	0	1
13	AD	0	1
14	AE	0	4
17	D	0	1
21	H	0	5
24	K	0	2
26	M	0	1
28	O	0	1
31	R	0	1
40	a	0	3
48	i	0	1
50	k	0	1
53	n	0	1
60	u	0	1
62	w	0	1
All	All	0	34

The worst 5 of 410 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
40	a	1262	A	N1-C2	104.77	2.28	1.34
40	a	88	G	N9-C8	71.95	1.88	1.37
40	a	88	G	N7-C5	64.86	1.78	1.39
40	a	88	G	C8-N7	64.12	1.69	1.30
40	a	88	G	N9-C4	45.00	1.74	1.38

The worst 5 of 1573 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	a	336	C	N3-C2-O2	-87.70	60.51	121.90
40	a	789	A	C8-N9-C4	-73.67	76.33	105.80
40	a	1262	A	N9-C4-C5	69.03	133.41	105.80
40	a	1262	A	C8-N9-C4	-65.11	79.76	105.80
17	D	958	A	C5-C6-N1	62.10	148.75	117.70

There are no chirality outliers.

5 of 34 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	9	107	GLU	Peptide
9	9	79	PRO	Peptide
9	9	92	ALA	Peptide
10	A	37	A	Sidechain
10	A	76	A	Sidechain

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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%)	95 (94%)	6 (6%)	0	100	100
2	1	108/110 (98%)	105 (97%)	3 (3%)	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%)	91 (99%)	1 (1%)	0	100	100
9	9	146/165 (88%)	101 (69%)	33 (23%)	12 (8%)	1	10
11	AA	1338/1342 (100%)	1220 (91%)	114 (8%)	4 (0%)	37	72
12	AB	173/181 (96%)	137 (79%)	27 (16%)	9 (5%)	1	15
13	AC	217/329 (66%)	203 (94%)	12 (6%)	2 (1%)	14	51
13	AD	214/329 (65%)	198 (92%)	16 (8%)	0	100	100
14	AE	1331/1407 (95%)	1219 (92%)	109 (8%)	3 (0%)	44	78
15	AF	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
16	C	64/75 (85%)	62 (97%)	2 (3%)	0	100	100
18	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
19	F	68/71 (96%)	68 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	G	223/241 (92%)	212 (95%)	10 (4%)	1 (0%)	30	68
21	H	255/557 (46%)	192 (75%)	52 (20%)	11 (4%)	2	17
22	I	206/233 (88%)	197 (96%)	9 (4%)	0	100	100
23	J	203/206 (98%)	200 (98%)	3 (2%)	0	100	100
24	K	154/167 (92%)	144 (94%)	8 (5%)	2 (1%)	10	42
25	L	102/135 (76%)	98 (96%)	3 (3%)	1 (1%)	13	49
26	M	149/179 (83%)	144 (97%)	4 (3%)	1 (1%)	19	56
27	N	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
28	O	125/130 (96%)	116 (93%)	8 (6%)	1 (1%)	16	54
29	P	97/103 (94%)	87 (90%)	10 (10%)	0	100	100
30	Q	115/129 (89%)	106 (92%)	9 (8%)	0	100	100
31	R	117/124 (94%)	116 (99%)	0	1 (1%)	14	51
32	S	98/101 (97%)	96 (98%)	1 (1%)	1 (1%)	13	49
33	T	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
34	U	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
35	V	78/84 (93%)	75 (96%)	3 (4%)	0	100	100
36	W	81/92 (88%)	78 (96%)	3 (4%)	0	100	100
37	X	114/118 (97%)	105 (92%)	7 (6%)	2 (2%)	7	34
38	Y	139/142 (98%)	107 (77%)	31 (22%)	1 (1%)	19	56
39	Z	28/121 (23%)	21 (75%)	7 (25%)	0	100	100
41	b	74/85 (87%)	72 (97%)	2 (3%)	0	100	100
42	c	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
44	e	60/63 (95%)	58 (97%)	2 (3%)	0	100	100
45	f	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
46	g	64/70 (91%)	63 (98%)	1 (2%)	0	100	100
47	h	269/273 (98%)	259 (96%)	10 (4%)	0	100	100
48	i	54/57 (95%)	48 (89%)	5 (9%)	1 (2%)	6	32
49	j	207/209 (99%)	196 (95%)	11 (5%)	0	100	100
50	k	50/55 (91%)	49 (98%)	0	1 (2%)	6	32
51	l	199/201 (99%)	192 (96%)	7 (4%)	0	100	100
52	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	n	175/179 (98%)	164 (94%)	10 (6%)	1 (1%)	22	60
54	o	62/65 (95%)	58 (94%)	3 (5%)	1 (2%)	8	38
55	p	173/177 (98%)	163 (94%)	10 (6%)	0	100	100
56	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
57	r	147/149 (99%)	137 (93%)	10 (7%)	0	100	100
58	s	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
59	t	121/123 (98%)	113 (93%)	8 (7%)	0	100	100
60	u	142/144 (99%)	133 (94%)	9 (6%)	0	100	100
61	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
62	w	117/127 (92%)	107 (92%)	10 (8%)	0	100	100
63	x	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
64	y	112/115 (97%)	106 (95%)	6 (5%)	0	100	100
65	z	115/118 (98%)	111 (96%)	4 (4%)	0	100	100
All	All	9526/10577 (90%)	8823 (93%)	646 (7%)	57 (1%)	24	60

5 of 57 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	9	88	HIS
9	9	108	VAL
11	AA	913	VAL
12	AB	44	VAL
12	AB	49	VAL

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%)	78 (93%)	6 (7%)	12	32
2	1	93/93 (100%)	85 (91%)	8 (9%)	8	27
3	2	81/84 (96%)	77 (95%)	4 (5%)	21	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	3	84/85 (99%)	78 (93%)	6 (7%)	12	32
5	4	78/78 (100%)	74 (95%)	4 (5%)	20	42
9	9	112/123 (91%)	73 (65%)	39 (35%)	0	1
11	AA	1155/1157 (100%)	1147 (99%)	8 (1%)	81	87
12	AB	150/158 (95%)	127 (85%)	23 (15%)	2	12
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%)	1106 (99%)	16 (1%)	62	76
15	AF	70/75 (93%)	70 (100%)	0	100	100
16	C	57/65 (88%)	55 (96%)	2 (4%)	31	52
18	E	65/66 (98%)	60 (92%)	5 (8%)	10	30
19	F	60/61 (98%)	56 (93%)	4 (7%)	13	34
20	G	187/199 (94%)	177 (95%)	10 (5%)	19	41
21	H	137/461 (30%)	129 (94%)	8 (6%)	17	38
22	I	171/190 (90%)	165 (96%)	6 (4%)	31	52
23	J	172/173 (99%)	165 (96%)	7 (4%)	26	48
24	K	119/126 (94%)	112 (94%)	7 (6%)	16	38
25	L	91/116 (78%)	84 (92%)	7 (8%)	10	30
26	M	124/147 (84%)	115 (93%)	9 (7%)	11	32
27	N	104/105 (99%)	102 (98%)	2 (2%)	52	70
28	O	105/107 (98%)	99 (94%)	6 (6%)	17	39
29	P	86/90 (96%)	78 (91%)	8 (9%)	7	24
30	Q	90/99 (91%)	87 (97%)	3 (3%)	33	54
31	R	101/104 (97%)	94 (93%)	7 (7%)	13	34
32	S	83/84 (99%)	74 (89%)	9 (11%)	5	20
33	T	76/77 (99%)	64 (84%)	12 (16%)	2	11
34	U	65/65 (100%)	59 (91%)	6 (9%)	7	24
35	V	74/78 (95%)	72 (97%)	2 (3%)	40	60
36	W	72/79 (91%)	68 (94%)	4 (6%)	17	40
37	X	94/96 (98%)	86 (92%)	8 (8%)	8	28
38	Y	109/110 (99%)	77 (71%)	32 (29%)	0	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	Z	26/85 (31%)	12 (46%)	14 (54%)	0	0
41	b	58/63 (92%)	56 (97%)	2 (3%)	32	53
42	c	67/68 (98%)	65 (97%)	2 (3%)	36	56
44	e	54/55 (98%)	53 (98%)	1 (2%)	52	70
45	f	48/49 (98%)	46 (96%)	2 (4%)	25	47
46	g	59/62 (95%)	52 (88%)	7 (12%)	4	17
47	h	216/218 (99%)	200 (93%)	16 (7%)	11	31
48	i	47/48 (98%)	40 (85%)	7 (15%)	2	12
49	j	164/164 (100%)	156 (95%)	8 (5%)	21	43
50	k	47/49 (96%)	43 (92%)	4 (8%)	8	28
51	l	165/165 (100%)	155 (94%)	10 (6%)	15	38
52	m	38/38 (100%)	35 (92%)	3 (8%)	10	29
53	n	148/150 (99%)	134 (90%)	14 (10%)	7	23
54	o	51/52 (98%)	46 (90%)	5 (10%)	6	22
55	p	136/138 (99%)	131 (96%)	5 (4%)	29	51
56	q	34/34 (100%)	32 (94%)	2 (6%)	16	38
57	r	114/114 (100%)	104 (91%)	10 (9%)	8	26
58	s	116/116 (100%)	110 (95%)	6 (5%)	19	41
59	t	104/104 (100%)	98 (94%)	6 (6%)	17	38
60	u	103/103 (100%)	98 (95%)	5 (5%)	21	43
61	v	109/109 (100%)	103 (94%)	6 (6%)	18	40
62	w	99/103 (96%)	92 (93%)	7 (7%)	12	32
63	x	86/87 (99%)	82 (95%)	4 (5%)	22	45
64	y	99/100 (99%)	95 (96%)	4 (4%)	27	48
65	z	89/90 (99%)	87 (98%)	2 (2%)	47	66
All	All	7919/8739 (91%)	7489 (95%)	430 (5%)	21	41

5 of 430 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	U	20	VAL
39	Z	16	VAL
59	t	80	ASP

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Mol	Chain	Res	Type
37	X	11	ASP
38	Y	78	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
46	g	6	HIS
51	l	62	GLN
47	h	15	HIS
49	j	130	GLN
54	o	43	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	75/76 (98%)	29 (38%)	7 (9%)
10	B	75/76 (98%)	29 (38%)	6 (8%)
17	D	1515/1542 (98%)	295 (19%)	26 (1%)
40	a	2859/2904 (98%)	534 (18%)	0
43	d	119/120 (99%)	17 (14%)	0
8	7	33/44 (75%)	21 (63%)	3 (9%)
All	All	4676/4762 (98%)	925 (19%)	42 (0%)

5 of 925 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	-18	G
8	7	-17	U
8	7	-16	U
8	7	-15	U
8	7	-14	U

5 of 42 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
17	D	991	U
17	D	1213	A
17	D	992	U
17	D	1196	A
17	D	1299	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.

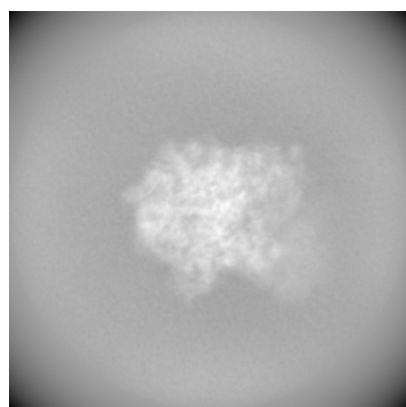
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22142. These allow visual inspection of the internal detail of the map and identification of artifacts.

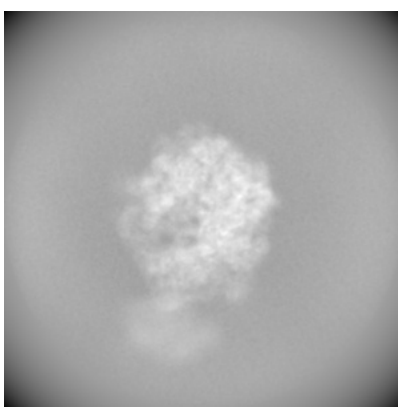
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

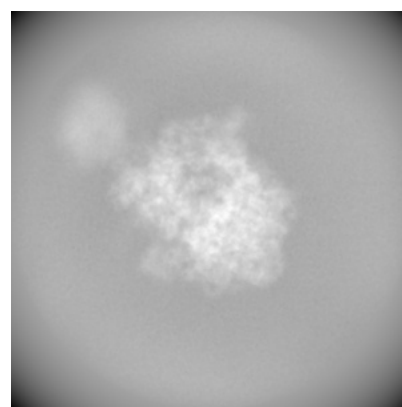
6.1.1 Primary map



X



Y

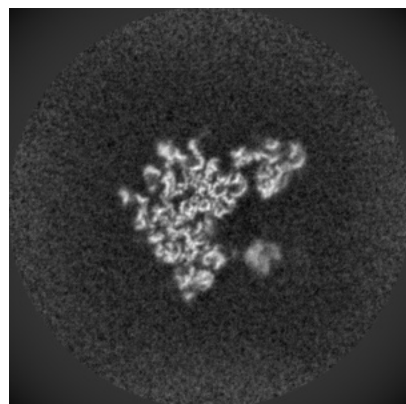


Z

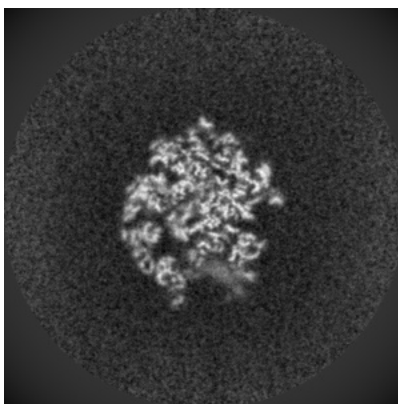
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

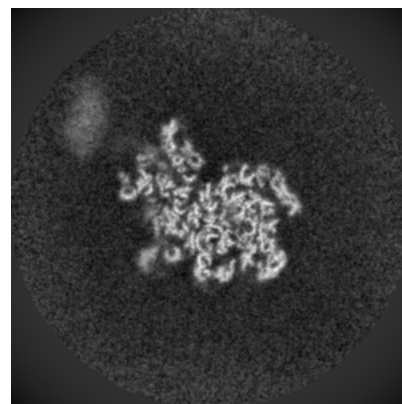
6.2.1 Primary map



X Index: 256



Y Index: 256

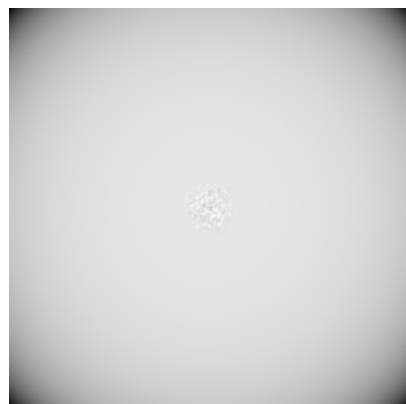


Z Index: 256

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

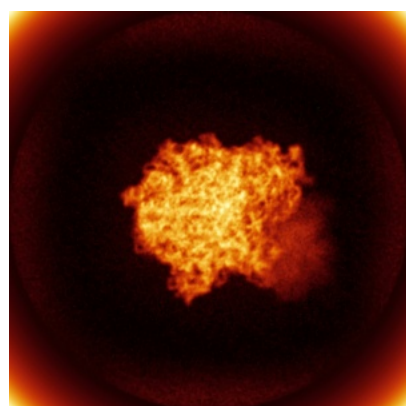


Z Index: 0

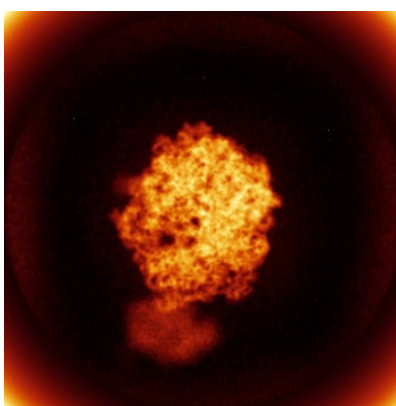
The images above show the largest variance slices of the map in three orthogonal directions.

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

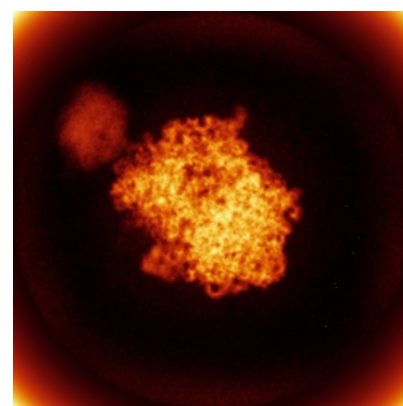
6.4.1 Primary map



X



Y

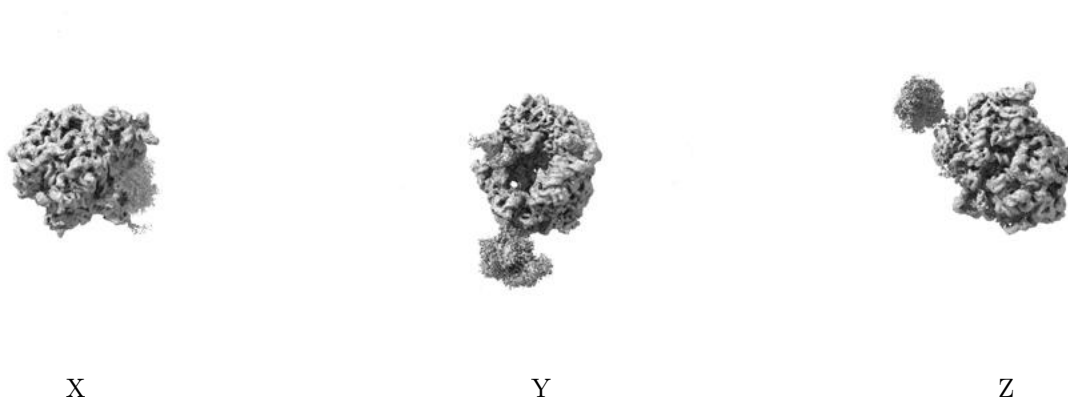


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00561. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

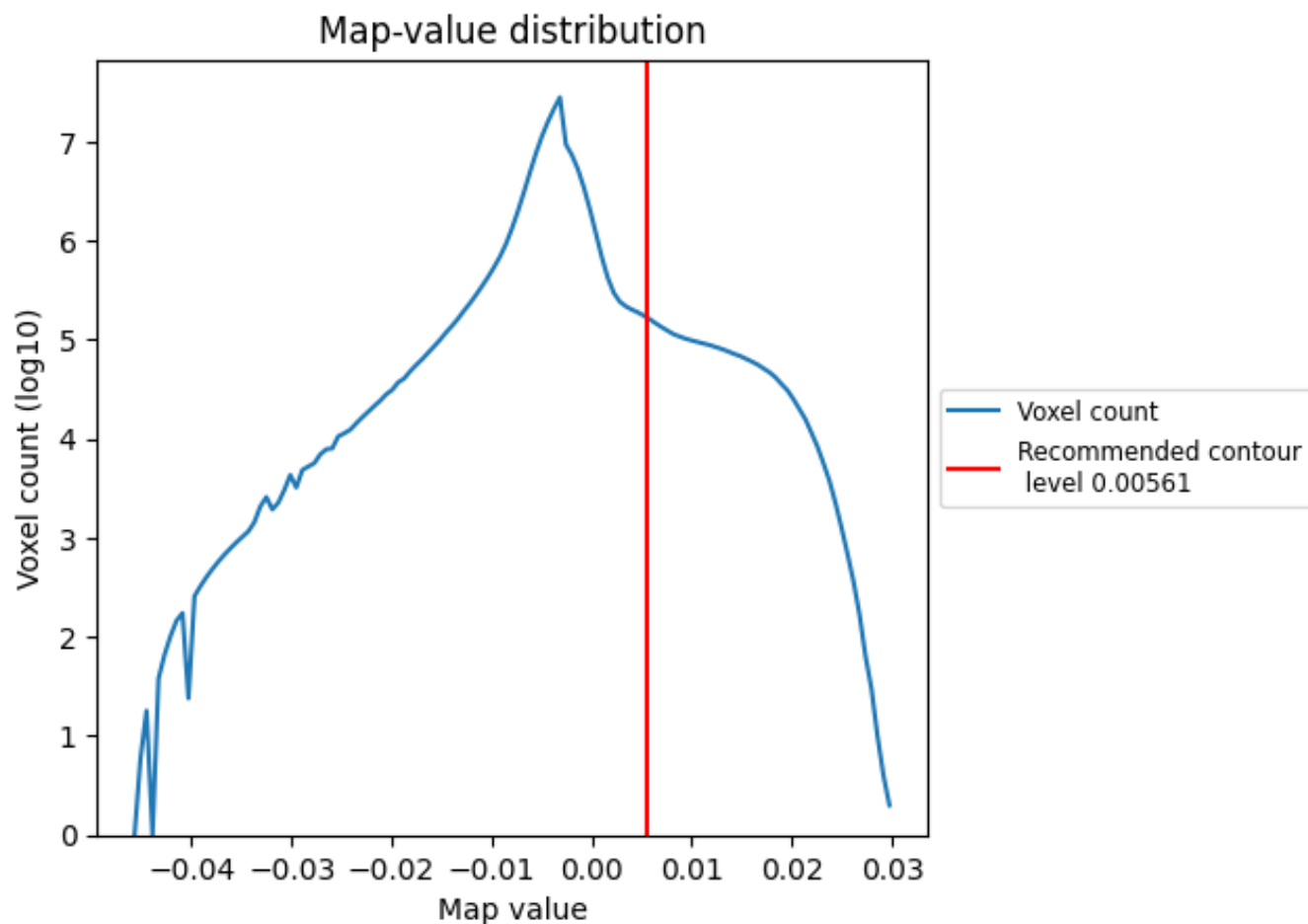
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

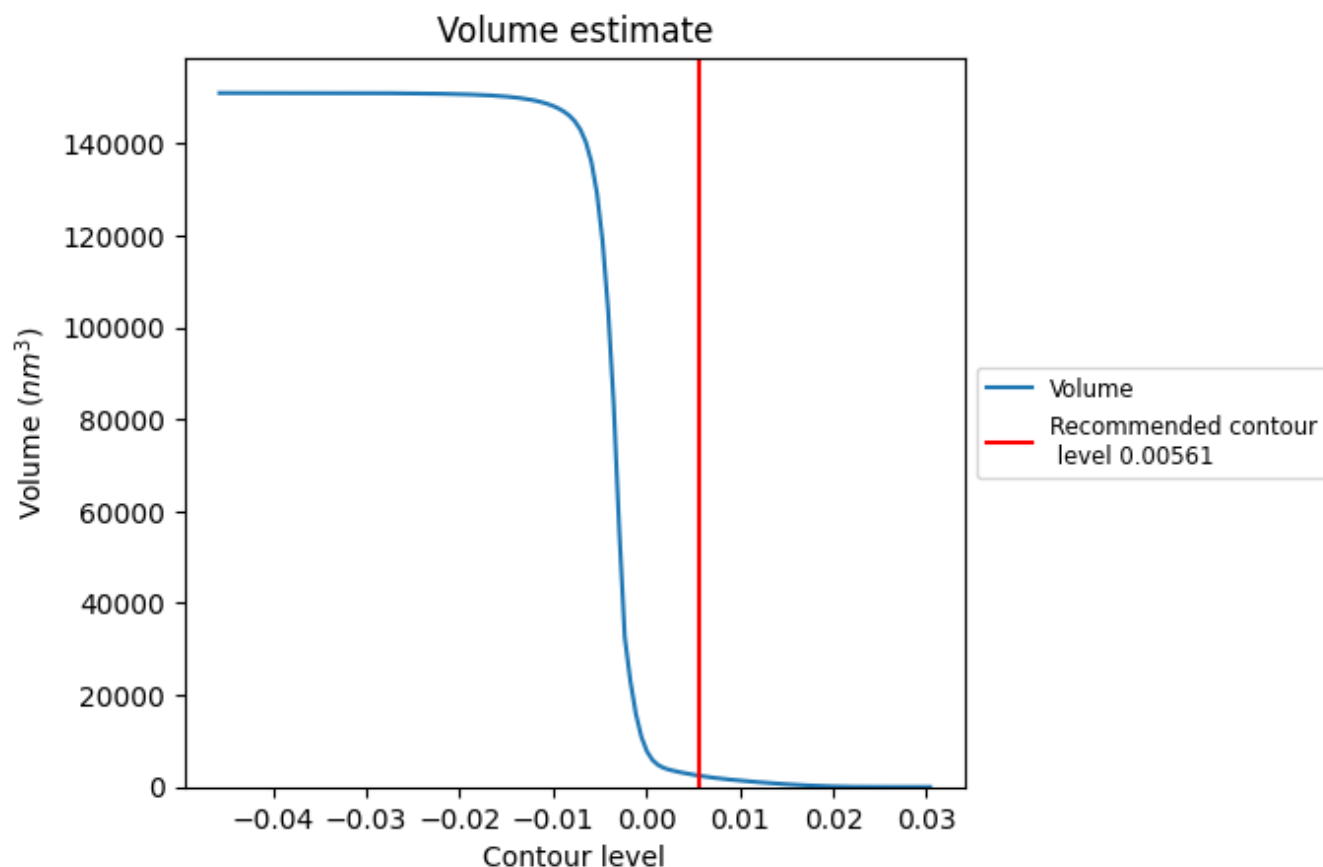
This section contains the results of statistical analysis of the map.

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.

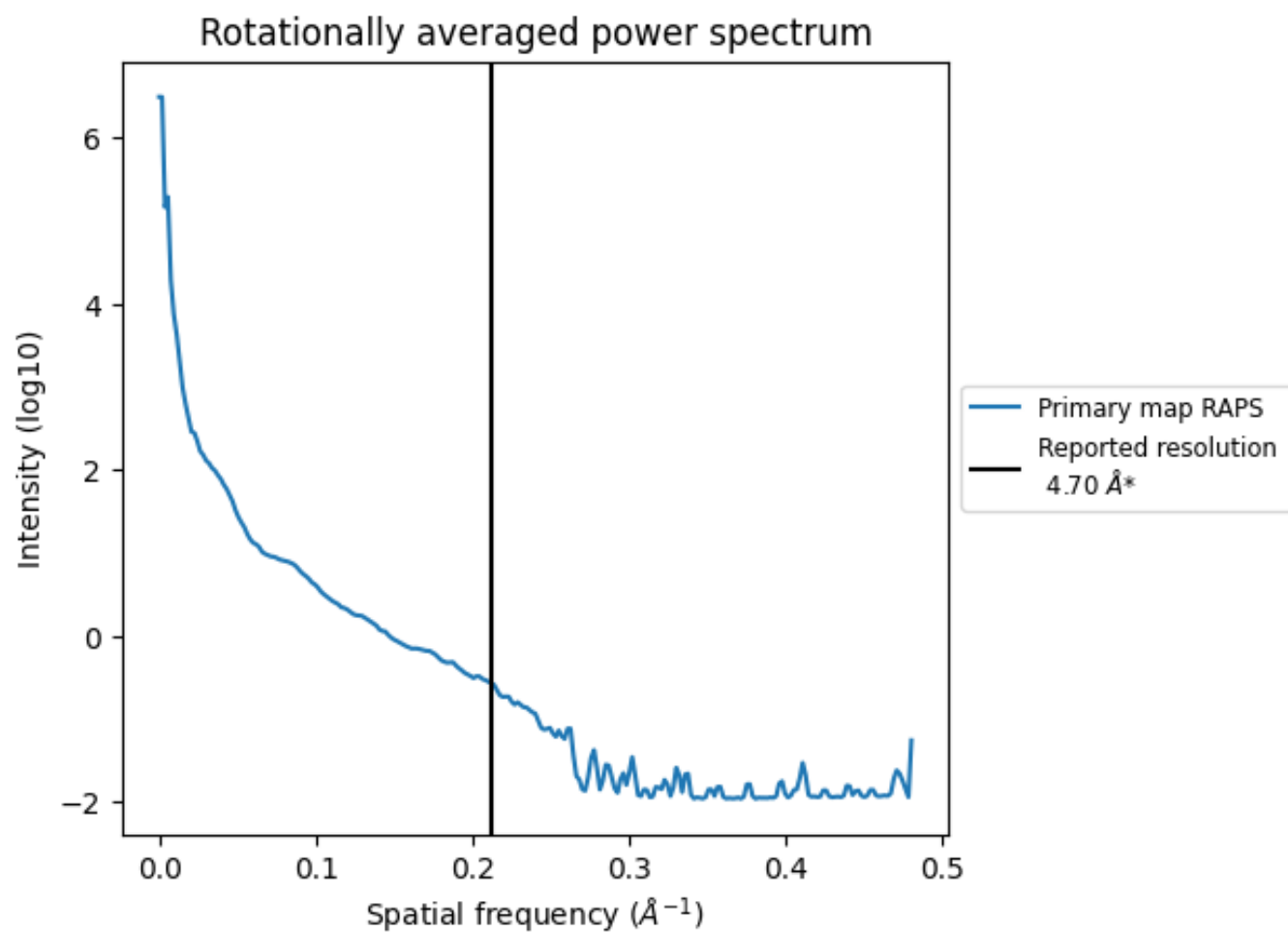
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2463 nm³; this corresponds to an approximate mass of 2225 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 0.213 Å⁻¹

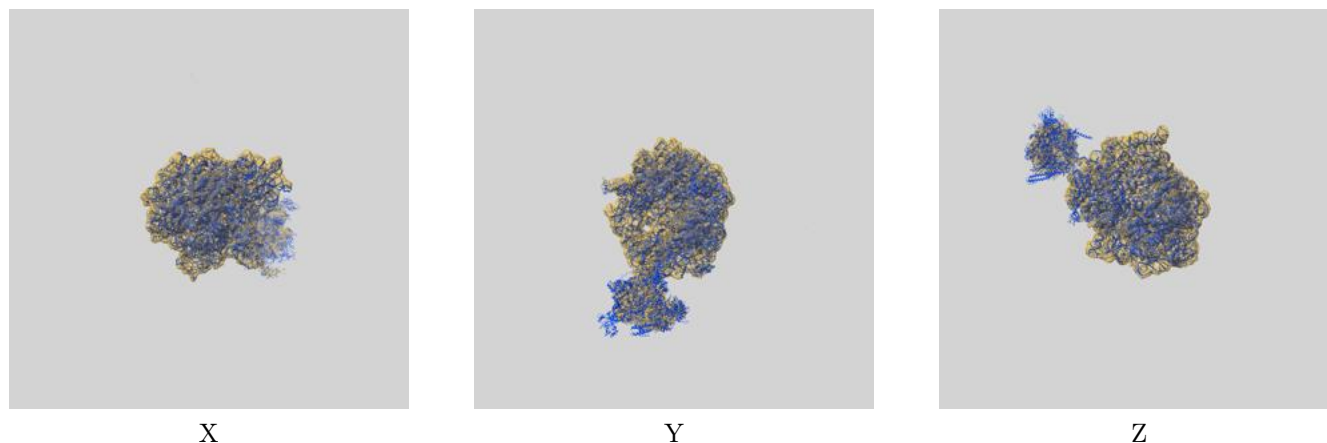
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

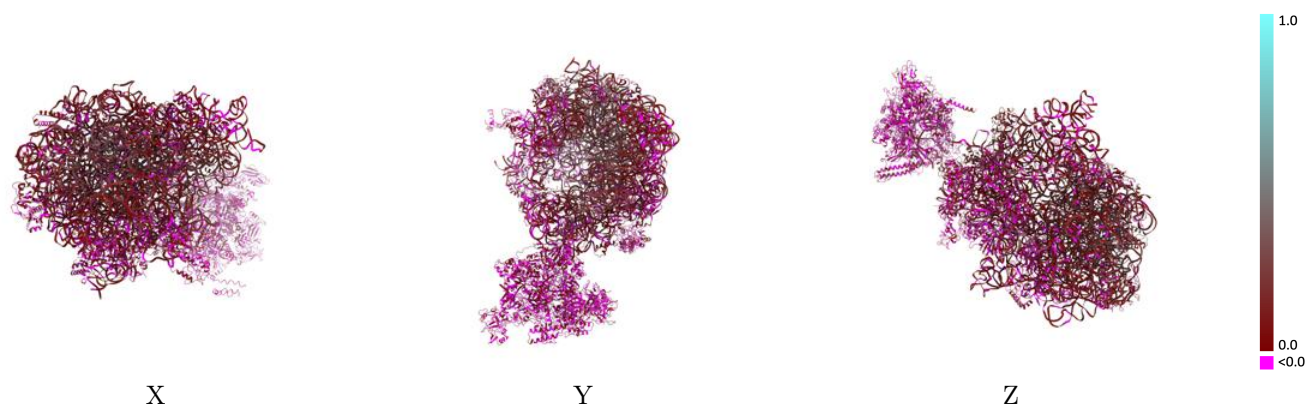
This section contains information regarding the fit between EMDB map EMD-22142 and PDB model 6XDR. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



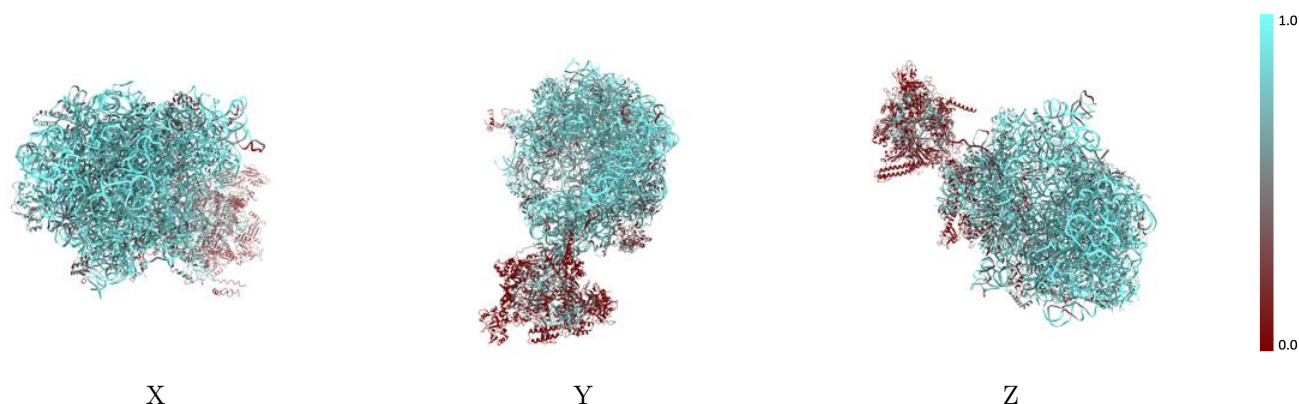
The images above show the 3D surface view of the map at the recommended contour level 0.00561 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



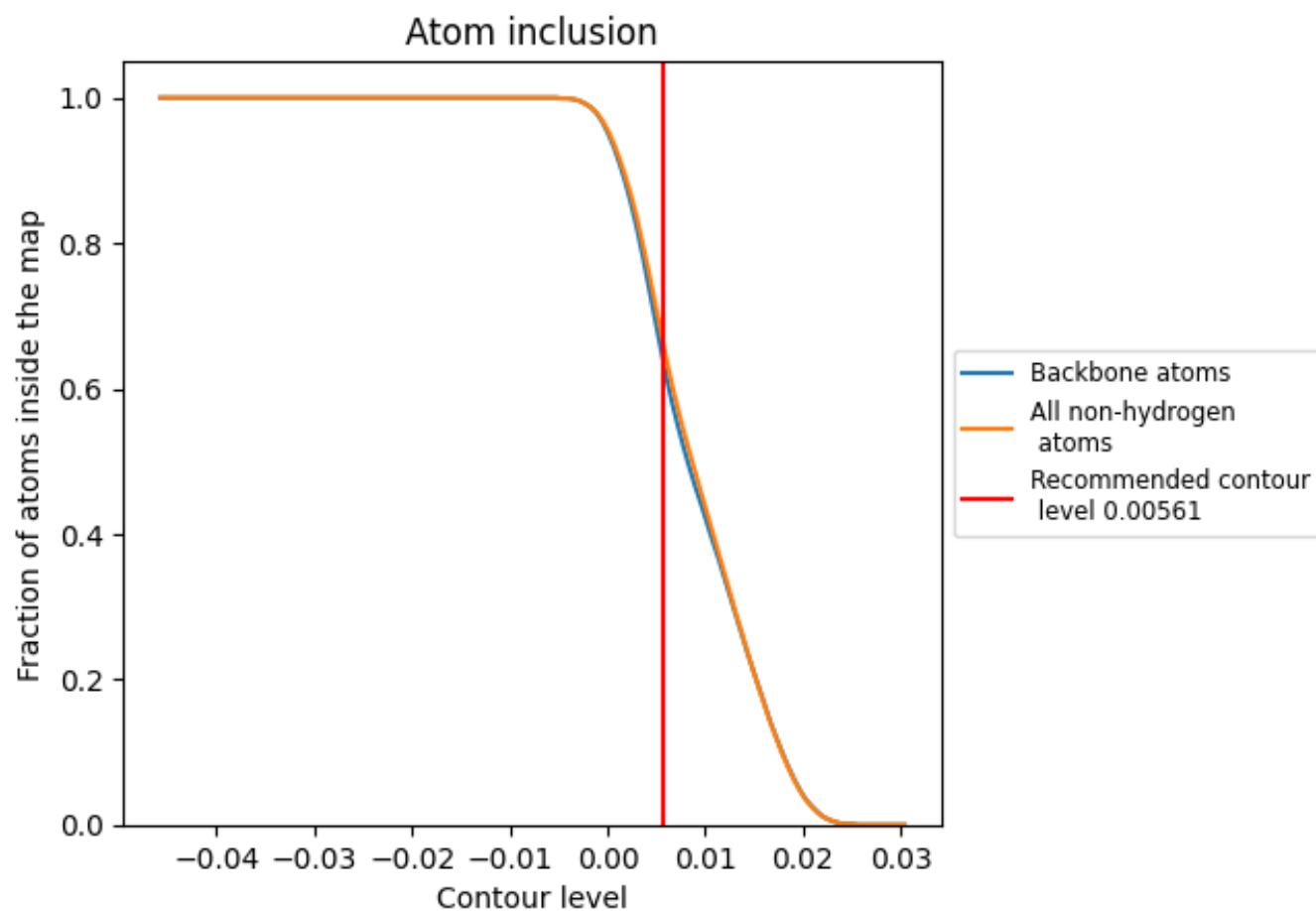
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00561).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 64% of all backbone atoms, 67% 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 (0.00561) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6680	 0.1070
0	 0.7420	 0.1220
1	 0.7890	 0.2450
2	 0.7220	 0.1010
3	 0.7710	 0.1020
4	 0.7560	 0.1040
5	 0.2730	 0.0330
6	 0.4170	 0.0410
7	 0.3970	 0.0630
9	 0.5570	 0.0390
A	 0.7780	 0.1070
AA	 0.2720	 0.0290
AB	 0.1760	 0.0840
AC	 0.1270	 0.0270
AD	 0.0540	 0.0130
AE	 0.2270	 0.0200
AF	 0.0270	 0.0140
B	 0.7760	 0.1310
C	 0.5330	 0.0400
D	 0.8660	 0.1230
E	 0.6710	 0.0850
F	 0.4720	 0.0640
G	 0.5050	 0.0490
H	 0.1990	 0.0420
I	 0.7480	 0.2030
J	 0.7610	 0.1840
K	 0.7430	 0.1450
L	 0.6500	 0.1040
M	 0.5250	 0.0530
N	 0.6290	 0.0660
O	 0.6230	 0.0370
P	 0.6650	 0.1190
Q	 0.6720	 0.0630
R	 0.6570	 0.1250
S	 0.6370	 0.0020



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Chain	Atom inclusion	Q-score
T	 0.5380	 0.0560
U	 0.7100	 0.0890
V	 0.6900	 0.0850
W	 0.6290	 0.0210
X	 0.6570	 0.0940
Y	 0.5290	 0.0530
Z	 0.0440	 0.0440
a	 0.8870	 0.1450
b	 0.6500	 -0.0120
c	 0.6790	 0.1070
d	 0.8570	 0.0770
e	 0.6830	 0.1190
f	 0.7870	 0.1190
g	 0.4250	 0.0960
h	 0.7240	 0.0940
i	 0.5440	 -0.0090
j	 0.7170	 0.1020
k	 0.3590	 0.0070
l	 0.6570	 0.0690
m	 0.7830	 0.1470
n	 0.6420	 0.0630
o	 0.6580	 0.0380
p	 0.7330	 0.1220
q	 0.7300	 0.0820
r	 0.5010	 0.0700
s	 0.8180	 0.1770
t	 0.7420	 0.2010
u	 0.5350	 0.0160
v	 0.7390	 0.1140
w	 0.7870	 0.1490
x	 0.5540	 -0.0010
y	 0.6910	 0.0980
z	 0.8390	 0.1820