



wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 11:01 PM UTC

PDB ID : 6VYS / pdb_00006vys
EMDB ID : EMD-21470
Title : Escherichia coli transcription-translation complex A1 (TTC-A1) containing a 21 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 : 2020-02-27
Resolution : 3.70 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:

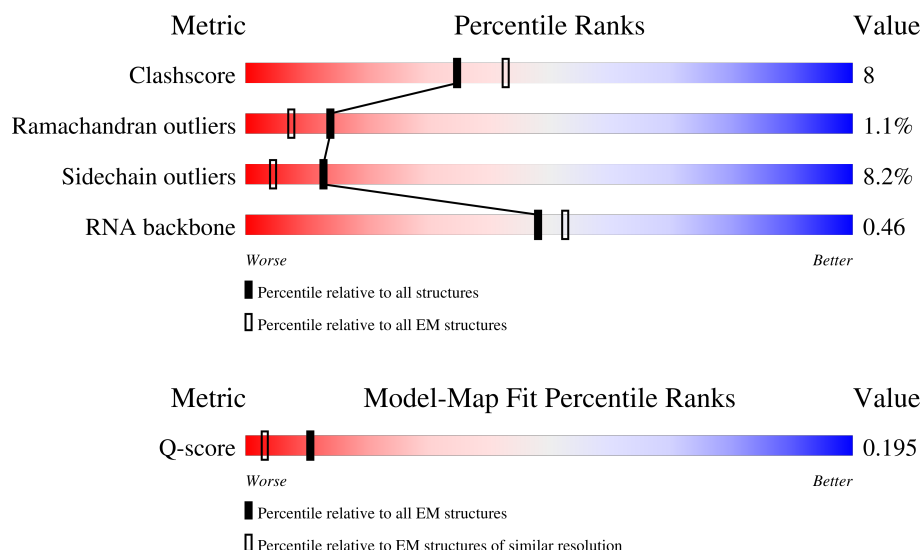
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

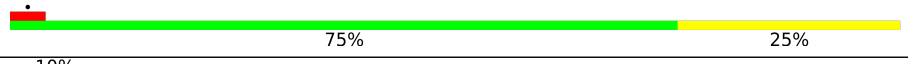
The reported resolution of this entry is 3.70 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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

Mol	Chain	Length	Quality of chain
1	0	103	
2	1	110	
3	2	100	

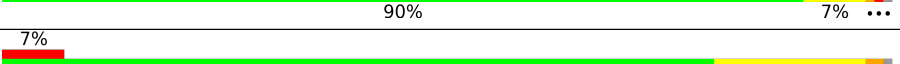
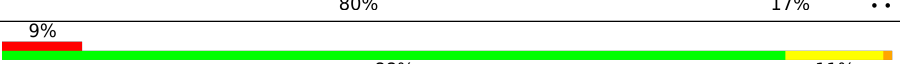
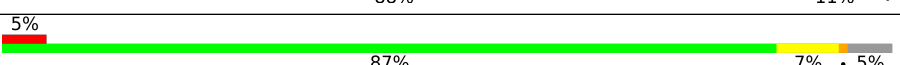
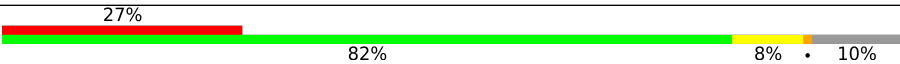
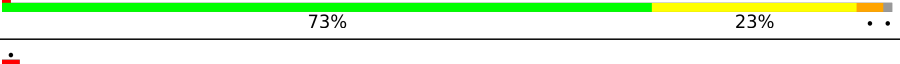
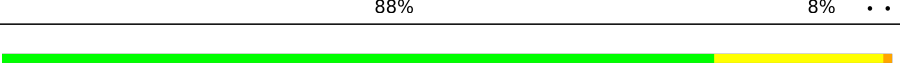
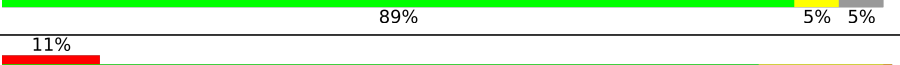
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Mol	Chain	Length	Quality of chain
4	3	104	
5	4	94	
6	5	36	
7	6	36	
8	7	37	
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AB	181	
13	AC	329	
13	AD	329	
14	AE	1358	
15	C	75	
16	D	1542	
17	E	87	
18	F	71	
19	G	241	
20	H	557	
21	I	233	
22	J	206	
23	K	167	
24	L	135	
25	M	179	
26	N	130	

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Mol	Chain	Length	Quality of chain
27	O	130	
28	P	103	
29	Q	129	
30	R	124	
31	S	101	
32	T	89	
33	U	82	
34	V	84	
35	W	92	
36	X	118	
37	Y	142	
38	Z	121	
39	a	2904	
40	b	85	
41	c	78	
42	d	120	
43	e	63	
44	f	59	
45	g	70	
46	h	273	
47	i	57	
48	j	209	
49	k	55	
50	l	201	
51	m	46	

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

2 Entry composition

There are 66 unique types of molecules in this entry. The entry contains 300543 atoms, of which 124723 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 21 nt long spacer.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	26	Total	C	H	N	O	P	0	0
			644	244	97	82	195	26		

- 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	1322	Total	C	H	N	O	S	0	0
			20851	6539	10426	1817	2026	43		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
12	AB	98	Total	C	H	N	O	S	0	0
			1573	505	783	139	140	6		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
13	AC	230	Total	C	H	N	O	S	0	0
			3599	1112	1813	317	351	6		

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Mol	Chain	Residues	Atoms						AltConf	Trace
13	AD	228	Total	C	H	N	O	S	0	0
			3556	1100	1789	312	349	6		

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

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 30S ribosomal protein S18.

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

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

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

- Molecule 17 is a protein called 30S ribosomal protein S20.

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

- Molecule 18 is a protein called 30S ribosomal protein S21.

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

- Molecule 19 is a protein called 30S ribosomal protein S2.

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

- Molecule 20 is a protein called 30S ribosomal protein S1.

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

- Molecule 21 is a protein called 30S ribosomal protein S3.

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

- Molecule 22 is a protein called 30S ribosomal protein S4.

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

- Molecule 23 is a protein called 30S ribosomal protein S5.

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

- Molecule 24 is a protein called 30S ribosomal protein S6.

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

- Molecule 25 is a protein called 30S ribosomal protein S7.

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

- Molecule 26 is a protein called 30S ribosomal protein S8.

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

- Molecule 27 is a protein called 30S ribosomal protein S9.

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

- Molecule 28 is a protein called 30S ribosomal protein S10.

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

- Molecule 29 is a protein called 30S ribosomal protein S11.

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

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

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

- Molecule 31 is a protein called 30S ribosomal protein S14.

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

- Molecule 32 is a protein called 30S ribosomal protein S15.

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

- Molecule 33 is a protein called 30S ribosomal protein S16.

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

- Molecule 34 is a protein called 30S ribosomal protein S17.

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

- Molecule 35 is a protein called 30S ribosomal protein S19.

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

- Molecule 36 is a protein called 30S ribosomal protein S13.

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

- Molecule 37 is a protein called 50S ribosomal protein L11.

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

- Molecule 38 is a protein called 50S ribosomal protein L7/L12.

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

- Molecule 39 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	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	variant	GB 937521852

- Molecule 40 is a protein called 50S ribosomal protein L27.

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

- Molecule 41 is a protein called 50S ribosomal protein L28.

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

- Molecule 42 is a RNA chain called 5S rRNA.

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

- Molecule 43 is a protein called 50S ribosomal protein L29.

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

- Molecule 44 is a protein called 50S ribosomal protein L30.

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

- Molecule 45 is a protein called 50S ribosomal protein L31.

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

- Molecule 46 is a protein called 50S ribosomal protein L2.

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

- Molecule 47 is a protein called 50S ribosomal protein L32.

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

- Molecule 48 is a protein called 50S ribosomal protein L3.

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

- Molecule 49 is a protein called 50S ribosomal protein L33.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L34.

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

- Molecule 52 is a protein called 50S ribosomal protein L5.

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

- Molecule 53 is a protein called 50S ribosomal protein L35.

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

- Molecule 54 is a protein called 50S ribosomal protein L6.

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

- Molecule 55 is a protein called 50S ribosomal protein L36.

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

- Molecule 56 is a protein called 50S ribosomal protein L9.

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

- Molecule 57 is a protein called 50S ribosomal protein L13.

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

- Molecule 58 is a protein called 50S ribosomal protein L14.

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

- Molecule 59 is a protein called 50S ribosomal protein L15.

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

- Molecule 60 is a protein called 50S ribosomal protein L16.

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

- Molecule 61 is a protein called 50S ribosomal protein L17.

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

- Molecule 62 is a protein called 50S ribosomal protein L18.

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

- Molecule 63 is a protein called 50S ribosomal protein L19.

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

- Molecule 64 is a protein called 50S ribosomal protein L20.

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

- Molecule 65 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

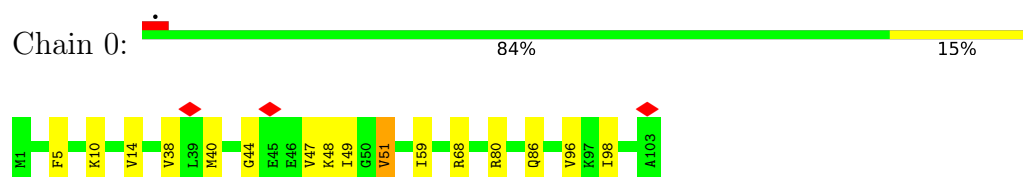
- Molecule 66 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

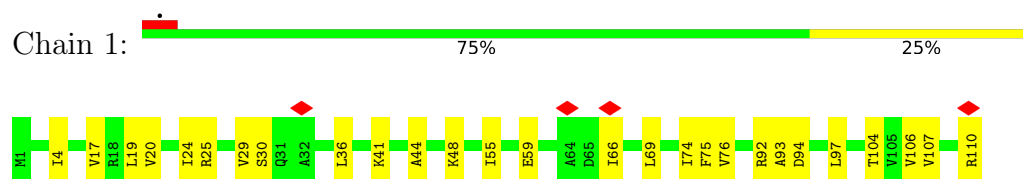
3 Residue-property plots [i](#)

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.

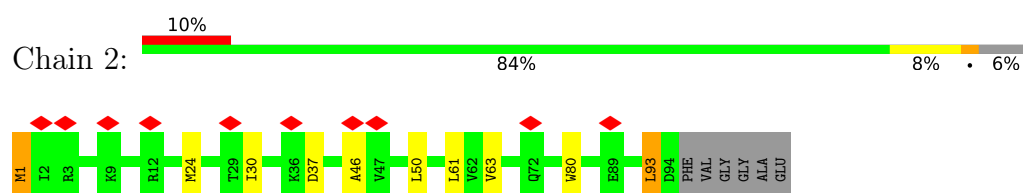
- Molecule 1: 50S ribosomal protein L21



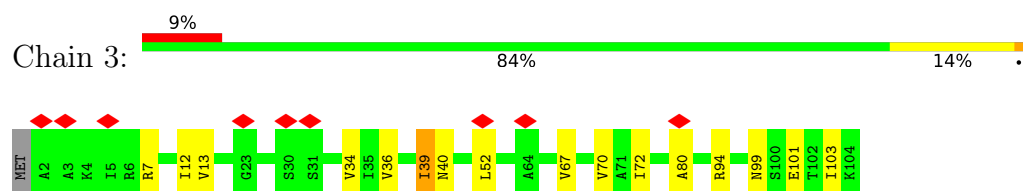
- Molecule 2: 50S ribosomal protein L22



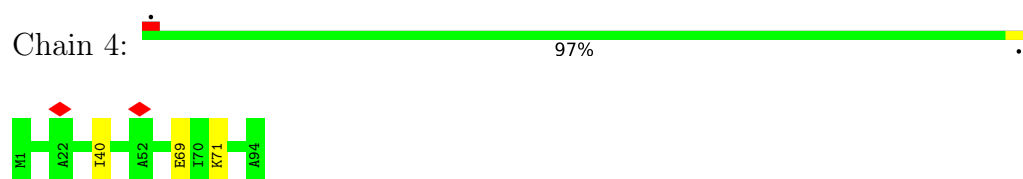
- Molecule 3: 50S ribosomal protein L23



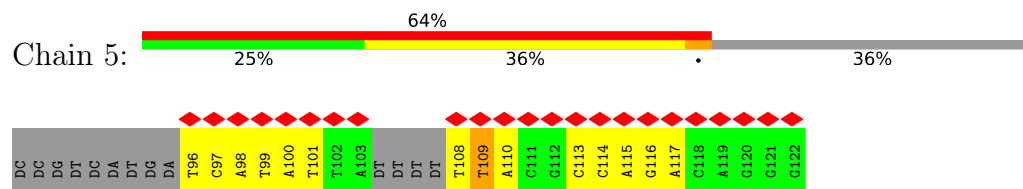
- Molecule 4: 50S ribosomal protein L24



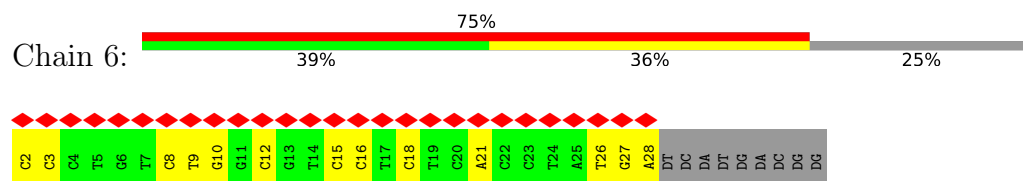
- Molecule 5: 50S ribosomal protein L25



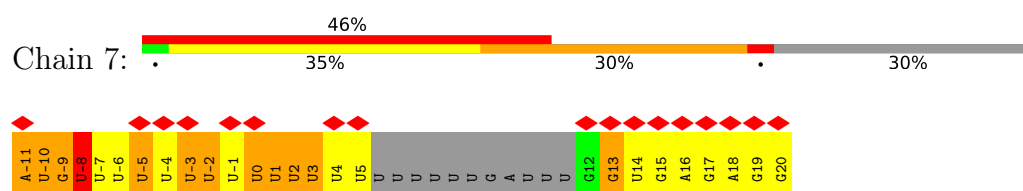
- Molecule 6: NT DNA



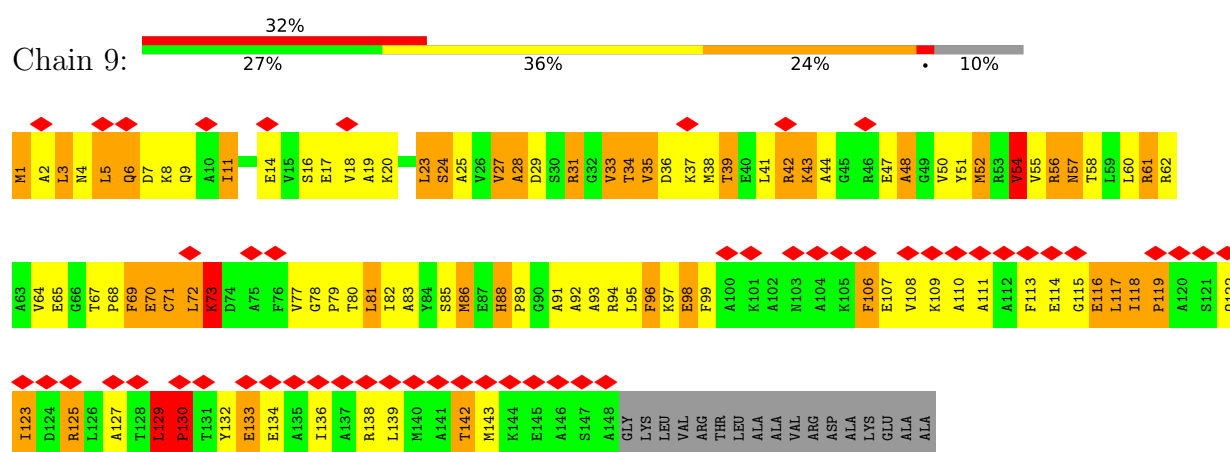
- Molecule 7: T DNA



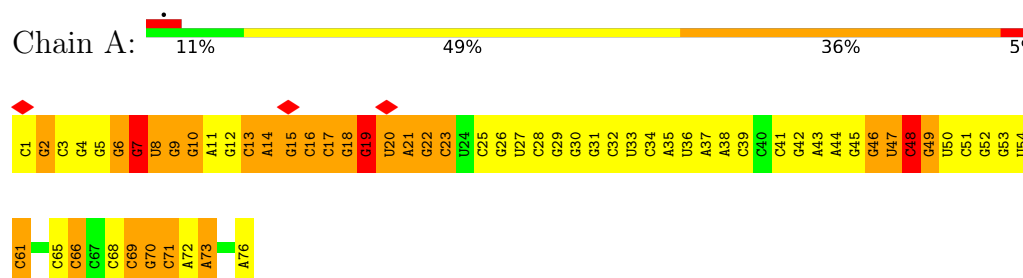
- Molecule 8: mRNA with 21 nt long spacer



- Molecule 9: 50S ribosomal protein L10

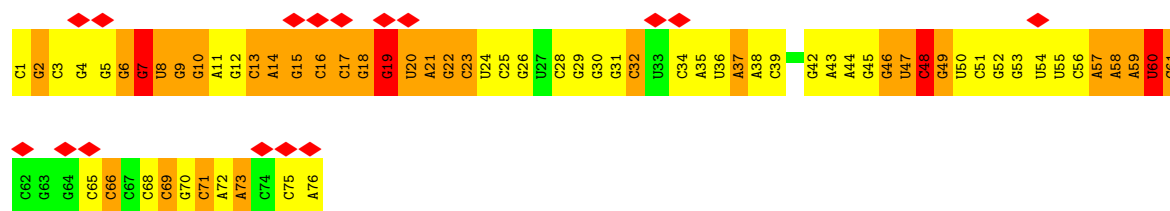


- Molecule 10: E-site and P-site tRNA (fMet)

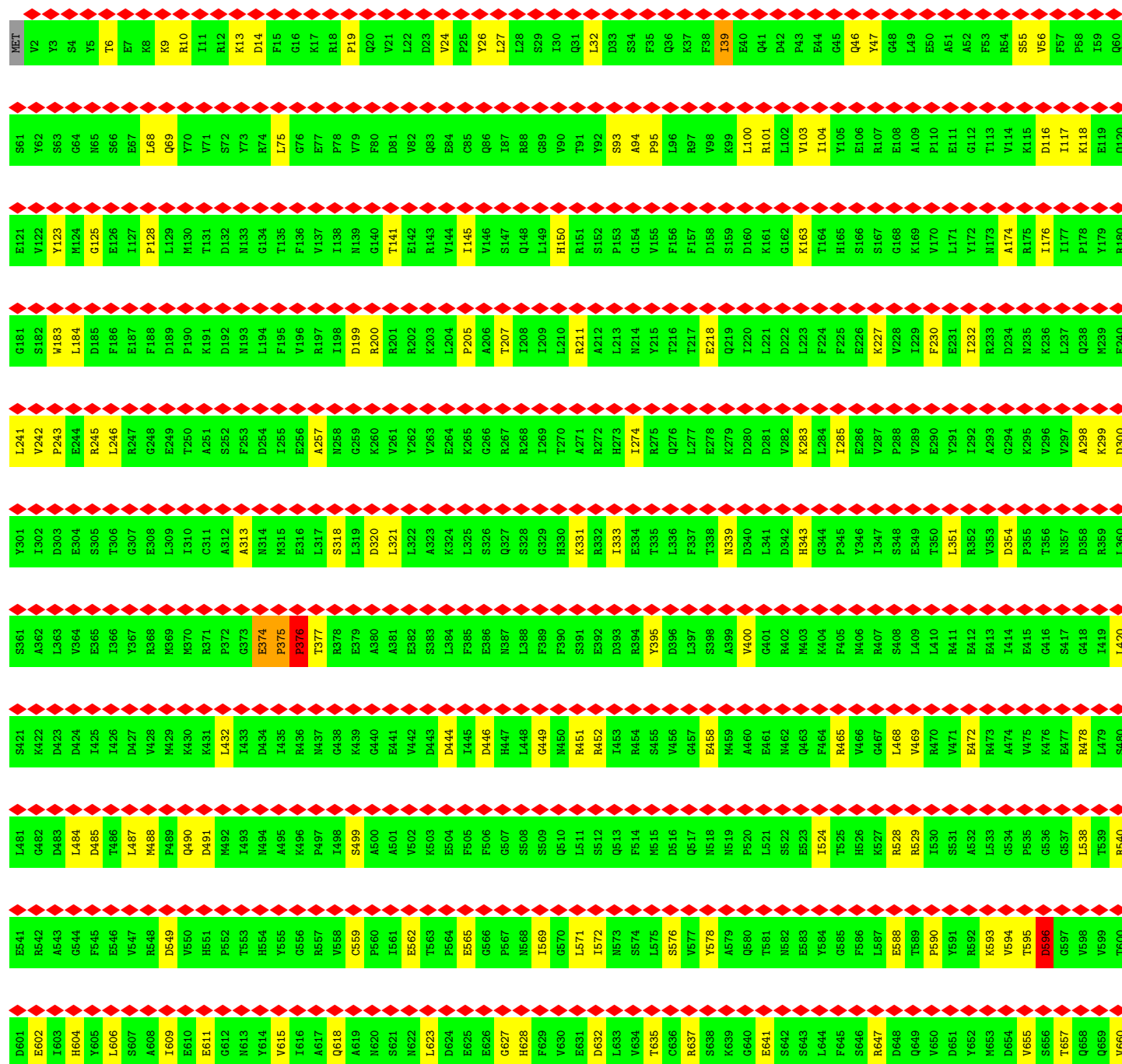


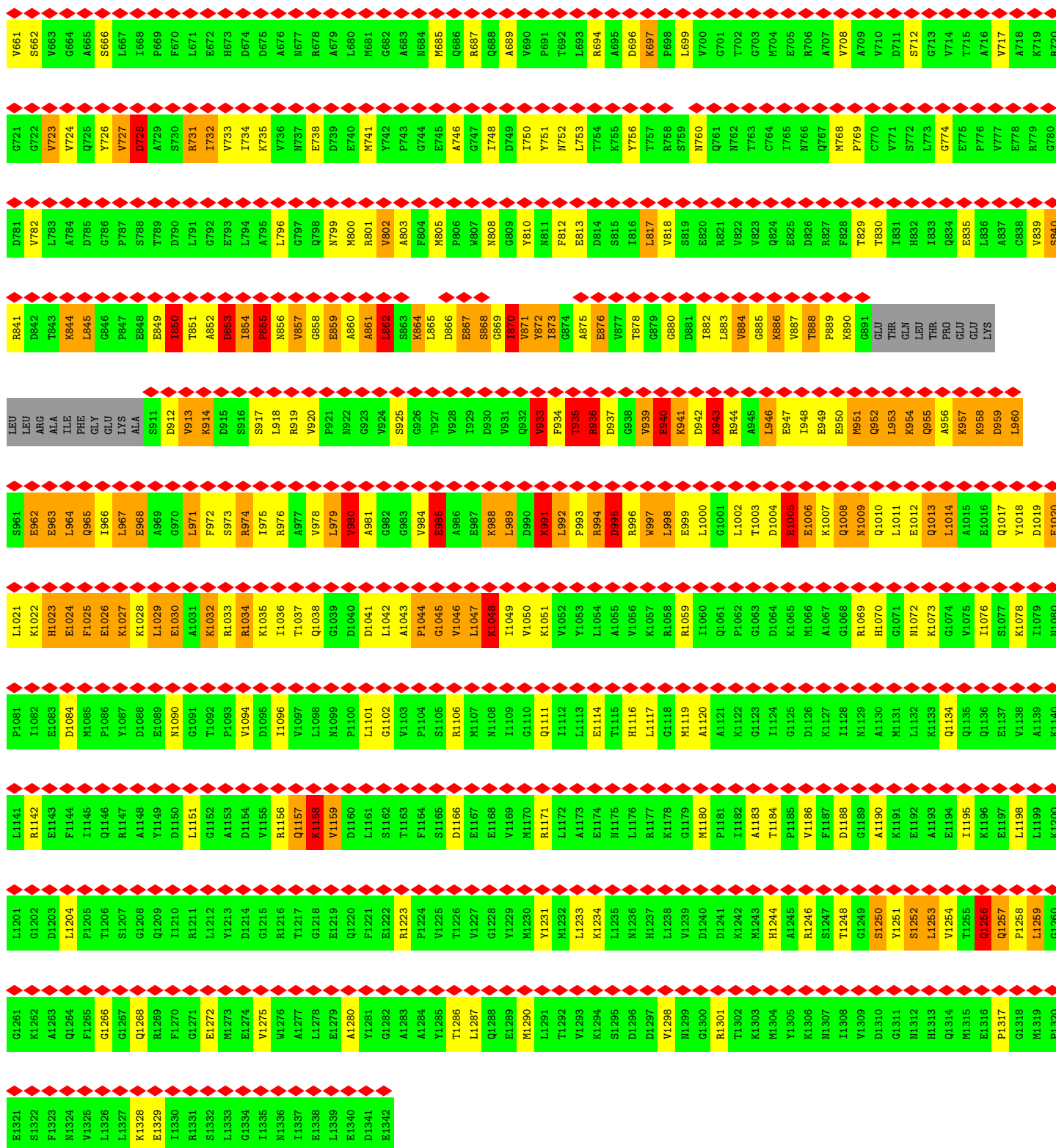
- Molecule 10: E-site and P-site tRNA (fMet)





● Molecule 11: DNA-directed RNA polymerase subunit beta





● Molecule 12: Transcription termination/antitermination protein NusG



																																	E181	R182	I183	A184	Y185	N186	V187	E188	A189	A190	R191	V192	E193	Q194	R195	T196	D197	L198	D199	K200	L201	V202	I203	E204	M205	E206	T207	N208	G209	T210	I211	D212	P213	E214	E215	A216	L217	R218	R219	A220	A221	T222	I223	L224	A225	E226	Q227	L228	E229	A230	F231	V232	D233	LEU	ARG	ASP	VAL	ARG	GLN	PRO																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
THR	GLU	ILE	LYS	ASP	VAL	LEU	ALA	SER	ARG	GLY	LEU	SER	GLY	MET	ARG	VAL	LEU	GLU	ASN	TRP	PRO	PRO	ALA	SER	ILE	ASP	ASP	GLU	ILE	HIS	TYR	ILE	GLY	ASP	LEU	VAL	GLN	ARG	THR	THR	GLU	VAL	GLU	LEU	LYS	THR	PRO	ASN	LEU	GLY	LYS	LYS	SER	LEU																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				

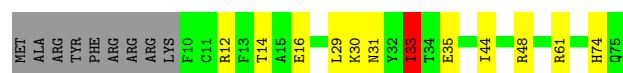
• Molecule 14: DNA-directed RNA polymerase subunit



E556	K557	D558	A559	N560	G561	E562	L563	Y564	A565	K566	T567	S568	L569	K570	D571	T572	T573	Y574	G575	R576	A577	L578	L579	W580	M581	L582	W583	D584	K585	G586	L587	Y588	Y589	S590	L591	E592	N593	Q594	A595	L596	G597	K598	K599	A600	T601	S602	K603	M604	L605	M606	T607	C608	Y609	R610	L611	L612	G613	L614	K615
G496	E497	P498	T499	W500	V501	P502	S503	Q504	D505	W506	V507	L508	G509	L510	V511	Y512	W513	T514	R515	D516	C517	W518	N519	A520	K521	S522	E523	G524	M525	W526	L527	Y528	W529	P530	K531	E532	A533	E534	R535	L536	Y537	R538	S539	G540	L541	A542	S543	L544	H545	A546	R547	Y548	Y549	W550	R551	I552	T553	E554	Y555
A436	P437	E438	P439	V440	L441	L442	E443	G444	K445	A446	L447	Q448	L449	H450	P451	L452	V453	C454	A455	A456	A457	N458	A459	D460	P461	D462	G463	D464	Q465	M466	A467	W468	H469	V470	P471	L472	T473	L474	E475	A476	L477	E478	H479	A480	R481	A482	L483	M484	M485	S486	T487	N488	Y489	T490	L491	S492	P493	A494	N495
L376	F377	K378	P379	F380	L381	Y382	G383	K384	L385	E386	L387	R388	G389	L390	A391	T392	T393	I394	K395	A396	A397	K398	K399	M400	V401	E402	R403	E404	A405	A406	V407	W408	W409	D410	T411	L412	D413	E414	V415	I416	R417	E418	H419	P420	V421	L422	L423	N424	R425	A426	P427	T428	L429	H430	R431	L432	Q433	T434	Q435
I316	T317	G318	S319	N320	K321	R322	P323	L324	K325	S326	L327	A328	K329	M330	I331	K332	G333	K334	Q335	G336	F337	R338	K339	Q340	N341	L342	L343	G344	K345	R346	V347	D348	W349	D350	G351	R352	S353	V354	L355	T356	V357	G358	P359	Y360	L361	R362	L363	H364	Q365	C366	G367	L368	P369	K370	K371	M372	A373	L374	E375
D256	G257	G258	R259	F260	A261	T262	S263	D264	L265	N266	D267	L268	Y269	R270	R271	V272	L273	M274	R275	N276	N277	R278	L279	K280	R281	L282	L283	D284	L285	A286	A287	P288	D289	I290	G291	V292	R293	N294	E295	K296	R297	M298	L299	Q300	E301	A302	V303	D304	A305	L306	L307	D308	N309	G310	R311	R312	G313	R314	A315
Q196	E197	C198	E199	Q200	L201	R202	E203	E204	L205	N206	E207	T208	N209	S210	E211	T212	K213	R214	K215	L216	L217	T218	K219	R220	I221	K222	L223	L224	E225	A226	F227	V228	Q229	S230	G231	N232	K233	P234	E235	M236	L237	T238	I239	T240	V241	L242	V243	L245	P246	P247	D248	L249	R250	P251	L252	V253	P254	L255	
E136	R137	V138	L139	Y140	F141	E142	S143	I144	V145	V146	I147	E148	G149	G150	M151	T152	K153	L154	E155	R156	Q157	Q158	I159	L160	T161	E162	E163	Q164	Y165	L166	D167	A168	L169	E170	E171	T172	G173	D174	E175	F176	M177	A178	K179	M180	L181	A182	E183	A184	I185	Q186	A187	L188	L189	K190	S191	M192	D193	L194	E195
K76	R77	L78	K79	H80	R81	G82	W83	I84	C85	E86	K87	C88	G89	V90	E91	V92	Q93	Q94	T95	K96	V97	R98	R99	E100	R101	M102	G103	H104	I105	E106	L107	A108	S109	P110	T111	A112	H113	I114	W115	F116	L117	K118	S119	L120	P121	S122	R123	I124	G125	L126	L127	L128	L129	M130	P131	L132	R133	D134	I135
E16	F17	D18	A19	I20	K21	I22	A23	A25	S26	P27	D28	M29	I30	R31	S32	W33	S34	F35	G36	E37	V38	K39	K40	P41	E42	T43	I44	M45	Y46	R47	T48	S49	K50	P51	E52	R53	D54	G55	L56	F57	C58	A59	R60	I61	F62	G63	P64	V65	K66	D67	Y68	E69	C70	L71	C72	G73	K74	Y75	

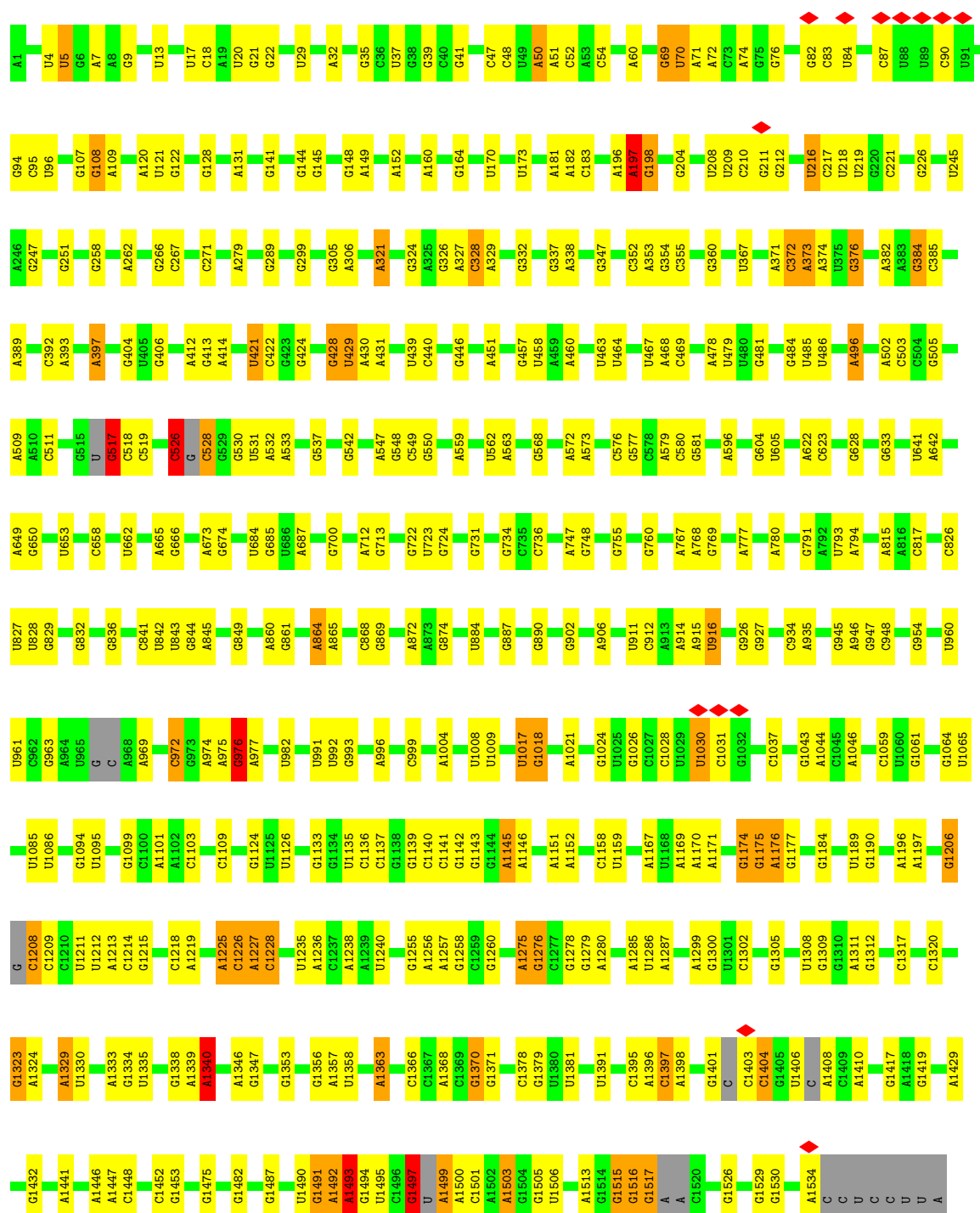
- Molecule 15: 30S ribosomal protein S18

Chain C:  72% 15% 12%

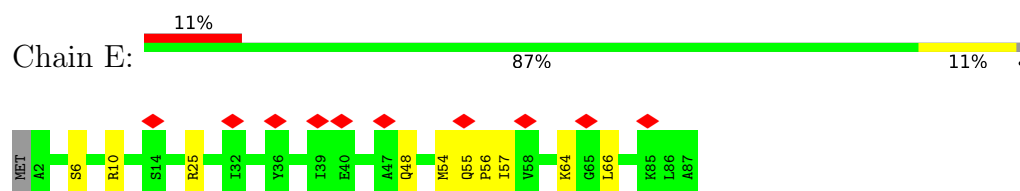


• Molecule 16: 16S rRNA

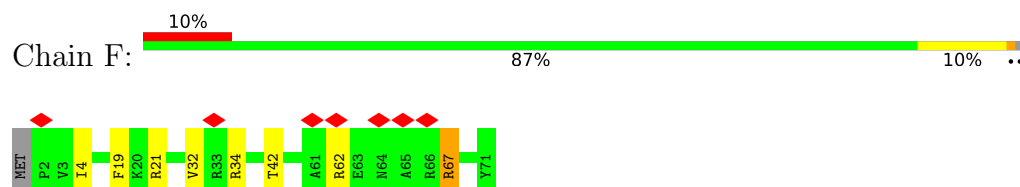
Chain D:  70% 25%



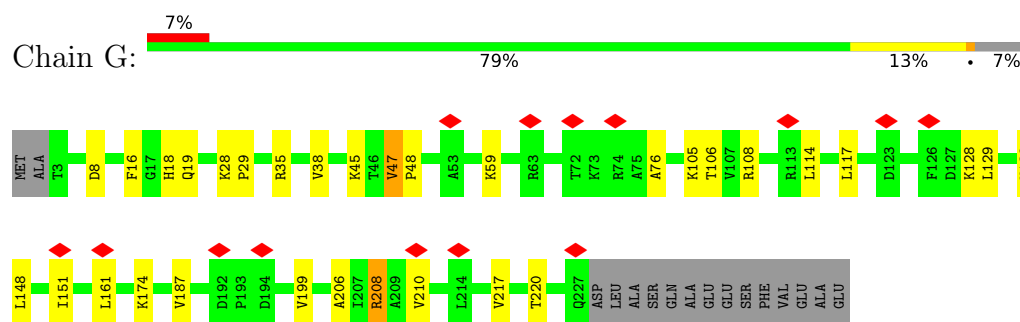
- Molecule 17: 30S ribosomal protein S20



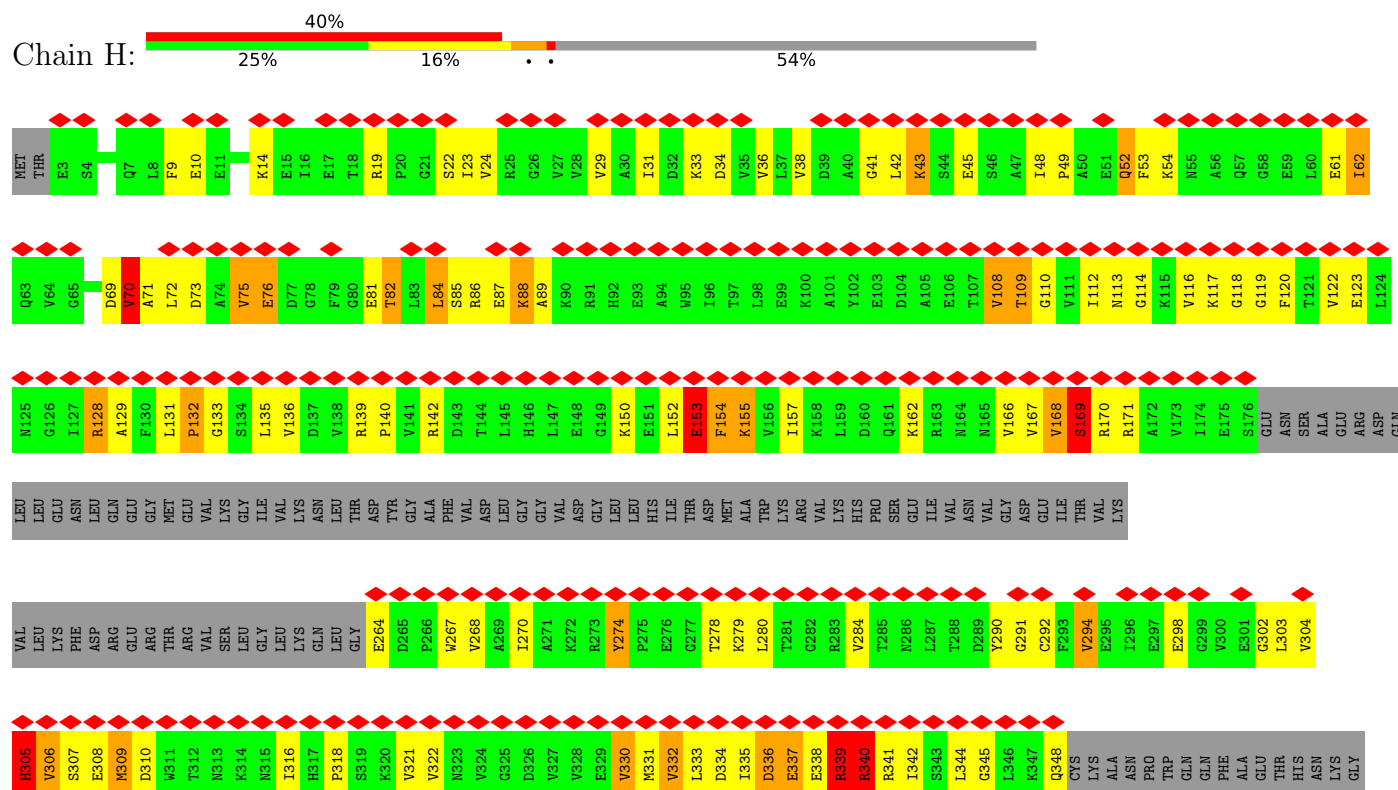
- Molecule 18: 30S ribosomal protein S21

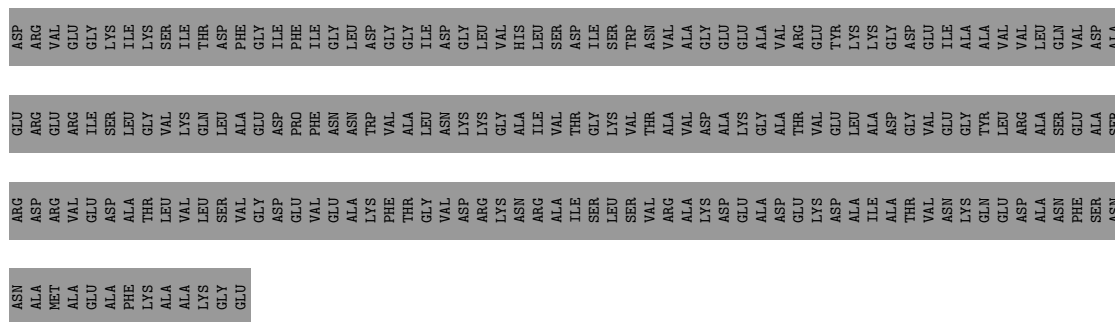


- Molecule 19: 30S ribosomal protein S2

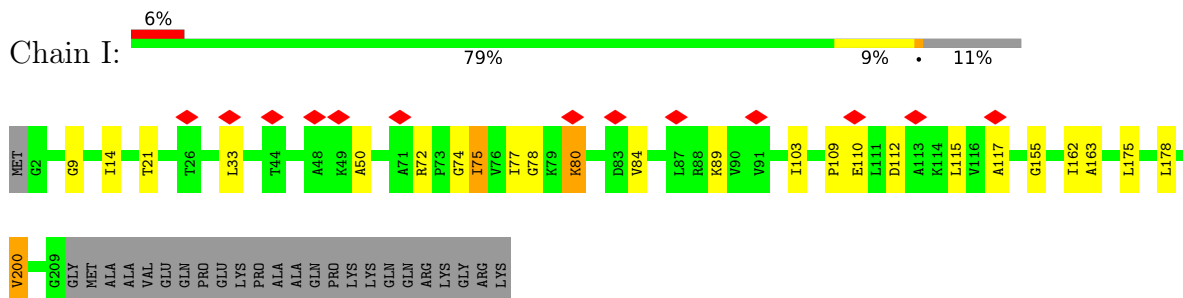


- Molecule 20: 30S ribosomal protein S1

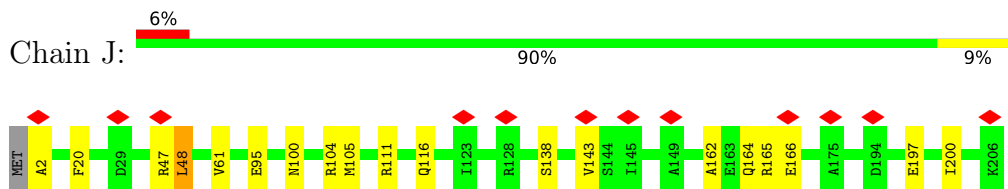




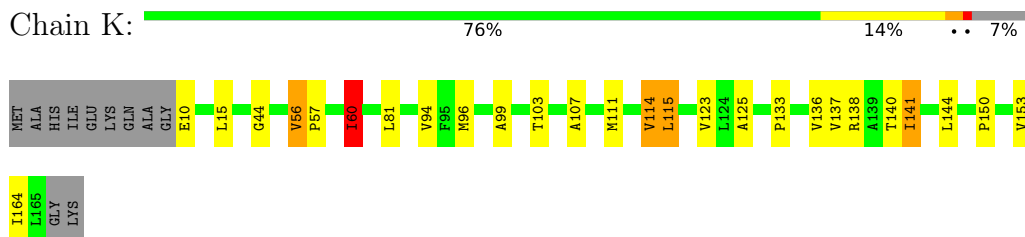
- Molecule 21: 30S ribosomal protein S3



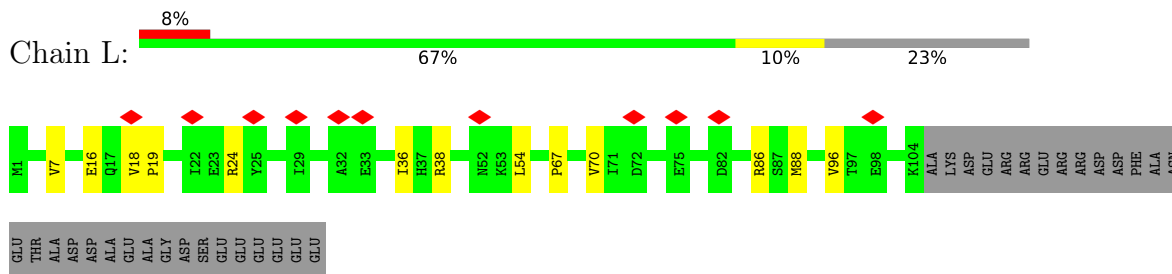
- Molecule 22: 30S ribosomal protein S4



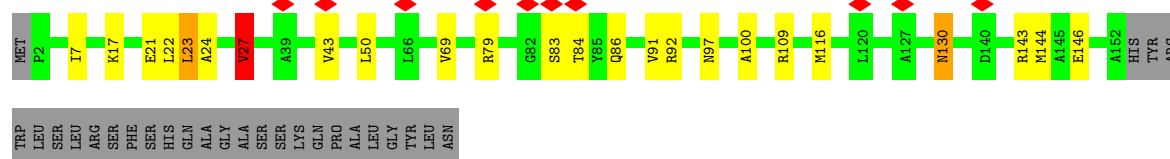
- Molecule 23: 30S ribosomal protein S5



- Molecule 24: 30S ribosomal protein S6



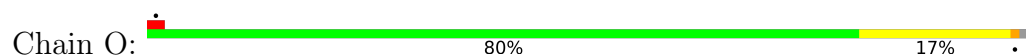
- Molecule 25: 30S ribosomal protein S7



- Molecule 26: 30S ribosomal protein S8



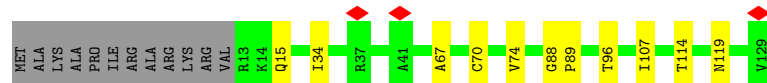
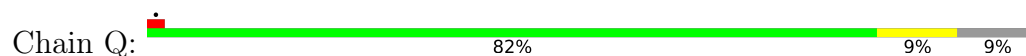
- Molecule 27: 30S ribosomal protein S9



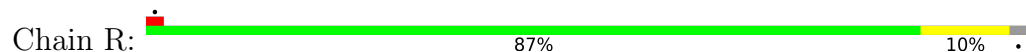
- Molecule 28: 30S ribosomal protein S10



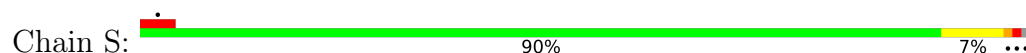
- Molecule 29: 30S ribosomal protein S11



- Molecule 30: 30S ribosomal protein S12

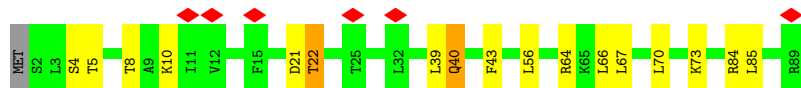
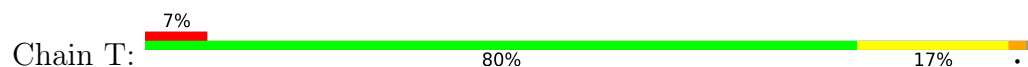


- Molecule 31: 30S ribosomal protein S14

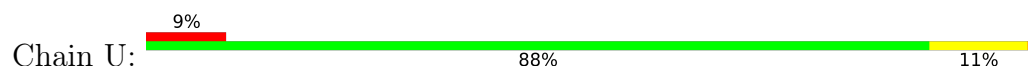




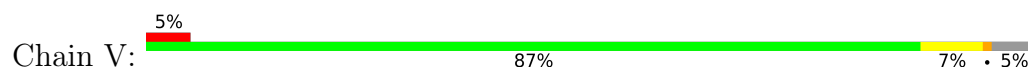
- Molecule 32: 30S ribosomal protein S15



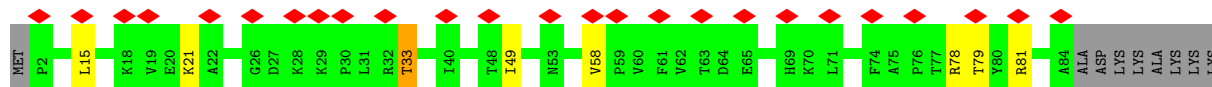
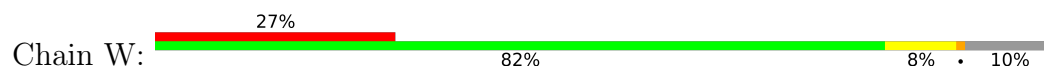
- Molecule 33: 30S ribosomal protein S16



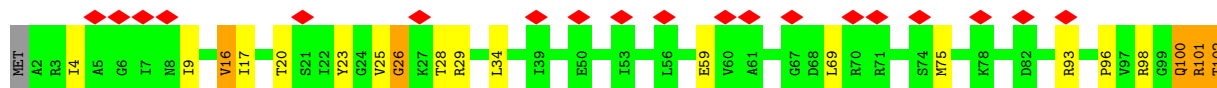
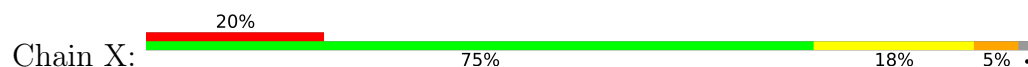
- Molecule 34: 30S ribosomal protein S17



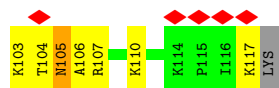
- Molecule 35: 30S ribosomal protein S19

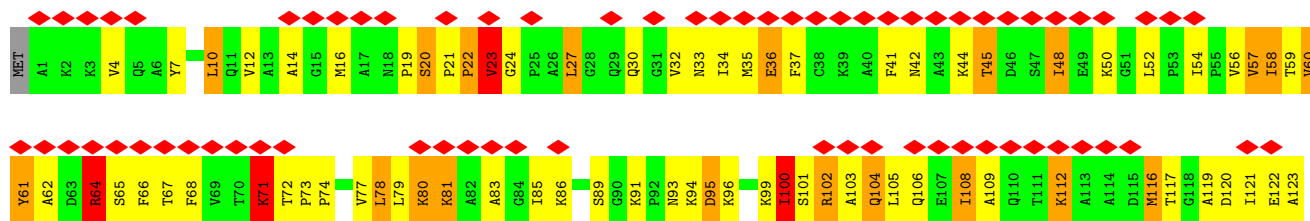


- Molecule 36: 30S ribosomal protein S13

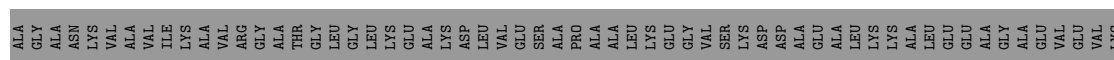
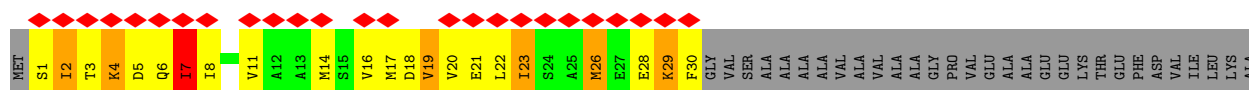


- Molecule 37: 50S ribosomal protein L11

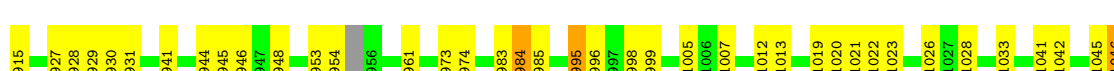
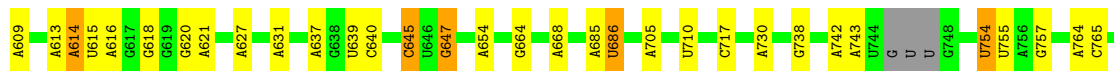
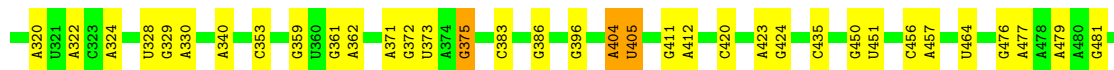
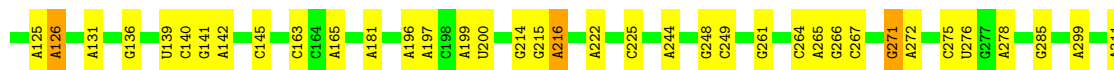


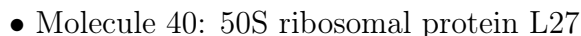


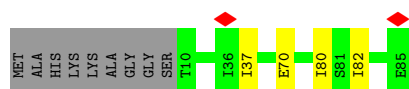
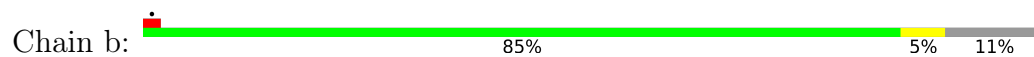
• Molecule 38: 50S ribosomal protein L7/L12



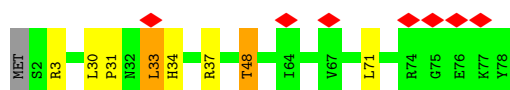
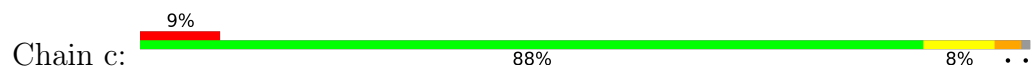
• Molecule 39: 23S rRNA



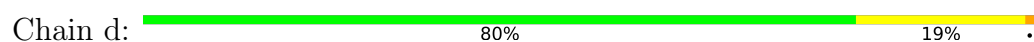




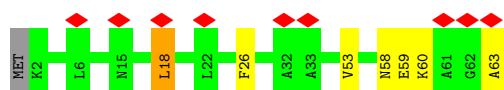
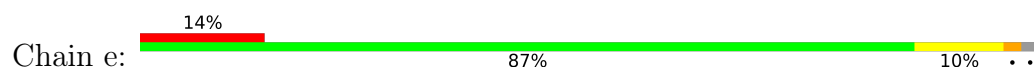
- Molecule 41: 50S ribosomal protein L28



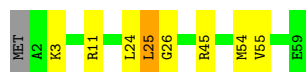
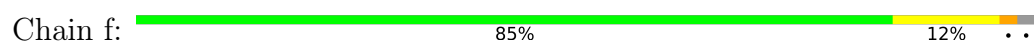
- Molecule 42: 5S rRNA



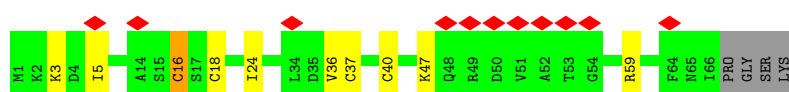
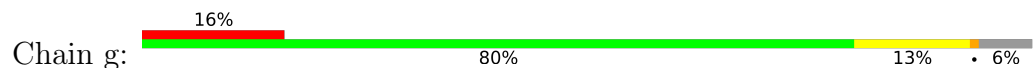
- Molecule 43: 50S ribosomal protein L29



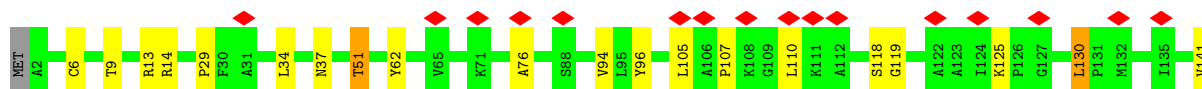
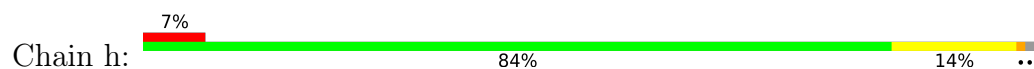
- Molecule 44: 50S ribosomal protein L30

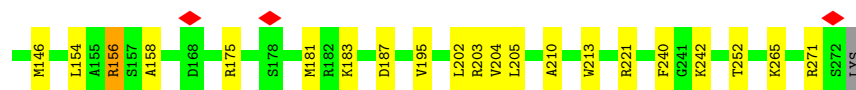


- Molecule 45: 50S ribosomal protein L31

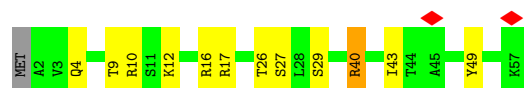
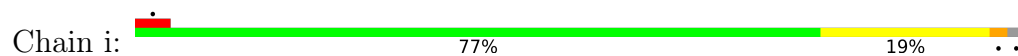


- Molecule 46: 50S ribosomal protein L2

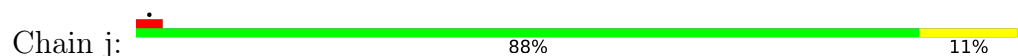




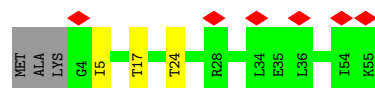
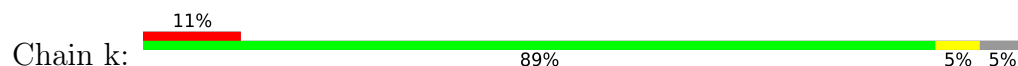
- Molecule 47: 50S ribosomal protein L32



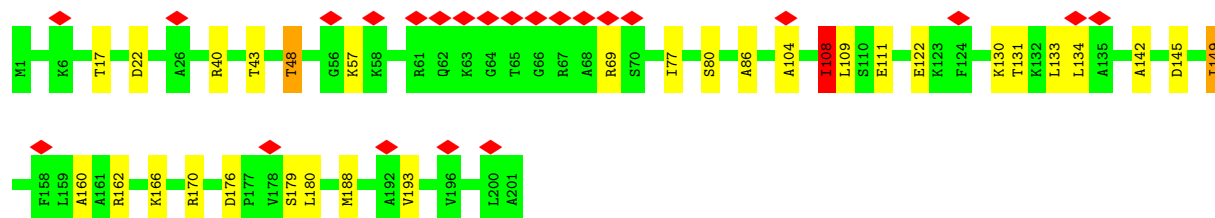
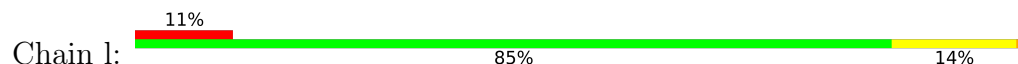
- Molecule 48: 50S ribosomal protein L3



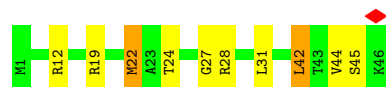
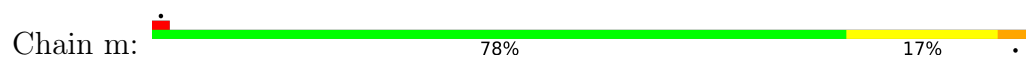
- Molecule 49: 50S ribosomal protein L33



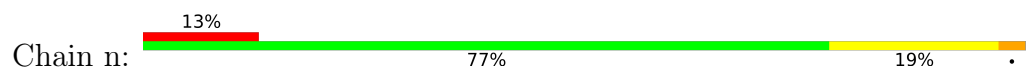
- Molecule 50: 50S ribosomal protein L4

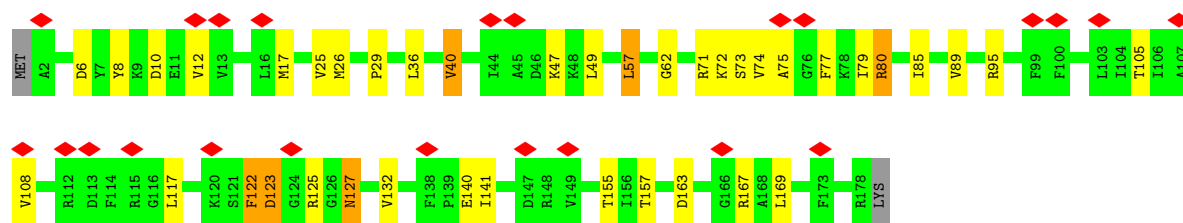


- Molecule 51: 50S ribosomal protein L34

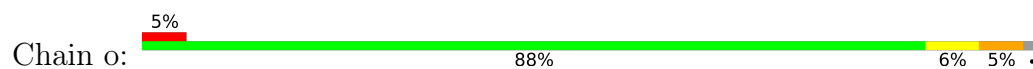


- Molecule 52: 50S ribosomal protein L5

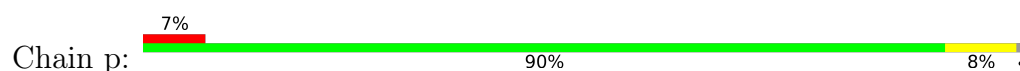




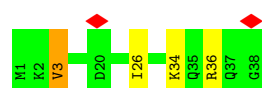
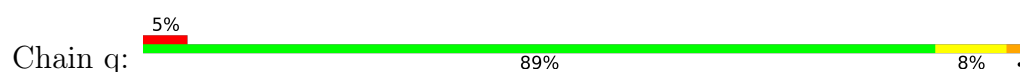
- Molecule 53: 50S ribosomal protein L35



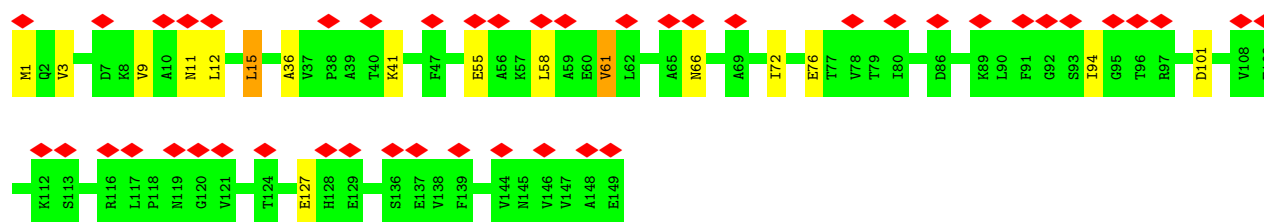
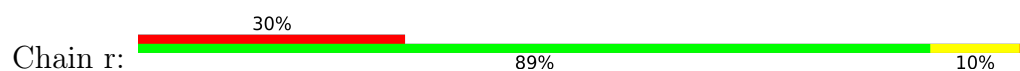
- Molecule 54: 50S ribosomal protein L6



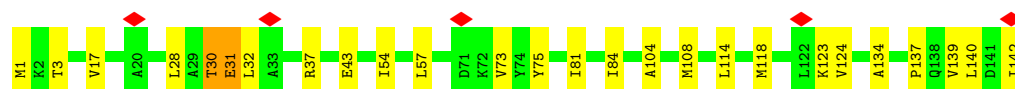
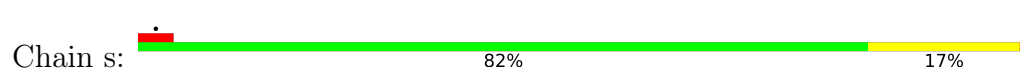
- Molecule 55: 50S ribosomal protein L36



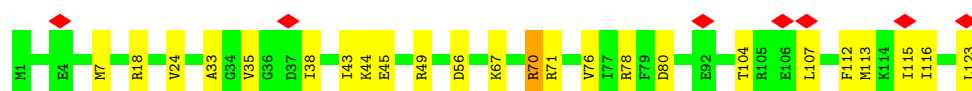
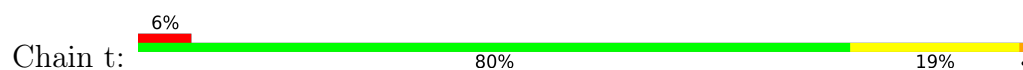
- Molecule 56: 50S ribosomal protein L9



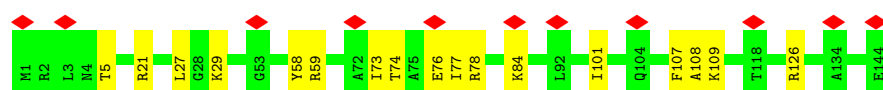
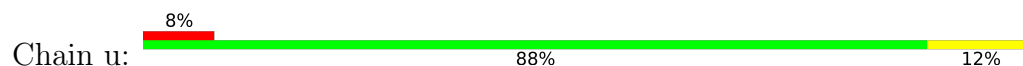
- Molecule 57: 50S ribosomal protein L13



- Molecule 58: 50S ribosomal protein L14



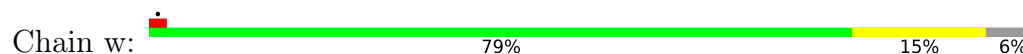
- Molecule 59: 50S ribosomal protein L15



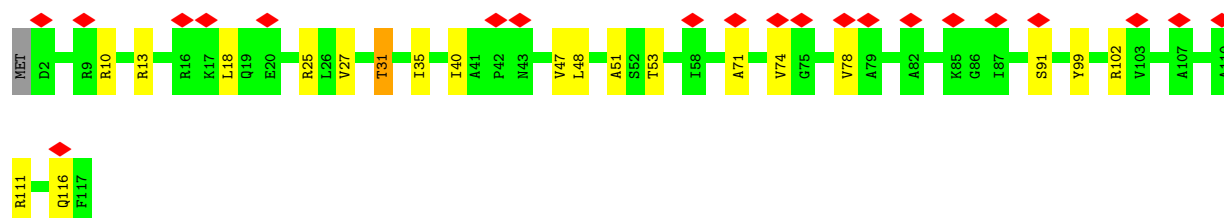
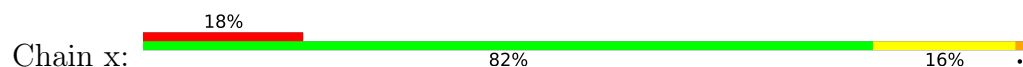
- Molecule 60: 50S ribosomal protein L16



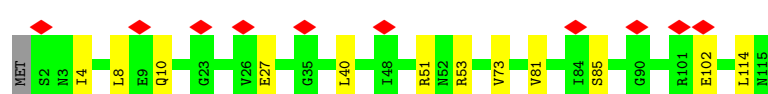
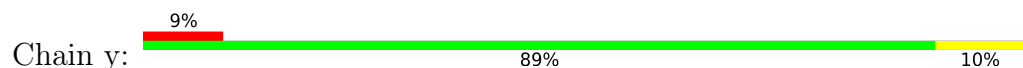
- Molecule 61: 50S ribosomal protein L17



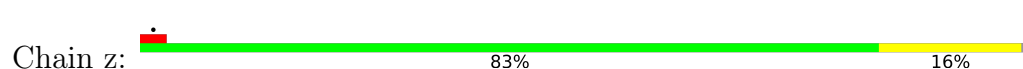
- Molecule 62: 50S ribosomal protein L18



- Molecule 63: 50S ribosomal protein L19



- Molecule 64: 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	29704	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	0.042	Depositor
Minimum map value	-0.010	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.00868	Depositor
Map size (Å)	520.0, 520.0, 520.0	wwPDB
Map dimensions	500, 500, 500	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	0.50	0/829	0.73	0/1107
2	1	0.67	0/864	1.08	0/1156
3	2	0.54	0/752	0.90	0/1005
4	3	0.47	0/796	0.78	0/1062
5	4	0.52	0/766	0.88	0/1025
6	5	0.63	1/528 (0.2%)	0.55	0/810
7	6	0.55	1/603 (0.2%)	0.56	0/926
8	7	0.60	2/607 (0.3%)	0.84	2/940 (0.2%)
9	9	1.15	3/1131 (0.3%)	1.30	4/1524 (0.3%)
10	A	0.36	0/1810	0.72	2/2821 (0.1%)
10	B	0.43	0/1810	0.86	9/2821 (0.3%)
11	AA	0.67	13/10591 (0.1%)	0.96	54/14289 (0.4%)
12	AB	0.43	1/808 (0.1%)	0.70	2/1088 (0.2%)
13	AC	0.60	4/1808 (0.2%)	0.73	9/2450 (0.4%)
13	AD	0.40	0/1789	0.56	0/2425
14	AE	0.54	8/10545 (0.1%)	0.74	25/14236 (0.2%)
15	C	0.66	0/553	1.15	2/743 (0.3%)
16	D	0.40	9/36610 (0.0%)	0.75	39/57091 (0.1%)
17	E	0.76	0/675	1.32	0/895
18	F	0.71	0/597	1.20	0/792
19	G	0.65	0/1791	1.08	1/2413 (0.0%)
20	H	0.76	4/1746 (0.2%)	1.58	34/2382 (1.4%)
21	I	0.58	0/1663	0.98	0/2241
22	J	0.63	0/1665	1.08	0/2227
23	K	0.63	1/1165 (0.1%)	1.06	2/1568 (0.1%)
24	L	0.58	0/867	0.94	0/1171
25	M	0.68	0/1195	1.19	3/1602 (0.2%)
26	N	0.55	0/989	0.91	0/1326
27	O	0.59	0/1034	1.02	1/1375 (0.1%)
28	P	0.60	0/800	1.10	4/1082 (0.4%)
29	Q	0.55	0/893	0.91	0/1205
30	R	0.49	0/952	0.81	0/1274

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	S	0.64	0/817	1.11	1/1088 (0.1%)
32	T	0.69	0/722	1.21	0/964
33	U	0.57	0/659	0.99	0/884
34	V	0.45	0/657	0.73	0/881
35	W	0.51	0/680	0.83	0/915
36	X	0.67	0/909	1.21	3/1215 (0.2%)
37	Y	1.03	0/1046	1.08	0/1410
38	Z	1.03	0/227	1.12	0/304
39	a	0.40	3/69247 (0.0%)	0.75	55/107985 (0.1%)
40	b	0.51	0/589	0.76	0/779
41	c	0.63	0/635	0.97	0/848
42	d	0.37	0/2872	0.69	0/4478
43	e	0.69	0/502	1.19	0/667
44	f	0.62	0/452	1.02	0/605
45	g	0.55	0/531	0.99	1/709 (0.1%)
46	h	0.54	0/2121	0.85	0/2852
47	i	0.52	0/450	0.94	0/599
48	j	0.60	0/1586	0.87	0/2134
49	k	0.47	0/433	0.80	0/576
50	l	0.61	0/1571	1.03	1/2113 (0.0%)
51	m	0.68	0/380	1.21	0/498
52	n	0.62	0/1434	1.18	10/1926 (0.5%)
53	o	0.64	0/513	1.10	1/676 (0.1%)
54	p	0.58	0/1333	0.89	0/1805
55	q	0.50	0/303	0.88	0/397
56	r	0.63	0/1122	0.97	1/1515 (0.1%)
57	s	0.68	0/1152	1.02	2/1551 (0.1%)
58	t	0.57	0/955	0.88	0/1279
59	u	0.55	0/1062	0.96	1/1413 (0.1%)
60	v	0.60	0/1093	0.97	0/1460
61	w	0.67	0/964	1.13	0/1289
62	x	0.61	0/902	1.09	0/1209
63	y	0.53	0/929	0.79	0/1242
64	z	0.80	0/960	1.25	0/1278
All	All	0.50	50/189040 (0.0%)	0.84	269/278616 (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

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Mol	Chain	#Chirality outliers	#Planarity outliers
10	B	0	2
11	AA	0	10
14	AE	0	5
20	H	0	3
36	X	0	1
All	All	0	23

The worst 5 of 50 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	9	130	PRO	N-CA	18.24	1.70	1.47
11	AA	374	GLU	C-N	17.62	1.54	1.33
11	AA	850	ILE	N-CA	-13.15	1.29	1.46
14	AE	93	THR	CA-C	12.13	1.69	1.52
20	H	169	SER	N-CA	11.81	1.61	1.46

The worst 5 of 269 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	D	1516	G	O3'-P-O5'	17.48	130.22	104.00
11	AA	727	VAL	N-CA-C	-17.09	95.18	110.74
20	H	88	LYS	CA-C-N	16.96	143.61	120.38
20	H	88	LYS	C-N-CA	16.96	143.61	120.38
10	B	29	G	C3'-C2'-O2'	15.96	134.64	110.70

There are no chirality outliers.

5 of 23 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	A	19	G	Sidechain
10	A	7	G	Sidechain
11	AA	205	PRO	Peptide
11	AA	594	VAL	Peptide
11	AA	595	THR	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	7	0
4	3	788	844	844	10	0
5	4	753	780	780	0	0
6	5	472	260	261	22	0
7	6	542	305	306	24	0
8	7	547	97	271	74	0
9	9	1117	0	1153	160	0
10	A	1620	826	826	171	0
10	B	1620	813	827	137	0
11	AA	10425	10426	10428	388	0
12	AB	790	783	783	8	0
13	AC	1786	1813	1813	78	0
13	AD	1767	1789	1789	48	0
14	AE	10388	10612	10611	373	0
15	C	544	559	560	23	0
16	D	32703	16423	16459	227	0
17	E	669	719	719	3	0
18	F	589	629	629	8	0
19	G	1760	1785	1785	47	0
20	H	1730	1454	1454	211	0
21	I	1636	1710	1710	39	0
22	J	1643	1707	1707	29	0
23	K	1152	1196	1196	22	0
24	L	848	846	846	3	0
25	M	1181	1235	1235	33	0
26	N	979	1031	1031	5	0
27	O	1022	1070	1070	12	0
28	P	790	831	831	37	0
29	Q	877	887	887	4	0
30	R	939	1001	1001	7	0
31	S	805	844	844	5	0
32	T	714	734	734	7	0
33	U	649	666	666	3	0
34	V	648	691	691	4	0
35	W	663	688	688	2	0
36	X	900	964	964	57	0
37	Y	1032	0	1088	88	0
38	Z	227	0	237	18	0
39	a	61841	31077	31123	293	0
40	b	582	599	599	2	0
41	c	625	652	652	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	d	2569	1301	1301	5	0
43	e	501	531	531	4	0
44	f	448	488	488	5	0
45	g	522	520	520	11	0
46	h	2082	2154	2154	20	0
47	i	444	459	458	6	0
48	j	1565	1617	1616	15	0
49	k	426	464	464	0	0
50	l	1552	1619	1619	14	0
51	m	377	418	418	11	0
52	n	1410	1443	1444	27	0
53	o	504	572	572	4	0
54	p	1313	1358	1358	7	0
55	q	302	343	343	1	0
56	r	1111	1148	1148	4	0
57	s	1129	1162	1162	14	0
58	t	946	1023	1023	12	0
59	u	1053	1129	1129	8	0
60	v	1074	1157	1157	5	0
61	w	951	994	994	7	0
62	x	892	923	923	10	0
63	y	917	962	962	4	0
64	z	947	1020	1019	13	0
65	AE	1	0	0	0	0
66	AE	2	0	0	0	0
All	All	175820	124723	127473	2425	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 8.

The worst 5 of 2425 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)
20:H:131:LEU:CB	20:H:167:VAL:CA	1.78	1.58
15:C:12:ARG:HG3	20:H:264:GLU:CB	1.30	1.53
20:H:131:LEU:CB	20:H:167:VAL:HA	1.03	1.46
9:9:31:ARG:NE	39:a:1054:A:H5'	1.31	1.45
11:AA:1026:GLU:HG3	16:D:1030:U:C2	1.54	1.42

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	101/103 (98%)	97 (96%)	3 (3%)	1 (1%)	12	43
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%)	12	43
5	4	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
9	9	146/165 (88%)	95 (65%)	37 (25%)	14 (10%)	0	7
11	AA	1318/1342 (98%)	1149 (87%)	137 (10%)	32 (2%)	4	29
12	AB	94/181 (52%)	88 (94%)	6 (6%)	0	100	100
13	AC	228/329 (69%)	215 (94%)	11 (5%)	2 (1%)	14	45
13	AD	226/329 (69%)	212 (94%)	13 (6%)	1 (0%)	30	60
14	AE	1329/1358 (98%)	1200 (90%)	120 (9%)	9 (1%)	18	50
15	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
17	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
18	F	68/71 (96%)	68 (100%)	0	0	100	100
19	G	223/241 (92%)	210 (94%)	13 (6%)	0	100	100
20	H	255/557 (46%)	188 (74%)	55 (22%)	12 (5%)	2	18
21	I	206/233 (88%)	196 (95%)	9 (4%)	1 (0%)	24	56
22	J	203/206 (98%)	198 (98%)	5 (2%)	0	100	100
23	K	154/167 (92%)	146 (95%)	7 (4%)	1 (1%)	21	52
24	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	12	43
25	M	149/179 (83%)	144 (97%)	4 (3%)	1 (1%)	18	50
26	N	127/130 (98%)	121 (95%)	5 (4%)	1 (1%)	16	48
27	O	125/130 (96%)	115 (92%)	9 (7%)	1 (1%)	16	48
28	P	97/103 (94%)	88 (91%)	8 (8%)	1 (1%)	12	43
29	Q	115/129 (89%)	104 (90%)	9 (8%)	2 (2%)	7	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	R	117/124 (94%)	116 (99%)	1 (1%)	0	100	100
31	S	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
32	T	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
33	U	80/82 (98%)	76 (95%)	3 (4%)	1 (1%)	9	38
34	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
35	W	81/92 (88%)	78 (96%)	3 (4%)	0	100	100
36	X	114/118 (97%)	107 (94%)	5 (4%)	2 (2%)	6	34
37	Y	139/142 (98%)	102 (73%)	25 (18%)	12 (9%)	0	8
38	Z	28/121 (23%)	19 (68%)	7 (25%)	2 (7%)	1	12
40	b	74/85 (87%)	69 (93%)	5 (7%)	0	100	100
41	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
43	e	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
44	f	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
45	g	64/70 (91%)	63 (98%)	1 (2%)	0	100	100
46	h	269/273 (98%)	259 (96%)	9 (3%)	1 (0%)	30	60
47	i	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
48	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
49	k	50/55 (91%)	50 (100%)	0	0	100	100
50	l	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	24	56
51	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
52	n	175/179 (98%)	162 (93%)	11 (6%)	2 (1%)	11	42
53	o	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
54	p	173/177 (98%)	161 (93%)	12 (7%)	0	100	100
55	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
56	r	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
57	s	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
58	t	121/123 (98%)	111 (92%)	10 (8%)	0	100	100
59	u	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
60	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
61	w	117/127 (92%)	107 (92%)	10 (8%)	0	100	100
62	x	114/117 (97%)	108 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	y	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
64	z	115/118 (98%)	110 (96%)	4 (4%)	1 (1%)	14	45
All	All	9368/10437 (90%)	8605 (92%)	660 (7%)	103 (1%)	14	42

5 of 103 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	9	88	HIS
11	AA	596	ASP
11	AA	853	ASP
11	AA	859	GLU
11	AA	862	LEU

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%)	8	31
2	1	93/93 (100%)	86 (92%)	7 (8%)	12	39
3	2	81/84 (96%)	77 (95%)	4 (5%)	22	48
4	3	84/85 (99%)	79 (94%)	5 (6%)	17	44
5	4	78/78 (100%)	75 (96%)	3 (4%)	29	53
9	9	112/123 (91%)	63 (56%)	49 (44%)	0	0
11	AA	1140/1157 (98%)	1027 (90%)	113 (10%)	7	30
12	AB	86/158 (54%)	85 (99%)	1 (1%)	63	72
13	AC	198/286 (69%)	183 (92%)	15 (8%)	12	38
13	AD	196/286 (68%)	193 (98%)	3 (2%)	57	68
14	AE	1120/1134 (99%)	1046 (93%)	74 (7%)	15	42
15	C	57/65 (88%)	55 (96%)	2 (4%)	32	54
17	E	65/66 (98%)	61 (94%)	4 (6%)	16	44
18	F	60/61 (98%)	57 (95%)	3 (5%)	22	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	G	187/199 (94%)	174 (93%)	13 (7%)	14	41
20	H	137/461 (30%)	124 (90%)	13 (10%)	8	31
21	I	171/190 (90%)	163 (95%)	8 (5%)	23	48
22	J	172/173 (99%)	164 (95%)	8 (5%)	23	48
23	K	119/126 (94%)	111 (93%)	8 (7%)	15	42
24	L	91/116 (78%)	84 (92%)	7 (8%)	12	38
25	M	124/147 (84%)	113 (91%)	11 (9%)	9	33
26	N	104/105 (99%)	101 (97%)	3 (3%)	37	57
27	O	105/107 (98%)	99 (94%)	6 (6%)	18	45
28	P	86/90 (96%)	77 (90%)	9 (10%)	6	28
29	Q	90/99 (91%)	88 (98%)	2 (2%)	45	63
30	R	101/104 (97%)	95 (94%)	6 (6%)	18	44
31	S	83/84 (99%)	79 (95%)	4 (5%)	23	48
32	T	76/77 (99%)	65 (86%)	11 (14%)	3	17
33	U	65/65 (100%)	60 (92%)	5 (8%)	12	38
34	V	74/78 (95%)	71 (96%)	3 (4%)	27	52
35	W	72/79 (91%)	66 (92%)	6 (8%)	10	35
36	X	94/96 (98%)	87 (93%)	7 (7%)	13	39
37	Y	109/110 (99%)	69 (63%)	40 (37%)	0	1
38	Z	26/85 (31%)	10 (38%)	16 (62%)	0	0
40	b	58/63 (92%)	57 (98%)	1 (2%)	53	67
41	c	67/68 (98%)	64 (96%)	3 (4%)	24	49
43	e	54/55 (98%)	51 (94%)	3 (6%)	19	46
44	f	48/49 (98%)	43 (90%)	5 (10%)	7	28
45	g	59/62 (95%)	54 (92%)	5 (8%)	10	35
46	h	216/218 (99%)	199 (92%)	17 (8%)	11	37
47	i	47/48 (98%)	41 (87%)	6 (13%)	4	21
48	j	164/164 (100%)	156 (95%)	8 (5%)	22	48
49	k	47/49 (96%)	44 (94%)	3 (6%)	16	43
50	l	165/165 (100%)	151 (92%)	14 (8%)	10	35
51	m	38/38 (100%)	36 (95%)	2 (5%)	20	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	n	148/150 (99%)	130 (88%)	18 (12%)	5	22
53	o	51/52 (98%)	47 (92%)	4 (8%)	11	37
54	p	136/138 (99%)	130 (96%)	6 (4%)	25	50
55	q	34/34 (100%)	31 (91%)	3 (9%)	9	33
56	r	114/114 (100%)	102 (90%)	12 (10%)	6	28
57	s	116/116 (100%)	106 (91%)	10 (9%)	10	34
58	t	104/104 (100%)	98 (94%)	6 (6%)	18	45
59	u	103/103 (100%)	96 (93%)	7 (7%)	14	42
60	v	109/109 (100%)	105 (96%)	4 (4%)	30	54
61	w	99/103 (96%)	91 (92%)	8 (8%)	11	36
62	x	86/87 (99%)	80 (93%)	6 (7%)	14	41
63	y	99/100 (99%)	91 (92%)	8 (8%)	11	36
64	z	89/90 (99%)	85 (96%)	4 (4%)	24	49
All	All	7791/8630 (90%)	7151 (92%)	640 (8%)	13	36

5 of 640 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	Z	3	THR
55	q	26	ILE
38	Z	30	PHE
38	Z	2	ILE
48	j	99	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 72 such sidechains are listed below:

Mol	Chain	Res	Type
46	h	70	ASN
63	y	77	HIS
47	i	5	GLN
55	q	35	GLN
14	AE	865	HIS

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%)
16	D	1515/1542 (98%)	289 (19%)	35 (2%)
39	a	2859/2904 (98%)	541 (18%)	0
42	d	119/120 (99%)	17 (14%)	0
8	7	24/37 (64%)	15 (62%)	3 (12%)
All	All	4667/4755 (98%)	926 (19%)	50 (1%)

5 of 926 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	-9	G
8	7	-8	U
8	7	-7	U
8	7	-5	U
8	7	-4	U

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	D	532	A
16	D	1109	C
16	D	1493	A
16	D	562	U
16	D	793	U

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

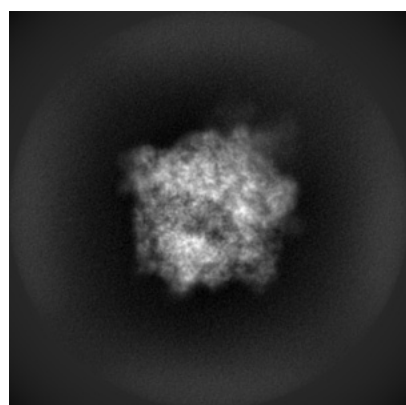
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21470. These allow visual inspection of the internal detail of the map and identification of artifacts.

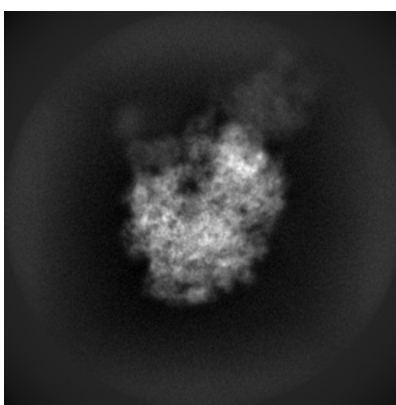
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

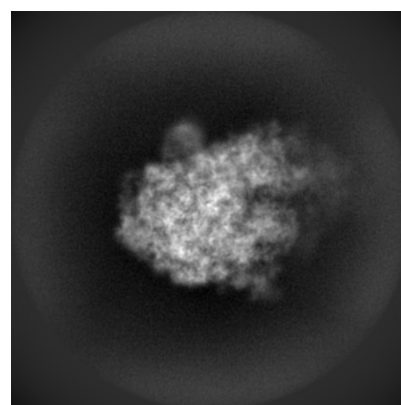
6.1.1 Primary map



X



Y

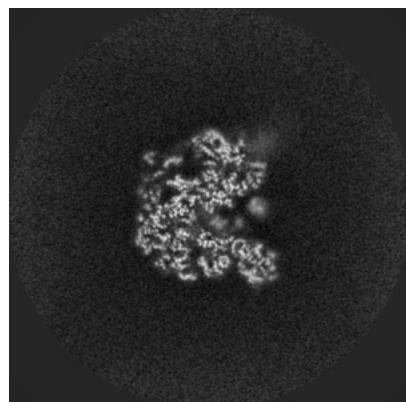


Z

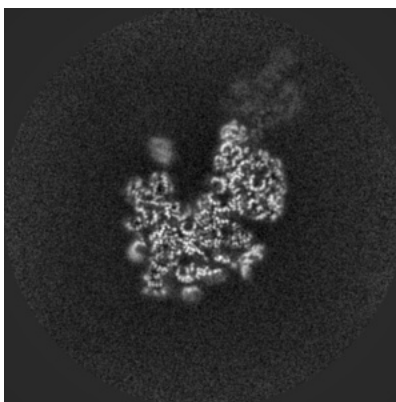
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

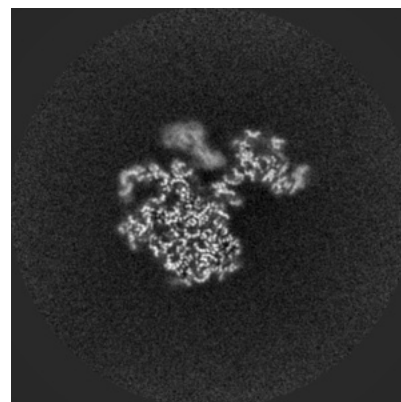
6.2.1 Primary map



X Index: 250



Y Index: 250

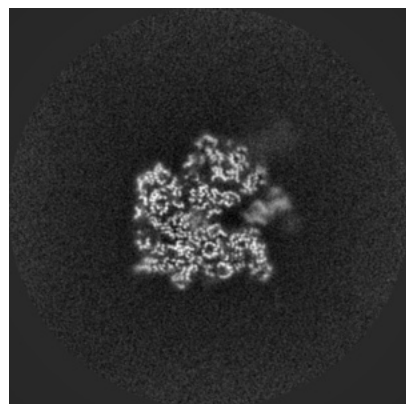


Z Index: 250

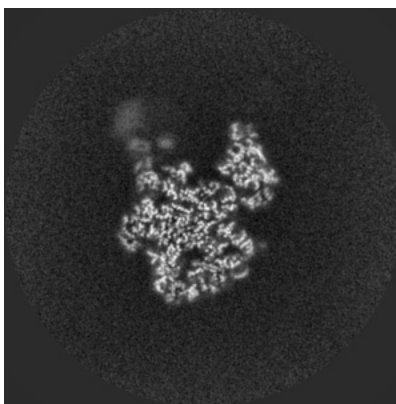
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

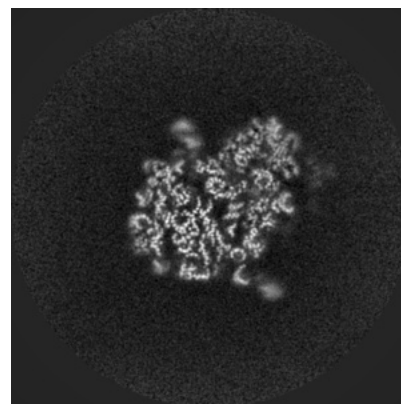
6.3.1 Primary map



X Index: 238



Y Index: 213

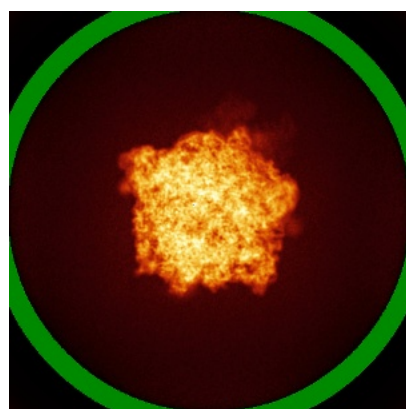


Z Index: 276

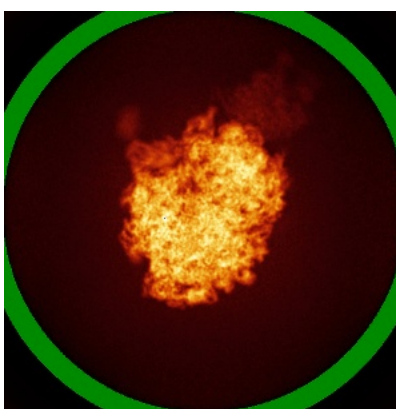
The images above show the largest variance slices of the map in three orthogonal directions.

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 0.00868. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

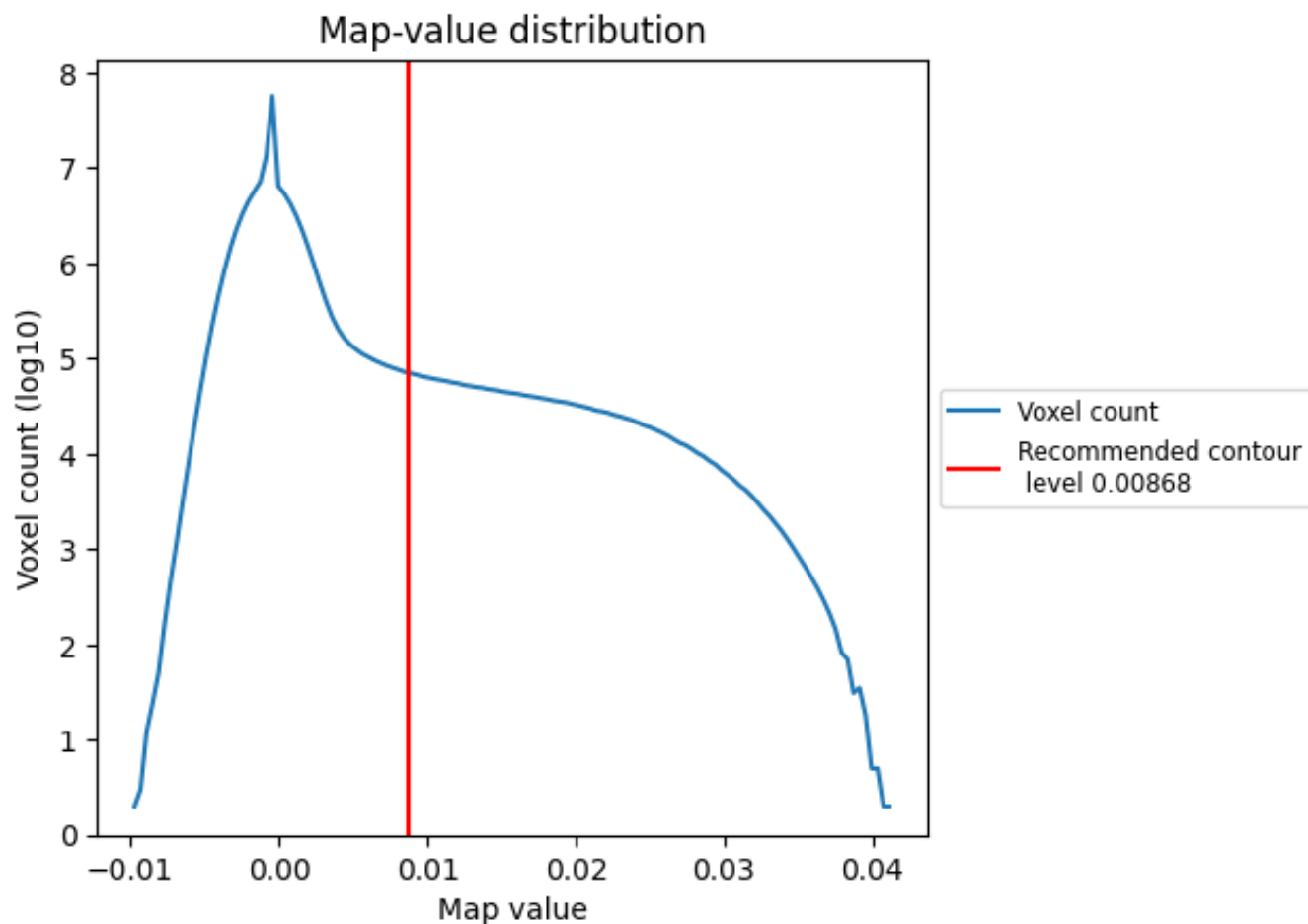
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

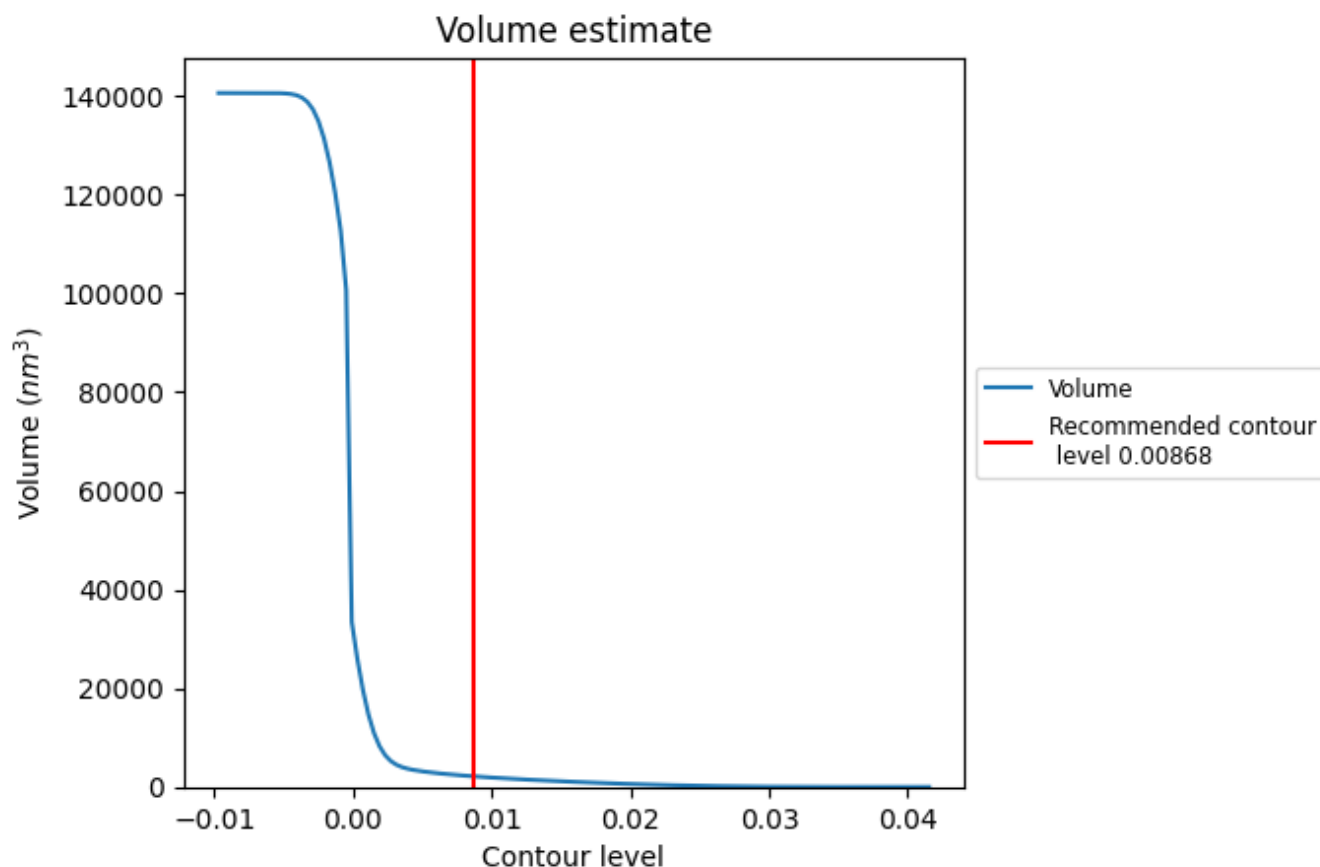
This section contains the results of statistical analysis of the map.

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.

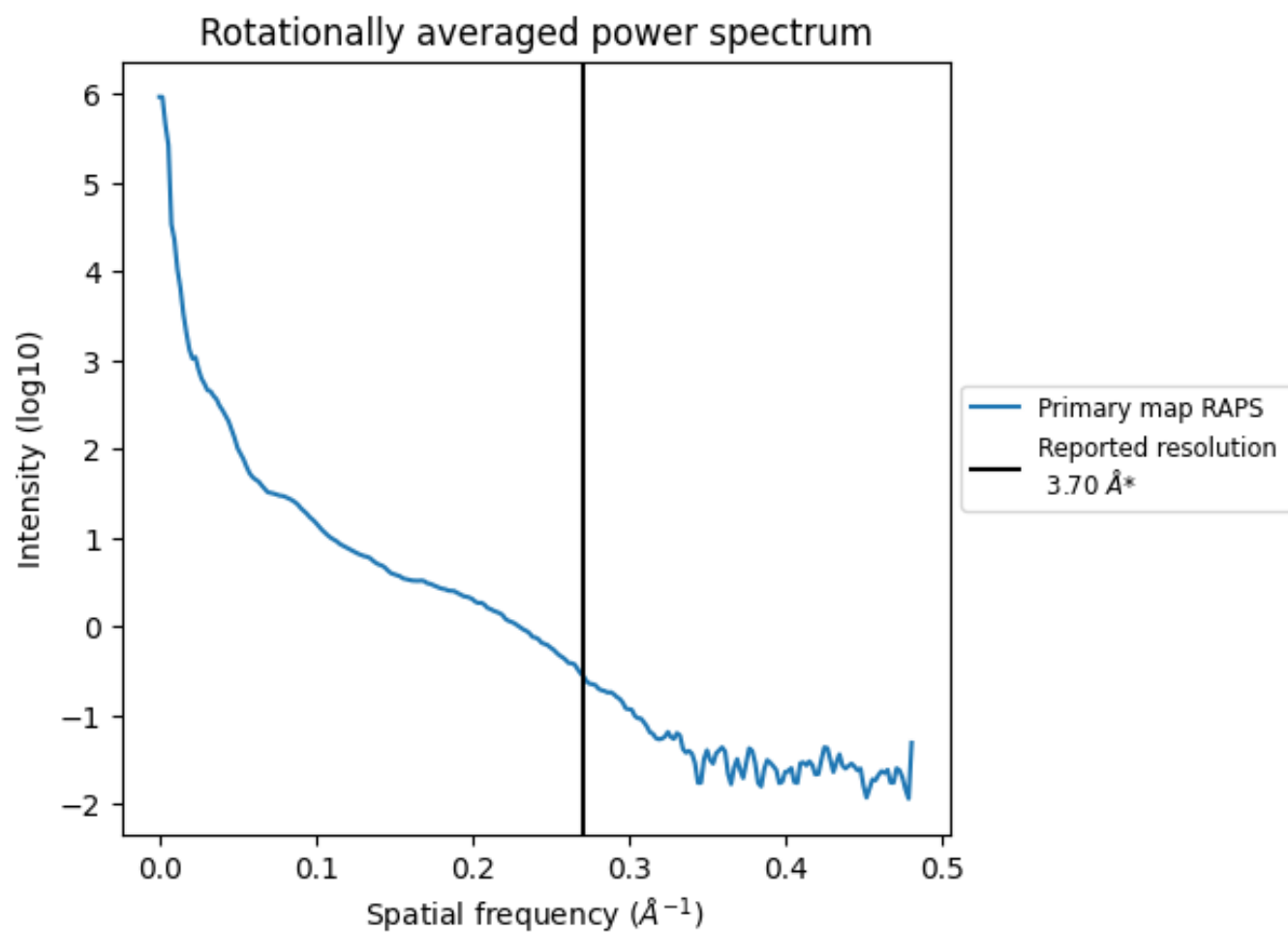
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2155 nm^3 ; this corresponds to an approximate mass of 1947 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 0.270 Å⁻¹

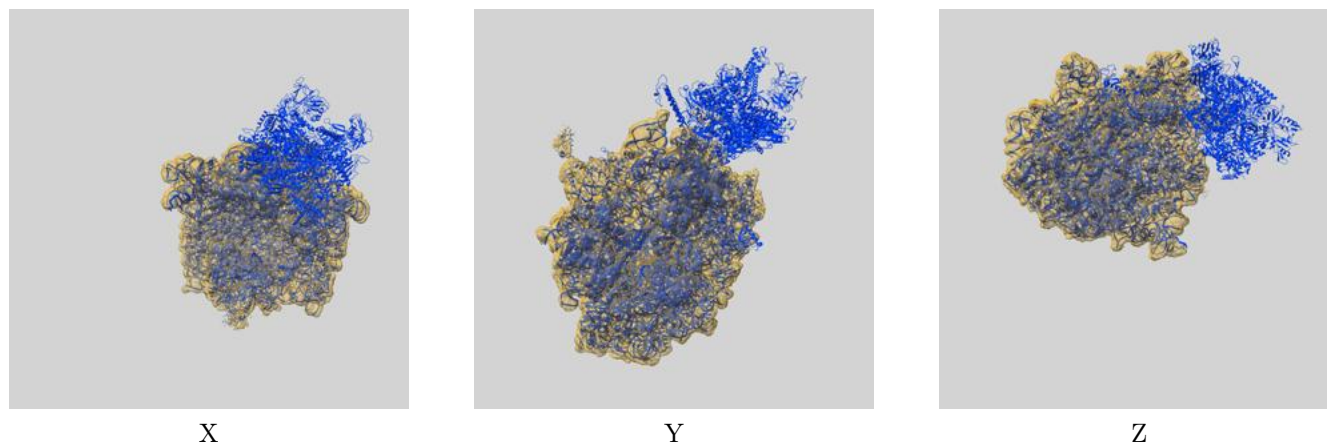
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

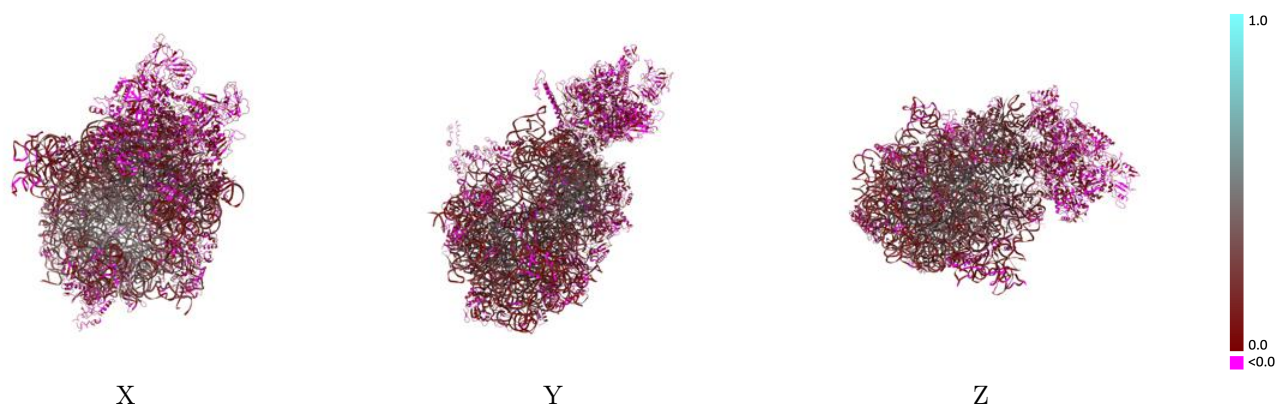
This section contains information regarding the fit between EMDB map EMD-21470 and PDB model 6VYS. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



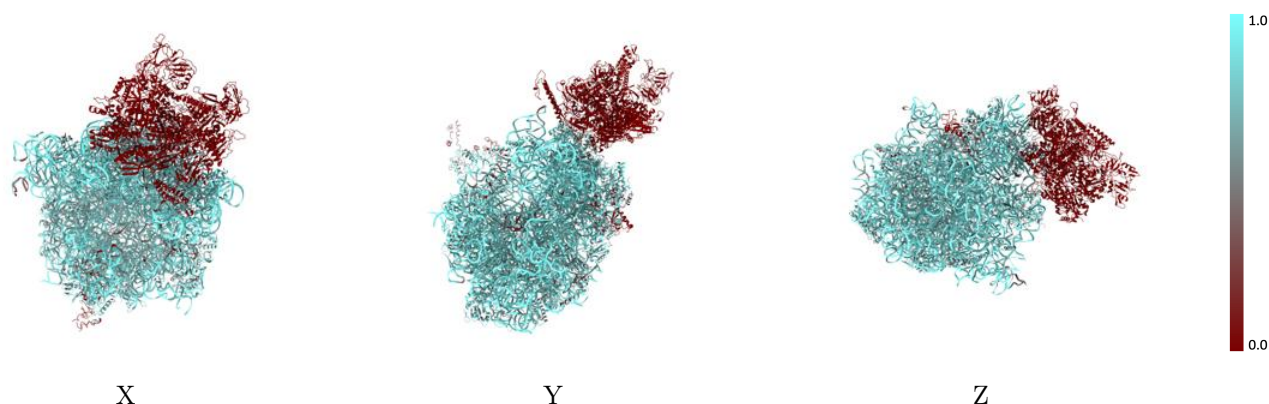
The images above show the 3D surface view of the map at the recommended contour level 0.00868 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



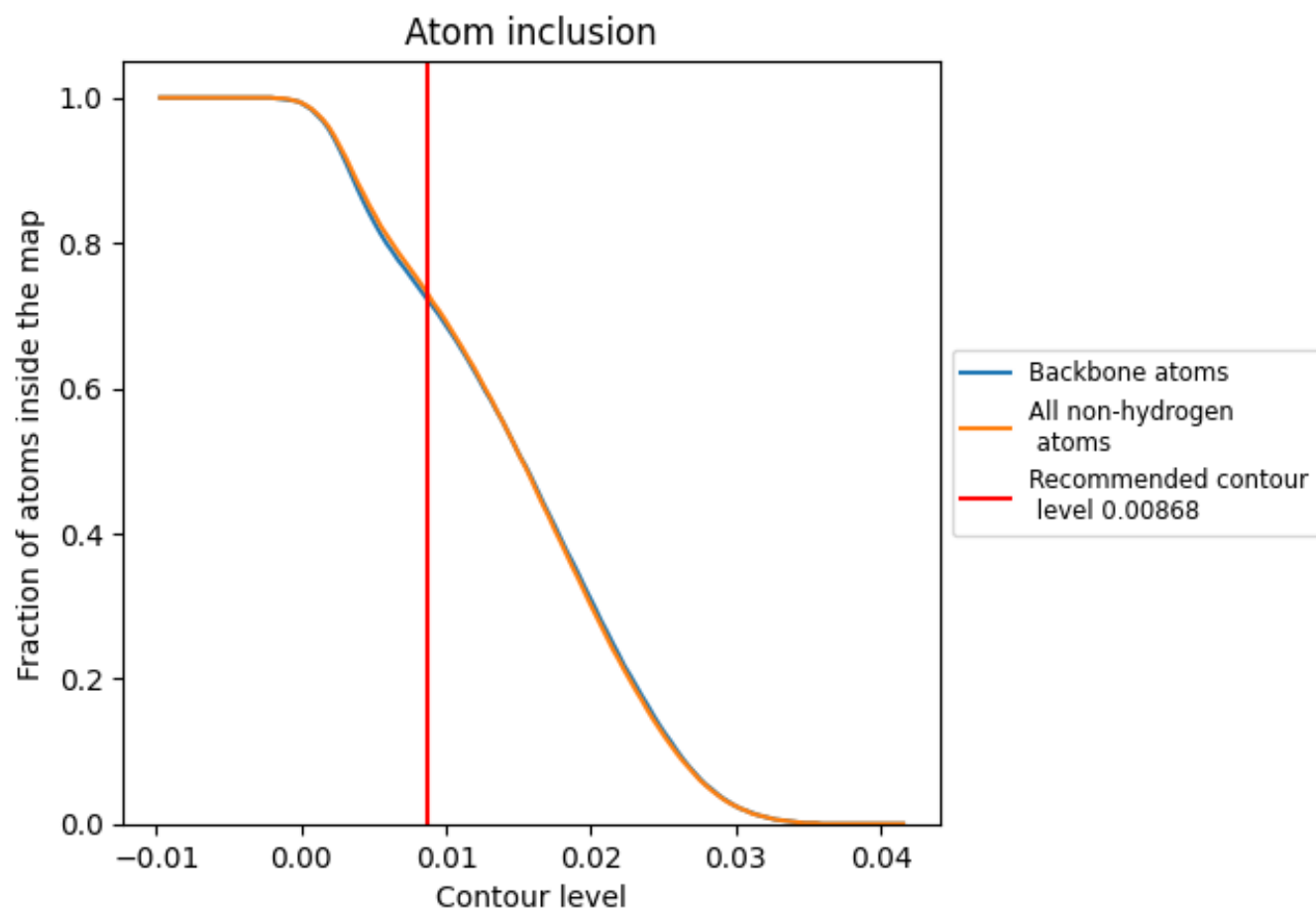
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00868).

9.4 Atom inclusion ⓘ



At the recommended contour level, 72% of all backbone atoms, 73% 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 (0.00868) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7320	 0.1950
0	 0.8140	 0.1990
1	 0.7810	 0.2550
2	 0.7000	 0.1110
3	 0.7650	 0.0900
4	 0.8100	 0.1990
5	 0.0000	 0.0130
6	 0.0180	 0.1500
7	 0.3070	 0.1010
9	 0.5580	 0.0400
A	 0.8900	 0.1870
AA	 0.0080	 0.0770
AB	 0.0000	 0.0340
AC	 0.0180	 0.1010
AD	 0.0000	 0.0460
AE	 0.0010	 0.0650
B	 0.6520	 0.0930
C	 0.7840	 0.1820
D	 0.9470	 0.2610
E	 0.7200	 0.0870
F	 0.7080	 0.2360
G	 0.7490	 0.1920
H	 0.1450	 0.0410
I	 0.7550	 0.2330
J	 0.7790	 0.1880
K	 0.8300	 0.3220
L	 0.7150	 0.1180
M	 0.7510	 0.1930
N	 0.8120	 0.2400
O	 0.8210	 0.1920
P	 0.7490	 0.1880
Q	 0.7690	 0.2140
R	 0.8290	 0.3250
S	 0.7930	 0.1770
T	 0.7800	 0.1690



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Chain	Atom inclusion	Q-score
U	 0.7370	 0.1070
V	 0.7780	 0.2040
W	 0.6270	 0.0470
X	 0.6820	 0.1050
Y	 0.4350	 0.0490
Z	 0.1760	 0.0610
a	 0.9340	 0.2370
b	 0.7900	 0.1940
c	 0.7390	 0.1720
d	 0.9290	 0.1880
e	 0.7490	 0.0770
f	 0.8100	 0.2460
g	 0.6970	 0.0790
h	 0.7390	 0.1500
i	 0.8110	 0.2560
j	 0.7950	 0.2150
k	 0.7030	 0.1200
l	 0.7300	 0.1640
m	 0.8280	 0.2680
n	 0.7170	 0.1030
o	 0.7430	 0.2070
p	 0.7690	 0.1100
q	 0.7980	 0.1930
r	 0.5710	 0.0620
s	 0.8150	 0.2330
t	 0.7320	 0.2060
u	 0.7800	 0.1890
v	 0.7810	 0.2590
w	 0.7930	 0.1840
x	 0.7520	 0.0520
y	 0.7420	 0.1430
z	 0.8410	 0.2700