



wwPDB EM Validation Summary Report ⓘ

Oct 12, 2024 – 10:26 pm BST

PDB ID : 5GAK
EMDB ID : EMD-3227
Title : Yeast 60S ribosomal subunit with A-site tRNA, P-site tRNA and eIF-5A
Authors : Schmidt, C.; Becker, T.
Deposited on : 2015-12-09
Resolution : 3.88 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
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
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

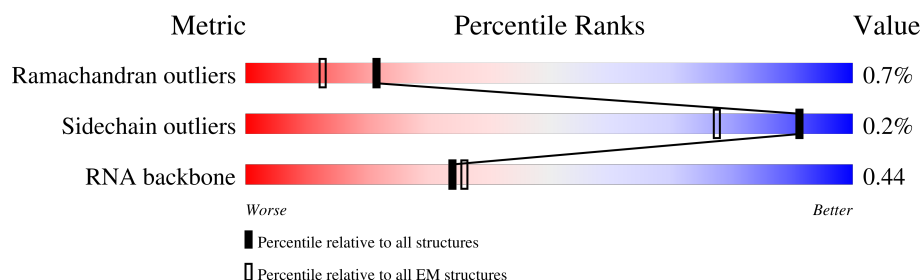
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.88 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	1	3396	<div> <div>70%</div> <div>56%</div> <div>36%</div> <div>7%</div> </div>
2	X	137	<div> <div>81%</div> <div>99%</div> <div>.</div> </div>
3	3	121	<div> <div>66%</div> <div>72%</div> <div>28%</div> </div>
4	Y	155	<div> <div>52%</div> <div>63%</div> <div>37%</div> </div>
5	4	158	<div> <div>78%</div> <div>59%</div> <div>39%</div> <div>.</div> </div>
6	Z	142	<div> <div>65%</div> <div>85%</div> <div>15%</div> <div>.</div> </div>
7	A	76	<div> <div>86%</div> <div>45%</div> <div>53%</div> <div>.</div> </div>
8	a	127	<div> <div>80%</div> <div>98%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
9	B	77	<div>81%</div> <div>51% 48%</div>
10	b	136	<div>77%</div> <div>99%</div>
11	C	106	<div>89%</div> <div>99%</div>
12	c	149	<div>79%</div> <div>97%</div>
13	D	92	<div>84%</div> <div>99%</div>
14	d	59	<div>83%</div> <div>97%</div>
15	E	254	<div>78%</div> <div>99%</div>
16	e	105	<div>82%</div> <div>92% 8%</div>
17	F	387	<div>73%</div> <div>99%</div>
18	f	109	<div>81%</div> <div>100%</div>
19	G	362	<div>82%</div> <div>99%</div>
20	g	130	<div>77%</div> <div>98%</div>
21	H	297	<div>82%</div> <div>98%</div>
22	h	107	<div>71%</div> <div>99%</div>
23	I	176	<div>74%</div> <div>88% 11%</div>
24	i	121	<div>66%</div> <div>93% 7%</div>
25	J	244	<div>73%</div> <div>91% 9%</div>
26	j	120	<div>78%</div> <div>99%</div>
27	K	256	<div>74%</div> <div>89% 9%</div>
28	k	100	<div>80%</div> <div>98%</div>
29	L	191	<div>79%</div> <div>100%</div>
30	l	88	<div>77%</div> <div>98%</div>
31	M	174	<div>79%</div> <div>96%</div>
32	m	78	<div>85%</div> <div>99%</div>
33	N	199	<div>78%</div> <div>97%</div>

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Mol	Chain	Length	Quality of chain
34	n	51	<div>80%</div> <div>98%</div> <div>.</div>
35	O	138	<div>86%</div> <div>98%</div> <div>..</div>
36	o	128	<div>34%</div> <div>41%</div> <div>59%</div>
37	P	204	<div>71%</div> <div>100%</div>
38	p	25	<div>80%</div> <div>100%</div>
39	Q	199	<div>78%</div> <div>98%</div> <div>..</div>
40	q	157	<div>94%</div> <div>89%</div> <div>8%</div> <div>..</div>
41	R	184	<div>78%</div> <div>99%</div> <div>.</div>
42	r	210	<div>88%</div> <div>100%</div>
43	S	186	<div>81%</div> <div>99%</div> <div>..</div>
44	s	221	<div>81%</div> <div>94%</div> <div>.</div> <div>.</div>
45	T	189	<div>83%</div> <div>99%</div> <div>..</div>
46	U	172	<div>83%</div> <div>99%</div> <div>.</div>
47	V	160	<div>84%</div> <div>99%</div> <div>..</div>
48	W	121	<div>61%</div> <div>82%</div> <div>.</div> <div>17%</div>
49	z	23	<div>96%</div> <div>100%</div>

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 128975 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	3165	Total	C	N	O	P	0	0
			67695	30238	12201	22091	3165		

- Molecule 2 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	X	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 4 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Y	98	Total	C	N	O	S	0	0
			699	443	137	118	1		

- Molecule 5 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 6 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Z	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 7 is a RNA chain called The A-site tRNA was modeled based on an E. coli tRNA-Lys.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	76	Total	C	N	O	P	0	0
			1611	721	281	534	75		

- Molecule 8 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	a	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 9 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	77	Total	C	N	O	P	0	0
			1644	731	290	546	77		

- Molecule 10 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	b	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 11 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 12 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	c	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 13 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 14 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	d	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 15 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	E	252	Total	C	N	O	S	0	0
			1914	1191	388	334	1		

- Molecule 16 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	e	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 17 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	F	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 18 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	f	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 19 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	G	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 20 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	g	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 21 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	H	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 22 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	h	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 23 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	I	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 24 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	i	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 25 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	J	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 26 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	j	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 27 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	K	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 28 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	k	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 29 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 30 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	l	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 31 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	M	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 32 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	m	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 33 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	N	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 34 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	n	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 35 is a protein called 60S ribosomal protein L14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	O	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 36 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	o	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 37 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	P	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 38 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	p	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 39 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Q	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 40 is a protein called Eukaryotic translation initiation factor 5A-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	q	154	Total	C	N	O	S	0	0
			1143	709	195	230	9		

- Molecule 41 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	R	183	Total	C	N	O		0	0
			1420	882	281	257			

- Molecule 42 is a protein called ribosomal protein RPL1.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	r	210	Total	C	N	O	0	0
			1050	630	210	210		

- Molecule 43 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	S	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 44 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	s	220	Total	C	N	O	S	0	0
			1770	1121	335	307	7		

- Molecule 45 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	T	188	Total	C	N	O	0	0
			1521	935	326	260		

- Molecule 46 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	U	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 47 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	V	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

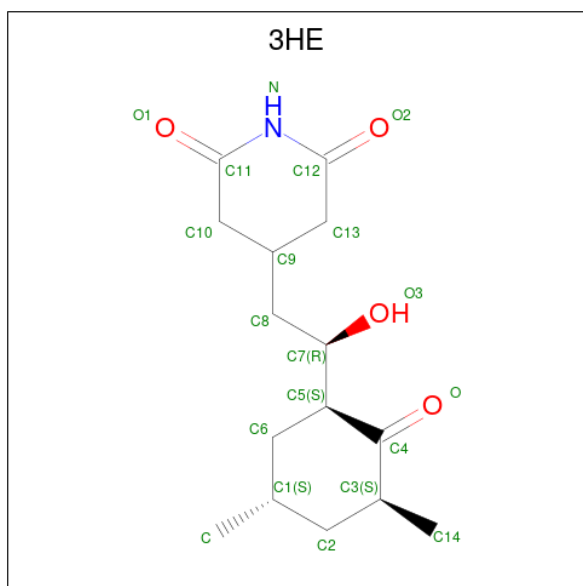
- Molecule 48 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	W	100	Total	C	N	O	0	0
			796	516	131	149		

- Molecule 49 is a protein called nascent polypeptide chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	z	23	Total	C	N	O	0	0
			115	69	23	23		

- Molecule 50 is 4-{(2R)-2-[(1S,3S,5S)-3,5-dimethyl-2-oxocyclohexyl]-2-hydroxyethyl}piperidine-2,6-dione (three-letter code: 3HE) (formula: C₁₅H₂₃NO₄).

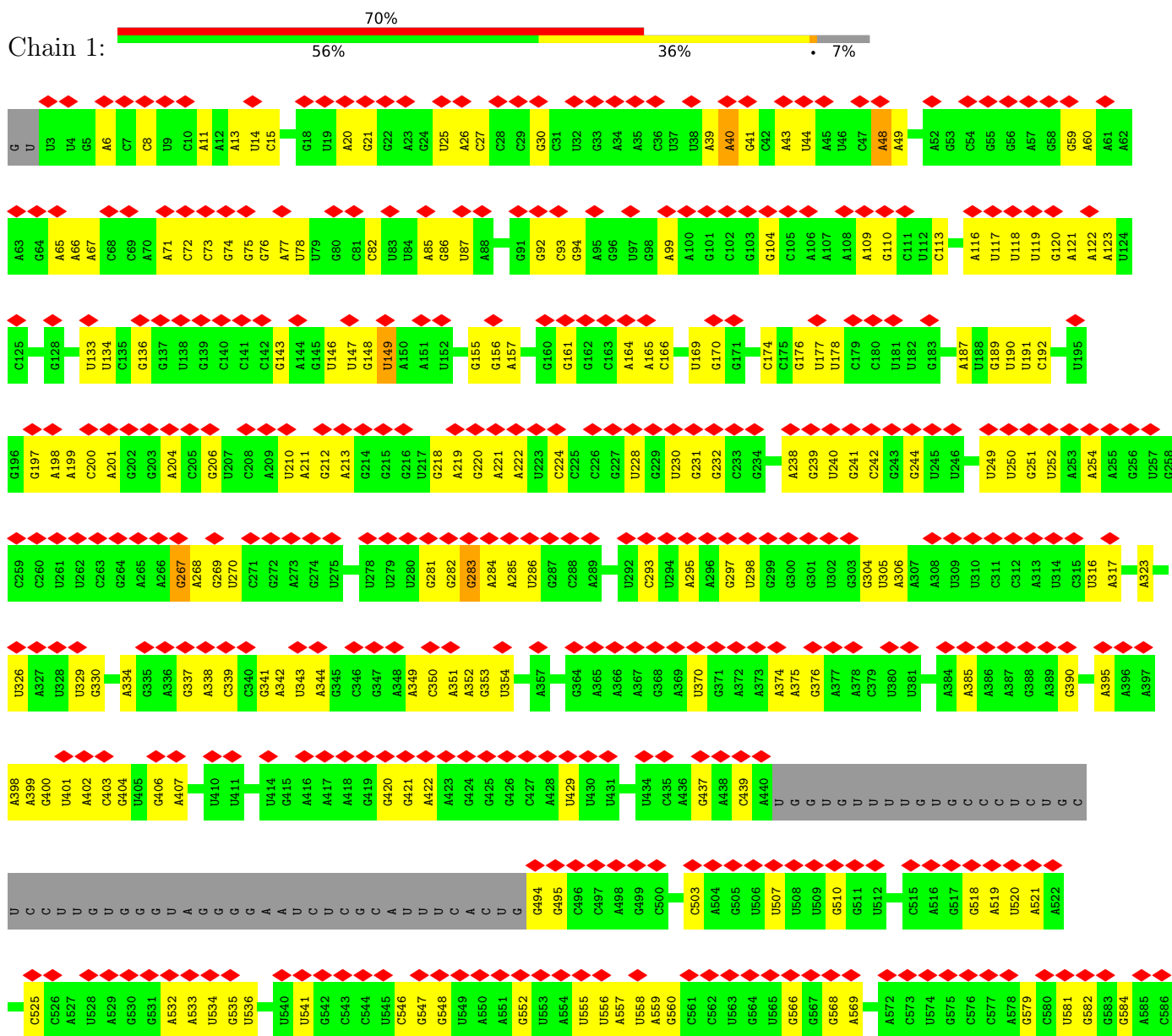


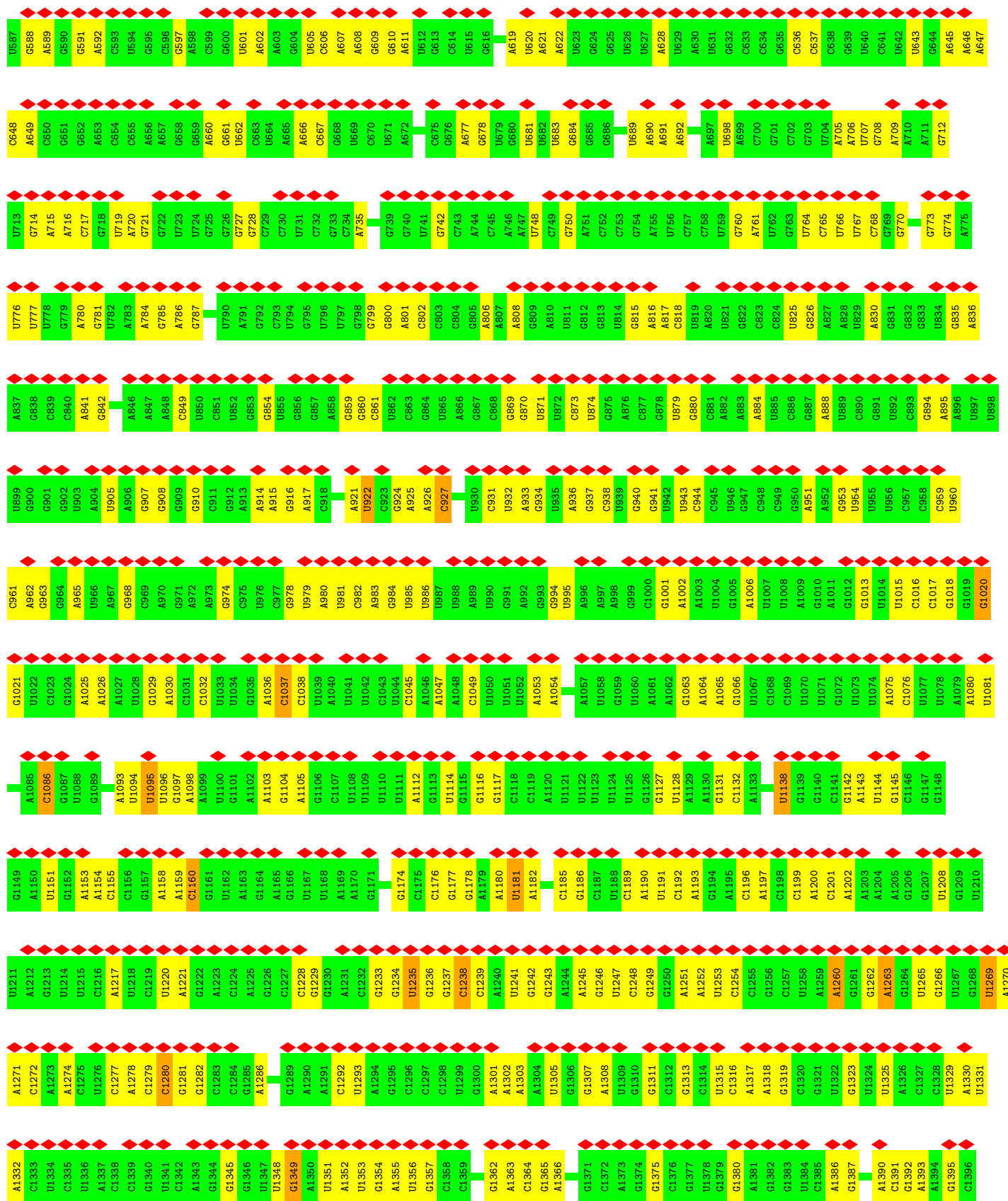
Mol	Chain	Residues	Atoms				AltConf
50	1	1	Total	C	N	O	0
			20	15	1	4	

3 Residue-property plots

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

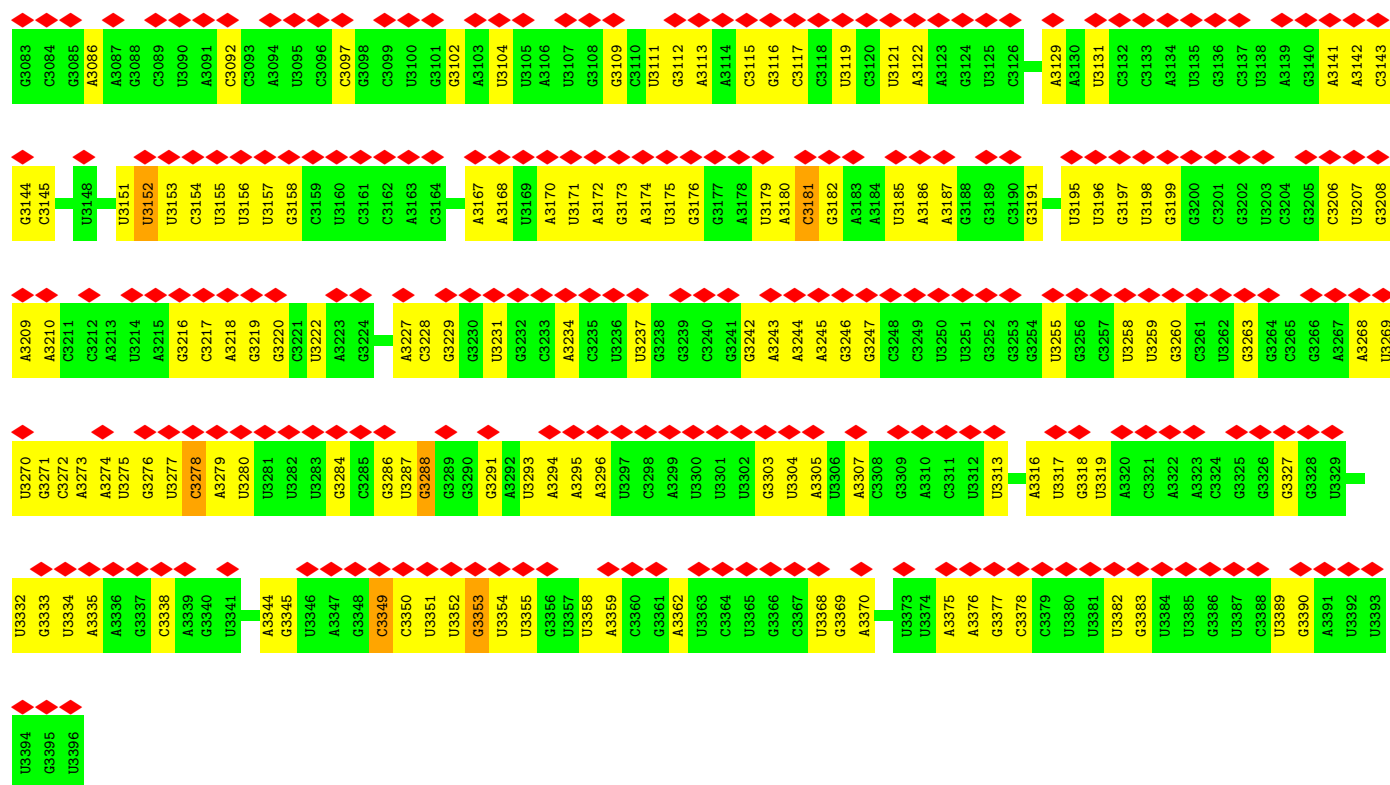
• Molecule 1: 25S rRNA



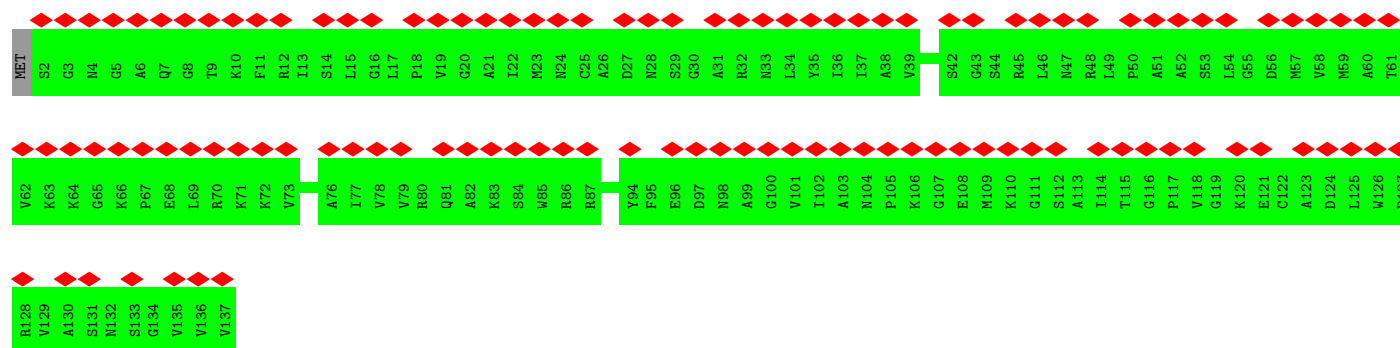
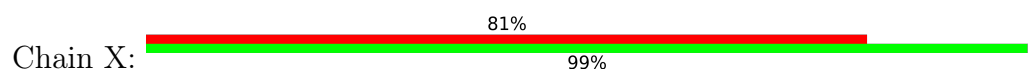




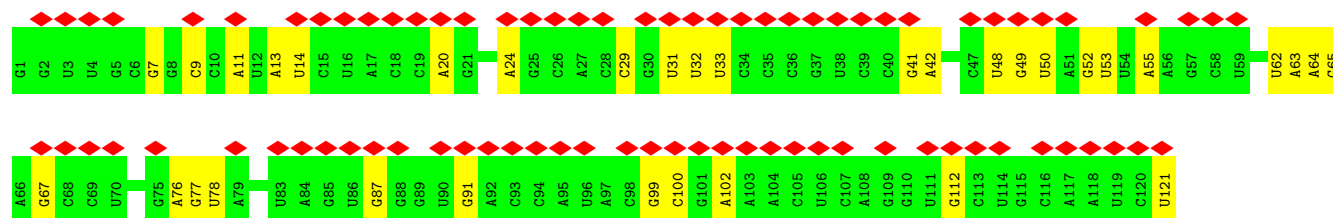
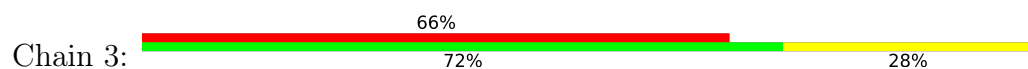
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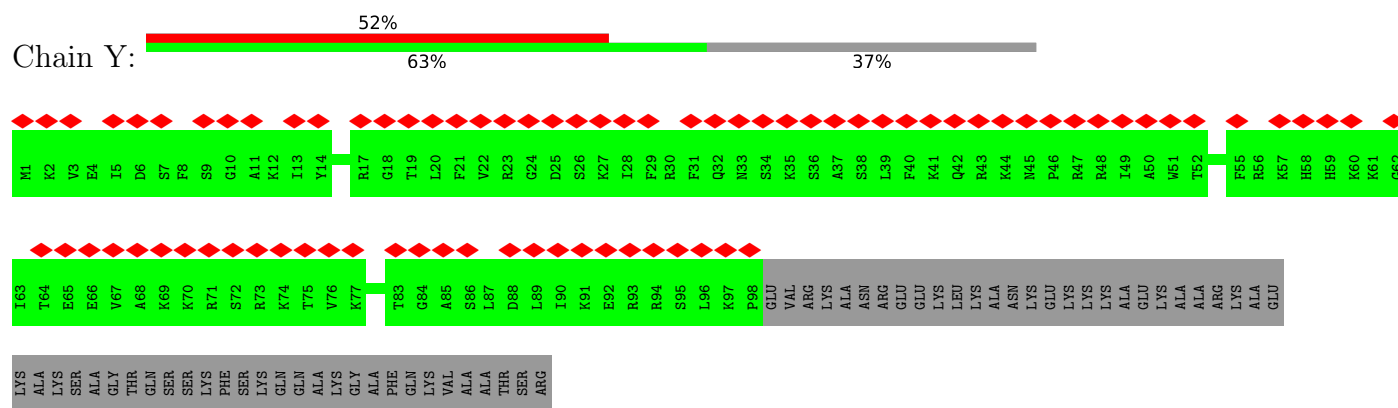
• Molecule 2: 60S ribosomal protein L23-A



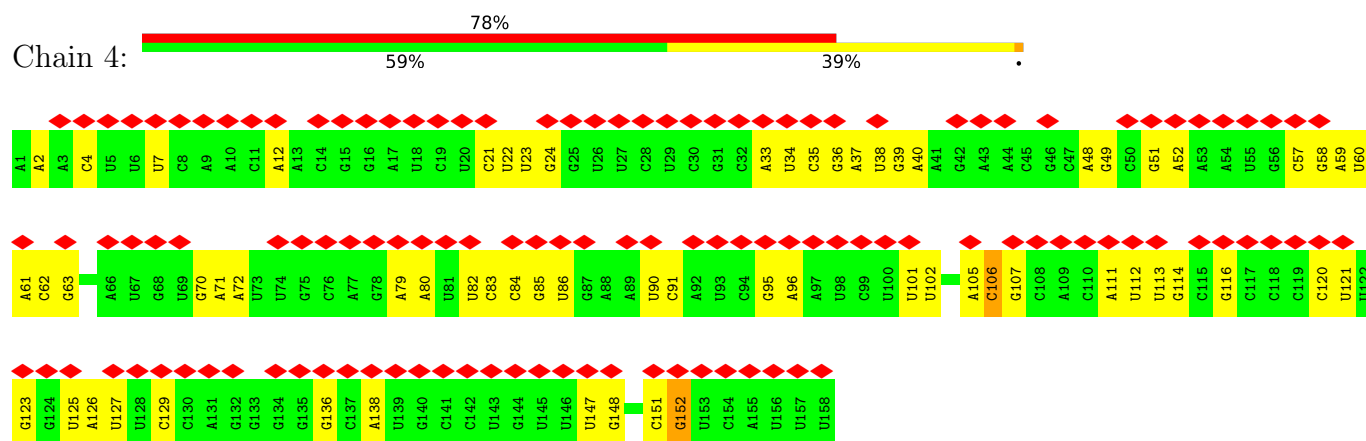
• Molecule 3: 5S rRNA



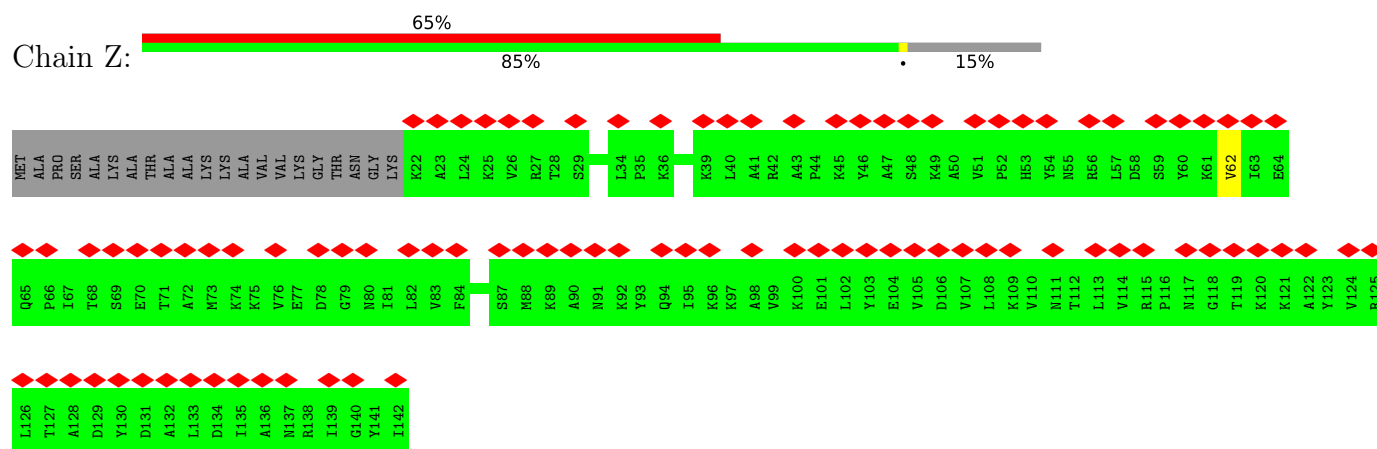
• Molecule 4: 60S ribosomal protein L24-A



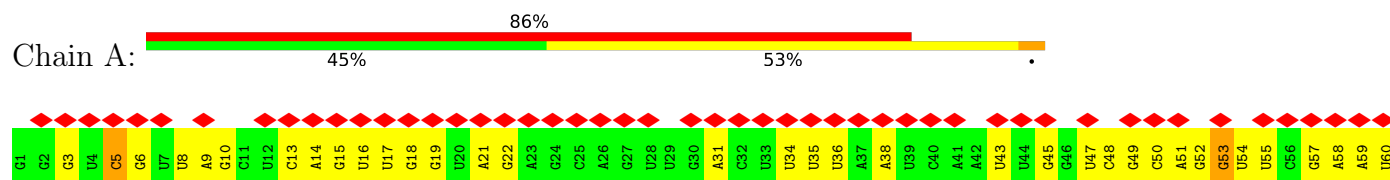
• Molecule 5: 5.8S rRNA

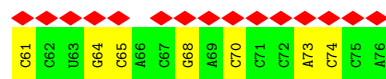


• Molecule 6: 60S ribosomal protein L25

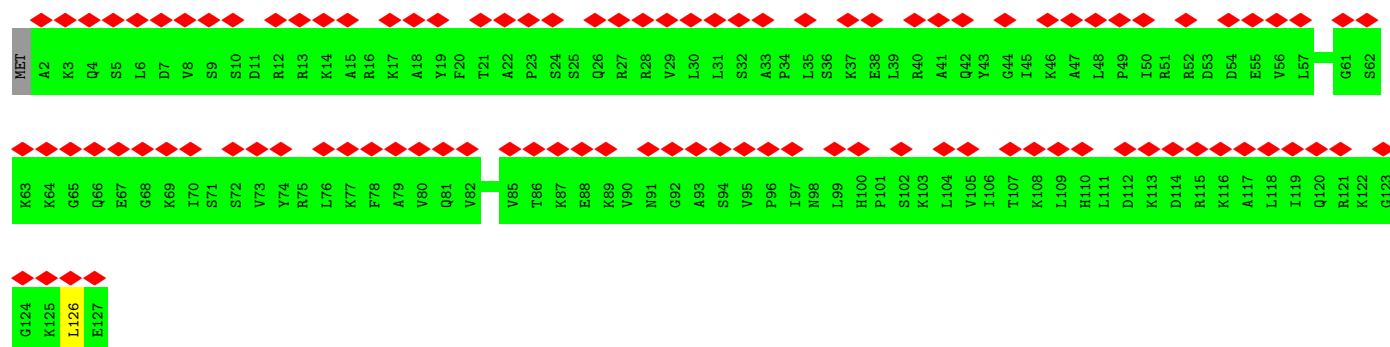
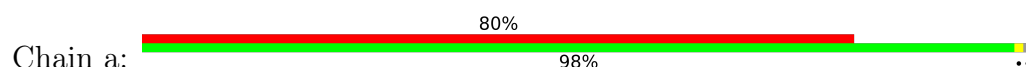


• Molecule 7: The A-site tRNA was modeled based on an E. coli tRNA-Lys

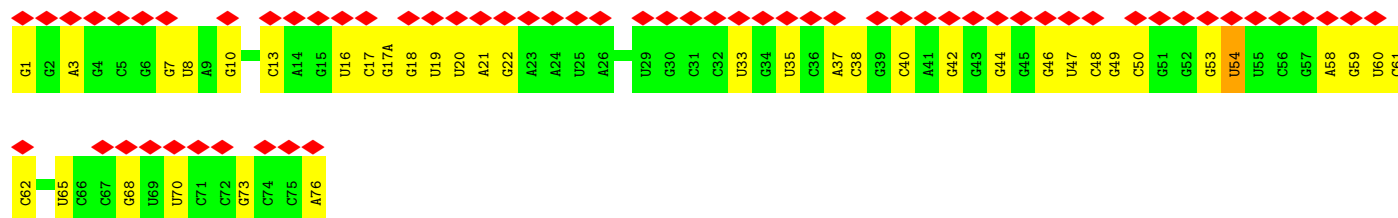
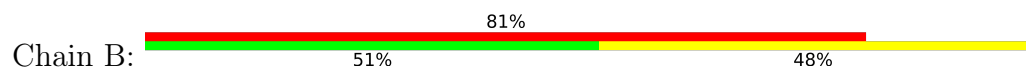




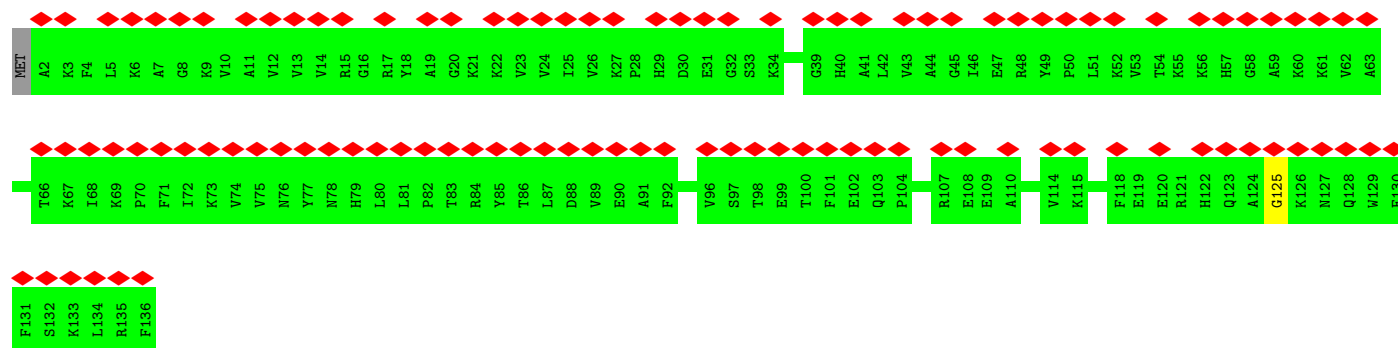
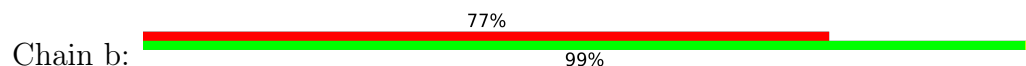
• Molecule 8: 60S ribosomal protein L26-A



• Molecule 9: P-site tRNA

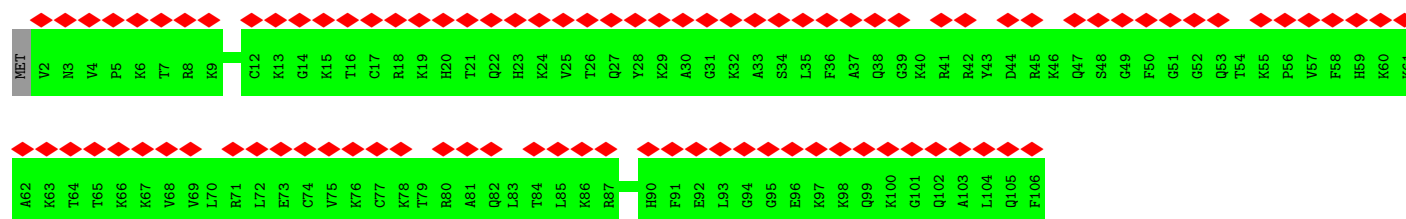


• Molecule 10: 60S ribosomal protein L27-A

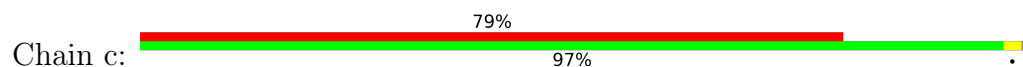


• Molecule 11: 60S ribosomal protein L42-A

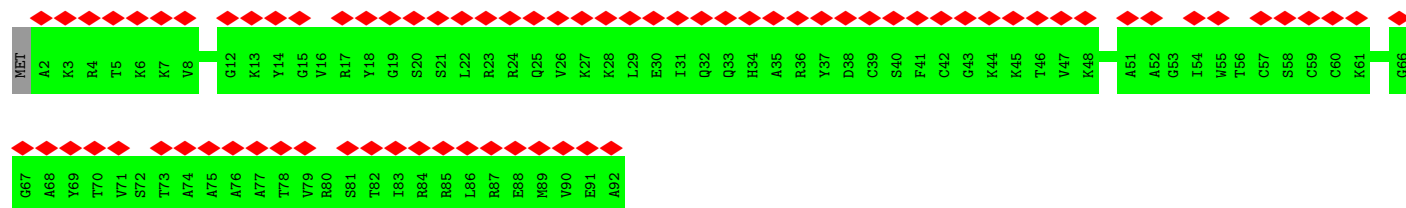
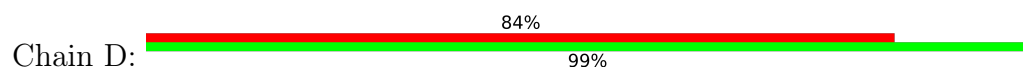




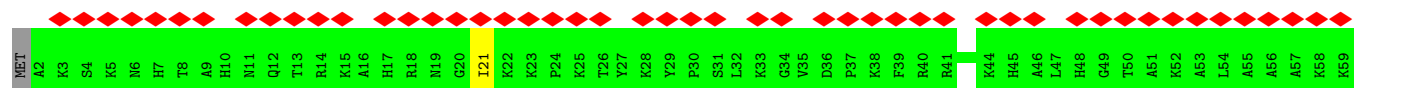
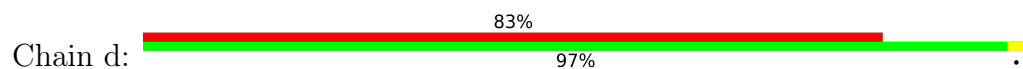
• Molecule 12: 60S ribosomal protein L28



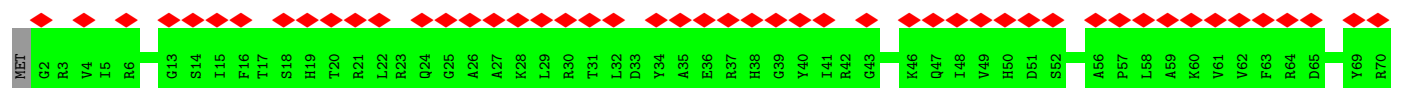
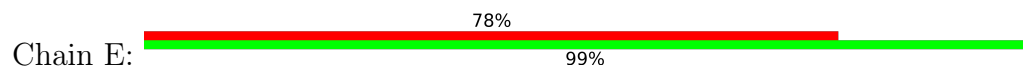
• Molecule 13: 60S ribosomal protein L43-A

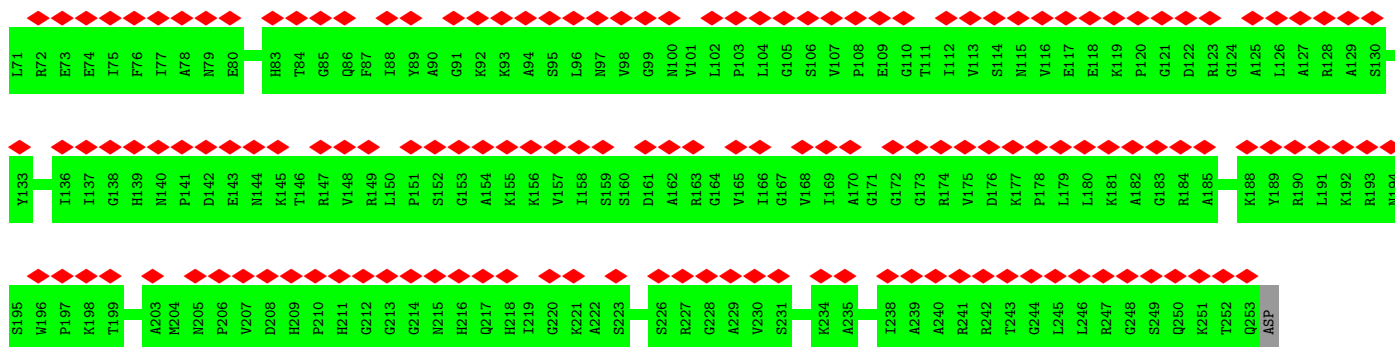


• Molecule 14: 60S ribosomal protein L29

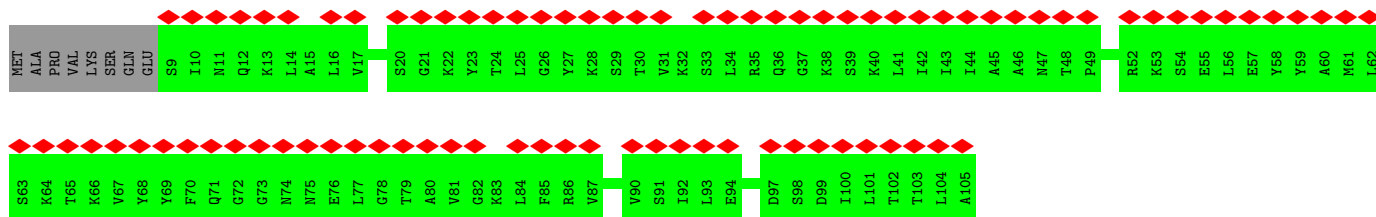
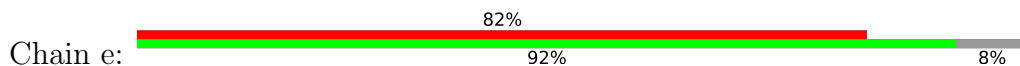


• Molecule 15: 60S ribosomal protein L2-A

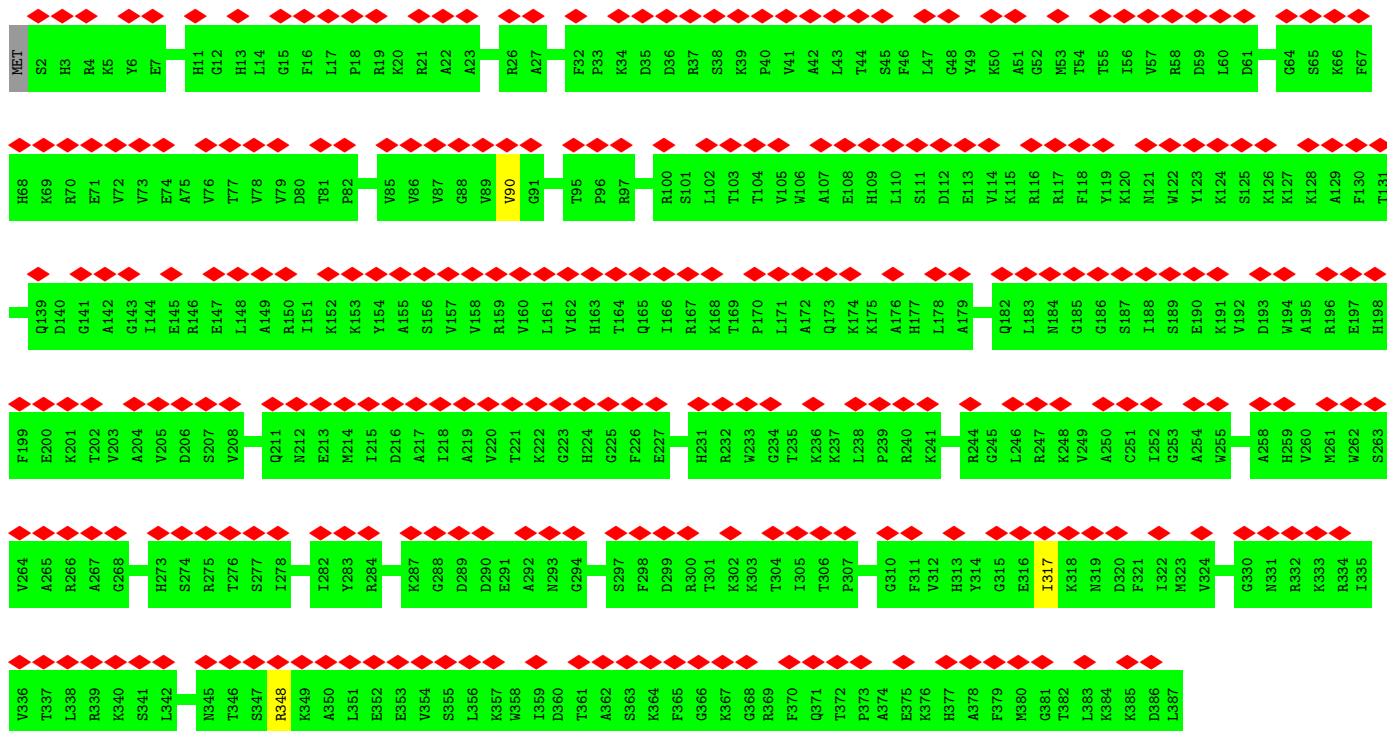
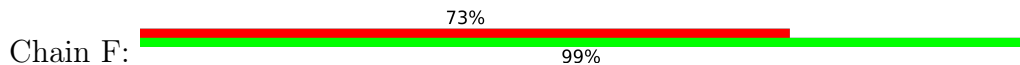




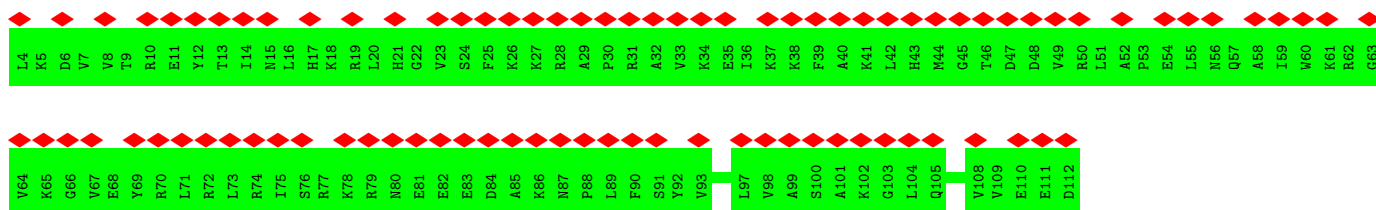
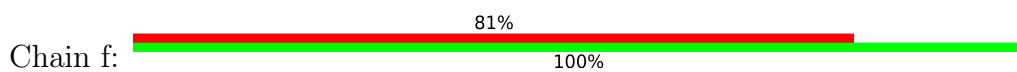
• Molecule 16: 60S ribosomal protein L30



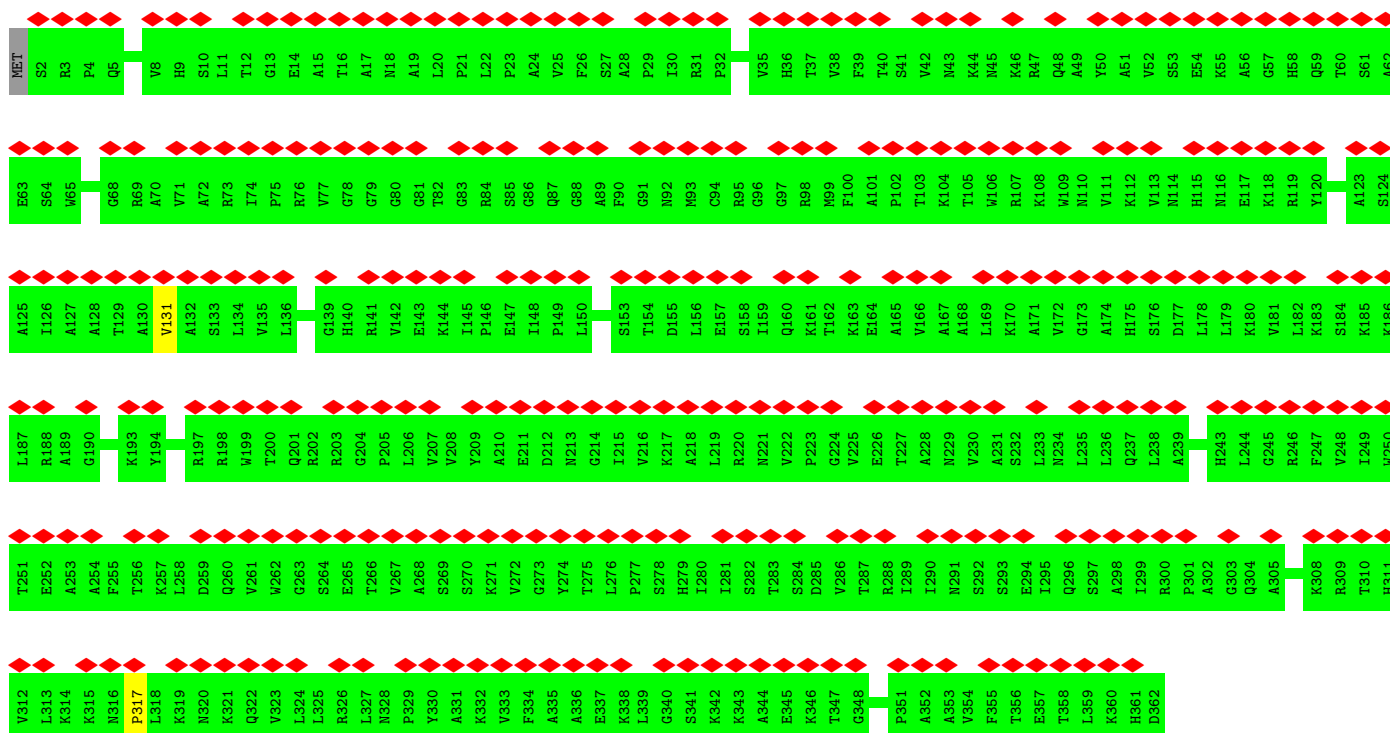
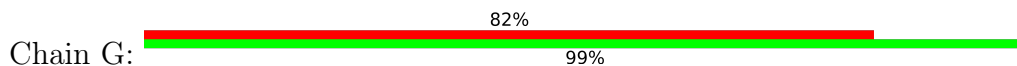
• Molecule 17: 60S ribosomal protein L3



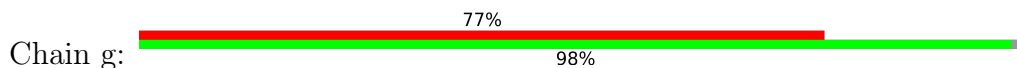
• Molecule 18: 60S ribosomal protein L31-A



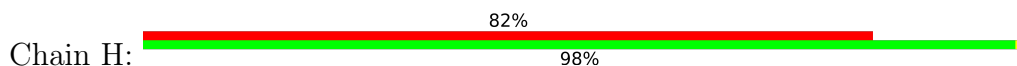
• Molecule 19: 60S ribosomal protein L4-A

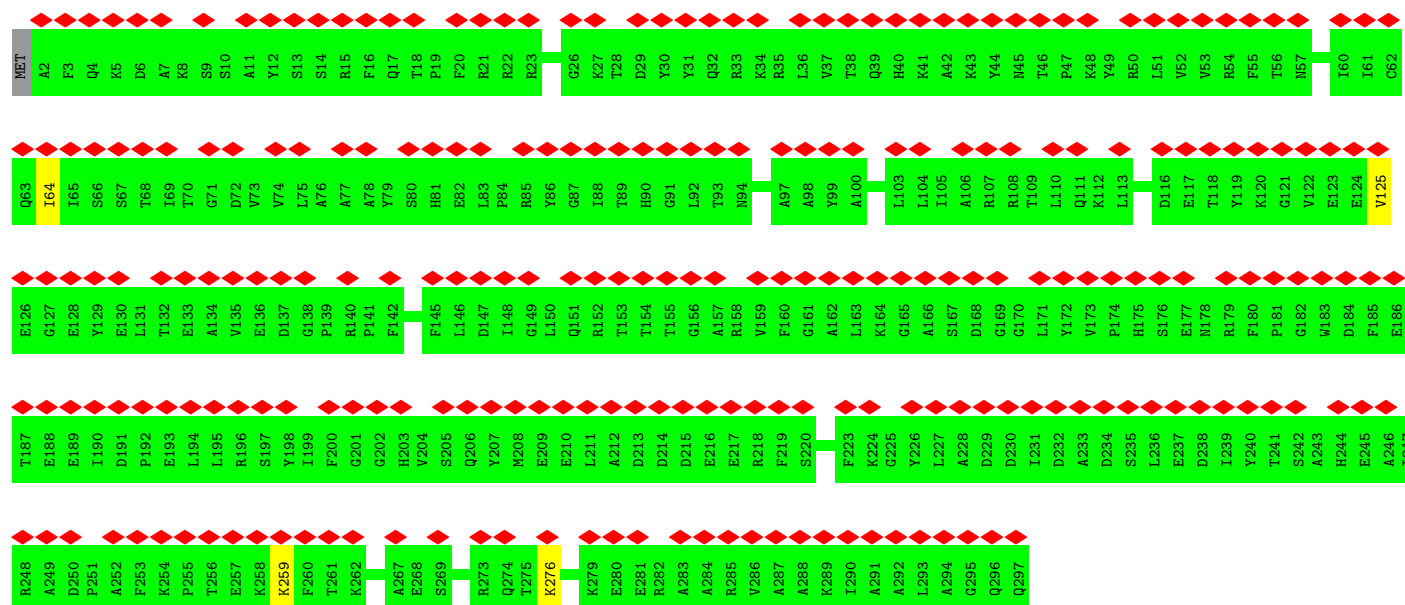


• Molecule 20: 60S ribosomal protein L32

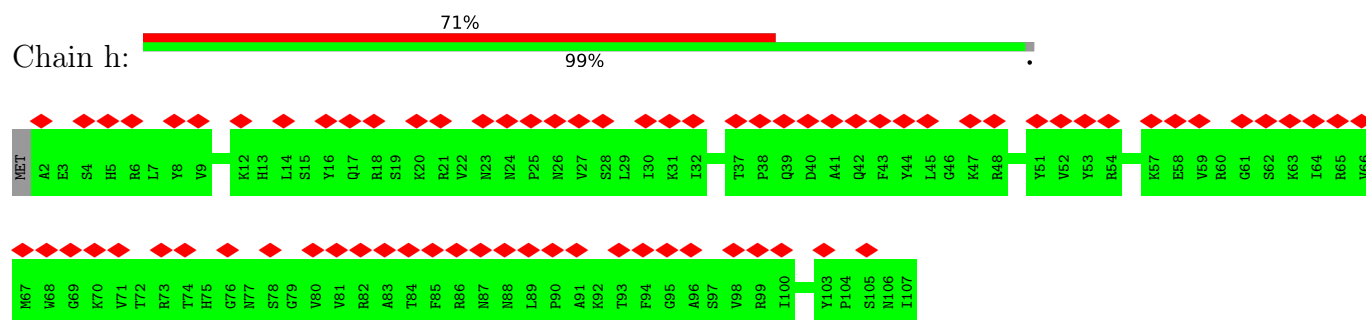


• Molecule 21: 60S ribosomal protein L5





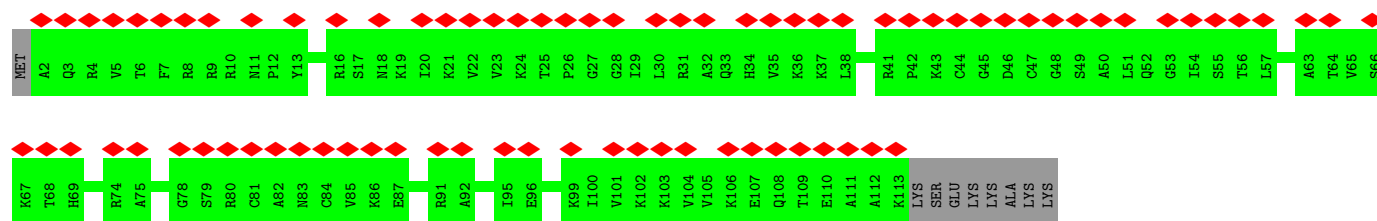
• Molecule 22: 60S ribosomal protein L33-A



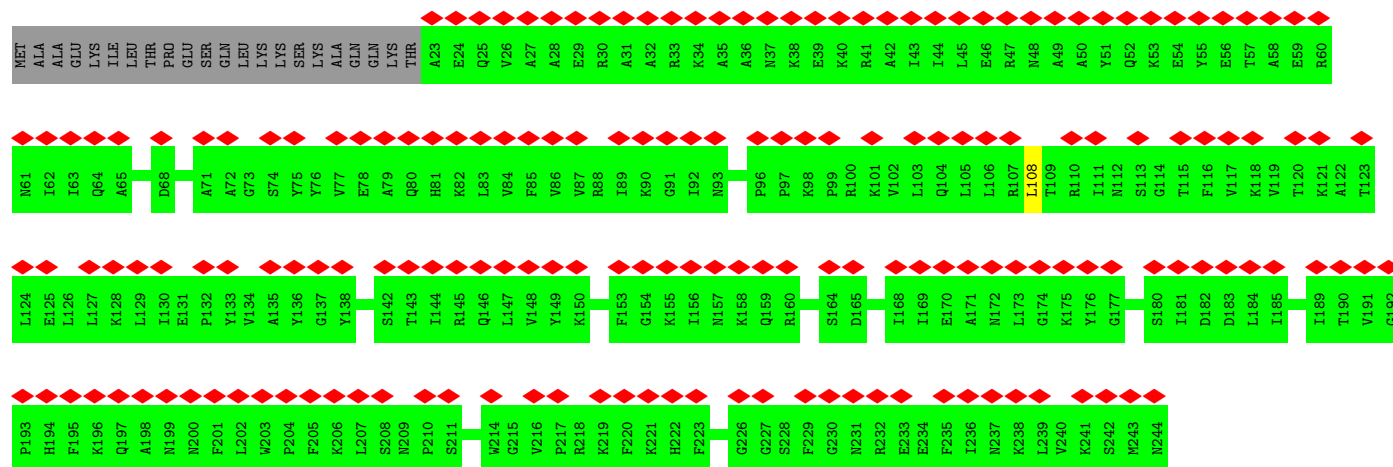
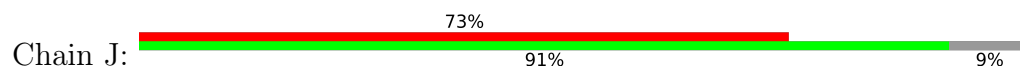
• Molecule 23: 60S ribosomal protein L6-A



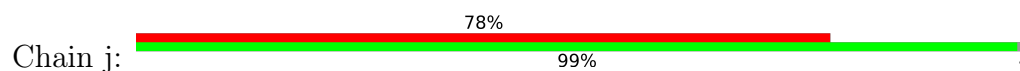
• Molecule 24: 60S ribosomal protein L34-A



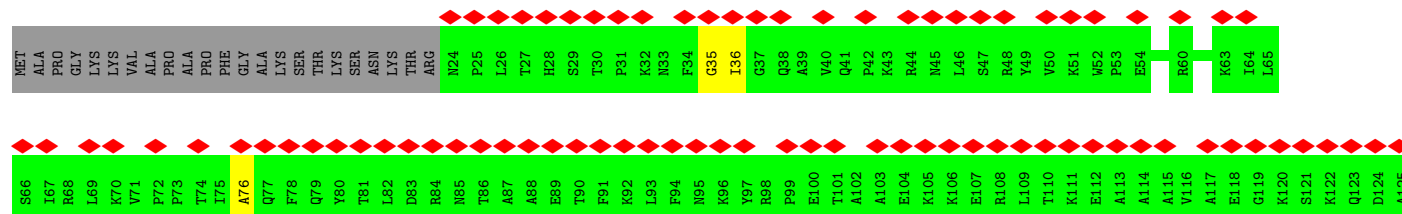
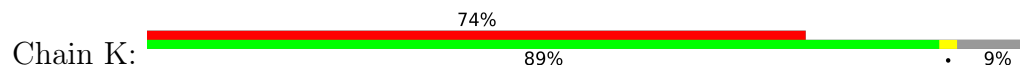
• Molecule 25: 60S ribosomal protein L7-A

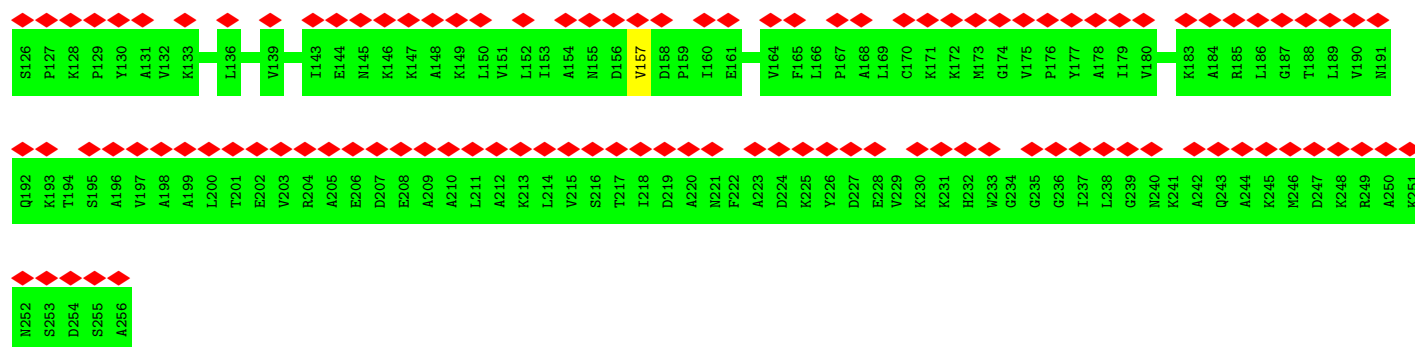


• Molecule 26: 60S ribosomal protein L35-A

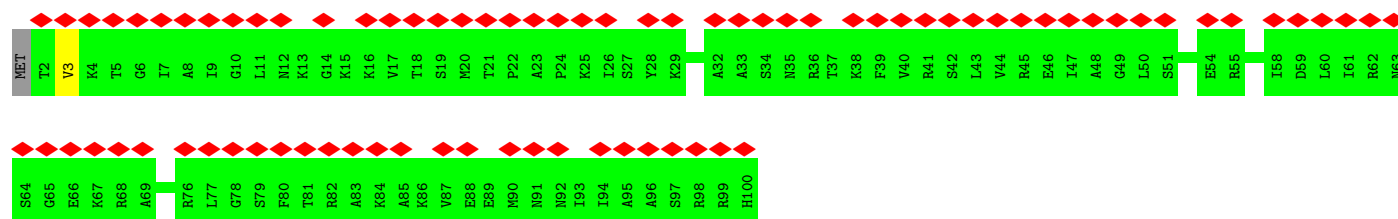
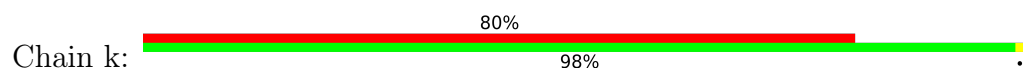


• Molecule 27: 60S ribosomal protein L8-A

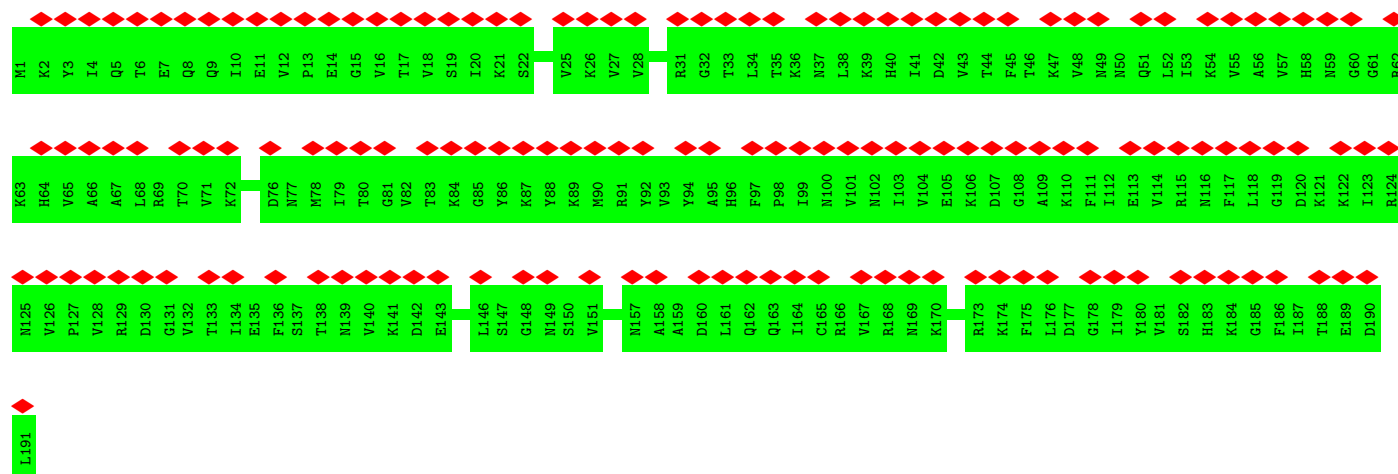
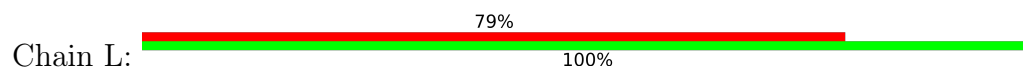




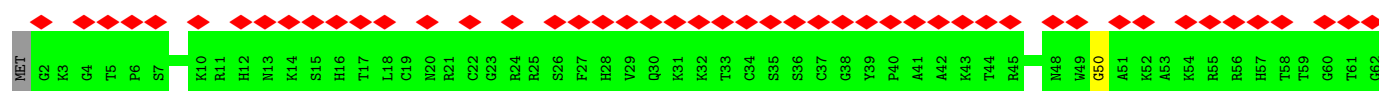
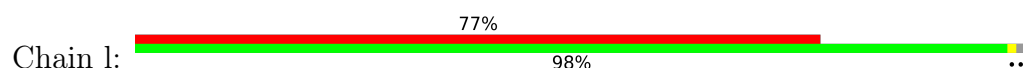
• Molecule 28: 60S ribosomal protein L36-A

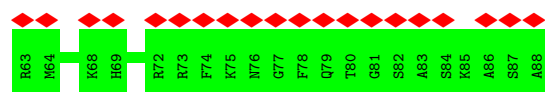


• Molecule 29: 60S ribosomal protein L9-A

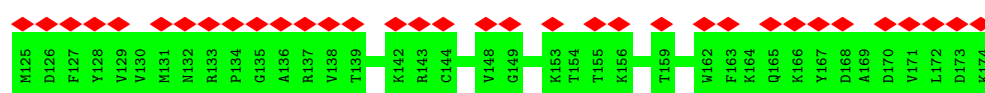
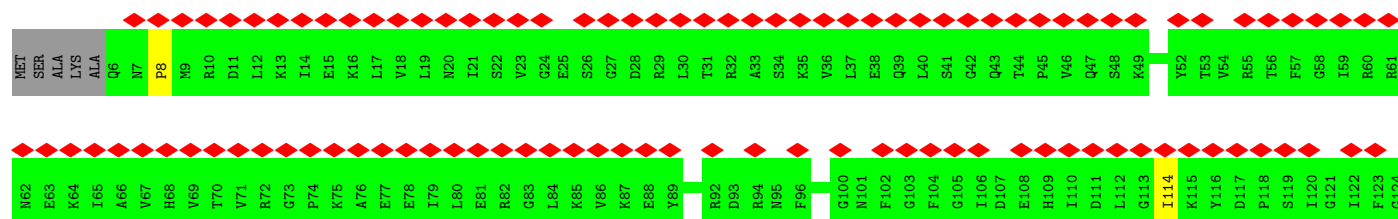
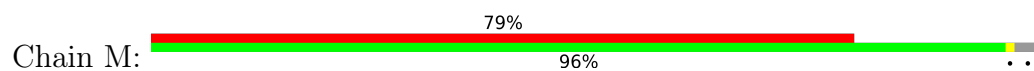


• Molecule 30: 60S ribosomal protein L37-A

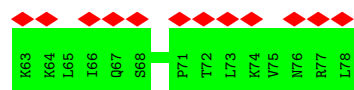
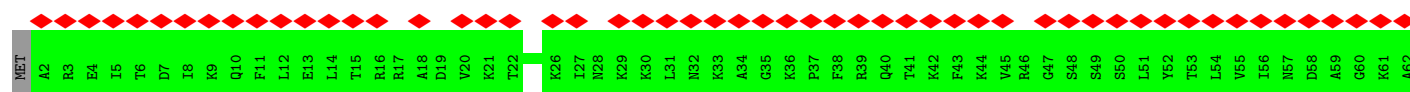
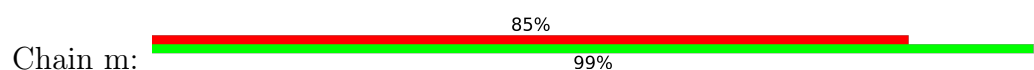




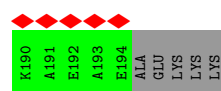
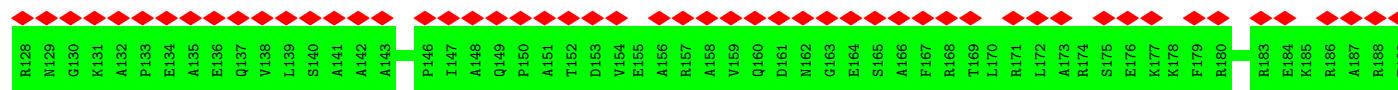
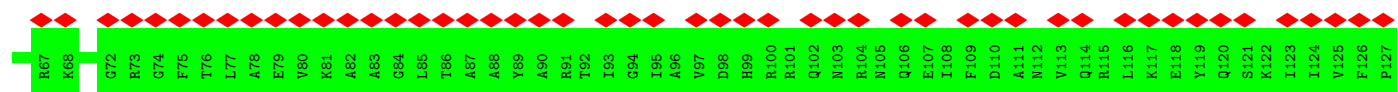
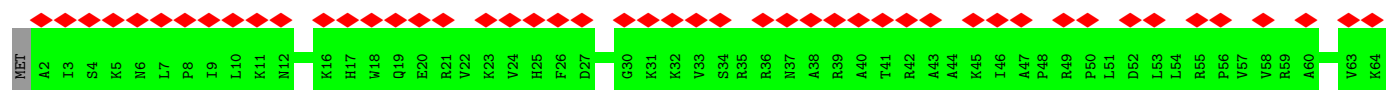
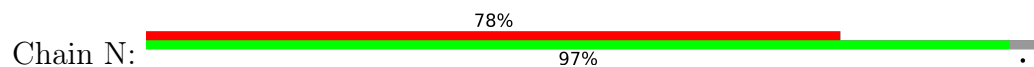
- Molecule 31: 60S ribosomal protein L11-A



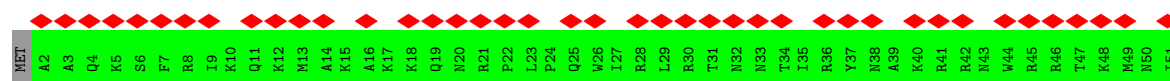
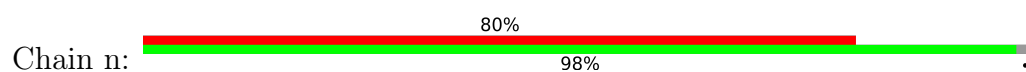
- Molecule 32: 60S ribosomal protein L38



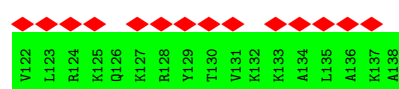
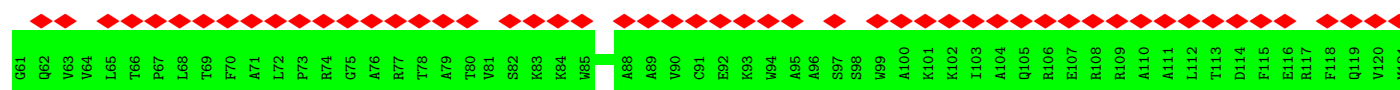
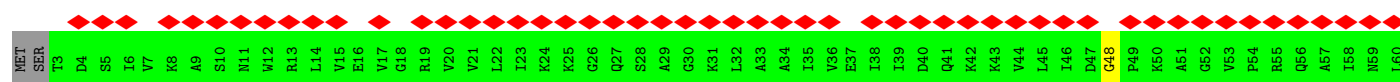
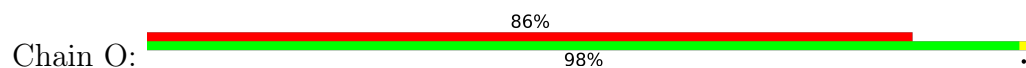
- Molecule 33: 60S ribosomal protein L13-A



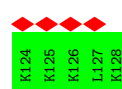
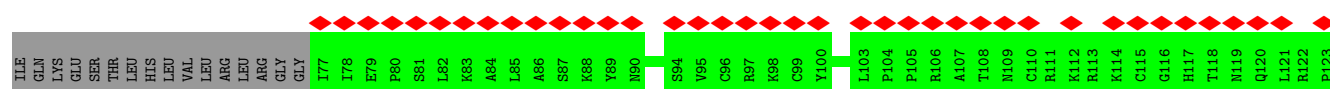
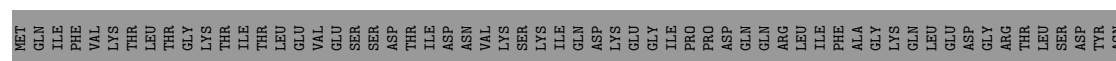
- Molecule 34: 60S ribosomal protein L39



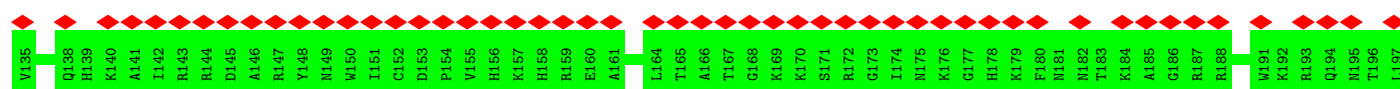
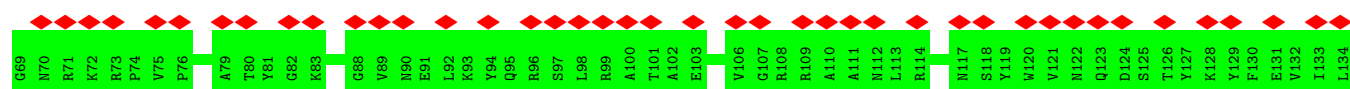
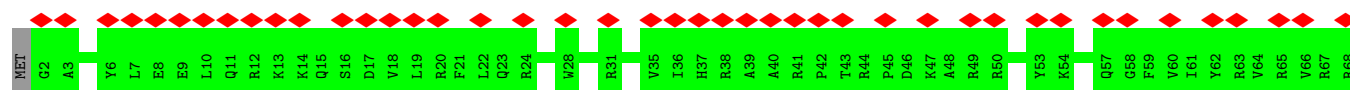
• Molecule 35: 60S ribosomal protein L14-B

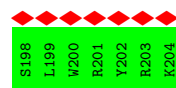


• Molecule 36: Ubiquitin-60S ribosomal protein L40

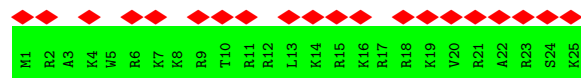
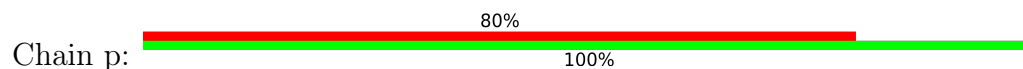


• Molecule 37: 60S ribosomal protein L15-A

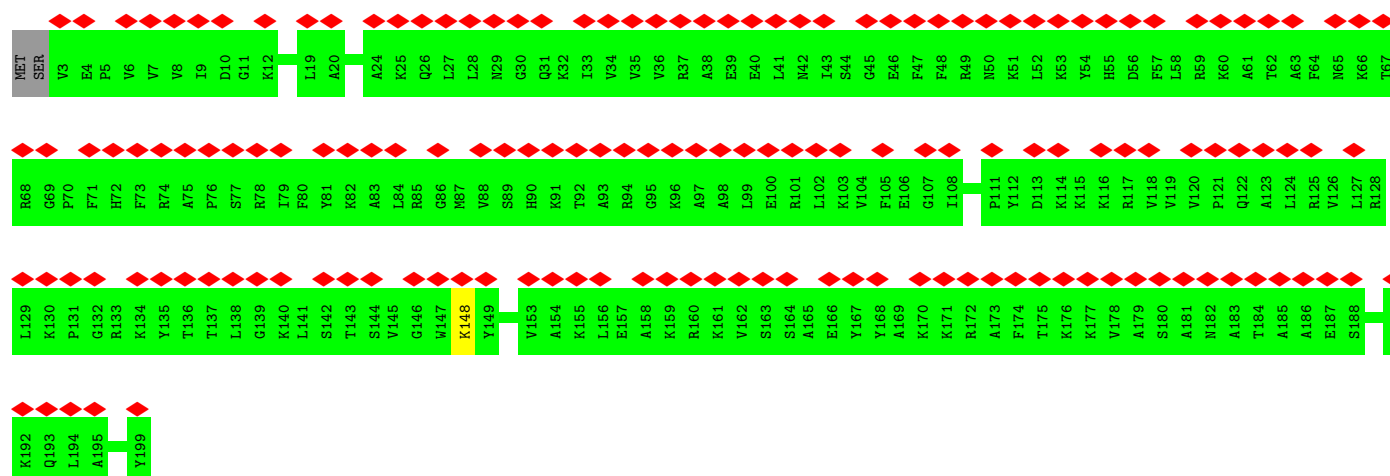
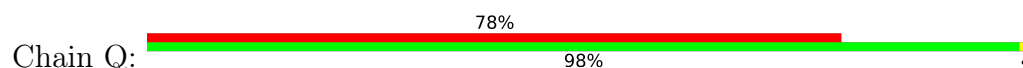




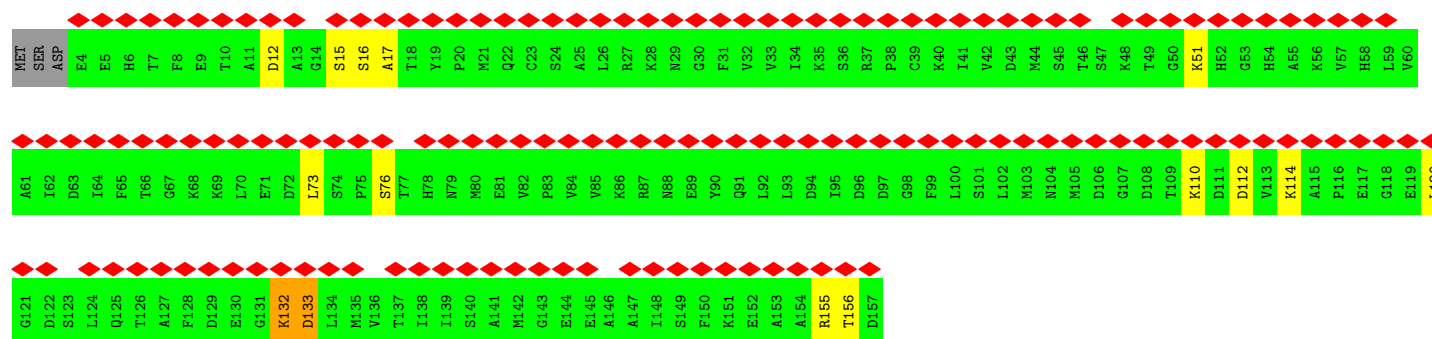
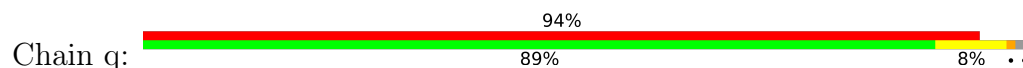
- Molecule 38: 60S ribosomal protein L41-A



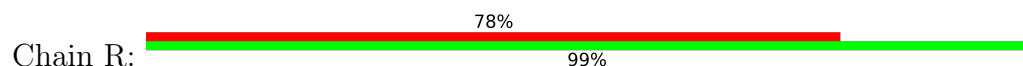
- Molecule 39: 60S ribosomal protein L16-A

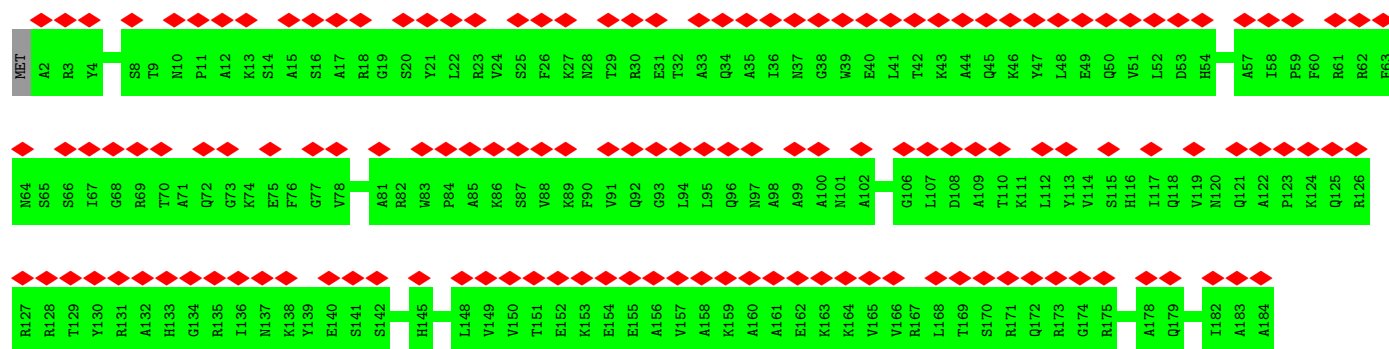


- Molecule 40: Eukaryotic translation initiation factor 5A-1

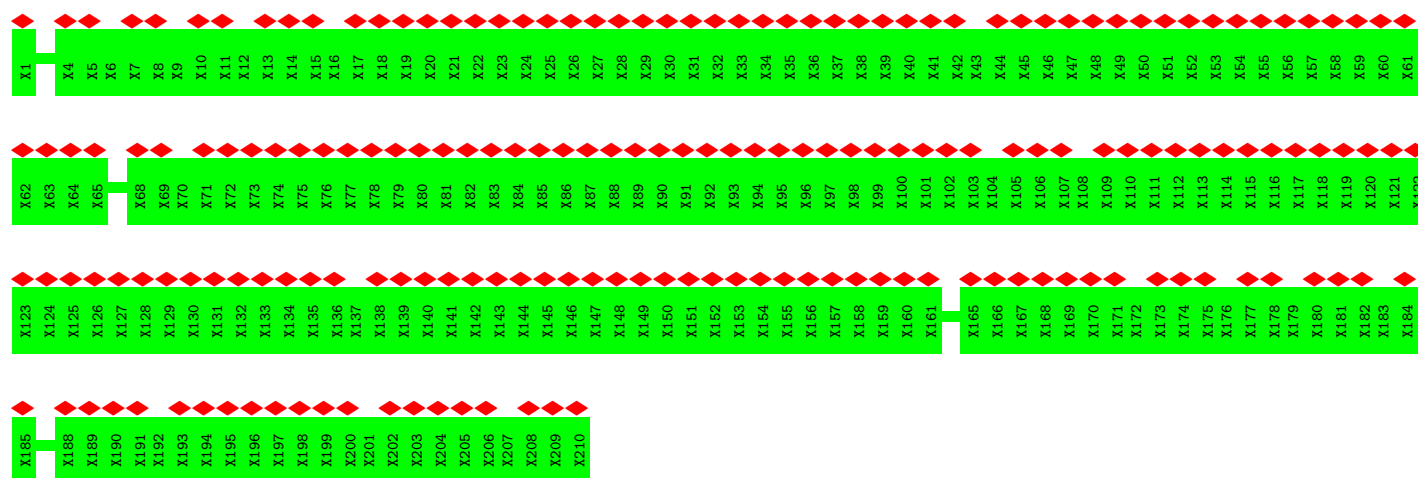
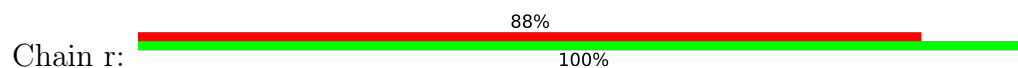


- Molecule 41: 60S ribosomal protein L17-A

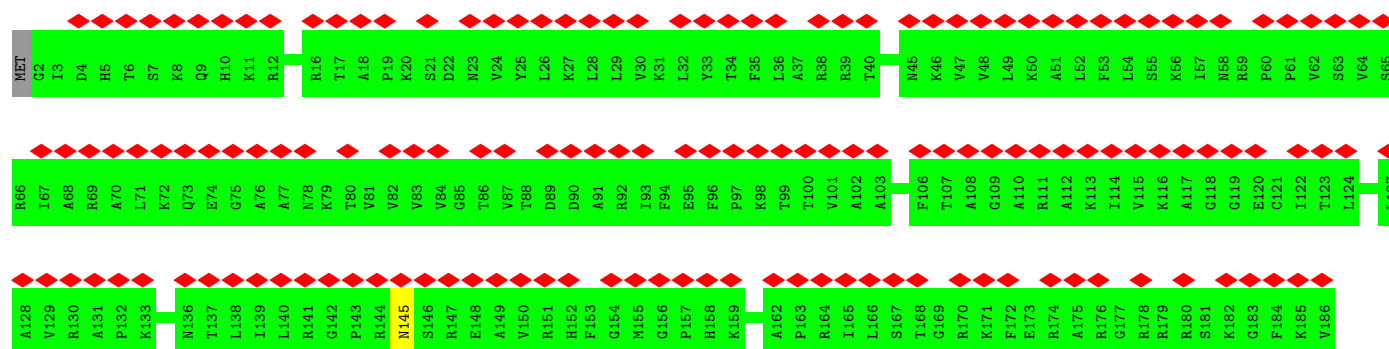
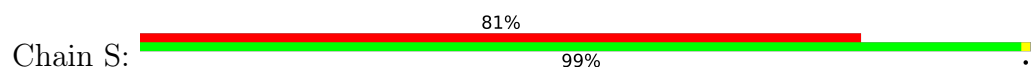




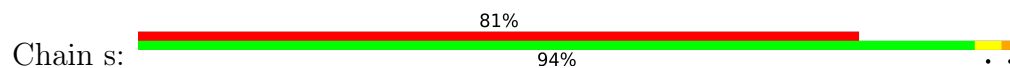
- Molecule 42: ribosomal protein RPL1

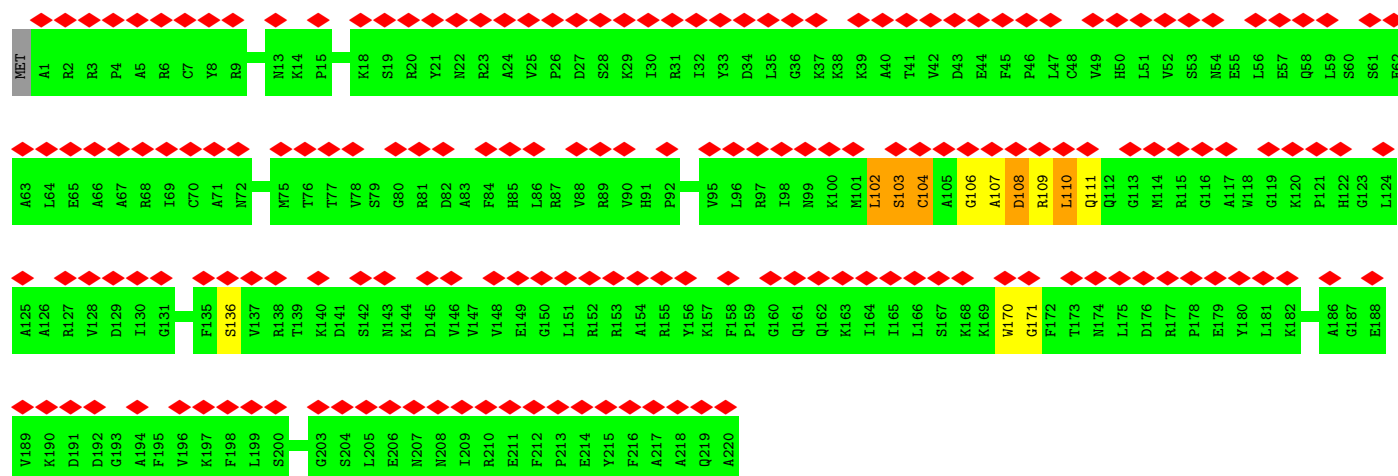


- Molecule 43: 60S ribosomal protein L18-A



- Molecule 44: 60S ribosomal protein L10





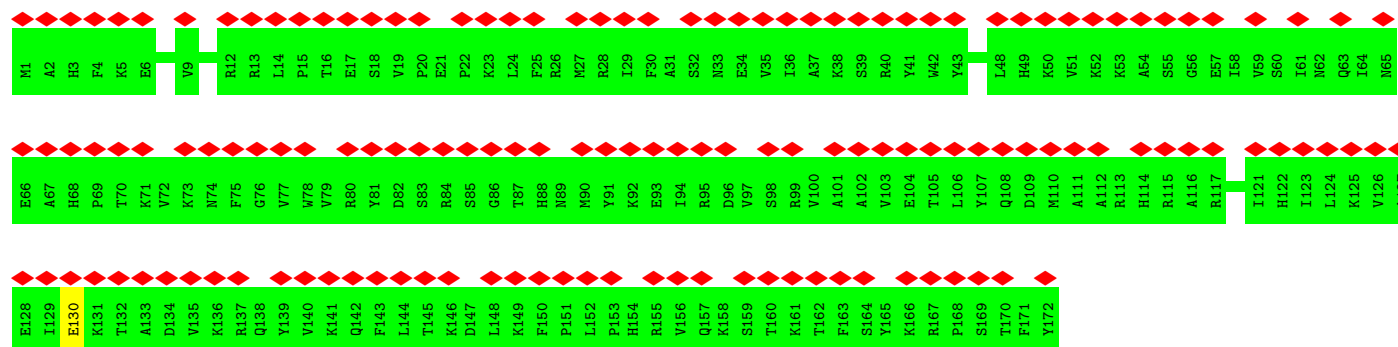
- Molecule 45: 60S ribosomal protein L19-A

Chain T: 83% 99%



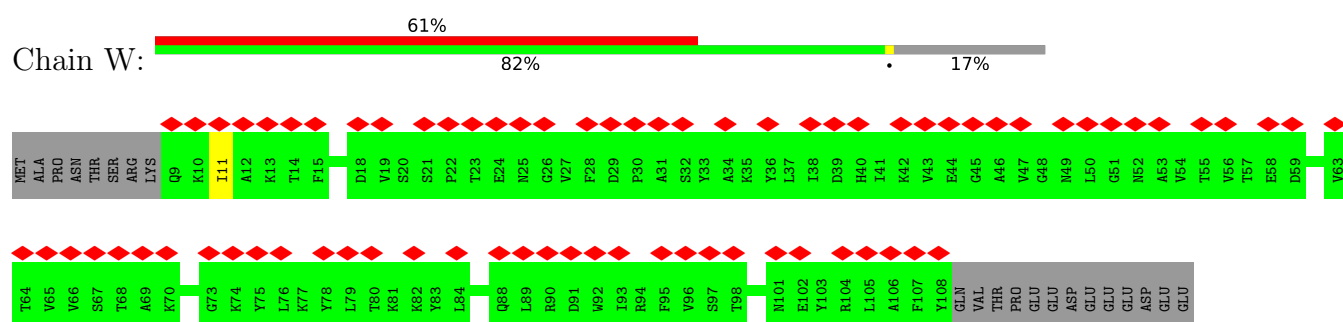
- Molecule 46: 60S ribosomal protein L20-A

Chain U: 83% 99%

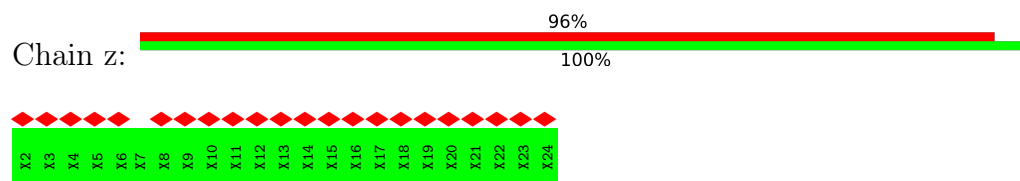


- Molecule 47: 60S ribosomal protein L21-A

- Molecule 48: 60S ribosomal protein L22-A



- Molecule 49: nascent polypeptide chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	62532	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY; Each Particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.404	Depositor
Minimum map value	-0.244	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.06	Depositor
Map size (\AA)	401.08, 401.08, 401.08	wwPDB
Map dimensions	370, 370, 370	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.084, 1.084, 1.084	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 3HE, 5CT

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	1	0.73	0/75774	1.03	156/118137 (0.1%)
2	X	0.39	0/1018	0.52	0/1369
3	3	0.61	0/2883	0.94	0/4491
4	Y	0.32	0/712	0.50	0/958
5	4	0.73	0/3746	0.99	8/5832 (0.1%)
6	Z	0.39	0/979	0.54	0/1321
7	A	0.52	0/1799	1.03	4/2801 (0.1%)
8	a	0.34	0/1004	0.55	1/1341 (0.1%)
9	B	0.57	1/1835 (0.1%)	1.01	1/2858 (0.0%)
10	b	0.35	0/1118	0.51	0/1497
11	C	0.37	0/860	0.53	0/1136
12	c	0.40	0/1204	0.54	0/1612
13	D	0.42	0/701	0.60	0/934
14	d	0.36	0/473	0.48	0/629
15	E	0.41	0/1948	0.56	0/2617
16	e	0.34	0/751	0.50	0/1008
17	F	0.40	0/3146	0.55	0/4228
18	f	0.40	0/890	0.54	0/1196
19	G	0.39	0/2800	0.53	0/3790
20	g	0.39	0/1041	0.54	0/1394
21	H	0.34	0/2425	0.50	0/3271
22	h	0.45	0/868	0.53	0/1168
23	I	0.34	0/1260	0.47	0/1694
24	i	0.39	0/890	0.52	0/1189
25	J	0.41	0/1821	0.50	0/2451
26	j	0.33	0/978	0.47	0/1301
27	K	0.35	0/1836	0.52	0/2481
28	k	0.31	0/778	0.50	0/1034
29	L	0.37	0/1539	0.53	0/2073
30	l	0.44	0/696	0.54	0/923
31	M	0.33	0/1374	0.51	0/1842
32	m	0.31	0/618	0.53	0/826

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	N	0.36	0/1568	0.52	0/2106
34	n	0.36	0/443	0.51	0/588
35	O	0.34	0/1068	0.52	0/1438
36	o	0.37	0/423	0.52	0/562
37	P	0.45	0/1757	0.58	0/2354
38	p	0.29	0/234	0.52	0/300
39	Q	0.41	0/1585	0.54	0/2128
40	q	0.32	0/1142	0.61	0/1537
41	R	0.40	0/1443	0.55	0/1944
43	S	0.37	0/1465	0.54	0/1965
44	s	0.40	0/1807	0.54	0/2425
45	T	0.34	0/1538	0.48	0/2050
46	U	0.43	0/1481	0.55	0/1990
47	V	0.39	0/1300	0.54	0/1743
48	W	0.36	0/812	0.52	0/1099
All	All	0.61	1/137831 (0.0%)	0.89	170/203631 (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
17	F	0	1
25	J	0	1
27	K	0	1
30	l	0	1
35	O	0	1
39	Q	0	1
40	q	0	1
43	S	0	1
44	s	0	2
All	All	0	10

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	B	1	G	OP3-P	-10.85	1.48	1.61

The worst 5 of 170 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	922	U	C2-N1-C1'	8.41	127.79	117.70
1	1	3278	C	C2-N1-C1'	7.92	127.51	118.80
1	1	1836	C	N3-C2-O2	-7.81	116.43	121.90
1	1	2867	C	N1-C2-O2	7.79	123.57	118.90
1	1	1836	C	N1-C2-O2	7.77	123.56	118.90

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
17	F	348	ARG	Peptide
25	J	108	LEU	Peptide
27	K	76	ALA	Peptide
35	O	48	GLY	Peptide
30	l	50	GLY	Peptide

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	
2	X	134/137 (98%)	130 (97%)	4 (3%)	0	100	100
4	Y	96/155 (62%)	86 (90%)	10 (10%)	0	100	100
6	Z	119/142 (84%)	111 (93%)	7 (6%)	1 (1%)	16	51
8	a	124/127 (98%)	109 (88%)	15 (12%)	0	100	100
10	b	133/136 (98%)	120 (90%)	12 (9%)	1 (1%)	16	51
11	C	103/106 (97%)	88 (85%)	15 (15%)	0	100	100
12	c	146/149 (98%)	128 (88%)	15 (10%)	3 (2%)	5	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	D	89/92 (97%)	79 (89%)	10 (11%)	0	100	100
14	d	56/59 (95%)	48 (86%)	7 (12%)	1 (2%)	7	35
15	E	250/254 (98%)	230 (92%)	20 (8%)	0	100	100
16	e	95/105 (90%)	88 (93%)	7 (7%)	0	100	100
17	F	384/387 (99%)	358 (93%)	25 (6%)	1 (0%)	37	70
18	f	107/109 (98%)	99 (92%)	8 (8%)	0	100	100
19	G	359/362 (99%)	319 (89%)	38 (11%)	2 (1%)	22	56
20	g	125/130 (96%)	115 (92%)	10 (8%)	0	100	100
21	H	294/297 (99%)	260 (88%)	31 (10%)	3 (1%)	13	46
22	h	104/107 (97%)	100 (96%)	4 (4%)	0	100	100
23	I	152/176 (86%)	145 (95%)	6 (4%)	1 (1%)	19	54
24	i	110/121 (91%)	106 (96%)	4 (4%)	0	100	100
25	J	220/244 (90%)	202 (92%)	18 (8%)	0	100	100
26	j	117/120 (98%)	103 (88%)	14 (12%)	0	100	100
27	K	231/256 (90%)	205 (89%)	23 (10%)	3 (1%)	10	41
28	k	97/100 (97%)	80 (82%)	16 (16%)	1 (1%)	13	46
29	L	189/191 (99%)	169 (89%)	20 (11%)	0	100	100
30	l	85/88 (97%)	74 (87%)	11 (13%)	0	100	100
31	M	167/174 (96%)	145 (87%)	20 (12%)	2 (1%)	11	43
32	m	75/78 (96%)	69 (92%)	6 (8%)	0	100	100
33	N	191/199 (96%)	171 (90%)	20 (10%)	0	100	100
34	n	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
35	O	134/138 (97%)	119 (89%)	15 (11%)	0	100	100
36	o	50/128 (39%)	46 (92%)	4 (8%)	0	100	100
37	P	201/204 (98%)	176 (88%)	25 (12%)	0	100	100
38	p	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
39	Q	195/199 (98%)	179 (92%)	16 (8%)	0	100	100
40	q	151/157 (96%)	127 (84%)	14 (9%)	10 (7%)	1	15
41	R	181/184 (98%)	166 (92%)	15 (8%)	0	100	100
43	S	183/186 (98%)	169 (92%)	14 (8%)	0	100	100
44	s	218/221 (99%)	180 (83%)	29 (13%)	9 (4%)	2	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	T	186/189 (98%)	169 (91%)	16 (9%)	1 (0%)	25	60
46	U	170/172 (99%)	151 (89%)	18 (11%)	1 (1%)	22	56
47	V	157/160 (98%)	150 (96%)	6 (4%)	1 (1%)	22	56
48	W	98/121 (81%)	86 (88%)	11 (11%)	1 (1%)	13	46
All	All	6347/6736 (94%)	5722 (90%)	583 (9%)	42 (1%)	21	54

5 of 42 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	c	48	TYR
23	I	98	VAL
40	q	110	LYS
40	q	112	ASP
40	q	133	ASP

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	
2	X	104/105 (99%)	104 (100%)	0	100	100
4	Y	57/129 (44%)	57 (100%)	0	100	100
6	Z	104/118 (88%)	104 (100%)	0	100	100
8	a	109/110 (99%)	109 (100%)	0	100	100
10	b	115/116 (99%)	115 (100%)	0	100	100
11	C	90/91 (99%)	90 (100%)	0	100	100
12	c	118/119 (99%)	118 (100%)	0	100	100
13	D	71/72 (99%)	71 (100%)	0	100	100
14	d	46/47 (98%)	46 (100%)	0	100	100
15	E	193/196 (98%)	193 (100%)	0	100	100
16	e	81/88 (92%)	81 (100%)	0	100	100
17	F	320/323 (99%)	319 (100%)	1 (0%)	91	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	f	92/96 (96%)	92 (100%)	0	100	100
19	G	288/289 (100%)	288 (100%)	0	100	100
20	g	109/111 (98%)	109 (100%)	0	100	100
21	H	244/245 (100%)	243 (100%)	1 (0%)	89	92
22	h	90/91 (99%)	90 (100%)	0	100	100
23	I	134/153 (88%)	134 (100%)	0	100	100
24	i	95/103 (92%)	95 (100%)	0	100	100
25	J	186/205 (91%)	186 (100%)	0	100	100
26	j	104/105 (99%)	104 (100%)	0	100	100
27	K	187/208 (90%)	187 (100%)	0	100	100
28	k	81/82 (99%)	81 (100%)	0	100	100
29	L	171/171 (100%)	171 (100%)	0	100	100
30	l	70/71 (99%)	70 (100%)	0	100	100
31	M	147/150 (98%)	147 (100%)	0	100	100
32	m	68/69 (99%)	68 (100%)	0	100	100
33	N	154/159 (97%)	154 (100%)	0	100	100
34	n	45/46 (98%)	45 (100%)	0	100	100
35	O	107/109 (98%)	107 (100%)	0	100	100
36	o	47/116 (40%)	47 (100%)	0	100	100
37	P	175/176 (99%)	175 (100%)	0	100	100
38	p	23/23 (100%)	23 (100%)	0	100	100
39	Q	160/162 (99%)	160 (100%)	0	100	100
40	q	118/132 (89%)	113 (96%)	5 (4%)	25	49
41	R	140/146 (96%)	140 (100%)	0	100	100
43	S	150/151 (99%)	150 (100%)	0	100	100
44	s	184/187 (98%)	178 (97%)	6 (3%)	33	56
45	T	153/154 (99%)	153 (100%)	0	100	100
46	U	156/156 (100%)	156 (100%)	0	100	100
47	V	136/137 (99%)	136 (100%)	0	100	100
48	W	87/107 (81%)	87 (100%)	0	100	100
All	All	5309/5624 (94%)	5296 (100%)	13 (0%)	91	94

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	s	102	LEU
44	s	103	SER
44	s	110	LEU
44	s	108	ASP
44	s	109	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 79 such sidechains are listed below:

Mol	Chain	Res	Type
36	o	109	ASN
44	s	54	ASN
37	P	87	GLN
40	q	125	GLN
46	U	46	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3162/3396 (93%)	1117 (35%)	336 (10%)
3	3	120/121 (99%)	30 (25%)	7 (5%)
5	4	157/158 (99%)	58 (36%)	20 (12%)
7	A	75/76 (98%)	40 (53%)	7 (9%)
9	B	76/77 (98%)	35 (46%)	6 (7%)
All	All	3590/3828 (93%)	1280 (35%)	376 (10%)

5 of 1280 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	6	A
1	1	11	A
1	1	13	A
1	1	14	U
1	1	15	C

5 of 376 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2403	G
1	1	2850	G

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Mol	Chain	Res	Type
1	1	2500	A
1	1	2635	A
1	1	3115	C

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
40	5CT	q	51	40	13,14,15	0.35	0	9,15,17	1.21	2 (22%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
40	5CT	q	51	40	-	5/13/14/16	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	q	51	5CT	C1-NZ-CE	-2.32	108.23	113.42
40	q	51	5CT	C4-C3-C2	-2.05	109.16	113.47

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
40	q	51	5CT	O-C-CA-CB

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Mol	Chain	Res	Type	Atoms
40	q	51	5CT	C2-C3-C4-N1
40	q	51	5CT	CG-CD-CE-NZ
40	q	51	5CT	C2-C1-NZ-CE
40	q	51	5CT	CD-CE-NZ-C1

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
50	3HE	1	3401	-	21,21,21	0.87	1 (4%)	19,30,30	0.76	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
50	3HE	1	3401	-	-	3/8/36/36	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	1	3401	3HE	C5-C7	3.30	1.58	1.53

There are no bond angle outliers.

There are no chirality outliers.

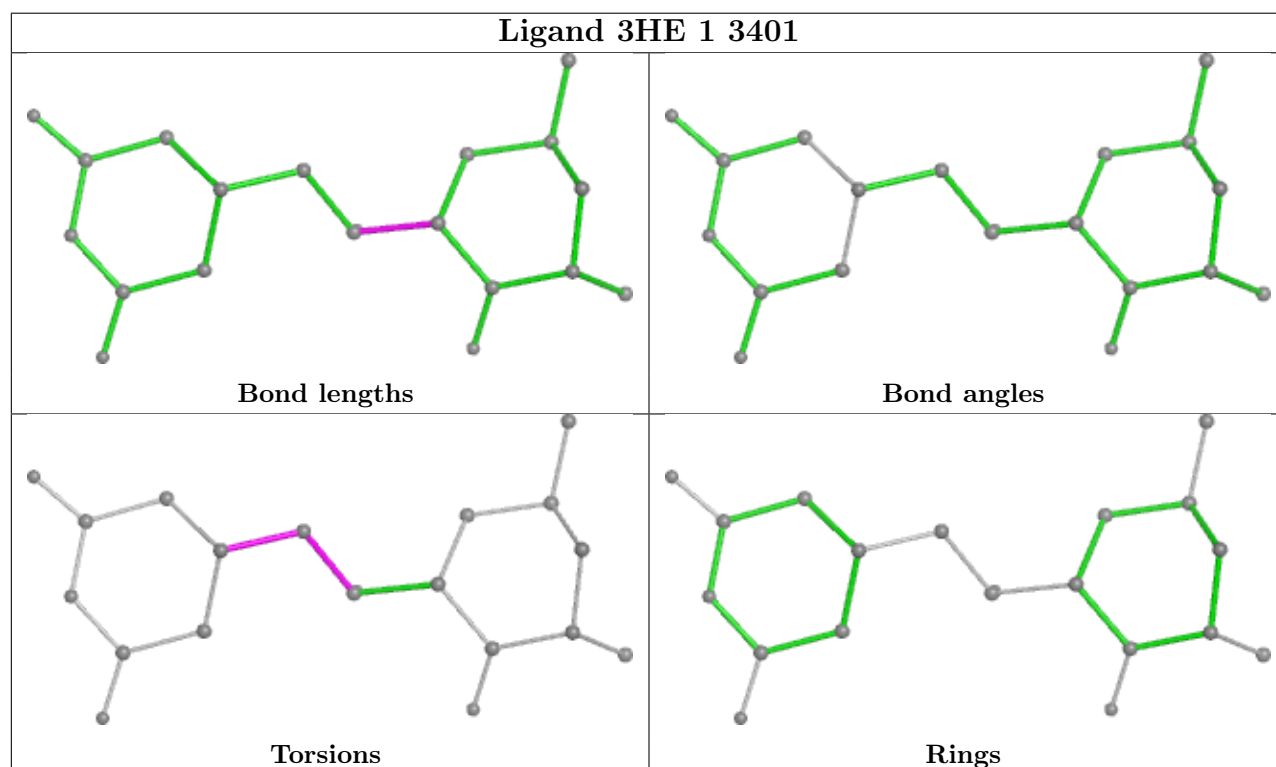
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
50	1	3401	3HE	C7-C8-C9-C10
50	1	3401	3HE	C7-C8-C9-C13
50	1	3401	3HE	O3-C7-C8-C9

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

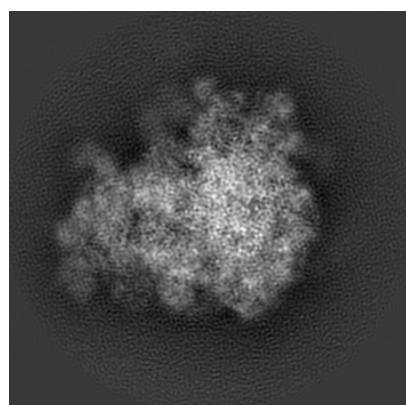
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3227. These allow visual inspection of the internal detail of the map and identification of artifacts.

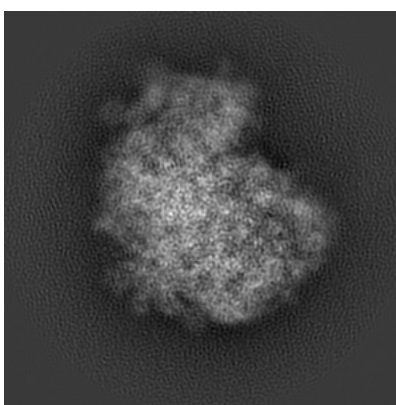
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

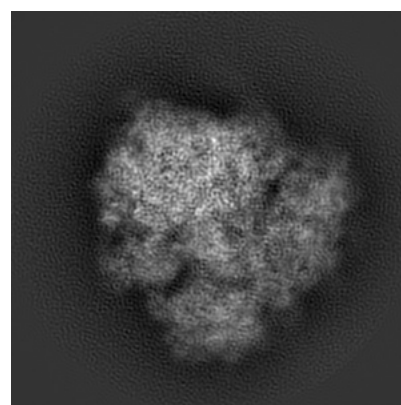
6.1.1 Primary map



X



Y

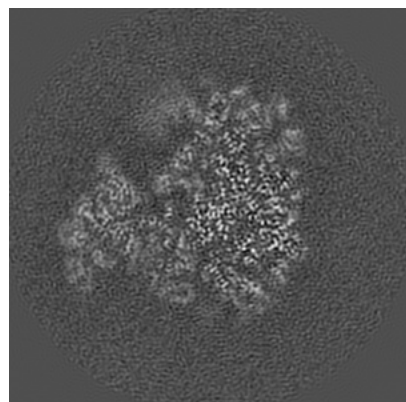


Z

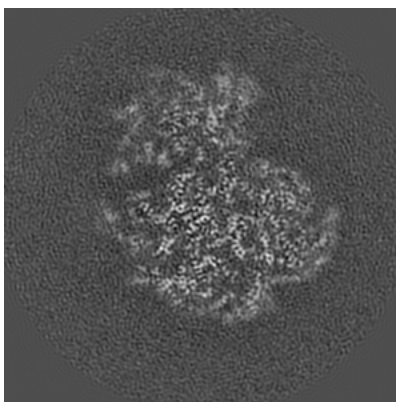
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

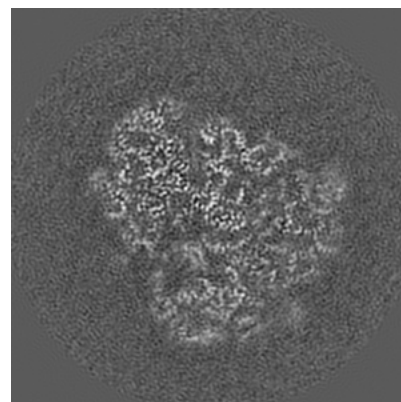
6.2.1 Primary map



X Index: 185



Y Index: 185

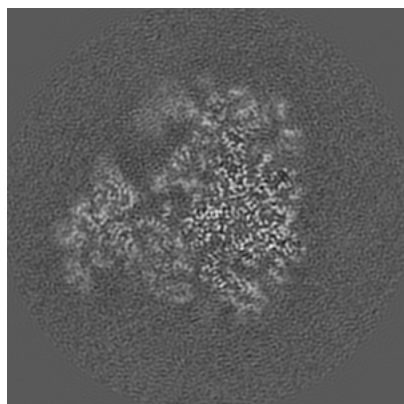


Z Index: 185

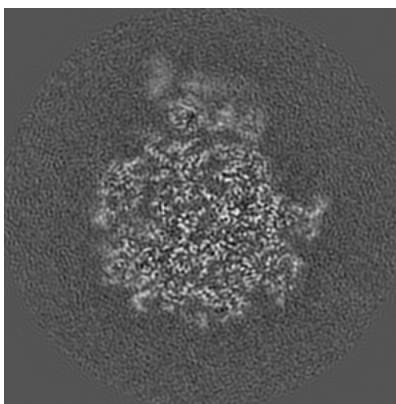
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

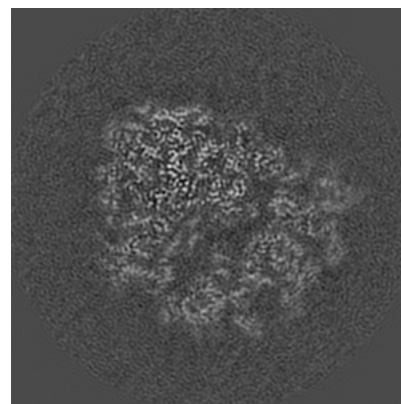
6.3.1 Primary map



X Index: 184



Y Index: 216

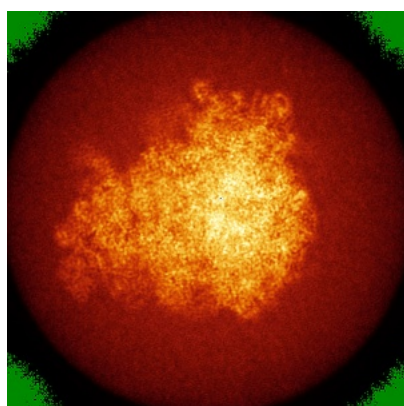


Z Index: 198

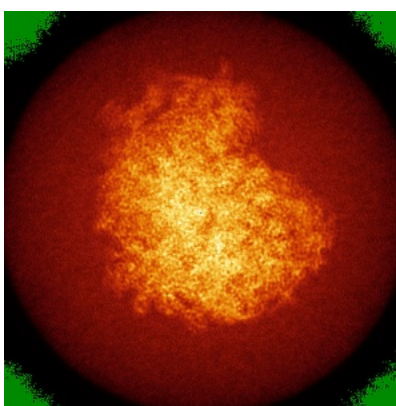
The images above show the largest variance slices of the map in three orthogonal directions.

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

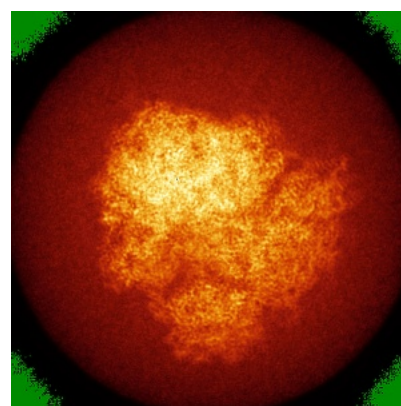
6.4.1 Primary map



X



Y

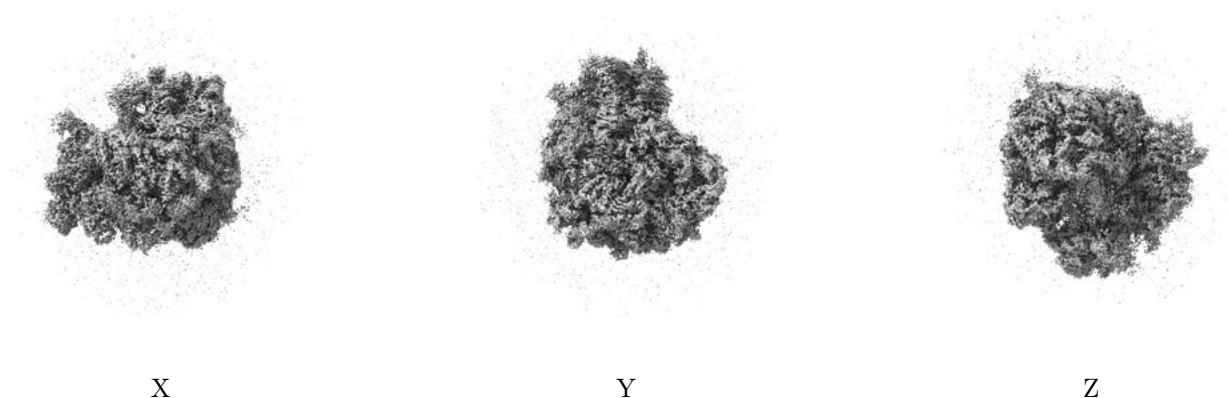


Z

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

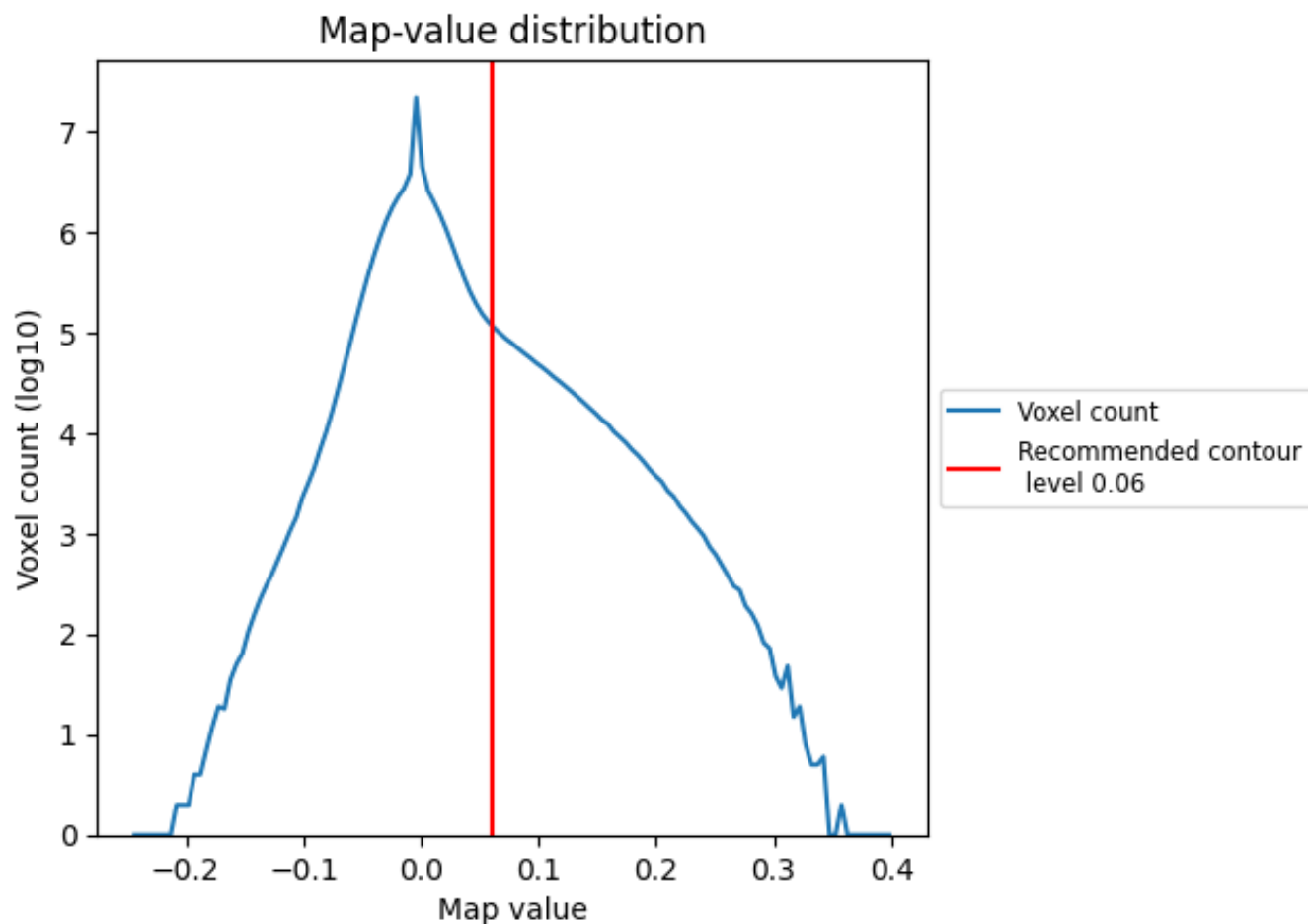
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

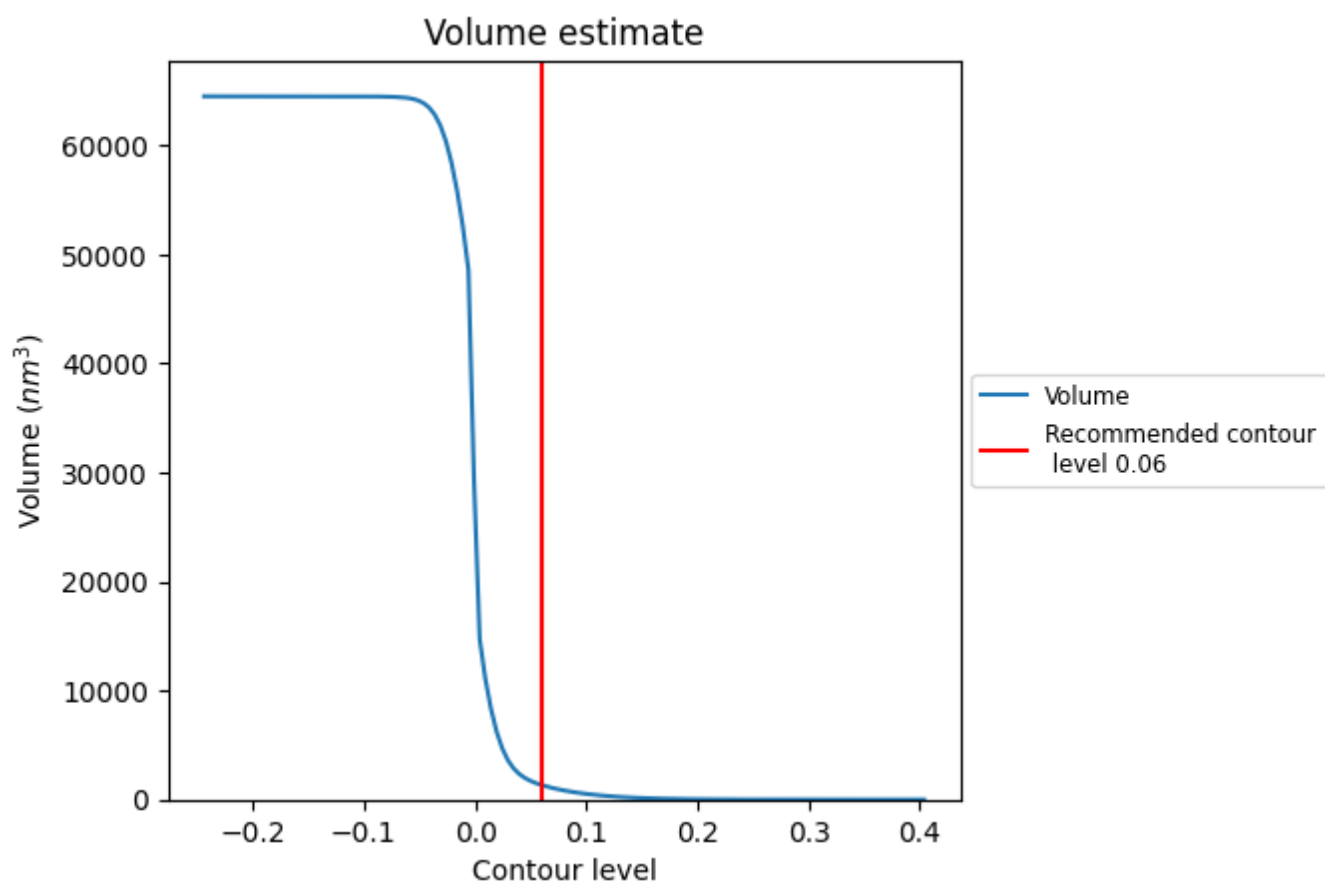
This section contains the results of statistical analysis of the map.

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.

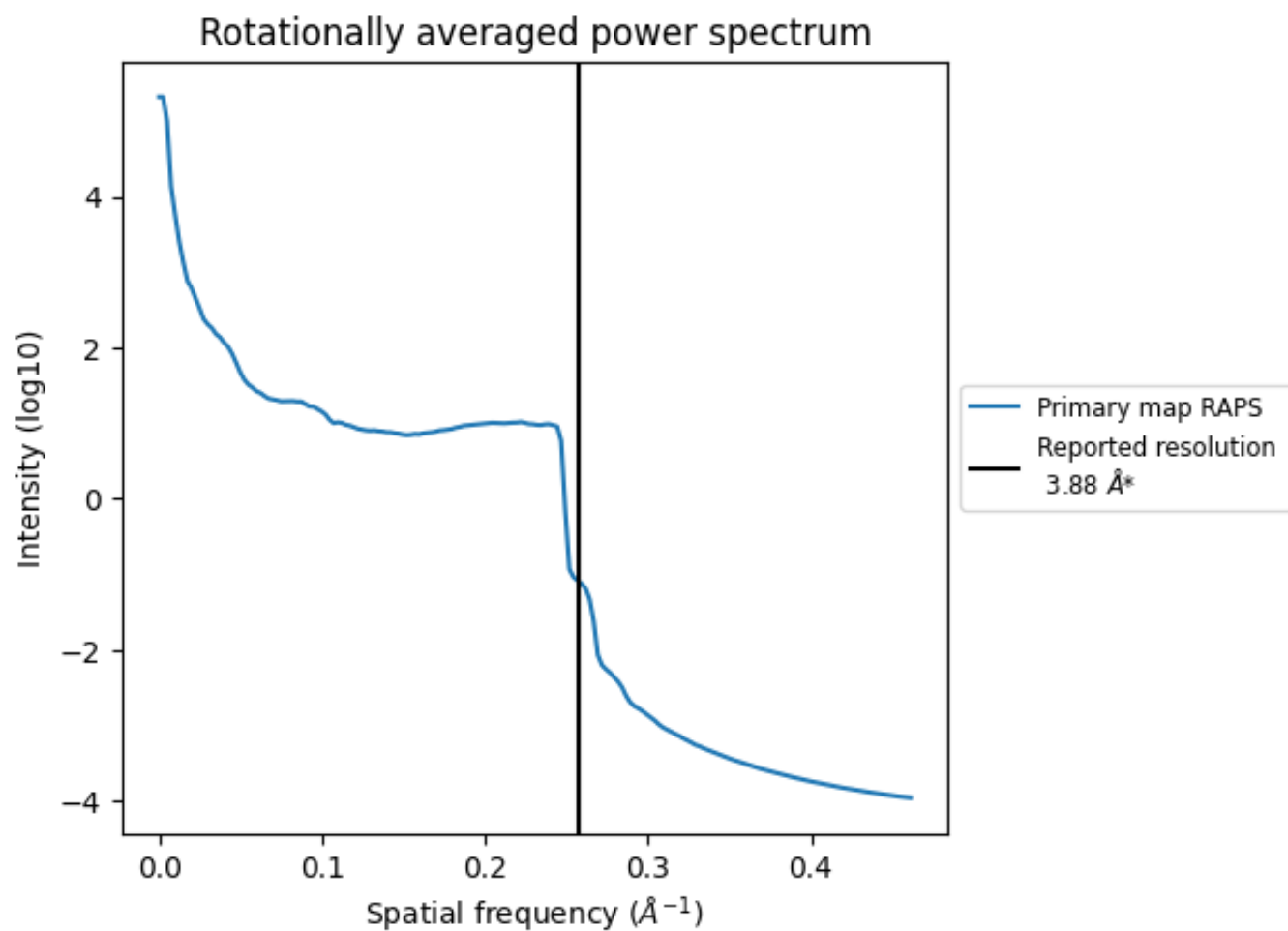
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1328 nm³; this corresponds to an approximate mass of 1199 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 0.258 Å⁻¹

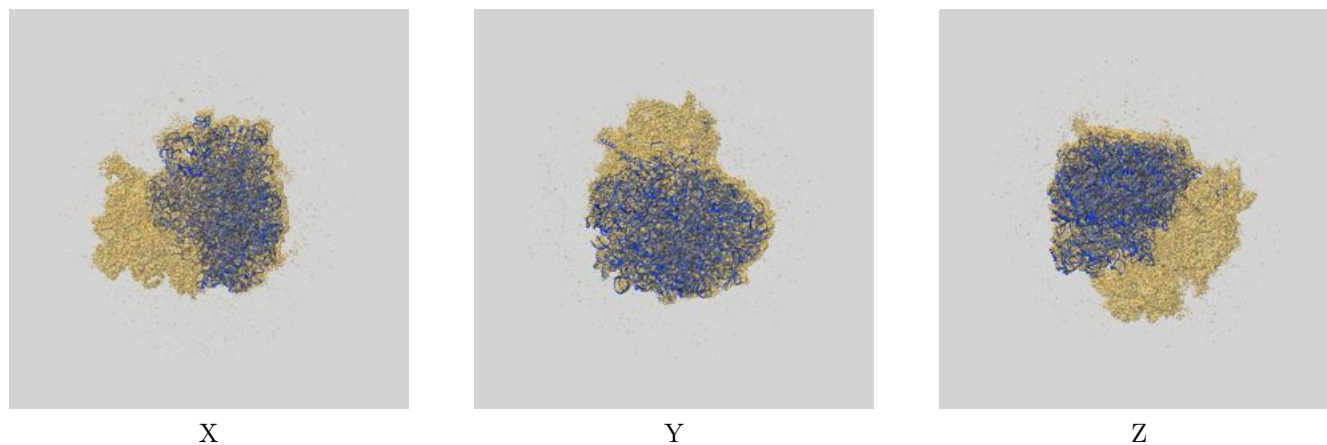
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

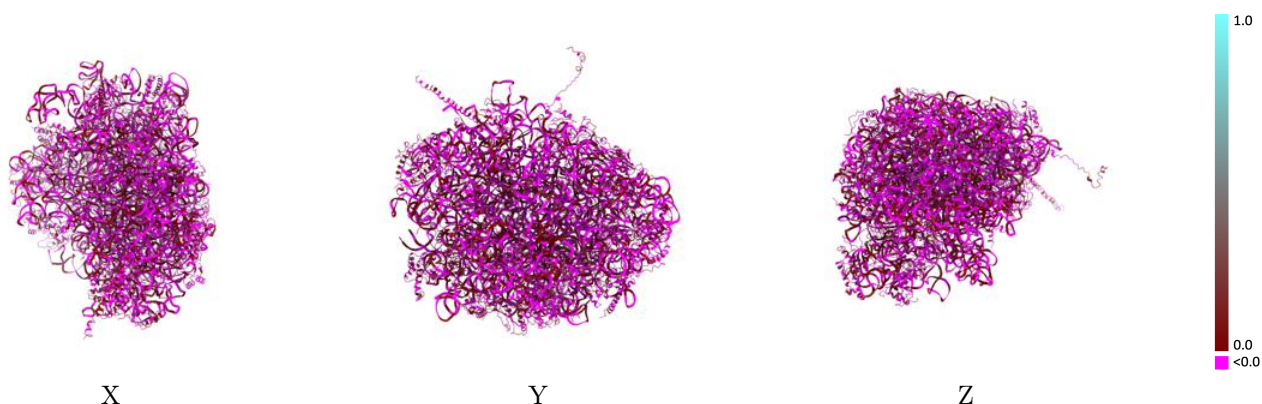
This section contains information regarding the fit between EMDB map EMD-3227 and PDB model 5GAK. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



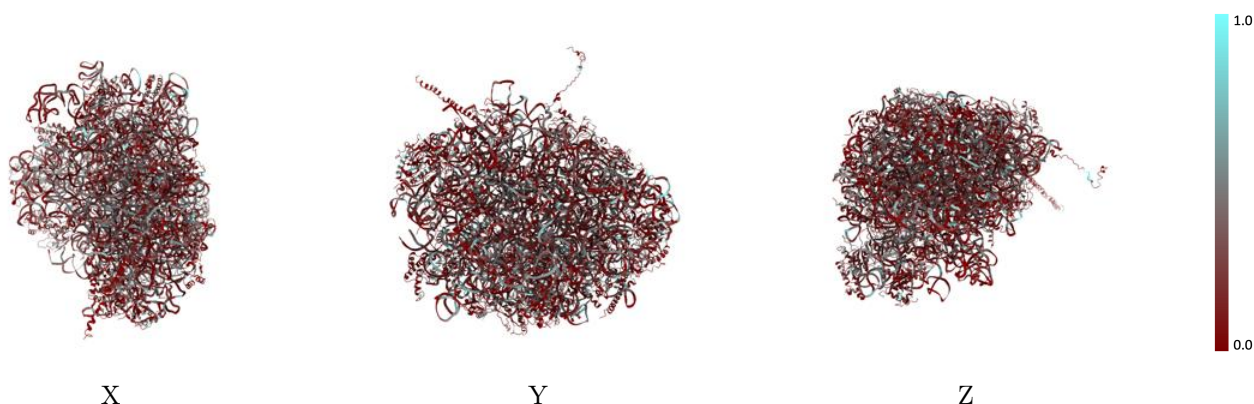
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



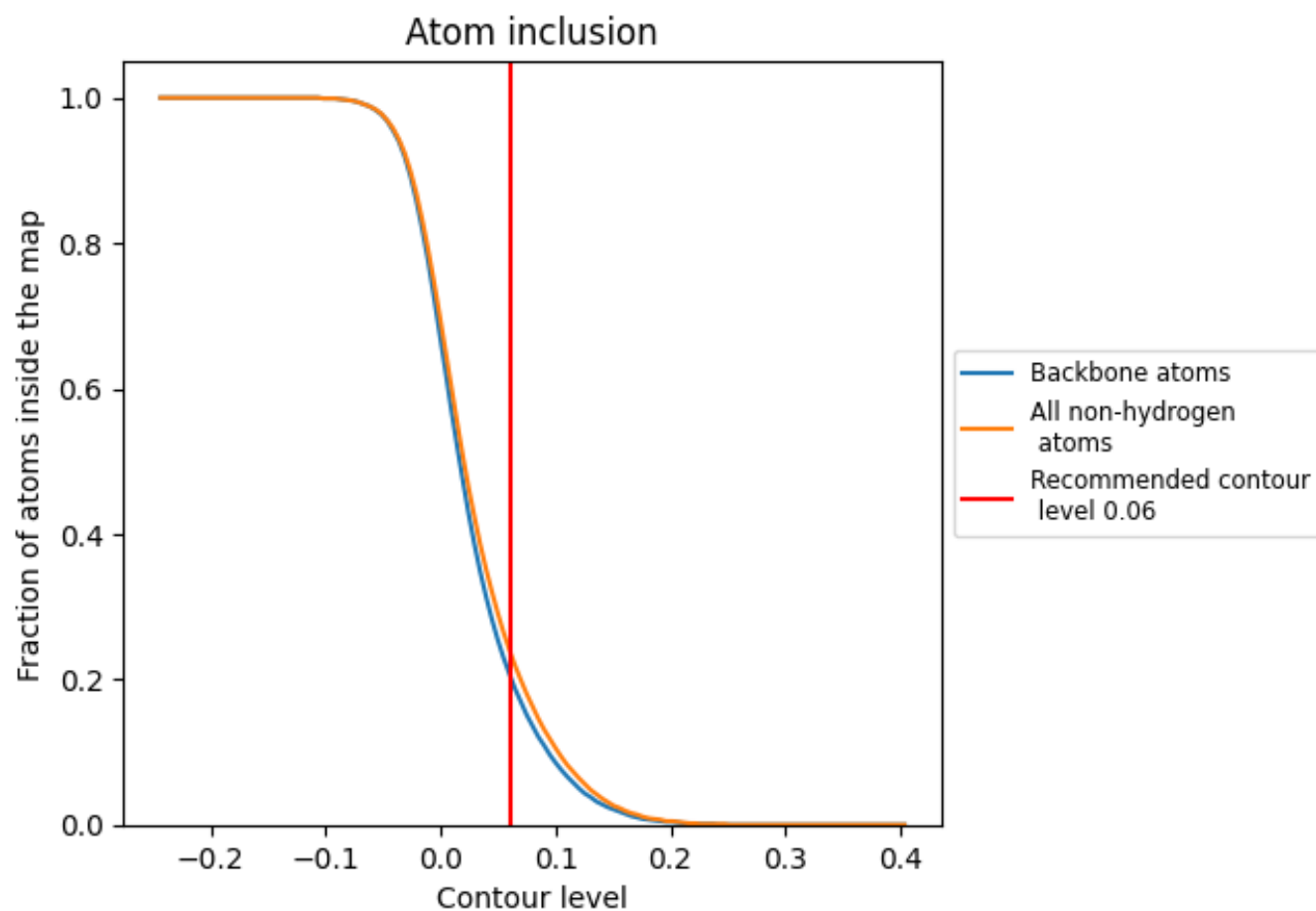
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.06).

9.4 Atom inclusion [i](#)



At the recommended contour level, 21% of all backbone atoms, 24% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.2400	-0.0120
1	0.2670	-0.0130
3	0.3180	-0.0210
4	0.2430	-0.0250
A	0.1680	-0.0150
B	0.2310	0.0010
C	0.1280	-0.0020
D	0.1460	-0.0120
E	0.2090	0.0100
F	0.2590	-0.0090
G	0.2020	-0.0280
H	0.2010	0.0080
I	0.1980	-0.0340
J	0.1910	-0.0280
K	0.1750	0.0320
L	0.2110	-0.0230
M	0.1910	0.0130
N	0.2140	0.0110
O	0.1550	-0.0430
P	0.2680	0.0110
Q	0.2360	-0.0320
R	0.2340	-0.0260
S	0.2140	-0.0210
T	0.1870	-0.0350
U	0.1950	-0.0200
V	0.1790	-0.0200
W	0.2200	-0.0260
X	0.1650	-0.0310
Y	0.1980	0.0080
Z	0.2210	-0.0080
a	0.2010	-0.0390
b	0.2180	0.0030
c	0.2090	-0.0130
d	0.1640	-0.0330
e	0.1350	-0.0040



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Chain	Atom inclusion	Q-score
f	 0.2130	 -0.0140
g	 0.2300	 -0.0230
h	 0.2750	 -0.0160
i	 0.2640	 0.0200
j	 0.2110	 0.0010
k	 0.1680	 0.0600
l	 0.2180	 -0.0270
m	 0.1520	 -0.0310
n	 0.1900	 -0.0230
o	 0.1840	 0.0130
p	 0.1930	 -0.0010
q	 0.1040	 0.0100
r	 0.1510	 -0.0060
s	 0.1900	 -0.0110
z	 0.0700	 -0.0450