



wwPDB EM Validation Summary Report ⓘ

Nov 10, 2025 – 02:22 PM EST

PDB ID : 8UXA / pdb_00008uxa
EMDB ID : EMD-42720
Title : Glucose treated mitochondrial ribosome of saccharomyces cerevisiae class I
Authors : Yu, Z.; Zheng, F.; Zhou, C.
Deposited on : 2023-11-09
Resolution : 3.20 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:

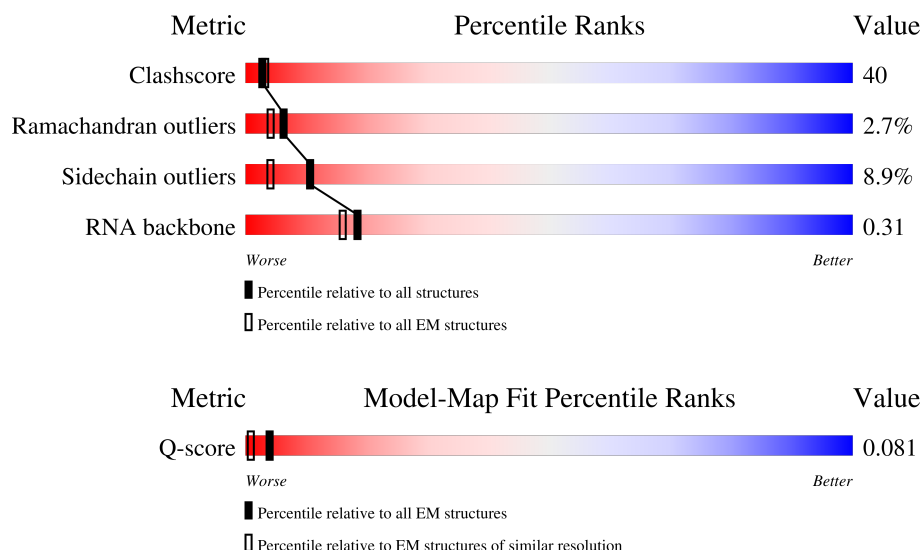
EMDB validation analysis : 0.0.1.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.46

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.20 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	AA	34	<div> <div>65%</div> <div>24%</div> <div>68%</div> <div>9%</div> </div>
2	AB	101	<div> <div>90%</div> <div>20%</div> <div>51%</div> <div>22%</div> <div>6%</div> </div>
3	AC	259	<div> <div>93%</div> <div>28%</div> <div>58%</div> <div>13%</div> </div>

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Mol	Chain	Length	Quality of chain
4	AD	321	
5	AE	339	
6	AF	320	
7	AG	236	
8	AH	234	
9	AI	405	
10	AJ	96	
11	AK	273	
12	AL	1649	
13	AM	76	
14	AN	13	
15	Z	91	
16	g	344	
17	h	267	
18	i	398	
19	j	486	
20	k	293	
21	l	131	
22	m	161	
23	n	155	
24	o	244	
25	p	186	
26	q	152	
27	r	125	
28	s	120	

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Mol	Chain	Length	Quality of chain
29	t	115	
30	u	253	
31	v	120	
32	w	237	
33	x	99	
34	y	80	
35	z	92	
36	0	38	
37	1	348	
38	2	113	
39	3	130	
40	4	138	
41	5	324	
42	6	281	
43	7	106	
44	8	264	
45	9	215	
46	A	3296	
47	B	393	
48	C	249	
49	D	252	
50	E	274	
51	F	196	
52	G	74	
53	H	160	

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Mol	Chain	Length	Quality of chain
54	I	138	
55	J	220	
56	K	195	
57	L	237	
58	M	151	
59	N	118	
60	O	225	
61	P	207	
62	Q	296	
63	R	337	
64	S	216	
65	T	225	
66	U	82	
67	V	177	
68	W	112	
69	X	64	
70	Y	46	
71	a	177	
72	b	155	
73	c	119	
74	d	215	
75	e	249	
76	f	158	

2 Entry composition

There are 76 unique types of molecules in this entry. The entry contains 201764 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 protein called Small ribosomal subunit protein mS38.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	34	Total	C	N	O	S	0	0
			304	183	75	44	2		

- Molecule 2 is a protein called Small ribosomal subunit protein mS41.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	95	Total	C	N	O	S	0	0
			808	512	153	142	1		

- Molecule 3 is a protein called Small ribosomal subunit protein mS42.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	259	Total	C	N	O	S	0	0
			2079	1335	352	387	5		

- Molecule 4 is a protein called 37S ribosomal protein MRP1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	301	Total	C	N	O	S	0	0
			2422	1530	418	464	10		

- Molecule 5 is a protein called 37S ribosomal protein MRP13, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	298	Total	C	N	O	S	0	0
			2432	1569	421	438	4		

- Molecule 6 is a protein called Small ribosomal subunit protein mS45.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	252	Total	C	N	O	S	0	0
			2079	1327	377	369	6		

- Molecule 7 is a protein called Small ribosomal subunit protein mS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	236	Total	C	N	O	S	0	0
			1931	1224	337	363	7		

- Molecule 8 is a protein called Small ribosomal subunit protein mS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	234	Total	C	N	O	S	0	0
			1887	1197	339	347	4		

- Molecule 9 is a protein called Small ribosomal subunit protein mS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	405	Total	C	N	O	S	0	0
			3243	2087	545	603	8		

- Molecule 10 is a protein called Small ribosomal subunit protein mS33.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	96	Total	C	N	O	S	0	0
			774	496	140	135	3		

- Molecule 11 is a protein called Small ribosomal subunit protein mS35.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	264	Total	C	N	O	S	0	0
			2212	1397	399	412	4		

- Molecule 12 is a RNA chain called Small ribosomal subunit rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	1501	Total	C	N	O	P	0	0
			31883	14338	5633	10411	1501		

- Molecule 13 is a RNA chain called Small ribosomal subunit tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	76	Total	C	N	O	P	0	0
			1615	723	289	528	75		

- Molecule 14 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	13	Total	C	N	O	P	0	0
			270	123	49	86	12		

- Molecule 15 is a protein called Small ribosomal subunit protein mS37.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Z	87	Total	C	N	O	S	0	0
			687	435	128	118	6		

- Molecule 16 is a protein called 37S ribosomal protein MRP51, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	g	198	Total	C	N	O	S	0	0
			1577	1014	278	280	5		

- Molecule 17 is a protein called Small ribosomal subunit protein uS2m.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	h	267	Total	C	N	O	S	0	0
			2095	1319	368	406	2		

- Molecule 18 is a protein called Ribosomal protein VAR1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	i	293	Total	C	N	O	S	0	0
			2461	1554	432	452	23		

- Molecule 19 is a protein called 37S ribosomal protein NAM9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	j	287	Total	C	N	O	S	0	0
			2370	1542	420	404	4		

- Molecule 20 is a protein called Small ribosomal subunit protein uS5m.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	k	288	Total	C	N	O	S	0	0
			2306	1473	408	417	8		

- Molecule 21 is a protein called 37S ribosomal protein MRP17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	l	131	Total	C	N	O	S	0	0
			1055	671	189	191	4		

- Molecule 22 is a protein called Small ribosomal subunit protein uS7m.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	m	161	Total	C	N	O	S	0	0
			1282	811	238	228	5		

- Molecule 23 is a protein called 37S ribosomal protein S8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	n	155	Total	C	N	O	S	0	0
			1221	772	218	221	10		

- Molecule 24 is a protein called Small ribosomal subunit protein uS9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	o	226	Total	C	N	O	S	0	0
			1820	1167	332	316	5		

- Molecule 25 is a protein called Small ribosomal subunit protein uS10m.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	p	134	Total	C	N	O	S	0	0
			1108	719	192	193	4		

- Molecule 26 is a protein called Small ribosomal subunit protein uS11m.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	q	152	Total	C	N	O	S	0	0
			1208	775	211	216	6		

- Molecule 27 is a protein called Small ribosomal subunit protein uS12m.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	r	125	Total	C	N	O	S	0	0
			955	588	195	168	4		

- Molecule 28 is a protein called Small ribosomal subunit protein uS13m.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	s	120	Total	C	N	O	S	0	0
			942	596	179	161	6		

- Molecule 29 is a protein called 37S ribosomal protein MRP2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	t	113	Total	C	N	O	S	0	0
			942	605	180	153	4		

- Molecule 30 is a protein called Small ribosomal subunit protein uS15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	u	253	Total	C	N	O	S	0	0
			2070	1292	387	383	8		

- Molecule 31 is a protein called Small ribosomal subunit protein bS16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	v	106	Total	C	N	O	S	0	0
			830	529	155	144	2		

- Molecule 32 is a protein called 37S ribosomal protein S17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	w	204	Total	C	N	O	S	0	0
			1683	1055	315	308	5		

- Molecule 33 is a protein called Small ribosomal subunit protein bS18m.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	x	91	Total	C	N	O	S	0	0
			738	463	143	128	4		

- Molecule 34 is a protein called Small ribosomal subunit protein uS19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	y	80	Total	C	N	O	S	0	0
			636	408	115	111	2		

- Molecule 35 is a protein called Small ribosomal subunit protein bS21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	z	92	Total	C	N	O	S	0	0
			760	475	150	130	5		

- Molecule 36 is a protein called Large ribosomal subunit protein bL36m.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	0	38	Total	C	N	O	S	0	0
			324	205	66	50	3		

- Molecule 37 is a protein called Large ribosomal subunit protein mL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	1	348	Total	C	N	O	S	0	0
			2875	1847	499	523	6		

- Molecule 38 is a protein called Large ribosomal subunit protein mL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	2	113	Total	C	N	O	S	0	0
			944	597	174	168	5		

- Molecule 39 is a protein called Large ribosomal subunit protein mL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	3	130	Total	C	N	O	S	0	0
			1046	671	189	183	3		

- Molecule 40 is a protein called Large ribosomal subunit protein mL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	4	138	Total	C	N	O	S	0	0
			1117	700	219	193	5		

- Molecule 41 is a protein called Large ribosomal subunit protein mL44.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	5	324	Total	C	N	O	S	0	0
			2552	1630	431	480	11		

- Molecule 42 is a protein called Large ribosomal subunit protein mL46.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	6	234	Total	C	N	O	S	0	0
			1932	1250	327	353	2		

- Molecule 43 is a protein called Large ribosomal subunit protein mL49.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	7	106	Total	C	N	O	S	0	0
			858	553	151	152	2		

- Molecule 44 is a protein called Large ribosomal subunit protein mL50.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	8	199	Total	C	N	O	S	0	0
			1629	1032	278	315	4		

- Molecule 45 is a protein called Large ribosomal subunit protein mL57.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	9	202	Total	C	N	O	S	0	0
			1587	1014	279	289	5		

- Molecule 46 is a RNA chain called Large ribosomal subunit rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	A	2876	Total	C	N	O	P	0	0
			61141	27507	10875	19889	2870		

- Molecule 47 is a protein called Large ribosomal subunit protein uL2m.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	B	321	Total	C	N	O	S	0	0
			2527	1575	507	436	9		

- Molecule 48 is a protein called Large ribosomal subunit protein uL3m.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	C	249	Total	C	N	O	S	0	0
			1932	1218	360	344	10		

- Molecule 49 is a protein called Large ribosomal subunit protein uL4m.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	D	252	Total	C	N	O	S	0	0
			1989	1262	355	369	3		

- Molecule 50 is a protein called Large ribosomal subunit protein uL5m.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	E	274	Total	C	N	O	S	0	0
			2187	1396	391	394	6		

- Molecule 51 is a protein called Large ribosomal subunit protein uL6m.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	F	196	Total	C	N	O	S	0	0
			1524	967	273	280	4		

- Molecule 52 is a protein called Large ribosomal subunit protein bL9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	G	74	Total	C	N	O	S	0	0
			617	393	110	113	1		

- Molecule 53 is a protein called Large ribosomal subunit protein uL13m.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	H	160	Total	C	N	O	S	0	0
			1275	807	240	224	4		

- Molecule 54 is a protein called Large ribosomal subunit protein uL14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	I	127	Total	C	N	O	S	0	0
			956	595	180	170	11		

- Molecule 55 is a protein called Large ribosomal subunit protein uL15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	J	220	Total	C	N	O	S	0	0
			1746	1119	326	298	3		

- Molecule 56 is a protein called Large ribosomal subunit protein uL16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	K	195	Total	C	N	O	S	0	0
			1573	1001	297	270	5		

- Molecule 57 is a protein called Large ribosomal subunit protein bL17m.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	L	229	Total	C	N	O	S	0	0
			1817	1140	333	336	8		

- Molecule 58 is a protein called Large ribosomal subunit protein bL19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	M	151	Total	C	N	O	S	0	0
			1206	766	220	217	3		

- Molecule 59 is a protein called Large ribosomal subunit protein bL21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	N	118	Total	C	N	O	S	0	0
			948	598	177	171	2		

- Molecule 60 is a protein called Large ribosomal subunit protein uL22m.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	O	225	Total	C	N	O	S	0	0
			1826	1169	332	320	5		

- Molecule 61 is a protein called Large ribosomal subunit protein uL23m.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	P	207	Total	C	N	O	S	0	0
			1729	1104	310	309	6		

- Molecule 62 is a protein called Large ribosomal subunit protein uL24m.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Q	284	Total	C	N	O	S	0	0
			2272	1451	396	417	8		

- Molecule 63 is a protein called Large ribosomal subunit protein bL27m.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	R	331	Total	C	N	O	S	0	0
			2738	1728	497	509	4		

- Molecule 64 is a protein called Large ribosomal subunit protein bL28m.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	S	185	Total	C	N	O	S	0	0
			1543	994	281	265	3		

- Molecule 65 is a protein called Large ribosomal subunit protein uL29m.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	T	216	Total	C	N	O	S	0	0
			1792	1139	324	325	4		

- Molecule 66 is a protein called Large ribosomal subunit protein uL30m.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	U	82	Total	C	N	O		0	0
			639	410	116	113			

- Molecule 67 is a protein called Large ribosomal subunit protein bL31m.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	V	66	Total	C	N	O	S	0	0
			543	340	110	92	1		

- Molecule 68 is a protein called Large ribosomal subunit protein bL32m.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	W	112	Total	C	N	O	S	0	0
			937	587	181	163	6		

- Molecule 69 is a protein called Large ribosomal subunit protein bL33m.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	X	64	Total	C	N	O		0	0
			512	330	96	86			

- Molecule 70 is a protein called Large ribosomal subunit protein bL34m.

Mol	Chain	Residues	Atoms				AltConf	Trace
70	Y	46	Total	C	N	O		
			385	245	82	58	0	0

- Molecule 71 is a protein called Large ribosomal subunit protein mL58.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	a	177	Total	C	N	O	S		
			1440	907	267	260	6	0	0

- Molecule 72 is a protein called Large ribosomal subunit protein mL59.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	b	155	Total	C	N	O	S		
			1299	850	225	221	3	0	0

- Molecule 73 is a protein called Large ribosomal subunit protein mL60.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	c	119	Total	C	N	O	S		
			1004	645	191	164	4	0	0

- Molecule 74 is a protein called Large ribosomal subunit protein mL67.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	d	206	Total	C	N	O	S		
			1746	1117	318	304	7	0	0

- Molecule 75 is a protein called Large ribosomal subunit protein uL10m.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	e	165	Total	C	N	O	S		
			1340	862	234	238	6	0	0

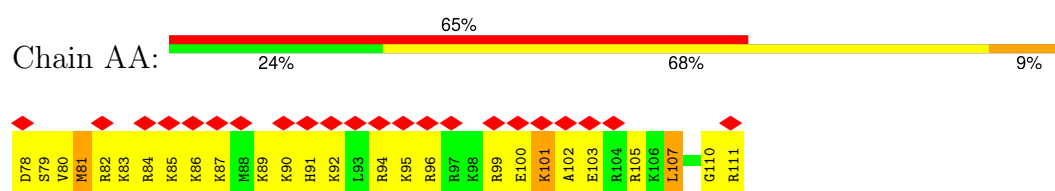
- Molecule 76 is a protein called Large ribosomal subunit protein uL11m.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	f	138	Total	C	N	O	S		
			1032	668	176	183	5	0	0

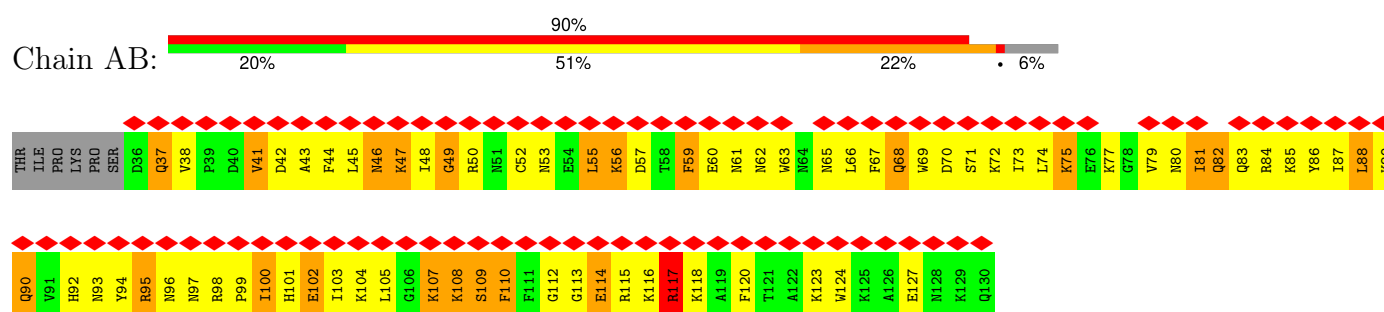
3 Residue-property plots

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.

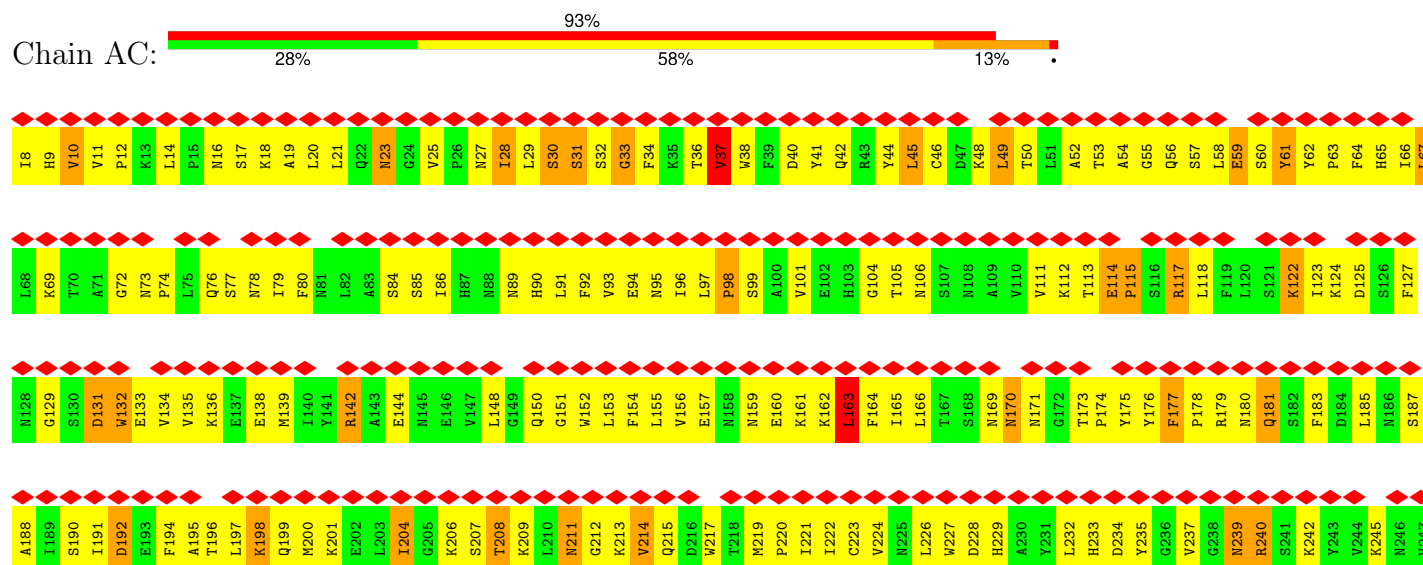
- Molecule 1: Small ribosomal subunit protein mS38

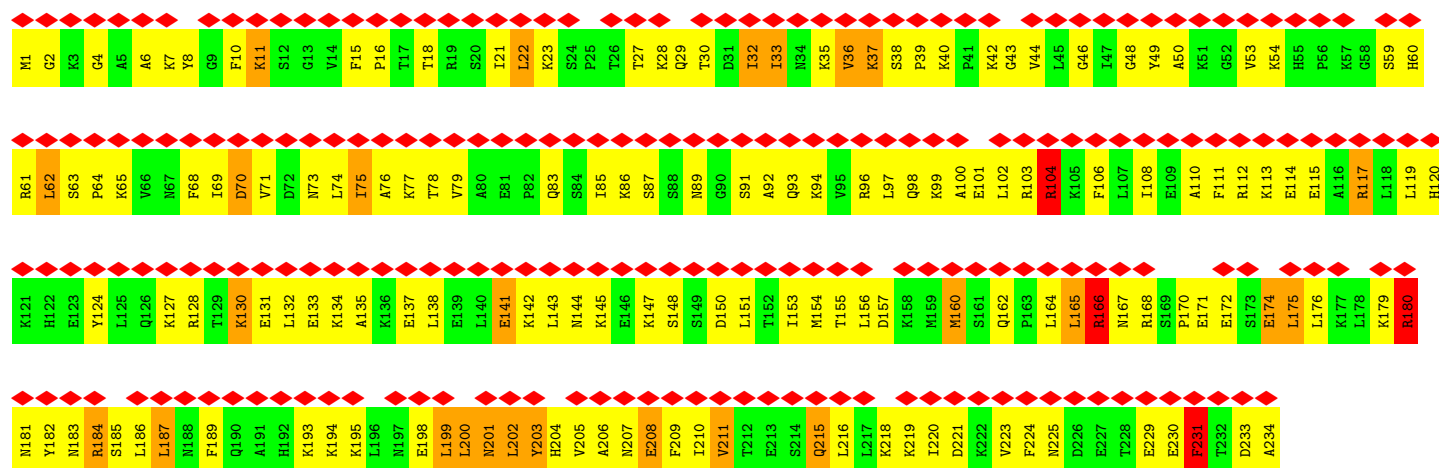


- Molecule 2: Small ribosomal subunit protein mS41



- Molecule 3: Small ribosomal subunit protein mS42

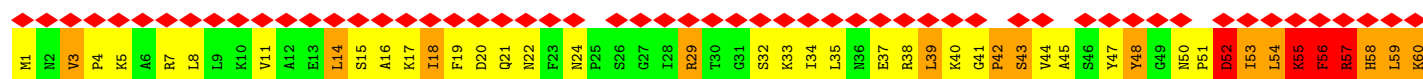
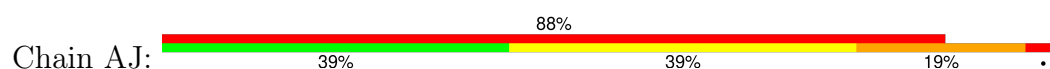


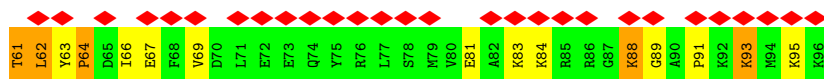


• Molecule 9: Small ribosomal subunit protein mS29

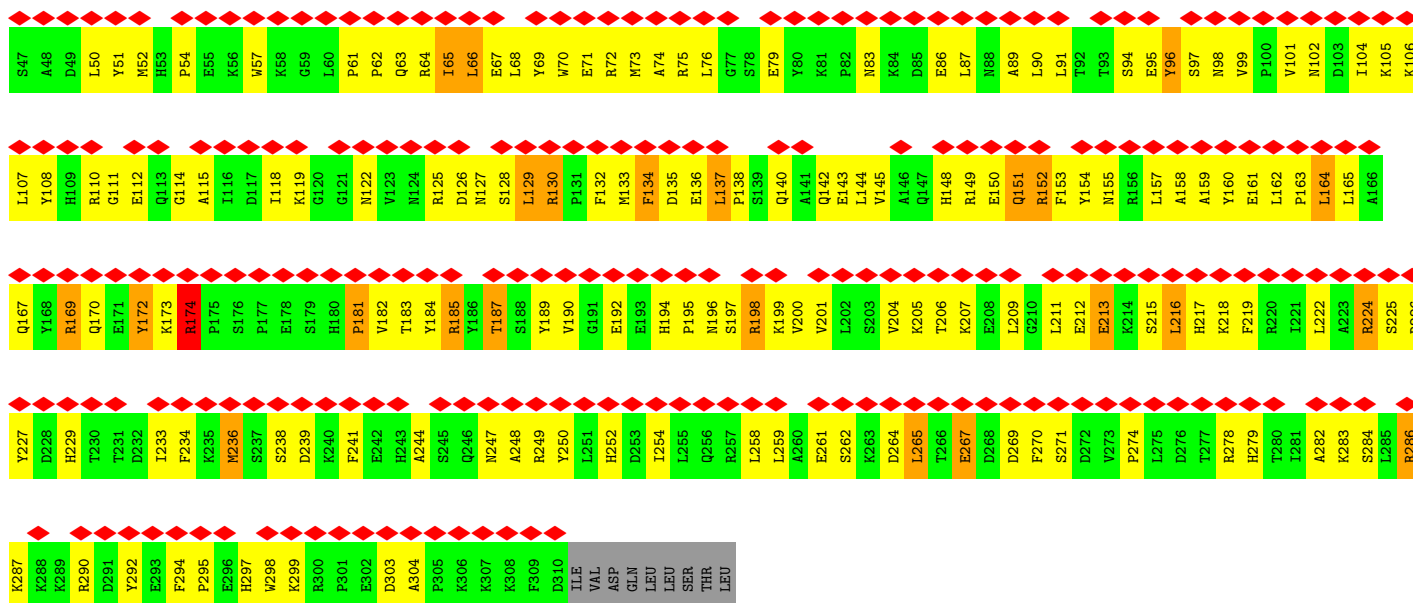
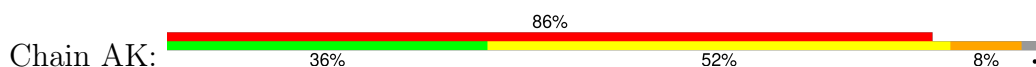


• Molecule 10: Small ribosomal subunit protein mS33

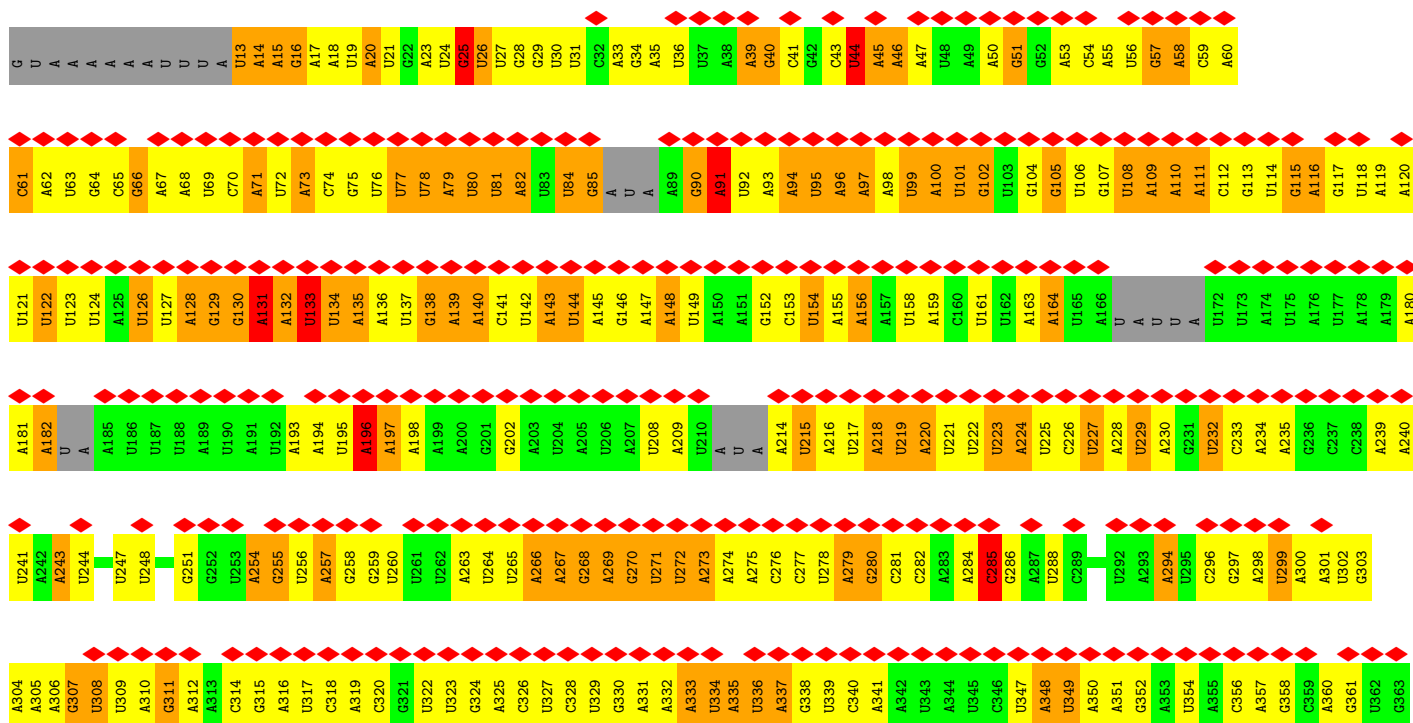
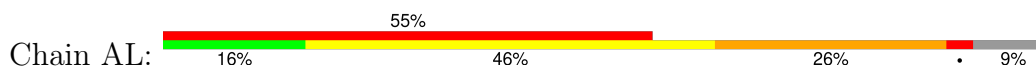




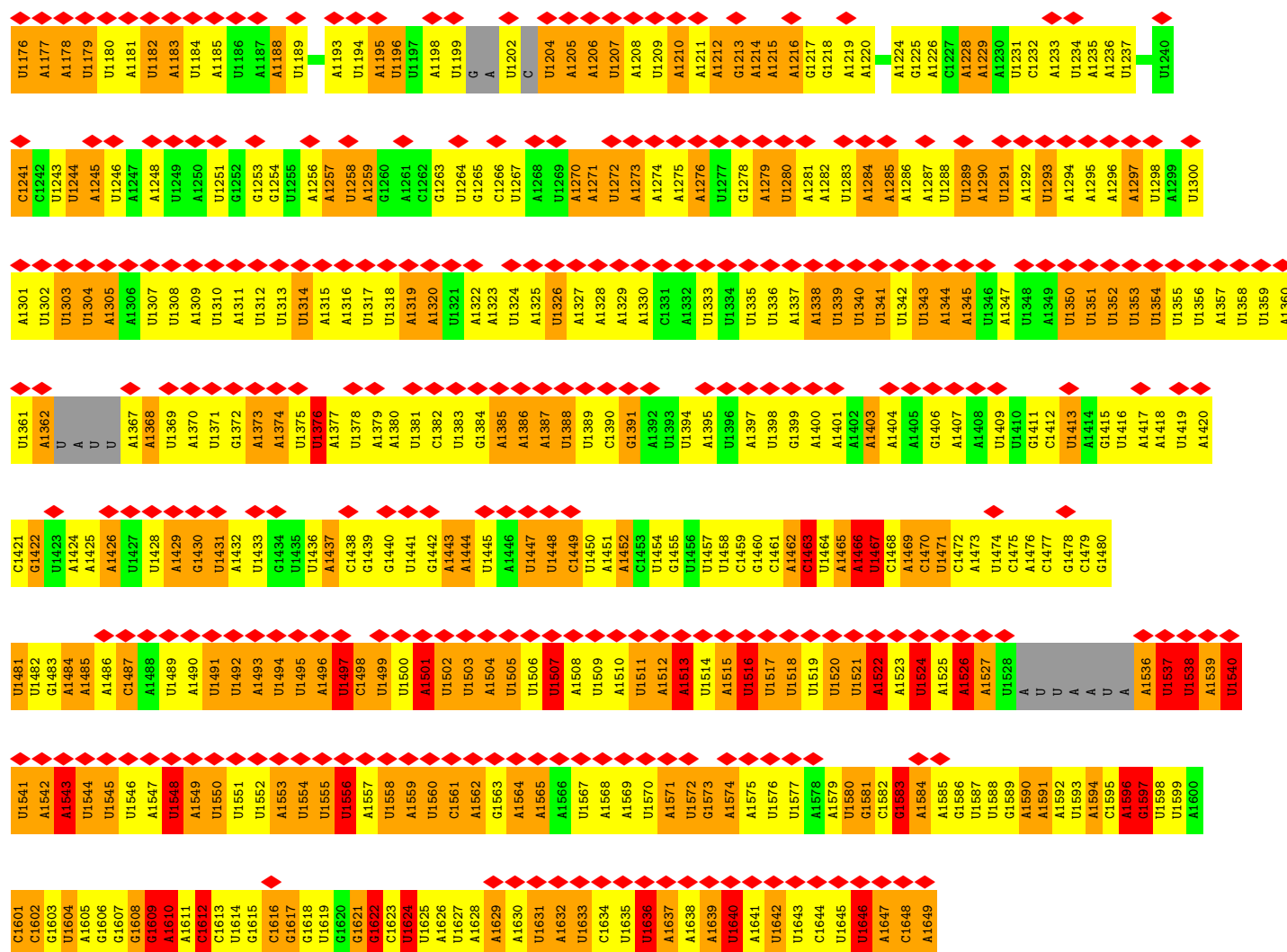
• Molecule 11: Small ribosomal subunit protein mS35



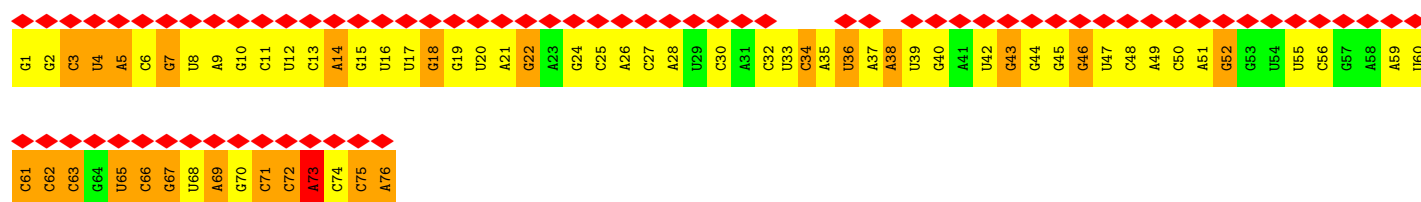
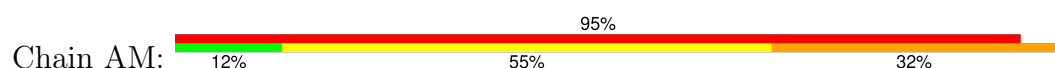
• Molecule 12: Small ribosomal subunit rRNA



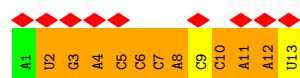
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U1117	U1056	U993	U921	A859	U800	G739	A671	A609	U	U489	U369
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A1136	A1072	G939	G939	A876	U816	A754	U691	U628	A	A505	A385
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G1141	U1074	A941	A941	U878	A818	U756	G693	U630	U	A507	U387
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C1144	A1077	C944	C944	U881	U821	U759	U696	C633	U	U510	U390
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A1156	A1087	U959	U959	U894	A831	U769	U705	U643	U	A520	A401
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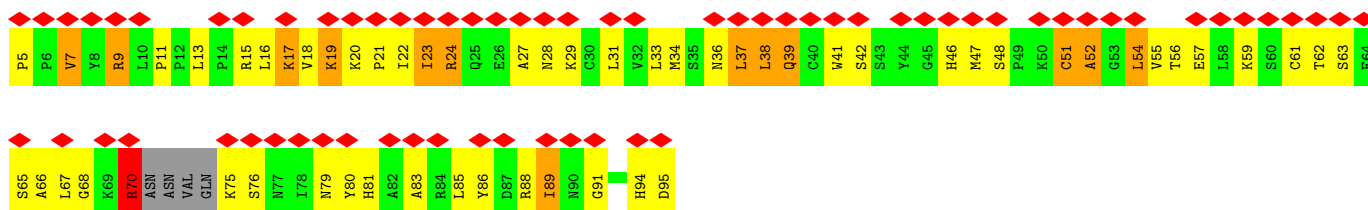
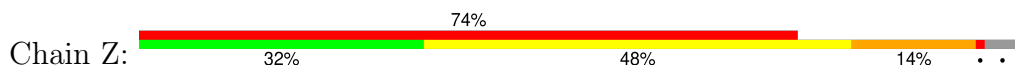
• Molecule 13: Small ribosomal subunit tRNA



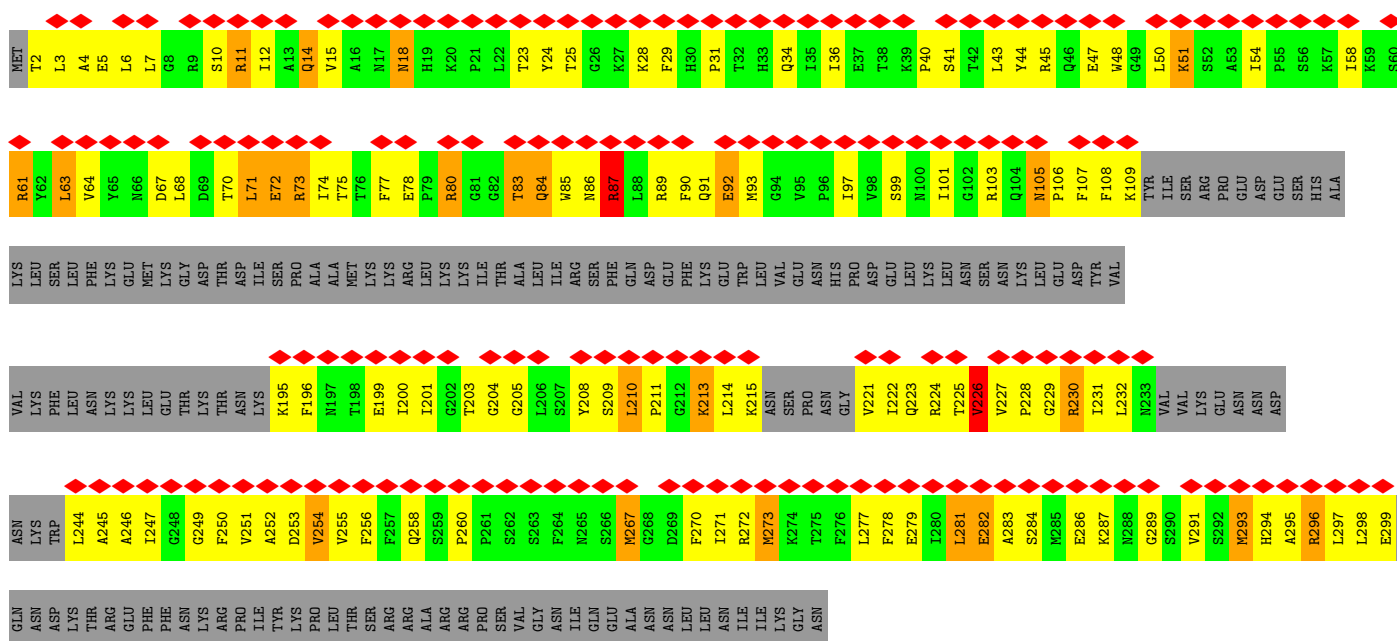
• Molecule 14: mRNA



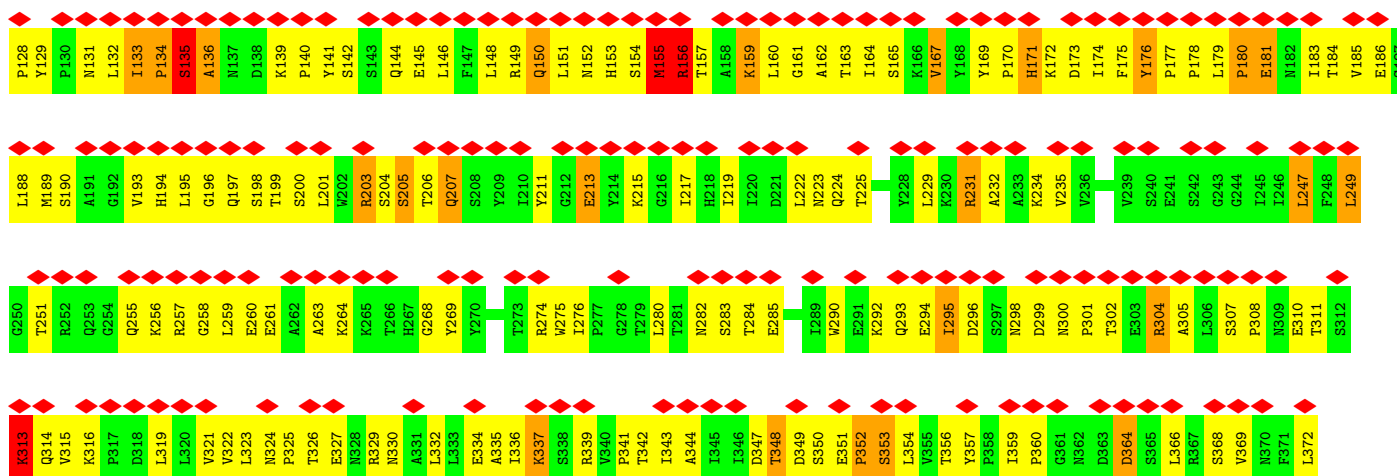
• Molecule 15: Small ribosomal subunit protein mS37

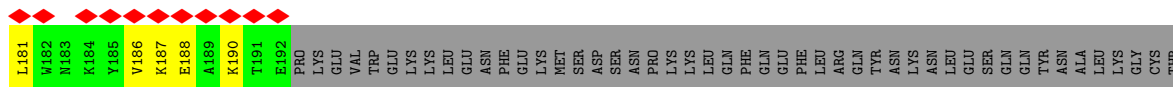


• Molecule 16: 37S ribosomal protein MRP51, mitochondrial



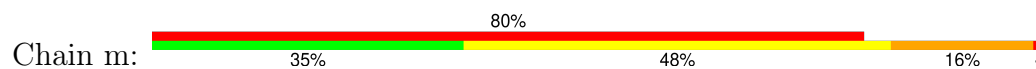
• Molecule 17: Small ribosomal subunit protein uS2m





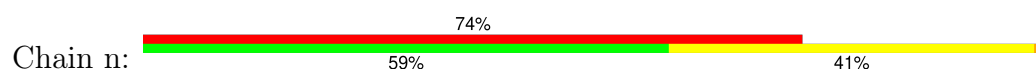
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• Molecule 22: Small ribosomal subunit protein uS7m



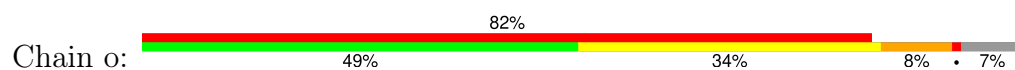
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• Molecule 23: 37S ribosomal protein S8, mitochondrial

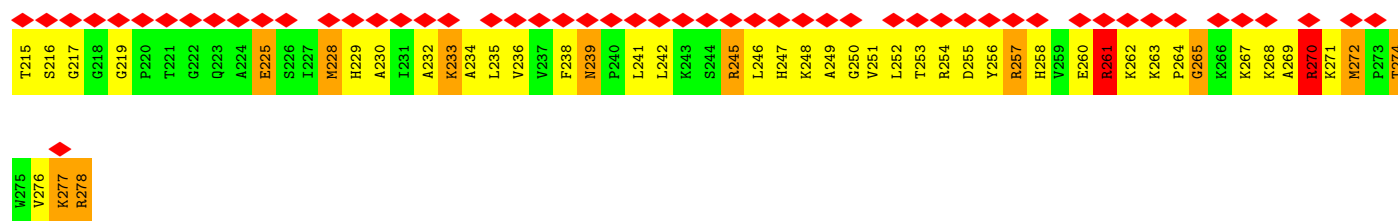


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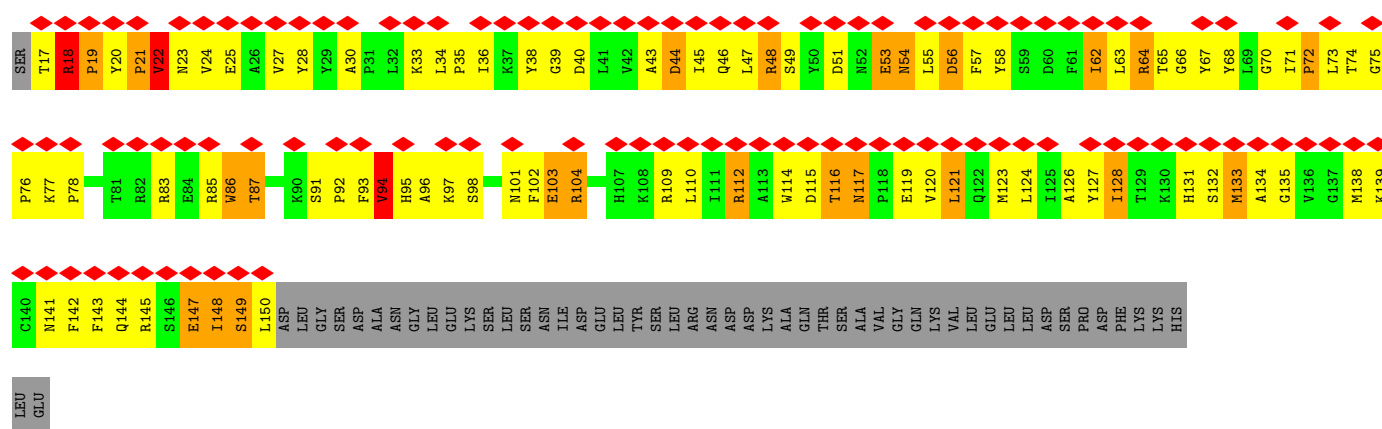
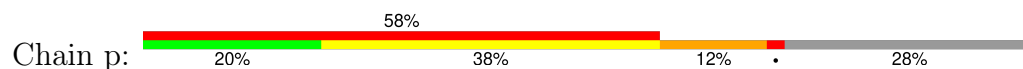
• Molecule 24: Small ribosomal subunit protein uS9m



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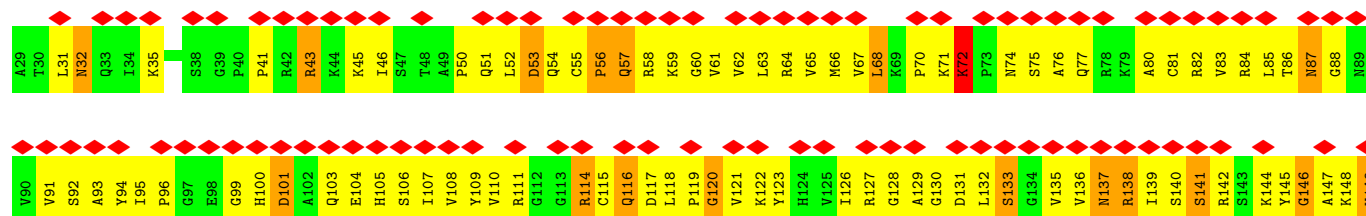
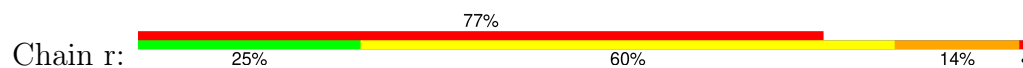
- Molecule 25: Small ribosomal subunit protein uS10m



- Molecule 26: Small ribosomal subunit protein uS11m

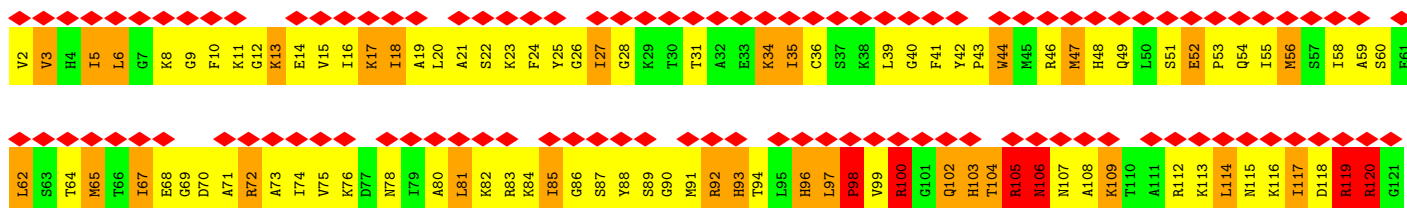
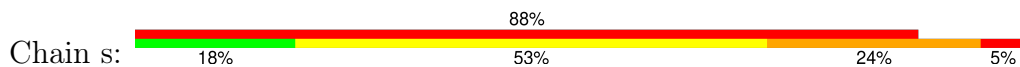


- Molecule 27: Small ribosomal subunit protein uS12m

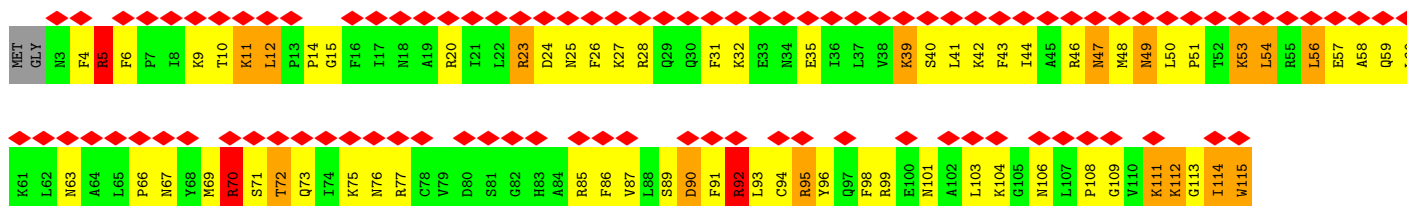
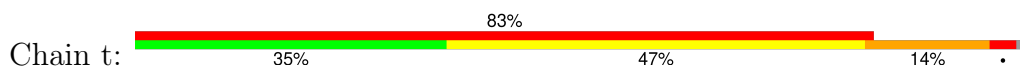




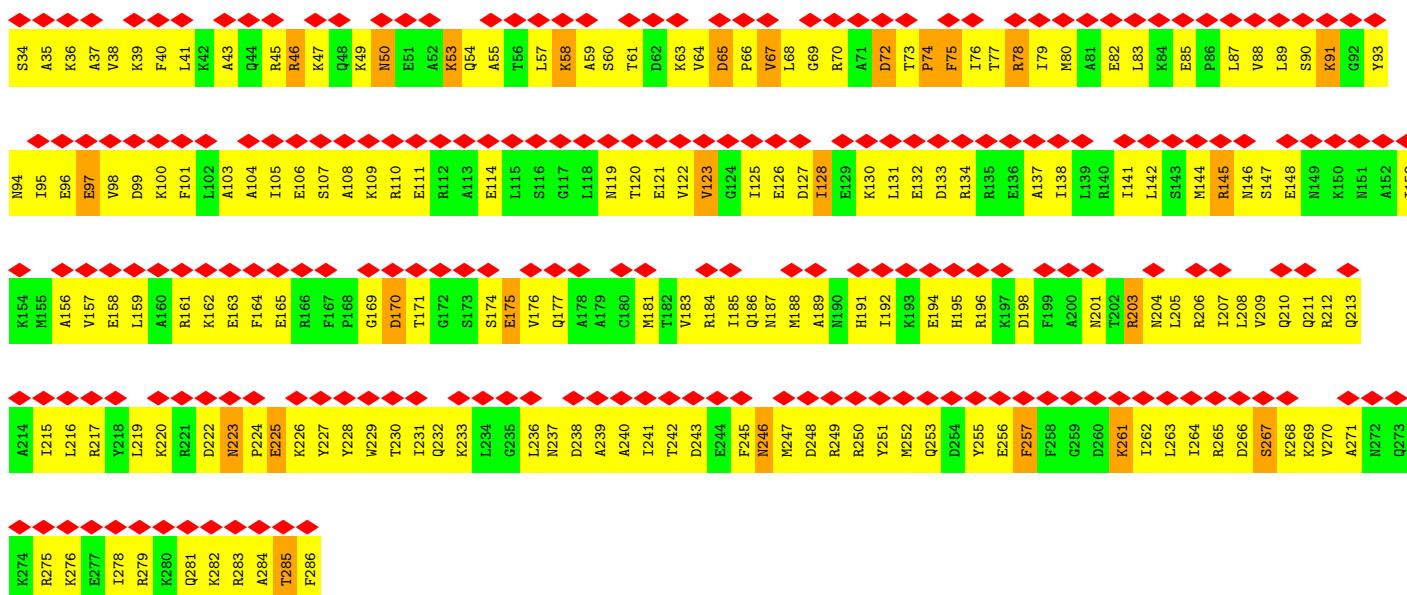
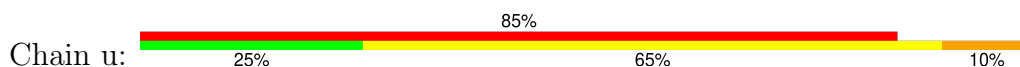
• Molecule 28: Small ribosomal subunit protein uS13m



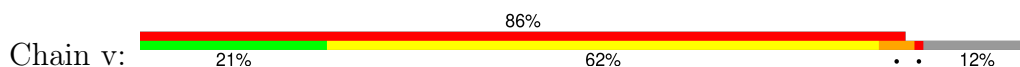
• Molecule 29: 37S ribosomal protein MRP2, mitochondrial



• Molecule 30: Small ribosomal subunit protein uS15m

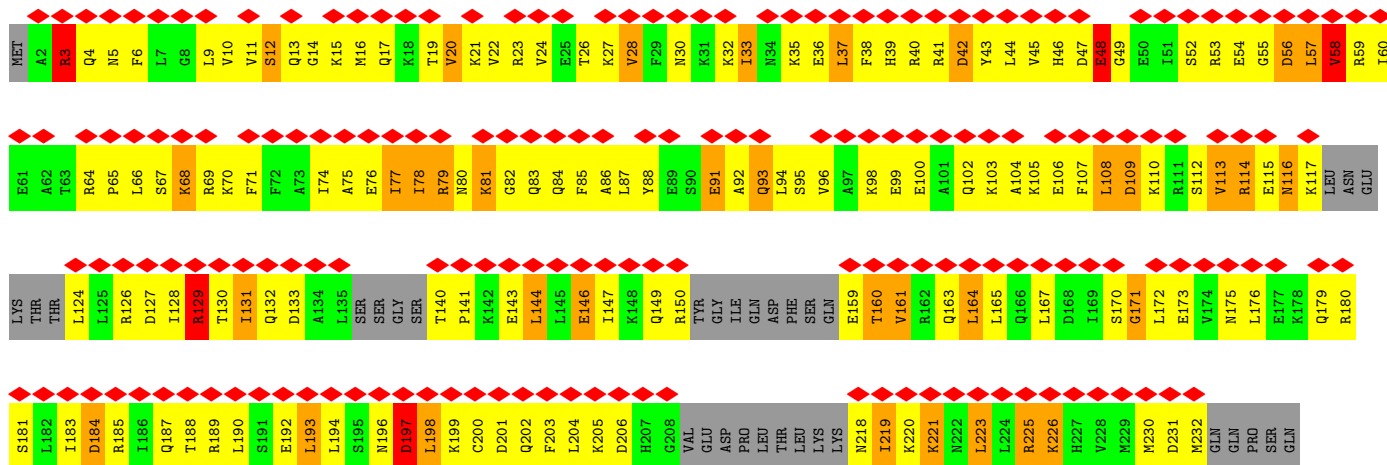
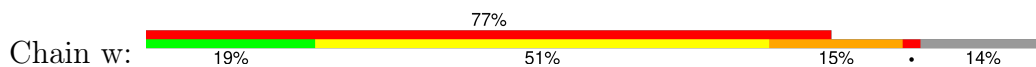


• Molecule 31: Small ribosomal subunit protein bS16m

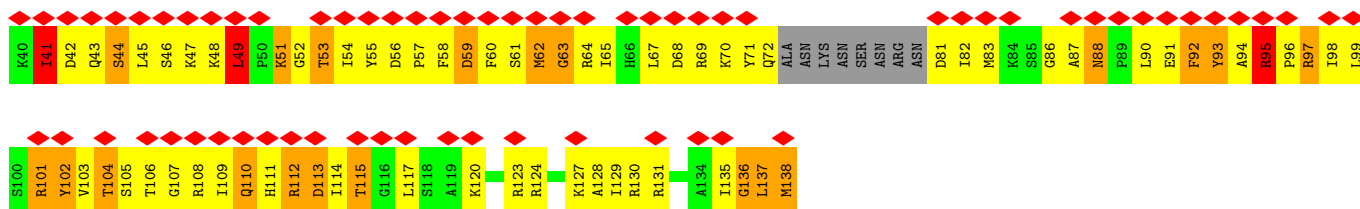
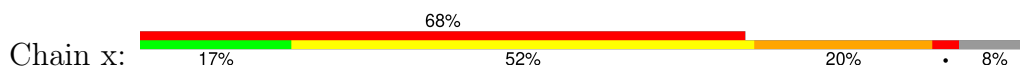




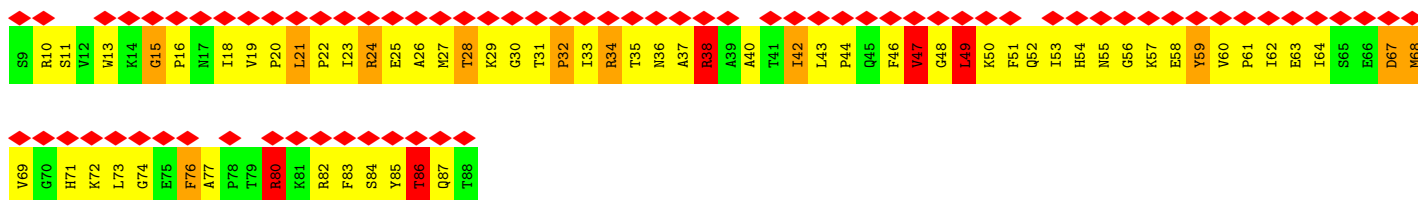
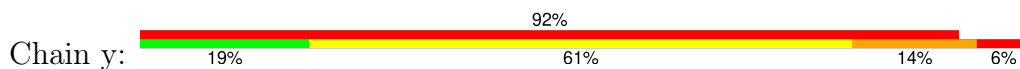
• Molecule 32: 37S ribosomal protein S17, mitochondrial



• Molecule 33: Small ribosomal subunit protein bS18m

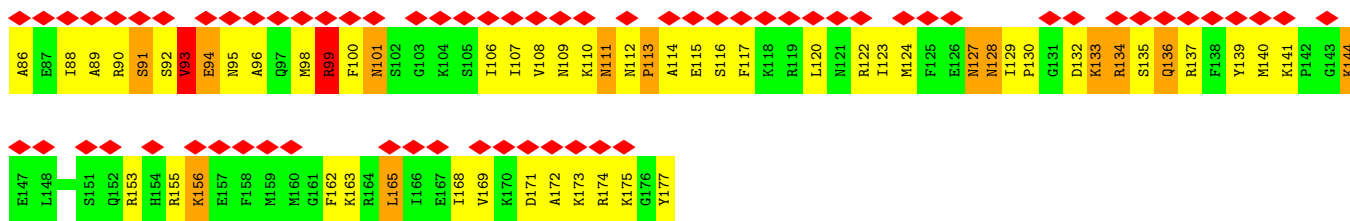


• Molecule 34: Small ribosomal subunit protein uS19m

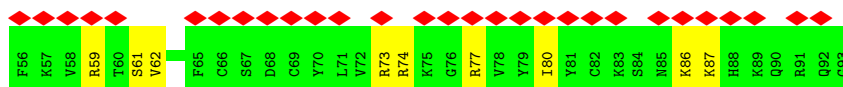
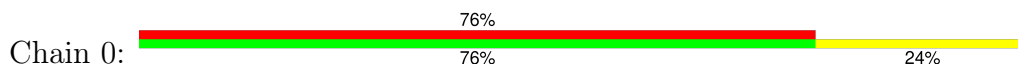


• Molecule 35: Small ribosomal subunit protein bS21m

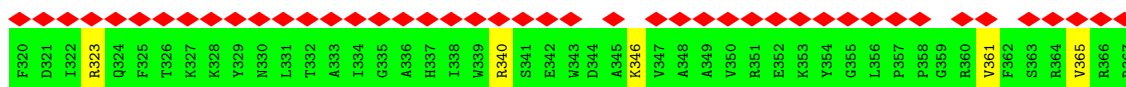
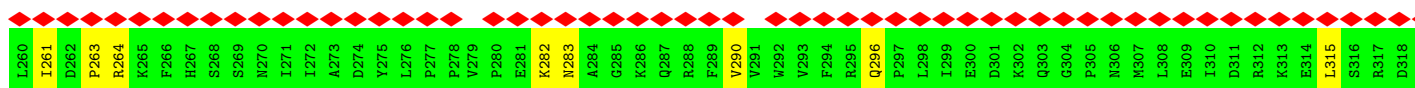
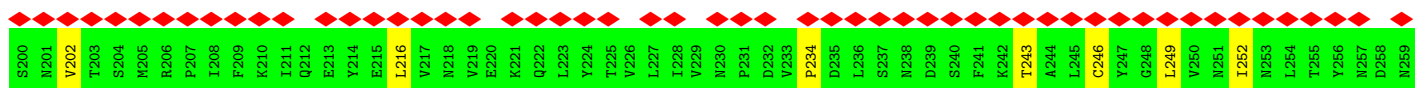
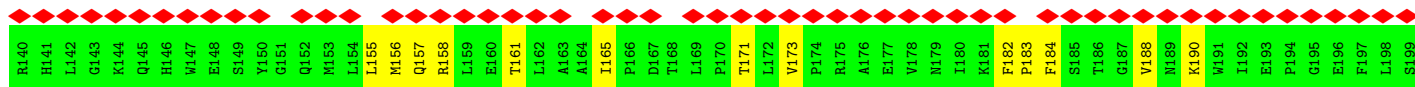
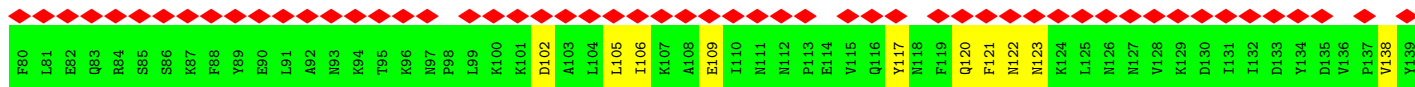
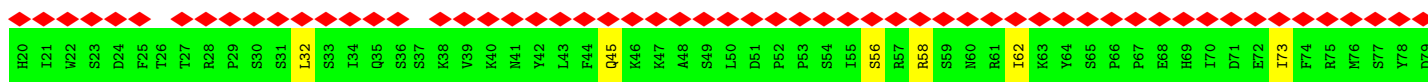
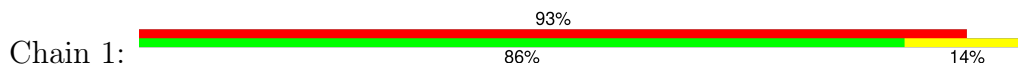




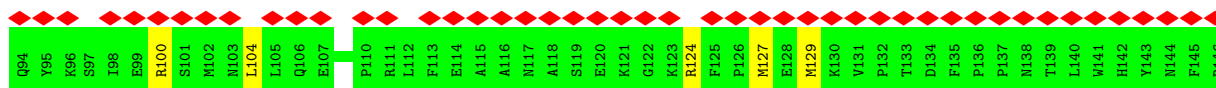
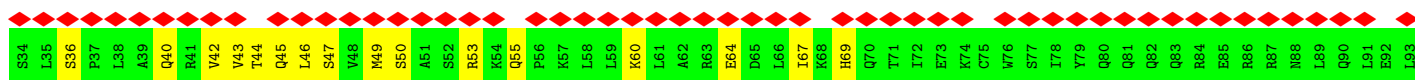
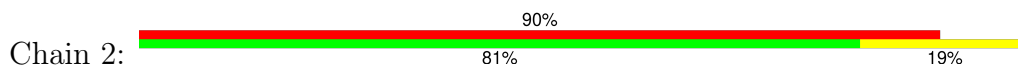
• Molecule 36: Large ribosomal subunit protein bL36m



• Molecule 37: Large ribosomal subunit protein mL38

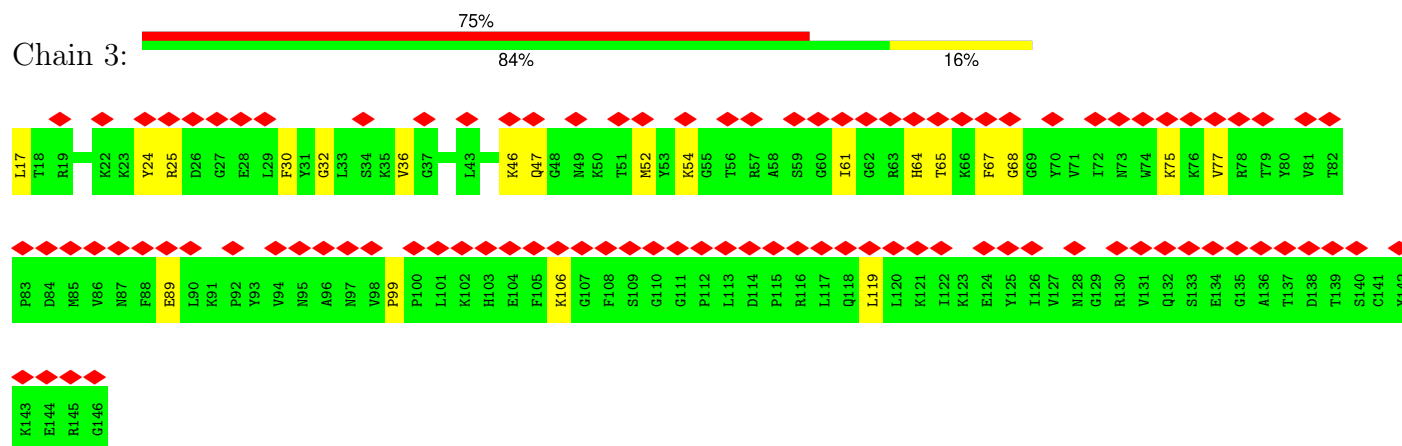


• Molecule 38: Large ribosomal subunit protein mL40



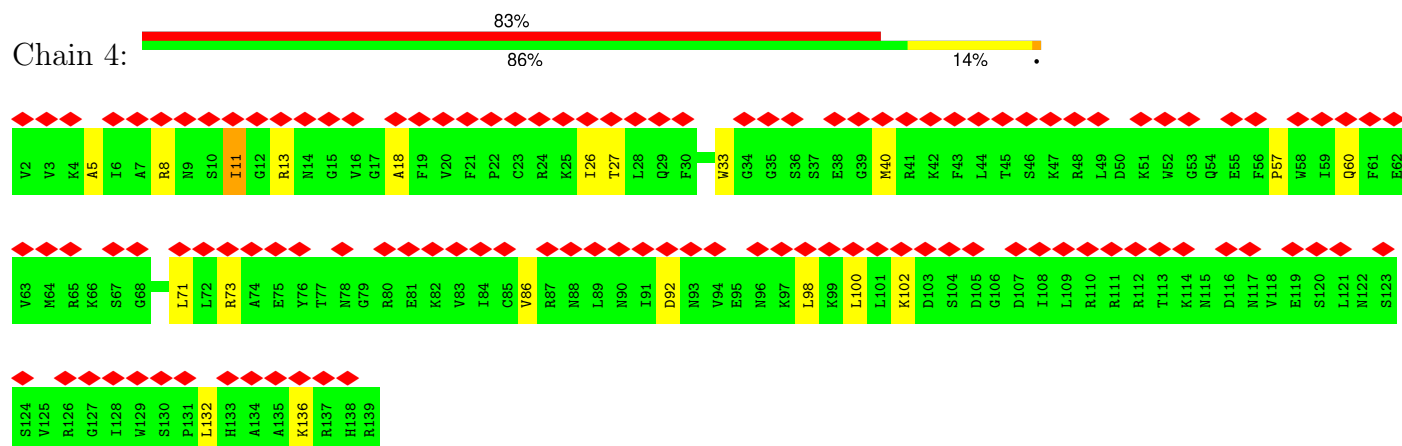
- Molecule 39: Large ribosomal subunit protein mL41

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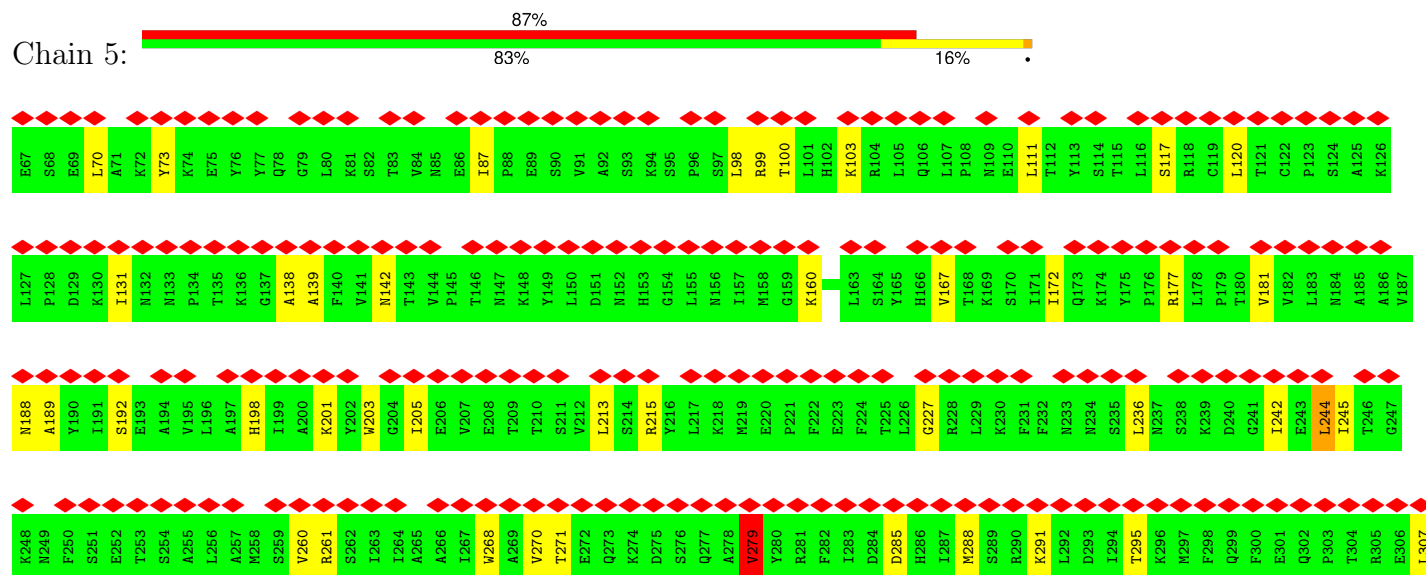
- Molecule 40: Large ribosomal subunit protein mL43

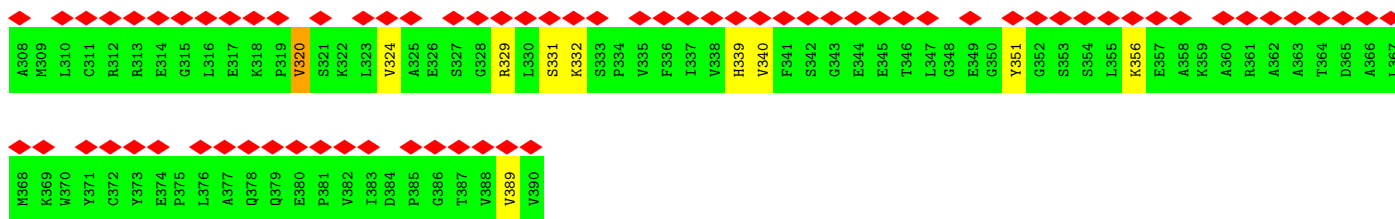
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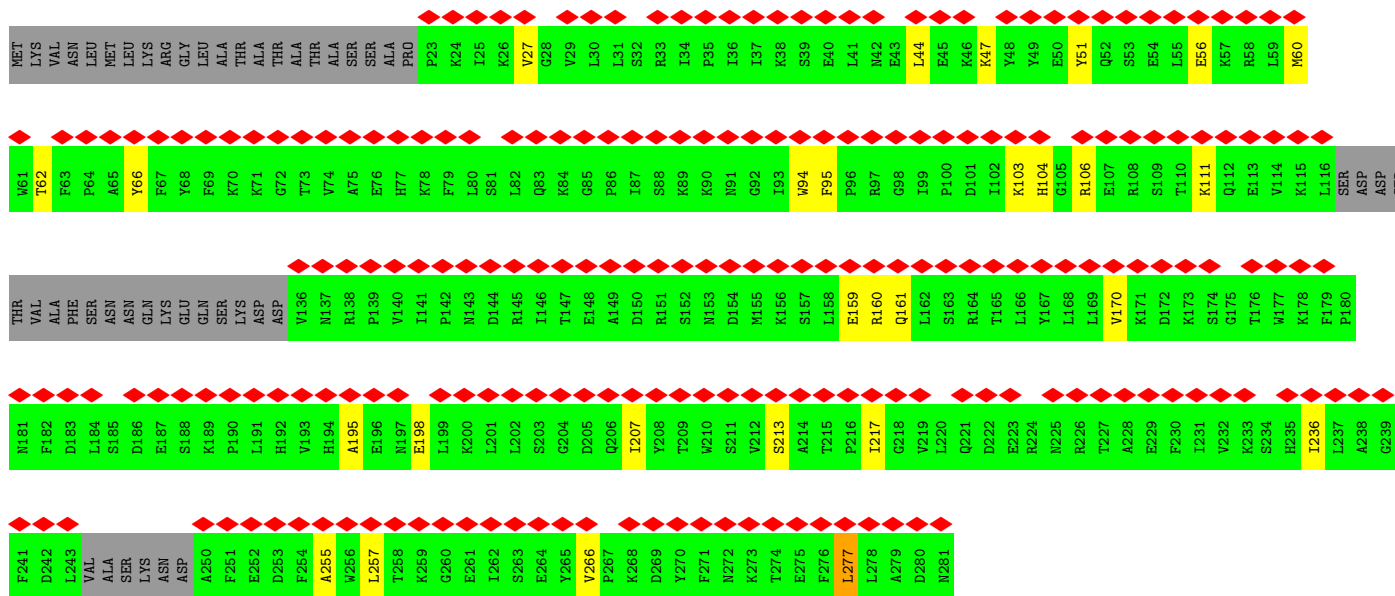
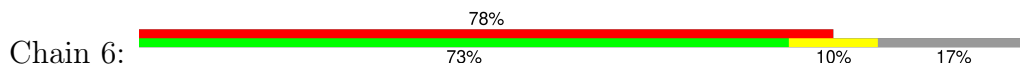
- Molecule 41: Large ribosomal subunit protein mL44

Chain 5:

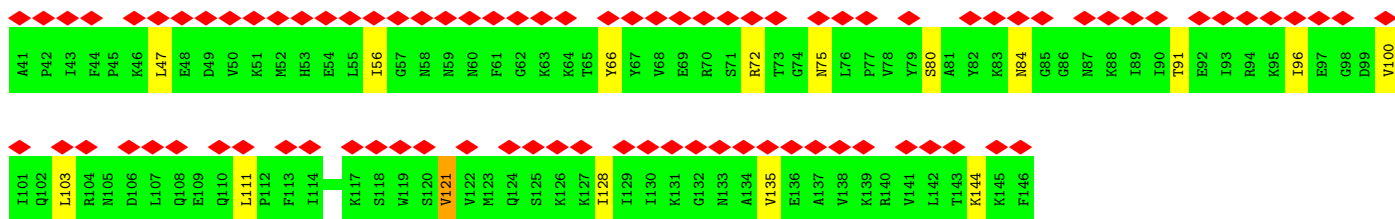
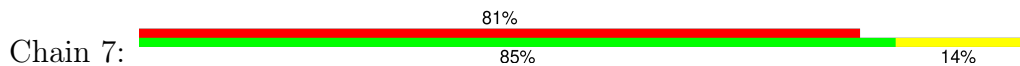




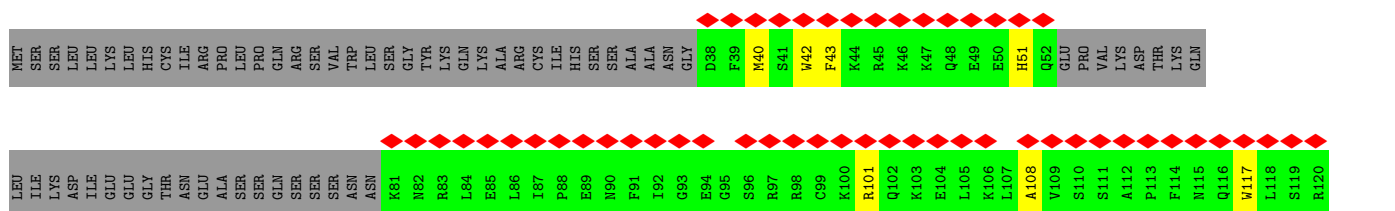
• Molecule 42: Large ribosomal subunit protein mL46

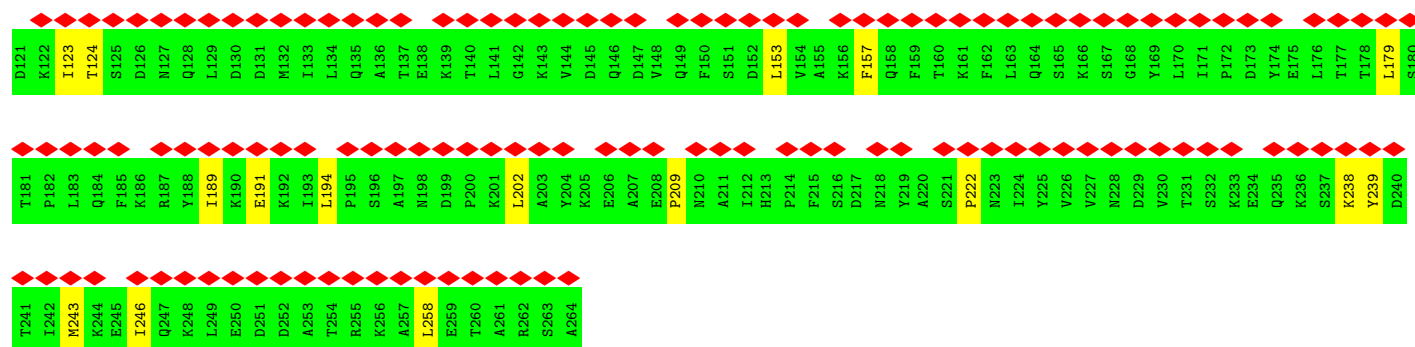


• Molecule 43: Large ribosomal subunit protein mL49

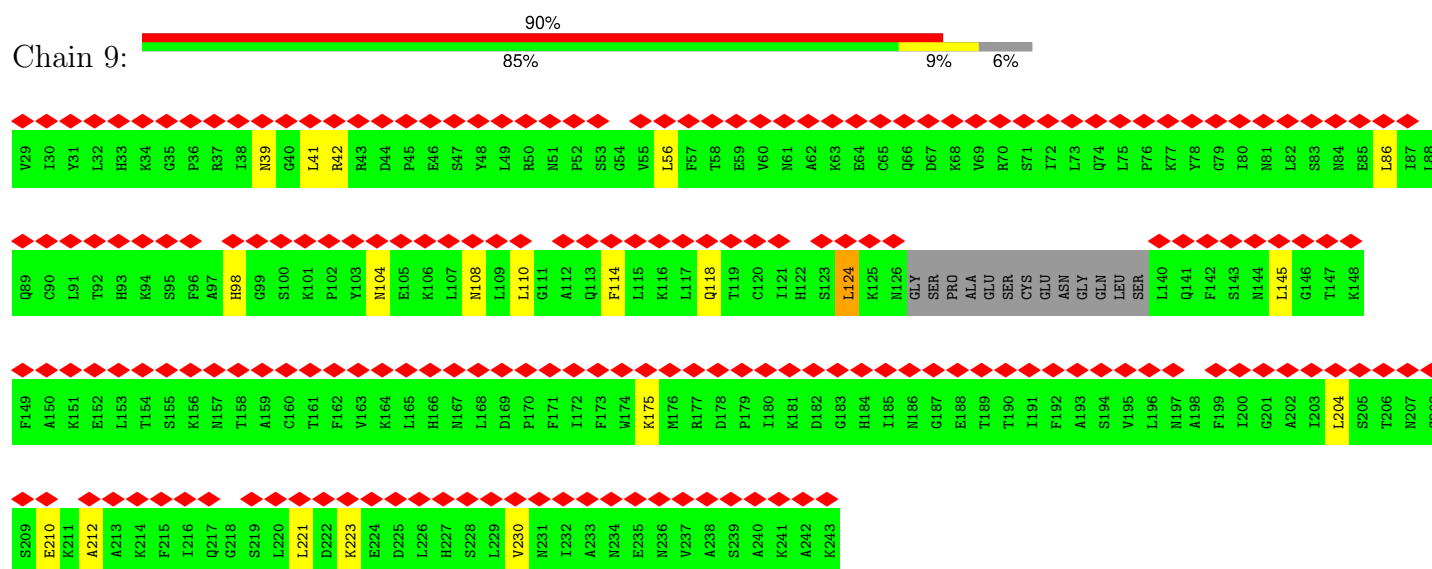


• Molecule 44: Large ribosomal subunit protein mL50

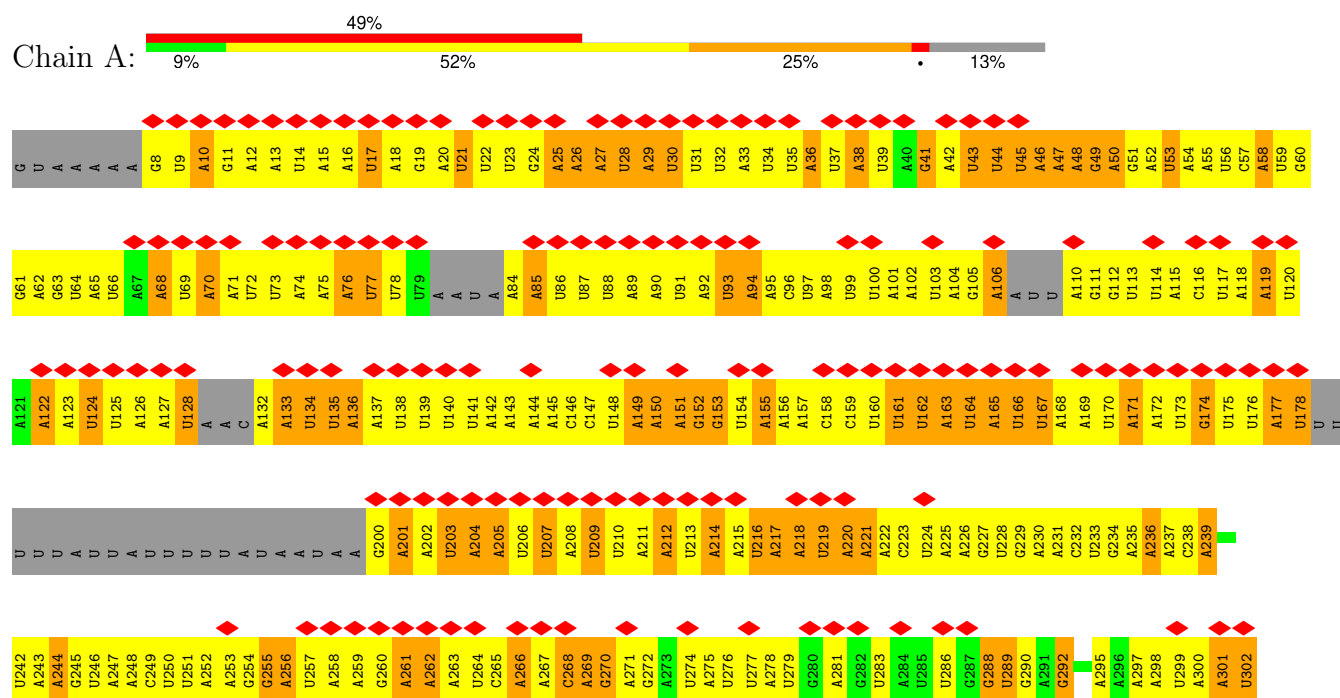




• Molecule 45: Large ribosomal subunit protein mL57



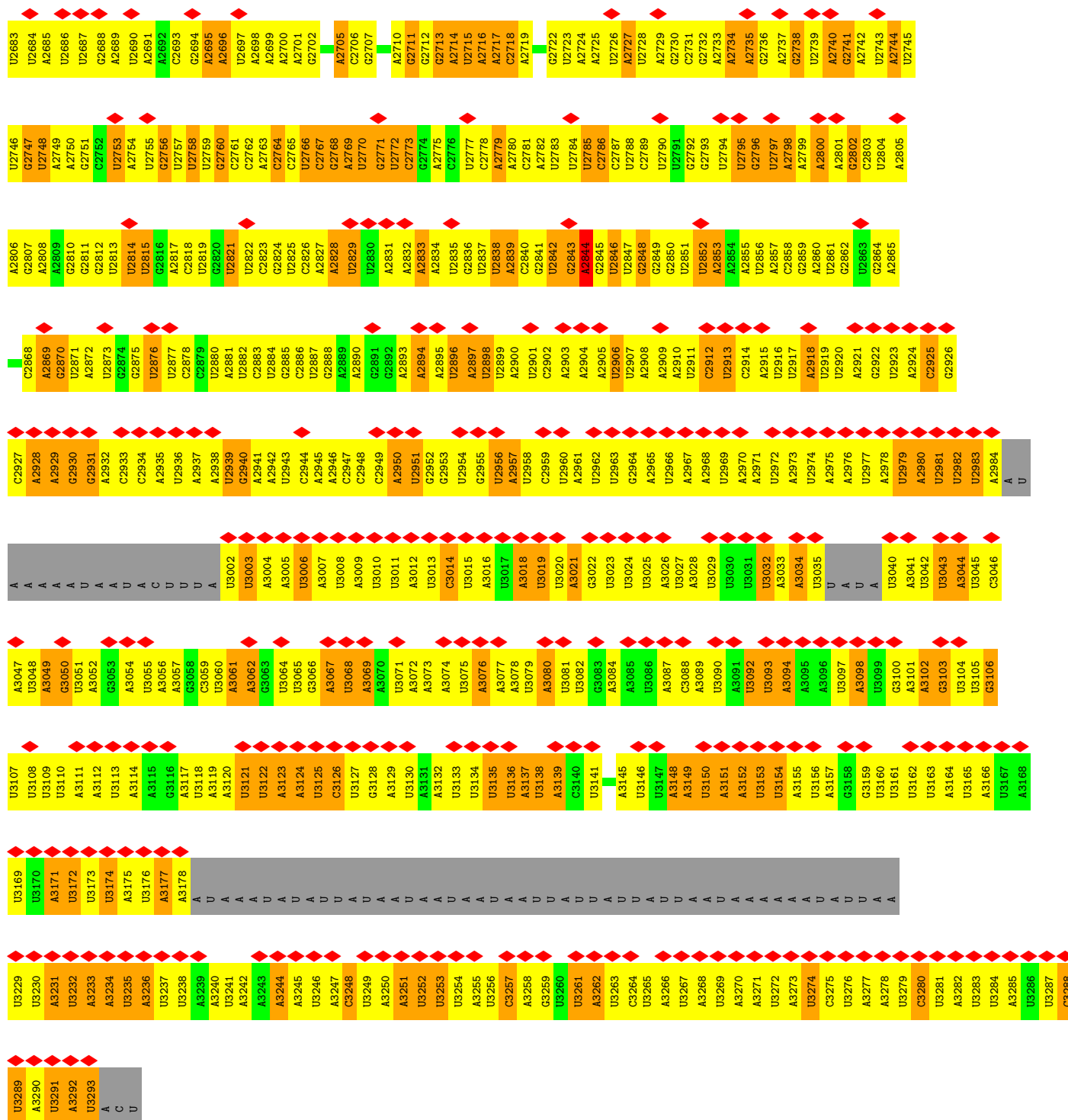
• Molecule 46: Large ribosomal subunit rRNA

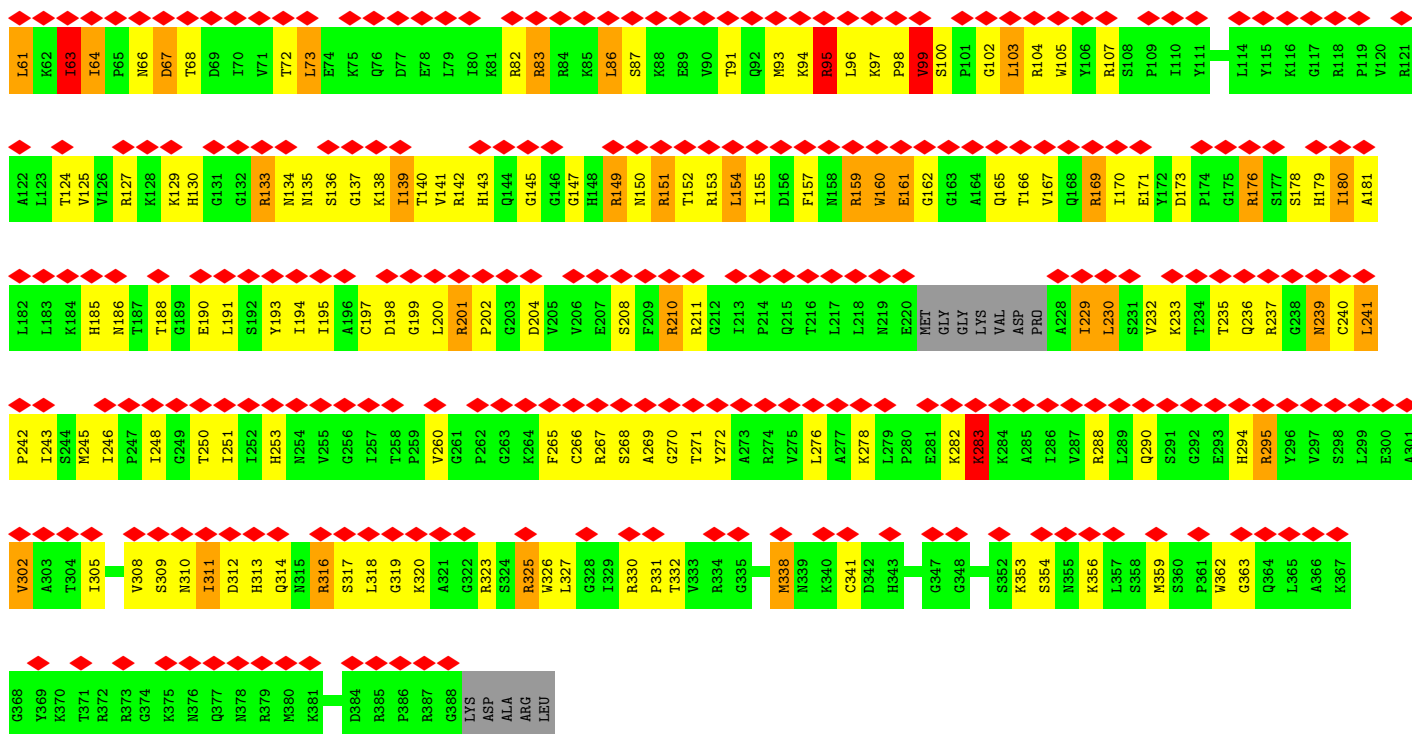


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A856	U857	A858	U859	A860	A861	U862	A863	A864	A865	G866	A867	G868	U869	C870	A871	A872	U873	U874	U875	A876	U877	U878	C879	A880	U881	A882	U883	A884	U885	G886	U887	A888	A889	A890	A891	A892	U893	A894	A895	U896	U897	A898	A899	A900	G901	G902	G903	G904	A905	A906	A907	C908	U909	G910	C911	C912	C913	A914	G915		
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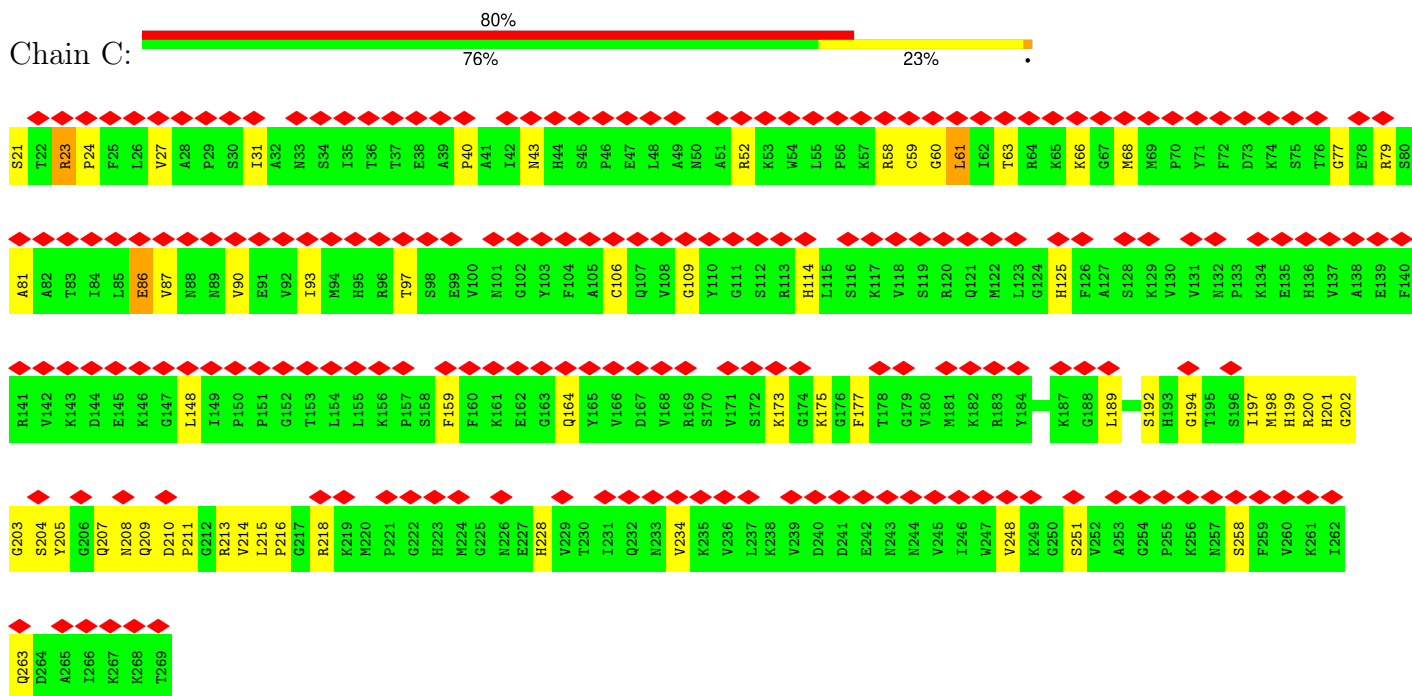
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		A1767	A1710	A1650	G1585	U		A1277	U147		
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		A1768	C1712	U1652	A1587	U		U1337	U1211		
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		U1773		U1523		U		U1400	A1216		
		U1774		U1524		U		A1278	A1217		
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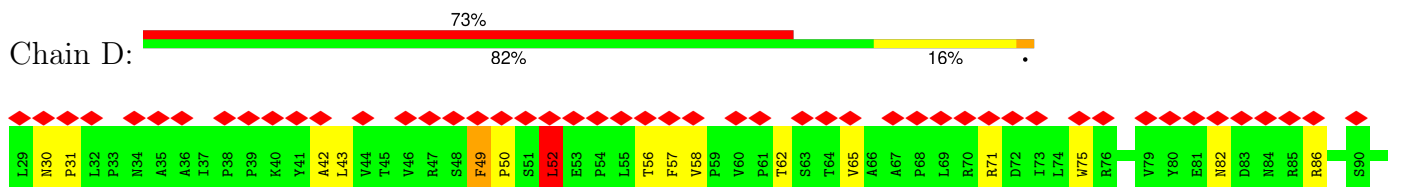


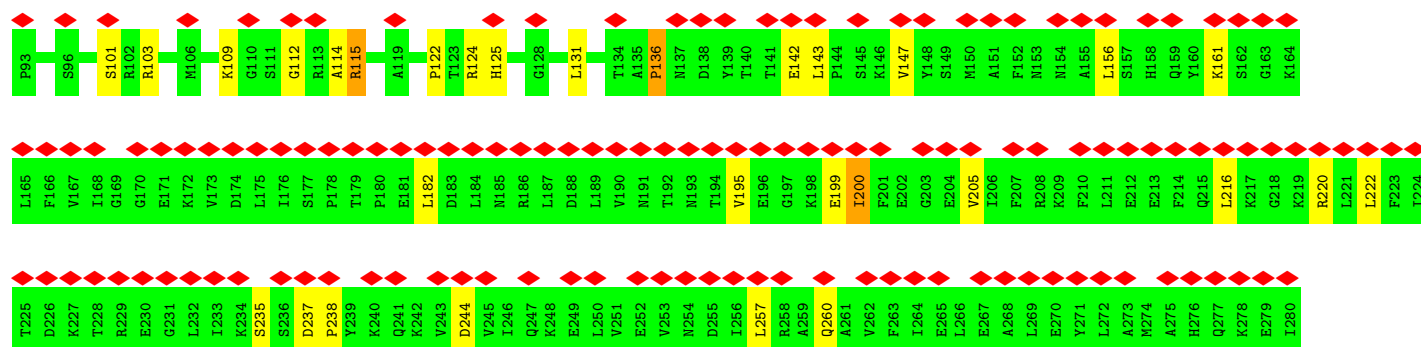


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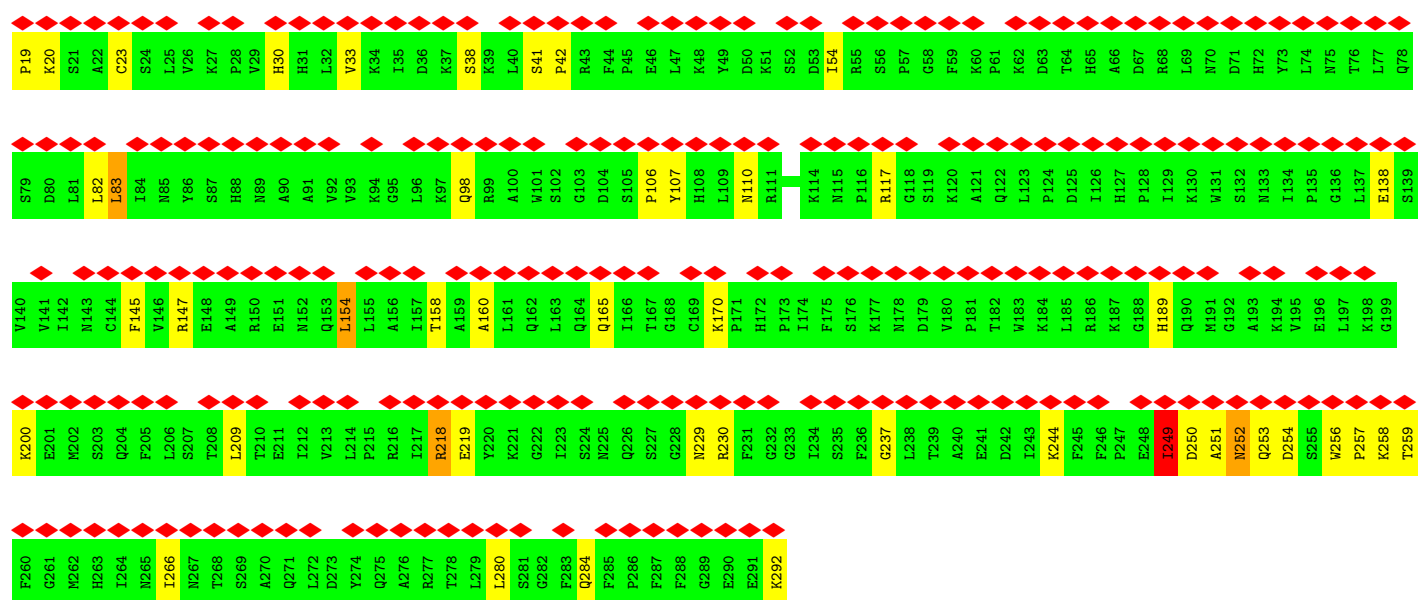
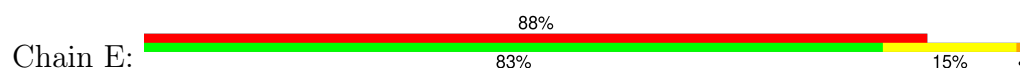


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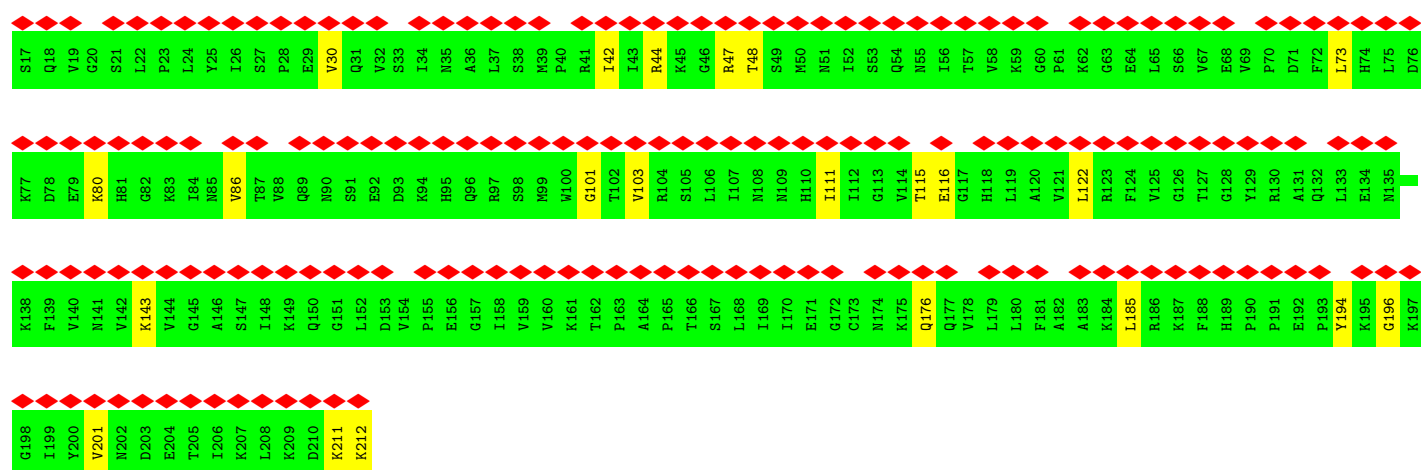
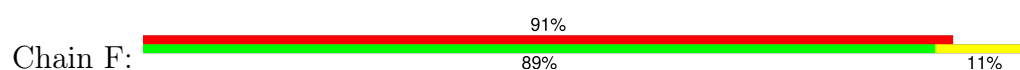




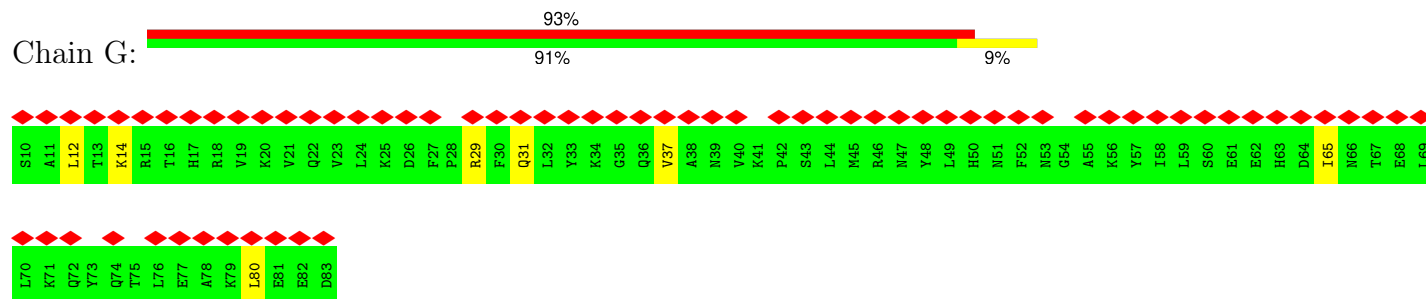
- Molecule 50: Large ribosomal subunit protein uL5m



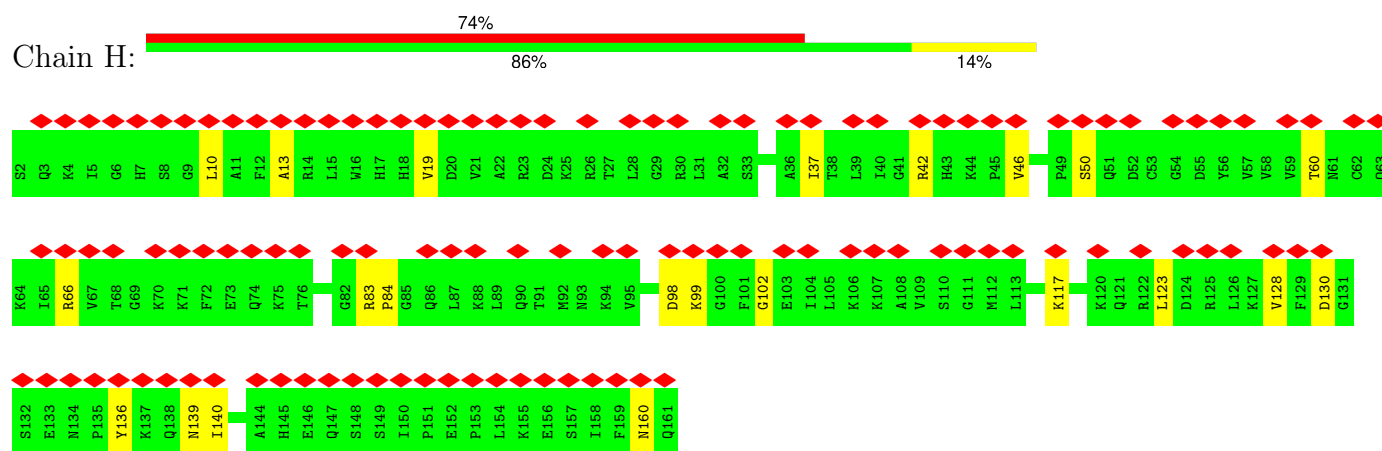
- Molecule 51: Large ribosomal subunit protein uL6m



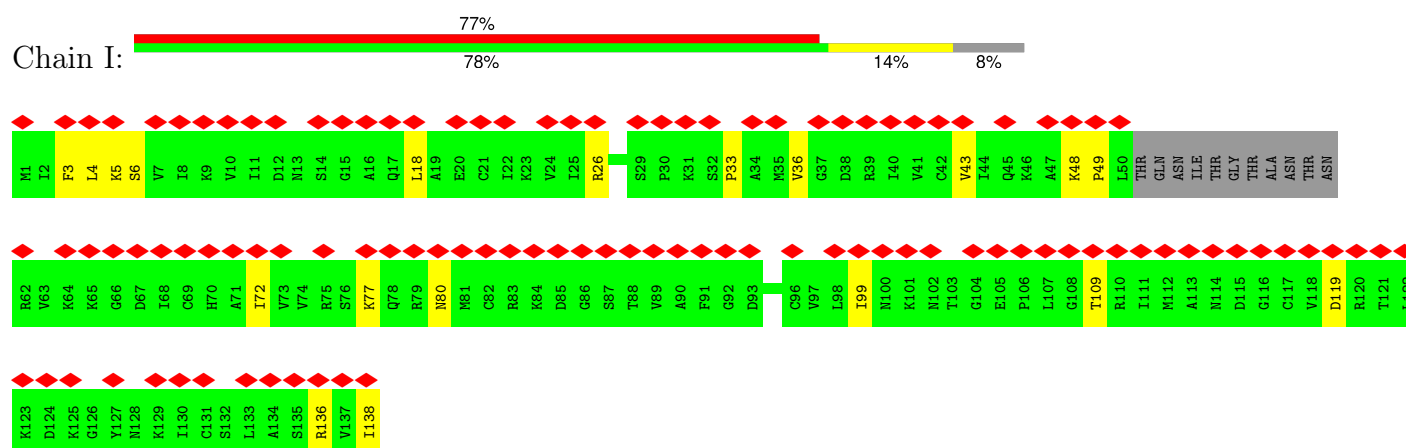
- Molecule 52: Large ribosomal subunit protein bL9m



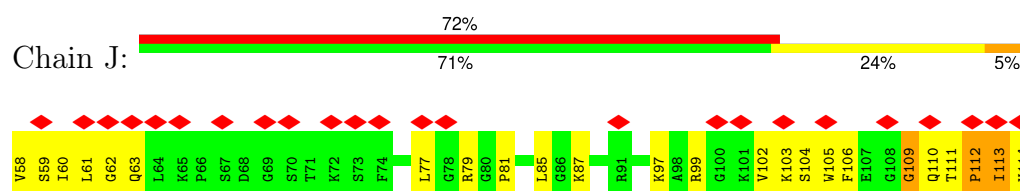
- Molecule 53: Large ribosomal subunit protein uL13m

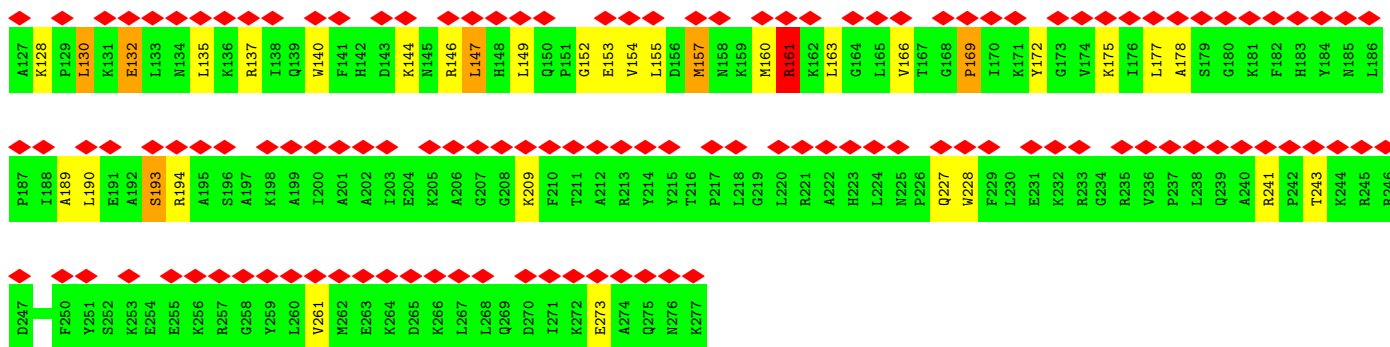


- Molecule 54: Large ribosomal subunit protein uL14m



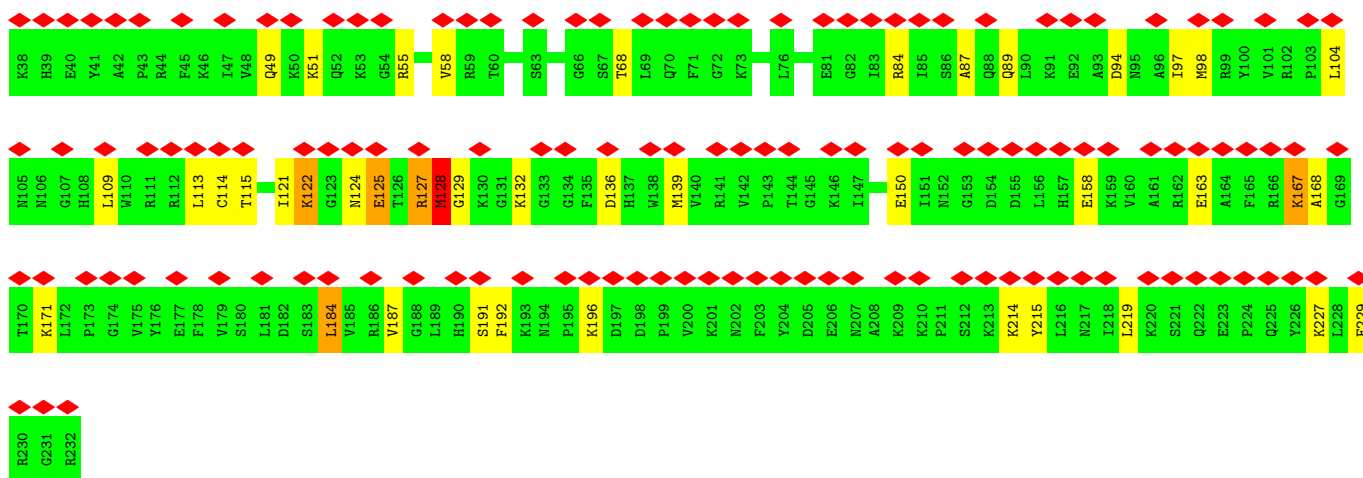
- Molecule 55: Large ribosomal subunit protein uL15m





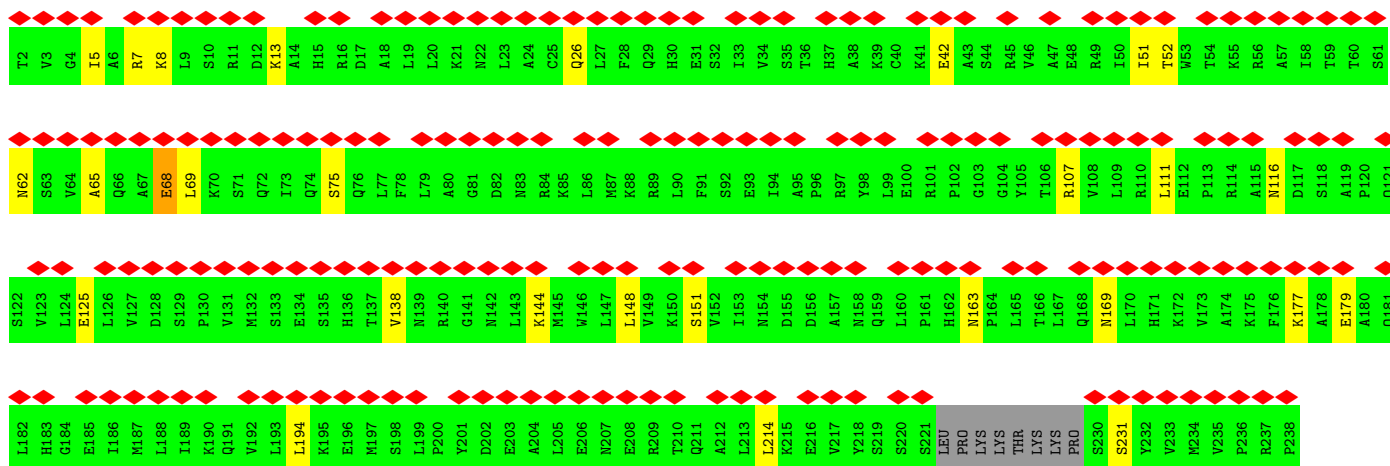
- Molecule 56: Large ribosomal subunit protein uL16m

Chain K:

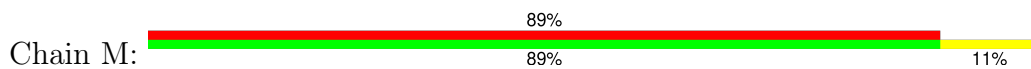


- Molecule 57: Large ribosomal subunit protein bL17m

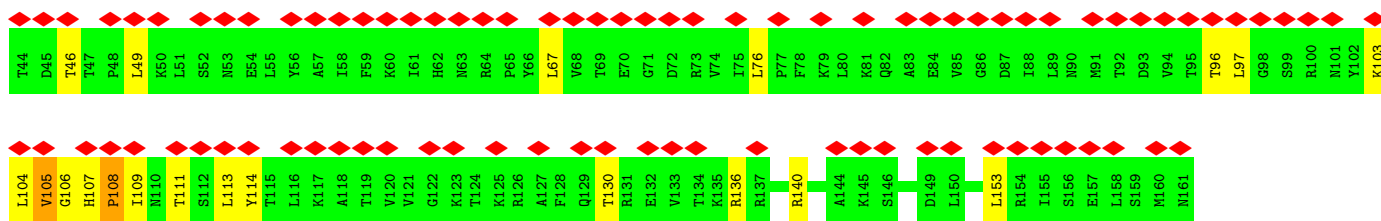
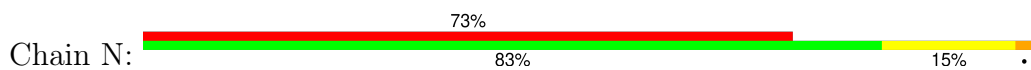
Chain L:



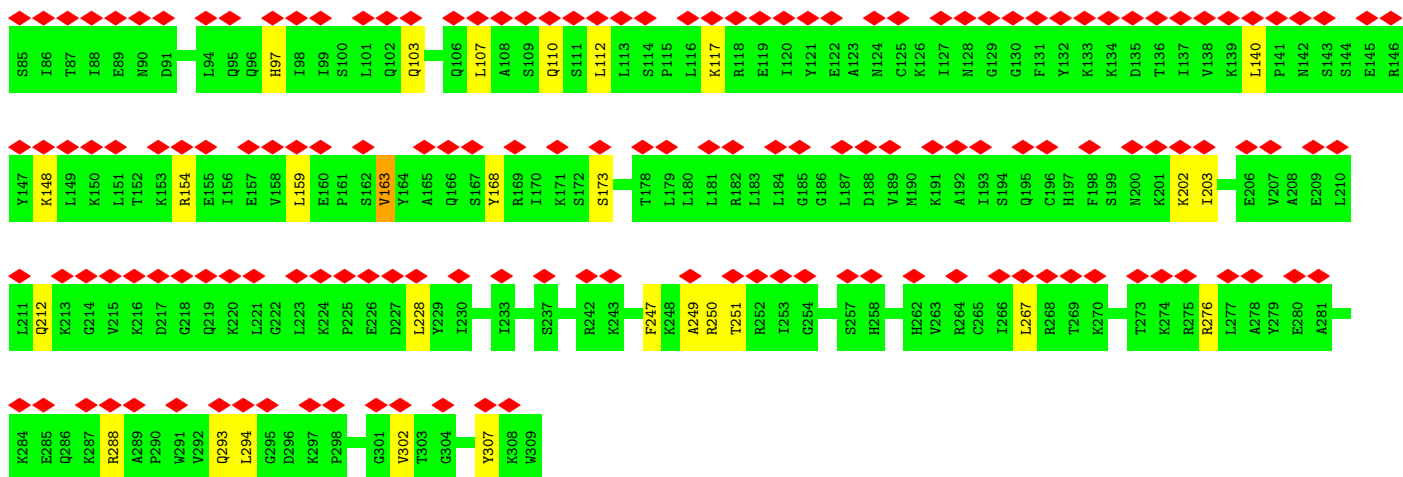
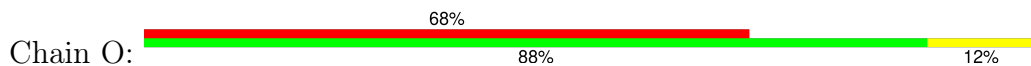
- Molecule 58: Large ribosomal subunit protein bL19m



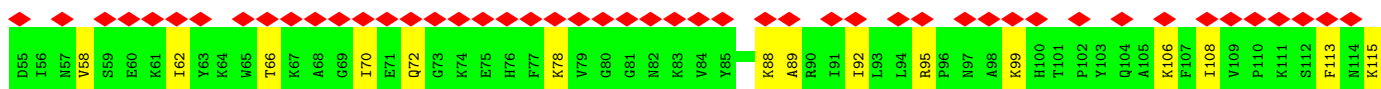
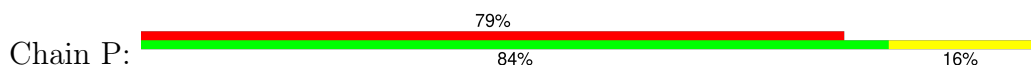
• Molecule 59: Large ribosomal subunit protein bL21m

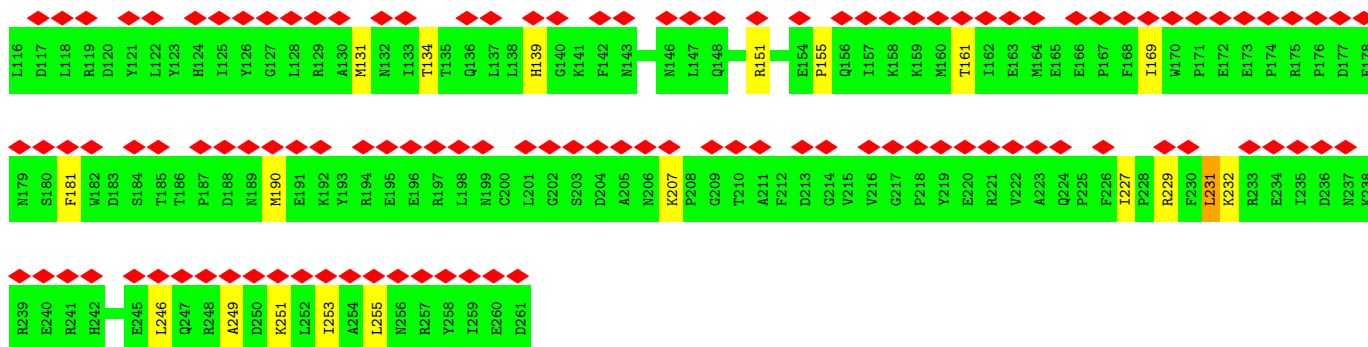


• Molecule 60: Large ribosomal subunit protein uL22m

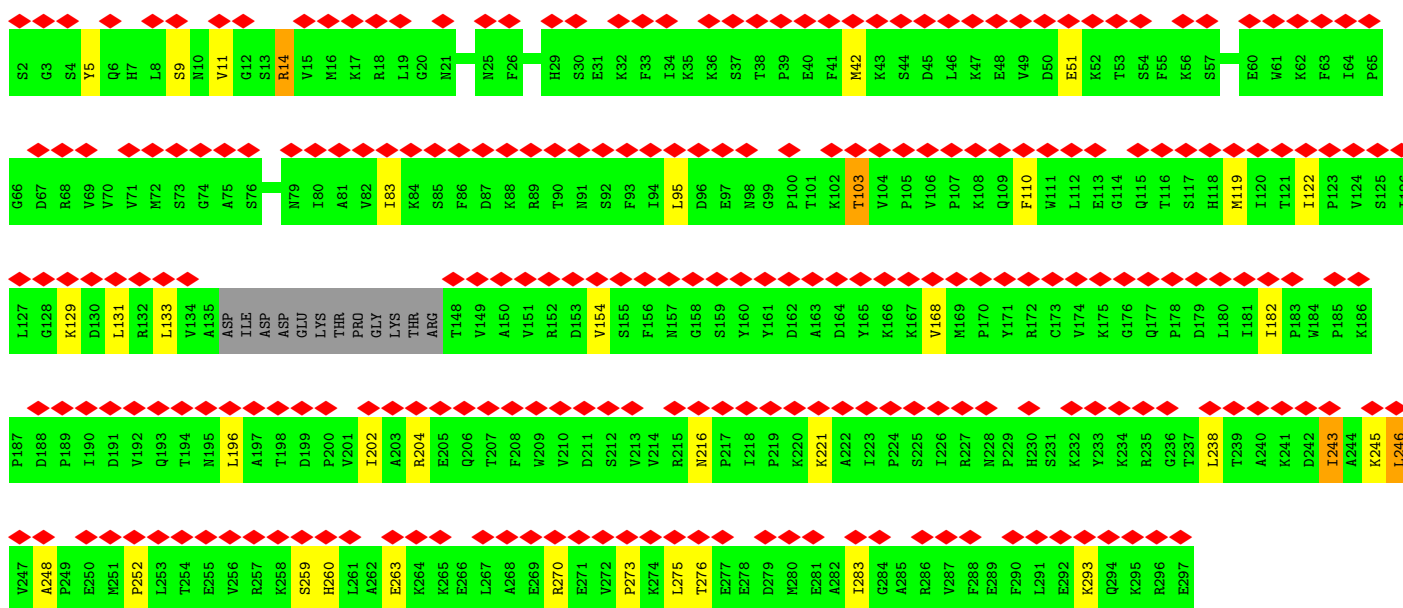
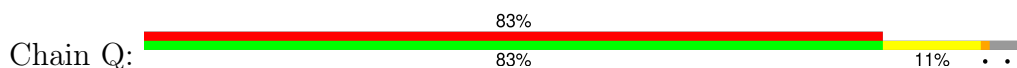


• Molecule 61: Large ribosomal subunit protein uL23m

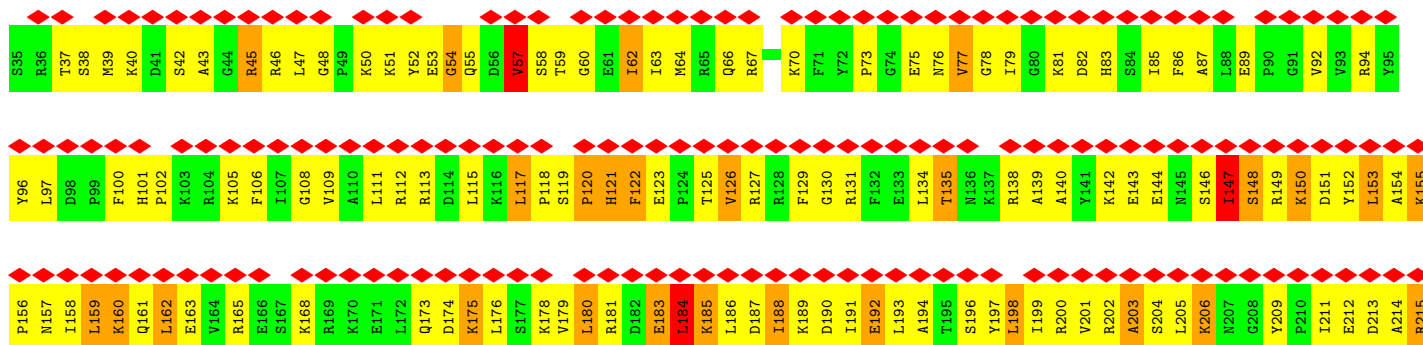


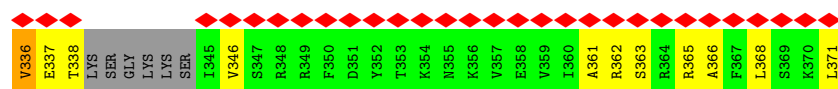
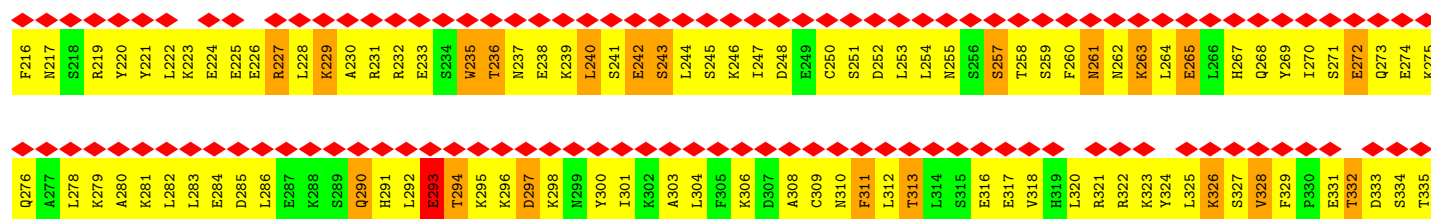


- Molecule 62: Large ribosomal subunit protein uL24m

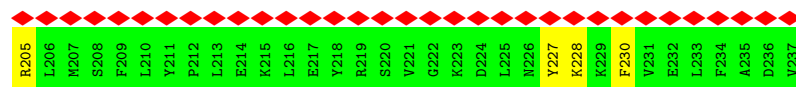
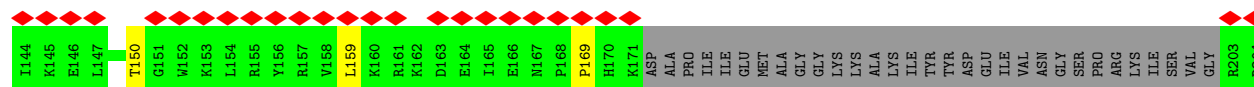
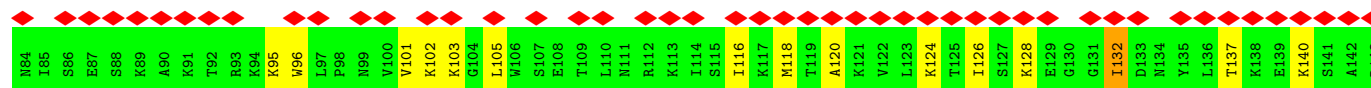
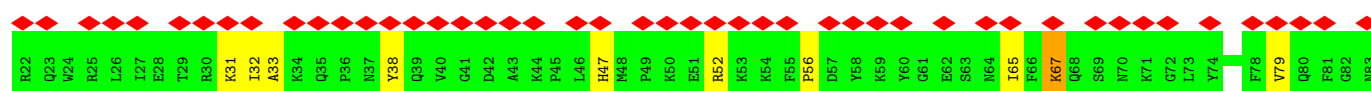


- Molecule 63: Large ribosomal subunit protein bL27m

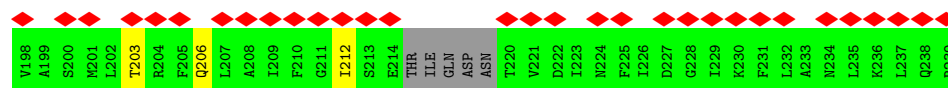
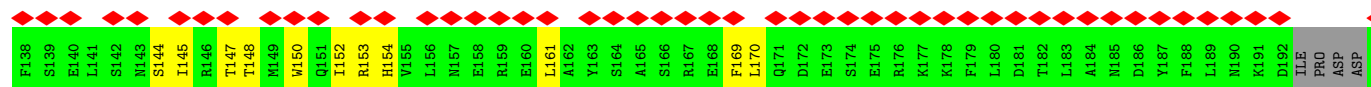
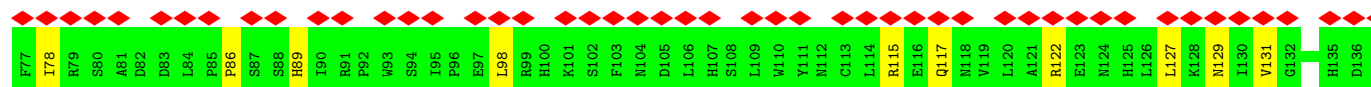
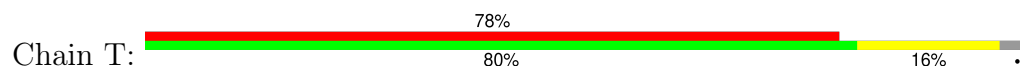




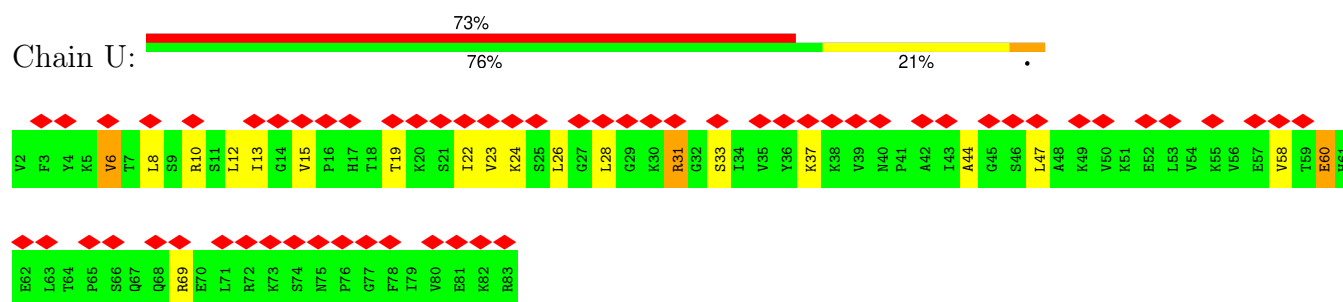
• Molecule 64: Large ribosomal subunit protein bL28m



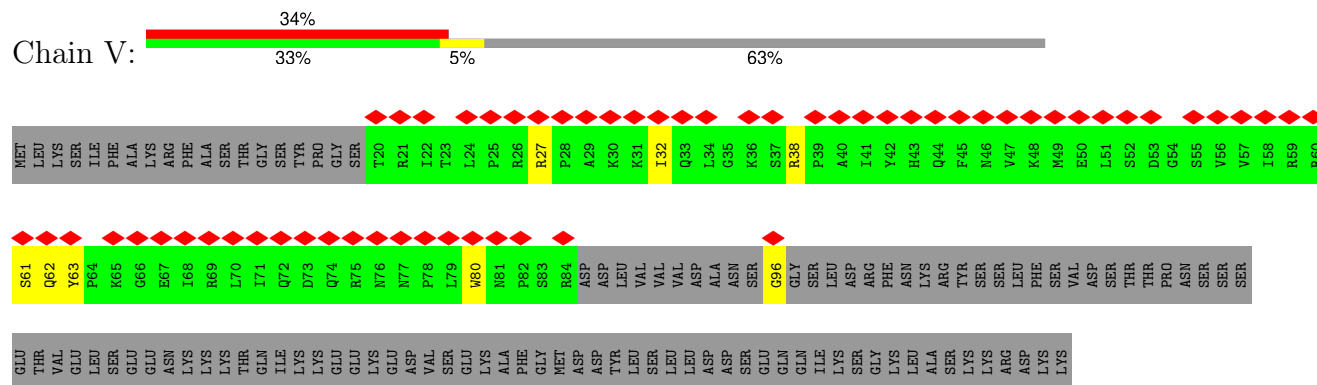
• Molecule 65: Large ribosomal subunit protein uL29m



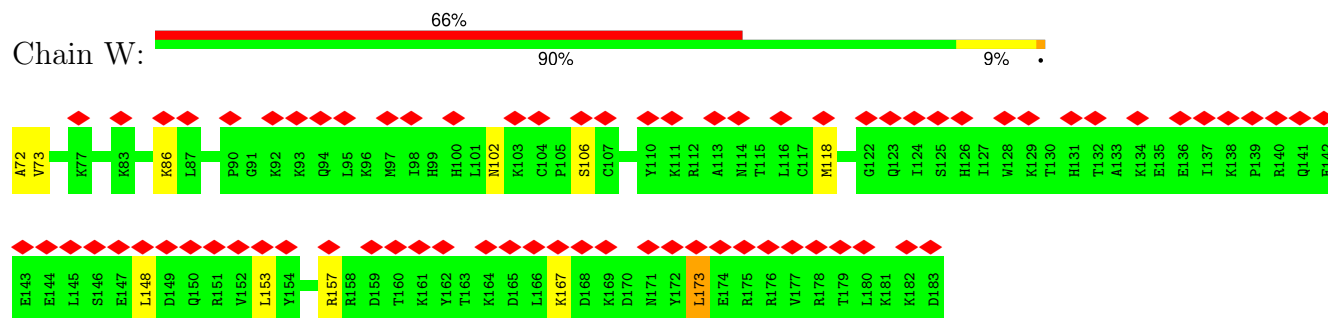
• Molecule 66: Large ribosomal subunit protein uL30m



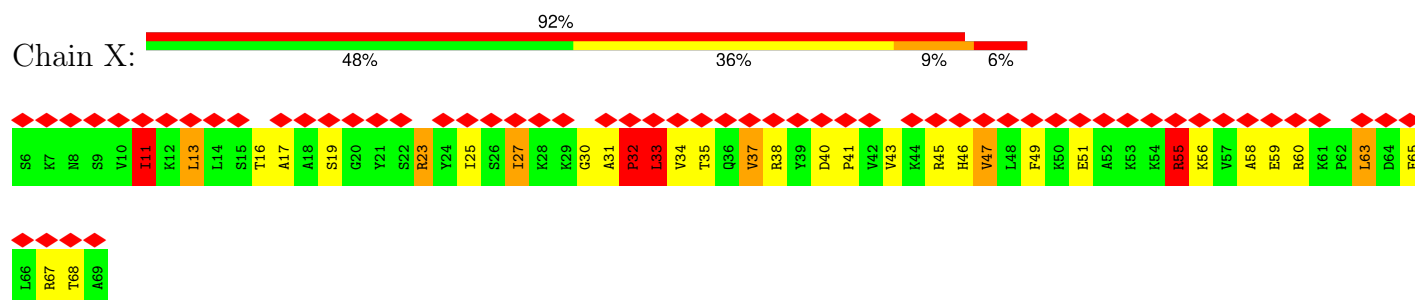
- Molecule 67: Large ribosomal subunit protein bL31m



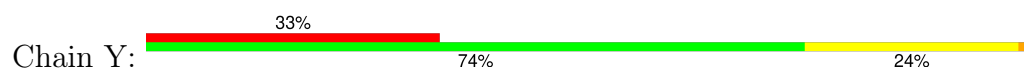
- Molecule 68: Large ribosomal subunit protein bL32m

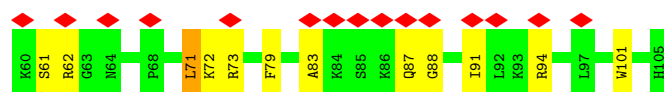


- Molecule 69: Large ribosomal subunit protein bL33m

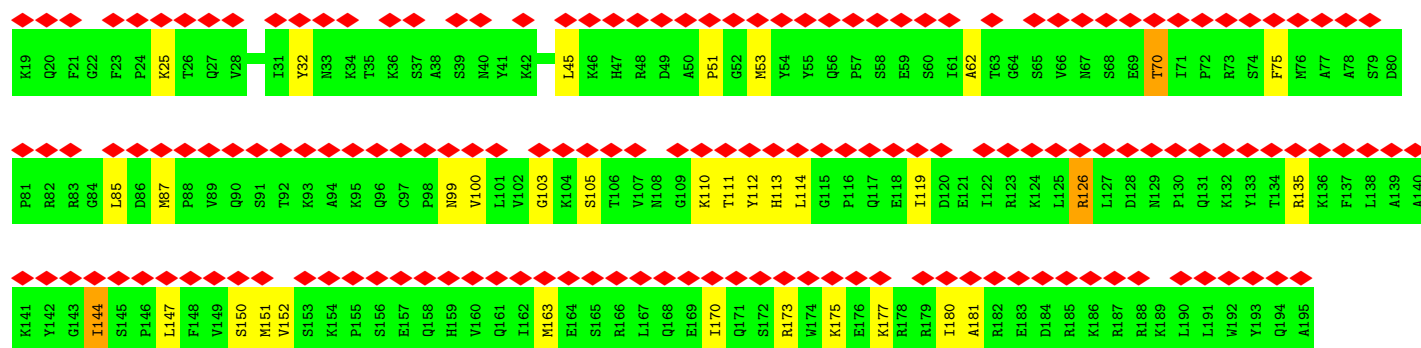
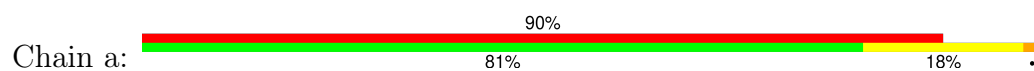


- Molecule 70: Large ribosomal subunit protein bL34m

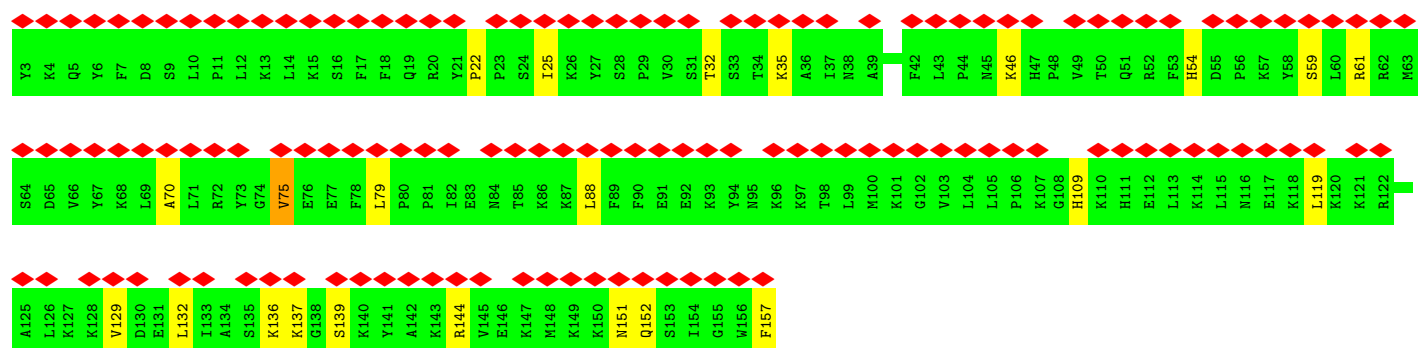
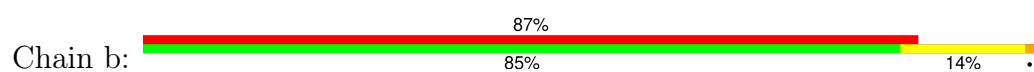




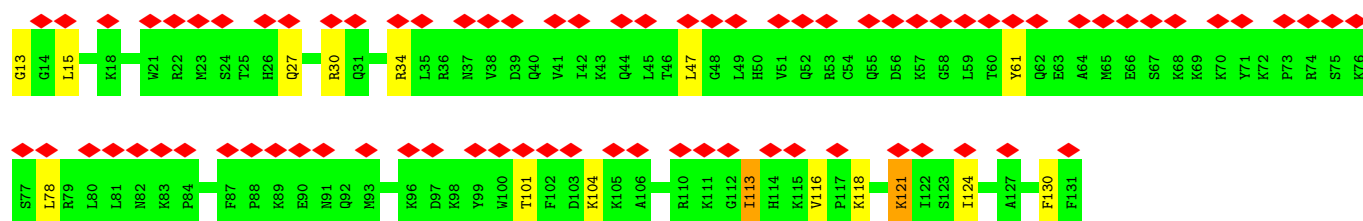
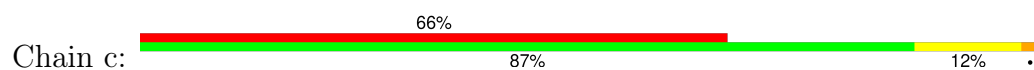
- Molecule 71: Large ribosomal subunit protein mL58



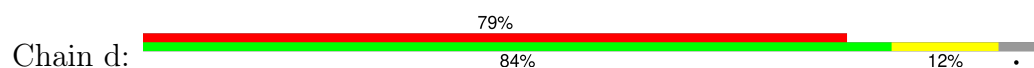
- Molecule 72: Large ribosomal subunit protein mL59

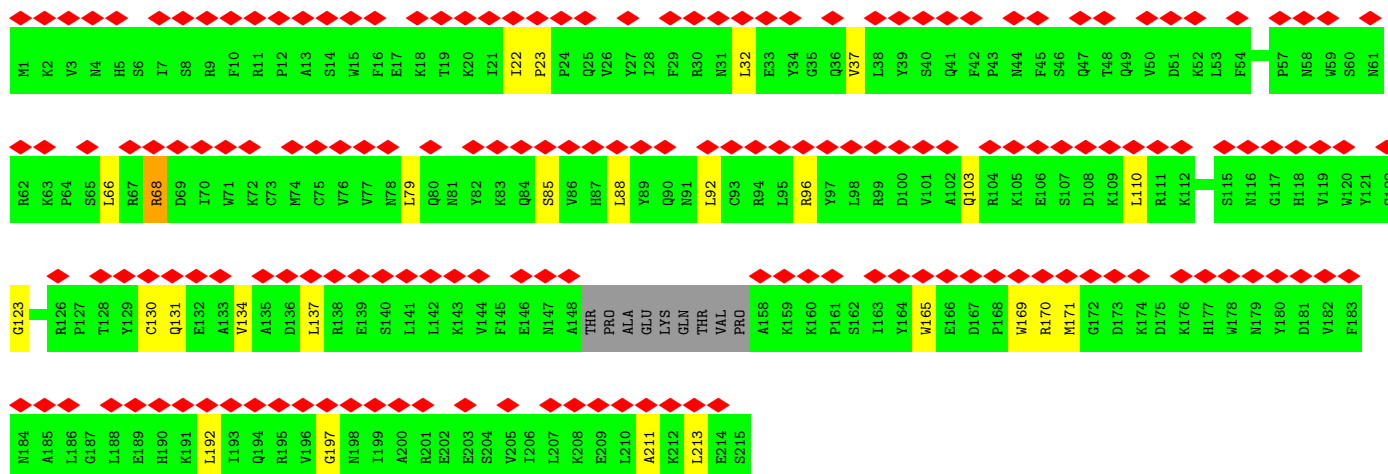


- Molecule 73: Large ribosomal subunit protein mL60

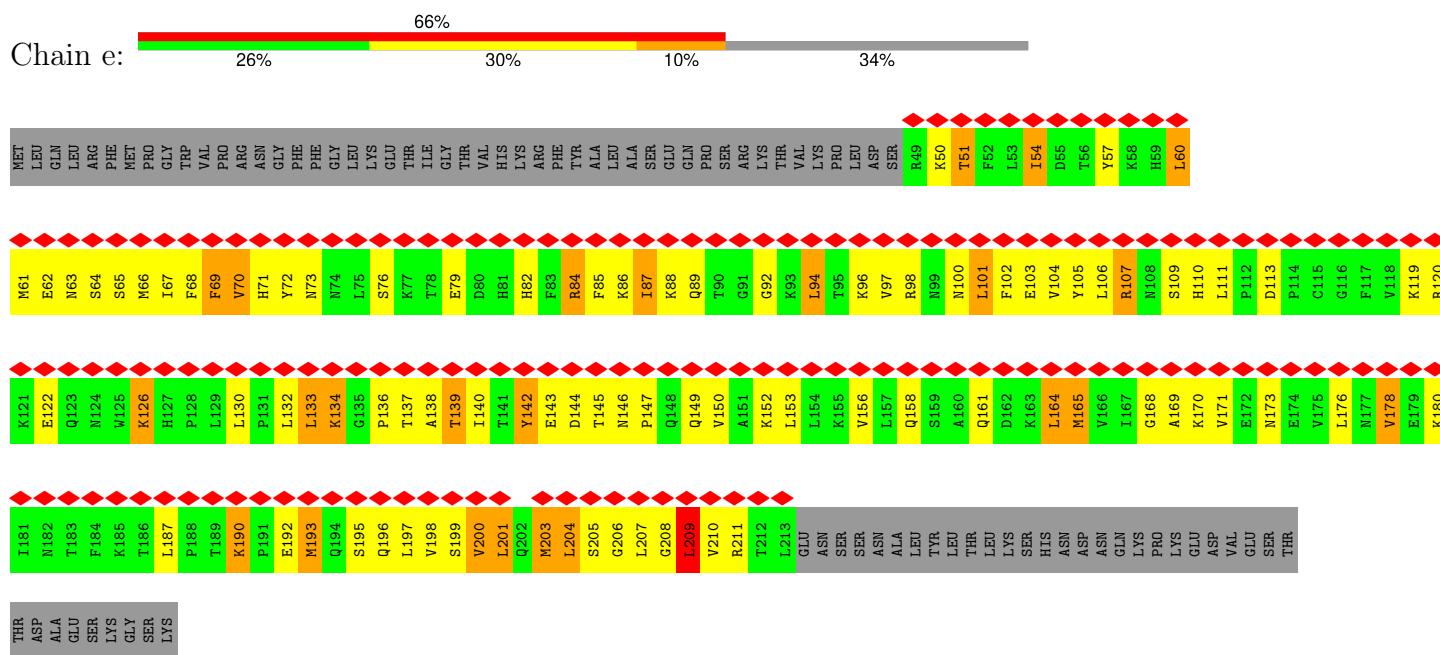


- Molecule 74: Large ribosomal subunit protein mL67





- Molecule 75: Large ribosomal subunit protein uL10m



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	12907	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	19.881	Depositor
Minimum map value	-12.977	Depositor
Average map value	0.066	Depositor
Map value standard deviation	1.736	Depositor
Recommended contour level	4.3	Depositor
Map size (\AA)	427.52, 427.52, 427.52	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.835, 0.835, 0.835	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	AA	0.84	0/304	1.30	1/386 (0.3%)
2	AB	0.78	0/825	1.05	4/1101 (0.4%)
3	AC	0.89	0/2130	1.21	1/2891 (0.0%)
4	AD	0.89	0/2472	1.24	4/3338 (0.1%)
5	AE	0.84	0/2490	1.27	35/3372 (1.0%)
6	AF	0.88	0/2130	1.20	4/2867 (0.1%)
7	AG	0.88	0/1974	1.20	1/2668 (0.0%)
8	AH	0.92	0/1915	1.23	3/2559 (0.1%)
9	AI	0.94	0/3309	1.13	19/4472 (0.4%)
10	AJ	0.75	0/788	1.08	1/1052 (0.1%)
11	AK	0.94	0/2268	1.13	4/3058 (0.1%)
12	AL	0.49	1/35699 (0.0%)	0.83	182/55529 (0.3%)
13	AM	0.72	0/1805	0.96	3/2811 (0.1%)
14	AN	0.70	0/301	1.13	0/466
15	Z	0.90	0/702	1.24	5/945 (0.5%)
16	g	0.91	0/1610	1.16	2/2168 (0.1%)
17	h	0.88	0/2138	1.27	2/2903 (0.1%)
18	i	0.88	0/2503	1.14	1/3375 (0.0%)
19	j	0.91	0/2435	1.19	4/3281 (0.1%)
20	k	0.89	0/2360	1.21	7/3180 (0.2%)
21	l	0.97	0/1068	1.13	2/1430 (0.1%)
22	m	1.01	0/1305	1.29	13/1763 (0.7%)
23	n	0.73	0/1240	1.20	1/1670 (0.1%)
24	o	0.65	0/1855	1.04	0/2492
25	p	0.88	0/1140	1.17	0/1547
26	q	1.06	2/1228 (0.2%)	1.09	5/1638 (0.3%)
27	r	0.92	0/970	1.20	7/1300 (0.5%)
28	s	0.90	0/957	1.35	3/1277 (0.2%)
29	t	0.96	1/961 (0.1%)	1.19	4/1285 (0.3%)
30	u	1.00	0/2094	1.12	10/2796 (0.4%)
31	v	0.88	0/845	1.10	1/1143 (0.1%)
32	w	0.91	0/1694	1.18	9/2252 (0.4%)
33	x	0.90	0/749	1.25	7/998 (0.7%)
34	y	0.91	0/652	1.18	1/882 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	z	0.87	0/771	1.20	5/1019 (0.5%)
36	0	0.41	0/329	0.57	0/432
37	1	0.48	0/2949	0.84	0/3998
38	2	0.44	0/963	0.95	0/1295
39	3	0.48	0/1072	0.79	0/1442
40	4	0.47	0/1138	0.88	0/1526
41	5	0.46	0/2604	0.92	1/3526 (0.0%)
42	6	0.48	0/1978	0.83	0/2664
43	7	0.51	0/873	0.84	0/1170
44	8	0.46	0/1659	0.95	0/2230
45	9	0.48	0/1616	0.95	0/2177
46	A	0.45	0/68489	0.75	114/106553 (0.1%)
47	B	0.80	0/2573	1.18	3/3456 (0.1%)
48	C	0.50	0/1975	0.79	0/2657
49	D	0.52	0/2028	0.92	1/2746 (0.0%)
50	E	0.48	0/2244	0.82	1/3033 (0.0%)
51	F	0.50	0/1551	0.82	0/2093
52	G	0.44	0/628	0.88	0/844
53	H	0.48	0/1302	0.90	0/1749
54	I	0.46	0/962	0.80	0/1285
55	J	0.62	0/1783	1.03	1/2384 (0.0%)
56	K	0.50	0/1606	0.93	0/2148
57	L	0.45	0/1845	0.96	0/2489
58	M	0.51	0/1224	0.83	0/1651
59	N	0.50	0/961	0.75	0/1295
60	O	0.45	0/1859	0.89	0/2495
61	P	0.44	0/1773	0.89	0/2390
62	Q	0.51	0/2323	0.84	0/3135
63	R	0.96	1/2783 (0.0%)	1.13	20/3723 (0.5%)
64	S	0.48	0/1576	0.88	0/2104
65	T	0.49	0/1837	0.96	0/2486
66	U	0.60	0/648	0.89	2/870 (0.2%)
67	V	0.48	0/553	0.69	0/742
68	W	0.44	0/955	0.84	0/1273
69	X	0.93	0/520	1.25	0/696
70	Y	0.43	0/392	0.98	0/515
71	a	0.48	0/1471	0.97	0/1976
72	b	0.46	0/1333	0.92	0/1783
73	c	0.46	0/1028	0.91	0/1372
74	d	0.44	0/1791	0.90	0/2415
75	e	0.97	0/1367	1.12	1/1844 (0.1%)
76	f	0.97	0/1051	1.19	0/1416
All	All	0.62	5/215299 (0.0%)	0.92	495/311992 (0.2%)

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
2	AB	0	1
3	AC	0	4
4	AD	0	7
5	AE	0	5
6	AF	0	6
7	AG	0	8
8	AH	0	8
9	AI	0	2
10	AJ	0	3
11	AK	0	9
15	Z	0	2
16	g	0	5
17	h	0	5
18	i	0	1
19	j	0	10
20	k	0	5
21	l	0	1
22	m	0	3
24	o	0	6
25	p	0	5
26	q	0	1
27	r	0	2
28	s	0	6
29	t	0	5
30	u	0	2
31	v	0	2
32	w	0	3
33	x	0	1
34	y	0	5
35	z	0	1
47	B	0	16
48	C	0	1
55	J	0	1
56	K	0	1
63	R	0	1
69	X	0	3
75	e	0	2
76	f	0	1
All	All	0	150

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	AL	482	U	O3'-P	-19.09	1.32	1.61
63	R	148	SER	CA-C	-6.40	1.49	1.52
26	q	147	THR	CA-C	-5.19	1.46	1.52
29	t	47	ASN	CA-C	5.07	1.59	1.53
26	q	142	GLU	CA-C	-5.05	1.46	1.52

The worst 5 of 495 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	AL	44	U	C3'-C2'-O2'	16.77	135.86	110.70
12	AL	44	U	C2'-C3'-O3'	-16.37	89.15	113.70
46	A	2067	A	P-O3'-C3'	-15.88	96.38	120.20
46	A	2072	U	P-O3'-C3'	-15.36	97.16	120.20
46	A	2018	C	P-O3'-C3'	-13.26	100.31	120.20

There are no chirality outliers.

5 of 150 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	117	ARG	Sidechain
3	AC	117	ARG	Sidechain
3	AC	142	ARG	Sidechain
3	AC	240	ARG	Sidechain
3	AC	259	ARG	Sidechain

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	AA	304	0	357	64	0
2	AB	808	0	809	138	0
3	AC	2079	0	2057	482	0
4	AD	2422	0	2395	424	0
5	AE	2432	0	2480	451	0
6	AF	2079	0	2104	448	0
7	AG	1931	0	1923	588	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	AH	1887	0	1994	495	0
9	AI	3243	0	3342	494	0
10	AJ	774	0	821	183	0
11	AK	2212	0	2170	524	0
12	AL	31883	0	15998	2046	0
13	AM	1615	0	820	84	0
14	AN	270	0	141	41	0
15	Z	687	0	719	154	0
16	g	1577	0	1611	527	0
17	h	2095	0	2101	535	0
18	i	2461	0	2450	637	0
19	j	2370	0	2435	364	0
20	k	2306	0	2323	428	0
21	l	1055	0	1129	281	0
22	m	1282	0	1342	253	0
23	n	1221	0	1287	167	0
24	o	1820	0	1906	331	0
25	p	1108	0	1115	369	0
26	q	1208	0	1262	206	0
27	r	955	0	1010	109	0
28	s	942	0	1001	194	0
29	t	942	0	992	254	0
30	u	2070	0	2138	327	0
31	v	830	0	890	258	0
32	w	1683	0	1769	330	0
33	x	738	0	771	240	0
34	y	636	0	654	87	0
35	z	760	0	791	157	0
36	0	324	0	347	20	0
37	1	2875	0	2881	79	0
38	2	944	0	969	38	0
39	3	1046	0	1071	32	0
40	4	1117	0	1142	19	0
41	5	2552	0	2600	47	0
42	6	1932	0	1950	43	0
43	7	858	0	908	10	0
44	8	1629	0	1633	15	0
45	9	1587	0	1628	17	0
46	A	61141	0	30666	4457	0
47	B	2527	0	2649	197	0
48	C	1932	0	1969	109	0
49	D	1989	0	2026	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	E	2187	0	2203	56	0
51	F	1524	0	1587	24	0
52	G	617	0	626	6	0
53	H	1275	0	1310	18	0
54	I	956	0	1037	13	0
55	J	1746	0	1840	80	0
56	K	1573	0	1628	35	0
57	L	1817	0	1878	22	0
58	M	1206	0	1283	13	0
59	N	948	0	1006	19	0
60	O	1826	0	1933	19	0
61	P	1729	0	1724	42	0
62	Q	2272	0	2334	43	0
63	R	2738	0	2811	405	0
64	S	1543	0	1621	43	0
65	T	1792	0	1782	29	0
66	U	639	0	699	16	0
67	V	543	0	568	39	0
68	W	937	0	978	13	0
69	X	512	0	563	47	0
70	Y	385	0	423	22	0
71	a	1440	0	1473	44	0
72	b	1299	0	1367	42	0
73	c	1004	0	1065	21	0
74	d	1746	0	1743	20	0
75	e	1340	0	1397	158	0
76	f	1032	0	1115	126	0
All	All	201764	0	157540	14173	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 40.

The worst 5 of 14173 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)
3:AC:9:HIS:CE1	17:h:164:ILE:CD1	1.76	1.65
8:AH:210:ILE:CG2	21:l:39:VAL:HB	1.29	1.62
17:h:247:LEU:HD11	24:o:45:TYR:CD2	1.28	1.61
18:i:180:MET:HG2	20:k:92:TRP:CG	1.33	1.60
7:AG:114:TRP:CZ2	16:g:87:ARG:HB2	1.31	1.59

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	32/34 (94%)	30 (94%)	2 (6%)	0	100	100
2	AB	93/101 (92%)	70 (75%)	15 (16%)	8 (9%)	0	3
3	AC	257/259 (99%)	209 (81%)	32 (12%)	16 (6%)	1	9
4	AD	299/321 (93%)	215 (72%)	63 (21%)	21 (7%)	1	6
5	AE	296/339 (87%)	220 (74%)	58 (20%)	18 (6%)	1	9
6	AF	248/320 (78%)	178 (72%)	49 (20%)	21 (8%)	0	3
7	AG	234/236 (99%)	196 (84%)	31 (13%)	7 (3%)	3	23
8	AH	232/234 (99%)	192 (83%)	34 (15%)	6 (3%)	4	27
9	AI	403/405 (100%)	316 (78%)	62 (15%)	25 (6%)	1	9
10	AJ	94/96 (98%)	75 (80%)	7 (7%)	12 (13%)	0	1
11	AK	262/273 (96%)	237 (90%)	22 (8%)	3 (1%)	12	44
15	Z	83/91 (91%)	63 (76%)	17 (20%)	3 (4%)	3	20
16	g	190/344 (55%)	159 (84%)	29 (15%)	2 (1%)	12	44
17	h	265/267 (99%)	215 (81%)	38 (14%)	12 (4%)	2	15
18	i	287/398 (72%)	236 (82%)	37 (13%)	14 (5%)	2	14
19	j	281/486 (58%)	253 (90%)	23 (8%)	5 (2%)	7	35
20	k	284/293 (97%)	219 (77%)	54 (19%)	11 (4%)	2	18
21	l	129/131 (98%)	104 (81%)	19 (15%)	6 (5%)	2	14
22	m	159/161 (99%)	128 (80%)	24 (15%)	7 (4%)	2	15
23	n	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
24	o	220/244 (90%)	196 (89%)	17 (8%)	7 (3%)	3	22
25	p	132/186 (71%)	100 (76%)	25 (19%)	7 (5%)	1	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	q	150/152 (99%)	117 (78%)	22 (15%)	11 (7%)	1	6
27	r	123/125 (98%)	91 (74%)	22 (18%)	10 (8%)	1	4
28	s	118/120 (98%)	87 (74%)	21 (18%)	10 (8%)	0	3
29	t	111/115 (96%)	102 (92%)	8 (7%)	1 (1%)	14	49
30	u	251/253 (99%)	205 (82%)	37 (15%)	9 (4%)	3	20
31	v	104/120 (87%)	94 (90%)	9 (9%)	1 (1%)	13	47
32	w	194/237 (82%)	155 (80%)	29 (15%)	10 (5%)	1	12
33	x	87/99 (88%)	67 (77%)	11 (13%)	9 (10%)	0	2
34	y	78/80 (98%)	54 (69%)	15 (19%)	9 (12%)	0	2
35	z	90/92 (98%)	72 (80%)	12 (13%)	6 (7%)	1	7
36	0	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
37	1	346/348 (99%)	329 (95%)	17 (5%)	0	100	100
38	2	111/113 (98%)	106 (96%)	5 (4%)	0	100	100
39	3	128/130 (98%)	122 (95%)	6 (5%)	0	100	100
40	4	136/138 (99%)	130 (96%)	6 (4%)	0	100	100
41	5	322/324 (99%)	306 (95%)	16 (5%)	0	100	100
42	6	228/281 (81%)	221 (97%)	7 (3%)	0	100	100
43	7	104/106 (98%)	97 (93%)	7 (7%)	0	100	100
44	8	195/264 (74%)	192 (98%)	3 (2%)	0	100	100
45	9	198/215 (92%)	186 (94%)	12 (6%)	0	100	100
47	B	317/393 (81%)	273 (86%)	34 (11%)	10 (3%)	3	22
48	C	247/249 (99%)	233 (94%)	13 (5%)	1 (0%)	30	64
49	D	250/252 (99%)	235 (94%)	10 (4%)	5 (2%)	6	32
50	E	272/274 (99%)	254 (93%)	15 (6%)	3 (1%)	12	44
51	F	194/196 (99%)	183 (94%)	10 (5%)	1 (0%)	25	60
52	G	72/74 (97%)	70 (97%)	2 (3%)	0	100	100
53	H	158/160 (99%)	152 (96%)	6 (4%)	0	100	100
54	I	123/138 (89%)	114 (93%)	9 (7%)	0	100	100
55	J	218/220 (99%)	193 (88%)	19 (9%)	6 (3%)	4	25
56	K	193/195 (99%)	181 (94%)	10 (5%)	2 (1%)	13	47
57	L	225/237 (95%)	217 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
58	M	149/151 (99%)	139 (93%)	10 (7%)	0	100	100
59	N	116/118 (98%)	106 (91%)	9 (8%)	1 (1%)	14	49
60	O	223/225 (99%)	211 (95%)	12 (5%)	0	100	100
61	P	205/207 (99%)	196 (96%)	9 (4%)	0	100	100
62	Q	280/296 (95%)	268 (96%)	12 (4%)	0	100	100
63	R	327/337 (97%)	268 (82%)	45 (14%)	14 (4%)	2	16
64	S	181/216 (84%)	171 (94%)	10 (6%)	0	100	100
65	T	210/225 (93%)	199 (95%)	11 (5%)	0	100	100
66	U	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
67	V	63/177 (36%)	61 (97%)	2 (3%)	0	100	100
68	W	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
69	X	62/64 (97%)	50 (81%)	8 (13%)	4 (6%)	1	8
70	Y	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
71	a	175/177 (99%)	163 (93%)	12 (7%)	0	100	100
72	b	153/155 (99%)	146 (95%)	7 (5%)	0	100	100
73	c	117/119 (98%)	112 (96%)	4 (3%)	1 (1%)	14	49
74	d	202/215 (94%)	189 (94%)	13 (6%)	0	100	100
75	e	163/249 (66%)	136 (83%)	23 (14%)	4 (2%)	4	28
76	f	134/158 (85%)	104 (78%)	21 (16%)	9 (7%)	1	7
All	All	13006/14441 (90%)	11375 (88%)	1283 (10%)	348 (3%)	6	26

5 of 348 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	82	GLN
2	AB	95	ARG
3	AC	33	GLY
3	AC	59	GLU
3	AC	170	ASN

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	AA	32/32 (100%)	28 (88%)	4 (12%)	3	18
2	AB	86/92 (94%)	73 (85%)	13 (15%)	2	12
3	AC	234/234 (100%)	206 (88%)	28 (12%)	4	19
4	AD	265/281 (94%)	235 (89%)	30 (11%)	4	22
5	AE	266/303 (88%)	213 (80%)	53 (20%)	1	5
6	AF	230/290 (79%)	189 (82%)	41 (18%)	1	7
7	AG	211/211 (100%)	189 (90%)	22 (10%)	5	25
8	AH	211/211 (100%)	177 (84%)	34 (16%)	2	9
9	AI	371/371 (100%)	347 (94%)	24 (6%)	14	45
10	AJ	84/84 (100%)	68 (81%)	16 (19%)	1	6
11	AK	241/250 (96%)	221 (92%)	20 (8%)	9	35
15	Z	78/82 (95%)	65 (83%)	13 (17%)	2	9
16	g	173/309 (56%)	143 (83%)	30 (17%)	1	8
17	h	234/234 (100%)	210 (90%)	24 (10%)	6	25
18	i	287/385 (74%)	236 (82%)	51 (18%)	1	7
19	j	256/437 (59%)	233 (91%)	23 (9%)	8	30
20	k	249/252 (99%)	220 (88%)	29 (12%)	4	21
21	l	120/120 (100%)	111 (92%)	9 (8%)	11	40
22	m	138/138 (100%)	124 (90%)	14 (10%)	6	26
23	n	142/142 (100%)	137 (96%)	5 (4%)	31	63
24	o	196/215 (91%)	173 (88%)	23 (12%)	4	21
25	p	121/167 (72%)	103 (85%)	18 (15%)	2	12
26	q	131/131 (100%)	122 (93%)	9 (7%)	13	43
27	r	104/104 (100%)	94 (90%)	10 (10%)	7	28
28	s	100/100 (100%)	73 (73%)	27 (27%)	0	1
29	t	102/103 (99%)	89 (87%)	13 (13%)	3	17
30	u	220/220 (100%)	206 (94%)	14 (6%)	14	46
31	v	91/105 (87%)	87 (96%)	4 (4%)	24	57
32	w	187/218 (86%)	160 (86%)	27 (14%)	2	13
33	x	80/87 (92%)	64 (80%)	16 (20%)	1	5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	y	69/69 (100%)	54 (78%)	15 (22%)	1	4
35	z	81/81 (100%)	71 (88%)	10 (12%)	4	19
36	0	36/36 (100%)	36 (100%)	0	100	100
37	1	323/323 (100%)	308 (95%)	15 (5%)	23	56
38	2	106/106 (100%)	100 (94%)	6 (6%)	17	50
39	3	112/112 (100%)	110 (98%)	2 (2%)	54	77
40	4	121/121 (100%)	116 (96%)	5 (4%)	26	59
41	5	284/284 (100%)	278 (98%)	6 (2%)	48	74
42	6	213/252 (84%)	203 (95%)	10 (5%)	22	55
43	7	95/95 (100%)	90 (95%)	5 (5%)	19	52
44	8	182/240 (76%)	174 (96%)	8 (4%)	24	57
45	9	176/186 (95%)	168 (96%)	8 (4%)	23	56
47	B	272/337 (81%)	240 (88%)	32 (12%)	4	20
48	C	210/210 (100%)	197 (94%)	13 (6%)	15	47
49	D	217/218 (100%)	195 (90%)	22 (10%)	6	26
50	E	242/242 (100%)	227 (94%)	15 (6%)	15	47
51	F	172/172 (100%)	167 (97%)	5 (3%)	37	67
52	G	68/68 (100%)	65 (96%)	3 (4%)	24	57
53	H	138/138 (100%)	131 (95%)	7 (5%)	20	53
54	I	108/117 (92%)	104 (96%)	4 (4%)	29	62
55	J	181/181 (100%)	167 (92%)	14 (8%)	10	39
56	K	167/167 (100%)	149 (89%)	18 (11%)	5	23
57	L	203/211 (96%)	195 (96%)	8 (4%)	27	60
58	M	136/136 (100%)	131 (96%)	5 (4%)	29	62
59	N	107/107 (100%)	103 (96%)	4 (4%)	29	62
60	O	200/200 (100%)	187 (94%)	13 (6%)	14	45
61	P	185/185 (100%)	180 (97%)	5 (3%)	40	69
62	Q	256/267 (96%)	244 (95%)	12 (5%)	22	55
63	R	303/308 (98%)	270 (89%)	33 (11%)	5	23
64	S	167/191 (87%)	157 (94%)	10 (6%)	16	48
65	T	204/213 (96%)	197 (97%)	7 (3%)	32	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	U	73/73 (100%)	68 (93%)	5 (7%)	13	43
67	V	60/161 (37%)	58 (97%)	2 (3%)	33	64
68	W	104/104 (100%)	102 (98%)	2 (2%)	52	76
69	X	56/56 (100%)	45 (80%)	11 (20%)	1	6
70	Y	40/40 (100%)	39 (98%)	1 (2%)	42	71
71	a	158/158 (100%)	150 (95%)	8 (5%)	20	53
72	b	144/144 (100%)	138 (96%)	6 (4%)	25	58
73	c	110/110 (100%)	108 (98%)	2 (2%)	54	77
74	d	191/199 (96%)	186 (97%)	5 (3%)	41	70
75	e	154/229 (67%)	129 (84%)	25 (16%)	2	9
76	f	113/127 (89%)	100 (88%)	13 (12%)	4	21
All	All	11777/12882 (91%)	10733 (91%)	1044 (9%)	10	31

5 of 1044 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
63	R	180	LEU
64	S	124	LYS
63	R	175	LYS
76	f	56	VAL
18	i	306	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 285 such sidechains are listed below:

Mol	Chain	Res	Type
50	E	253	GLN
55	J	110	GLN
63	R	267	HIS
18	i	103	ASN
18	i	91	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
12	AL	1490/1649 (90%)	523 (35%)	97 (6%)
13	AM	75/76 (98%)	43 (57%)	7 (9%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	AN	12/13 (92%)	12 (100%)	7 (58%)
46	A	2851/3296 (86%)	977 (34%)	187 (6%)
All	All	4428/5034 (87%)	1555 (35%)	298 (6%)

5 of 1555 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
12	AL	14	A
12	AL	15	A
12	AL	16	G
12	AL	20	A
12	AL	25	G

5 of 298 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
46	A	2039	U
46	A	3018	A
46	A	2056	A
46	A	2437	U
13	AM	7	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
12	AL	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AL	482:U	O3'	483:A	P	1.32

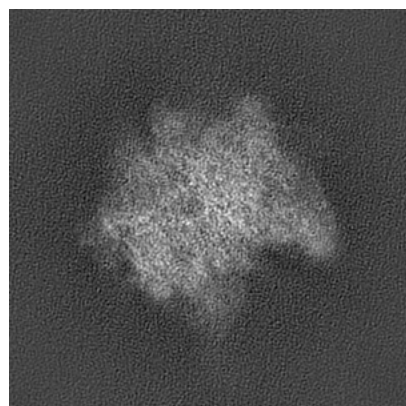
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42720. These allow visual inspection of the internal detail of the map and identification of artifacts.

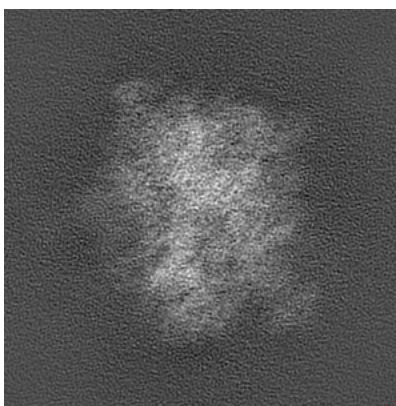
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

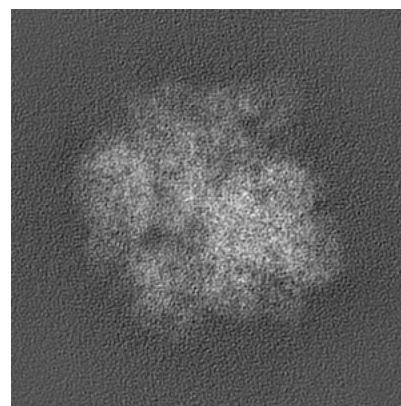
6.1.1 Primary map



X

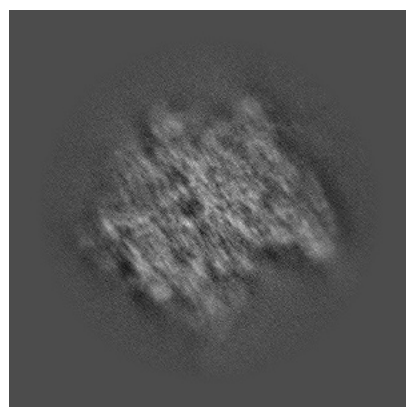


Y

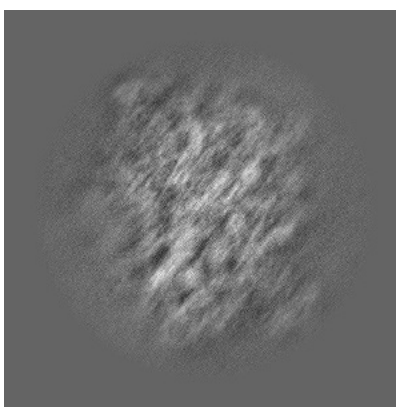


Z

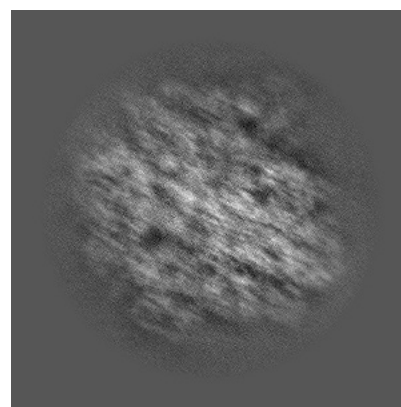
6.1.2 Raw map



X



Y

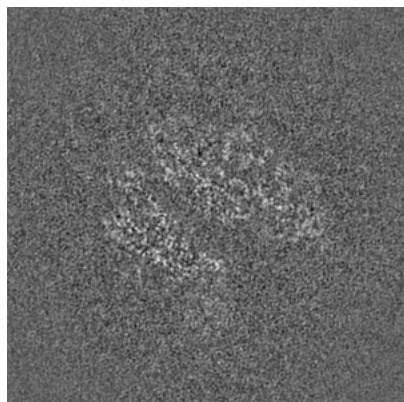


Z

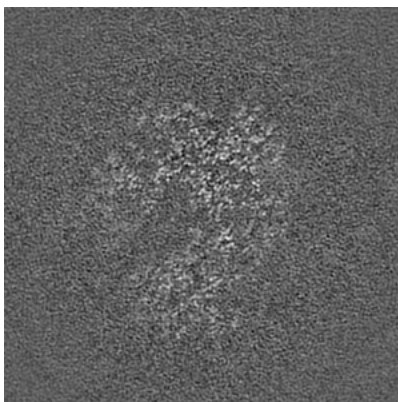
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

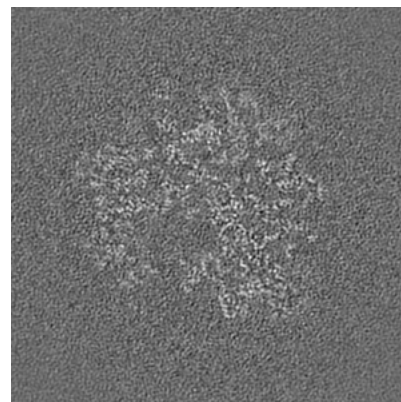
6.2.1 Primary map



X Index: 256

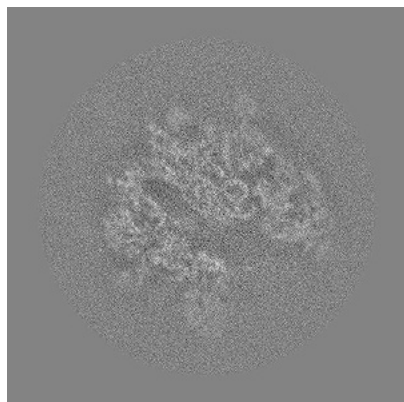


Y Index: 256

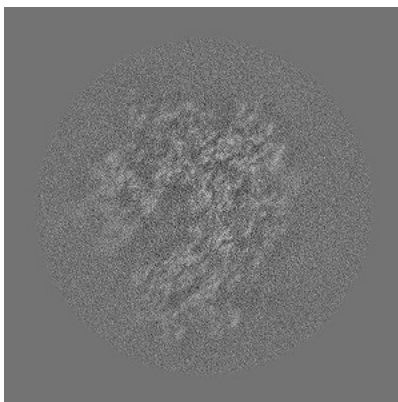


Z Index: 256

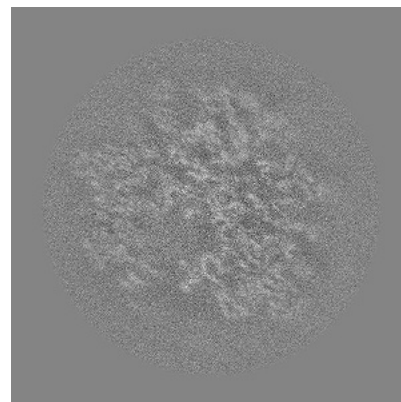
6.2.2 Raw map



X Index: 256



Y Index: 256

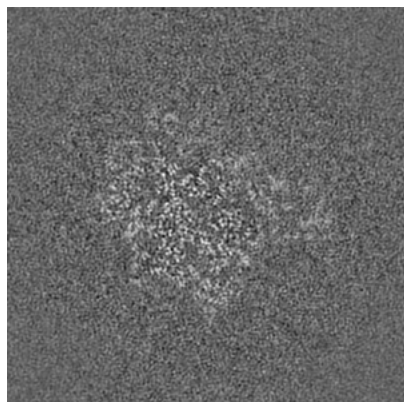


Z Index: 256

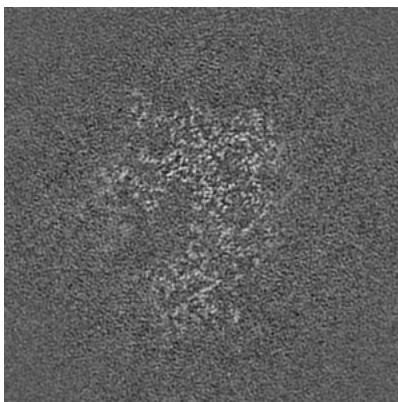
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

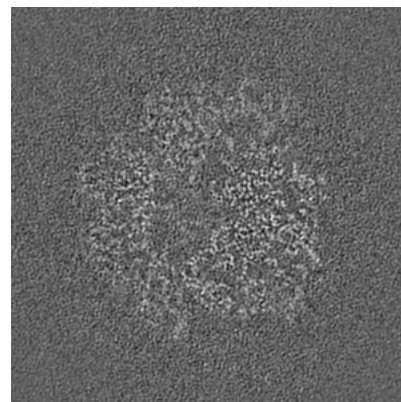
6.3.1 Primary map



X Index: 296

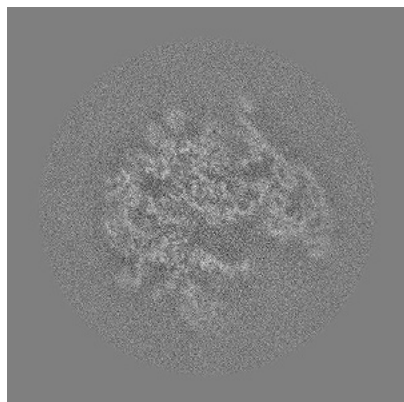


Y Index: 254

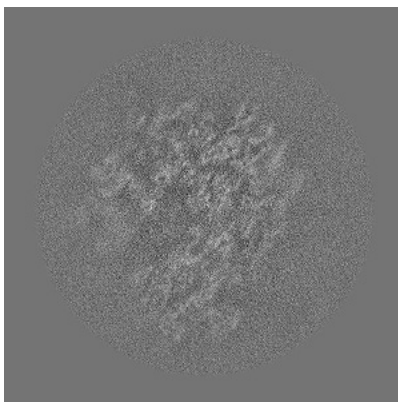


Z Index: 236

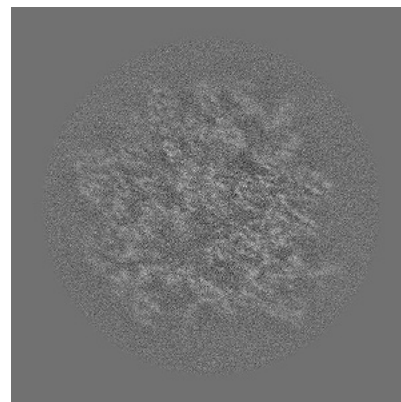
6.3.2 Raw map



X Index: 262



Y Index: 257

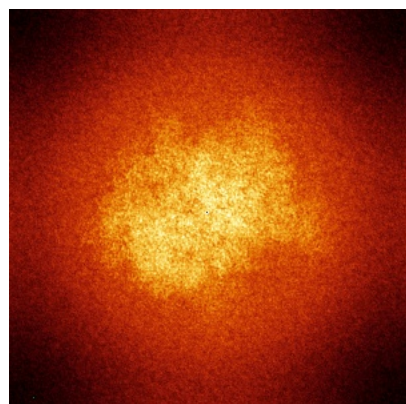


Z Index: 244

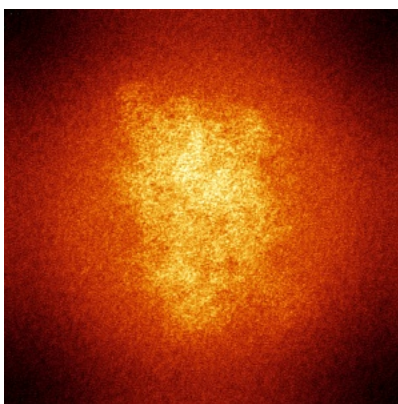
The images above show the largest variance slices of the map in three orthogonal directions.

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

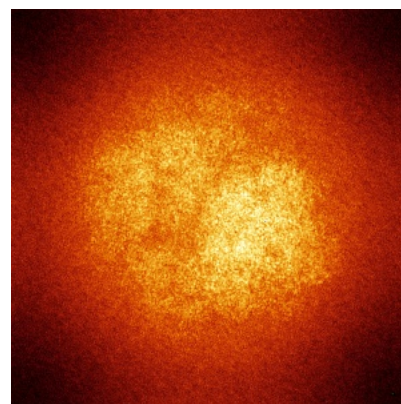
6.4.1 Primary map



X

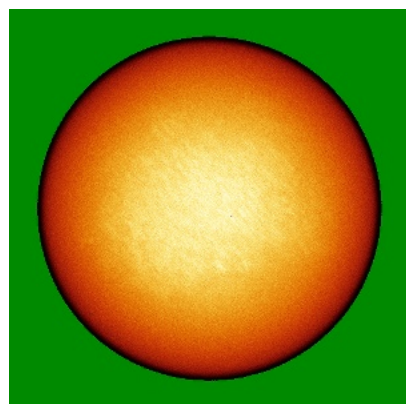


Y

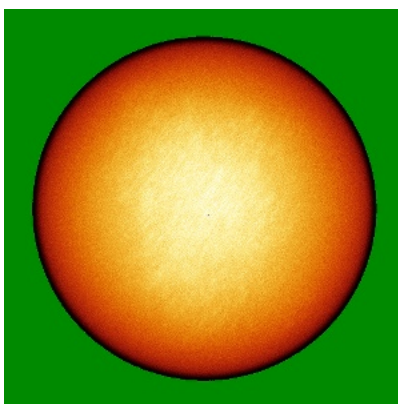


Z

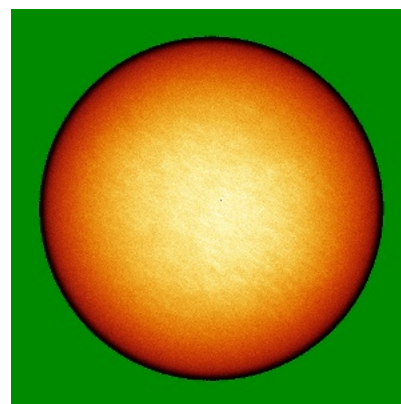
6.4.2 Raw map



X



Y

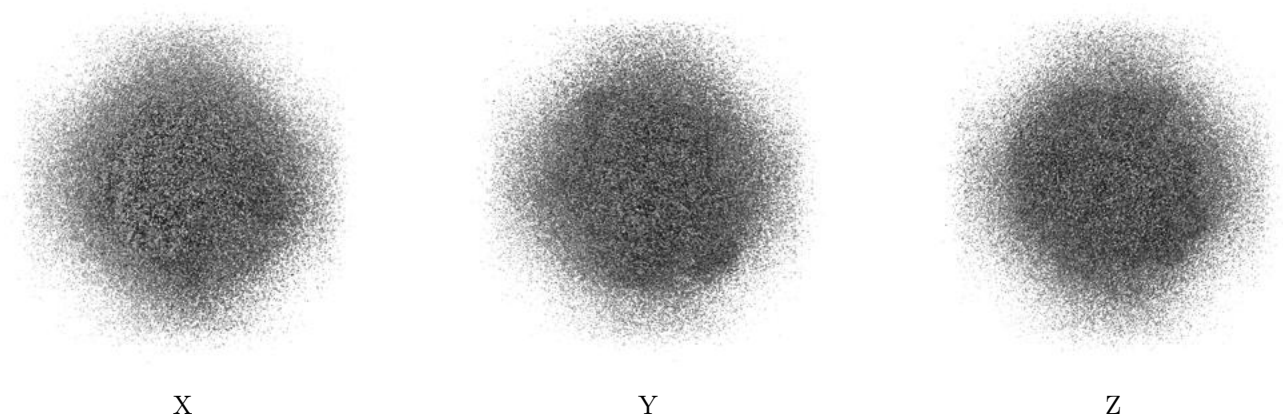


Z

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

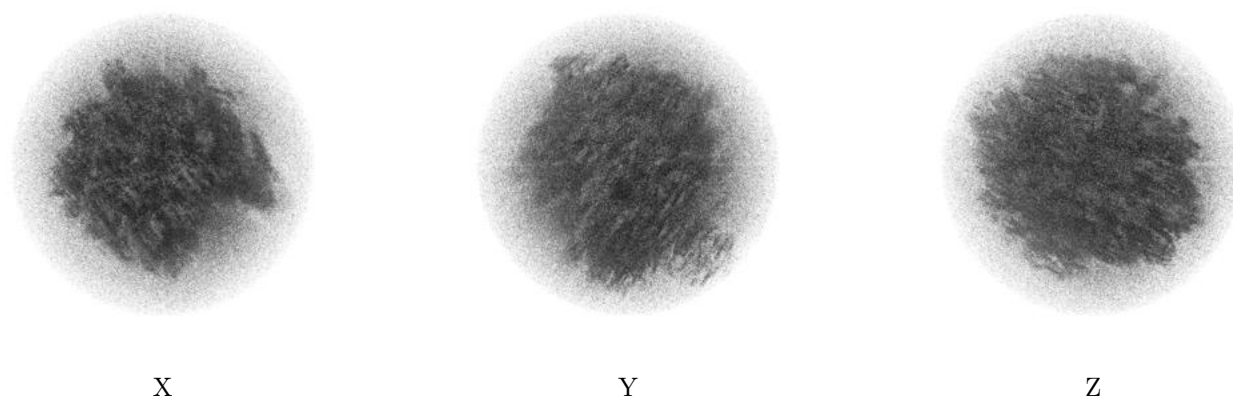
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

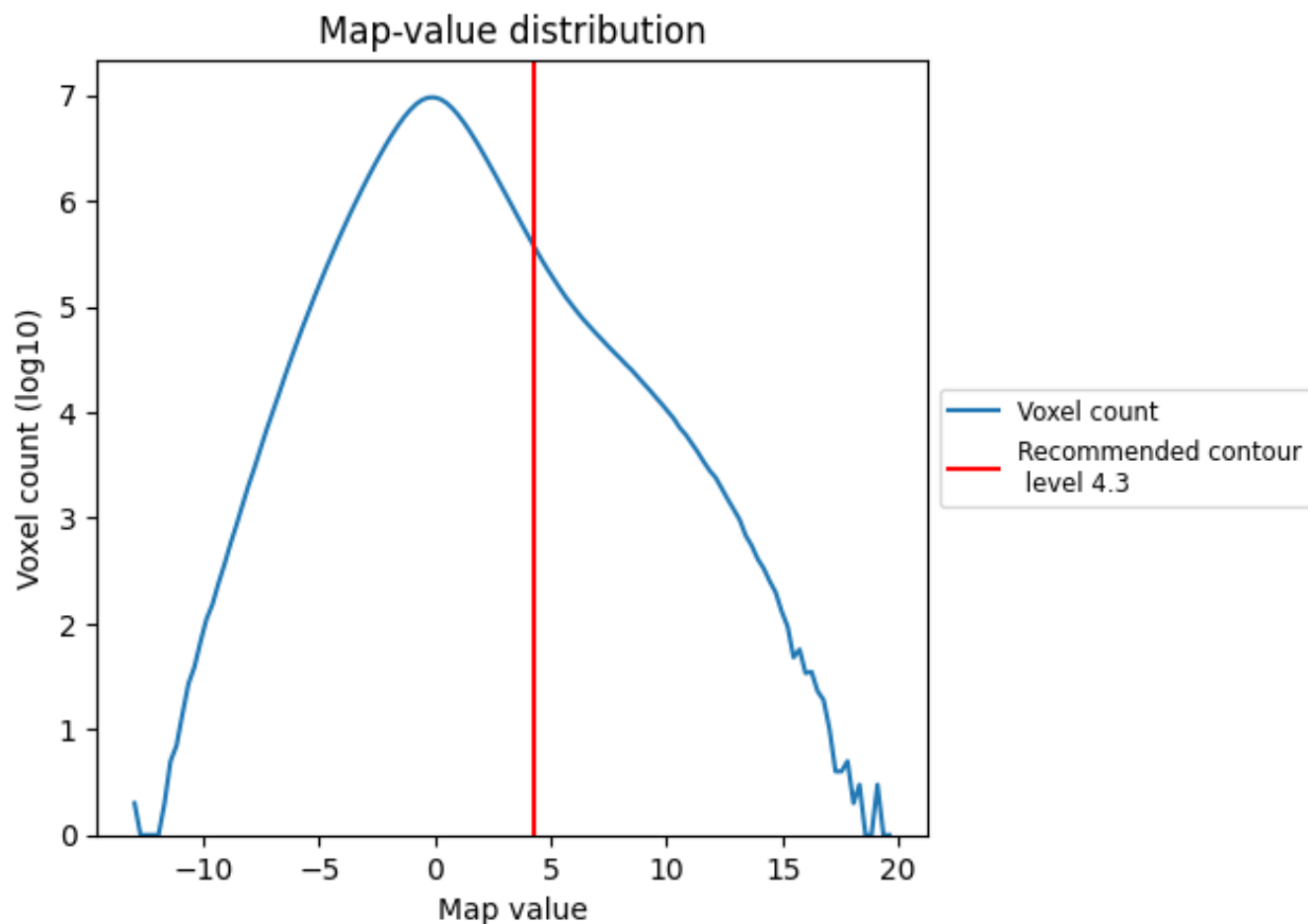
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

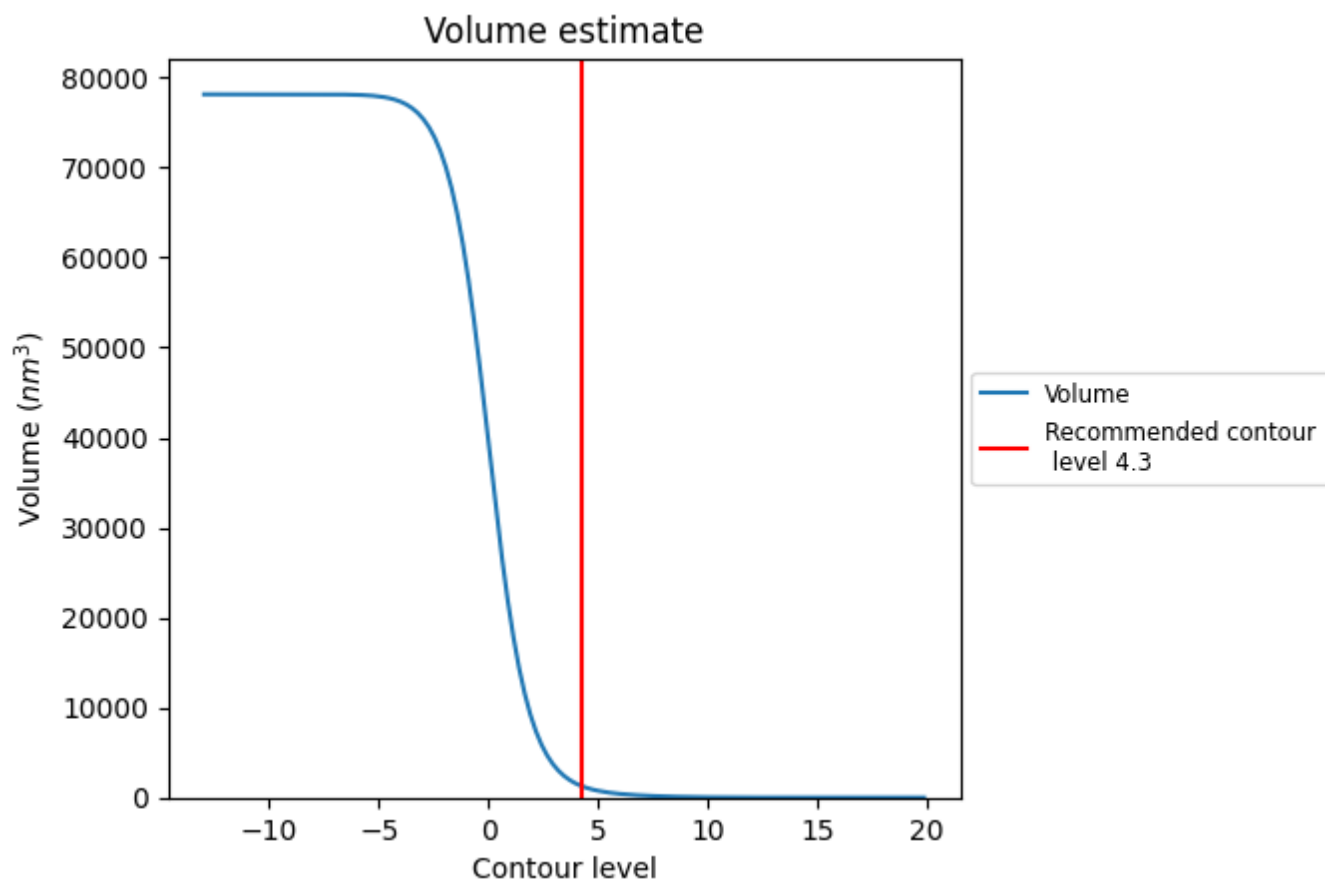
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

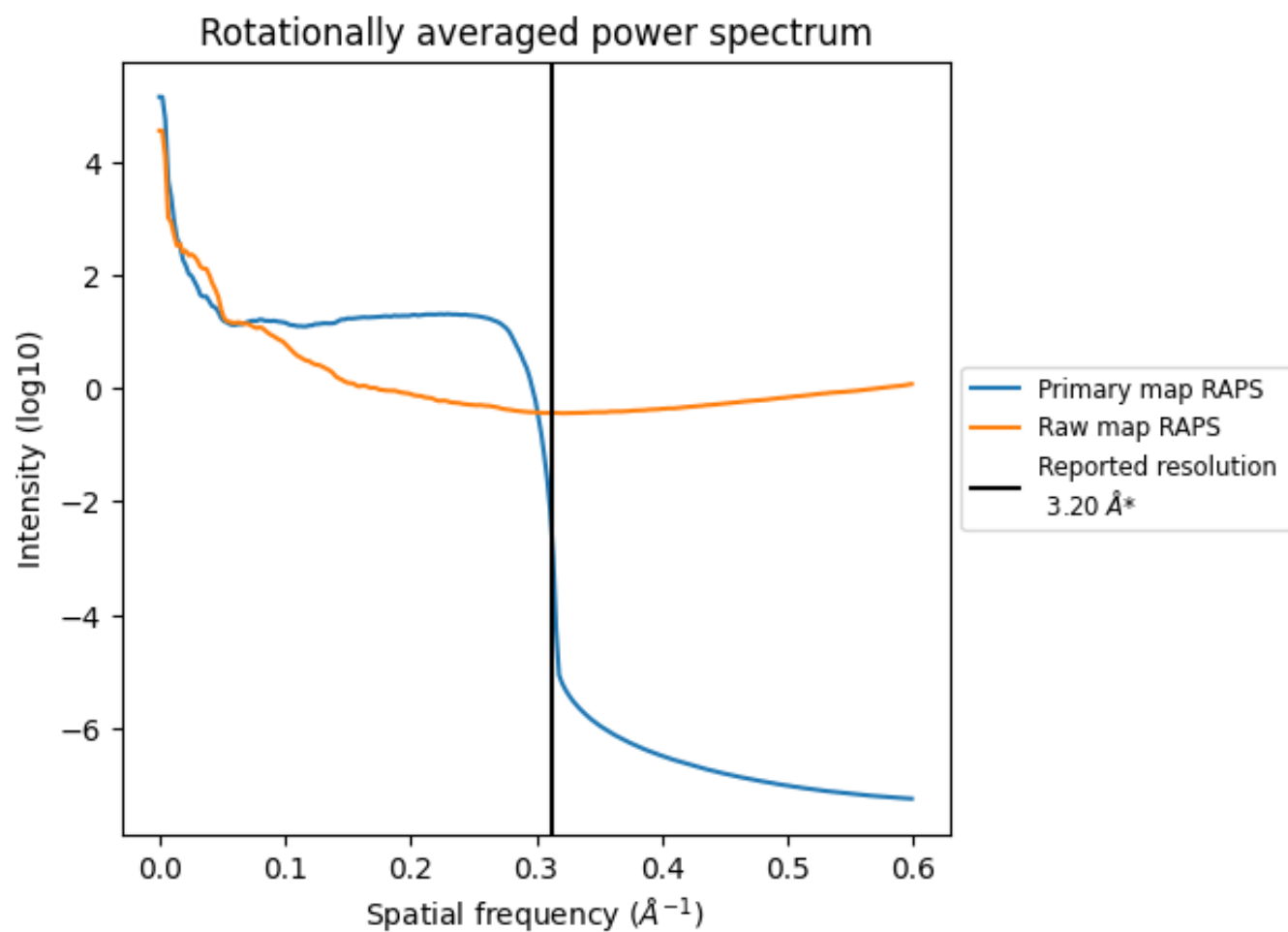
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1241 nm³; this corresponds to an approximate mass of 1121 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 ⓘ

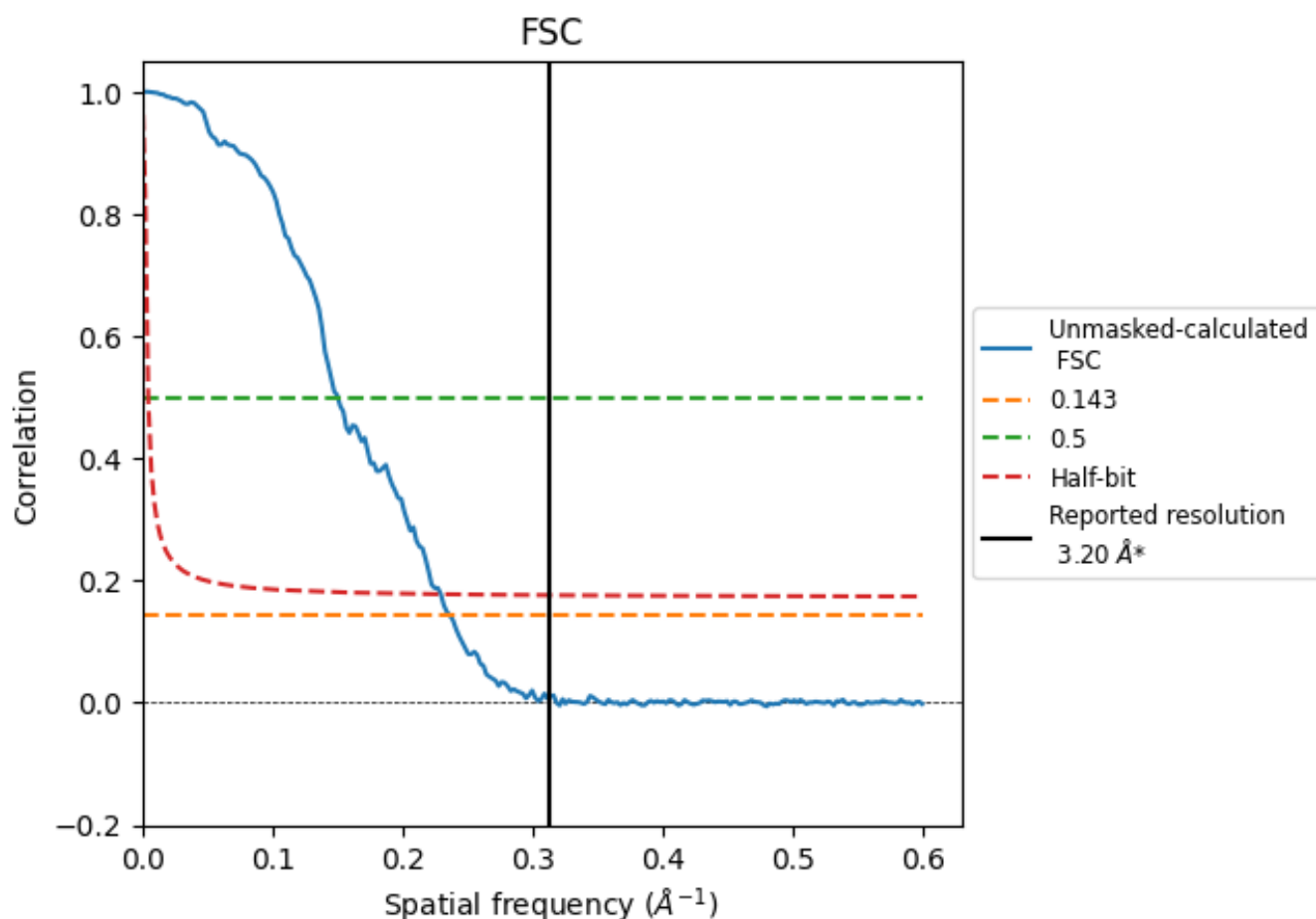


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

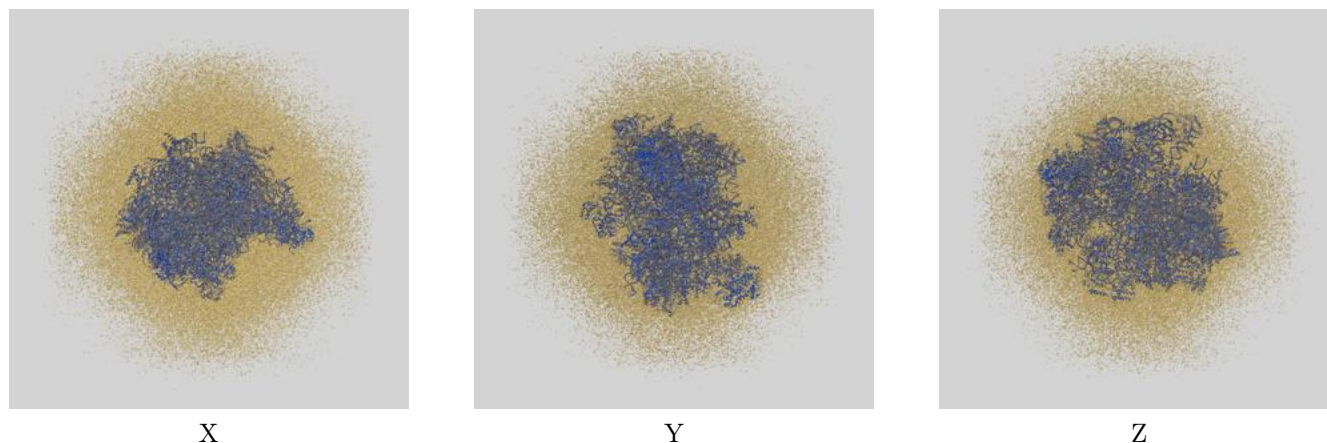
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.23	6.66	4.36

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.23 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

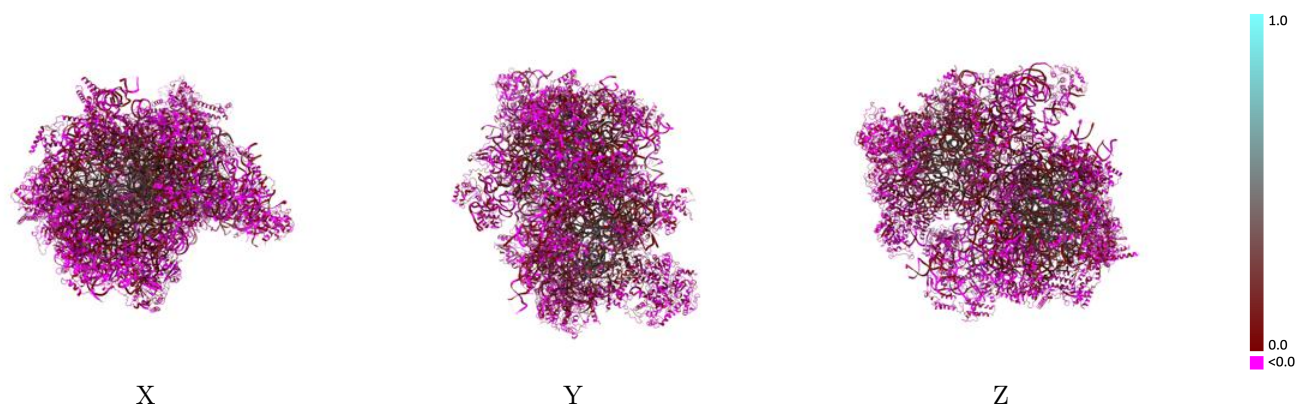
This section contains information regarding the fit between EMDB map EMD-42720 and PDB model 8UXA. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



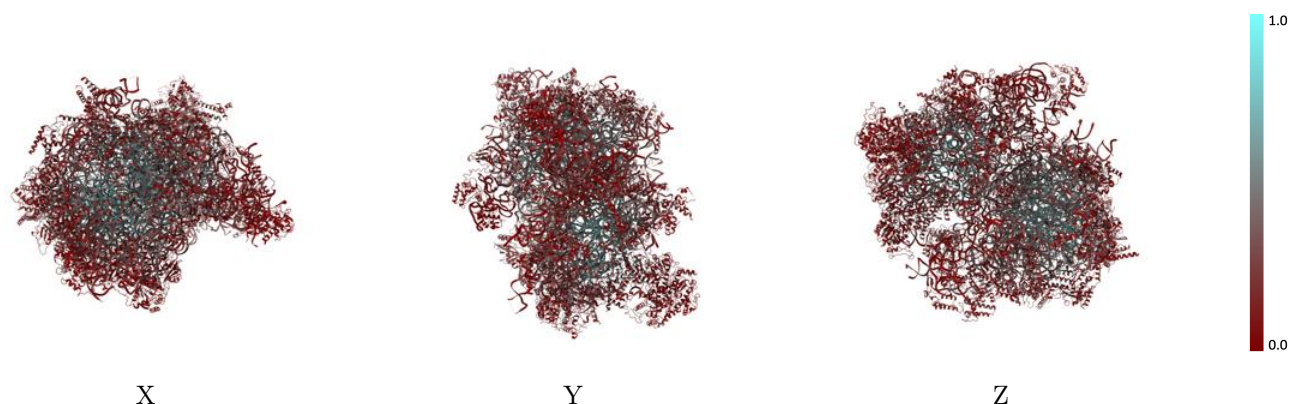
The images above show the 3D surface view of the map at the recommended contour level 4.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



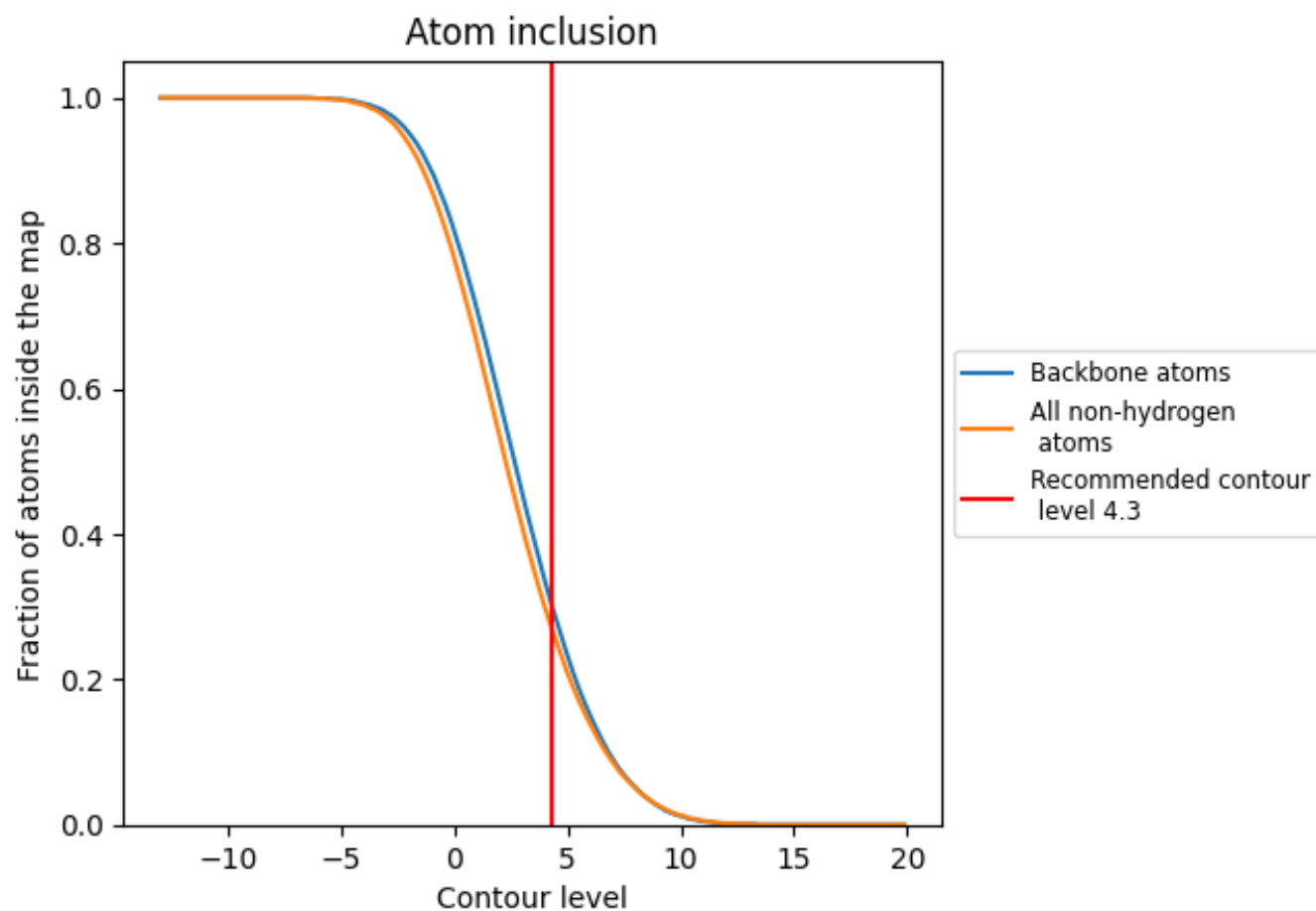
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 30% of all backbone atoms, 27% 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 (4.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.2700	0.0810
0	0.2610	0.0530
1	0.1270	-0.0450
2	0.1240	-0.0420
3	0.2550	0.0750
4	0.2190	0.0190
5	0.1670	-0.0180
6	0.1160	-0.0400
7	0.2050	-0.0030
8	0.1440	-0.0140
9	0.0880	-0.0550
A	0.3720	0.1290
AA	0.3530	0.1610
AB	0.0860	-0.0290
AC	0.1120	-0.0300
AD	0.0790	-0.0240
AE	0.0550	-0.0000
AF	0.1470	0.0480
AG	0.2040	0.0500
AH	0.1250	0.0140
AI	0.1210	-0.0410
AJ	0.1840	0.0820
AK	0.1510	0.0190
AL	0.3490	0.1360
AM	0.1400	0.0840
AN	0.2740	0.1610
B	0.2350	0.0230
C	0.2400	0.0400
D	0.2570	0.0880
E	0.1560	-0.0290
F	0.1420	-0.0180
G	0.1410	-0.0740
H	0.2740	0.0940
I	0.2080	0.0490
J	0.2510	0.0610



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Chain	Atom inclusion	Q-score
K	0.3040	0.1040
L	0.2110	0.0210
M	0.1580	-0.0290
N	0.2570	0.0620
O	0.3150	0.1580
P	0.2730	0.1030
Q	0.1800	0.0590
R	0.1370	-0.0110
S	0.2130	0.0240
T	0.2130	0.0240
U	0.2550	0.0410
V	0.1340	-0.0330
W	0.3080	0.1450
X	0.1330	-0.0630
Y	0.4630	0.2740
Z	0.2640	0.1370
a	0.1590	-0.0290
b	0.1660	-0.0290
c	0.3160	0.1000
d	0.2170	0.0080
e	0.0610	0.0030
f	0.0350	-0.0030
g	0.1530	0.0320
h	0.2830	0.1290
i	0.2280	0.1230
j	0.1670	0.0520
k	0.3150	0.1960
l	0.1930	0.0450
m	0.2250	0.0820
n	0.2680	0.1090
o	0.1760	0.0380
p	0.2240	0.0940
q	0.2830	0.1260
r	0.2650	0.1550
s	0.1540	-0.0260
t	0.2220	0.0840
u	0.2200	0.0720
v	0.0940	-0.0100
w	0.1450	0.0160
x	0.2470	0.1060
y	0.1550	0.0340
z	0.3290	0.1900