



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:22 PM UTC

PDB ID : 8XU8 / pdb_00008xu8
EMDB ID : EMD-38660
Title : State 2c(S2c) of yeast 80S ribosome bound to compact eEF2 and 2 tRNAs during peptidyl transferation
Authors : Cheng, J.; Wu, C.L.; Li, J.X.; Zhang, X.Z.
Deposited on : 2024-01-12
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

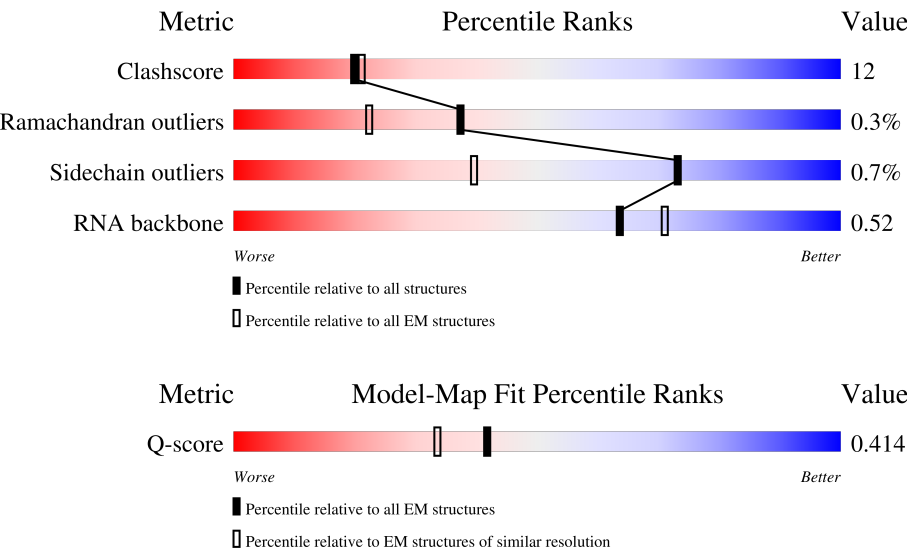
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	2	1799	
2	A	3394	
3	B	121	

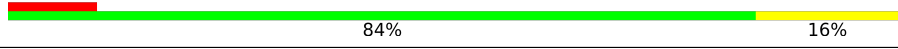
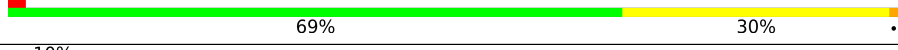
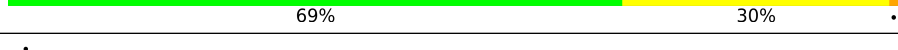
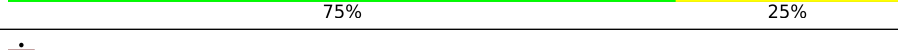
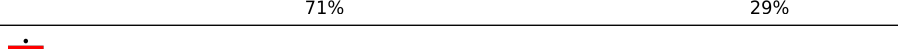
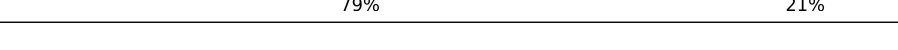
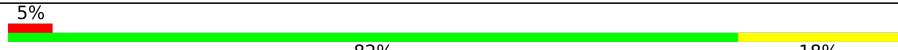
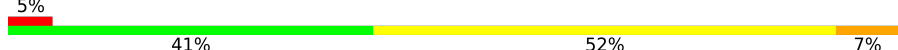
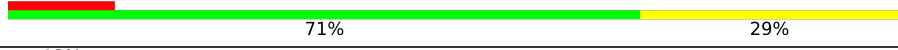
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Mol	Chain	Length	Quality of chain
4	C	158	
5	D	251	
6	E	386	
7	F	361	
8	G	294	
9	H	175	
10	I	222	
11	J	233	
12	K	191	
13	L	218	
14	M	169	
15	N	193	
16	O	136	
17	P	203	
18	Q	197	
19	R	183	
20	S	185	
21	T	188	
22	U	171	
23	V	159	
24	W	100	
25	X	136	
26	Y	126	
27	Z	121	
28	a	125	

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Mol	Chain	Length	Quality of chain
29	b	135	
30	c	148	
31	d	58	
32	e	96	
33	f	109	
34	g	127	
35	h	106	
36	i	112	
37	j	119	
38	k	99	
39	l	81	
40	m	77	
41	n	50	
42	o	52	
43	p	25	
44	q	103	
45	r	91	
46	s	75	
46	t	75	
47	x	842	
48	SD	121	
49	SZ	127	
50	Se	94	
51	SC	92	
52	SE	117	

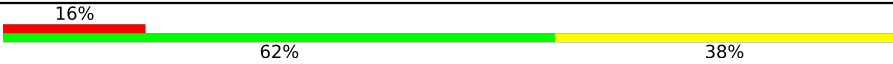
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Mol	Chain	Length	Quality of chain
53	SA	222	
54	SI	143	
55	SJ	100	
56	SL	63	
57	SM	53	
58	SB	206	
59	SF	141	
60	SH	145	
61	SO	312	
62	SN	73	
63	SG	121	
64	SP	206	
65	SQ	232	
66	SR	216	
67	SS	258	
68	ST	228	
69	SU	184	
70	SV	198	
71	SW	184	
72	SX	142	
73	SY	150	
74	Sa	87	
75	Sb	129	
76	Sc	144	
77	Sd	134	

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Mol	Chain	Length	Quality of chain
78	Sf	81	
79	Sg	60	
80	SK	108	

2 Entry composition

There are 80 unique types of molecules in this entry. The entry contains 209284 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 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1767	Total	C	N	O	P	0	0
			37653	16834	6668	12384	1767		

- Molecule 2 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	3189	Total	C	N	O	P	0	0
			68216	30470	12302	22255	3189		

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

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

- Molecule 4 is a RNA chain called 5.8S rRNA.

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

- Molecule 5 is a protein called Large ribosomal subunit protein uL2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	251	Total	C	N	O	S	0	0
			1899	1182	385	331	1		

- Molecule 6 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 7 is a protein called Large ribosomal subunit protein uL4A.

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

- Molecule 8 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 9 is a protein called Large ribosomal subunit protein eL6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	167	Total	C	N	O	S	0	0
			1307	843	234	230			

- Molecule 10 is a protein called Large ribosomal subunit protein uL30A.

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

- Molecule 11 is a protein called Large ribosomal subunit protein eL8A.

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

- Molecule 12 is a protein called Large ribosomal subunit protein uL6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 13 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 14 is a protein called Large ribosomal subunit protein uL5B.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	169	Total	C	N	O	S	0	0
			1346	843	252	247	4		

- Molecule 15 is a protein called Large ribosomal subunit protein eL13A.

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

- Molecule 16 is a protein called Large ribosomal subunit protein eL14A.

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

- Molecule 17 is a protein called Large ribosomal subunit protein eL15A.

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

- Molecule 18 is a protein called Large ribosomal subunit protein uL13A.

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

- Molecule 19 is a protein called Large ribosomal subunit protein uL22A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	183	Total	C	N	O		0	0
			1416	879	284	253			

- Molecule 20 is a protein called Large ribosomal subunit protein eL18A.

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

- Molecule 21 is a protein called Large ribosomal subunit protein eL19A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	T	188	Total	C	N	O	0	0
			1515	932	323	260		

- Molecule 22 is a protein called Large ribosomal subunit protein eL20A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 23 is a protein called Large ribosomal subunit protein eL21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	159	Total	C	N	O	S	0	0
			1272	802	245	221	4		

- Molecule 24 is a protein called Large ribosomal subunit protein eL22A.

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

- Molecule 25 is a protein called Large ribosomal subunit protein uL14A.

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

- Molecule 26 is a protein called Large ribosomal subunit protein eL24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	126	Total	C	N	O	S	0	0
			836	525	165	145	1		

- Molecule 27 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 28 is a protein called Large ribosomal subunit protein uL24A.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	a	125	Total	C	N	O	0	0
			984	620	191	173		

- Molecule 29 is a protein called Large ribosomal subunit protein eL27A.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	b	135	Total	C	N	O	0	0
			1080	701	199	180		

- Molecule 30 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	148	Total	C	N	O	S	0	0
			1169	747	231	188	3		

- Molecule 31 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 32 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 33 is a protein called Large ribosomal subunit protein eL31A.

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

- Molecule 34 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	127	Total	C	N	O	S	0	0
			1013	642	205	165	1		

- Molecule 35 is a protein called Large ribosomal subunit protein eL33A.

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

- Molecule 36 is a protein called Large ribosomal subunit protein eL34A.

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

- Molecule 37 is a protein called Large ribosomal subunit protein uL29A.

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

- Molecule 38 is a protein called Large ribosomal subunit protein eL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 39 is a protein called Large ribosomal subunit protein eL37A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	81	Total	C	N	O	S	0	0
			645	393	141	106	5		

- Molecule 40 is a protein called Large ribosomal subunit protein eL38.

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

- Molecule 41 is a protein called Large ribosomal subunit protein eL39.

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

- Molecule 42 is a protein called Large ribosomal subunit protein eL40A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	52	Total	C	N	O	S	0	0
			410	254	86	65	5		

- Molecule 43 is a protein called Large ribosomal subunit protein eL41A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	25	Total	C	N	O	S	0	0
			229	139	62	27	1		

- Molecule 44 is a protein called Large ribosomal subunit protein eL42A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 45 is a protein called Large ribosomal subunit protein eL43A.

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

- Molecule 46 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	s	75	Total	C	N	O	P	0	0
			1605	716	297	517	75		
46	t	75	Total	C	N	O	P	0	0
			1606	716	297	518	75		

- Molecule 47 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	x	842	Total	C	N	O	S	0	0
			6559	4166	1124	1238	31		

- Molecule 48 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SD	121	Total	C	N	O	S	0	0
			875	551	153	169	2		

- Molecule 49 is a protein called Small ribosomal subunit protein uS11B.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SZ	127	Total	C	N	O	S	0	0
			891	545	182	163	1		

- Molecule 50 is a protein called Small ribosomal subunit protein eS26A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Se	94	Total	C	N	O	S	0	0
			750	462	157	126	5		

- Molecule 51 is a protein called Small ribosomal subunit protein eS10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SC	92	Total	C	N	O	S	0	0
			752	487	122	141	2		

- Molecule 52 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SE	117	Total	C	N	O	S	0	0
			916	583	171	155	7		

- Molecule 53 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SA	222	Total	C	N	O	S	0	0
			1729	1098	312	313	6		

- Molecule 54 is a protein called Small ribosomal subunit protein eS19A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SI	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 55 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SJ	100	Total	C	N	O	S	0	0
			797	506	144	146	1		

- Molecule 56 is a protein called Small ribosomal subunit protein eS28A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SL	63	Total	C	N	O	S	0	0
			491	303	96	91	1		

- Molecule 57 is a protein called Small ribosomal subunit protein uS14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SM	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 58 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SB	206	Total	C	N	O	S	0	0
			1605	1005	299	298	3		

- Molecule 59 is a protein called Small ribosomal subunit protein uS9A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SF	141	Total	C	N	O	S	0	0
			1105	708	203	194			

- Molecule 60 is a protein called Small ribosomal subunit protein uS13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SH	145	Total	C	N	O	S	0	0
			1188	741	237	208	2		

- Molecule 61 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SO	304	Total	C	N	O	S	0	0
			2326	1477	401	440	8		

- Molecule 62 is a protein called Small ribosomal subunit protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SN	73	Total	C	N	O	S	0	0
			560	355	106	95	4		

- Molecule 63 is a protein called Small ribosomal subunit protein eS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SG	121	Total	C	N	O	S	0	0
			961	599	182	178	2		

- Molecule 64 is a protein called Small ribosomal subunit protein uS2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SP	206	Total	C	N	O	S	0	0
			1603	1030	284	287	2		

- Molecule 65 is a protein called Small ribosomal subunit protein eS1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SQ	226	Total	C	N	O	S	0	0
			1798	1139	330	325	4		

- Molecule 66 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SR	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		

- Molecule 67 is a protein called Small ribosomal subunit protein eS4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SS	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		

- Molecule 68 is a protein called Small ribosomal subunit protein eS6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	ST	228	Total	C	N	O	S	0	0
			1815	1138	351	323	3		

- Molecule 69 is a protein called Small ribosomal subunit protein eS7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SU	184	Total	C	N	O		0	0
			1473	946	263	264			

- Molecule 70 is a protein called Small ribosomal subunit protein eS8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SV	187	Total	C	N	O	S	0	0
			1476	916	295	263	2		

- Molecule 71 is a protein called Small ribosomal subunit protein uS4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SW	184	Total	C	N	O	S	0	0
			1479	935	285	258	1		

- Molecule 72 is a protein called Small ribosomal subunit protein uS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SX	142	Total	C	N	O	S	0	0
			1142	733	217	189	3		

- Molecule 73 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SY	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 74 is a protein called Small ribosomal subunit protein eS21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sa	87	Total	C	N	O	S	0	0
			673	415	125	131	2		

- Molecule 75 is a protein called Small ribosomal subunit protein uS8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Sb	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 76 is a protein called Small ribosomal subunit protein uS12A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sc	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 77 is a protein called Small ribosomal subunit protein eS24A.

Mol	Chain	Residues	Atoms				AltConf	Trace
77	Sd	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 78 is a protein called Small ribosomal subunit protein eS27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sf	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 79 is a protein called Small ribosomal subunit protein eS30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sg	60	Total	C	N	O	S	0	0
			472	298	97	76	1		

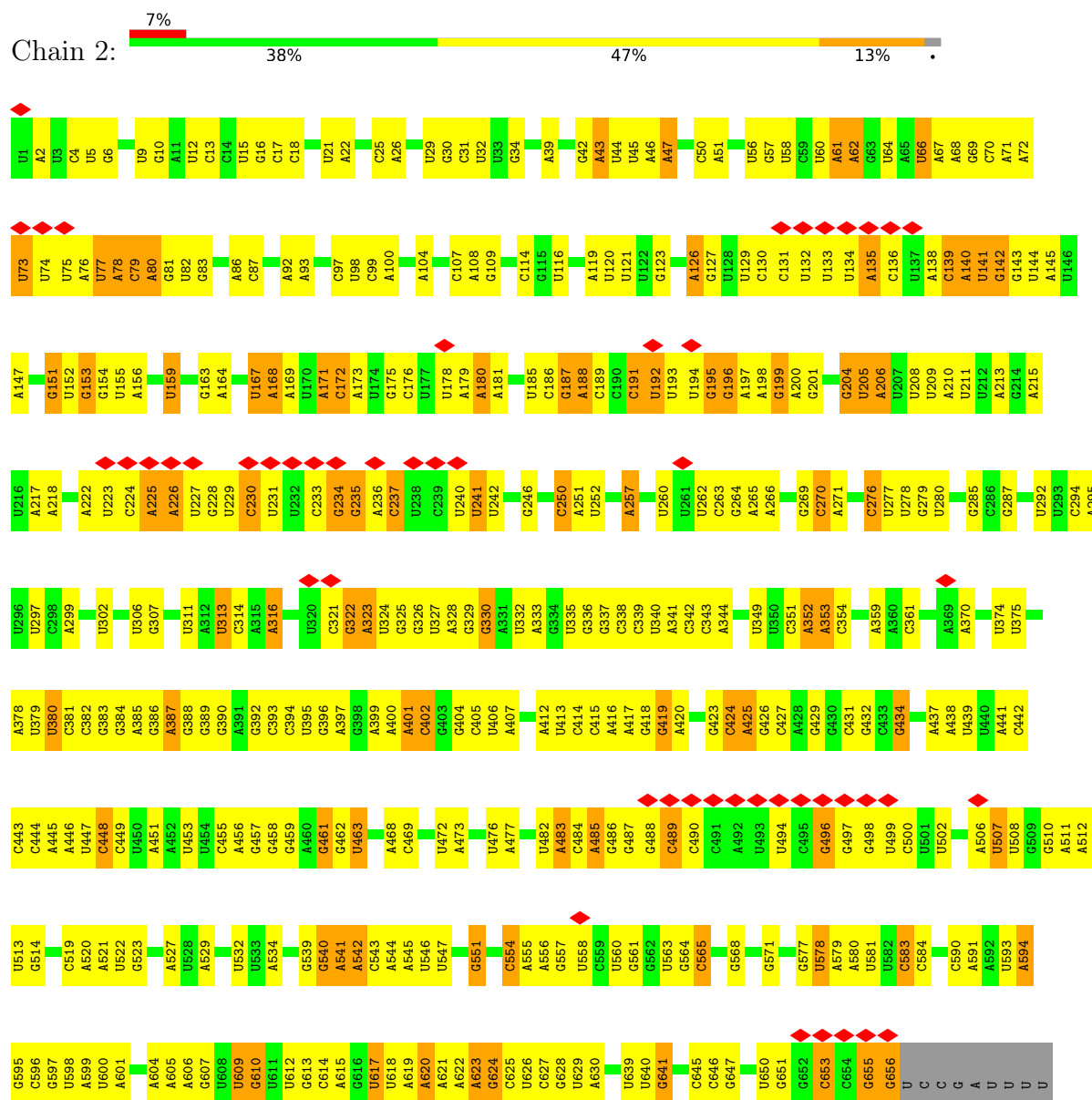
- Molecule 80 is a protein called Small ribosomal subunit protein eS25A.

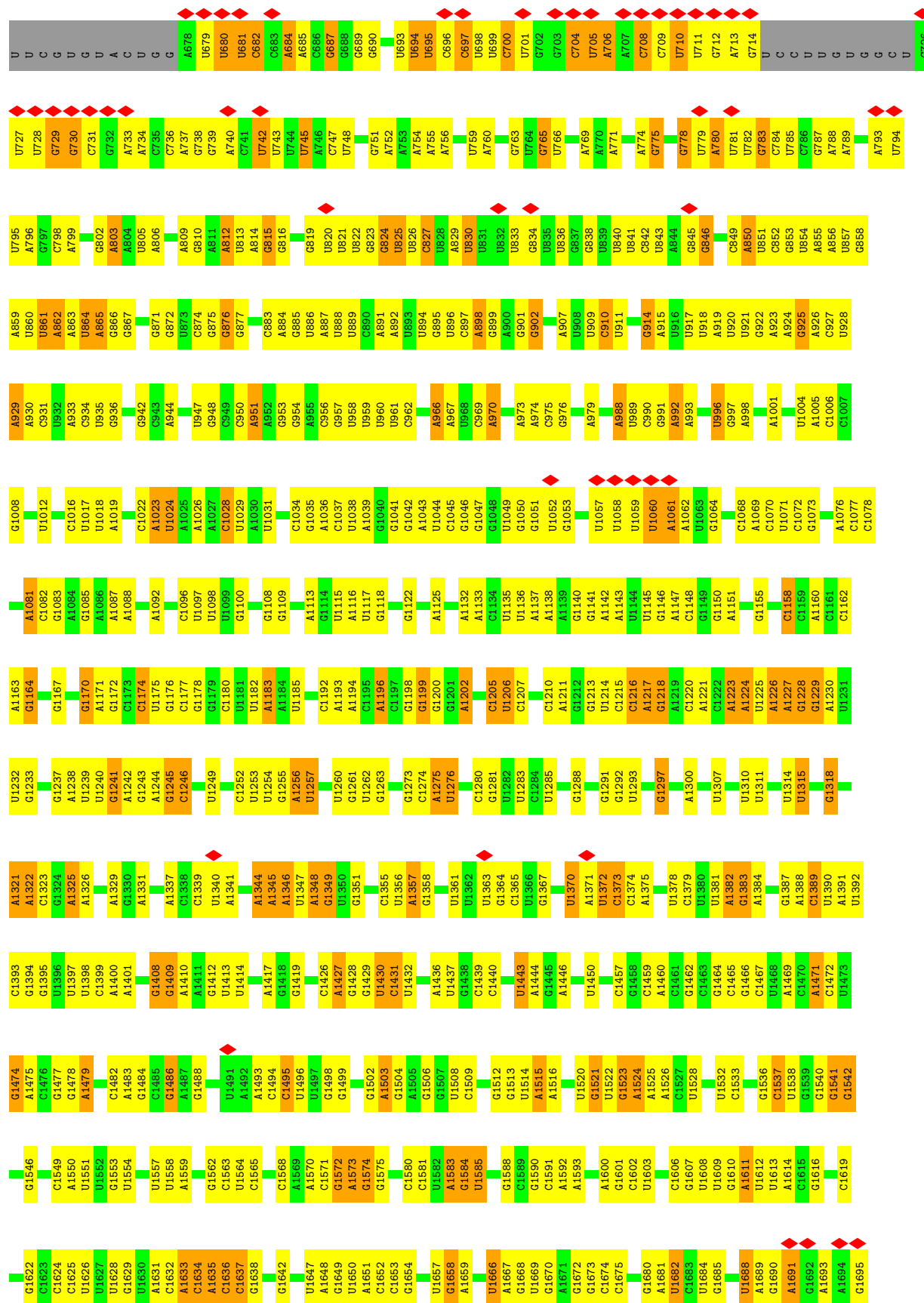
Mol	Chain	Residues	Atoms					AltConf	Trace
80	SK	103	Total	C	N	O	S	0	0
			810	514	151	143	2		

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.

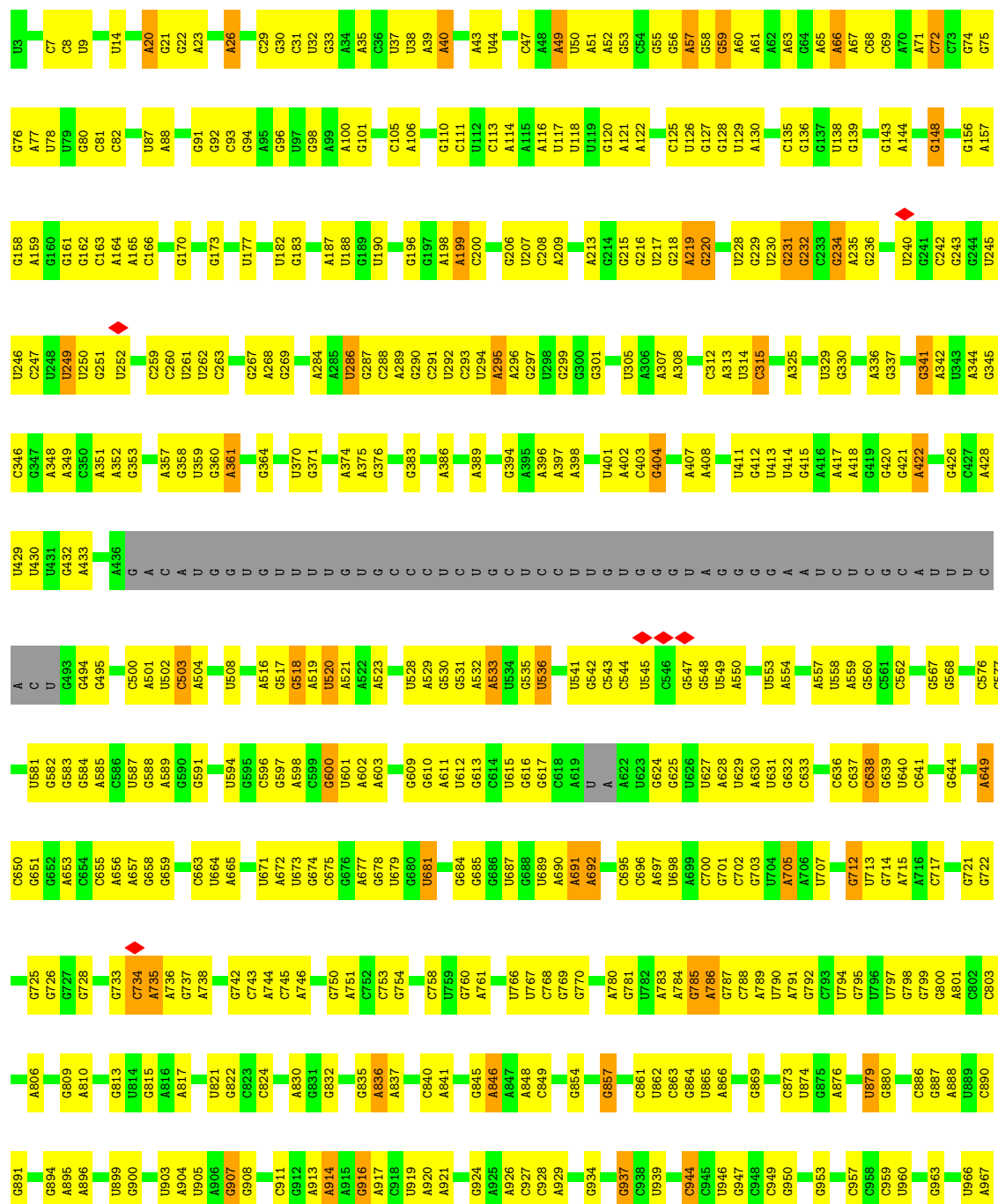
• Molecule 1: 18S rRNA





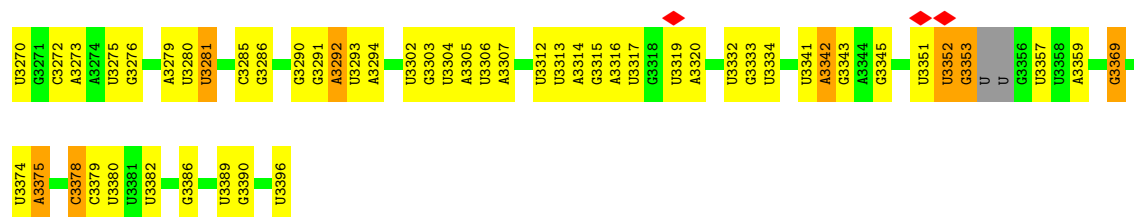
- Molecule 2: 25S rRNA

Chain A:

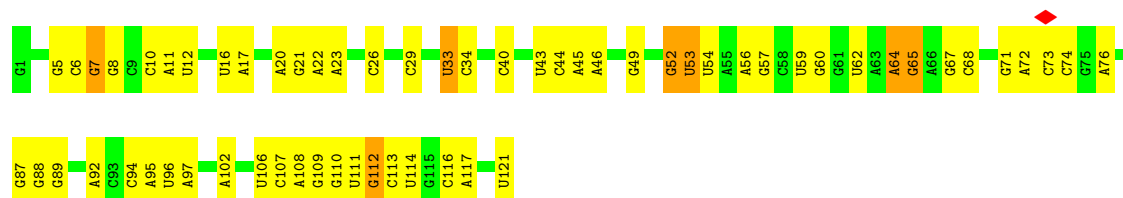




U3195	C2114	C2855	C3682	G2440	U2499	G2575	A2673	A2769	U2860	G2961	A3040	C3117	U3195
U3196	G2115	U2285	A2363	G2441	A2500	G2576	A2674	G2770	U2866	U2962	U3041	C3118	U3196
U3198	A2117	U2287	C2364	A2442	U2501	G2577	A2678	U2771	C2867	G2963	U3042	C3119	G3197
C3201	C2118	C2288	C2366	G2443	G2502	G2578	C2682	C2772	U2868	G2964	G3045	U3121	U3198
C3202	G2122	U2289	A2367	A2444	U2503	G2579	U2683	G2773	G2871	A2967	A3046	A3122	C3201
C3203	C2204	C2290	A2368	C2445	U2504	G2584	C2684	G2774	A2872	C2968	U3047	C3126	G3202
C3204	U2205	A2291	C2369	U2446	U2505	G2585	C2685	A2775	U2873	A2969	A3048	A3127	U3203
U2129	G2130	A2296	G2370	U2447	U2506	G2586	A2686	G2776	G2877	C2970	U3049	C3128	C3204
A2131	A2206	A2207	A2372	A2448	C2507	U2588	G2687	U2782	G2878	A2971	U3050	A3129	G3205
U2137	A2208	U2209	C2374	G2449	U2510	U2589	U2688	G2786	G2879	U2975	U3051	A3130	C3206
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			G2333	C2470	A2531	U2633	U2710	C2812	U2889	C3004	C3083	C3162	C3233
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			C2336	G2473	A2534	G2636	U2713	C2815	A2932	H3007	C3086	U3169	U3238
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			C2338	C2475	A2536	U2638	U2715	G2817	U2934	G3009	C3088	A3171	A3243
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			U2357	U2493	A2556	U2668	U2735	U2837	U2954	A3032			
			A2358	U2494	A2557	U2669	U2736	C2838	U2955	C3033			
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			U2365	U2501	A2564		U2743	U2845	U2962				
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			C2413	U2549	A2612		U2791	U2893	C3019				
			U2414	U2550	A2613		U2792	U2894	C3020				
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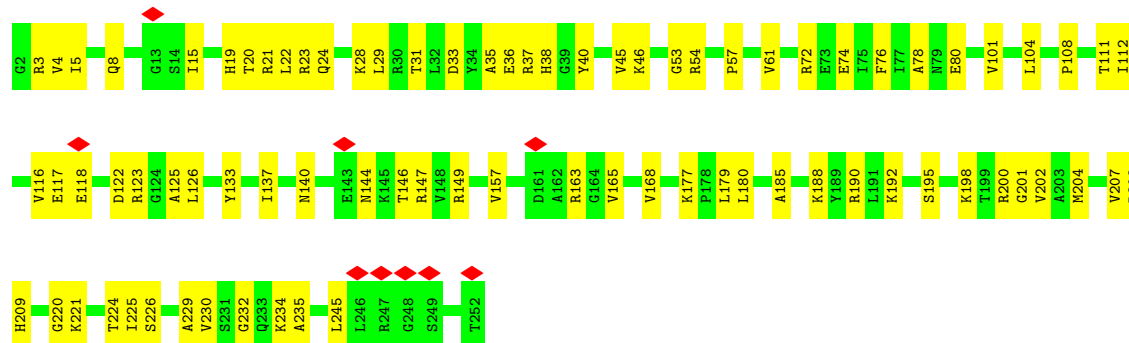
• Molecule 3: 5S rRNA



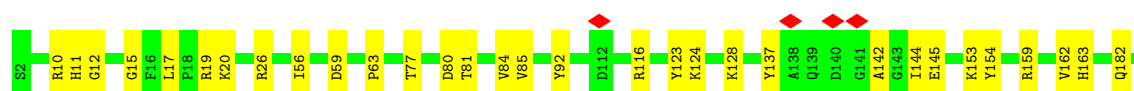
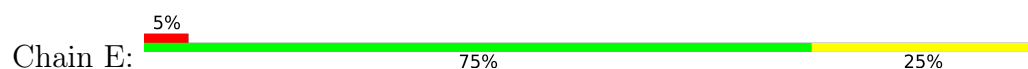
• Molecule 4: 5.8S rRNA

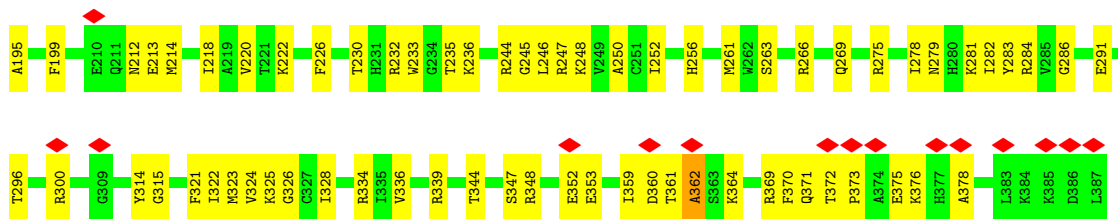


• Molecule 5: Large ribosomal subunit protein uL2A

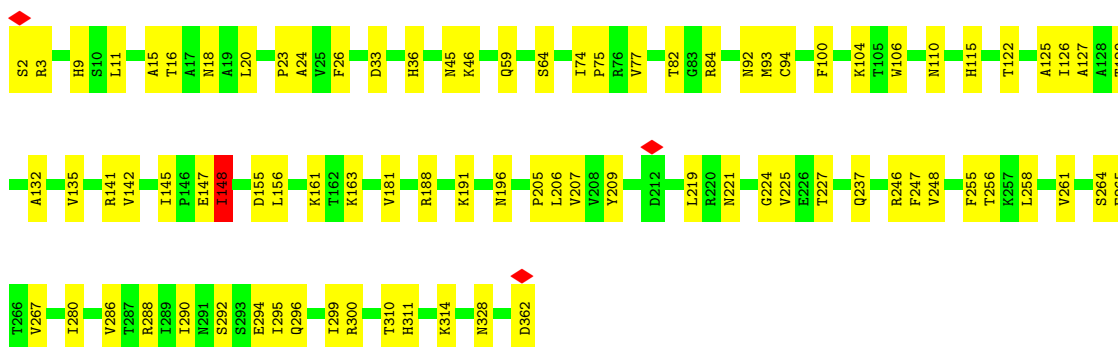
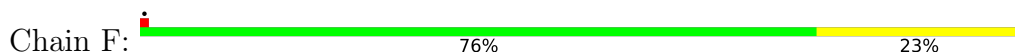


• Molecule 6: Large ribosomal subunit protein uL3

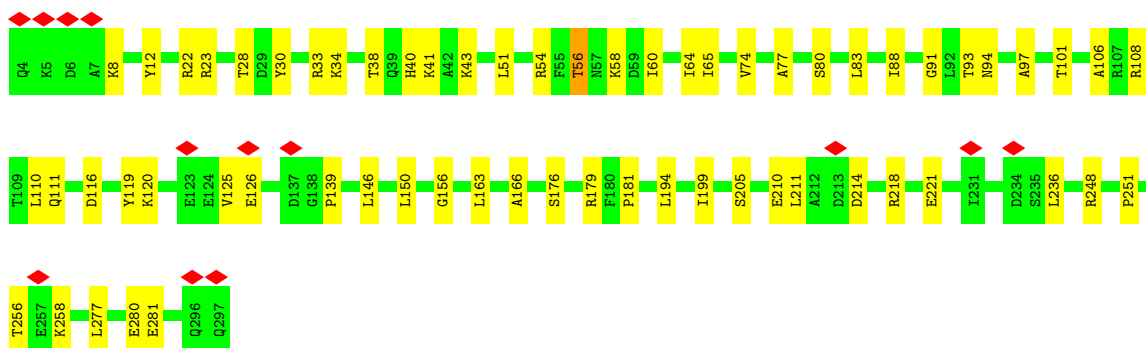
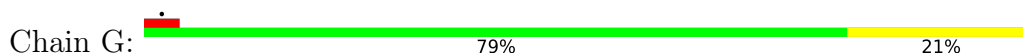




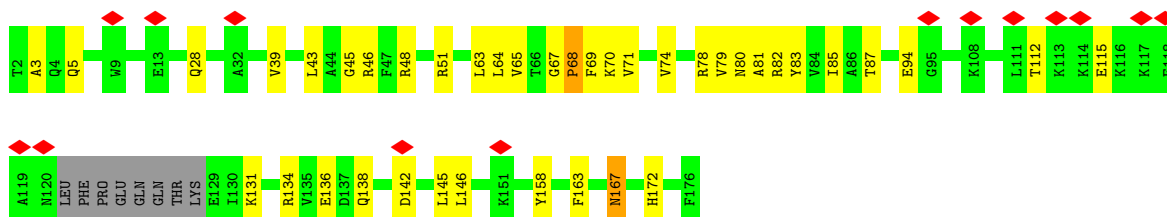
- Molecule 7: Large ribosomal subunit protein uL4A



- Molecule 8: Large ribosomal subunit protein uL18

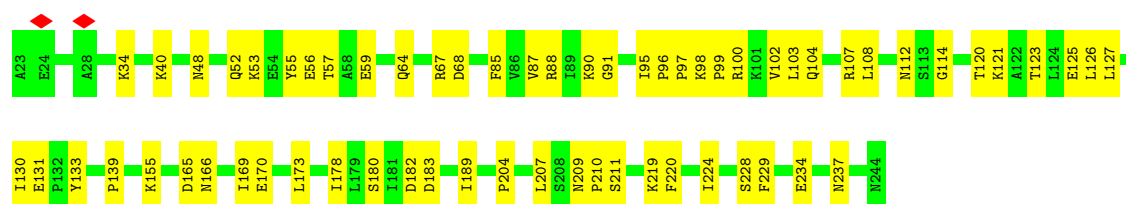


- Molecule 9: Large ribosomal subunit protein eL6B



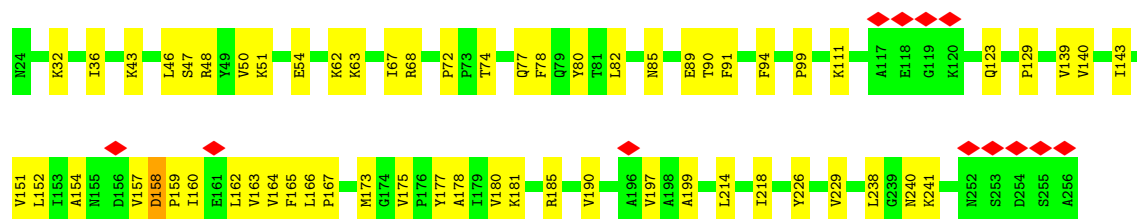
- Molecule 10: Large ribosomal subunit protein uL30A

Chain I:  72% 28%



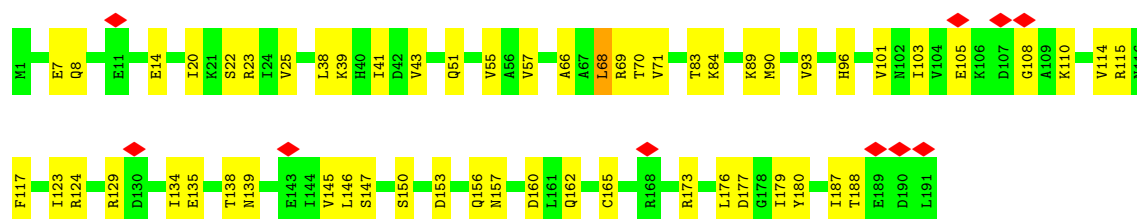
- Molecule 11: Large ribosomal subunit protein eL8A

Chain J:  5% 74% 26%



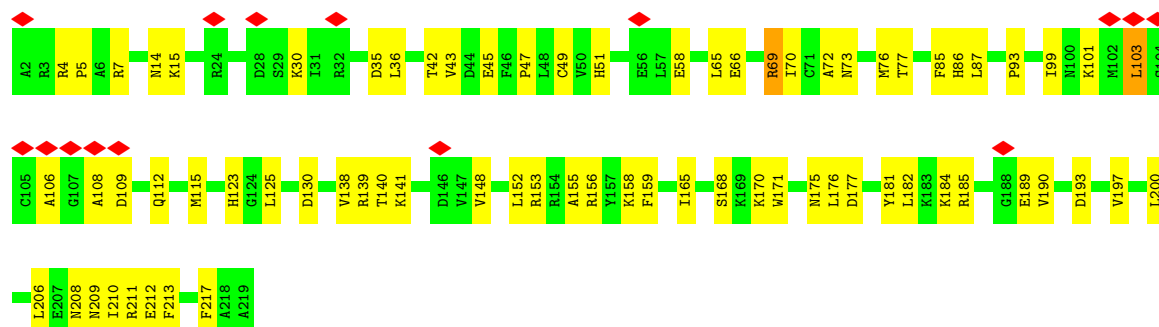
- Molecule 12: Large ribosomal subunit protein uL6A

Chain K:  5% 70% 29%



- Molecule 13: Large ribosomal subunit protein uL16

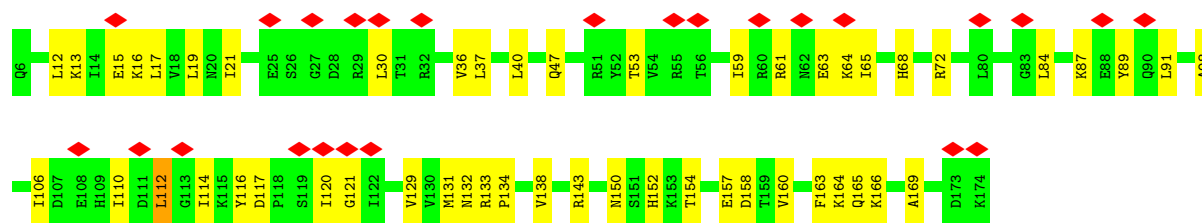
Chain L:  7% 67% 33%



- Molecule 14: Large ribosomal subunit protein uL5B

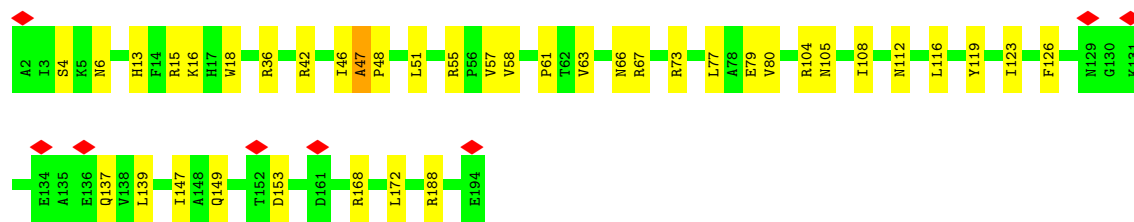
Chain M:  15% 70% 30%





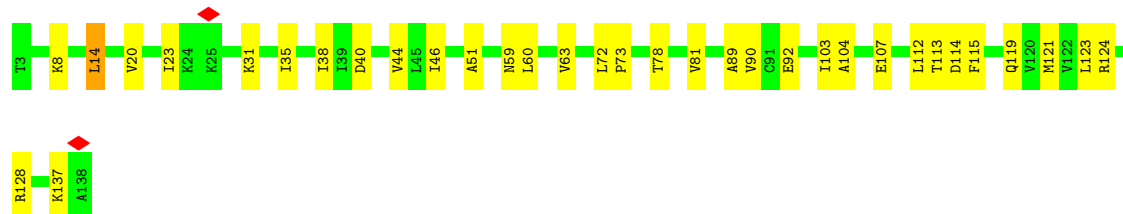
- Molecule 15: Large ribosomal subunit protein eL13A

Chain N: 80% 20%



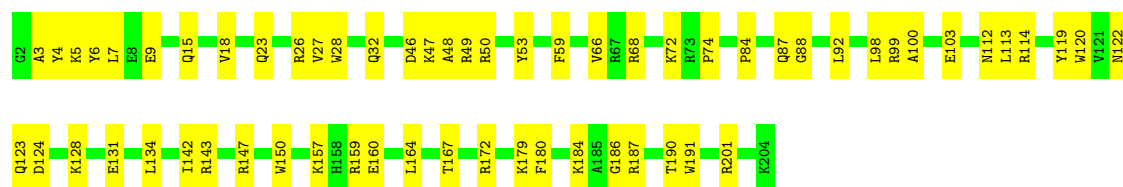
- Molecule 16: Large ribosomal subunit protein eL14A

Chain O: 75% 24%



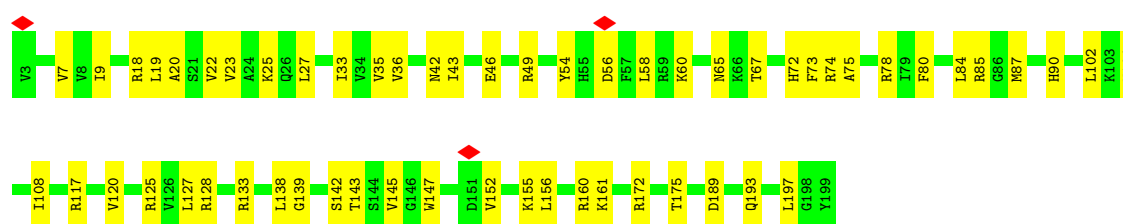
- Molecule 17: Large ribosomal subunit protein eL15A

Chain P: 70% 30%

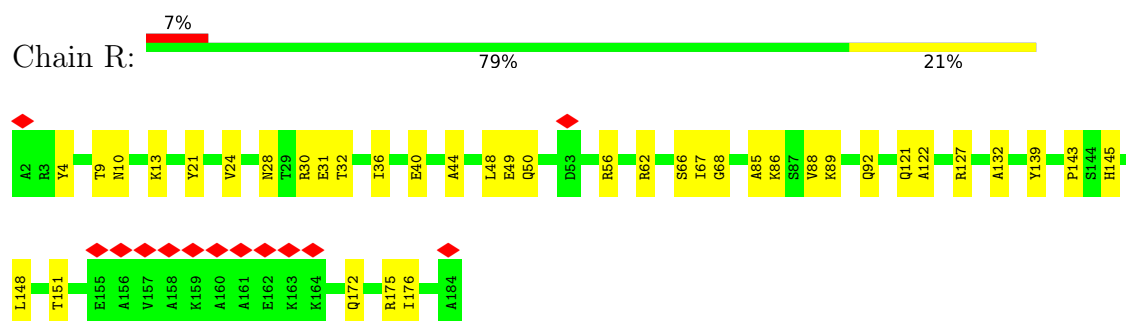


- Molecule 18: Large ribosomal subunit protein uL13A

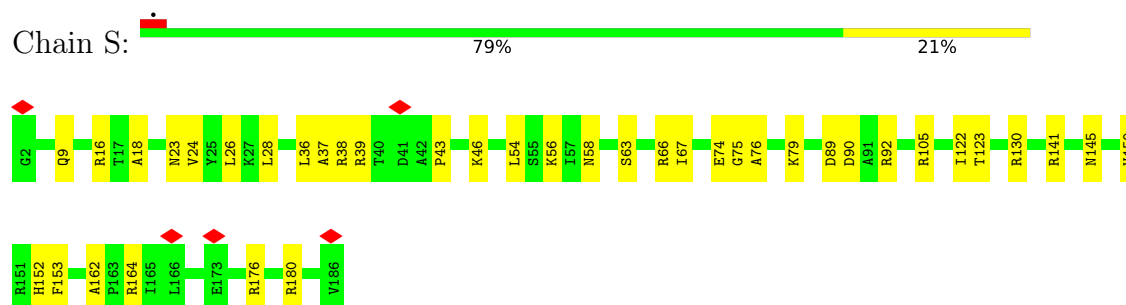
Chain Q: 71% 29%



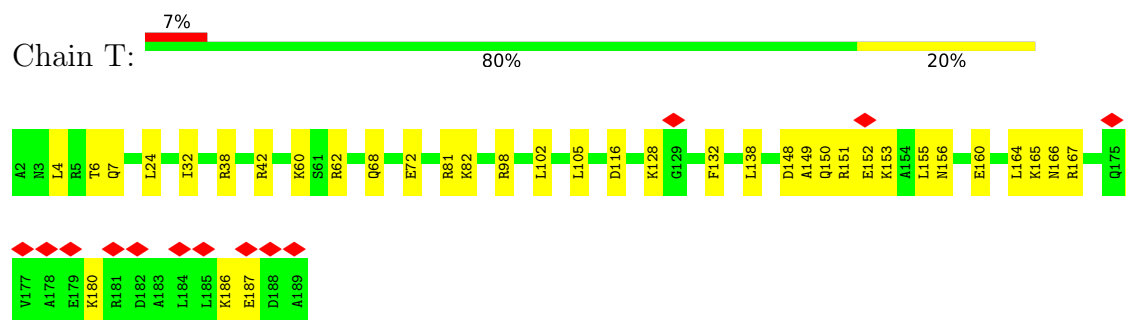
- Molecule 19: Large ribosomal subunit protein uL22A



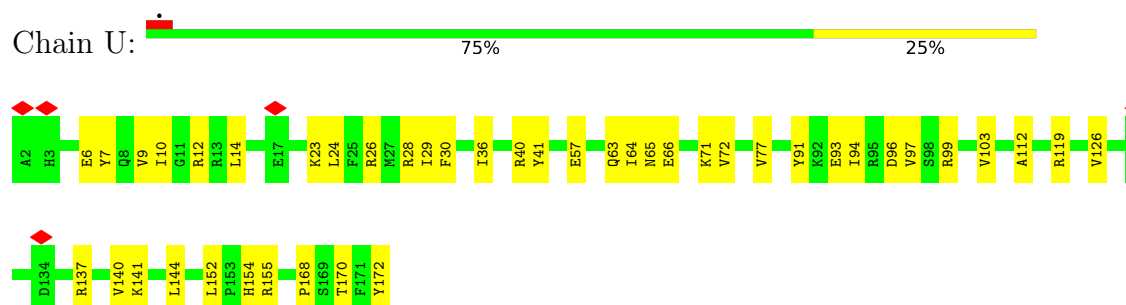
- Molecule 20: Large ribosomal subunit protein eL18A



- Molecule 21: Large ribosomal subunit protein eL19A

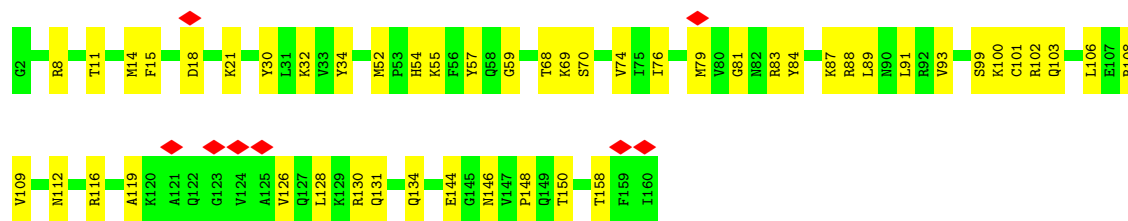


- Molecule 22: Large ribosomal subunit protein eL20A



- Molecule 23: Large ribosomal subunit protein eL21A

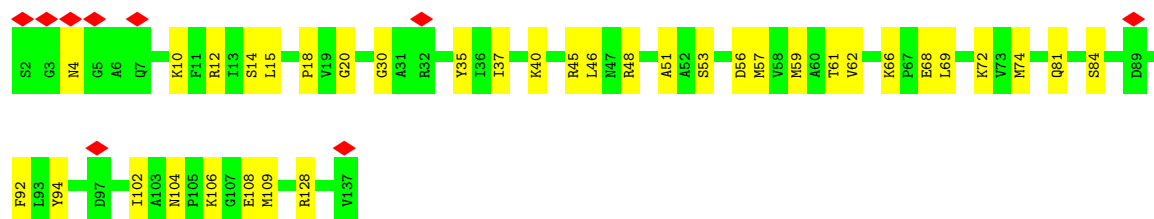
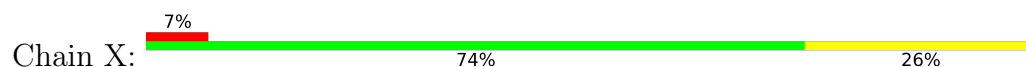




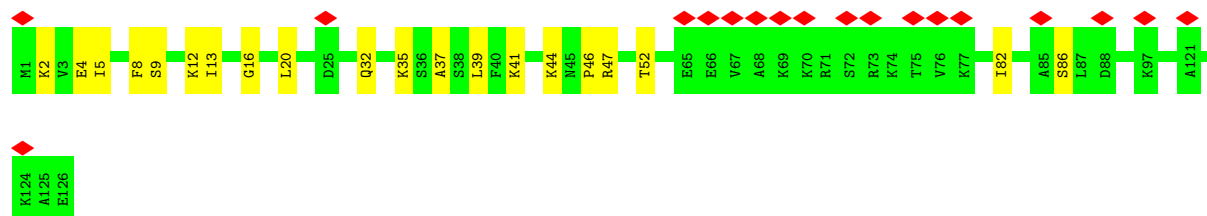
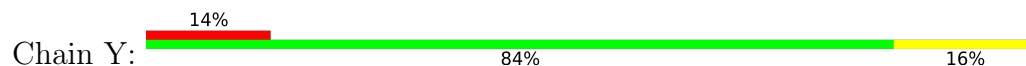
- Molecule 24: Large ribosomal subunit protein eL22A



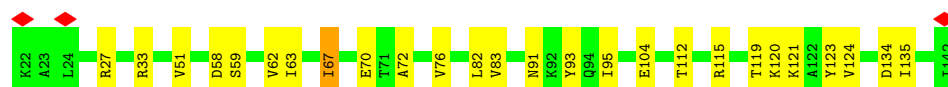
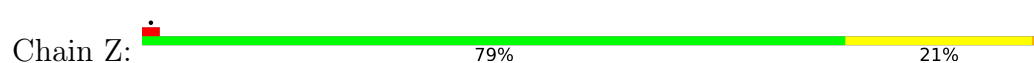
- Molecule 25: Large ribosomal subunit protein uL14A



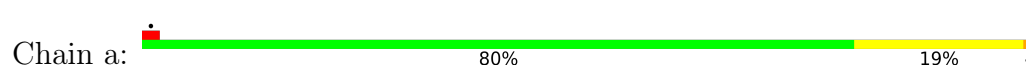
- Molecule 26: Large ribosomal subunit protein eL24A



- Molecule 27: Large ribosomal subunit protein uL23

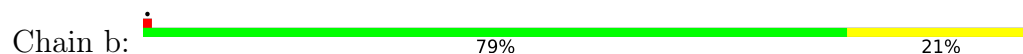


- Molecule 28: Large ribosomal subunit protein uL24A





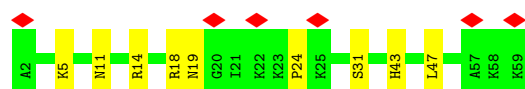
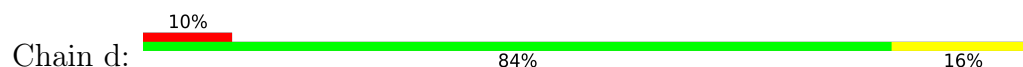
- Molecule 29: Large ribosomal subunit protein eL27A



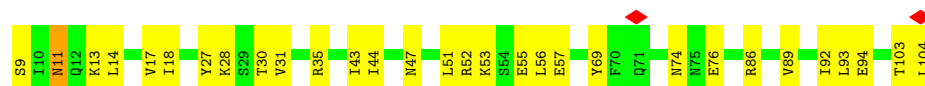
- Molecule 30: Large ribosomal subunit protein uL15



- Molecule 31: Large ribosomal subunit protein eL29



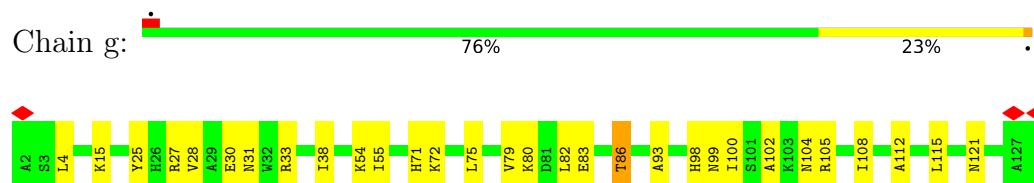
- Molecule 32: Large ribosomal subunit protein eL30



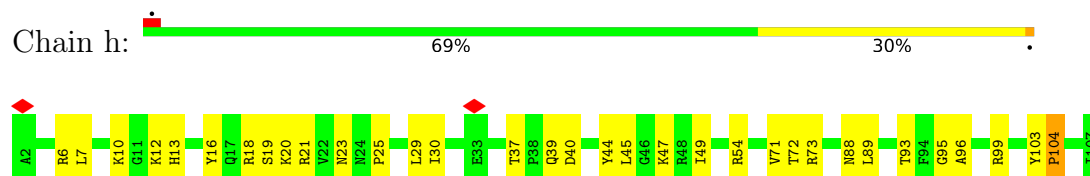
- Molecule 33: Large ribosomal subunit protein eL31A



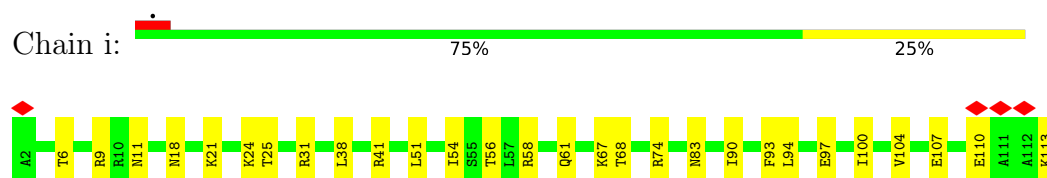
- Molecule 34: Large ribosomal subunit protein eL32



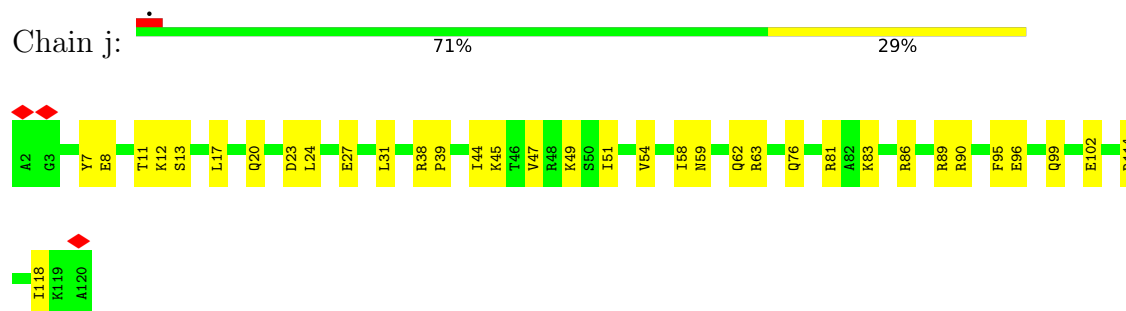
- Molecule 35: Large ribosomal subunit protein eL33A



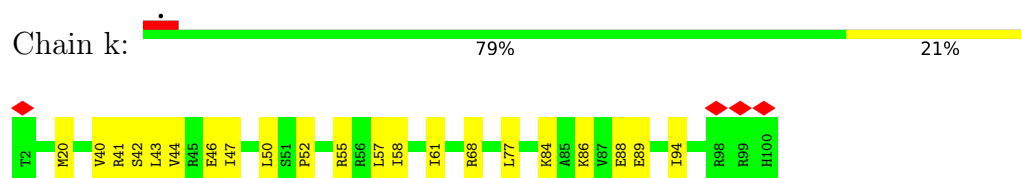
- Molecule 36: Large ribosomal subunit protein eL34A



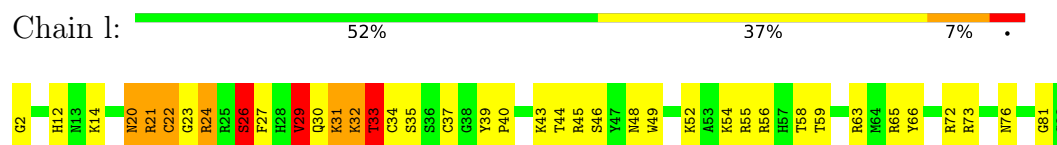
- Molecule 37: Large ribosomal subunit protein uL29A



- Molecule 38: Large ribosomal subunit protein eL36A



- Molecule 39: Large ribosomal subunit protein eL37A

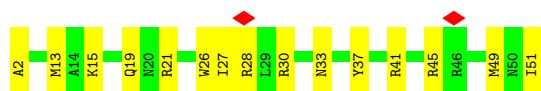


- Molecule 40: Large ribosomal subunit protein eL38





- Molecule 41: Large ribosomal subunit protein eL39



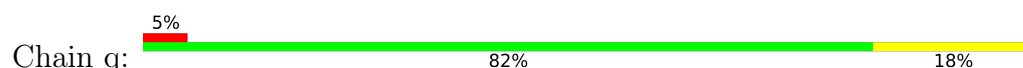
- Molecule 42: Large ribosomal subunit protein eL40A



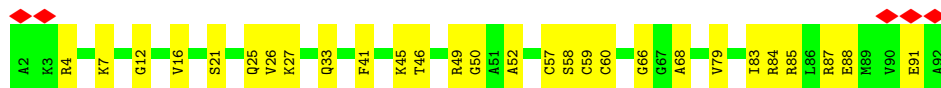
- Molecule 43: Large ribosomal subunit protein eL41A



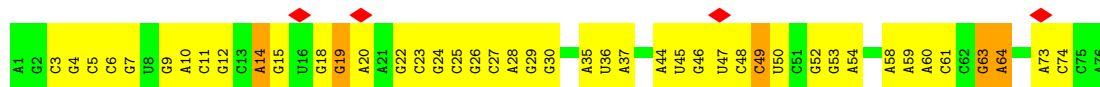
- Molecule 44: Large ribosomal subunit protein eL42A



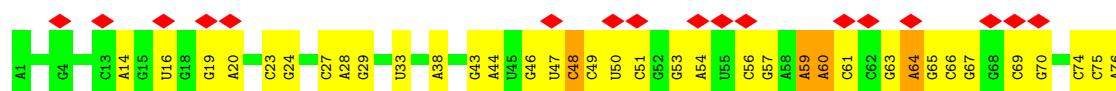
- Molecule 45: Large ribosomal subunit protein eL43A



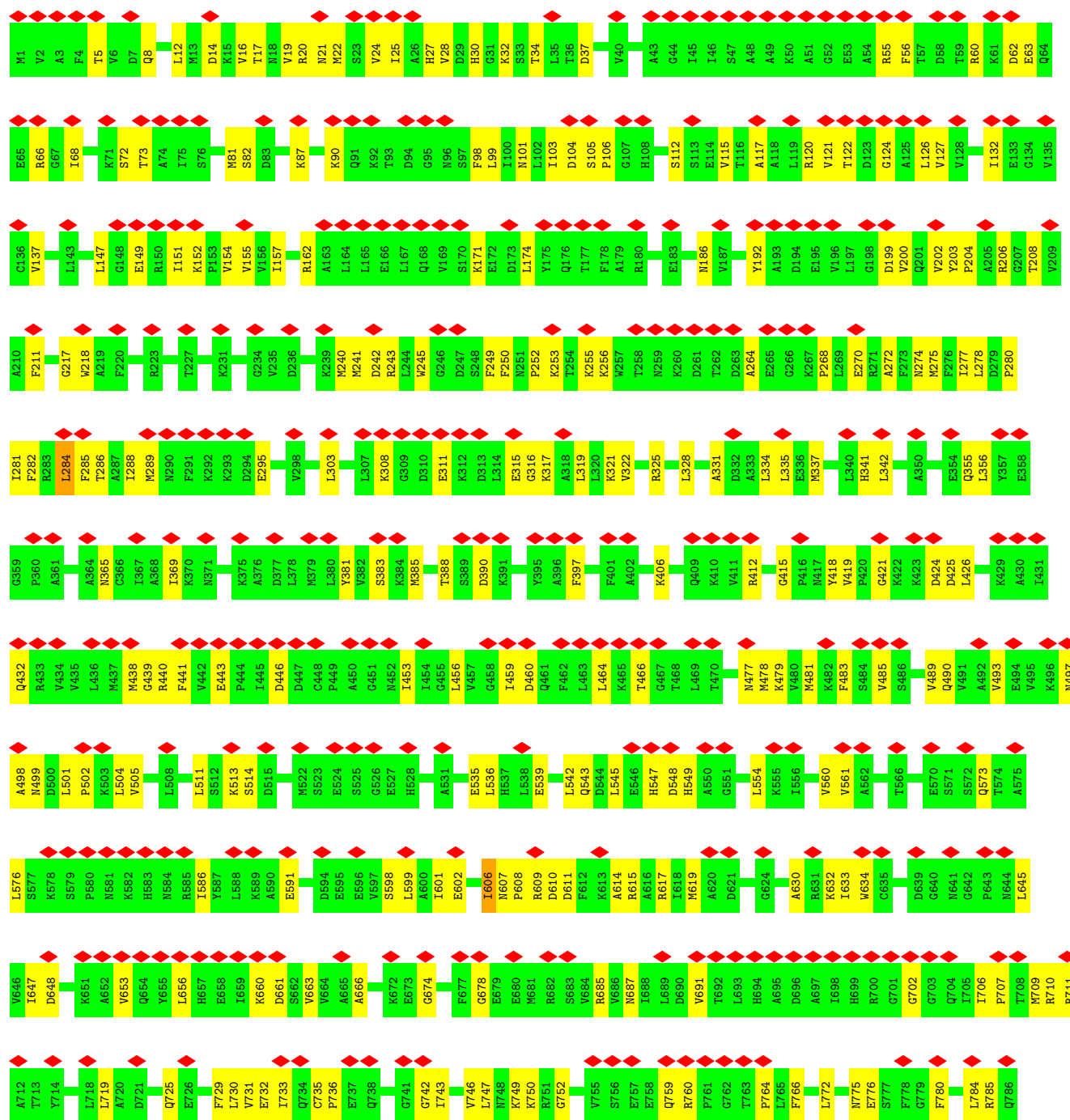
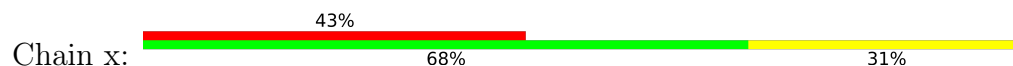
- Molecule 46: tRNA

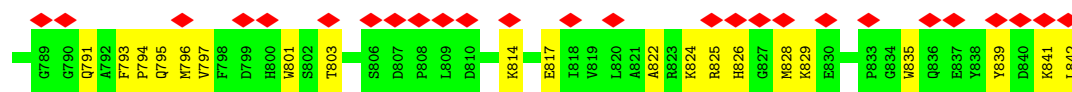


- Molecule 46: tRNA

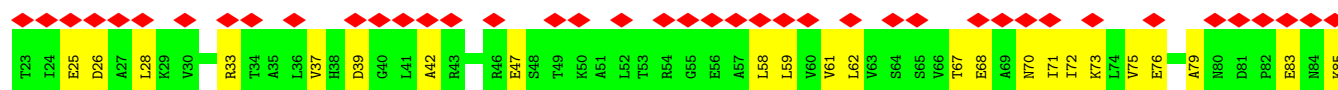
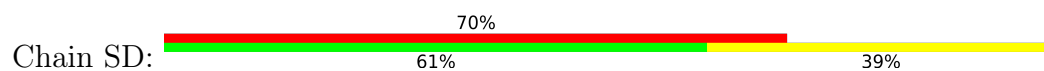


• Molecule 47: Elongation factor 2

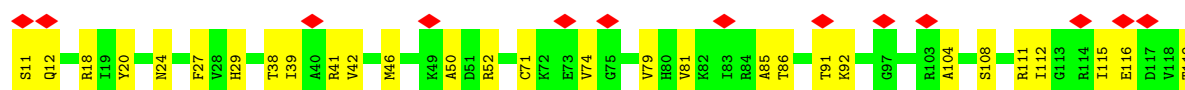
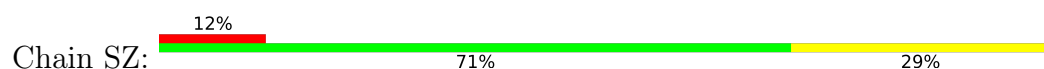




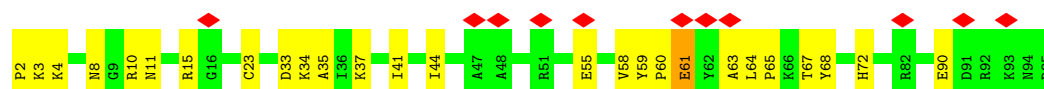
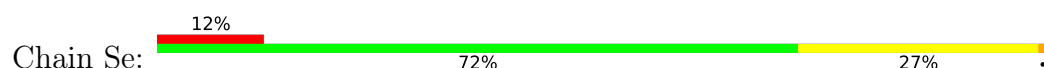
- Molecule 48: Small ribosomal subunit protein eS12



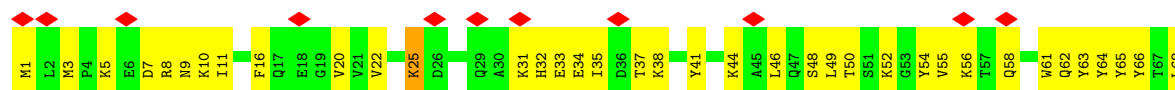
- Molecule 49: Small ribosomal subunit protein uS11B



- Molecule 50: Small ribosomal subunit protein eS26A

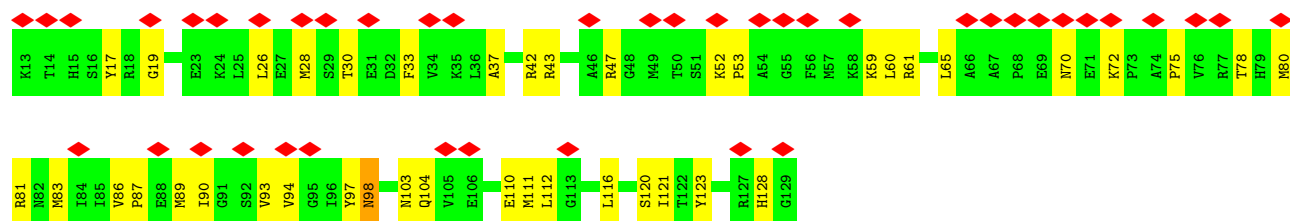


- Molecule 51: Small ribosomal subunit protein eS10A

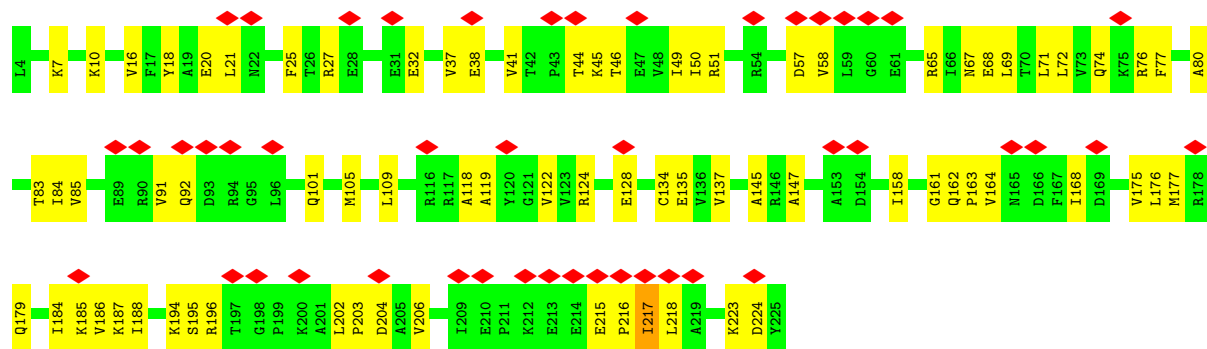


- Molecule 52: Small ribosomal subunit protein uS19

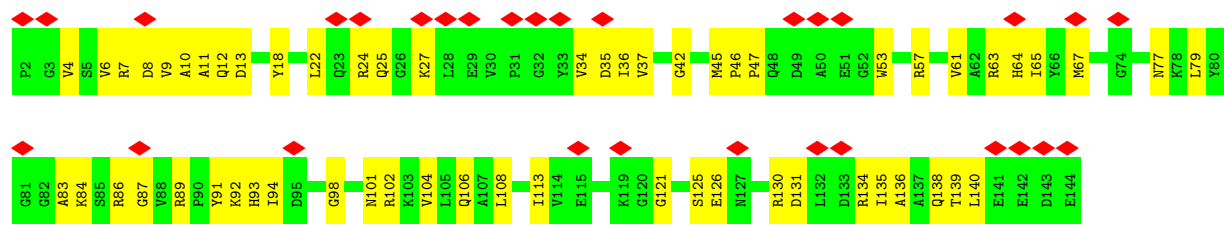




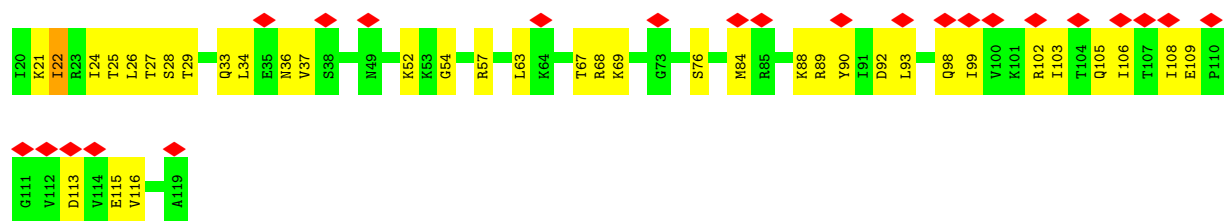
• Molecule 53: Small ribosomal subunit protein uS3



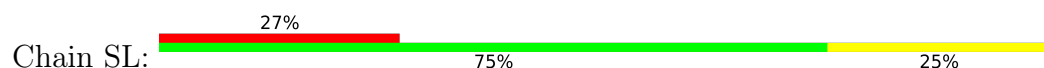
• Molecule 54: Small ribosomal subunit protein eS19A

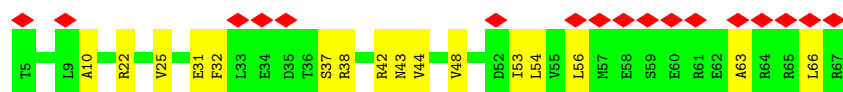


• Molecule 55: Small ribosomal subunit protein uS10

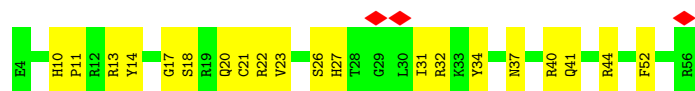


• Molecule 56: Small ribosomal subunit protein eS28A

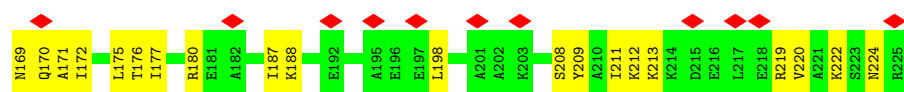
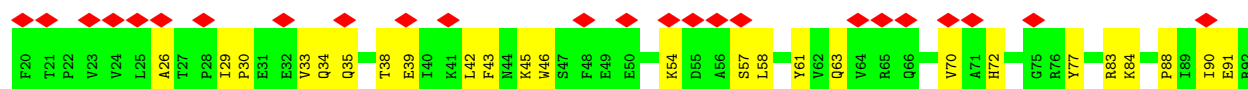




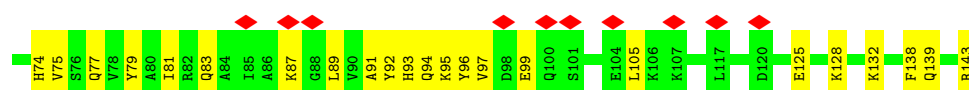
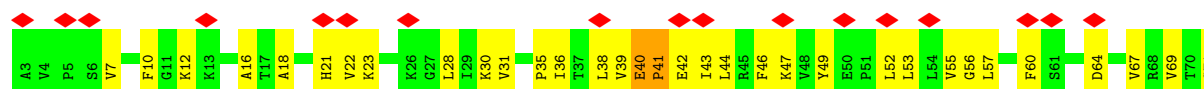
- Molecule 57: Small ribosomal subunit protein uS14A



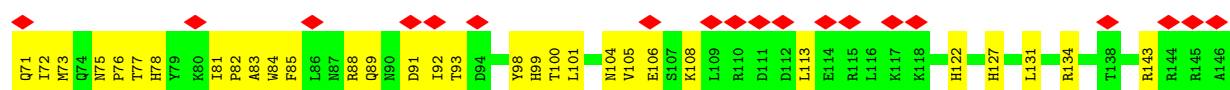
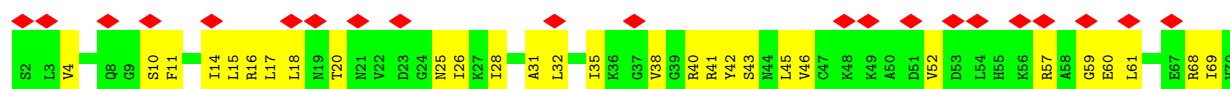
- Molecule 58: Small ribosomal subunit protein uS7



- Molecule 59: Small ribosomal subunit protein uS9A

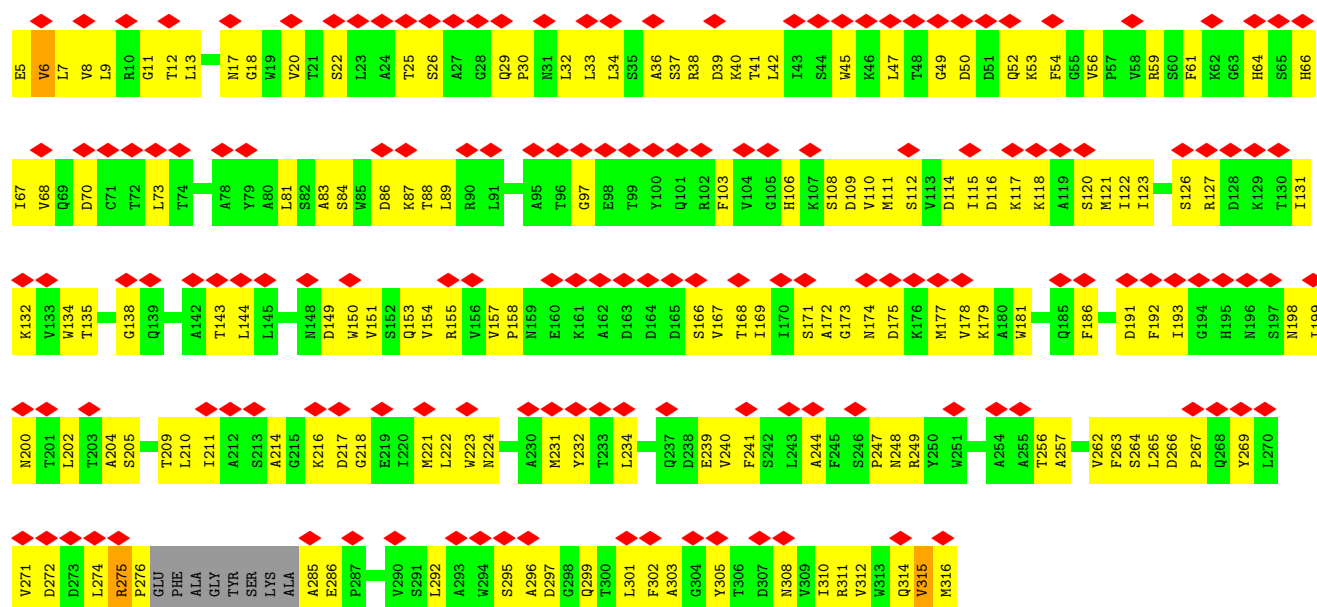


- Molecule 60: Small ribosomal subunit protein uS13A



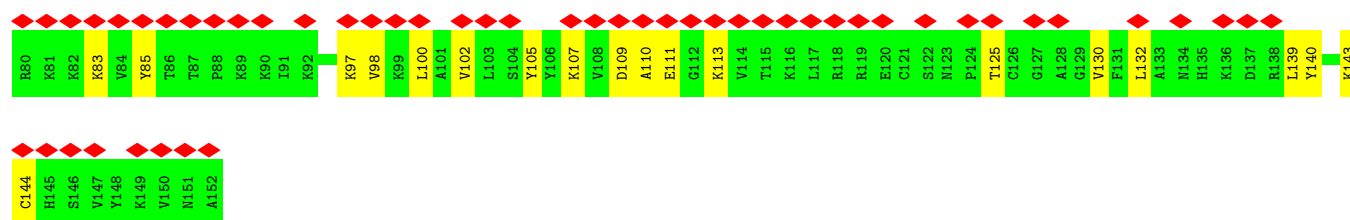
- Molecule 61: Small ribosomal subunit protein RACK1

Chain SO: 



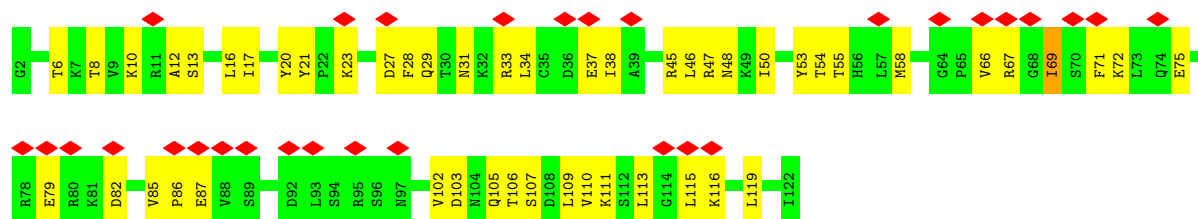
• Molecule 62: Small ribosomal subunit protein eS31

Chain SN: 



• Molecule 63: Small ribosomal subunit protein eS17A

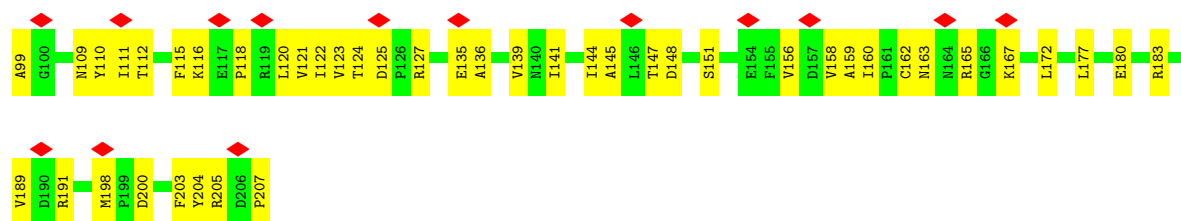
Chain SG: 



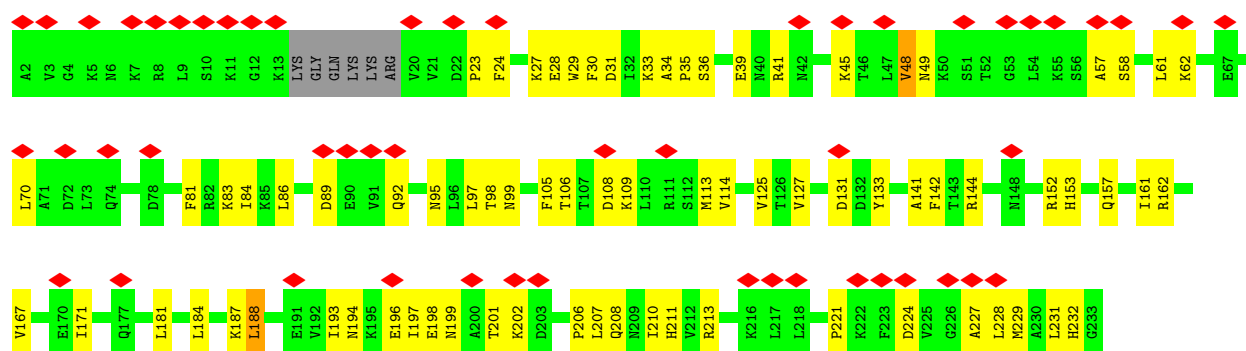
• Molecule 64: Small ribosomal subunit protein uS2A

Chain SP: 

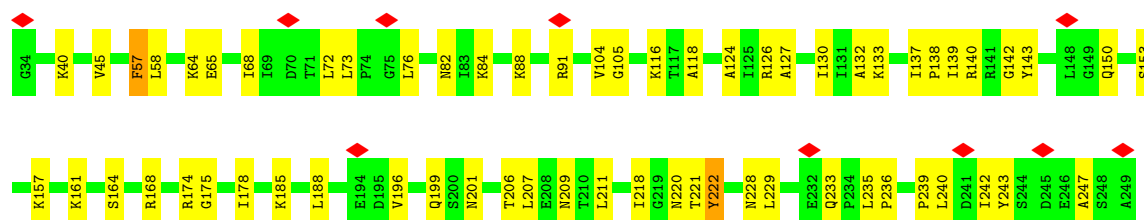
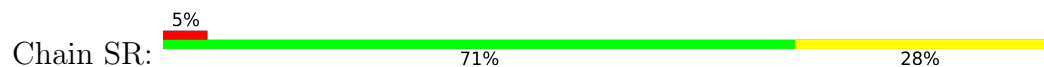




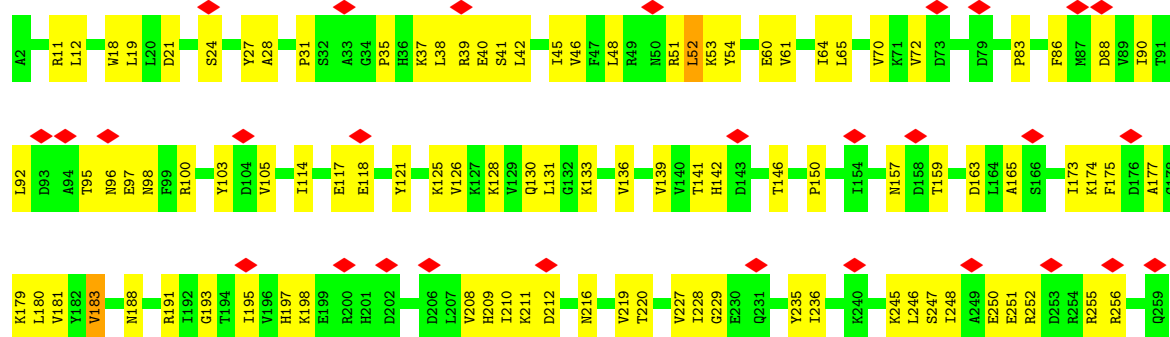
- Molecule 65: Small ribosomal subunit protein eS1A



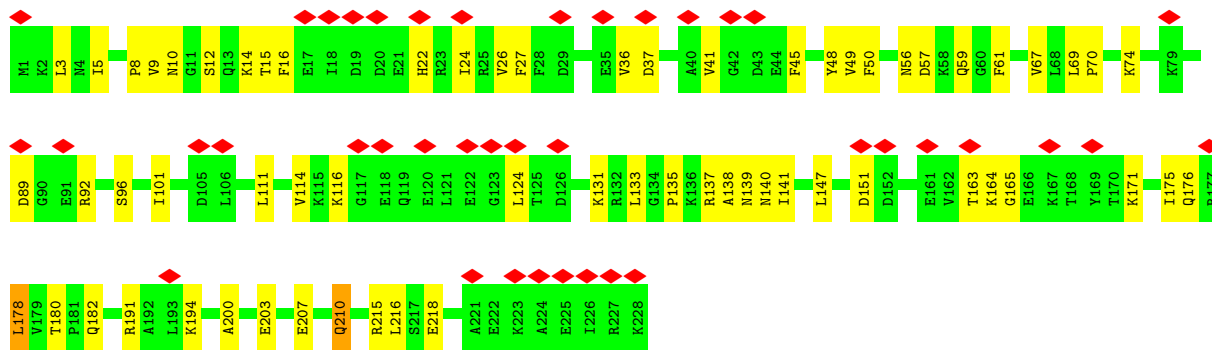
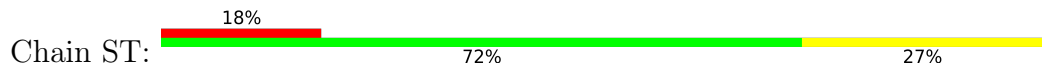
- Molecule 66: Small ribosomal subunit protein uS5



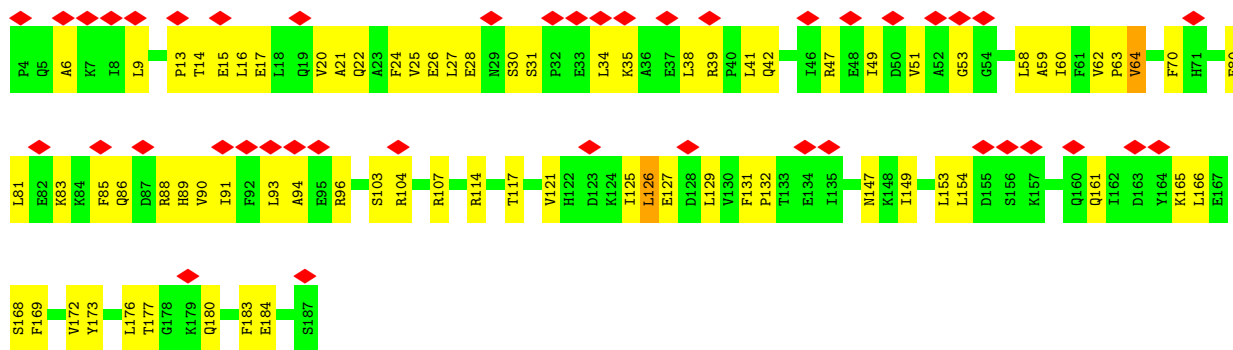
- Molecule 67: Small ribosomal subunit protein eS4A



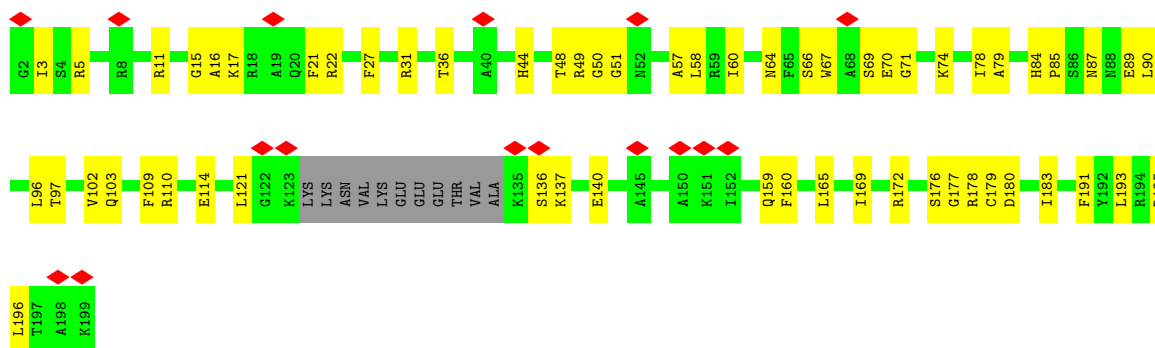
- Molecule 68: Small ribosomal subunit protein eS6A



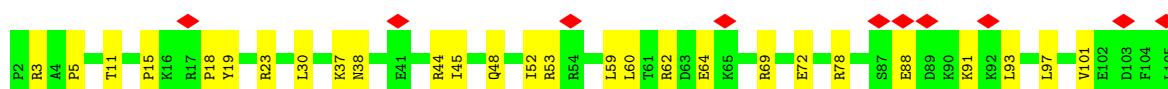
• Molecule 69: Small ribosomal subunit protein eS7A

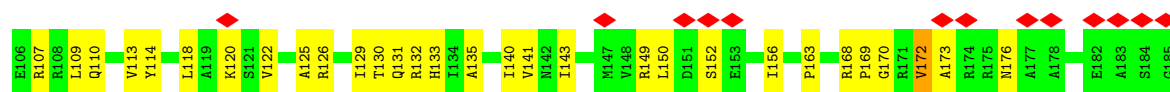


• Molecule 70: Small ribosomal subunit protein eS8A

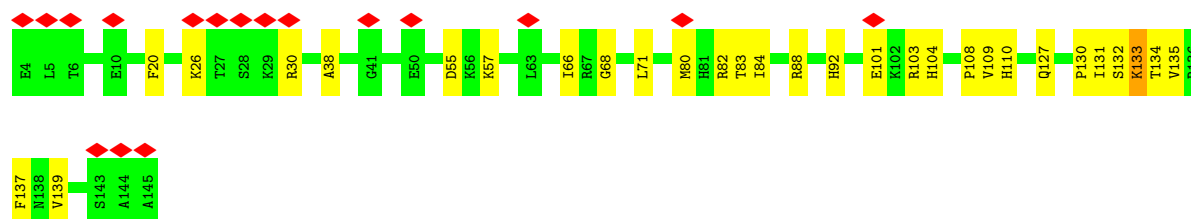
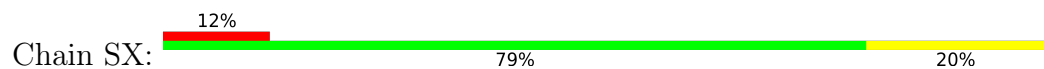


• Molecule 71: Small ribosomal subunit protein uS4A

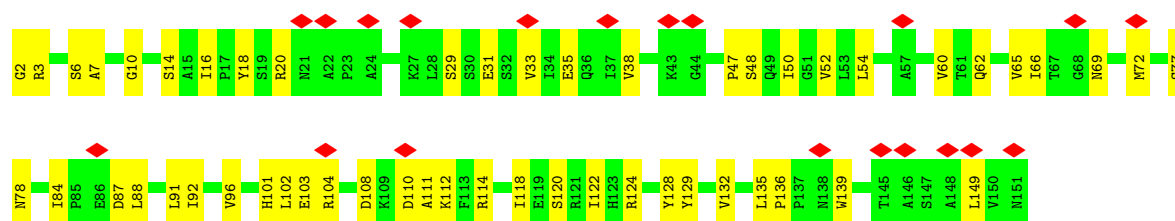




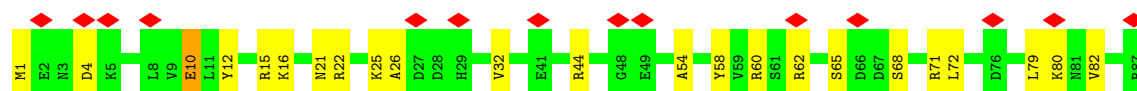
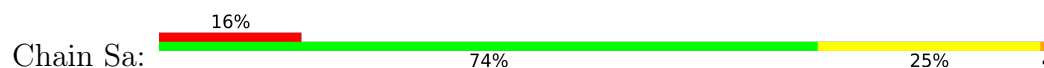
- Molecule 72: Small ribosomal subunit protein uS17A



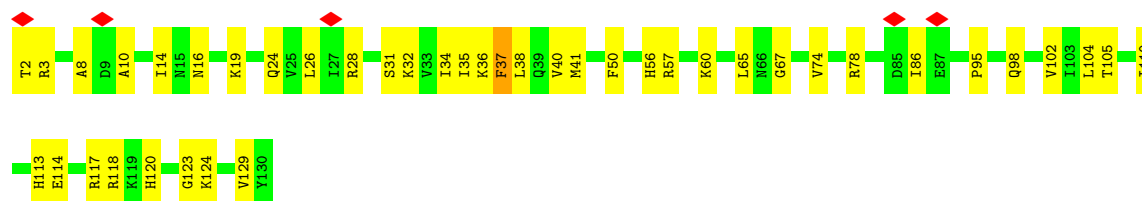
- Molecule 73: Small ribosomal subunit protein uS15



- Molecule 74: Small ribosomal subunit protein eS21A

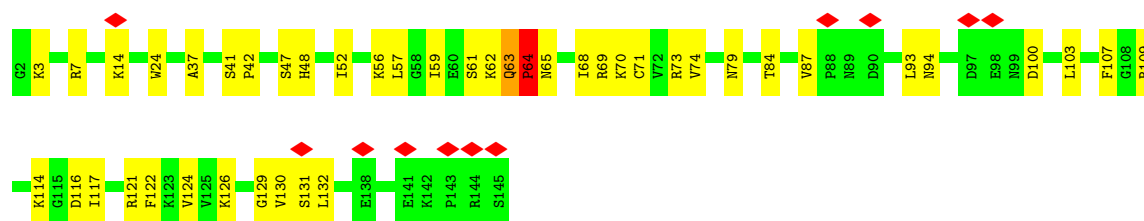


- Molecule 75: Small ribosomal subunit protein uS8A

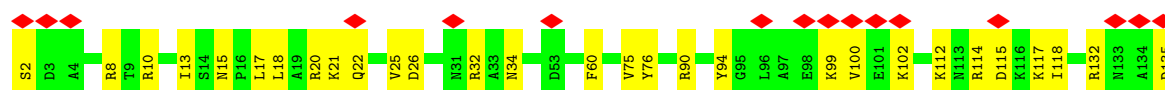
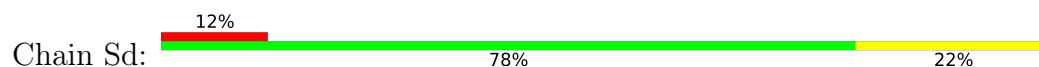


- Molecule 76: Small ribosomal subunit protein uS12A

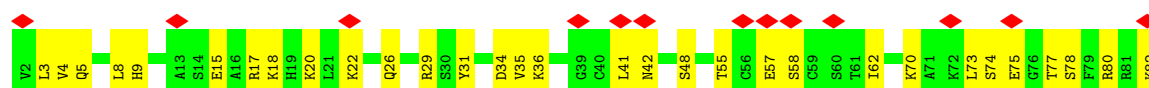




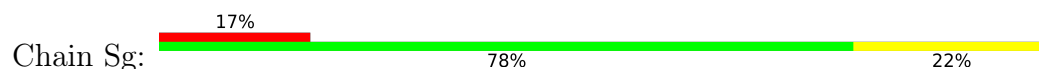
- Molecule 77: Small ribosomal subunit protein eS24A



- Molecule 78: Small ribosomal subunit protein eS27A



- Molecule 79: Small ribosomal subunit protein eS30A



- Molecule 80: Small ribosomal subunit protein eS25A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	39857	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	1.933	Depositor
Minimum map value	-0.938	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.086	Depositor
Recommended contour level	0.295	Depositor
Map size ($\text{\AA}$)	528.0, 528.0, 528.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.32, 1.32, 1.32	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	2	0.09	0/42115	0.24	0/65623
2	A	0.08	0/76357	0.20	0/119043
3	B	0.07	0/2883	0.21	0/4491
4	C	0.09	0/3746	0.21	0/5832
5	D	0.13	0/1933	0.29	0/2598
6	E	0.10	0/3146	0.30	0/4228
7	F	0.19	2/2800 (0.1%)	0.30	0/3790
8	G	0.13	0/2400	0.34	1/3239 (0.0%)
9	H	0.14	0/1329	0.33	0/1794
10	I	0.15	0/1821	0.35	0/2451
11	J	0.12	0/1836	0.32	0/2481
12	K	0.13	0/1529	0.29	0/2060
13	L	0.17	0/1801	0.40	0/2416
14	M	0.13	0/1367	0.33	0/1834
15	N	0.11	0/1568	0.28	0/2106
16	O	0.16	0/1068	0.34	0/1438
17	P	0.13	0/1757	0.27	0/2354
18	Q	0.15	0/1585	0.34	0/2128
19	R	0.09	0/1439	0.27	0/1938
20	S	0.25	0/1465	0.34	0/1965
21	T	0.13	0/1532	0.29	0/2043
22	U	0.10	0/1473	0.27	0/1980
23	V	0.14	0/1296	0.33	0/1739
24	W	0.15	0/812	0.39	0/1099
25	X	0.08	0/1018	0.23	0/1369
26	Y	0.11	0/850	0.28	0/1152
27	Z	0.13	0/979	0.32	0/1321
28	a	0.10	0/995	0.25	0/1329
29	b	0.16	0/1106	0.36	0/1485
30	c	0.09	0/1200	0.24	0/1607
31	d	0.12	0/473	0.32	0/629
32	e	0.15	0/745	0.38	0/1001
33	f	0.12	0/890	0.29	0/1196
34	g	0.09	0/1034	0.24	0/1385

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	h	0.15	0/868	0.37	0/1168
36	i	0.10	0/890	0.24	0/1189
37	j	0.20	0/978	0.32	0/1301
38	k	0.12	0/772	0.35	0/1026
39	l	0.65	0/660	0.59	1/875 (0.1%)
40	m	0.13	0/618	0.36	0/826
41	n	0.09	0/443	0.29	0/588
42	o	0.14	0/416	0.30	0/553
43	p	0.08	0/230	0.17	0/296
44	q	0.12	0/836	0.30	0/1104
45	r	0.11	0/701	0.29	0/934
46	s	0.07	0/1795	0.19	0/2797
46	t	0.09	0/1796	0.21	0/2799
47	x	0.17	0/6685	0.46	2/9050 (0.0%)
48	SD	0.16	0/883	0.47	0/1199
49	SZ	0.16	0/901	0.45	0/1217
50	Se	0.15	0/761	0.43	0/1016
51	SC	0.30	0/769	0.50	0/1039
52	SE	0.22	0/936	0.46	0/1259
53	SA	0.19	0/1754	0.42	0/2361
54	SI	0.26	0/1130	0.50	0/1517
55	SJ	0.17	0/807	0.42	0/1091
56	SL	0.13	0/493	0.34	0/663
57	SM	0.12	0/452	0.28	0/600
58	SB	0.15	0/1625	0.40	0/2197
59	SF	0.23	0/1125	0.50	2/1510 (0.1%)
60	SH	0.19	0/1207	0.49	0/1623
61	SO	0.22	0/2376	0.51	1/3235 (0.0%)
62	SN	0.16	0/571	0.48	0/768
63	SG	0.17	0/971	0.46	0/1303
64	SP	0.15	0/1644	0.35	0/2249
65	SQ	0.14	0/1823	0.39	0/2447
66	SR	0.15	0/1656	0.36	0/2251
67	SS	0.16	0/2097	0.41	0/2823
68	ST	0.14	0/1839	0.31	0/2460
69	SU	0.21	0/1498	0.47	0/2019
70	SV	0.12	0/1501	0.33	0/2006
71	SW	0.14	0/1504	0.33	0/2016
72	SX	0.11	0/1168	0.32	0/1575
73	SY	0.14	0/1215	0.35	0/1638
74	Sa	0.16	0/682	0.42	0/921
75	Sb	0.18	0/1038	0.40	0/1395
76	Sc	0.18	0/1139	0.45	0/1518

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
77	Sd	0.14	0/1087	0.34	0/1449
78	Sf	0.10	0/620	0.30	0/838
79	Sg	0.13	0/480	0.35	0/639
80	SK	0.13	0/821	0.36	0/1096
All	All	0.13	2/224609 (0.0%)	0.28	7/329588 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	F	147	GLU	C-N	-7.01	1.25	1.33
7	F	148	ILE	C-N	5.26	1.44	1.34

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	SF	41	PRO	N-CA-C	7.62	123.75	113.84
8	G	251	PRO	CA-N-CD	-5.77	103.92	112.00
61	SO	265	LEU	CB-CA-C	-5.58	110.13	116.54
59	SF	41	PRO	CB-CA-C	-5.34	104.27	111.85
47	x	606	ILE	CA-C-N	5.15	127.80	120.49

There are no chirality outliers.

There are no planarity outliers.

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	2	37653	0	18945	747	0
2	A	68216	0	34282	1149	0
3	B	2579	0	1304	47	0
4	C	3353	0	1695	64	0
5	D	1899	0	1957	72	0
6	E	3075	0	3142	81	0
7	F	2748	0	2859	64	0
8	G	2351	0	2294	49	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	H	1307	0	1377	29	0
10	I	1784	0	1862	50	0
11	J	1804	0	1877	47	0
12	K	1508	0	1572	44	0
13	L	1764	0	1804	56	0
14	M	1346	0	1370	36	0
15	N	1543	0	1608	34	0
16	O	1053	0	1149	32	0
17	P	1720	0	1779	53	0
18	Q	1555	0	1659	45	0
19	R	1416	0	1433	26	0
20	S	1441	0	1543	34	0
21	T	1515	0	1606	35	0
22	U	1437	0	1475	34	0
23	V	1272	0	1312	38	0
24	W	796	0	812	19	0
25	X	1003	0	1048	28	0
26	Y	836	0	706	15	0
27	Z	964	0	1025	19	0
28	a	984	0	1075	20	0
29	b	1080	0	1122	28	0
30	c	1169	0	1211	37	0
31	d	462	0	491	8	0
32	e	737	0	792	22	0
33	f	876	0	912	24	0
34	g	1013	0	1077	25	0
35	h	850	0	880	32	0
36	i	880	0	945	23	0
37	j	969	0	1078	24	0
38	k	766	0	844	18	0
39	l	645	0	649	43	0
40	m	612	0	682	17	0
41	n	436	0	475	10	0
42	o	410	0	446	14	0
43	p	229	0	273	7	0
44	q	824	0	892	25	0
45	r	694	0	738	26	0
46	s	1605	0	816	34	0
46	t	1606	0	816	20	0
47	x	6559	0	6627	203	0
48	SD	875	0	878	39	0
49	SZ	891	0	883	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	Se	750	0	799	20	0
51	SC	752	0	719	47	0
52	SE	916	0	941	38	0
53	SA	1729	0	1812	61	0
54	SI	1112	0	1124	66	0
55	SJ	797	0	863	40	0
56	SL	491	0	524	12	0
57	SM	442	0	432	17	0
58	SB	1605	0	1669	58	0
59	SF	1105	0	1166	58	0
60	SH	1188	0	1218	59	0
61	SO	2326	0	2287	152	0
62	SN	560	0	560	19	0
63	SG	961	0	999	41	0
64	SP	1603	0	1610	68	0
65	SQ	1798	0	1890	56	0
66	SR	1626	0	1715	53	0
67	SS	2056	0	2140	81	0
68	ST	1815	0	1894	58	0
69	SU	1473	0	1555	68	0
70	SV	1476	0	1501	50	0
71	SW	1479	0	1556	44	0
72	SX	1142	0	1209	24	0
73	SY	1192	0	1255	41	0
74	Sa	673	0	662	29	0
75	Sb	1021	0	1060	41	0
76	Sc	1121	0	1196	40	0
77	Sd	1073	0	1132	23	0
78	Sf	610	0	633	28	0
79	Sg	472	0	521	13	0
80	SK	810	0	875	26	0
All	All	209284	0	155614	4444	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 12.

The worst 5 of 4444 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)
66:SR:242:ILE:HG13	66:SR:243:TYR:CD1	1.99	0.98
1:2:222:A:H61	1:2:838:G:H1	1.03	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:I:22:CYS:HB2	39:I:37:CYS:SG	2.03	0.97
53:SA:20:GLU:HG2	53:SA:77:PHE:HZ	1.28	0.97
54:SI:47:PRO:HG3	54:SI:53:TRP:CZ3	1.99	0.96

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	
5	D	249/251 (99%)	236 (95%)	13 (5%)	0	100	100
6	E	384/386 (100%)	363 (94%)	20 (5%)	1 (0%)	36	65
7	F	359/361 (99%)	350 (98%)	9 (2%)	0	100	100
8	G	292/294 (99%)	280 (96%)	12 (4%)	0	100	100
9	H	163/175 (93%)	155 (95%)	7 (4%)	1 (1%)	21	50
10	I	220/222 (99%)	216 (98%)	4 (2%)	0	100	100
11	J	231/233 (99%)	223 (96%)	7 (3%)	1 (0%)	30	59
12	K	189/191 (99%)	178 (94%)	11 (6%)	0	100	100
13	L	216/218 (99%)	208 (96%)	8 (4%)	0	100	100
14	M	167/169 (99%)	162 (97%)	5 (3%)	0	100	100
15	N	191/193 (99%)	180 (94%)	10 (5%)	1 (0%)	24	54
16	O	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
17	P	201/203 (99%)	200 (100%)	1 (0%)	0	100	100
18	Q	195/197 (99%)	190 (97%)	5 (3%)	0	100	100
19	R	181/183 (99%)	176 (97%)	5 (3%)	0	100	100
20	S	183/185 (99%)	178 (97%)	4 (2%)	1 (0%)	24	54
21	T	186/188 (99%)	184 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	U	169/171 (99%)	166 (98%)	3 (2%)	0	100	100
23	V	157/159 (99%)	150 (96%)	7 (4%)	0	100	100
24	W	98/100 (98%)	92 (94%)	6 (6%)	0	100	100
25	X	134/136 (98%)	134 (100%)	0	0	100	100
26	Y	124/126 (98%)	121 (98%)	2 (2%)	1 (1%)	16	44
27	Z	119/121 (98%)	114 (96%)	5 (4%)	0	100	100
28	a	123/125 (98%)	121 (98%)	2 (2%)	0	100	100
29	b	133/135 (98%)	128 (96%)	5 (4%)	0	100	100
30	c	146/148 (99%)	141 (97%)	5 (3%)	0	100	100
31	d	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
32	e	94/96 (98%)	93 (99%)	1 (1%)	0	100	100
33	f	107/109 (98%)	104 (97%)	3 (3%)	0	100	100
34	g	125/127 (98%)	123 (98%)	2 (2%)	0	100	100
35	h	104/106 (98%)	97 (93%)	6 (6%)	1 (1%)	12	40
36	i	110/112 (98%)	106 (96%)	4 (4%)	0	100	100
37	j	117/119 (98%)	115 (98%)	2 (2%)	0	100	100
38	k	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
39	l	79/81 (98%)	68 (86%)	6 (8%)	5 (6%)	1	7
40	m	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
41	n	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
42	o	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
43	p	23/25 (92%)	23 (100%)	0	0	100	100
44	q	101/103 (98%)	96 (95%)	5 (5%)	0	100	100
45	r	89/91 (98%)	87 (98%)	2 (2%)	0	100	100
47	x	840/842 (100%)	755 (90%)	84 (10%)	1 (0%)	48	78
48	SD	119/121 (98%)	95 (80%)	24 (20%)	0	100	100
49	SZ	125/127 (98%)	101 (81%)	23 (18%)	1 (1%)	16	44
50	Se	92/94 (98%)	81 (88%)	9 (10%)	2 (2%)	5	24
51	SC	90/92 (98%)	78 (87%)	10 (11%)	2 (2%)	5	24
52	SE	115/117 (98%)	96 (84%)	18 (16%)	1 (1%)	14	42
53	SA	220/222 (99%)	206 (94%)	11 (5%)	3 (1%)	9	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	SI	141/143 (99%)	132 (94%)	8 (6%)	1 (1%)	18	47
55	SJ	98/100 (98%)	91 (93%)	7 (7%)	0	100	100
56	SL	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
57	SM	51/53 (96%)	47 (92%)	4 (8%)	0	100	100
58	SB	204/206 (99%)	182 (89%)	21 (10%)	1 (0%)	24	54
59	SF	139/141 (99%)	131 (94%)	6 (4%)	2 (1%)	9	31
60	SH	143/145 (99%)	123 (86%)	20 (14%)	0	100	100
61	SO	300/312 (96%)	238 (79%)	57 (19%)	5 (2%)	7	28
62	SN	71/73 (97%)	52 (73%)	19 (27%)	0	100	100
63	SG	119/121 (98%)	106 (89%)	13 (11%)	0	100	100
64	SP	204/206 (99%)	191 (94%)	13 (6%)	0	100	100
65	SQ	222/232 (96%)	201 (90%)	21 (10%)	0	100	100
66	SR	214/216 (99%)	205 (96%)	9 (4%)	0	100	100
67	SS	256/258 (99%)	226 (88%)	29 (11%)	1 (0%)	30	59
68	ST	226/228 (99%)	213 (94%)	12 (5%)	1 (0%)	30	59
69	SU	182/184 (99%)	174 (96%)	7 (4%)	1 (0%)	24	54
70	SV	183/198 (92%)	171 (93%)	12 (7%)	0	100	100
71	SW	182/184 (99%)	166 (91%)	15 (8%)	1 (0%)	24	54
72	SX	140/142 (99%)	132 (94%)	8 (6%)	0	100	100
73	SY	148/150 (99%)	144 (97%)	4 (3%)	0	100	100
74	Sa	85/87 (98%)	80 (94%)	4 (5%)	1 (1%)	10	35
75	Sb	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
76	Sc	142/144 (99%)	127 (89%)	13 (9%)	2 (1%)	9	31
77	Sd	132/134 (98%)	129 (98%)	3 (2%)	0	100	100
78	Sf	79/81 (98%)	79 (100%)	0	0	100	100
79	Sg	58/60 (97%)	56 (97%)	2 (3%)	0	100	100
80	SK	99/108 (92%)	98 (99%)	1 (1%)	0	100	100
All	All	11826/12024 (98%)	11092 (94%)	696 (6%)	38 (0%)	37	65

5 of 38 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	E	362	ALA

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Mol	Chain	Res	Type
9	H	68	PRO
35	h	104	PRO
49	SZ	42	VAL
51	SC	87	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	D	190/193 (98%)	190 (100%)	0	100	100
6	E	319/322 (99%)	319 (100%)	0	100	100
7	F	288/288 (100%)	286 (99%)	2 (1%)	76	78
8	G	241/243 (99%)	240 (100%)	1 (0%)	84	83
9	H	139/154 (90%)	138 (99%)	1 (1%)	76	78
10	I	186/186 (100%)	186 (100%)	0	100	100
11	J	187/191 (98%)	187 (100%)	0	100	100
12	K	168/171 (98%)	166 (99%)	2 (1%)	63	72
13	L	185/185 (100%)	183 (99%)	2 (1%)	65	74
14	M	145/147 (99%)	144 (99%)	1 (1%)	76	78
15	N	154/154 (100%)	154 (100%)	0	100	100
16	O	107/107 (100%)	106 (99%)	1 (1%)	70	76
17	P	175/175 (100%)	175 (100%)	0	100	100
18	Q	160/160 (100%)	160 (100%)	0	100	100
19	R	138/145 (95%)	138 (100%)	0	100	100
20	S	150/150 (100%)	150 (100%)	0	100	100
21	T	152/153 (99%)	152 (100%)	0	100	100
22	U	155/155 (100%)	155 (100%)	0	100	100
23	V	135/136 (99%)	134 (99%)	1 (1%)	76	78
24	W	87/87 (100%)	86 (99%)	1 (1%)	65	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	X	104/104 (100%)	104 (100%)	0	100	100
26	Y	56/108 (52%)	56 (100%)	0	100	100
27	Z	104/105 (99%)	103 (99%)	1 (1%)	68	75
28	a	108/108 (100%)	106 (98%)	2 (2%)	50	66
29	b	112/115 (97%)	112 (100%)	0	100	100
30	c	117/118 (99%)	117 (100%)	0	100	100
31	d	46/46 (100%)	46 (100%)	0	100	100
32	e	81/81 (100%)	80 (99%)	1 (1%)	63	72
33	f	92/96 (96%)	92 (100%)	0	100	100
34	g	107/109 (98%)	105 (98%)	2 (2%)	50	66
35	h	90/90 (100%)	90 (100%)	0	100	100
36	i	95/95 (100%)	94 (99%)	1 (1%)	65	74
37	j	104/104 (100%)	103 (99%)	1 (1%)	68	75
38	k	80/81 (99%)	77 (96%)	3 (4%)	29	54
39	l	67/67 (100%)	58 (87%)	9 (13%)	4	15
40	m	68/68 (100%)	67 (98%)	1 (2%)	57	69
41	n	45/45 (100%)	45 (100%)	0	100	100
42	o	45/47 (96%)	45 (100%)	0	100	100
43	p	22/23 (96%)	22 (100%)	0	100	100
44	q	87/88 (99%)	85 (98%)	2 (2%)	44	63
45	r	71/71 (100%)	71 (100%)	0	100	100
47	x	715/715 (100%)	709 (99%)	6 (1%)	73	77
48	SD	88/98 (90%)	87 (99%)	1 (1%)	65	74
49	SZ	81/96 (84%)	80 (99%)	1 (1%)	63	72
50	Se	81/81 (100%)	80 (99%)	1 (1%)	63	72
51	SC	77/85 (91%)	76 (99%)	1 (1%)	61	71
52	SE	95/98 (97%)	95 (100%)	0	100	100
53	SA	182/182 (100%)	182 (100%)	0	100	100
54	SI	115/115 (100%)	113 (98%)	2 (2%)	53	67
55	SJ	93/93 (100%)	91 (98%)	2 (2%)	45	63
56	SL	55/56 (98%)	54 (98%)	1 (2%)	51	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	SM	47/47 (100%)	47 (100%)	0	100	100
58	SB	172/173 (99%)	171 (99%)	1 (1%)	78	80
59	SF	117/117 (100%)	117 (100%)	0	100	100
60	SH	127/128 (99%)	127 (100%)	0	100	100
61	SO	246/257 (96%)	246 (100%)	0	100	100
62	SN	57/64 (89%)	57 (100%)	0	100	100
63	SG	105/110 (96%)	102 (97%)	3 (3%)	37	60
64	SP	170/173 (98%)	170 (100%)	0	100	100
65	SQ	200/205 (98%)	198 (99%)	2 (1%)	68	75
66	SR	175/175 (100%)	173 (99%)	2 (1%)	65	74
67	SS	220/220 (100%)	218 (99%)	2 (1%)	70	76
68	ST	189/195 (97%)	186 (98%)	3 (2%)	55	68
69	SU	163/165 (99%)	161 (99%)	2 (1%)	63	72
70	SV	148/159 (93%)	148 (100%)	0	100	100
71	SW	156/157 (99%)	156 (100%)	0	100	100
72	SX	126/127 (99%)	125 (99%)	1 (1%)	73	77
73	SY	127/127 (100%)	127 (100%)	0	100	100
74	Sa	71/74 (96%)	71 (100%)	0	100	100
75	Sb	110/110 (100%)	108 (98%)	2 (2%)	51	67
76	Sc	119/119 (100%)	117 (98%)	2 (2%)	53	67
77	Sd	112/112 (100%)	112 (100%)	0	100	100
78	Sf	70/70 (100%)	70 (100%)	0	100	100
79	Sg	50/51 (98%)	50 (100%)	0	100	100
80	SK	85/89 (96%)	85 (100%)	0	100	100
All	All	9906/10114 (98%)	9836 (99%)	70 (1%)	73	78

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
66	SR	222	TYR
67	SS	197	HIS
72	SX	133	LYS
39	l	21	ARG
39	l	14	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 133 such sidechains are listed below:

Mol	Chain	Res	Type
72	SX	16	GLN
72	SX	138	ASN
78	Sf	42	ASN
25	X	28	ASN
23	V	146	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1764/1799 (98%)	502 (28%)	32 (1%)
2	A	3183/3394 (93%)	526 (16%)	12 (0%)
3	B	120/121 (99%)	12 (10%)	1 (0%)
4	C	157/158 (99%)	30 (19%)	1 (0%)
46	s	74/75 (98%)	14 (18%)	0
46	t	74/75 (98%)	14 (18%)	0
All	All	5372/5622 (95%)	1098 (20%)	46 (0%)

5 of 1098 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	9	U
1	2	10	G
1	2	25	C

5 of 46 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	1584	G
2	A	1814	A
1	2	1633	A
2	A	601	U
2	A	2450	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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 [i](#)

There are no chain breaks in this entry.

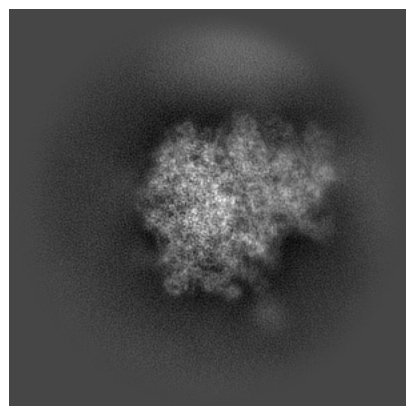
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38660. These allow visual inspection of the internal detail of the map and identification of artifacts.

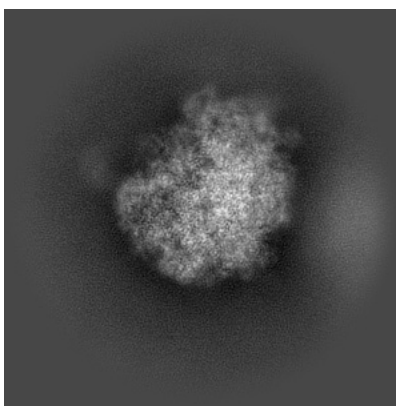
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

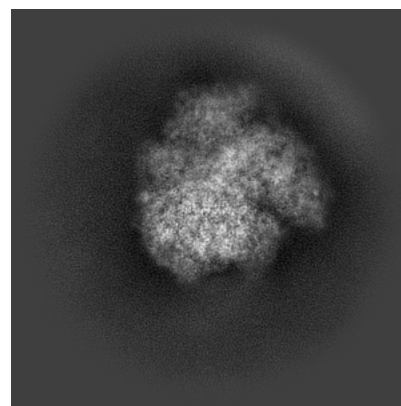
6.1.1 Primary map



X

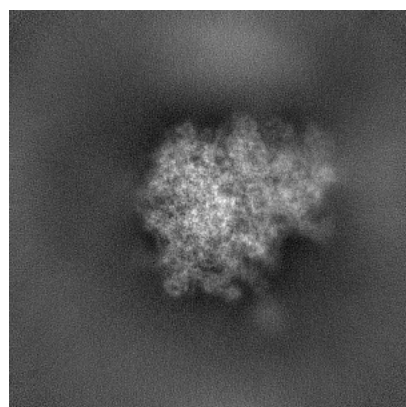


Y

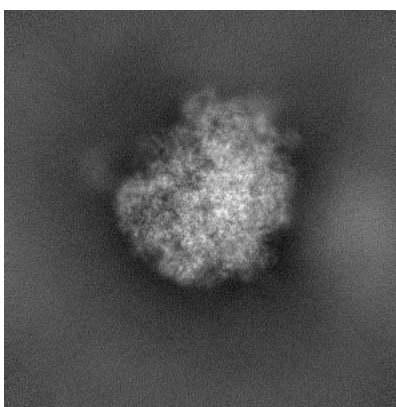


Z

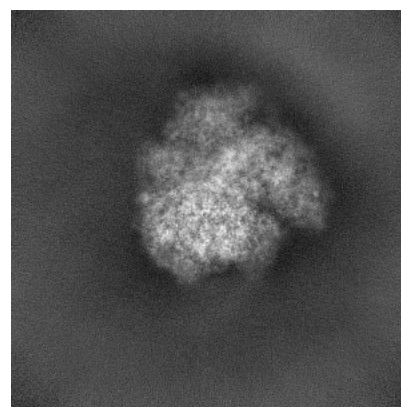
6.1.2 Raw map



X



Y

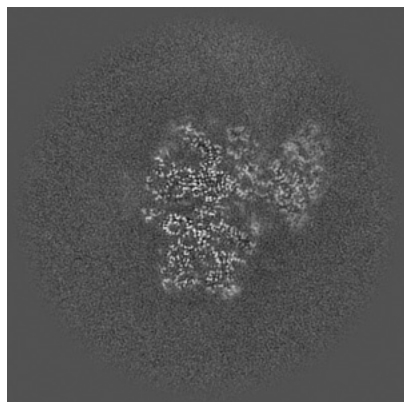


Z

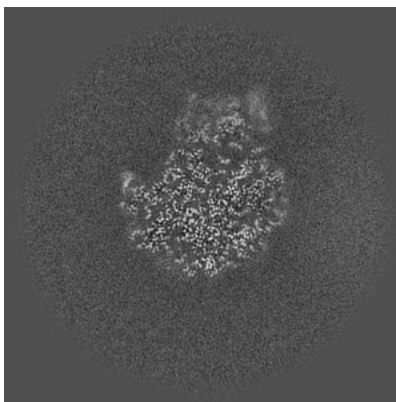
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

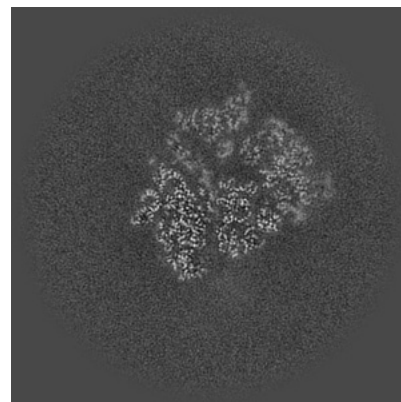
6.2.1 Primary map



X Index: 200

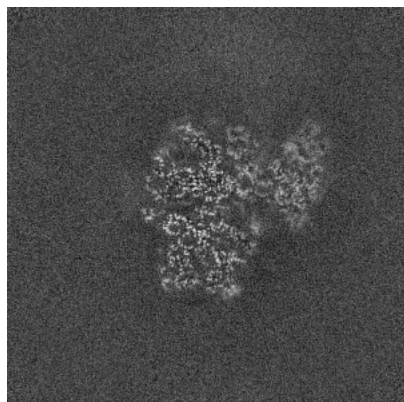


Y Index: 200

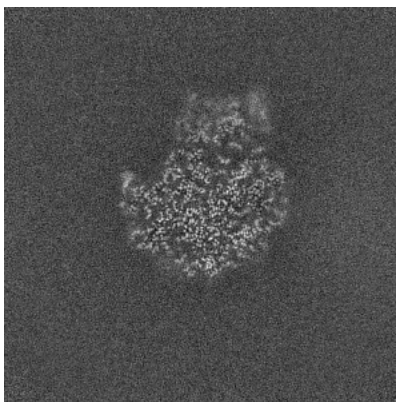


Z Index: 200

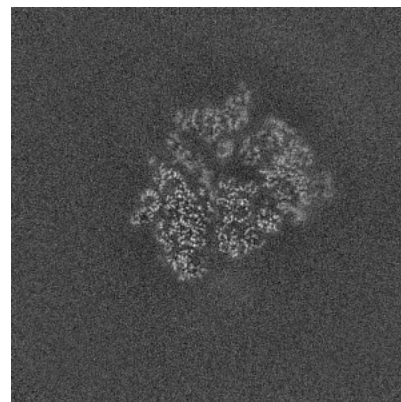
6.2.2 Raw map



X Index: 200



Y Index: 200

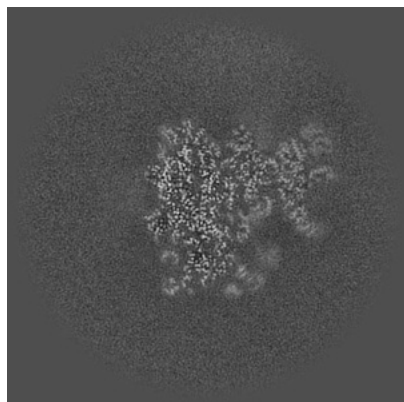


Z Index: 200

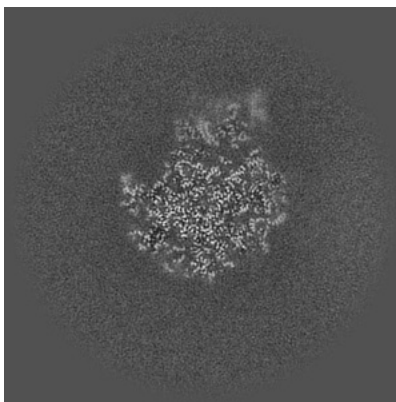
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

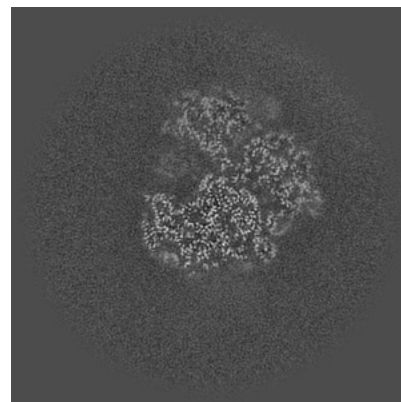
6.3.1 Primary map



X Index: 212

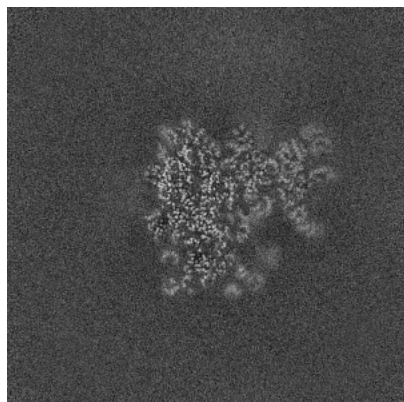


Y Index: 198

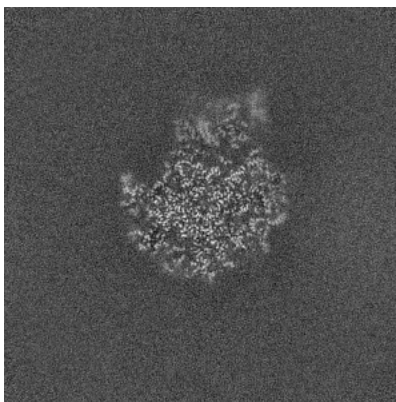


Z Index: 222

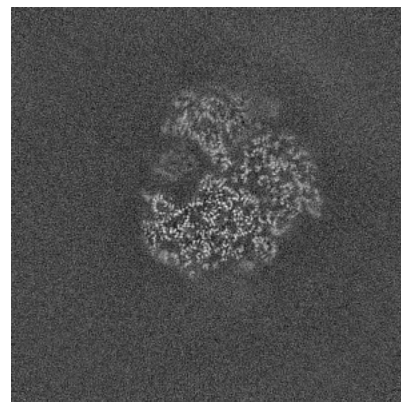
6.3.2 Raw map



X Index: 212



Y Index: 198

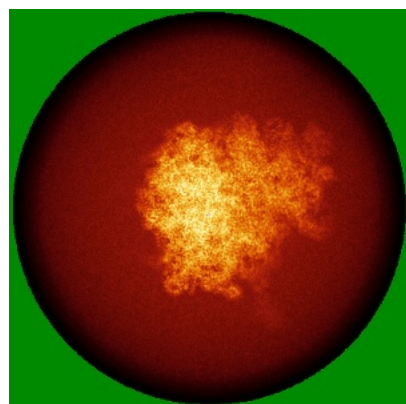


Z Index: 223

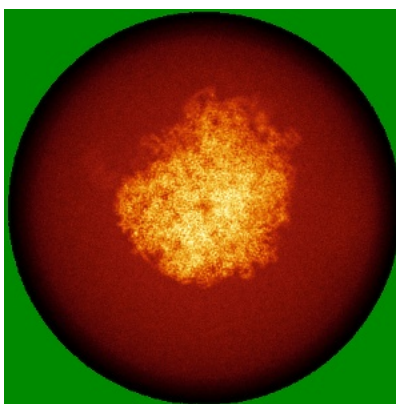
The images above show the largest variance slices of the map in three orthogonal directions.

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

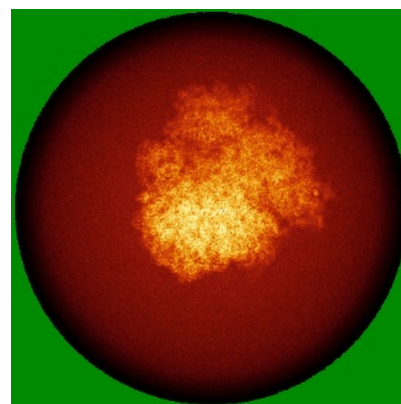
6.4.1 Primary map



X

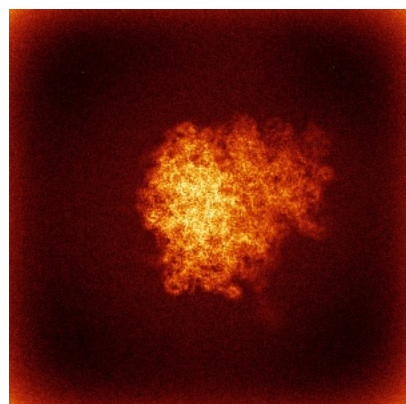


Y

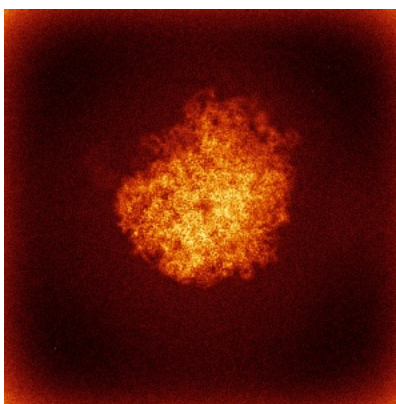


Z

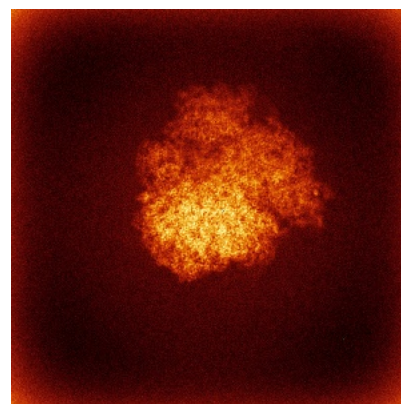
6.4.2 Raw map



X



Y

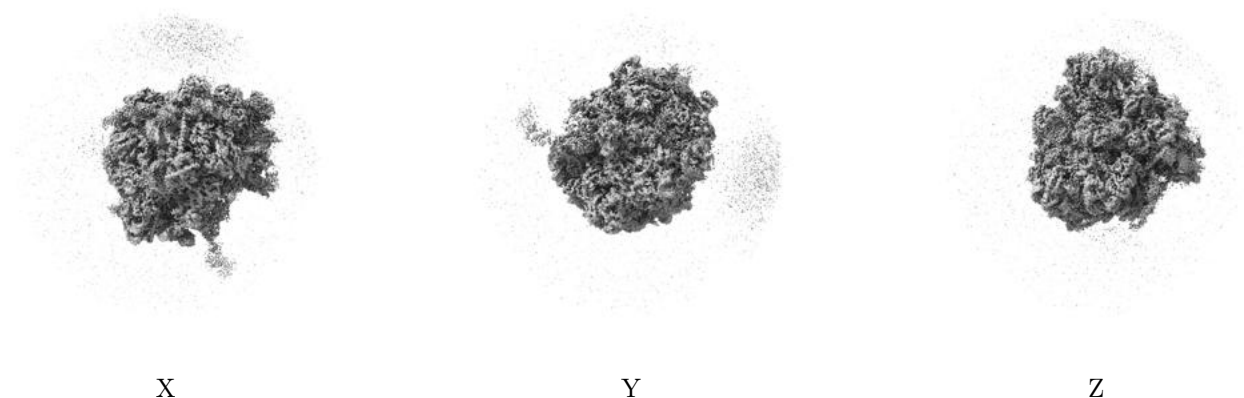


Z

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

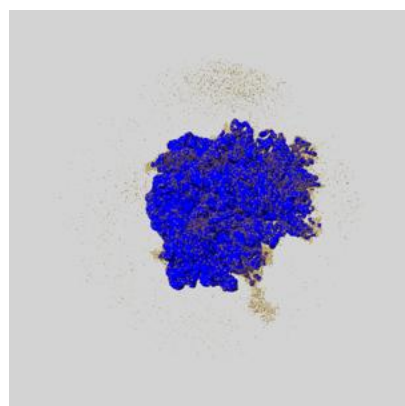
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

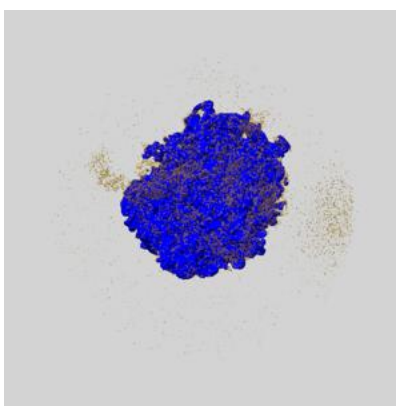
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

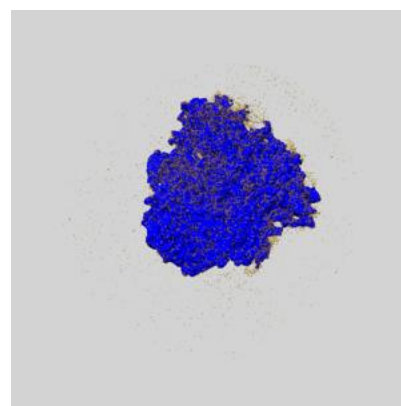
6.6.1 emd_38660_msk_1.map [i](#)



X



Y

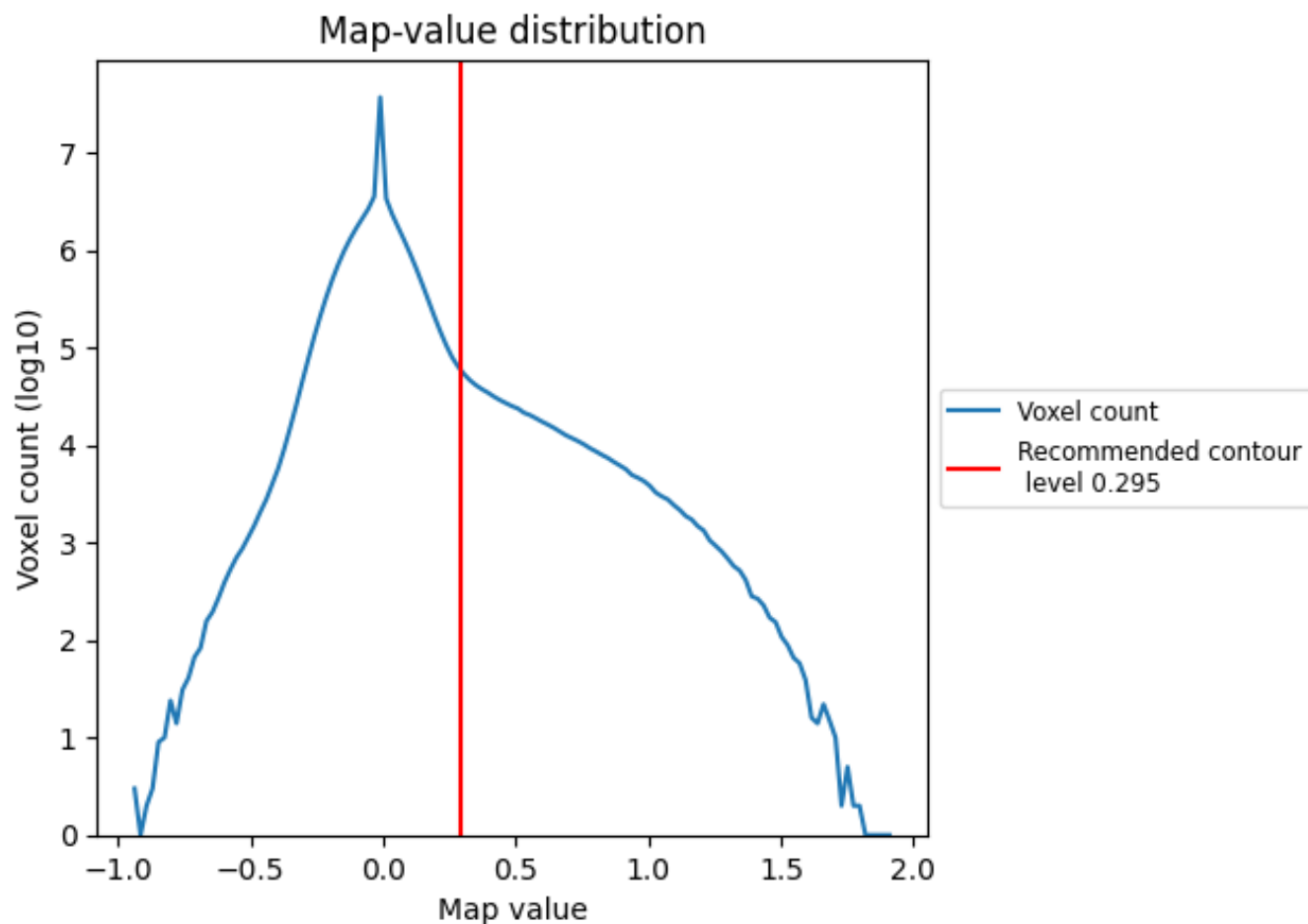


Z

7 Map analysis [i](#)

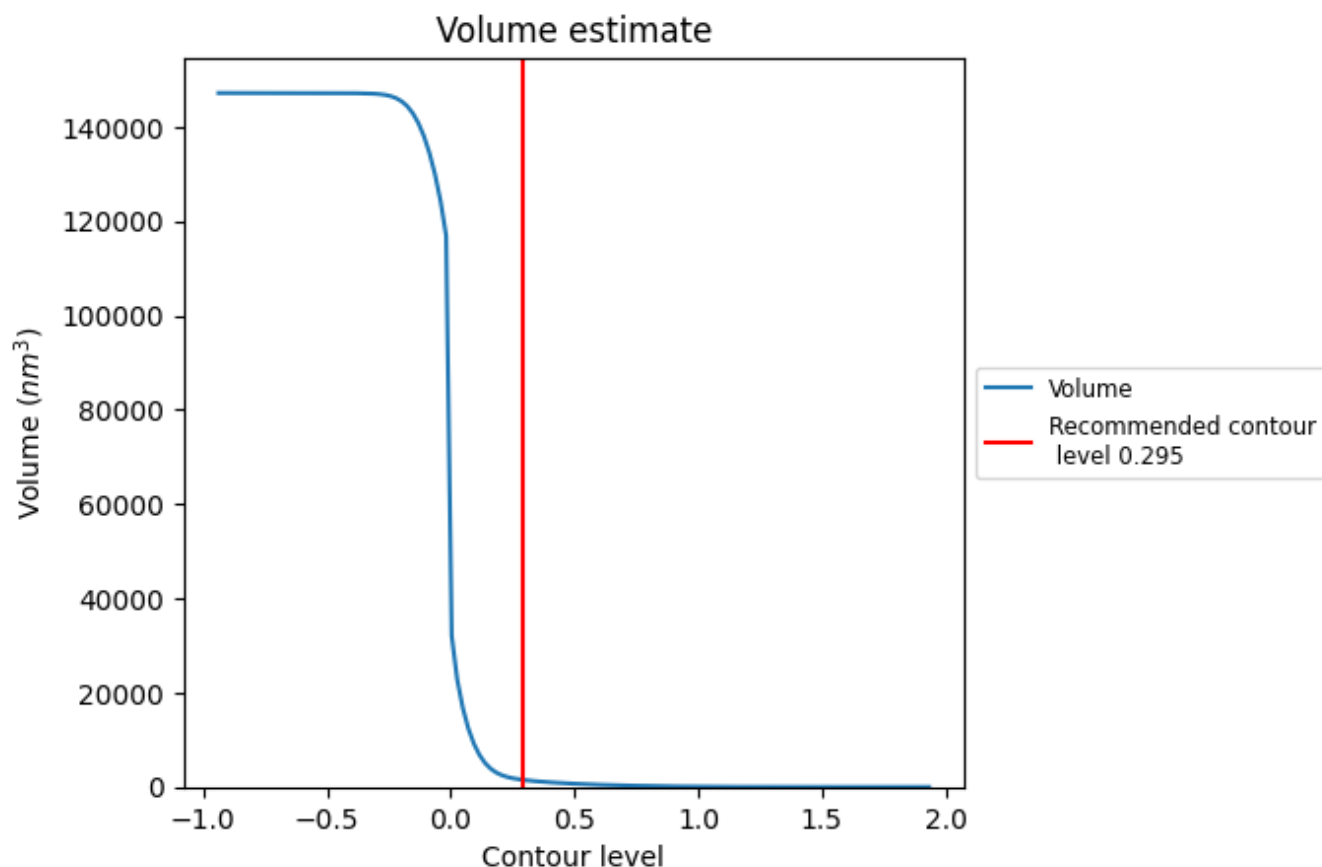
This section contains the results of statistical analysis of the map.

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.

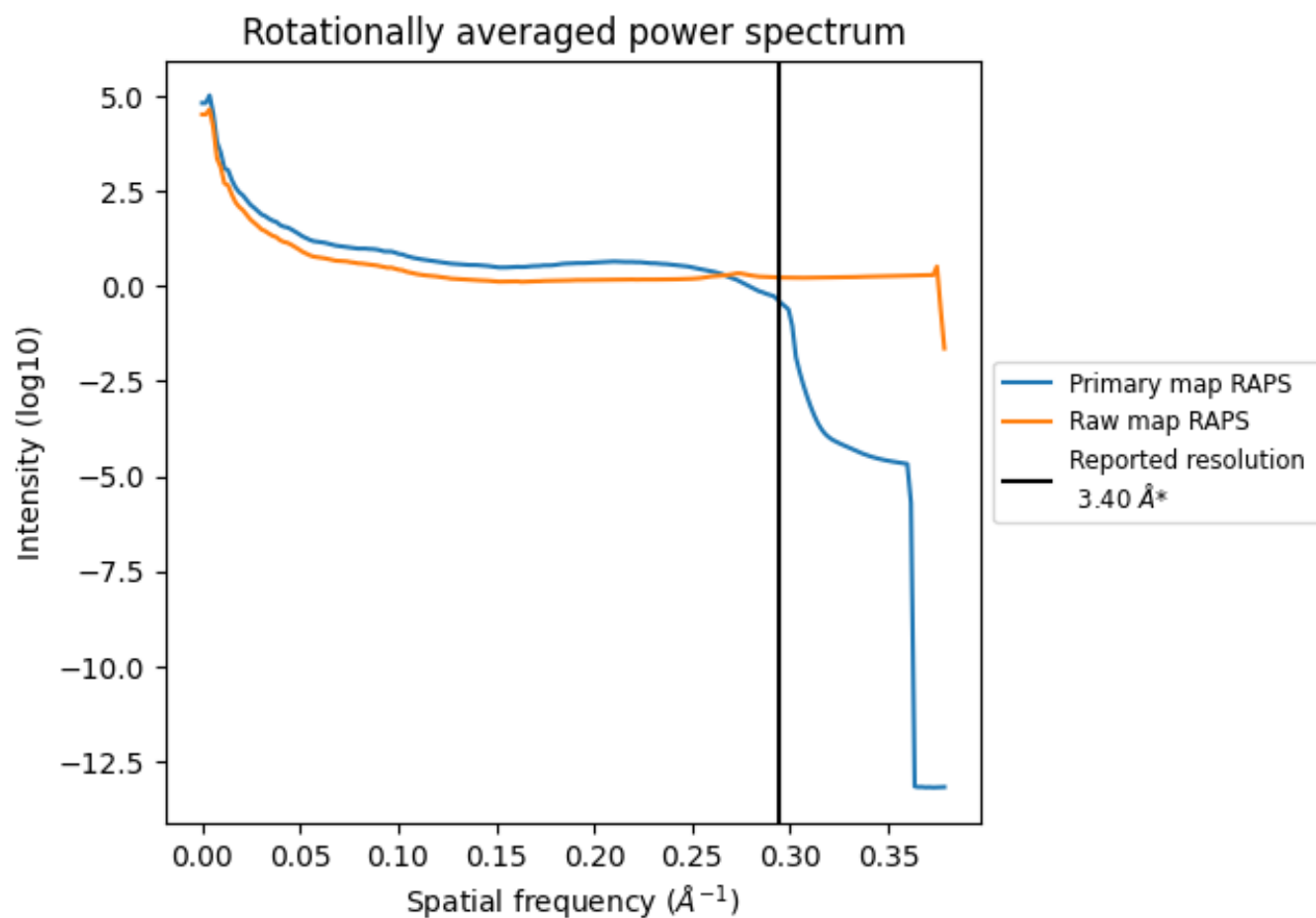
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1478 nm³; this corresponds to an approximate mass of 1335 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 ⓘ

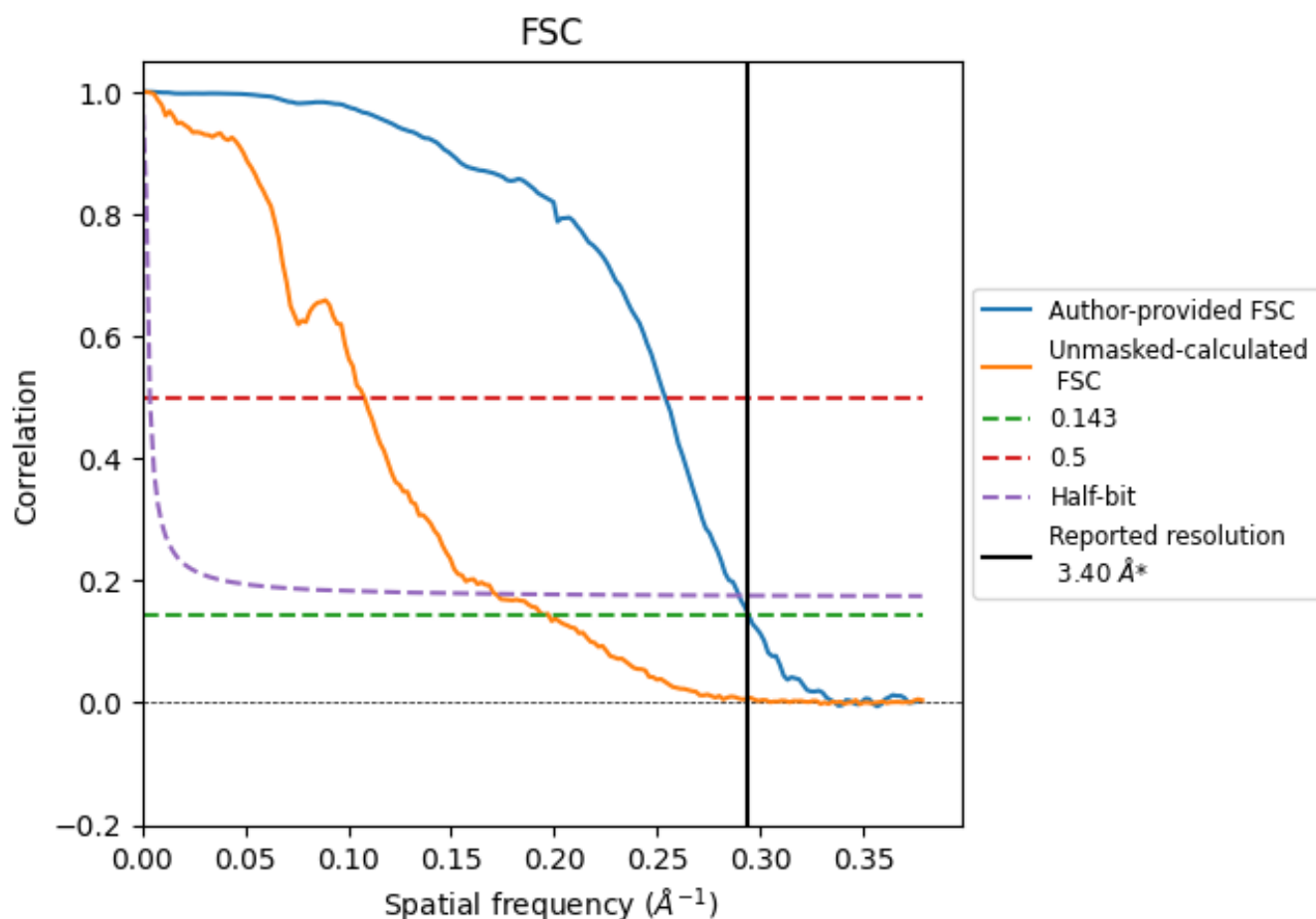


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 $0.294 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

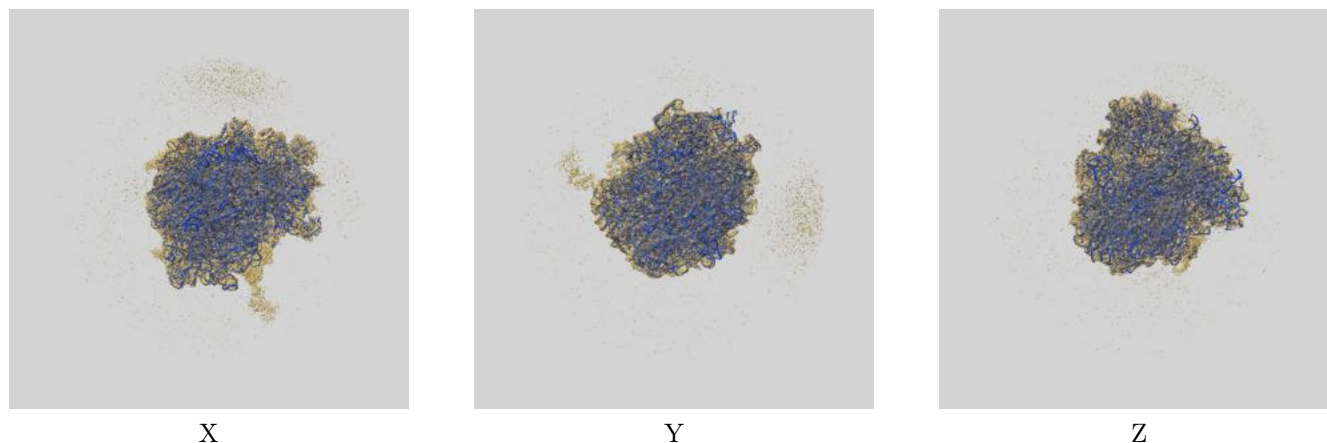
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.39	3.94	3.45
Unmasked-calculated*	5.07	9.29	5.83

*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 5.07 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

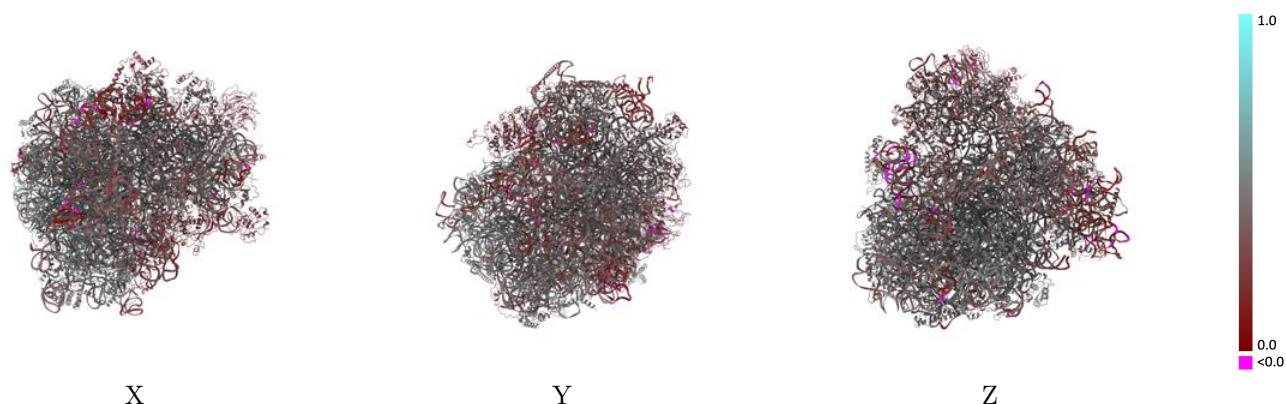
This section contains information regarding the fit between EMDB map EMD-38660 and PDB model 8XU8. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

9.1 Map-model overlay [i](#)



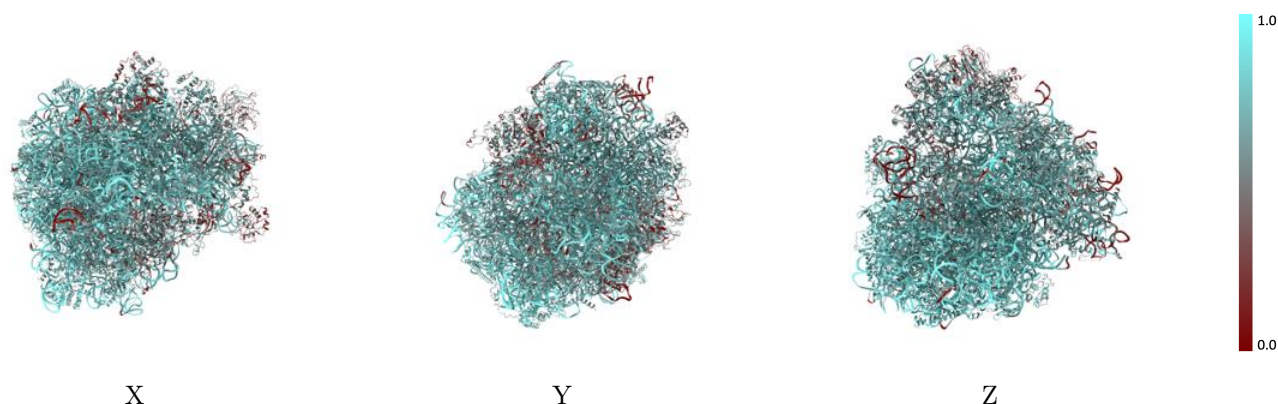
The images above show the 3D surface view of the map at the recommended contour level 0.295 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



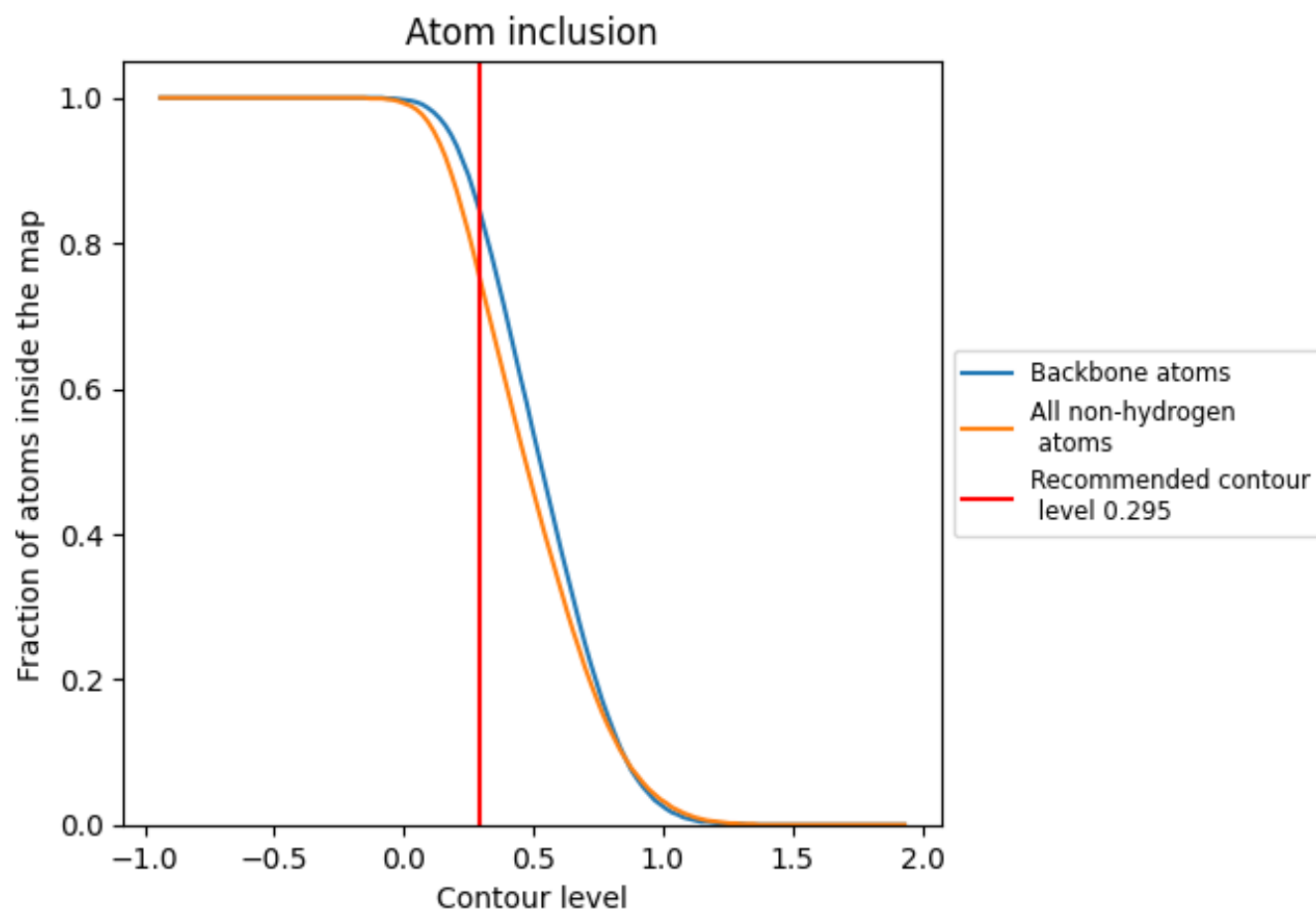
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.295).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 75% 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 (0.295) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7500	 0.4140
2	 0.7930	 0.3750
A	 0.8510	 0.4220
B	 0.8930	 0.4220
C	 0.8730	 0.4380
D	 0.7310	 0.5010
E	 0.7570	 0.4770
F	 0.7650	 0.4880
G	 0.7330	 0.4310
H	 0.7220	 0.4460
I	 0.7620	 0.4740
J	 0.7270	 0.4500
K	 0.7240	 0.4610
L	 0.6960	 0.4560
M	 0.6140	 0.3900
N	 0.7610	 0.4880
O	 0.7620	 0.4670
P	 0.7800	 0.5040
Q	 0.7510	 0.4770
R	 0.7540	 0.4960
S	 0.7570	 0.4980
SA	 0.5610	 0.4110
SB	 0.5240	 0.3680
SC	 0.5770	 0.3500
SD	 0.3090	 0.2760
SE	 0.5070	 0.3480
SF	 0.5710	 0.3770
SG	 0.5640	 0.3770
SH	 0.5420	 0.3580
SI	 0.5780	 0.3640
SJ	 0.5260	 0.3810
SK	 0.4300	 0.3110
SL	 0.5070	 0.3940
SM	 0.7090	 0.4250
SN	 0.3090	 0.1940



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Chain	Atom inclusion	Q-score
SO	 0.4070	 0.2720
SP	 0.6190	 0.3890
SQ	 0.5420	 0.3890
SR	 0.6570	 0.4430
SS	 0.6430	 0.4290
ST	 0.5980	 0.3940
SU	 0.5550	 0.3530
SV	 0.6820	 0.4410
SW	 0.6450	 0.4070
SX	 0.6630	 0.4660
SY	 0.6490	 0.4340
SZ	 0.6350	 0.4260
Sa	 0.6200	 0.4120
Sb	 0.6820	 0.4530
Sc	 0.6460	 0.4650
Sd	 0.6460	 0.4080
Se	 0.6570	 0.4400
Sf	 0.6060	 0.4050
Sg	 0.6140	 0.4140
T	 0.7050	 0.4540
U	 0.7600	 0.4940
V	 0.7340	 0.4830
W	 0.6960	 0.4330
X	 0.6970	 0.4970
Y	 0.6900	 0.4240
Z	 0.7400	 0.4910
a	 0.7670	 0.4920
b	 0.7560	 0.4740
c	 0.7920	 0.4980
d	 0.7190	 0.4710
e	 0.7030	 0.4510
f	 0.7190	 0.4780
g	 0.7480	 0.5070
h	 0.7710	 0.4970
i	 0.7200	 0.4870
j	 0.7300	 0.4680
k	 0.7100	 0.4490
l	 0.8300	 0.5260
m	 0.7250	 0.4490
n	 0.7280	 0.4890
o	 0.7500	 0.4930
p	 0.7500	 0.5070

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Chain	Atom inclusion	Q-score
q	 0.7290	 0.4970
r	 0.7090	 0.4810
s	 0.7250	 0.3220
t	 0.5790	 0.2830
x	 0.4480	 0.2750