



wwPDB EM Validation Summary Report ⓘ

Dec 11, 2022 – 09:06 am GMT

PDB ID : 6RXU
EMDB ID : EMD-10052
Title : Cryo-EM structure of the 90S pre-ribosome (Kre33-Noc4) from *Chaetomium thermophilum*, state B1
Authors : Cheng, J.; Kellner, N.; Griesel, S.; Berninghausen, O.; Beckmann, R.; Hurt, E.
Deposited on : 2019-06-10
Resolution : 3.50 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:

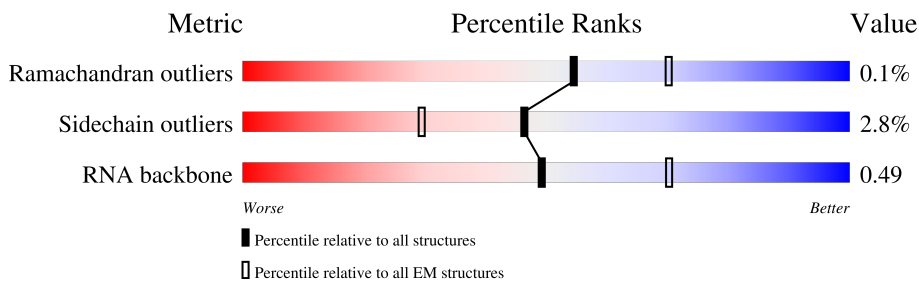
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance

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

The reported resolution of this entry is 3.50 Å.

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









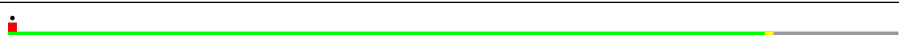
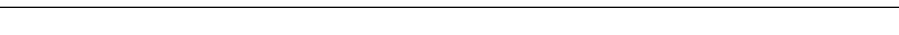
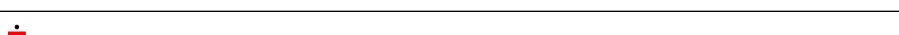
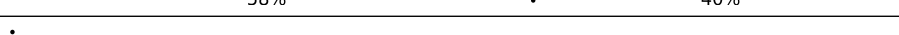
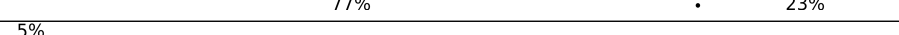
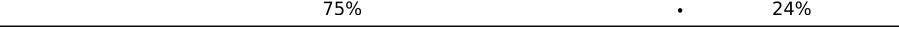


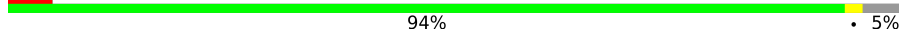








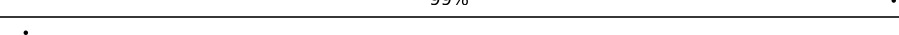

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	UA	904	
2	UB	907	
3	UC	648	
4	UD	884	
5	UF	414	
6	UG	558	
7	UJ	1802	
8	UK	270	




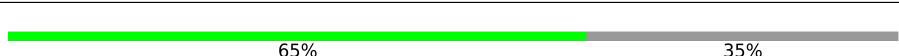
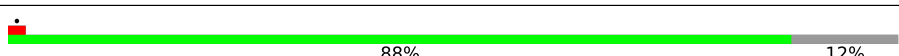
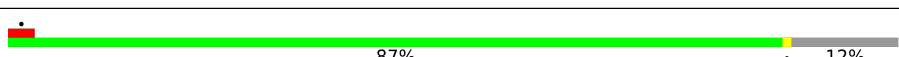
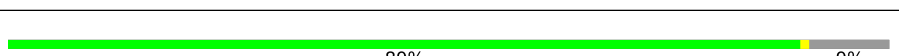
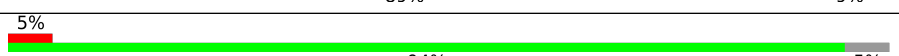
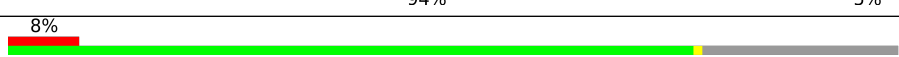

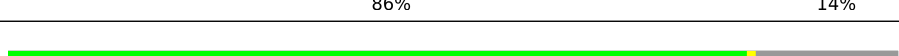
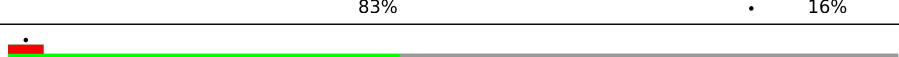

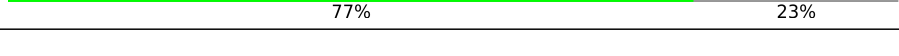
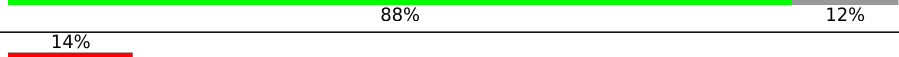

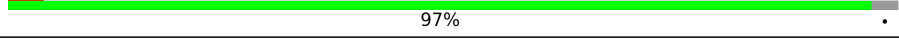


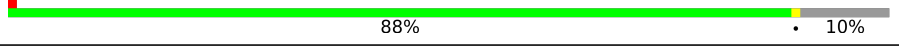

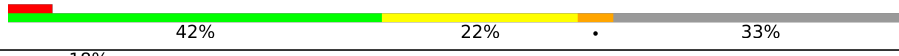



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Mol	Chain	Length	Quality of chain
9	UL	962	 81% 18%
10	UM	912	 79% 20%
11	UN	938	 19% 81%
12	UO	557	 89% 10%
13	UQ	960	 81% 18%
14	UR	618	 72% 28%
15	UU	1049	 85% 14%
16	UX	193	 98%
17	UZ	391	 58% 40%
18	CA	313	 77% 23%
18	CB	313	 5% 75% 24%
19	CC	523	 74% 26%
20	CD	582	 6% 72% 28%
21	CE	127	 5% 94% 5%
21	CF	127	 91% 6%
22	CG	630	 66% 34%
23	CH	411	 93% 5%
24	CI	1163	 70% 29%
25	CJ	183	 98%
26	CK	297	 97%
27	CL	785	 29% 71%
28	CM	446	 99%
29	CN	252	 89% 10%
29	CO	252	 13% 83% 15%
30	CP	322	 72% 28%









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Mol	Chain	Length	Quality of chain
31	CQ	259	 67% 32%
32	CR	1073	 13% 51% 19% 29%
32	CS	1073	 42% 51% 19% 29%
33	CT	203	 65% 35%
34	Ca	255	 88% 12%
35	Cb	264	 87% 12%
36	Cc	212	 89% 9%
37	Cd	239	 5% 94% 5%
38	Ce	203	 8% 77% 22%
39	Cf	202	 5% 86% 14%
40	Cg	190	 83% 16%
41	Ch	151	 44% 56%
42	Ci	150	 77% 23%
43	Cj	143	 88% 12%
44	Ck	161	 14% 87% 13%
45	Cm	130	 97%
46	Cn	145	 66% 34%
47	Co	136	 68% 32%
48	Cp	68	 88% 10%
49	CU	311	 56% 43%
50	C1	2352	 5% 42% 22% 33%
51	C2	230	 18% 63% 31% 7%
52	CW	668	 56% 43%
53	UT	2612	 11% 77% 22%
54	UH	930	 38% 61%

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Mol	Chain	Length	Quality of chain
55	UE	410	 30% 70%
55	UI	410	 30% 70%
56	US	549	 82% 18%
57	CI	156	 19% 50% 49%
58	CX	480	 44% 55% 44%
59	CY	381	 30% 68%
60	CZ	609	 7% 93%
61	UP	364	 15% 85%

2 Entry composition [i](#)

There are 64 unique types of molecules in this entry. The entry contains 211834 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 Periodic tryptophan protein 2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	UA	839	6366	4101	1136	1105	24	0	0

- Molecule 2 is a protein called Utp2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	UB	512	4079	2576	781	711	11	0	0

- Molecule 3 is a protein called Utp3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	UC	74	588	371	120	97	0	0

- Molecule 4 is a protein called Utp4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	UD	772	6071	3851	1093	1103	24	0	0

- Molecule 5 is a protein called Utp6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	UF	331	2591	1674	504	399	14	0	0

- Molecule 6 is a protein called Utp7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	UG	479	3717	2369	700	636	12	0	0

- Molecule 7 is a protein called UTP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	UJ	1090	8416	5408	1452	1525	31	0	0

- Molecule 8 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	UK	217	1687	1062	351	269	5	0	0

- Molecule 9 is a protein called Utp12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	UL	785	6175	3940	1088	1130	17	0	0

- Molecule 10 is a protein called Utp13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	UM	729	5643	3590	995	1045	13	0	0

- Molecule 11 is a protein called Utp14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	UN	177	1401	892	263	239	7	0	0

- Molecule 12 is a protein called Utp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	UO	504	3819	2422	699	684	14	0	0

- Molecule 13 is a protein called Utp17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	UQ	789	6008	3831	1037	1119	21	0	0

- Molecule 14 is a protein called Utp18.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	UR	447	Total	C	N	O	S	0	0
			3491	2209	656	616	10		

- Molecule 15 is a protein called Putative U3 snoRNP protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	UU	902	Total	C	N	O	S	0	0
			6734	4336	1236	1136	26		

- Molecule 16 is a protein called Utp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	UX	190	Total	C	N	O	S	0	0
			1470	932	282	246	10		

- Molecule 17 is a protein called Utp30.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	UZ	235	Total	C	N	O	S	0	0
			1819	1186	331	299	3		

- Molecule 18 is a protein called Nop1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	CA	242	Total	C	N	O	S	0	0
			1778	1149	327	293	9		
18	CB	237	Total	C	N	O	S	0	0
			1816	1154	318	335	9		

- Molecule 19 is a protein called Nop56.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	CC	387	Total	C	N	O	S	0	0
			2866	1836	527	492	11		

- Molecule 20 is a protein called Nop58.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	CD	420	Total	C	N	O	S	0	0
			3150	2023	560	557	10		

- Molecule 21 is a protein called Snu13.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CE	121	Total	C	N	O	S	0	0
			879	557	165	154	3		
21	CF	120	Total	C	N	O	S	0	0
			864	550	161	150	3		

- Molecule 22 is a protein called Rrp9.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	CG	416	Total	C	N	O	S	0	0
			3245	2065	587	580	13		

- Molecule 23 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	CH	389	Total	C	N	O	S	0	0
			2888	1827	526	525	10		

- Molecule 24 is a protein called Bms1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	CI	822	Total	C	N	O	S	0	0
			6486	4169	1213	1077	27		

- Molecule 25 is a protein called Imp3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	CJ	179	Total	C	N	O	S	0	0
			1434	918	283	226	7		

- Molecule 26 is a protein called Putative U3 small nucleolar ribonucleoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	CK	297	Total	C	N	O	S	0	0
			2329	1476	445	400	8		

- Molecule 27 is a protein called Putative U3 small nucleolar ribonucleoprotein protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	CL	231	Total	C	N	O	S	0	0
			1786	1114	339	327	6		

- Molecule 28 is a protein called Sof1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	CM	445	3501	2195	672	619	15	0	0

- Molecule 29 is a protein called Emg1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	CN	226	1762	1119	306	327	10	0	0
29	CO	215	1683	1067	293	313	10	0	0

- Molecule 30 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	CP	233	1893	1209	340	335	9	0	0

- Molecule 31 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	CQ	175	1361	862	250	242	7	0	0

- Molecule 32 is a protein called Kre33.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	CR	760	5989	3851	1024	1087	27	0	0
32	CS	760	5989	3851	1024	1087	27	0	0

- Molecule 33 is a protein called Fcf2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	CT	131	1035	656	197	178	4	0	0

- Molecule 34 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	Ca	225	1821	1160	341	315	5	0	0

- Molecule 35 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	Cb	232	1851	1179	340	325	7	0	0

- Molecule 36 is a protein called 40S ribosomal protein s5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	Cc	192	1464	926	278	253	7	0	0

- Molecule 37 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	Cd	226	1819	1138	363	313	5	0	0

- Molecule 38 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	Ce	159	1279	810	237	232		0	0

- Molecule 39 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	Cf	174	1398	872	283	242	1	0	0

- Molecule 40 is a protein called 40S ribosomal protein s9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	Cg	159	1242	801	255	184	2	0	0

- Molecule 41 is a protein called 40S ribosomal protein S13-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	Ch	66	546	355	101	90		0	0

- Molecule 42 is a protein called 40S ribosomal protein S14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ci	115	Total	C	N	O	S	0	0
			808	506	156	141	5		

- Molecule 43 is a protein called 40S ribosomal protein S16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Cj	126	Total	C	N	O	S	0	0
			943	613	177	151	2		

- Molecule 44 is a protein called 40S ribosomal protein S11-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ck	140	Total	C	N	O	S	0	0
			1163	750	224	184	5		

- Molecule 45 is a protein called 40S ribosomal protein S22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Cm	126	Total	C	N	O	S	0	0
			985	632	184	164	5		

- Molecule 46 is a protein called 40S ribosomal protein s23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Cn	96	Total	C	N	O	S	0	0
			702	456	134	110	2		

- Molecule 47 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Co	92	Total	C	N	O	S	0	0
			741	474	139	126	2		

- Molecule 48 is a protein called 40S ribosomal protein S28-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	Cp	61	Total	C	N	O	0	0
			455	284	97	74		

- Molecule 49 is a protein called Faf1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	CU	176	Total	C	N	O	S	0	0
			1337	822	265	244	6		

- Molecule 50 is a RNA chain called 35S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	C1	1575	Total	C	N	O	P	0	0
			33604	14992	6023	11014	1575		

- Molecule 51 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	C2	230	Total	C	N	O	P	0	0
			4891	2182	856	1623	230		

- Molecule 52 is a protein called Ribosome biogenesis protein ENP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	CW	382	Total	C	N	O	S	0	0
			2924	1857	530	524	13		

- Molecule 53 is a protein called Utp20.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	UT	2033	Total	C	N	O	S	0	0
			16053	10338	2819	2828	68		

- Molecule 54 is a protein called Utp8.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	UH	359	Total	C	N	O	S	0	0
			2809	1773	496	527	13		

- Molecule 55 is a protein called Utp5.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	UE	125	Total	C	N	O	S	0	0
			972	608	183	175	6		
55	UI	125	Total	C	N	O	S	0	0
			972	608	183	175	6		

- Molecule 56 is a protein called Noc4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	US	451	3672	2389	608	660	15	0	0

- Molecule 57 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	Cl	80	633	400	115	117	1	0	0

- Molecule 58 is a protein called Enp1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	CX	267	2130	1384	374	362	10	0	0

- Molecule 59 is a protein called U3 small nucleolar ribonucleoprotein protein lcp5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	CY	123	979	592	195	189	3	0	0

- Molecule 60 is a protein called Bfr2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	CZ	44	376	235	76	64	1	0	0

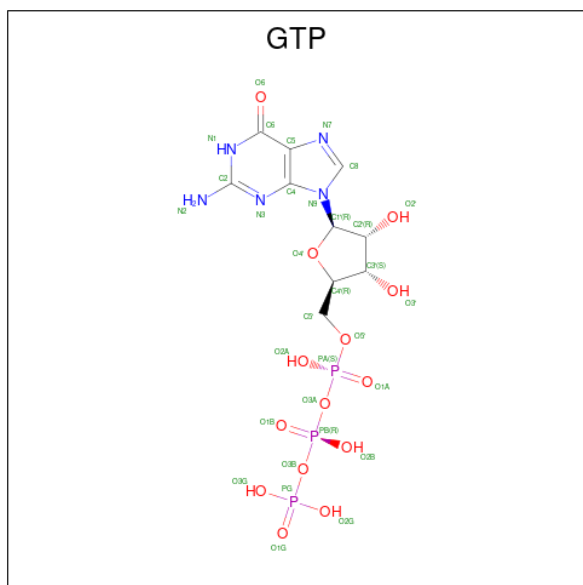
- Molecule 61 is a protein called Utp16.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
61	UP	54	422	264	88	70	0	0

- Molecule 62 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
62	UX	1	1	1	0

- Molecule 63 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
63	CI	1	32	10	5	14	3	0

- Molecule 64 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

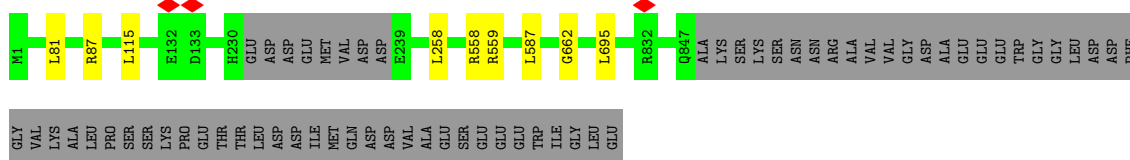
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
64	CI	1	1	1	0

3 Residue-property plots [i](#)

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

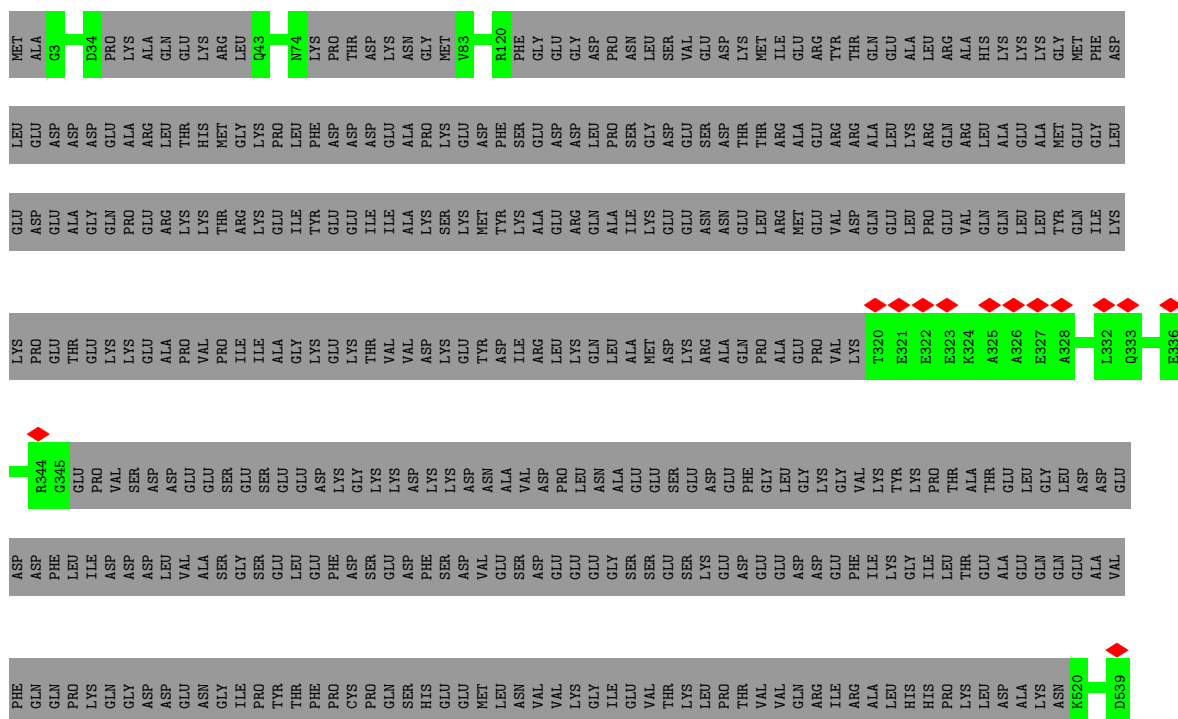
- Molecule 1: Periodic tryptophan protein 2-like protein

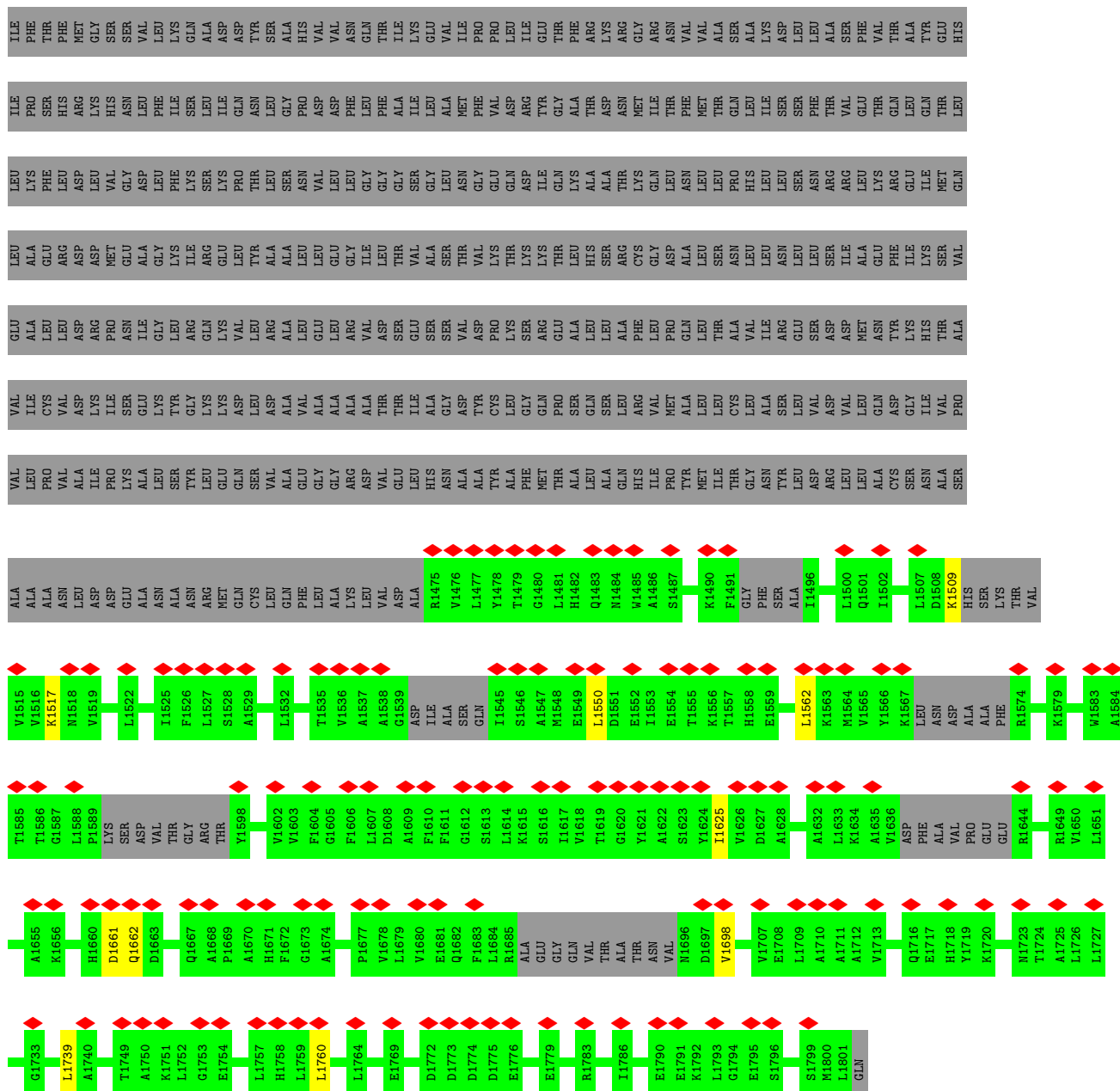
Chain UA:  92% 7%



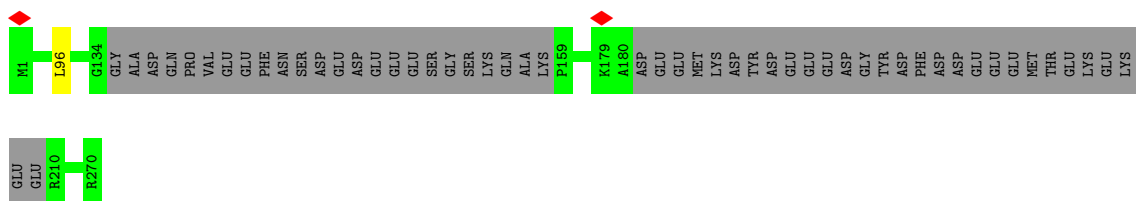
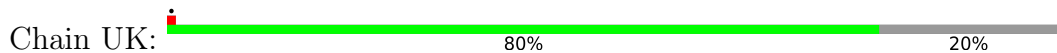
- Molecule 2: Utp2

Chain UB:  56% 44%

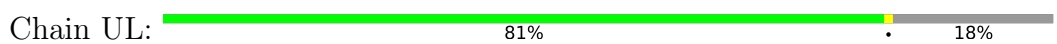


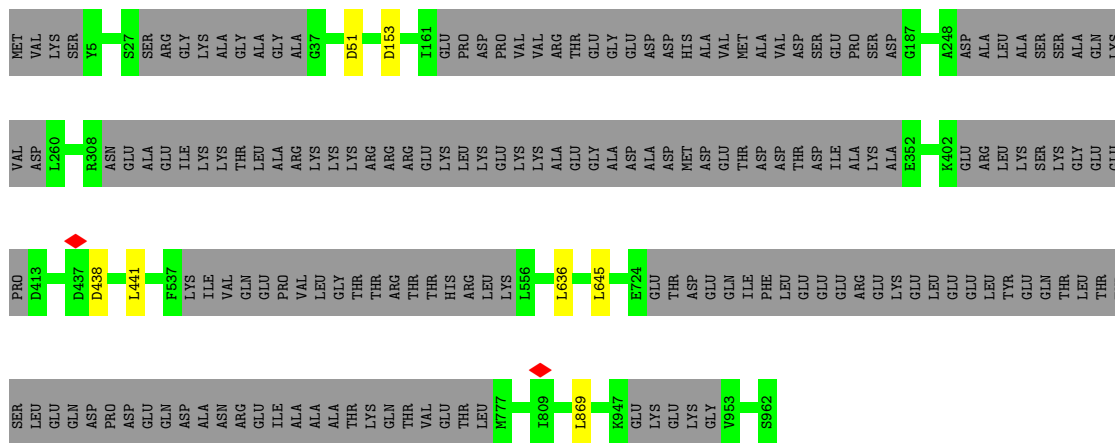


• Molecule 8: U3 small nucleolar RNA-associated protein 11

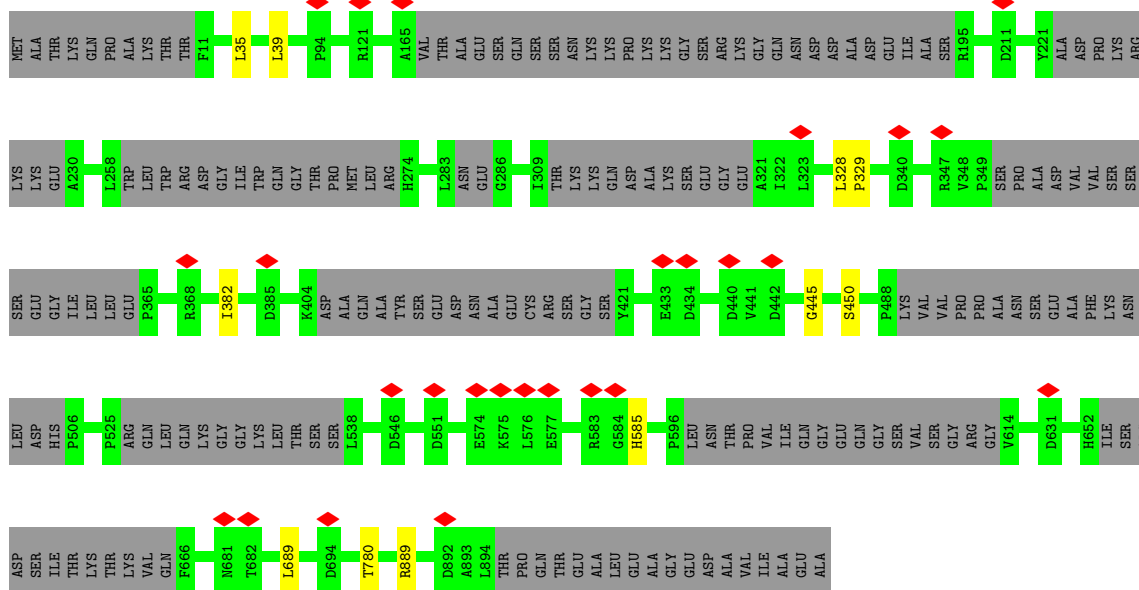
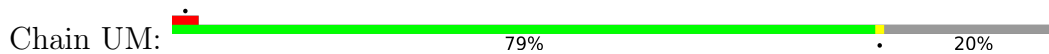


• Molecule 9: Utp12

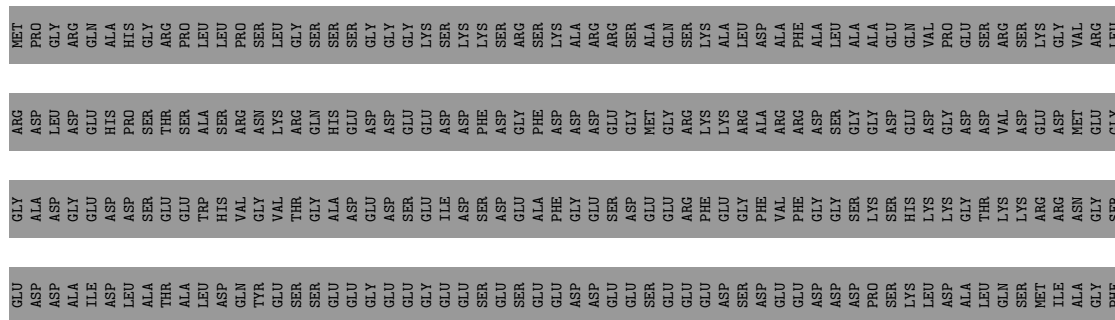


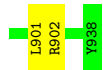
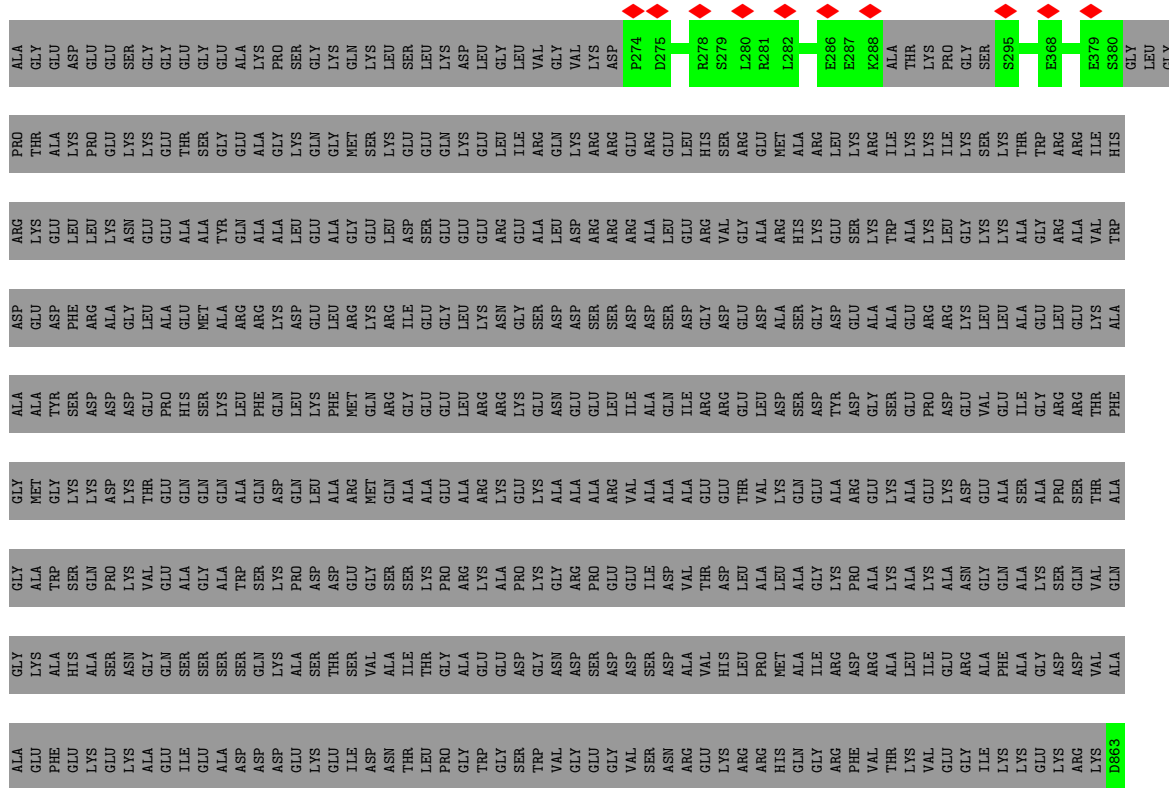


• Molecule 10: Utp13

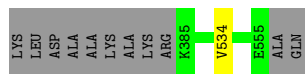


• Molecule 11: Utp14

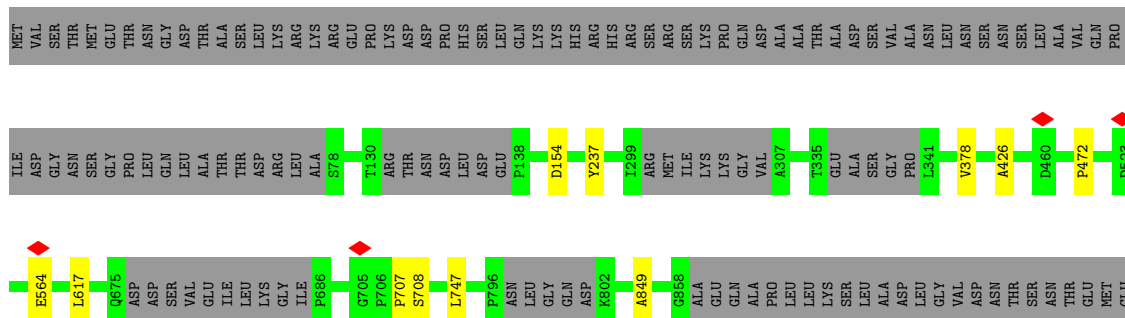
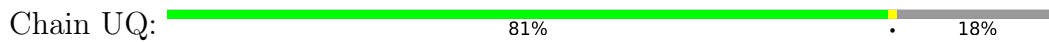


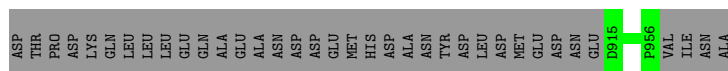


• Molecule 12: Utp15



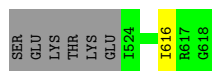
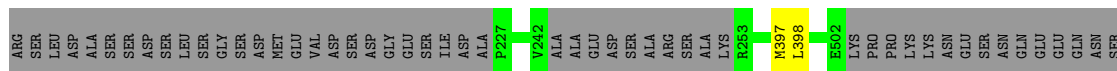
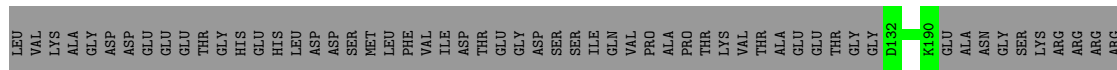
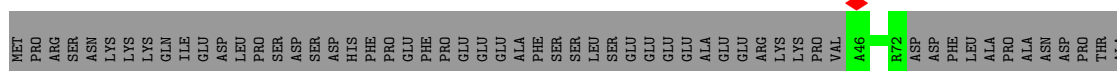
• Molecule 13: Utp17






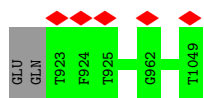
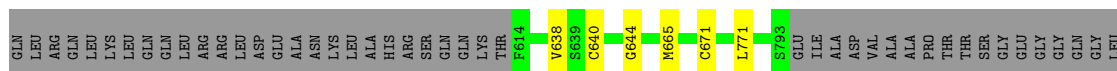
- Molecule 14: Utp18

Chain UR:  72% 28%



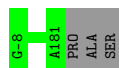
- Molecule 15: Putative U3 snoRNP protein

Chain UU:  85% 14%



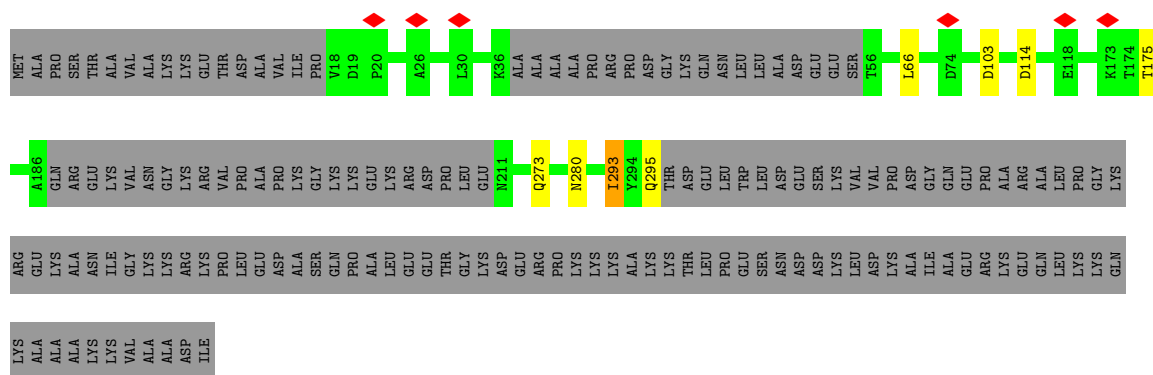
- Molecule 16: Utp24

Chain UX:  98%

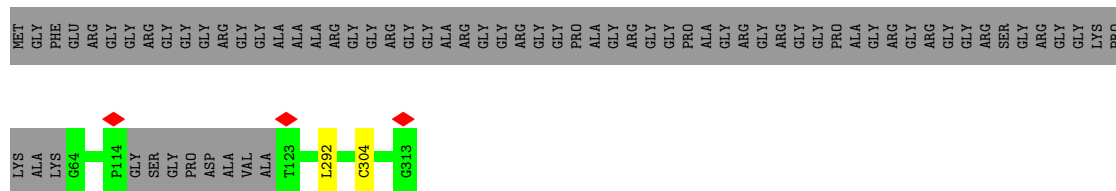
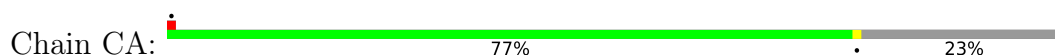


- Molecule 17: Utp30

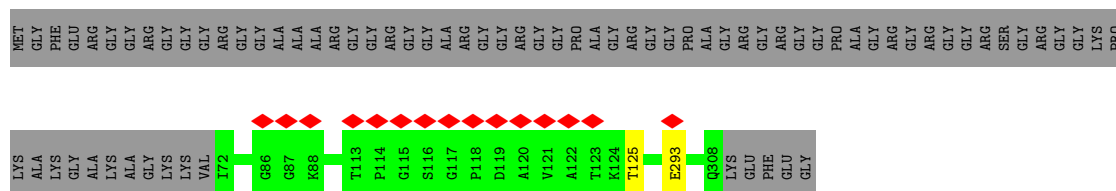
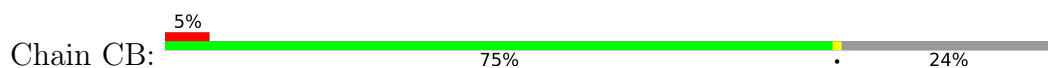
Chain UZ:  58% 40%



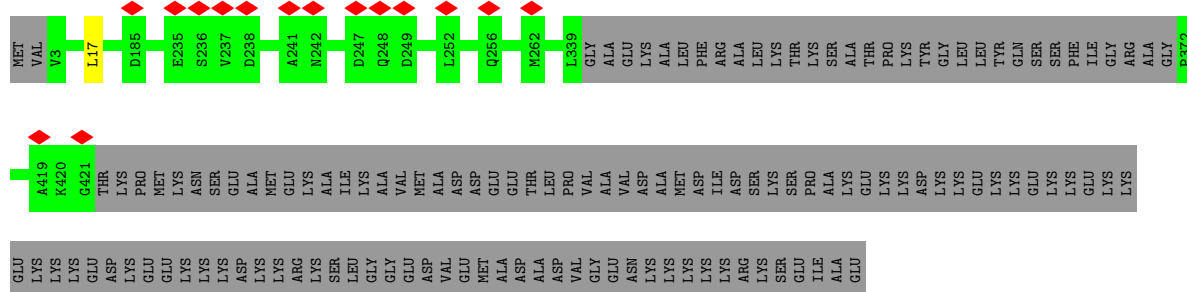
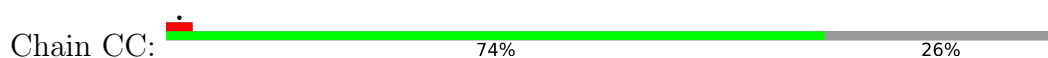
● Molecule 18: Nop1



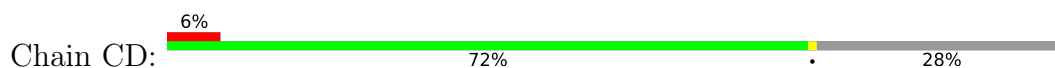
● Molecule 18: Nop1

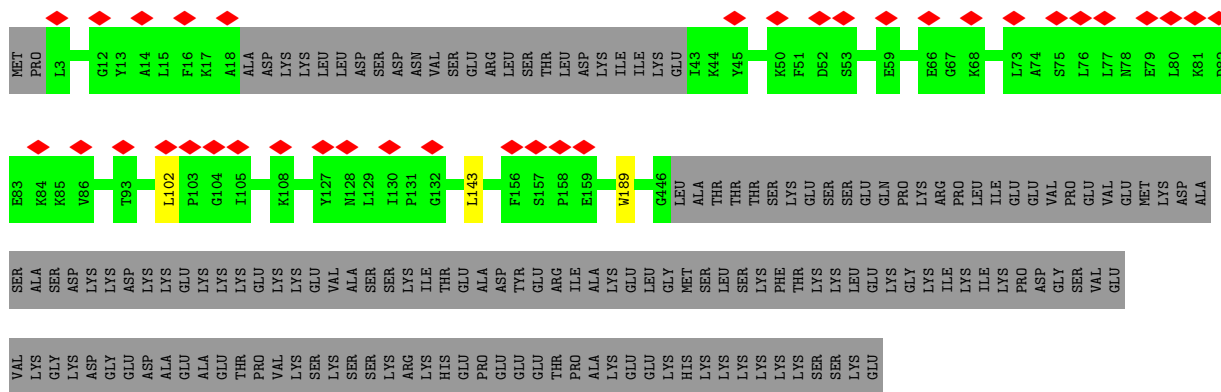


● Molecule 19: Nop56

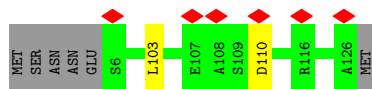


● Molecule 20: Nop58

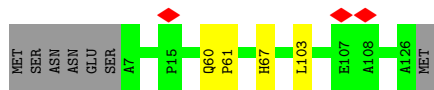




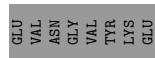
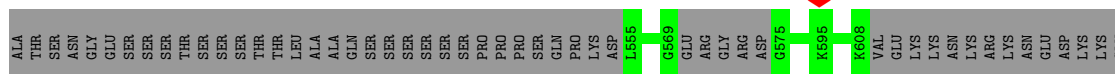
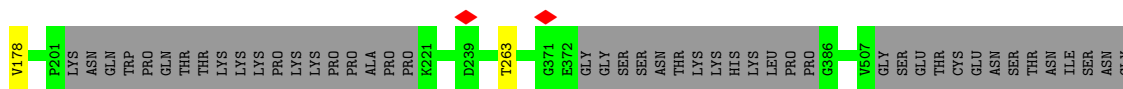
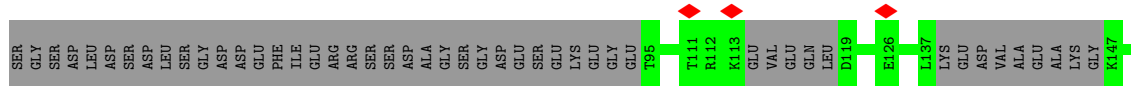
• Molecule 21: Snu13



• Molecule 21: Snu13



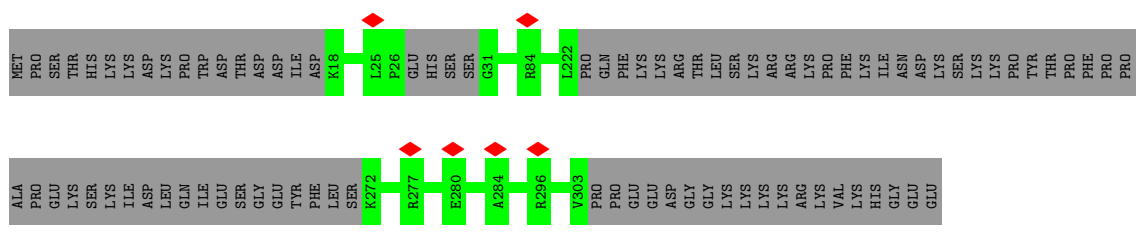
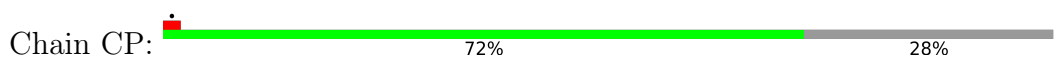
• Molecule 22: Rrp9



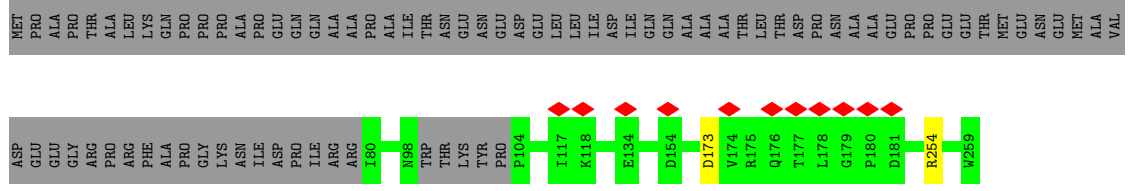
• Molecule 23: RNA 3'-terminal phosphate cyclase-like protein



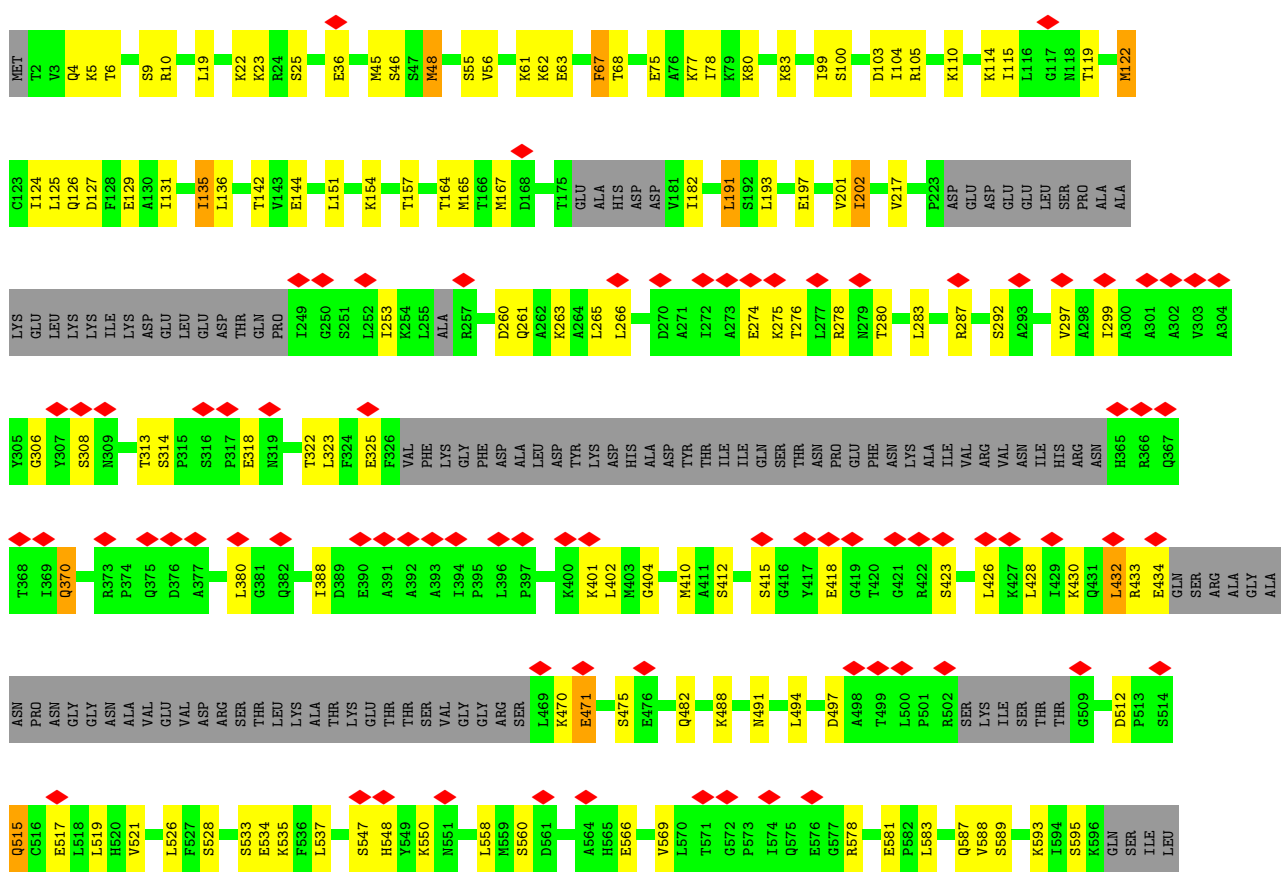
• Molecule 30: KRR1 small subunit processome component

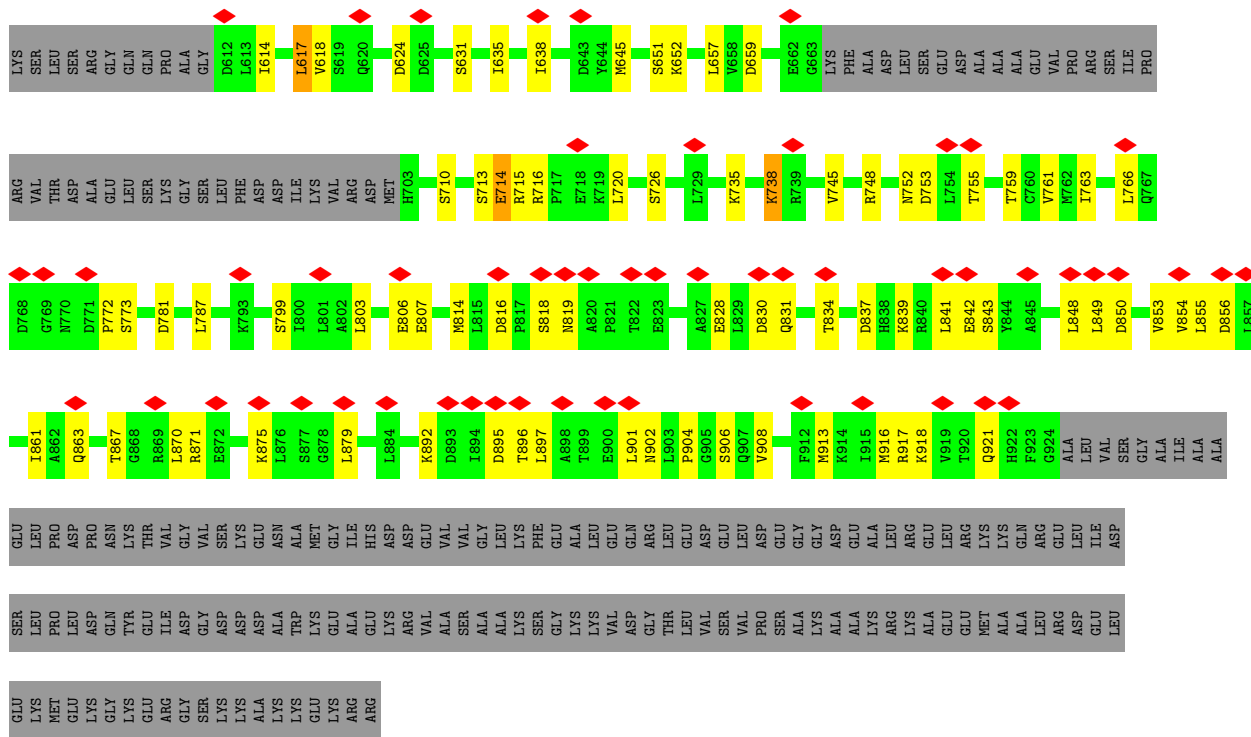


• Molecule 31: Pre-rRNA-processing protein PNO1

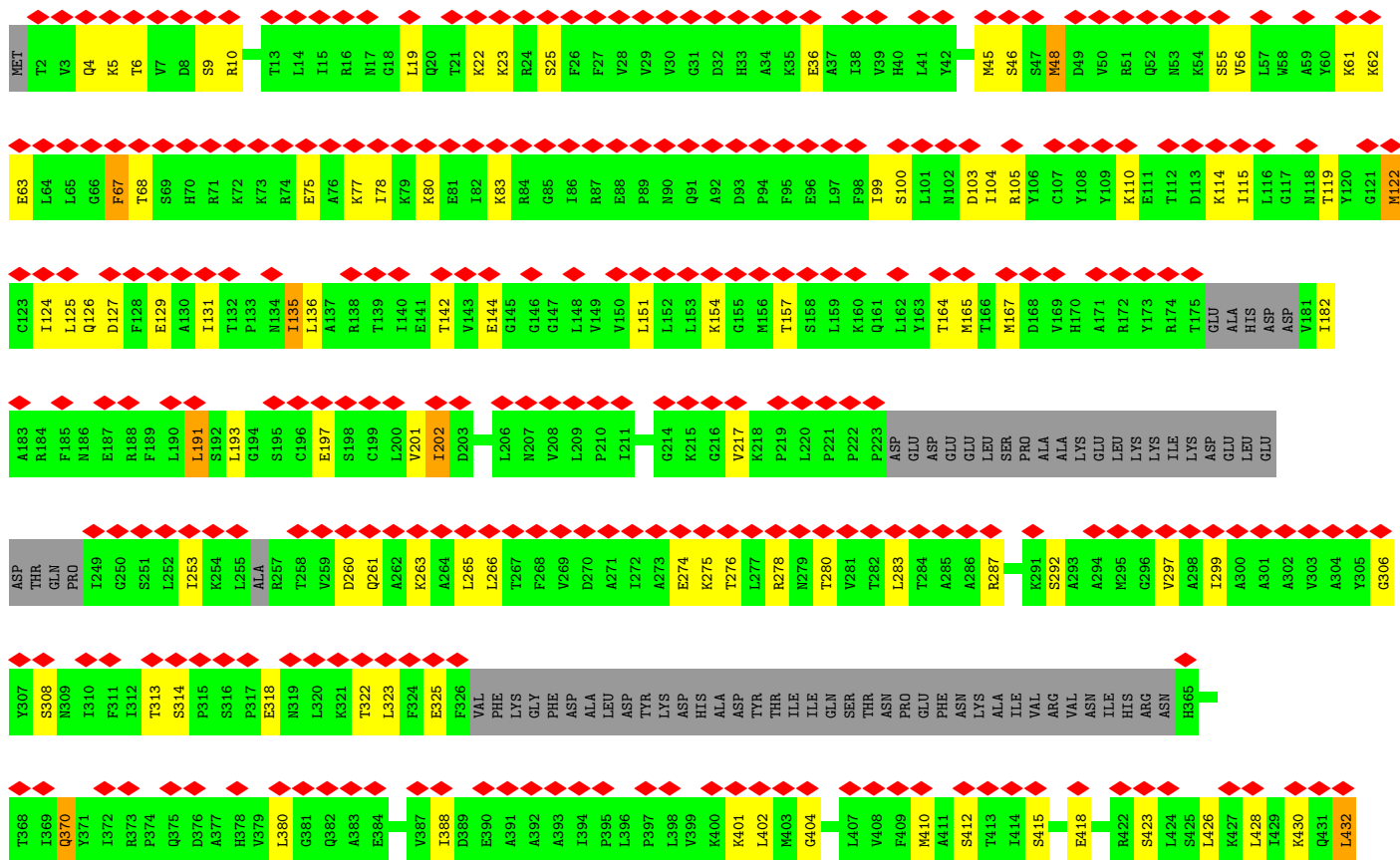
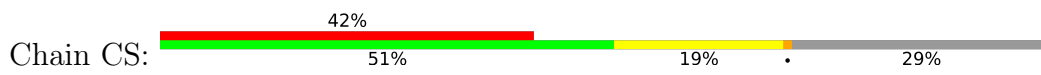


• Molecule 32: Kre33





● Molecule 32: Kre33



R433	E434	GLN	SER	ARG	ALA	GLY	ALA	ASN	PRO	SER	VAL	VAL	ASP	ARG	SER	THR	LEU	LYS	ALA	THR	LYS	LYS	GLU	THR	THR	THR	SER	SER	VAL	GLY	GLY	ARG	SER	L469	K470	E471	I472	T473	L474	S475	E476	P477	I478	R479	Y480	A481	Q482	G483	D484	E487	K488	W489	L490	W491	L494										
C495	L496	D497	T499	L500	P501	R502	SER	LYS	ILE	GLY	THR	THR	G509	D512	Q515	C516	E517	L518	L519	V521	W522	T525	L526	F527	S528	F529	H530	P531	V532	S533	E534	K535	F536	L537	Q538	A546	S547	H548	Y549	K550	N551	S552	P553	N554	D555	L556	Q557	L558	S560	P563															
E566	L567	F568	V569	T571	G572	P573	I574	Q575	E576	G577	R578	L579	P580	E581	P582	L583	C584	V585	I586	Q587	H520	L588	S589	L590	E591	G592	K593	I594	S595	K596	GLN	SER	ILE	LEU	LYS	SER	LEU	SER	LEU	SER	VAL	PRO	GLN	GLN	PRO	ALA	D612	L613	I614	L617	V618	S619	F622	Q623	D624	D625	E626	F627							
A628	S629	L630	S631	R634	I635	V636	R637	I638	P642	D643	Y644	M645	S646	H647	S651	K652	A653	L656	L657	V658	D659	G663	LYS	PHE	ALA	ASP	LEU	LEU	GLU	ASP	ALA	ALA	ALA	VAL	PRO	ARG	SER	ILE	PRO	ARG	VAL	THR	ASP	ALA	GLU	LEU	LYS	GLY	SER	LEU	PHE	ASP													
ASP	ILE	LYS	VAL	ARG	ASP	MET	H703	E704	L708	F709	S710	K711	L712	S713	E714	R715	R716	K719	L720	D721	Y722	V723	G724	V725	S726	Y727	G728	L729	T730	Q731	Q732	L733	H734	K735	K738	R739	V745	R748	Q749	T750	A751	N752	D753	L754	T755	T759	C760	V761	M762	I763	R764	P765	L766												
Q767	D768	G769	N770	D771	F772	S773	G776	A777	F778	A779	D781	L787	K793	E796	F797	S798	L800	L803	E806	E807	A811	G812	A813	M814	L815	D816	S818	M819	A820	E823	L824	E828	L829	D830	Q831	T834	F835	F836	D837	H838	K839	R840	L841	E842	S843																				
G847	L848	L849	D850	V853	L855	L856	L857	H858	I861	A862	Q863	T867	G868	R869	L870	R871	K875	L879	L883	L887	K882	D893	L894	D895	T896	L897	A898	T899	E900	L901	N902	L903	P904	G905	S906	S907	V908	F912	M913	M916	R917	X918	Q921	H922	F923	G924	ALA																		
LEU	VAL	SER	GLY	ALA	ILE	ALA	ALA	PRO	PRO	ASP	ASN	LYS	VAL	VAL	SER	LYS	GLU	ALA	ASN	ALA	TRP	LYS	MET	GLY	ILE	HIS	ASP	ASP	VAL	VAL	VAL	GLY	ALA	LEU	LYS	PHE	SER	GLY	ALA	VAL	GLN	ARG	LEU	LEU	ASP	VAL	VAL	VAL	PRO	PRO	PRO	ALA	ALA	ALA	LYS	ALA	ALA	ARG	LYS	ALA	GLU	LEU	ARG		
LYS	LYS	GLN	ARG	LEU	GLU	ILE	ASP	ASP	LEU	PRO	ASP	LEU	ASP	GLN	TYR	THR	ILE	ASP	GLY	VAL	ASP	ASP	LYS	ASP	GLU	ALA	ALA	ALA	ALA	VAL	ALA	ALA	ALA	LEU	LEU	GLY	THR	GLY	GLN	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
MET	ALA	ALA	LEU	ARG	GLY	LEU	GLU	GLY	LYS	GLY	LYS	GLY	SER	LYS	LYS	ASP	ALA	LYS	ALA	ALA	LYS	GLY	LYS	ARG	ARG	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA		

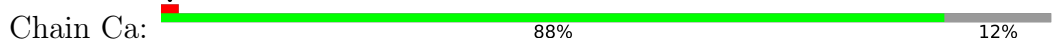
• Molecule 33: Fcf2



MET	ALA	THR	THR	LEU	GLY	LEU	PRO	ASP	GLU	GLU	GLU	ILE	ASP	ARG	LEU	ALA	ALA	ALA	GLU	VAL	GLY	VAL	VAL	ALA	ALA	GLY	GLY	ALA	ALA	VAL	VAL	THR	LEU	VAL	VAL	VAL	PRO	ALA	ALA	ALA	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

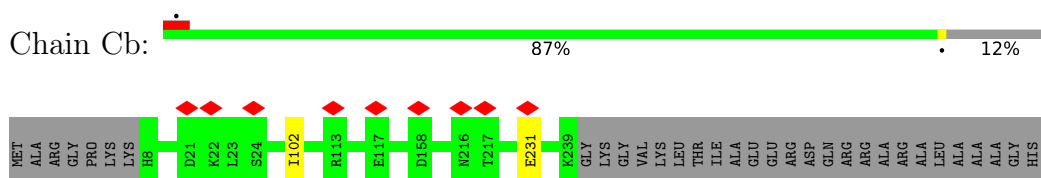
PRO	GLN	VAL	LYS	LYS	ALA	GLU	E866	P777	GLN	LYS	LYS	LYS	G82	R202	LYS
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• Molecule 34: 40S ribosomal protein S1

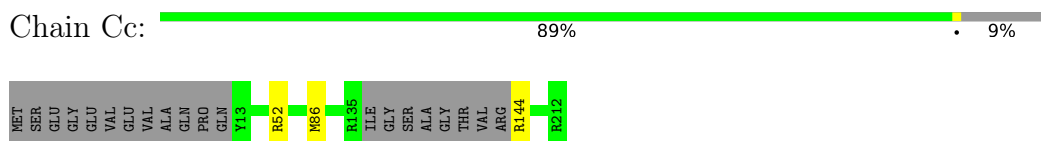


MET	ALA	VAL	GLY	LYS	ASN	LYS	R9	Q21	D42	D59	A230	L231	H232	GLY	GLU	SER	SER	GLU	GLY	GLY	LYS	LYS	VAL	VAL	GLU	ARG	ARG	GLU	PHE	ARG	GLN	GLN	VAL	VAL	LEU	GLU	LEU	SER	VAL
-----	-----	-----	-----	-----	-----	-----	----	-----	-----	-----	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

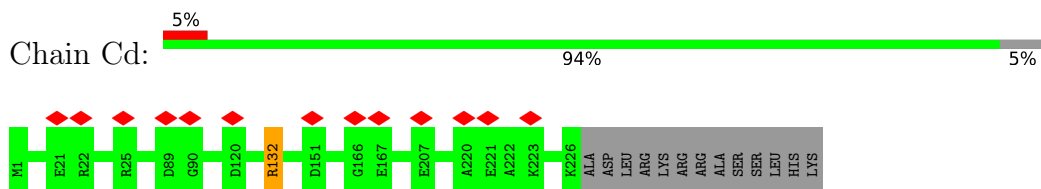
- Molecule 35: 40S ribosomal protein S4



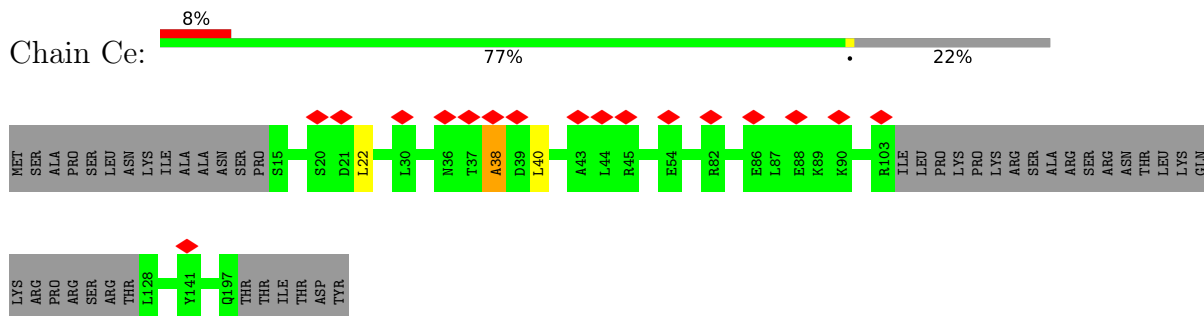
- Molecule 36: 40S ribosomal protein s5-like protein



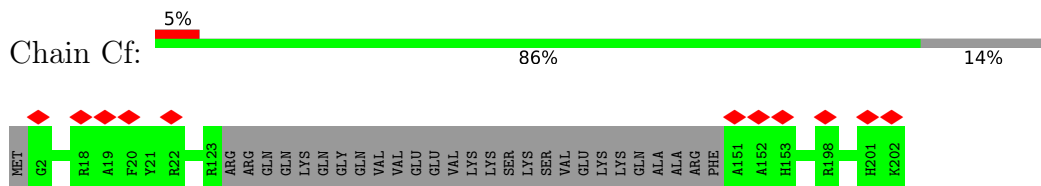
- Molecule 37: 40S ribosomal protein S6



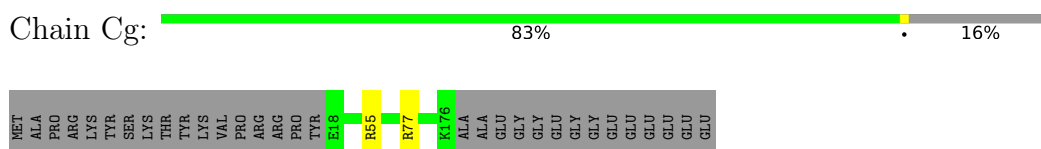
- Molecule 38: 40S ribosomal protein S7



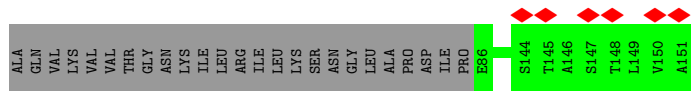
- Molecule 39: 40S ribosomal protein S8



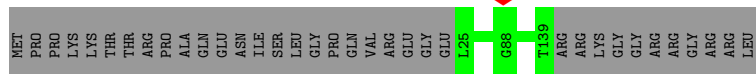
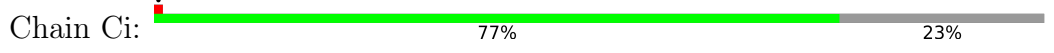
- Molecule 40: 40S ribosomal protein s9-like protein



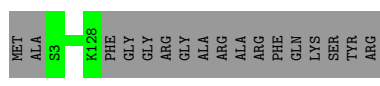
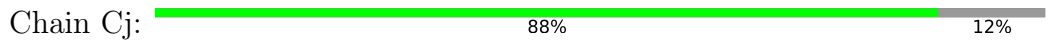
- Molecule 41: 40S ribosomal protein S13-like protein



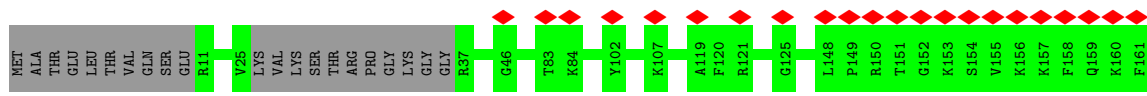
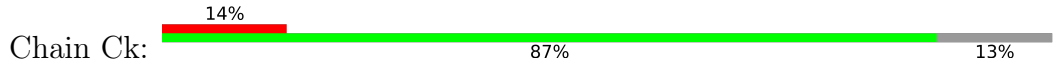
• Molecule 42: 40S ribosomal protein S14-like protein



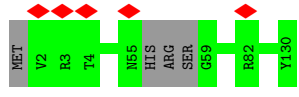
• Molecule 43: 40S ribosomal protein S16-like protein



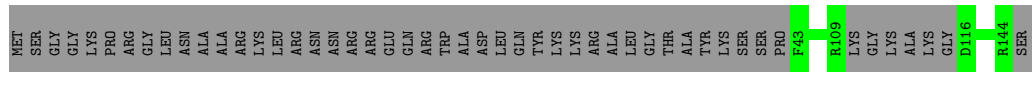
• Molecule 44: 40S ribosomal protein S11-like protein



• Molecule 45: 40S ribosomal protein S22-like protein

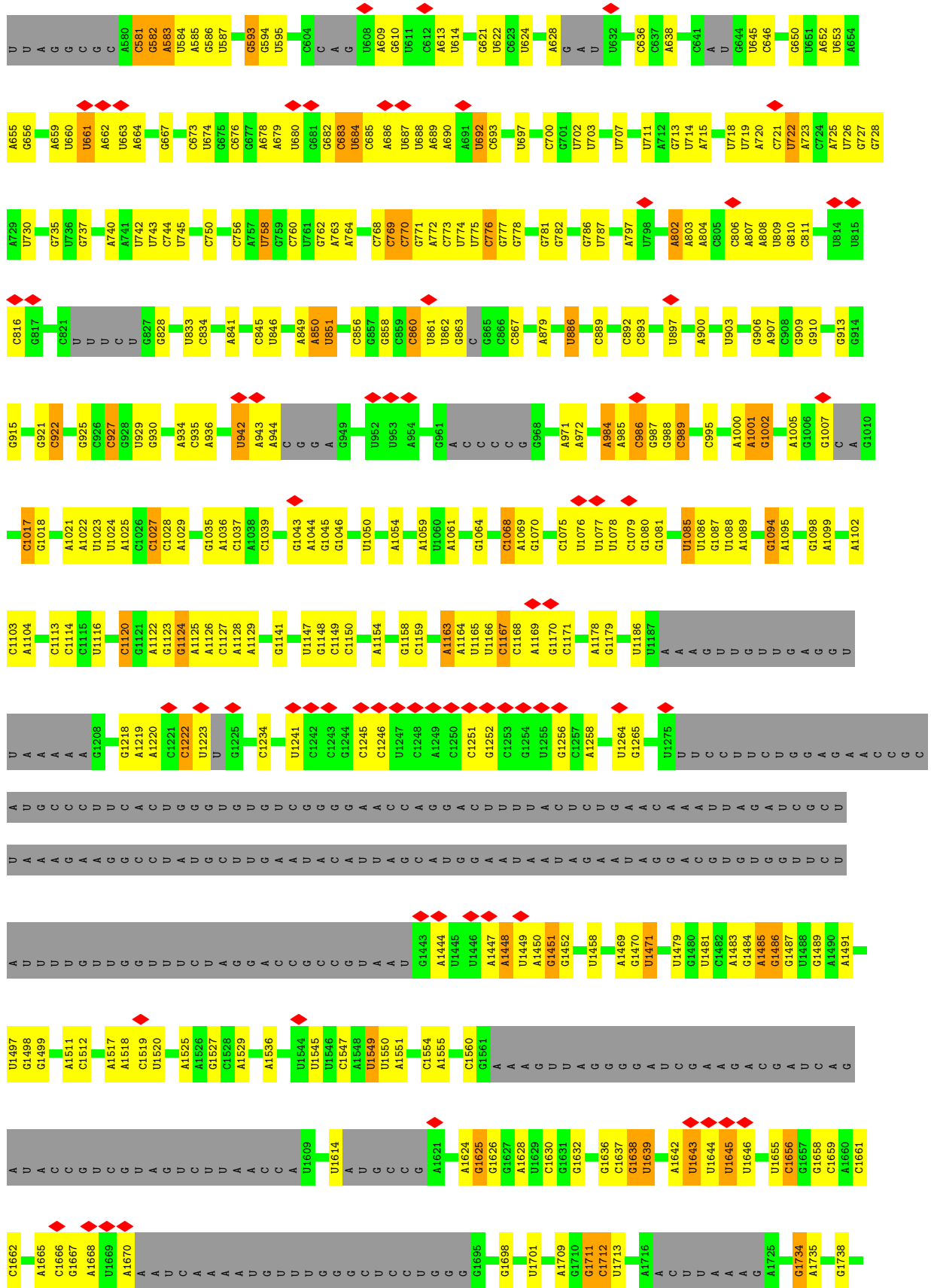


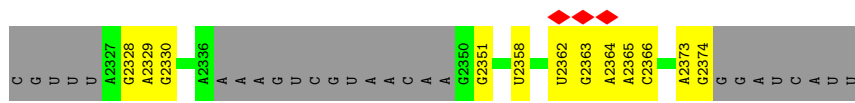
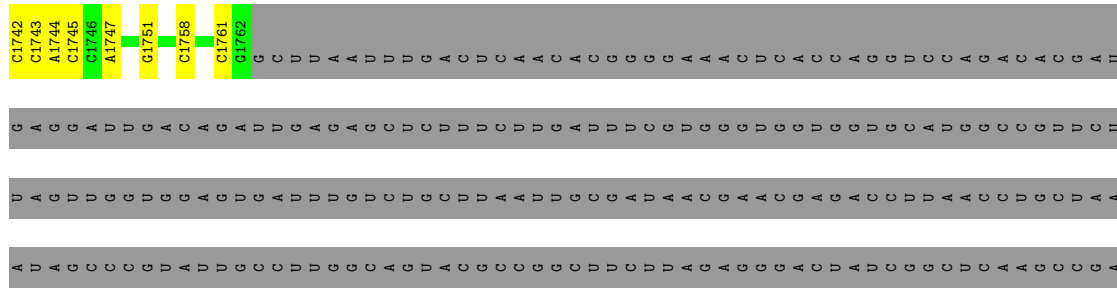
• Molecule 46: 40S ribosomal protein s23-like protein



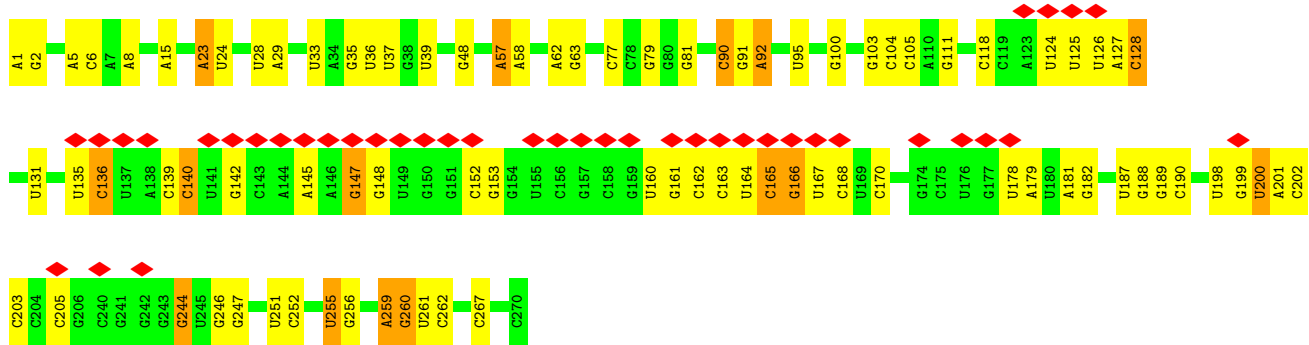
• Molecule 47: 40S ribosomal protein S24



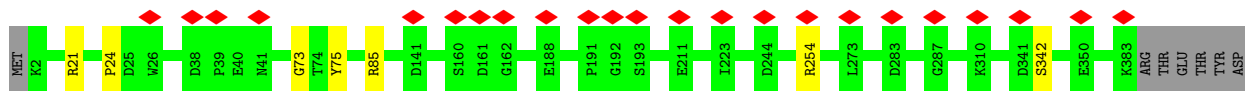


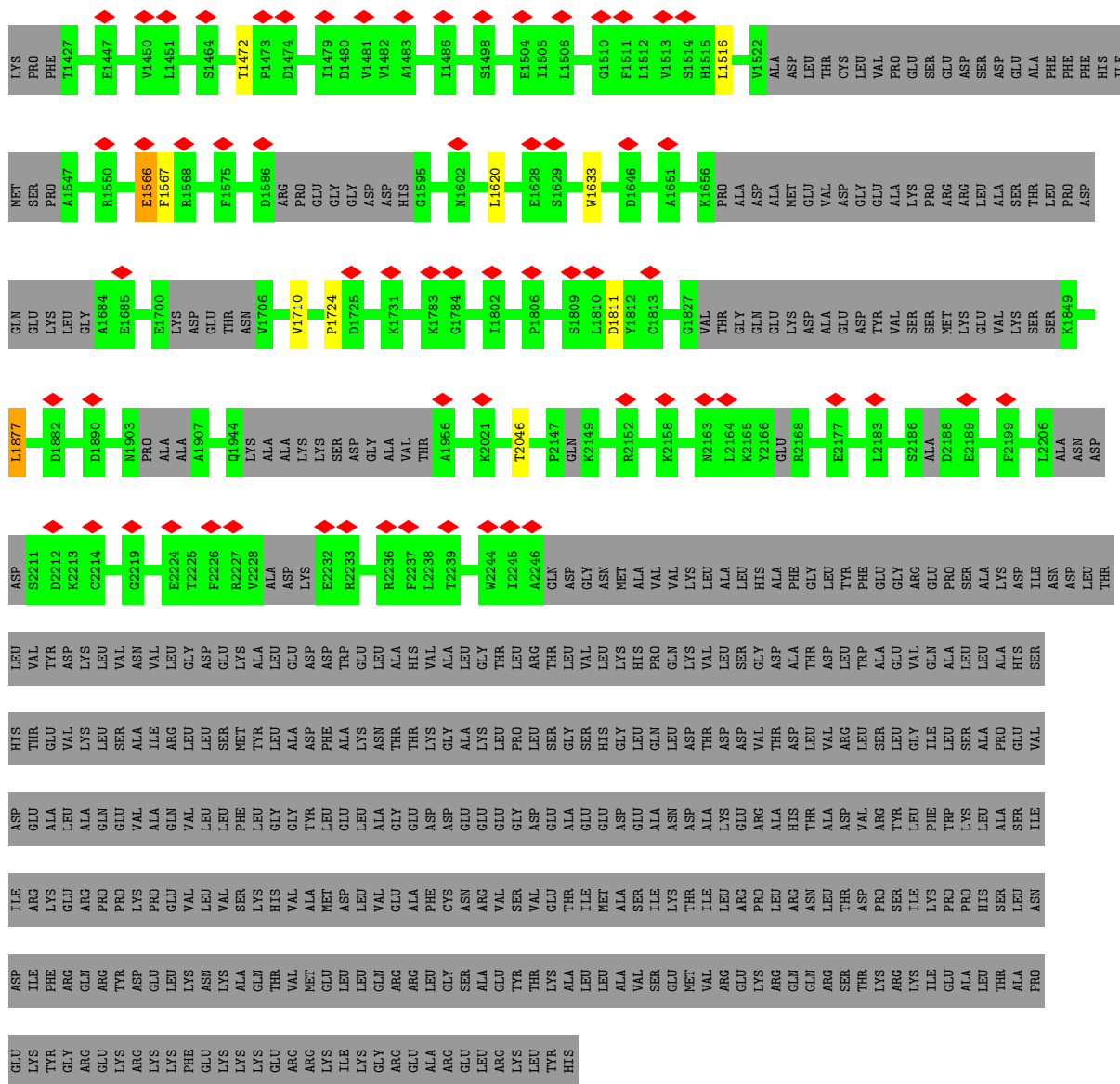


● Molecule 51: U3 snoRNA

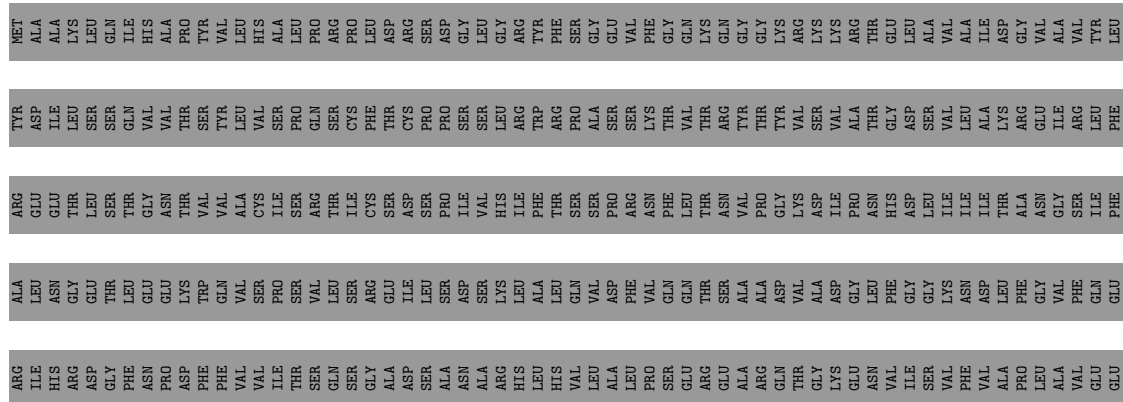


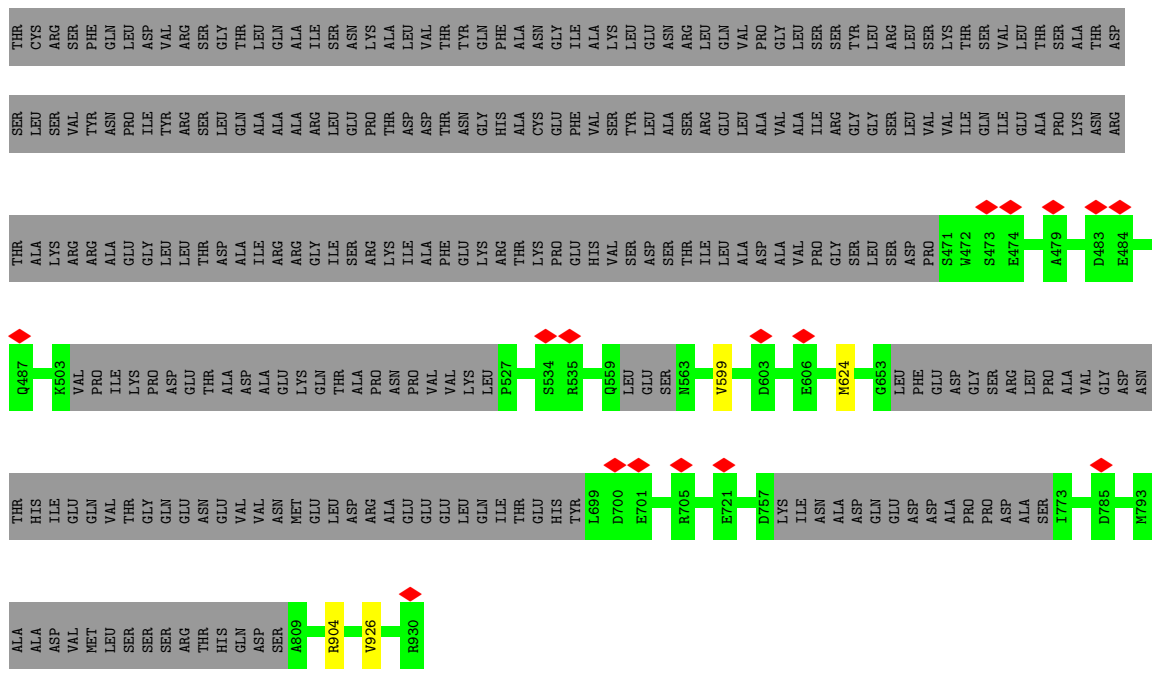
● Molecule 52: Ribosome biogenesis protein ENP2



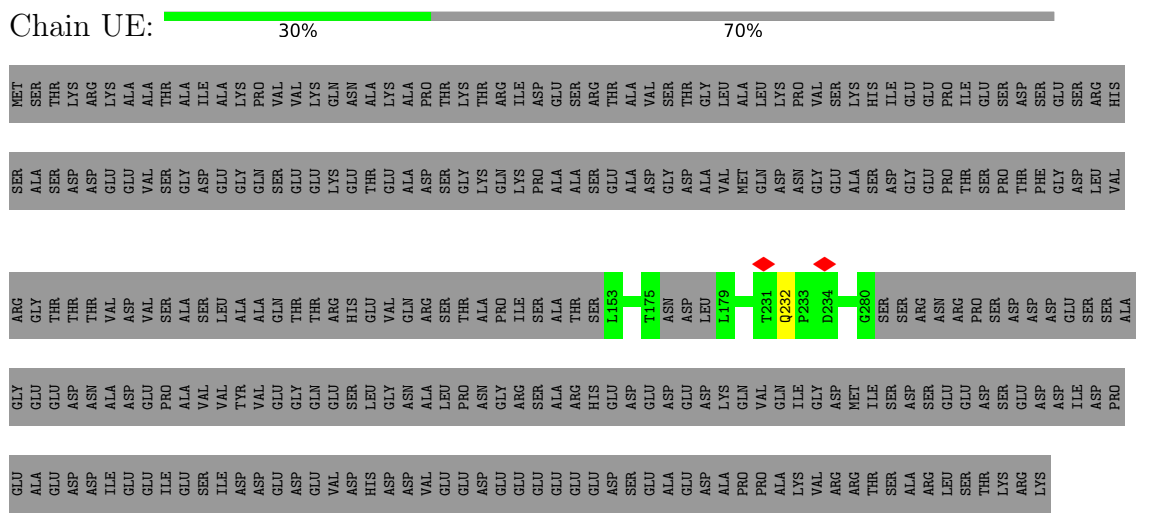


• Molecule 54: Utp8

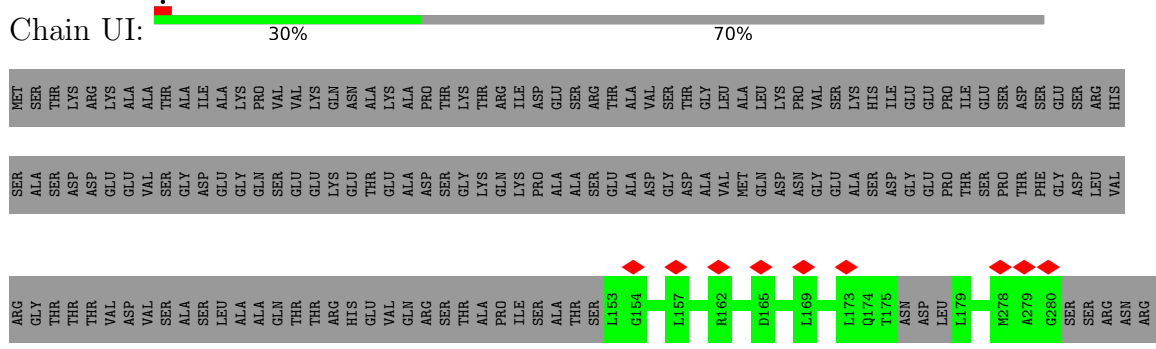


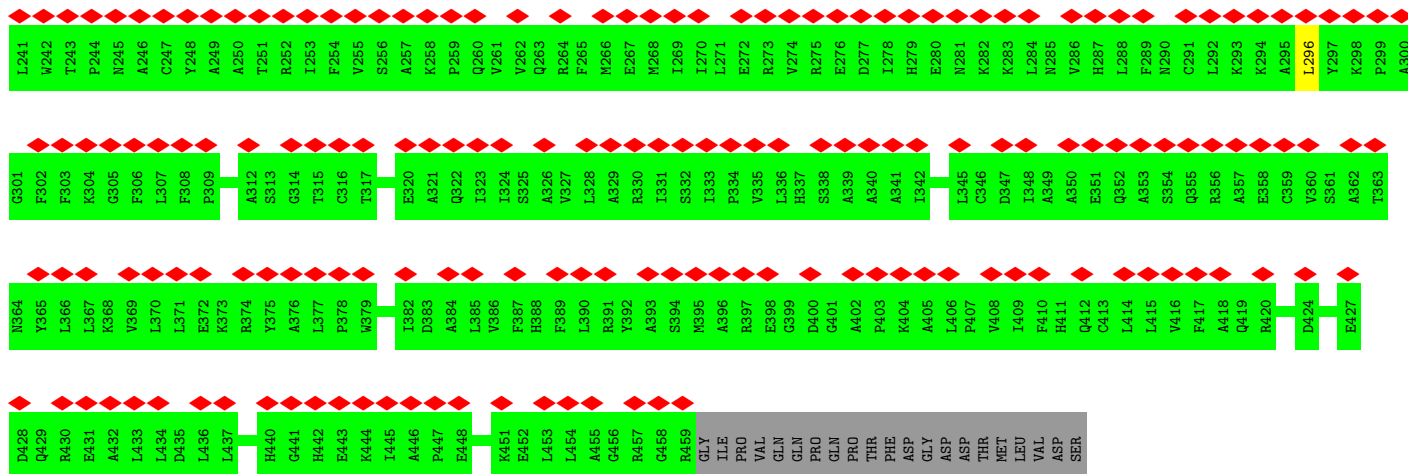


• Molecule 55: Utp5

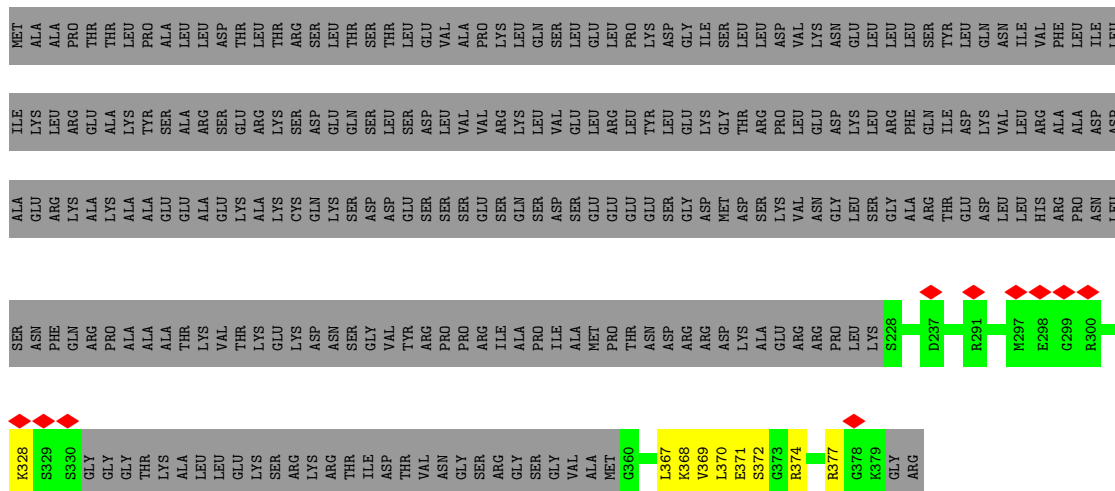


• Molecule 55: Utp5

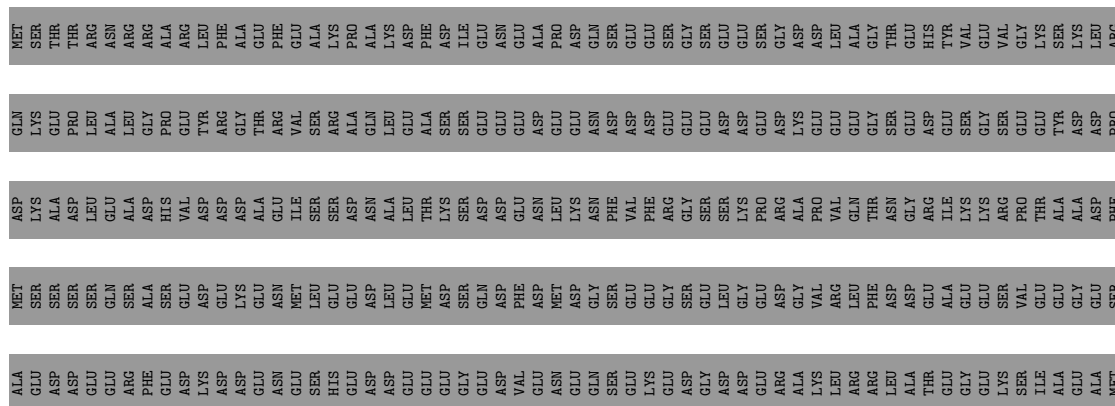




• Molecule 59: U3 small nucleolar ribonucleoprotein protein lcp5-like protein



• Molecule 60: Bfr2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	343726	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.359	Depositor
Minimum map value	-0.237	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	520.32, 520.32, 520.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, GTP

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	UA	0.47	0/6521	0.65	5/8867 (0.1%)
2	UB	0.33	0/4154	0.54	2/5583 (0.0%)
3	UC	0.40	0/595	0.52	0/786
4	UD	0.38	0/6211	0.56	2/8408 (0.0%)
5	UF	0.35	0/2657	0.54	1/3596 (0.0%)
6	UG	0.47	0/3790	0.62	3/5120 (0.1%)
7	UJ	0.34	0/8567	0.61	5/11619 (0.0%)
8	UK	0.41	0/1701	0.52	1/2251 (0.0%)
9	UL	0.37	0/6299	0.63	4/8531 (0.0%)
10	UM	0.33	0/5755	0.61	2/7827 (0.0%)
11	UN	0.39	0/1425	0.55	1/1913 (0.1%)
12	UO	0.41	0/3903	0.61	3/5312 (0.1%)
13	UQ	0.40	0/6136	0.63	4/8348 (0.0%)
14	UR	0.43	0/3564	0.59	1/4816 (0.0%)
15	UU	0.45	1/6903 (0.0%)	0.60	2/9392 (0.0%)
16	UX	0.42	0/1493	0.59	0/2011
17	UZ	0.34	0/1861	0.61	1/2531 (0.0%)
18	CA	0.46	0/1814	0.60	0/2456
18	CB	0.34	0/1853	0.54	0/2511
19	CC	0.37	0/2911	0.58	1/3937 (0.0%)
20	CD	0.36	0/3205	0.60	3/4338 (0.1%)
21	CE	0.45	0/891	0.66	2/1214 (0.2%)
21	CF	0.41	0/876	0.64	1/1195 (0.1%)
22	CG	0.36	0/3307	0.59	0/4462
23	CH	0.38	0/2939	0.58	1/3988 (0.0%)
24	CI	0.42	0/6631	0.58	1/8943 (0.0%)
25	CJ	0.48	0/1462	0.56	0/1967
26	CK	0.45	0/2376	0.64	2/3214 (0.1%)
27	CL	0.37	0/1812	0.51	0/2437
28	CM	0.48	0/3573	0.60	0/4829
29	CN	0.36	0/1797	0.56	1/2443 (0.0%)
29	CO	0.31	0/1714	0.55	0/2325

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	CP	0.34	0/1923	0.56	0/2577
31	CQ	0.30	0/1379	0.57	0/1850
32	CR	0.40	0/6108	0.80	14/8266 (0.2%)
32	CS	0.40	0/6108	0.80	14/8266 (0.2%)
33	CT	0.43	0/1053	0.58	0/1413
34	Ca	0.35	0/1850	0.61	0/2486
35	Cb	0.32	0/1890	0.61	1/2548 (0.0%)
36	Cc	0.40	0/1485	0.54	0/2008
37	Cd	0.34	0/1850	0.55	0/2474
38	Ce	0.34	0/1298	0.66	3/1750 (0.2%)
39	Cf	0.33	0/1429	0.54	0/1915
40	Cg	0.39	0/1259	0.55	0/1687
41	Ch	0.32	0/557	0.51	0/749
42	Ci	0.34	0/819	0.54	0/1107
43	Cj	0.49	0/958	0.60	0/1293
44	Ck	0.30	0/1190	0.54	0/1592
45	Cm	0.41	0/1001	0.57	0/1345
46	Cn	0.44	0/712	0.56	0/954
47	Co	0.32	0/754	0.59	0/1011
48	Cp	0.44	0/458	0.61	1/617 (0.2%)
49	CU	0.32	0/1350	0.53	0/1810
50	C1	0.61	1/37546 (0.0%)	1.24	401/58475 (0.7%)
51	C2	0.64	0/5459	1.40	72/8498 (0.8%)
52	CW	0.33	0/2996	0.67	2/4075 (0.0%)
53	UT	0.34	0/16371	0.63	10/22154 (0.0%)
54	UH	0.33	0/2852	0.56	0/3846
55	UE	0.31	0/980	0.58	0/1316
55	UI	0.26	0/980	0.52	0/1316
56	US	0.33	0/3765	0.57	1/5100 (0.0%)
57	CI	0.30	0/638	0.60	0/857
58	CX	0.28	0/2180	0.55	1/2956 (0.0%)
59	CY	0.36	0/986	0.53	0/1303
60	CZ	0.39	0/384	0.68	0/511
61	UP	0.34	0/428	0.60	0/570
All	All	0.44	2/219692 (0.0%)	0.80	569/305865 (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
1	UA	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
4	UD	0	1
7	UJ	0	2
9	UL	0	2
10	UM	0	4
12	UO	0	1
13	UQ	0	4
14	UR	0	1
15	UU	0	3
17	UZ	0	3
18	CB	0	1
21	CF	0	1
22	CG	0	1
23	CH	0	1
24	CI	0	2
26	CK	0	1
28	CM	0	1
29	CO	0	2
31	CQ	0	1
32	CR	0	3
32	CS	0	3
35	Cb	0	1
36	Cc	0	1
37	Cd	0	1
38	Ce	0	1
52	CW	0	2
53	UT	0	10
55	UE	0	1
56	US	0	1
57	CI	0	1
59	CY	0	1
All	All	0	59

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	C1	1081	G	C2-N3	-5.49	1.28	1.32
15	UU	640	CYS	CB-SG	-5.31	1.73	1.81

The worst 5 of 569 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	C2	2	G	O5'-P-OP1	-30.49	74.11	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	C2	2	G	OP1-P-OP2	-27.27	78.70	119.60
51	C2	2	G	O5'-P-OP2	18.13	132.46	110.70
51	C2	1	A	OP1-P-O3'	13.81	135.58	105.20
51	C2	1	A	OP2-P-O3'	-13.14	76.29	105.20

There are no chirality outliers.

5 of 59 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	UA	115	LEU	Peptide
4	UD	387	TRP	Peptide
7	UJ	1661	ASP	Peptide
7	UJ	1662	GLN	Peptide
9	UL	153	ASP	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	UA	835/904 (92%)	768 (92%)	67 (8%)	0	100	100
2	UB	502/907 (55%)	470 (94%)	32 (6%)	0	100	100
3	UC	72/648 (11%)	64 (89%)	8 (11%)	0	100	100
4	UD	754/884 (85%)	722 (96%)	32 (4%)	0	100	100
5	UF	325/414 (78%)	310 (95%)	14 (4%)	1 (0%)	41	75
6	UG	475/558 (85%)	441 (93%)	32 (7%)	2 (0%)	34	72
7	UJ	1062/1802 (59%)	1010 (95%)	52 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	UK	211/270 (78%)	210 (100%)	1 (0%)	0	100	100
9	UL	767/962 (80%)	711 (93%)	56 (7%)	0	100	100
10	UM	705/912 (77%)	656 (93%)	48 (7%)	1 (0%)	51	84
11	UN	171/938 (18%)	167 (98%)	3 (2%)	1 (1%)	25	64
12	UO	498/557 (89%)	474 (95%)	24 (5%)	0	100	100
13	UQ	775/960 (81%)	712 (92%)	61 (8%)	2 (0%)	41	75
14	UR	437/618 (71%)	416 (95%)	21 (5%)	0	100	100
15	UU	890/1049 (85%)	832 (94%)	58 (6%)	0	100	100
16	UX	188/193 (97%)	176 (94%)	12 (6%)	0	100	100
17	UZ	229/391 (59%)	212 (93%)	16 (7%)	1 (0%)	34	72
18	CA	238/313 (76%)	225 (94%)	13 (6%)	0	100	100
18	CB	235/313 (75%)	220 (94%)	15 (6%)	0	100	100
19	CC	383/523 (73%)	367 (96%)	16 (4%)	0	100	100
20	CD	416/582 (72%)	393 (94%)	23 (6%)	0	100	100
21	CE	119/127 (94%)	111 (93%)	8 (7%)	0	100	100
21	CF	118/127 (93%)	110 (93%)	7 (6%)	1 (1%)	19	58
22	CG	402/630 (64%)	375 (93%)	27 (7%)	0	100	100
23	CH	383/411 (93%)	344 (90%)	38 (10%)	1 (0%)	41	75
24	CI	812/1163 (70%)	761 (94%)	49 (6%)	2 (0%)	47	81
25	CJ	177/183 (97%)	166 (94%)	11 (6%)	0	100	100
26	CK	295/297 (99%)	284 (96%)	11 (4%)	0	100	100
27	CL	225/785 (29%)	212 (94%)	12 (5%)	1 (0%)	34	72
28	CM	443/446 (99%)	417 (94%)	26 (6%)	0	100	100
29	CN	222/252 (88%)	210 (95%)	12 (5%)	0	100	100
29	CO	211/252 (84%)	197 (93%)	12 (6%)	2 (1%)	17	56
30	CP	227/322 (70%)	221 (97%)	6 (3%)	0	100	100
31	CQ	171/259 (66%)	164 (96%)	7 (4%)	0	100	100
32	CR	746/1073 (70%)	682 (91%)	60 (8%)	4 (0%)	29	68
32	CS	746/1073 (70%)	682 (91%)	60 (8%)	4 (0%)	29	68
33	CT	127/203 (63%)	119 (94%)	8 (6%)	0	100	100
34	Ca	223/255 (88%)	211 (95%)	12 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	Cb	230/264 (87%)	204 (89%)	26 (11%)	0	100	100
36	Cc	188/212 (89%)	179 (95%)	9 (5%)	0	100	100
37	Cd	224/239 (94%)	211 (94%)	13 (6%)	0	100	100
38	Ce	155/203 (76%)	140 (90%)	15 (10%)	0	100	100
39	Cf	170/202 (84%)	164 (96%)	6 (4%)	0	100	100
40	Cg	157/190 (83%)	152 (97%)	5 (3%)	0	100	100
41	Ch	64/151 (42%)	61 (95%)	3 (5%)	0	100	100
42	Ci	113/150 (75%)	106 (94%)	7 (6%)	0	100	100
43	Cj	124/143 (87%)	116 (94%)	8 (6%)	0	100	100
44	Ck	136/161 (84%)	129 (95%)	7 (5%)	0	100	100
45	Cm	122/130 (94%)	117 (96%)	5 (4%)	0	100	100
46	Cn	92/145 (63%)	89 (97%)	3 (3%)	0	100	100
47	Co	90/136 (66%)	82 (91%)	8 (9%)	0	100	100
48	Cp	59/68 (87%)	55 (93%)	4 (7%)	0	100	100
49	CU	168/311 (54%)	156 (93%)	12 (7%)	0	100	100
52	CW	380/668 (57%)	349 (92%)	31 (8%)	0	100	100
53	UT	1987/2612 (76%)	1871 (94%)	110 (6%)	6 (0%)	41	75
54	UH	349/930 (38%)	340 (97%)	9 (3%)	0	100	100
55	UE	121/410 (30%)	117 (97%)	4 (3%)	0	100	100
55	UI	121/410 (30%)	121 (100%)	0	0	100	100
56	US	443/549 (81%)	415 (94%)	28 (6%)	0	100	100
57	Cl	78/156 (50%)	73 (94%)	5 (6%)	0	100	100
58	CX	265/480 (55%)	255 (96%)	10 (4%)	0	100	100
59	CY	119/381 (31%)	109 (92%)	10 (8%)	0	100	100
60	CZ	42/609 (7%)	34 (81%)	8 (19%)	0	100	100
61	UP	52/364 (14%)	46 (88%)	5 (10%)	1 (2%)	8	40
All	All	21864/32830 (67%)	20513 (94%)	1321 (6%)	30 (0%)	54	84

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
29	CO	85	SER
53	UT	487	ILE

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Mol	Chain	Res	Type
6	UG	580	GLU
13	UQ	708	SER
17	UZ	293	ILE

5.3.2 Protein sidechains [i](#)

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	UA	651/775 (84%)	648 (100%)	3 (0%)	88	94
2	UB	425/788 (54%)	423 (100%)	2 (0%)	88	94
3	UC	61/536 (11%)	61 (100%)	0	100	100
4	UD	653/738 (88%)	652 (100%)	1 (0%)	93	98
5	UF	248/341 (73%)	248 (100%)	0	100	100
6	UG	373/474 (79%)	370 (99%)	3 (1%)	81	91
7	UJ	898/1526 (59%)	893 (99%)	5 (1%)	86	94
8	UK	159/227 (70%)	159 (100%)	0	100	100
9	UL	667/821 (81%)	666 (100%)	1 (0%)	93	98
10	UM	606/770 (79%)	602 (99%)	4 (1%)	84	93
11	UN	146/765 (19%)	146 (100%)	0	100	100
12	UO	404/456 (89%)	402 (100%)	2 (0%)	88	94
13	UQ	650/817 (80%)	649 (100%)	1 (0%)	93	98
14	UR	360/524 (69%)	359 (100%)	1 (0%)	92	97
15	UU	672/863 (78%)	669 (100%)	3 (0%)	91	96
16	UX	150/167 (90%)	150 (100%)	0	100	100
17	UZ	187/329 (57%)	183 (98%)	4 (2%)	53	79
18	CA	175/228 (77%)	173 (99%)	2 (1%)	73	88
18	CB	195/228 (86%)	194 (100%)	1 (0%)	88	94
19	CC	287/435 (66%)	287 (100%)	0	100	100
20	CD	319/489 (65%)	319 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	CE	91/108 (84%)	91 (100%)	0	100	100
21	CF	88/108 (82%)	87 (99%)	1 (1%)	73	88
22	CG	331/525 (63%)	330 (100%)	1 (0%)	92	97
23	CH	303/320 (95%)	301 (99%)	2 (1%)	84	93
24	CI	661/1009 (66%)	656 (99%)	5 (1%)	81	91
25	CJ	147/169 (87%)	147 (100%)	0	100	100
26	CK	245/266 (92%)	239 (98%)	6 (2%)	49	76
27	CL	181/642 (28%)	181 (100%)	0	100	100
28	CM	364/383 (95%)	362 (100%)	2 (0%)	88	94
29	CN	202/223 (91%)	202 (100%)	0	100	100
29	CO	193/223 (86%)	191 (99%)	2 (1%)	76	88
30	CP	202/287 (70%)	202 (100%)	0	100	100
31	CQ	145/215 (67%)	144 (99%)	1 (1%)	84	93
32	CR	654/916 (71%)	449 (69%)	205 (31%)	0	2
32	CS	654/916 (71%)	449 (69%)	205 (31%)	0	2
33	CT	108/167 (65%)	108 (100%)	0	100	100
34	Ca	198/223 (89%)	198 (100%)	0	100	100
35	Cb	199/221 (90%)	199 (100%)	0	100	100
36	Cc	149/178 (84%)	147 (99%)	2 (1%)	69	86
37	Cd	192/204 (94%)	191 (100%)	1 (0%)	88	94
38	Ce	137/177 (77%)	137 (100%)	0	100	100
39	Cf	139/164 (85%)	139 (100%)	0	100	100
40	Cg	122/162 (75%)	120 (98%)	2 (2%)	62	83
41	Ch	58/130 (45%)	58 (100%)	0	100	100
42	Ci	78/117 (67%)	78 (100%)	0	100	100
43	Cj	92/115 (80%)	92 (100%)	0	100	100
44	Ck	126/143 (88%)	126 (100%)	0	100	100
45	Cm	103/113 (91%)	103 (100%)	0	100	100
46	Cn	70/116 (60%)	70 (100%)	0	100	100
47	Co	79/115 (69%)	79 (100%)	0	100	100
48	Cp	46/61 (75%)	46 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	CU	137/260 (53%)	135 (98%)	2 (2%)	65	84
52	CW	309/587 (53%)	306 (99%)	3 (1%)	76	88
53	UT	1732/2276 (76%)	1719 (99%)	13 (1%)	81	91
54	UH	301/788 (38%)	297 (99%)	4 (1%)	69	86
55	UE	105/346 (30%)	105 (100%)	0	100	100
55	UI	105/346 (30%)	105 (100%)	0	100	100
56	US	404/493 (82%)	403 (100%)	1 (0%)	93	98
57	CI	71/135 (53%)	70 (99%)	1 (1%)	67	85
58	CX	227/411 (55%)	227 (100%)	0	100	100
59	CY	100/322 (31%)	92 (92%)	8 (8%)	12	41
60	CZ	38/519 (7%)	37 (97%)	1 (3%)	46	74
61	UP	44/314 (14%)	44 (100%)	0	100	100
All	All	18216/27810 (66%)	17715 (97%)	501 (3%)	46	72

5 of 501 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	CR	842	GLU
32	CS	856	ASP
32	CS	104	ILE
32	CS	848	LEU
53	UT	147	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 208 such sidechains are listed below:

Mol	Chain	Res	Type
28	CM	77	ASN
33	CT	107	GLN
57	CI	21	ASN
29	CN	243	HIS
32	CR	655	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	C1	1550/2352 (65%)	483 (31%)	33 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	C2	226/230 (98%)	68 (30%)	4 (1%)
All	All	1776/2582 (68%)	551 (31%)	37 (2%)

5 of 551 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	C1	4	G
50	C1	5	G
50	C1	7	A
50	C1	13	G
50	C1	14	G

5 of 37 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	C1	2054	A
51	C2	91	G
50	C1	2077	C
50	C1	2219	C
50	C1	684	U

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
63	GTP	CI	1201	-	26,34,34	0.97	1 (3%)	32,54,54	1.79	5 (15%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
63	GTP	CI	1201	-	-	2/18/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
63	CI	1201	GTP	C6-N1	-2.87	1.33	1.37

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
63	CI	1201	GTP	PA-O3A-PB	-5.41	114.27	132.83
63	CI	1201	GTP	PB-O3B-PG	-4.84	116.23	132.83
63	CI	1201	GTP	C3'-C2'-C1'	2.86	105.28	100.98
63	CI	1201	GTP	C5-C6-N1	2.76	118.83	113.95
63	CI	1201	GTP	C8-N7-C5	2.50	107.75	102.99

There are no chirality outliers.

All (2) torsion outliers are listed below:

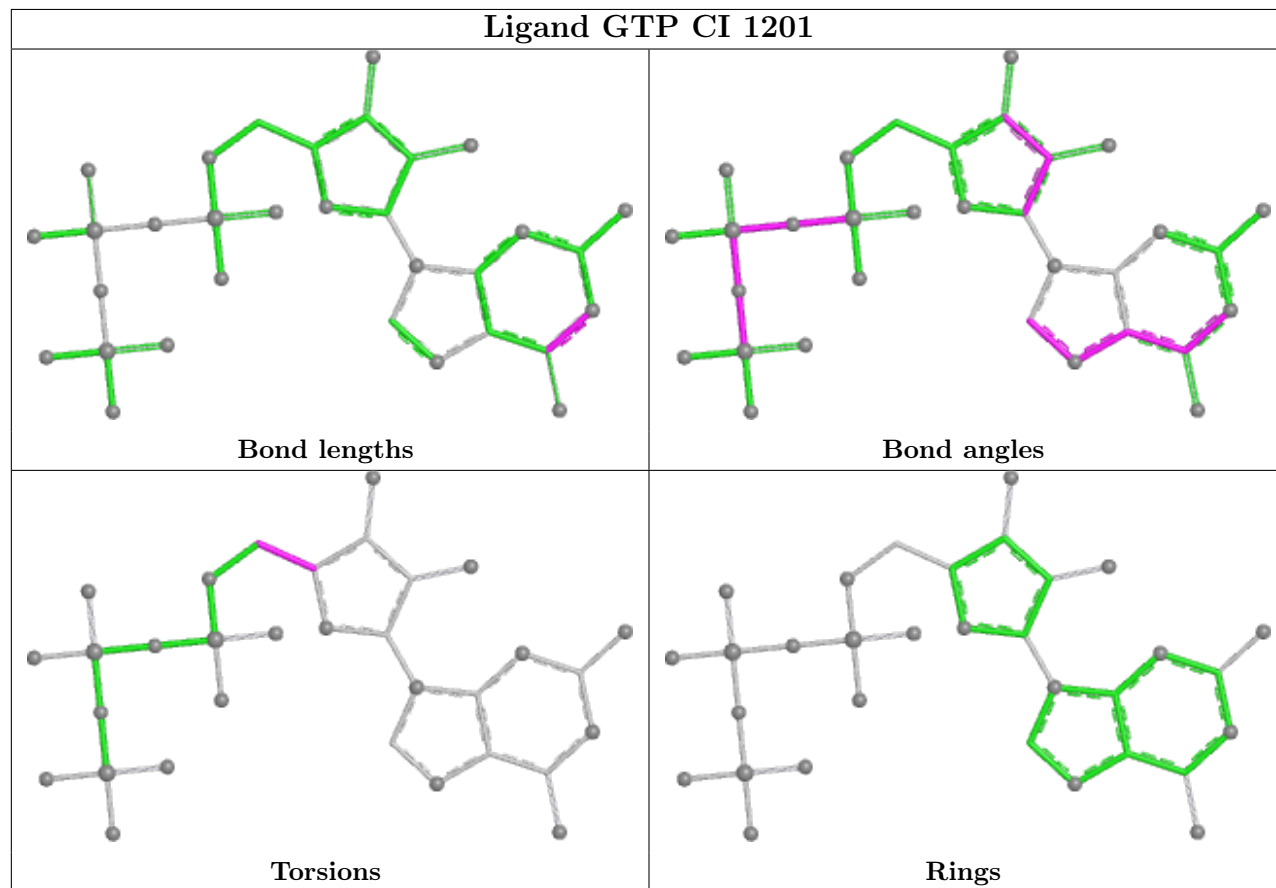
Mol	Chain	Res	Type	Atoms
63	CI	1201	GTP	O4'-C4'-C5'-O5'
63	CI	1201	GTP	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [\(i\)](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
51	C2	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C2	206:G	O3'	240:C	P	18.77

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C2	105:C	O3'	110:A	P	16.05
1	C2	119:C	O3'	123:A	P	11.95

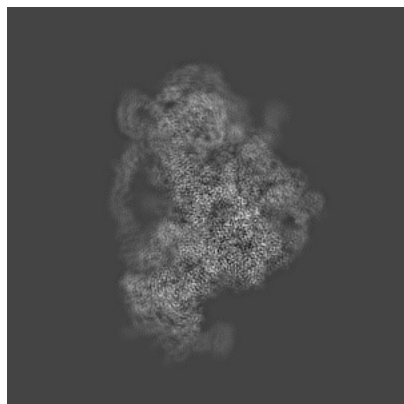
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10052. These allow visual inspection of the internal detail of the map and identification of artifacts.

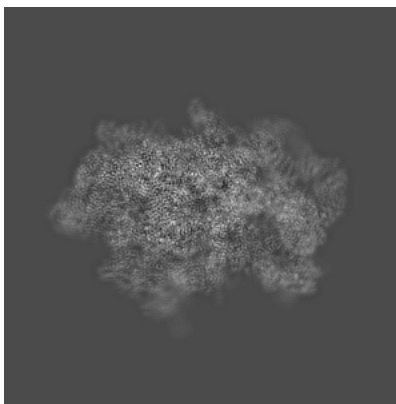
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

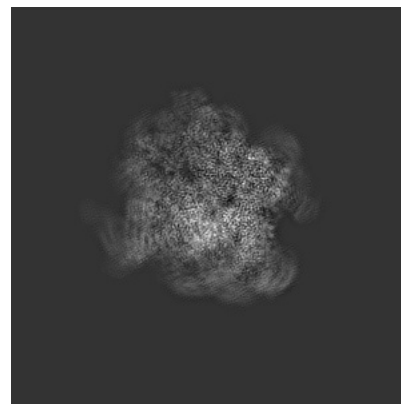
6.1.1 Primary map



X

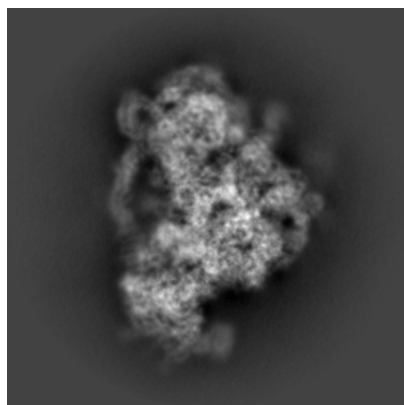


Y

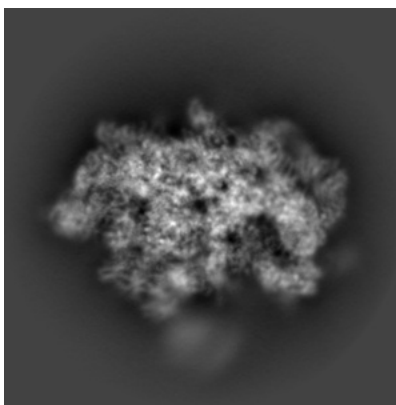


Z

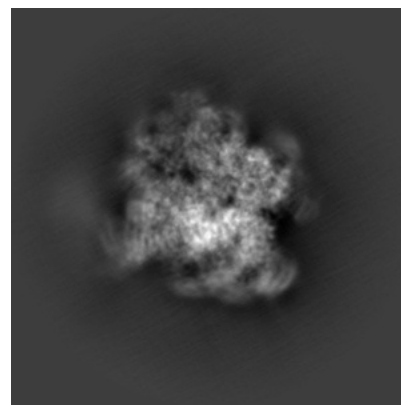
6.1.2 Raw map



X



Y

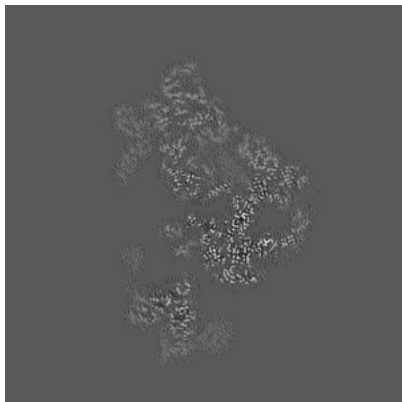


Z

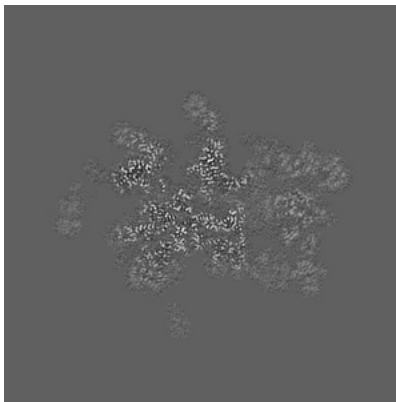
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

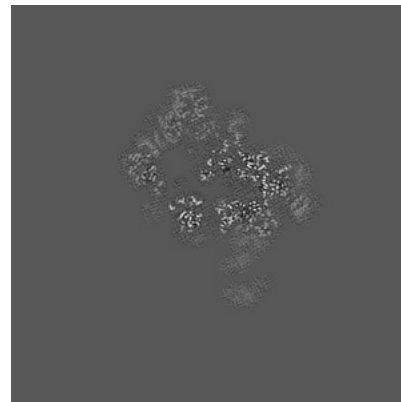
6.2.1 Primary map



X Index: 240

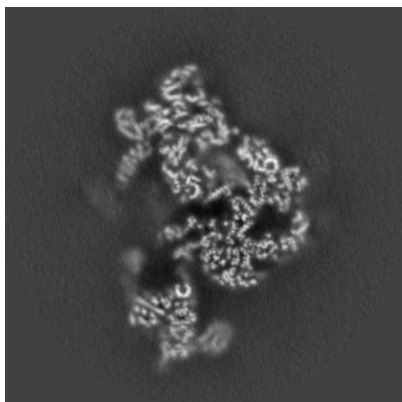


Y Index: 240

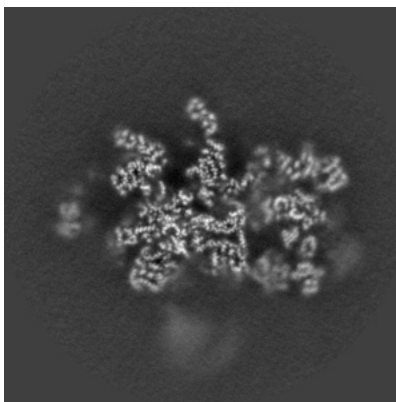


Z Index: 240

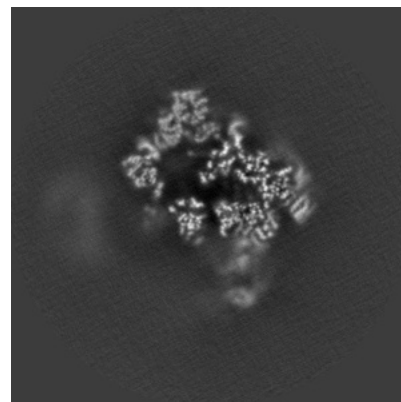
6.2.2 Raw map



X Index: 240



Y Index: 240

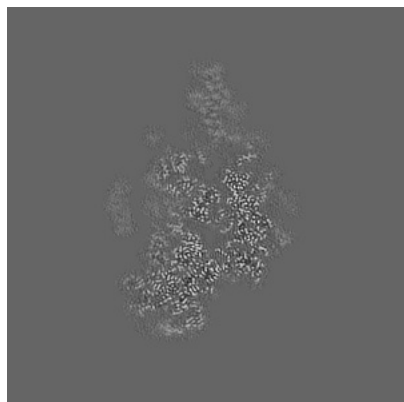


Z Index: 240

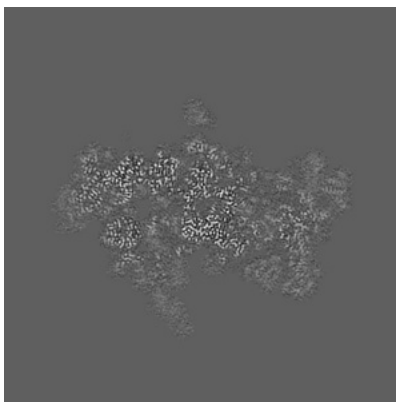
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

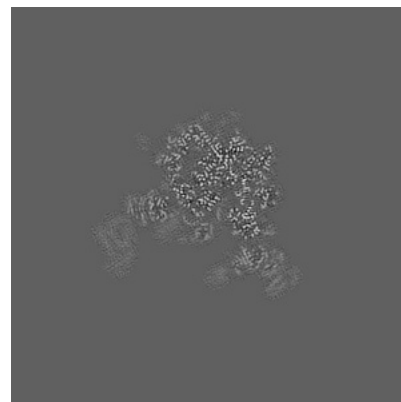
6.3.1 Primary map



X Index: 282

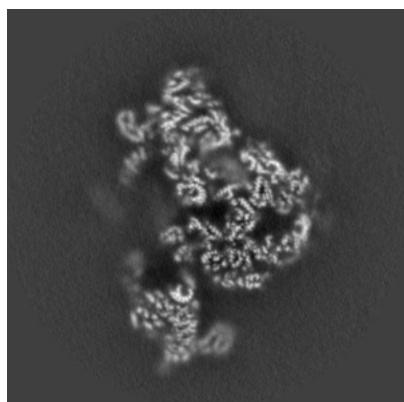


Y Index: 224

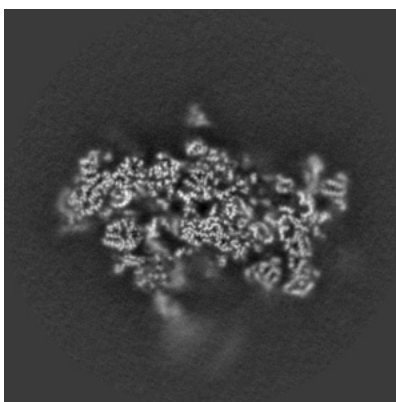


Z Index: 183

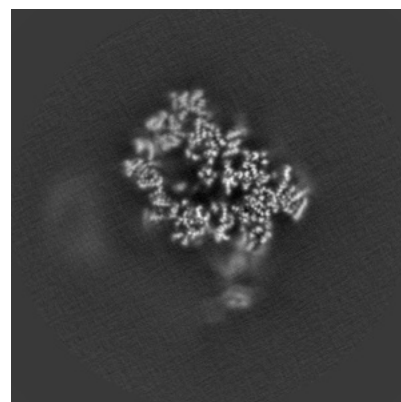
6.3.2 Raw map



X Index: 237



Y Index: 224

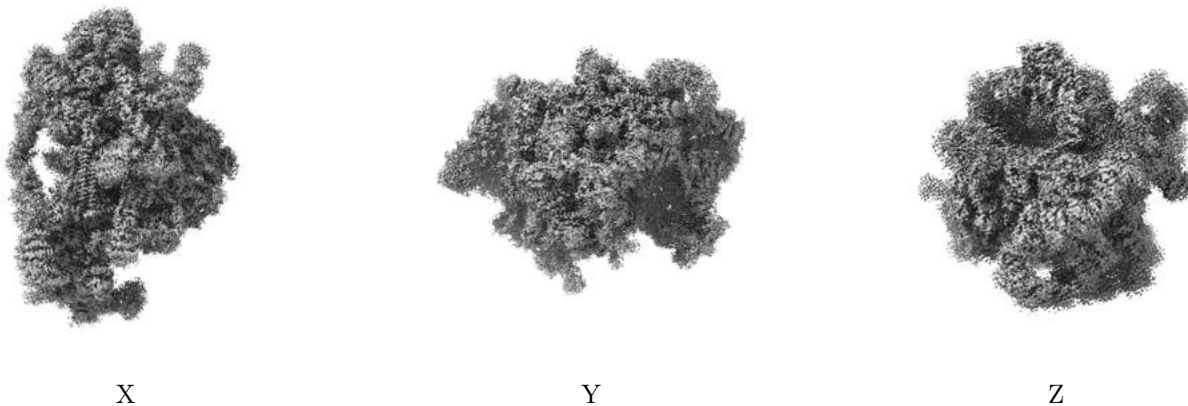


Z Index: 247

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

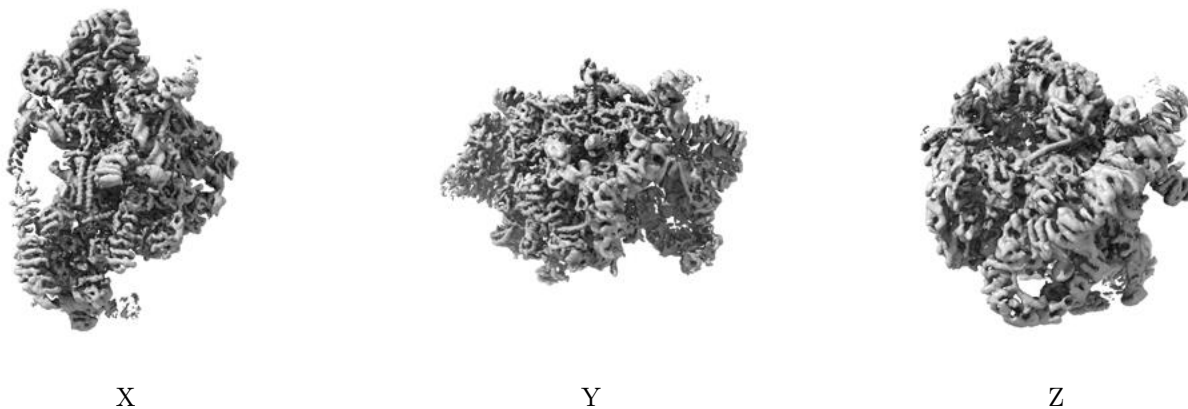
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

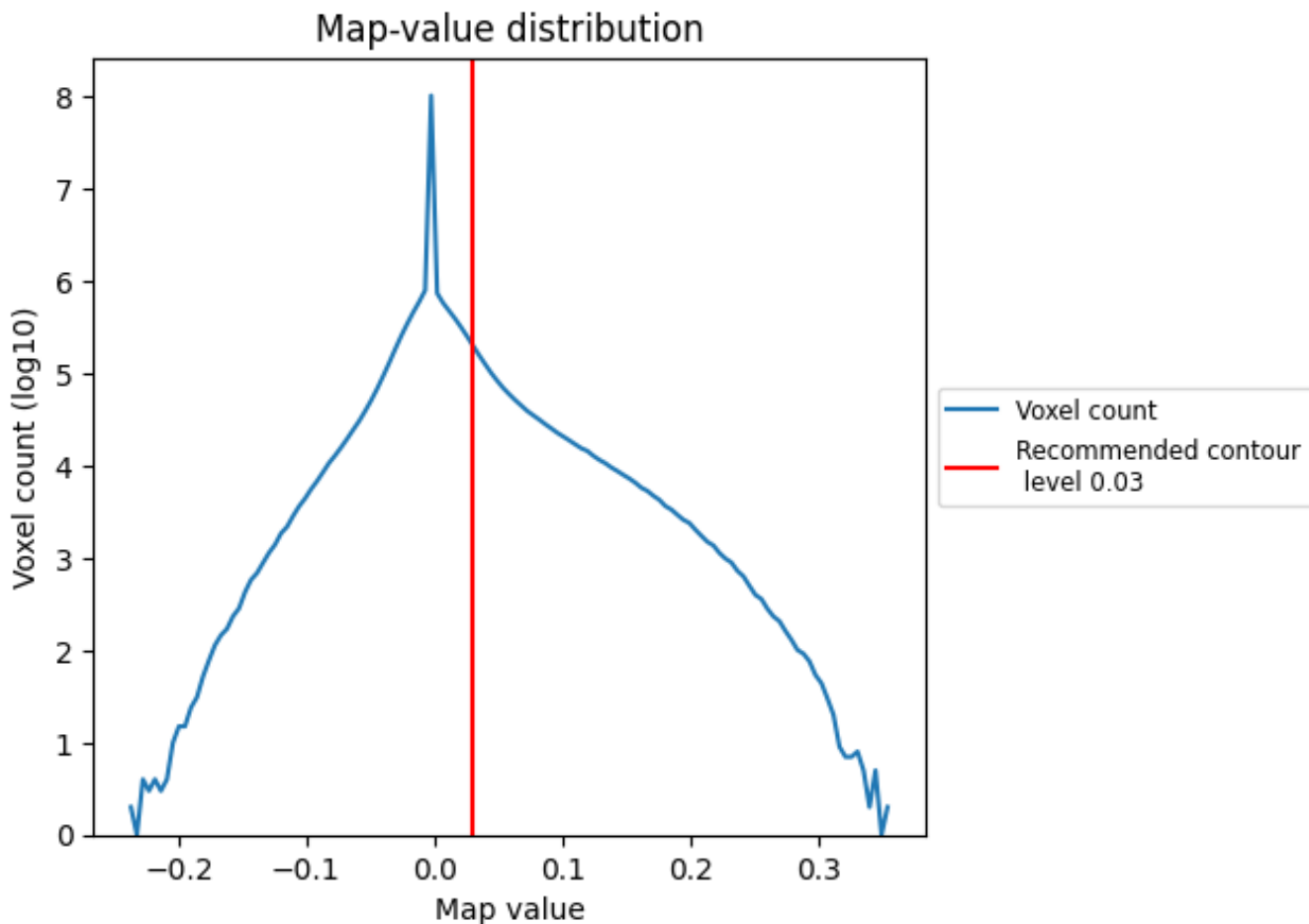
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

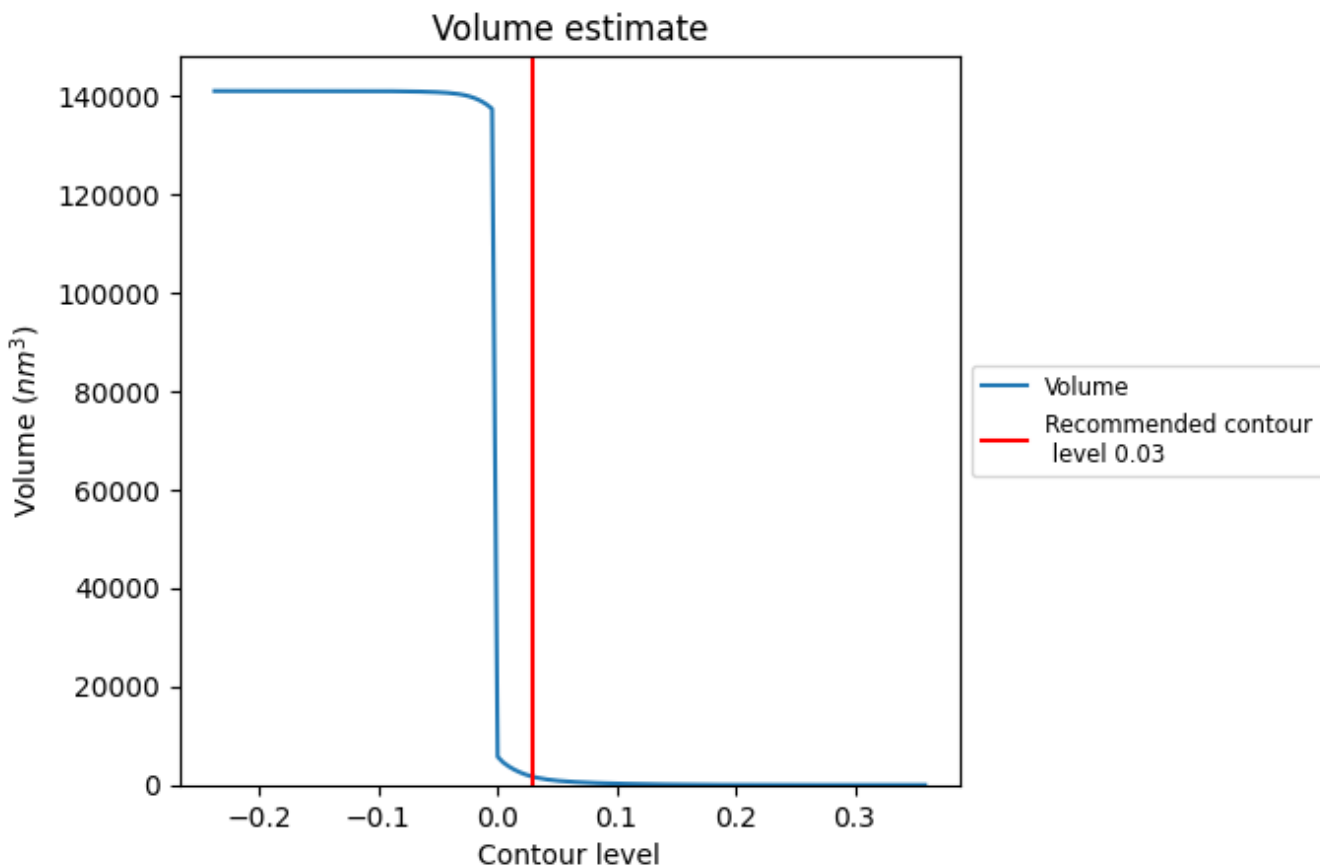
This section contains the results of statistical analysis of the map.

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.

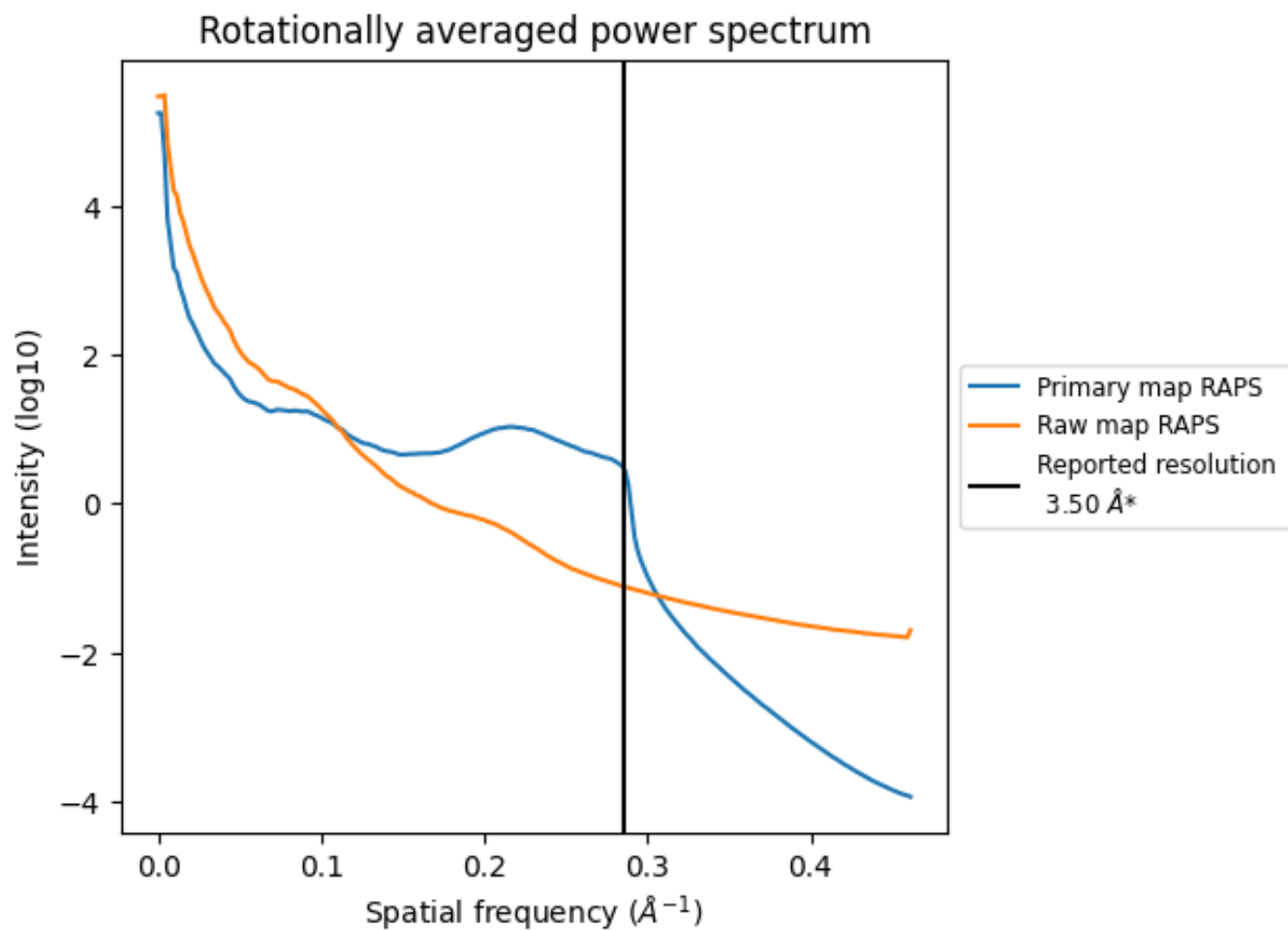
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1676 nm³; this corresponds to an approximate mass of 1514 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 i

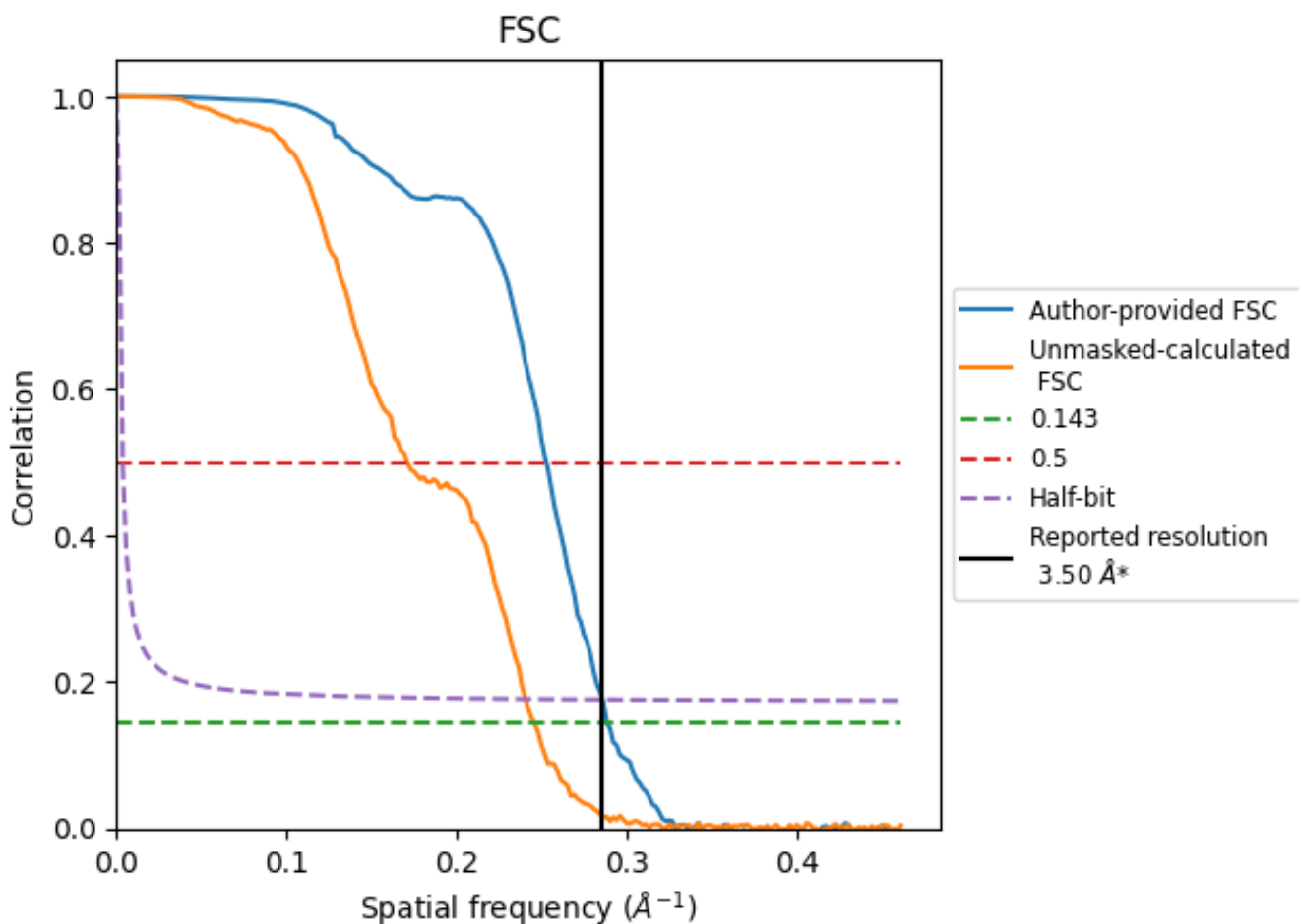


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

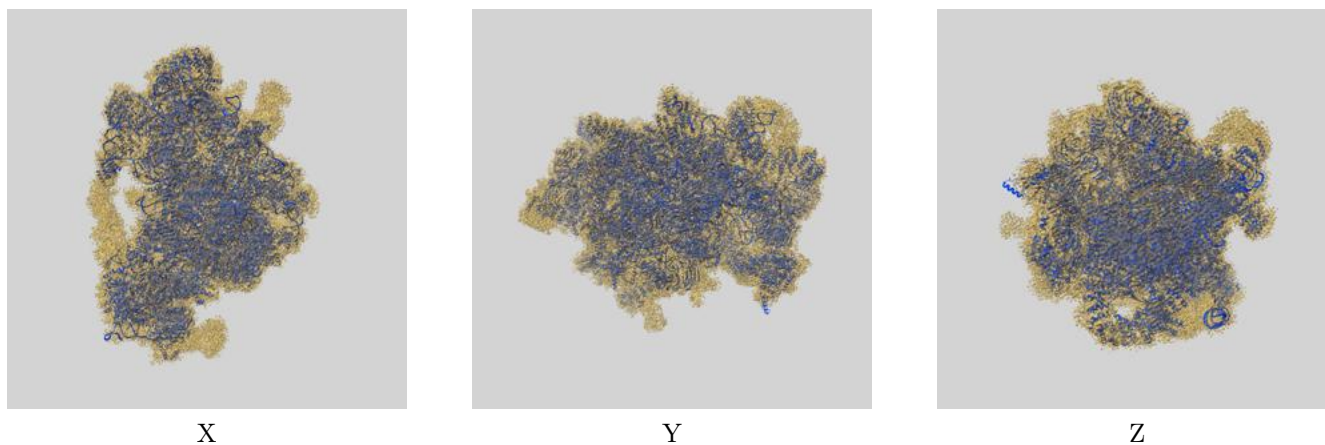
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.47	3.96	3.50
Unmasked-calculated*	4.07	5.85	4.16

*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 4.07 differs from the reported value 3.5 by more than 10 %

9 Map-model fit [i](#)

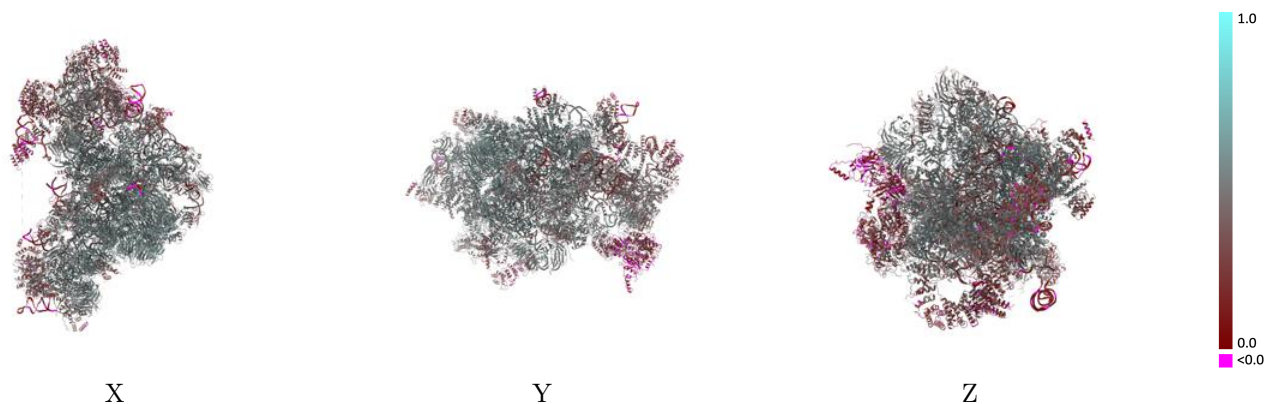
This section contains information regarding the fit between EMDB map EMD-10052 and PDB model 6RXU. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



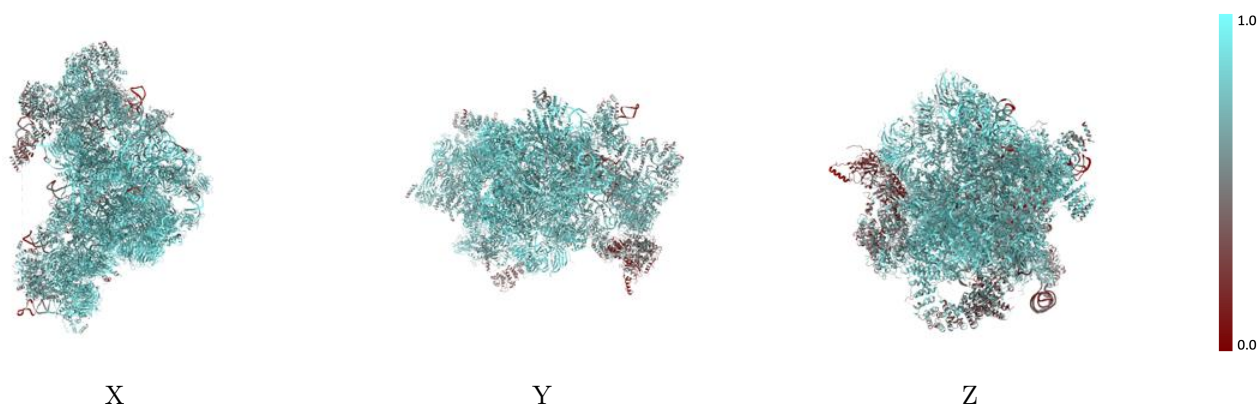
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



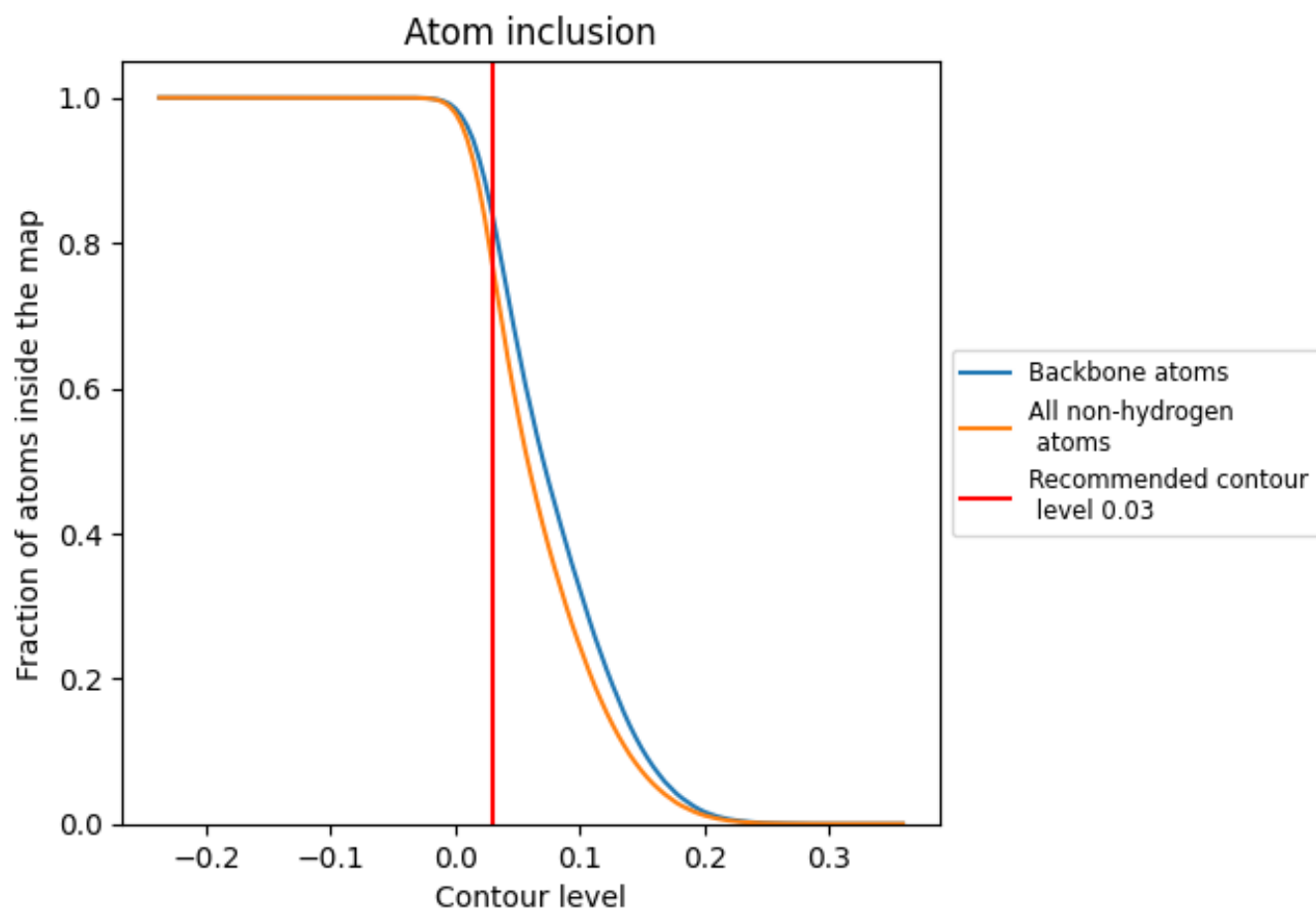
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 77% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7704	0.4400
C1	0.8229	0.4110
C2	0.7414	0.3660
CA	0.8781	0.5410
CB	0.7490	0.4650
CC	0.8016	0.4770
CD	0.7539	0.4500
CE	0.8583	0.5240
CF	0.8361	0.5030
CG	0.8047	0.4810
CH	0.8443	0.5140
CI	0.8511	0.5170
CJ	0.9058	0.5520
CK	0.8583	0.5350
CL	0.8264	0.5230
CM	0.8812	0.5460
CN	0.7698	0.4780
CO	0.6590	0.3720
CP	0.7881	0.4850
CQ	0.7442	0.4110
CR	0.6341	0.3440
CS	0.3496	0.1330
CT	0.8403	0.5180
CU	0.8023	0.5020
CW	0.7410	0.4390
CX	0.2706	0.1710
CY	0.7167	0.4500
CZ	0.6417	0.3770
Ca	0.7971	0.4700
Cb	0.7353	0.4470
Cc	0.8540	0.5260
Cd	0.7651	0.4640
Ce	0.6968	0.4030
Cf	0.7560	0.4560
Cg	0.8618	0.5290



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Chain	Atom inclusion	Q-score
Ch	 0.7609	 0.4240
Ci	 0.8517	 0.5120
Cj	 0.8818	 0.5460
Ck	 0.6575	 0.3810
Cl	 0.4597	 0.3680
Cm	 0.8004	 0.5000
Cn	 0.8900	 0.5390
Co	 0.7336	 0.4210
Cp	 0.8690	 0.5350
UA	 0.8927	 0.5450
UB	 0.7551	 0.4400
UC	 0.8706	 0.5420
UD	 0.8453	 0.5090
UE	 0.7725	 0.4560
UF	 0.8188	 0.4510
UG	 0.8819	 0.5360
UH	 0.7242	 0.4060
UI	 0.7206	 0.4200
UJ	 0.6234	 0.3650
UK	 0.8548	 0.5260
UL	 0.8301	 0.4840
UM	 0.7500	 0.4370
UN	 0.8304	 0.5090
UO	 0.8539	 0.5150
UP	 0.7690	 0.4730
UQ	 0.8436	 0.5040
UR	 0.8885	 0.5400
US	 0.7584	 0.4300
UT	 0.6453	 0.3360
UU	 0.8965	 0.5390
UX	 0.8604	 0.5340
UZ	 0.7618	 0.4480