



wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 06:42 PM UTC

PDB ID : 6RXT / pdb_00006rxt
EMDB ID : EMD-10051
Title : Cryo-EM structure of the 90S pre-ribosome (Kre33-Noc4) from *Chaetomium thermophilum*, state A
Authors : Cheng, J.; Kellner, N.; Griesel, S.; Berninghausen, O.; Beckmann, R.; Hurt, E.
Deposited on : 2019-06-10
Resolution : 7.00 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:

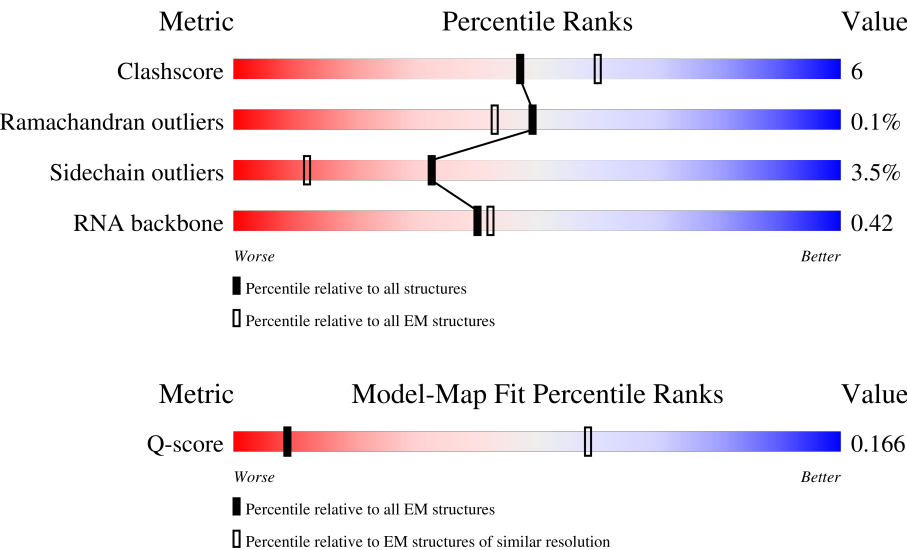
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 7.00 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	483 (6.50 - 7.50)

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	

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Mol	Chain	Length	Quality of chain
4	UD	884	
5	UF	414	
6	UG	558	
7	UJ	1802	
8	UK	270	
9	UL	962	
10	UM	912	
11	UN	938	
12	UO	557	
13	UQ	960	
14	UR	618	
15	UU	1049	
16	UX	193	
17	UZ	391	
18	CA	313	
18	CB	313	
19	CC	523	
20	CD	582	
21	CE	127	
21	CF	127	
22	CG	630	
23	CH	411	
24	CI	1163	
25	CJ	183	
26	CK	297	

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Mol	Chain	Length	Quality of chain
27	CL	785	
28	CM	446	
29	CN	252	
29	CO	252	
30	CP	322	
31	CQ	259	
32	CR	1073	
32	CS	1073	
33	CT	203	
34	Ca	255	
35	Cc	212	
36	Ce	203	
37	Cg	190	
38	Ch	151	
39	Ci	150	
40	Cj	143	
41	Cm	130	
42	Cn	145	
43	Cp	68	
44	CU	311	
45	C1	2352	
46	C2	230	
47	UH	930	
48	UE	410	
48	UI	410	

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Mol	Chain	Length	Quality of chain
49	US	549	
50	CI	156	
51	CX	480	
52	UP	364	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
54	GTP	CI	1201	-	-	X	-

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 169690 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
1	UA	839	Total	C	N	O	S	0	0
			6366	4101	1136	1105	24		

- Molecule 2 is a protein called Utp2.

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

- Molecule 3 is a protein called Utp3.

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

- Molecule 4 is a protein called Utp4.

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

- Molecule 5 is a protein called Utp6.

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

- Molecule 6 is a protein called Utp7.

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

- Molecule 7 is a protein called UTP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	UJ	445	Total	C	N	O	S	0	0
			3377	2169	604	590	14		

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

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

- Molecule 9 is a protein called Utp12.

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

- Molecule 10 is a protein called Utp13".

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

- Molecule 11 is a protein called Utp14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	UN	154	Total	C	N	O	S	0	0
			1209	770	228	206	5		

- Molecule 12 is a protein called Utp15.

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

- Molecule 13 is a protein called Utp17.

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

- 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
			1815	1184	330	298	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 Putative nucleolar protein.

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	378	Total	C	N	O	S	0	0
			2922	1865	527	517	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
28	CM	445	Total	C	N	O	S	0	0
			3501	2195	672	619	15		

- Molecule 29 is a protein called Emg1.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	CP	201	Total	C	N	O	S	0	0
			1625	1047	286	283	9		

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

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

- Molecule 32 is a protein called Kre33.

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

- Molecule 33 is a protein called Fcf2.

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

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

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

- Molecule 35 is a protein called 40S ribosomal protein s5-like protein.

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

- Molecule 36 is a protein called 40S ribosomal protein S7.

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

- Molecule 37 is a protein called 40S ribosomal protein s9-like protein.

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

- Molecule 38 is a protein called 40S ribosomal protein S13-like protein.

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

- Molecule 39 is a protein called 40S ribosomal protein S14-like protein.

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

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

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

- Molecule 41 is a protein called 40S ribosomal protein S22-like protein.

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

- Molecule 42 is a protein called 40S ribosomal protein s23-like protein.

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

- Molecule 43 is a protein called 40S ribosomal protein S28-like protein.

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

- Molecule 44 is a protein called Faf1.

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

- Molecule 45 is a RNA chain called 35S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	C1	1152	Total	C	N	O	P	0	0
			24590	10964	4415	8059	1152		

- Molecule 46 is a RNA chain called U3 snoRNA.

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

- Molecule 47 is a protein called Utp8.

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

- Molecule 48 is a protein called Utp5".

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

- Molecule 49 is a protein called Noc4.

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

- Molecule 50 is a protein called Putative ribosomal protein.

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

- Molecule 51 is a protein called Enp1.

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

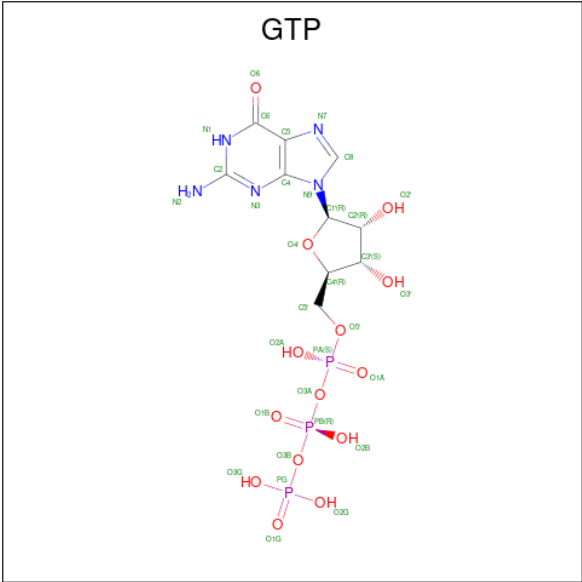
- Molecule 52 is a protein called Utp16.

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

- Molecule 53 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

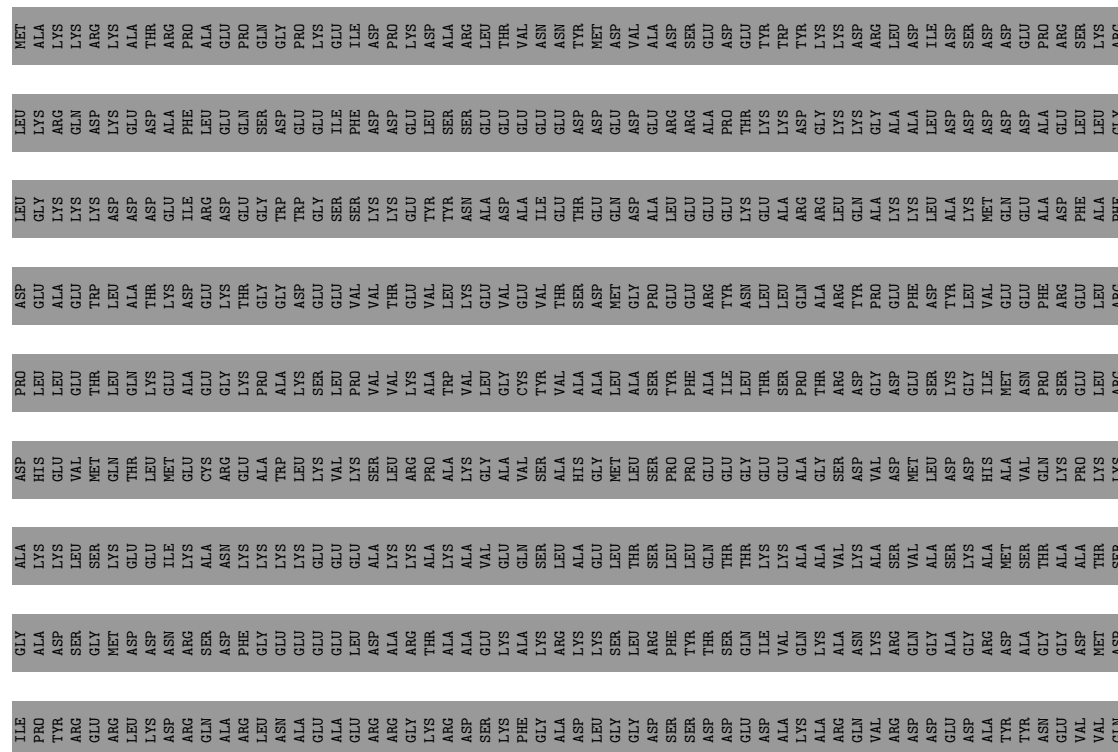
- Molecule 54 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

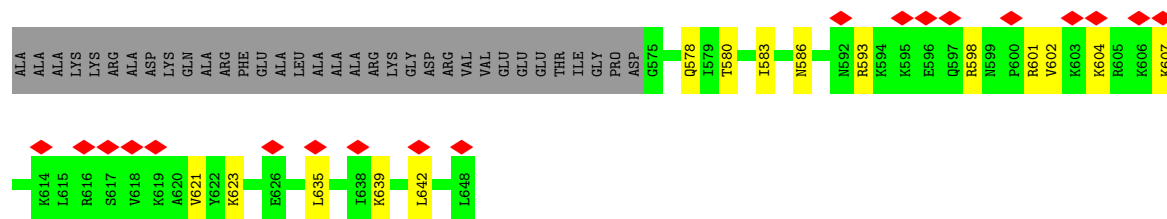


Mol	Chain	Residues	Atoms					AltConf
54	CI	1	Total	C	N	O	P	0
			32	10	5	14	3	

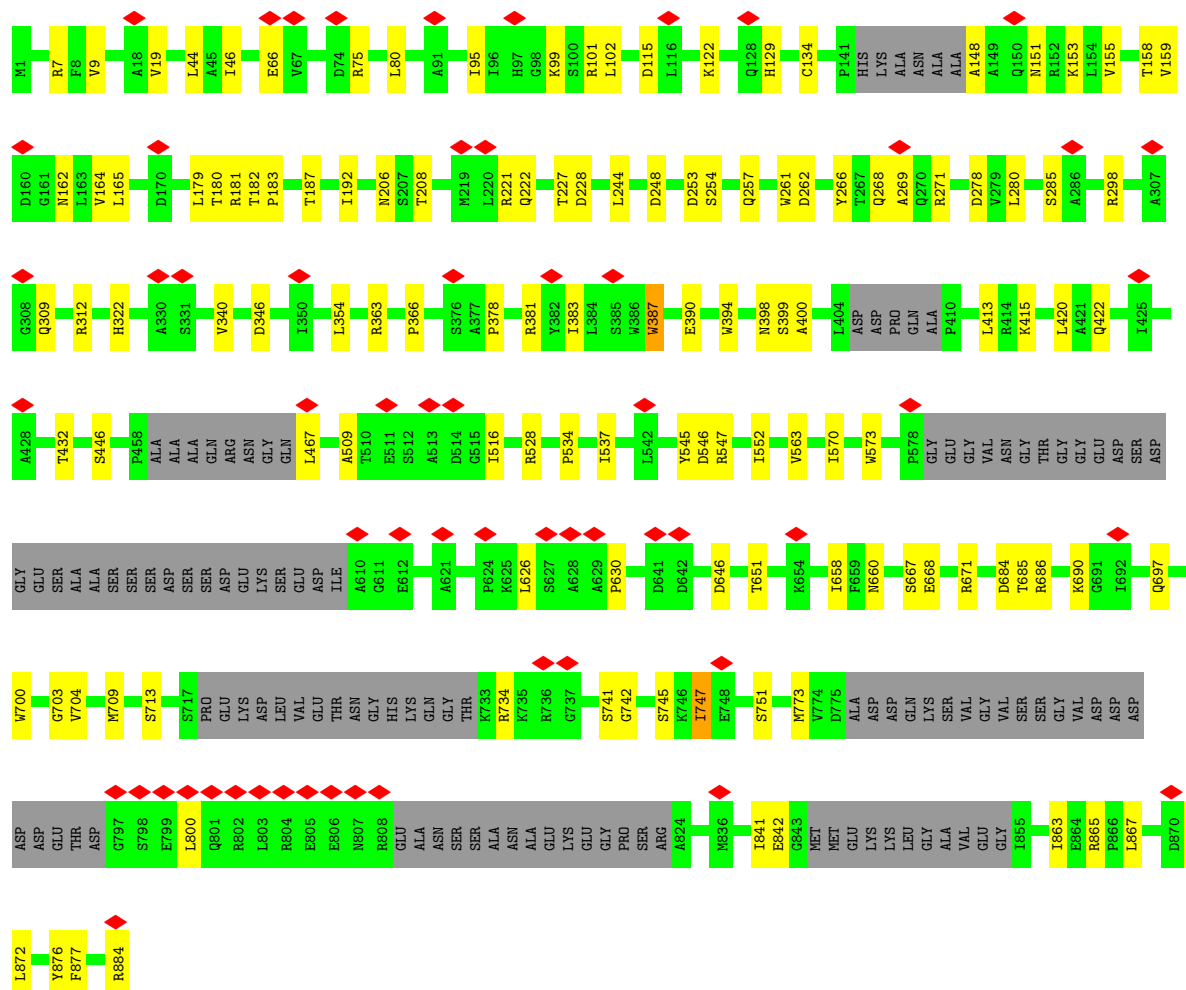
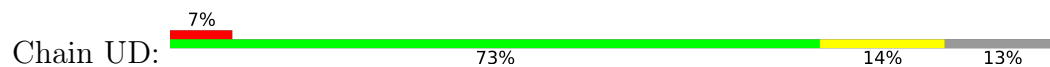
- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

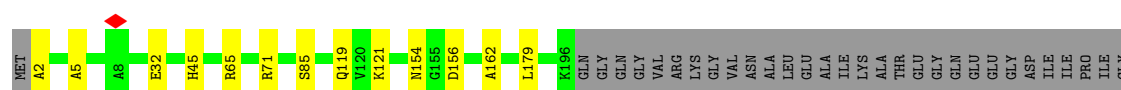
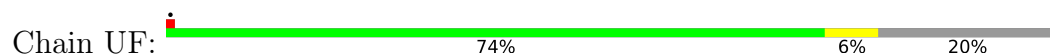


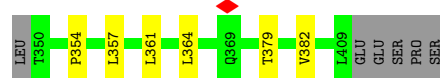
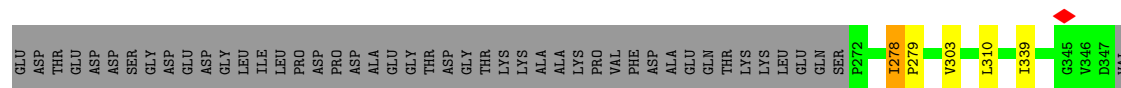


• Molecule 4: Utp4

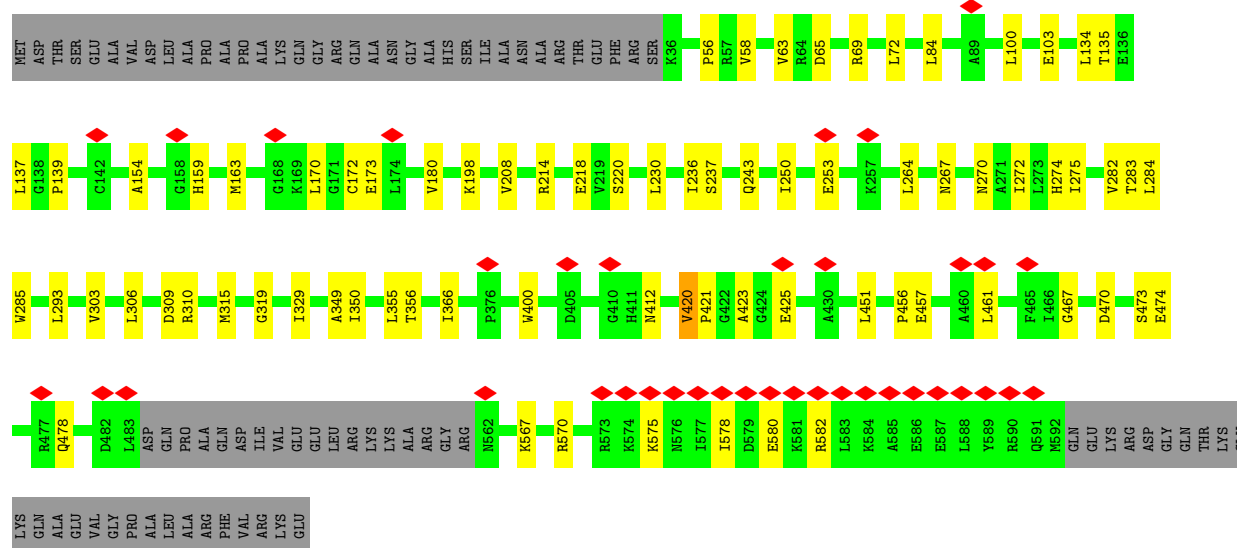
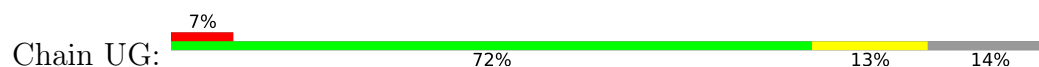


• Molecule 5: Utp6

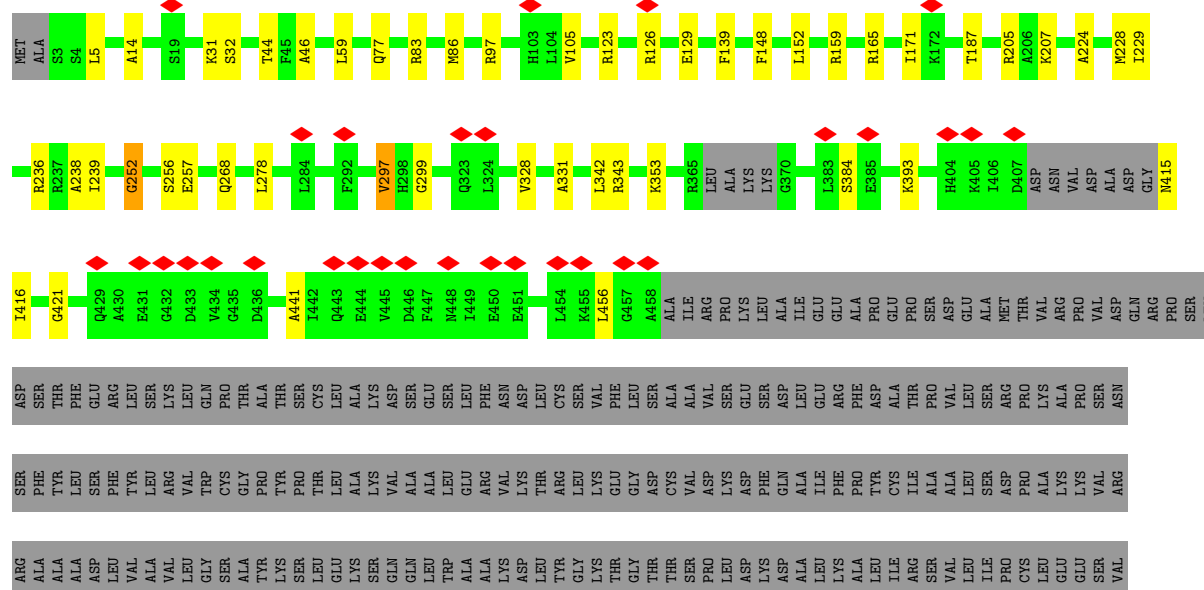




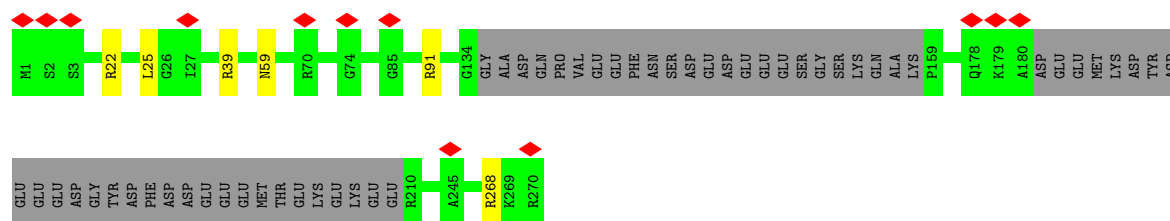
• Molecule 6: Utp7



• Molecule 7: UTP10

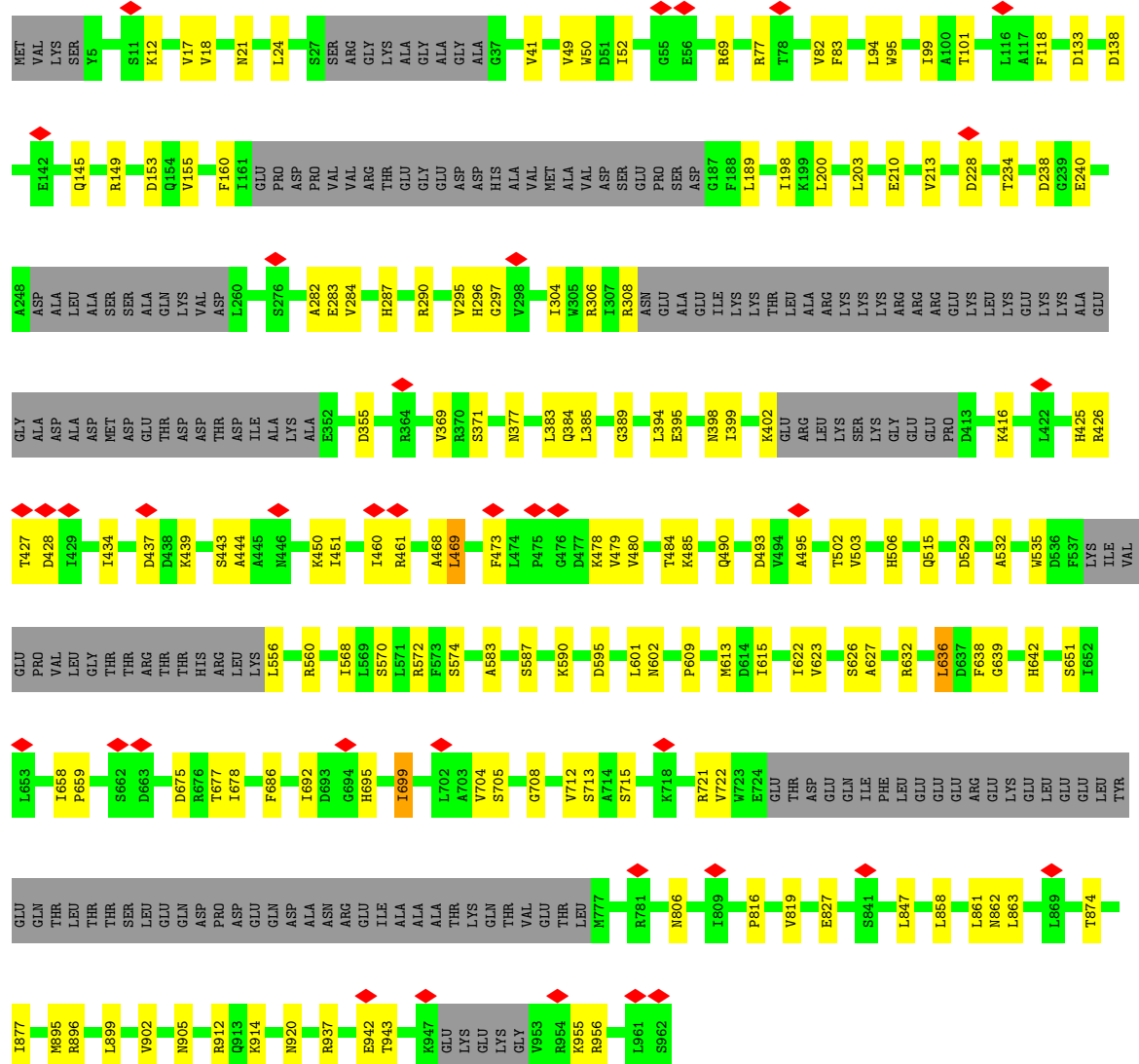






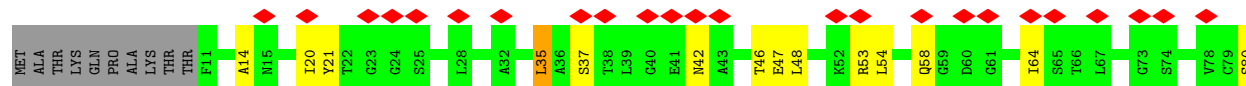
• Molecule 9: Utp12

Chain UL: 65% 16% 18%



• Molecule 10: Utp13"

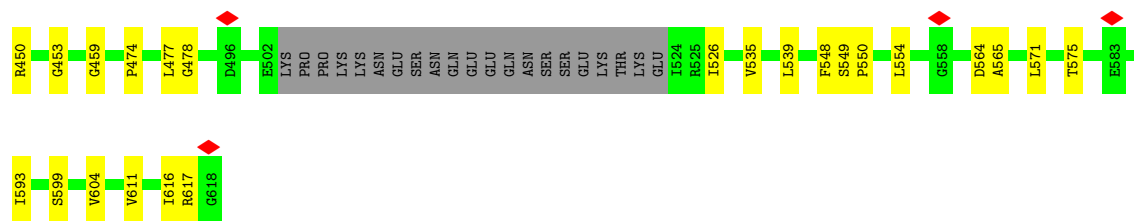
Chain UM: 18% 62% 17% 20%





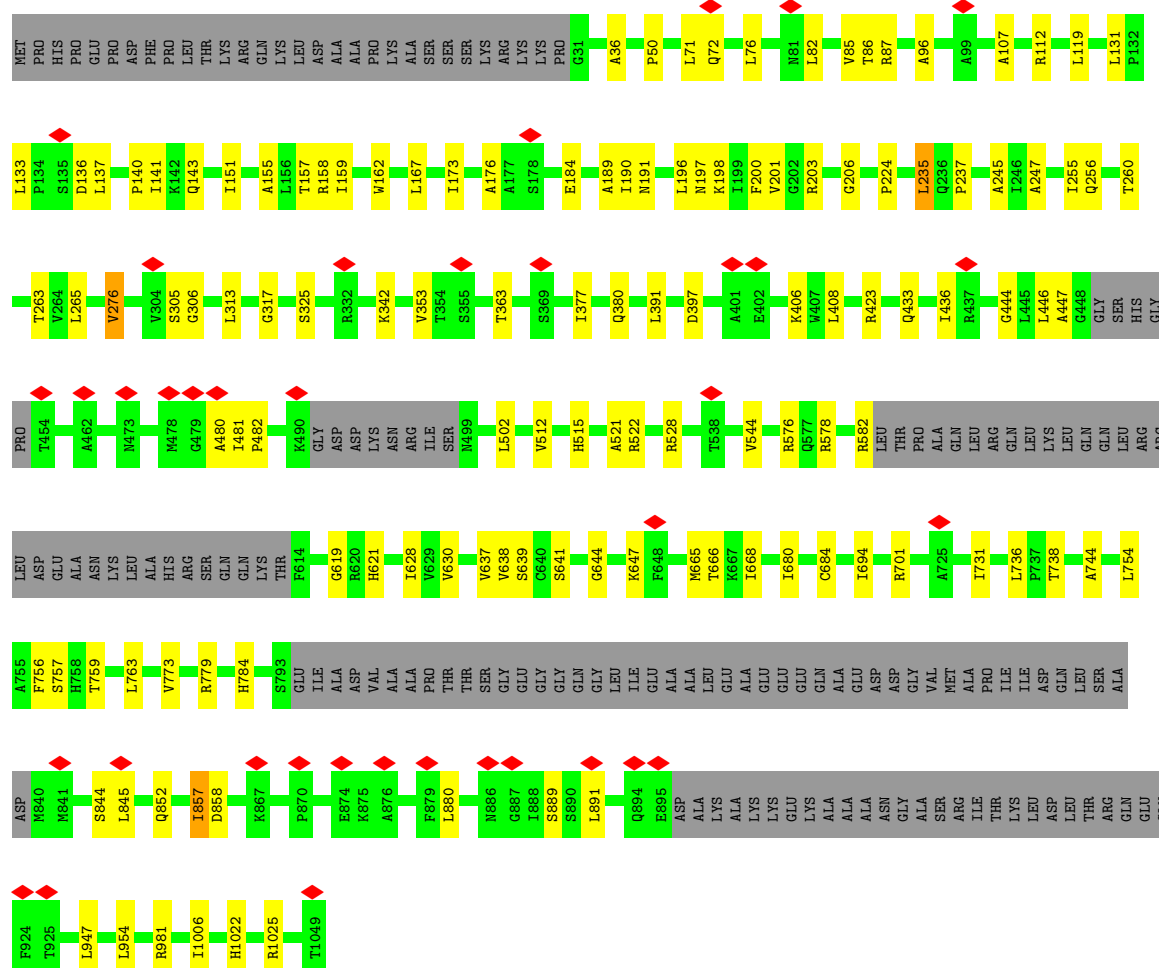
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ASP	ALA	ASP	PRO
ASP	ASP	LEU	LEU
ILE	GLY	ASP	ARG
LEU	GLU	GLU	GLN
ASP	ASP	HIS	ALA
LEU	ASP	PRO	HIS
ALA	SER	SER	GLY
THR	GLU	THR	ARG
ALA	GLU	SER	PRO
LEU	TRP	ALA	LEU
ASP	HIS	SER	LEU
GLN	VAL	ARG	PRO
TYR	GLY	ASN	SER
GLU	VAL	LYS	LEU
SER	THR	ARG	GLY
SER	GLY	GLN	SER
GLU	ALA	HIS	SER
GLU	ASP	GLU	SER
GLY	GLU	ASP	GLY
GLU	ASP	ASP	GLY
GLU	SER	GLU	GLY
GLY	GLU	ASP	LYS
GLU	ILE	GLU	ASP
GLU	ASP	ASP	LYS
SER	SER	PHE	LYS
GLU	ASP	ASP	SER
SER	GLU	GLY	ARG
GLU	ALA	PHE	SER
GLU	PHE	ASP	LYS
ASP	GLY	ASP	ALA
ASP	GLU	ASP	ARG
GLU	SER	GLU	ARG
GLU	ASP	GLY	SER
SER	GLU	MET	ALA
GLU	GLU	GLY	GLN
GLU	ARG	ARG	SER
GLU	PHE	LYS	LYS
ASP	GLU	LYS	ALA
SER	GLY	ARG	LEU
ASP	PHE	ALA	ASP
GLU	VAL	ARG	ALA
GLU	PHE	ARG	PHE
ASP	GLY	ASP	ALA
ASP	GLY	SER	LEU
ASP	SER	GLY	ALA
PRO	LYS	GLY	ALA
LEU	THR	VAL	GLU
GLN	LYS	VAL	ARG
LEU	HIS	GLU	GLN
ASP	LYS	GLY	VAL
ALA	GLY	ASP	PRO
LEU	THR	ASP	GLU
GLY	LYS	SER	SER
ARG	LYS	ASP	ARG
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ALA	ASN	ASP	GLY
PHE	GLY	MET	VAL
GLY	SER	GLY	LEU
ASP	SER	GLY	ARG





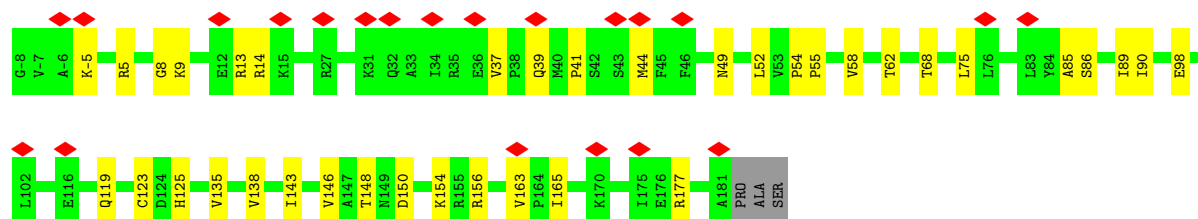
• Molecule 15: Putative U3 snoRNP protein

Chain UU: 74% 12% 14%

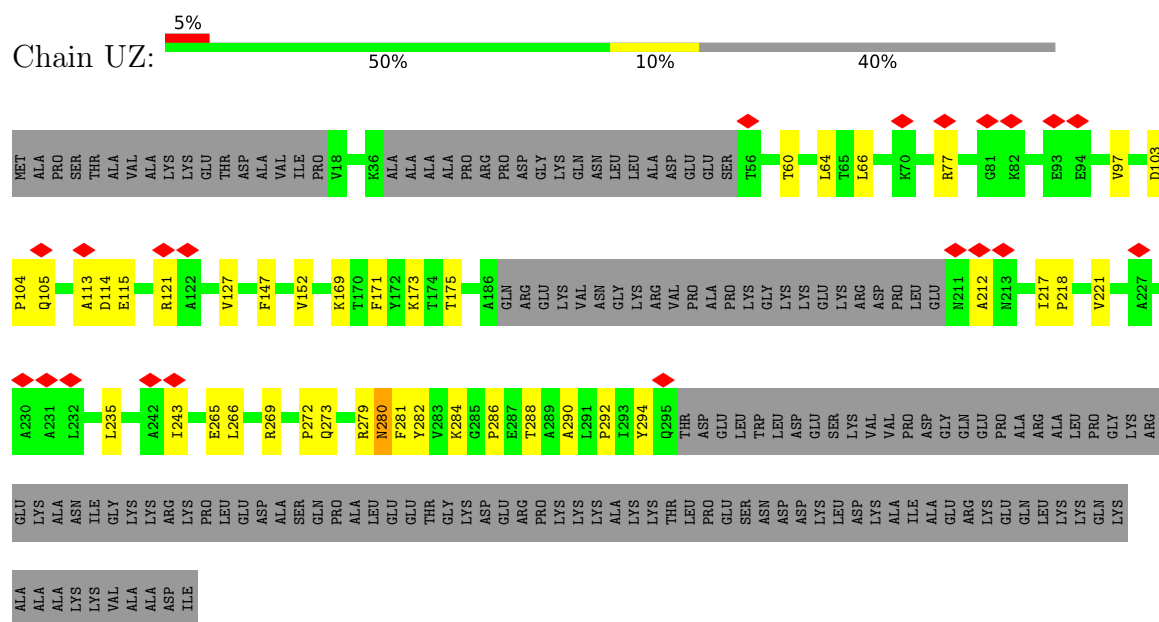


• Molecule 16: Utp24

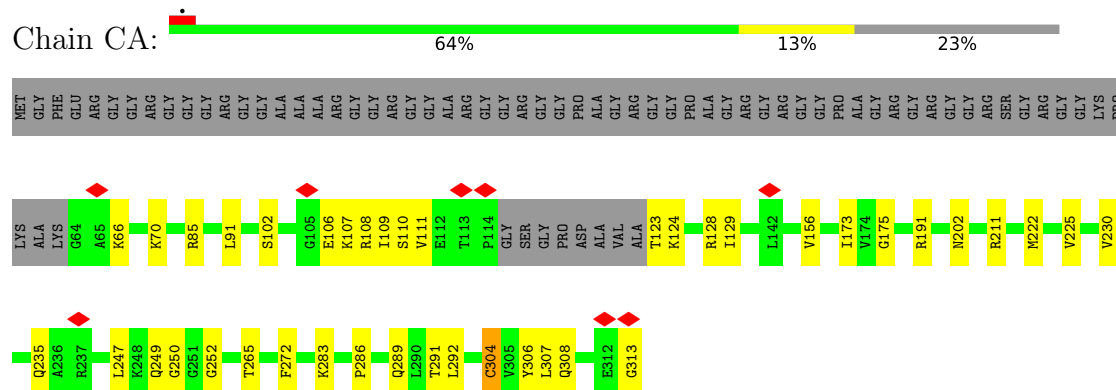
Chain UX: 11% 79% 19%



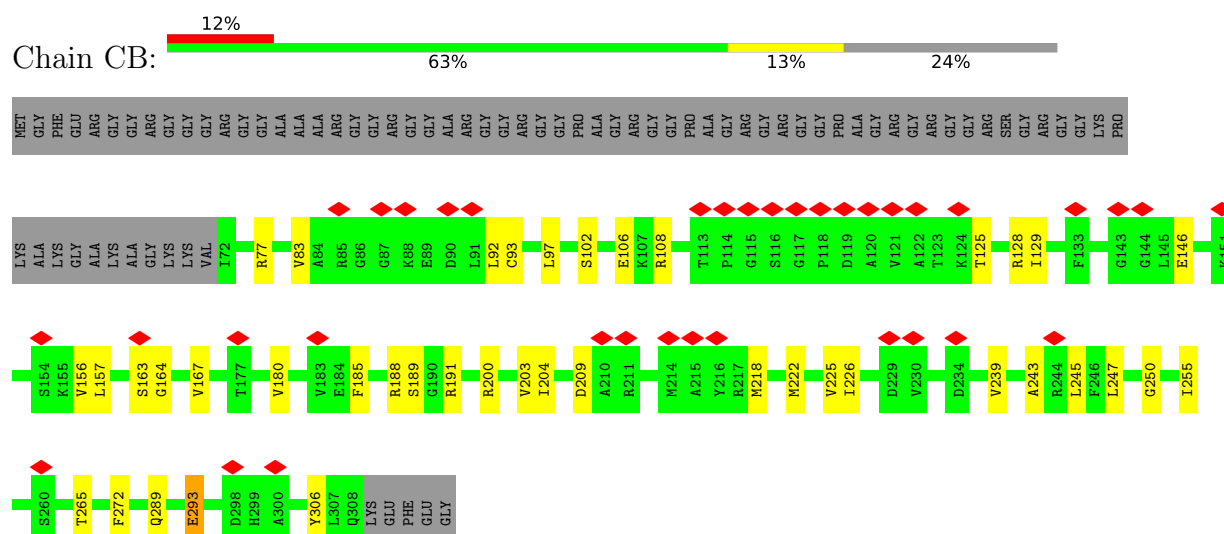
- Molecule 17: Utp30



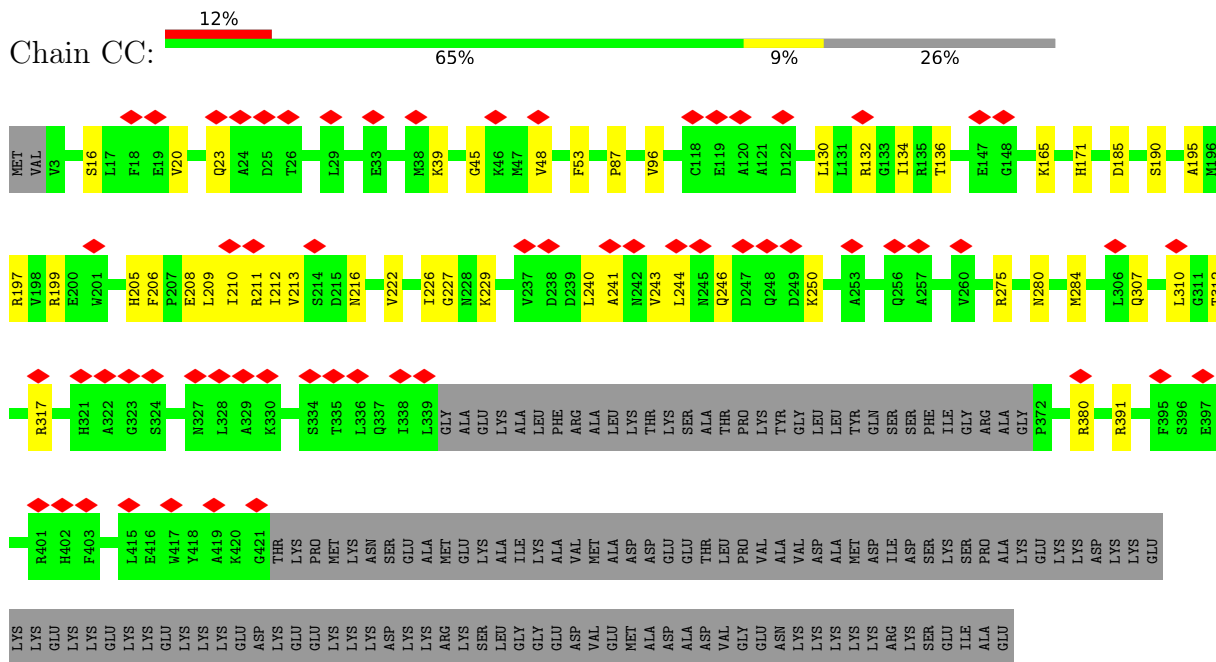
- Molecule 18: Nop1



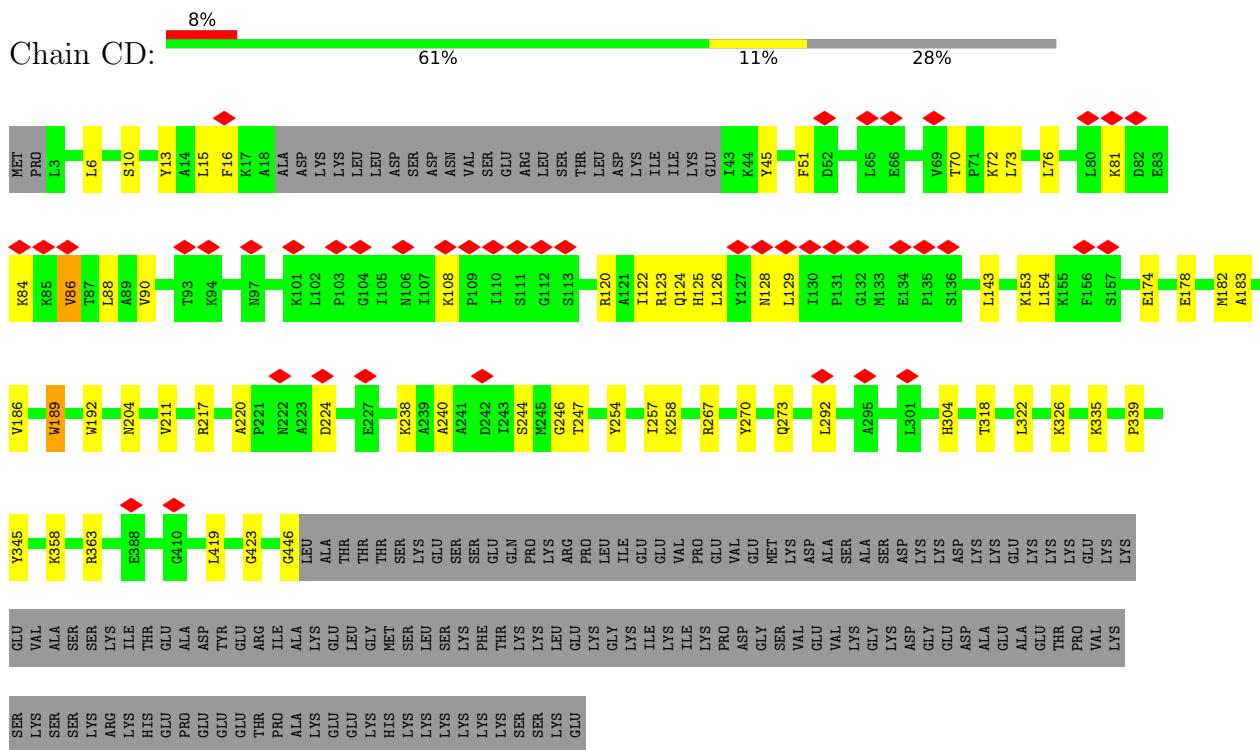
- Molecule 18: Nop1



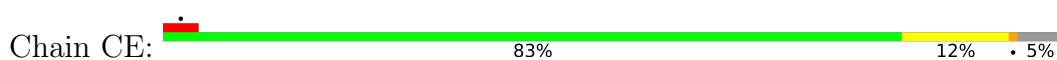
- Molecule 19: Putative nucleolar protein

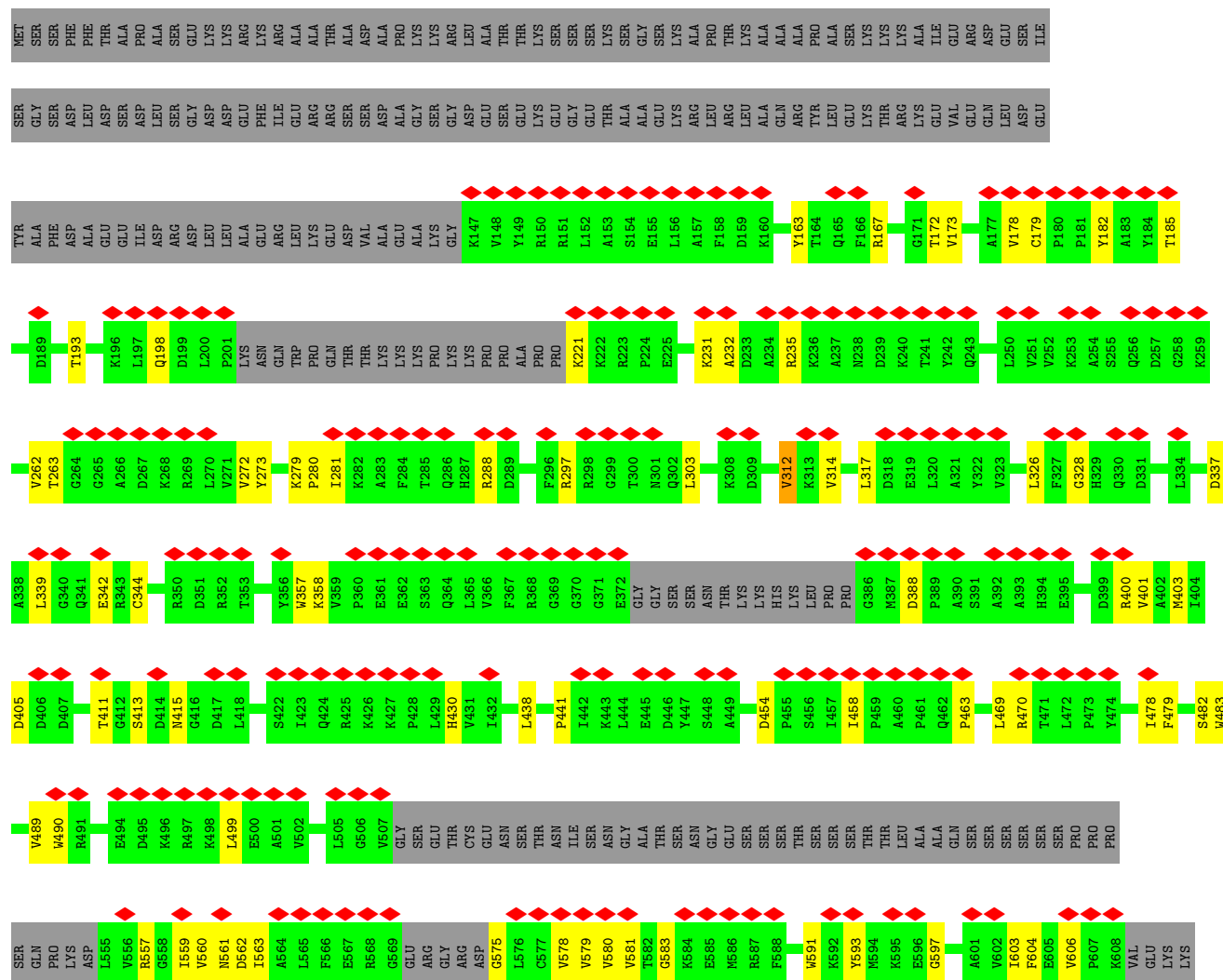


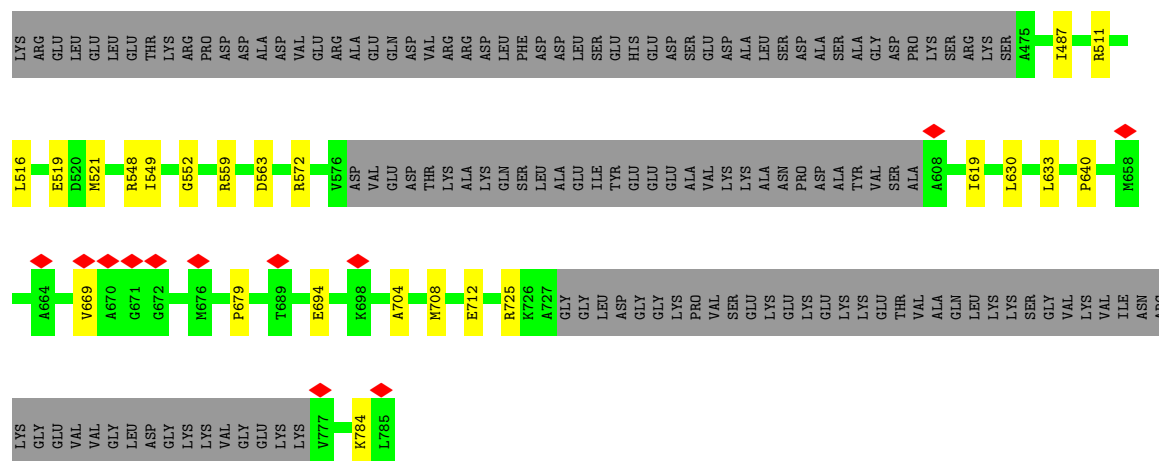
- Molecule 20: Nop58



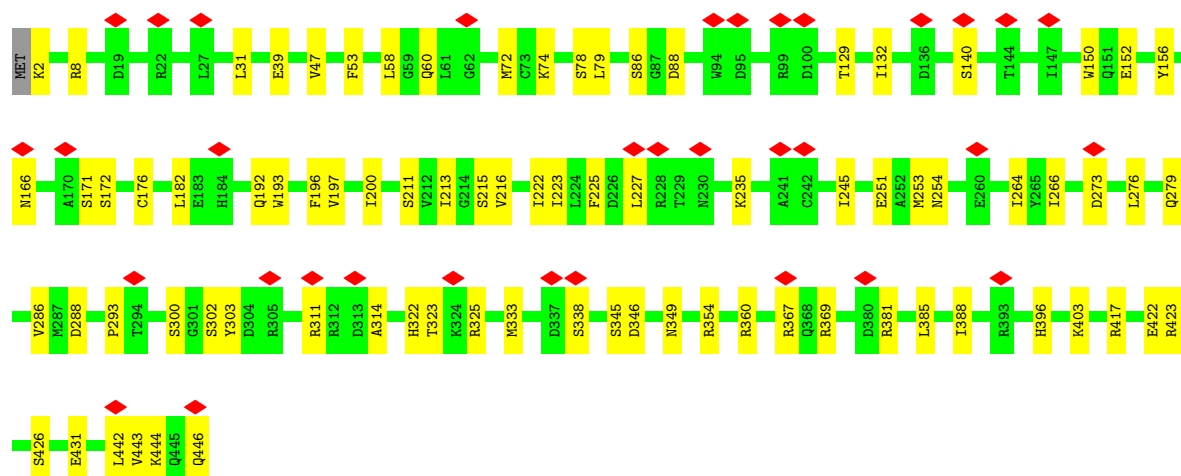
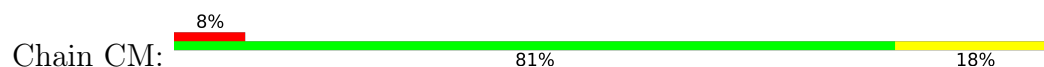
- Molecule 21: `snu13`



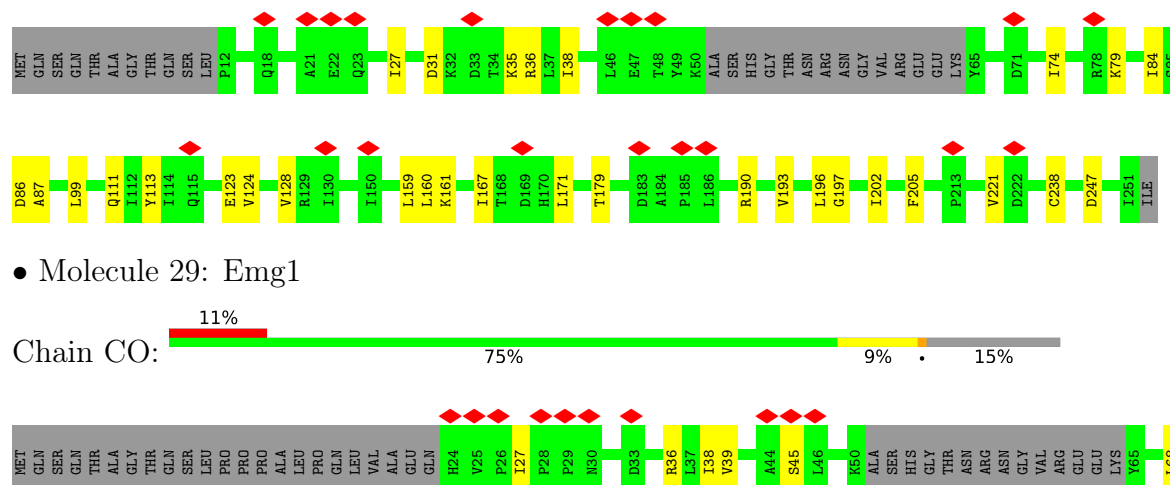
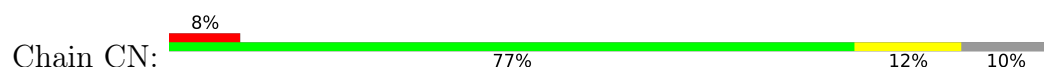




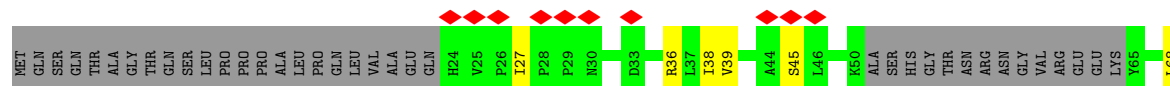
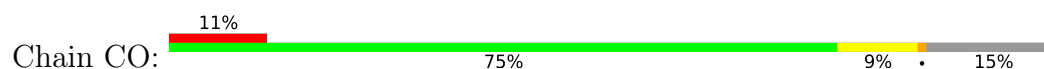
• Molecule 28: Sof1

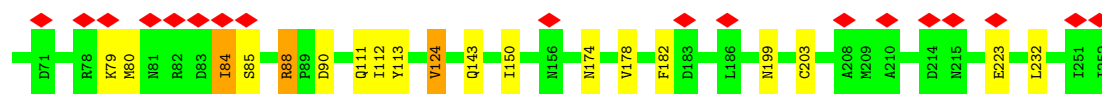


• Molecule 29: Emg1

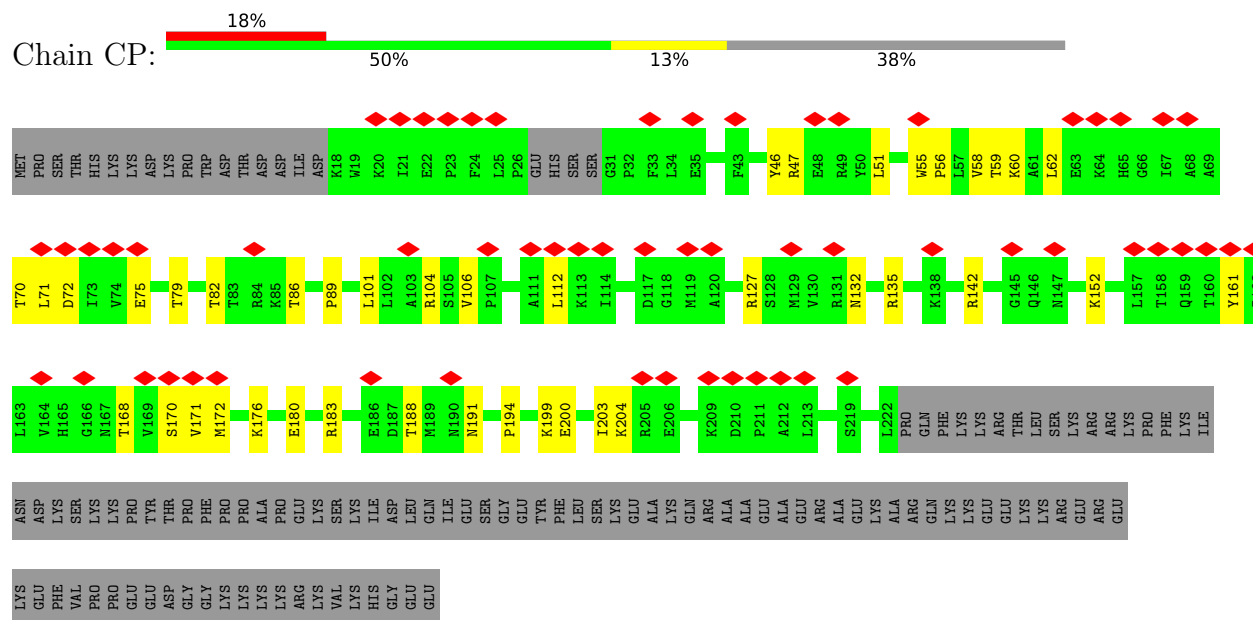


• Molecule 29: Emg1

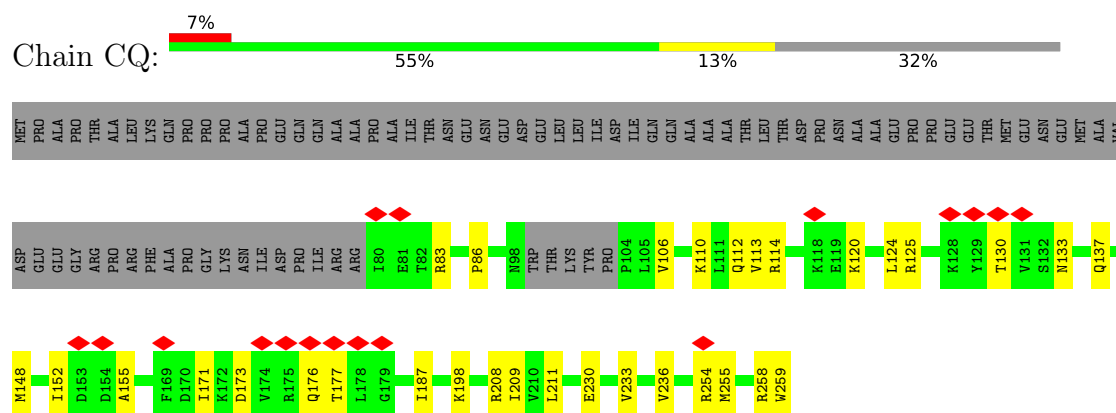




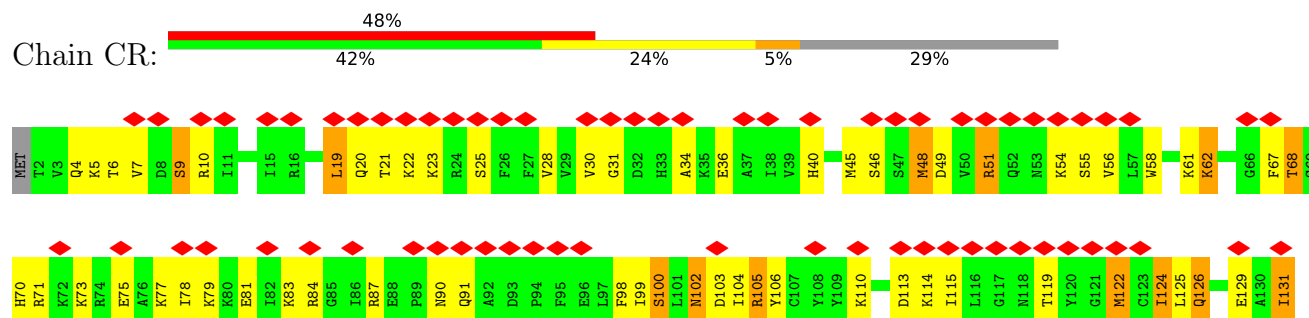
- Molecule 30: KRR1 small subunit processome component



- Molecule 31: Pre-rRNA-processing protein PNO1



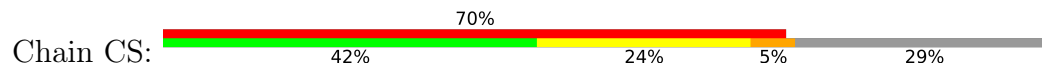
- Molecule 32: Kre33



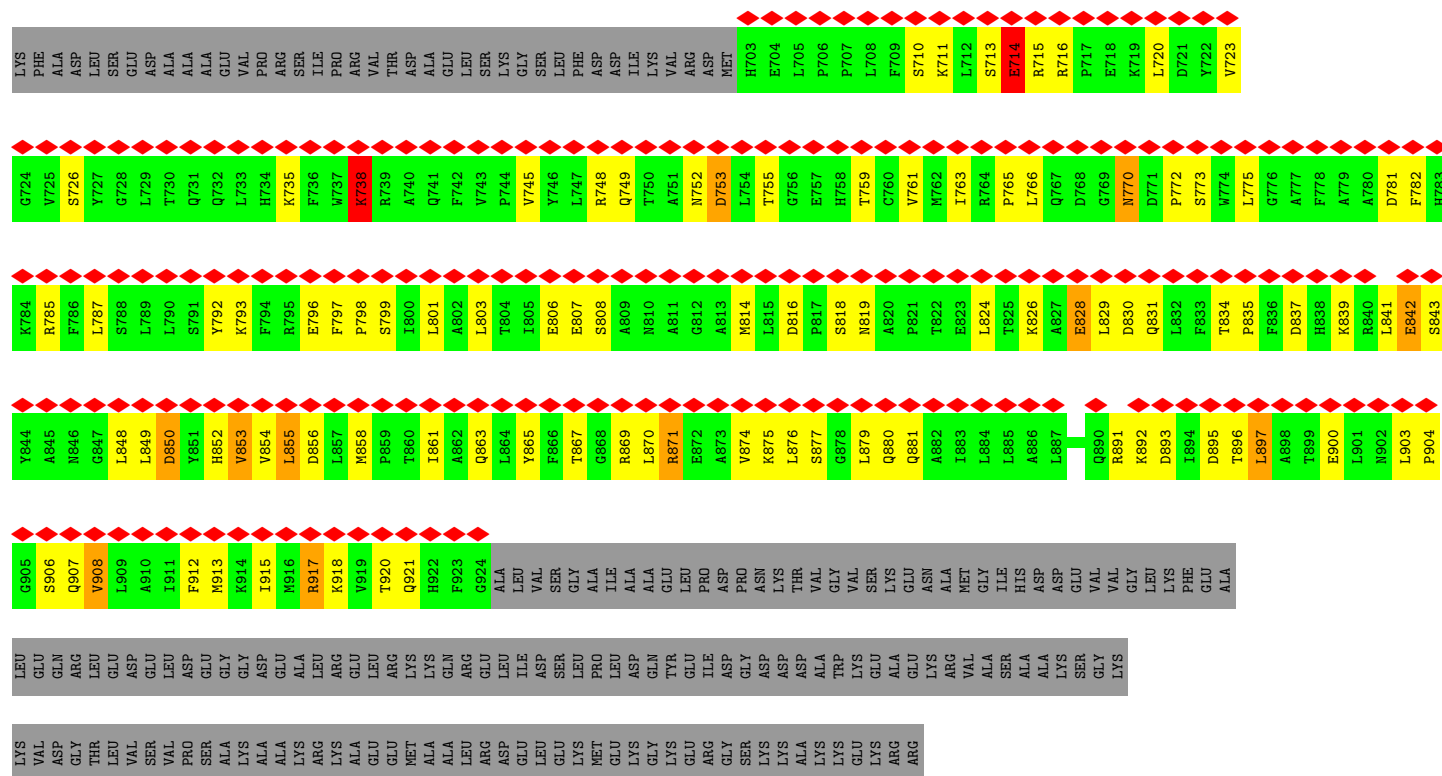


GLU	LYS	ARG	VAL	ALA	SER	ALA	ALA	LYS	SER	GLY	LYS	LYS	VAL	ASP	GLY	THR	LEU	VAL	SER	VAL	PRO	SER	SER	ALA	LYS	ALA	ALA	ALA	ARG	LYS	LYS	ALA	GLU	GLU	GLU	GLU	LYS	LYS	GLY	LYS	GLU	ARG	GLY	SER	LYS	LYS	LYS	ALA	LYS	LYS	GLU	LYS	ARG
ARG																																																					

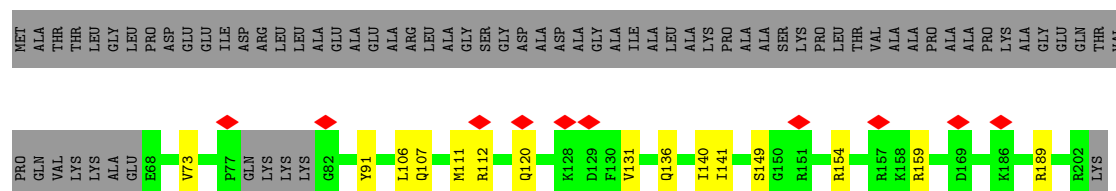
• Molecule 32: Kre33



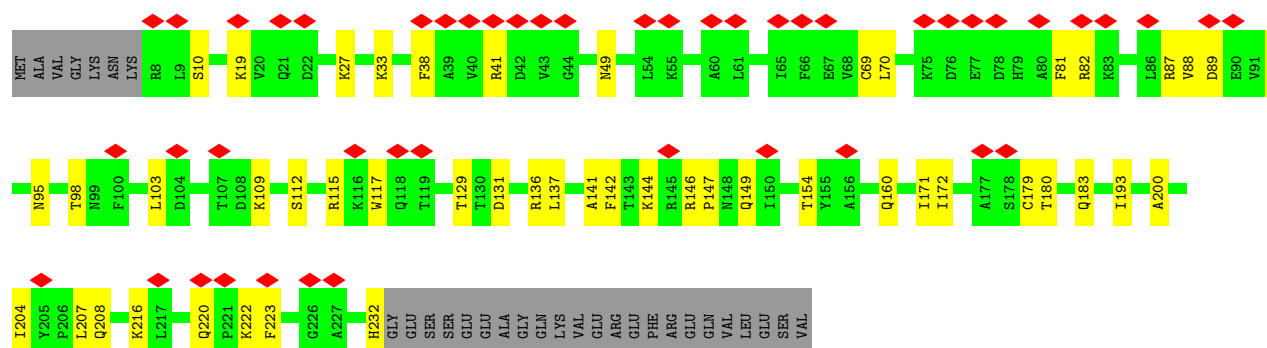
LYS	SER	LEU	SER	ARG	GLY	GLN	PRO	ALA	GLY	D612	L613	I614	P615	W616	L617	V618	S619	Q620	F621	F622	Q623	D624	D625	E626	F627	A628	S629	L630	S631	G632	A633	R634	I635	V636	I637	I638	A639	T640	N641	P642	D643	Y644	M645	S646	M647	V648	G649	G650	S651	K652	L657	V658	D659	Y660	Y661	S662	G663		
V541	A542	Q482	G483	D484	N485	V486	E487	K488	W489	L490	N491	T492	L493	L494	C495	L496	D497	A498	T499	L500	P501	R502	SER	LYS	ILE	ALA	VAL	THR	THR	L567	F568	V569	L570	T571	G572	P573	I574	Q575	E576	L578	L579	H580	V521	N522	D524	L526	F527	S528	F529	H530	P531	V532	E534	K535	F536	L537	Q538	N540	
G421	R422	S423	L424	S425	L426	K427	L428	I429	K430	Q431	L432	R433	E434	GLN	SER	ARG	ALA	GLY	ALA	ASN	PRO	ASN	GLY	GLY	ASN	ALA	VAL	VAL	VAL	ASP	ARG	P511	D512	P513	S514	THR	LYS	GLU	THR	THR	THR	VAL	GLY	GLY	ARG	SER	L469	K470	E471	L472	T473	S475	E476	P477	I478	R479	Y480		
ILE	HIS	ARG	ASN	R365	R366	Q367	T368	I369	Q370	Y371	I372	R373	P374	Q375	D376	A377	H378	V379	L380	G381	Q382	A383	E384	L385	V386	V387	I388	D389	E390	A391	A392	A393	I394	P395	L396	P397	L398	V399	K400	K401	L402	M403	G404	P405	L406	L407	V408	F409	M410	A411	S412	T413	I414	S415	G416	Y417	E418	G419	T420
A301	A302	V303	A304	Y305	G306	Y307	S308	N309	I310	F311	I312	T313	S314	P315	S316	P317	E318	N319	K320	K321	T322	L323	F324	E325	F326	VAL	PHE	LYS	GLY	PHE	ASP	ALA	LEU	ASP	TYR	LYS	ASP	HIS	ALA	ASP	THR	ILE	ILE	GLN	SER	THR	ASN	PRO	GLU	PHE	ASN	LYS	ILE	VAL	ARG	VAL	ASN		
ASP	GLU	LEU	GLU	ASP	THR	GLN	PRO	I249	G250	S251	L252	I253	K254	L255	ALA	R257	T258	V259	D260	Q261	A262	K263	A264	L265	L266	T267	F268	V269	D270	A271	I272	A273	E274	K275	T276	L277	R278	N279	T280	V281	T282	L283	T284	A285	A286	R287	G288	R289	Q290	K291	S292	A293	A294	M295	G296	V297	I298	A300	
V181	I182	A183	R184	F185	N186	E187	R188	F189	L190	L191	S192	L193	G194	S195	C196	E197	S198	C199	L200	V201	I202	D203	D204	E205	L206	N207	V208	L209	P210	I211	S212	G213	G214	K215	G216	V217	K218	P219	L220	P221	P222	P223	ASP	GLU	ASP	GLU	LEU	SER	PRO	ALA	ALA	LYS	GLU	LEU	LYS	LYS	ILE	LYS	
G121	M122	C123	I124	L125	Q126	D127	F128	E129	A130	I131	T132	P133	R134	I135	L136	A137	R138	T139	I140	E141	T142	V143	E144	G145	G146	G147	L148	V149	V150	Q151	L152	L153	D154	K155	M156	T157	S158	L159	K160	Q161	L162	Y163	T164	R165	T166	M167	D168	V169	H170	E171	R172	Y173	R174	T175	GLU	ALA	HIS	ASP	ASP
K61	K62	E63	L64	L65	G66	F67	T68	S69	H70	R71	K72	K73	R74	E75	A76	K77	T78	K79	K80	E81	I82	K83	R84	G85	I86	R87	E88	P89	N90	Q91	A92	D93	P94	F95	E96	L97	F98	I99	S100	L101	M102	D103	I104	R105	Y106	C107	Y108	Y109	K110	E111	T112	D113	K114	I115	L116	G117	N118	T119	V120
MET	T2	V3	Q4	K5	T6	V7	D8	S9	R10	I11	P12	T13	L14	I15	R16	M17	G18	L19	Q20	T21	K22	K23	R24	S25	F26	F27	V28	V29	V30	G31	D32	H33	A34	K35	E36	A37	T38	V39	H40	L41	Y42	Y43	T44	M45	S46	S47	N48	D49	V50	R51	Q52	N53	K54	S55	V56	L57	W58	A59	Y60



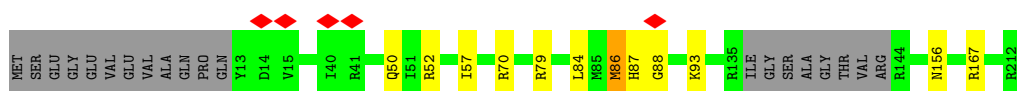
- Molecule 33: Fcf2



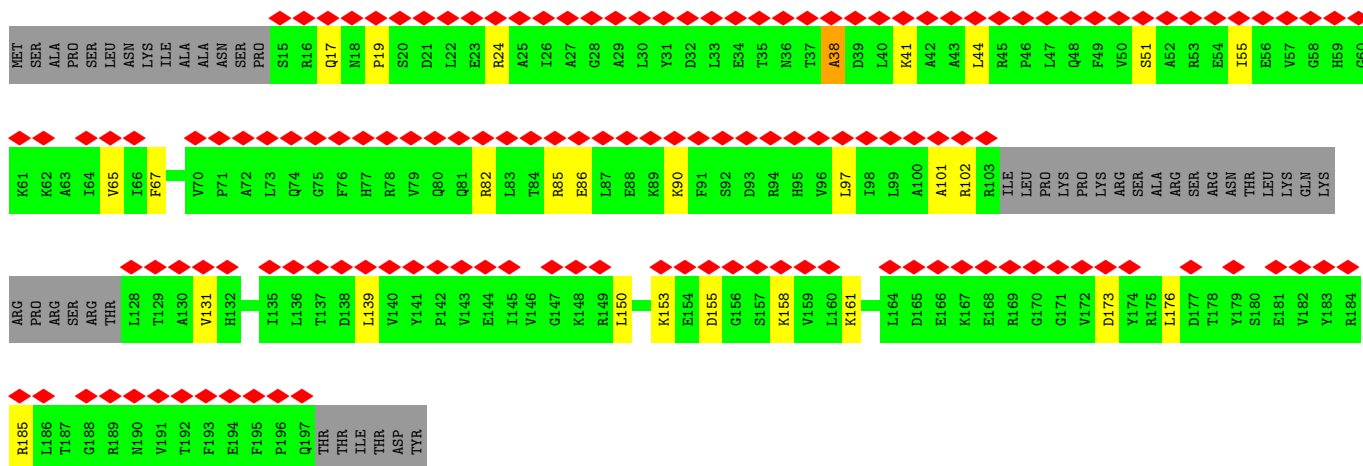
- Molecule 34: 40S ribosomal protein S1



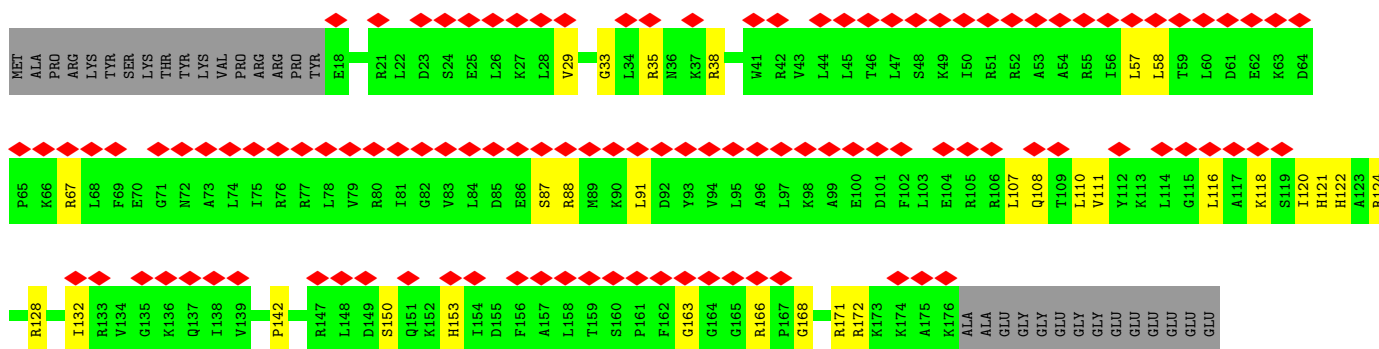
- Molecule 35: 40S ribosomal protein s5-like protein



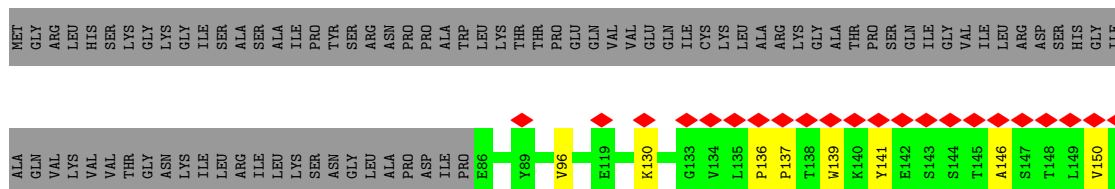
Chain Ce:

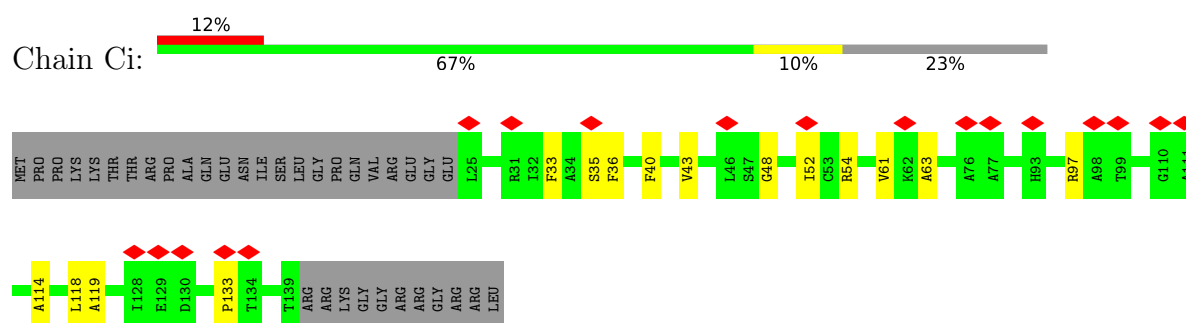


Chain Cg:

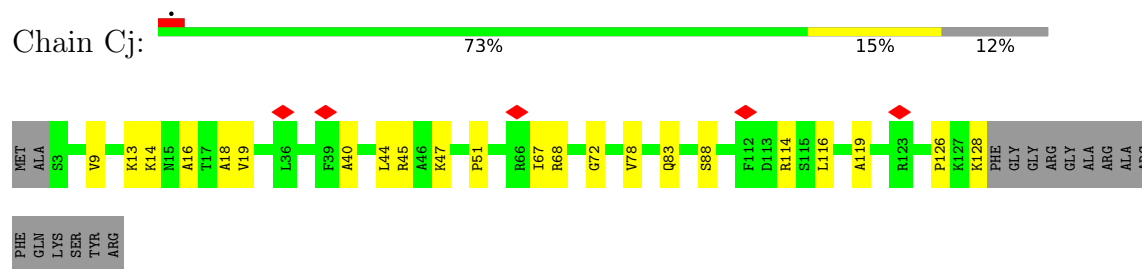


Chain Ch:

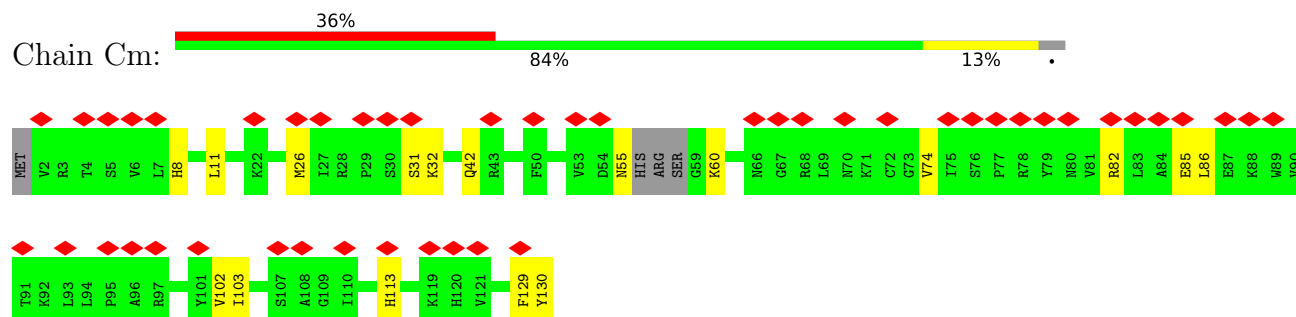




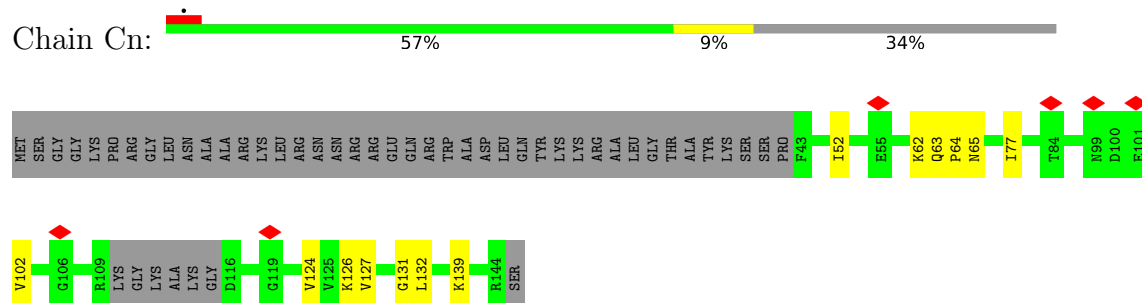
- Molecule 40: 40S ribosomal protein S16-like protein



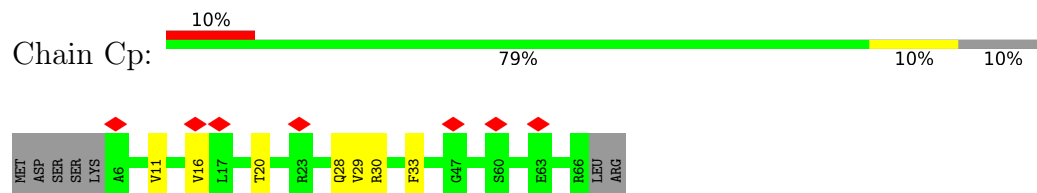
- Molecule 41: 40S ribosomal protein S22-like protein



- Molecule 42: 40S ribosomal protein s23-like protein

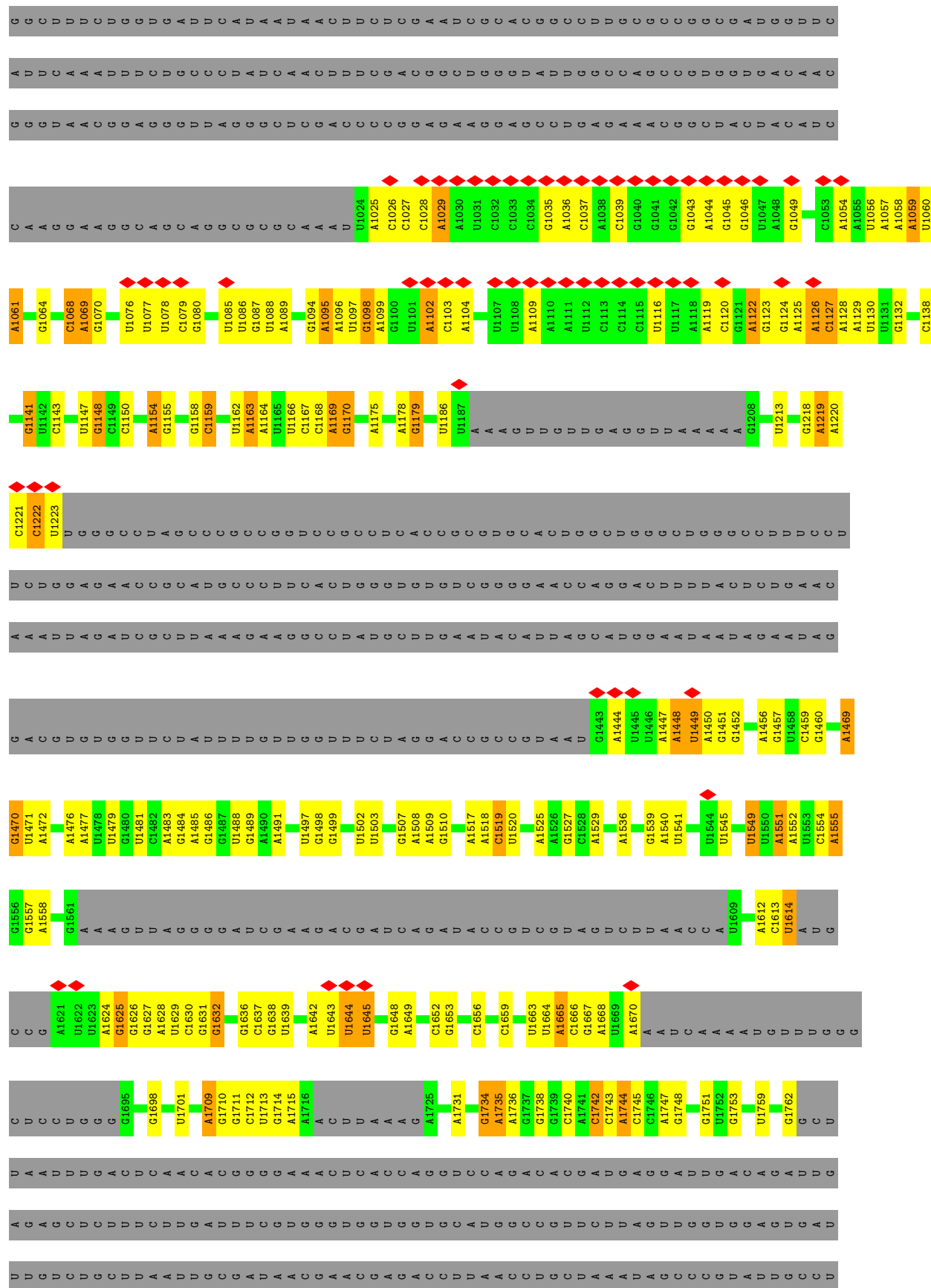


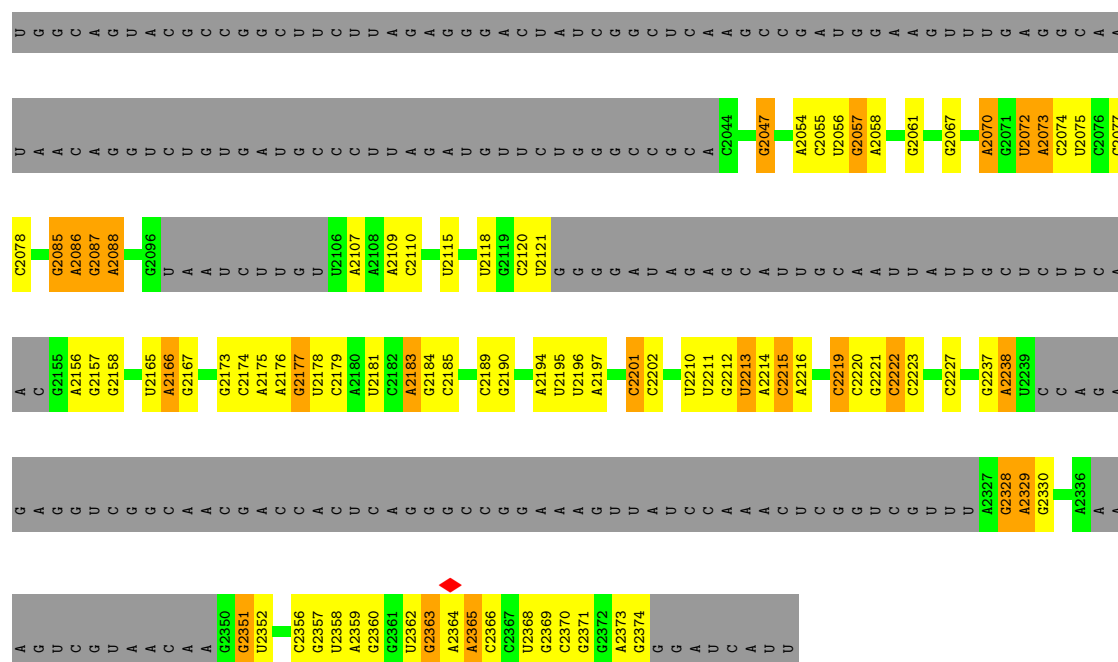
- Molecule 43: 40S ribosomal protein S28-like protein



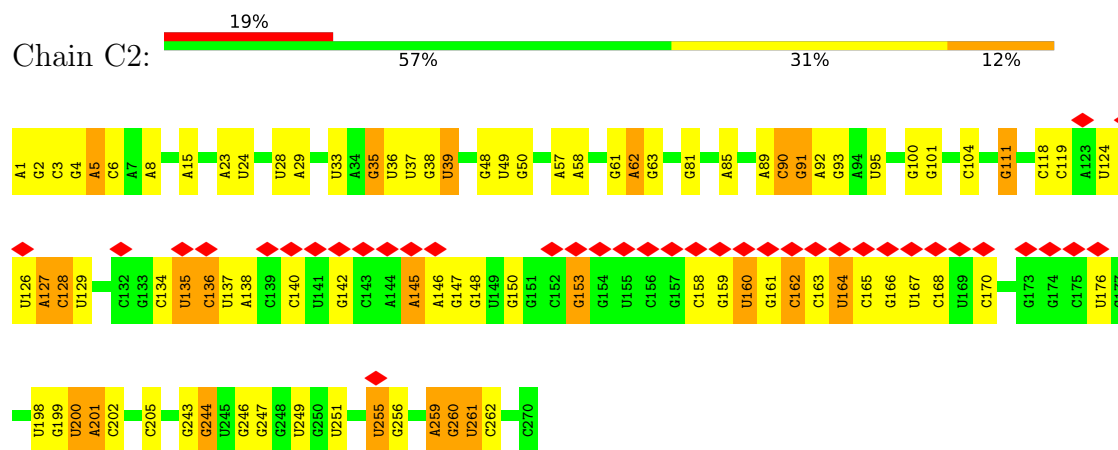
Chain CU:



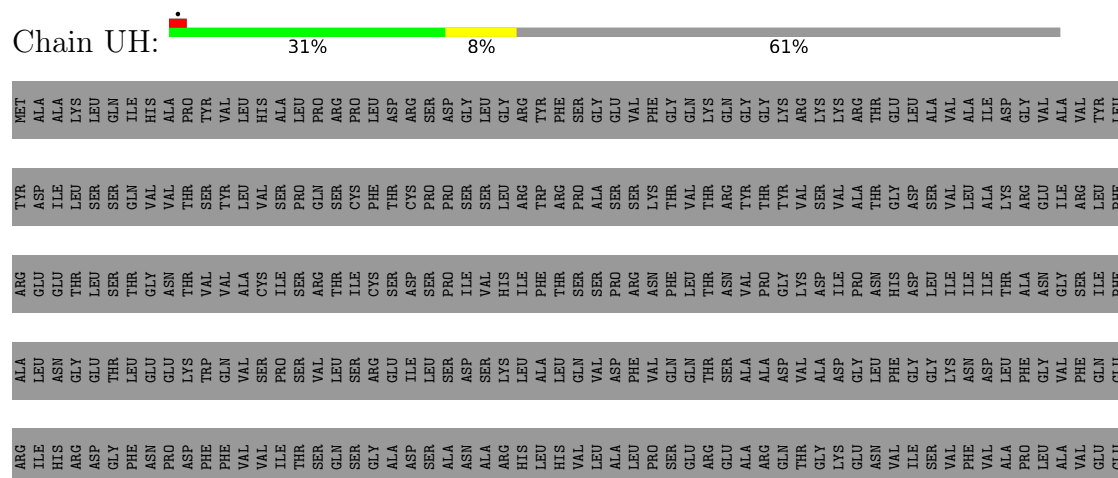




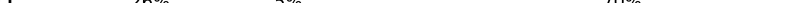
• Molecule 46: U3 snoRNA

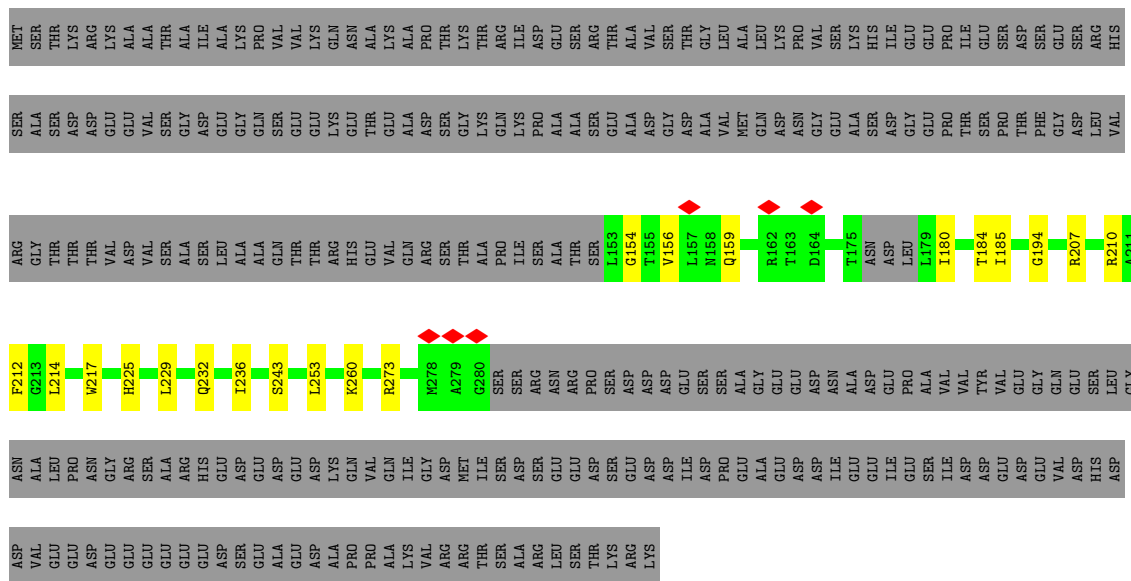


• Molecule 47: Utp8



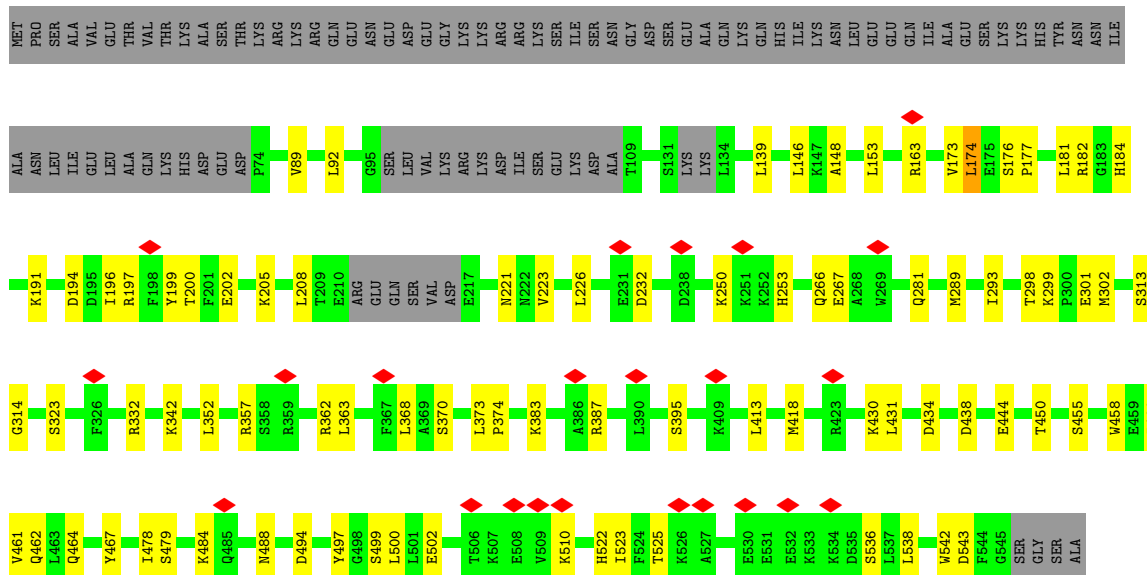


Chain UI: 



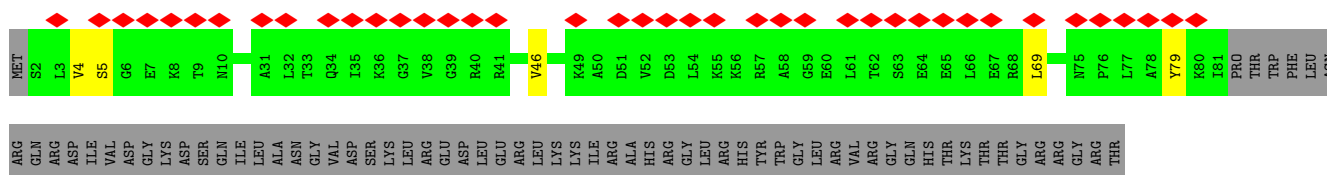
- Molecule 49: Noc4

Chain US:



- Molecule 50: Putative ribosomal protein

Chain Cl: 26% 48% 1% 25%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	8415	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	0.232	Depositor
Minimum map value	-0.184	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.03	Depositor
Map size ($\text{\AA}$)	520.32, 520.32, 520.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.42	0/6521	0.66	1/8867 (0.0%)
2	UB	0.28	0/4154	0.58	0/5583
3	UC	0.35	0/595	0.57	0/786
4	UD	0.32	0/6211	0.55	0/8408
5	UF	0.31	0/2657	0.58	0/3596
6	UG	0.42	0/3790	0.66	2/5120 (0.0%)
7	UJ	0.34	0/3435	0.59	1/4661 (0.0%)
8	UK	0.35	0/1701	0.51	0/2251
9	UL	0.33	0/6299	0.70	4/8531 (0.0%)
10	UM	0.29	0/5755	0.68	2/7827 (0.0%)
11	UN	0.37	0/1232	0.60	0/1662
12	UO	0.35	0/3903	0.63	0/5312
13	UQ	0.34	0/6136	0.64	5/8348 (0.1%)
14	UR	0.39	0/3564	0.60	0/4816
15	UU	0.40	0/6903	0.63	0/9392
16	UX	0.38	0/1493	0.63	1/2011 (0.0%)
17	UZ	0.29	0/1857	0.64	0/2526
18	CA	0.40	0/1814	0.60	2/2456 (0.1%)
18	CB	0.27	0/1853	0.54	0/2511
19	CC	0.33	0/2911	0.59	0/3937
20	CD	0.32	0/3205	0.66	3/4338 (0.1%)
21	CE	0.40	0/891	0.65	0/1214
21	CF	0.36	0/876	0.67	0/1195
22	CG	0.31	0/2983	0.62	2/4032 (0.0%)
23	CH	0.32	0/2939	0.59	0/3988
24	CI	0.37	0/6631	0.61	0/8943
25	CJ	0.43	0/1462	0.62	0/1967
26	CK	0.41	0/2376	0.64	1/3214 (0.0%)
27	CL	0.32	0/1812	0.54	0/2437
28	CM	0.42	0/3573	0.62	0/4829
29	CN	0.30	0/1797	0.59	0/2443
29	CO	0.25	0/1714	0.60	2/2325 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	CP	0.32	0/1655	0.57	0/2229
31	CQ	0.26	0/1379	0.60	0/1850
32	CR	0.37	1/6108 (0.0%)	0.92	15/8266 (0.2%)
32	CS	0.37	1/6108 (0.0%)	0.92	15/8266 (0.2%)
33	CT	0.35	0/1053	0.64	0/1413
34	Ca	0.32	0/1850	0.64	0/2486
35	Cc	0.35	0/1485	0.56	0/2008
36	Ce	0.31	0/1298	0.76	2/1750 (0.1%)
37	Cg	0.36	0/1259	0.58	0/1687
38	Ch	0.25	0/557	0.54	0/749
39	Ci	0.31	0/819	0.58	0/1107
40	Cj	0.41	0/958	0.63	0/1293
41	Cm	0.33	0/1001	0.57	0/1345
42	Cn	0.37	0/712	0.55	0/954
43	Cp	0.35	0/458	0.57	0/617
44	CU	0.28	0/1350	0.60	0/1810
45	C1	0.32	0/27472	0.48	7/42792 (0.0%)
46	C2	0.32	0/5459	0.56	6/8498 (0.1%)
47	UH	0.27	0/2852	0.59	0/3846
48	UE	0.31	0/980	0.64	0/1316
48	UI	0.22	0/980	0.56	0/1316
49	US	0.28	0/3765	0.61	0/5100
50	Cl	0.24	0/638	0.70	0/857
51	CX	0.27	1/2180 (0.0%)	0.62	0/2956
52	UP	0.30	0/428	0.66	0/570
All	All	0.34	3/175847 (0.0%)	0.62	71/244607 (0.0%)

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
4	UD	0	1
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

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
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	Cc	0	1
36	Ce	0	1
48	UE	0	1
49	US	0	1
50	Cl	0	1
All	All	0	42

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	CX	402	ALA	C-N	5.50	1.38	1.33
32	CR	714	GLU	CA-CB	5.26	1.59	1.52
32	CS	714	GLU	CA-CB	5.23	1.59	1.52

The worst 5 of 71 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	C2	2	G	OP1-P-OP2	-13.64	78.67	119.60
46	C2	2	G	O5'-P-OP1	-11.29	74.13	108.00
46	C2	1	A	OP2-P-O3'	-10.57	76.28	108.00
45	C1	55	G	OP1-P-O3'	-9.88	78.35	108.00
45	C1	45	U	OP1-P-O3'	-9.29	80.14	108.00

There are no chirality outliers.

5 of 42 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	UA	115	LEU	Peptide
4	UD	387	TRP	Peptide
9	UL	153	ASP	Peptide

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Mol	Chain	Res	Type	Group
9	UL	636	LEU	Peptide
10	UM	328	LEU	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	UA	6366	0	6273	88	0
2	UB	4079	0	4201	45	0
3	UC	588	0	647	12	0
4	UD	6071	0	6080	86	0
5	UF	2591	0	2642	15	0
6	UG	3717	0	3756	48	0
7	UJ	3377	0	3472	31	0
8	UK	1687	0	1820	6	0
9	UL	6175	0	6188	94	0
10	UM	5643	0	5643	97	0
11	UN	1209	0	1234	10	0
12	UO	3819	0	3873	59	0
13	UQ	6008	0	6033	88	0
14	UR	3491	0	3507	44	0
15	UU	6734	0	6745	78	0
16	UX	1470	0	1533	20	0
17	UZ	1815	0	1896	30	0
18	CA	1778	0	1830	30	0
18	CB	1816	0	1847	28	0
19	CC	2866	0	2960	30	0
20	CD	3150	0	3262	46	0
21	CE	879	0	918	11	0
21	CF	864	0	900	4	0
22	CG	2922	0	2939	45	0
23	CH	2888	0	2979	56	0
24	CI	6486	0	6649	82	0
25	CJ	1434	0	1482	18	0
26	CK	2329	0	2373	34	0
27	CL	1786	0	1826	20	0
28	CM	3501	0	3498	54	0
29	CN	1762	0	1807	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	CO	1683	0	1726	14	0
30	CP	1625	0	1718	28	0
31	CQ	1361	0	1431	22	0
32	CR	5989	0	6130	110	0
32	CS	5989	0	6130	107	0
33	CT	1035	0	1063	15	0
34	Ca	1821	0	1936	38	0
35	Cc	1464	0	1504	10	0
36	Ce	1279	0	1322	17	0
37	Cg	1242	0	1354	23	0
38	Ch	546	0	580	6	0
39	Ci	808	0	831	10	0
40	Cj	943	0	1002	15	0
41	Cm	985	0	1021	12	0
42	Cn	702	0	750	12	0
43	Cp	455	0	482	5	0
44	CU	1337	0	1376	15	0
45	C1	24590	0	12457	216	0
46	C2	4891	0	2476	39	0
47	UH	2809	0	2843	55	0
48	UE	972	0	1032	12	0
48	UI	972	0	1032	13	0
49	US	3672	0	3679	64	0
50	CI	633	0	676	3	0
51	CX	2130	0	2219	29	0
52	UP	422	0	457	10	0
53	UX	1	0	0	0	0
54	CI	32	0	12	11	0
55	CI	1	0	0	0	0
All	All	169690	0	158052	1941	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 6.

The worst 5 of 1941 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)
47:UH:557:GLU:O	47:UH:565:GLY:HA2	1.36	1.25
47:UH:555:GLY:O	47:UH:567:LEU:HA	1.37	1.20
24:CI:80:GLY:HA2	54:CI:1201:GTP:O2A	1.01	1.15
24:CI:80:GLY:CA	54:CI:1201:GTP:O2A	1.95	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:UZ:280:ASN:ND2	17:UZ:282:TYR:HE2	1.47	1.11

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	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%)	36	72
6	UG	475/558 (85%)	441 (93%)	32 (7%)	2 (0%)	30	67
7	UJ	439/1802 (24%)	422 (96%)	17 (4%)	0	100	100
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%)	48	83
11	UN	150/938 (16%)	146 (97%)	3 (2%)	1 (1%)	18	56
12	UO	498/557 (89%)	474 (95%)	24 (5%)	0	100	100
13	UQ	775/960 (81%)	712 (92%)	61 (8%)	2 (0%)	36	72
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%)	215 (94%)	14 (6%)	0	100	100
18	CA	238/313 (76%)	225 (94%)	13 (6%)	0	100	100
18	CB	235/313 (75%)	220 (94%)	15 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	16	54
22	CG	368/630 (58%)	343 (93%)	25 (7%)	0	100	100
23	CH	383/411 (93%)	346 (90%)	36 (9%)	1 (0%)	36	72
24	CI	812/1163 (70%)	760 (94%)	50 (6%)	2 (0%)	43	78
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%)	30	67
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%)	14	51
30	CP	197/322 (61%)	191 (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%)	24	63
32	CS	746/1073 (70%)	682 (91%)	60 (8%)	4 (0%)	24	63
33	CT	127/203 (63%)	119 (94%)	8 (6%)	0	100	100
34	Ca	223/255 (88%)	212 (95%)	11 (5%)	0	100	100
35	Cc	188/212 (89%)	179 (95%)	9 (5%)	0	100	100
36	Ce	155/203 (76%)	139 (90%)	16 (10%)	0	100	100
37	Cg	157/190 (83%)	152 (97%)	5 (3%)	0	100	100
38	Ch	64/151 (42%)	61 (95%)	3 (5%)	0	100	100
39	Ci	113/150 (75%)	106 (94%)	7 (6%)	0	100	100
40	Cj	124/143 (87%)	116 (94%)	8 (6%)	0	100	100
41	Cm	122/130 (94%)	117 (96%)	5 (4%)	0	100	100
42	Cn	92/145 (63%)	89 (97%)	3 (3%)	0	100	100
43	Cp	59/68 (87%)	55 (93%)	4 (7%)	0	100	100
44	CU	168/311 (54%)	156 (93%)	12 (7%)	0	100	100
47	UH	349/930 (38%)	340 (97%)	9 (3%)	0	100	100
48	UE	121/410 (30%)	117 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	UI	121/410 (30%)	121 (100%)	0	0	100	100
49	US	443/549 (81%)	415 (94%)	28 (6%)	0	100	100
50	CI	78/156 (50%)	73 (94%)	5 (6%)	0	100	100
51	CX	265/480 (55%)	255 (96%)	10 (4%)	0	100	100
52	UP	52/364 (14%)	46 (88%)	5 (10%)	1 (2%)	6	32
All	All	17778/27558 (64%)	16693 (94%)	1062 (6%)	23 (0%)	49	83

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
29	CO	85	SER
6	UG	580	GLU
13	UQ	708	SER
6	UG	56	PRO
32	CR	48	MET

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	UA	651/775 (84%)	649 (100%)	2 (0%)	86	86
2	UB	425/788 (54%)	425 (100%)	0	100	100
3	UC	61/536 (11%)	61 (100%)	0	100	100
4	UD	653/738 (88%)	649 (99%)	4 (1%)	78	83
5	UF	248/341 (73%)	247 (100%)	1 (0%)	84	84
6	UG	373/474 (79%)	370 (99%)	3 (1%)	73	80
7	UJ	351/1526 (23%)	350 (100%)	1 (0%)	86	86
8	UK	159/227 (70%)	159 (100%)	0	100	100
9	UL	667/821 (81%)	661 (99%)	6 (1%)	70	79
10	UM	606/770 (79%)	599 (99%)	7 (1%)	63	75
11	UN	123/765 (16%)	123 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	UO	404/456 (89%)	395 (98%)	9 (2%)	45	64
13	UQ	650/817 (80%)	646 (99%)	4 (1%)	78	83
14	UR	360/524 (69%)	358 (99%)	2 (1%)	78	83
15	UU	672/863 (78%)	666 (99%)	6 (1%)	70	79
16	UX	150/167 (90%)	147 (98%)	3 (2%)	48	66
17	UZ	186/329 (56%)	184 (99%)	2 (1%)	65	76
18	CA	175/228 (77%)	172 (98%)	3 (2%)	53	69
18	CB	195/228 (86%)	193 (99%)	2 (1%)	68	78
19	CC	287/435 (66%)	287 (100%)	0	100	100
20	CD	319/489 (65%)	318 (100%)	1 (0%)	86	86
21	CE	91/108 (84%)	90 (99%)	1 (1%)	65	76
21	CF	88/108 (82%)	87 (99%)	1 (1%)	65	76
22	CG	299/525 (57%)	294 (98%)	5 (2%)	53	69
23	CH	303/320 (95%)	299 (99%)	4 (1%)	61	74
24	CI	661/1009 (66%)	653 (99%)	8 (1%)	63	75
25	CJ	147/169 (87%)	146 (99%)	1 (1%)	76	81
26	CK	245/266 (92%)	238 (97%)	7 (3%)	37	58
27	CL	181/642 (28%)	181 (100%)	0	100	100
28	CM	364/383 (95%)	363 (100%)	1 (0%)	86	86
29	CN	202/223 (91%)	202 (100%)	0	100	100
29	CO	193/223 (86%)	192 (100%)	1 (0%)	81	83
30	CP	177/287 (62%)	177 (100%)	0	100	100
31	CQ	145/215 (67%)	145 (100%)	0	100	100
32	CR	654/916 (71%)	446 (68%)	208 (32%)	0	2
32	CS	654/916 (71%)	446 (68%)	208 (32%)	0	2
33	CT	108/167 (65%)	107 (99%)	1 (1%)	70	79
34	Ca	198/223 (89%)	197 (100%)	1 (0%)	81	83
35	Cc	149/178 (84%)	149 (100%)	0	100	100
36	Ce	137/177 (77%)	137 (100%)	0	100	100
37	Cg	122/162 (75%)	122 (100%)	0	100	100
38	Ch	58/130 (45%)	58 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	Ci	78/117 (67%)	78 (100%)	0	100	100
40	Cj	92/115 (80%)	92 (100%)	0	100	100
41	Cm	103/113 (91%)	103 (100%)	0	100	100
42	Cn	70/116 (60%)	70 (100%)	0	100	100
43	Cp	46/61 (75%)	46 (100%)	0	100	100
44	CU	137/260 (53%)	137 (100%)	0	100	100
47	UH	301/788 (38%)	298 (99%)	3 (1%)	68	78
48	UE	105/346 (30%)	105 (100%)	0	100	100
48	UI	105/346 (30%)	105 (100%)	0	100	100
49	US	404/493 (82%)	403 (100%)	1 (0%)	87	87
50	Cl	71/135 (53%)	71 (100%)	0	100	100
51	CX	227/411 (55%)	227 (100%)	0	100	100
52	UP	44/314 (14%)	44 (100%)	0	100	100
All	All	14674/23259 (63%)	14167 (96%)	507 (4%)	32	53

5 of 507 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	CR	713	SER
32	CS	723	VAL
32	CR	900	GLU
32	CS	710	SER
32	CS	837	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 237 such sidechains are listed below:

Mol	Chain	Res	Type
19	CC	321	HIS
49	US	151	GLN
24	CI	791	ASN
47	UH	898	HIS
52	UP	341	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	C1	1134/2352 (48%)	347 (30%)	26 (2%)
46	C2	226/230 (98%)	68 (30%)	4 (1%)
All	All	1360/2582 (52%)	415 (30%)	30 (2%)

5 of 415 RNA backbone outliers are listed below:

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

5 of 30 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
45	C1	1085	U
46	C2	35	G
45	C1	1485	A
46	C2	255	U
45	C1	2177	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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
54	GTP	CI	1201	-	33,34,34	1.09	3 (9%)	50,54,54	1.80	9 (18%)

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
54	GTP	CI	1201	-	-	2/22/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	CI	1201	GTP	C6-N1	-2.77	1.33	1.38
54	CI	1201	GTP	C5-C4	2.74	1.46	1.38
54	CI	1201	GTP	C5-N7	-2.27	1.34	1.39

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	CI	1201	GTP	C5-C4-N3	-6.31	118.34	128.39
54	CI	1201	GTP	C2-N3-C4	5.13	121.14	112.30
54	CI	1201	GTP	N9-C4-N3	4.67	135.29	125.95
54	CI	1201	GTP	C6-C5-N7	3.33	136.34	130.29
54	CI	1201	GTP	C4-C5-N7	-2.60	106.56	110.67

There are no chirality outliers.

All (2) torsion outliers are listed below:

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

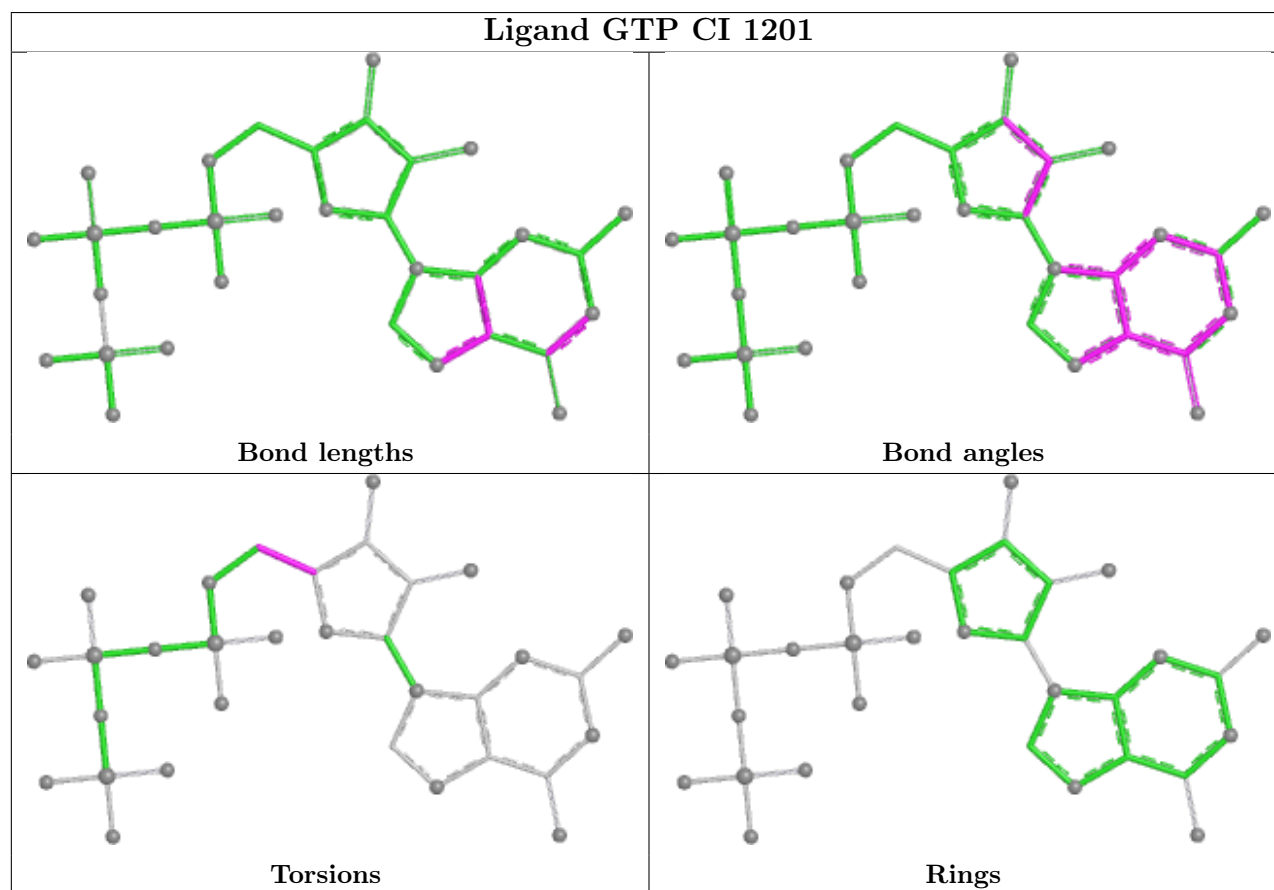
There are no ring outliers.

1 monomer is involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	CI	1201	GTP	11	0

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
46	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
1	C2	105:C	O3'	110:A	P	16.05
1	C2	119:C	O3'	123:A	P	11.95

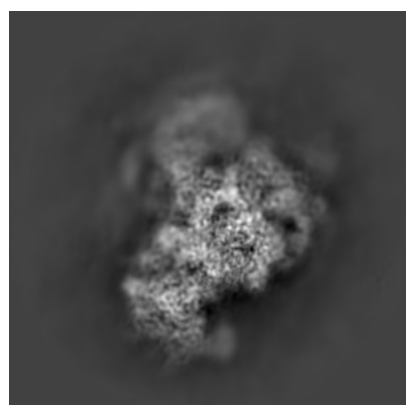
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10051. These allow visual inspection of the internal detail of the map and identification of artifacts.

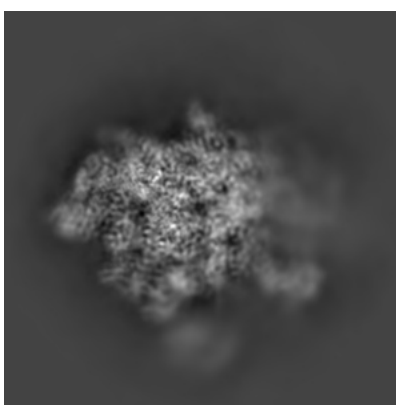
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

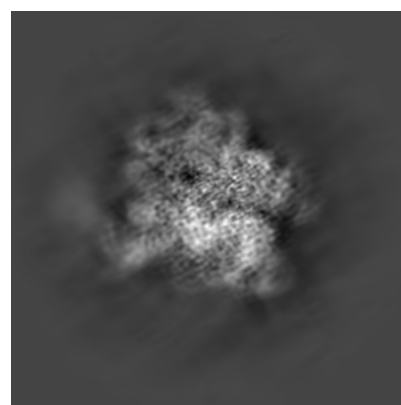
6.1.1 Primary map



X



Y

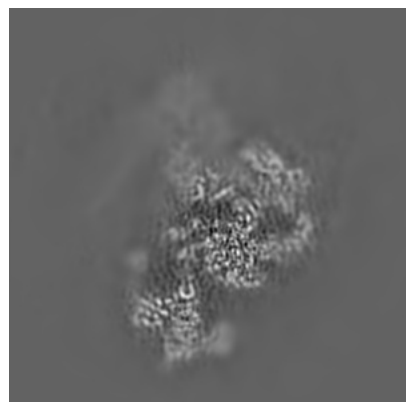


Z

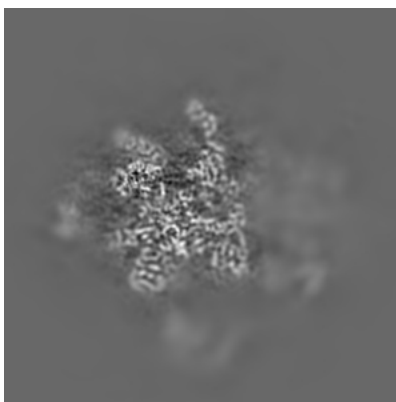
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

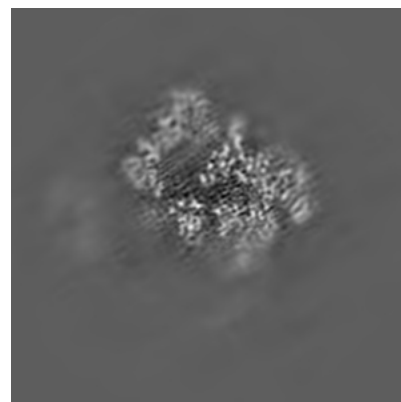
6.2.1 Primary map



X Index: 240



Y Index: 240

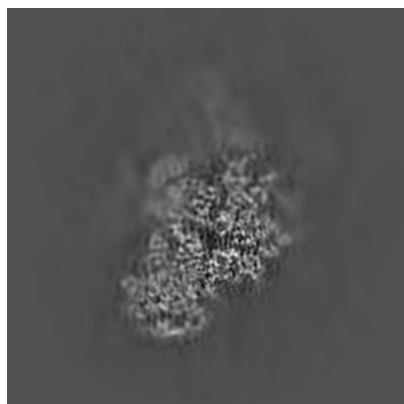


Z Index: 240

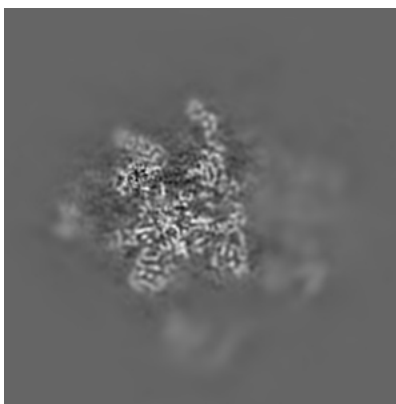
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

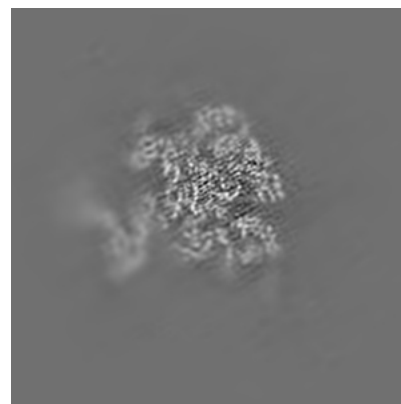
6.3.1 Primary map



X Index: 280



Y Index: 241

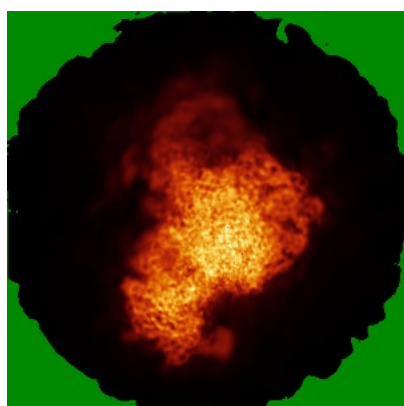


Z Index: 204

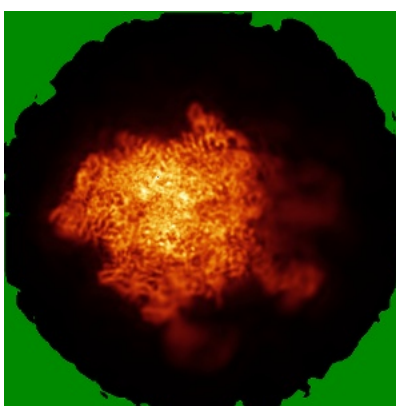
The images above show the largest variance slices of the map in three orthogonal directions.

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

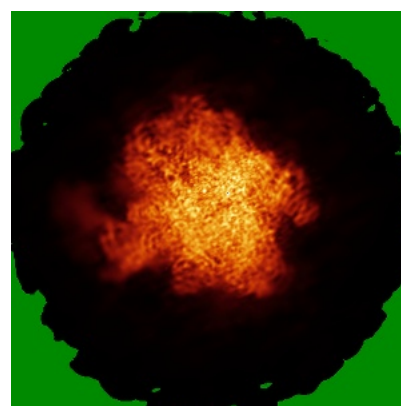
6.4.1 Primary map



X



Y



Z

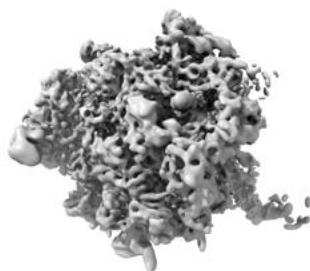
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

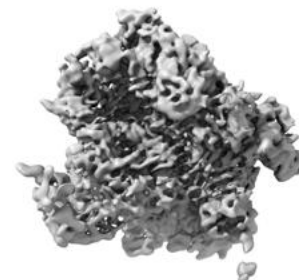
6.5.1 Primary map



X



Y



Z

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.

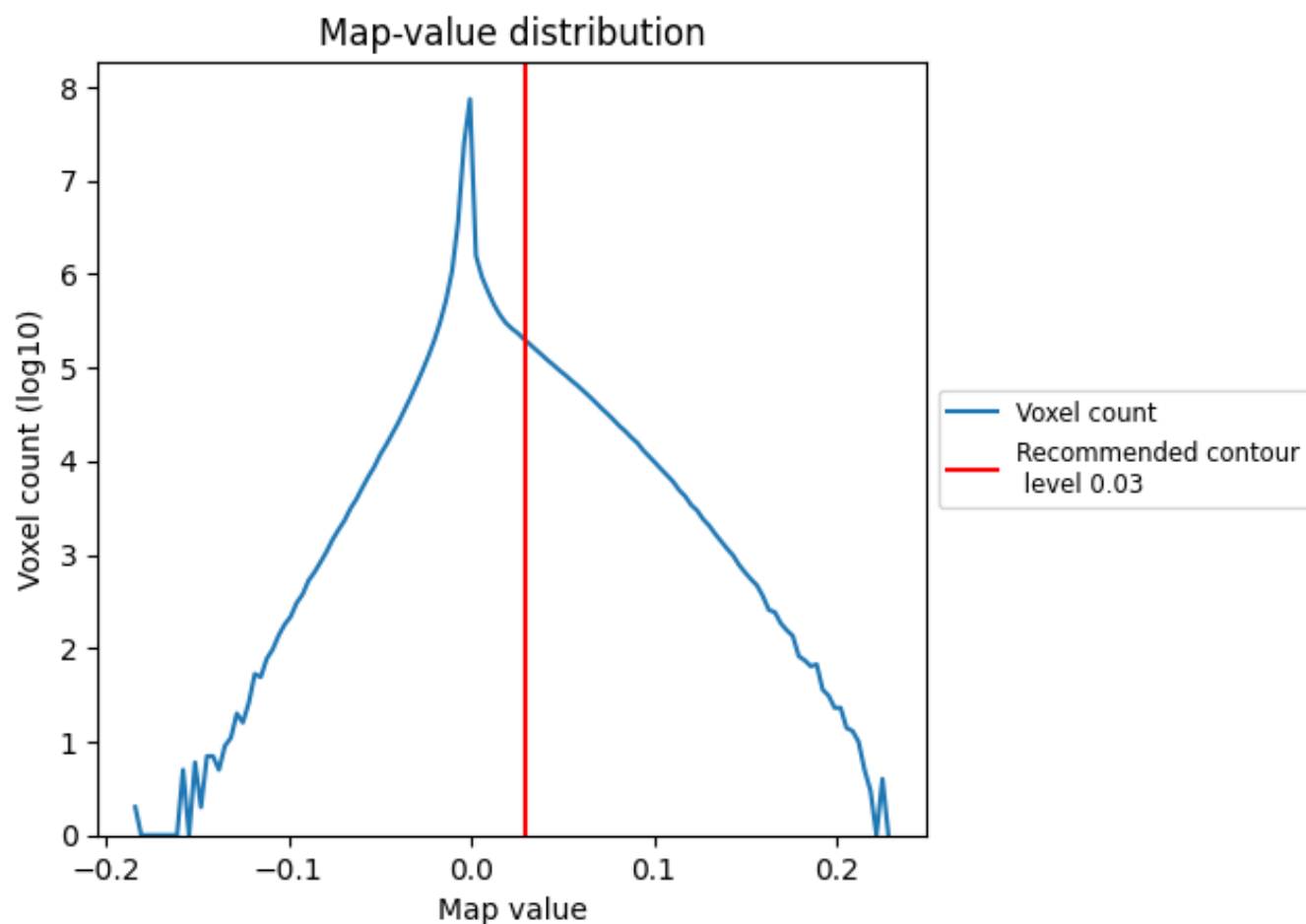
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

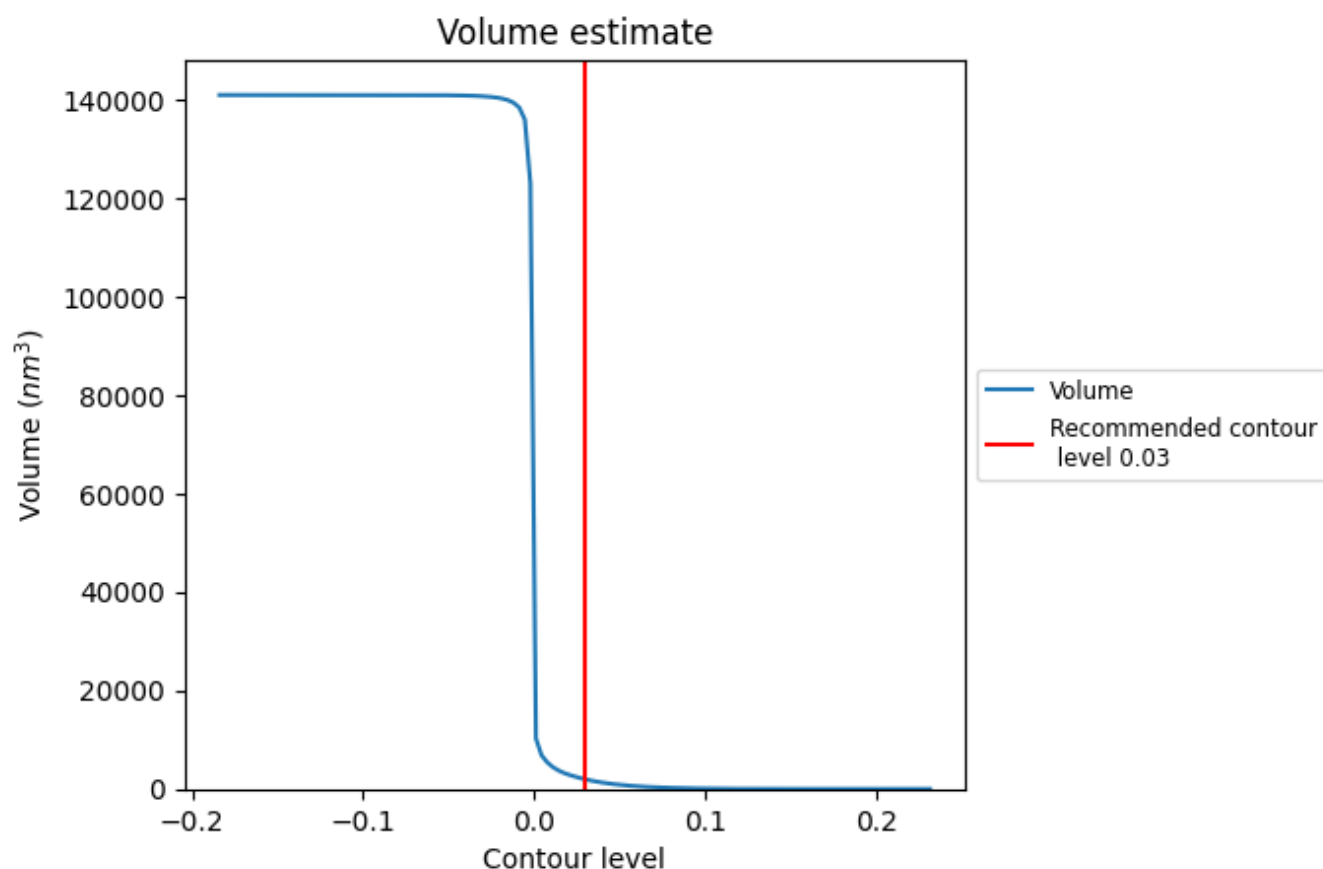
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

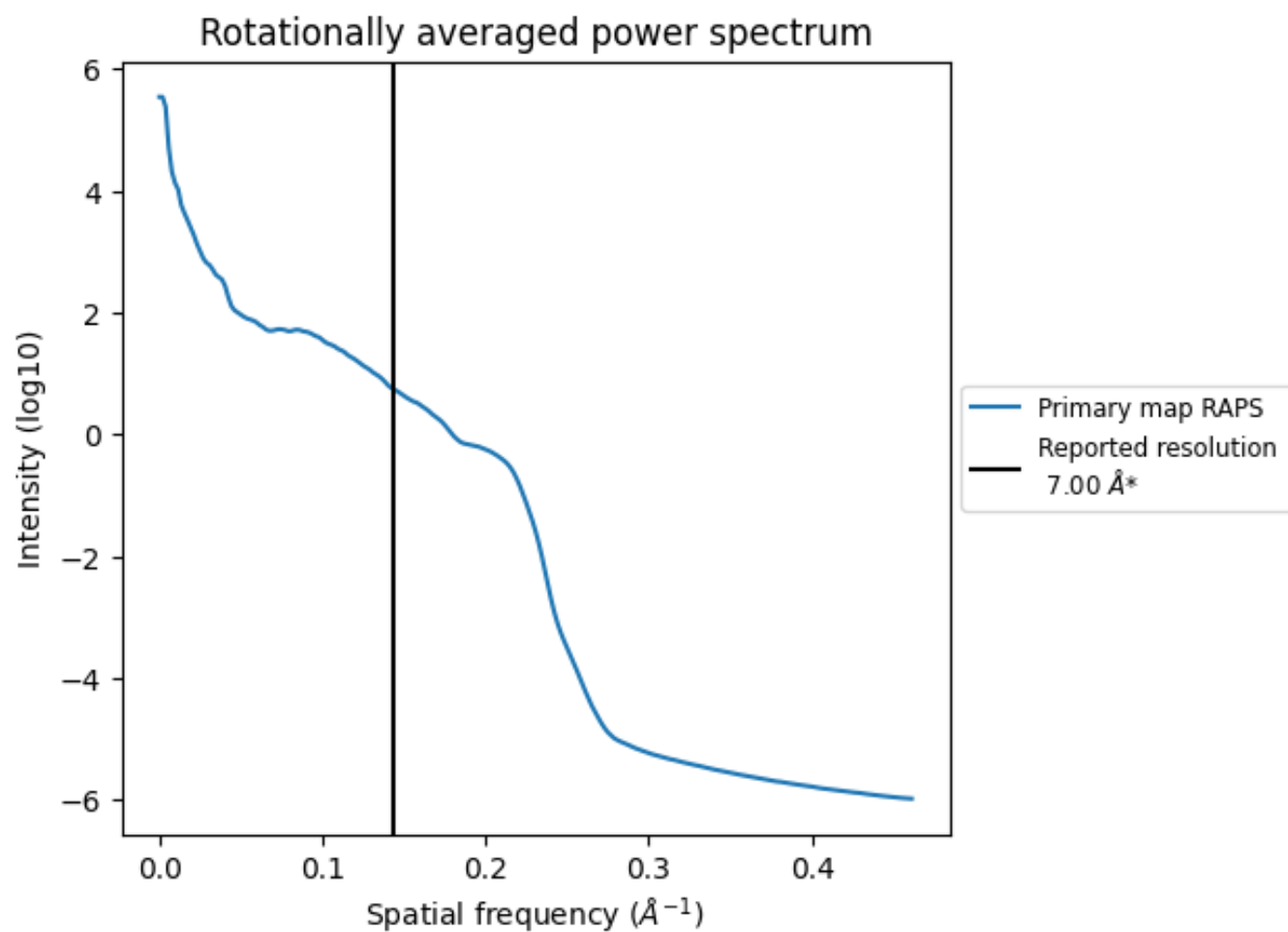
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1958 nm³; this corresponds to an approximate mass of 1768 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 ⓘ

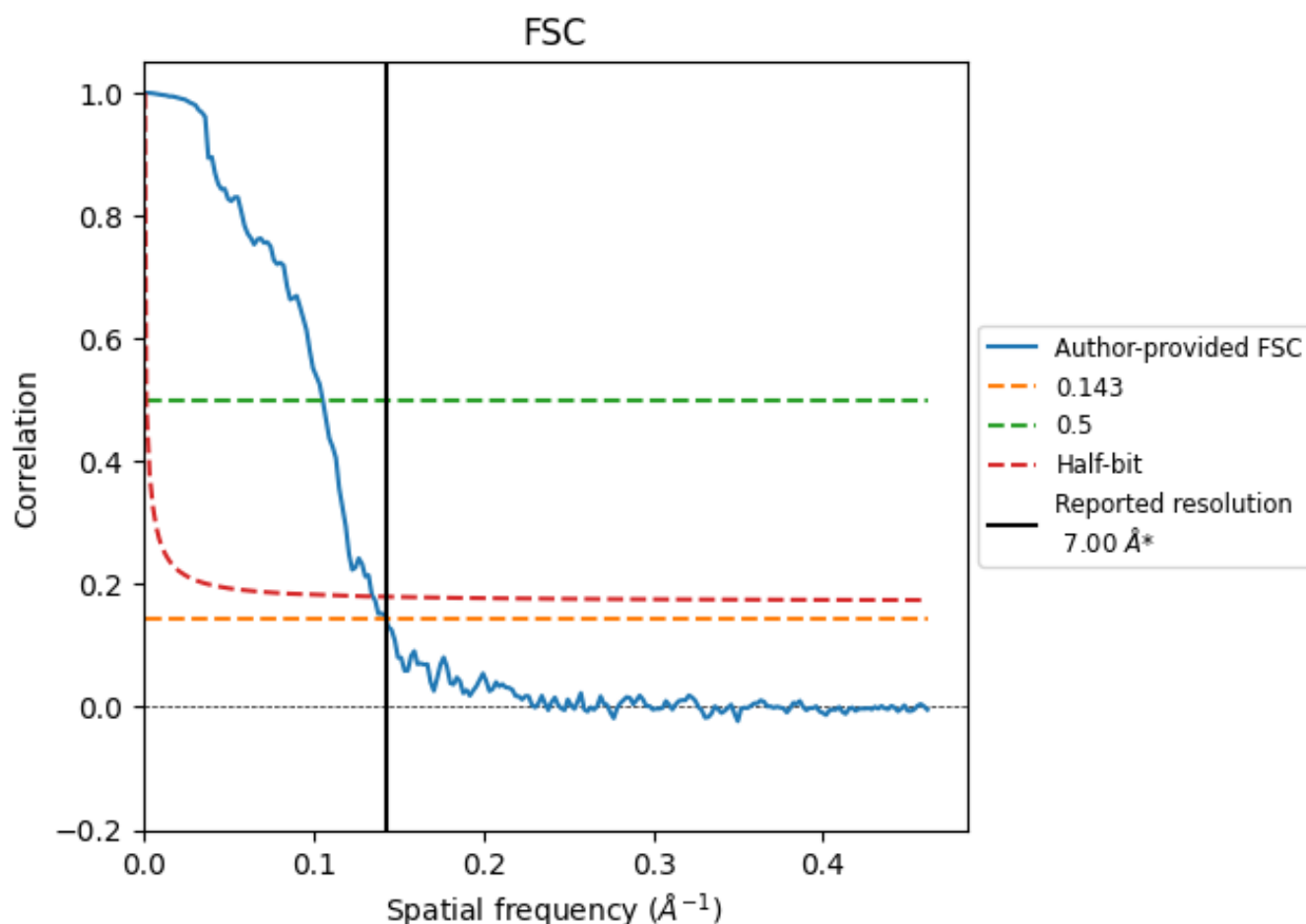


*Reported resolution corresponds to spatial frequency of 0.143 Å⁻¹

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 0.143 Å⁻¹

8.2 Resolution estimates [i](#)

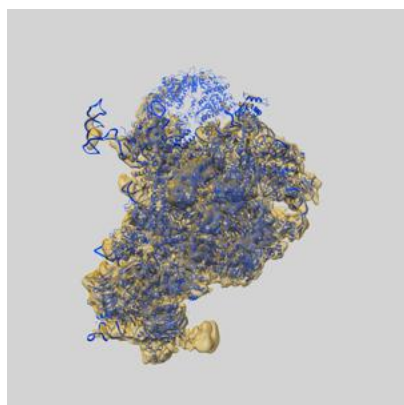
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.00	-	-
Author-provided FSC curve	7.00	9.47	7.40
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

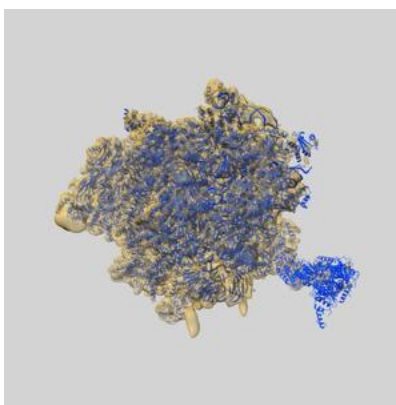
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10051 and PDB model 6RXT. Per-residue inclusion information can be found in section [3](#) on page [15](#).

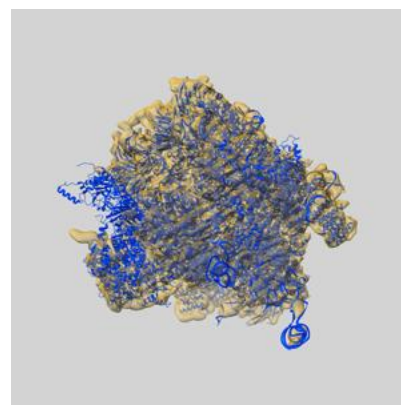
9.1 Map-model overlay [i](#)



X



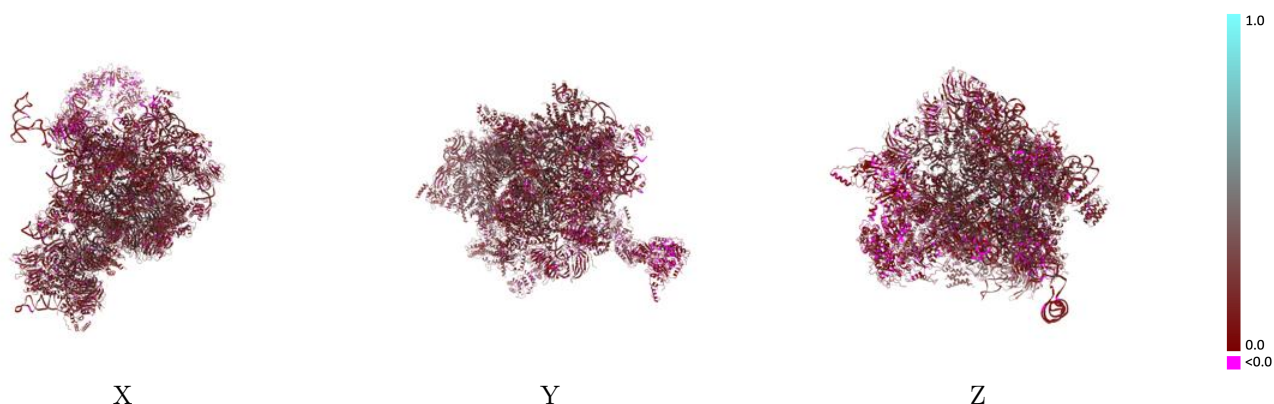
Y



Z

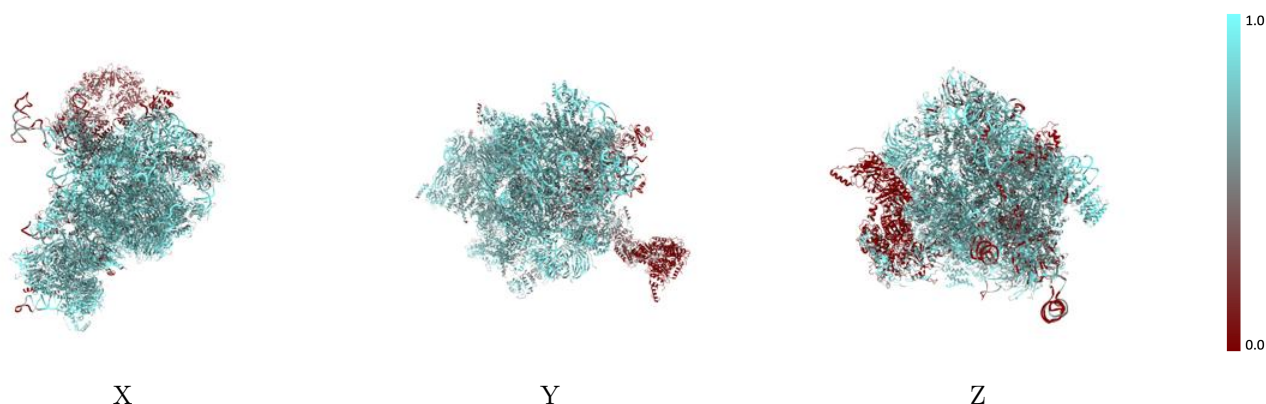
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



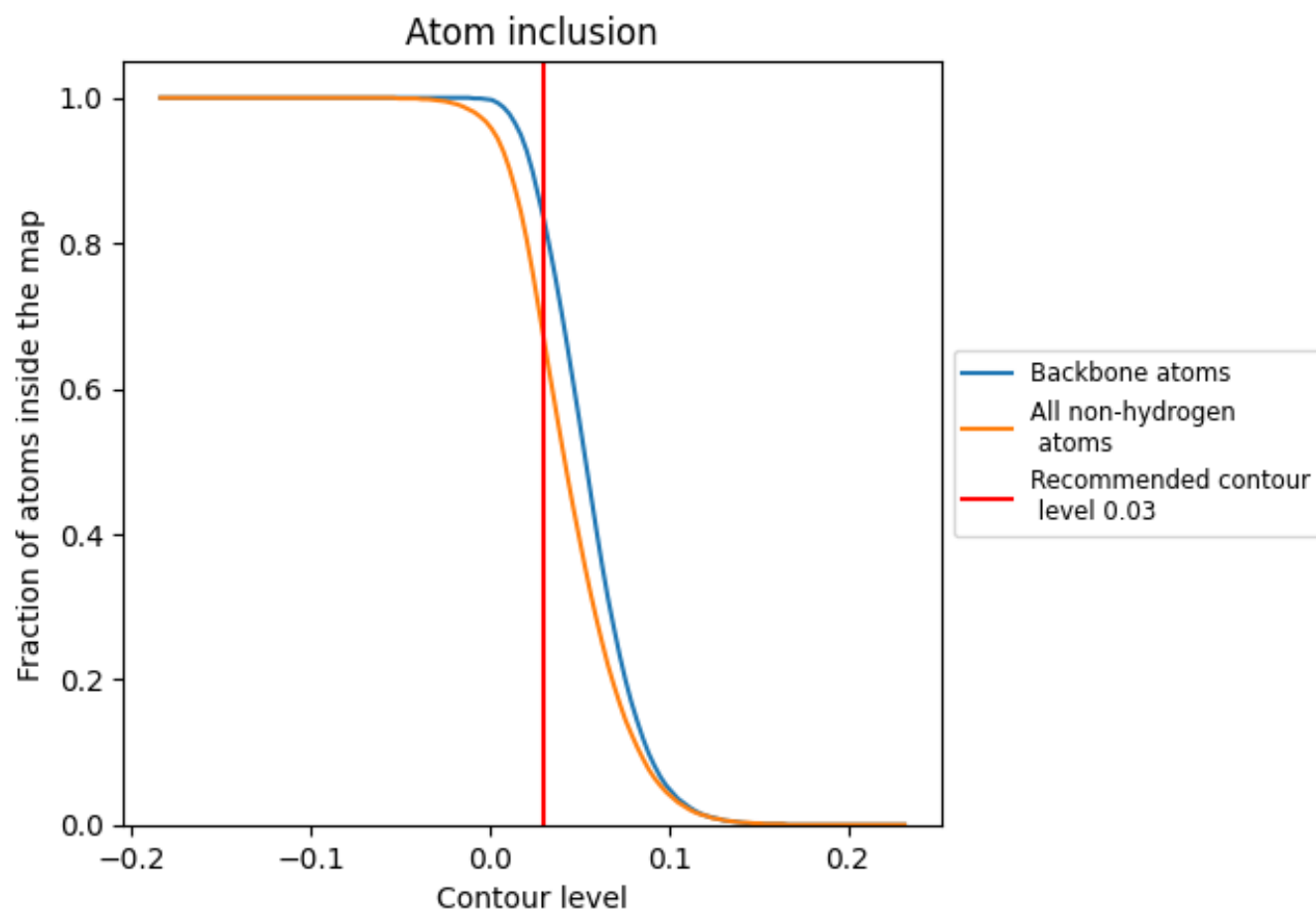
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 67% 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	 0.6710	 0.1660
C1	 0.8420	 0.2100
C2	 0.7280	 0.1970
CA	 0.7010	 0.1750
CB	 0.6540	 0.1480
CC	 0.6640	 0.1560
CD	 0.7060	 0.1610
CE	 0.7090	 0.1920
CF	 0.5920	 0.1310
CG	 0.4090	 0.0860
CH	 0.6830	 0.1430
CI	 0.6700	 0.1600
CJ	 0.7190	 0.2240
CK	 0.6880	 0.2120
CL	 0.7070	 0.1960
CM	 0.7080	 0.1460
CN	 0.6700	 0.1560
CO	 0.6970	 0.1380
CP	 0.5310	 0.1470
CQ	 0.7070	 0.1590
CR	 0.2890	 0.0920
CS	 0.0150	 0.0450
CT	 0.6710	 0.1670
CU	 0.5220	 0.1560
CX	 0.6420	 0.0950
Ca	 0.6210	 0.1280
Cc	 0.6990	 0.1800
Ce	 0.1150	 0.0970
Cg	 0.2770	 0.1210
Ch	 0.4740	 0.1070
Ci	 0.6500	 0.1360
Cj	 0.7220	 0.2320
Cl	 0.3870	 0.1290
Cm	 0.4820	 0.1310
Cn	 0.6610	 0.1730



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Chain	Atom inclusion	Q-score
Cp	 0.7150	 0.1790
UA	 0.7410	 0.2100
UB	 0.7300	 0.1640
UC	 0.5660	 0.1530
UD	 0.7270	 0.1680
UE	 0.6910	 0.1540
UF	 0.7680	 0.1560
UG	 0.7000	 0.1990
UH	 0.7500	 0.1490
UI	 0.7160	 0.1460
UJ	 0.7050	 0.1730
UK	 0.7070	 0.1910
UL	 0.7640	 0.1500
UM	 0.6370	 0.1240
UN	 0.7150	 0.1700
UO	 0.7170	 0.1750
UP	 0.7050	 0.1730
UQ	 0.7570	 0.1870
UR	 0.7620	 0.2290
US	 0.7280	 0.1490
UU	 0.7640	 0.2090
UX	 0.6630	 0.1610
UZ	 0.6900	 0.1550