



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 06:16 AM UTC

PDB ID : 6RXY / pdb_00006rxy
EMDB ID : EMD-10055
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 : 4.70 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

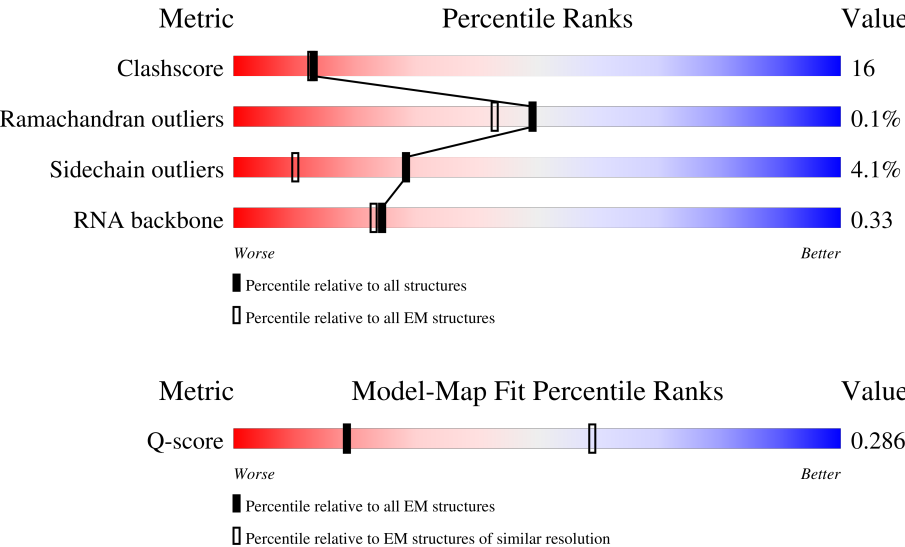
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.70 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.



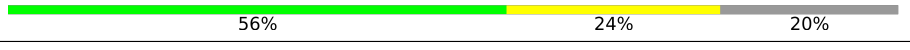
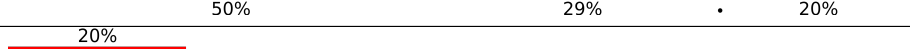
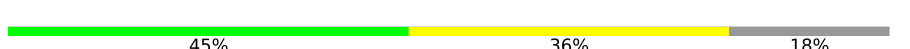
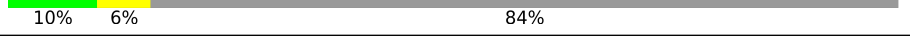
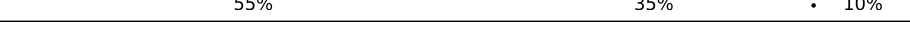
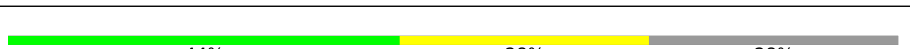
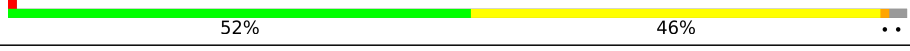
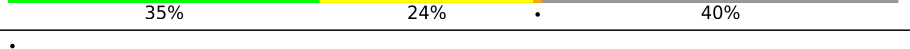
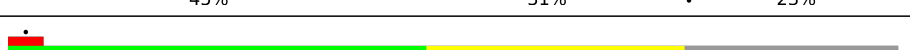
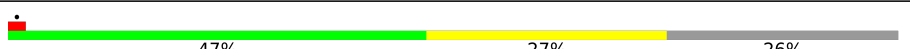
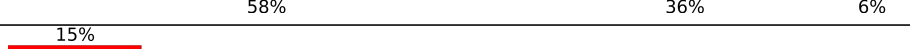
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1989 (4.20 - 5.20)

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	Cc	212	
35	Ce	203	
36	Cg	190	
37	Ch	151	
38	Ci	150	
39	Cj	143	
40	Cm	130	
41	Cn	145	
42	Cp	68	
43	CU	311	
44	C1	2323	
45	C2	230	
46	UV	1171	
47	CV	322	
48	UH	930	
49	UE	410	

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Mol	Chain	Length	Quality of chain
49	UI	410	13%13%70%
50	US	549	51%31%18%
51	Cl	156	8%39%12%49%
52	CX	480	9%36%19%44%
53	UP	364	10%5%85%
54	Cz	1796	13%11%85%

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 180242 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	448	Total	C	N	O	S	0	0
			3444	2197	646	590	11		

- Molecule 7 is a protein called Utp10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	UJ	808	Total	C	N	O	S	0	0
			6180	3965	1077	1115	23		

- 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	679	Total	C	N	O	S	0	0
			5273	3351	924	986	12		

- 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 Utp21.

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 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	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 Imp4.

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 Mpp10.

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	187	Total	C	N	O	S	0	0
			1504	961	269	265	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 s5-like protein.

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

- Molecule 35 is a protein called 40S ribosomal protein S7.

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

- Molecule 36 is a protein called 40S ribosomal protein s9-like protein.

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

- Molecule 37 is a protein called 40S ribosomal protein S13-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	Ch	49	Total	C	N	O	0	0
			416	270	82	64		

- Molecule 38 is a protein called 40S ribosomal protein S14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ci	115	Total	C	N	O	S	0	0
			791	492	154	141	4		

- Molecule 39 is a protein called 40S ribosomal protein S16-like protein.

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

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

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

- Molecule 41 is a protein called 40S ribosomal protein s23-like protein.

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

- Molecule 42 is a protein called 40S ribosomal protein S28-like protein.

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

- Molecule 43 is a protein called Faf1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	CU	131	Total	C	N	O	S	0	0
			1009	623	205	175	6		

- Molecule 44 is a RNA chain called 35S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	C1	1106	Total	C	N	O	P	0	0
			23604	10525	4233	7740	1106		

- Molecule 45 is a RNA chain called U3 snoRNA.

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

- Molecule 46 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	UV	1061	Total	C	N	O	S	0	0
			8424	5399	1480	1523	22		

- Molecule 47 is a protein called Rrp7.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	CV	148	Total	C	N	O	S	0	0
			1145	729	198	216	2		

- Molecule 48 is a protein called Utp8.

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

- Molecule 49 is a protein called Utp5.

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

- Molecule 50 is a protein called Noc4.

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

- Molecule 51 is a protein called Rps18.

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

- Molecule 52 is a protein called Enp1.

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

- Molecule 53 is a protein called Utp16.

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

- Molecule 54 is a protein called Rrp5.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Cz	275	Total	C	N	O	S	0	0
			2259	1435	401	420	3		

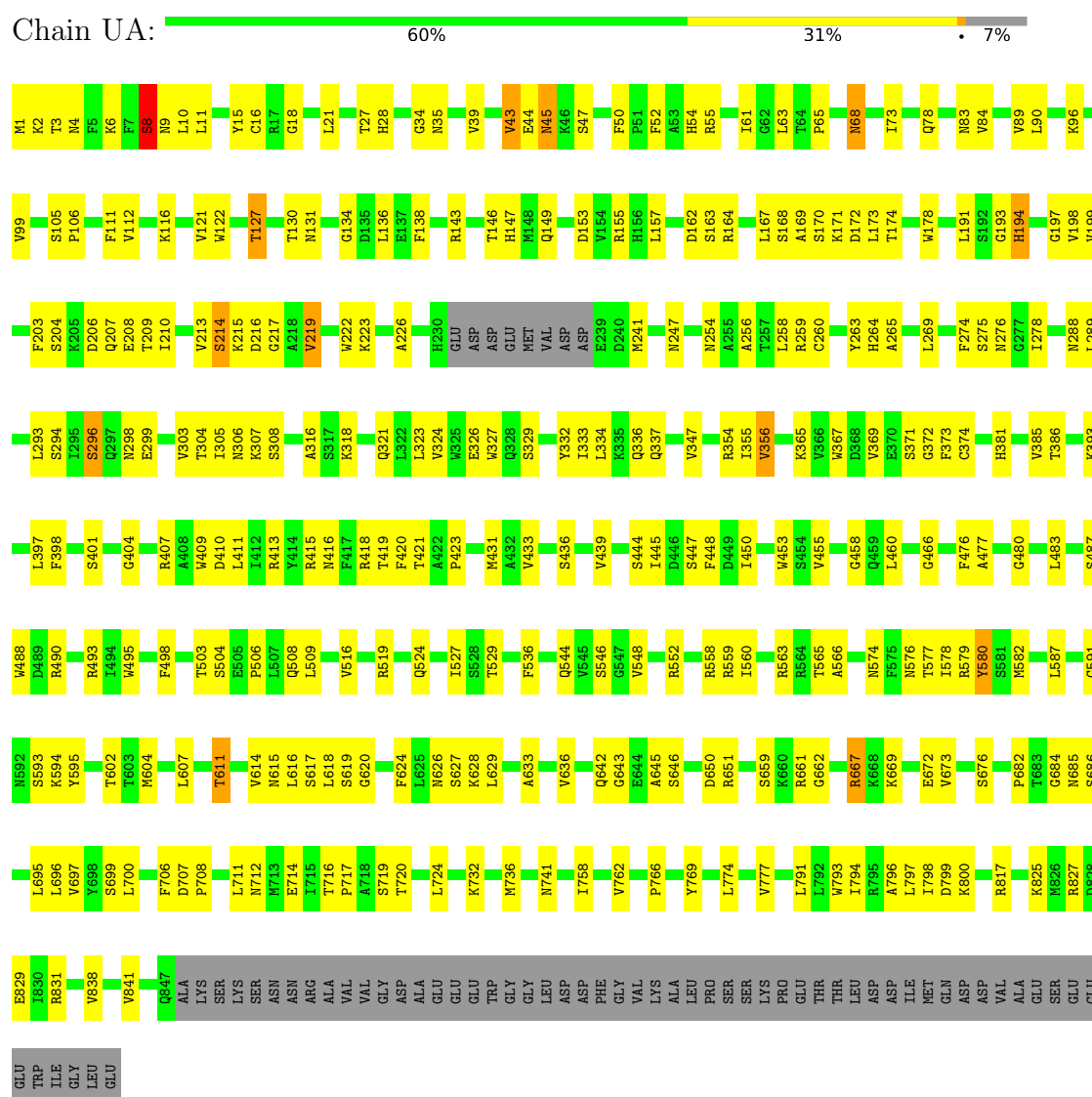
- Molecule 55 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

3 Residue-property plots

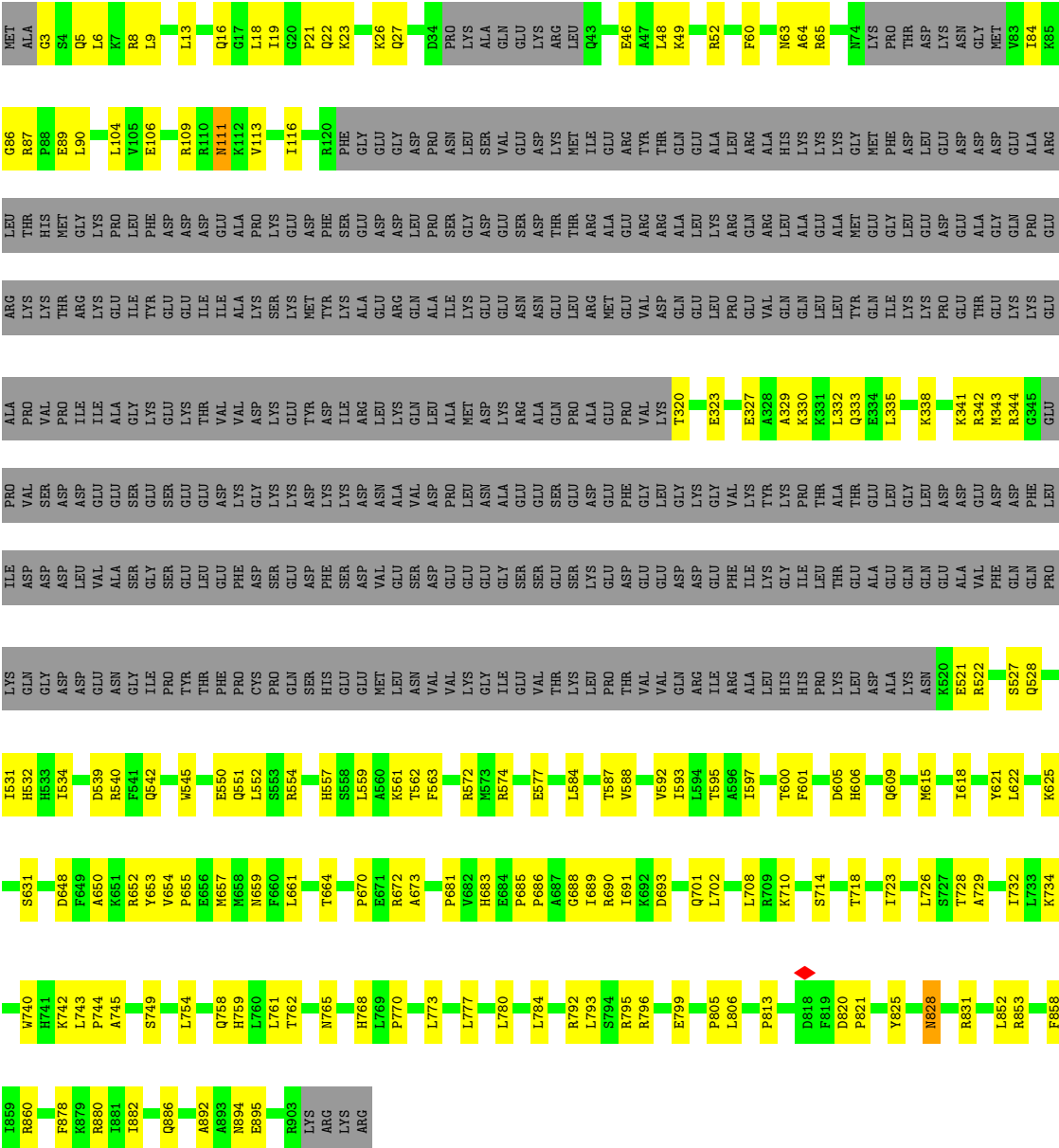
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: Periodic tryptophan protein 2-like protein

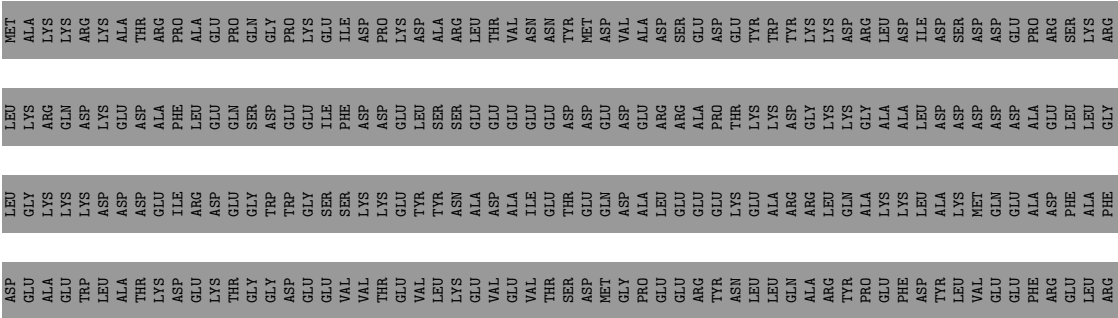


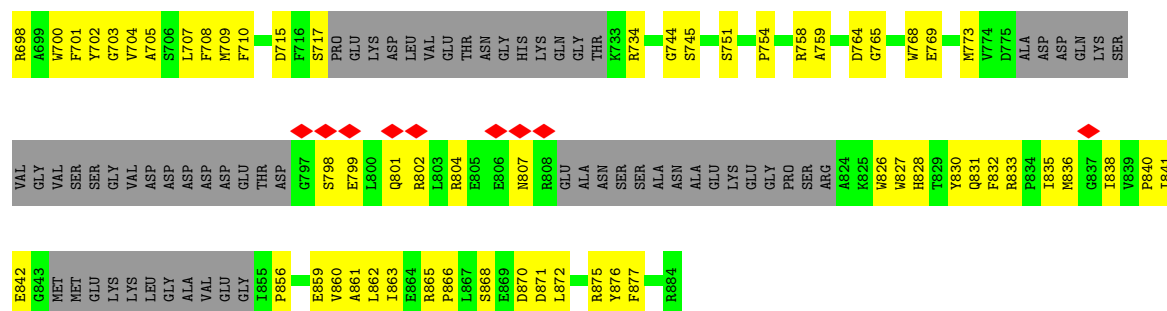
- Molecule 2: Utp2





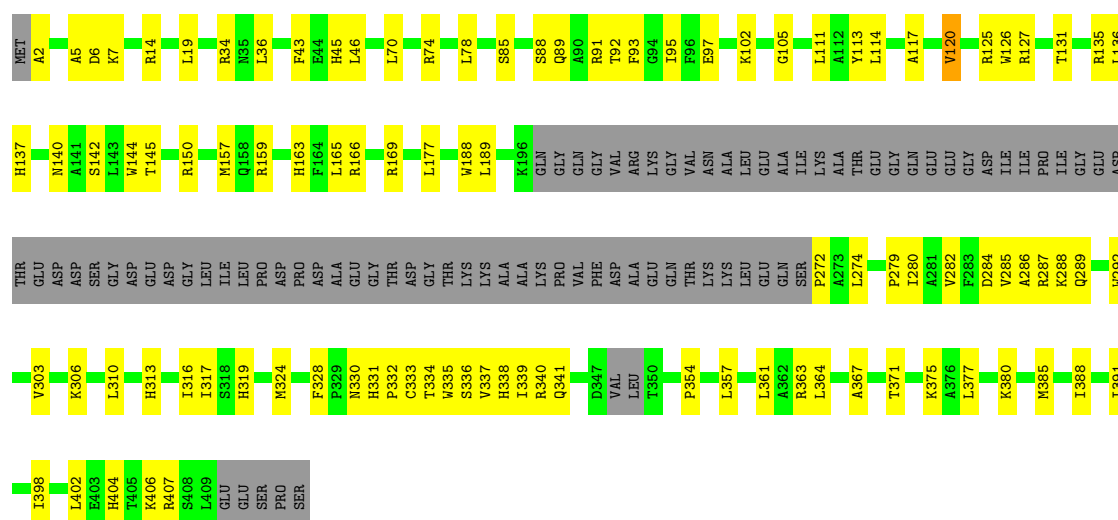
● Molecule 3: Utp3





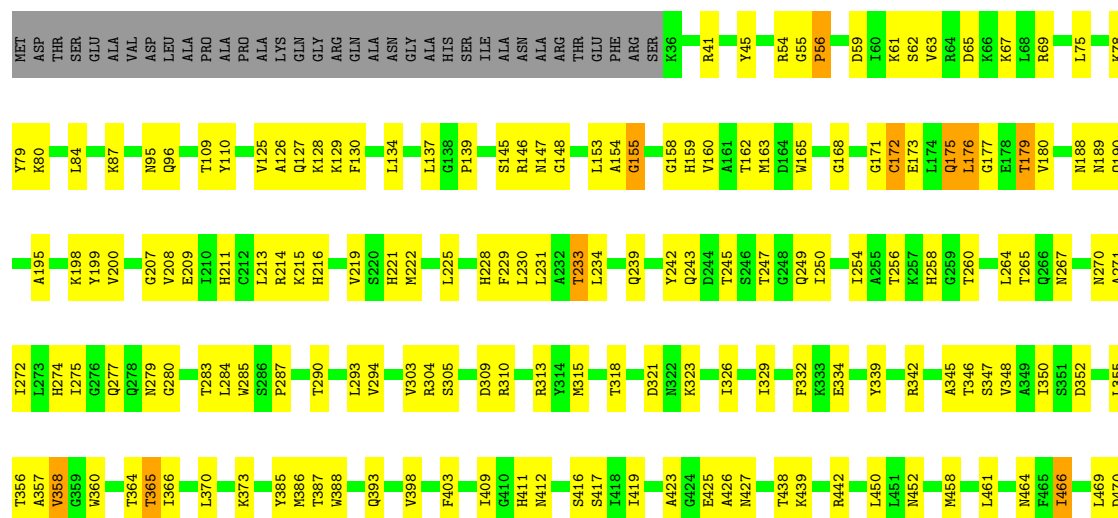
• Molecule 5: Utp6

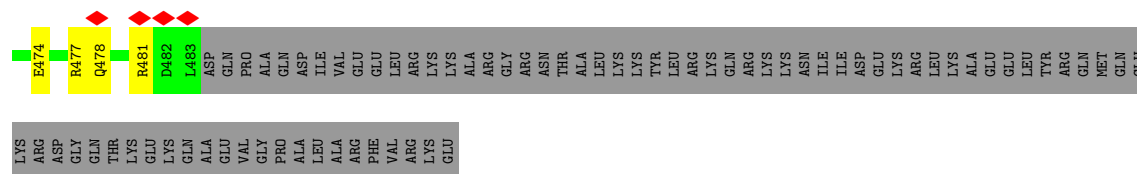
Chain UF: 56% 24% 20%



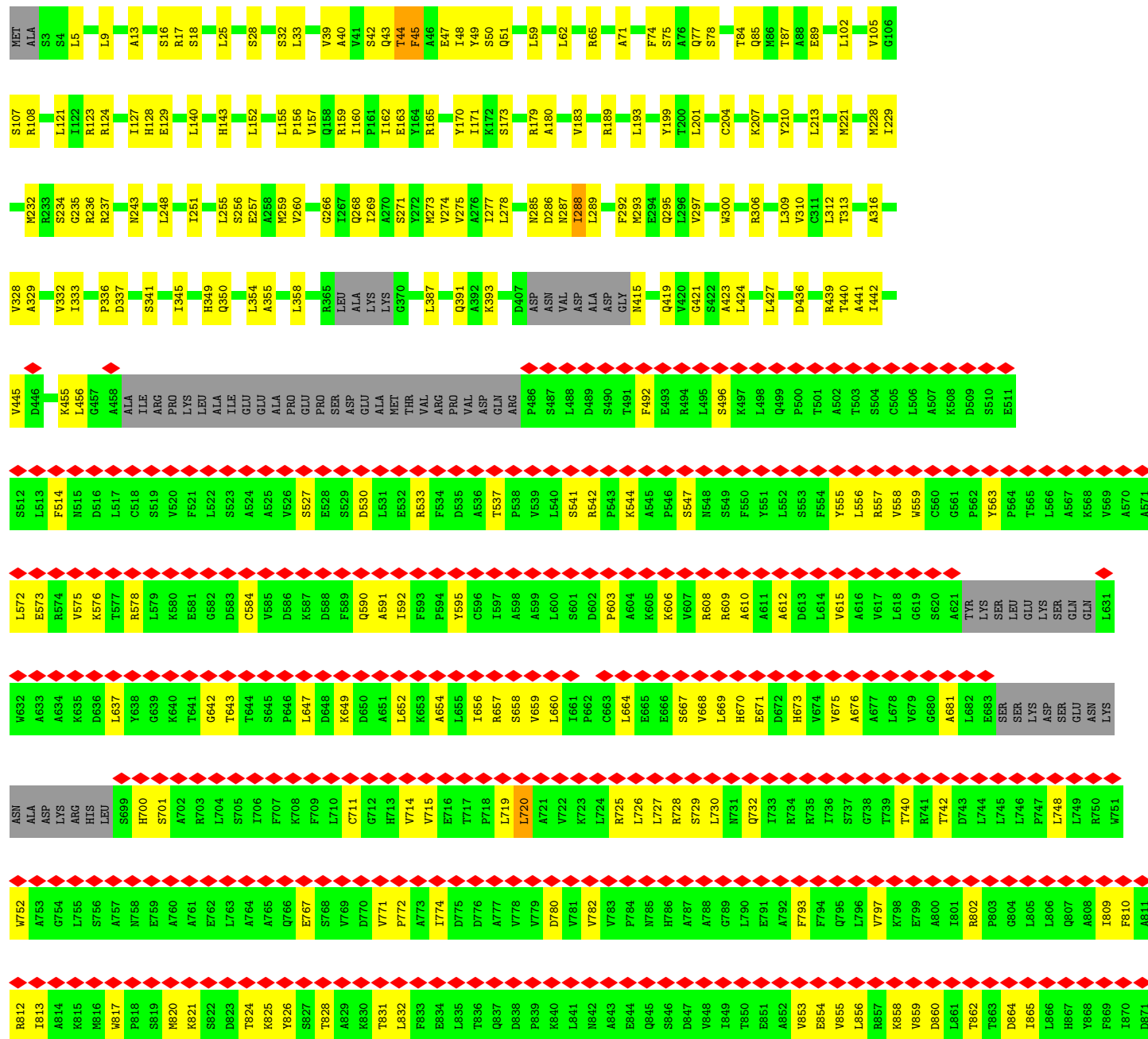
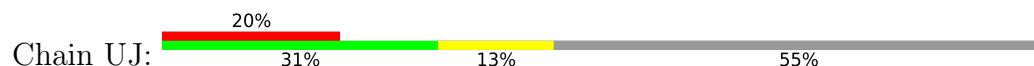
• Molecule 6: Utp7

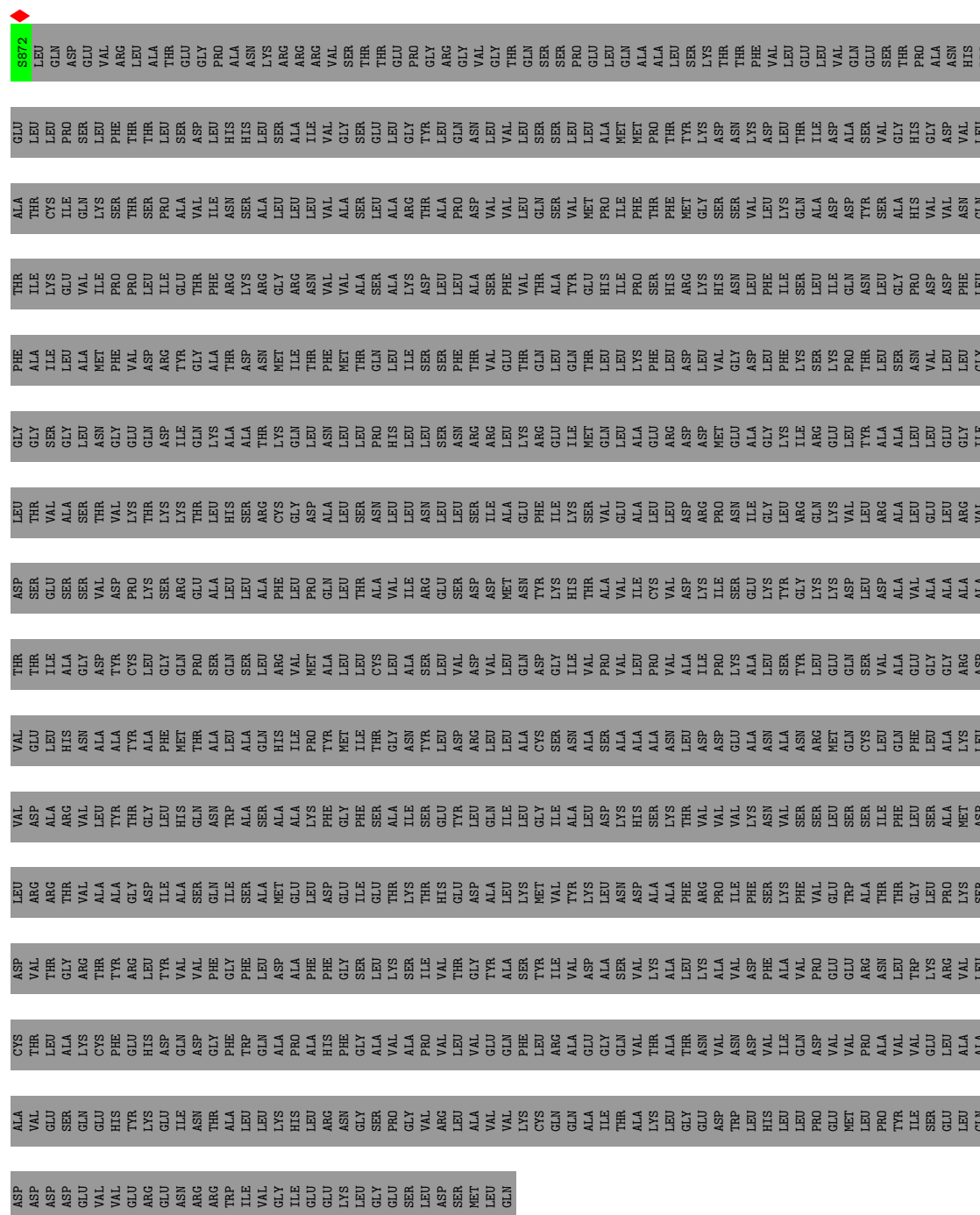
Chain UG: 50% 29% 20%



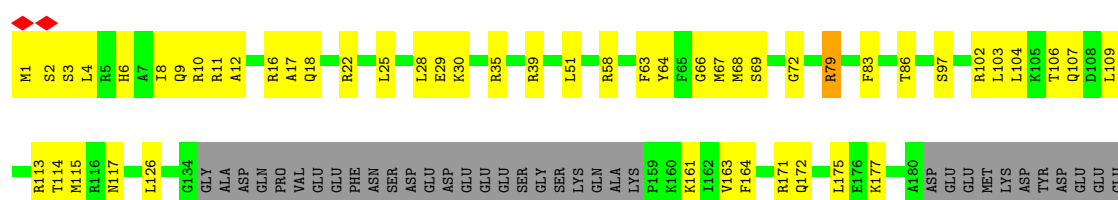


• Molecule 7: Utp10

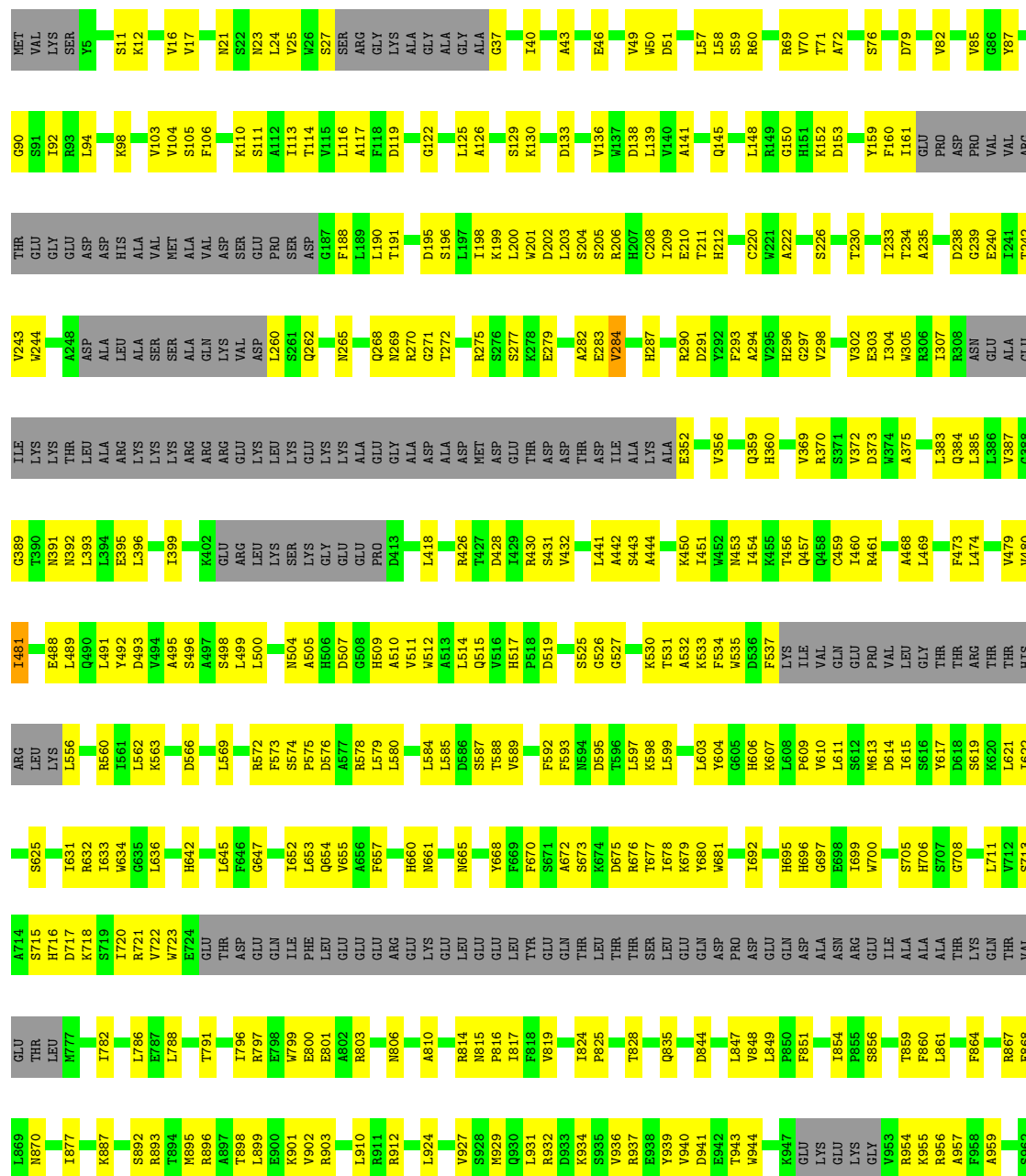




- Molecule 8: U3 small nucleolar RNA-associated protein 11



Chain UL:



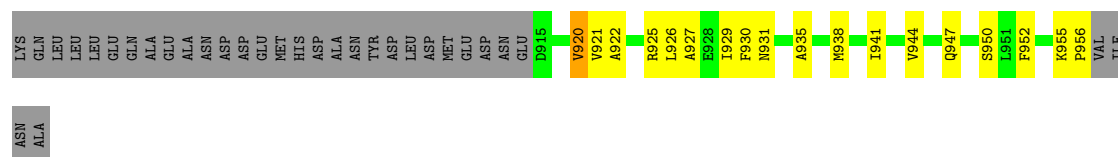
Chain UM:



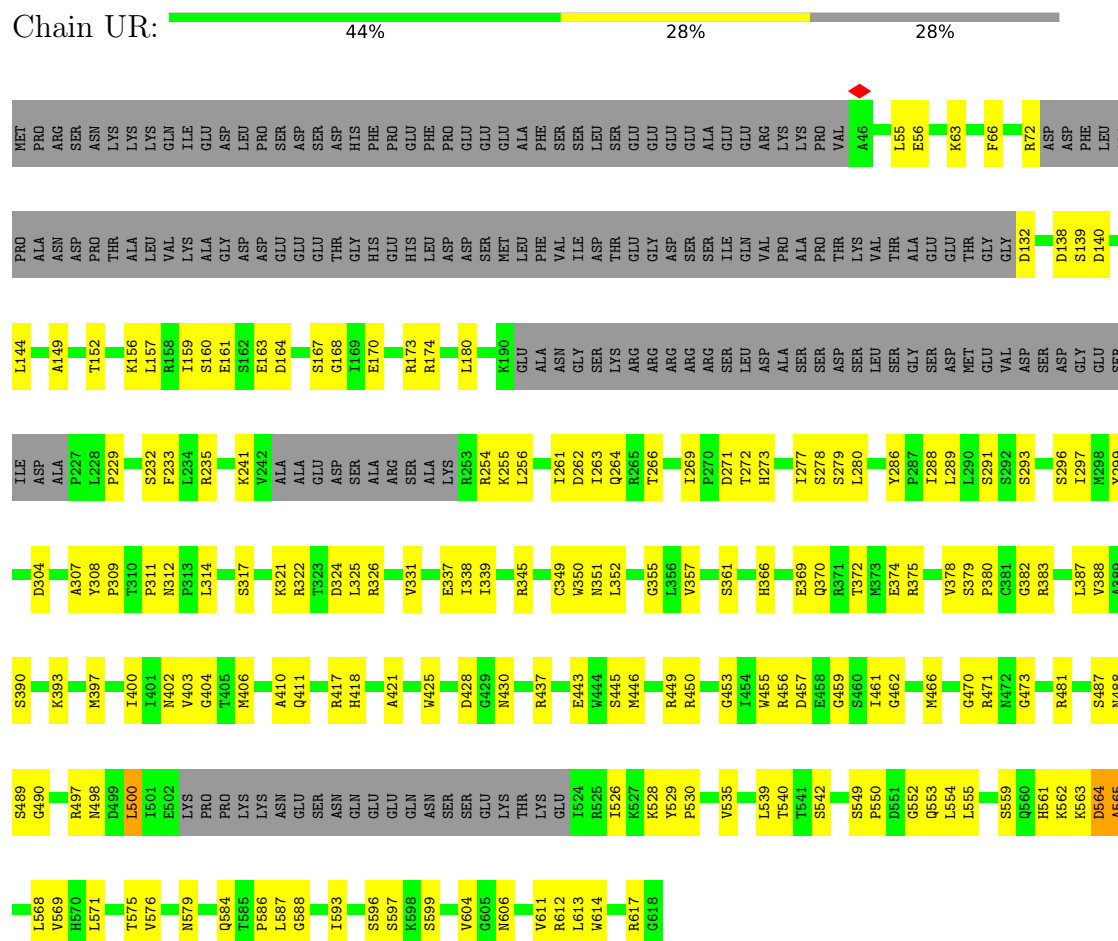
Y852	T855	G886	L887	S893	Q896	R899	S900	L901	R902	L903	P904	V905	M910	T911	K912	Q916	D917	R922	V923	I929	I930	K935	P936	M937	Y938
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

Chain UO: 55% 35% 10%

[illegible]

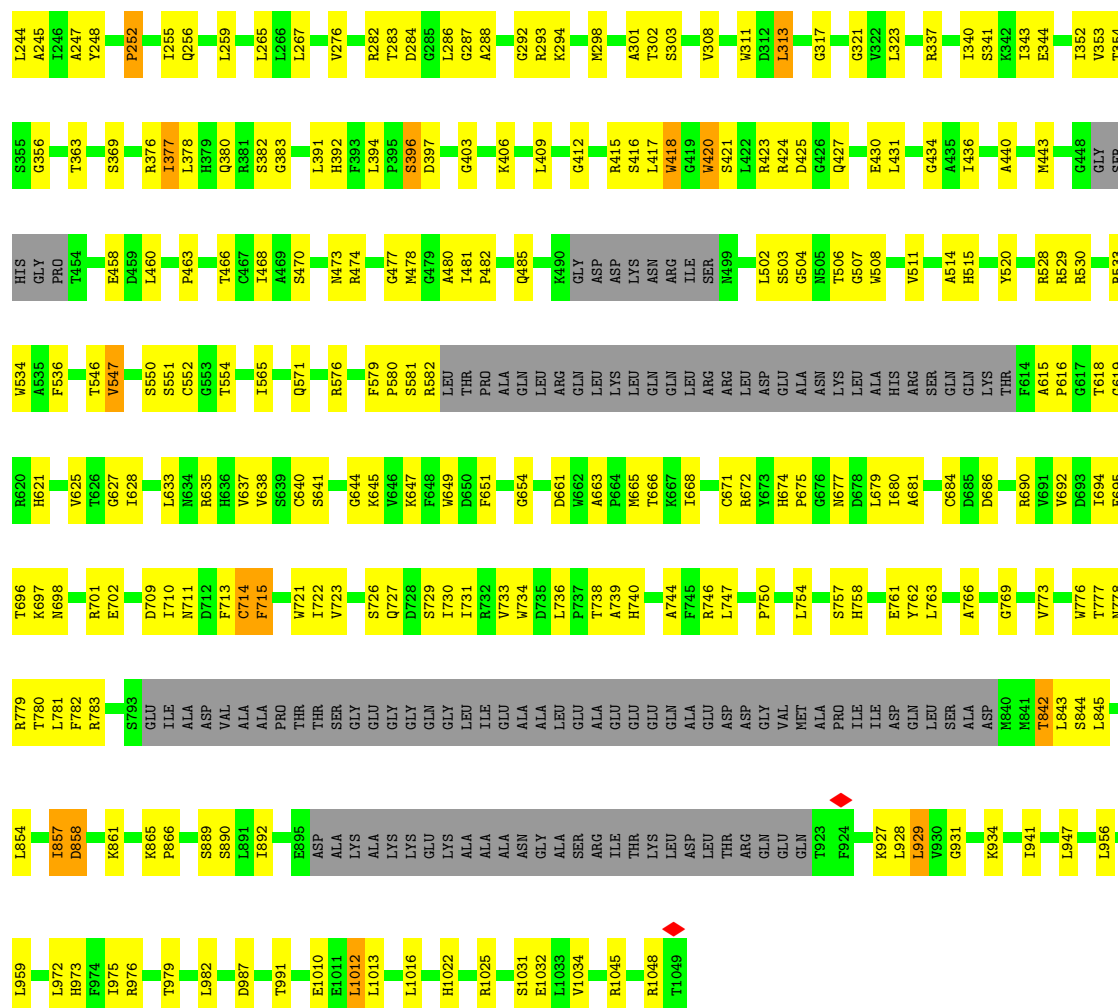


• Molecule 14: Utp18

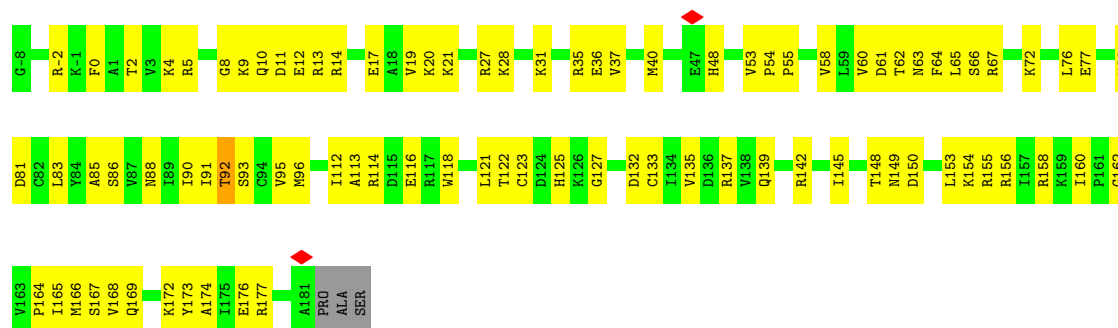


• Molecule 15: Utp21

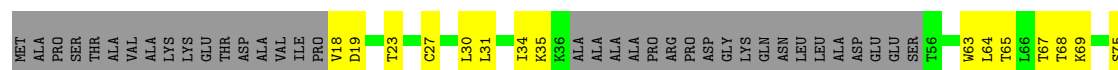


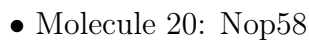


• Molecule 16: Utp24



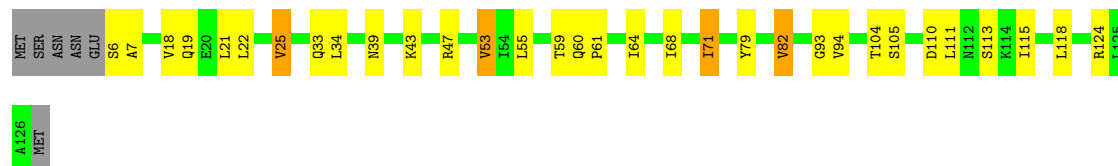
• Molecule 17: Utp30





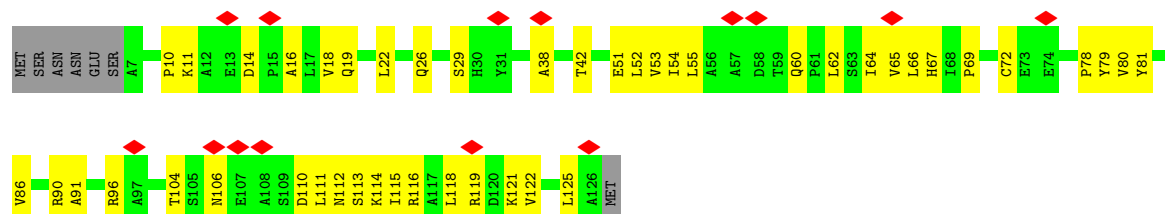
- Molecule 21: Snu13

Chain CE:  70% 22% 5%

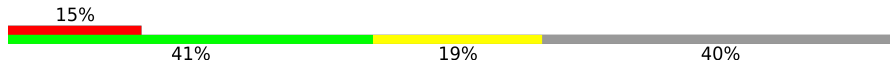


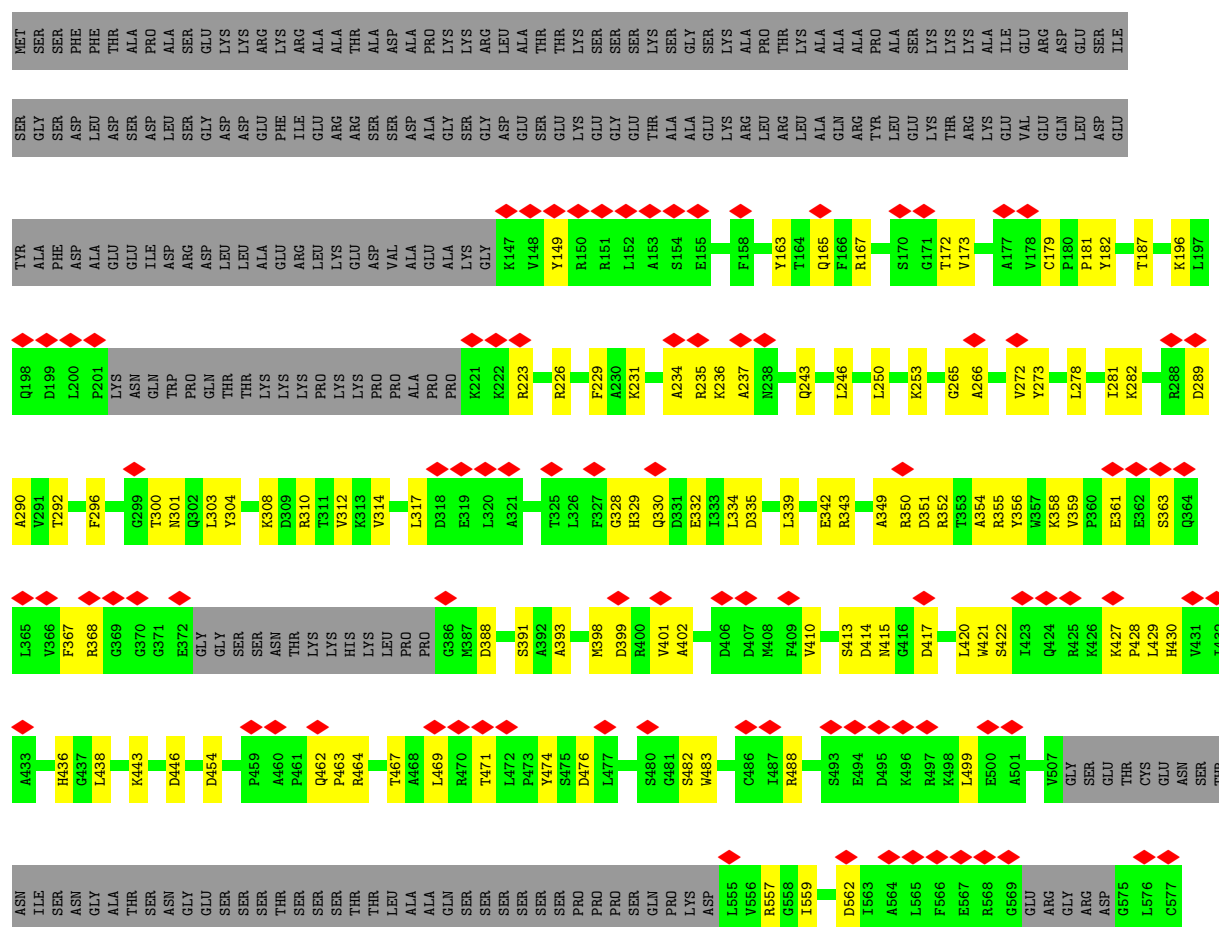
- Molecule 21: Snu13

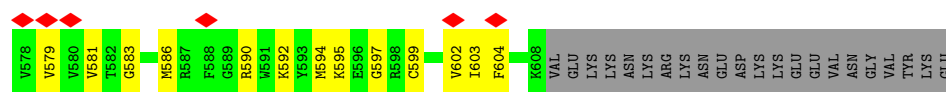
Chain CF:  11% 58% 36% 6%



- Molecule 22: Rrp9

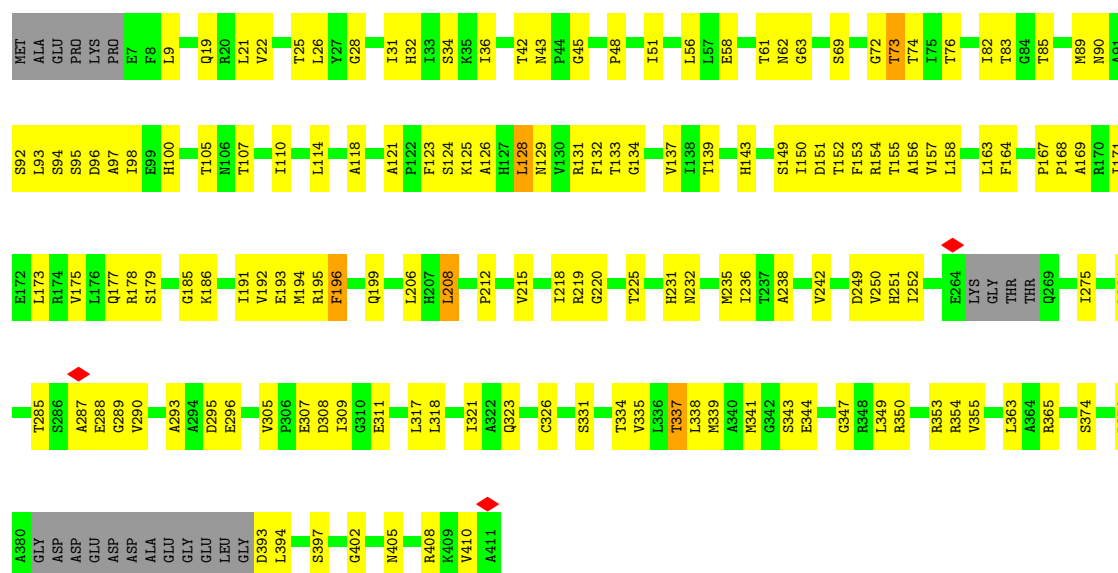
Chain CG:  15% 41% 19% 40%





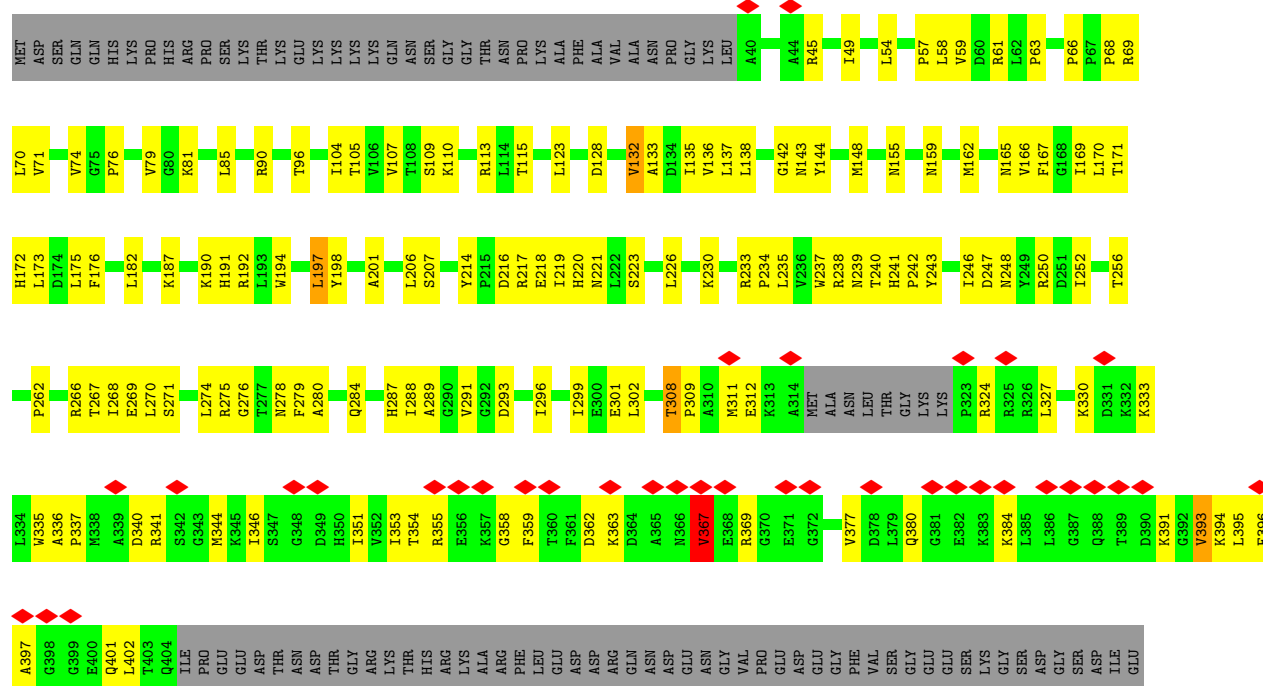
- Molecule 23: RNA 3'-terminal phosphate cyclase-like protein

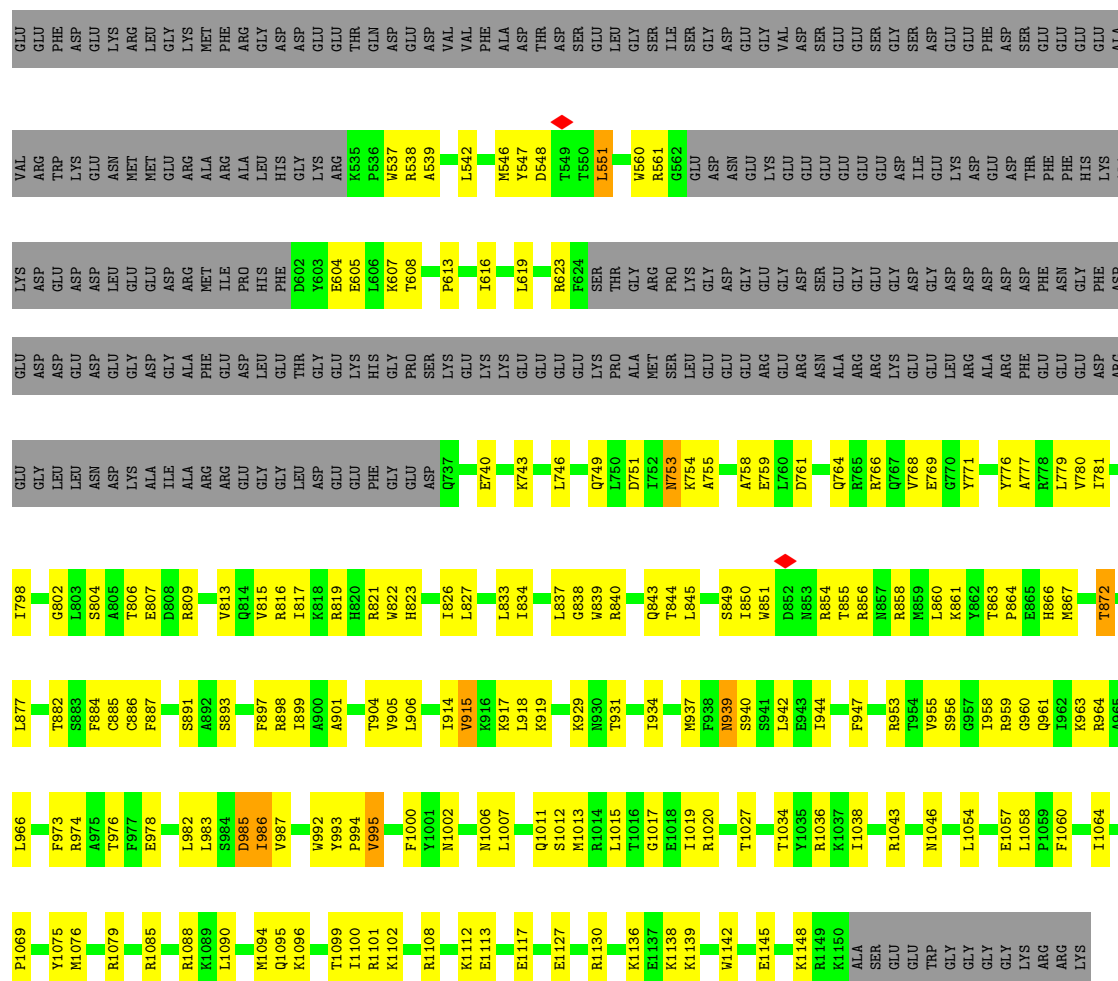
Chain CH: 58% 36% 5%



- Molecule 24: Bms1

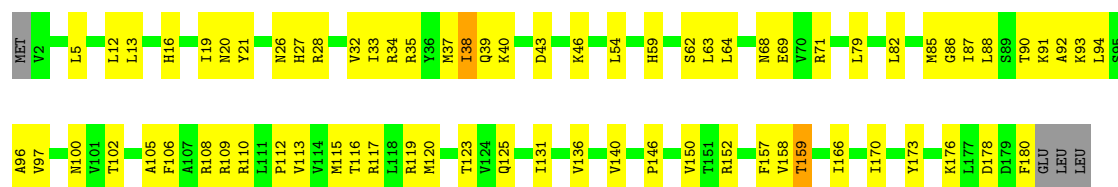
Chain CI: 43% 27% 29%





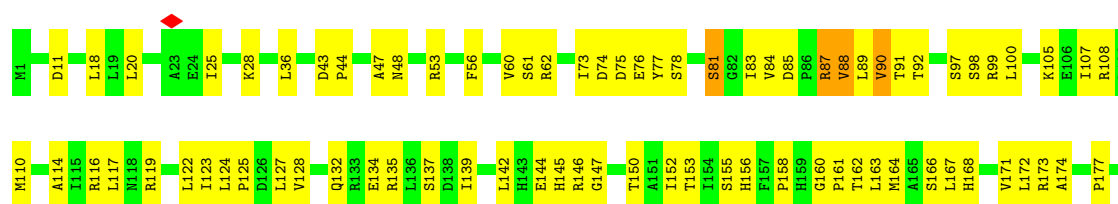
• Molecule 25: Imp3

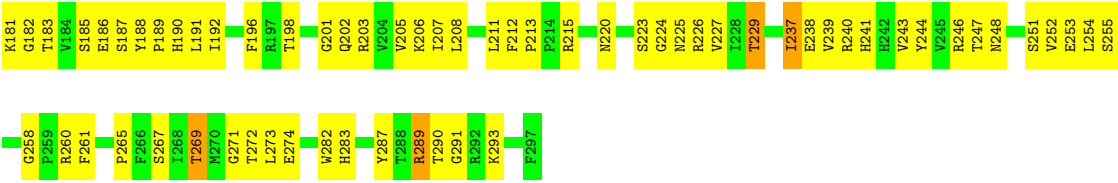
Chain CJ:  58% 38%



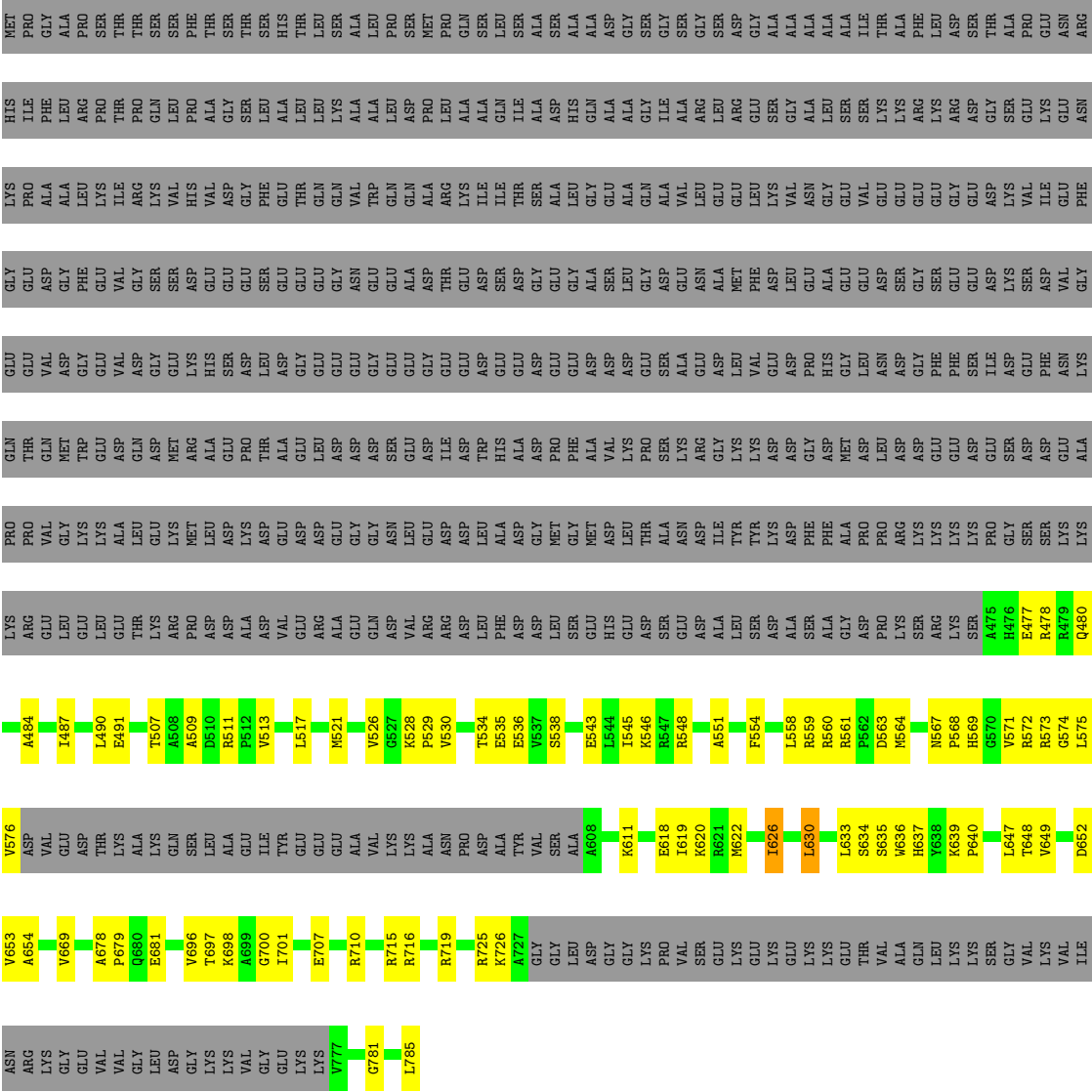
• Molecule 26: Imp4

Chain CK:  53% 45%



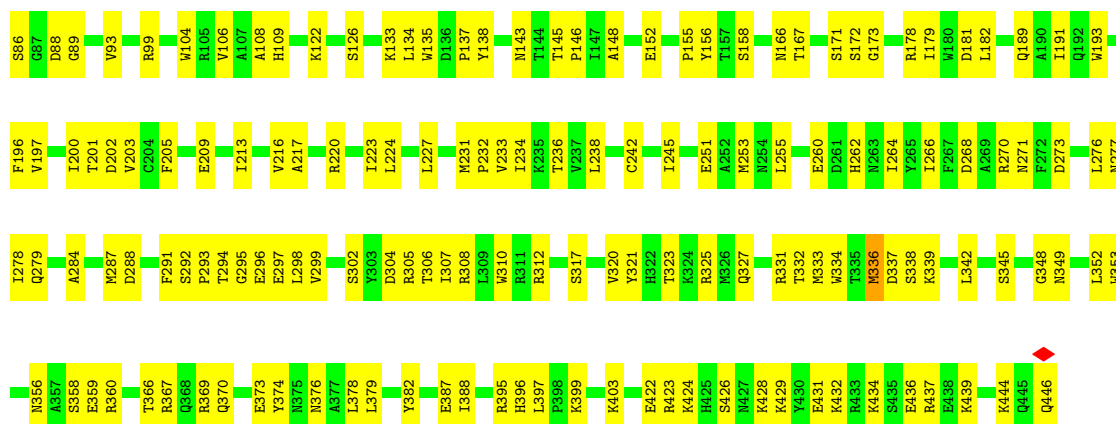


• Molecule 27: Mpp10

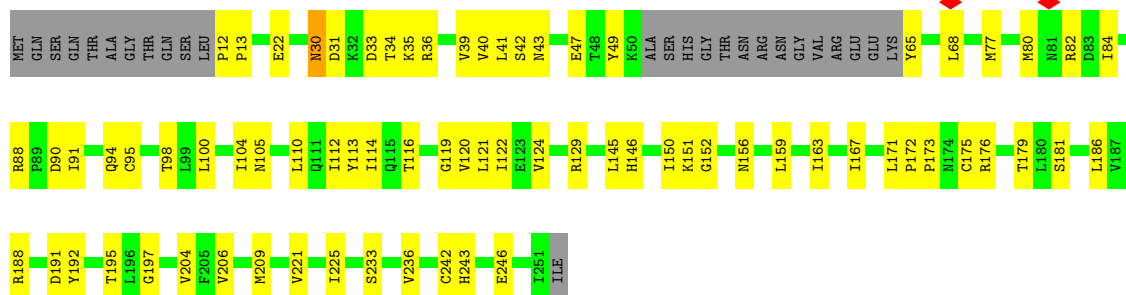


• Molecule 28: Sof1

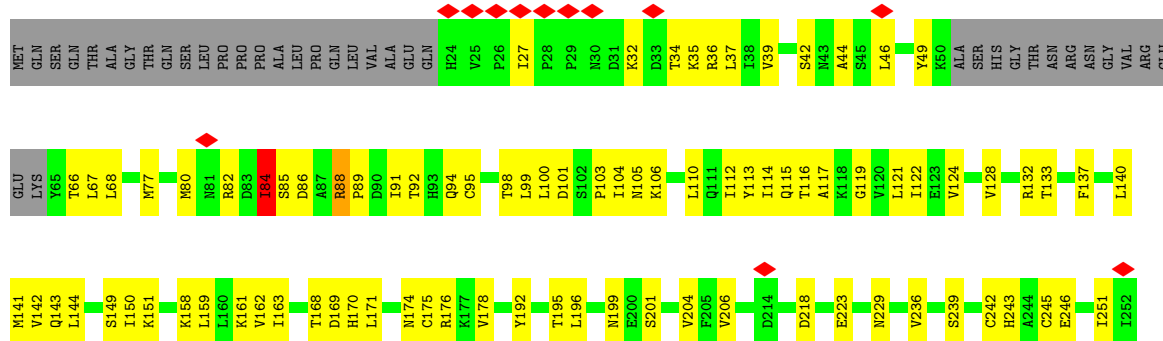




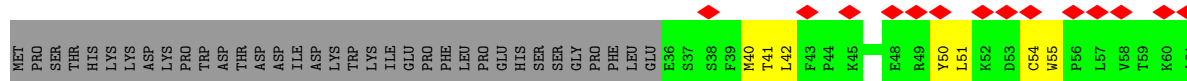
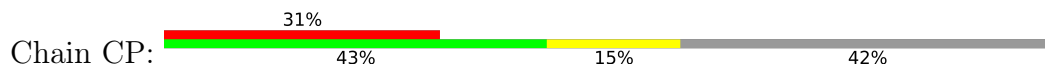
• Molecule 29: Emg1

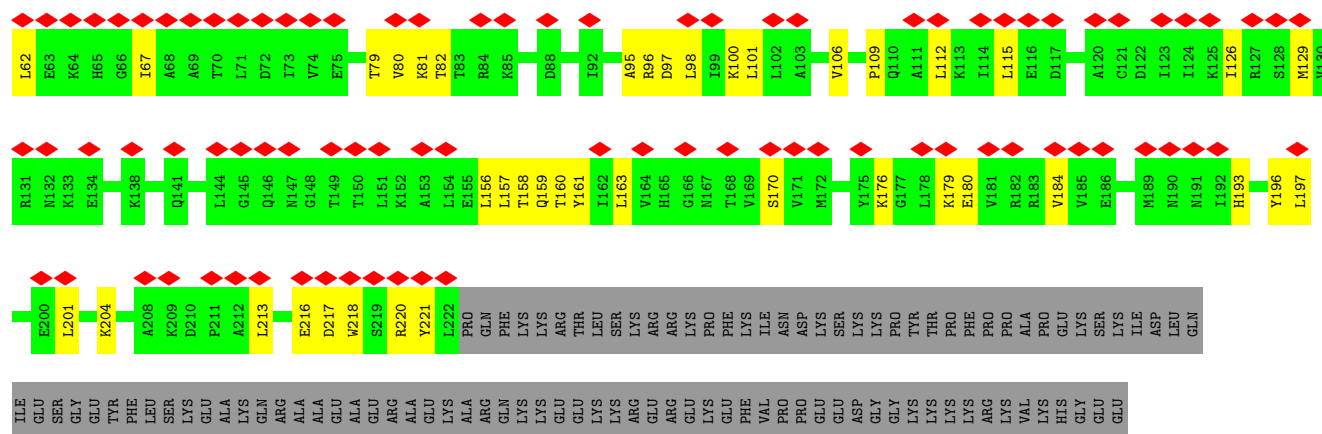


• Molecule 29: Emg1

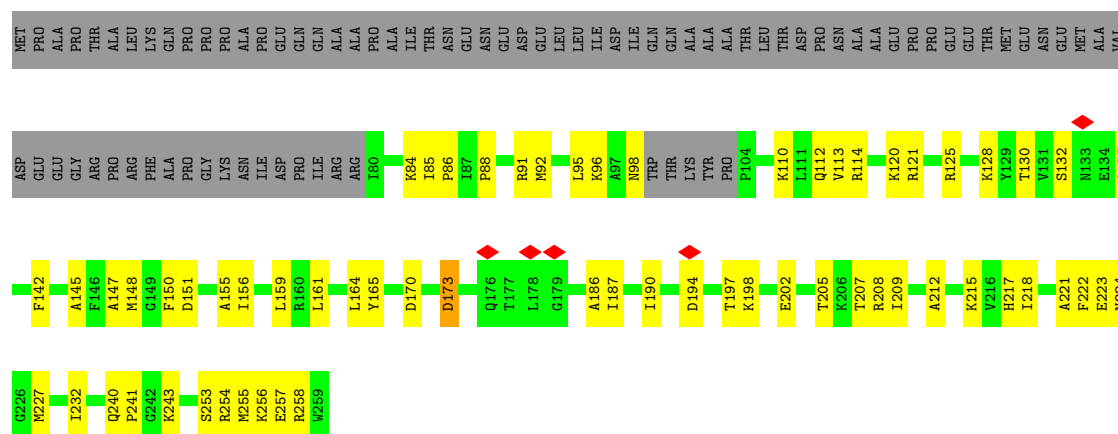


• Molecule 30: KRR1 small subunit processome component

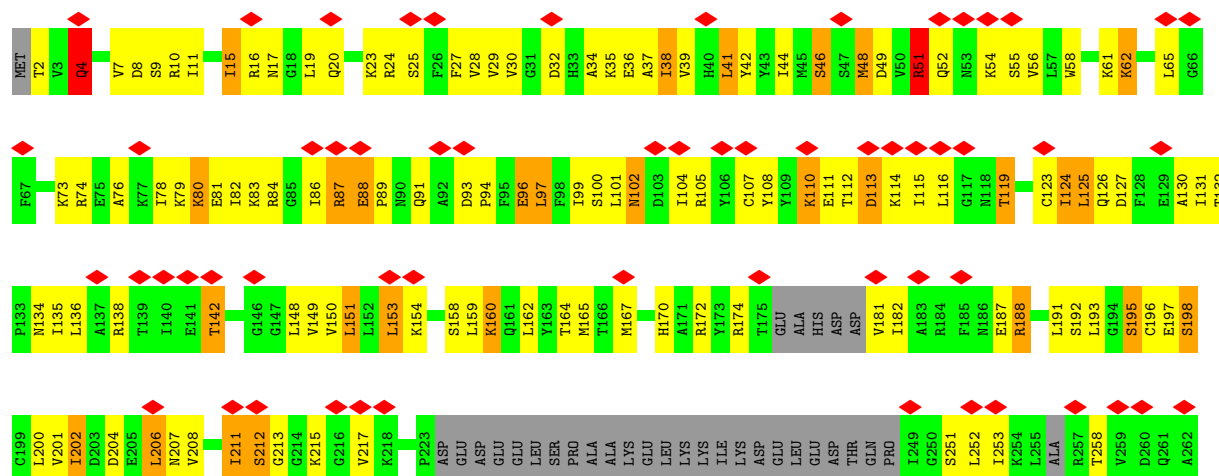


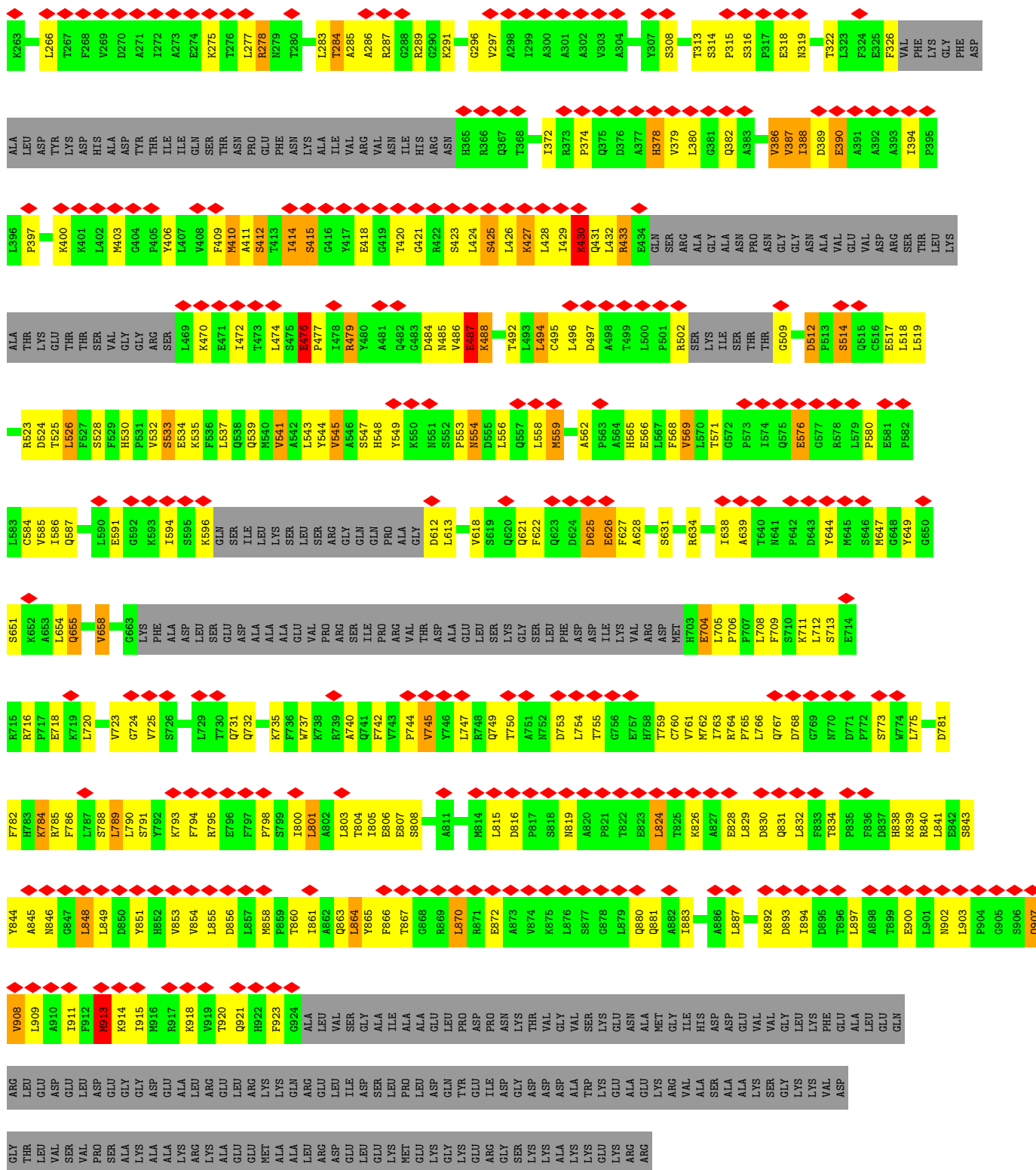


• Molecule 31: Pre-rRNA-processing protein PNO1



• Molecule 32: Kre33

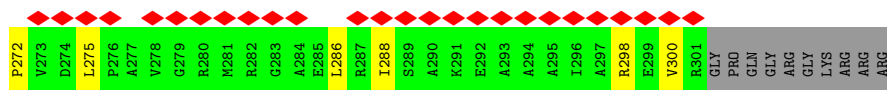




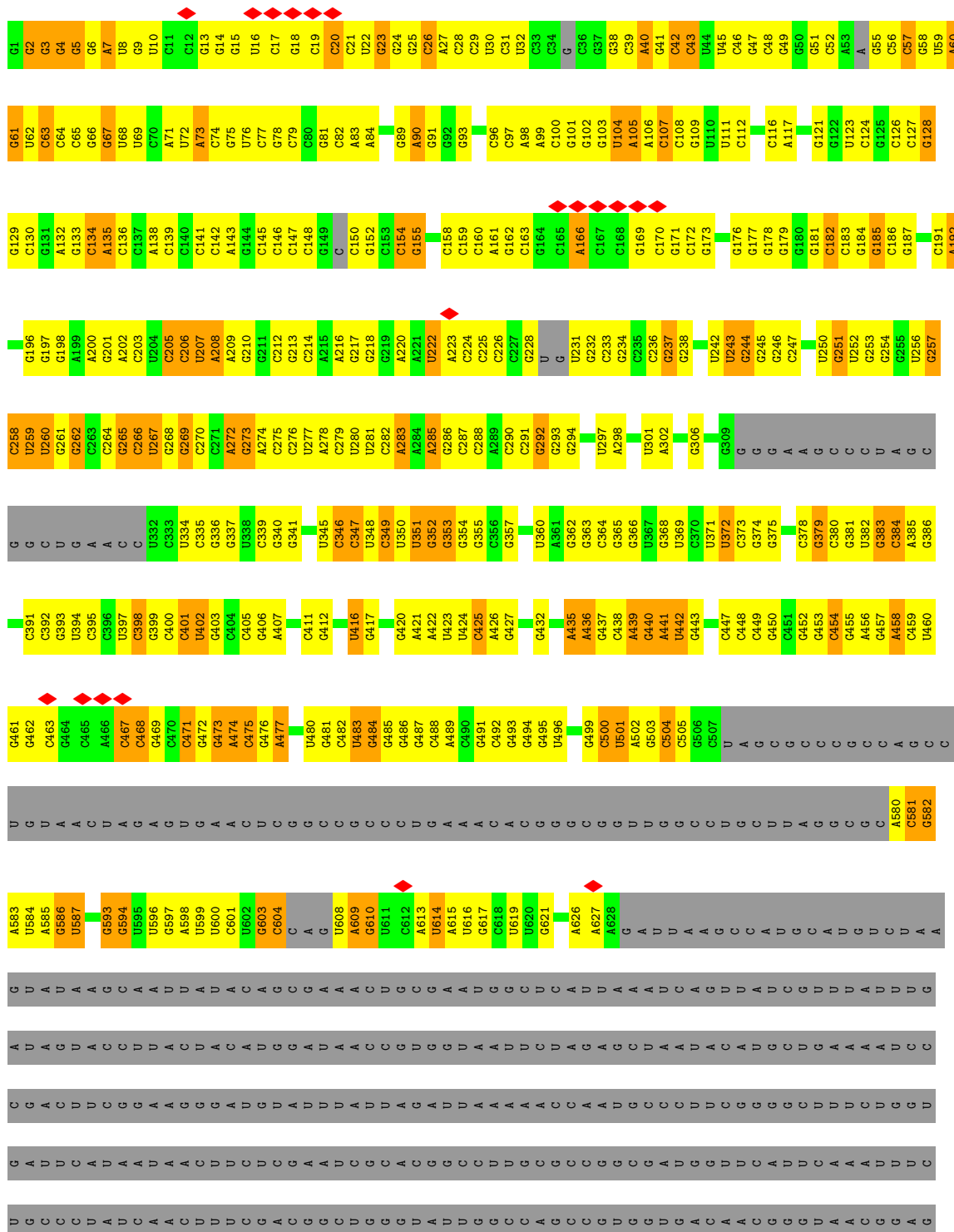
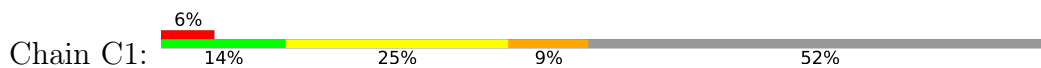
• Molecule 32: Kre33



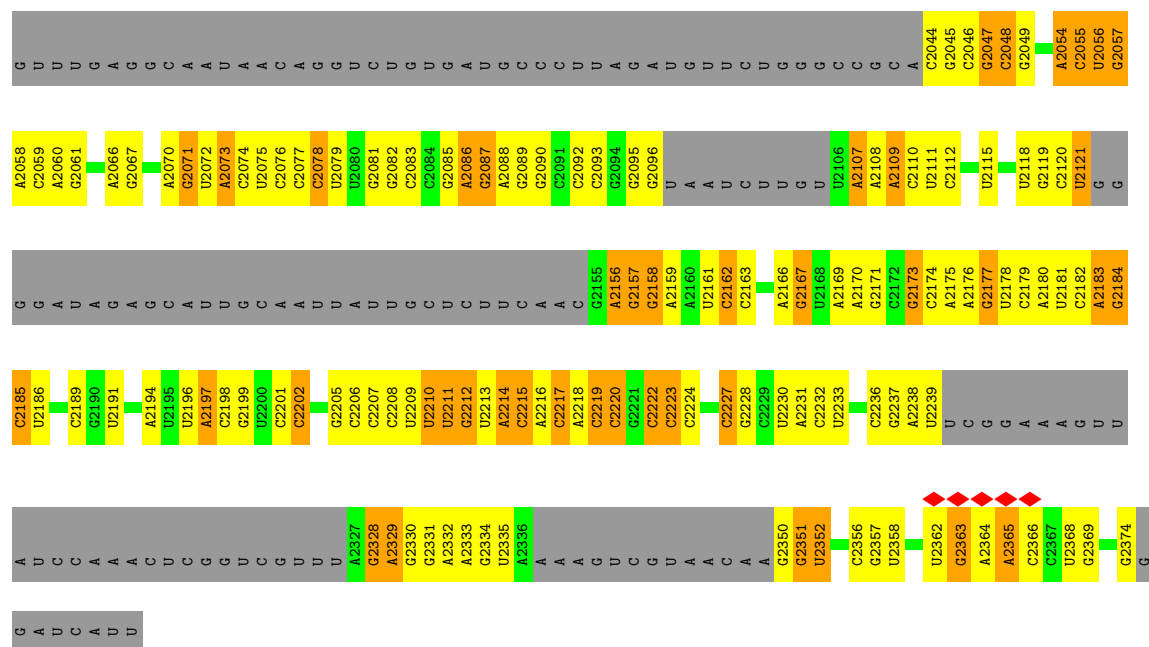
L789	L790	S791	K793	F794	R795	E796	F797	P798	S799	I800	L801	A802	L803	T804	I805	E806	E807	S808	A809	N810	A811	G812	A813	N814	L815	D816	P817	S818	N819	A820	P821	T822	E823	L824	T825	K826	A827	E828	L829	D830	Q831	L832	F833	T834	P835		H838	K839	R840	L841	E842	S843	Y844	A845	N846	G847	L848	L849			
L729	T730	Q731	Q732	L733	H734	K735	F736	W737	K738	R739	A740	Q741	F742	V743	P744	V745	Y746	E747	R748	Q749	T750	A751	N752	D753	L754	T755	G756	E757	H758	T759	C760	V761	M762	I763	R764	P765	L766	Q767	D768	G769	N770	D771	P772	S773	T774	L775	G776	A777	F778	A779	A780	D781	F782	H783	K784	R785	F786	L787	S788		
SER	GLU	ASP	ALA	ALA	ALA	GLU	VAL	PRO	ARG	ARG	VAL	THR	ASP	ALA	GLU	LEU	SER	GLY	SER	LEU	PHE	ASP	ASP	ILE	LYS	VAL	ARG	MET	H703	E704	L705	P706	P707	L708	F709	S710	K711	L712	S713	E714	R715	R716	P717	E718	K719	L720	D721	Y722	V723	G724	V725	S726	Y727	G728							
GLY	GLN	GLN	PRO	ALA	GLY	D612	L613	I614	L617	V618	Q621	F622	Q623	D624	D625	E626	F627	A628	S629	L630	S631	R634	I635	V636	R637	I638	A639	T640	N641	D642	D643	Y644	M645	S646	M647	G648	Y649	G650	S651	K652	A653	L654	Q655	L656	L657	V658	D659	Y660	Y661	E662	G663	LYS	PHE	ALA	ASP	LEU					
G483	D484	N485	A486	E487	K488	W489	L490	N491	T492	L493	L494	C495	L496	D497	A498	T499	L500	P501	R502	SER	LYS	ILE	SER	THR	THR	G509	C510	P511	D512	P513	S514	Q515	C516	E517	L518	L519	H520	V521	N522	D523	D524	T525	L526	F527	S528	F529	H530	P531	V532	S533	E534	K535	F536	L537	Q538	Q539	M540	V541	A542		
S423	L424	S425	A426	K427	L428	I429	K430	Q431	L432	R433	E434	GLN	SER	ARG	ALA	GLY	ASN	PRO	ASN	GLY	GLY	ASN	ALA	VAL	VAL	ASP	ARG	SER	THR	LEU	LYS	ALA	LYS	THR	SER	VAL	GLY	ARG	SER	L469	K470	E471	I472	T473	L474	S475	E476	P477	I478	R479	Y480	A481	Q482								
HIS	ARG	ASN	H365	R366	Q367	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	L398	V399	K400	K401	L402	M403	G404	P405	Y406	L407	V408	F409	M410	A411	S412	T413	I414	S415	G416	Y417	E418	T420	G421	R422					
GLU	LEU	GLU	THR	GLN	PRO	T249	G250	S251	L252	T253	K254	L255	ALA	R257	T258	V259	D260	Q261	K263	A264	L265	L266	T267	V268	D270	A271	I272	A273	E274	G275	T276	L277	R278	N279	T280	V281	T282	L283	T284	A285	A286	R287	G288	R289	G290	K291	S292	A293	A294	A295	G296	V297	A298	I299	A300	A301					
A302	V303	A304	Y305	G306	Y307	S308	N309	I310	F311	I312	T313	S314	P315	S316	P317	E318	N319	L320	K321	T322	L323	F324	E325	F326	VAL	PHE	LYS	GLY	PHE	ASP	ALA	LEU	TYR	LYS	ASP	HIS	ALA	ASP	GLY	K400	K401	L402	M403	G404	P405	Y406	L407	V408	F409	M410	A411	S412	T413	I414	S415	G416	Y417	E418	T420	G421	R422
G121	M122	C123	I124	L125	Q126	D127	F128	E129	A130	I131	T132	P133	N134	I135	L136	A137	I138	T139	I140	E141	T142	V143	E144	G145	G146	G147	L148	V149	V150	L151	L152	L153	G155	M156	T157	S158	L159	K160	Q161	L162	Y163	T164	M165	T166	M167	D168	V169	A170	A171	R172	Y173	T175	GLU	ALA	HIS	ASP	ASP				
V181	I182	F185	H186	E187	R188	F189	L190	L191	S192	L193	G194	S195	C196	E197	S198	C199	L200	V201	I202	D203	D204	L206	N207	V208	L209	P210	T211	S212	G213	G214	K215	G216	V217	K218	P219	L220	P221	P222	P223	ASP	GLU	ASP	GLU	GLU	LEU	SER	PRO	ALA	ALA	LYS	GLU	LEU	LYS	LYS	ILE	ASP					
K61	K62	E63	L64	L65	G66	F67	T68	S69	H70	R71	K72	K73	R74	E75	A76	K77	I78	K79	K80	E81	I82	K83	R84	G85	I86	R87	E88	P89	N90	Q91	A92	D93	P94	F95	E96	L97	F98	I99	S100	L101	L102	D103	I104	R105	Y106	C107	Y108	K109	V110	E111	T112	D113	I115	L116	G117	N118	T119	Y120			
MET	T2	V3	Q4	K5	T6	V7	D8	S9	R10	I11	P12	T13	I14	I15	R16	N17	G18	L19	Q20	T21	K22	K23	R24	S25	F26	F27	V28	V29	V30	G31	D32	H33	A34	K35	E36	A37	I38	V39	H40	L41	Y42	Y43	I44	H45	S46	S47	M48	D49	V50	R51	Q52	N53	K54	S55	V56	L57	N58	A59	Y60		



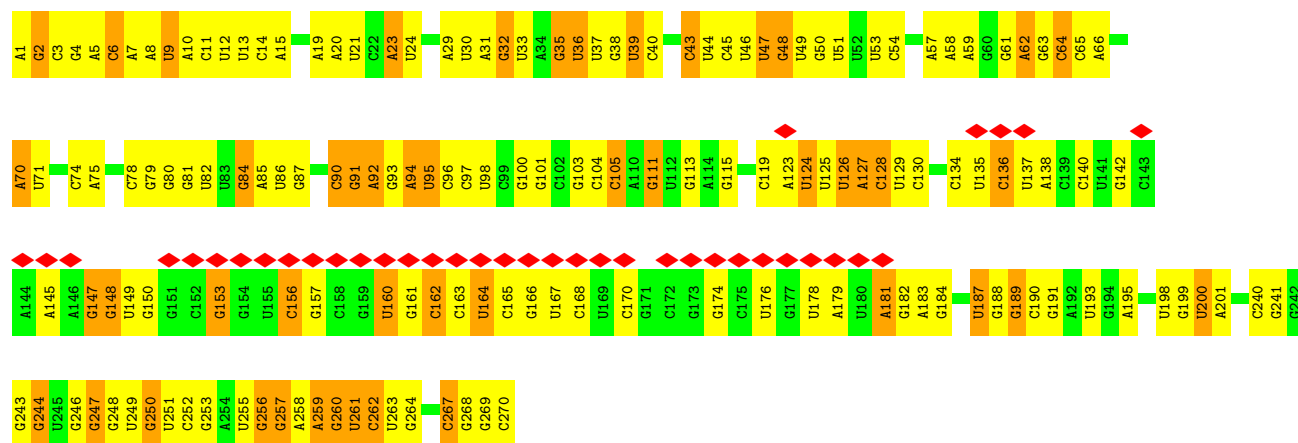
• Molecule 44: 35S rRNA



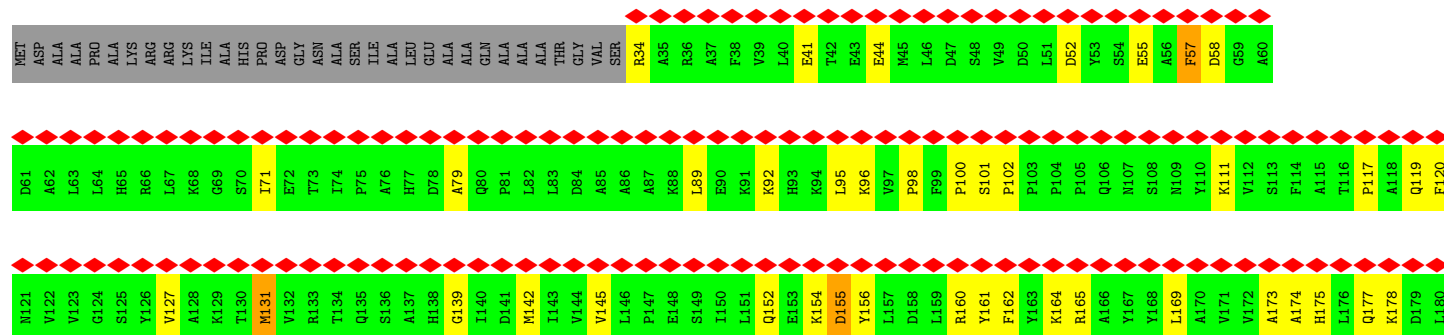




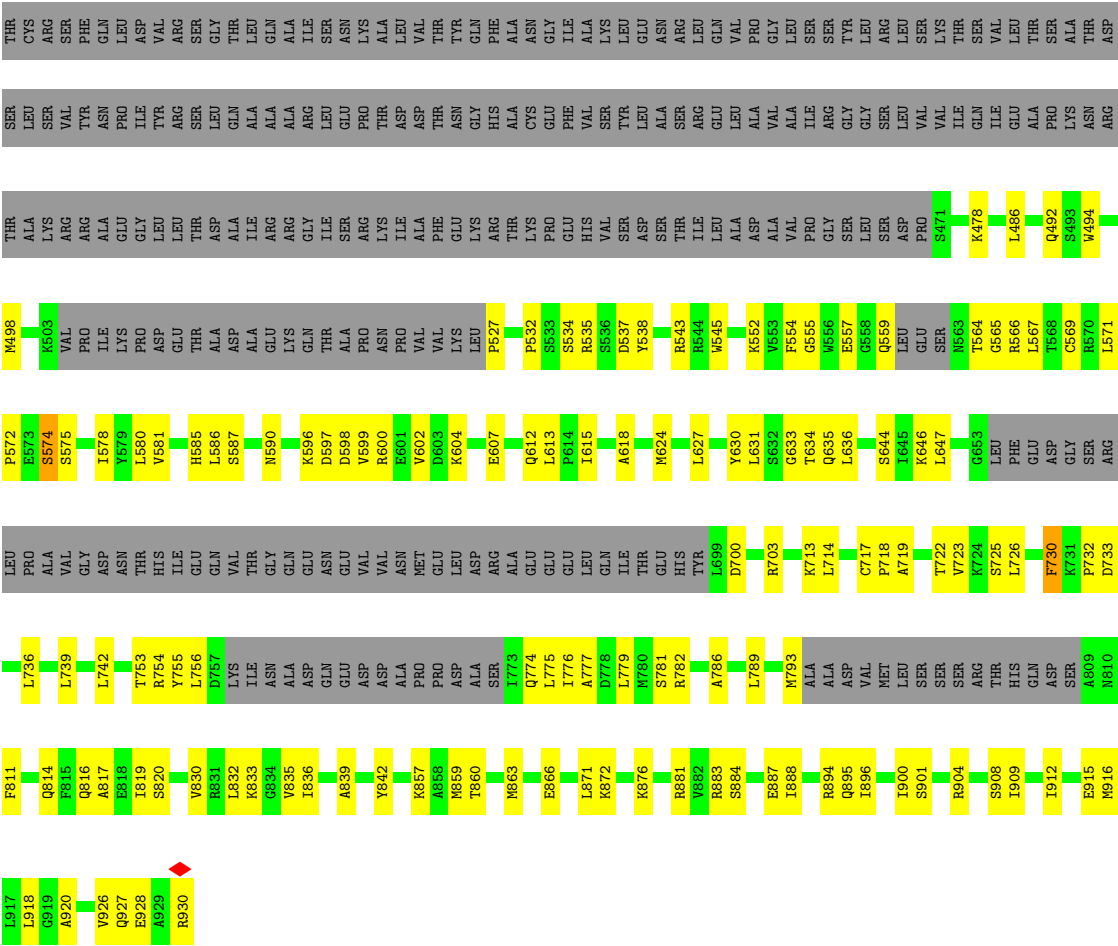
• Molecule 45: U3 snoRNA



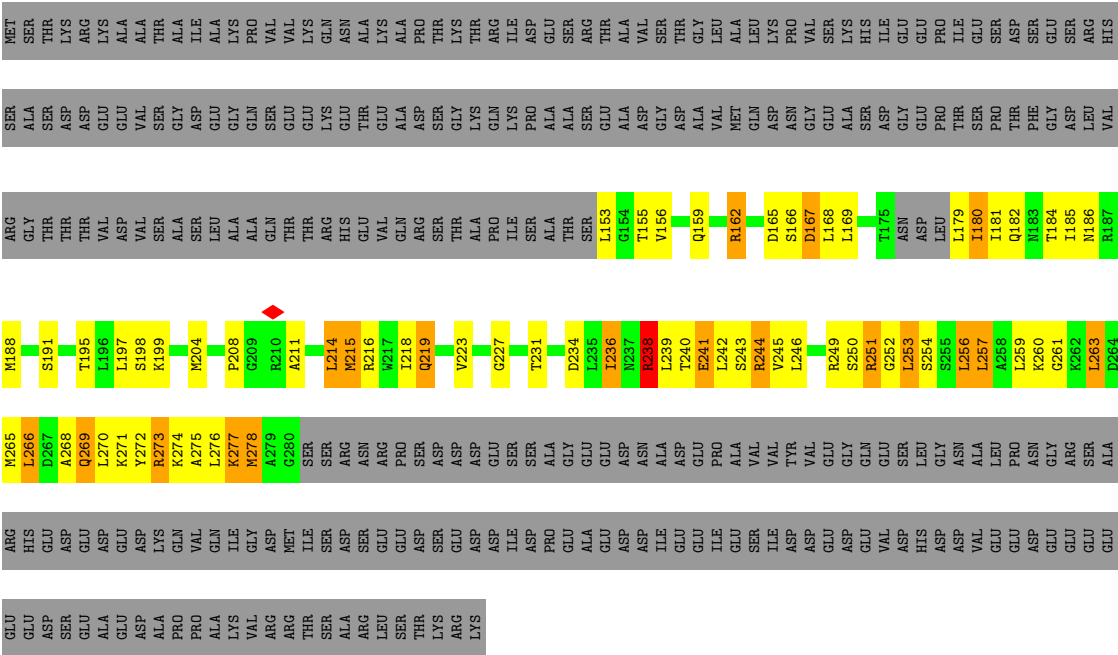
• Molecule 46: U3 small nucleolar RNA-associated protein 22







● Molecule 49: Utp5



Chain UI: 13% 13% 70%



Chain Cl:



PRO	LVS	LEU	LEU	VAL	GLU	PRO	K308	K313	R314	V315	G316	S317	T318	A319	Y320	R321	G327	D328	P329	R330	L331	A332	P333	K334	L340	K343	R348	R351	R356	V361	ASN	LVS	ARG
-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----

Chain Cz: 13% 11% 85%

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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	20250	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	0.437	Depositor
Minimum map value	-0.319	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	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

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	0.96	1/6521 (0.0%)	1.01	10/8867 (0.1%)
2	UB	0.46	0/4154	0.66	0/5583
3	UC	0.45	0/595	0.69	0/786
4	UD	0.65	2/6211 (0.0%)	0.78	2/8408 (0.0%)
5	UF	0.52	0/2657	0.69	0/3596
6	UG	0.91	3/3516 (0.1%)	0.93	5/4761 (0.1%)
7	UJ	0.52	0/6291	0.74	0/8543
8	UK	0.81	0/1701	0.90	5/2251 (0.2%)
9	UL	0.45	0/6299	0.69	0/8531
10	UM	0.33	0/5366	0.63	0/7282
11	UN	0.60	0/1232	0.72	0/1662
12	UO	0.73	1/3903 (0.0%)	0.84	4/5312 (0.1%)
13	UQ	0.71	1/6136 (0.0%)	0.85	4/8348 (0.0%)
14	UR	0.95	2/3564 (0.1%)	0.95	3/4816 (0.1%)
15	UU	0.82	5/6903 (0.1%)	0.89	7/9392 (0.1%)
16	UX	0.64	0/1493	0.75	0/2011
17	UZ	0.44	0/1857	0.74	2/2526 (0.1%)
18	CA	0.77	1/1814 (0.1%)	0.86	0/2456
18	CB	0.44	0/1853	0.68	0/2511
19	CC	0.53	0/2911	0.72	0/3937
20	CD	0.55	0/3205	0.76	2/4338 (0.0%)
21	CE	0.90	1/891 (0.1%)	0.91	0/1214
21	CF	0.37	0/876	0.68	0/1195
22	CG	0.25	0/2983	0.58	0/4032
23	CH	0.51	0/2939	0.72	2/3988 (0.1%)
24	CI	0.60	0/6631	0.77	9/8943 (0.1%)
25	CJ	1.04	0/1462	1.00	0/1967
26	CK	0.96	1/2376 (0.0%)	0.97	3/3214 (0.1%)
27	CL	0.68	0/1812	0.76	0/2437
28	CM	0.71	0/3573	0.83	0/4829
29	CN	0.53	0/1797	0.73	0/2443
29	CO	0.39	0/1714	0.65	0/2325

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	CP	0.29	0/1528	0.77	1/2057 (0.0%)
31	CQ	0.36	0/1379	0.62	0/1850
32	CR	0.37	1/6108 (0.0%)	0.88	22/8266 (0.3%)
32	CS	0.37	1/6108 (0.0%)	0.88	22/8266 (0.3%)
33	CT	0.63	0/1053	0.82	0/1413
34	Cc	0.82	0/1485	0.90	0/2008
35	Ce	0.36	0/1298	0.83	2/1750 (0.1%)
36	Cg	0.33	0/1259	0.66	0/1687
37	Ch	0.23	0/422	0.71	0/561
38	Ci	0.27	0/801	0.74	1/1087 (0.1%)
39	Cj	1.03	0/958	1.00	0/1293
40	Cm	0.30	0/1001	0.67	0/1345
41	Cn	0.60	0/712	0.75	0/954
42	Cp	0.58	0/458	0.79	0/617
43	CU	0.37	0/1015	0.65	0/1351
44	C1	0.63	0/26369	0.61	4/41071 (0.0%)
45	C2	0.65	0/5459	0.66	7/8498 (0.1%)
46	UV	0.32	0/8638	0.80	6/11725 (0.1%)
47	CV	0.31	0/1172	0.76	1/1592 (0.1%)
48	UH	0.48	1/2852 (0.0%)	0.72	0/3846
49	UE	0.53	0/980	0.96	2/1316 (0.2%)
49	UI	0.53	0/980	0.96	2/1316 (0.2%)
50	US	0.50	0/3765	0.70	0/5100
51	Cl	0.38	0/638	0.74	0/857
52	CX	0.25	0/2180	0.62	0/2956
53	UP	0.56	0/428	0.74	0/570
54	Cz	0.26	0/2310	0.62	0/3120
All	All	0.61	21/186592 (0.0%)	0.77	128/258976 (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	4
4	UD	0	2
5	UF	0	1
6	UG	0	2
9	UL	0	1
10	UM	0	3
12	UO	0	2

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
13	UQ	0	6
15	UU	0	8
17	UZ	0	3
18	CA	0	1
18	CB	0	1
21	CF	0	1
23	CH	0	1
24	CI	0	2
26	CK	0	1
29	CO	0	2
31	CQ	0	1
32	CR	0	2
32	CS	0	2
34	Cc	0	2
35	Ce	0	1
38	Ci	0	1
39	Cj	0	2
46	UV	0	5
47	CV	0	2
48	UH	0	2
50	US	0	1
51	Cl	0	1
54	Cz	0	1
All	All	0	64

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	UQ	394	HIS	CA-CB	-17.11	1.23	1.53
15	UU	1048	ARG	CA-CB	-10.32	1.39	1.52
1	UA	4	ASN	CA-CB	-9.34	1.37	1.52
14	UR	565	ALA	CA-CB	-8.64	1.40	1.52
26	CK	186	GLU	CA-CB	-8.22	1.41	1.52

The worst 5 of 128 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	C2	2	G	OP1-P-OP2	-13.18	80.07	119.60
24	CI	995	VAL	CA-C-N	12.59	151.76	122.31
24	CI	995	VAL	C-N-CA	12.59	151.76	122.31
45	C2	2	G	O5'-P-OP1	-12.07	71.78	108.00
45	C2	1	A	OP2-P-O3'	-10.20	77.40	108.00

There are no chirality outliers.

5 of 64 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	UA	214	SER	Peptide
1	UA	386	THR	Peptide
1	UA	667	ARG	Peptide
1	UA	8	SER	Peptide
4	UD	309	GLN	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	209	0
2	UB	4079	0	4201	125	0
3	UC	588	0	647	18	0
4	UD	6071	0	6080	232	0
5	UF	2591	0	2642	80	0
6	UG	3444	0	3454	135	0
7	UJ	6180	0	6341	188	0
8	UK	1687	0	1820	62	0
9	UL	6175	0	6188	260	0
10	UM	5273	0	5284	169	0
11	UN	1209	0	1234	58	0
12	UO	3819	0	3873	154	0
13	UQ	6008	0	6033	228	0
14	UR	3491	0	3507	129	0
15	UU	6734	0	6745	248	0
16	UX	1470	0	1533	80	0
17	UZ	1815	0	1896	69	0
18	CA	1778	0	1830	82	0
18	CB	1816	0	1847	68	0
19	CC	2866	0	2960	108	0
20	CD	3150	0	3262	117	0
21	CE	879	0	918	22	0
21	CF	864	0	900	34	0
22	CG	2922	0	2939	87	0
23	CH	2888	0	2979	118	0
24	CI	6486	0	6650	261	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	CJ	1434	0	1482	63	0
26	CK	2329	0	2373	110	0
27	CL	1786	0	1826	78	0
28	CM	3501	0	3498	144	0
29	CN	1762	0	1807	52	0
29	CO	1683	0	1726	62	0
30	CP	1504	0	1596	33	0
31	CQ	1361	0	1431	47	0
32	CR	5989	0	6130	202	0
32	CS	5989	0	6130	192	0
33	CT	1035	0	1063	32	0
34	Cc	1464	0	1504	53	0
35	Ce	1279	0	1322	43	0
36	Cg	1242	0	1354	49	0
37	Ch	416	0	451	11	0
38	Ci	791	0	795	13	0
39	Cj	943	0	1002	28	0
40	Cm	985	0	1021	31	0
41	Cn	702	0	750	19	0
42	Cp	455	0	482	15	0
43	CU	1009	0	1070	39	0
44	C1	23604	0	11955	691	0
45	C2	4891	0	2476	136	0
46	UV	8424	0	8502	254	0
47	CV	1145	0	1155	33	0
48	UH	2809	0	2843	122	0
49	UE	972	0	1032	61	0
49	UI	972	0	1032	68	0
50	US	3672	0	3679	121	0
51	Cl	633	0	676	14	0
52	CX	2130	0	2219	59	0
53	UP	422	0	457	19	0
54	Cz	2259	0	2235	54	0
55	UX	1	0	0	0	0
All	All	180242	0	169110	5636	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 16.

The worst 5 of 5636 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)
48:UH:555:GLY:O	48:UH:567:LEU:HA	1.43	1.17
48:UH:557:GLU:O	48:UH:565:GLY:HA2	1.45	1.16
44:C1:2238:A:N6	44:C1:2328:G:N3	1.97	1.10
17:UZ:133:LEU:O	17:UZ:137:PHE:HB2	1.52	1.07
44:C1:2238:A:H62	44:C1:2328:G:N2	1.53	1.07

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	UA	835/904 (92%)	730 (87%)	103 (12%)	2 (0%)	43	78
2	UB	502/907 (55%)	466 (93%)	36 (7%)	0	100	100
3	UC	72/648 (11%)	67 (93%)	5 (7%)	0	100	100
4	UD	754/884 (85%)	689 (91%)	65 (9%)	0	100	100
5	UF	325/414 (78%)	304 (94%)	21 (6%)	0	100	100
6	UG	446/558 (80%)	384 (86%)	60 (14%)	2 (0%)	30	67
7	UJ	796/1802 (44%)	750 (94%)	45 (6%)	1 (0%)	48	83
8	UK	211/270 (78%)	201 (95%)	10 (5%)	0	100	100
9	UL	767/962 (80%)	685 (89%)	82 (11%)	0	100	100
10	UM	645/912 (71%)	605 (94%)	39 (6%)	1 (0%)	43	78
11	UN	150/938 (16%)	143 (95%)	6 (4%)	1 (1%)	18	55
12	UO	498/557 (89%)	450 (90%)	48 (10%)	0	100	100
13	UQ	775/960 (81%)	691 (89%)	81 (10%)	3 (0%)	30	67
14	UR	437/618 (71%)	399 (91%)	38 (9%)	0	100	100
15	UU	890/1049 (85%)	786 (88%)	103 (12%)	1 (0%)	48	83
16	UX	188/193 (97%)	174 (93%)	14 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	UZ	229/391 (59%)	211 (92%)	18 (8%)	0	100	100
18	CA	238/313 (76%)	213 (90%)	25 (10%)	0	100	100
18	CB	235/313 (75%)	211 (90%)	24 (10%)	0	100	100
19	CC	383/523 (73%)	353 (92%)	30 (8%)	0	100	100
20	CD	416/582 (72%)	382 (92%)	34 (8%)	0	100	100
21	CE	119/127 (94%)	107 (90%)	12 (10%)	0	100	100
21	CF	118/127 (93%)	110 (93%)	8 (7%)	0	100	100
22	CG	368/630 (58%)	342 (93%)	26 (7%)	0	100	100
23	CH	383/411 (93%)	348 (91%)	35 (9%)	0	100	100
24	CI	812/1163 (70%)	737 (91%)	73 (9%)	2 (0%)	43	78
25	CJ	177/183 (97%)	151 (85%)	26 (15%)	0	100	100
26	CK	295/297 (99%)	271 (92%)	24 (8%)	0	100	100
27	CL	225/785 (29%)	200 (89%)	24 (11%)	1 (0%)	30	67
28	CM	443/446 (99%)	398 (90%)	44 (10%)	1 (0%)	43	78
29	CN	222/252 (88%)	207 (93%)	15 (7%)	0	100	100
29	CO	211/252 (84%)	193 (92%)	16 (8%)	2 (1%)	14	49
30	CP	185/322 (58%)	179 (97%)	6 (3%)	0	100	100
31	CQ	171/259 (66%)	165 (96%)	6 (4%)	0	100	100
32	CR	746/1073 (70%)	699 (94%)	47 (6%)	0	100	100
32	CS	746/1073 (70%)	699 (94%)	47 (6%)	0	100	100
33	CT	127/203 (63%)	111 (87%)	16 (13%)	0	100	100
34	Cc	188/212 (89%)	170 (90%)	18 (10%)	0	100	100
35	Ce	155/203 (76%)	140 (90%)	15 (10%)	0	100	100
36	Cg	157/190 (83%)	153 (98%)	4 (2%)	0	100	100
37	Ch	47/151 (31%)	46 (98%)	1 (2%)	0	100	100
38	Ci	113/150 (75%)	103 (91%)	10 (9%)	0	100	100
39	Cj	124/143 (87%)	104 (84%)	20 (16%)	0	100	100
40	Cm	122/130 (94%)	116 (95%)	6 (5%)	0	100	100
41	Cn	92/145 (63%)	86 (94%)	6 (6%)	0	100	100
42	Cp	59/68 (87%)	53 (90%)	6 (10%)	0	100	100
43	CU	123/311 (40%)	108 (88%)	15 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	UV	1057/1171 (90%)	946 (90%)	108 (10%)	3 (0%)	36	72
47	CV	144/322 (45%)	130 (90%)	13 (9%)	1 (1%)	18	55
48	UH	349/930 (38%)	327 (94%)	22 (6%)	0	100	100
49	UE	121/410 (30%)	109 (90%)	12 (10%)	0	100	100
49	UI	121/410 (30%)	109 (90%)	12 (10%)	0	100	100
50	US	443/549 (81%)	414 (94%)	28 (6%)	1 (0%)	43	78
51	Cl	78/156 (50%)	72 (92%)	6 (8%)	0	100	100
52	CX	265/480 (55%)	252 (95%)	13 (5%)	0	100	100
53	UP	52/364 (14%)	42 (81%)	9 (17%)	1 (2%)	6	32
54	Cz	273/1796 (15%)	257 (94%)	15 (6%)	1 (0%)	30	67
All	All	19223/30592 (63%)	17548 (91%)	1651 (9%)	24 (0%)	49	83

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	UG	176	LEU
29	CO	85	SER
46	UV	1059	ASP
13	UQ	708	SER
11	UN	902	ARG

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%)	630 (97%)	21 (3%)	34	56
2	UB	425/788 (54%)	421 (99%)	4 (1%)	70	77
3	UC	61/536 (11%)	60 (98%)	1 (2%)	55	69
4	UD	653/738 (88%)	645 (99%)	8 (1%)	63	74
5	UF	248/341 (73%)	248 (100%)	0	100	100
6	UG	344/474 (73%)	330 (96%)	14 (4%)	27	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	UJ	658/1526 (43%)	651 (99%)	7 (1%)	65	74
8	UK	159/227 (70%)	157 (99%)	2 (1%)	61	72
9	UL	667/821 (81%)	661 (99%)	6 (1%)	70	77
10	UM	569/770 (74%)	565 (99%)	4 (1%)	76	79
11	UN	123/765 (16%)	122 (99%)	1 (1%)	73	78
12	UO	404/456 (89%)	396 (98%)	8 (2%)	48	66
13	UQ	650/817 (80%)	638 (98%)	12 (2%)	51	67
14	UR	360/524 (69%)	350 (97%)	10 (3%)	38	59
15	UU	672/863 (78%)	651 (97%)	21 (3%)	35	56
16	UX	150/167 (90%)	146 (97%)	4 (3%)	39	60
17	UZ	186/329 (56%)	184 (99%)	2 (1%)	65	74
18	CA	175/228 (77%)	168 (96%)	7 (4%)	28	49
18	CB	195/228 (86%)	194 (100%)	1 (0%)	81	82
19	CC	287/435 (66%)	287 (100%)	0	100	100
20	CD	319/489 (65%)	314 (98%)	5 (2%)	55	69
21	CE	91/108 (84%)	85 (93%)	6 (7%)	15	37
21	CF	88/108 (82%)	88 (100%)	0	100	100
22	CG	299/525 (57%)	298 (100%)	1 (0%)	86	84
23	CH	303/320 (95%)	296 (98%)	7 (2%)	44	64
24	CI	661/1009 (66%)	647 (98%)	14 (2%)	47	65
25	CJ	147/169 (87%)	138 (94%)	9 (6%)	17	39
26	CK	245/266 (92%)	232 (95%)	13 (5%)	20	42
27	CL	181/642 (28%)	175 (97%)	6 (3%)	33	55
28	CM	364/383 (95%)	358 (98%)	6 (2%)	55	69
29	CN	202/223 (91%)	201 (100%)	1 (0%)	81	82
29	CO	193/223 (86%)	191 (99%)	2 (1%)	68	76
30	CP	164/287 (57%)	164 (100%)	0	100	100
31	CQ	145/215 (67%)	145 (100%)	0	100	100
32	CR	654/916 (71%)	471 (72%)	183 (28%)	0	3
32	CS	654/916 (71%)	471 (72%)	183 (28%)	0	3
33	CT	108/167 (65%)	107 (99%)	1 (1%)	70	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	Cc	149/178 (84%)	148 (99%)	1 (1%)	76	79
35	Ce	137/177 (77%)	135 (98%)	2 (2%)	57	71
36	Cg	122/162 (75%)	121 (99%)	1 (1%)	73	78
37	Ch	43/130 (33%)	43 (100%)	0	100	100
38	Ci	74/117 (63%)	73 (99%)	1 (1%)	59	72
39	Cj	92/115 (80%)	90 (98%)	2 (2%)	45	64
40	Cm	103/113 (91%)	102 (99%)	1 (1%)	68	76
41	Cn	70/116 (60%)	70 (100%)	0	100	100
42	Cp	46/61 (75%)	45 (98%)	1 (2%)	45	64
43	CU	103/260 (40%)	98 (95%)	5 (5%)	22	44
46	UV	908/989 (92%)	900 (99%)	8 (1%)	70	77
47	CV	129/276 (47%)	129 (100%)	0	100	100
48	UH	301/788 (38%)	300 (100%)	1 (0%)	86	84
49	UE	105/346 (30%)	74 (70%)	31 (30%)	0	3
49	UI	105/346 (30%)	74 (70%)	31 (30%)	0	3
50	US	404/493 (82%)	402 (100%)	2 (0%)	81	82
51	Cl	71/135 (53%)	71 (100%)	0	100	100
52	CX	227/411 (55%)	227 (100%)	0	100	100
53	UP	44/314 (14%)	44 (100%)	0	100	100
54	Cz	235/1533 (15%)	235 (100%)	0	100	100
All	All	15923/25834 (62%)	15266 (96%)	657 (4%)	28	49

5 of 657 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	CS	319	ASN
36	Cg	97	LEU
32	CS	414	ILE
32	CS	318	GLU
32	CS	655	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 316 such sidechains are listed below:

Mol	Chain	Res	Type
32	CS	565	HIS
49	UE	219	GLN
32	CS	902	ASN
46	UV	192	ASN
52	CX	290	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
44	C1	1088/2323 (46%)	374 (34%)	31 (2%)
45	C2	226/230 (98%)	84 (37%)	8 (3%)
All	All	1314/2553 (51%)	458 (34%)	39 (2%)

5 of 458 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
44	C1	2	G
44	C1	3	G
44	C1	4	G
44	C1	5	G
44	C1	7	A

5 of 39 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
44	C1	2177	G
45	C2	91	G
44	C1	2214	A
45	C2	35	G
45	C2	255	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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
45	C2	3
2	UB	1
48	UH	1

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	18.53
1	C2	105:C	O3'	110:A	P	15.27
1	C2	119:C	O3'	123:A	P	11.89
1	UB	679:ASN	C	680:PHE	N	1.20
1	UH	730:PHE	C	731:LYS	N	1.18

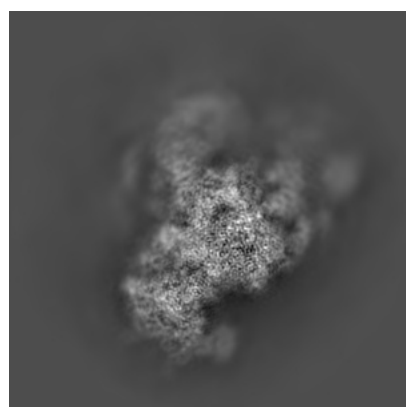
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10055. These allow visual inspection of the internal detail of the map and identification of artifacts.

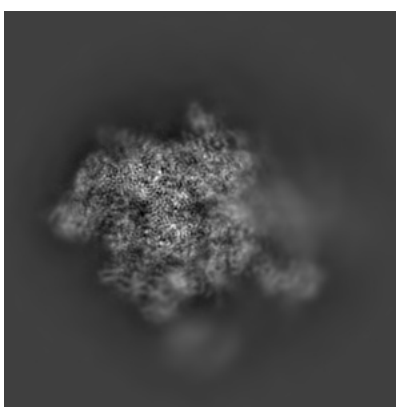
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

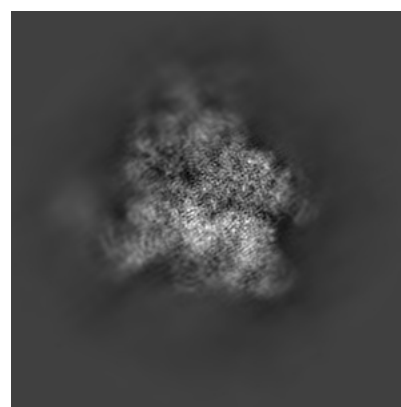
6.1.1 Primary map



X



Y

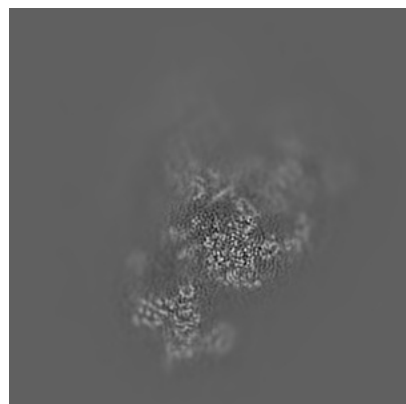


Z

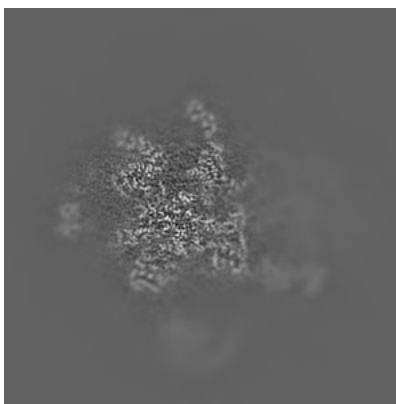
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

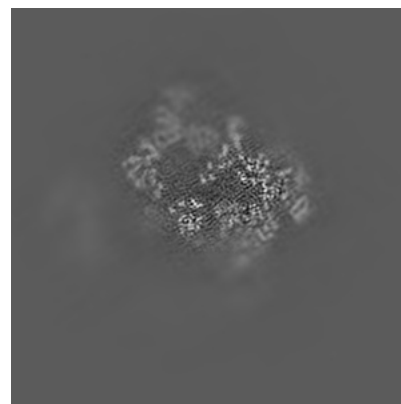
6.2.1 Primary map



X Index: 240



Y Index: 240

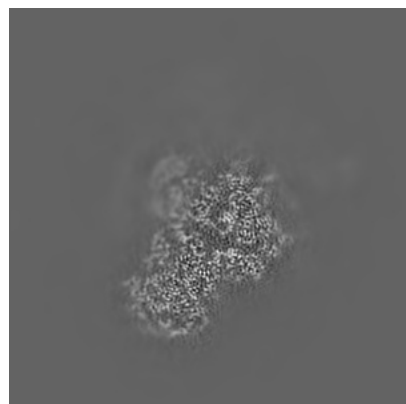


Z Index: 240

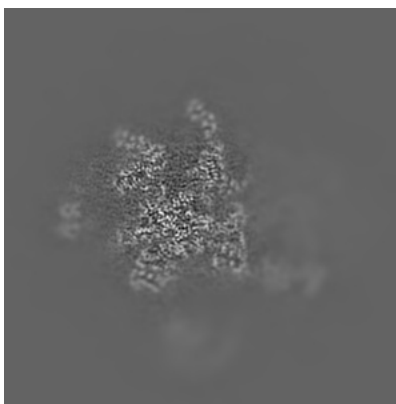
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

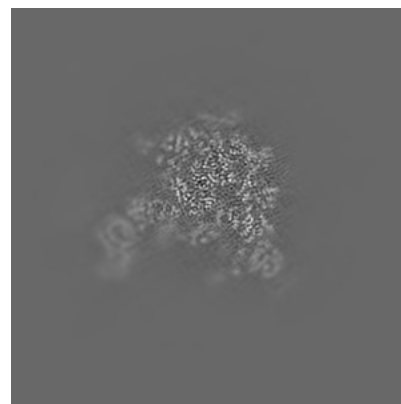
6.3.1 Primary map



X Index: 279



Y Index: 241

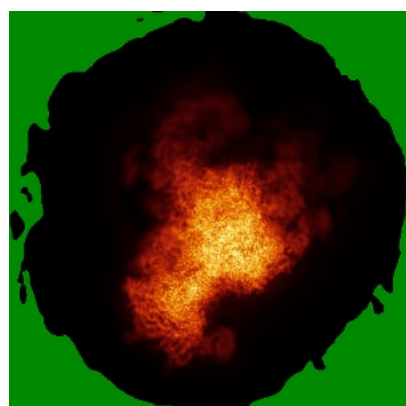


Z Index: 187

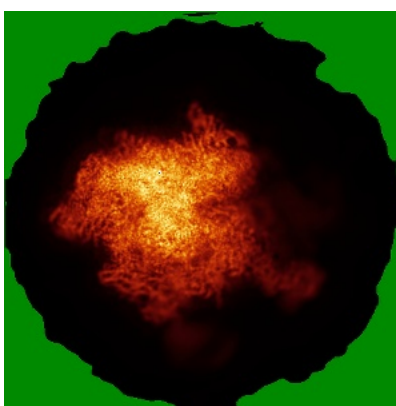
The images above show the largest variance slices of the map in three orthogonal directions.

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

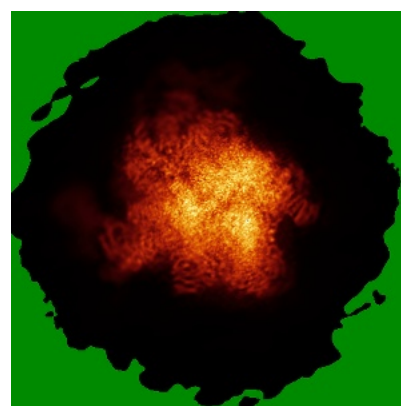
6.4.1 Primary map



X



Y

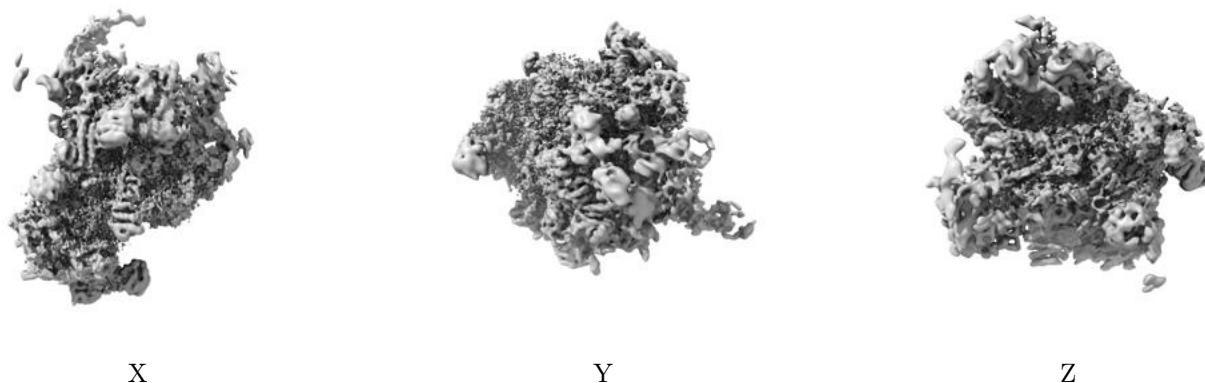


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

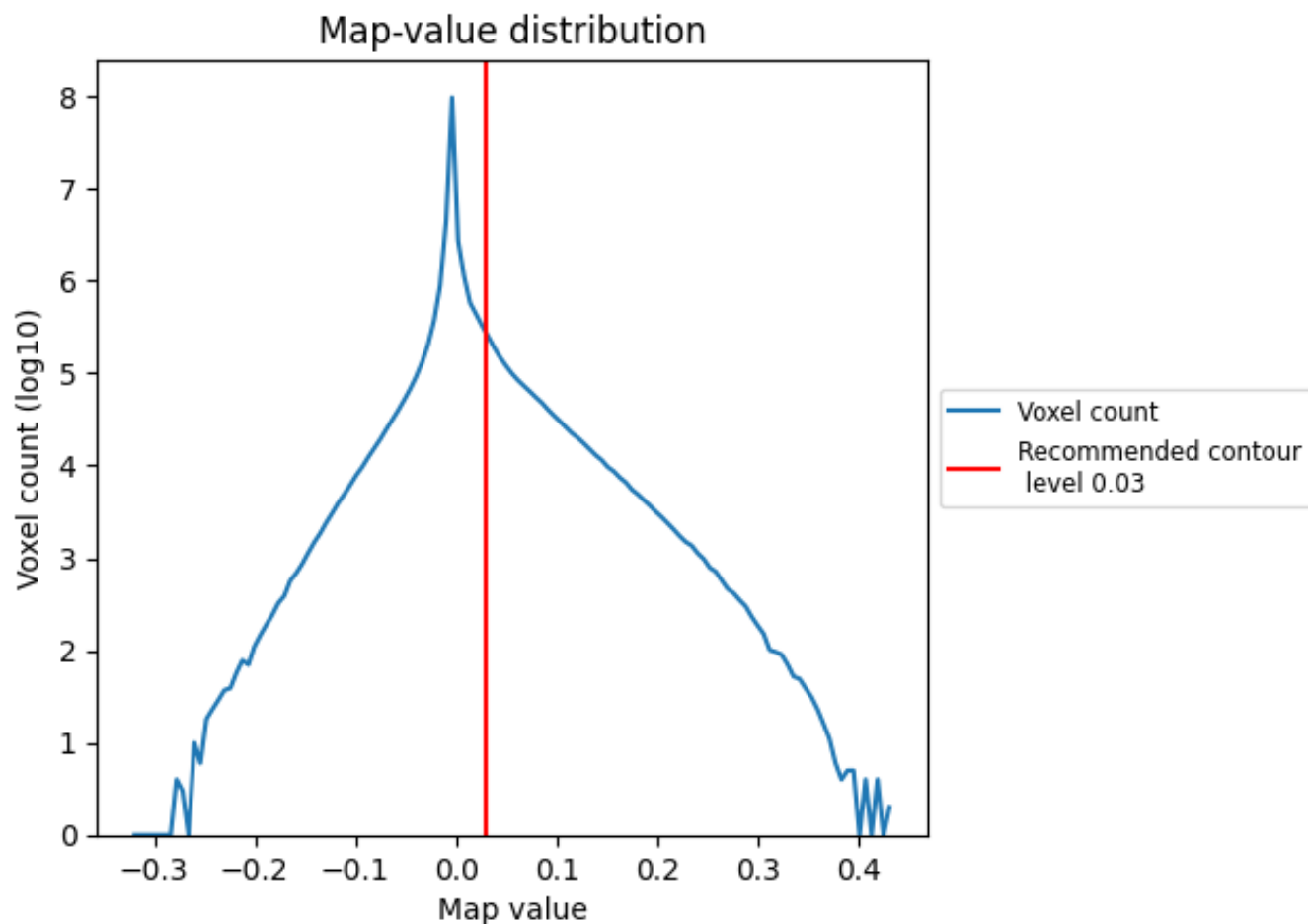
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

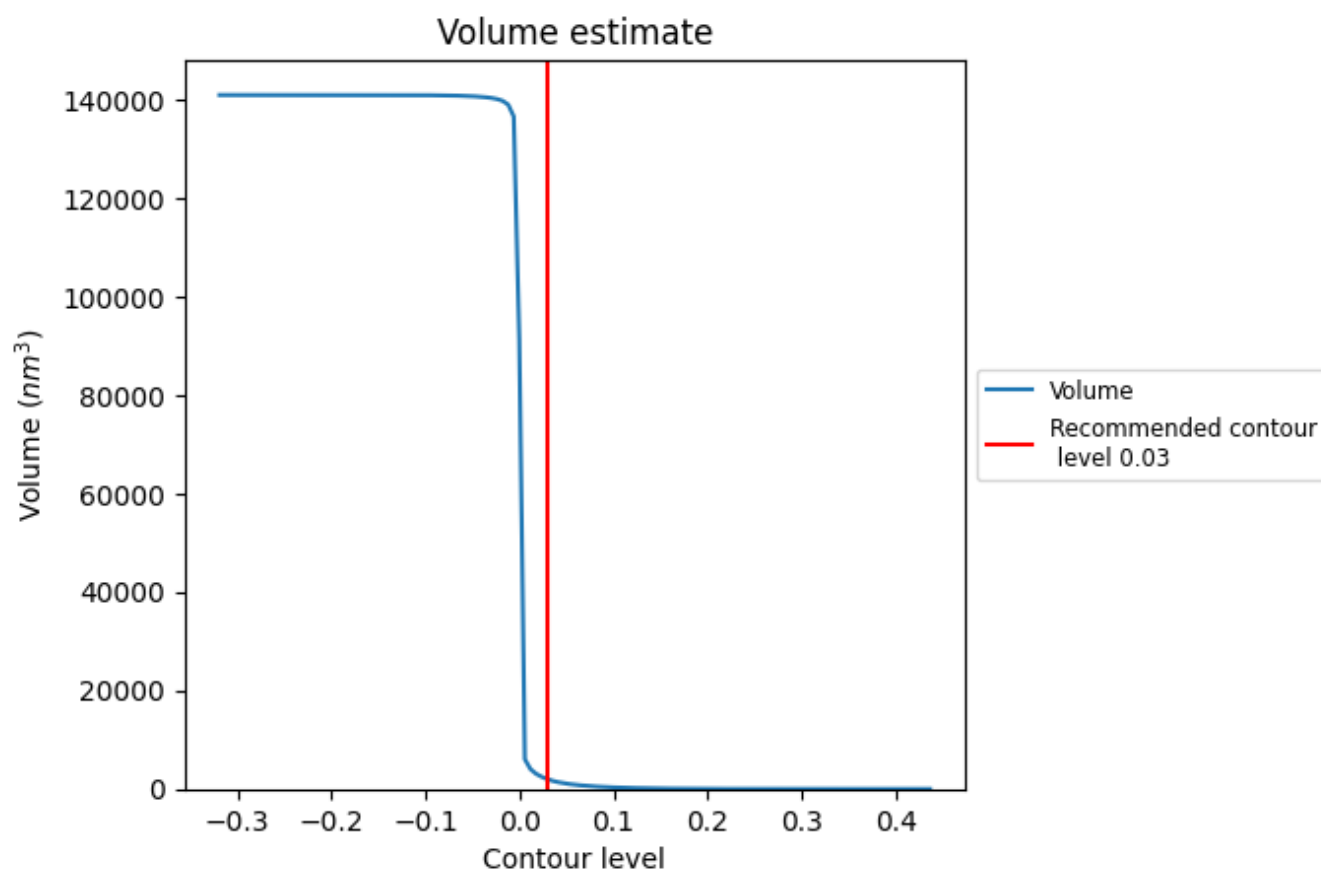
This section contains the results of statistical analysis of the map.

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.

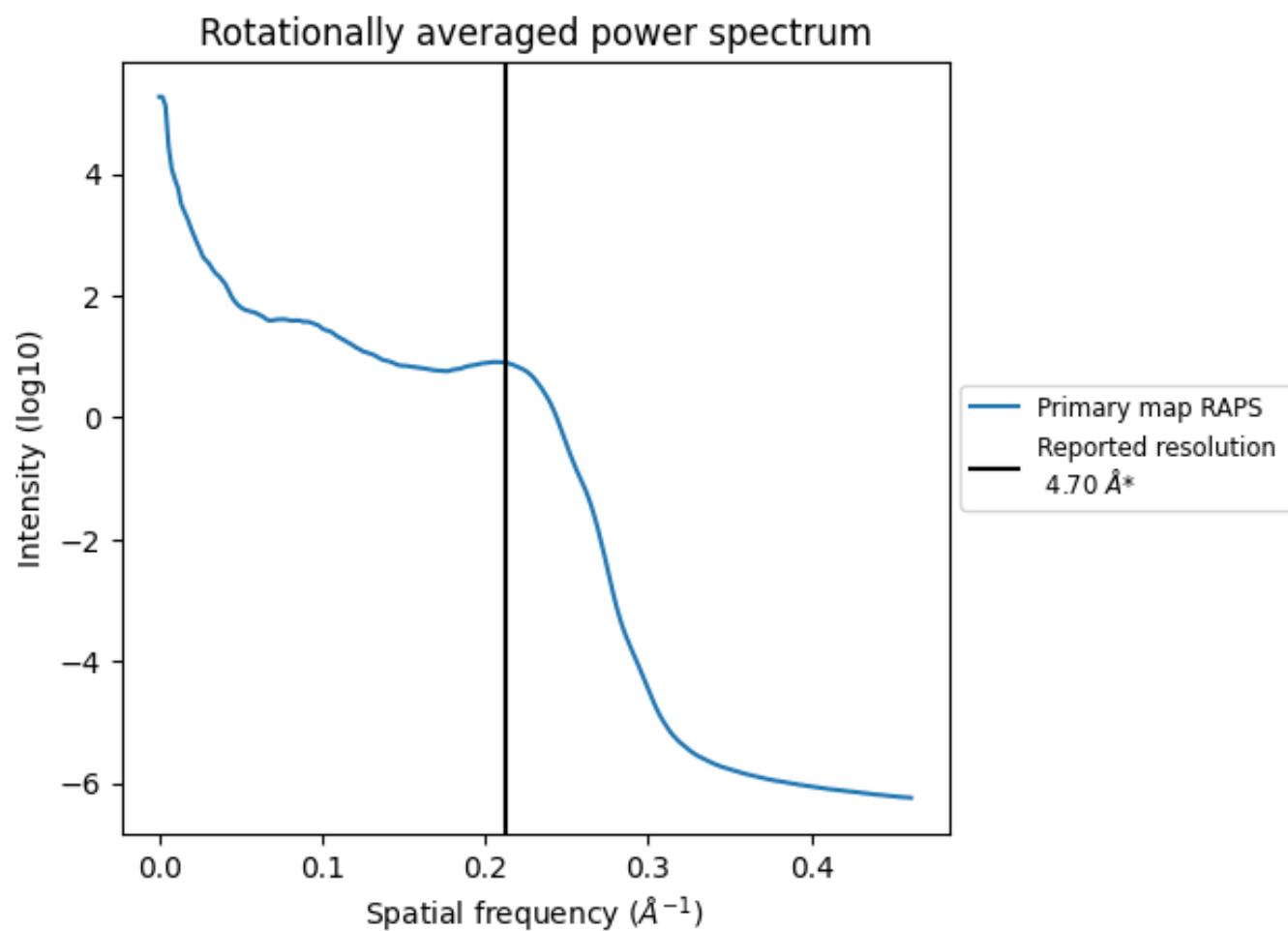
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1965 nm^3 ; this corresponds to an approximate mass of 1775 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 ⓘ

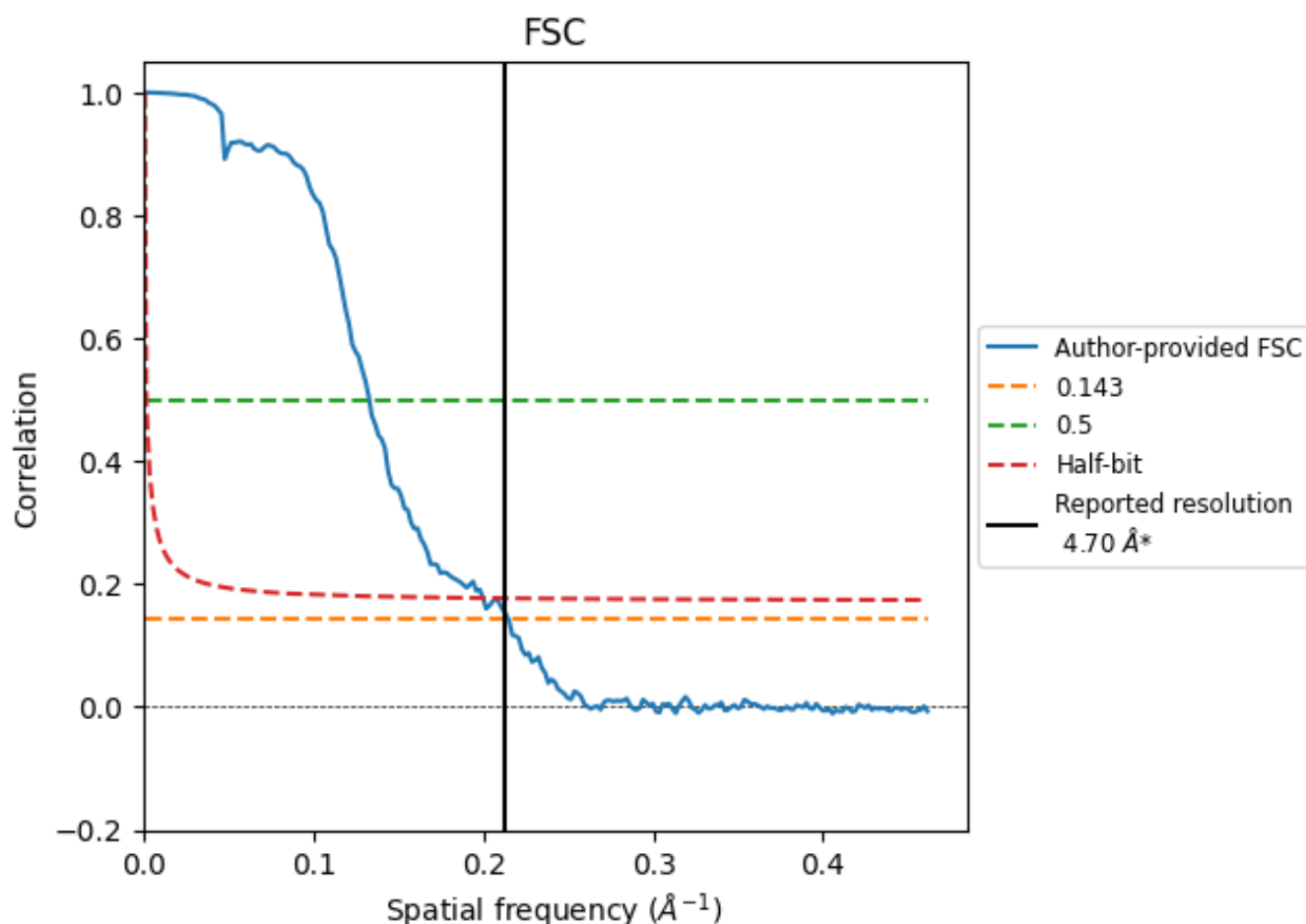


*Reported resolution corresponds to spatial frequency of 0.213 Å⁻¹

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 0.213 Å⁻¹

8.2 Resolution estimates [i](#)

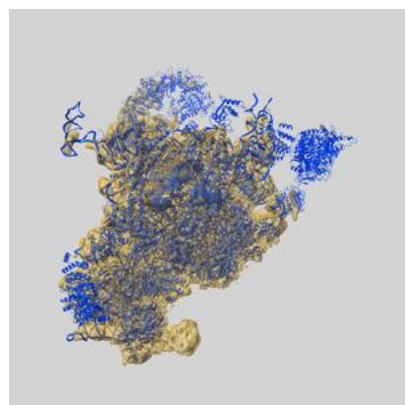
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.70	-	-
Author-provided FSC curve	4.66	7.52	5.00
Unmasked-calculated*	-	-	-

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

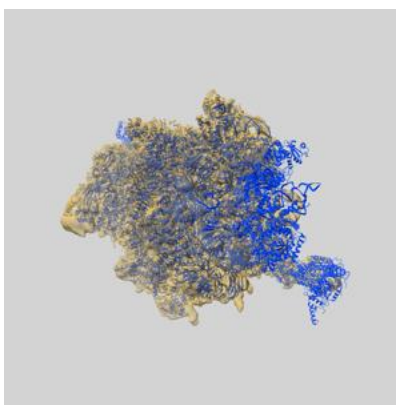
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10055 and PDB model 6RXY. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

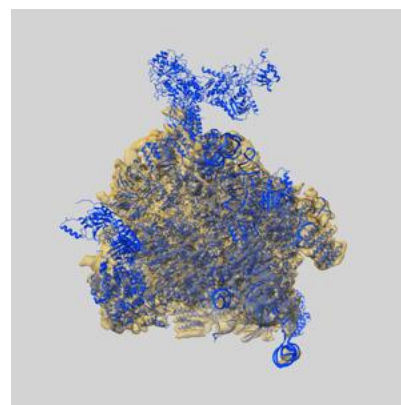
9.1 Map-model overlay [i](#)



X



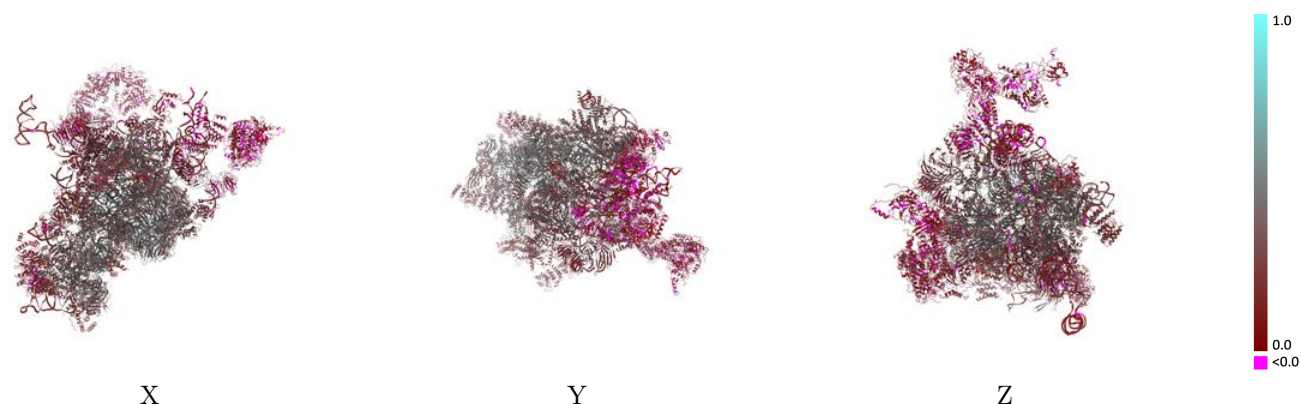
Y



Z

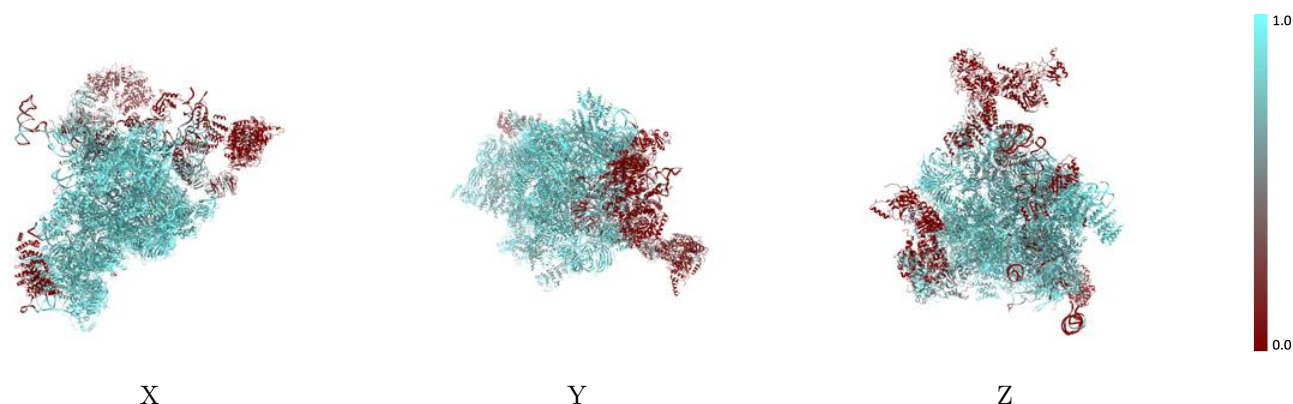
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



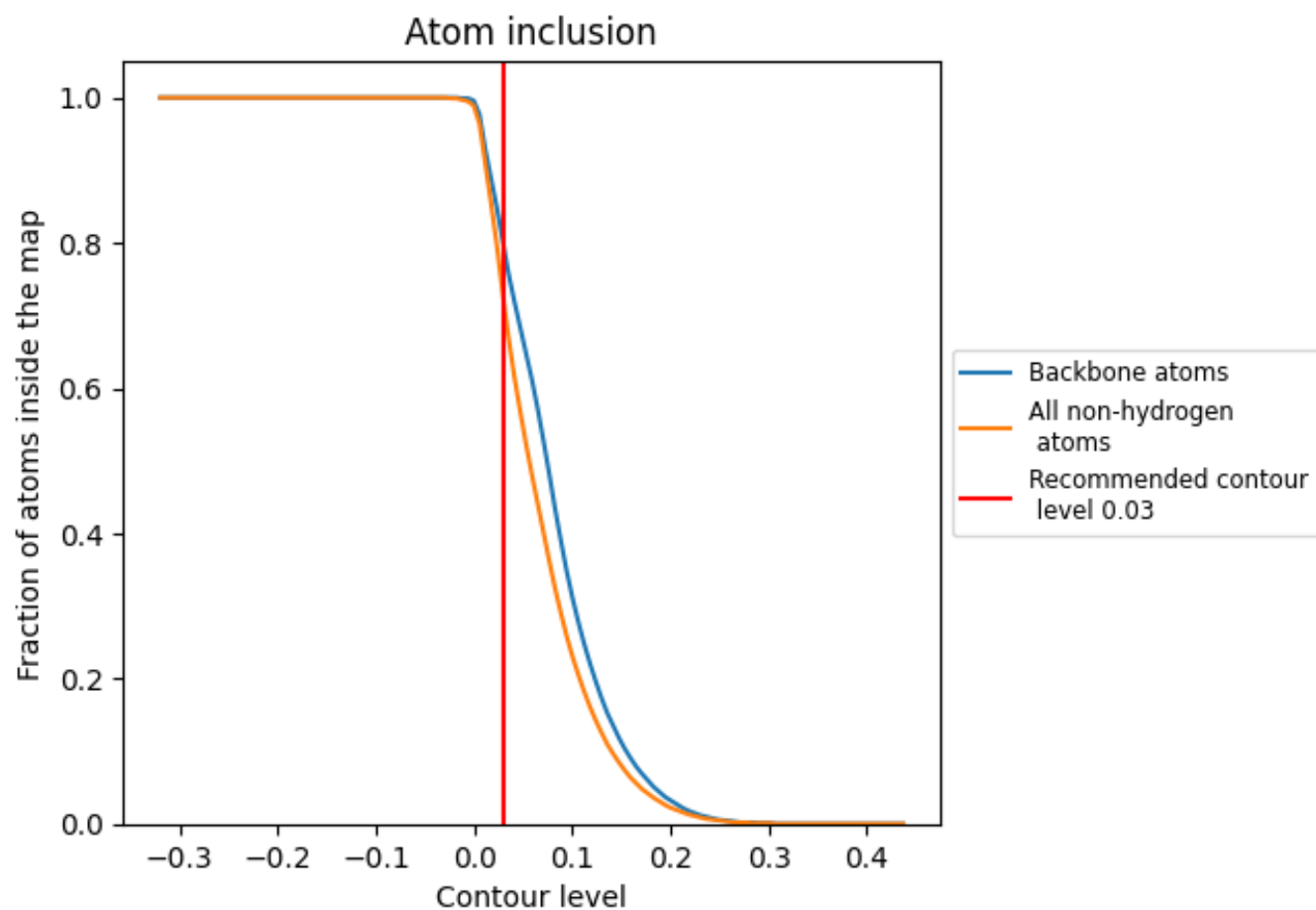
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 80% of all backbone atoms, 72% 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	 0.7220	 0.2860
C1	 0.8230	 0.2910
C2	 0.7840	 0.2890
CA	 0.8910	 0.4010
CB	 0.7880	 0.2650
CC	 0.8330	 0.2940
CD	 0.8600	 0.3010
CE	 0.9210	 0.4520
CF	 0.6880	 0.2260
CG	 0.6170	 0.1410
CH	 0.8490	 0.3060
CI	 0.8290	 0.3190
CJ	 0.9340	 0.4690
CK	 0.9170	 0.4410
CL	 0.9010	 0.3840
CM	 0.9090	 0.3920
CN	 0.8400	 0.3450
CO	 0.7810	 0.2220
CP	 0.4010	 0.1470
CQ	 0.8350	 0.2360
CR	 0.4630	 0.1440
CS	 0.0680	 0.0790
CT	 0.8930	 0.4100
CU	 0.6210	 0.2920
CV	 0.0000	 0.0470
CX	 0.6830	 0.1390
Cc	 0.9180	 0.4140
Ce	 0.0050	 0.1440
Cg	 0.4200	 0.1990
Ch	 0.1500	 0.0740
Ci	 0.4970	 0.1250
Cj	 0.9350	 0.4730
Cl	 0.6350	 0.2730
Cm	 0.2660	 0.2370
Cn	 0.8600	 0.3770



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Chain	Atom inclusion	Q-score
Cp	 0.9150	 0.4210
Cz	 0.1530	 0.1050
UA	 0.9300	 0.4450
UB	 0.8650	 0.2900
UC	 0.7850	 0.3260
UD	 0.8940	 0.3560
UE	 0.8470	 0.3050
UF	 0.8890	 0.2880
UG	 0.9090	 0.4320
UH	 0.8530	 0.2590
UI	 0.7400	 0.1610
UJ	 0.4900	 0.2670
UK	 0.9130	 0.4090
UL	 0.8620	 0.2650
UM	 0.5660	 0.1270
UN	 0.8970	 0.3630
UO	 0.9160	 0.4160
UP	 0.8970	 0.3780
UQ	 0.9150	 0.3900
UR	 0.9330	 0.4440
US	 0.8450	 0.2750
UU	 0.9310	 0.4210
UV	 0.0000	 0.0550
UX	 0.8750	 0.3830
UZ	 0.8520	 0.3060