



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 03:41 AM UTC

PDB ID : 6RXZ / pdb_00006rxz
EMDB ID : EMD-10056
Title : Cryo-EM structure of the 90S pre-ribosome (Kre33-Noc4) from *Chaetomium thermophilum*, state b
Authors : Cheng, J.; Kellner, N.; Griesel, S.; Berninghausen, O.; Beckmann, R.; Hurt, E.
Deposited on : 2019-06-10
Resolution : 4.40 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

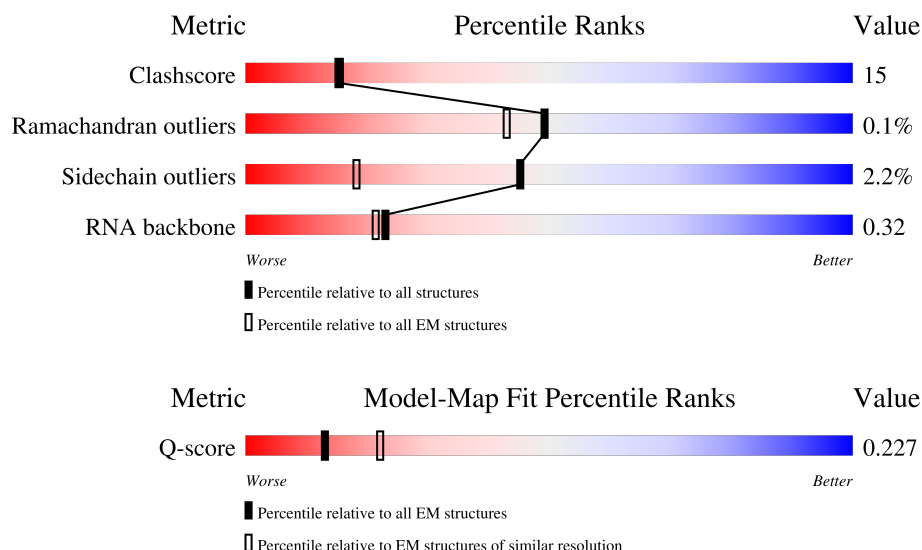
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	3132 (3.91 - 4.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

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1	UA	904	
2	UB	907	
3	UC	648	

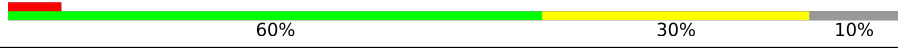
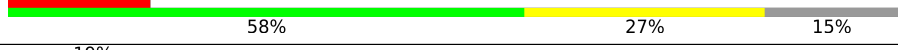
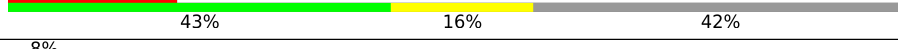
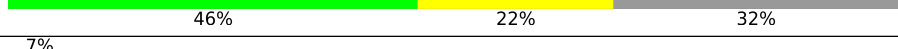
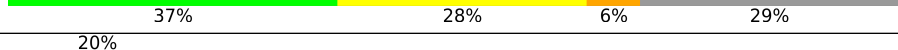
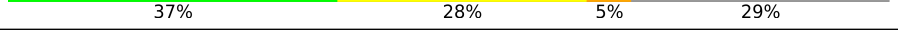
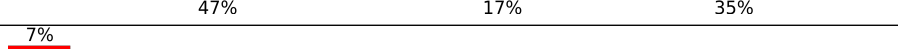
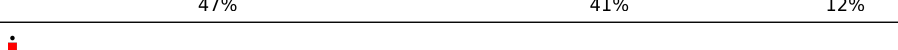
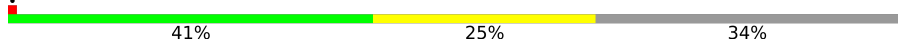
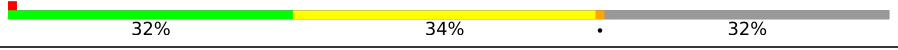
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Mol	Chain	Length	Quality of chain
4	UD	884	
5	UF	414	
6	UG	558	
7	UJ	1802	
8	UK	270	
9	UL	962	
10	UM	912	
11	UN	938	
12	UO	557	
13	UQ	960	
14	UR	618	
15	UU	1049	
16	UX	193	
17	UZ	391	
18	CA	313	
18	CB	313	
19	CC	523	
20	CD	582	
21	CE	127	
21	CF	127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

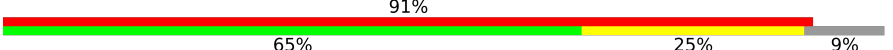
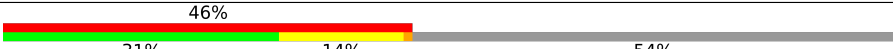
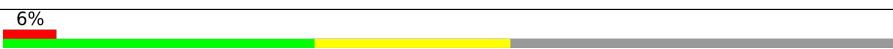
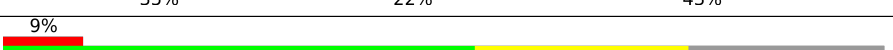
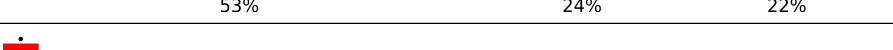
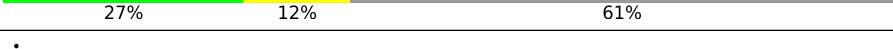
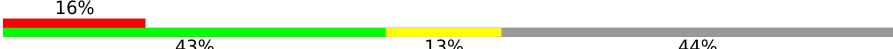
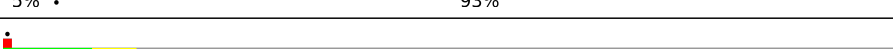
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Mol	Chain	Length	Quality of chain
27	CL	785	
28	CM	446	
29	CN	252	
29	CO	252	
30	CP	322	
31	CQ	259	
32	CR	1073	
32	CS	1073	
33	CT	203	
34	Cb	264	
35	Cc	212	
36	Cd	239	
37	Ce	203	
38	Cf	202	
39	Cg	190	
40	Ch	151	
41	Ci	150	
42	Cj	143	
43	Ck	161	
44	Cm	130	
45	Cn	145	
46	Co	136	
47	Cp	68	
48	CU	311	
49	C1	2323	

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Mol	Chain	Length	Quality of chain
50	C2	230	
51	UV	1171	
52	CV	322	
53	CW	668	
54	UT	2612	
55	UH	930	
56	UE	410	
56	UI	410	
57	US	549	
58	Cl	156	
59	CX	480	
60	CY	381	
61	CZ	609	
62	UP	364	
63	Cz	1796	

2 Entry composition

There are 64 unique types of molecules in this entry. The entry contains 218474 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	1090	Total	C	N	O	S	0	0
			8416	5408	1452	1525	31		

- 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	177	Total	C	N	O	S	0	0
			1401	892	263	239	7		

- 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	416	Total	C	N	O	S	0	0
			3245	2065	587	580	13		

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

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

- Molecule 24 is a protein called Bms1.

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

- Molecule 25 is a protein called Imp3.

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

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

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

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

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

- Molecule 28 is a protein called Sof1.

Mol	Chain	Residues	Atoms					AltConf	Trace
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 S4.

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

- 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 S6.

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

- Molecule 37 is a protein called 40S ribosomal protein S7.

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

- Molecule 38 is a protein called 40S ribosomal protein S8.

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

- Molecule 39 is a protein called 40S ribosomal protein s9-like protein.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ch	49	Total	C	N	O	S	0	0
			406	265	79	62			

- Molecule 41 is a protein called 40S ribosomal protein S14-like protein.

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

- Molecule 42 is a protein called 40S ribosomal protein S16-like protein.

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

- Molecule 43 is a protein called 40S ribosomal protein S11-like protein.

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

- Molecule 44 is a protein called 40S ribosomal protein S22-like protein.

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

- Molecule 45 is a protein called 40S ribosomal protein s23-like protein.

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

- Molecule 46 is a protein called 40S ribosomal protein S24.

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

- Molecule 47 is a protein called 40S ribosomal protein S28-like protein.

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

- Molecule 48 is a protein called Faf1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	CU	114	Total	C	N	O	S	0	0
			882	544	178	154	6		

- Molecule 49 is a RNA chain called 35S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	C1	1487	Total	C	N	O	P	0	0
			31732	14158	5691	10396	1487		

- Molecule 50 is a RNA chain called U3 snoRNA.

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

- Molecule 51 is a protein called U3 small nucleolar RNA-associated protein 22.

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

- Molecule 52 is a protein called Rrp7.

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

- Molecule 53 is a protein called Ribosome biogenesis protein ENP2.

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

- Molecule 54 is a protein called Utp20.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	UT	2028	Total	C	N	O	S	0	0
			16000	10303	2813	2816	68		

- Molecule 55 is a protein called Utp8.

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

- Molecule 56 is a protein called Utp5.

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

- Molecule 57 is a protein called Noc4.

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

- Molecule 58 is a protein called Rps18.

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

- Molecule 59 is a protein called Enp1.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	CX	267	Total	C	N	O	S	0	0
			2122	1380	374	358	10		

- Molecule 60 is a protein called U3 small nucleolar ribonucleoprotein protein lcp5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	CY	122	Total	C	N	O	S	0	0
			975	590	194	188	3		

- Molecule 61 is a protein called Bfr2.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	CZ	42	Total	C	N	O	S	0	0
			354	223	68	62	1		

- Molecule 62 is a protein called Utp16.

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

- Molecule 63 is a protein called Rrp5.

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

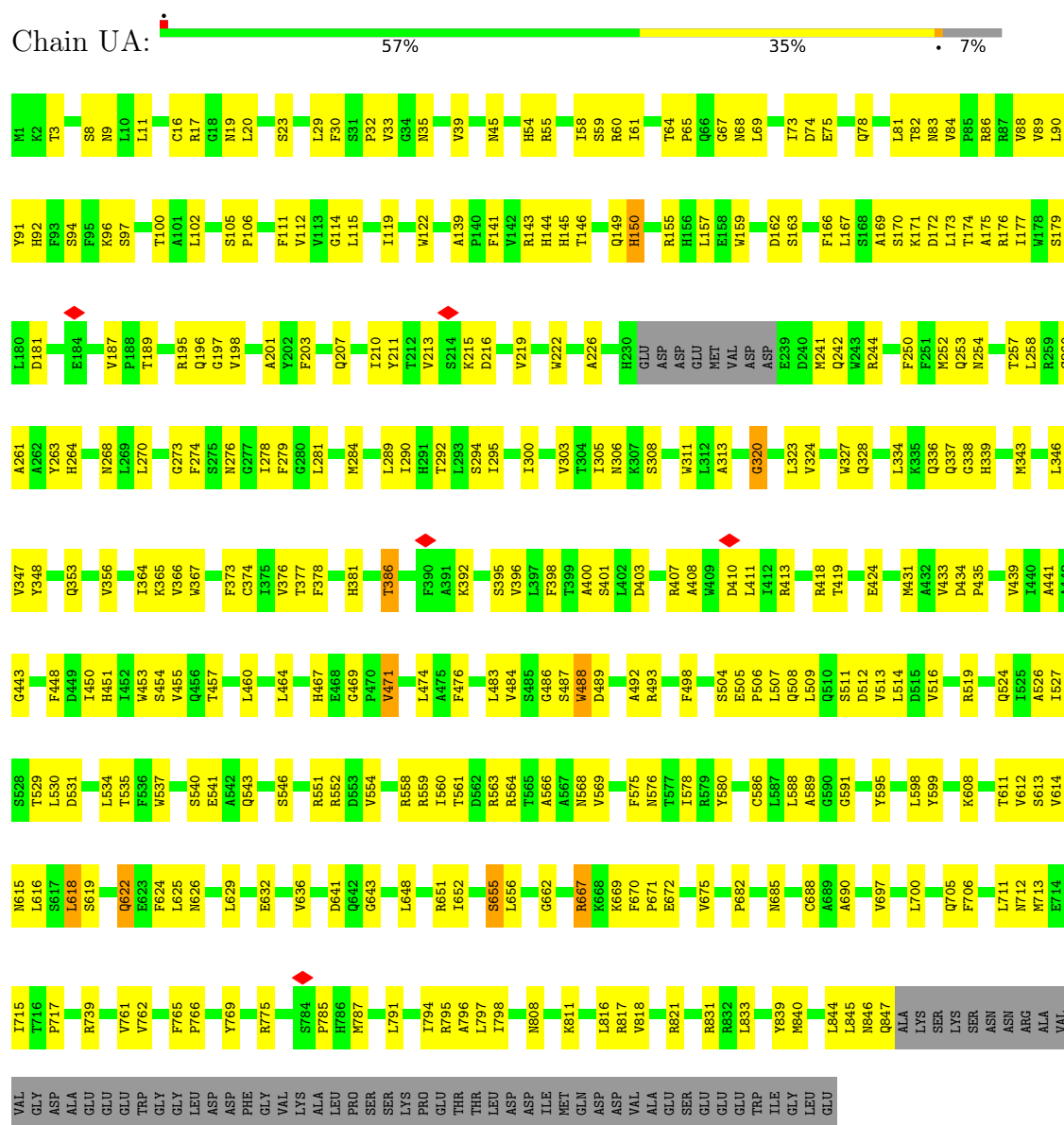
- Molecule 64 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

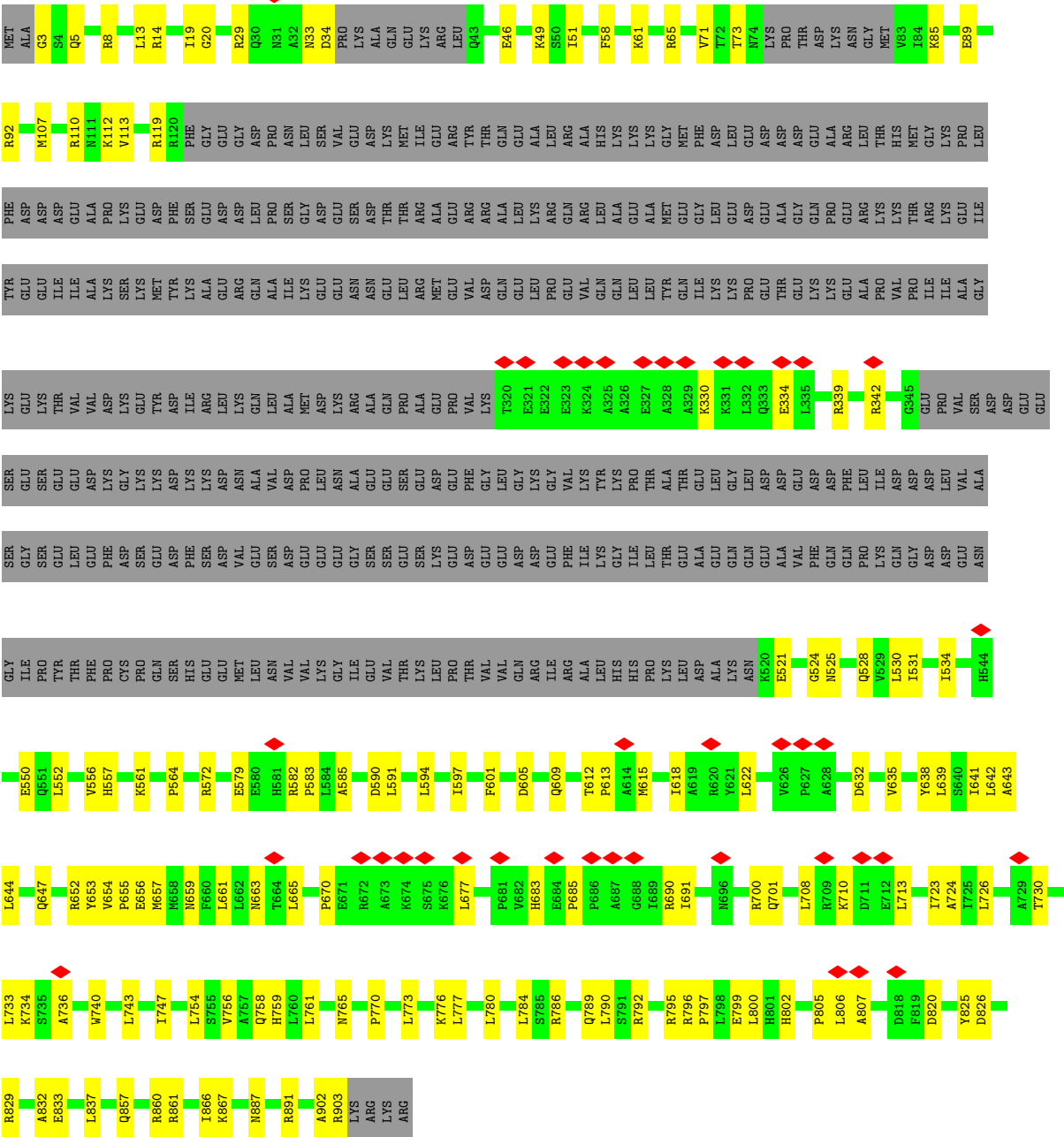
3 Residue-property plots

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.

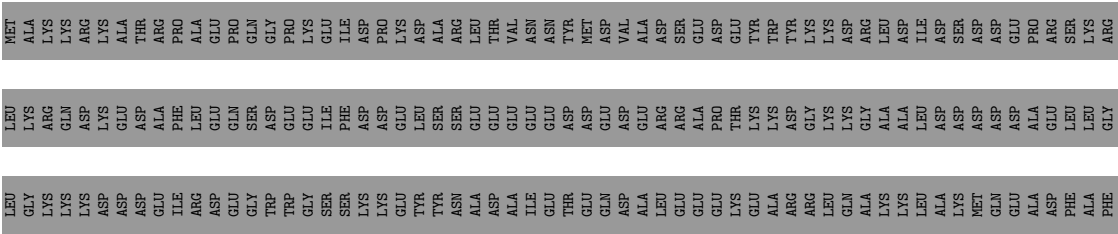
- Molecule 1: Periodic tryptophan protein 2-like protein

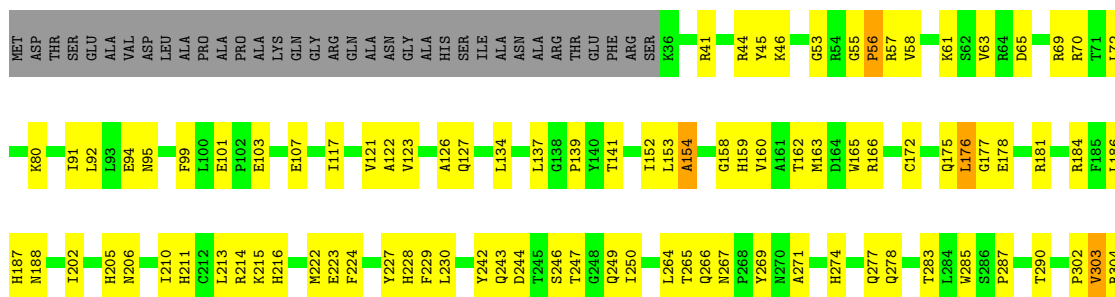


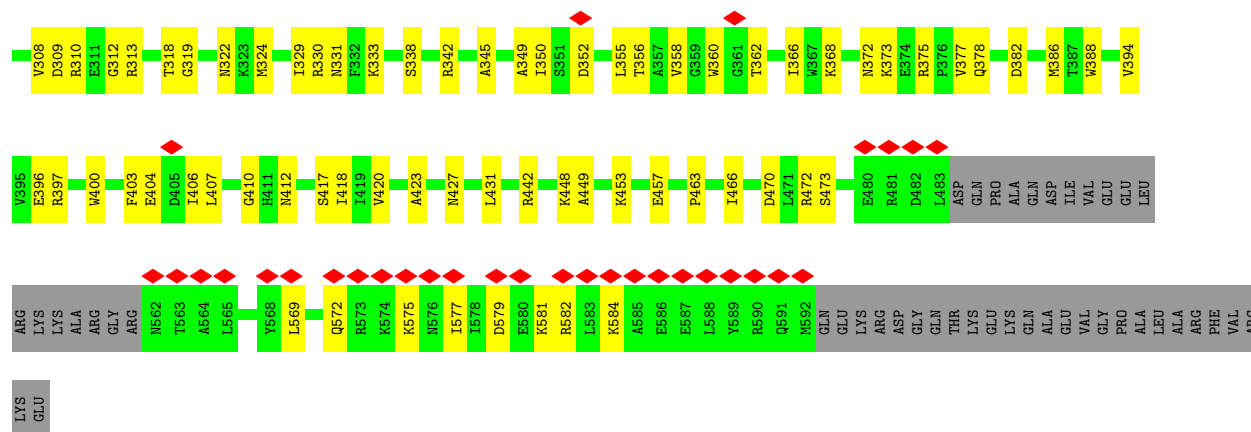
- Molecule 2: Utp2



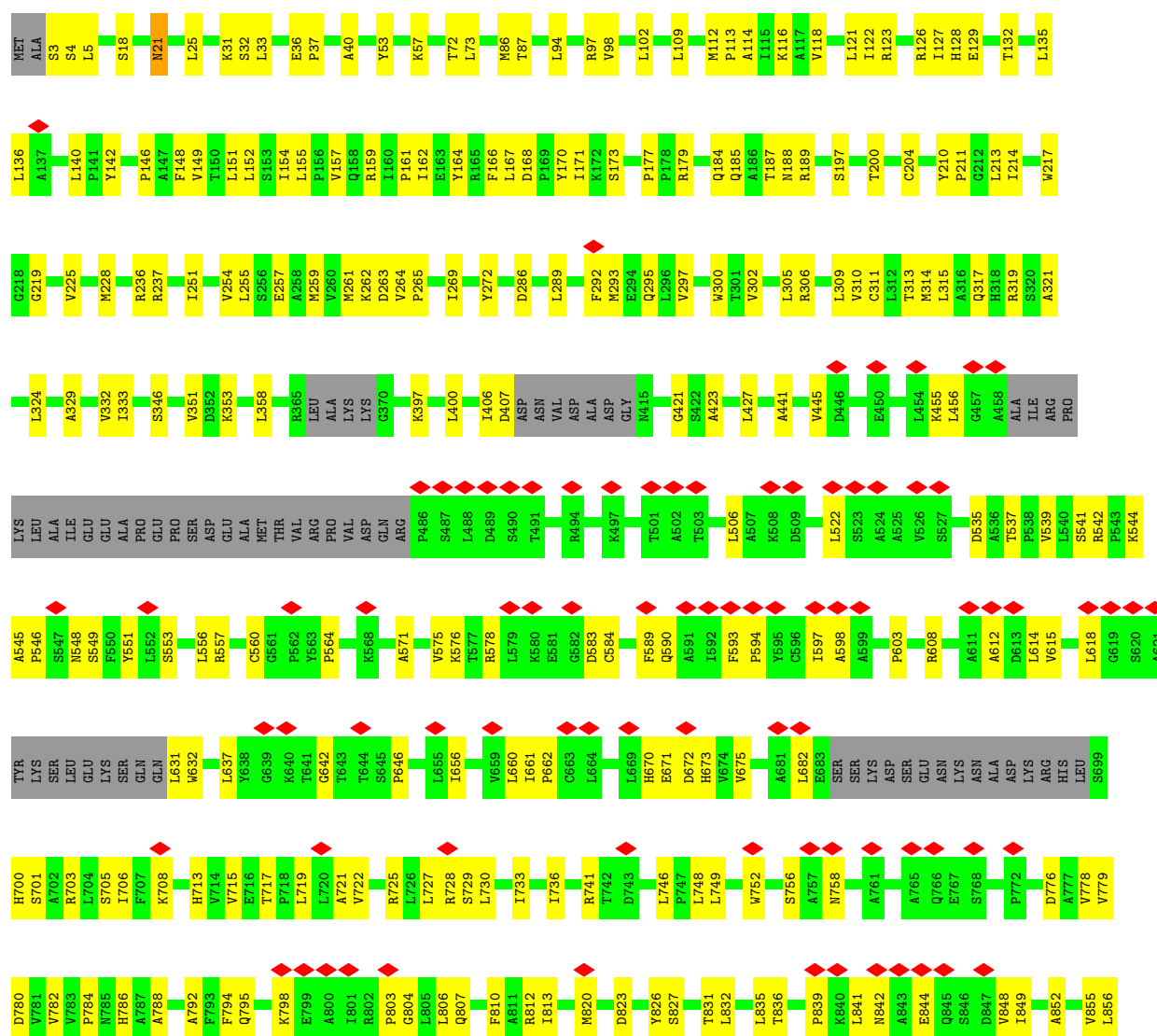
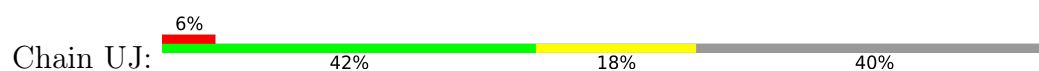
● Molecule 3: Utp3



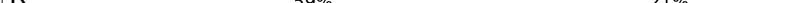


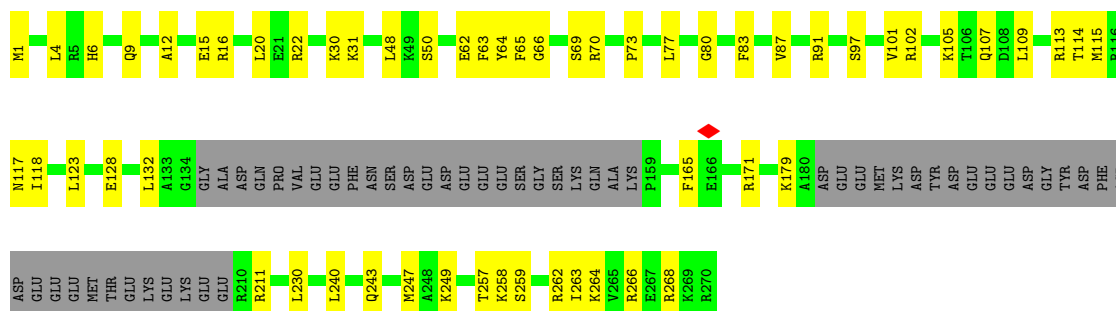


• Molecule 7: UTP10

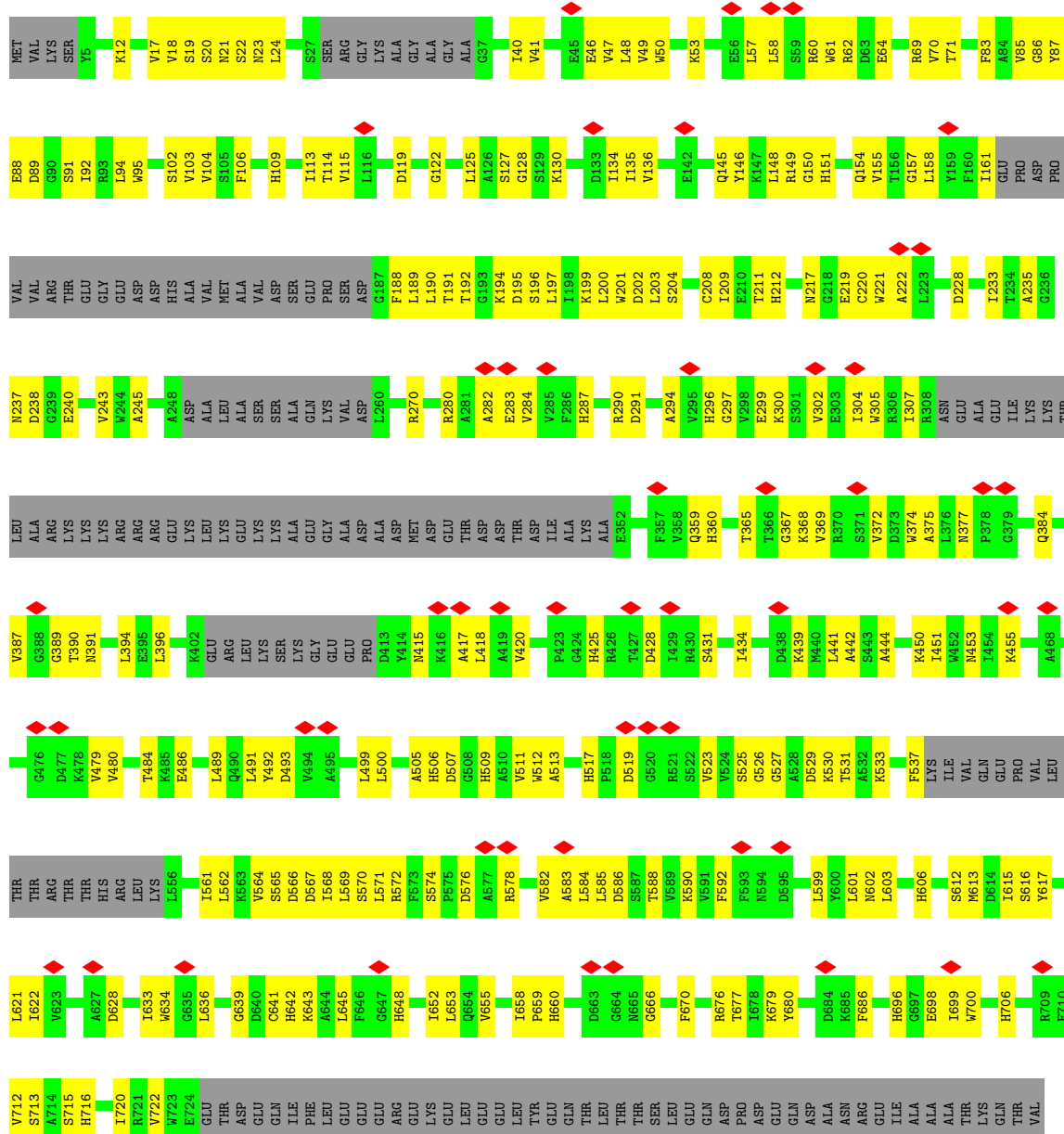


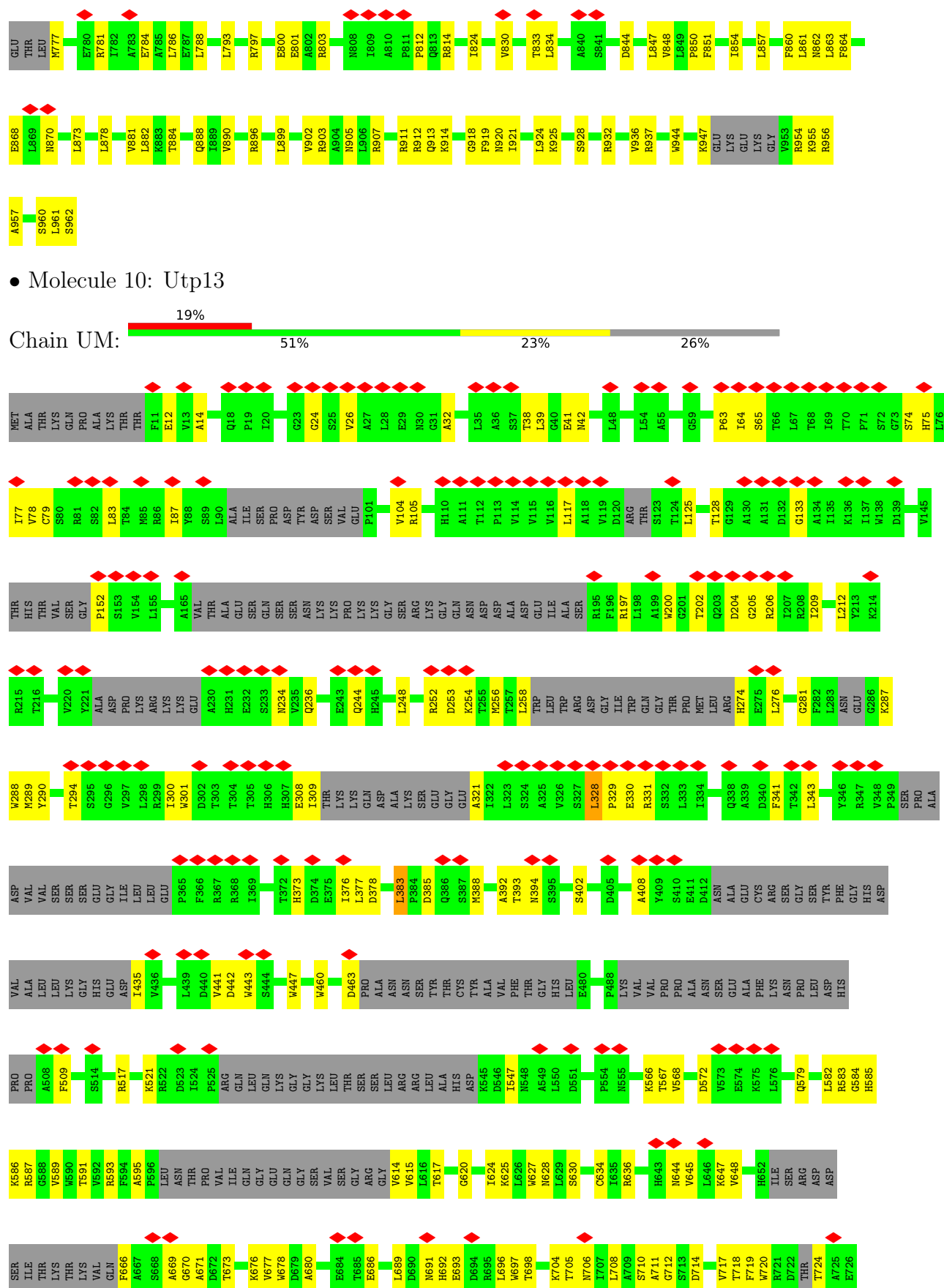
- Molecule 8: U3 small nucleolar RNA-associated protein 11

Chain UK:  59% 21% 20%

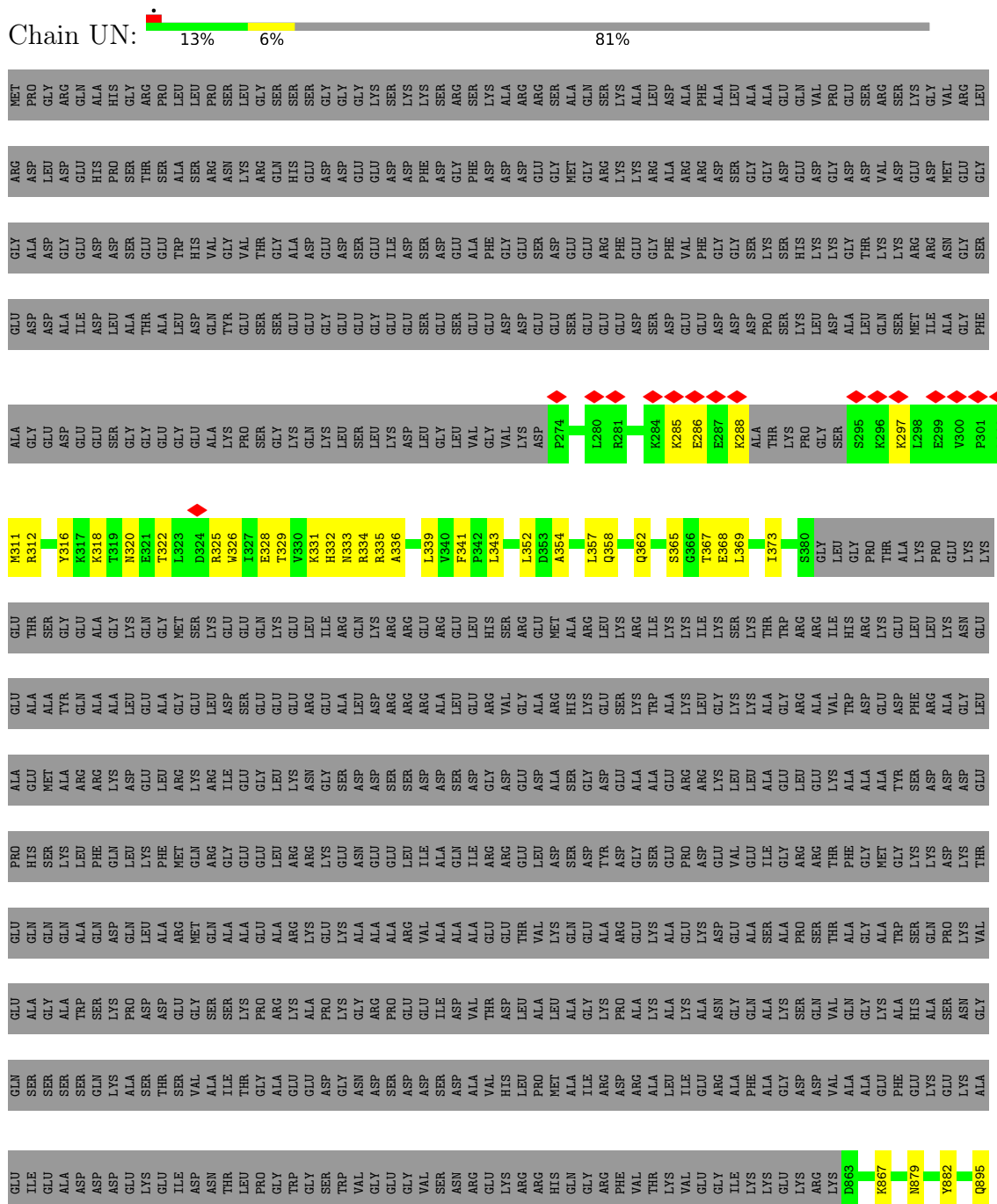


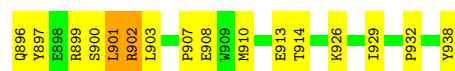
• Molecule 9: Utp12





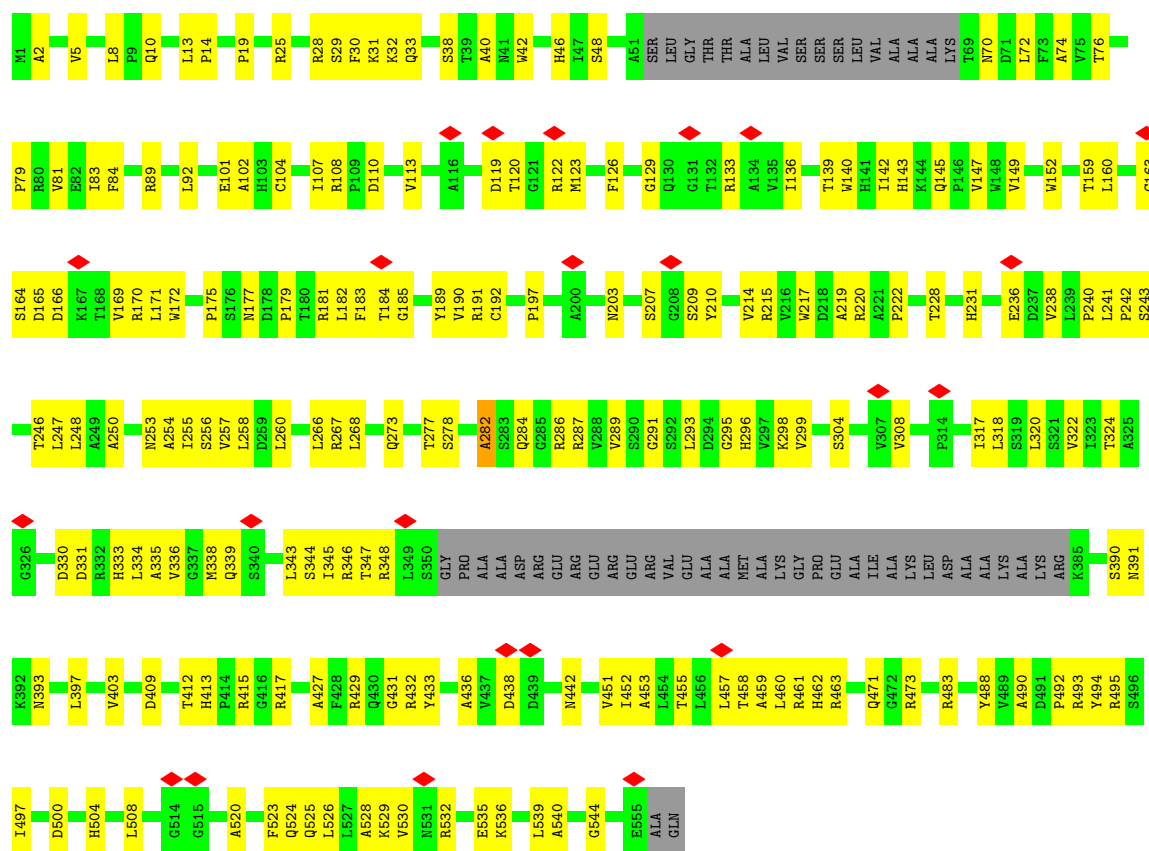
- Molecule 11: Utp14





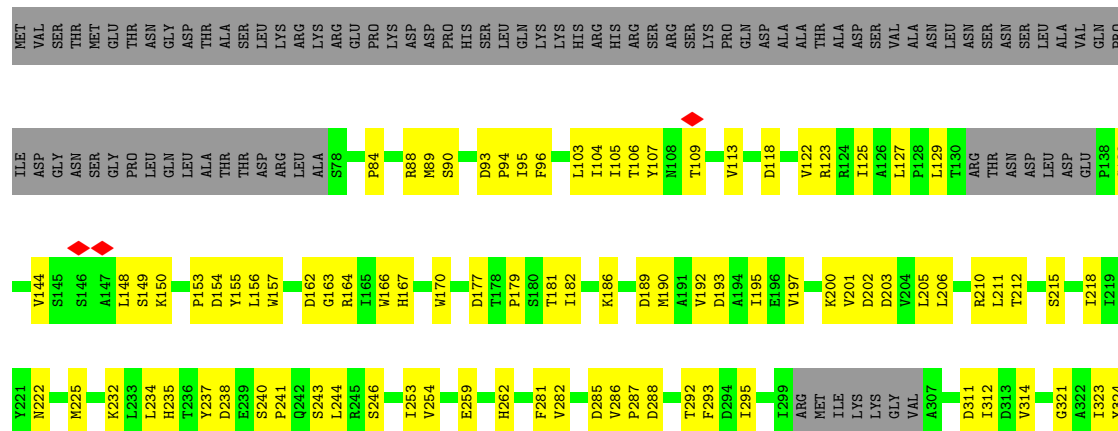
• Molecule 12: Utp15

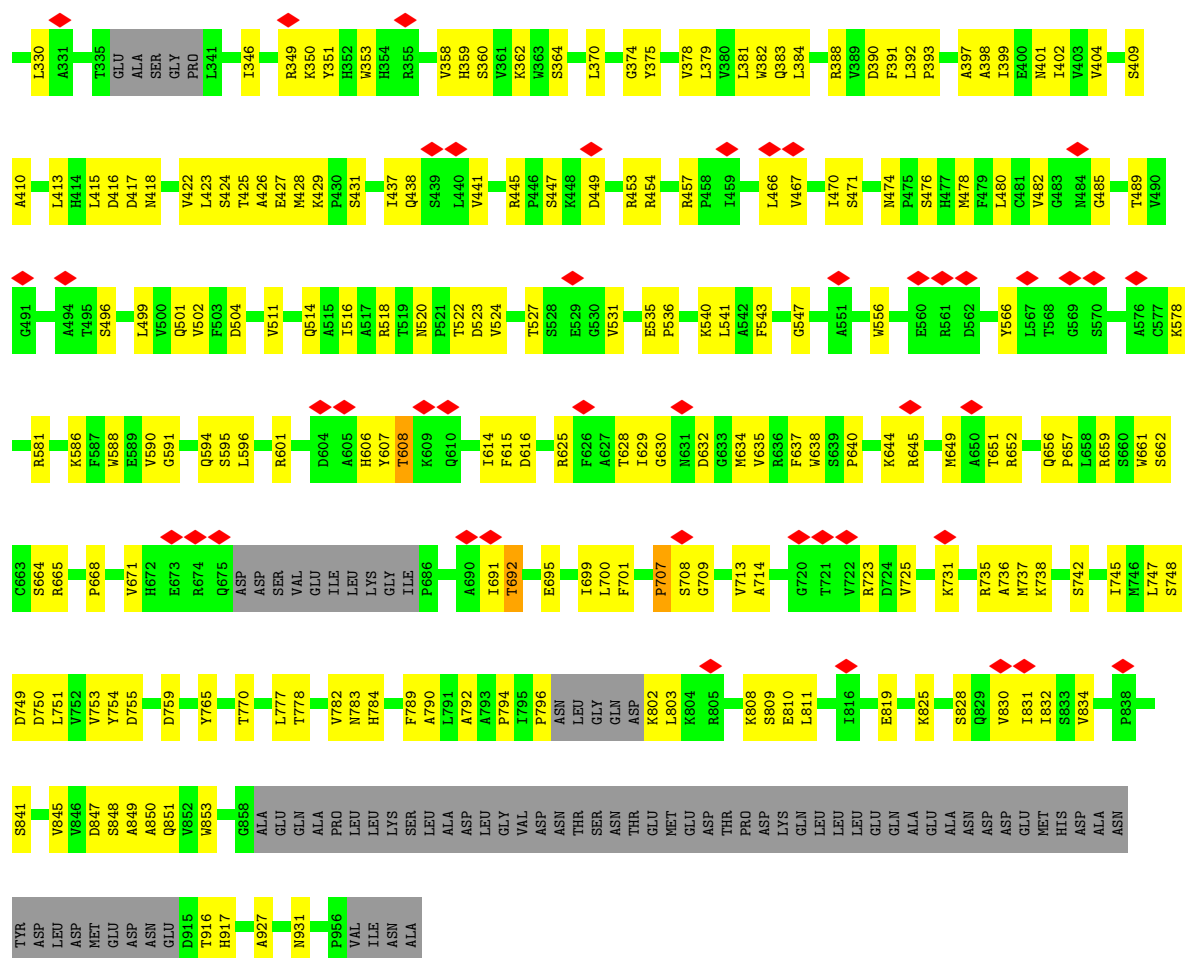
Chain UO: 55% 35% 10%



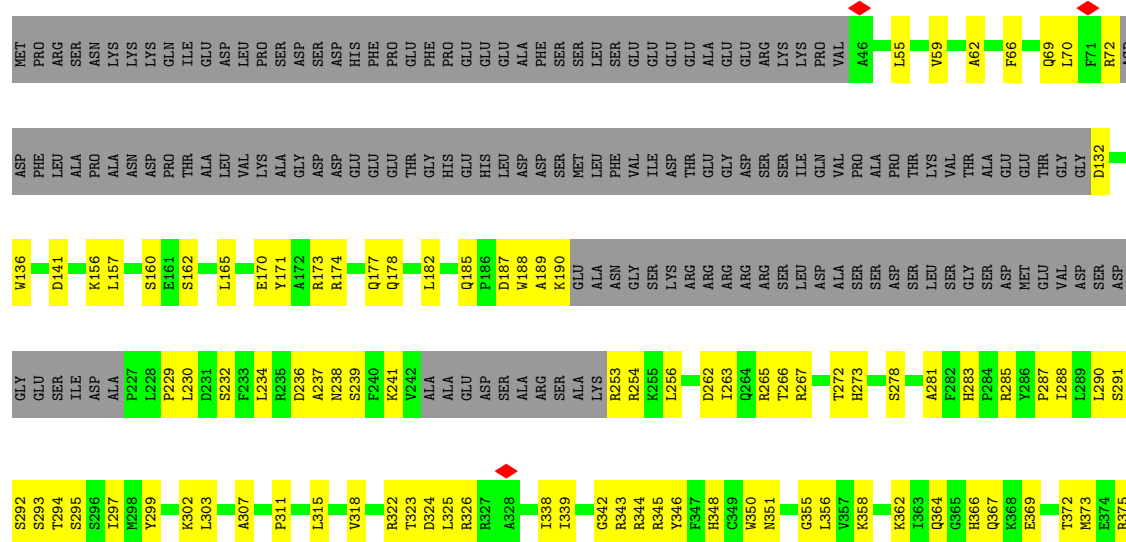
• Molecule 13: Utp17

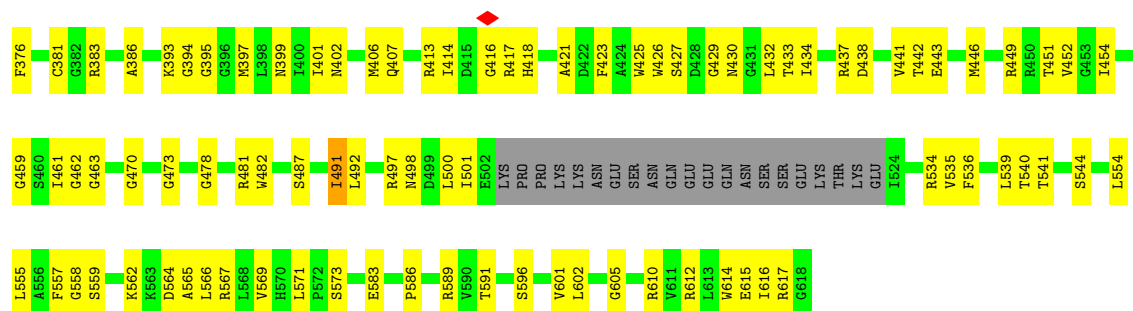
Chain UQ: 5% 52% 30% 18%



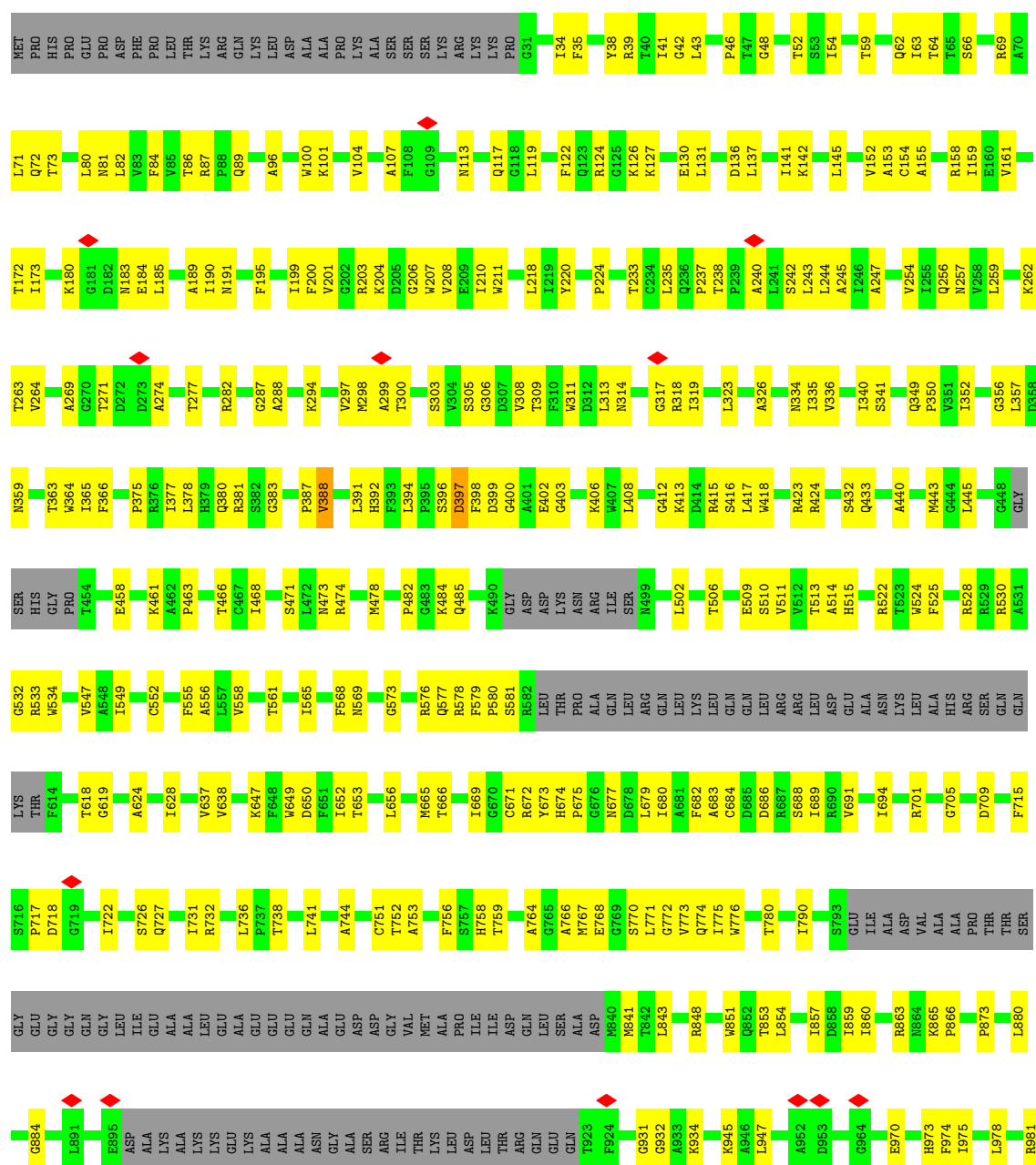


• Molecule 14: Utp18

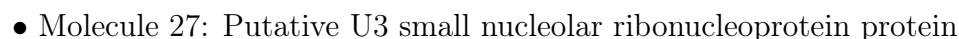




• Molecule 15: Putative U3 snoRNP protein



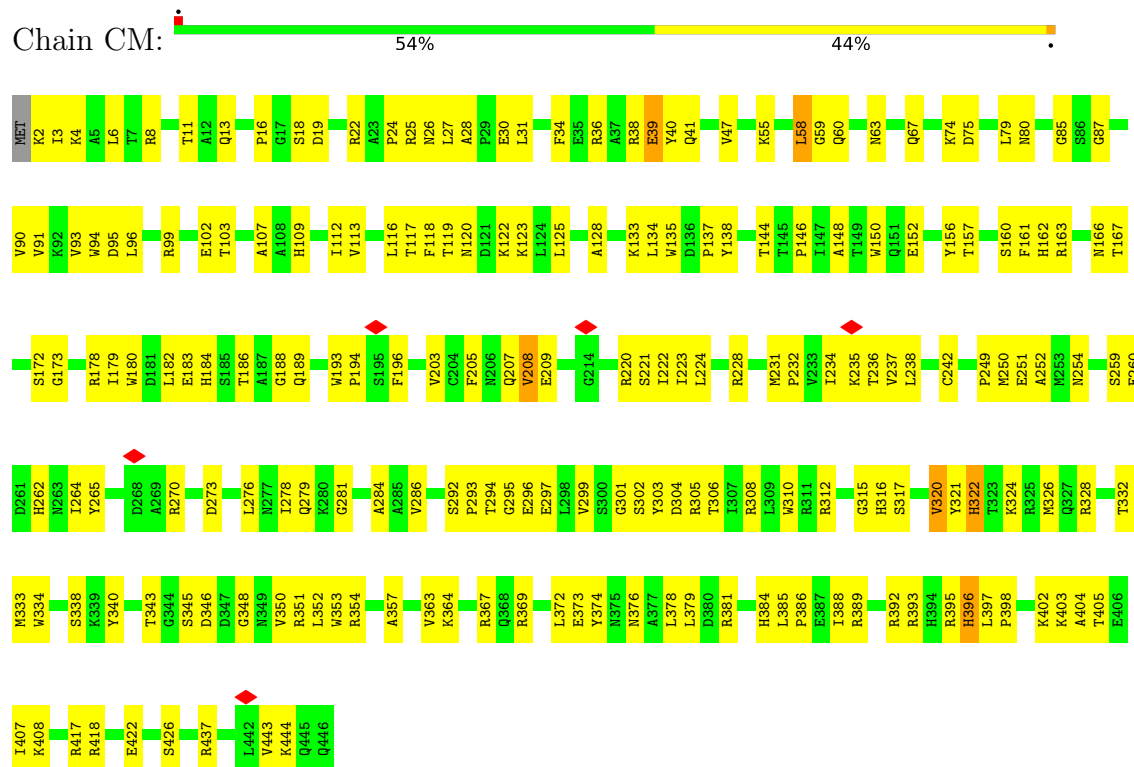
Response	Percentage
U.S. should take more action to protect the environment	62%
U.S. should take less action to protect the environment	37%



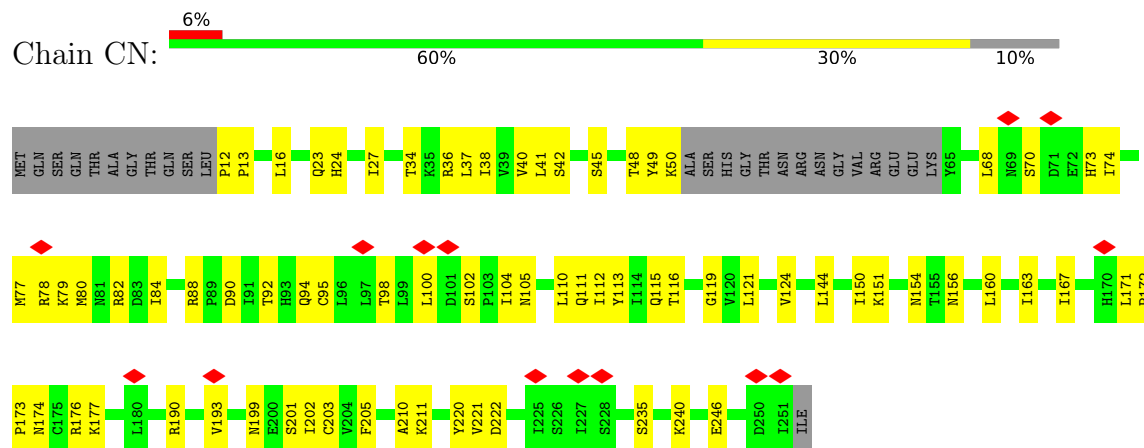
Frequency	Percentage
Often	20%
Sometimes	9%
Rarely/Not at all	71%



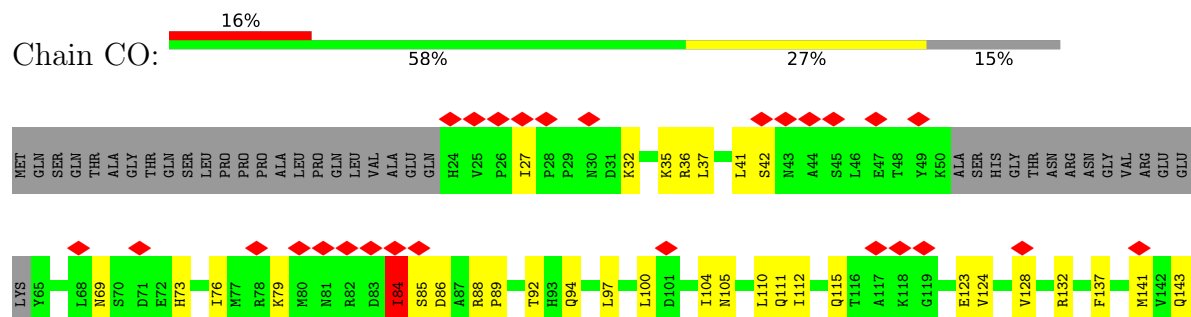
- Molecule 28: Sof1



- Molecule 29: Emg1

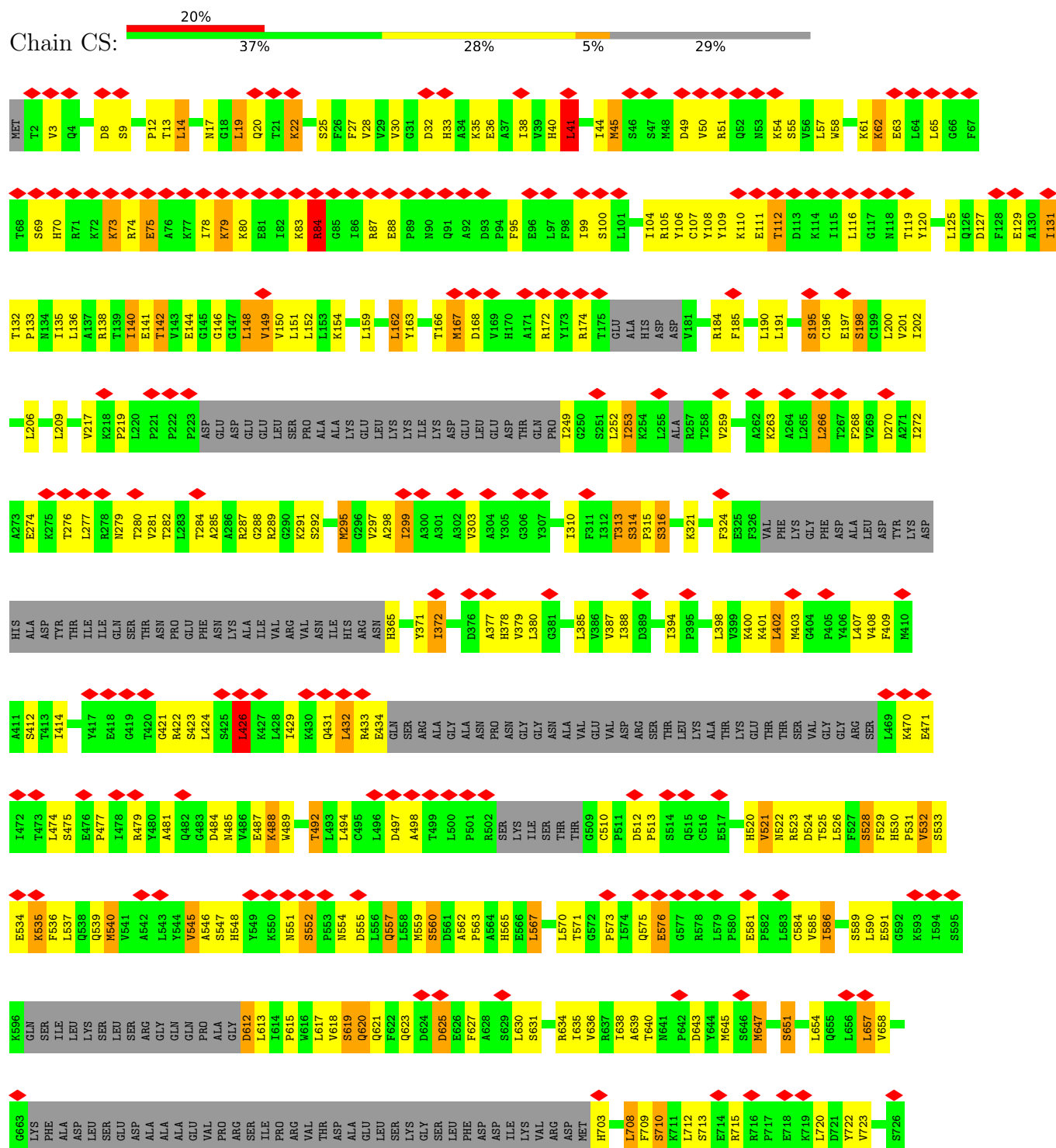


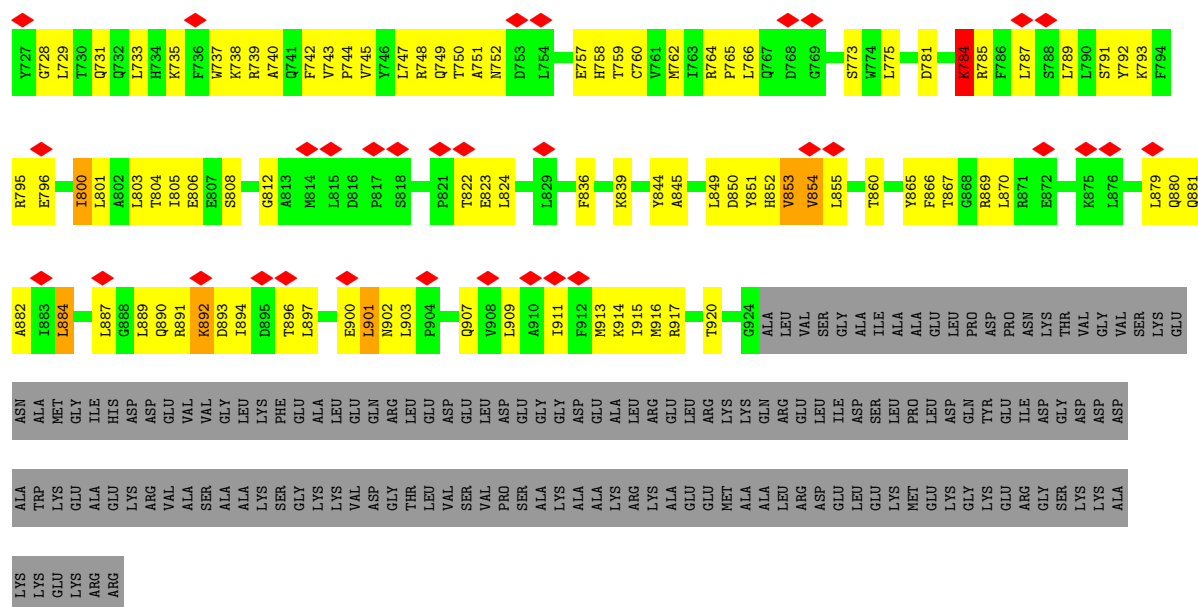
- Molecule 29: Emg1





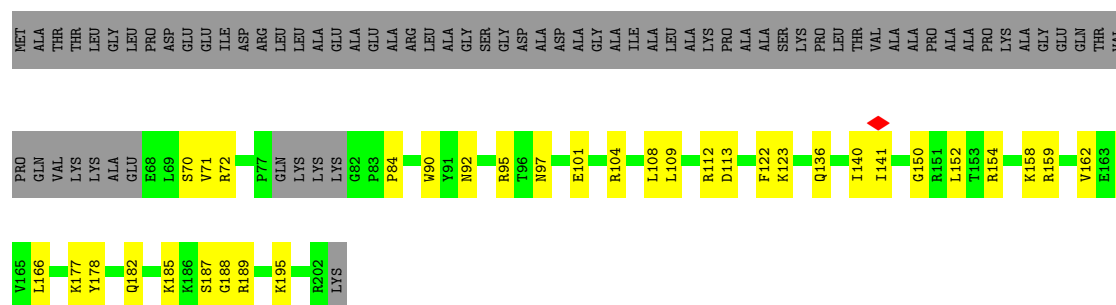
- Molecule 32: Kre33





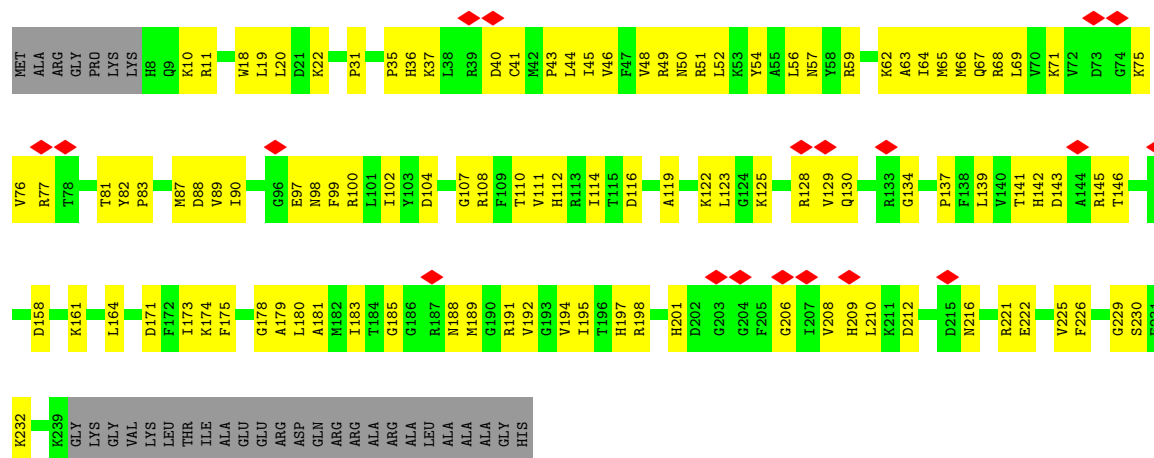
• Molecule 33: Fcf2

Chain CT: 47% 17% 35%



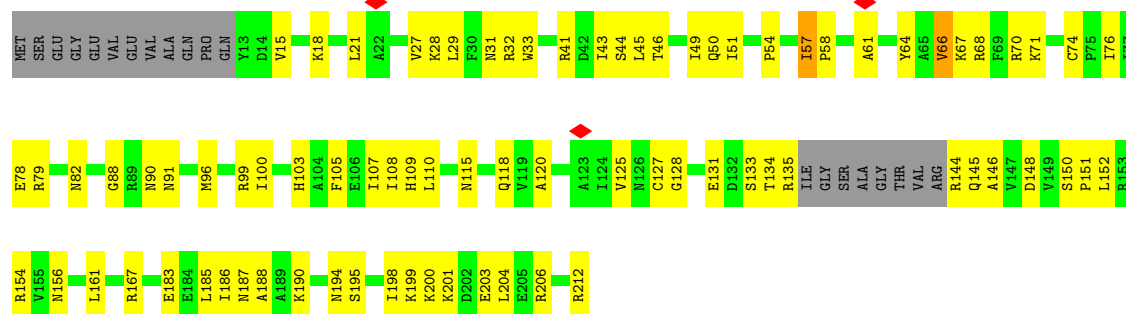
• Molecule 34: 40S ribosomal protein S4

Chain Cb: 7% 47% 41% 12%



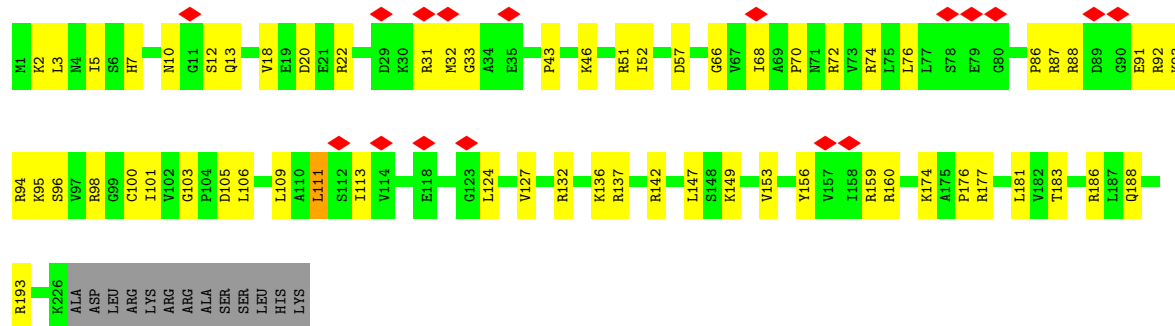
• Molecule 35: 40S ribosomal protein s5-like protein

Chain Cc: 

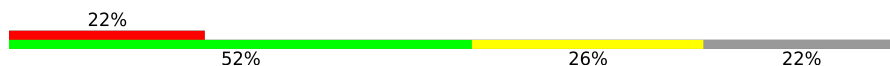


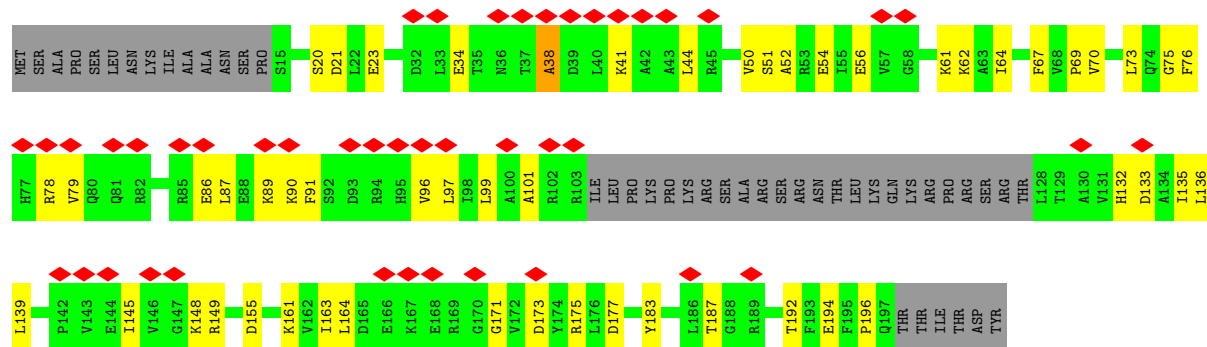
• Molecule 36: 40S ribosomal protein S6

Chain Cd: 



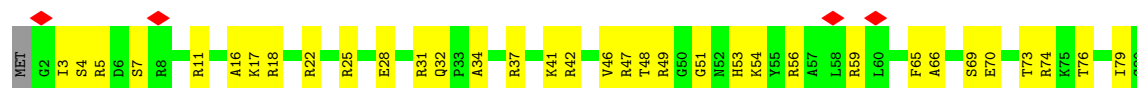
• Molecule 37: 40S ribosomal protein S7

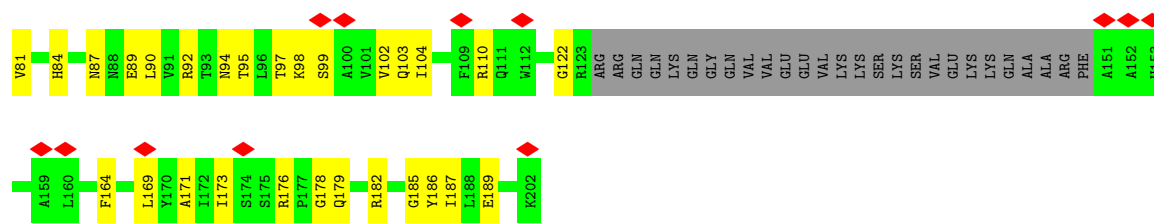
Chain Ce: 



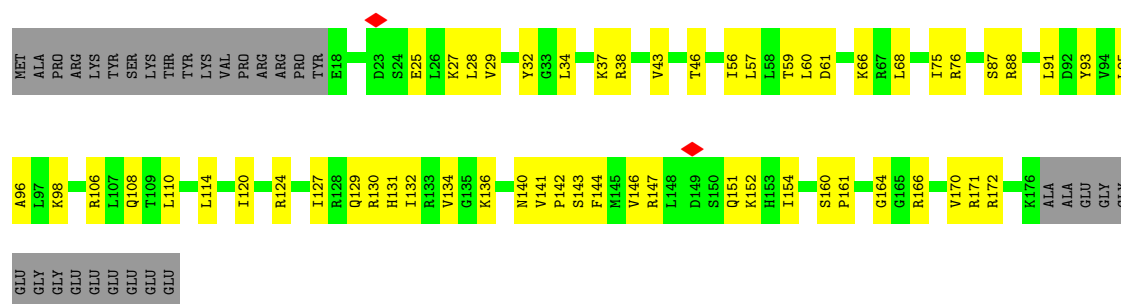
• Molecule 38: 40S ribosomal protein S8

Chain Cf: 

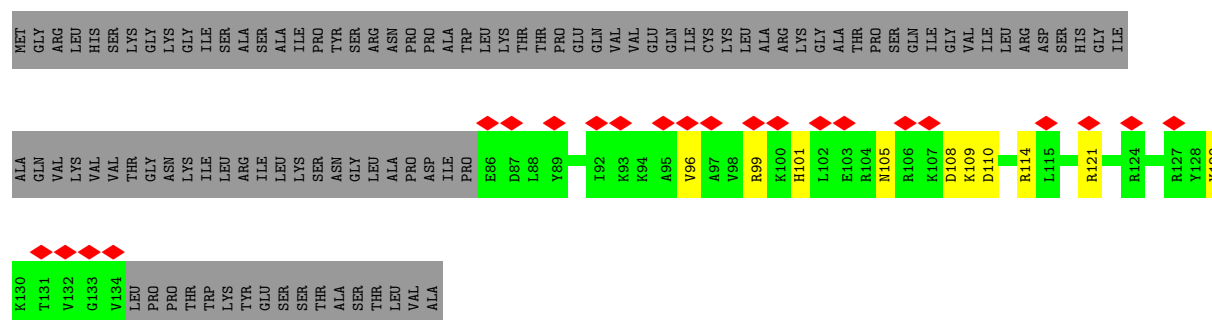




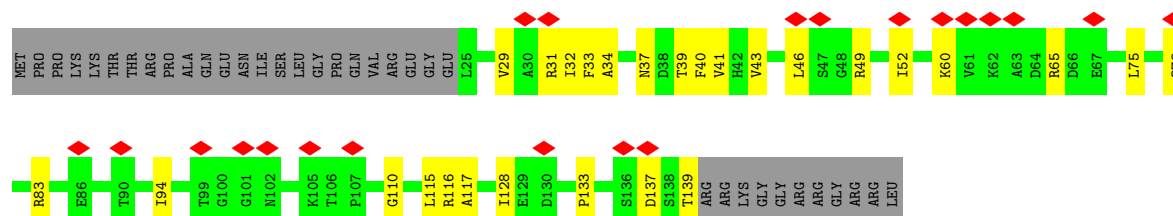
- Molecule 39: 40S ribosomal protein s9-like protein



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

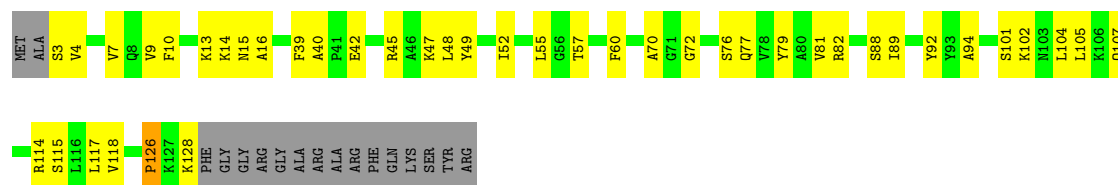


- Molecule 41: 40S ribosomal protein S14-like protein

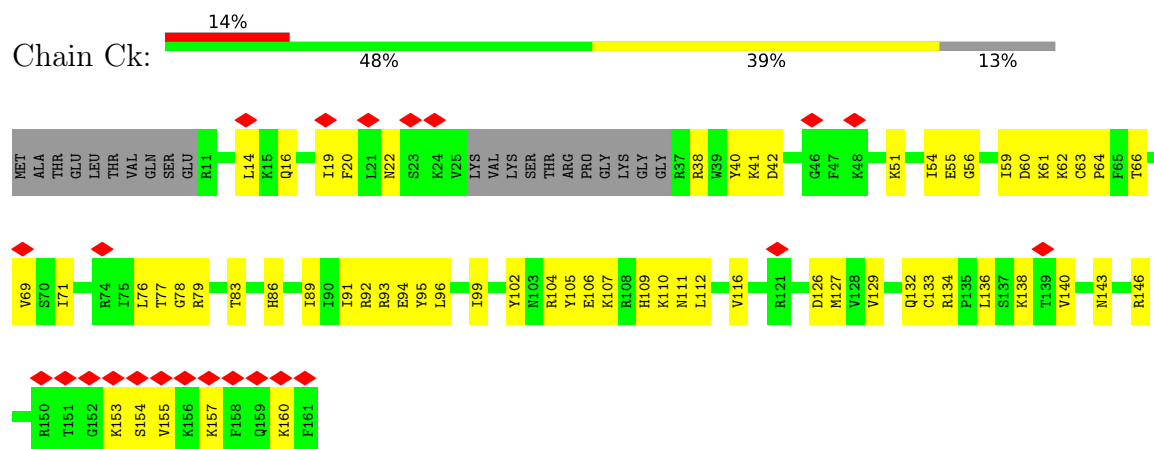


- Molecule 42: 40S ribosomal protein S16-like protein

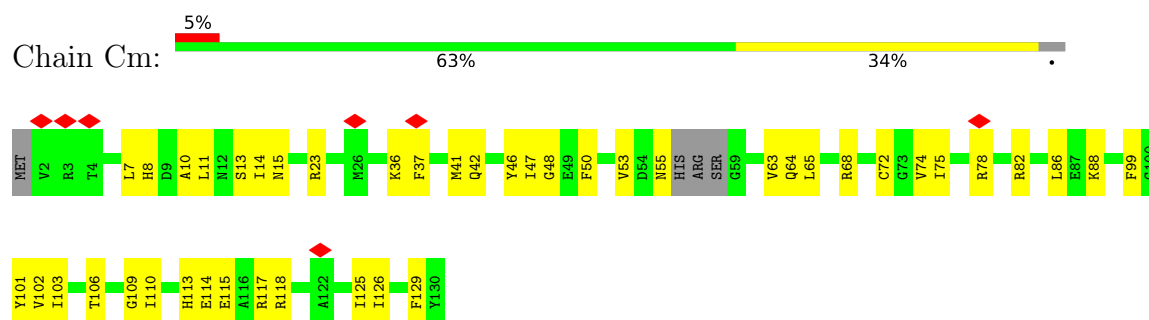




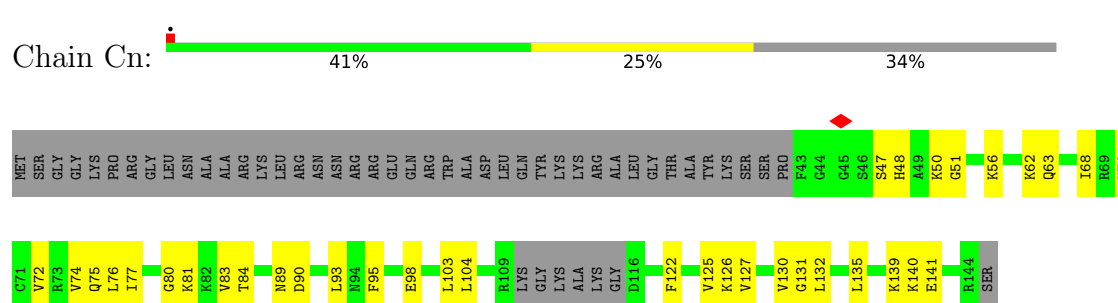
- Molecule 43: 40S ribosomal protein S11-like protein



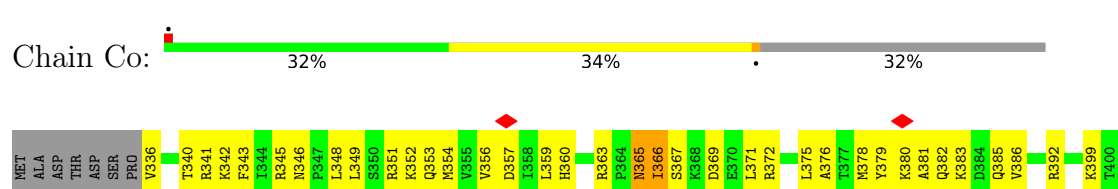
- Molecule 44: 40S ribosomal protein S22-like protein



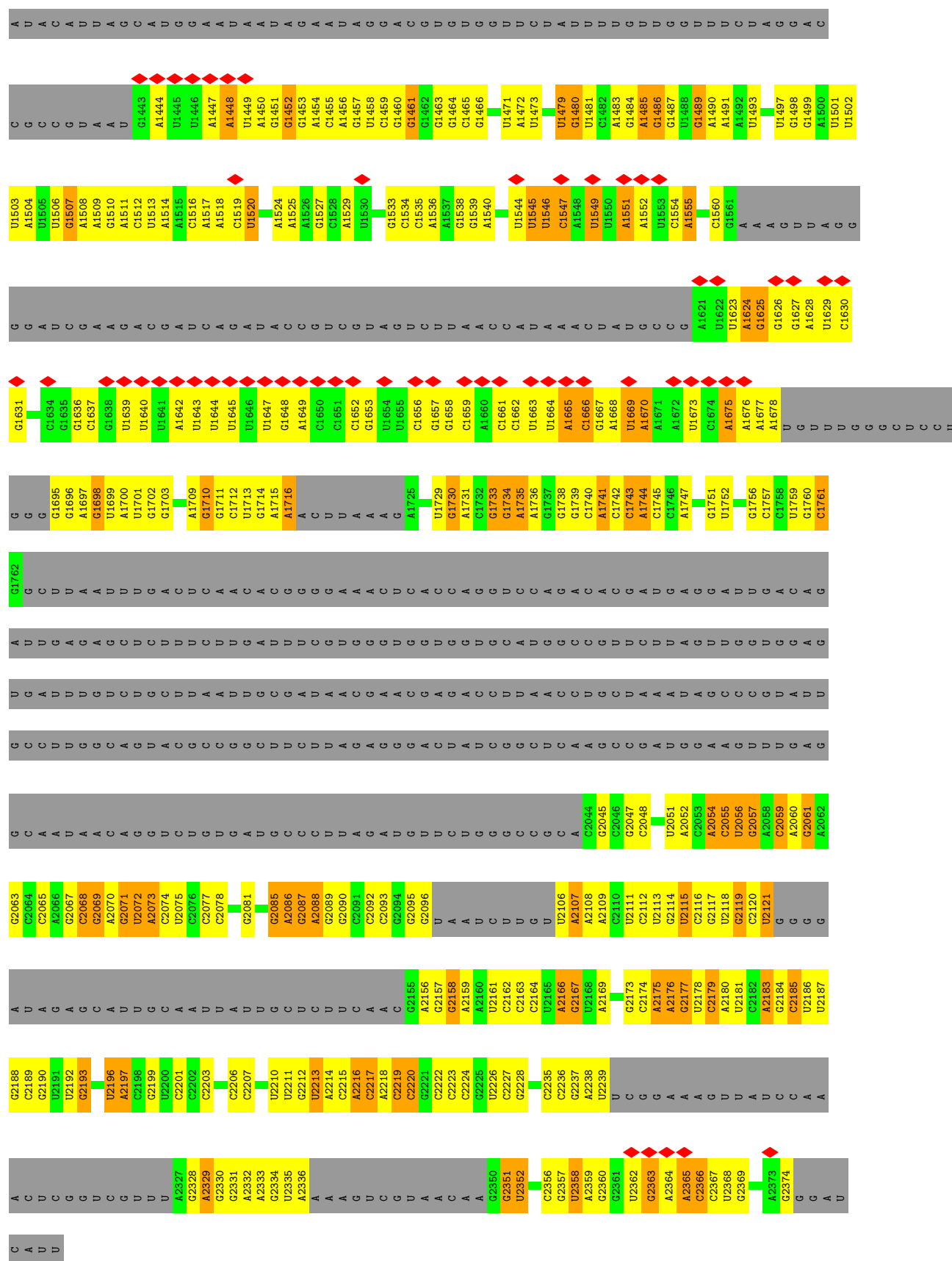
- Molecule 45: 40S ribosomal protein s23-like protein



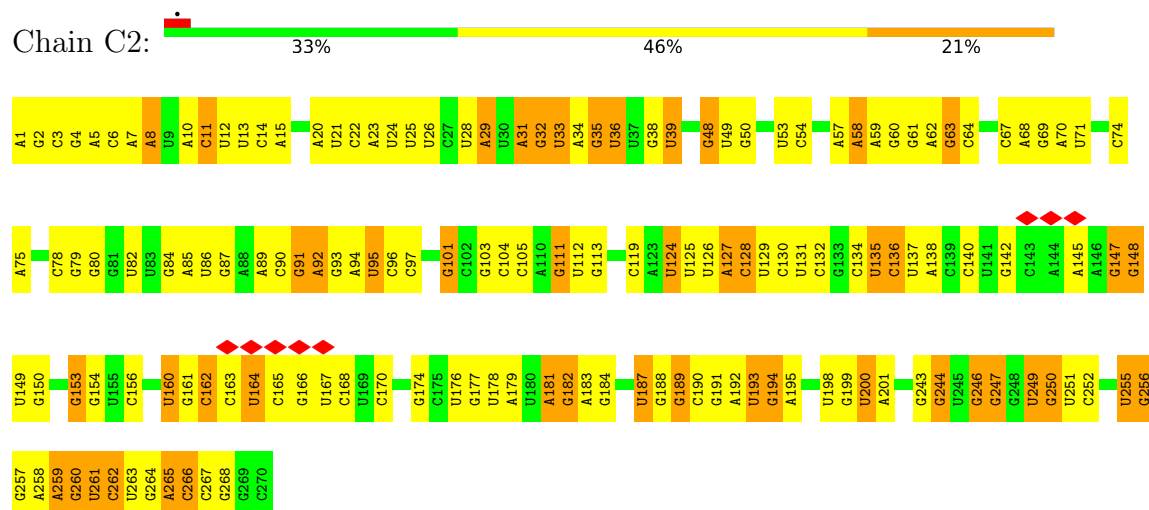
- Molecule 46: 40S ribosomal protein S24



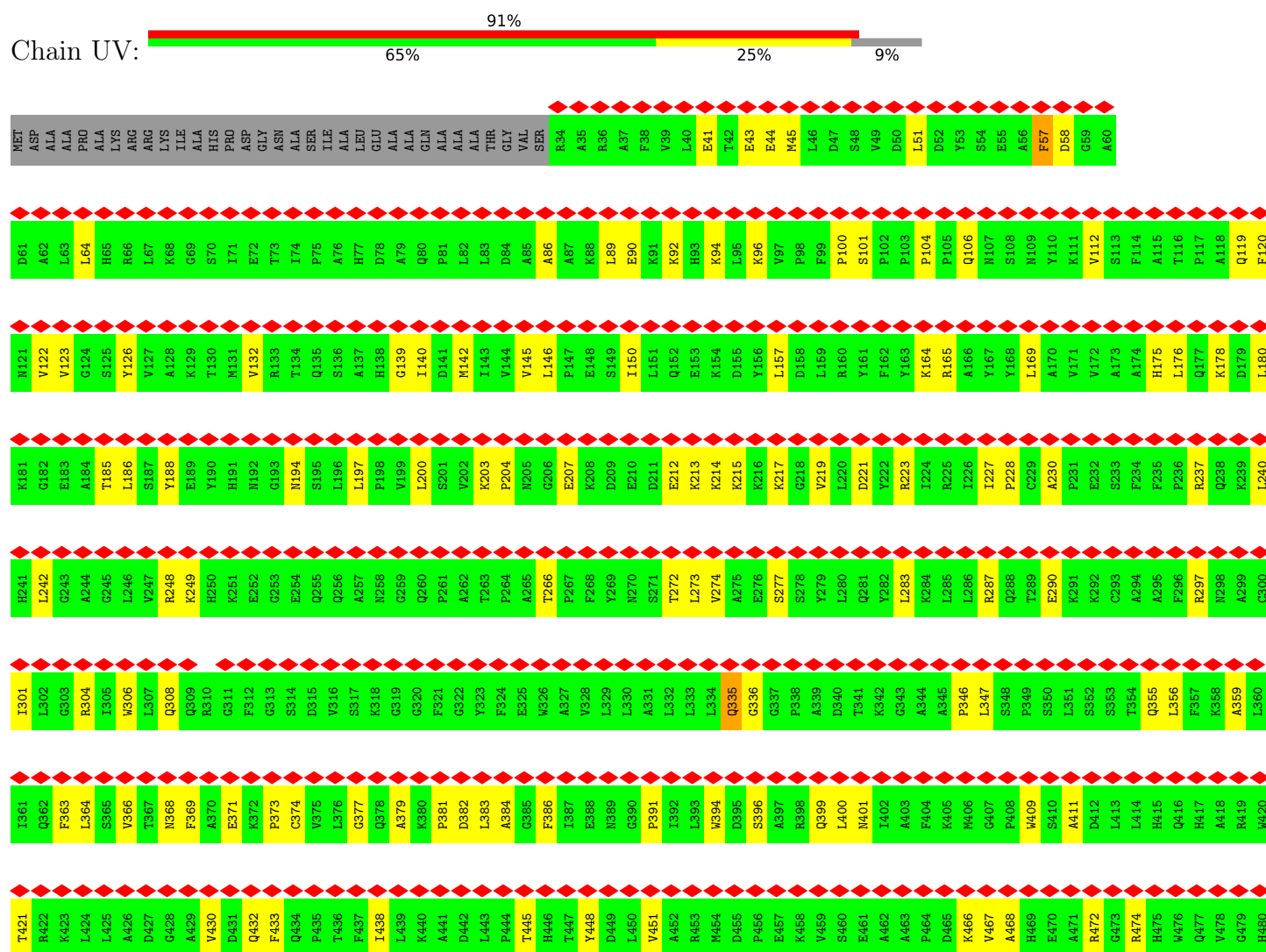


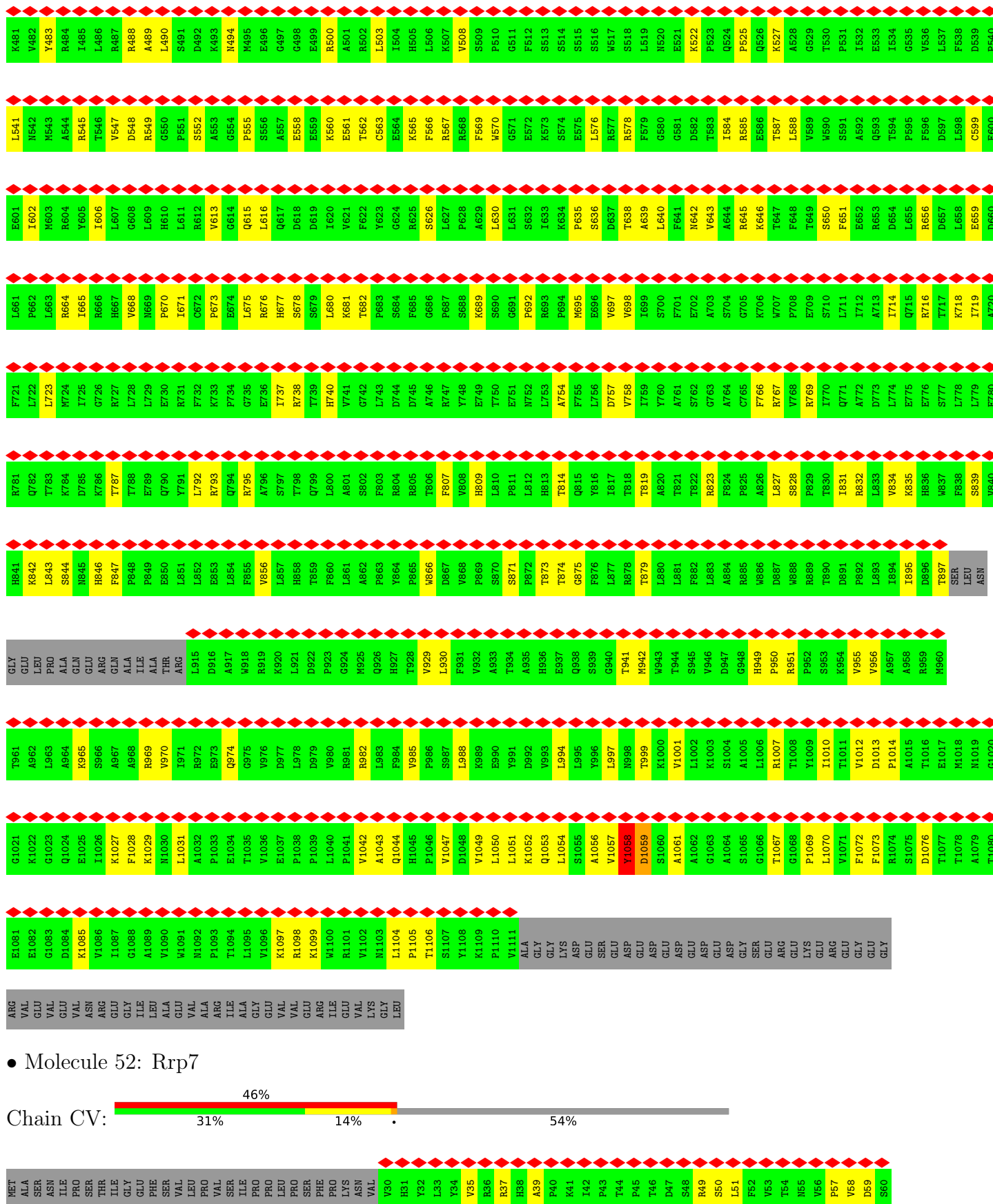


● Molecule 50: U3 snoRNA



• Molecule 51: U3 small nucleolar RNA-associated protein 22

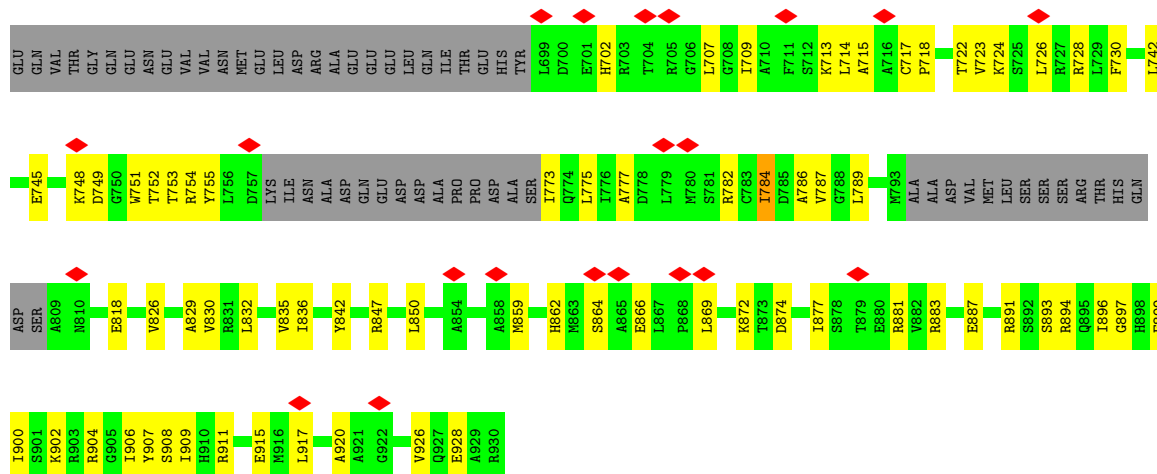




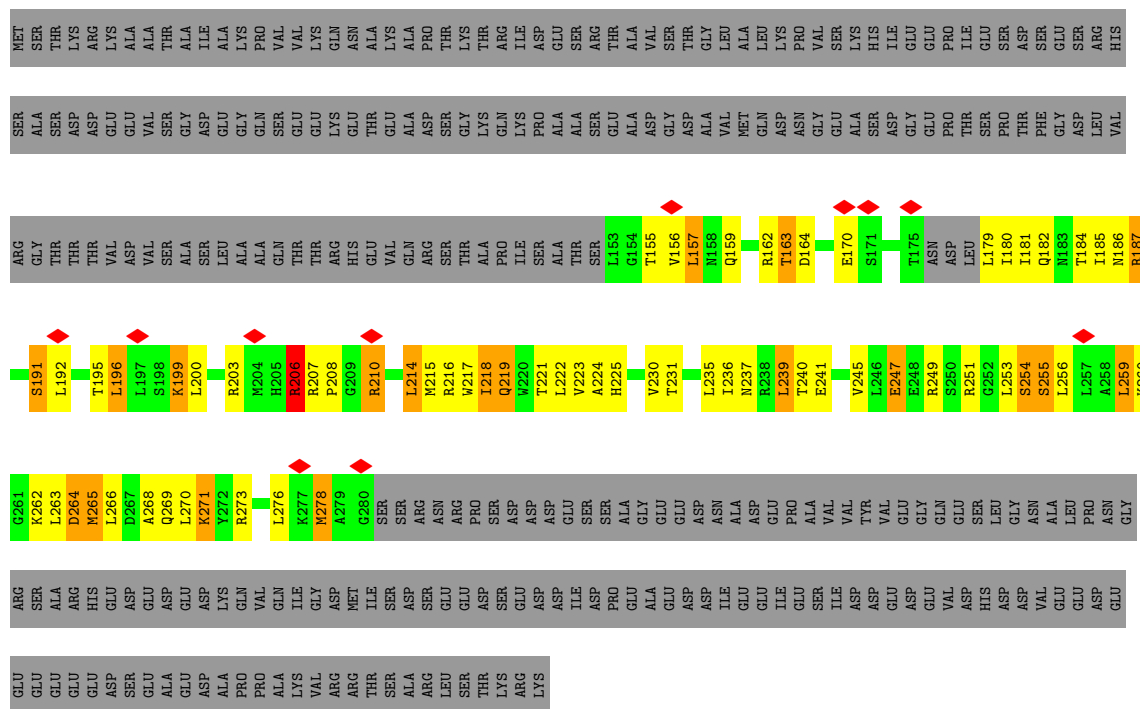
Chain UT:



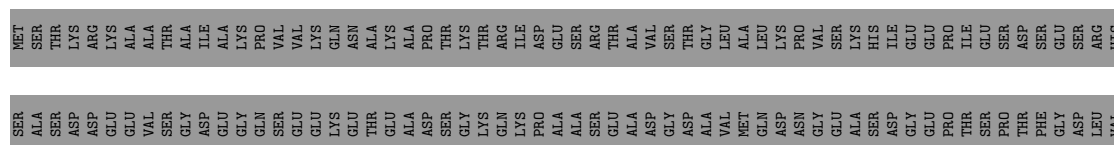


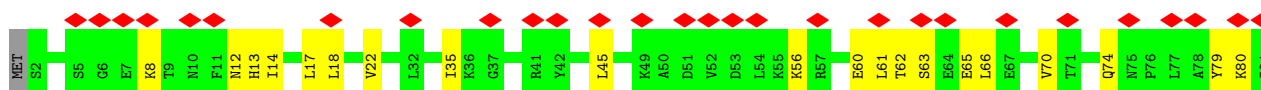


• Molecule 56: Utp5



• Molecule 56: Utp5





[illegible]

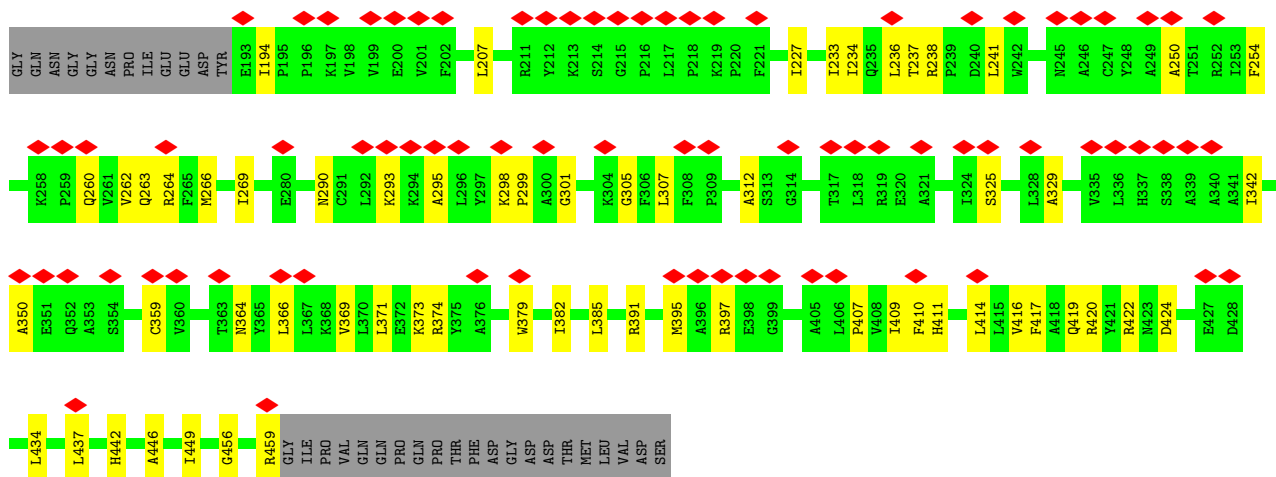
- Molecule 59: Enp1



MET	PRO	LYS	ALA	ALA	SER	SER	HIS	LYS	ARG	ARG	HIS	ASN	PRO	GLU	ASP	ASP	LEU	LEU	LYS	ASN	ARG	GLU	GLY	THR	ALA	THR	GLY	ILE	LEU	LEU	LYS	ASN	ARG	GLU	GLY	ARG	PRO	PRO	SER	SER	LYS	LYS	VAL	VAL	ALA	GLU	GLU	GLU	ASN	TYR	VAL	ASP	ASP	LYS	LYS	ALA	SER	ARG	LYS	ILE	LEU	LEU	ALA	MET
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SER	ARG	GLU	LEU	MET	ASP	GLU	GLU	GLN	GLN	LEU	LYS	ASN	LYS	GLN	VAL	THR	VAL	ALA	SER	THR	THR	ALA	PHE	ASP	PHE	ASP	PRO	SER	ARG	MET	ASP	HIS	GLU	GLU	ASP	ASP	VAL	ASN	ASN	GLU	GLU	TRP	GLY	ASP	GLU	ASP	GLU	GLU	ASP	ASP	ALA	GLY	ASP	ASN	ASN	ASP	ASP	ASP	GLU
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VAL	ASP	ALA	ALA	ALA	ASP	LEU	GLU	ILE	PHE	ASN	ARG	PHE	VAL	GLN	PRO	PRO	THR	MET	LYS	ASP	ASP	LEU	LEU	THR	HIS	GLY	TRP	ASP	GLN	LYS	PRO	ALA	ASP	GLY	GLY	GLU	GLU	GLU	LYS	THR	ASN	LEU	ALA	ASP	LEU	ILE	ALA	GLU	LYS	GLU	ALA	MET	THR	LYS
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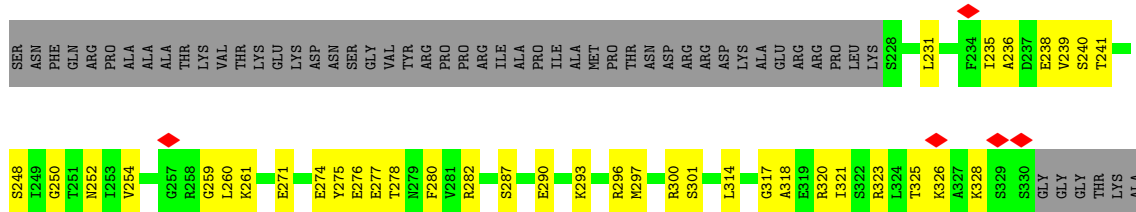
- Molecule 60: U3 small nucleolar ribonucleoprotein protein lcp5-like protein



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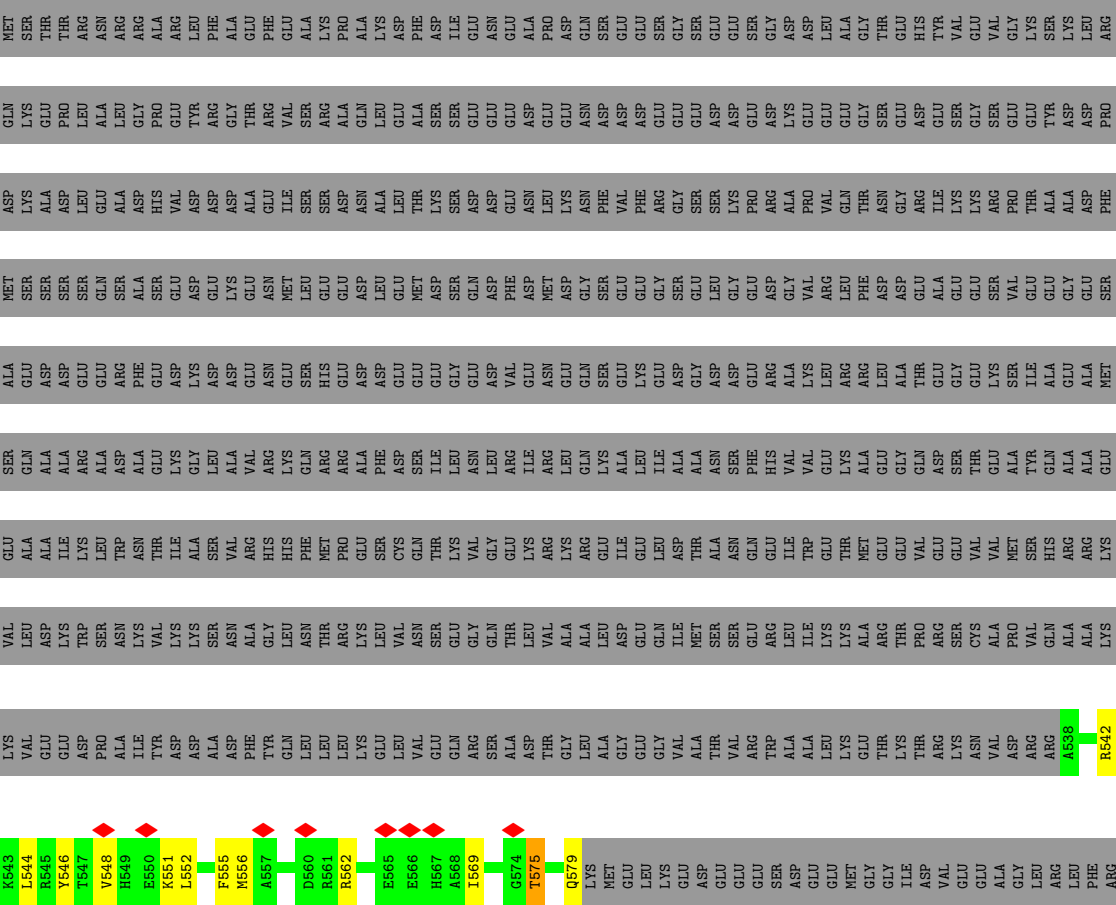
TLE	LYS	LEU	ARG	GLU	LYS	ALA	LYS	TYR	SER	ALA	ARG	SER	GLU	LYS	SER	ASP	ASP	GLU	GLN	SER	LEU	SER	ASP	LEU	VAL	VAL	ARG	LYS	VAL	GLU	ARG	LEU	TYR	LEU	GLY	LYS	THR	ARG	PRO	LEU	GLU	ASP	LYS	LEU	ARG	PHE	GLN	ILE	ASP	LYS	VAL	LEU	ARG	ALA	ALA	ASP	ASP
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ALA	GLU	ARG	LYS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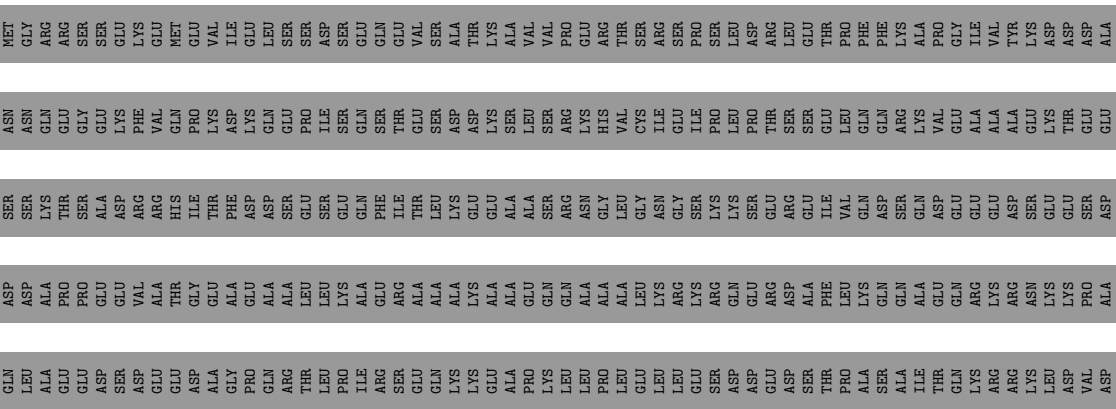


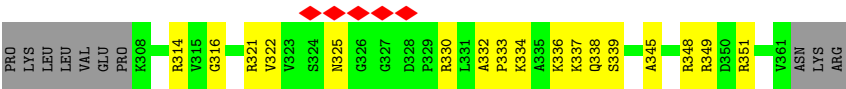


• Molecule 61: Bfr2

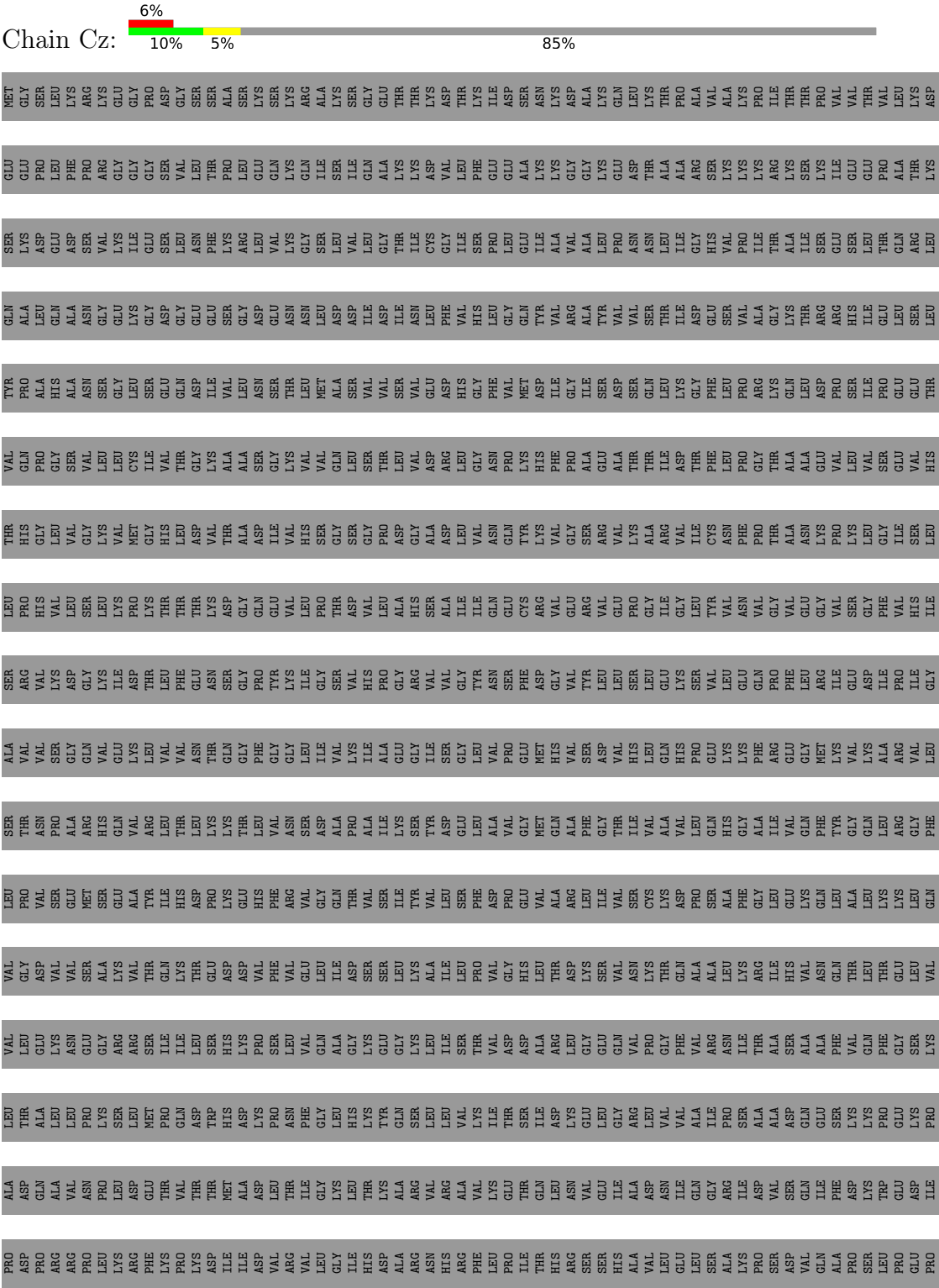


• Molecule 62: Utp16





• Molecule 63: Rrp5





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24283	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	0.834	Depositor
Minimum map value	-0.505	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.012	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	0.53	1/6521 (0.0%)	0.83	9/8867 (0.1%)
2	UB	0.31	0/4154	0.60	0/5583
3	UC	0.57	0/595	0.79	0/786
4	UD	0.29	1/6211 (0.0%)	0.60	0/8408
5	UF	0.29	0/2657	0.55	0/3596
6	UG	0.51	2/3790 (0.1%)	0.75	2/5120 (0.0%)
7	UJ	0.29	0/8567	0.63	0/11619
8	UK	0.59	0/1701	0.82	3/2251 (0.1%)
9	UL	0.29	0/6299	0.67	2/8531 (0.0%)
10	UM	0.25	0/5366	0.60	0/7282
11	UN	0.35	0/1425	0.63	0/1913
12	UO	0.31	0/3903	0.64	0/5312
13	UQ	0.26	0/6136	0.63	3/8348 (0.0%)
14	UR	0.36	0/3564	0.68	0/4816
15	UU	0.39	0/6903	0.71	4/9392 (0.0%)
16	UX	0.58	0/1493	0.81	0/2011
17	UZ	0.35	0/1857	0.74	4/2526 (0.2%)
18	CA	0.49	0/1814	0.74	0/2456
18	CB	0.30	0/1853	0.61	0/2511
19	CC	0.36	0/2911	0.66	0/3937
20	CD	0.34	0/3205	0.66	0/4338
21	CE	0.42	0/891	0.66	0/1214
21	CF	0.37	0/876	0.74	0/1195
22	CG	0.28	0/3307	0.63	0/4462
23	CH	0.40	0/2939	0.69	0/3988
24	CI	0.56	0/6631	0.96	7/8943 (0.1%)
25	CJ	0.70	0/1462	0.91	2/1967 (0.1%)
26	CK	0.70	0/2376	0.92	3/3214 (0.1%)
27	CL	0.44	0/1812	0.70	0/2437
28	CM	0.52	0/3573	0.81	6/4829 (0.1%)
29	CN	0.30	0/1797	0.66	0/2443
29	CO	0.27	0/1714	0.64	2/2325 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	CP	0.28	0/1528	0.78	0/2057
31	CQ	0.25	0/1379	0.59	0/1850
32	CR	0.32	0/6108	0.83	10/8266 (0.1%)
32	CS	0.32	0/6108	0.83	10/8266 (0.1%)
33	CT	0.47	0/1053	0.74	2/1413 (0.1%)
34	Cb	0.25	0/1890	0.61	0/2548
35	Cc	0.42	0/1485	0.68	0/2008
36	Cd	0.26	0/1850	0.60	0/2474
37	Ce	0.33	0/1298	0.76	2/1750 (0.1%)
38	Cf	0.23	0/1429	0.58	0/1915
39	Cg	0.45	0/1259	0.72	0/1687
40	Ch	0.23	0/412	0.72	0/549
41	Ci	0.25	0/801	0.72	0/1087
42	Cj	0.57	0/958	0.83	0/1293
43	Ck	0.23	0/1190	0.55	0/1592
44	Cm	0.35	0/1001	0.66	0/1345
45	Cn	0.74	0/712	0.90	0/954
46	Co	0.29	0/754	0.63	1/1011 (0.1%)
47	Cp	0.32	0/458	0.70	0/617
48	CU	0.33	0/887	0.72	0/1178
49	C1	0.40	0/35454	0.55	9/55209 (0.0%)
50	C2	0.42	0/5459	0.61	5/8498 (0.1%)
51	UV	0.30	0/8638	0.77	6/11725 (0.1%)
52	CV	0.34	0/1172	0.84	0/1592
53	CW	0.26	0/2996	0.63	1/4075 (0.0%)
54	UT	0.26	0/16314	0.60	1/22075 (0.0%)
55	UH	0.28	0/2852	0.61	2/3846 (0.1%)
56	UE	0.36	0/980	0.88	2/1316 (0.2%)
56	UI	0.36	0/980	0.88	2/1316 (0.2%)
57	US	0.25	0/3765	0.59	2/5100 (0.0%)
58	CI	0.28	0/638	0.76	1/857 (0.1%)
59	CX	0.21	0/2172	0.56	0/2946
60	CY	0.33	0/982	0.74	0/1298
61	CZ	0.31	0/362	0.82	0/483
62	UP	0.28	0/428	0.62	0/570
63	Cz	0.25	0/2310	0.59	0/3120
All	All	0.37	4/226365 (0.0%)	0.68	103/314506 (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	10
5	UF	0	1
6	UG	0	2
8	UK	0	2
9	UL	0	2
10	UM	0	4
11	UN	0	1
12	UO	0	1
13	UQ	0	2
15	UU	0	4
16	UX	0	2
17	UZ	0	2
18	CB	0	1
21	CE	0	1
21	CF	0	2
23	CH	0	1
24	CI	0	6
25	CJ	0	2
26	CK	0	1
28	CM	0	1
29	CO	0	2
32	CR	0	1
32	CS	0	1
37	Ce	0	1
41	Ci	0	1
42	Cj	0	3
45	Cn	0	1
46	Co	0	1
51	UV	0	4
52	CV	0	2
54	UT	0	5
55	UH	0	1
58	Cl	0	1
60	CY	0	1
63	Cz	0	1
All	All	0	74

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	UA	488	TRP	CA-C	-10.82	1.38	1.52
6	UG	154	ALA	C-N	-9.49	1.28	1.33
4	UD	496	ALA	CA-CB	-8.13	1.42	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	UG	290	THR	C-N	-6.87	1.23	1.33

The worst 5 of 103 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	CI	995	VAL	CA-C-N	37.54	171.29	121.74
24	CI	995	VAL	C-N-CA	37.54	171.29	121.74
32	CS	372	ILE	CA-C-N	17.81	145.15	120.39
32	CS	372	ILE	C-N-CA	17.81	145.15	120.39
32	CR	372	ILE	CA-C-N	17.79	145.12	120.39

There are no chirality outliers.

5 of 74 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	UA	273	GLY	Peptide
1	UA	320	GLY	Peptide
1	UA	386	THR	Peptide
1	UA	424	GLU	Peptide
1	UA	443	GLY	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	253	0
2	UB	4079	0	4201	112	0
3	UC	588	0	647	16	0
4	UD	6071	0	6080	206	0
5	UF	2591	0	2642	68	0
6	UG	3717	0	3756	134	0
7	UJ	8416	0	8591	233	0
8	UK	1687	0	1820	48	0
9	UL	6175	0	6188	217	0
10	UM	5273	0	5284	155	0
11	UN	1401	0	1455	55	0
12	UO	3819	0	3873	154	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	UQ	6008	0	6033	202	0
14	UR	3491	0	3507	141	0
15	UU	6734	0	6745	234	0
16	UX	1470	0	1532	52	0
17	UZ	1815	0	1896	59	0
18	CA	1778	0	1830	73	0
18	CB	1816	0	1847	59	0
19	CC	2866	0	2960	97	0
20	CD	3150	0	3262	109	0
21	CE	879	0	918	36	0
21	CF	864	0	900	33	0
22	CG	3245	0	3262	105	0
23	CH	2888	0	2979	103	0
24	CI	6486	0	6649	199	0
25	CJ	1434	0	1482	65	0
26	CK	2329	0	2373	88	0
27	CL	1786	0	1826	76	0
28	CM	3501	0	3498	172	0
29	CN	1762	0	1807	61	0
29	CO	1683	0	1726	42	0
30	CP	1504	0	1596	34	0
31	CQ	1361	0	1431	39	0
32	CR	5989	0	6130	206	0
32	CS	5989	0	6130	196	0
33	CT	1035	0	1063	33	0
34	Cb	1851	0	1905	78	0
35	Cc	1464	0	1504	54	0
36	Cd	1819	0	1920	54	0
37	Ce	1279	0	1322	40	0
38	Cf	1398	0	1401	49	0
39	Cg	1242	0	1354	49	0
40	Ch	406	0	436	8	0
41	Ci	791	0	795	20	0
42	Cj	943	0	1002	35	0
43	Ck	1163	0	1230	48	0
44	Cm	985	0	1021	30	0
45	Cn	702	0	750	27	0
46	Co	741	0	785	42	0
47	Cp	455	0	482	21	0
48	CU	882	0	944	39	0
49	C1	31732	0	16064	862	0
50	C2	4891	0	2476	128	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	UV	8424	0	8502	191	0
52	CV	1145	0	1155	44	0
53	CW	2924	0	2854	122	0
54	UT	16000	0	16404	429	0
55	UH	2809	0	2843	89	0
56	UE	972	0	1032	46	0
56	UI	972	0	1032	50	0
57	US	3672	0	3679	92	0
58	Cl	633	0	676	12	0
59	CX	2122	0	2211	38	0
60	CY	975	0	992	36	0
61	CZ	354	0	345	12	0
62	UP	422	0	457	19	0
63	Cz	2259	0	2235	67	0
64	UX	1	0	0	0	0
All	All	218474	0	204000	6157	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 15.

The worst 5 of 6157 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)
49:C1:2238:A:N6	49:C1:2328:G:C2	2.08	1.21
55:UH:555:GLY:O	55:UH:567:LEU:HA	1.42	1.14
49:C1:2238:A:N6	49:C1:2328:G:N3	1.95	1.13
49:C1:2169:A:H62	49:C1:2193:G:N2	1.54	1.06
7:UJ:185:GLN:O	7:UJ:189:ARG:HB3	1.59	1.01

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%)	733 (88%)	102 (12%)	0	100	100
2	UB	502/907 (55%)	472 (94%)	30 (6%)	0	100	100
3	UC	72/648 (11%)	58 (81%)	14 (19%)	0	100	100
4	UD	754/884 (85%)	708 (94%)	46 (6%)	0	100	100
5	UF	325/414 (78%)	303 (93%)	21 (6%)	1 (0%)	36	71
6	UG	475/558 (85%)	433 (91%)	39 (8%)	3 (1%)	21	58
7	UJ	1062/1802 (59%)	1000 (94%)	62 (6%)	0	100	100
8	UK	211/270 (78%)	196 (93%)	15 (7%)	0	100	100
9	UL	767/962 (80%)	704 (92%)	63 (8%)	0	100	100
10	UM	645/912 (71%)	595 (92%)	49 (8%)	1 (0%)	43	77
11	UN	171/938 (18%)	161 (94%)	9 (5%)	1 (1%)	21	58
12	UO	498/557 (89%)	459 (92%)	39 (8%)	0	100	100
13	UQ	775/960 (81%)	703 (91%)	71 (9%)	1 (0%)	48	83
14	UR	437/618 (71%)	400 (92%)	37 (8%)	0	100	100
15	UU	890/1049 (85%)	797 (90%)	93 (10%)	0	100	100
16	UX	188/193 (97%)	172 (92%)	16 (8%)	0	100	100
17	UZ	229/391 (59%)	206 (90%)	23 (10%)	0	100	100
18	CA	238/313 (76%)	218 (92%)	20 (8%)	0	100	100
18	CB	235/313 (75%)	216 (92%)	19 (8%)	0	100	100
19	CC	383/523 (73%)	361 (94%)	22 (6%)	0	100	100
20	CD	416/582 (72%)	384 (92%)	32 (8%)	0	100	100
21	CE	119/127 (94%)	112 (94%)	7 (6%)	0	100	100
21	CF	118/127 (93%)	109 (92%)	9 (8%)	0	100	100
22	CG	402/630 (64%)	366 (91%)	36 (9%)	0	100	100
23	CH	383/411 (93%)	344 (90%)	38 (10%)	1 (0%)	36	71
24	CI	812/1163 (70%)	732 (90%)	80 (10%)	0	100	100
25	CJ	177/183 (97%)	154 (87%)	23 (13%)	0	100	100
26	CK	295/297 (99%)	255 (86%)	40 (14%)	0	100	100
27	CL	225/785 (29%)	205 (91%)	20 (9%)	0	100	100
28	CM	443/446 (99%)	402 (91%)	41 (9%)	0	100	100
29	CN	222/252 (88%)	202 (91%)	20 (9%)	0	100	100
29	CO	211/252 (84%)	196 (93%)	13 (6%)	2 (1%)	14	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	CP	185/322 (58%)	181 (98%)	4 (2%)	0	100	100
31	CQ	171/259 (66%)	165 (96%)	6 (4%)	0	100	100
32	CR	746/1073 (70%)	692 (93%)	54 (7%)	0	100	100
32	CS	746/1073 (70%)	692 (93%)	54 (7%)	0	100	100
33	CT	127/203 (63%)	111 (87%)	16 (13%)	0	100	100
34	Cb	230/264 (87%)	211 (92%)	19 (8%)	0	100	100
35	Cc	188/212 (89%)	166 (88%)	22 (12%)	0	100	100
36	Cd	224/239 (94%)	208 (93%)	16 (7%)	0	100	100
37	Ce	155/203 (76%)	145 (94%)	10 (6%)	0	100	100
38	Cf	170/202 (84%)	162 (95%)	8 (5%)	0	100	100
39	Cg	157/190 (83%)	149 (95%)	8 (5%)	0	100	100
40	Ch	47/151 (31%)	47 (100%)	0	0	100	100
41	Ci	113/150 (75%)	100 (88%)	13 (12%)	0	100	100
42	Cj	124/143 (87%)	109 (88%)	15 (12%)	0	100	100
43	Ck	136/161 (84%)	131 (96%)	5 (4%)	0	100	100
44	Cm	122/130 (94%)	116 (95%)	6 (5%)	0	100	100
45	Cn	92/145 (63%)	83 (90%)	9 (10%)	0	100	100
46	Co	90/136 (66%)	82 (91%)	8 (9%)	0	100	100
47	Cp	59/68 (87%)	55 (93%)	4 (7%)	0	100	100
48	CU	106/311 (34%)	99 (93%)	7 (7%)	0	100	100
51	UV	1057/1171 (90%)	948 (90%)	108 (10%)	1 (0%)	48	83
52	CV	144/322 (45%)	129 (90%)	14 (10%)	1 (1%)	18	55
53	CW	380/668 (57%)	349 (92%)	31 (8%)	0	100	100
54	UT	1982/2612 (76%)	1878 (95%)	100 (5%)	4 (0%)	43	77
55	UH	349/930 (38%)	335 (96%)	14 (4%)	0	100	100
56	UE	121/410 (30%)	111 (92%)	9 (7%)	1 (1%)	16	52
56	UI	121/410 (30%)	111 (92%)	9 (7%)	1 (1%)	16	52
57	US	443/549 (81%)	420 (95%)	23 (5%)	0	100	100
58	Cl	78/156 (50%)	74 (95%)	4 (5%)	0	100	100
59	CX	265/480 (55%)	251 (95%)	14 (5%)	0	100	100
60	CY	118/381 (31%)	109 (92%)	9 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	CZ	40/609 (7%)	32 (80%)	8 (20%)	0	100	100
62	UP	52/364 (14%)	45 (86%)	7 (14%)	0	100	100
63	Cz	273/1796 (15%)	261 (96%)	12 (4%)	0	100	100
All	All	22926/35864 (64%)	21113 (92%)	1795 (8%)	18 (0%)	49	83

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	UG	176	LEU
29	CO	85	SER
51	UV	1059	ASP
54	UT	487	ILE
5	UF	121	LYS

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%)	647 (99%)	4 (1%)	78	80
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%)	650 (100%)	3 (0%)	81	81
5	UF	248/341 (73%)	247 (100%)	1 (0%)	84	82
6	UG	373/474 (79%)	371 (100%)	2 (0%)	81	81
7	UJ	898/1526 (59%)	896 (100%)	2 (0%)	87	85
8	UK	159/227 (70%)	158 (99%)	1 (1%)	78	80
9	UL	667/821 (81%)	666 (100%)	1 (0%)	88	88
10	UM	569/770 (74%)	569 (100%)	0	100	100
11	UN	146/765 (19%)	146 (100%)	0	100	100
12	UO	404/456 (89%)	402 (100%)	2 (0%)	81	81
13	UQ	650/817 (80%)	648 (100%)	2 (0%)	86	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	UR	360/524 (69%)	358 (99%)	2 (1%)	78	80
15	UU	672/863 (78%)	669 (100%)	3 (0%)	84	82
16	UX	150/167 (90%)	147 (98%)	3 (2%)	48	66
17	UZ	186/329 (56%)	184 (99%)	2 (1%)	65	74
18	CA	175/228 (77%)	172 (98%)	3 (2%)	53	67
18	CB	195/228 (86%)	193 (99%)	2 (1%)	68	76
19	CC	287/435 (66%)	287 (100%)	0	100	100
20	CD	319/489 (65%)	317 (99%)	2 (1%)	78	80
21	CE	91/108 (84%)	91 (100%)	0	100	100
21	CF	88/108 (82%)	88 (100%)	0	100	100
22	CG	331/525 (63%)	330 (100%)	1 (0%)	86	84
23	CH	303/320 (95%)	297 (98%)	6 (2%)	48	66
24	CI	661/1009 (66%)	655 (99%)	6 (1%)	70	76
25	CJ	147/169 (87%)	146 (99%)	1 (1%)	76	79
26	CK	245/266 (92%)	242 (99%)	3 (1%)	63	73
27	CL	181/642 (28%)	178 (98%)	3 (2%)	53	67
28	CM	364/383 (95%)	359 (99%)	5 (1%)	59	71
29	CN	202/223 (91%)	202 (100%)	0	100	100
29	CO	193/223 (86%)	193 (100%)	0	100	100
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%)	513 (78%)	141 (22%)	1	6
32	CS	654/916 (71%)	513 (78%)	141 (22%)	1	6
33	CT	108/167 (65%)	108 (100%)	0	100	100
34	Cb	199/221 (90%)	199 (100%)	0	100	100
35	Cc	149/178 (84%)	146 (98%)	3 (2%)	48	66
36	Cd	192/204 (94%)	191 (100%)	1 (0%)	81	81
37	Ce	137/177 (77%)	137 (100%)	0	100	100
38	Cf	139/164 (85%)	139 (100%)	0	100	100
39	Cg	122/162 (75%)	122 (100%)	0	100	100
40	Ch	41/130 (32%)	41 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	Ci	74/117 (63%)	74 (100%)	0	100	100
42	Cj	92/115 (80%)	92 (100%)	0	100	100
43	Ck	126/143 (88%)	126 (100%)	0	100	100
44	Cm	103/113 (91%)	103 (100%)	0	100	100
45	Cn	70/116 (60%)	70 (100%)	0	100	100
46	Co	79/115 (69%)	79 (100%)	0	100	100
47	Cp	46/61 (75%)	45 (98%)	1 (2%)	45	64
48	CU	92/260 (35%)	92 (100%)	0	100	100
51	UV	908/989 (92%)	902 (99%)	6 (1%)	76	79
52	CV	129/276 (47%)	129 (100%)	0	100	100
53	CW	309/587 (53%)	308 (100%)	1 (0%)	86	84
54	UT	1724/2276 (76%)	1721 (100%)	3 (0%)	87	85
55	UH	301/788 (38%)	300 (100%)	1 (0%)	86	84
56	UE	105/346 (30%)	75 (71%)	30 (29%)	0	3
56	UI	105/346 (30%)	75 (71%)	30 (29%)	0	3
57	US	404/493 (82%)	403 (100%)	1 (0%)	87	85
58	Cl	71/135 (53%)	70 (99%)	1 (1%)	59	71
59	CX	225/411 (55%)	225 (100%)	0	100	100
60	CY	100/322 (31%)	100 (100%)	0	100	100
61	CZ	36/519 (7%)	34 (94%)	2 (6%)	19	41
62	UP	44/314 (14%)	44 (100%)	0	100	100
63	Cz	235/1533 (15%)	233 (99%)	2 (1%)	70	76
All	All	19136/30385 (63%)	18712 (98%)	424 (2%)	45	64

5 of 424 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	CS	116	LEU
32	CS	537	LEU
56	UI	199	LYS
32	CS	142	THR
32	CS	313	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 344 such sidechains are listed below:

Mol	Chain	Res	Type
42	Cj	32	ASN
54	UT	768	ASN
44	Cm	42	GLN
51	UV	542	ASN
54	UT	1436	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
49	C1	1461/2323 (62%)	560 (38%)	35 (2%)
50	C2	226/230 (98%)	86 (38%)	6 (2%)
All	All	1687/2553 (66%)	646 (38%)	41 (2%)

5 of 646 RNA backbone outliers are listed below:

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

5 of 41 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	C1	1734	G
50	C2	23	A
49	C1	2054	A
49	C1	2156	A
50	C2	35	G

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

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

5.5 Carbohydrates ⓘ

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
50	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	18.94
1	C2	105:C	O3'	110:A	P	15.09
1	C2	119:C	O3'	123:A	P	11.47

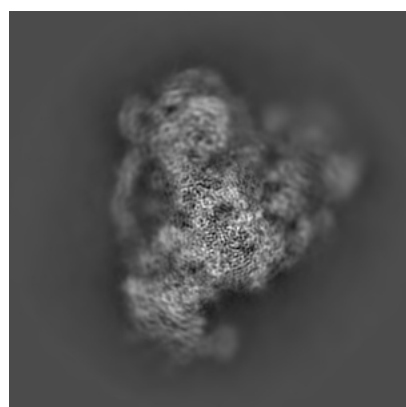
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10056. These allow visual inspection of the internal detail of the map and identification of artifacts.

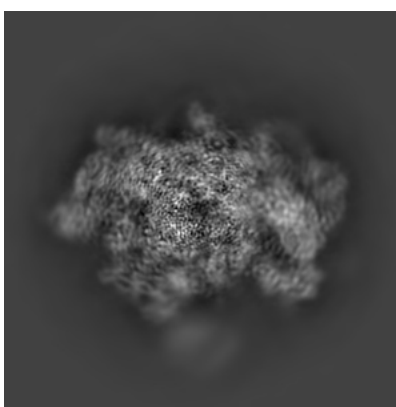
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

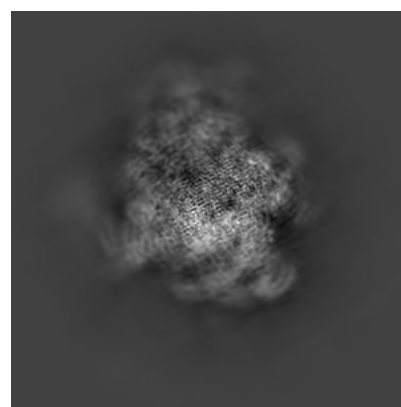
6.1.1 Primary map



X



Y

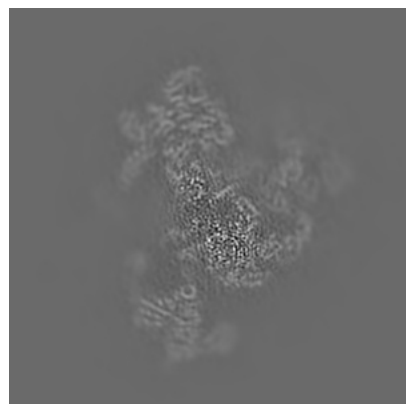


Z

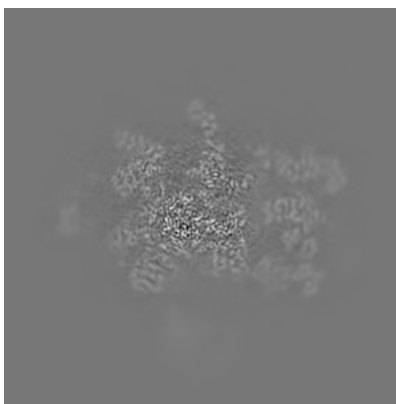
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

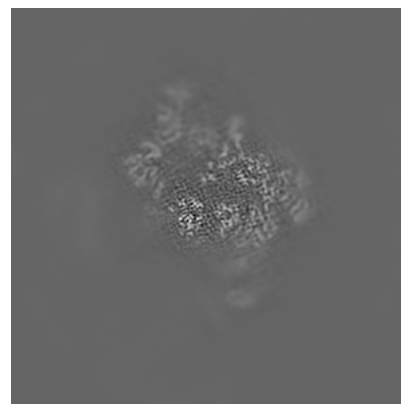
6.2.1 Primary map



X Index: 240



Y Index: 240

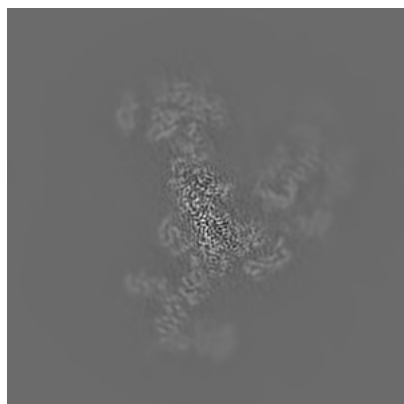


Z Index: 240

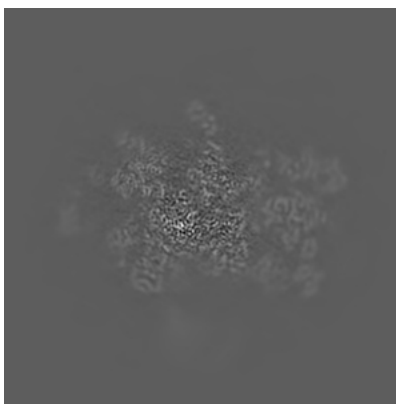
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

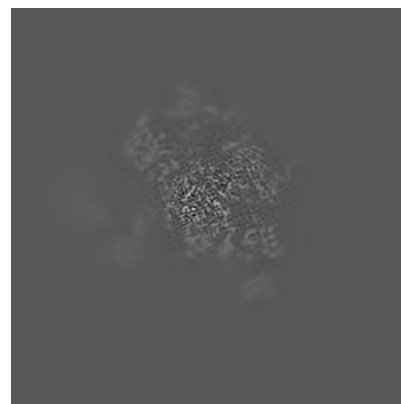
6.3.1 Primary map



X Index: 217



Y Index: 238

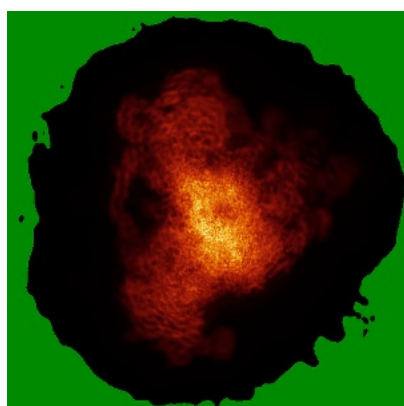


Z Index: 214

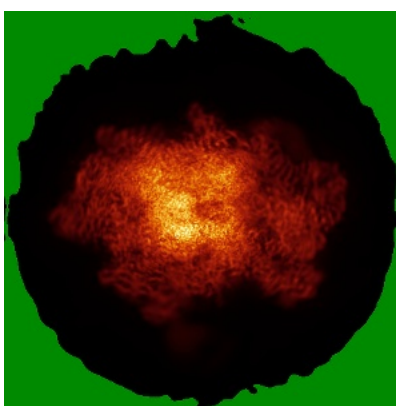
The images above show the largest variance slices of the map in three orthogonal directions.

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

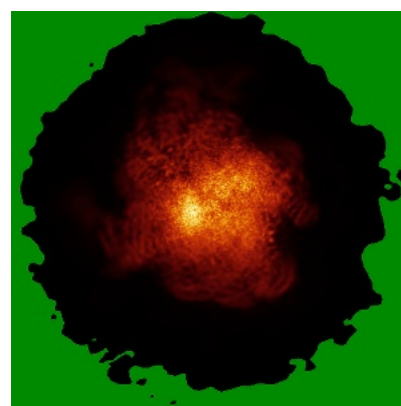
6.4.1 Primary map



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.

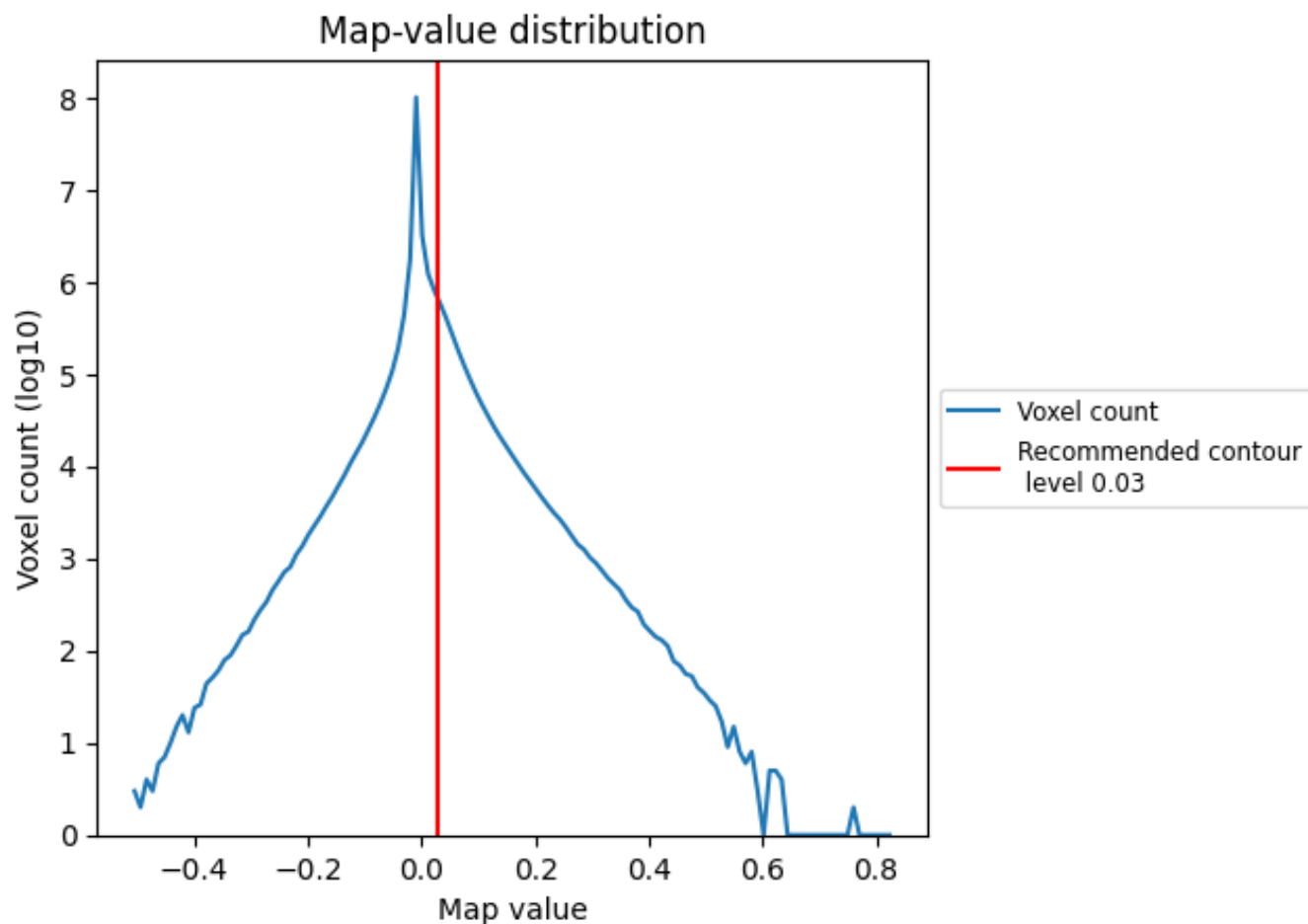
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

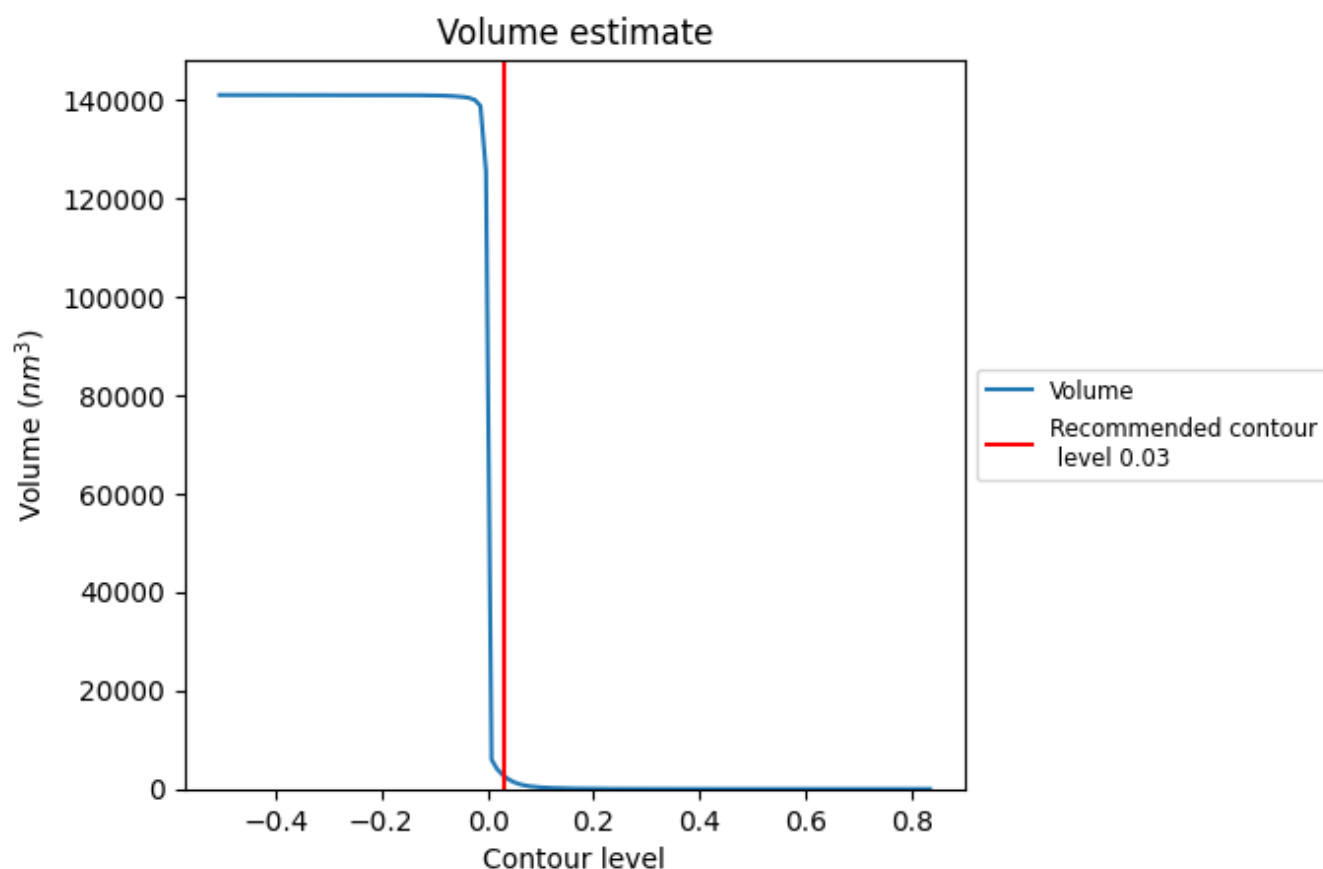
This section contains the results of statistical analysis of the map.

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.

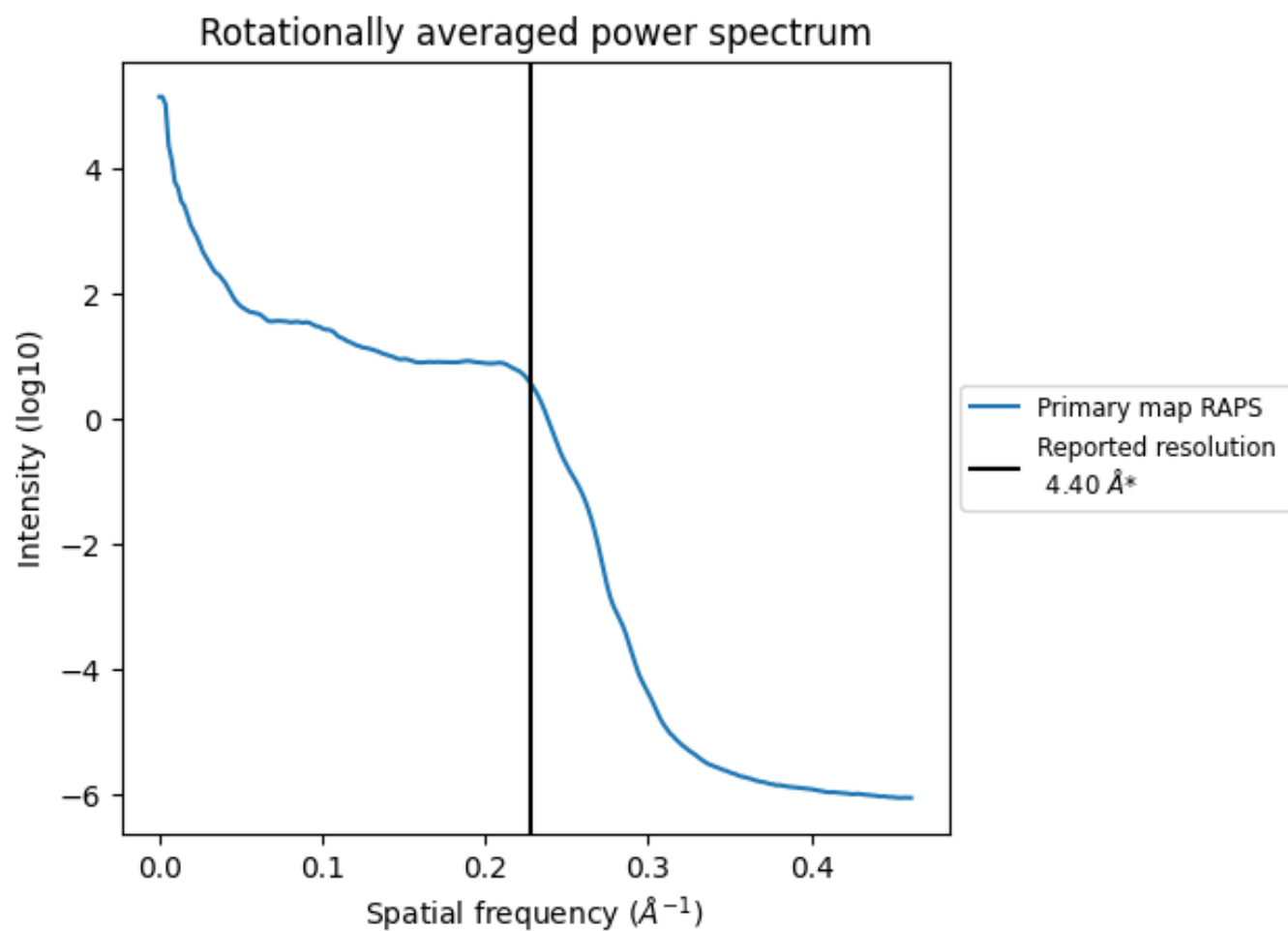
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2721 nm^3 ; this corresponds to an approximate mass of 2458 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 ⓘ

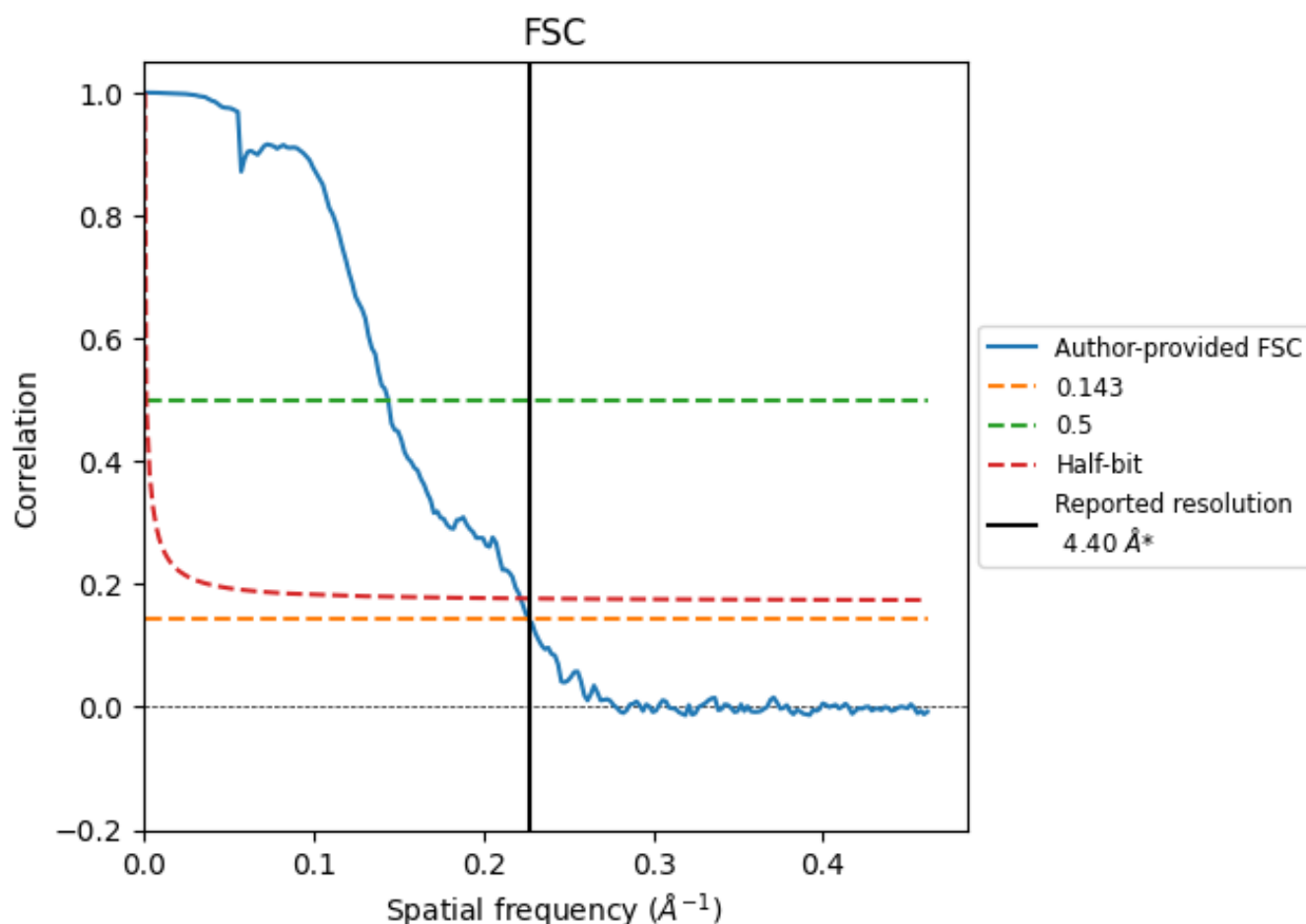


*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

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 0.227 Å⁻¹

8.2 Resolution estimates [i](#)

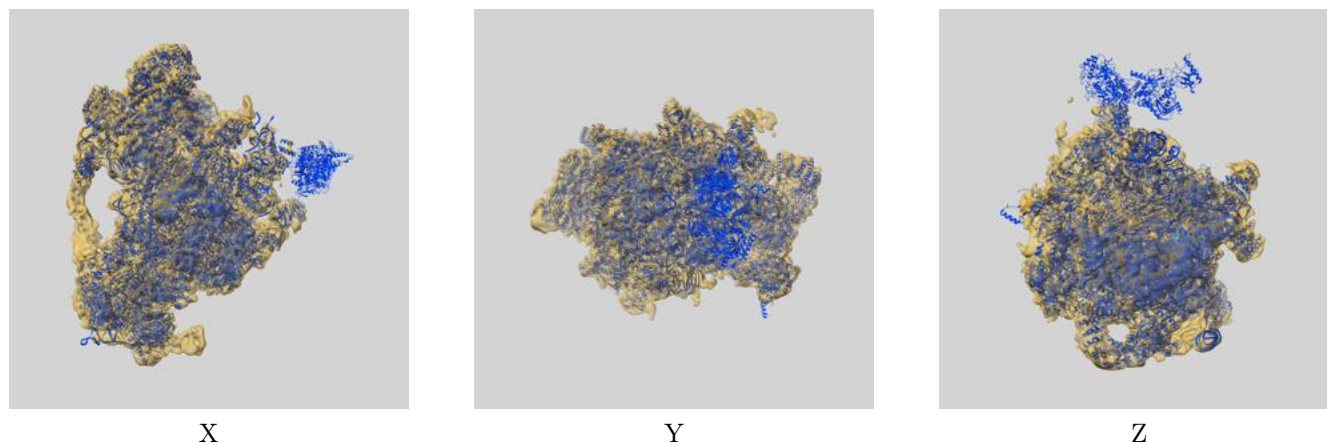
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.40	-	-
Author-provided FSC curve	4.42	6.93	4.50
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

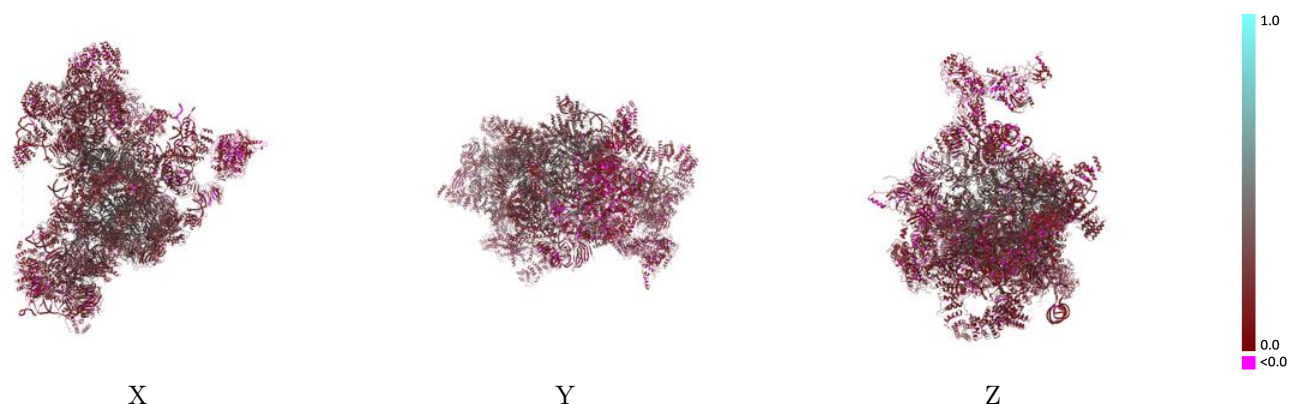
This section contains information regarding the fit between EMDB map EMD-10056 and PDB model 6RXZ. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



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

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

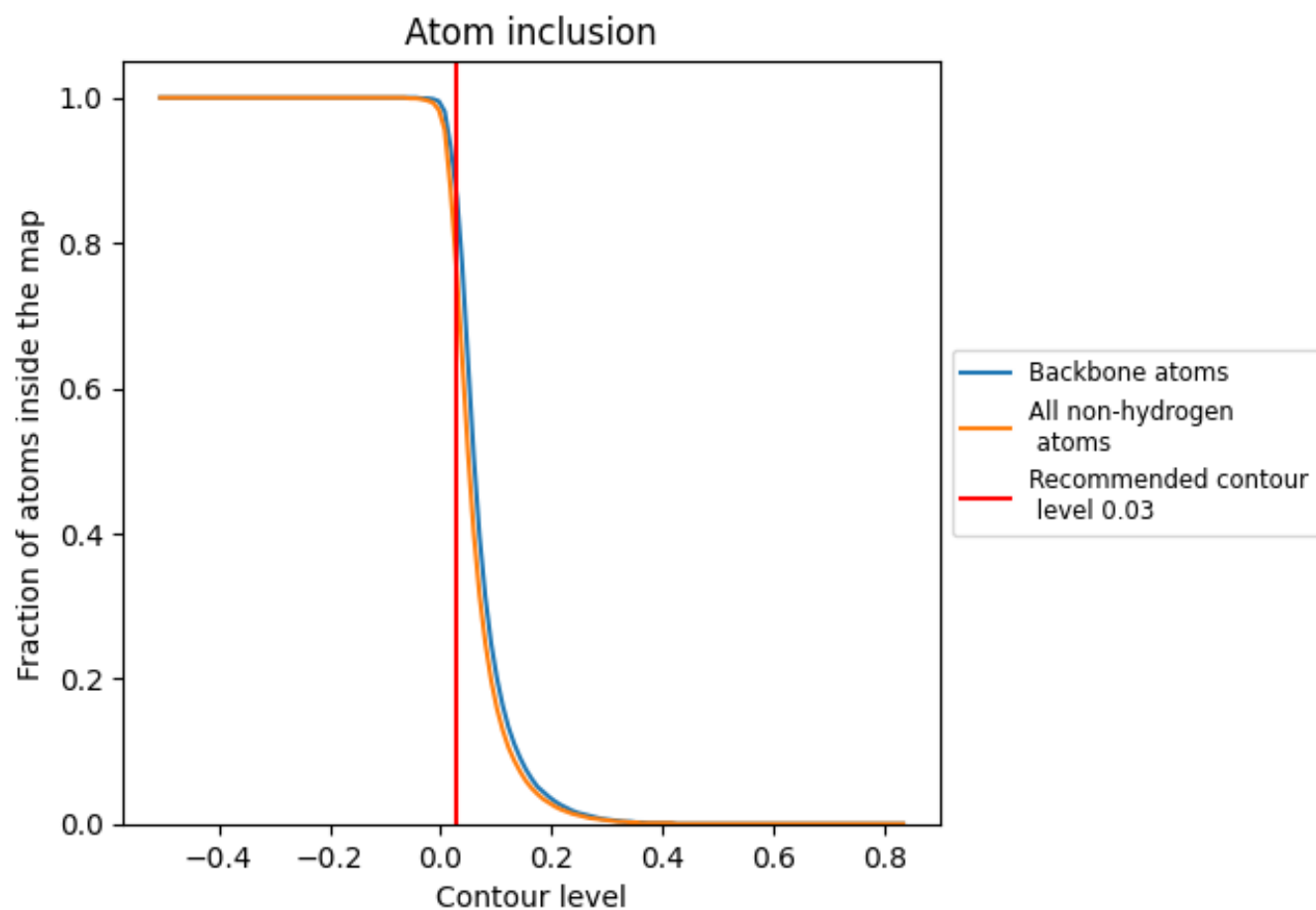


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 75% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7520	 0.2270
C1	 0.8700	 0.2580
C2	 0.9050	 0.2760
CA	 0.8720	 0.3590
CB	 0.7420	 0.2130
CC	 0.8130	 0.2470
CD	 0.7940	 0.2420
CE	 0.8610	 0.3370
CF	 0.8180	 0.2680
CG	 0.7830	 0.2070
CH	 0.8130	 0.2770
CI	 0.8790	 0.3550
CJ	 0.9150	 0.4170
CK	 0.8980	 0.4110
CL	 0.8390	 0.3190
CM	 0.8580	 0.3350
CN	 0.7370	 0.2190
CO	 0.6650	 0.1760
CP	 0.5340	 0.1610
CQ	 0.7250	 0.1670
CR	 0.7260	 0.1710
CS	 0.6120	 0.1210
CT	 0.8940	 0.3680
CU	 0.7960	 0.2810
CV	 0.0000	 0.0660
CW	 0.7380	 0.1660
CX	 0.6190	 0.1010
CY	 0.7510	 0.2410
CZ	 0.6960	 0.1540
Cb	 0.7140	 0.1810
Cc	 0.8230	 0.2950
Cd	 0.7370	 0.1700
Ce	 0.5820	 0.1730
Cf	 0.7440	 0.1410
Cg	 0.8540	 0.3460



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Chain	Atom inclusion	Q-score
Ch	 0.5340	 0.1030
Ci	 0.6460	 0.1590
Cj	 0.8910	 0.4000
Ck	 0.6730	 0.1430
Cl	 0.5030	 0.2250
Cm	 0.7760	 0.2740
Cn	 0.9170	 0.4400
Co	 0.7560	 0.2010
Cp	 0.8020	 0.2540
Cz	 0.4380	 0.1550
UA	 0.8580	 0.3350
UB	 0.7750	 0.2200
UC	 0.8880	 0.3970
UD	 0.7720	 0.2150
UE	 0.7200	 0.1650
UF	 0.8260	 0.2180
UG	 0.8040	 0.3170
UH	 0.7480	 0.1680
UI	 0.6510	 0.1390
UJ	 0.7460	 0.2010
UK	 0.8760	 0.3630
UL	 0.7580	 0.1780
UM	 0.6520	 0.1240
UN	 0.7670	 0.2770
UO	 0.7730	 0.2240
UP	 0.7540	 0.2410
UQ	 0.7900	 0.2070
UR	 0.8520	 0.3000
US	 0.7560	 0.1660
UT	 0.7440	 0.1570
UU	 0.8530	 0.2850
UV	 0.0030	 0.0740
UX	 0.8960	 0.4090
UZ	 0.8150	 0.2630