wwPDB EM Validation Summary Report (i)

May 18, 2024 – 05:35 pm BST

PDB ID	:	6RXY
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 (i) 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 (i)) were used in the production of this report:

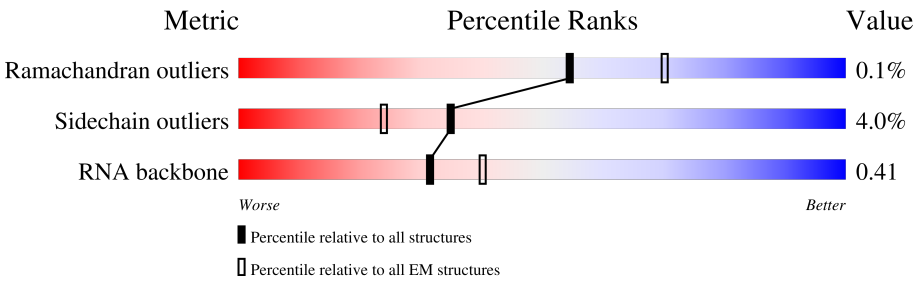
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 4.70 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	89% • 7%
2	UB	907	56% • 44%
3	UC	648	11% 89%
4	UD	884	• 86% • 13%
5	UF	414	80% 20%
6	UG	558	• 76% • 20%
7	UJ	1802	20% 44% • 55%
8	UK	270	• 79% • 20%

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Mol	Chain	Length	Quality of chain
9	UL	962	81% 18%
10	UM	912	25% 73% 26%
11	UN	938	16% 84%
12	UO	557	88% 10%
13	UQ	960	80% 18%
14	UR	618	71% 28%
15	UU	1049	83% 14%
16	UX	193	97%
17	UZ	391	58% 40%
18	CA	313	75% 23%
18	CB	313	75% 24%
19	CC	523	74% 26%
20	CD	582	71% 28%
21	CE	127	94% 5%
21	CF	127	11% 94% 6%
22	CG	630	15% 60% 40%
23	CH	411	93% 5%
24	CI	1163	69% 29%
25	CJ	183	94%
26	CK	297	95% 5%
27	CL	785	29% 71%
28	CM	446	97%
29	CN	252	89% 10%
29	CO	252	5% 83% 15%
30	CP	322	31% 57% 42%

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Mol	Chain	Length	Quality of chain
31	CQ	259	66% 32%
32	CR	1073	30% 53% 16% 29%
32	CS	1073	66% 53% 16% 29%
33	CT	203	64% 35%
34	Cc	212	89% 9%
35	Ce	203	78% 76% 22%
36	Cg	190	41% 83% 16%
37	Ch	151	27% 32% 68%
38	Ci	150	33% 76% 23%
39	Cj	143	85% 12%
40	Cm	130	68% 95%
41	Cn	145	66% 34%
42	Cp	68	90% 10%
43	CU	311	11% 40% 58%
44	C1	2323	6% 24% 19% 5% 52%
45	C2	230	17% 48% 37% 15%
46	UV	1171	91% 88% 9%
47	CV	322	46% 44% 54%
48	UH	930	38% 61%
49	UE	410	23% 7% 70%
49	UI	410	23% 7% 70%
50	US	549	81% 18%
51	Cl	156	8% 49% 49%
52	CX	480	9% 55% 44%
53	UP	364	15% 85%

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Mol	Chain	Length	Quality of chain
54	Cz	1796	13% 15% 85%

2 Entry composition (i)

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
			Total	C	N	O	S		
1	UA	839	6366	4101	1136	1105	24	0	0

- Molecule 2 is a protein called Utp2.

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

- Molecule 3 is a protein called Utp3.

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

- Molecule 4 is a protein called Utp4.

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

- Molecule 5 is a protein called Utp6.

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

- Molecule 6 is a protein called Utp7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	UG	448	3444	2197	646	590	11	0	0

- Molecule 7 is a protein called Utp10.

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

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

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

- Molecule 9 is a protein called Utp12.

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

- Molecule 10 is a protein called Utp13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	UM	679	5273	3351	924	986	12	0	0

- Molecule 11 is a protein called Utp14.

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

- Molecule 12 is a protein called Utp15.

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

- Molecule 13 is a protein called Utp17.

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

- Molecule 14 is a protein called Utp18.

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

- Molecule 15 is a protein called Utp21.

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

- Molecule 16 is a protein called Utp24.

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

- Molecule 17 is a protein called Utp30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	UZ	235	1815	1184	330	298	3	0	0

- Molecule 18 is a protein called Nop1.

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

- Molecule 19 is a protein called Nop56.

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

- Molecule 20 is a protein called Nop58.

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

- Molecule 21 is a protein called Snu13.

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

- Molecule 22 is a protein called Rrp9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	CG	378	2922	1865	527	517	13	0	0

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

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

- Molecule 24 is a protein called Bms1.

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

- Molecule 25 is a protein called Imp3.

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

- Molecule 26 is a protein called Imp4.

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

- Molecule 27 is a protein called Mpp10.

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

- Molecule 28 is a protein called Sof1.

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

- Molecule 29 is a protein called Emg1.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	CP	187	1504	961	269	265	9	0	0

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

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

- Molecule 32 is a protein called Kre33.

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

- Molecule 33 is a protein called Fcf2.

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

- Molecule 34 is a protein called 40S ribosomal protein s5-like protein.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 43 is a protein called Faf1.

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

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

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

- Molecule 45 is a RNA chain called U3 snoRNA.

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

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

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

- Molecule 47 is a protein called Rrp7.

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

- Molecule 48 is a protein called Utp8.

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

- Molecule 49 is a protein called Utp5.

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

- Molecule 50 is a protein called Noc4.

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

- Molecule 51 is a protein called Rps18.

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

- Molecule 52 is a protein called Enp1.

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

- Molecule 53 is a protein called Utp16.

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

- Molecule 54 is a protein called Rrp5.

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

- Molecule 55 is ZINC ION (three-letter code: ZN) (formula: Zn).

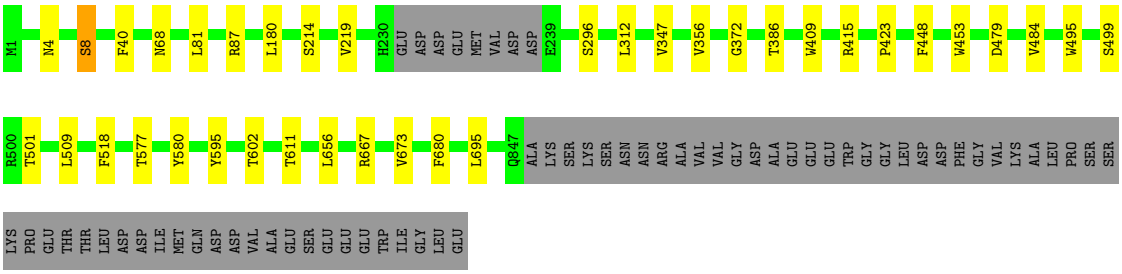
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
55	UX	1	1	1	0

3 Residue-property plots (i)

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

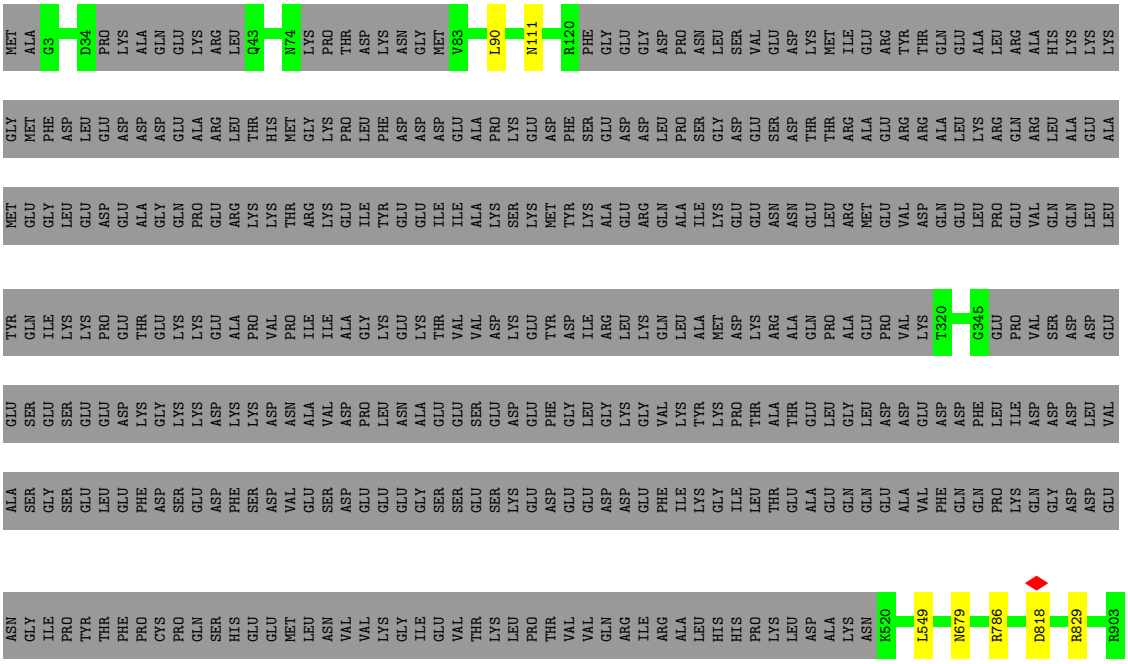
- Molecule 1: Periodic tryptophan protein 2-like protein

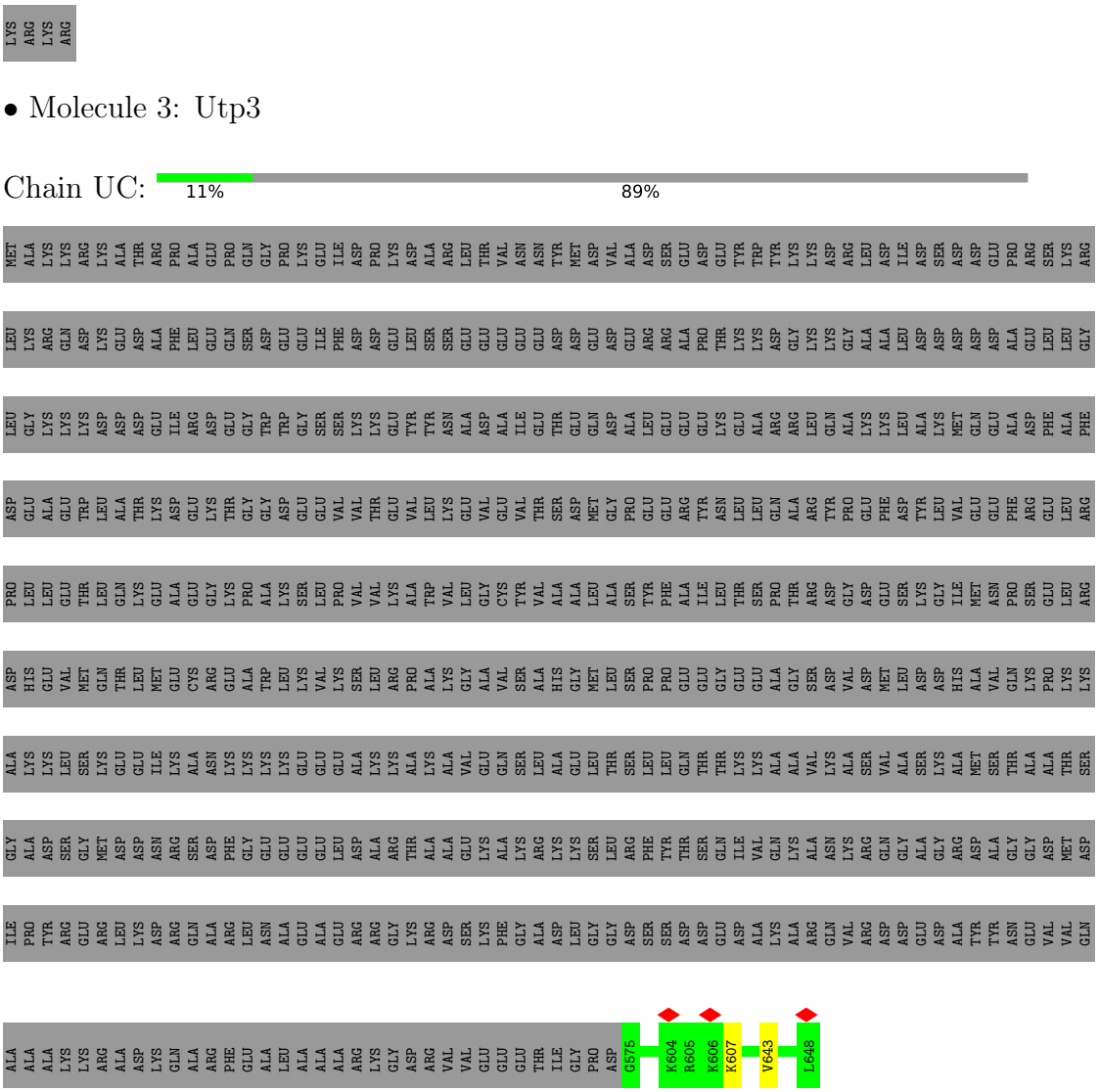
Chain UA: 89% 7%

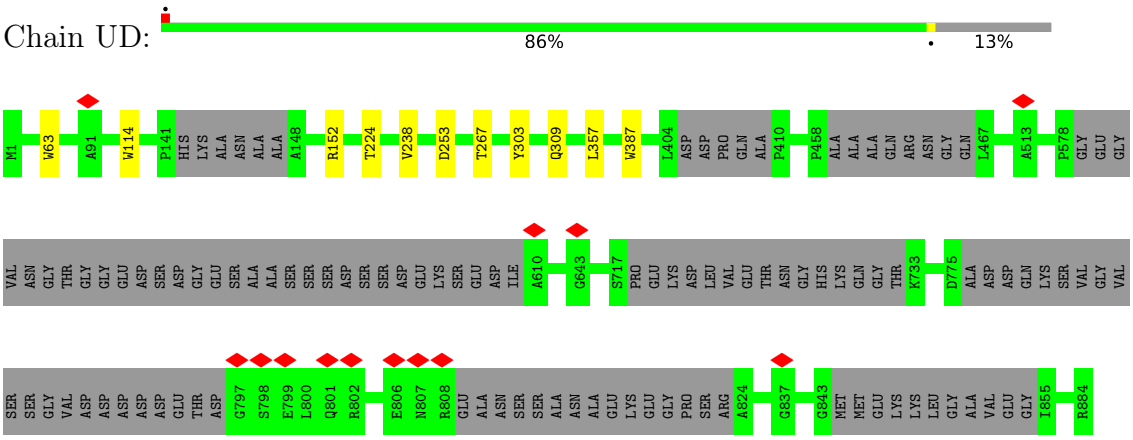


- Molecule 2: Utp2

Chain UB: 56% 44%




LYS ARG LYS ARG
• Molecule 3: Utp3
Chain UC:
11%
89%
G575
K604
R605
K606
K607
V643
L648


• Molecule 4: Utp4
Chain UD:
86%
13%
M1
W63
A91
W114
P141
A148
R152
T224
V238
D253
T267
Y303
Q309
L357
W387
L404
P410
P458
L467
A513
P578
A610
G643
S717
K733
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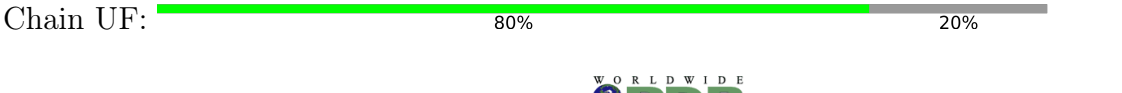
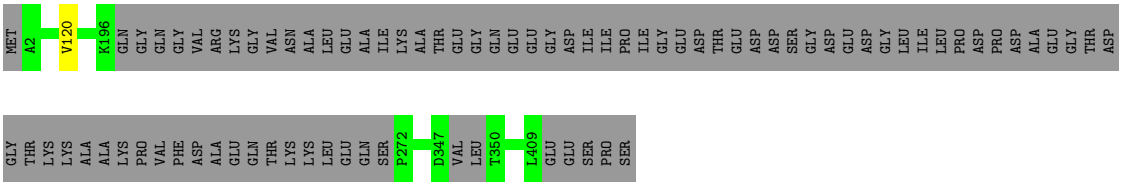
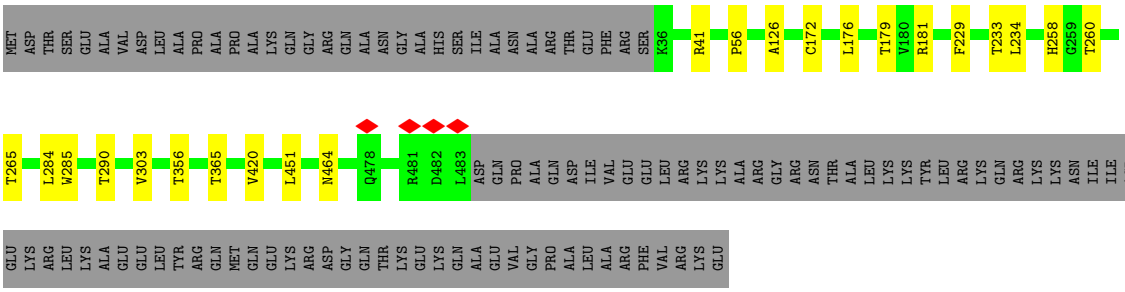
N807
R808
A824
G837
G843
I855
R884


• Molecule 5: Utp6
Chain UF:
80%
20%



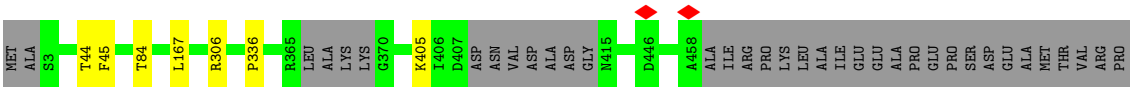
- Molecule 6: Utp7

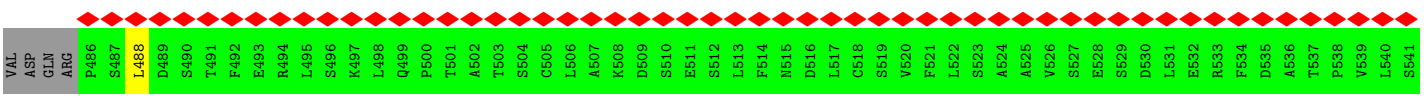
Chain UG:

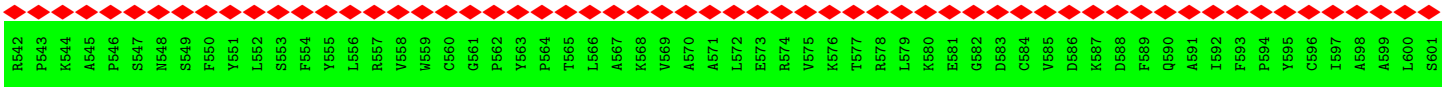


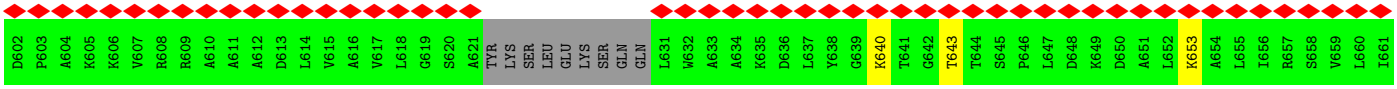
- Molecule 7: Utp10

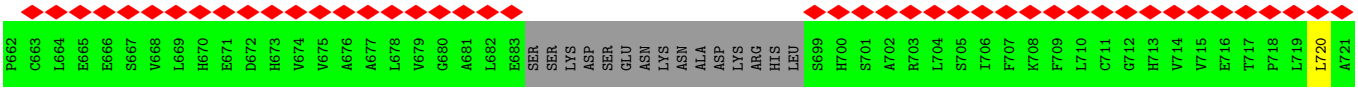
Chain UJ:

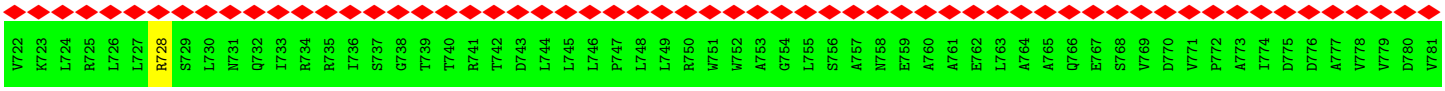


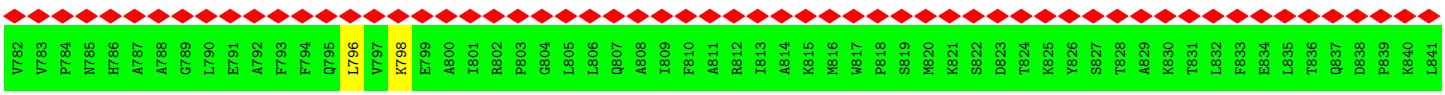


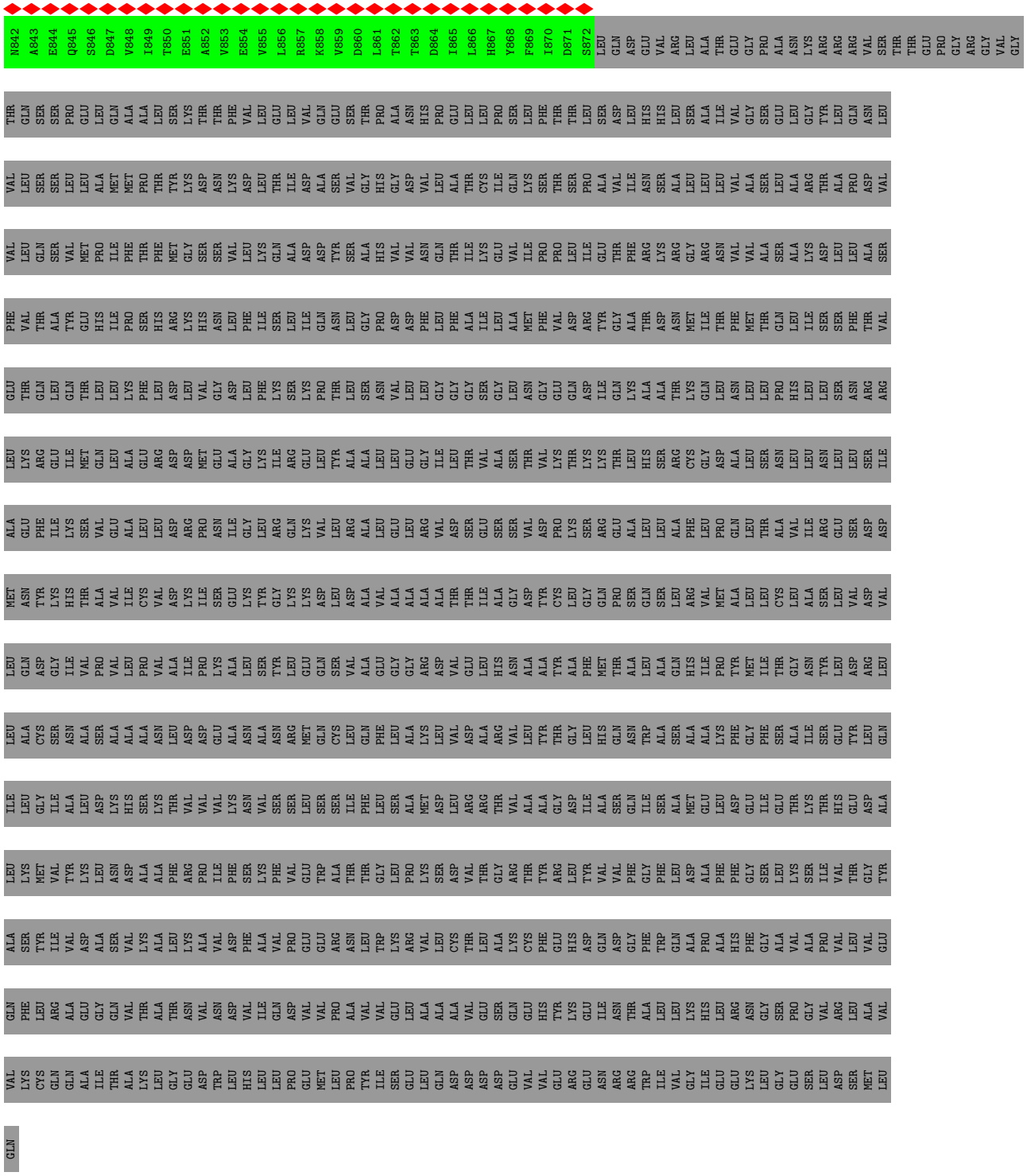






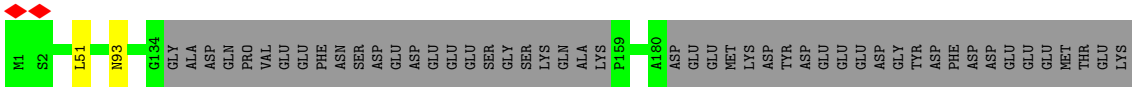






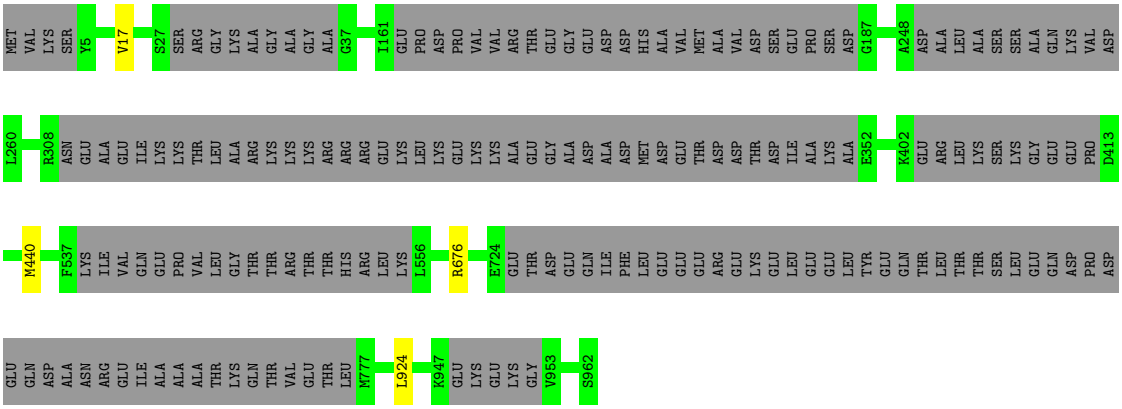
• Molecule 8: U3 small nucleolar RNA-associated protein 11

Chain UK:



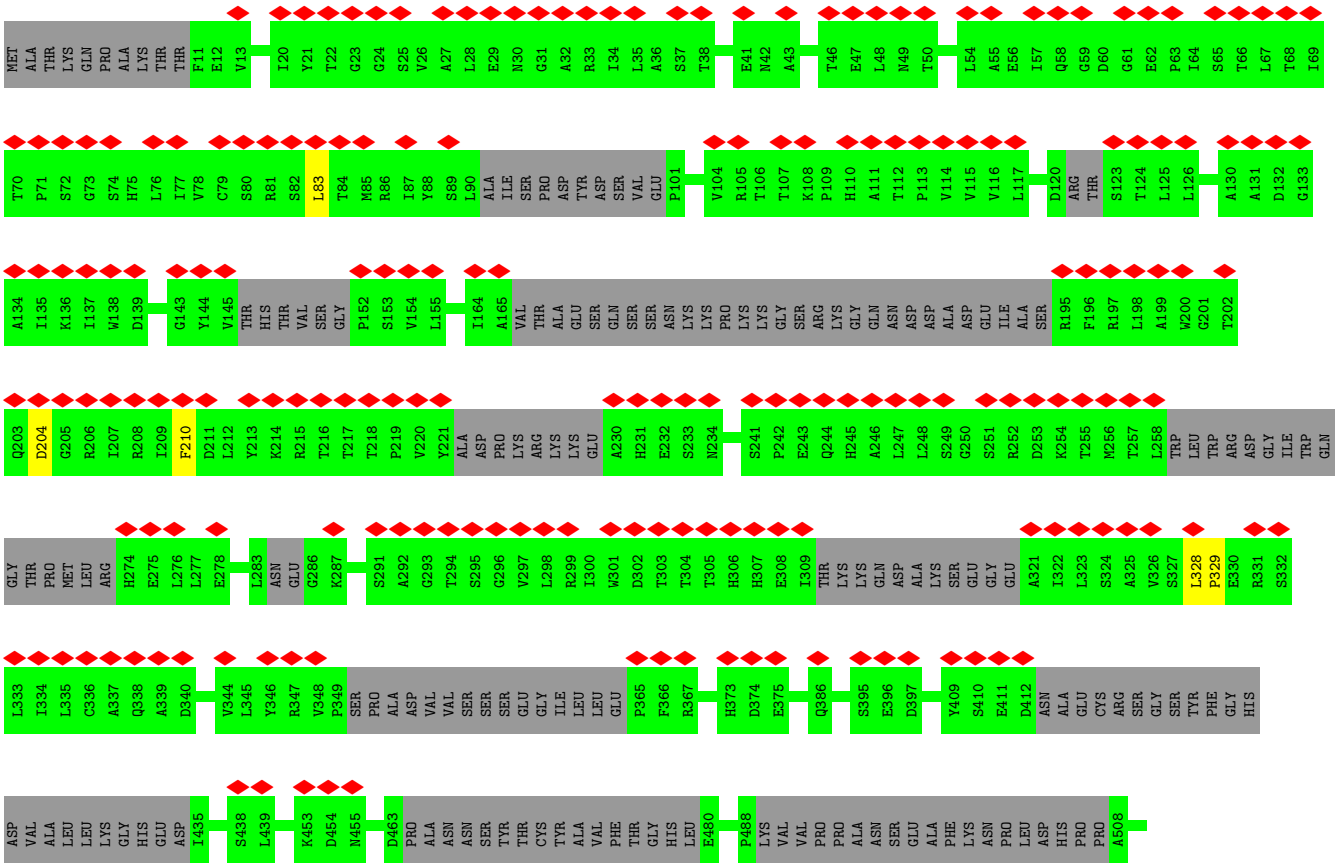
• Molecule 9: Utp12

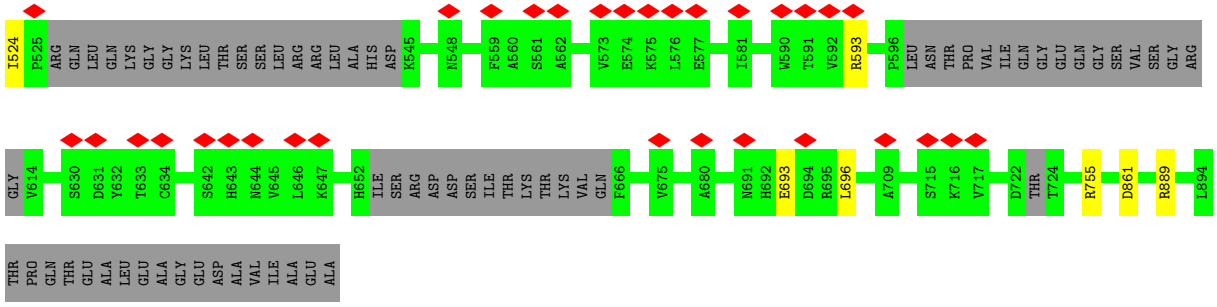
Chain UL:



• Molecule 10: Utp13

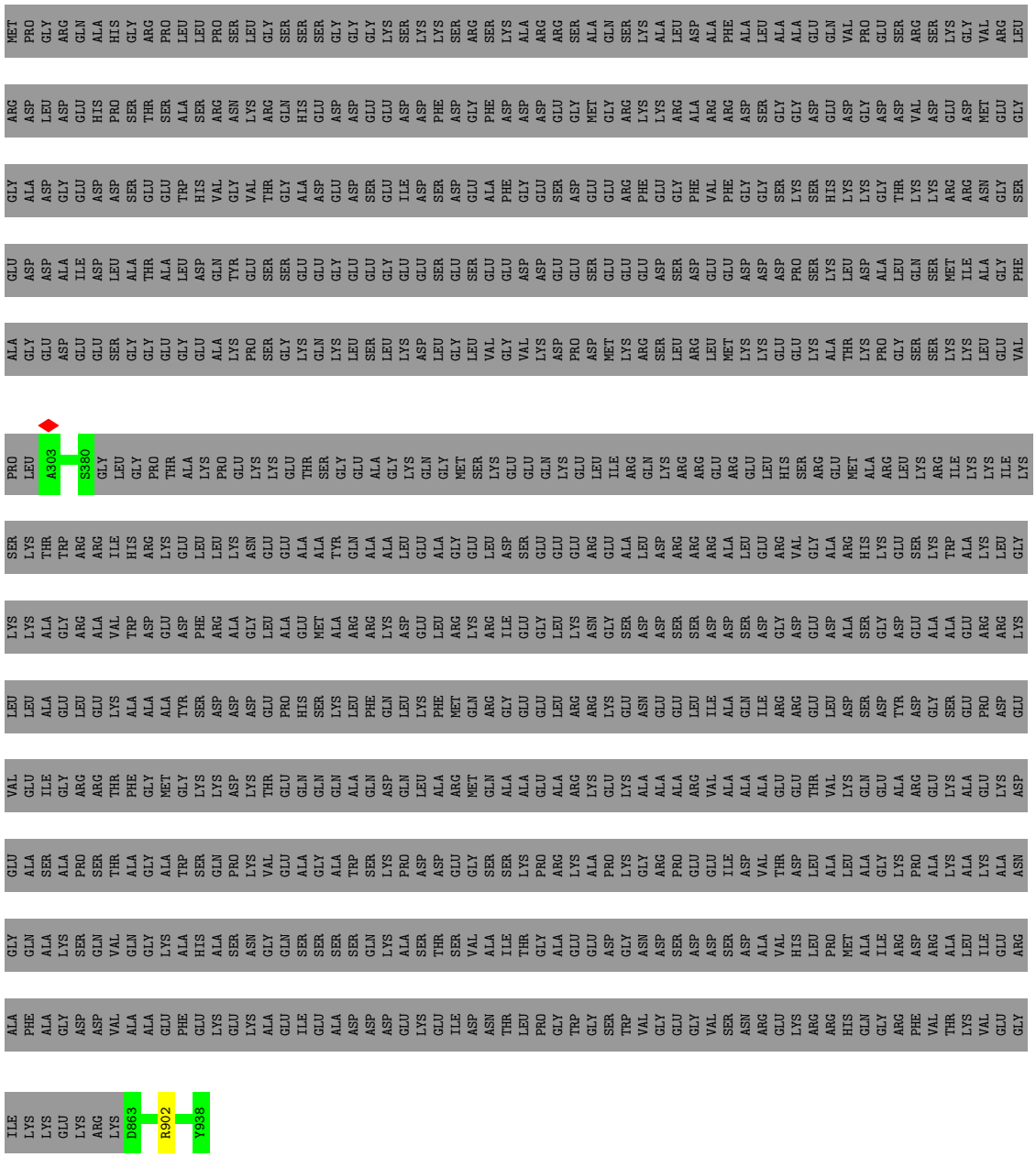
Chain UM:





- Molecule 11: Utp14

Chain UN: 16% 84%



- Molecule 12: Utp15

Chain UO: 88% 10%

M1 A51 SER LEU GLY THR THR ALA LEU VAL SER SER LEU VAL ALA ALA ALA LYS T69 D110 V149 K167 W172 V190 T270 T277 A282 S350 GLY PRO ALA ALA ASP ARG GLU ARG GLU ARG GLU ARG VAL GLU ALA ALA MET ALA LYS GLY PRO

GLU ALA ILE ALA LYS LEU ASP ALA ALA LYS ALA LYS ARG K385 R417 R432 L457 D474 E555 ALA GLN

- Molecule 13: Utp17

Chain UQ: 80% 18%

MET VAL SER THR MET GLU THR ASN GLY ASP THR ALA SER LEU LYS ARG LYS ARG GLU PRO LYS ASP ASP PRO HIS SER LEU GLN LYS LYS HIS ARG HIS ARG SER ARG SER LYS PRO GLN ASP ALA ALA THR ALA ASP SER VAL ALA ASN LEU ASN SER ASN SER LEU ALA VAL GLN PRO

ILE ASP GLY ASN SER GLY PRO LEU GLN LEU ALA THR THR ASP ARG LEU ALA S78 T130 ARG THR ASN ASP LEU ASP GLU P138 S149 W170 Y237 L244 I299 ARG MET ILE LYS LYS GLY VAL A307 T335 GLU ALA SER GLY PRO L341 V358 S364 G365

H394 L423 D449 V452 W456 L466 T497 T537 T563 E564 T622 Q675 ASP ASP SER VAL GLU ILE LEU LYS GLY ILE P686 Y687 P707 S708 P796 ASN LEU GLY GLN ASP K802 A849 G858 ALA GLU GLN ALA PRO LEU LEU LYS SER LEU ALA

ASP LEU GLY VAL ASP ASN THR SER ASN THR GLU MET GLU ASP THR PRO ASP LYS GLN LEU LEU LEU GLU GLN ALA GLU ALA ASN ASP ASP GLU MET HIS ASP ALA ASN TYR ASP LEU ASP MET GLU ASP ASN GLU D915 V920 P956 VAL ILE ASN ALA

- Molecule 14: Utp18

Chain UR: 71% 28%

MET PRO ARG SER ASN LYS LYS LYS GLN ILE GLU ASP LEU PRO SER ASP SER ASP HIS PHE PRO GLU PHE PRO GLU GLU GLU ALA PHE SER SER LEU SER GLU GLU GLU GLU ALA GLU GLU ARG LYS LYS PRO VAL A46 K63 R72 ASP ASP PHE LEU ALA PRO ALA ASN ASP PRO

THR ALA LEU VAL LYS ALA GLY ASP ASP GLU GLU GLU THR GLY HIS GLU HIS LEU ASP ASP SER MET LEU PHE VAL ILE ASP THR GLU GLY ASP SER SER ILE GLN VAL PRO ALA PRO THR LYS VAL THR ALA GLU GLU THR GLY GLY D132 T152 K190 GLU ALA ASN GLY SER LYS

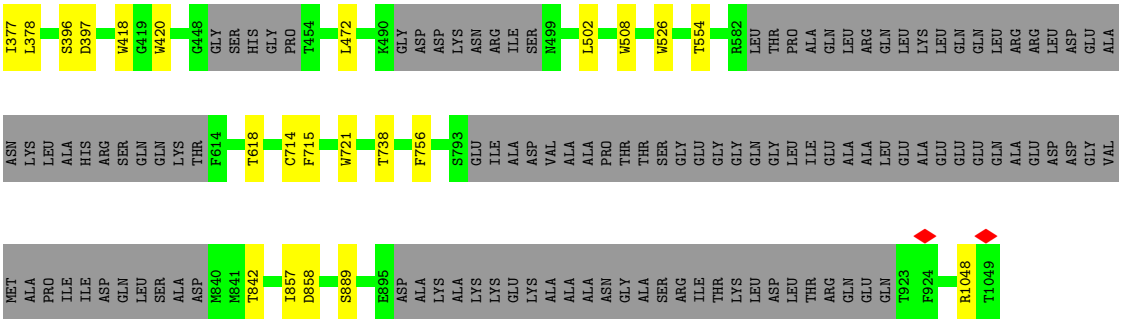
ARG ARG ARG ARG SER LEU ASP ALA SER SER ASP SER LEU SER GLY SER ASP MET GLU VAL ASP SER ASP GLY GLU SER ILE ASP ALA P227 V242 ALA ALA GLU ASP SER ALA ARG SER ALA LYS R253 S279 L314 K393 M397 L432 R471 E502 LYS PRO

PRO LYS LYS ASN GLU SER ASN GLN GLU GLU GLU GLN ASN SER SER GLU LYS THR LYS GLU I524 A565 W580 L587 G618

- Molecule 15: Utp21

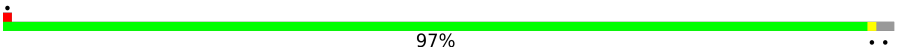
Chain UU: 83% 14%

MET PRO HIS PRO GLU PRO ASP PHE PRO LEU THR LYS ARG GLN LYS LEU ASP ALA ALA PRO LYS ALA SER SER SER LYS ARG LYS LYS PRO G31 T40 K58 Y74 N81 T86 W100 E130 I190 N191 M192 L222 P252 L313 T354 S369



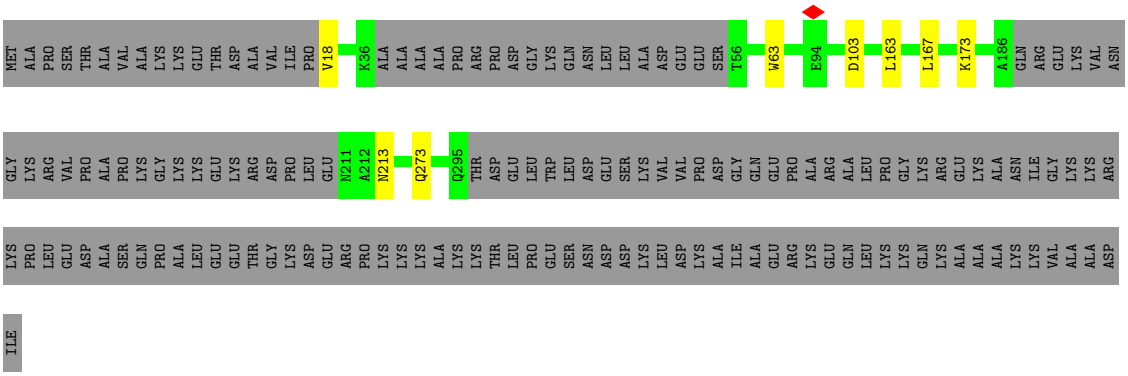
- Molecule 16: Utp24

Chain UX:



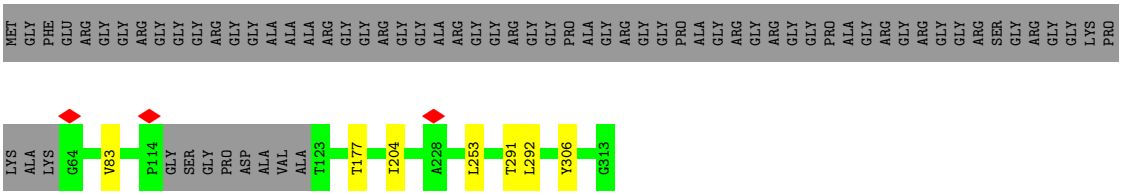
- Molecule 17: Utp30

Chain UZ:



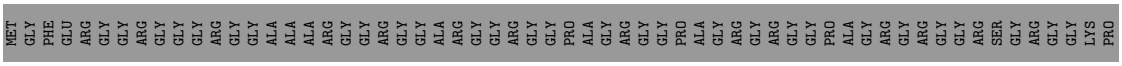
- Molecule 18: Nop1

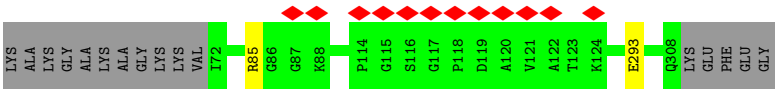
Chain CA:



- Molecule 18: Nop1

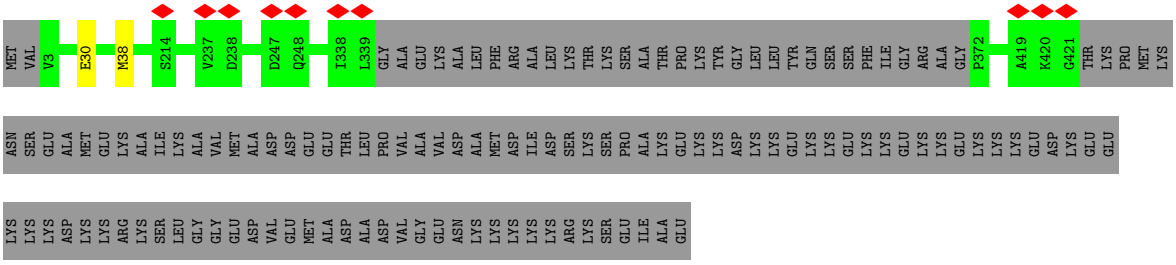
Chain CB:





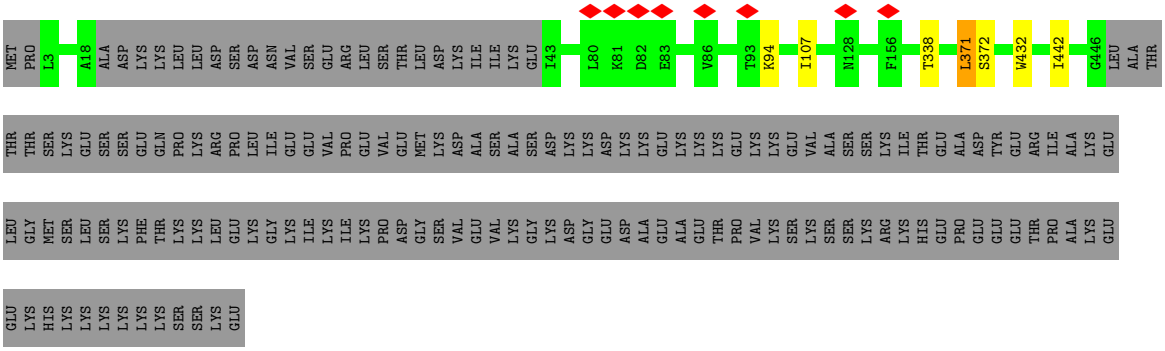
- Molecule 19: Nop56

Chain CC:



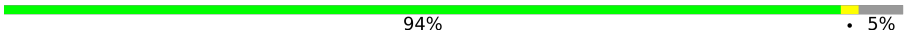
- Molecule 20: Nop58

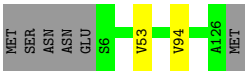
Chain CD:



- Molecule 21: Snu13

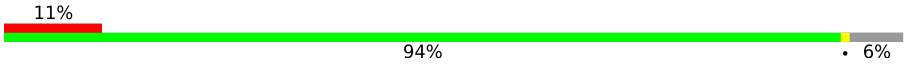
Chain CE:

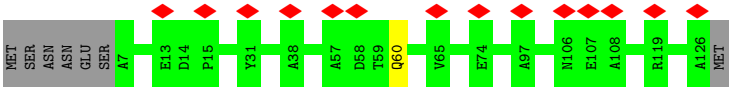




- Molecule 21: Snu13

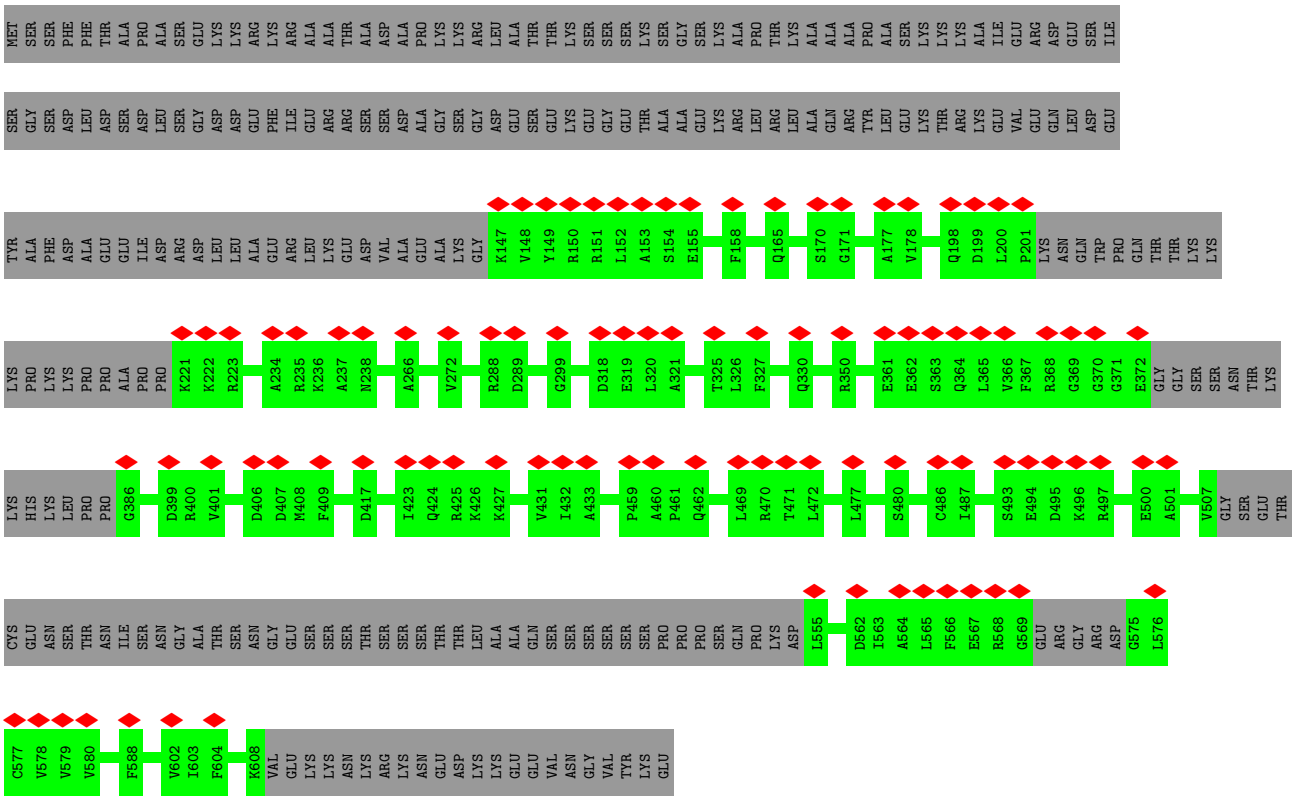
Chain CF:





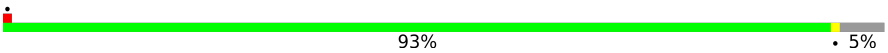
- Molecule 22: Rrp9

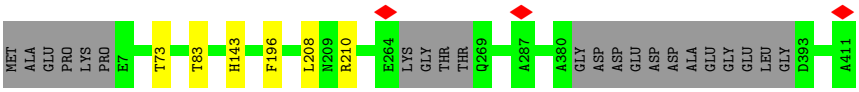
Chain CG:



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

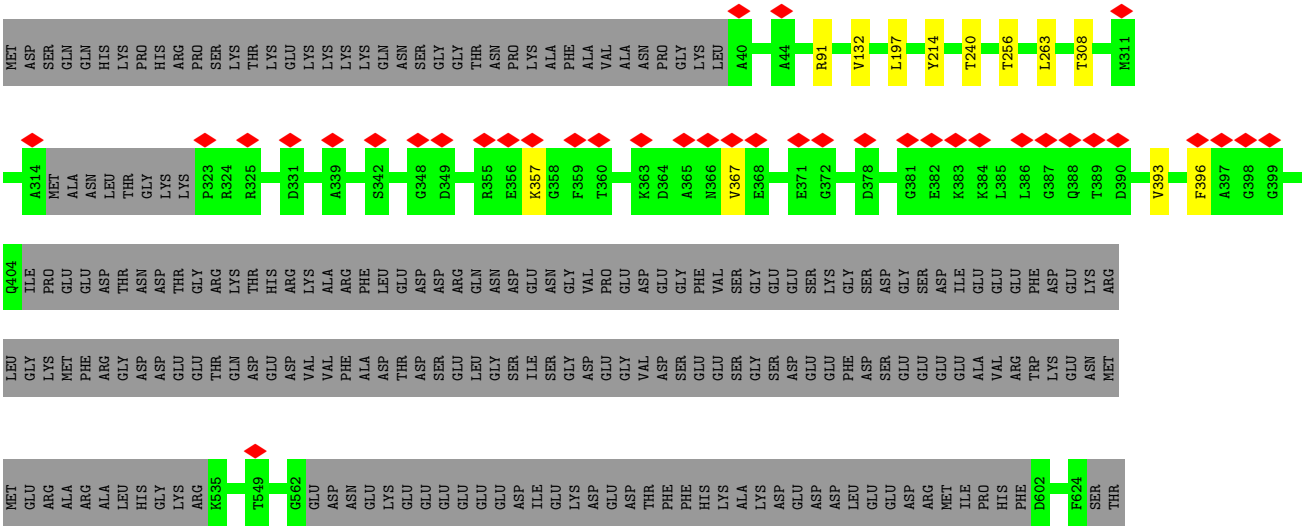
Chain CH:

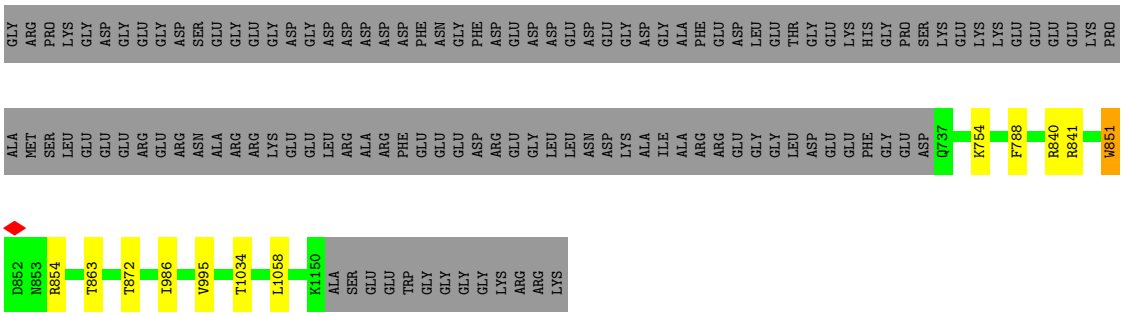




- Molecule 24: Bms1

Chain CI:



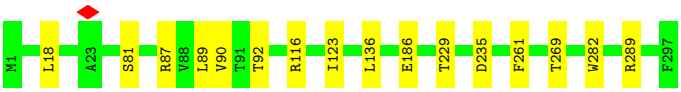


- Molecule 25: Imp3

Chain CJ: 94%

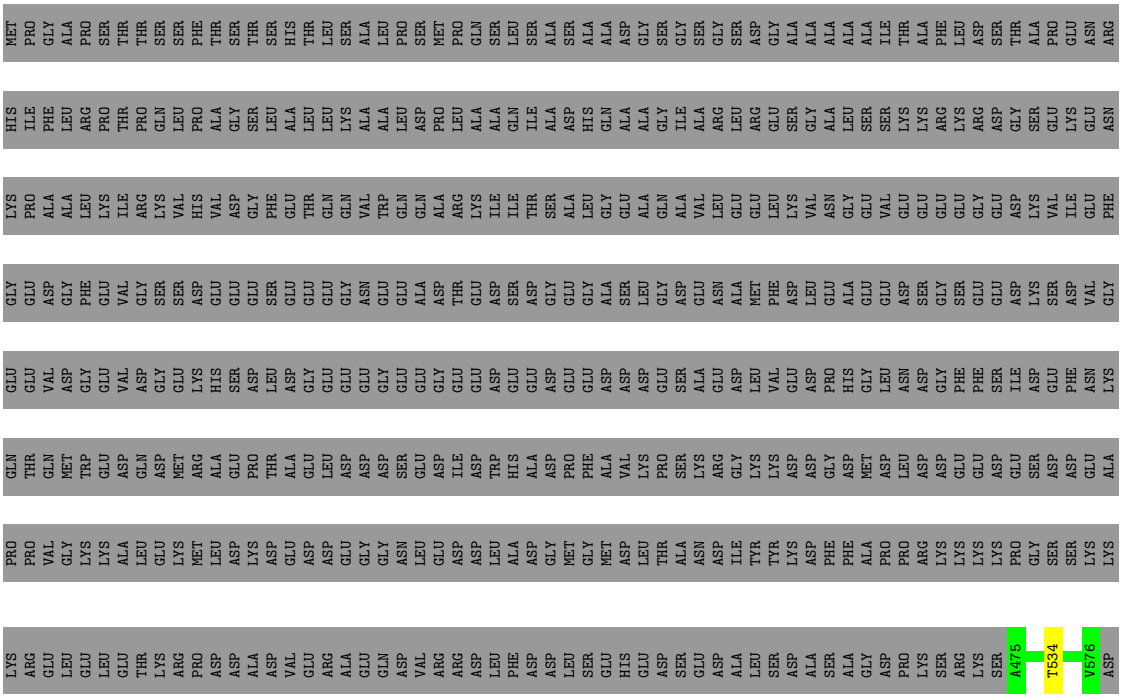
- Molecule 26: Imp4

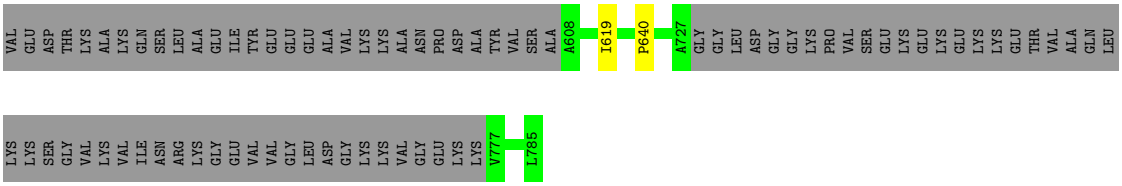
Chain CK: 95% 5%



- Molecule 27: Mpp10

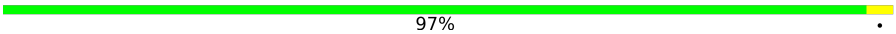
Chain CL: 29% 71%

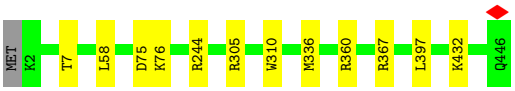




- Molecule 28: Sof1

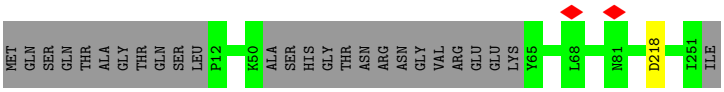
Chain CM:





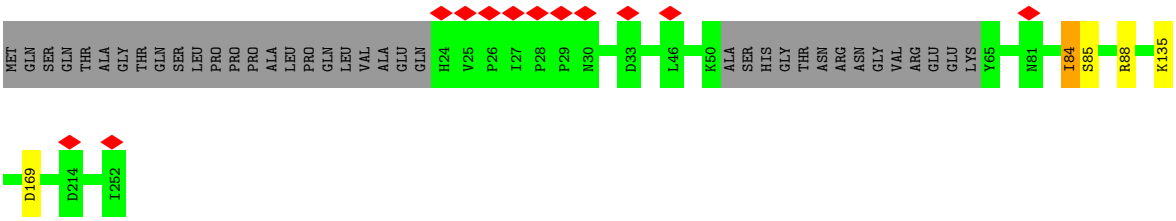
- Molecule 29: Emg1

Chain CN:



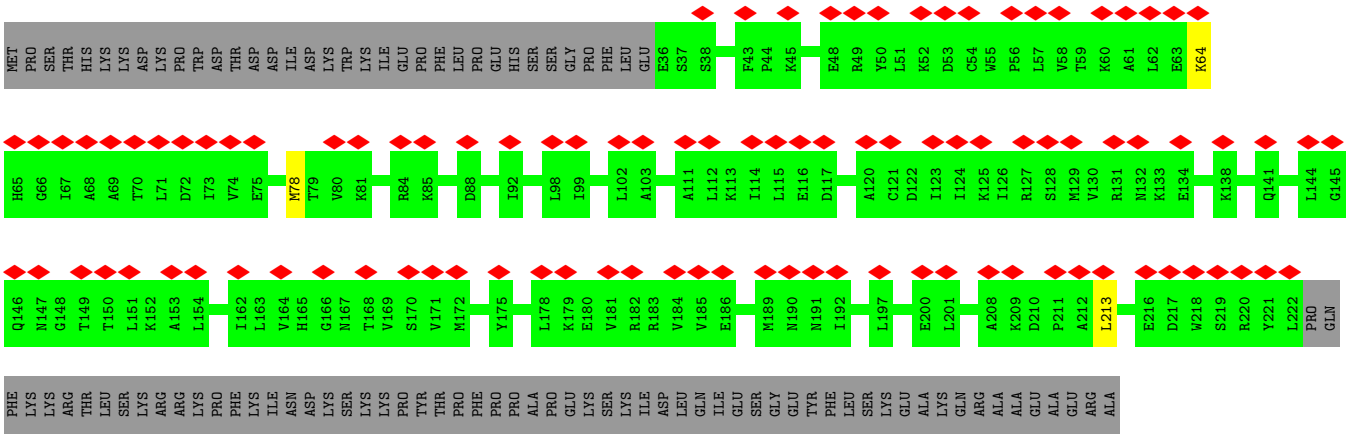
- Molecule 29: Emg1

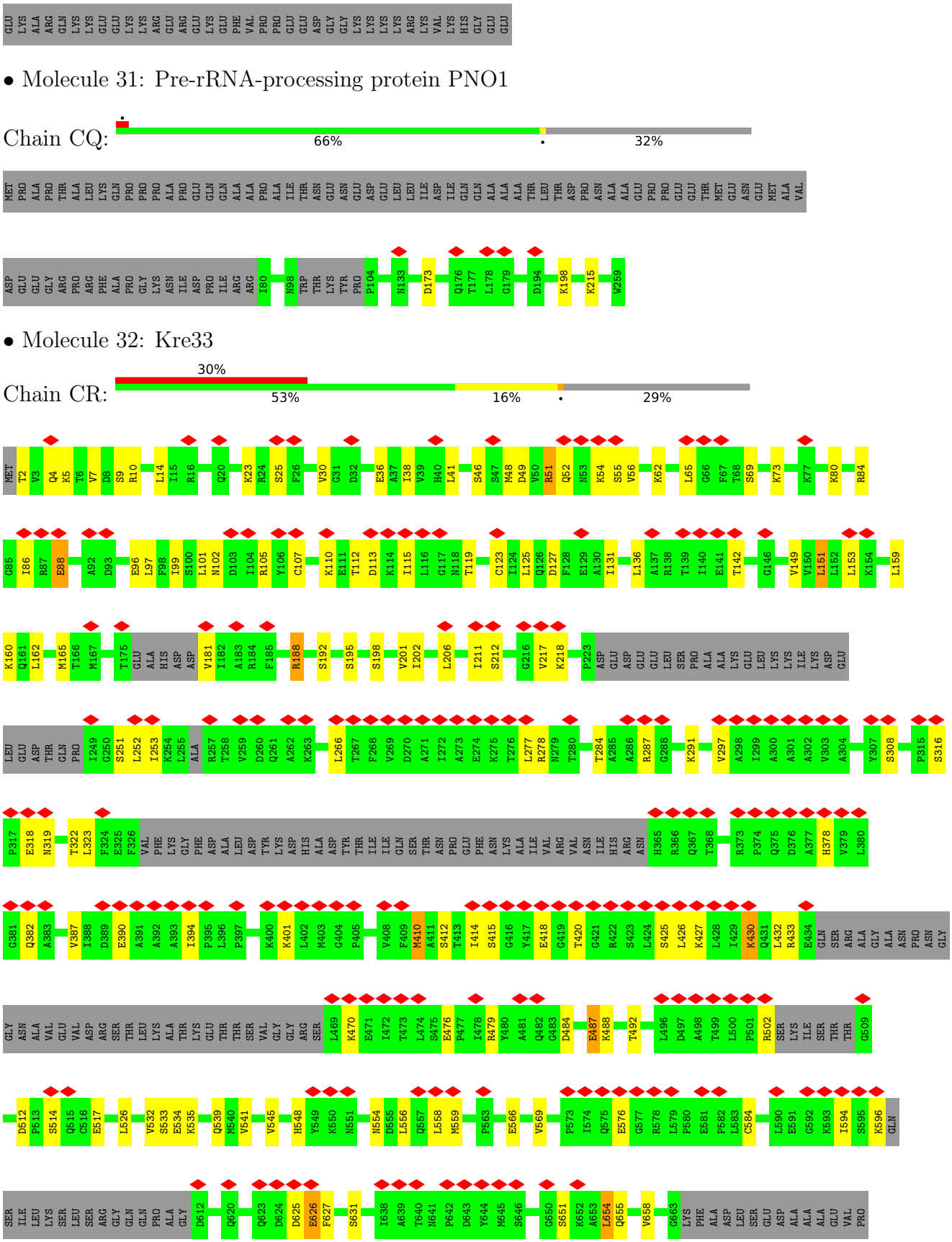
Chain CO:

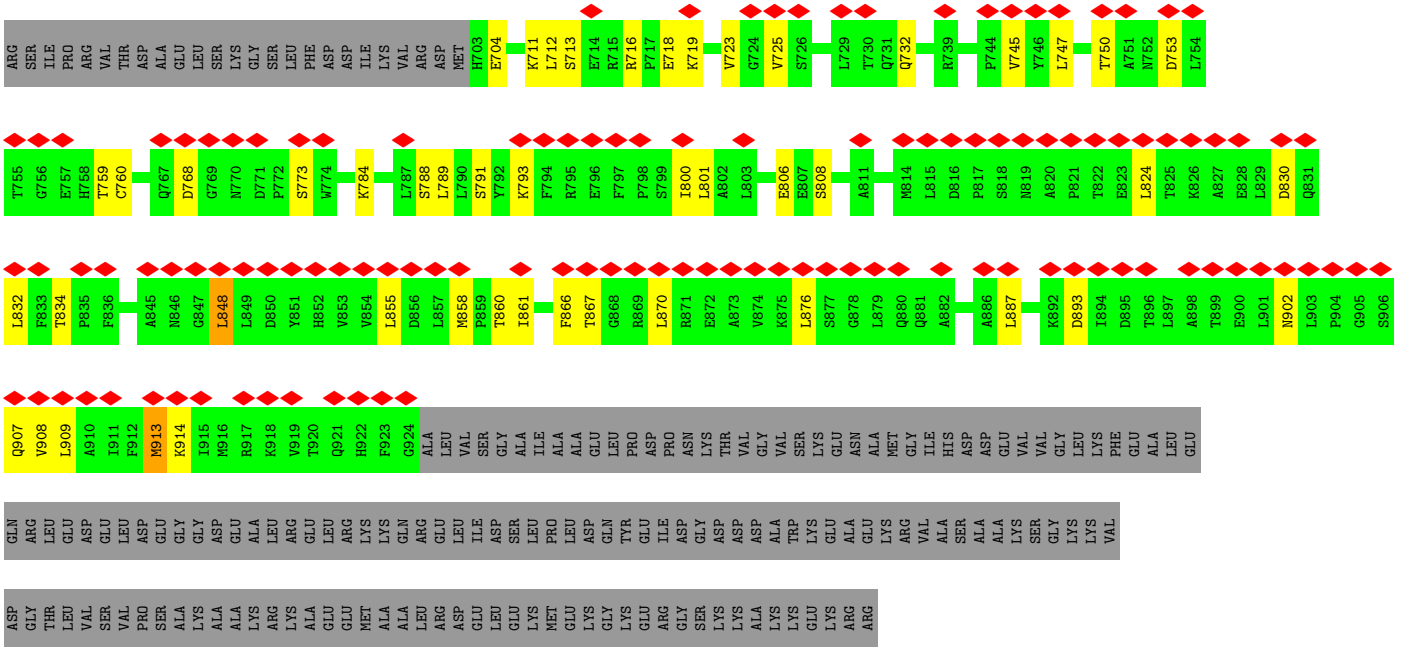


- Molecule 30: KRR1 small subunit processome component

Chain CP:

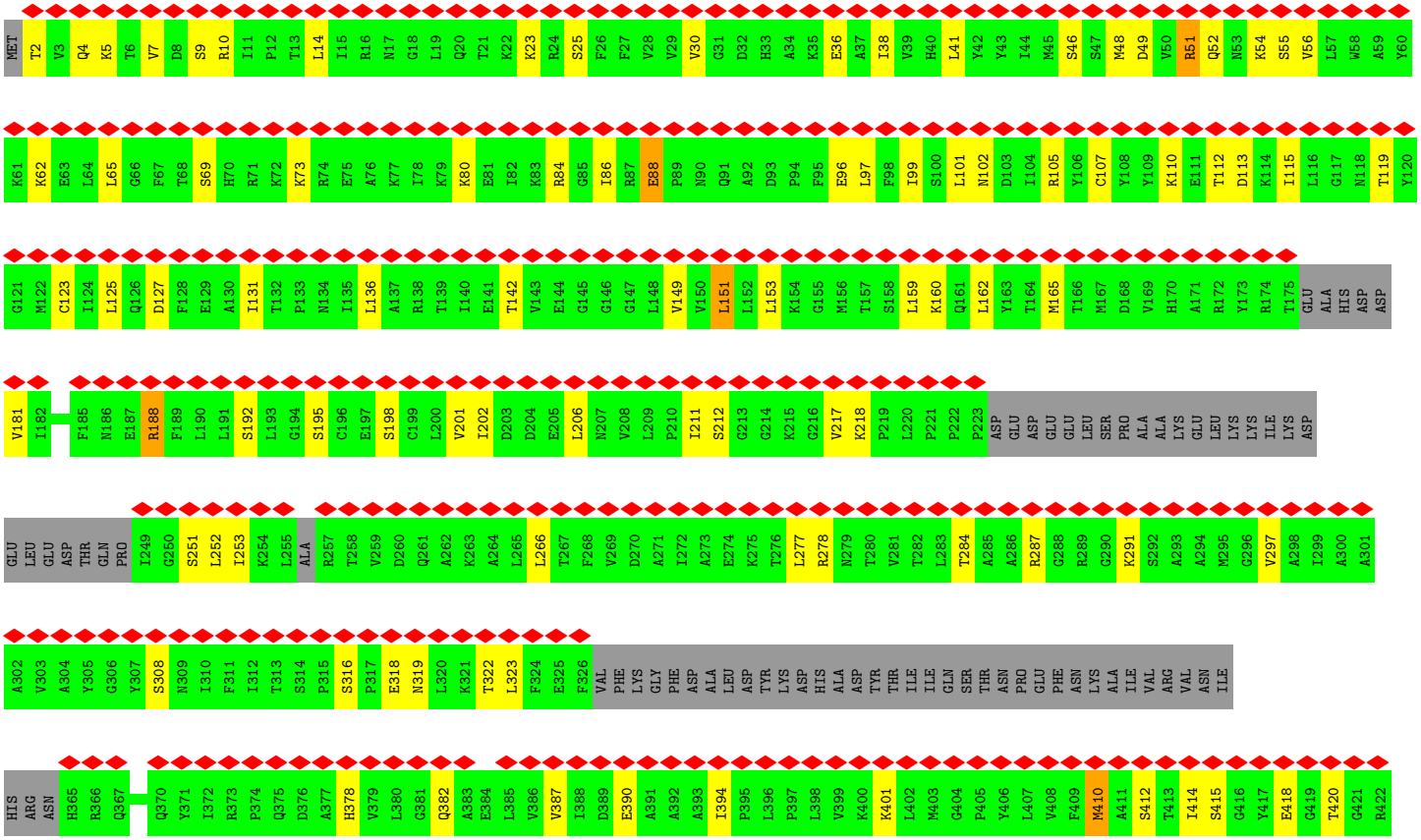


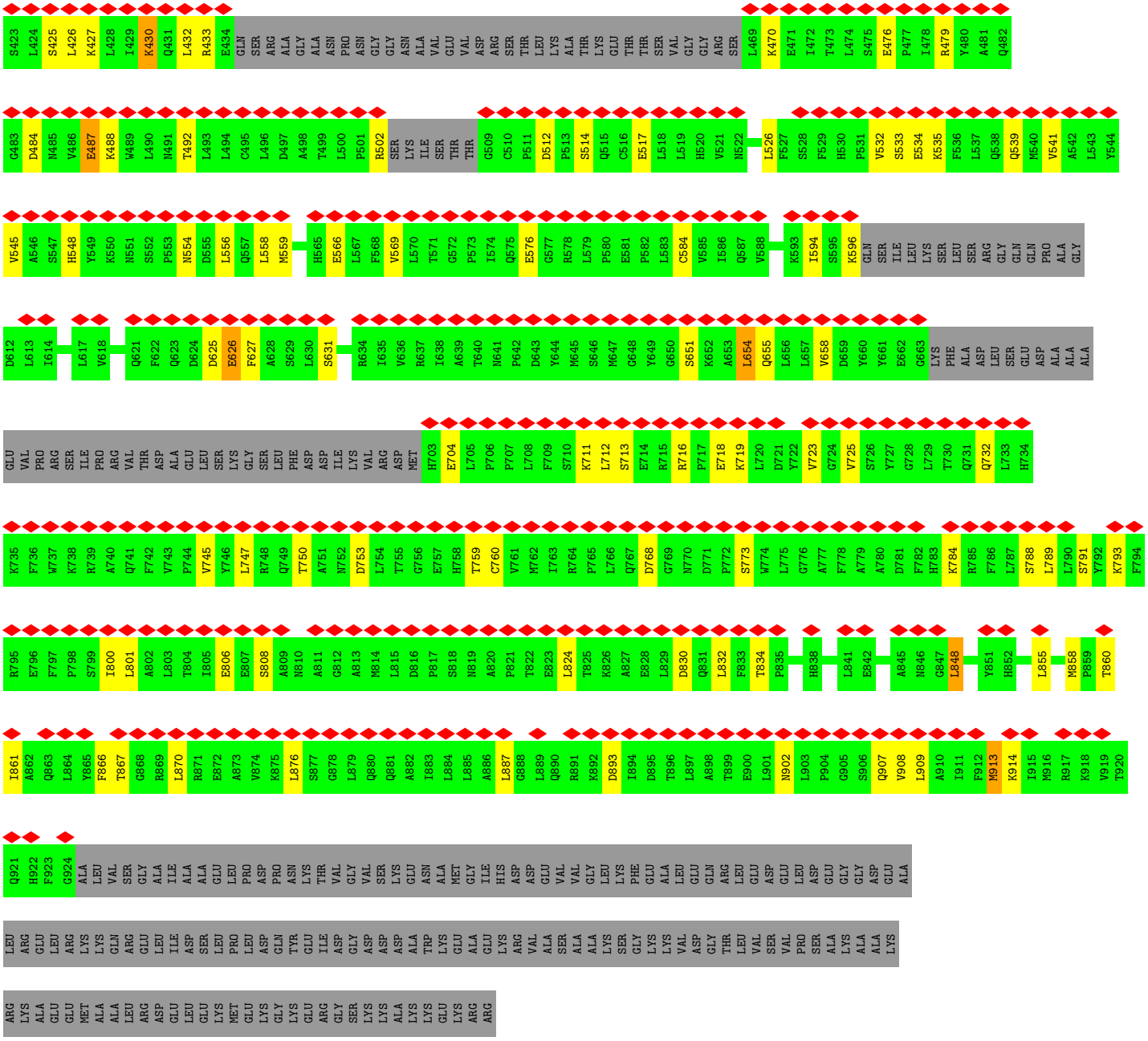

• Molecule 31: Pre-rRNA-processing protein PNO1
Chain CQ:
66%
32%
• Molecule 32: Kre33
Chain CR:
30%
53%
16%
29%



- Molecule 32: Kre33

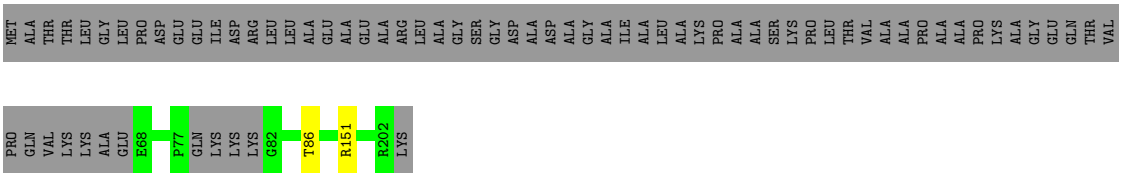
Chain CS:





- Molecule 33: Fcf2

Chain CT: 64% • 35%



- Molecule 34: 40S ribosomal protein s5-like protein

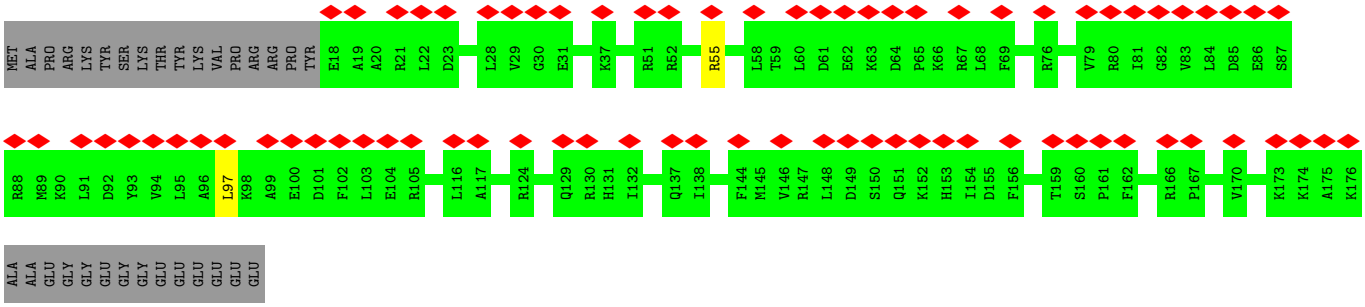
Chain Cc: 89% • 9%

• Molecule 35: 40S ribosomal protein S7

Chain Ce:

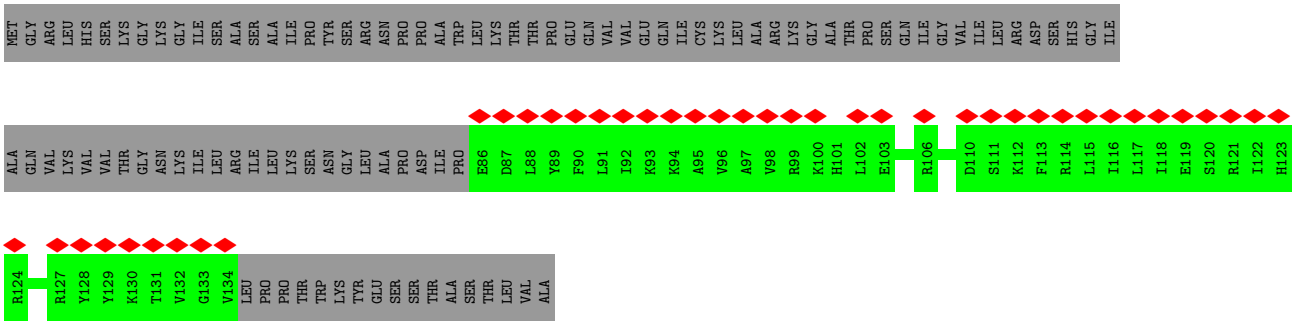
• Molecule 36: 40S ribosomal protein s9-like protein

Chain Cg:



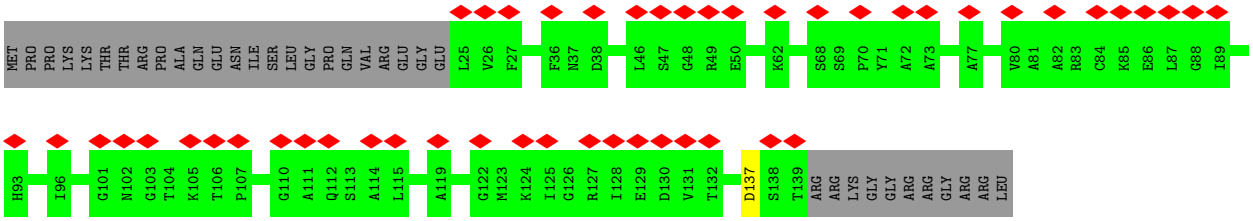
• Molecule 37: 40S ribosomal protein S13-like protein

Chain Ch:



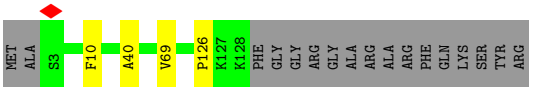
• Molecule 38: 40S ribosomal protein S14-like protein

Chain Ci:



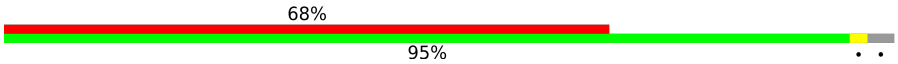
- Molecule 39: 40S ribosomal protein S16-like protein

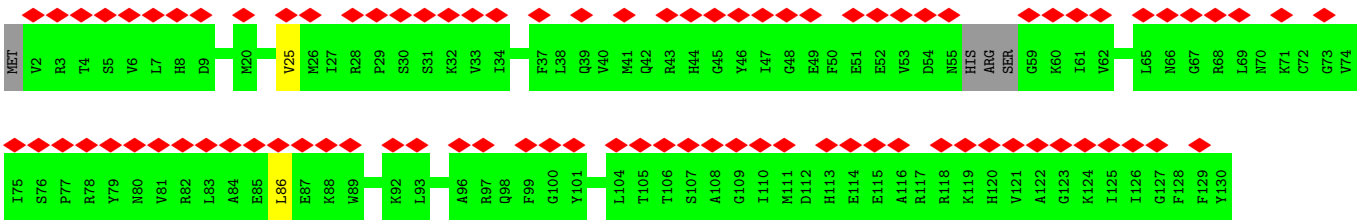
Chain Cj:



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

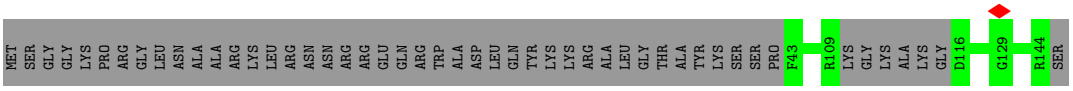
Chain Cm:





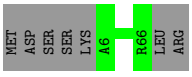
- Molecule 41: 40S ribosomal protein s23-like protein

Chain Cn:



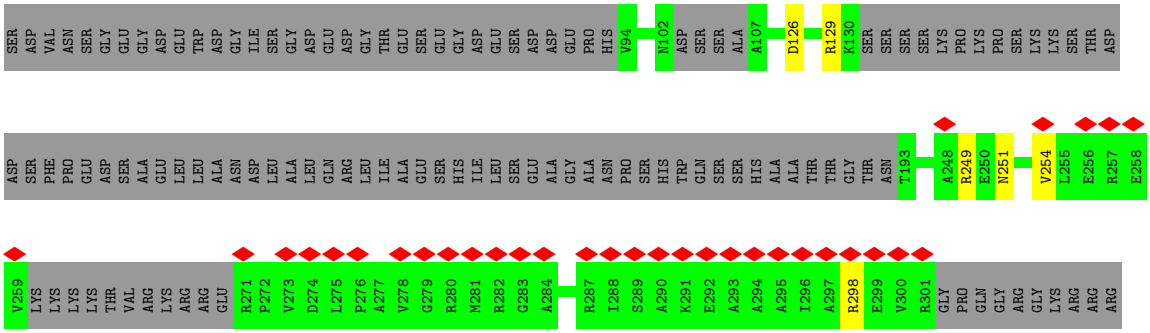
- Molecule 42: 40S ribosomal protein S28-like protein

Chain Cp:



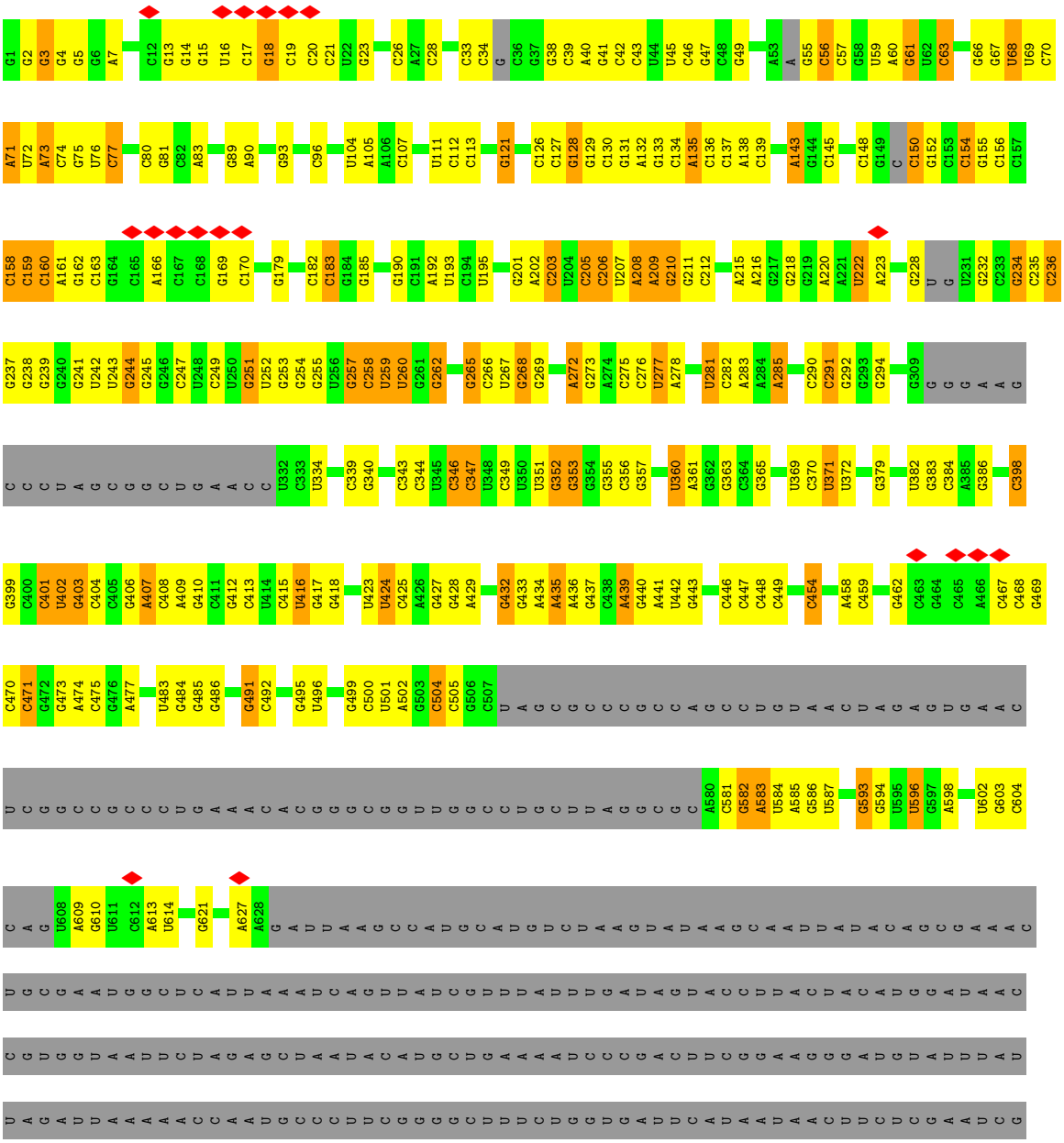
- Molecule 43: Faf1

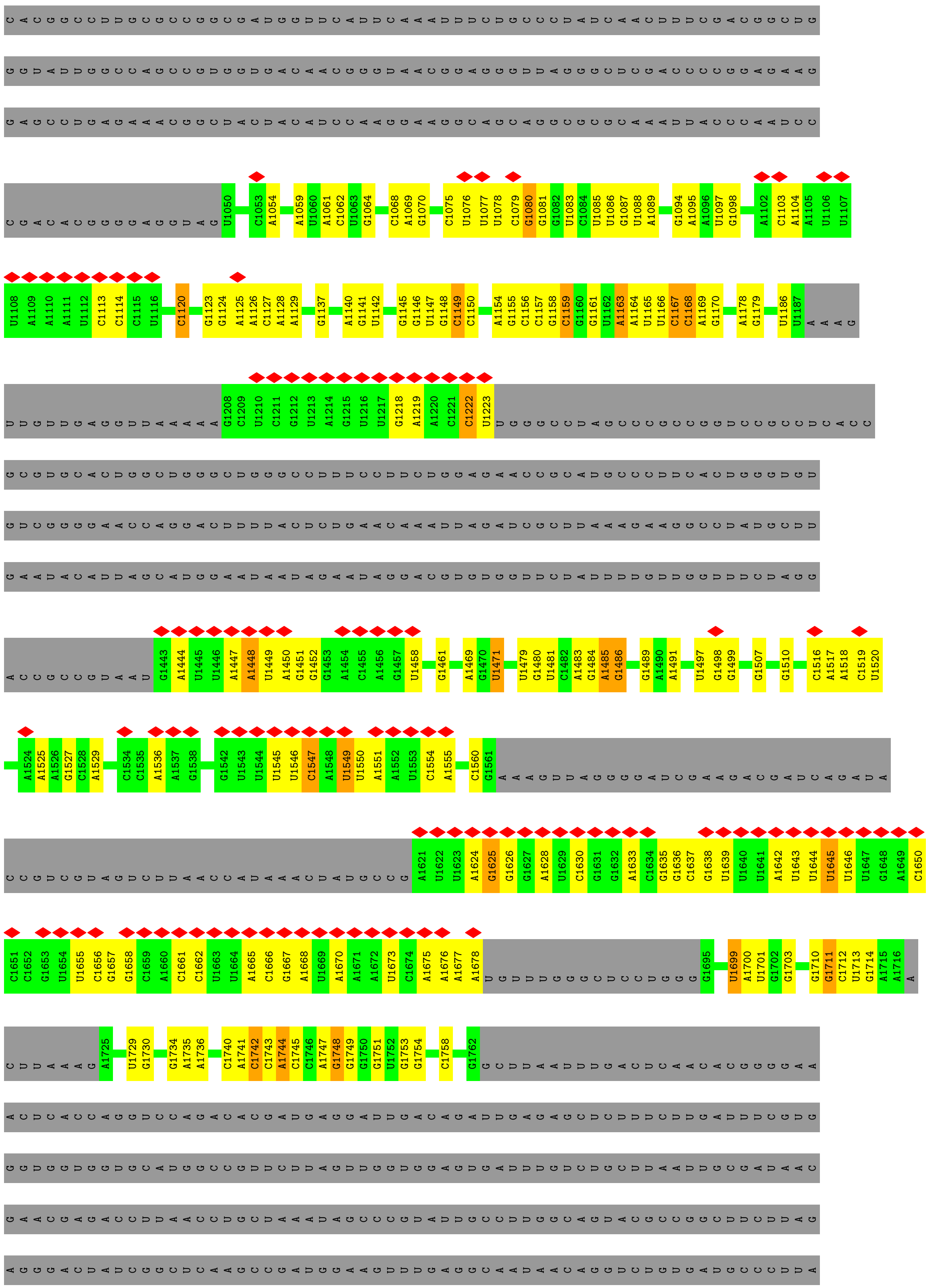
Chain CU:

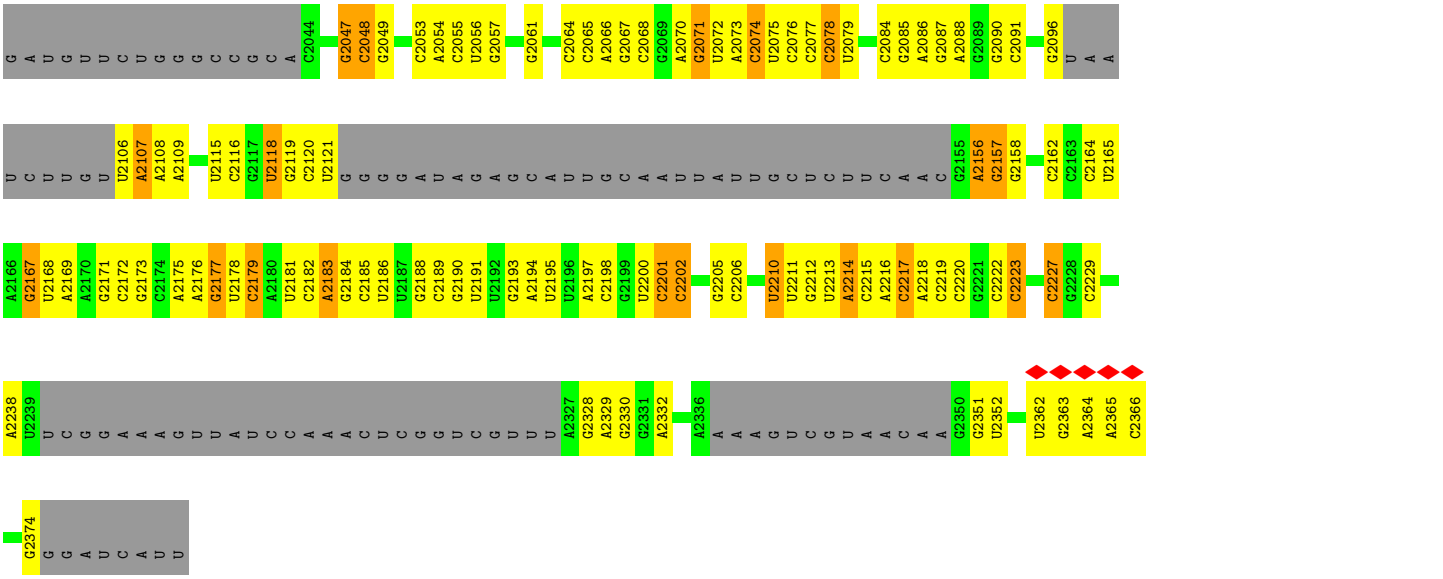


- Molecule 44: 35S rRNA

Chain C1: 6% 24% 19% 5% 52%

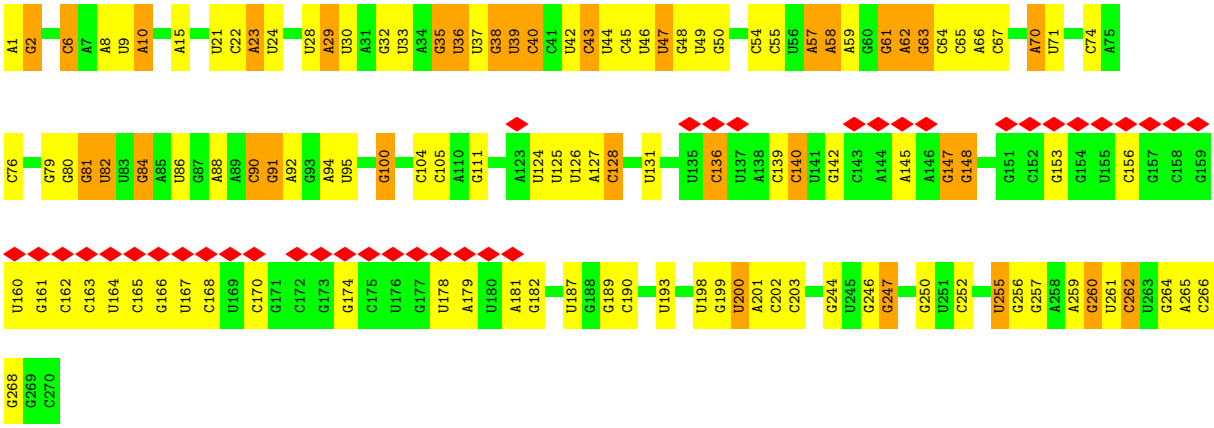






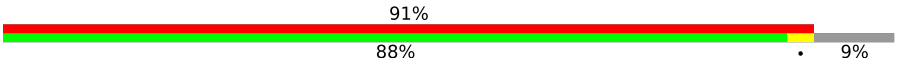
- Molecule 45: U3 snoRNA

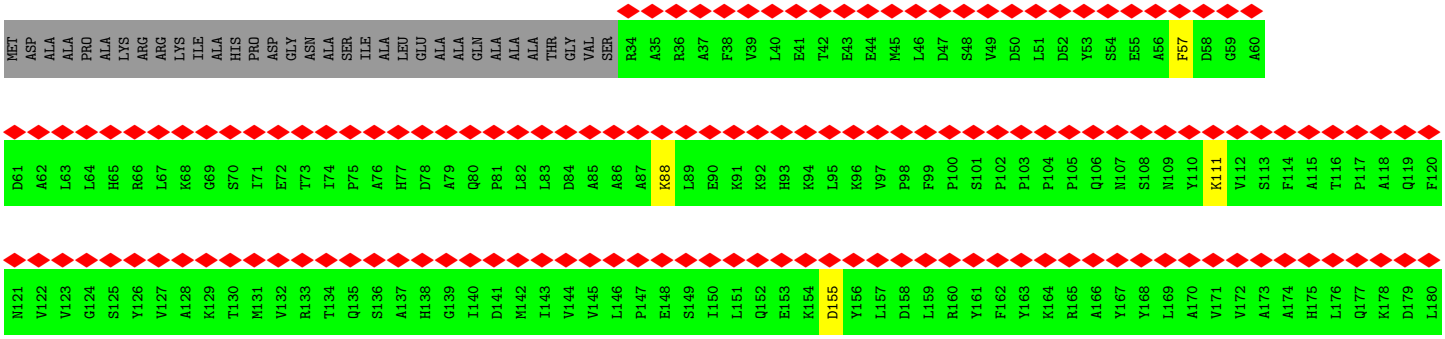
Chain C2:



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

Chain UV:





K181 G182 E183 A184 T185 L186 S187 Y188 E189 Y190 H191 N192 G193 N194 S195 L196 L197 P198 V199 L200 S201 V202 K203 P204 N205 G206 E207 K208 D209 E210 D211 E212 K213 K214 K215 K216 K217 G218 V219 L220 D221 Y222 R223 I224 R225 I226 I227 P228 C229 A230 P231 E232 S233 F234 F235 P236 R237 Q238 K239 L240

H241 L242 G243 A244 T245 L246 V247 R248 K249 H250 K251 E252 G253 E254 Q255 Q256 A257 N258 G259 Q260 P261 A262 T263 P264 A265 T266 P267 F268 Y269 N270 S271 T272 L273 V274 A275 E276 S277 S278 Y279 L280 Q281 Y282 L283 K284 L285 L286 R287 Q288 T289 E290 K291 K292 C293 A294 A295 F296 R297 N298 A299 C300

I301 L302 G303 R304 I305 W306 L307 Q308 Q309 R310 G311 F312 G313 S314 D315 V316 S317 K318 G319 G320 F321 G322 Y323 F324 E325 W326 A327 V328 L329 L330 A331 L332 L333 L334 Q335 G336 G337 P338 A339 D340 T341 K342 G343 A344 A345 P346 L347 S348 P349 S350 L351 S352 S353 T354 Q355 L356 F357 K358 A359 L360

I361 Q362 F363 L364 S365 V366 T367 N368 F369 A370 E371 K372 P373 C374 V375 L376 G377 Q378 A379 G319 K380 P381 D382 L383 A384 G385 F386 I387 E388 N389 G390 P391 I392 L393 W394 D395 S396 A397 R398 Q399 L400 N401 I402 A403 F404 K405 M406 G407 P408 W409 S410 A411 D412 L413 L414 H415 Q416 H417 A418 R419 W420

T421 R422 K423 L424 L425 A426 D427 G428 A429 V430 D431 Q432 F433 Q434 P435 T436 F437 I438 L439 K440 A441 D442 L443 P444 T445 H446 T447 Y448 D449 L450 V451 A452 R453 M454 D455 P456 E457 K458 V459 S460 E461 A462 A463 P464 D465 K466 V467 A468 H469 E470 A471 R472 G473 R474 H475 W476 Q477 V478 G479 H480

K481 V482 Y483 R484 I485 L486 R487 R488 A489 L490 S491 D492 K493 N494 M495 E496 G497 G498 E499 R500 A501 R502 L503 I504 H505 L506 K507 V508 S509 P510 G511 F512 S513 S514 S515 S516 W517 S518 L519 N520 E521 K522 P523 Q524 P525 Q526 K527 A528 G529 T530 P531 I532 E533 I534 G535 V536 L537 F538 D539 P540

L541 N542 M543 A544 R545 T546 V547 D548 R549 G550 P551 S552 A553 G554 P555 S556 A557 E558 E559 K560 E561 T562 C563 E564 K565 F566 R567 R568 F569 W570 G571 E572 K573 S574 E575 L576 R577 R578 P579 G580 G581 D582 T583 I584 R585 E586 T587 L588 V589 W590 S591 A592 Q593 T594 P595 F596 D597 L598 C599 E600

E601 I602 M603 R604 Y605 I606 L607 G608 L609 H610 L611 R612 V613 G614 Q615 L616 Q617 D618 D619 I620 V621 F622 Y623 G624 R625 S626 L627 P628 A629 L630 L631 S632 I633 K634 P635 S636 D637 T638 A639 L640 F641 N642 V643 A644 R645 K646 T647 F648 T649 S650 F651 E652 R653 D654 L655 R656 D657 L658 E659 D660

L661 P662 L663 R664 I665 R666 H667 V668 N669 P670 I671 C672 P673 E674 L675 R676 H677 S678 S679 L680 K681 T682 P683 S684 F685 G686 P687 S688 K689 S690 G691 P692 R693 P694 M695 E696 V697 V698 I699 S700 F701 E702 A703 S704 G705 K706 W707 P708 E709 S710 L711 I712 A713 I714 Q715 R716 T717 K718 I719 A720

F721 L722 L723 M724 I725 G726 R727 L728 L729 E730 R731 F732 K733 P734 G735 E736 I737 R738 T739 H740 V741 G742 L743 D744 D745 A746 R747 Y748 E749 T750 E751 N752 L753 A754 F755 L756 D757 V758 I759 Y760 A761 S762 G763 A764 C765 F766 R767 V768 R769 I770 Q771 A772 D773 L774 E775 E776 S777 L778 L779 E780

R781 Q782 T783 K784 D785 K786 T787 T788 E789 Q790 Y791 L792 R793 Q794 R795 A796 S797 T798 Q799 L800 A801 S802 F803 R804 R805 T806 F807 V808 H809 L810 P811 L812 H813 T814 Q815 Y816 I817 T818 T819 A820 T821 T822 R823 F824 P825 A826 L827 S828 P829 T830 I831 R832 L833 V834 K835 H836 W837 F838 S839 V840

H841 K842 L843 S844 N845 H846 F847 P848 P849 E850 L851 L852 E853 L854 F855 V856 L857 H858 T859 F860 L861 A862 P863 Y864 P865 W866 D867 V868 P869 S870 S871 P872 T873 T874 G875 F876 L877 R878 T879 L880 L881 F882 L883 A884 R885 W886 D887 W888 R889 T890 D891 P892 L893 I894 I895 D896 T897 SER LEU ASN

GLY GLU LEU PRO ALA GLN GLU ARG GLN ALA ILE ALA THR ARG L915 D916 A917 W918 R919 K920 L921 D922 P923 G924 M925 Q926 H927 T928 V929 L930 F931 V932 A933 T934 A935 H936 E937 Q938 S939 G940 T941 M942 W943 T944 S945 V946 D947 G948 H949 P950 R951 P952 S953 K954 V955 V956 A957 A958 R959 M960

T961 A962 L963 A964 K965 S966 A967 A968 R969 V970 I971 R972 E973 Q974 G975 V976 D977 L978 D979 V980 R981 R982 L983 F984 V985 P986 S987 L988 K989 E990 Y991 D992 V993 L994 L995 Y996 L997 N998 T999 K1000 V1001 L1002 K1003 S1004 A1005 L1006 R1007 T1008 Y1009 I1010 T1011 V1012 D1013 P1014 A1015 T1016 E1017 M1018 N1019 G1020

G1021 K1022 G1023 Q1024 E1025 I1026 K1027 F1028 K1029 N1030 L1031 A1032 P1033 E1034 T1035 V1036 E1037 P1038 P1039 L1040 P1041 V1042 A1043 Q1044 H1045 P1046 V1047 D1048 V1049 L1050 L1051 K1052 Q1053 L1054 S1055 A1056 V1057 Y1058 D1059 S1060 A1061 A1062 G1063 A1064 S1065 G1066 T1067 G1068 P1069 L1070 V1071 F1072 F1073 R1074 S1075 D1076 T1077 T1078 A1079 T1080

E1081 E1082 G1083 D1084 K1085 V1086 I1087 G1088 A1089 V1090 W1091 N1092 P1093 T1094 L1095 V1096 K1097 R1098 K1099 W1100 R1101 V1102 N1103 L1104 P1105 T1106 S1107 Y1108 K1109 P1110 V1111 ALA GLY GLY LYS ASP GLU SER GLU ASP GLU ASP GLU ASP GLU ASP GLU ASP GLY SER GLU ARG GLU LYS GLU ARG GLU GLY GLU GLY

ARG VAL GLU VAL GLU VAL ASN ARG GLU GLY ILE LEU ALA GLU VAL ALA ARG ILE ALA GLY GLU VAL VAL GLU ARG ILE GLU VAL LYS GLY LEU

- Molecule 47: Rrp7

Chain CV: 46% 44% 54%

MET ALA SER ASN ILE PRO SER THR ILE GLY GLU PHE SER VAL LEU PRO VAL SER ILE PRO PRO LEU PRO SER PHE PRO LYS ASN VAL V30 H31 Y32 L33 Y34 V35 R36 R37 H38 A39 P40 K41 I42 P43 T44 P45 T46 D47 S48 R49 S50 L51 F52 V53 T54 N55 V56 P57 V58 D59 S60

T61 E62 A63 H64 L65 R66 A67 L68 V69 T70 S71 L72 V73 G74 T75 G76 R77 F78 E79 K80 V81 T82 F83 E84 D85 E86 S87 K88 Q89 E90 H91 S92 L93 E94 G95 K96 S97 T98 I99 D100 A101 A102 Q103 PRO VAL HIS ALA ALA ARG LEU LEU GLN ALA HIS ILE LYS LYS ARG LYS ARG

ASP ASP GLU GLU ALA GLN GLU GLU GLU ALA ALA ARG LEU PRO SER THR TRP THR ARG PRO LEU ARG ARG SER G145 S146 T147 A148 V149 V150 L151 L152 A153 D154 E155 K156 S157 V158 E159 Q160 V161 L162 K163 A164 I165 A166 K167 V168 H169 K170 T171 K172 K173 Y174 P175 V176 W177 G178 G179 D180

G181 L182 P183 D184 S185 K186 M187 P188 P189 L190 G191 P192 V193 W194 L195 K196 S197 H198 N199 R200 L201 S202 F203 P204 D205 P206 S207 M208 L209 Q210 A211 S212 V213 D214 A215 F216 S217 T218 LEU PHE ALA ARG ARG GLU GLN GLU ALA ALA GLU ILE ALA LYS ARG LEU ARG ASN GLU PRO ASP GLU

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

PHE ASP GLU ASP ARG LYS LYS LEU GLU GLU LEU ARG ALA LYS LYS GLY LYS PHE VAL PRO GLU ALA

- Molecule 48: Utp8

Chain UH: 38% 61%

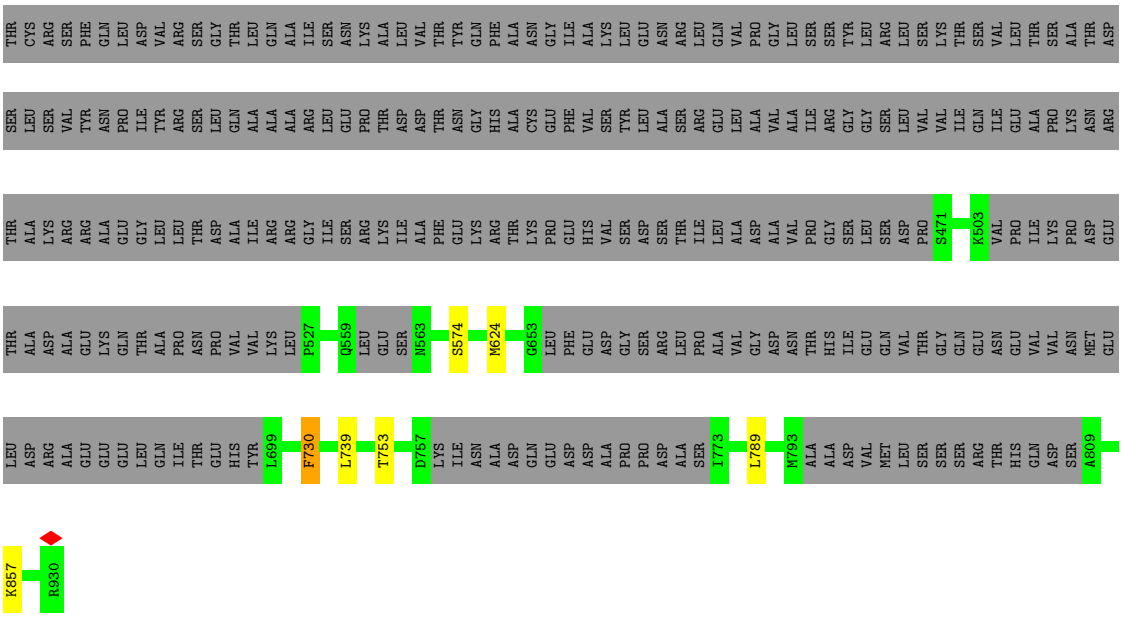
MET ALA ALA LYS LEU GLN ILE HIS ALA PRO TYR VAL LEU HIS ALA LEU PRO ARG PRO LEU ASP ARG SER PRO SER ASP GLY LEU GLY ARG TYR PHE SER GLY GLU VAL PHE GLY GLN LYS GLN GLY GLY LYS ARG LYS LYS ARG THR GLU LEU ALA VAL ALA ILE ASP GLY VAL ALA VAL TYR LEU

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

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

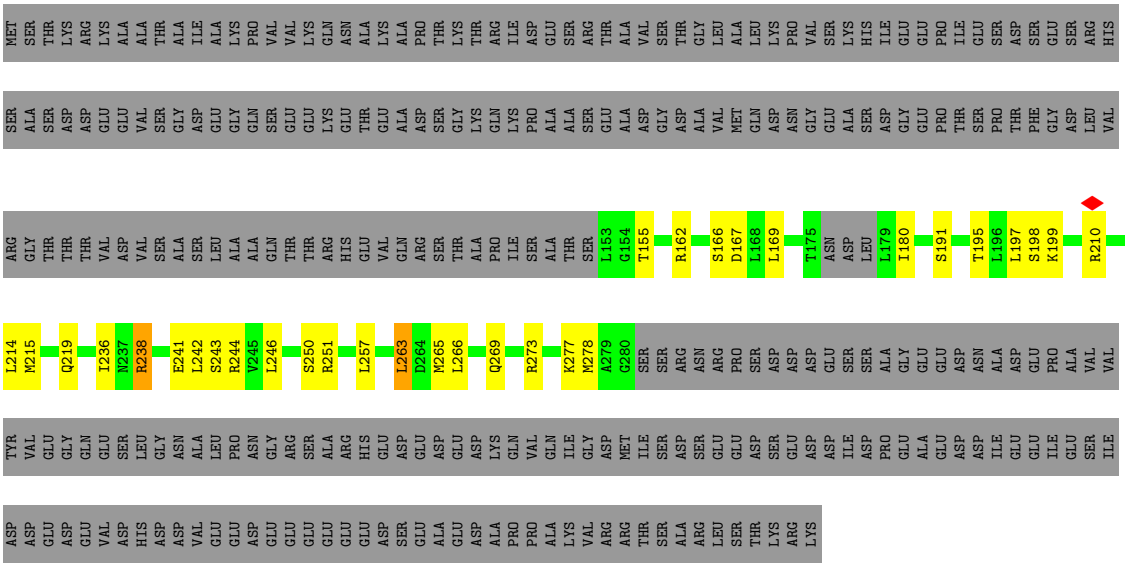
ALA LEU ASN GLY GLU THR LEU GLU LYS TRP GLN VAL SER PRO SER VAL LEU SER ARG GLU ILE LEU SER ASP SER LYS LEU ALA LEU GLN VAL ASP PHE VAL GLN GLN THR SER ALA ASP VAL ALA ASP GLY LEU PHE GLY GLY LYS VAL PHE GLN GLU

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



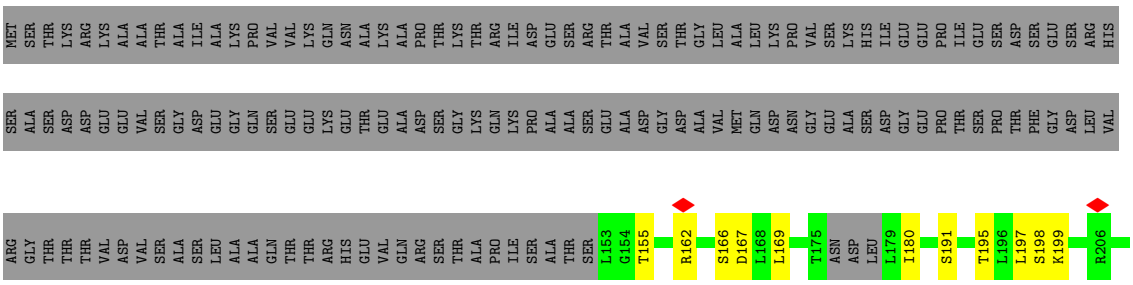
- Molecule 49: Utp5

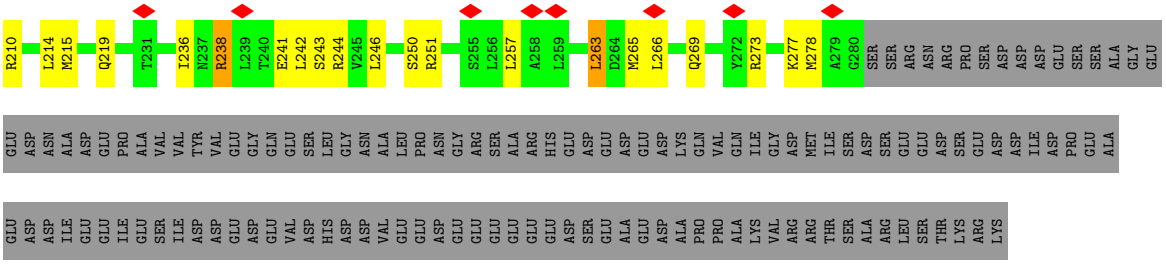
Chain UE: 23% 7% 70%



- Molecule 49: Utp5

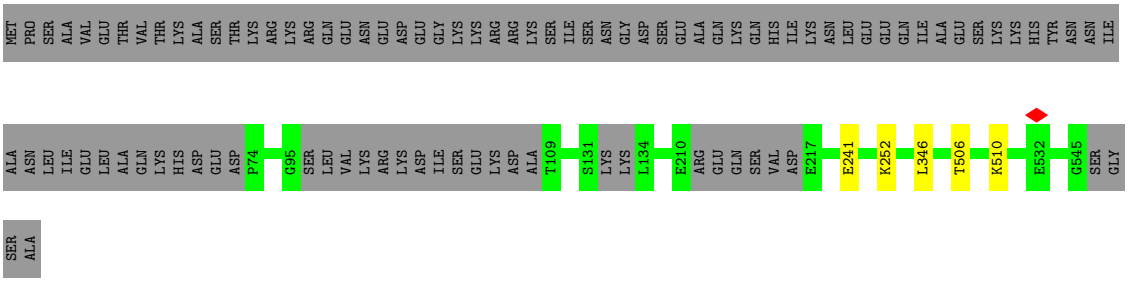
Chain UI: 23% 7% 70%





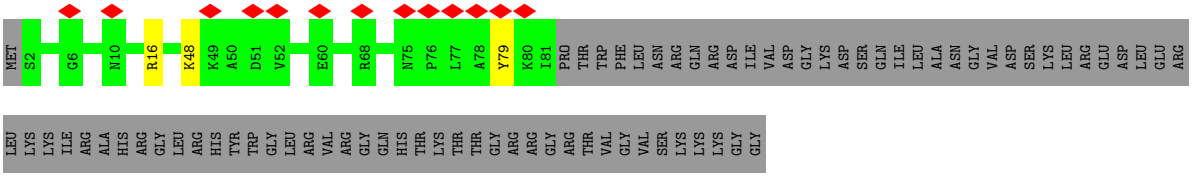
• Molecule 50: Noc4

Chain US:



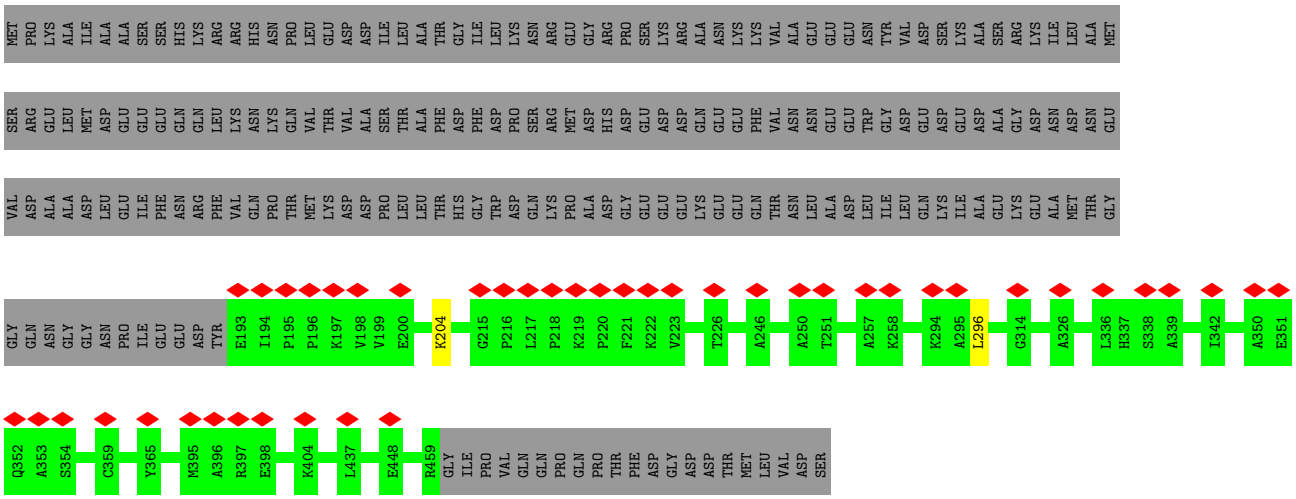
• Molecule 51: Rps18

Chain Cl:



• Molecule 52: Enp1

Chain CX:



• Molecule 53: Utp16

Chain UP: 15% 85%

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

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

SER SER LYS THR SER ALA ASP ARG ARG HIS ILE THR PHE ASP ASP SER GLU SER GLU GLN PHE ILE THR LEU LYS GLU GLU ALA ALA SER ARG ASN GLY LEU GLY ASN GLY SER LYS LYS SER GLU ARG GLU ILE VAL GLN ASP SER GLN ASP GLU GLU GLU ASP SER GLU GLU SER ASP

ASP ASP ALA PRO PRO GLU GLU VAL ALA THR GLY GLU ALA GLU ALA ALA LEU LEU LYS ALA GLU ARG ALA ALA ALA ALA GLU GLN GLN ALA ALA ALA LEU GLU LYS ARG LYS ARG GLN GLU ARG ASP ALA PHE LEU LYS GLN GLN ALA GLU GLN ARG LYS ARG ASN LYS LYS PRO ALA

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

PRO LYS LEU LEU VAL GLU PRO K308 G327 D328 P329 V361 ASN LYS ARG

- Molecule 54: Rrp5

Chain Cz: 13% 15% 85%

MET GLY SER LEU LYS ARG LYS GLU GLY PRO ASP GLY SER SER ALA SER LYS SER LYS ARG ALA LYS SER GLY GLU THR THR LYS ASP THR LYS ILE ASP SER ASN LYS ASP ALA LYS GLN LEU LYS THR PRO ALA VAL ALA LYS PRO ILE THR THR PRO VAL VAL THR VAL LEU LYS ASP

GLU GLU PRO LEU PHE PRO ARG GLY GLY GLY SER VAL LEU THR PRO LEU GLU GLN LYS GLN ILE SER ILE GLN ALA LYS LYS ASP VAL LEU PHE GLU GLU ALA LYS LYS GLY GLY LYS GLU ASP THR ALA ALA ARG SER LYS LYS LYS ARG LYS SER LYS ILE GLU GLU PRO ALA THR LYS

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

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

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

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

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

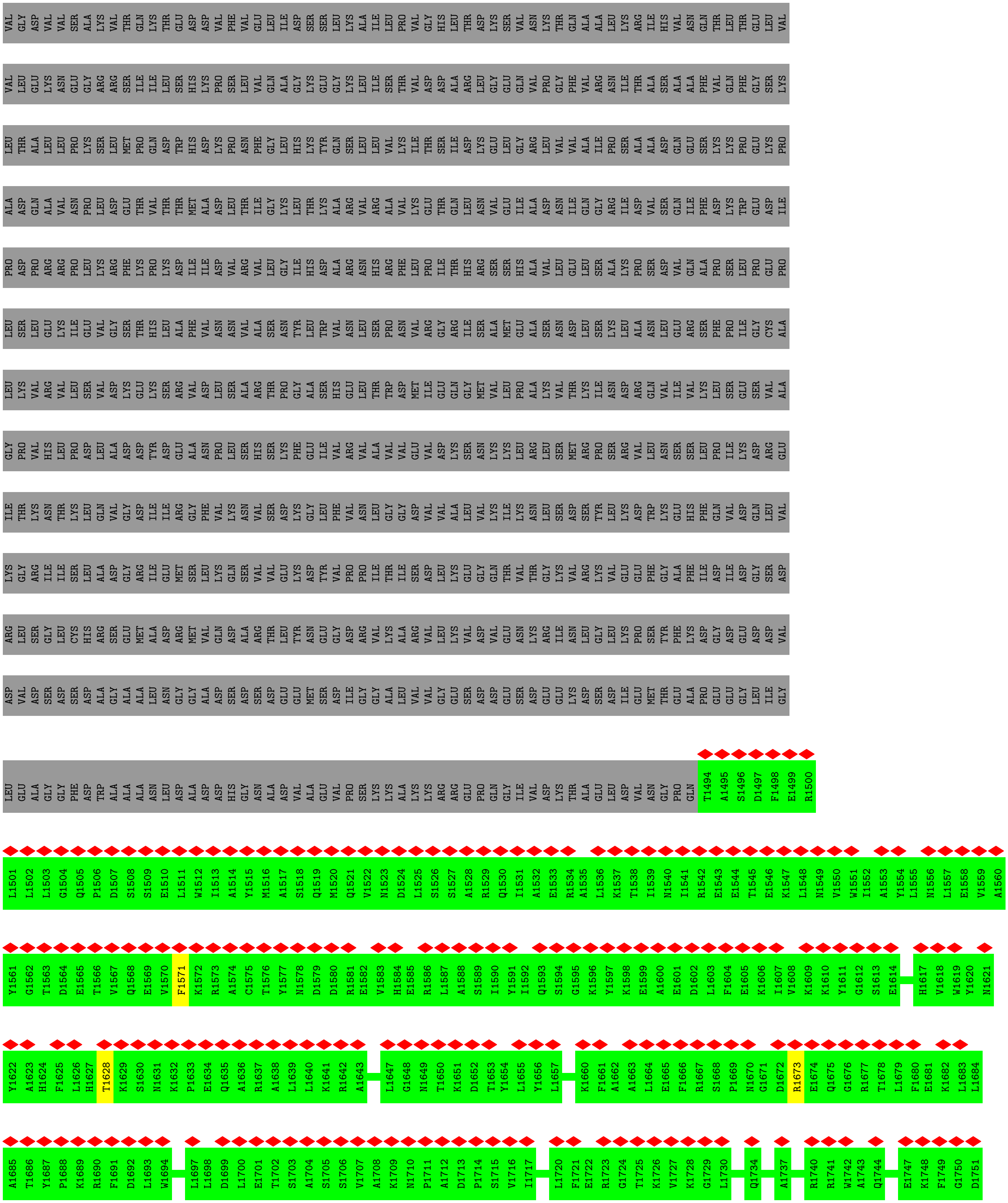
LEU PRO HIS VAL LEU SER LEU LYS PRO LYS THR THR THR LYS ASP GLY GLN GLU VAL LEU PRO THR ASP VAL LEU ALA HIS SER ALA ALA ILE ILE GLN GLU CYS ARG VAL GLU ARG VAL GLU PRO GLY ILE GLY LEU TYR VAL ASN VAL GLY VAL GLY GLY VAL SER GLY PHE VAL HIS ILE

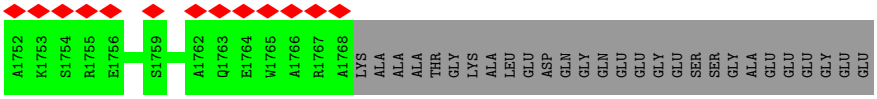
SER ARG VAL LYS ASP GLY LYS ILE ASP THR LEU PHE GLU ASN SER GLY PRO TYR LYS ILE GLY SER VAL VAL GLY TYR ASN SER PHE ASP GLY VAL TYR LEU LEU SER LEU GLU LYS SER VAL LEU GLU GLN PRO PHE LEU ARG ILE GLU ASP ILE PRO ILE GLY

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

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

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


VAL GLY ASP VAL VAL SER ALA LYS VAL THR GLN LYS THR GLU ASP ASP VAL PHE VAL GLU LEU ILE ASP SER SER LEU LYS ALA ILE LEU PRO VAL GLY HIS LEU THR ASP LYS SER VAL ASN LYS THR GLN ALA ALA LEU LYS ARG ILE HIS VAL ASN GLN THR LEU THR GLU LEU VAL
VAL LEU GLU LYS ASN GLU GLY ARG ARG SER ILE ILE LEU SER HIS LYS PRO SER LEU VAL GLN ALA GLY LYS GLU GLY LYS LEU ILE SER THR VAL ASP ASP ALA ARG LEU GLY GLU GLN VAL PRO GLY PHE VAL ARG ASN ILE THR ALA SER ALA ALA PHE VAL GLN PHE GLY SER LYS
LEU THR ALA LEU LEU PRO LYS SER LEU MET PRO GLN ASP TRP HIS ASP LYS PRO ASN PHE GLY LEU HIS LYS TYR GLN SER LEU LEU VAL LYS ILE THR SER ILE ASP LYS GLU LEU GLY ARG LEU VAL VAL ALA ILE PRO SER ALA ALA ASP GLN GLU SER LYS LYS PRO GLU LYS PRO
ALA ASP GLN ALA VAL ASN PRO LEU ASP GLU THR VAL THR THR MET ALA ASP LEU THR ILE GLY LYS LEU THR LYS ALA ARG VAL ARG ALA VAL LYS GLU THR GLN LEU ASN VAL GLU ILE ALA ASP ASN ILE GLN GLY ARG ILE ASP VAL SER GLN ILE PHE ASP LYS TRP GLU ASP ILE
PRO ASP PRO ARG ARG PRO LEU LYS ARG PHE LYS PRO LYS ASP ILE ILE ASP VAL ARG VAL LEU GLY ILE HIS ASP ALA ARG ASN HIS ARG PHE LEU PRO ILE THR HIS ARG SER SER HIS ALA VAL LEU GLU LEU SER ALA LYS PRO SER ASP VAL GLN ALA PRO SER LEU PRO GLU PRO
LEU SER LEU GLU LYS ILE GLU VAL GLY SER THR HIS LEU ALA PHE VAL ASN ASN VAL ALA SER ASN TYR LEU TRP VAL ASN LEU SER PRO ASN VAL ARG GLY ARG ILE SER ALA MET GLU ALA SER ASN ASP LEU SER LYS LEU ALA ASN LEU GLU ARG SER PHE PRO ILE GLY CYS ALA
LEU LYS VAL ARG VAL LEU SER VAL ASP LYS GLU LYS SER ARG VAL ASP LEU SER ALA ARG THR PRO GLY ALA SER HIS GLU LEU THR TRP ASP MET ILE GLU GLN GLY MET VAL LEU PRO ALA LYS VAL THR LYS ILE ASN ASP ARG GLN VAL ILE VAL LYS LEU SER GLU SER VAL ALA
GLY PRO VAL HIS LEU PRO ASP LEU ALA ASP ASP TYR ASP GLU ALA ASN PRO LEU SER HIS SER LYS PHE GLU ILE VAL ARG VAL ALA VAL VAL GLU VAL ASP LYS SER ASN LYS LYS LEU ARG LEU SER MET ARG PRO SER ARG VAL LEU ASN SER SER LEU PRO ILE LYS ASP ARG GLU
ILE THR LYS ASN THR LYS LEU GLN VAL GLY ASP ILE ILE ARG GLY PHE VAL LYS ASN VAL SER ASP LYS GLY LEU PHE VAL ASN LEU GLY GLY ASP VAL VAL ALA LEU VAL LYS ILE LYS ASN LEU SER ASP SER TYR LEU LYS ASP TRP LYS GLU HIS PHE GLN VAL ASP GLN LEU VAL
LYS GLY ARG ILE ILE SER LEU ALA ASP GLY ARG ILE GLU MET SER LEU LYS GLN SER VAL VAL GLU LYS ASP TYR VAL PRO PRO ILE THR ILE SER ASP LEU LYS GLU GLY GLN THR VAL THR GLY LYS VAL ARG LYS VAL GLU GLU PHE GLY ALA PHE ILE ASP ILE ASP GLY SER ASP
ARG LEU SER GLY LEU CYS HIS ARG SER GLU MET ALA ASP ARG MET VAL GLN ASP ALA ARG THR LEU TYR ASN GLU GLY ASP ARG VAL LYS ALA ARG VAL LEU LYS VAL ASP VAL GLU ASN LYS ARG ILE ASN LEU GLY LEU LYS PRO SER TYR PHE LYS ASP GLY ASP GLU ASP ASP VAL
ASP VAL ASP SER ASP SER ASP ALA GLY ALA ALA LEU ASN GLY GLY ALA ASP SER ASP SER ASP GLU GLU MET SER ASP ILE GLY GLY ALA LEU VAL VAL GLY GLU SER ASP ASP GLU SER ASP GLU GLU LYS ASP SER ASP ILE GLU MET THR GLU ALA PRO GLU GLU GLY LEU ILE GLY
LEU GLU ALA GLY GLY PHE ASP TRP ALA ALA ALA ASN LEU ASP ALA ASP ASP HIS GLY ASN ALA ASP VAL ALA GLU VAL PRO SER LYS LYS ALA LYS LYS ARG ARG GLU PRO GLN GLY ILE VAL ASP LYS THR ALA GLU LEU ASP VAL ASN GLY PRO GLN T1494 A1495 S1496 D1497 F1498 E1499 R1500
L1501 L1502 L1503 G1504 Q1505 P1506 D1507 S1508 S1509 E1510 L1511 W1512 I1513 A1514 Y1515 M1516 A1517 S1518 Q1519 M1520 Q1521 V1522 N1523 D1524 L1525 S1526 S1527 A1528 R1529 Q1530 I1531 A1532 E1533 R1534 A1535 L1536 K1537 T1538 I1539 N1540 I1541 R1542 E1543 E1544 T1545 E1546 K1547 L1548 N1549 V1550 W1551 I1552 A1553 Y1554 L1555 N1556 L1557 E1558 V1559 A1560
Y1561 G1562 T1563 D1564 E1565 T1566 V1567 Q1568 E1569 V1570 F1571 K1572 R1573 A1574 C1575 T1576 Y1577 N1578 D1579 D1580 R1581 E1582 V1583 H1584 E1585 R1586 L1587 A1588 S1589 I1590 Y1591 I1592 Q1593 S1594 G1595 K1596 Y1597 K1598 E1599 A1600 E1601 D1602 L1603 F1604 E1605 K1606 I1607 V1608 K1609 K1610 Y1611 G1612 S1613 E1614 H1617 V1618 W1619 Y1620 N1621
Y1622 A1623 H1624 F1625 L1626 H1627 T1628 K1629 S1630 N1631 K1632 P1633 E1634 Q1635 A1636 R1637 A1638 L1639 L1640 K1641 R1642 A1643 L1647 G1648 N1649 T1650 K1651 D1652 T1653 Y1654 L1655 Y1656 L1657 K1660 F1661 A1662 A1663 L1664 E1665 F1666 R1667 S1668 P1669 N1670 G1671 D1672 R1673 E1674 Q1675 G1676 R1677 T1678 L1679 F1680 E1681 K1682 L1683 L1684
A1685 T1686 Y1687 P1688 K1689 R1690 F1691 D1692 L1693 W1694 L1697 L1698 D1699 L1700 E1701 T1702 S1703 A1704 S1705 S1706 V1707 A1708 K1709 N1710 P1711 A1712 D1713 P1714 S1715 V1716 I1717 L1720 F1721 E1722 R1723 G1724 T1725 K1726 V1727 K1728 G1729 L1730 Q1734 A1737 R1740 R1741 W1742 A1743 Q1744 E1747 K1748 F1749 G1750 D1751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A1762
Q1763
E1764
W1765
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LYS
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GLU

4 Experimental information (i)

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 ($e^-/Å^2$)	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 (Å)	520.32, 520.32, 520.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.99	12/6521 (0.2%)	0.86	6/8867 (0.1%)
2	UB	0.48	1/4154 (0.0%)	0.60	1/5583 (0.0%)
3	UC	0.49	0/595	0.59	0/786
4	UD	0.68	4/6211 (0.1%)	0.70	3/8408 (0.0%)
5	UF	0.54	0/2657	0.60	0/3596
6	UG	0.88	4/3516 (0.1%)	0.79	3/4761 (0.1%)
7	UJ	0.52	0/6291	0.69	3/8543 (0.0%)
8	UK	0.80	0/1701	0.79	1/2251 (0.0%)
9	UL	0.47	0/6299	0.65	1/8531 (0.0%)
10	UM	0.38	0/5366	0.62	4/7282 (0.1%)
11	UN	0.60	0/1232	0.62	0/1662
12	UO	0.72	3/3903 (0.1%)	0.74	3/5312 (0.1%)
13	UQ	0.70	1/6136 (0.0%)	0.72	3/8348 (0.0%)
14	UR	0.94	2/3564 (0.1%)	0.80	2/4816 (0.0%)
15	UU	0.81	8/6903 (0.1%)	0.77	5/9392 (0.1%)
16	UX	0.63	0/1493	0.67	0/2011
17	UZ	0.48	1/1857 (0.1%)	0.66	3/2526 (0.1%)
18	CA	0.75	1/1814 (0.1%)	0.72	0/2456
18	CB	0.48	0/1853	0.61	0/2511
19	CC	0.53	0/2911	0.65	1/3937 (0.0%)
20	CD	0.53	1/3205 (0.0%)	0.68	2/4338 (0.0%)
21	CE	0.84	0/891	0.80	0/1214
21	CF	0.40	0/876	0.64	0/1195
22	CG	0.33	0/2983	0.58	0/4032
23	CH	0.51	0/2939	0.67	0/3988
24	CI	0.63	1/6631 (0.0%)	0.67	3/8943 (0.0%)
25	CJ	1.09	3/1462 (0.2%)	0.86	0/1967
26	CK	0.95	2/2376 (0.1%)	0.86	4/3214 (0.1%)
27	CL	0.70	0/1812	0.66	0/2437
28	CM	0.70	1/3573 (0.0%)	0.71	2/4829 (0.0%)
29	CN	0.52	0/1797	0.64	0/2443
29	CO	0.41	0/1714	0.62	0/2325

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
30	CP	0.31	0/1528	0.67	1/2057 (0.0%)
31	CQ	0.37	0/1379	0.58	0/1850
32	CR	0.42	1/6108 (0.0%)	0.84	20/8266 (0.2%)
32	CS	0.42	1/6108 (0.0%)	0.84	20/8266 (0.2%)
33	CT	0.67	0/1053	0.70	0/1413
34	Cc	0.78	0/1485	0.74	0/2008
35	Ce	0.36	0/1298	0.75	1/1750 (0.1%)
36	Cg	0.37	0/1259	0.63	0/1687
37	Ch	0.28	0/422	0.50	0/561
38	Ci	0.31	0/801	0.60	0/1087
39	Cj	1.02	0/958	0.88	0/1293
40	Cm	0.35	0/1001	0.65	1/1345 (0.1%)
41	Cn	0.62	0/712	0.67	0/954
42	Cp	0.58	0/458	0.68	0/617
43	CU	0.37	0/1015	0.60	0/1351
44	C1	1.32	203/26369 (0.8%)	1.49	504/41071 (1.2%)
45	C2	1.37	62/5459 (1.1%)	1.61	134/8498 (1.6%)
46	UV	0.35	1/8638 (0.0%)	0.72	9/11725 (0.1%)
47	CV	0.33	0/1172	0.69	0/1592
48	UH	0.50	1/2852 (0.0%)	0.68	2/3846 (0.1%)
49	UE	0.47	0/980	0.91	5/1316 (0.4%)
49	UI	0.47	0/980	0.91	5/1316 (0.4%)
50	US	0.52	0/3765	0.62	0/5100
51	Cl	0.42	0/638	0.66	0/857
52	CX	0.31	0/2180	0.57	1/2956 (0.0%)
53	UP	0.55	0/428	0.62	0/570
54	Cz	0.33	0/2310	0.58	0/3120
All	All	0.78	314/186592 (0.2%)	0.92	753/258976 (0.3%)

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

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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 314 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	UQ	394	HIS	CA-CB	-13.98	1.23	1.53
45	C2	57	A	N7-C5	-10.06	1.33	1.39
15	UU	418	TRP	CB-CG	-9.97	1.32	1.50
44	C1	2107	A	N9-C4	-9.80	1.31	1.37
44	C1	254	G	N7-C5	-9.57	1.33	1.39

The worst 5 of 753 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
45	C2	2	G	O5'-P-OP1	-32.44	71.78	110.70
45	C2	2	G	OP1-P-OP2	-26.35	80.07	119.60
45	C2	2	G	O5'-P-OP2	19.04	133.54	110.70
44	C1	258	C	N1-C2-O2	13.22	126.83	118.90
45	C2	1	A	OP1-P-O3'	13.10	134.03	105.20

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 (i)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	UA	835/904 (92%)	730 (87%)	103 (12%)	2 (0%)	47 81
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%)	34 72
7	UJ	796/1802 (44%)	750 (94%)	45 (6%)	1 (0%)	51 85
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%)	47 81
11	UN	150/938 (16%)	143 (95%)	6 (4%)	1 (1%)	22 62
12	UO	498/557 (89%)	450 (90%)	48 (10%)	0	100 100
13	UQ	775/960 (81%)	691 (89%)	81 (10%)	3 (0%)	34 72

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	UR	437/618 (71%)	399 (91%)	38 (9%)	0	100	100
15	UU	890/1049 (85%)	786 (88%)	103 (12%)	1 (0%)	51	85
16	UX	188/193 (97%)	174 (93%)	14 (7%)	0	100	100
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%)	47	81
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%)	34	72
28	CM	443/446 (99%)	398 (90%)	44 (10%)	1 (0%)	47	81
29	CN	222/252 (88%)	207 (93%)	15 (7%)	0	100	100
29	CO	211/252 (84%)	193 (92%)	16 (8%)	2 (1%)	17	56
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
46	UV	1057/1171 (90%)	946 (90%)	108 (10%)	3 (0%)	41	76
47	CV	144/322 (45%)	130 (90%)	13 (9%)	1 (1%)	22	62
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%)	47	81
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%)	8	40
54	Cz	273/1796 (15%)	257 (94%)	15 (6%)	1 (0%)	34	72
All	All	19223/30592 (63%)	17548 (91%)	1651 (9%)	24 (0%)	54	85

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 (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	UA	651/775 (84%)	635 (98%)	16 (2%)	47	68
2	UB	425/788 (54%)	420 (99%)	5 (1%)	71	84
3	UC	61/536 (11%)	59 (97%)	2 (3%)	38	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	UD	653/738 (88%)	650 (100%)	3 (0%)	88	93
5	UF	248/341 (73%)	248 (100%)	0	100	100
6	UG	344/474 (73%)	333 (97%)	11 (3%)	39	62
7	UJ	658/1526 (43%)	647 (98%)	11 (2%)	60	78
8	UK	159/227 (70%)	155 (98%)	4 (2%)	47	68
9	UL	667/821 (81%)	665 (100%)	2 (0%)	92	95
10	UM	569/770 (74%)	565 (99%)	4 (1%)	84	90
11	UN	123/765 (16%)	123 (100%)	0	100	100
12	UO	404/456 (89%)	400 (99%)	4 (1%)	76	86
13	UQ	650/817 (80%)	640 (98%)	10 (2%)	65	80
14	UR	360/524 (69%)	353 (98%)	7 (2%)	57	75
15	UU	672/863 (78%)	657 (98%)	15 (2%)	52	71
16	UX	150/167 (90%)	148 (99%)	2 (1%)	69	82
17	UZ	186/329 (56%)	185 (100%)	1 (0%)	88	93
18	CA	175/228 (77%)	170 (97%)	5 (3%)	42	64
18	CB	195/228 (86%)	194 (100%)	1 (0%)	88	93
19	CC	287/435 (66%)	286 (100%)	1 (0%)	92	95
20	CD	319/489 (65%)	314 (98%)	5 (2%)	62	79
21	CE	91/108 (84%)	89 (98%)	2 (2%)	52	71
21	CF	88/108 (82%)	88 (100%)	0	100	100
22	CG	299/525 (57%)	299 (100%)	0	100	100
23	CH	303/320 (95%)	298 (98%)	5 (2%)	60	78
24	CI	661/1009 (66%)	644 (97%)	17 (3%)	46	67
25	CJ	147/169 (87%)	142 (97%)	5 (3%)	37	61
26	CK	245/266 (92%)	236 (96%)	9 (4%)	34	59
27	CL	181/642 (28%)	179 (99%)	2 (1%)	73	85
28	CM	364/383 (95%)	356 (98%)	8 (2%)	52	71
29	CN	202/223 (91%)	201 (100%)	1 (0%)	88	93
29	CO	193/223 (86%)	191 (99%)	2 (1%)	76	86
30	CP	164/287 (57%)	162 (99%)	2 (1%)	71	84
31	CQ	145/215 (67%)	143 (99%)	2 (1%)	67	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	CR	654/916 (71%)	474 (72%)	180 (28%)	0	3
32	CS	654/916 (71%)	474 (72%)	180 (28%)	0	3
33	CT	108/167 (65%)	106 (98%)	2 (2%)	57	75
34	Cc	149/178 (84%)	147 (99%)	2 (1%)	69	82
35	Ce	137/177 (77%)	134 (98%)	3 (2%)	52	71
36	Cg	122/162 (75%)	120 (98%)	2 (2%)	62	79
37	Ch	43/130 (33%)	43 (100%)	0	100	100
38	Ci	74/117 (63%)	74 (100%)	0	100	100
39	Cj	92/115 (80%)	90 (98%)	2 (2%)	52	71
40	Cm	103/113 (91%)	102 (99%)	1 (1%)	76	86
41	Cn	70/116 (60%)	70 (100%)	0	100	100
42	Cp	46/61 (75%)	46 (100%)	0	100	100
43	CU	103/260 (40%)	97 (94%)	6 (6%)	20	47
46	UV	908/989 (92%)	891 (98%)	17 (2%)	57	75
47	CV	129/276 (47%)	127 (98%)	2 (2%)	62	79
48	UH	301/788 (38%)	298 (99%)	3 (1%)	76	86
49	UE	105/346 (30%)	74 (70%)	31 (30%)	0	2
49	UI	105/346 (30%)	74 (70%)	31 (30%)	0	2
50	US	404/493 (82%)	401 (99%)	3 (1%)	84	90
51	Cl	71/135 (53%)	69 (97%)	2 (3%)	43	65
52	CX	227/411 (55%)	226 (100%)	1 (0%)	91	94
53	UP	44/314 (14%)	44 (100%)	0	100	100
54	Cz	235/1533 (15%)	234 (100%)	1 (0%)	91	94
All	All	15923/25834 (62%)	15290 (96%)	633 (4%)	35	56

5 of 633 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	CS	559	MET
49	UE	198	SER
32	CS	655	GLN
32	CS	558	LEU
32	CS	908	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 265 such sidechains are listed below:

Mol	Chain	Res	Type
46	UV	520	ASN
46	UV	998	ASN
49	UI	183	ASN
15	UU	236	GLN
14	UR	370	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
44	C1	1088/2323 (46%)	373 (34%)	31 (2%)
45	C2	226/230 (98%)	83 (36%)	8 (3%)
All	All	1314/2553 (51%)	456 (34%)	39 (2%)

5 of 456 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 monosaccharides 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

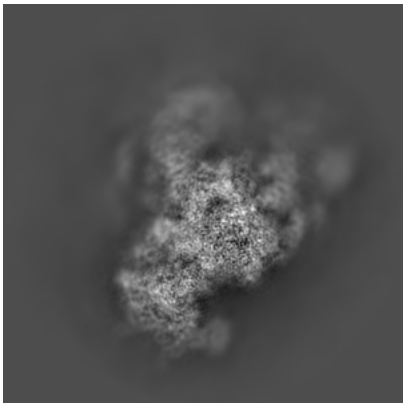
6 Map visualisation (i)

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.

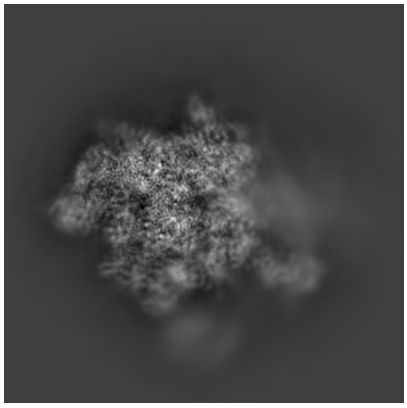
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

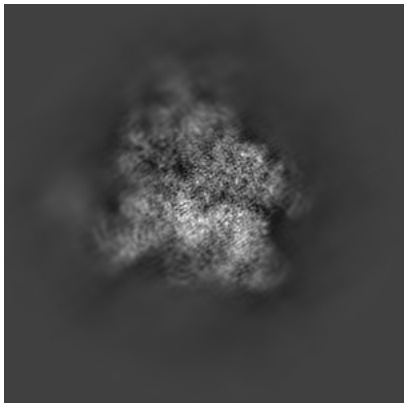
6.1.1 Primary map



X



Y

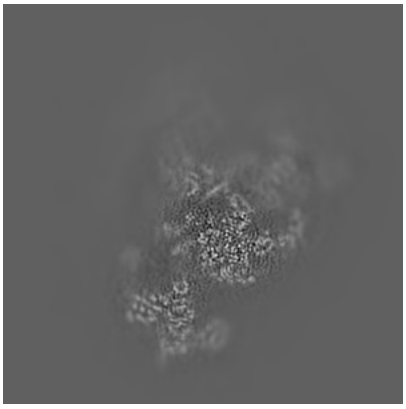


Z

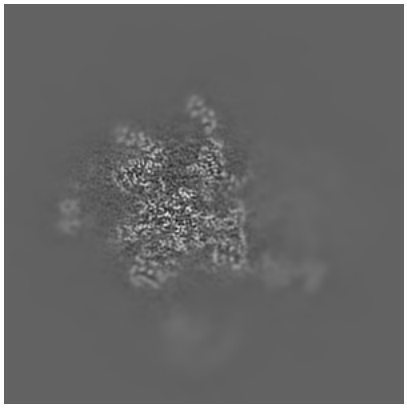
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

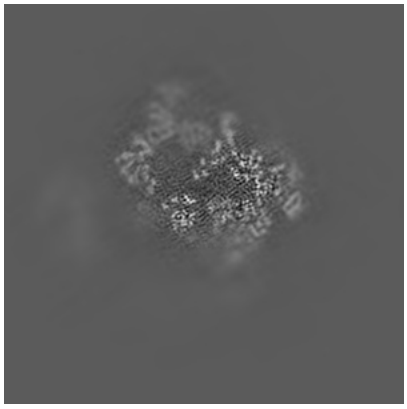
6.2.1 Primary map



X Index: 240



Y Index: 240

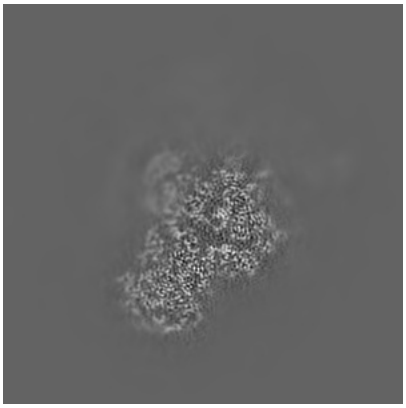


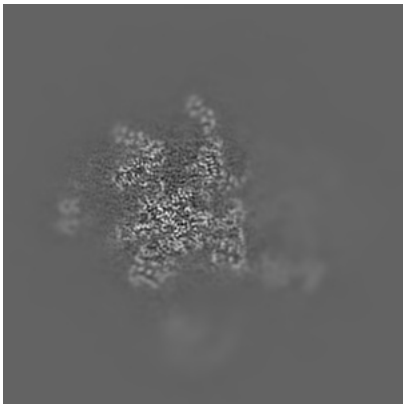
Z Index: 240

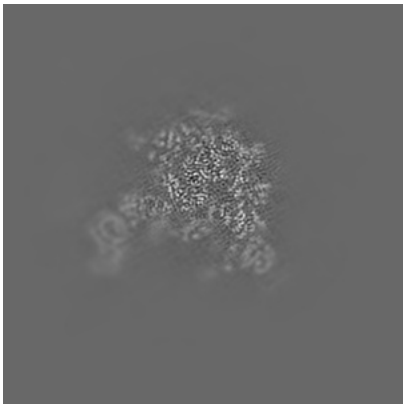
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map


X Index: 279

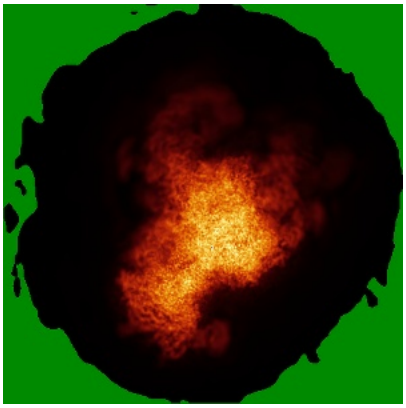

Y Index: 241

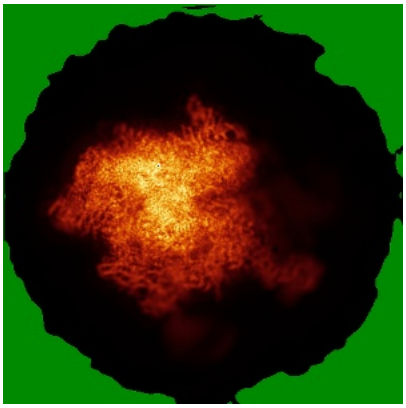

Z Index: 187

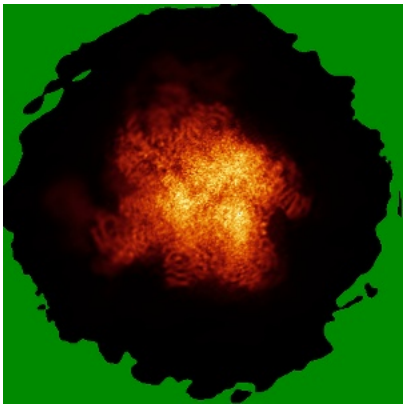
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map


X

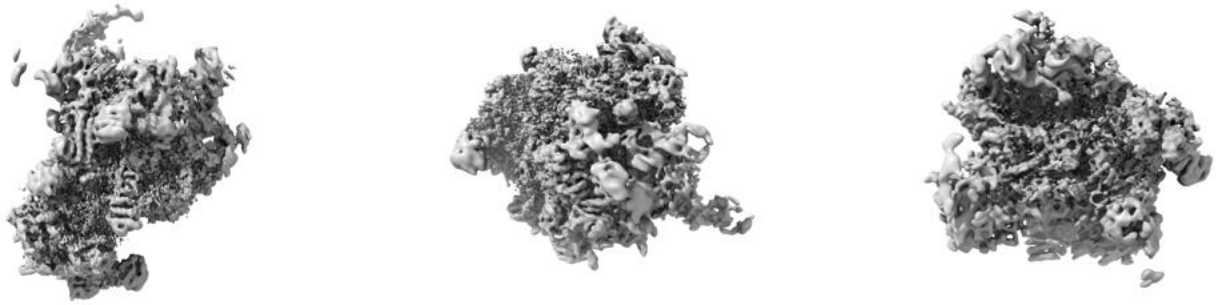

Y


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



X Y Z

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

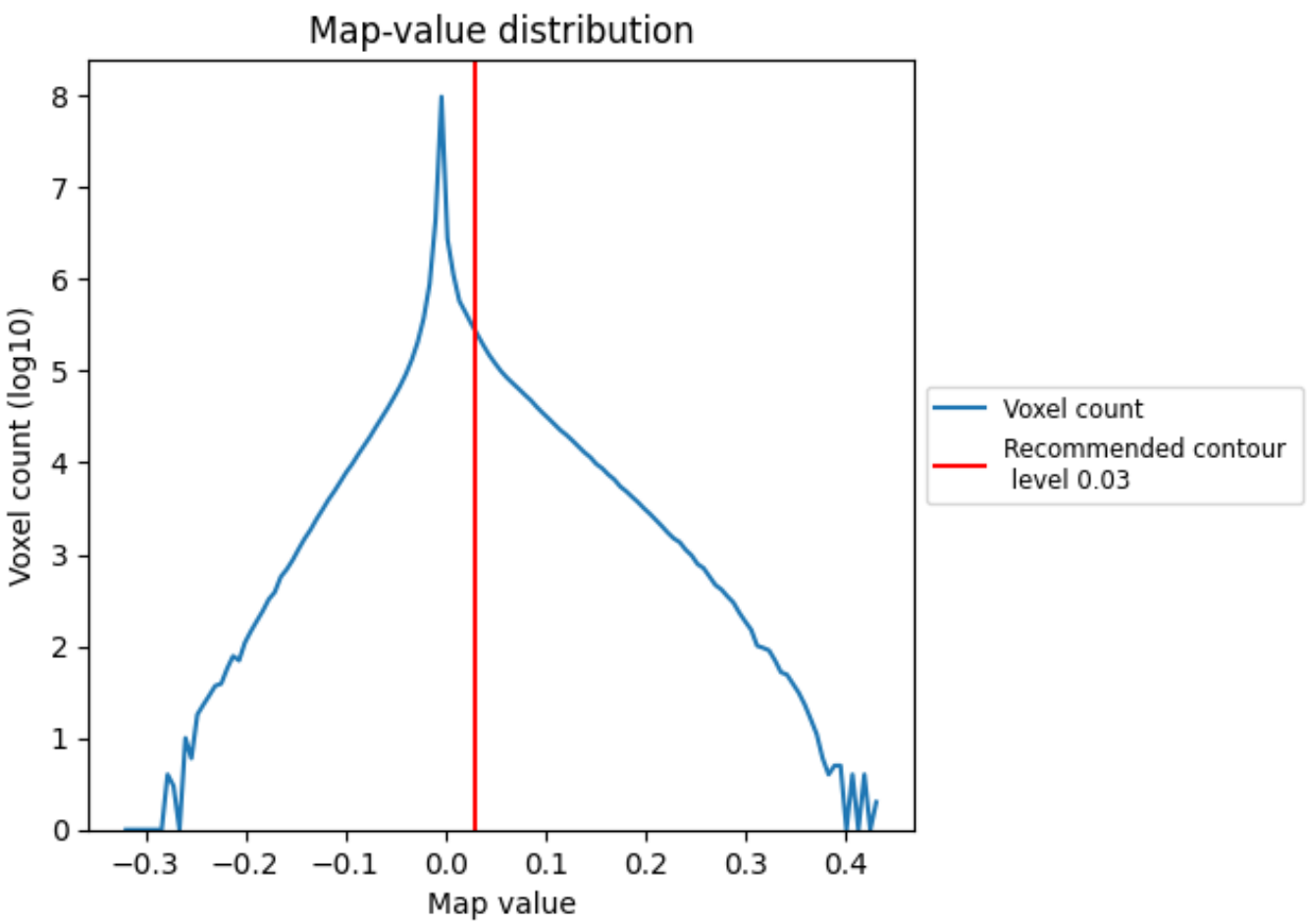
6.6 Mask visualisation (i)

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

7 Map analysis (i)

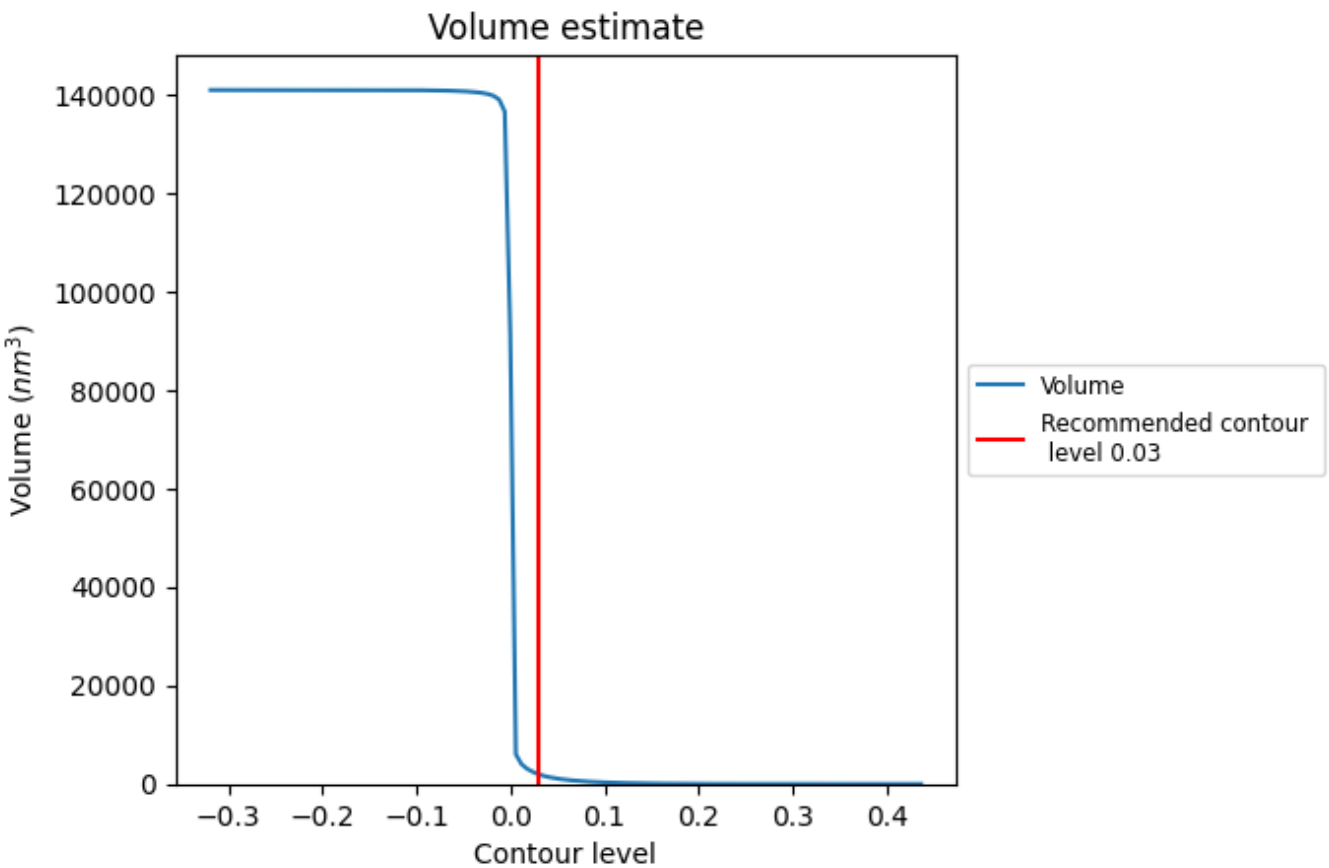
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

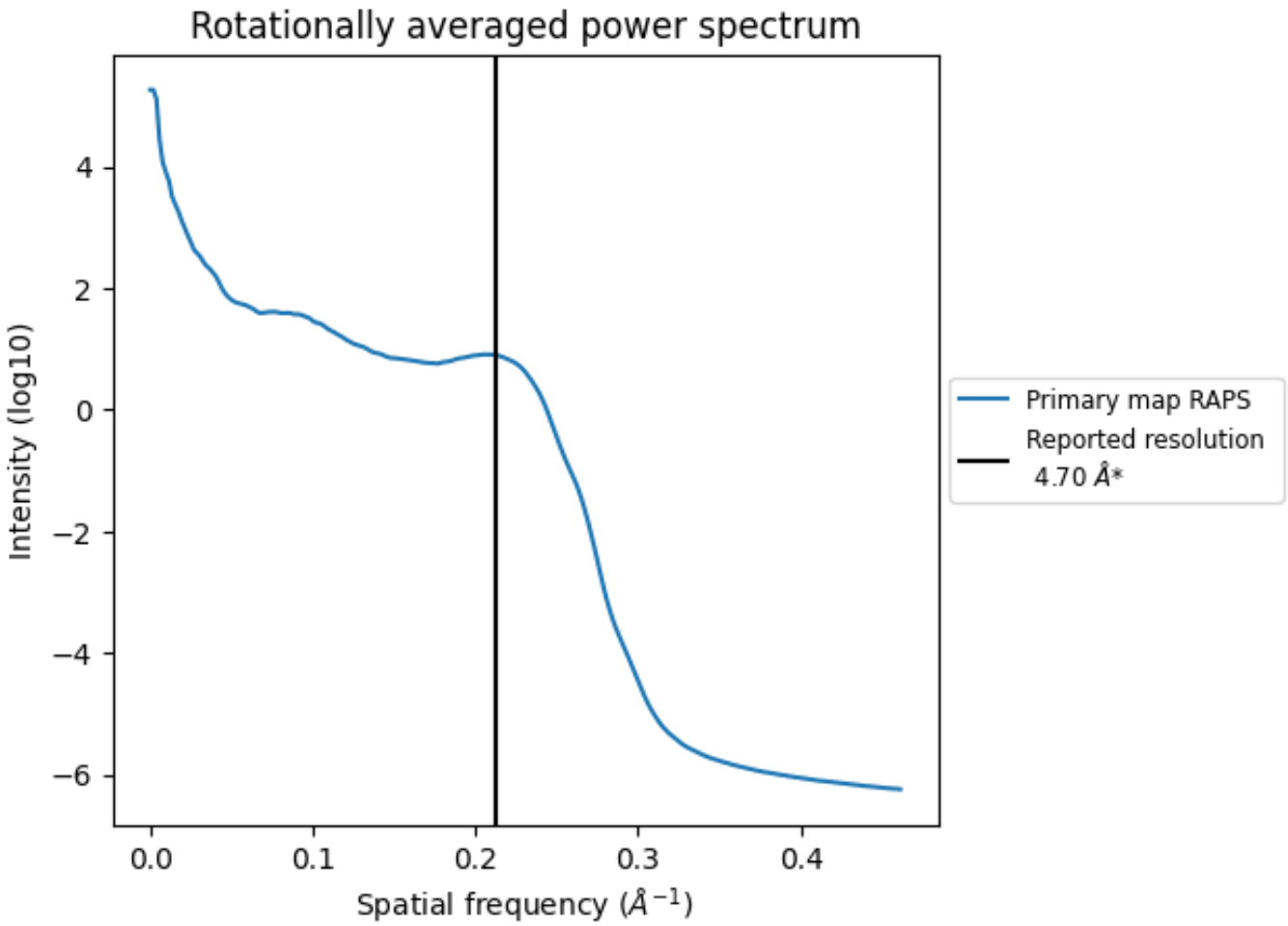
7.2 Volume estimate (i)



The volume at the recommended contour level is 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 (i)

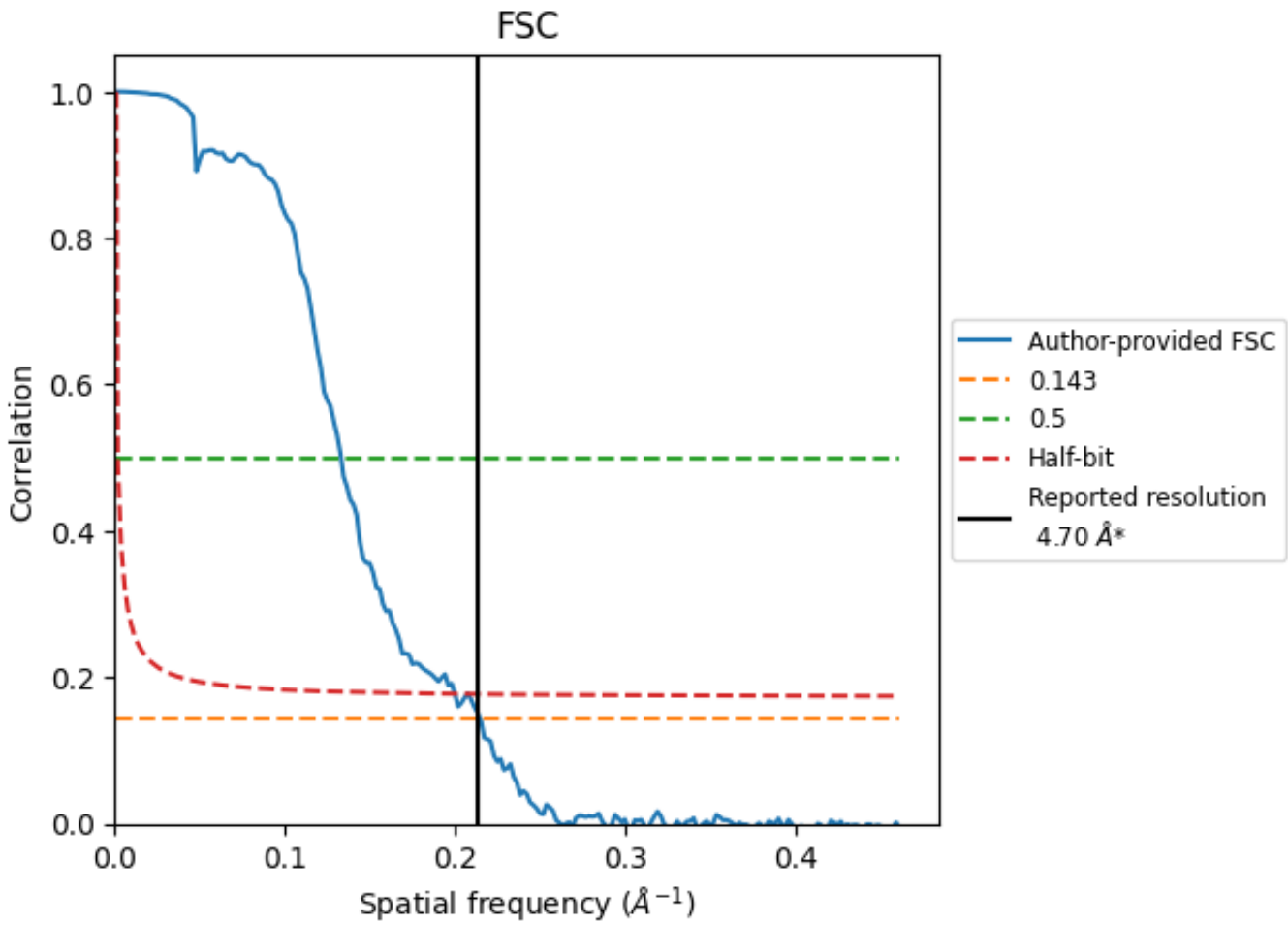


*Reported resolution corresponds to spatial frequency of 0.213 Å^{-1}

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)

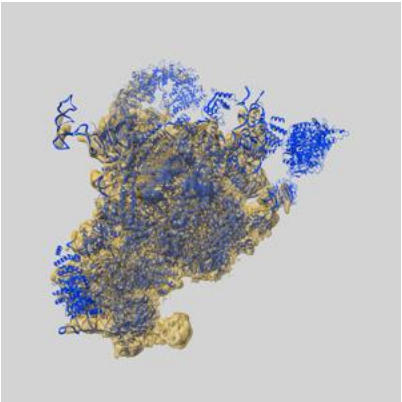
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.70	-	-
Author-provided FSC curve	4.66	7.52	5.00
Unmasked-calculated*	-	-	-

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

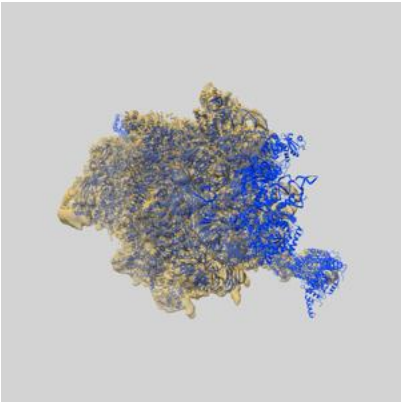
9 Map-model fit (i)

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.

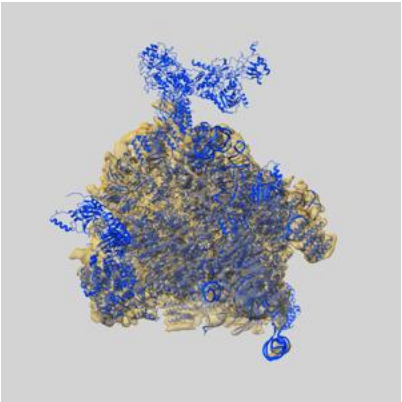
9.1 Map-model overlay (i)



X



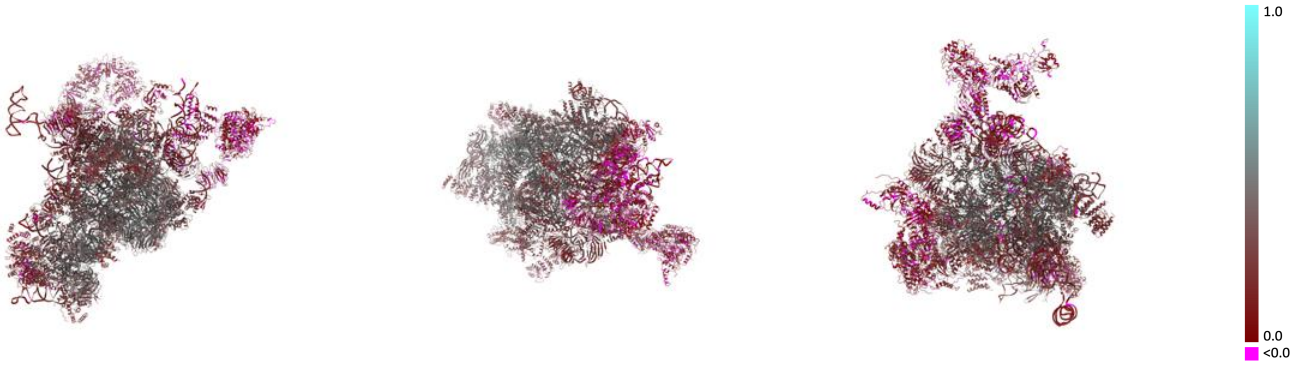
Y



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.

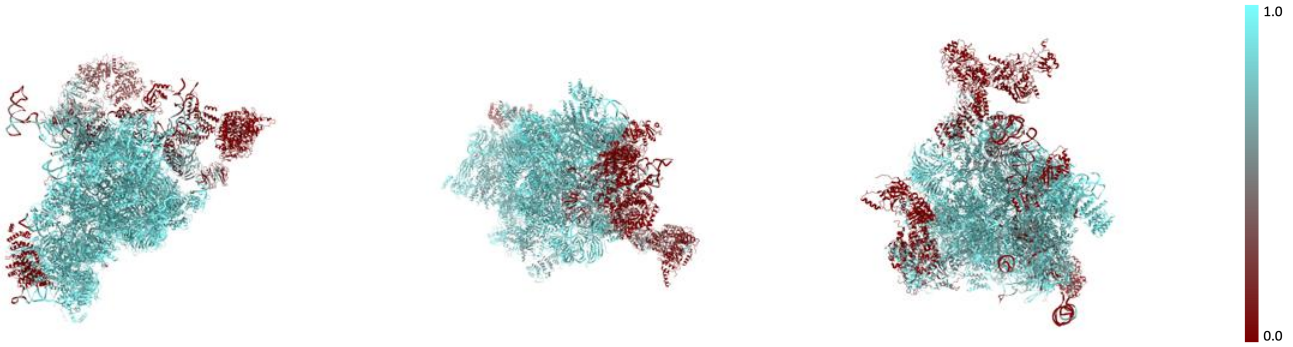
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

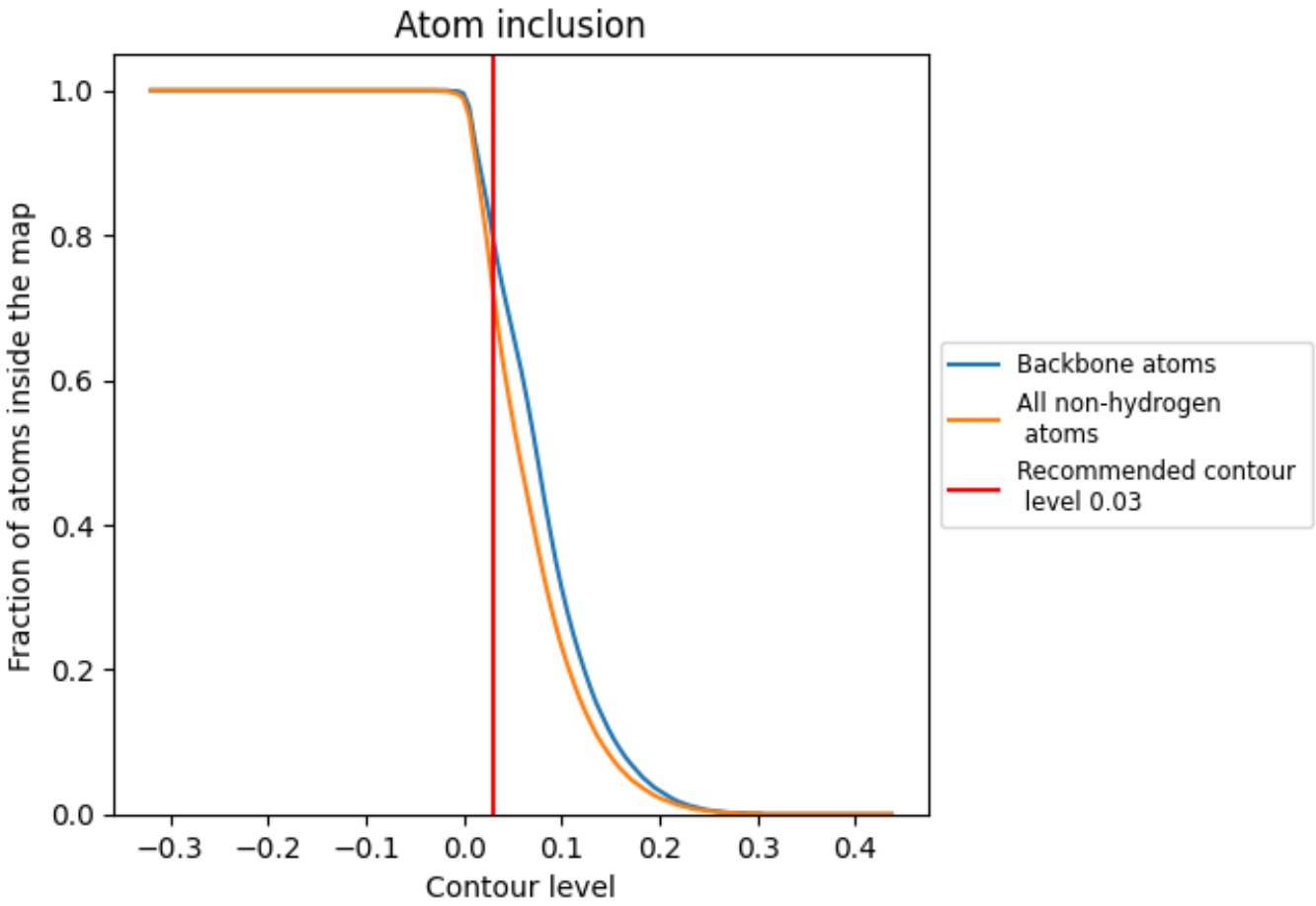
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (i)

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