



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 10:06 AM UTC

PDB ID : 5WLC / pdb_00005wlc
EMDB ID : EMD-8859
Title : The complete structure of the small subunit processome
Authors : Barandun, J.; Chaker-Margot, M.; Hunziker, M.; Klinge, S.
Deposited on : 2017-07-26
Resolution : 3.80 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:

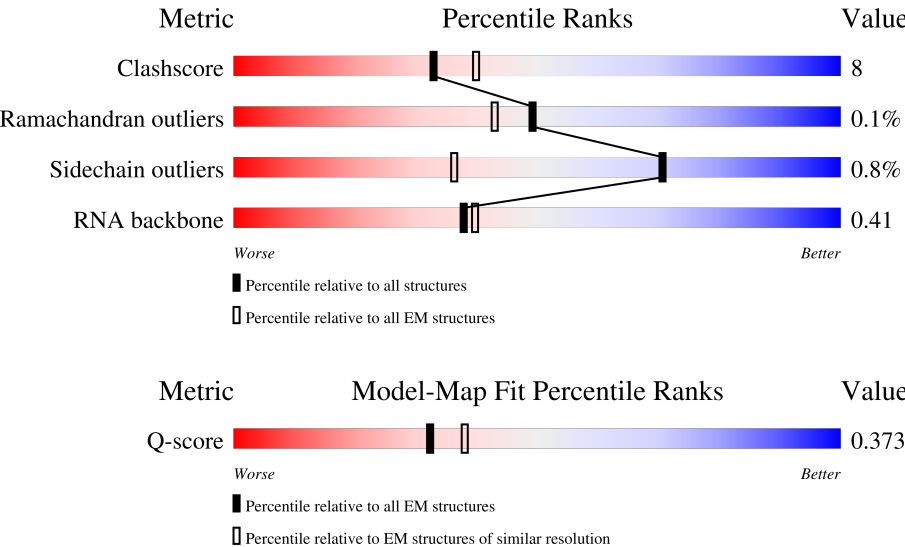
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.80 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	10198 (3.30 - 4.30)

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

Mol	Chain	Length	Quality of chain
1	L0	700	5% 38% 27% • 30%
2	L1	1807	23% 30% 21% 5% 43%
3	L2	333	• 29% 18% • 49%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	L3	146	
5	L4	261	
6	L5	225	
7	L6	236	
8	L7	190	
9	L8	200	
10	L9	197	
11	LC	143	
12	LD	156	
13	LE	130	
14	LF	135	
15	LG	67	
16	LH	896	
17	LI	713	
18	LJ	513	
19	LK	575	
20	LL	643	
21	LM	1769	
22	LN	776	
23	LO	923	
24	LP	440	
25	LQ	943	
26	LR	817	
27	LS	594	
28	LT	939	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	LU	489	
30	LV	707	
31	LW	554	
32	LX	1056	
32	LY	1056	
33	LZ	183	
34	NA	593	
35	NB	610	
36	NC	357	
37	ND	214	
38	NE	346	
39	NF	151	
40	NG	137	
41	NH	1237	
42	NI	297	
43	NJ	1729	
44	NK	316	
45	SA	504	
46	SB	511	
47	SC	327	
47	SD	327	
48	SE	126	
48	SF	126	
49	SG	573	
50	SH	367	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
51	SI	1184	
52	SJ	252	
52	SK	252	
53	SL	189	
54	SM	290	
55	SN	274	
56	SO	274	
57	SP	982	
58	SQ	217	
59	SR	145	
60	SS	898	
61	ST	792	
62	SU	552	
63	SV	206	
64	SX	103	
65	SY	250	
66	SZ	483	

2 Entry composition

There are 67 unique types of molecules in this entry. The entry contains 196921 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 RNA chain called 5' ETS.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L0	488	Total	C	N	O	P	0	0
			10405	4650	1838	3429	488		

- Molecule 2 is a RNA chain called 18S pre-rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L1	1025	Total	C	N	O	P	0	0
			21866	9773	3905	7163	1025		

- Molecule 3 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L2	169	Total	C	N	O	P	0	0
			3585	1605	629	1182	169		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L2	200	C	G	conflict	GB 176452

- Molecule 4 is a protein called rpS18_uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L3	113	Total	C	N	O	S	0	0
			901	569	168	162	2		

- Molecule 5 is a protein called rpS4_eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L4	228	Total	C	N	O	S	0	0
			1810	1158	330	319	3		

- Molecule 6 is a protein called rpS5_uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L5	213	Total	C	N	O	S	0	0
			1669	1045	307	314	3		

- Molecule 7 is a protein called rpS6_eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L6	113	Total	C	N	O	S	0	0
			888	567	156	163	2		

- Molecule 8 is a protein called rpS7_eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L7	165	Total	C	N	O		0	0
			1321	854	227	240			

- Molecule 9 is a protein called rpS8_eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L8	170	Total	C	N	O	S	0	0
			1349	839	267	241	2		

- Molecule 10 is a protein called rpS9_uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L9	175	Total	C	N	O	S	0	0
			1415	895	273	246	1		

- Molecule 11 is a protein called rpS16_uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LC	125	Total	C	N	O		0	0
			973	625	174	174			

- Molecule 12 is a protein called rpS11_uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LD	127	Total	C	N	O	S	0	0
			1027	660	194	170	3		

- Molecule 13 is a protein called rpS22_uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LE	127	Total	C	N	O	S	0	0
			1003	640	183	177	3		

- Molecule 14 is a protein called rpS24_eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LF	90	Total	C	N	O	S	0	0
			715	458	131	126			

- Molecule 15 is a protein called rpS28_eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LG	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 16 is a protein called Utp17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH	834	Total	C	N	O	S	0	0
			6633	4215	1121	1278	19		

- Molecule 17 is a protein called Utp8.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LI	487	Total	C	N	O	S	0	0
			2857	1763	529	562	3		

- Molecule 18 is a protein called Utp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LJ	493	Total	C	N	O	S	0	0
			3911	2462	702	735	12		

- Molecule 19 is a protein called Utp9.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LK	123	Total	C	N	O	S	0	0
			898	567	166	163	2		

- Molecule 20 is a protein called Utp5.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LL	475	Total	C	N	O	S	0	0
			3772	2400	649	710	13		

- Molecule 21 is a protein called Utp10.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LM	431	Total	C	N	O	S	0	0
			3443	2224	566	641	12		

- Molecule 22 is a protein called Utp4.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LN	678	Total	C	N	O	S	0	0
			5344	3384	930	1009	21		

- Molecule 23 is a protein called Utp1.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LO	834	Total	C	N	O	S	0	0
			6635	4223	1140	1253	19		

- Molecule 24 is a protein called Utp6.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LP	359	Total	C	N	O	S	0	0
			2709	1723	486	488	12		

- Molecule 25 is a protein called Utp12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LQ	848	Total	C	N	O	S	0	0
			6640	4244	1116	1253	27		

- Molecule 26 is a protein called Utp13.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LR	729	Total	C	N	O	S	0	0
			4144	2520	797	818	9		

- Molecule 27 is a protein called Utp18.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LS	481	Total	C	N	O	S	0	0
			3791	2399	668	714	10		

- Molecule 28 is a protein called Utp21.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LT	850	Total	C	N	O	S	0	0
			6697	4253	1154	1269	21		

- Molecule 29 is a protein called Sof1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LU	457	Total	C	N	O	S	0	0
			3725	2328	679	702	16		

- Molecule 30 is a protein called Enp2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LV	362	Total	C	N	O	S	0	0
			2840	1789	487	555	9		

- Molecule 31 is a protein called Utp7.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LW	438	Total	C	N	O	S	0	0
			3428	2163	601	652	12		

- Molecule 32 is a protein called Kre33.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LX	808	Total	C	N	O	S	0	0
			4583	2798	888	890	7		
32	LY	769	Total	C	N	O		0	0
			3823	2285	769	769			

- Molecule 33 is a protein called Imp3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LZ	182	Total	C	N	O	S	0	0
			1530	967	287	269	7		

- Molecule 34 is a protein called Mpp10.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	NA	207	Total	C	N	O	S	0	0
			1667	1034	297	332	4		

- Molecule 35 is a protein called Sas10.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	NB	142	Total	C	N	O		0	0
			1098	677	218	203			

- Molecule 36 is a protein called Lcp5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	NC	136	Total	C	N	O	S	0	0
			1125	674	231	217	3		

- Molecule 37 is a protein called Bud21.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	ND	81	Total	C	N	O		0	0
			600	373	122	105			

- Molecule 38 is a protein called Faf1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	NE	158	Total	C	N	O	S	0	0
			1192	731	246	212	3		

- Molecule 39 is a protein called rpS13_uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	NF	124	Total	C	N	O		0	0
			615	367	124	124			

- Molecule 40 is a protein called rpS14_uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	NG	111	Total	C	N	O		0	0
			543	321	111	111			

- Molecule 41 is a protein called Utp22.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	NH	1082	Total	C	N	O	0	0
			5362	3198	1082	1082		

- Molecule 42 is a protein called Rrp7.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	NI	169	Total	C	N	O	0	0
			841	503	169	169		

- Molecule 43 is a protein called Rrp5.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	NJ	265	Total	C	N	O	0	0
			1314	784	265	265		

- Molecule 44 is a protein called Krr1.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	NK	175	Total	C	N	O	0	0
			868	518	175	175		

- Molecule 45 is a protein called Nop56.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SA	370	Total	C	N	O	S	0	0
			2854	1815	490	541	8		

- Molecule 46 is a protein called Nop58.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SB	425	Total	C	N	O	S	0	0
			2937	1824	533	572	8		

- Molecule 47 is a protein called Nop1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SC	242	Total	C	N	O	S	0	0
			1881	1193	338	340	10		
47	SD	228	Total	C	N	O	S	0	0
			1782	1131	320	321	10		

- Molecule 48 is a protein called Snu13.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SE	121	Total	C	N	O	S	0	0
			916	583	158	171	4		
48	SF	121	Total	C	N	O	S	0	0
			916	583	158	171	4		

- Molecule 49 is a protein called Rrp9.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SG	429	Total	C	N	O	S	0	0
			3428	2185	596	637	10		

- Molecule 50 is a protein called Rcl1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SH	360	Total	C	N	O	S	0	0
			2781	1781	473	516	11		

- Molecule 51 is a protein called Bms1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SI	802	Total	C	N	O	S	0	0
			6412	4108	1142	1133	29		

- Molecule 52 is a protein called Emg1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SJ	216	Total	C	N	O	S	0	0
			1701	1079	296	315	11		
52	SK	230	Total	C	N	O	S	0	0
			1799	1142	313	333	11		

- Molecule 53 is a protein called Utp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SL	174	Total	C	N	O	S	0	0
			1395	890	255	240	10		

- Molecule 54 is a protein called Imp4.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SM	282	Total	C	N	O	S	0	0
			2296	1441	430	418	7		

- Molecule 55 is a protein called Utp30.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SN	247	Total	C	N	O	S	0	0
			2006	1284	356	358	8		

- Molecule 56 is a protein called Pno1.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SO	179	Total	C	N	O	S	0	0
			998	606	199	192	1		

- Molecule 57 is a protein called Utp20.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SP	982	Total	C	N	O		0	0
			4910	2946	982	982			

- Molecule 58 is a protein called Fcf2.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SQ	135	Total	C	N	O	S	0	0
			1137	721	211	201	4		

- Molecule 59 is a protein called rpS23_uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SR	104	Total	C	N	O	S	0	0
			792	506	145	139	2		

- Molecule 60 is a protein called Utp14.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SS	197	Total	C	N	O	S	0	0
			1466	905	282	277	2		

- Molecule 61 is a protein called Nop14.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	ST	599	Total	C	N	O	S	0	0
			4473	2830	809	823	11		

- Molecule 62 is a protein called Noc4.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SU	526	Total	C	N	O	S	0	0
			3781	2422	650	697	12		

- Molecule 63 is a protein called Rrt14.

Mol	Chain	Residues	Atoms				AltConf	Trace
63	SV	63	Total	C	N	O	0	0
			381	234	69	78		

- Molecule 64 is a protein called Unassigned peptides.

Mol	Chain	Residues	Atoms				AltConf	Trace
64	SX	103	Total	C	N	O	0	0
			515	309	103	103		

- Molecule 65 is a protein called Utp11.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SY	241	Total	C	N	O	S	0	0
			2016	1251	388	370	7		

- Molecule 66 is a protein called Enp1.

Mol	Chain	Residues	Atoms				AltConf	Trace
66	SZ	261	Total	C	N	O	0	0
			1295	773	261	261		

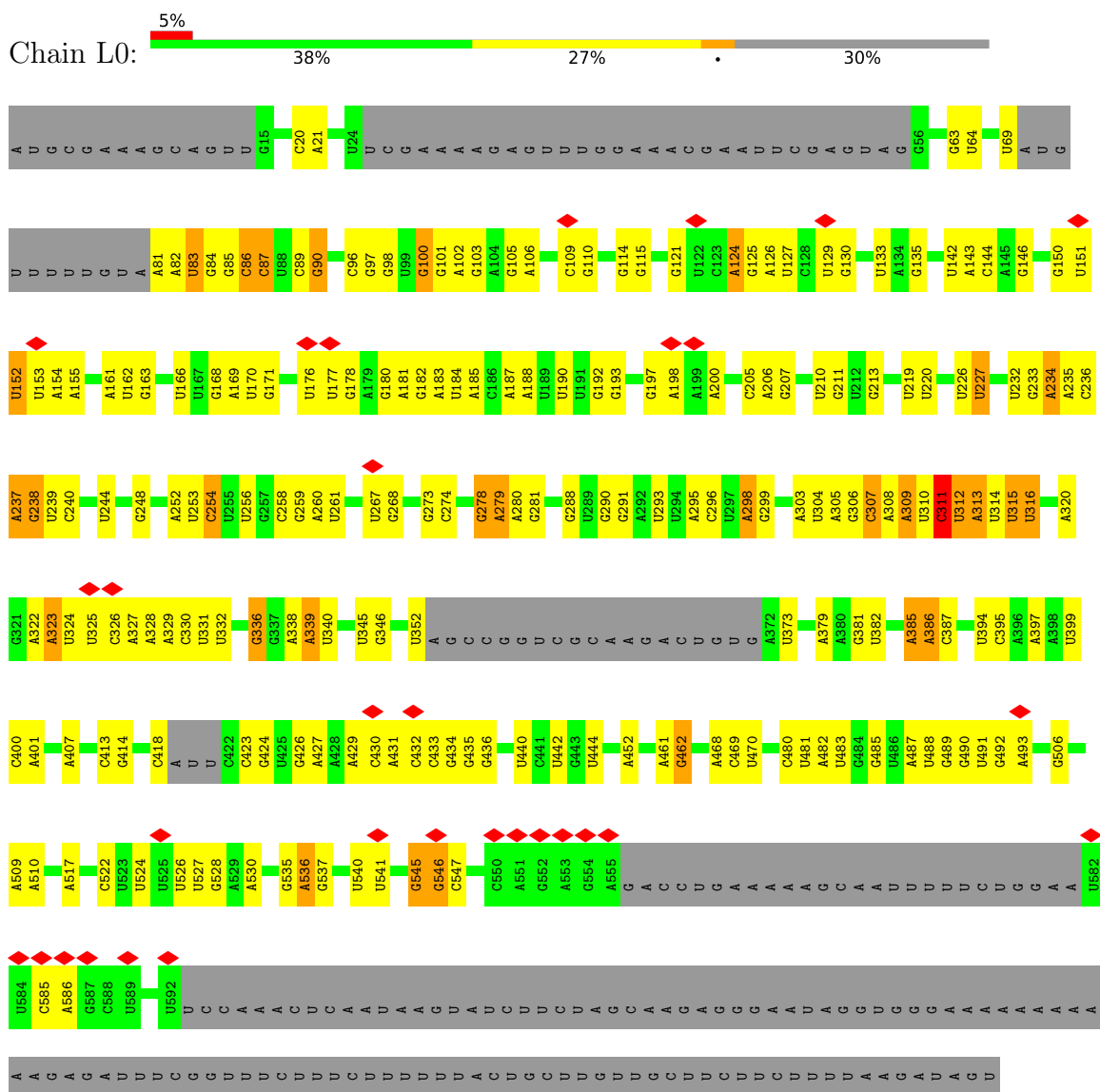
- Molecule 67 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
67	SL	1	Total	Zn	0
			1	1	

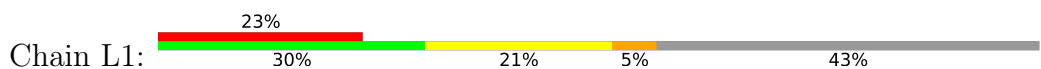
3 Residue-property plots

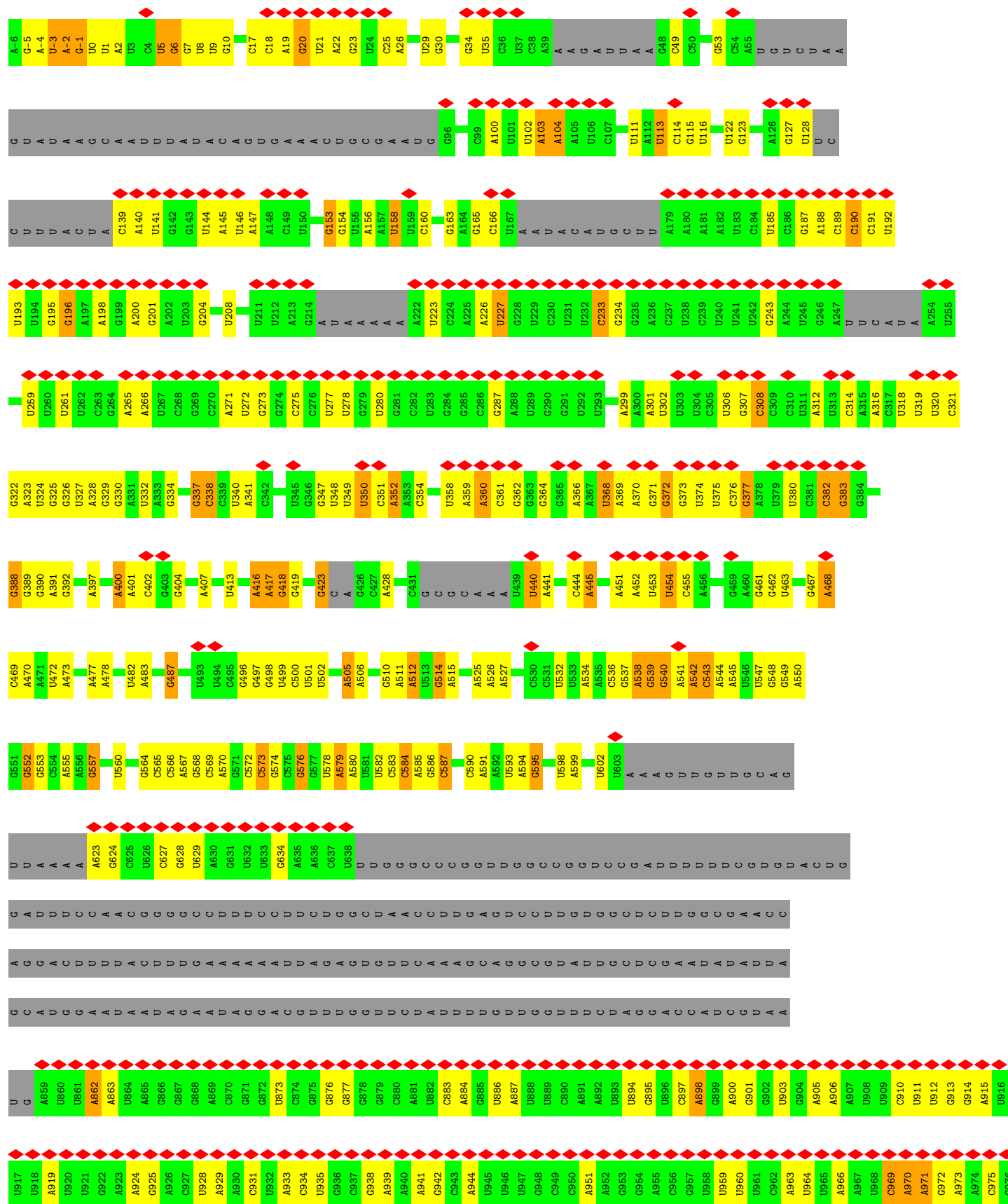
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 5' ETS

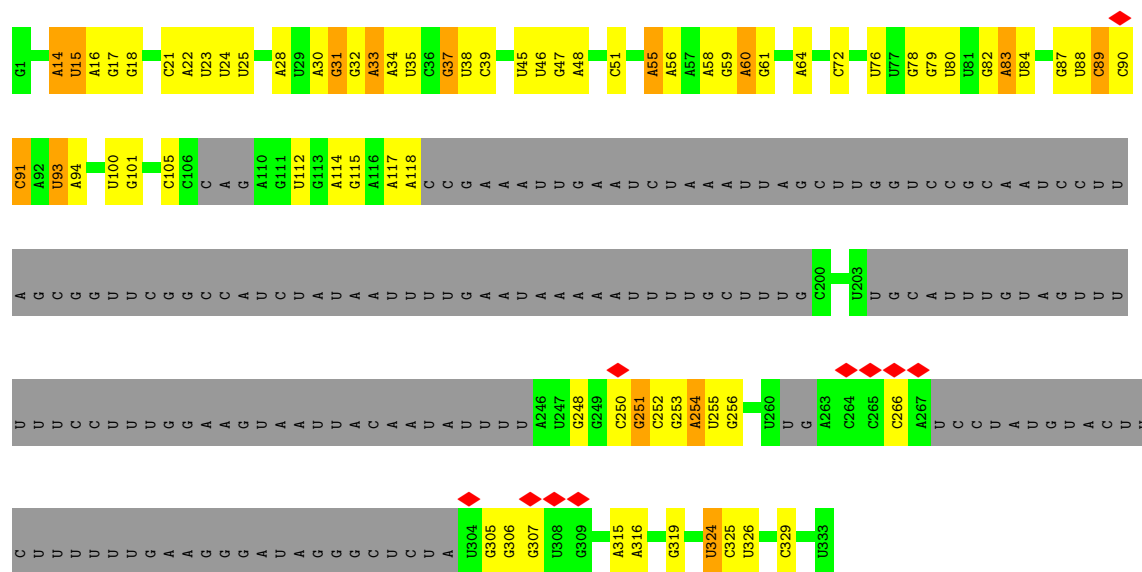


• Molecule 2: 18S pre-rRNA

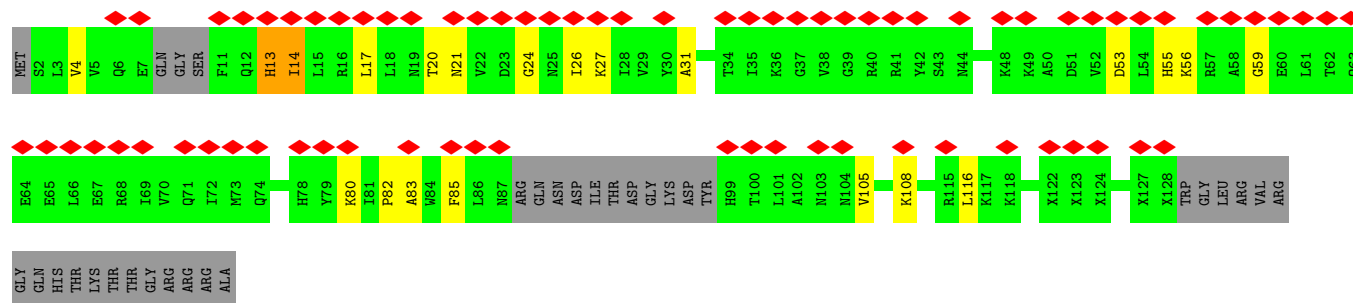




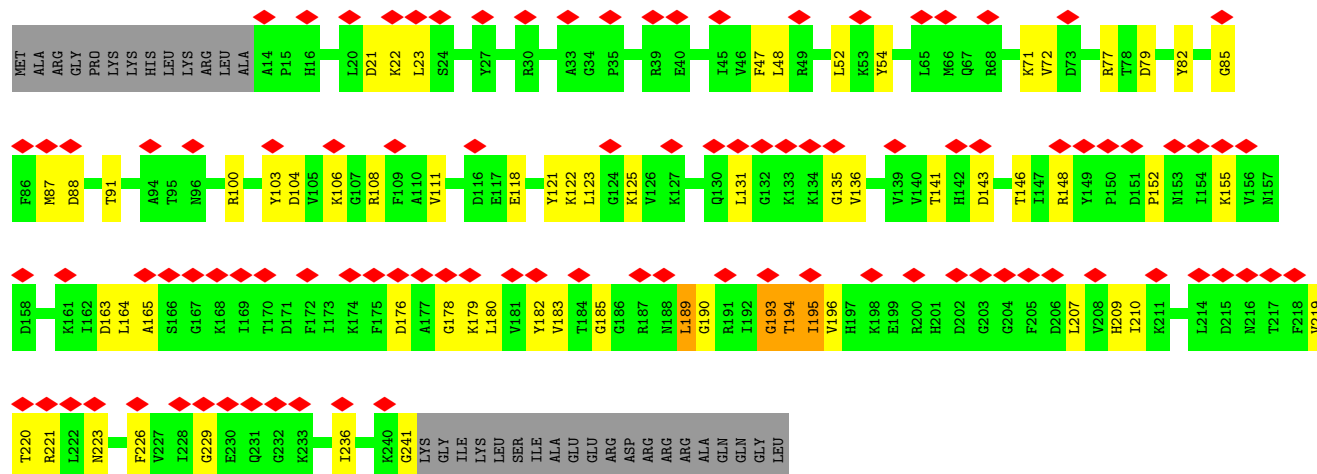
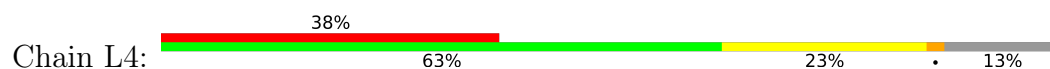




• Molecule 4: rpS18_uS13



• Molecule 5: rpS4_eS4



• Molecule 6: rpS5_uS7

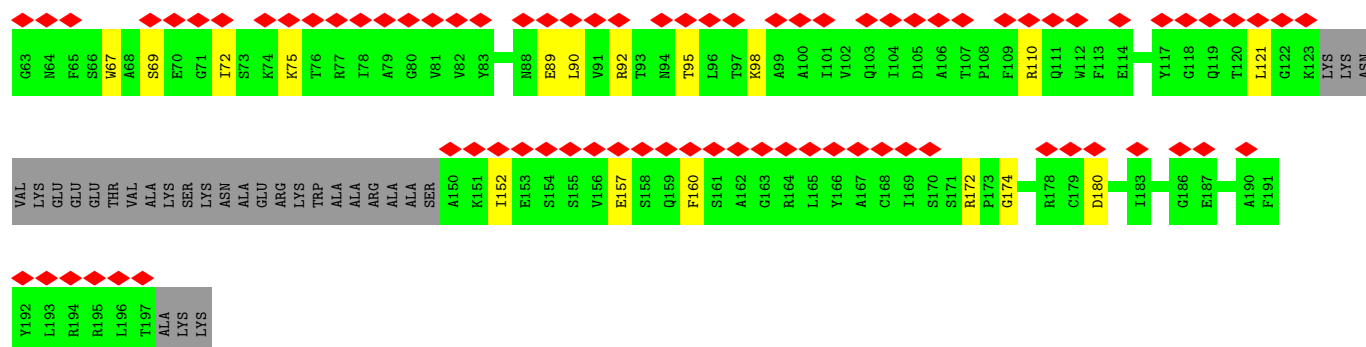
Chain L5:

Chain L6:

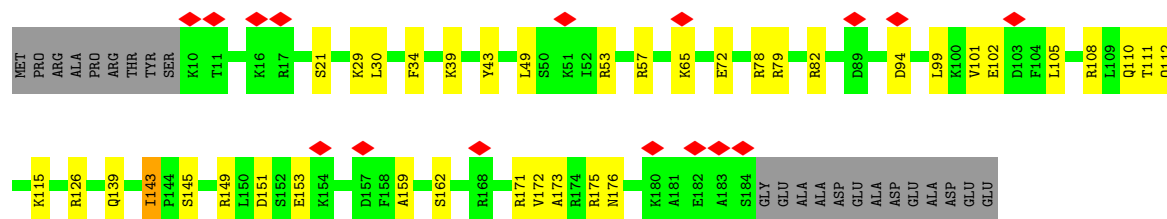
Chain L7:

Chain L8:

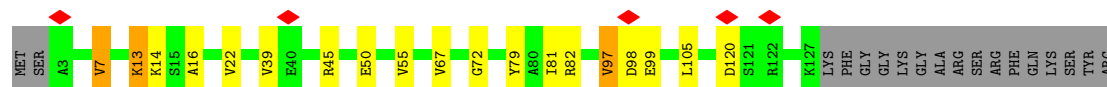
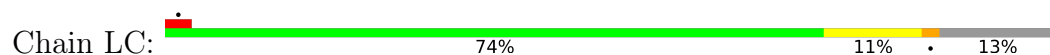




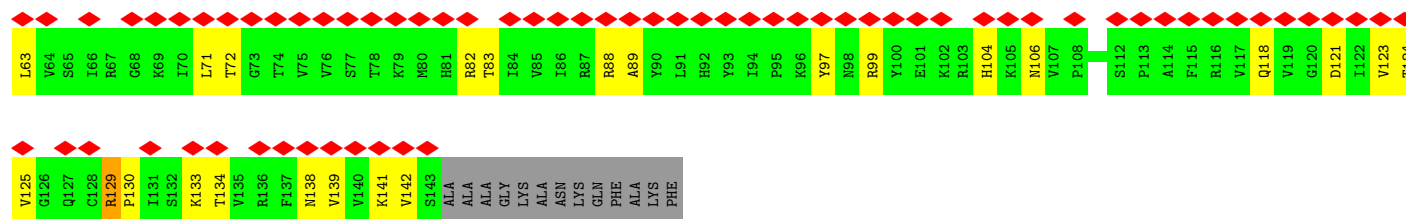
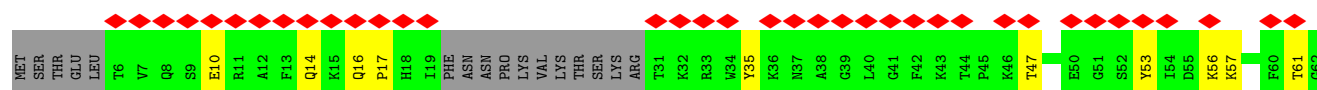
• Molecule 10: rpS9_uS4



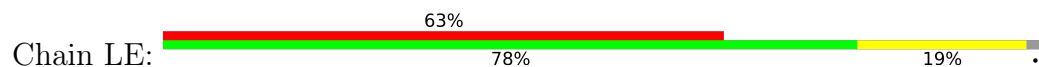
• Molecule 11: rpS16_uS9

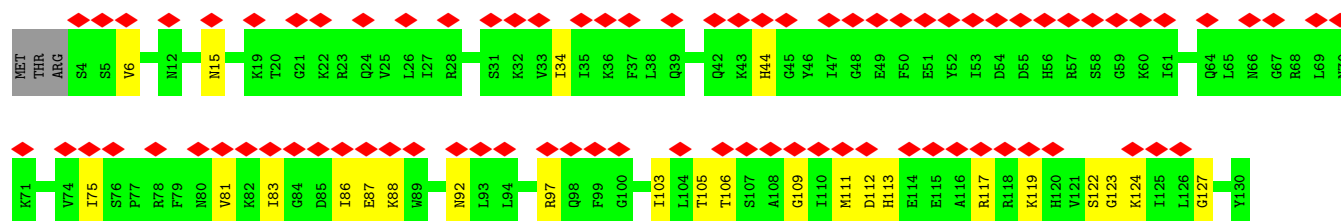


• Molecule 12: rpS11_uS17

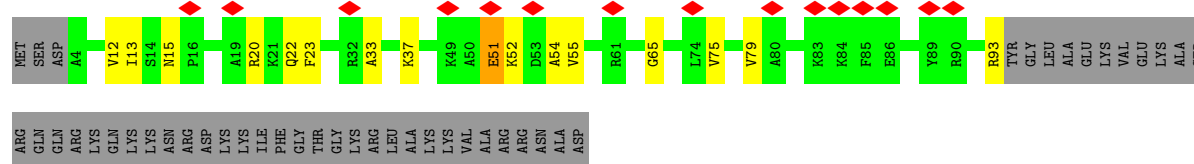


• Molecule 13: rpS22_uS8

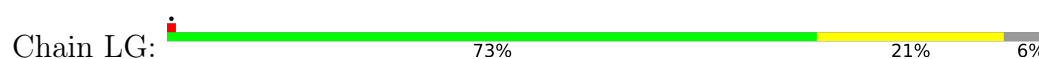




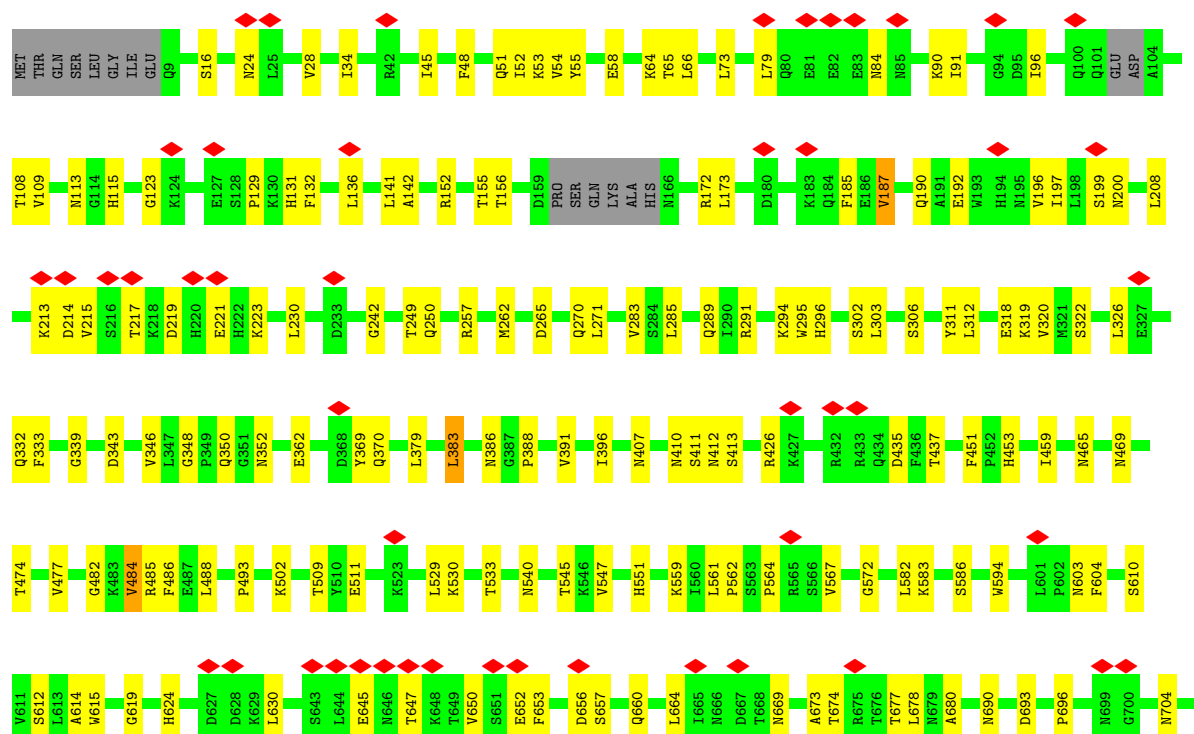
• Molecule 14: rpS24_eS24

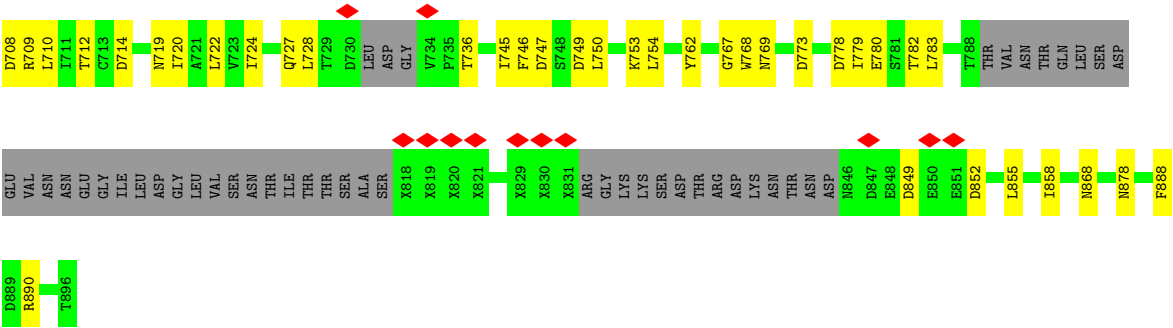


• Molecule 15: rpS28_eS28

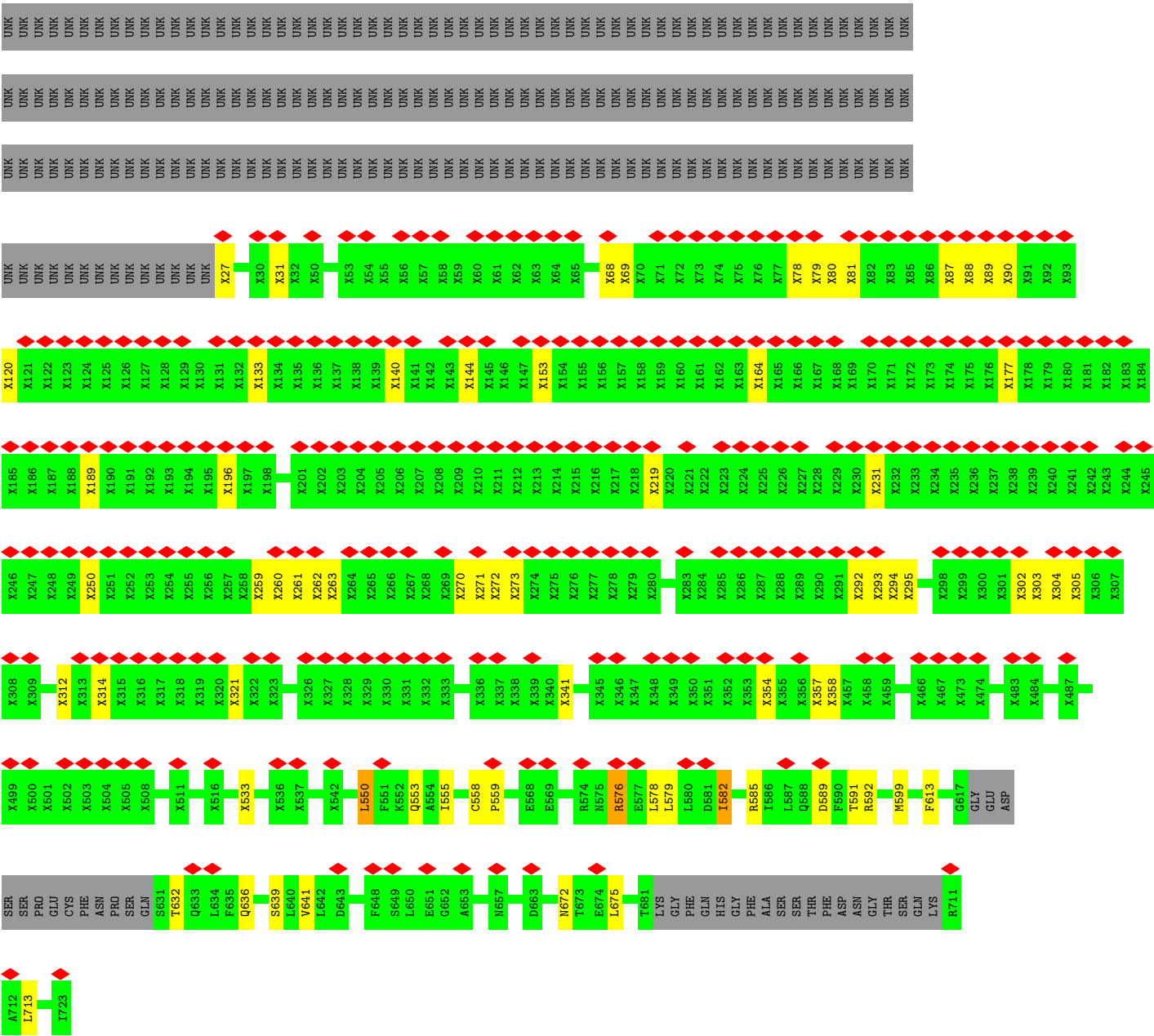


• Molecule 16: Utp17





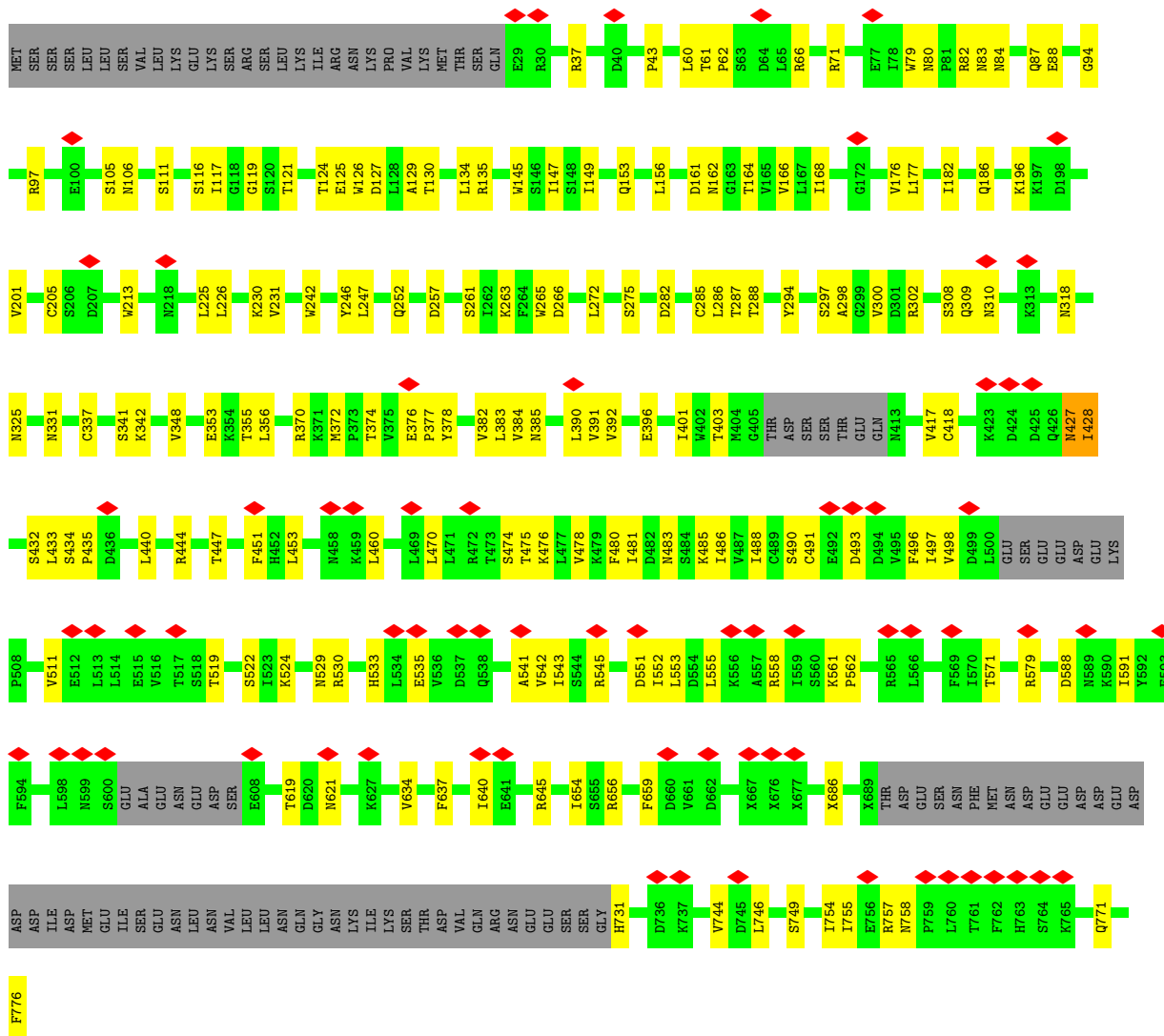
• Molecule 17: Utp8



Chain LJ: 70% 26% ..

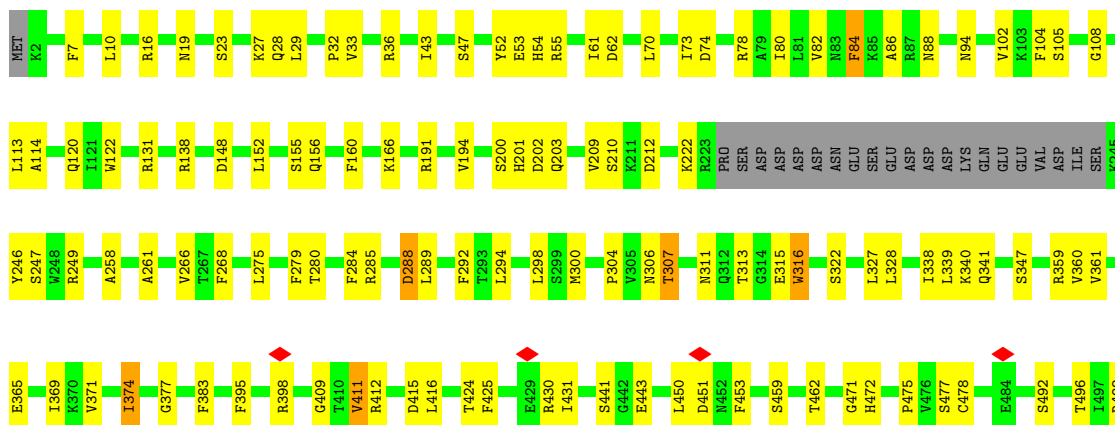


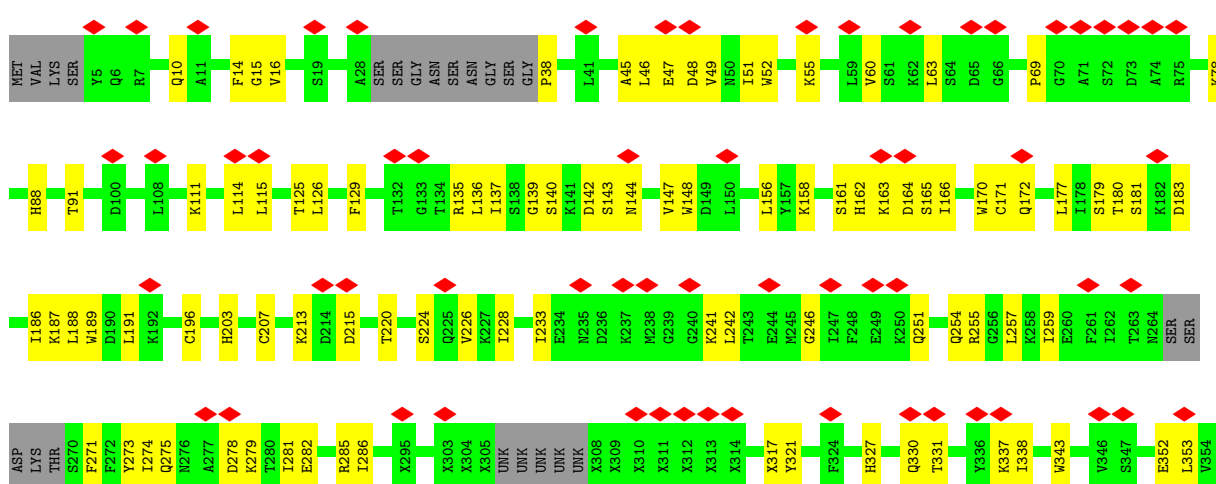


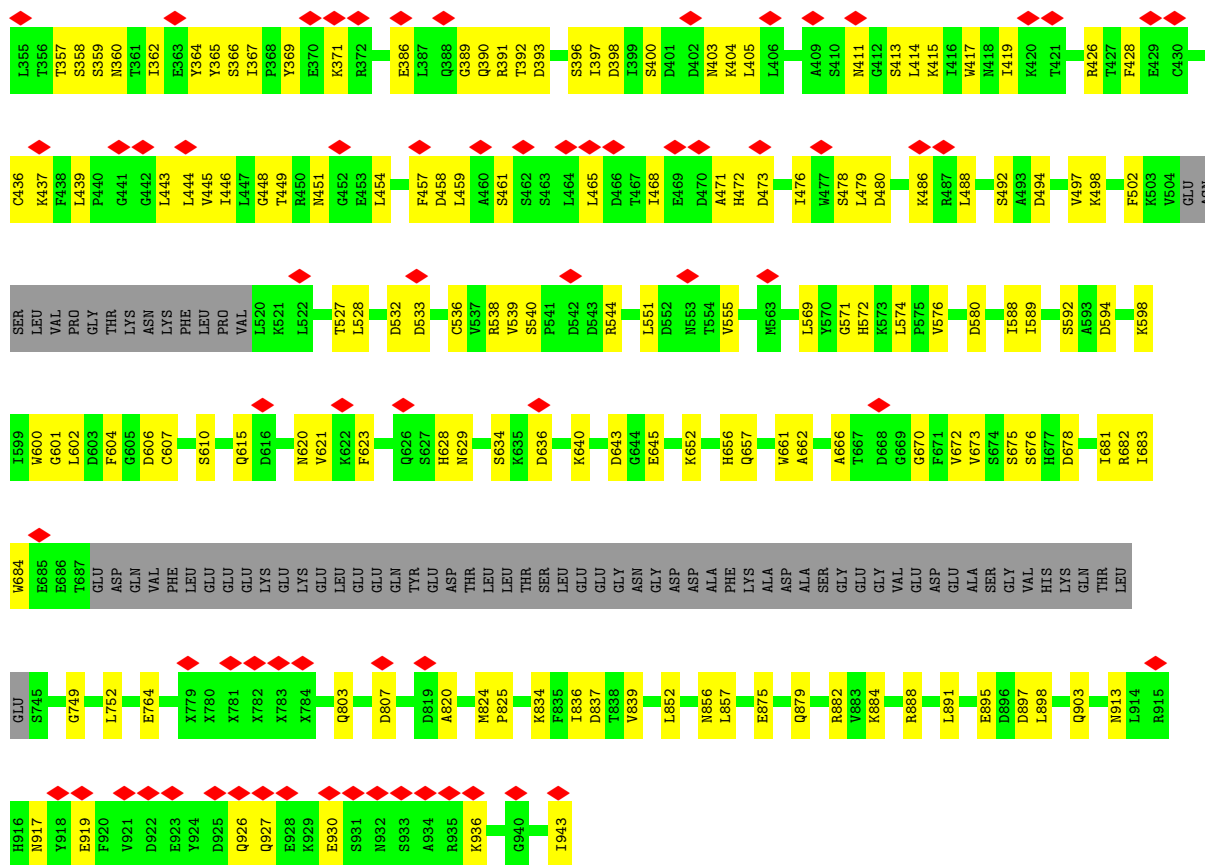


• Molecule 23: Utp1

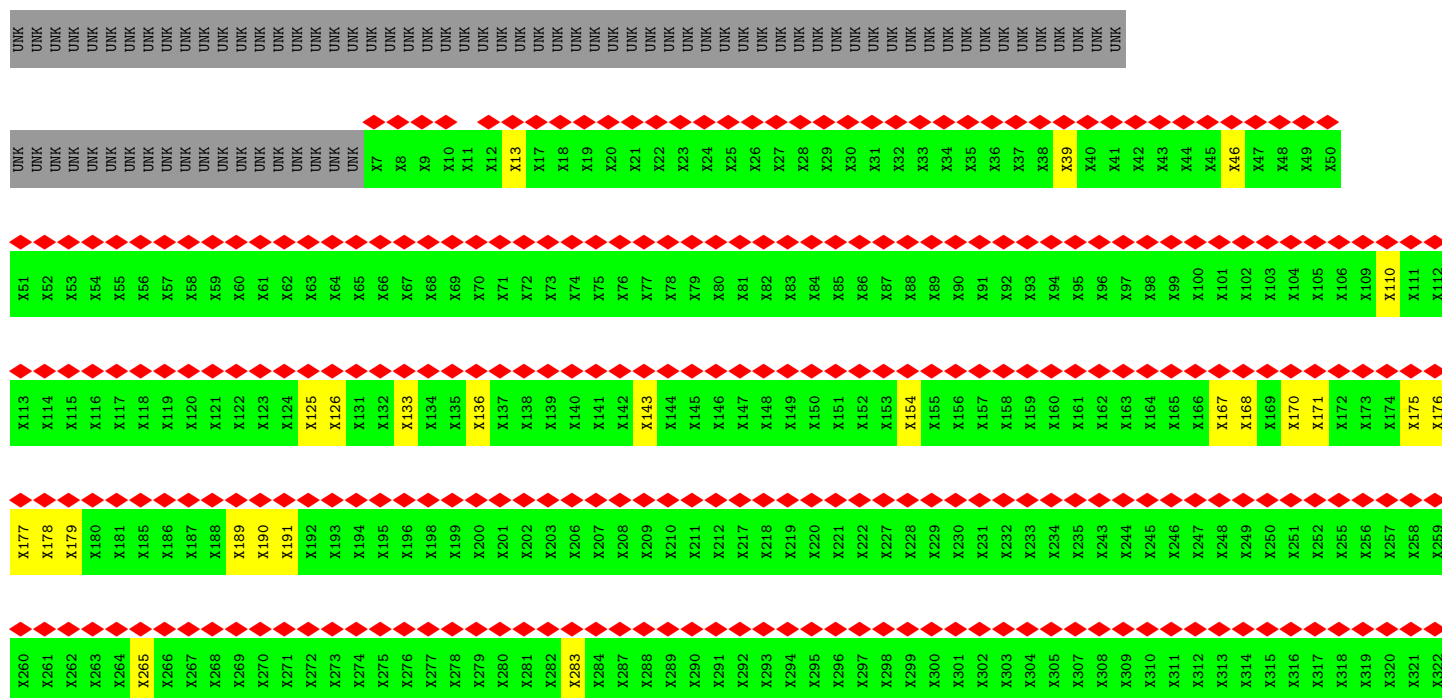
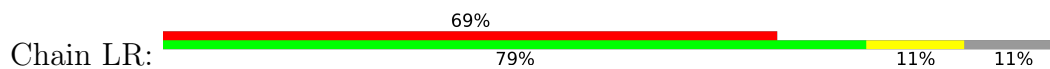
Chain LO: 69% 21% 10%

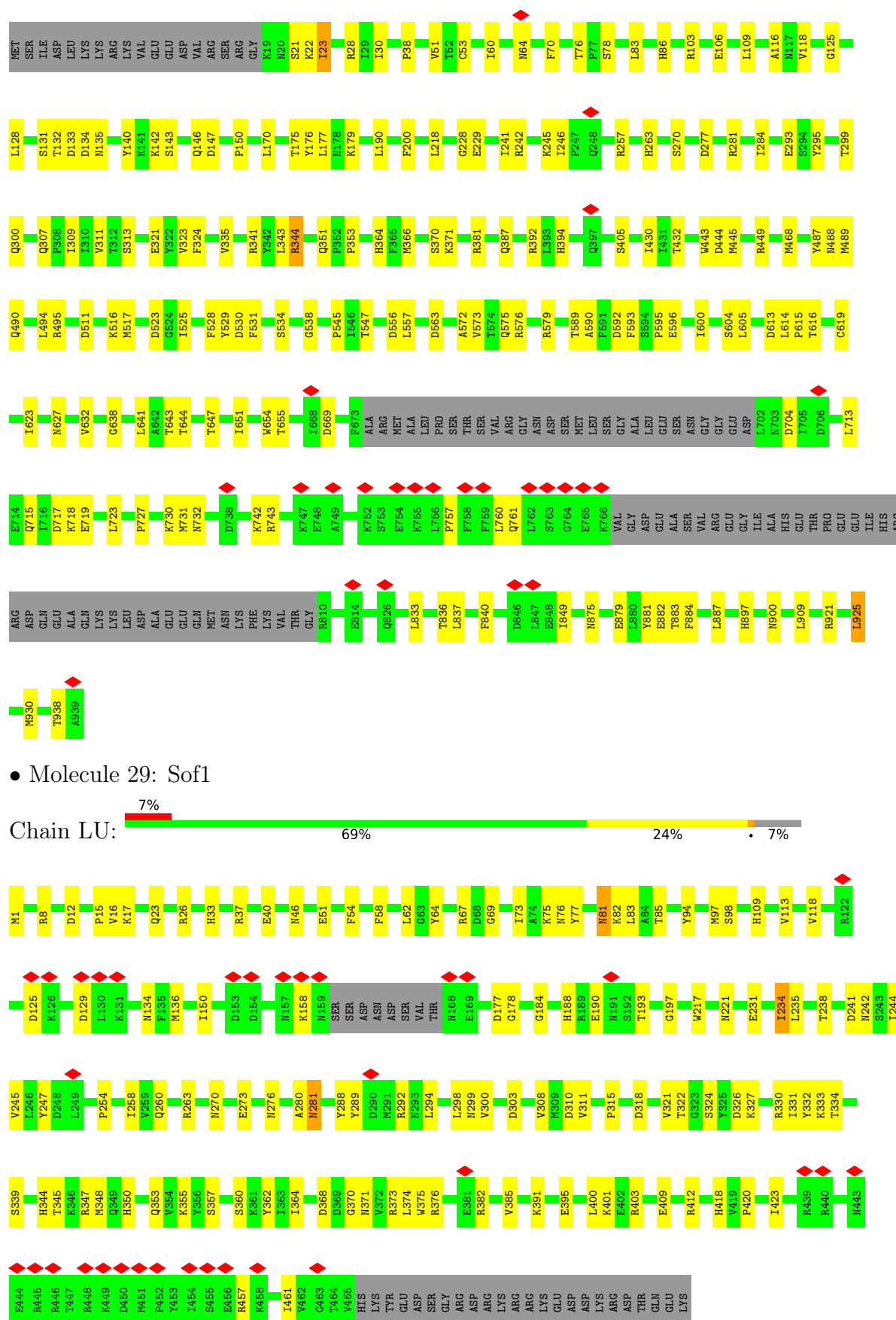


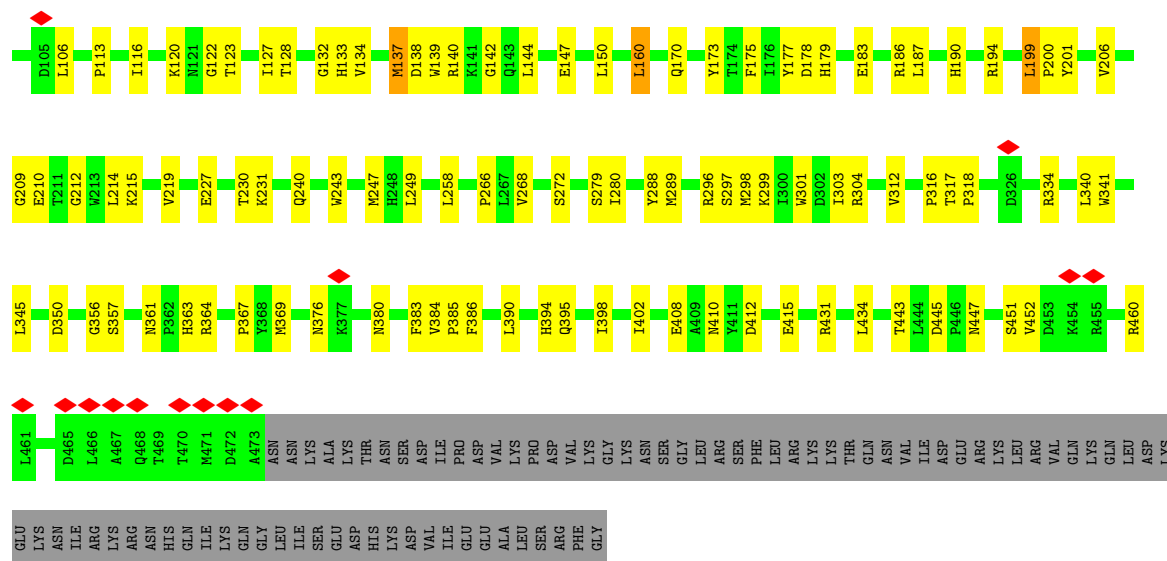




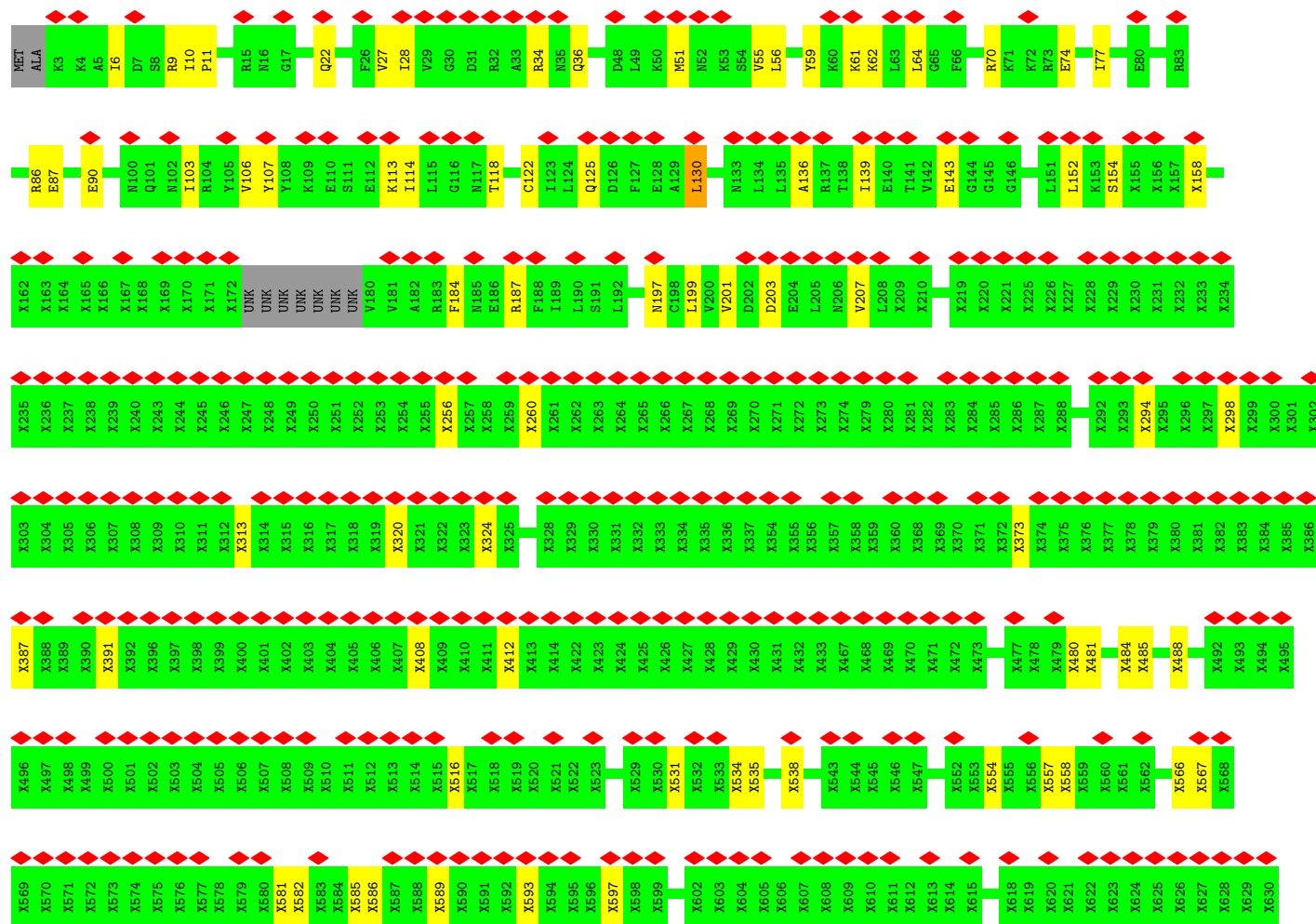
• Molecule 26: Utp13

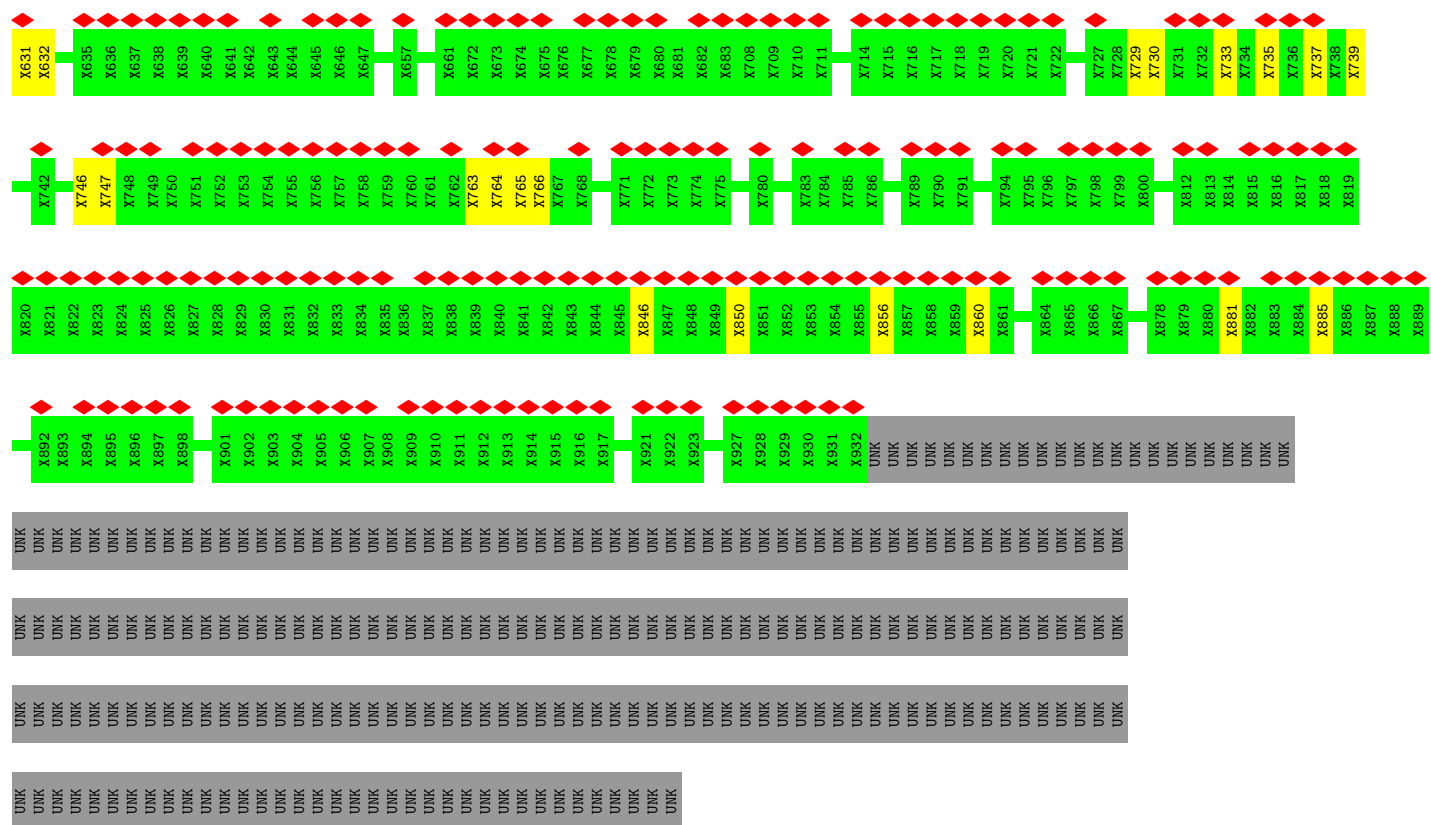




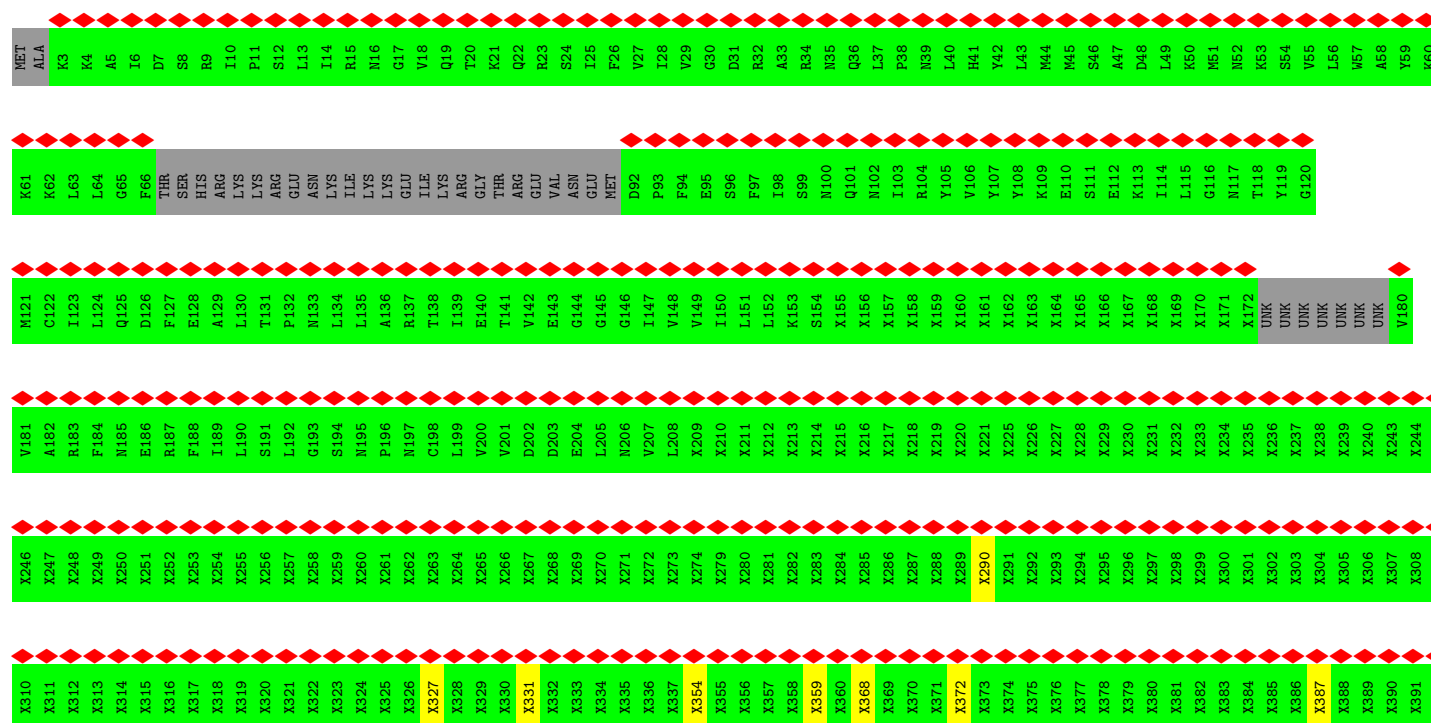


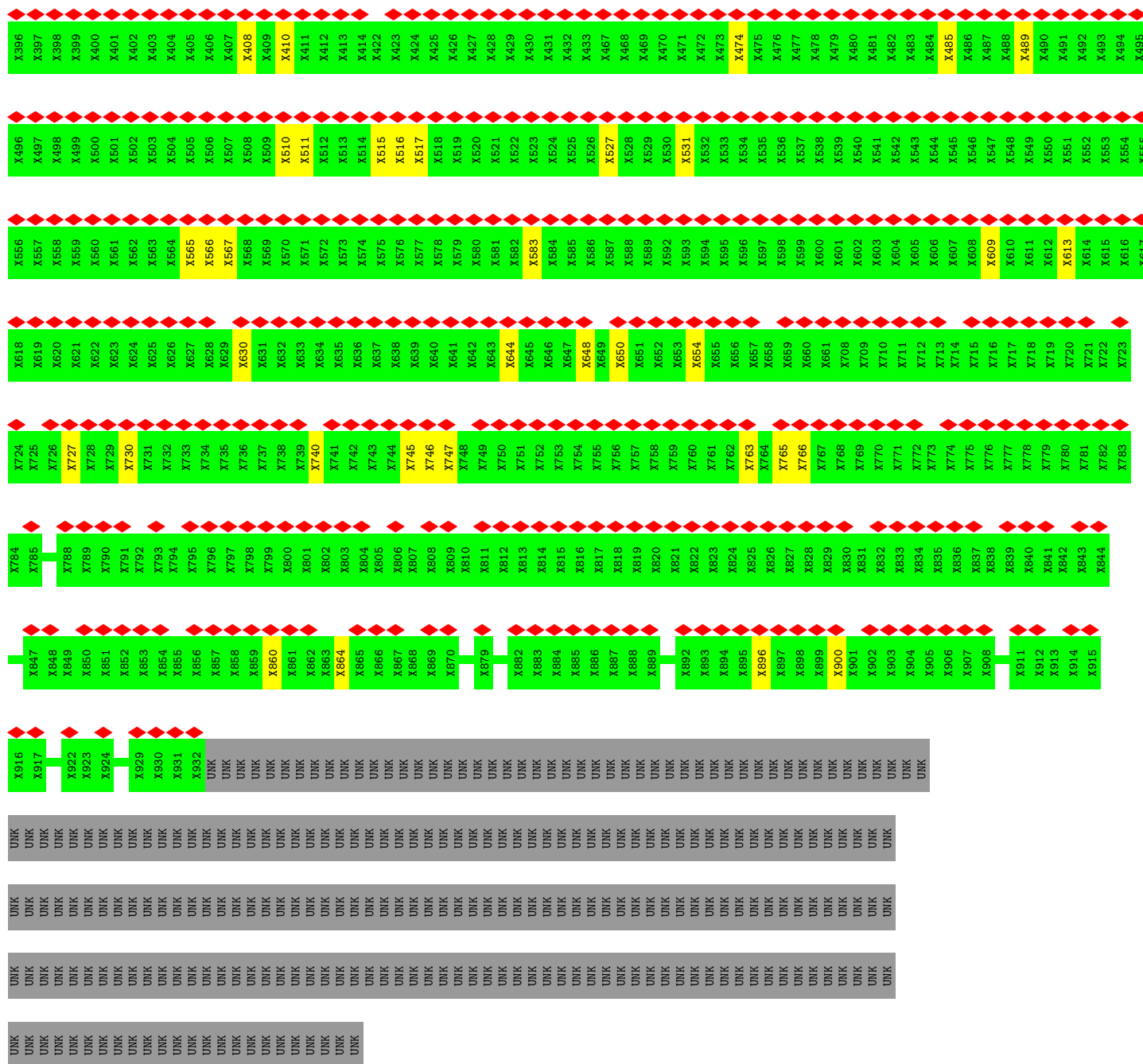
• Molecule 32: Kre33



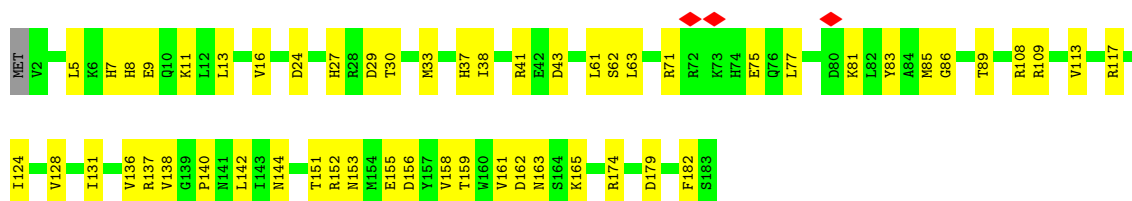


• Molecule 32: Kre33





Chain LZ: 70% 30%



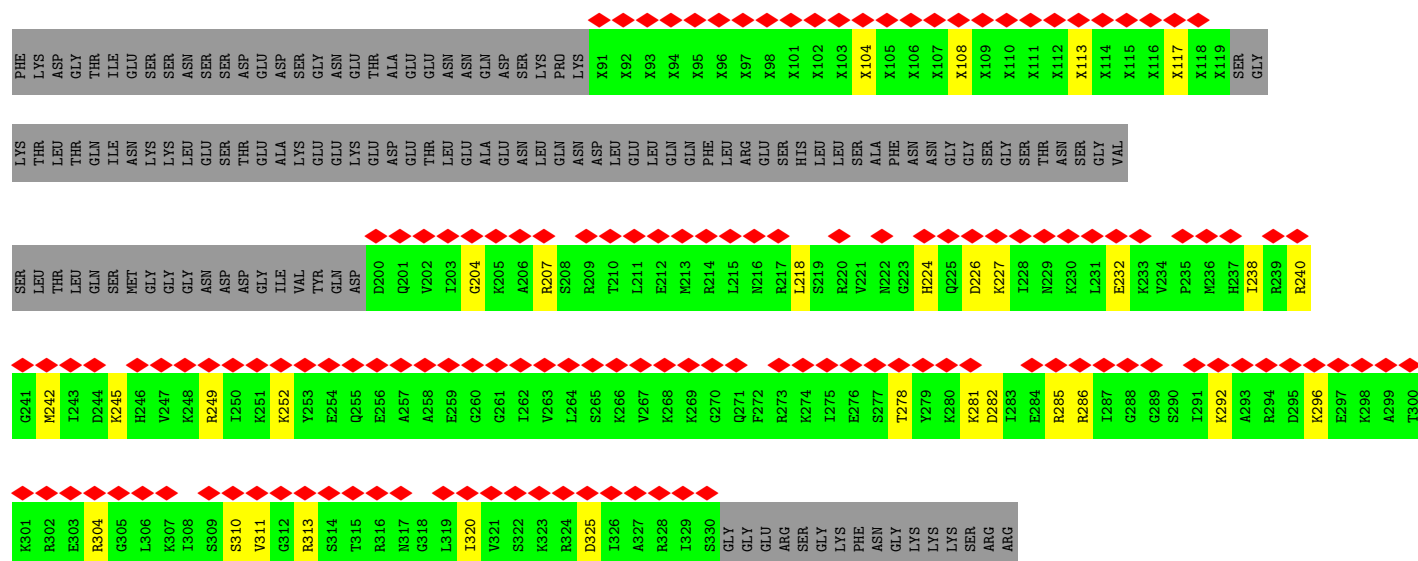
Frequency	Percentage
Daily	28%
Weekly	7%
Not at all	65%

A539	ASN	ASN	LEU	PRO	ASN	VAL	ASN	LYS	ARG	SER	LYS	ARG	ASN	ASP	VAL	VAL	ASP	THR	LEU	SER	LYS	ALA	LYS	LYS	ASN	ASN	ASN	GLN	LYS	GLY	GLY	LYS	LYS	ASP	VAL	SER	SER	LYS	GLY	THR	LYS	LYS	LYS	SER	SER	ARG	GLY	PRO	ASP	SER	THR	ASN	ILE	LYS	LEU
------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

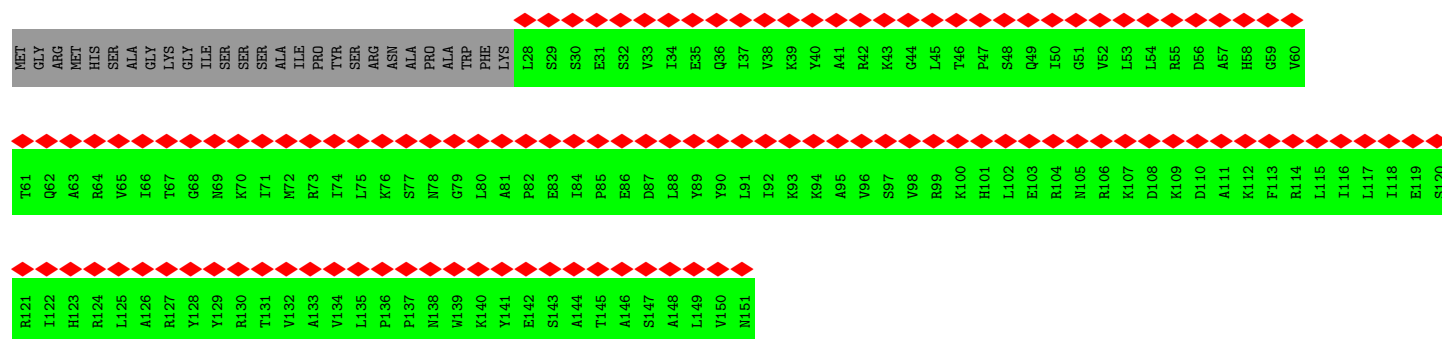
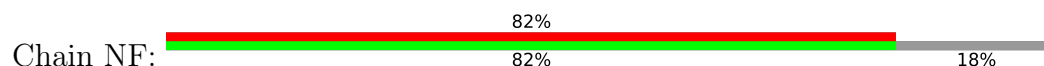
- Molecule 35: Sas10

Category	Percentage
Red	20%
Green	77%
Yellow	3%

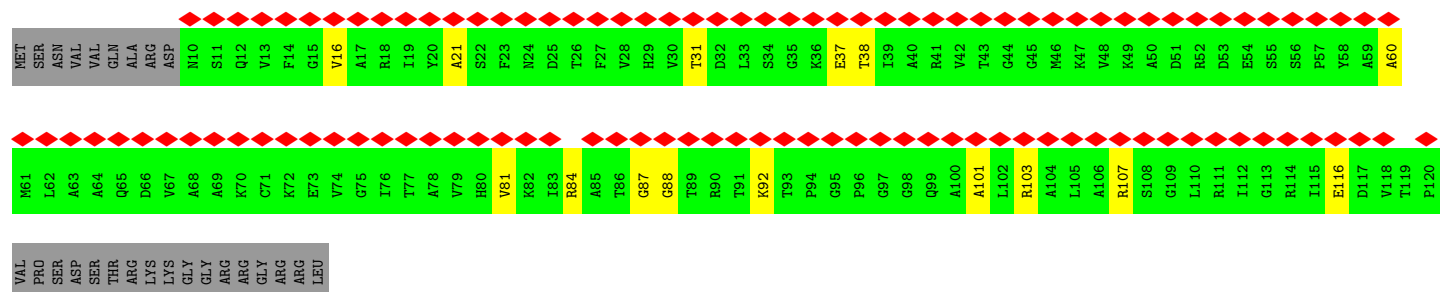
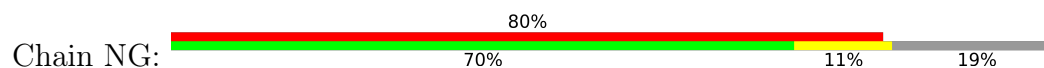
SER	LVS	ILE	ASP	GLN	GLU	ASN	LVS	LVS	T431	D432	R433	F434	K435	D436	T437	X446	X447	X448	X449	X450	X451	X452	X453	X454	ASP	GLU	ALA	ARG	LVS	ARG	GLY	MET	HIS	ASP	ASN	ASN	GLY	ALA	ASP	LEU	ASP	ASP	LVS	ASP	GLY	VAL	SER	ARG	ILE
-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



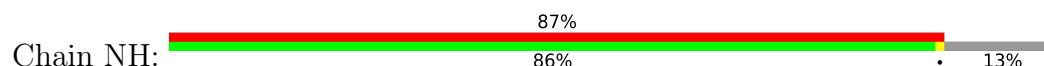
• Molecule 39: rpS13_uS15



• Molecule 40: rpS14_uS11



• Molecule 41: Utp22



MET	ALA	THR	SER	SER	VAL	GLY	LYS	ARG	LYS	ALA	SER	GLU	THR	SER	ASP	GLN	HIS	ASN	ILE	VAL	GLY	LYS	VAL	GLN	LYS	LYS	HIS	SER	THR	GLN	ASP	HIS	THR	THR	ASP	ASN	GLY	SER	LYS	GLU	ASN	ASP	HIS	SER	SER	GLN	ALA	ILE	ILE	GLU	ARG	THR	VAL	PRO	GLU	GLN	GLU	ASN	ASP	GLU	SER	THR					
SER	PRO	GLU	SER	ASN	GLU	VAL	ALA	THR	ALA	THR	THR	ALA	ALA	ALA	THR	ARG	HIS	ASN	ASN	GLY	GLY	LYS	VAL	THR	GLN	THR	ALA	THR	HIS	SER	THR	GLN	ASP	ILE	THR	THR	ALA	ARG	ASN	GLY	THR	ALA	SER	LYS	GLU	ASN	ASP	HIS	SER	SER	GLN	ALA	ILE	ILE	GLU	ARG	THR	VAL	PRO	GLU	GLN	GLU	ASN	ASP	GLU	SER	THR
V121	L122	K123	V124	E125	K126	F127	L128	H129	K130	L131	Y132	D133	I134	L135	Q136	E137	I138	P139	D140	W141	E142	E143	K144	S145	L146	A147	E148	V149	D150	S151	F152	F153	K154	N155	K156	I157	V158	S159	V160	P161	F162	L163	V163	D164	P165	K166	P167	I168	P169	Q170	M171	T172	N173	Y174	K175	F176	N177	K178	K179	K180							
P181	D182	I183	S184	L185	I186	G187	S188	F189	A190	L191	K192	A193	G194	I195	Y196	Q197	P198	N199	G200	S201	I202	D203	D204	T205	L206	L207	T208	M209	P210	K211	E212	L213	L214	E215	K216	K217	D218	F219	L220	N221	F222	N284	F285	Y286	K287	T288	R289	F290	S291	I292	N293	L294	L295	I296	G297	F298	H237	H238	L239	L240							
I241	L242	L243	K244	K245	D246	K247	L248	D249	S250	F251	L252	Q253	L254	E255	Y256	S257	Y258	F259	D260	N261	D262	G383	L264	L265	P266	I267	L268	R269	I270	S271	C272	S273	K274	PRO	THR	GLY	ASP	SER	LEU	SER	D282	Y283	N284	R285	Y286	K287	T288	R289	F290	K351	T352	K353	K354	Q355	T356	E357	S358	F359	V360	Y300							
K301	V302	F303	E304	P305	L306	K307	L308	L309	P310	N311	R312	K313	C314	I315	R316	I317	ALA	GLN	GLU	SER	LYS	GLN	SER	L326	P327	A328	T329	P330	L331	Y332	N333	F334	S335	V336	L337	S338	S339	S340	T341	H342	E343	N344	G403	G404	G405	I406	M407	S408	M409	K410	I411	L412	L413	H414	G415	F416	S417	S418	Y419	Q420							
E361	A362	T363	V364	L365	G366	R367	L368	W369	L370	N371	Q372	K373	G374	F375	S376	S377	N378	M379	S380	H381	S382	G383	S384	L385	G386	G387	F388	G389	T390	F391	E392	F393	T394	I395	L396	K397	A398	A399	L400	L401	M402	G403	G404	G405	I406	M407	S408	M409	K410	I411	L412	L413	H414	G415	F416	S417	S418	Y419	Q420								
L421	F422	K423	G424	V425	I426	K427	Y428	L429	A430	T431	M432	D433	L434	C435	H436	D437	G438	H439	L440	Q441	F442	H443	S444	M445	PRO	GLU	ASN	SER	SER	SER	P453	A454	S455	K456	Y457	I458	D459	E460	G461	F462	Q463	T464	P465	T466	L467	F468	D469	K470	S471	T472	K473	V474	M475	I476	L477	T478	K479	M480									
T481	V482	S483	S484	Y485	Q486	L487	L488	K489	F490	Y491	A492	G493	E494	T495	L496	R497	M498	L499	N500	N501	V502	V503	Q504	D505	Q506	F507	S508	N509	I510	F511	L512	T513	N514	I515	S516	R517	F518	D519	N520	L521	K522	Y523	D524	L525	C526	Y527	D528	V529	Q530	L531	P532	L533	G534	K535	Y536	N537	N538	L539	E540								
T541	S542	L543	A544	A545	T546	F547	G548	S549	M550	E551	R552	V553	K554	F555	I556	T557	L558	E559	N560	F561	S622	E623	O624	D625	I566	T567	N568	V569	A570	R571	Y572	A573	L574	G575	D576	R577	I578	K579	Y580	I581	Q582	L583	E584	M585	V586	G587	Q588	K589	S590	I591	F592	P593	I594	T595	K596	R597	K598	V599	Y600								
S601	N602	T603	G604	G605	N606	H607	F608	N609	F610	D611	F612	G613	R614	V615	K616	L617	I618	V619	N620	P621	S622	E623	O624	D625	I566	T567	N568	V569	A570	R571	Y572	A573	L574	G575	D576	R577	I578	K579	Y580	I581	Q582	L583	E584	M585	V586	G587	Q588	K589	S590	I591	F592	P593	I594	T595	K596	R597	K598	V599	Y600								
G661	S662	I663	T664	H665	C666	C667	V668	W669	S670	T671	S672	S673	S674	E675	P676	L677	I678	S679	S680	I681	V682	N683	F684	A685	L686	Q687	K688	H689	S690	S691	K692	K693	L694	Q695	I696	S697	N698	M698	S699	T700	I701	K702	K703	S704	F704	H705	N706	F707	L708	P709	V710	P711	N712	L713	S714	S715	S716	A717	K718	T719	S720						
V721	L722	N723	L724	S725	S726	F727	F728	N729	L730	K731	K732	S733	F734	D735	D736	L737	K738	K739	I740	I741	F742	Q743	M744	K745	L746	P747	L748	S749	V750	K751	S752	I753	L754	P755	V756	G757	S758	A759	F760	R761	Y762	T763	S764	L765	C766	F767	P768	V769	P770	F771	A772	Y773	S774	D775	P776	D777	F778	F779	Q780								
D781	V782	I783	L784	E785	F786	E787	T788	S789	P790	K791	S792	P793	D794	E795	I796	T797	S798	L799	E800	K801	A802	K803	T804	A805	F806	L807	L808	K809	I810	Q811	E812	E813	L814	S815	A816	N817	S818	S819	T820	Y821	R822	S823	F824	F825	S826	R827	D828	E829	I831	P832	Y833	N834	L835	E836	I837	V838	T839	L840									

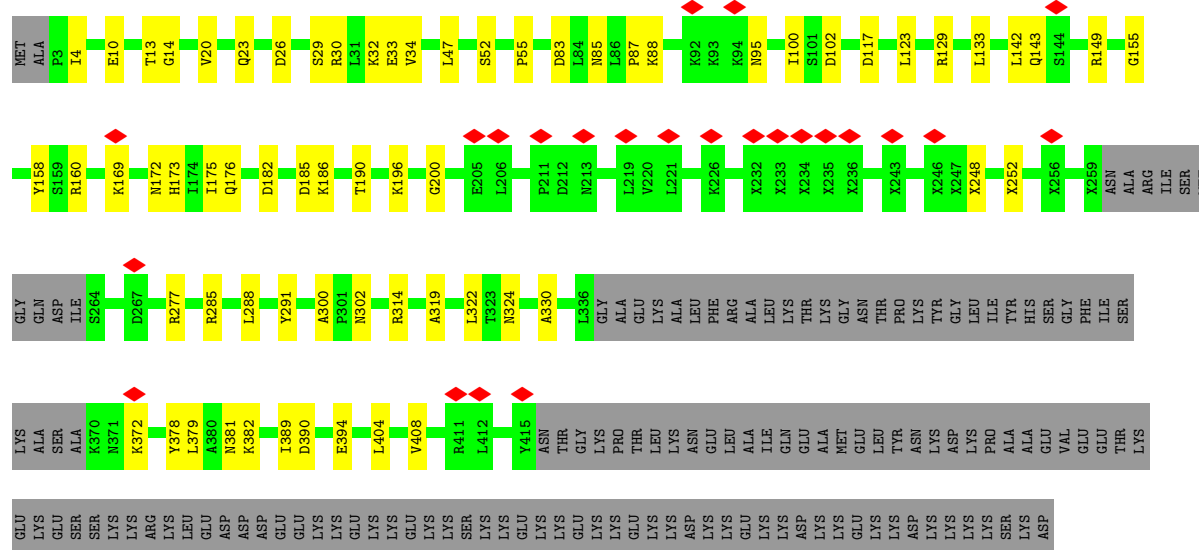




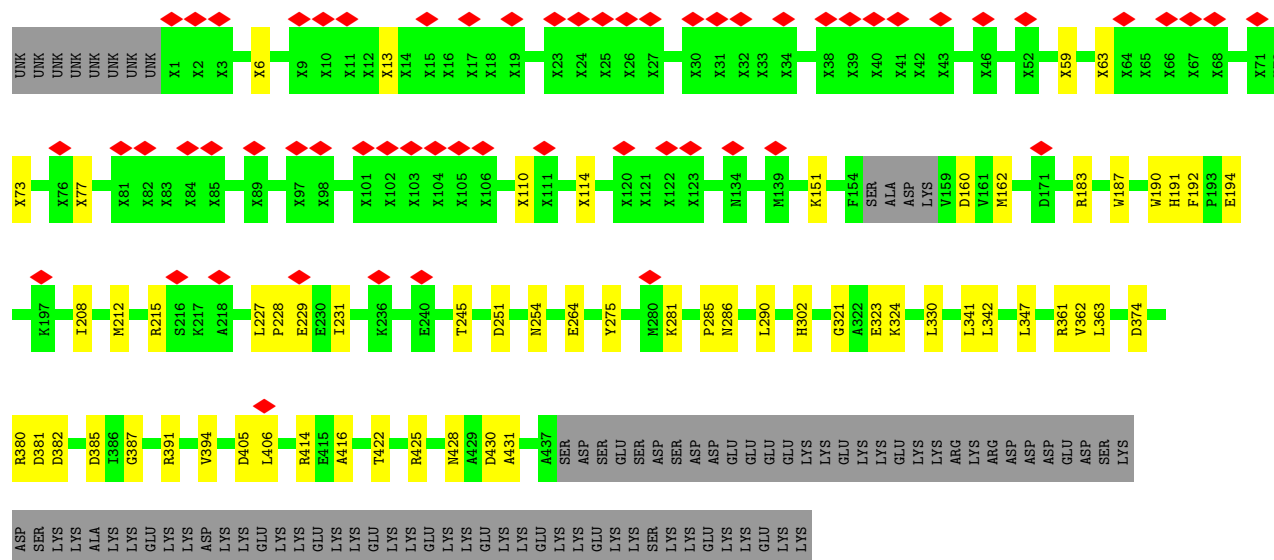


LYS
ASP
PHE
ILE
ALA
PRO
GLU
GLU
ALA
ALA
TYR
LYS
PRO
ASN
GLN
ASN

• Molecule 45: Nop56

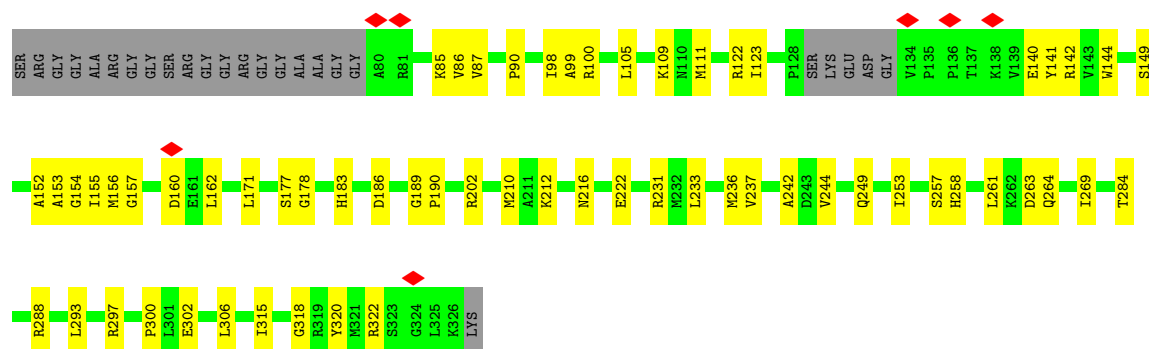


• Molecule 46: Nop58

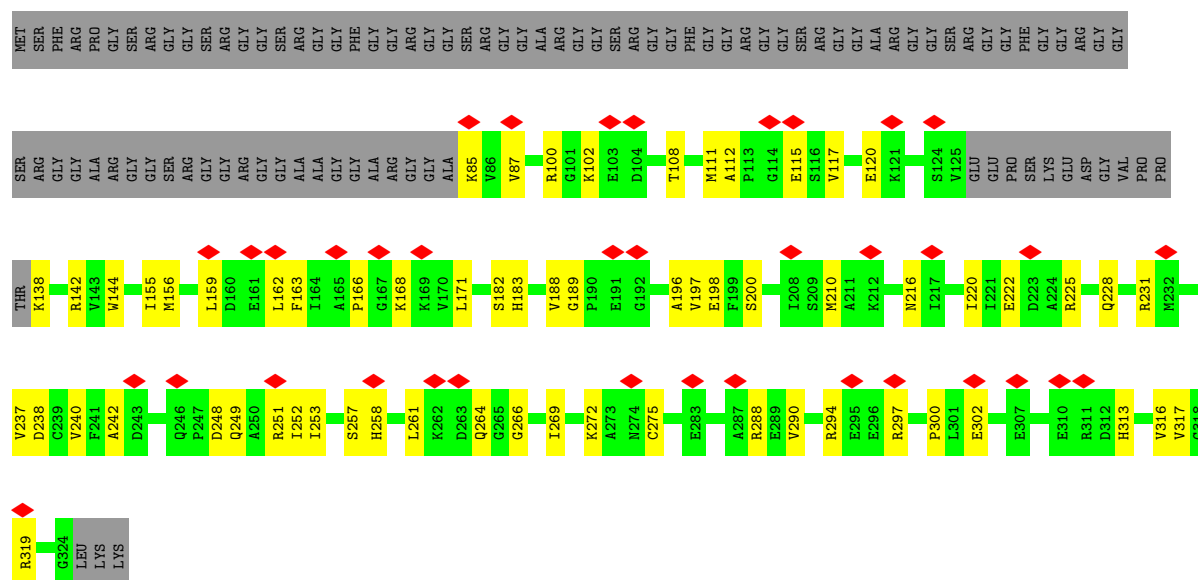


• Molecule 47: Nop1

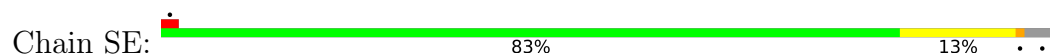




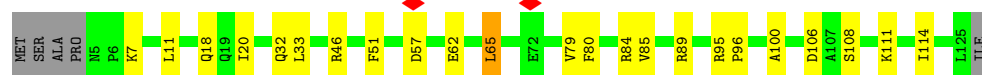
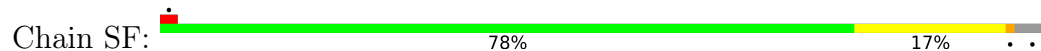
• Molecule 47: Nop1



• Molecule 48: Snu13

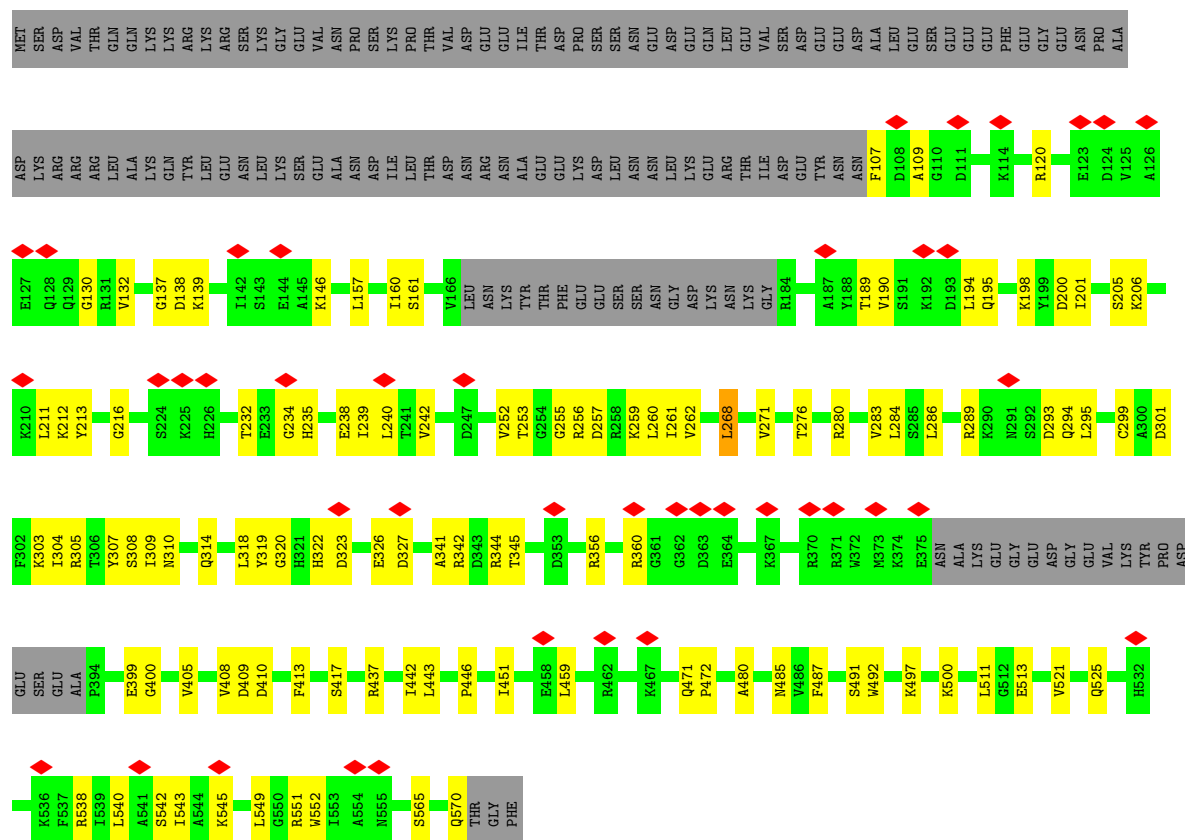


• Molecule 48: Snu13

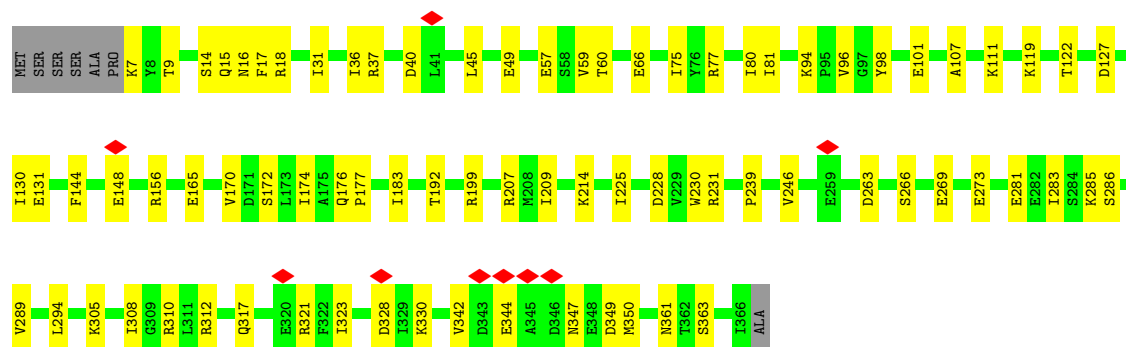
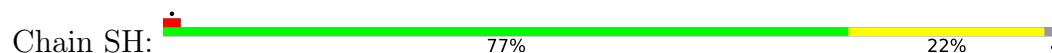


• Molecule 49: Rrp9

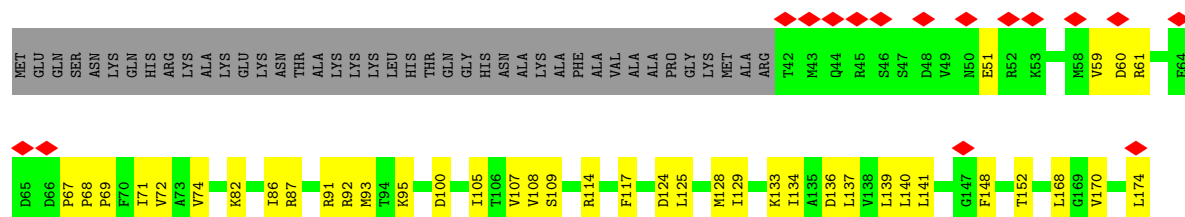


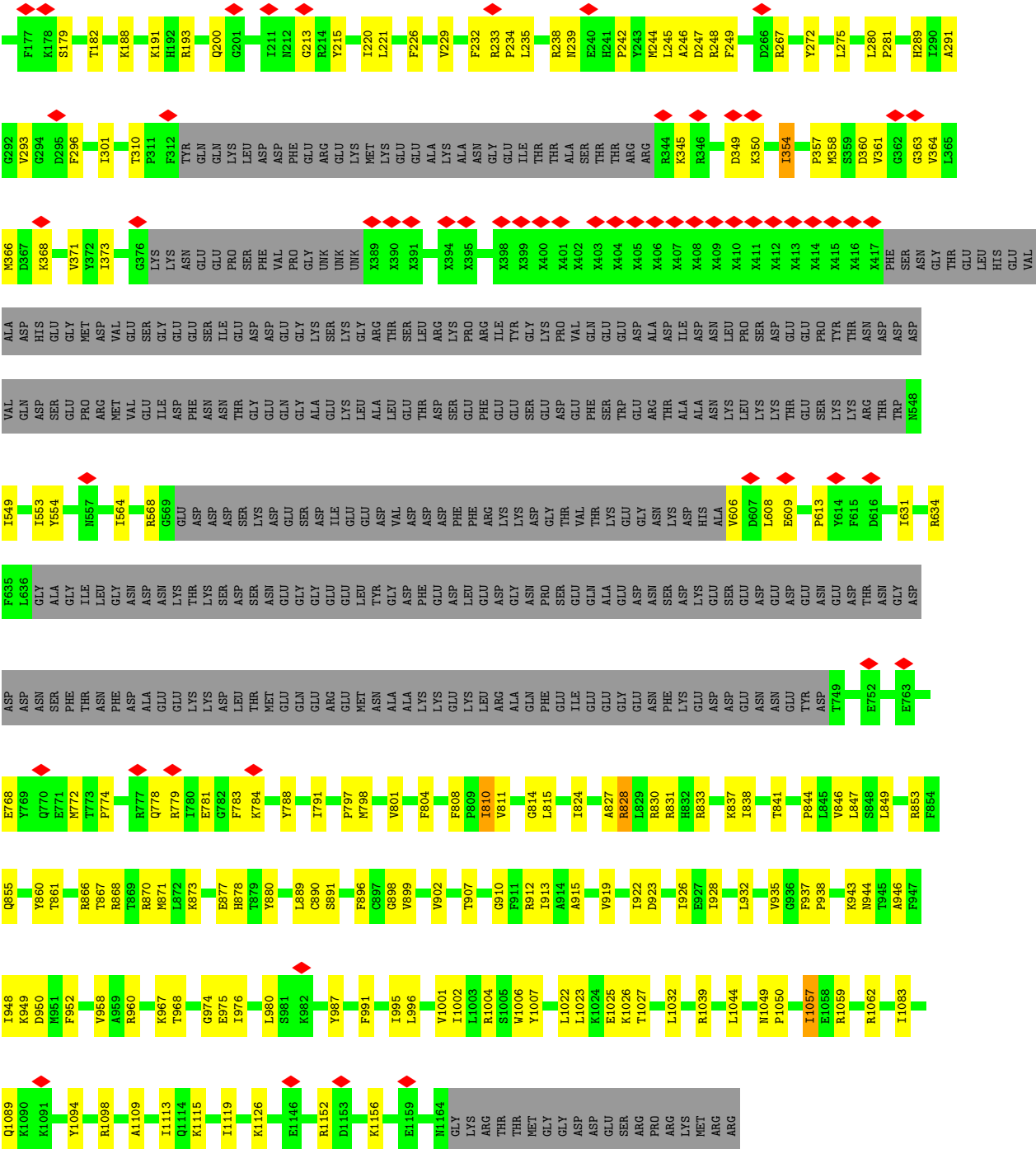


- Molecule 50: Rcl1

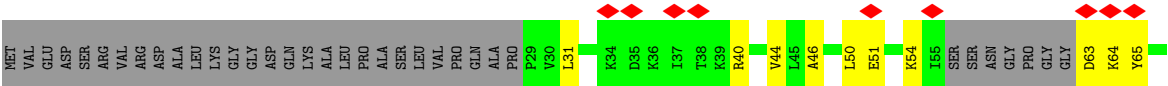


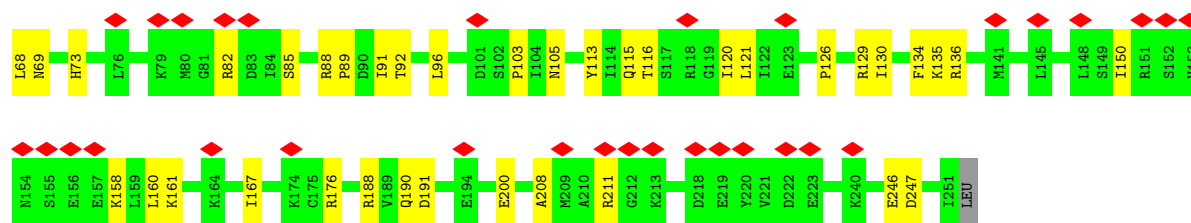
- Molecule 51: Bms1



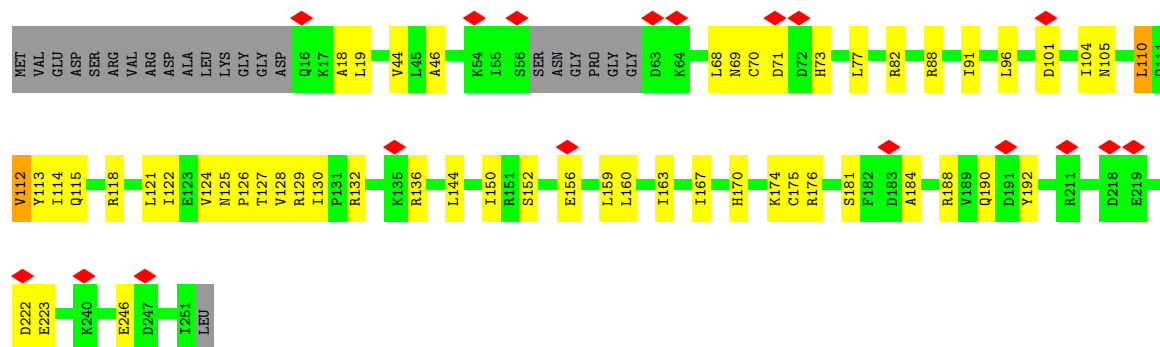


• Molecule 52: Emg1

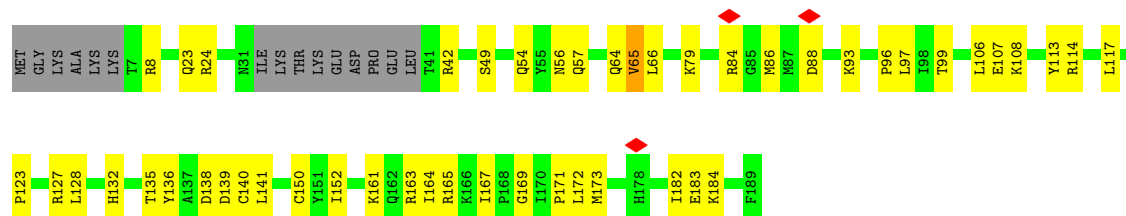




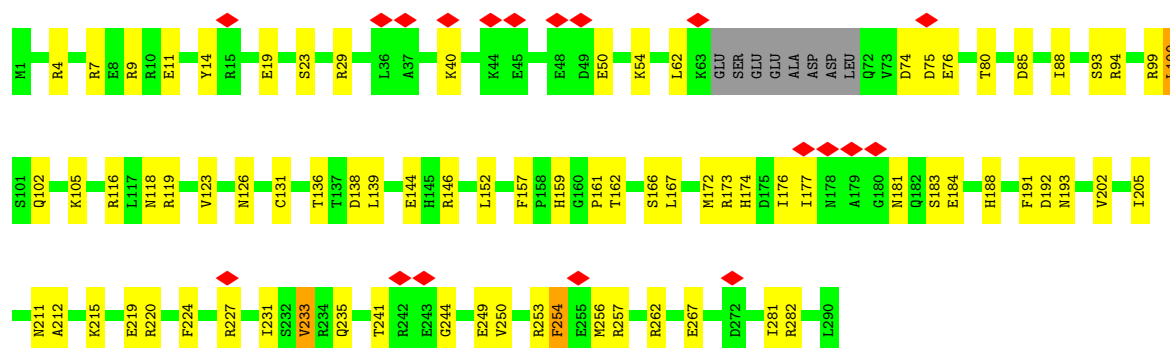
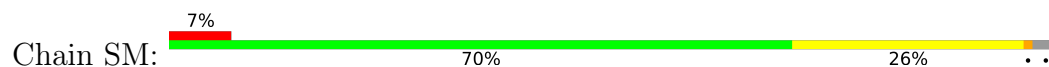
- Molecule 52: Emg1



- Molecule 53: Utp24

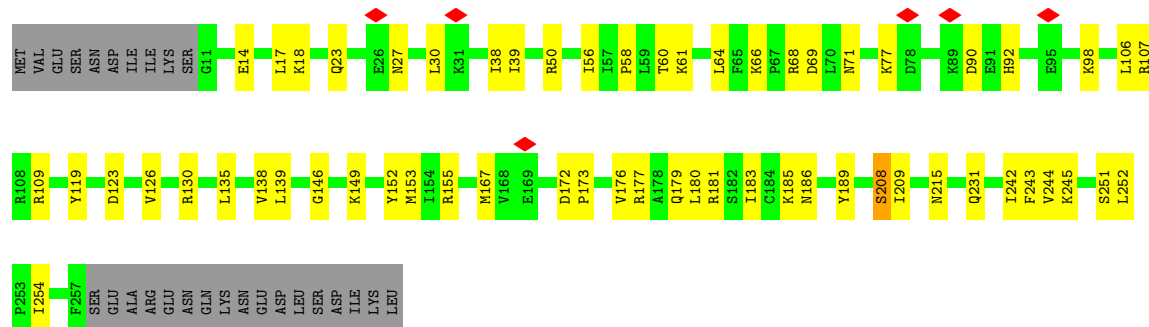


- Molecule 54: Imp4



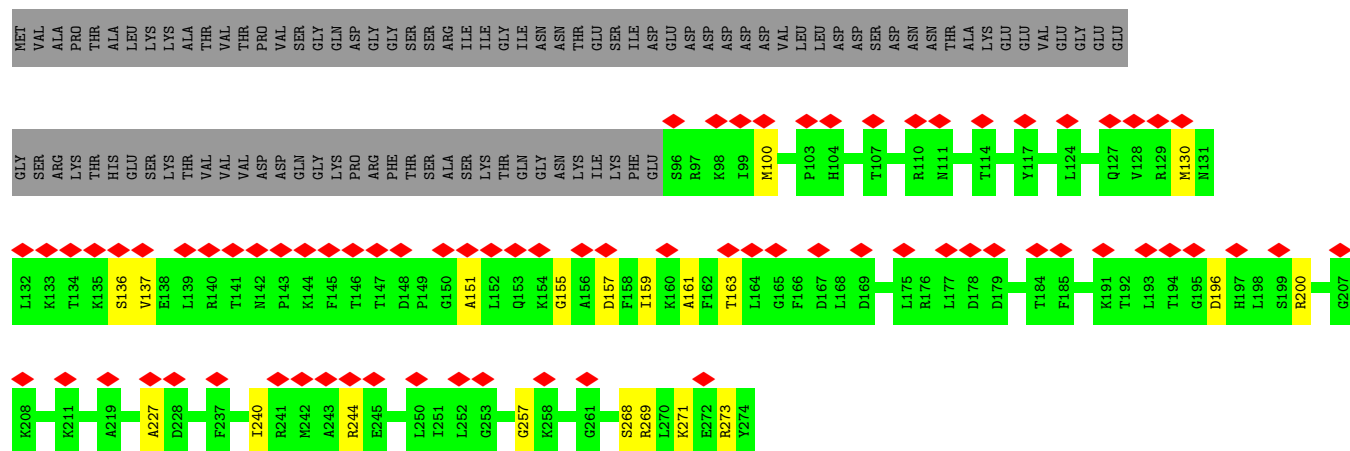
- Molecule 55: Utp30

Chain SN: 

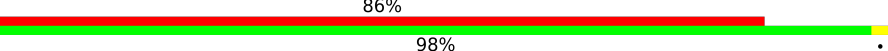


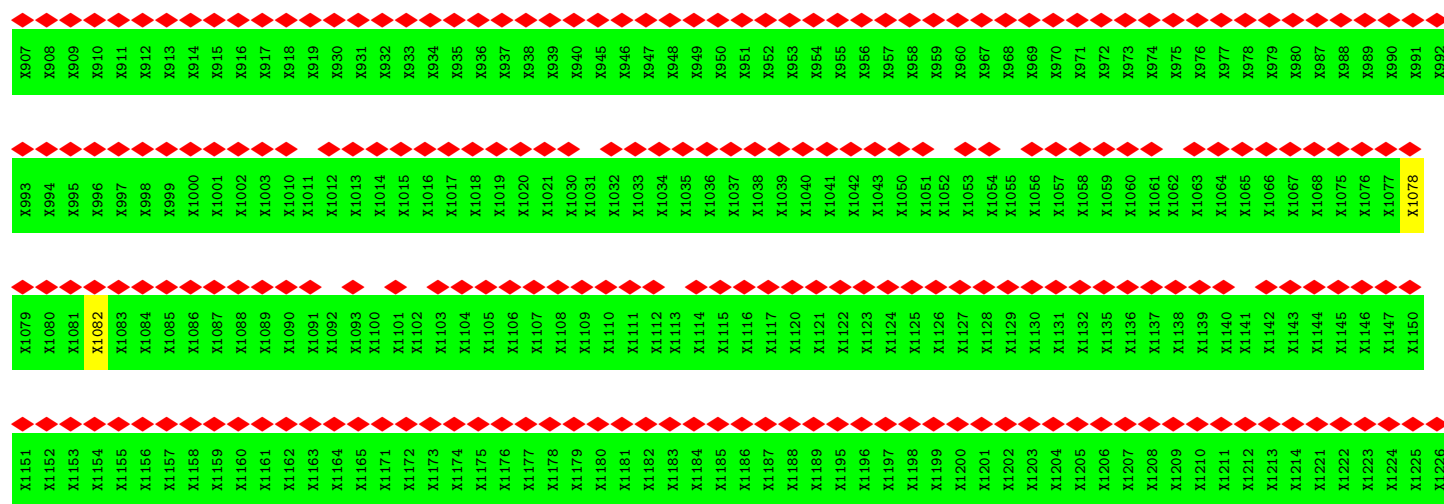
• Molecule 56: Pno1

Chain SO: 



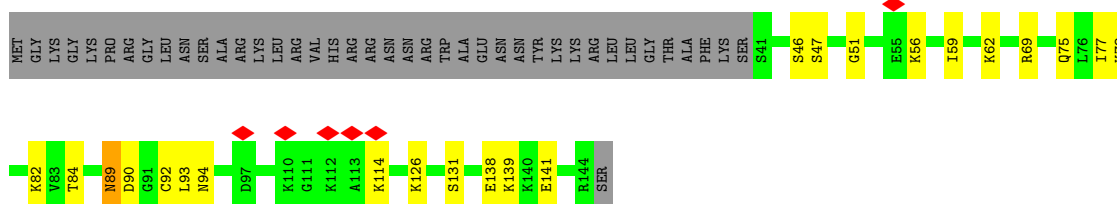
• Molecule 57: Utp20

Chain SP: 

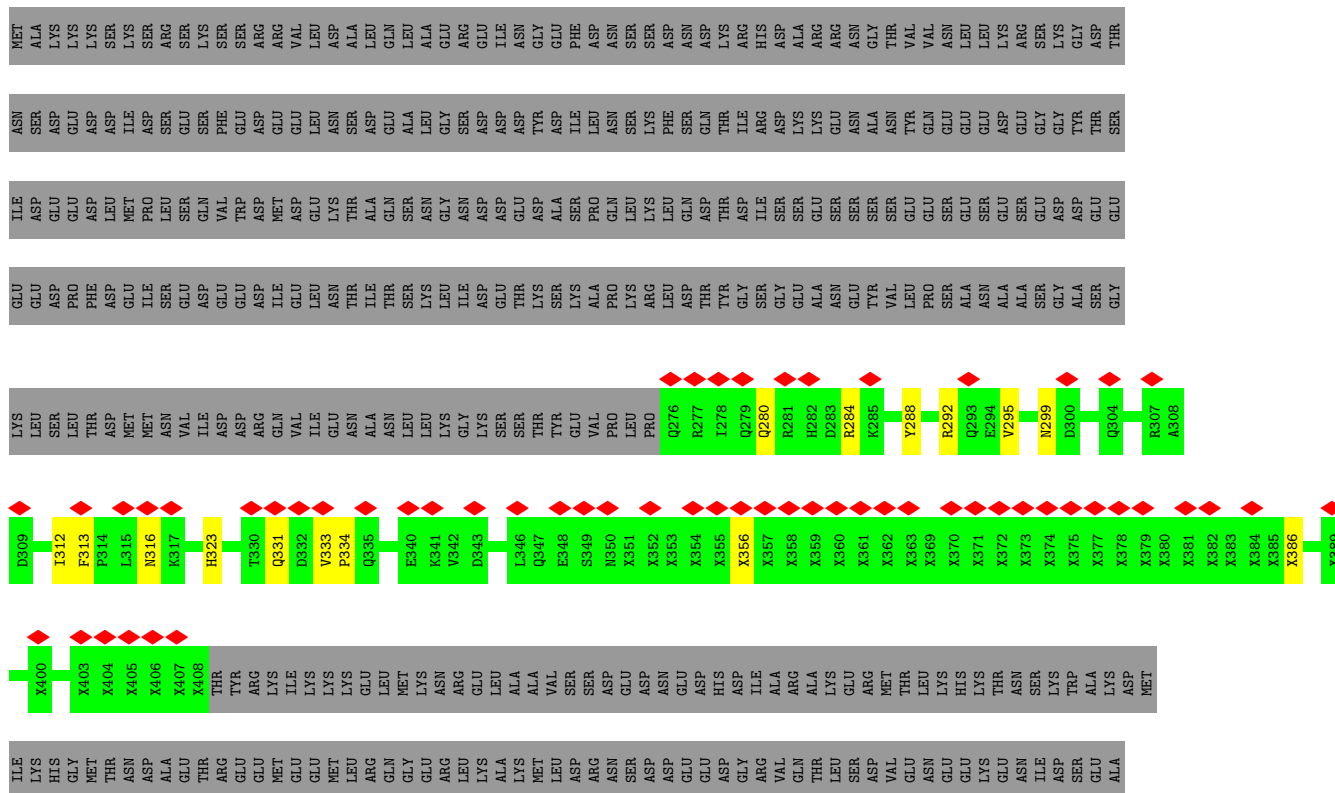




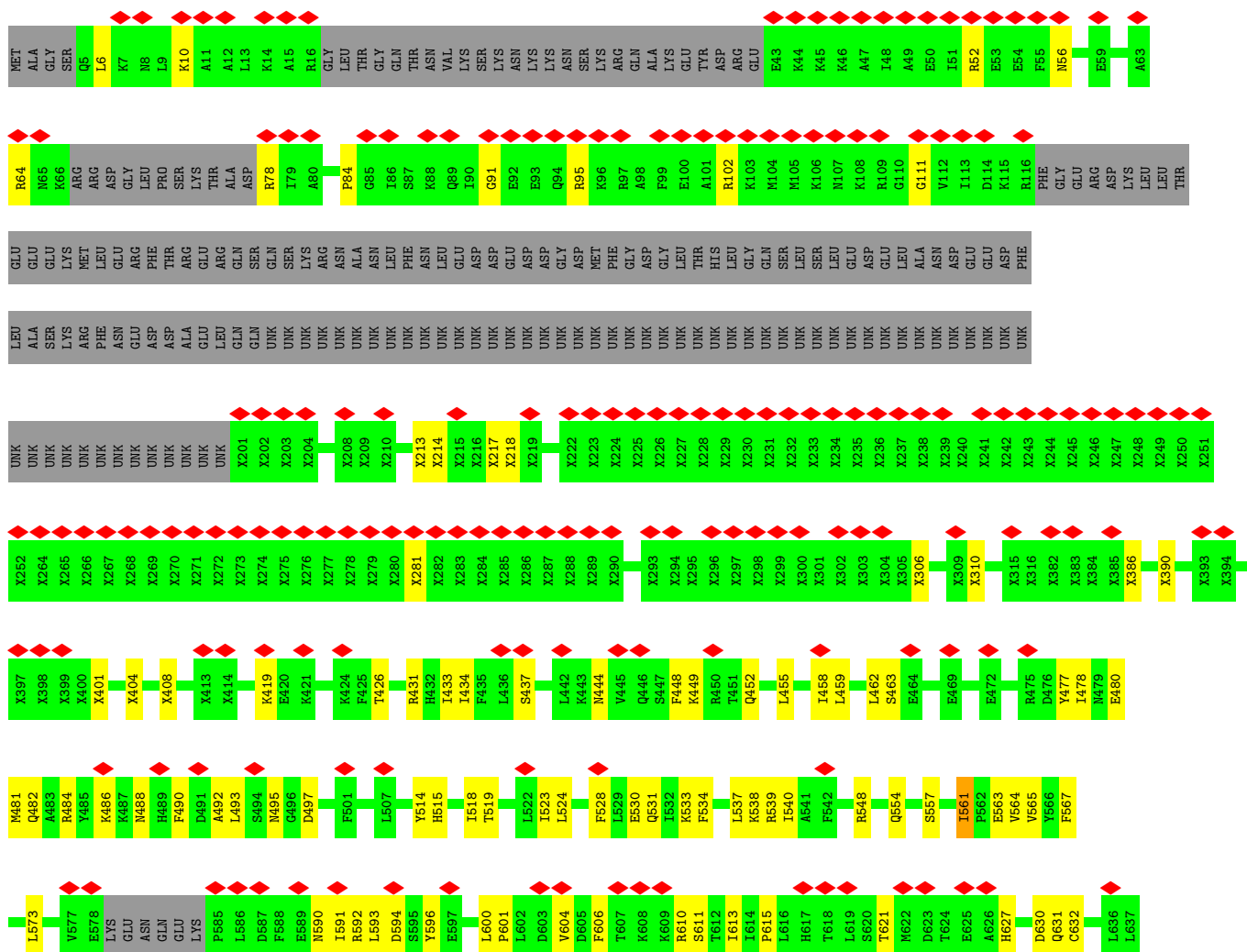
- Molecule 59: rpS23 uS12



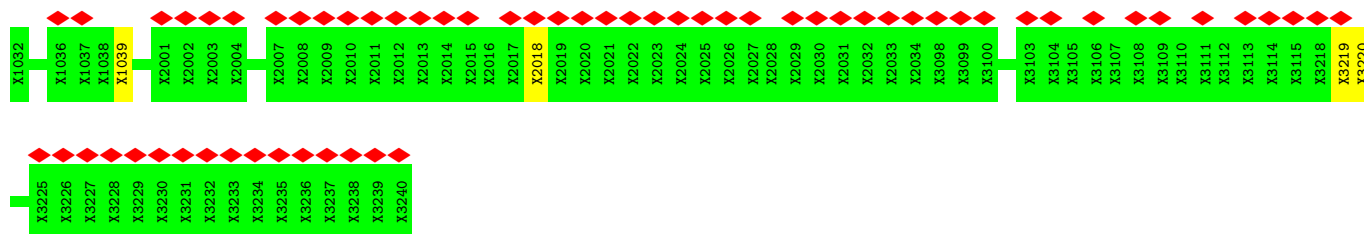
- Molecule 60: Utp14



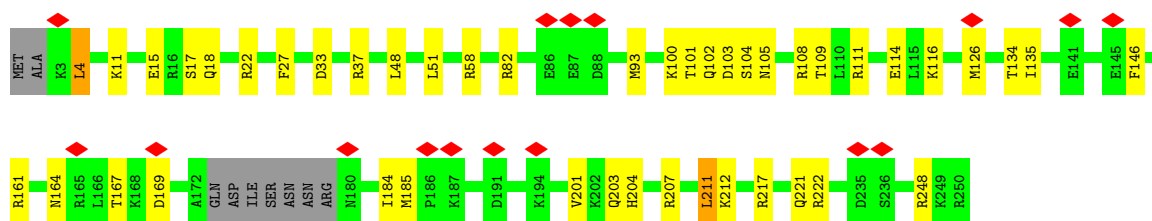
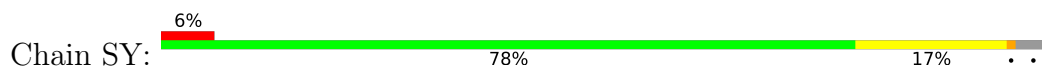
- Molecule 61: Nop14



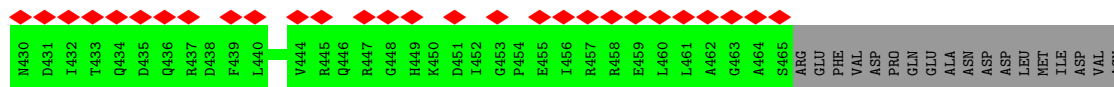
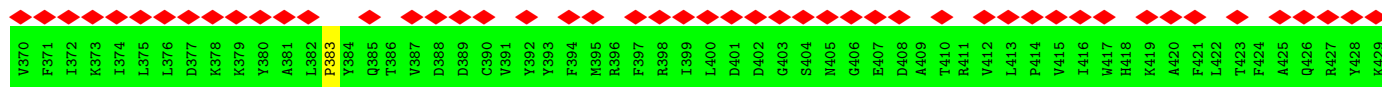
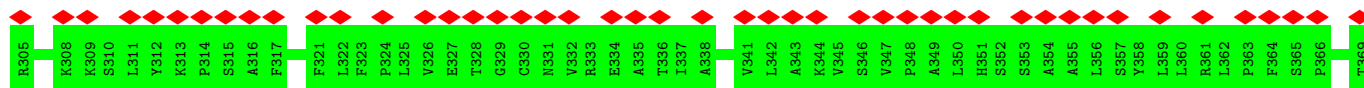
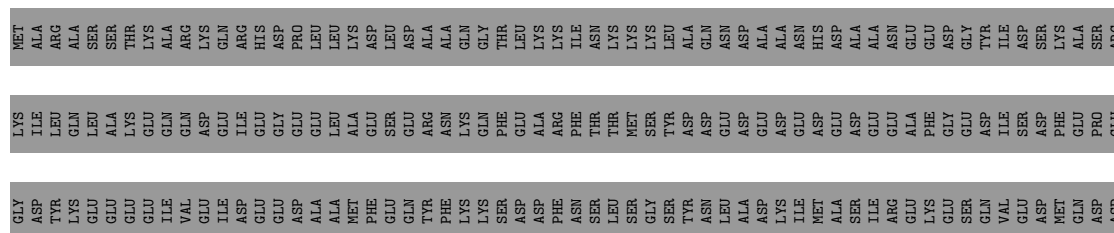
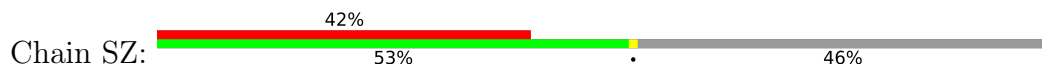




• Molecule 65: Utp11



• Molecule 66: Enp1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	284213	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.56	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.166	Depositor
Minimum map value	-0.105	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.023	Depositor
Map size ($\text{\AA}$)	520.0, 520.0, 520.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3, 1.3, 1.3	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	L0	0.35	0/11634	0.41	3/18120 (0.0%)
2	L1	0.27	0/24442	0.38	0/38042
3	L2	0.36	0/4001	0.37	0/6215
4	L3	0.23	0/871	0.56	0/1171
5	L4	0.26	0/1849	0.72	0/2497
6	L5	0.41	0/1690	0.68	0/2285
7	L6	0.21	0/899	0.60	2/1201 (0.2%)
8	L7	0.26	0/1342	0.71	0/1807
9	L8	0.21	0/1372	0.57	0/1834
10	L9	0.40	0/1437	0.67	0/1924
11	LC	0.54	0/990	0.77	0/1335
12	LD	0.25	0/1050	0.61	0/1415
13	LE	0.25	0/1020	0.51	0/1371
14	LF	0.31	0/727	0.78	0/977
15	LG	0.41	0/499	0.72	0/670
16	LH	0.33	0/6694	0.61	0/9070
17	LI	0.22	0/1105	0.56	2/1491 (0.1%)
18	LJ	0.40	0/3993	0.67	0/5413
19	LK	0.21	0/735	0.51	0/987
20	LL	0.37	0/3840	0.65	2/5208 (0.0%)
21	LM	0.41	0/3470	0.64	1/4694 (0.0%)
22	LN	0.34	0/5369	0.64	2/7272 (0.0%)
23	LO	0.50	0/6780	0.73	2/9175 (0.0%)
24	LP	0.33	0/2281	0.56	0/3059
25	LQ	0.30	0/6574	0.65	0/8881
26	LR	0.33	0/1336	0.57	0/1800
27	LS	0.47	0/3875	0.65	0/5254
28	LT	0.43	0/6834	0.62	0/9238
29	LU	0.43	0/3802	0.68	2/5118 (0.0%)
30	LV	0.27	0/2902	0.70	3/3941 (0.1%)
31	LW	0.53	0/3505	0.71	2/4748 (0.0%)
32	LX	0.26	0/1481	0.58	0/1987

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
32	LY	0.14	0/768	0.38	0/1065
33	LZ	0.53	0/1559	0.82	2/2097 (0.1%)
34	NA	0.36	0/1685	0.65	3/2261 (0.1%)
35	NB	0.36	0/1042	0.62	0/1377
36	NC	0.31	0/1139	0.77	1/1512 (0.1%)
37	ND	0.27	0/499	0.60	0/659
38	NE	0.23	0/1063	0.59	1/1402 (0.1%)
39	NF	0.17	0/614	0.57	0/855
40	NG	0.19	0/542	0.55	0/750
41	NH	0.16	0/5356	0.44	0/7460
42	NI	0.14	0/838	0.42	0/1166
43	NJ	0.14	0/1313	0.45	0/1830
44	NK	0.17	0/867	0.45	0/1208
45	SA	0.35	0/2769	0.62	0/3728
46	SB	0.38	0/2344	0.64	0/3160
47	SC	0.50	0/1917	0.71	1/2588 (0.0%)
47	SD	0.29	0/1815	0.65	0/2448
48	SE	0.42	0/928	0.63	0/1262
48	SF	0.37	0/928	0.65	0/1262
49	SG	0.30	0/3498	0.61	0/4712
50	SH	0.31	0/2832	0.55	0/3825
51	SI	0.40	0/6403	0.67	2/8616 (0.0%)
52	SJ	0.23	0/1727	0.52	0/2329
52	SK	0.31	0/1828	0.56	0/2470
53	SL	0.47	0/1418	0.69	0/1906
54	SM	0.46	0/2337	0.75	0/3148
55	SN	0.36	0/2041	0.69	2/2745 (0.1%)
56	SO	0.20	0/1003	0.51	0/1381
58	SQ	0.34	0/1156	0.60	0/1536
59	SR	0.41	0/804	0.72	2/1074 (0.2%)
60	SS	0.28	0/1230	0.60	1/1660 (0.1%)
61	ST	0.25	0/3826	0.56	0/5125
62	SU	0.30	0/3064	0.60	2/4163 (0.0%)
63	SV	0.32	0/201	0.65	0/273
65	SY	0.41	0/2042	0.69	0/2704
66	SZ	0.15	0/1294	0.44	0/1804
All	All	0.35	0/183089	0.58	38/255761 (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
4	L3	0	1
5	L4	0	2
8	L7	0	4
11	LC	0	1
12	LD	0	1
14	LF	0	1
16	LH	0	2
22	LN	0	2
23	LO	0	2
25	LQ	0	2
28	LT	0	1
29	LU	0	1
30	LV	0	3
31	LW	0	2
34	NA	0	1
36	NC	0	2
46	SB	0	1
48	SE	0	1
49	SG	0	1
54	SM	0	3
56	SO	0	1
58	SQ	0	2
All	All	0	37

There are no bond length outliers.

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L0	524	U	OP1-P-O3'	-8.80	81.59	108.00
1	L0	524	U	OP2-P-O3'	-7.43	85.72	108.00
22	LN	621	ASN	CA-C-N	7.33	132.59	120.86
22	LN	621	ASN	C-N-CA	7.33	132.59	120.86
55	SN	208	SER	CA-C-N	6.86	125.82	120.33

There are no chirality outliers.

5 of 37 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	L3	13	HIS	Peptide
5	L4	193	GLY	Peptide
5	L4	194	THR	Peptide
8	L7	10	SER	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
8	L7	12	ALA	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	L0	10405	0	5231	112	0
2	L1	21866	0	11031	254	0
3	L2	3585	0	1819	45	0
4	L3	901	0	904	16	0
5	L4	1810	0	1865	52	0
6	L5	1669	0	1724	36	0
7	L6	888	0	928	21	0
8	L7	1321	0	1390	18	0
9	L8	1349	0	1372	37	0
10	L9	1415	0	1497	32	0
11	LC	973	0	1029	17	0
12	LD	1027	0	1084	25	0
13	LE	1003	0	1040	14	0
14	LF	715	0	744	11	0
15	LG	497	0	535	12	0
16	LH	6633	0	6509	127	0
17	LI	2857	0	1520	47	0
18	LJ	3911	0	3906	97	0
19	LK	898	0	809	11	0
20	LL	3772	0	3806	93	0
21	LM	3443	0	3558	58	0
22	LN	5344	0	5303	113	0
23	LO	6635	0	6525	140	0
24	LP	2709	0	2363	46	0
25	LQ	6640	0	6501	171	0
26	LR	4144	0	1952	54	0
27	LS	3791	0	3772	108	0
28	LT	6697	0	6676	139	0
29	LU	3725	0	3679	98	0
30	LV	2840	0	2685	77	0
31	LW	3428	0	3407	87	0
32	LX	4583	0	2198	63	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	LY	3823	0	983	25	0
33	LZ	1530	0	1572	41	0
34	NA	1667	0	1701	44	0
35	NB	1098	0	1100	22	0
36	NC	1125	0	1101	18	0
37	ND	600	0	586	18	0
38	NE	1192	0	1184	24	0
39	NF	615	0	280	0	0
40	NG	543	0	277	9	0
41	NH	5362	0	2295	6	0
42	NI	841	0	365	1	0
43	NJ	1314	0	610	2	0
44	NK	868	0	379	3	0
45	SA	2854	0	2787	53	0
46	SB	2937	0	2512	44	0
47	SC	1881	0	1928	45	0
47	SD	1782	0	1826	45	0
48	SE	916	0	964	15	0
48	SF	916	0	964	18	0
49	SG	3428	0	3446	77	0
50	SH	2781	0	2878	59	0
51	SI	6412	0	6497	165	0
52	SJ	1701	0	1767	26	0
52	SK	1799	0	1872	41	0
53	SL	1395	0	1473	38	0
54	SM	2296	0	2325	61	0
55	SN	2006	0	2118	47	0
56	SO	998	0	631	11	0
57	SP	4910	0	1107	10	0
58	SQ	1137	0	1188	16	0
59	SR	792	0	847	24	0
60	SS	1466	0	1253	24	0
61	ST	4473	0	4053	72	0
62	SU	3781	0	3106	63	0
63	SV	381	0	224	8	0
64	SX	515	0	118	4	0
65	SY	2016	0	2093	40	0
66	SZ	1295	0	571	4	0
67	SL	1	0	0	0	0
All	All	196921	0	158343	2860	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 8.

The worst 5 of 2860 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)
2:L1:547:U:OP2	35:NB:554:ARG:NH1	1.81	1.12
1:L0:90:G:OP1	18:LJ:378:LYS:NZ	1.84	1.10
3:L2:253:G:OP2	48:SF:95:ARG:NH1	1.93	1.00
51:SI:1059:ARG:NH1	65:SY:33:ASP:OD2	1.95	0.99
29:LU:292:ARG:HH12	60:SS:299:ASN:HB2	1.28	0.98

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	
4	L3	100/146 (68%)	93 (93%)	6 (6%)	1 (1%)	12	43
5	L4	226/261 (87%)	206 (91%)	19 (8%)	1 (0%)	30	62
6	L5	211/225 (94%)	198 (94%)	13 (6%)	0	100	100
7	L6	109/236 (46%)	100 (92%)	8 (7%)	1 (1%)	14	45
8	L7	161/190 (85%)	149 (92%)	10 (6%)	2 (1%)	10	40
9	L8	166/200 (83%)	155 (93%)	11 (7%)	0	100	100
10	L9	173/197 (88%)	165 (95%)	8 (5%)	0	100	100
11	LC	123/143 (86%)	111 (90%)	12 (10%)	0	100	100
12	LD	123/156 (79%)	109 (89%)	13 (11%)	1 (1%)	16	48
13	LE	125/130 (96%)	119 (95%)	6 (5%)	0	100	100
14	LF	88/135 (65%)	73 (83%)	12 (14%)	3 (3%)	3	23
15	LG	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
16	LH	810/896 (90%)	760 (94%)	50 (6%)	0	100	100
17	LI	128/713 (18%)	121 (94%)	7 (6%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	LJ	489/513 (95%)	459 (94%)	30 (6%)	0	100	100
19	LK	86/575 (15%)	83 (96%)	3 (4%)	0	100	100
20	LL	465/643 (72%)	437 (94%)	28 (6%)	0	100	100
21	LM	424/1769 (24%)	407 (96%)	17 (4%)	0	100	100
22	LN	654/776 (84%)	600 (92%)	54 (8%)	0	100	100
23	LO	830/923 (90%)	762 (92%)	68 (8%)	0	100	100
24	LP	259/440 (59%)	253 (98%)	6 (2%)	0	100	100
25	LQ	798/943 (85%)	747 (94%)	51 (6%)	0	100	100
26	LR	156/817 (19%)	152 (97%)	4 (3%)	0	100	100
27	LS	473/594 (80%)	442 (93%)	31 (7%)	0	100	100
28	LT	844/939 (90%)	800 (95%)	44 (5%)	0	100	100
29	LU	453/489 (93%)	431 (95%)	22 (5%)	0	100	100
30	LV	360/707 (51%)	319 (89%)	40 (11%)	1 (0%)	36	67
31	LW	436/554 (79%)	405 (93%)	31 (7%)	0	100	100
32	LX	179/1056 (17%)	170 (95%)	9 (5%)	0	100	100
32	LY	152/1056 (14%)	139 (91%)	13 (9%)	0	100	100
33	LZ	180/183 (98%)	168 (93%)	11 (6%)	1 (1%)	21	54
34	NA	203/593 (34%)	188 (93%)	13 (6%)	2 (1%)	12	43
35	NB	126/610 (21%)	119 (94%)	7 (6%)	0	100	100
36	NC	134/357 (38%)	118 (88%)	16 (12%)	0	100	100
37	ND	58/214 (27%)	55 (95%)	3 (5%)	0	100	100
38	NE	129/346 (37%)	124 (96%)	5 (4%)	0	100	100
39	NF	122/151 (81%)	116 (95%)	6 (5%)	0	100	100
40	NG	109/137 (80%)	94 (86%)	15 (14%)	0	100	100
41	NH	1070/1237 (86%)	1019 (95%)	51 (5%)	0	100	100
42	NI	163/297 (55%)	159 (98%)	4 (2%)	0	100	100
43	NJ	263/1729 (15%)	256 (97%)	7 (3%)	0	100	100
44	NK	173/316 (55%)	164 (95%)	9 (5%)	0	100	100
45	SA	338/504 (67%)	326 (96%)	12 (4%)	0	100	100
46	SB	297/511 (58%)	283 (95%)	14 (5%)	0	100	100
47	SC	238/327 (73%)	220 (92%)	18 (8%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	SD	224/327 (68%)	216 (96%)	8 (4%)	0	100	100
48	SE	119/126 (94%)	114 (96%)	4 (3%)	1 (1%)	16	48
48	SF	119/126 (94%)	117 (98%)	2 (2%)	0	100	100
49	SG	423/573 (74%)	395 (93%)	28 (7%)	0	100	100
50	SH	358/367 (98%)	343 (96%)	15 (4%)	0	100	100
51	SI	763/1184 (64%)	721 (94%)	41 (5%)	1 (0%)	48	79
52	SJ	212/252 (84%)	208 (98%)	4 (2%)	0	100	100
52	SK	226/252 (90%)	219 (97%)	7 (3%)	0	100	100
53	SL	170/189 (90%)	157 (92%)	13 (8%)	0	100	100
54	SM	278/290 (96%)	252 (91%)	26 (9%)	0	100	100
55	SN	245/274 (89%)	230 (94%)	15 (6%)	0	100	100
56	SO	177/274 (65%)	167 (94%)	10 (6%)	0	100	100
58	SQ	129/217 (59%)	121 (94%)	8 (6%)	0	100	100
59	SR	102/145 (70%)	88 (86%)	13 (13%)	1 (1%)	12	43
60	SS	142/898 (16%)	134 (94%)	8 (6%)	0	100	100
61	ST	448/792 (57%)	432 (96%)	16 (4%)	0	100	100
62	SU	366/552 (66%)	349 (95%)	17 (5%)	0	100	100
63	SV	24/206 (12%)	20 (83%)	4 (17%)	0	100	100
65	SY	237/250 (95%)	218 (92%)	18 (8%)	1 (0%)	30	62
66	SZ	259/483 (54%)	245 (95%)	14 (5%)	0	100	100
All	All	18286/31778 (58%)	17177 (94%)	1092 (6%)	17 (0%)	49	79

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	L4	195	ILE
34	NA	454	VAL
59	SR	90	ASP
14	LF	52	LYS
30	LV	58	ALA

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	
4	L3	96/123 (78%)	96 (100%)	0	100	100
5	L4	196/222 (88%)	195 (100%)	1 (0%)	81	81
6	L5	180/191 (94%)	179 (99%)	1 (1%)	78	79
7	L6	96/201 (48%)	95 (99%)	1 (1%)	68	74
8	L7	146/170 (86%)	146 (100%)	0	100	100
9	L8	138/161 (86%)	136 (99%)	2 (1%)	59	70
10	L9	150/166 (90%)	148 (99%)	2 (1%)	61	71
11	LC	105/119 (88%)	103 (98%)	2 (2%)	50	66
12	LD	114/137 (83%)	114 (100%)	0	100	100
13	LE	108/111 (97%)	107 (99%)	1 (1%)	70	74
14	LF	76/113 (67%)	76 (100%)	0	100	100
15	LG	56/60 (93%)	56 (100%)	0	100	100
16	LH	758/813 (93%)	751 (99%)	7 (1%)	70	74
17	LI	126/153 (82%)	124 (98%)	2 (2%)	55	68
18	LJ	437/454 (96%)	429 (98%)	8 (2%)	51	67
19	LK	83/500 (17%)	83 (100%)	0	100	100
20	LL	428/574 (75%)	423 (99%)	5 (1%)	63	72
21	LM	391/1627 (24%)	386 (99%)	5 (1%)	61	71
22	LN	604/699 (86%)	600 (99%)	4 (1%)	76	77
23	LO	730/812 (90%)	722 (99%)	8 (1%)	65	73
24	LP	248/303 (82%)	248 (100%)	0	100	100
25	LQ	717/794 (90%)	717 (100%)	0	100	100
26	LR	147/155 (95%)	146 (99%)	1 (1%)	76	77
27	LS	424/529 (80%)	420 (99%)	4 (1%)	70	74
28	LT	745/819 (91%)	740 (99%)	5 (1%)	76	77
29	LU	412/443 (93%)	409 (99%)	3 (1%)	76	77
30	LV	307/636 (48%)	306 (100%)	1 (0%)	86	84
31	LW	373/480 (78%)	372 (100%)	1 (0%)	86	84
32	LX	164/165 (99%)	163 (99%)	1 (1%)	78	79

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	LZ	171/172 (99%)	168 (98%)	3 (2%)	51	67
34	NA	187/535 (35%)	185 (99%)	2 (1%)	65	73
35	NB	108/525 (21%)	108 (100%)	0	100	100
36	NC	119/315 (38%)	118 (99%)	1 (1%)	73	76
37	ND	57/176 (32%)	56 (98%)	1 (2%)	51	67
38	NE	114/278 (41%)	114 (100%)	0	100	100
45	SA	296/413 (72%)	295 (100%)	1 (0%)	86	84
46	SB	243/319 (76%)	240 (99%)	3 (1%)	63	72
47	SC	202/240 (84%)	202 (100%)	0	100	100
47	SD	192/240 (80%)	192 (100%)	0	100	100
48	SE	100/104 (96%)	100 (100%)	0	100	100
48	SF	100/104 (96%)	99 (99%)	1 (1%)	68	74
49	SG	373/503 (74%)	371 (100%)	2 (0%)	81	81
50	SH	307/312 (98%)	307 (100%)	0	100	100
51	SI	684/1014 (68%)	673 (98%)	11 (2%)	55	68
52	SJ	195/222 (88%)	195 (100%)	0	100	100
52	SK	206/222 (93%)	203 (98%)	3 (2%)	57	69
53	SL	156/169 (92%)	153 (98%)	3 (2%)	50	66
54	SM	251/258 (97%)	245 (98%)	6 (2%)	43	62
55	SN	230/256 (90%)	230 (100%)	0	100	100
56	SO	33/238 (14%)	33 (100%)	0	100	100
58	SQ	124/200 (62%)	124 (100%)	0	100	100
59	SR	86/120 (72%)	86 (100%)	0	100	100
60	SS	135/758 (18%)	135 (100%)	0	100	100
61	ST	417/534 (78%)	415 (100%)	2 (0%)	81	81
62	SU	330/338 (98%)	325 (98%)	5 (2%)	57	69
63	SV	22/117 (19%)	22 (100%)	0	100	100
65	SY	226/234 (97%)	222 (98%)	4 (2%)	51	67
All	All	14219/20646 (69%)	14106 (99%)	113 (1%)	70	76

5 of 113 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	LT	525	ILE
65	SY	48	LEU
37	ND	198	ILE
65	SY	4	LEU
54	SM	167	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 324 such sidechains are listed below:

Mol	Chain	Res	Type
49	SG	322	HIS
56	SO	239	HIS
51	SI	264	GLN
52	SK	53	HIS
61	ST	697	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L0	484/700 (69%)	123 (25%)	7 (1%)
2	L1	1004/1807 (55%)	282 (28%)	19 (1%)
3	L2	163/333 (48%)	45 (27%)	0
All	All	1651/2840 (58%)	450 (27%)	26 (1%)

5 of 450 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L0	63	G
1	L0	64	U
1	L0	82	A
1	L0	83	U
1	L0	85	G

5 of 26 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	L1	272	U
2	L1	542	A
2	L1	1620	C
2	L1	417	A
2	L1	579	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
57	SP	61
26	LR	14
32	LY	11
32	LX	11
17	LI	9
64	SX	3
61	ST	2
24	LP	2
19	LK	2
45	SA	2
46	SB	2
63	SV	1

Continued on next page...

Continued from previous page...

Mol	Chain	Number of breaks
22	LN	1
60	SS	1
38	NE	1
62	SU	1
37	ND	1
25	LQ	1

The worst 5 of 126 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	SX	2034:UNK	C	3098:UNK	N	257.52
1	SX	1058:UNK	C	2000:UNK	N	68.50
1	SX	3115:UNK	C	3218:UNK	N	49.43
1	LI	358:UNK	C	457:UNK	N	41.95
1	LR	323:UNK	C	329:UNK	N	40.86

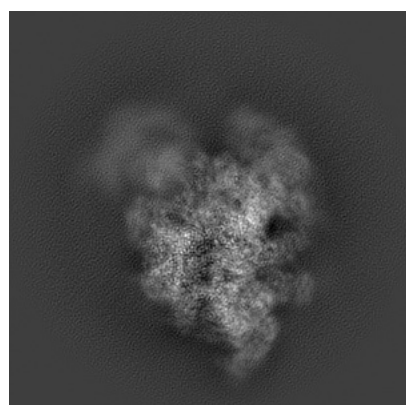
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8859. These allow visual inspection of the internal detail of the map and identification of artifacts.

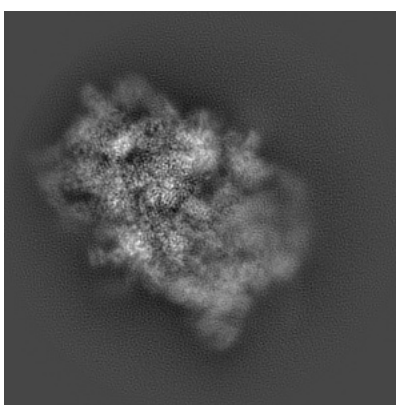
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

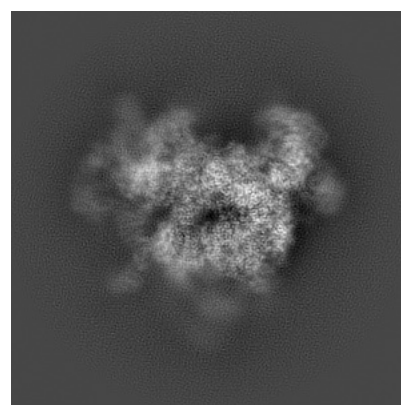
6.1.1 Primary map



X



Y

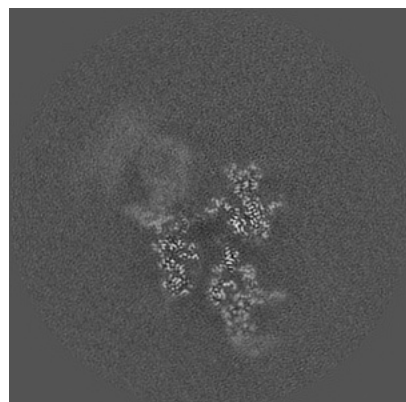


Z

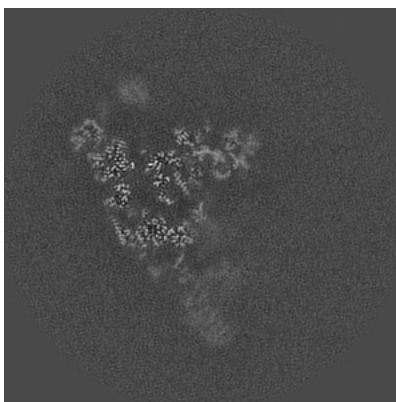
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

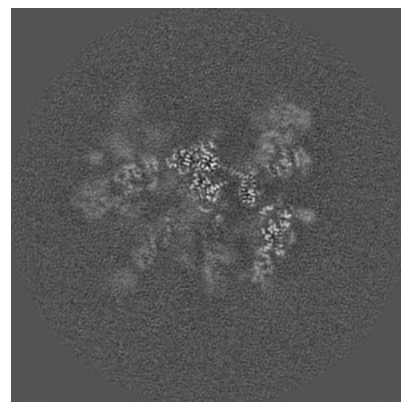
6.2.1 Primary map



X Index: 200



Y Index: 200

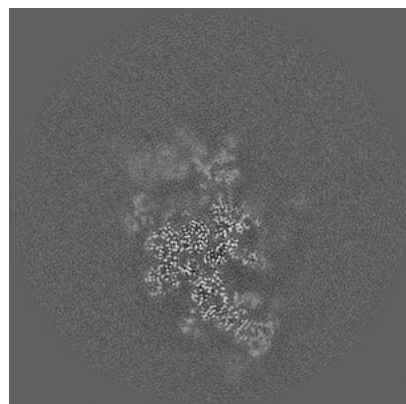


Z Index: 200

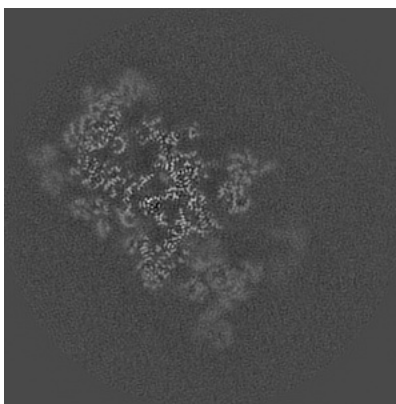
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

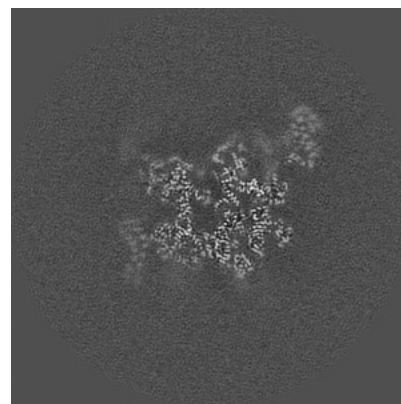
6.3.1 Primary map



X Index: 242



Y Index: 223

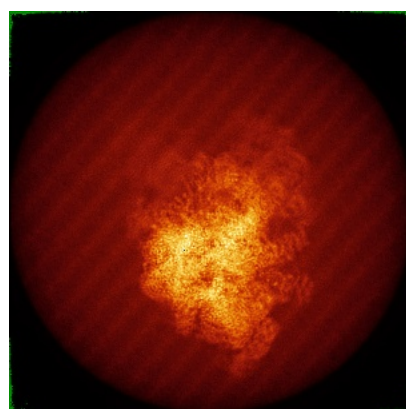


Z Index: 167

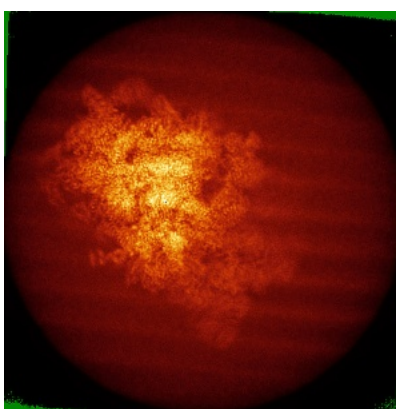
The images above show the largest variance slices of the map in three orthogonal directions.

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

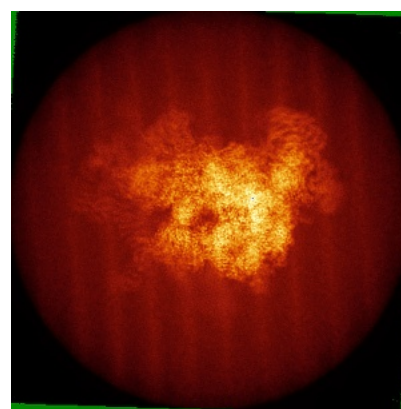
6.4.1 Primary map



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 0.023. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

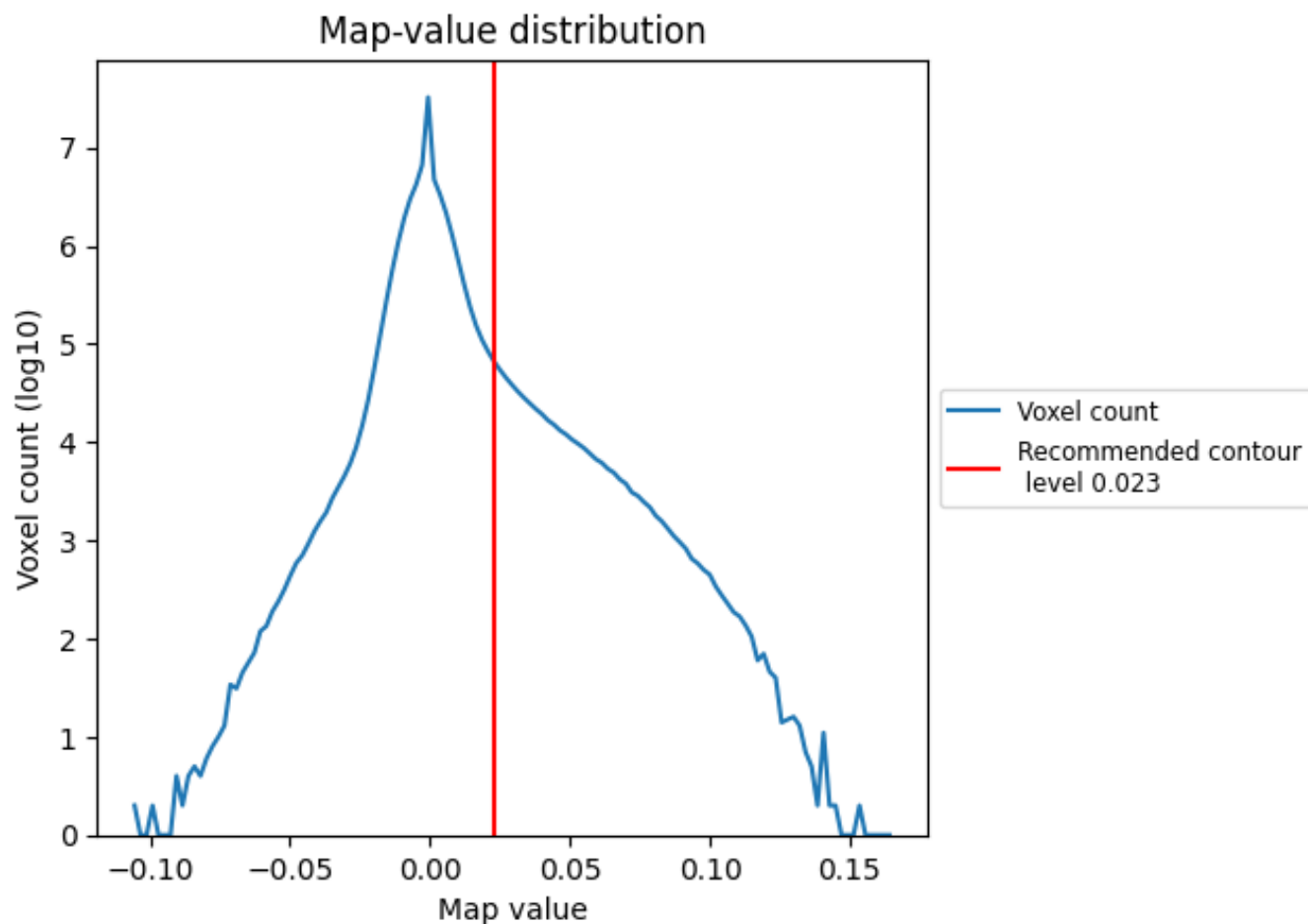
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

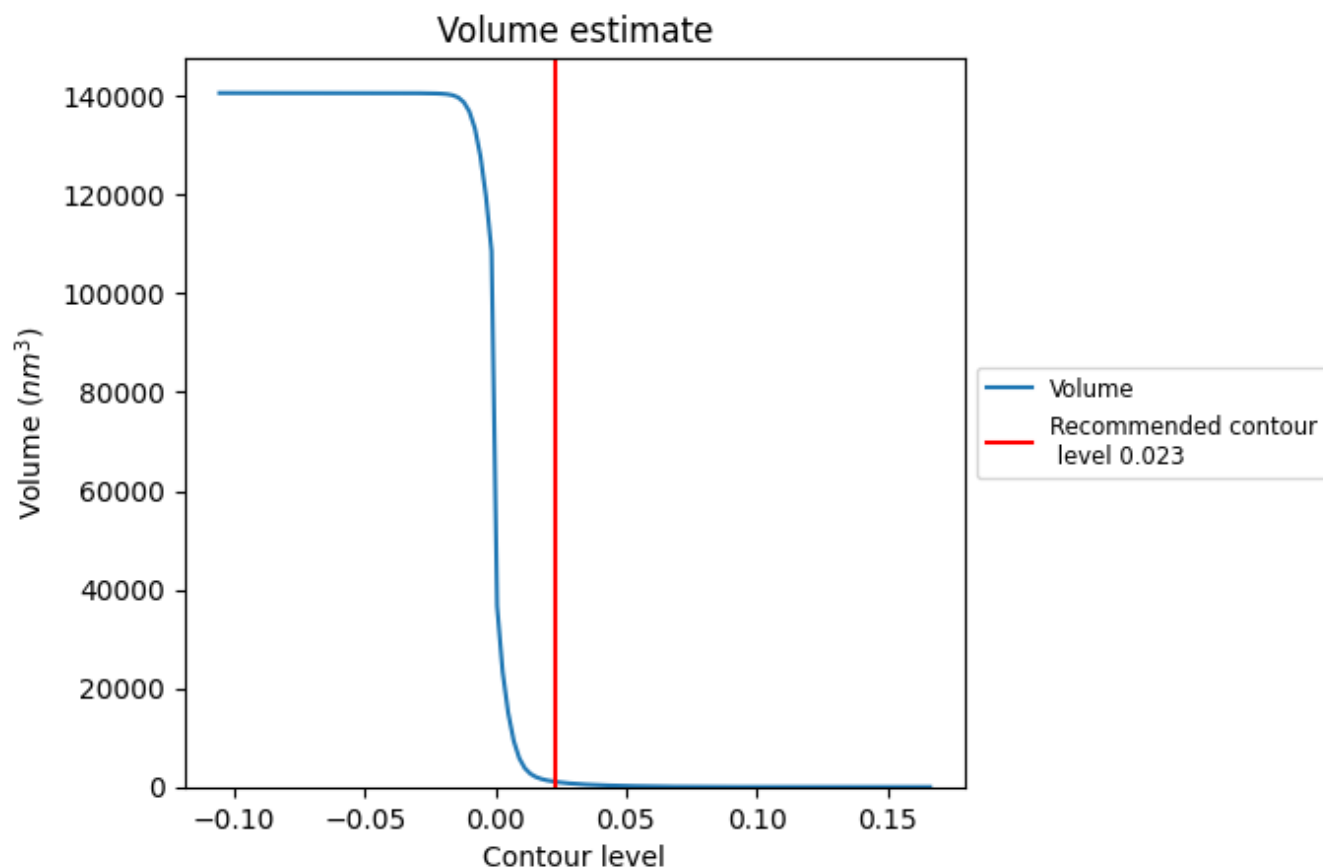
This section contains the results of statistical analysis of the map.

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.

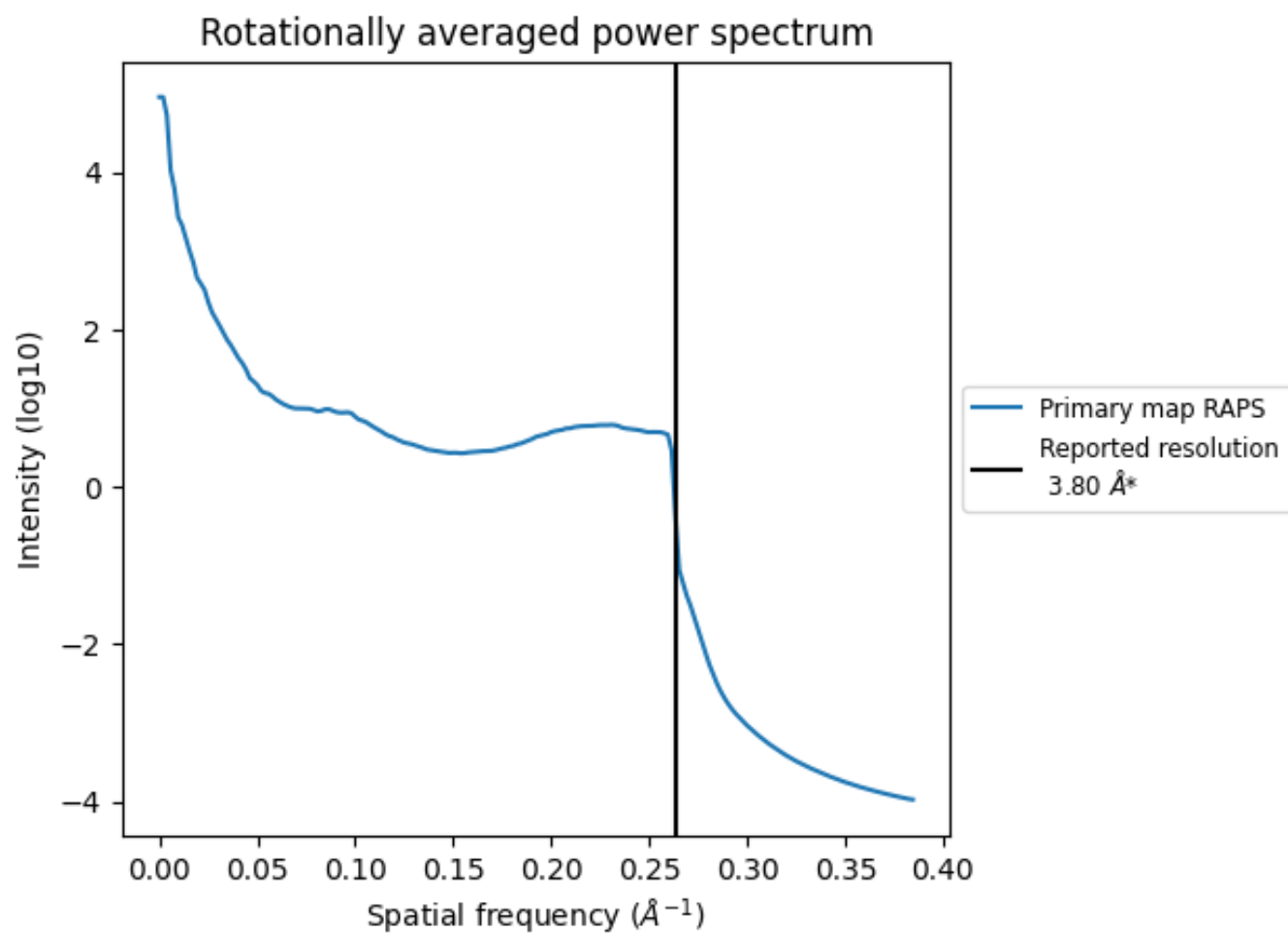
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1051 nm³; this corresponds to an approximate mass of 950 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 0.263 Å⁻¹

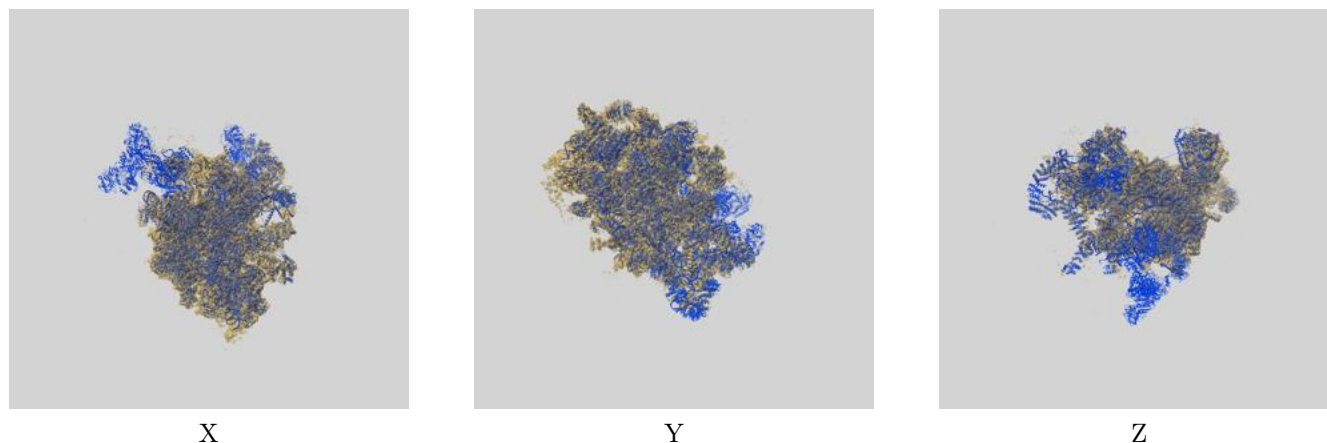
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

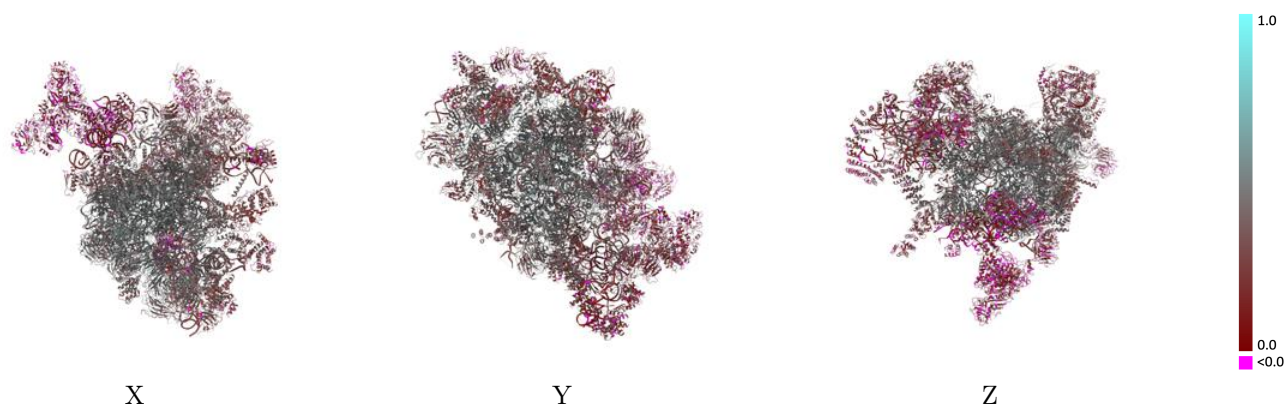
This section contains information regarding the fit between EMDB map EMD-8859 and PDB model 5WLC. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



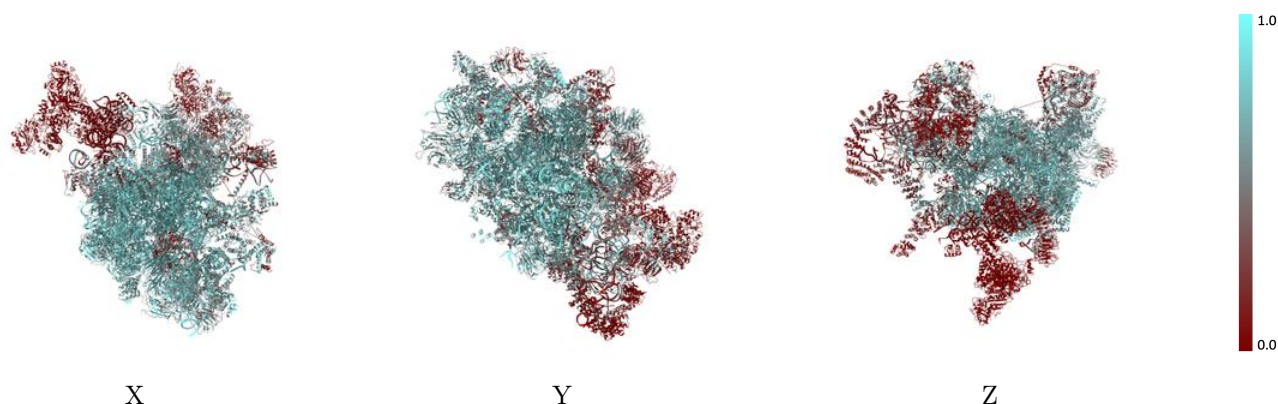
The images above show the 3D surface view of the map at the recommended contour level 0.023 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



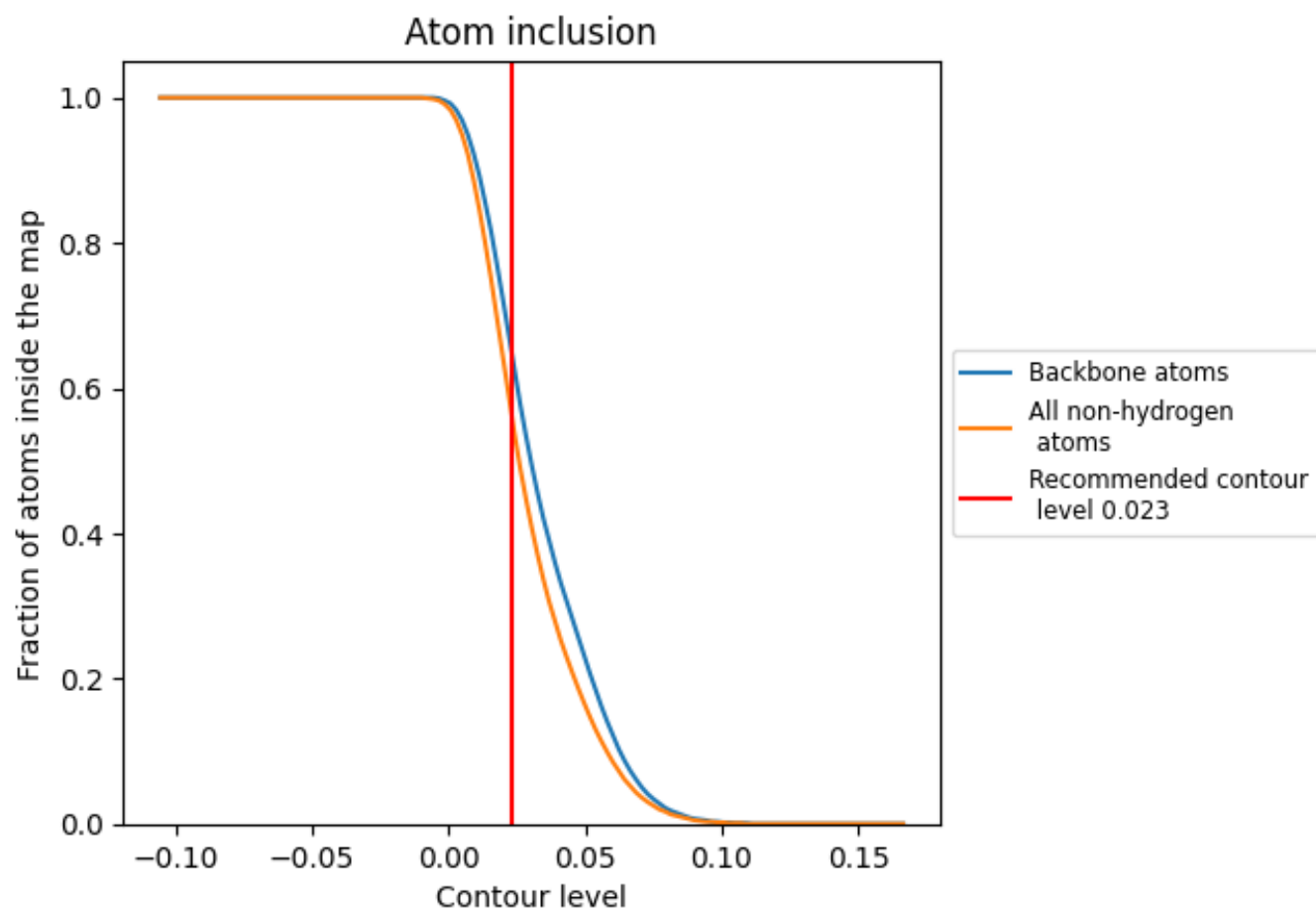
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.023).

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 56% 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 (0.023) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5650	 0.3730
L0	 0.8090	 0.4030
L1	 0.5150	 0.2950
L2	 0.8300	 0.4230
L3	 0.3460	 0.3430
L4	 0.4540	 0.3550
L5	 0.7190	 0.4610
L6	 0.2410	 0.2740
L7	 0.1010	 0.2740
L8	 0.2820	 0.2460
L9	 0.6940	 0.4630
LC	 0.7830	 0.5000
LD	 0.1950	 0.2040
LE	 0.3400	 0.3730
LF	 0.5690	 0.3810
LG	 0.7150	 0.4880
LH	 0.6650	 0.4140
LI	 0.4180	 0.2590
LJ	 0.7440	 0.4610
LK	 0.5910	 0.3190
LL	 0.7170	 0.4470
LM	 0.7370	 0.4510
LN	 0.6410	 0.3930
LO	 0.7680	 0.4850
LP	 0.7110	 0.3720
LQ	 0.6090	 0.3670
LR	 0.2600	 0.2480
LS	 0.7660	 0.4780
LT	 0.7600	 0.4740
LU	 0.7010	 0.4550
LV	 0.2140	 0.2370
LW	 0.7590	 0.4840
LX	 0.3660	 0.3050
LY	 0.0880	 0.2160
LZ	 0.7750	 0.4920



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
NA	 0.6390	 0.4320
NB	 0.6630	 0.4450
NC	 0.4820	 0.3750
ND	 0.4500	 0.3620
NE	 0.1180	 0.3550
NF	 0.0110	 0.1620
NG	 0.0350	 0.1830
NH	 0.0020	 0.1540
NI	 0.0000	 0.1450
NJ	 0.0090	 0.1660
NK	 0.0590	 0.2090
SA	 0.6830	 0.4210
SB	 0.6800	 0.4140
SC	 0.7530	 0.4900
SD	 0.5960	 0.4080
SE	 0.7460	 0.4860
SF	 0.6960	 0.4560
SG	 0.6520	 0.3940
SH	 0.6970	 0.4420
SI	 0.6950	 0.4410
SJ	 0.5630	 0.3460
SK	 0.6560	 0.4430
SL	 0.7730	 0.4890
SM	 0.7210	 0.4730
SN	 0.7190	 0.4400
SO	 0.5020	 0.3520
SP	 0.1840	 0.2730
SQ	 0.6440	 0.4410
SR	 0.7030	 0.4700
SS	 0.5080	 0.3900
ST	 0.5060	 0.3310
SU	 0.6330	 0.3490
SV	 0.5000	 0.4130
SX	 0.3690	 0.3230
SY	 0.7330	 0.4650
SZ	 0.2670	 0.2490