



wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 09:24 PM EST

PDB ID : 7MQ9
EMDB ID : EMD-23937
Title : Cryo-EM structure of the human SSU processome, state pre-A1*
Authors : Vanden Broeck, A.; Singh, S.; Klinge, S.
Deposited on : 2021-05-05
Resolution : 3.87 Å(reported)
Based on initial models : 6ZQD, 2OZB, 5FAI, 6G18, 5WLC, 6G4S, 4JXM, 6ZOJ, 2IPX

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:

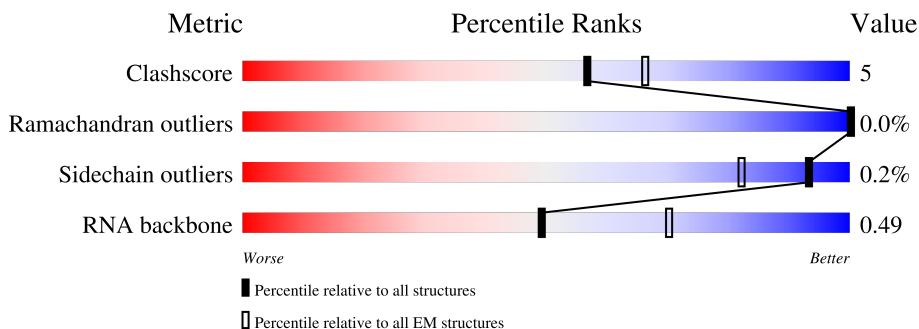
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 3.87 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.




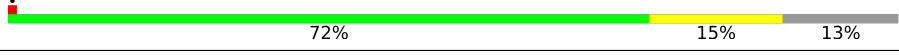
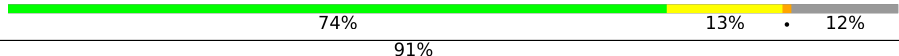
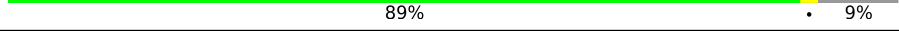
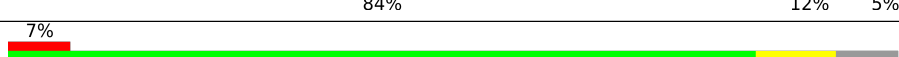
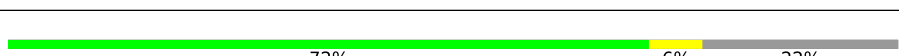












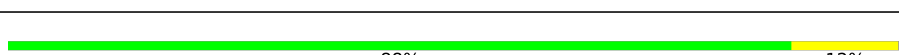
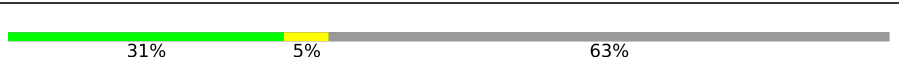





Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 $\leq 5\%$. 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	3617	 93%
2	L1	1872	 12% 35% 29% 5% 31%
3	L2	217	 43% 47% 9%
4	L3	116	 96% 99%
5	L4	263	 78% 13% 9%
6	L5	204	 80% 13% 7%
7	L6	249	 70% 19% 10%







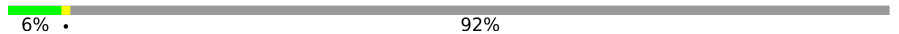


















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Mol	Chain	Length	Quality of chain
8	L7	194	 75% 11% 13%
9	L8	208	 72% 15% 13%
10	L9	194	 74% 13% 12%
11	LA	132	 91% 89% 9%
12	LC	146	 84% 12% 5%
13	LD	158	 7% 84% 9% 7%
14	LF	133	 72% 6% 22%
15	LG	69	 77% 12% 10%
16	LH	830	 74% 16% 10%
17	LI	699	 15% 76% 23%
18	LJ	518	 73% 18% 9%
19	LK	677	 14% 83%
19	LL	677	 61% 14% 25%
20	LN	686	 81% 17% 2%
21	LO	919	 79% 13% 8%
22	LP	597	 85% 10% 5%
23	LQ	943	 70% 18% 12%
24	LS	556	 67% 14% 19%
25	LT	951	 80% 11% 9%
26	LU	445	 82% 18%
27	LW	610	 64% 10% 26%
28	LZ	184	 88% 12%
29	NA	681	 31% 5% 63%
30	NB	479	 13% 85%
31	ND	257	 30% 67%




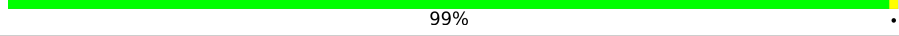

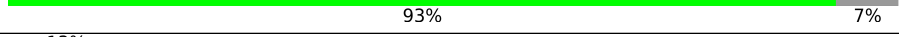


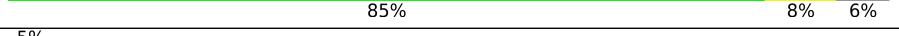

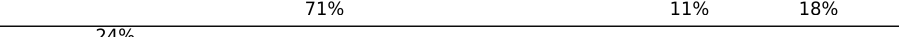
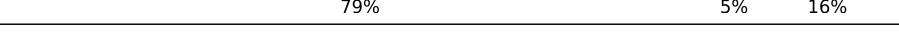

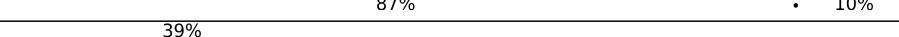

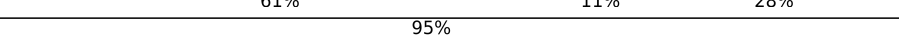
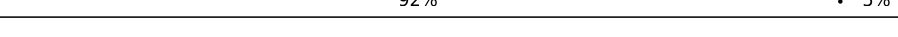
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Mol	Chain	Length	Quality of chain
32	NE	293	
33	NF	151	
34	NG	151	
35	NJ	1025	
35	NK	1025	
36	NM	264	
37	NN	560	
38	NO	130	
39	NQ	84	
40	NR	861	
41	NT	156	
42	NU	135	
43	NW	688	
44	SA	594	
45	SB	529	
46	SC	321	
46	SD	321	
47	SE	128	
47	SF	128	
48	SH	373	
49	SI	1282	
50	SJ	244	
50	SK	244	
51	SL	198	
52	SM	291	

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Mol	Chain	Length	Quality of chain
53	SQ	756	
54	SR	143	
55	SS	771	
56	SX	177	
57	SY	253	
58	NH	1146	
59	SP	2785	
60	LR	808	
61	LM	2144	
62	NO	22	
63	SG	475	
64	NI	280	
65	SW	252	
66	ST	632	
67	SU	472	
68	NY	381	
69	SZ	304	

2 Entry composition

There are 74 unique types of molecules in this entry. The entry contains 223184 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 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	L0	242	5152	2289	908	1713	242	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	L1	1301	27777	12396	5002	9078	1301	0	0

- Molecule 3 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	L2	215	4589	2047	809	1518	215	0	0

- Molecule 4 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	L3	115	571	341	115	115	0	0

- Molecule 5 is a protein called 40S ribosomal protein S4 X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	L4	239	1902	1220	350	324	8	0	0

- Molecule 6 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	L5	190	1501	939	285	270	7	0	0

- Molecule 7 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	L6	223	1811	1133	361	311	6	0	0

- Molecule 8 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	L7	168	1346	862	239	244	1	0	0

- Molecule 9 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	L8	180	1474	925	294	250	5	0	0

- Molecule 10 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	L9	171	1425	908	284	232	1	0	0

- Molecule 11 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	LA	120	593	353	120	120	0	0

- Molecule 12 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	LC	139	1098	699	207	189	3	0	0

- Molecule 13 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	LD	147	1204	767	225	206	6	0	0

- Molecule 14 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LF	104	Total	C	N	O	S	0	0
			851	543	158	145	5		

- Molecule 15 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LG	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 16 is a protein called WD repeat-containing protein 75.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH	746	Total	C	N	O	S	0	0
			5987	3846	1005	1101	35		

- Molecule 17 is a protein called Nucleolar protein 11.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	LI	537	Total	C	N	O	0	0
			2675	1601	537	537		

- Molecule 18 is a protein called U3 small nucleolar RNA-associated protein 15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LJ	469	Total	C	N	O	S	0	0
			3711	2372	637	688	14		

- Molecule 19 is a protein called WD repeat-containing protein 43.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LK	118	Total	C	N	O	S	0	0
			943	612	163	163	5		
19	LL	510	Total	C	N	O	S	0	0
			3982	2538	686	731	27		

- Molecule 20 is a protein called U3 small nucleolar RNA-associated protein 4 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LN	671	Total	C	N	O	S	0	0
			5299	3394	925	956	24		

- Molecule 21 is a protein called Periodic tryptophan protein 2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	LO	848	6676	4258	1151	1234	33	0	0

- Molecule 22 is a protein called U3 small nucleolar RNA-associated protein 6 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	LP	567	4705	3022	808	847	28	0	0

- Molecule 23 is a protein called WD repeat-containing protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	LQ	828	6438	4103	1108	1194	33	0	0

- Molecule 24 is a protein called U3 small nucleolar RNA-associated protein 18 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	LS	453	3560	2235	631	671	23	0	0

- Molecule 25 is a protein called WD repeat-containing protein 36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	LT	869	6756	4321	1158	1244	33	0	0

- Molecule 26 is a protein called DDB1- and CUL4-associated factor 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	LU	445	3611	2282	653	651	25	0	0

- Molecule 27 is a protein called WD repeat-containing protein 46.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	LW	453	3519	2221	637	646	15	0	0

- Molecule 28 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	LZ	183	1532	966	292	270	4	0	0

- Molecule 29 is a protein called U3 small nucleolar ribonucleoprotein protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	NA	249	2055	1299	359	391	6	0	0

- Molecule 30 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
30	NB	73	617	379	140	98	0	0

- Molecule 31 is a protein called Nucleolar protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	ND	84	696	438	143	114	1	0	0

- Molecule 32 is a protein called Uncharacterized protein C1orf131.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	NE	100	799	509	143	146	1	0	0

- Molecule 33 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	NF	149	1202	770	228	203	1	0	0

- Molecule 34 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	NG	116	861	531	159	165	6	0	0

- Molecule 35 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	NJ	827	Total	C	N	O	S	0	0
			6526	4187	1126	1178	35		
35	NK	815	Total	C	N	O		0	0
			4030	2400	815	815			

- Molecule 36 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	NM	233	Total	C	N	O	S	0	0
			1873	1186	339	334	14		

- Molecule 37 is a protein called Protein AATF.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	NN	42	Total	C	N	O	S	0	0
			340	215	63	60	2		

- Molecule 38 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	NO	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 39 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	NQ	82	Total	C	N	O	S	0	0
			640	402	118	113	7		

- Molecule 40 is a protein called RRP12-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace	
40	NR	861	Total	C	N	O		0	0
			4305	2583	861	861			

- Molecule 41 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms				AltConf	Trace	
41	NT	58	Total	C	N	O		0	0
			286	170	58	58			

- Molecule 42 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
42	NU	60	297	177	60	60	0	0

- Molecule 43 is a protein called Nucleolar protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	NW	311	2498	1599	413	472	14	0	0

- Molecule 44 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	SA	396	3077	1948	542	575	12	0	0

- Molecule 45 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	SB	440	3439	2179	596	642	22	0	0

- Molecule 46 is a protein called rRNA 2'-O-methyltransferase fibrillar.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	SC	229	1781	1129	322	323	7	0	0
46	SD	237	1841	1163	337	334	7	0	0

- Molecule 47 is a protein called NHP2-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	SE	125	968	611	172	180	5	0	0
47	SF	123	955	604	170	176	5	0	0

- Molecule 48 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	SH	368	2832	1803	495	518	16	0	0

- Molecule 49 is a protein called Ribosome biogenesis protein BMS1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	SI	844	6801	4349	1230	1188	34	0	0

- Molecule 50 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	SK	204	1579	1012	272	286	9	0	0
50	SJ	204	1008	600	204	204		0	0

- Molecule 51 is a protein called rRNA-processing protein FCF1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	SL	192	1586	1006	290	275	15	0	0

- Molecule 52 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	SM	290	2369	1485	451	424	9	0	0

- Molecule 53 is a protein called Deoxynucleotidyltransferase terminal-interacting protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	SQ	187	1533	972	278	277	6	0	0

- Molecule 54 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	SR	108	816	521	153	140	2	0	0

- Molecule 55 is a protein called U3 small nucleolar RNA-associated protein 14 homolog A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	SS	197	1626	1039	301	285	1	0	0

- Molecule 56 is a protein called Unassigned peptides.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
56	SX	177	885	531	177	177	0	0

- Molecule 57 is a protein called Probable U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	SY	238	2024	1280	385	353	6	0	0

- Molecule 58 is a protein called Nucleolar protein 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
58	NH	1066	5265	3133	1066	1066	0	0

- Molecule 59 is a protein called Small subunit processome component 20 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	SP	1993	11768	7248	2243	2262	15	0	0

- Molecule 60 is a protein called Transducin beta-like protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	LR	773	4321	2606	860	850	5	0	0

- Molecule 61 is a protein called HEAT repeat-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	LM	2005	13156	8305	2316	2493	42	0	0

- Molecule 62 is a RNA chain called 5' ETS rRNA.

Mol	Chain	Residues	Atoms			AltConf	Trace	
			Total	C	O			P
62	N0	22	264	110	132	22	0	0

- Molecule 63 is a protein called U3 small nucleolar RNA-interacting protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	SG	389	2878	1806	531	528	13	1	0

- Molecule 64 is a protein called Ribosomal RNA-processing protein 7 homolog A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	NI	234	1459	885	287	285	2	0	0

- Molecule 65 is a protein called RNA-binding protein PNO1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
65	SW	180	890	530	180	180	0	0

- Molecule 66 is a protein called Nucleolar protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	ST	568	3064	1844	620	598	2	0	0

- Molecule 67 is a protein called Nucleolar complex protein 4 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
67	SU	413	2057	1231	413	413	0	0

- Molecule 68 is a protein called KRR1 small subunit processome component homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	NY	274	2094	1337	366	383	8	0	0

- Molecule 69 is a protein called Bystin.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
69	SZ	290	1442	862	290	290	0	0

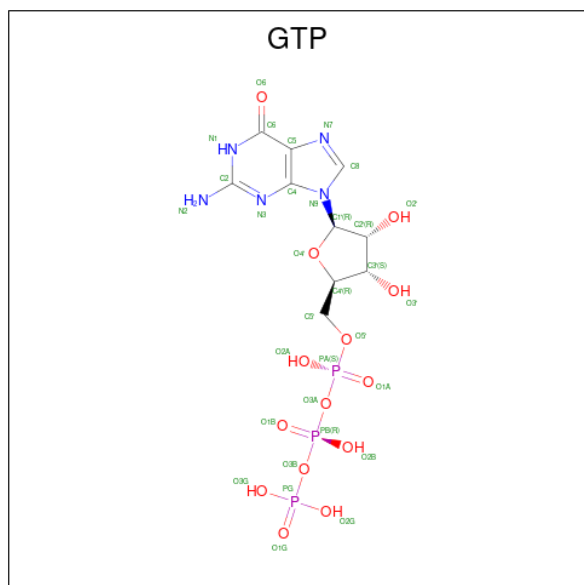
- Molecule 70 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
70	L1	19	Total Mg 19 19	0
70	SI	1	Total Mg 1 1	0
70	SL	1	Total Mg 1 1	0
70	NH	1	Total Mg 1 1	0

- Molecule 71 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
71	NQ	1	Total Zn 1 1	0
71	NT	1	Total Zn 1 1	0
71	SL	1	Total Zn 1 1	0

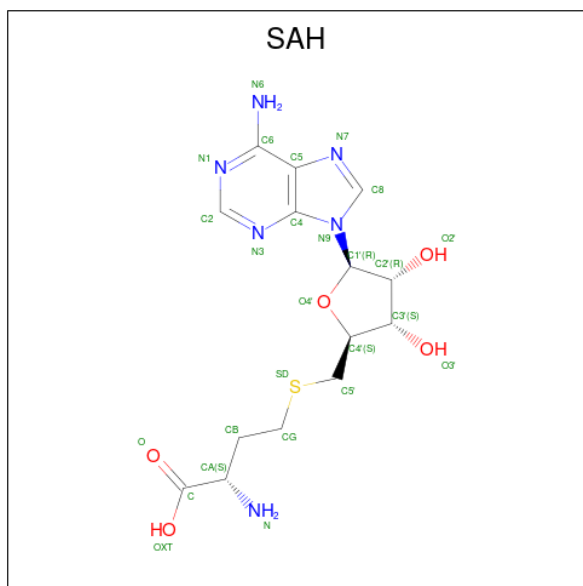
- Molecule 72 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



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

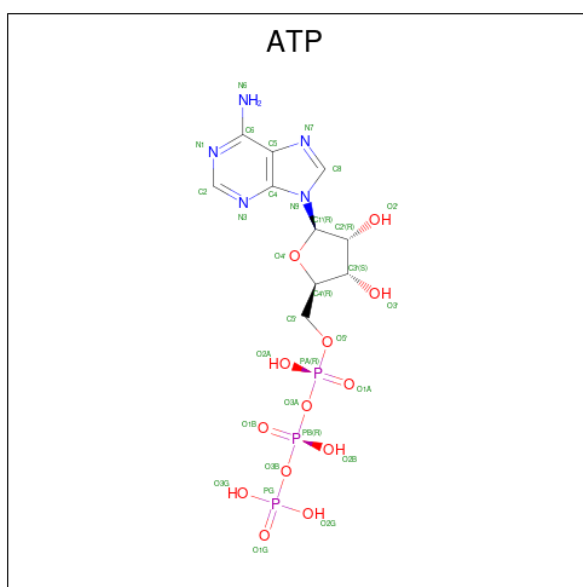
- Molecule 73 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula:

$C_{14}H_{20}N_6O_5S$).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
73	SK	1	Total	C	N	O	S	0
			26	14	6	5	1	
73	SJ	1	Total	C	N	O	S	0
			26	14	6	5	1	

- Molecule 74 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).

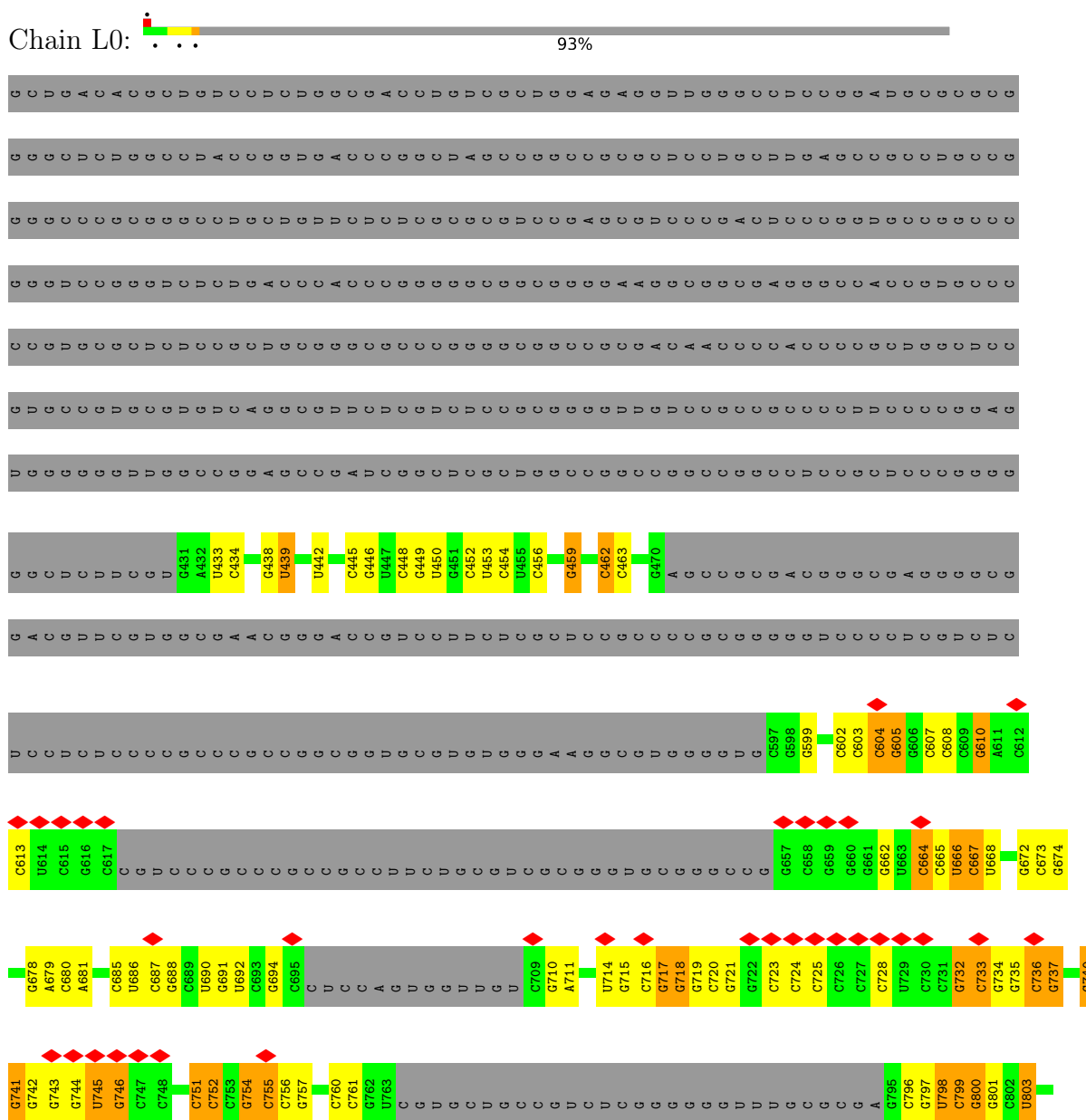


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
74	NH	1	31	10	5	13	3	0
74	NK	1	31	10	5	13	3	0

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 rRNA

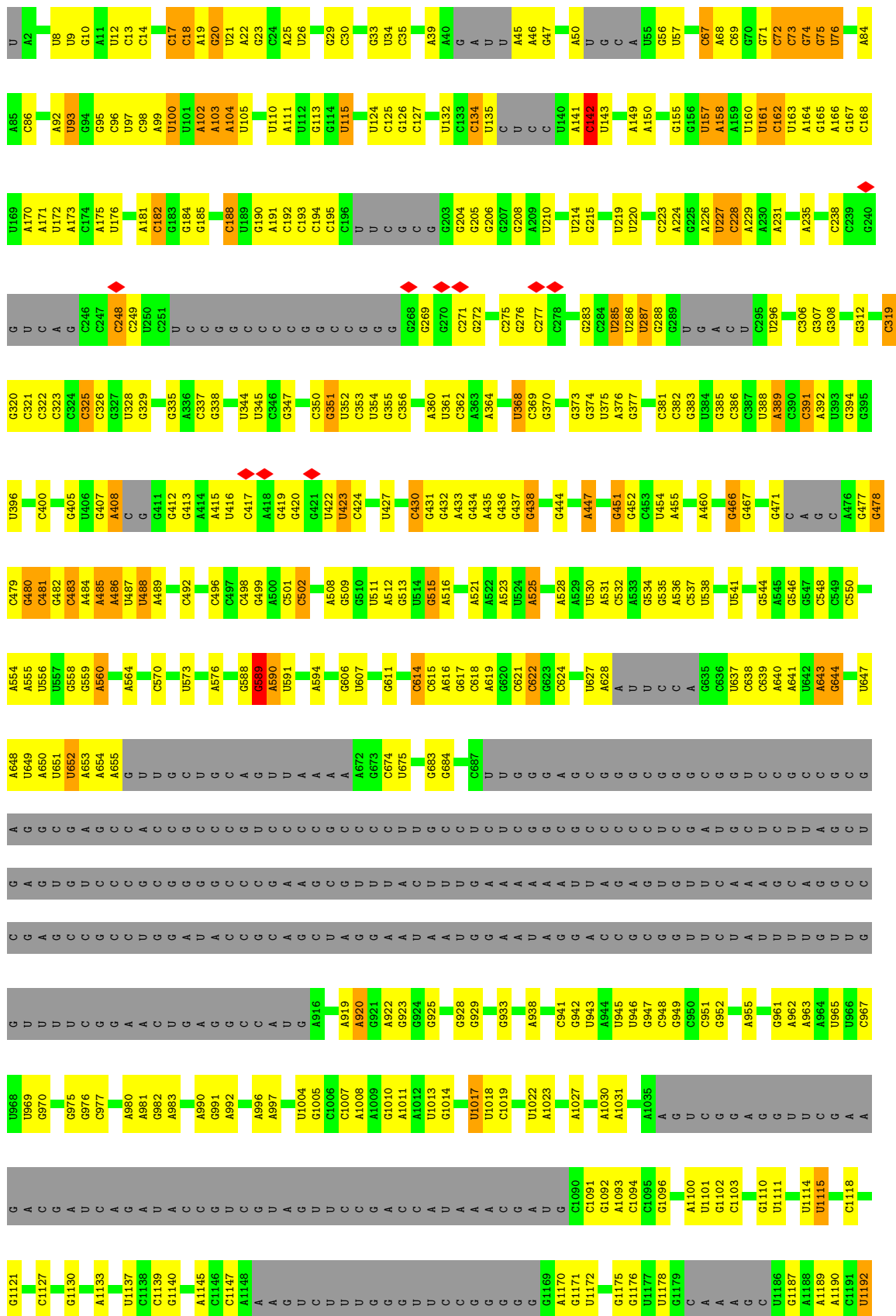


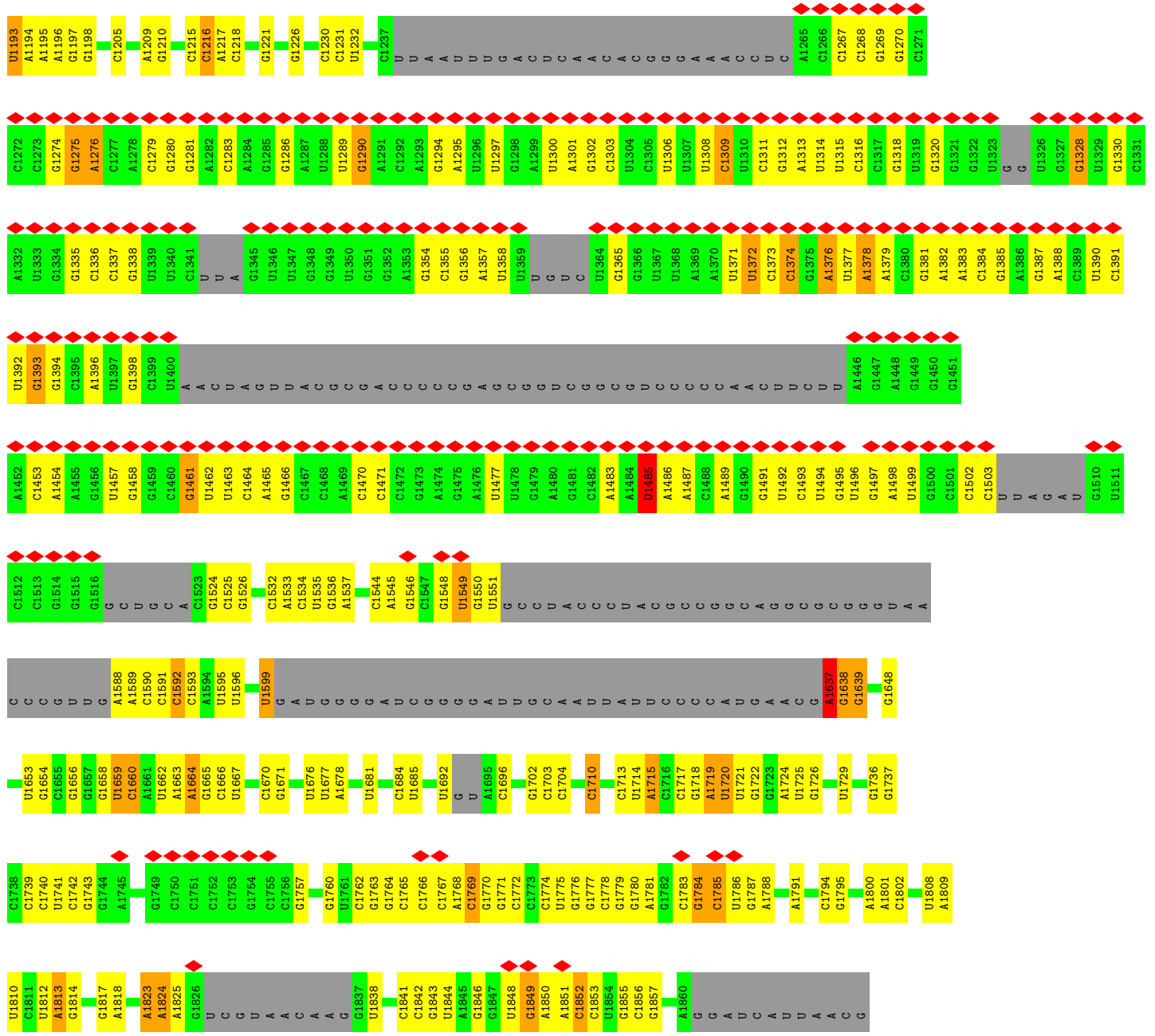
Residue ID	Atom Name	B-factor	Occupancy	Validation Status
G806	C	80.1	1.00	Green
C	C	81.2	1.00	Grey
U	C	82.3	1.00	Grey
G	C	83.4	1.00	Grey
G811	C	84.5	1.00	Yellow
G812	C	85.6	1.00	Yellow
G813	C	86.7	1.00	Yellow
C814	C	87.8	1.00	Orange
C815	C	88.9	1.00	Orange
U816	C	90.0	1.00	Green
U817	C	91.1	1.00	Green
G818	C	92.2	1.00	Green
C819	C	93.3	1.00	Orange
G820	C	94.4	1.00	Green
U821	C	95.5	1.00	Green
U822	C	96.6	1.00	Green
G823	C	97.7	1.00	Yellow
C	C	98.8	1.00	Grey
C827	C	99.9	1.00	Green
U828	C	101.0	1.00	Green
G829	C	102.1	1.00	Green
G830	C	103.2	1.00	Green
A831	C	104.3	1.00	Orange
G832	C	105.4	1.00	Yellow
C833	C	106.5	1.00	Yellow
C	C	107.6	1.00	Grey
C	C	108.7	1.00	Grey
C	C	109.8	1.00	Grey
U	C	110.9	1.00	Grey
C850	C	112.0	1.00	Green
A851	C	113.1	1.00	Green
G852	C	114.2	1.00	Green
C853	C	115.3	1.00	Green
U854	C	116.4	1.00	Orange
G855	C	117.5	1.00	Orange
C	C	118.6	1.00	Grey
C	C	119.7	1.00	Grey
G859	C	120.8	1.00	Green
A860	C	121.9	1.00	Green
G861	C	123.0	1.00	Green
G862	C	124.1	1.00	Green
C863	C	125.2	1.00	Green
C864	C	126.3	1.00	Green
G865	C	127.4	1.00	Yellow
A866	C	128.5	1.00	Green
A	C	129.6	1.00	Green
C	C	130.7	1.00	Grey
C	C	131.8	1.00	Grey
G	C	132.9	1.00	Grey
G	C	134.0	1.00	Grey
U	C	135.1	1.00	Grey
U	C	136.2	1.00	Grey
C	C	137.3	1.00	Grey
C	C	138.4	1.00	Grey
C	C	139.5	1.00	Grey
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C	C	146.1	1.00	Grey
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C	C	148.3	1.00	Grey
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C	C	165.9	1.00	Grey
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C	C	169.2	1.00	Grey
C	C	170.3	1.00	Grey
C	C	171.4	1.00	Grey
C	C	172.5	1.00	Grey
C	C	173.6	1.00	Grey
C	C	174.7	1.00	Grey
C	C	175.8	1.00	Grey
C	C	176.9	1.00	Grey
C	C	178.0	1.00	Grey
C	C	179.1	1.00	Grey
C	C	180.2	1.00	Grey
C	C	181.3	1.00	Grey
C	C	182.4	1.00	Grey
C	C	183.5	1.00	Grey
C	C	184.6	1.00	Grey
C	C	185.7	1.00	Grey
C	C	186.8	1.00	Grey
C	C	187.9	1.00	Grey
C	C	189.0	1.00	Grey
C	C	190.1	1.00	Grey
C	C	191.2	1.00	Grey
C	C	192.3	1.00	Grey
C	C	193.4	1.00	Grey
C	C	194.5	1.00	Grey
C	C	195.6	1.00	Grey
C	C	196.7	1.00	Grey
C	C	197.8	1.00	Grey
C	C	198.9	1.00	Grey
C	C	200.0	1.00	Grey
C	C	201.1	1.00	Grey
C	C	202.2	1.00	Grey
C	C	203.3	1.00	Grey
C	C	204.4	1.00	Grey
C	C	205.5	1.00	Grey
C	C	206.6	1.00	Grey
C	C	207.7	1.00	Grey
C	C	208.8	1.00	Grey
C	C	209.9	1.00	Grey
C	C	211.0	1.00	Grey
C	C	212.1	1.00	Grey
C	C	213.2	1.00	Grey
C	C	214.3	1.00	Grey
C	C	215.4	1.00	Grey
C	C	216.5	1.00	Grey
C	C	217.6	1.00	Grey
C	C	218.7	1.00	Grey
C	C	219.8	1.00	Grey
C	C	220.9	1.00	Grey
C	C	222.0	1.00	Grey
C	C	223.1	1.00	Grey
C	C	224.2	1.00	Grey
C	C	225.3	1.00	Grey
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C	C	227.5	1.00	Grey
C	C	228.6	1.00	Grey
C	C	229.7	1.00	Grey
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C	C	233.0	1.00	Grey
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C	C	235.2	1.00	Grey
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C	C	258.3	1.00	Grey
C	C	259.4	1.00	Grey
C	C	260.5	1.00	Grey
C	C	261.6	1.00	Grey
C	C	262.7	1.00	Grey
C	C	263.8	1.00	Grey
C	C	264.9	1.00	Grey
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C	C	267.1	1.00	Grey
C	C	268.2	1.00	Grey
C	C	269.3	1.00	Grey
C	C	270.4	1.00	Grey
C	C	271.5	1.00	Grey
C	C	272.6	1.00	Grey
C	C	273.7	1.00	Grey
C	C	274.8	1.00	Grey
C	C	275.9	1.00	Grey
C	C	277.0	1.00	Grey
C	C	278.1	1.00	Grey
C	C	279.2	1.00	Grey
C	C	280.3	1.00	Grey
C	C	281.4	1.00	Grey
C	C	282.5	1.00	Grey
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C	C	284.7	1.00	Grey
C	C	285.8	1.00	Grey
C	C	286.9	1.00	Grey
C	C	288.0	1.00	Grey
C	C	289.1	1.00	Grey
C	C	290.2	1.00	Grey
C	C	291.3	1.00	Grey
C	C	292.4	1.00	Grey
C	C	293.5	1.00	Grey
C	C	294.6	1.00	Grey
C	C	295.7	1.00	Grey
C	C	296.8	1.00	Grey
C	C	297.9	1.00	Grey
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C	C	317.7	1.00	Grey
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C	C	325.4	1.00	Grey
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C	C	328.7	1.00	Grey
C	C	329.8	1.00	Grey
C	C	330.9	1.00	Grey
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C	C	356.2	1.00	Grey
C	C	357.3	1.00	Grey
C	C	358.4	1.00	Grey
C	C	359.5	1.00	Grey
C	C	360.6	1.00	Grey
C	C	361.7	1.	

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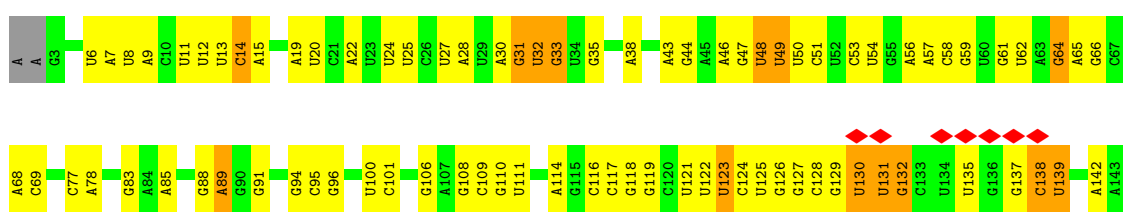
● Molecule 2: 18S rRNA

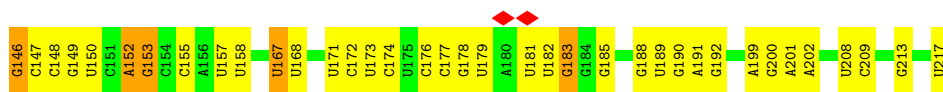




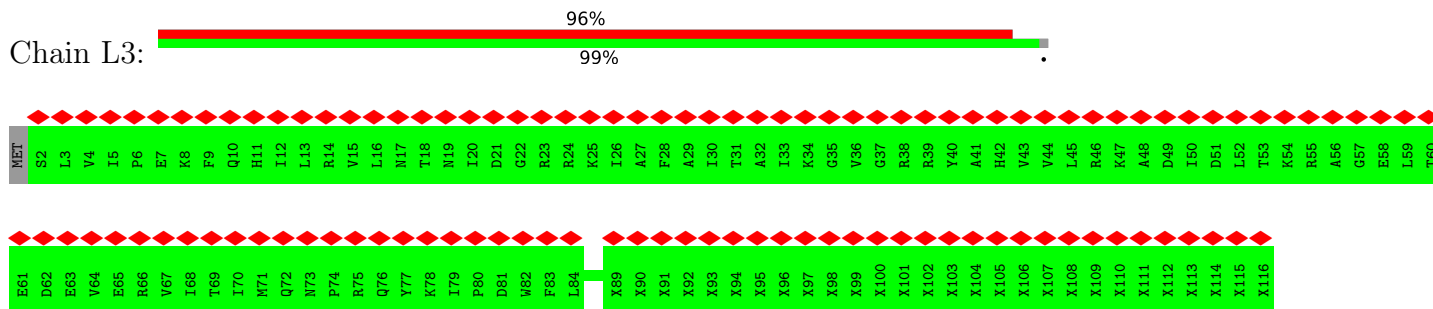


• Molecule 3: U3 snoRNA

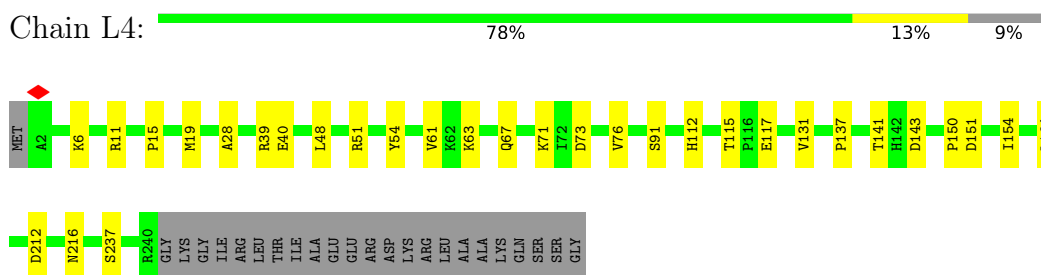




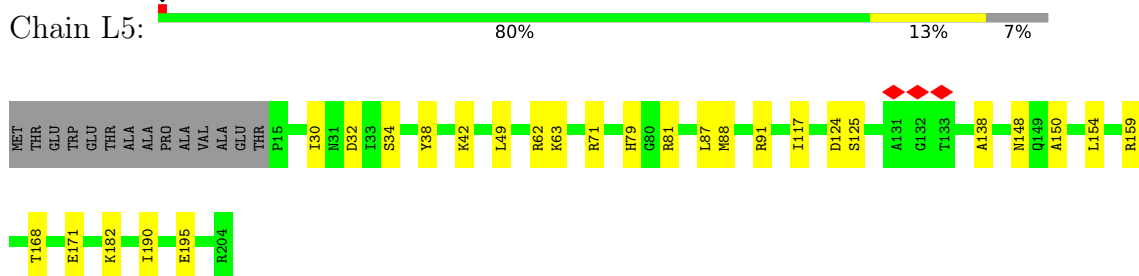
• Molecule 4: 40S ribosomal protein S18



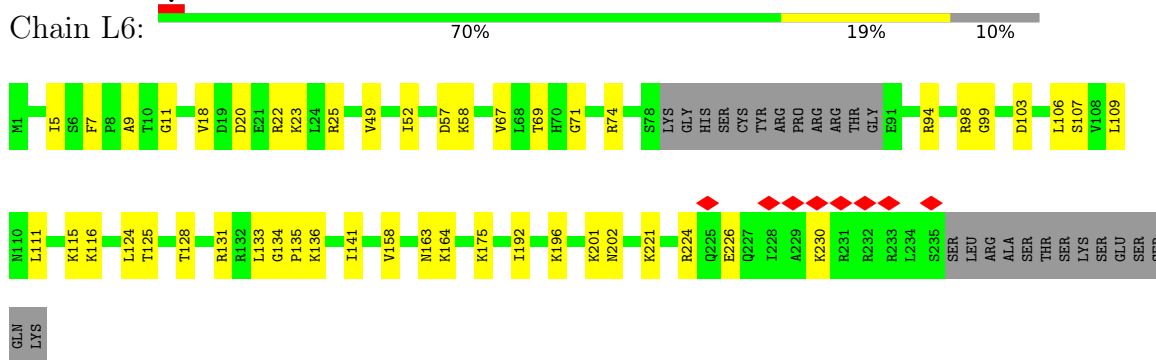
• Molecule 5: 40S ribosomal protein S4 X isoform



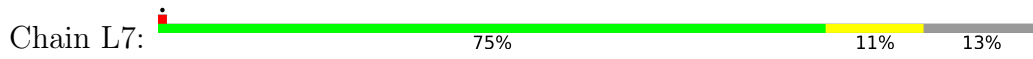
• Molecule 6: 40S ribosomal protein S5



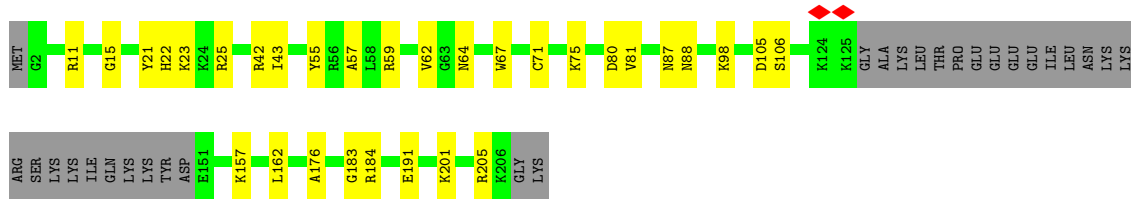
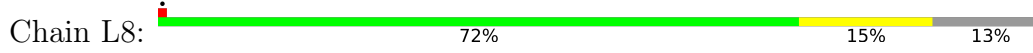
• Molecule 7: 40S ribosomal protein S6



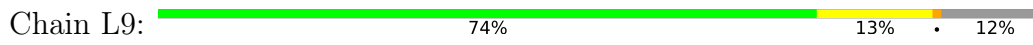
• Molecule 8: 40S ribosomal protein S7



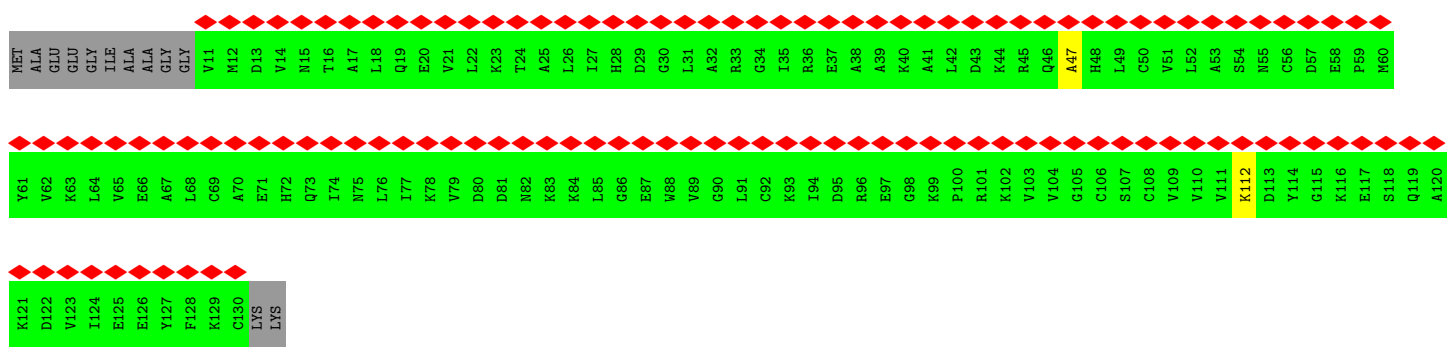
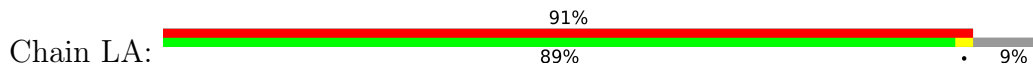
- Molecule 9: 40S ribosomal protein S8



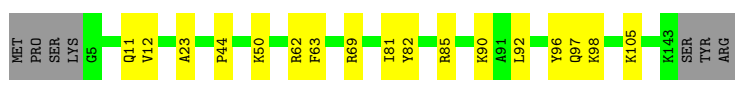
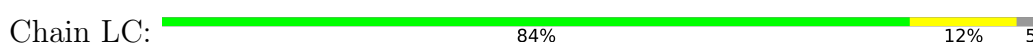
- Molecule 10: 40S ribosomal protein S9



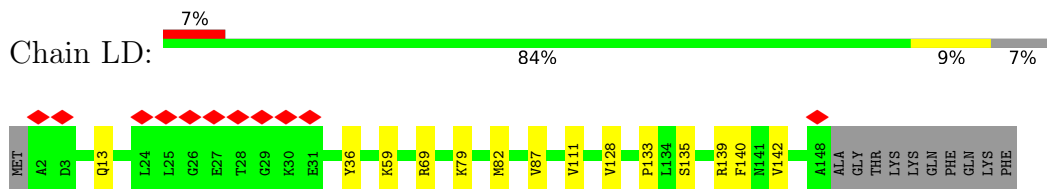
- Molecule 11: 40S ribosomal protein S12



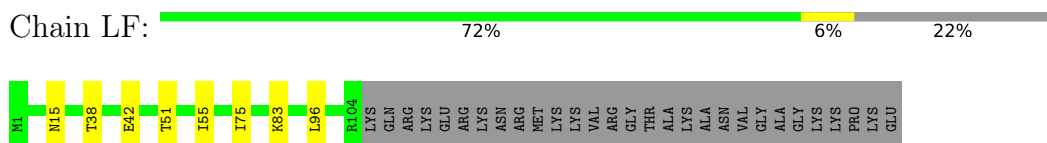
- Molecule 12: 40S ribosomal protein S16



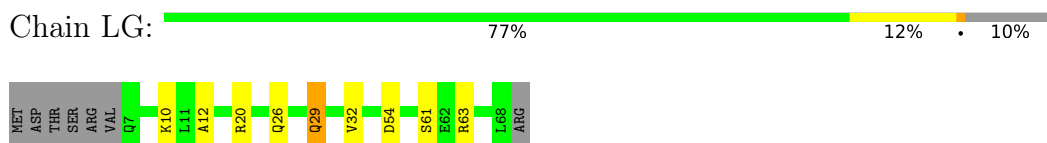
• Molecule 13: 40S ribosomal protein S11



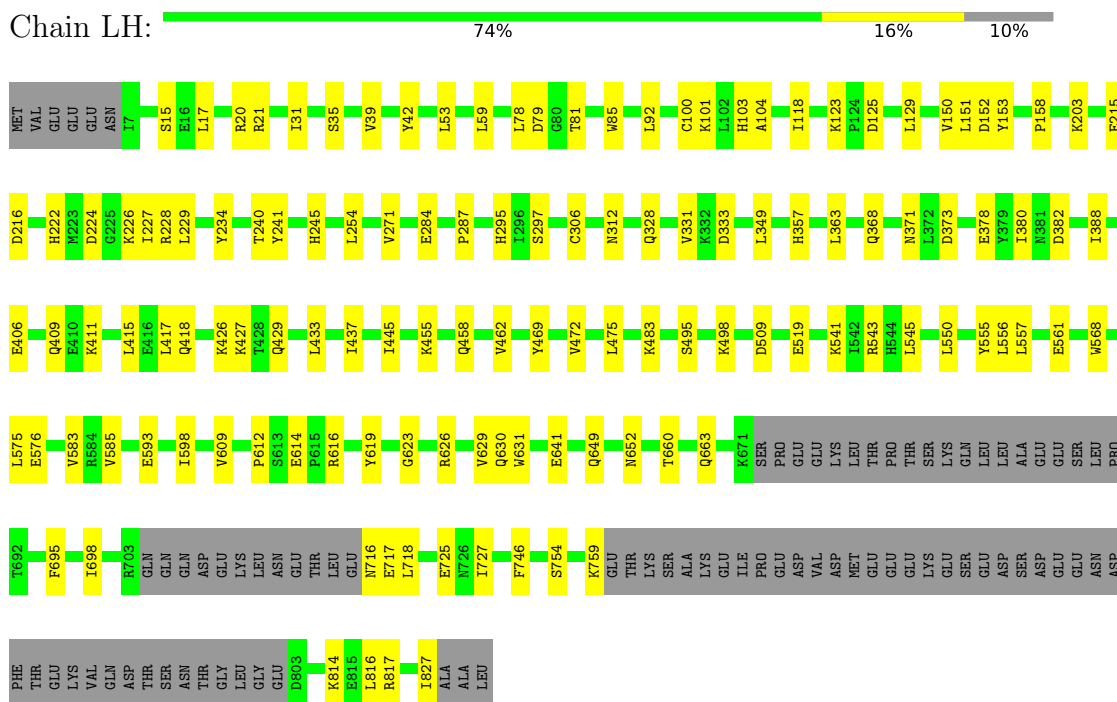
• Molecule 14: 40S ribosomal protein S24



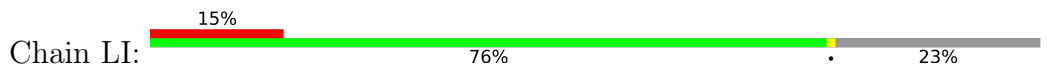
• Molecule 15: 40S ribosomal protein S28

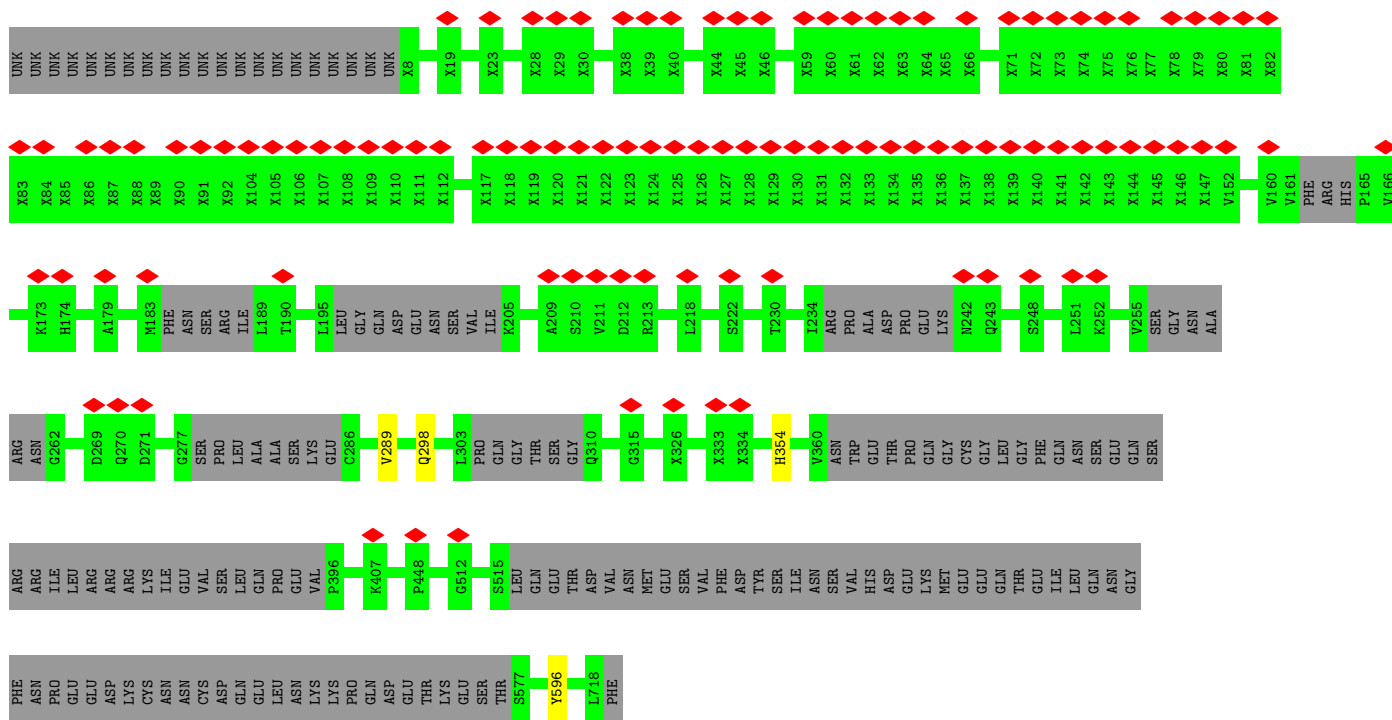


• Molecule 16: WD repeat-containing protein 75

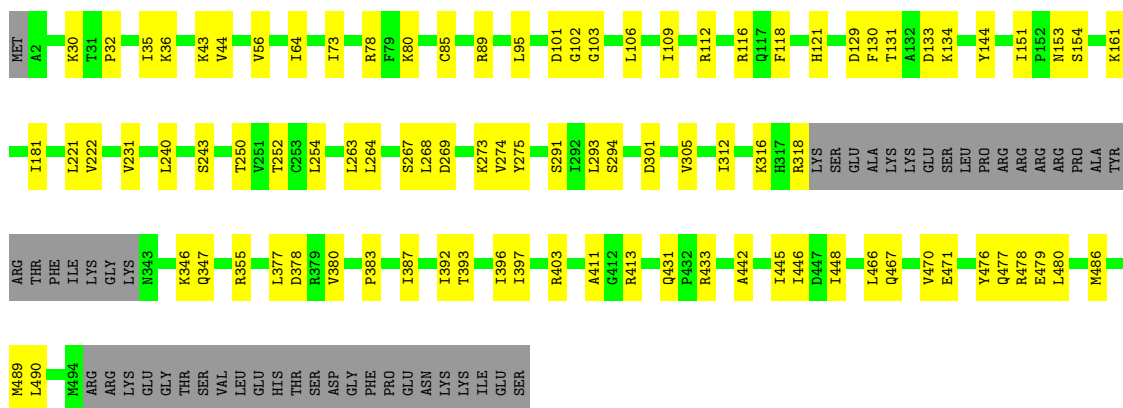


• Molecule 17: Nucleolar protein 11

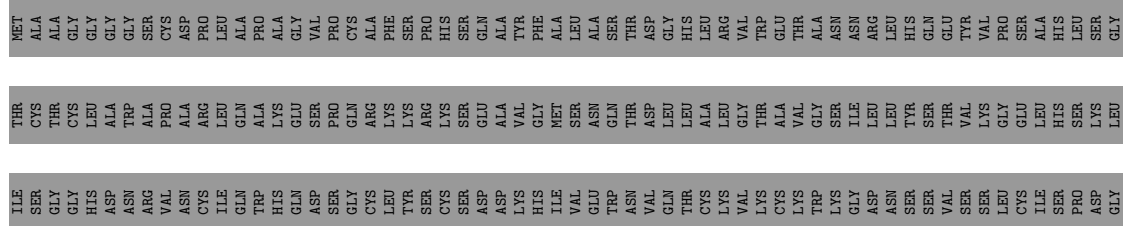


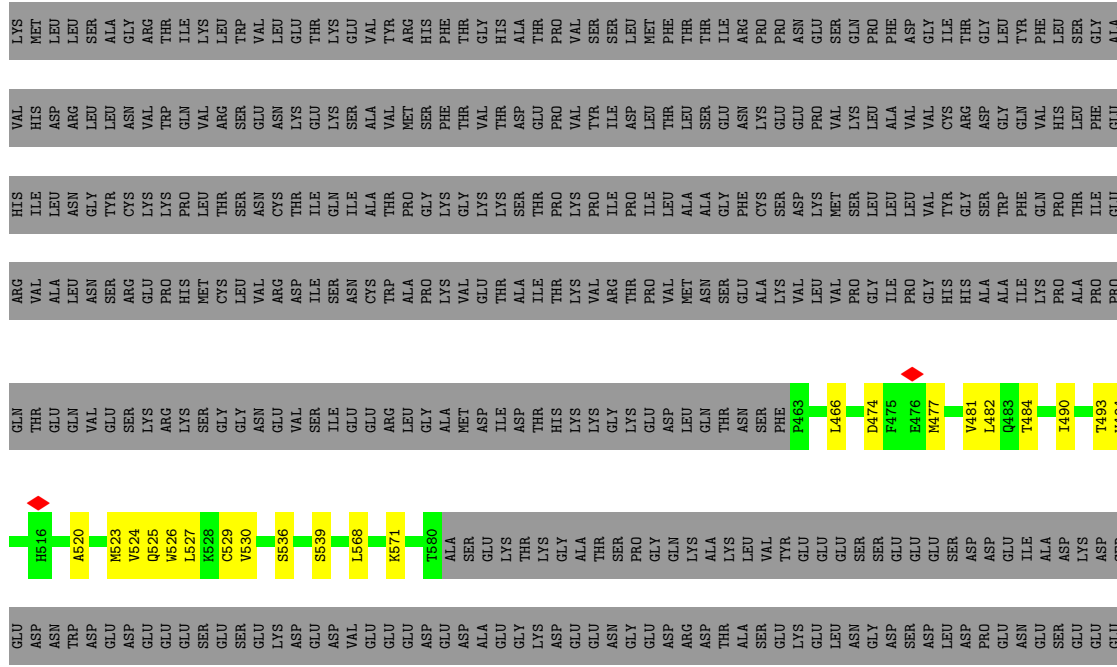


• Molecule 18: U3 small nucleolar RNA-associated protein 15 homolog

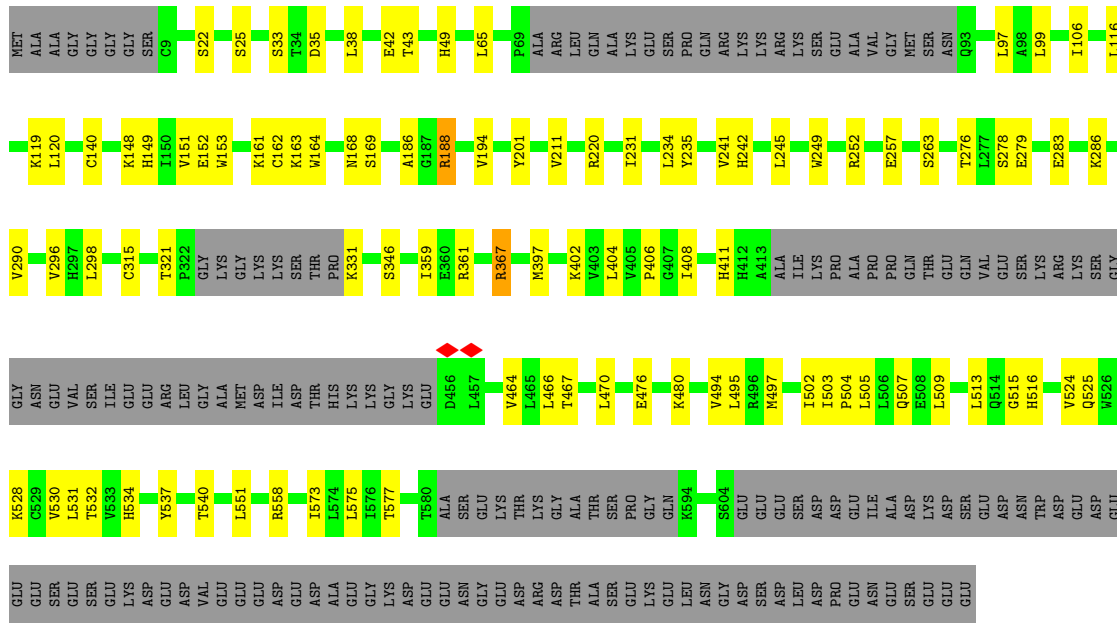


• Molecule 19: WD repeat-containing protein 43

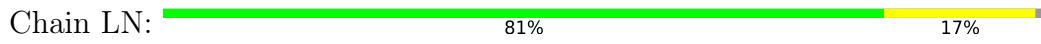


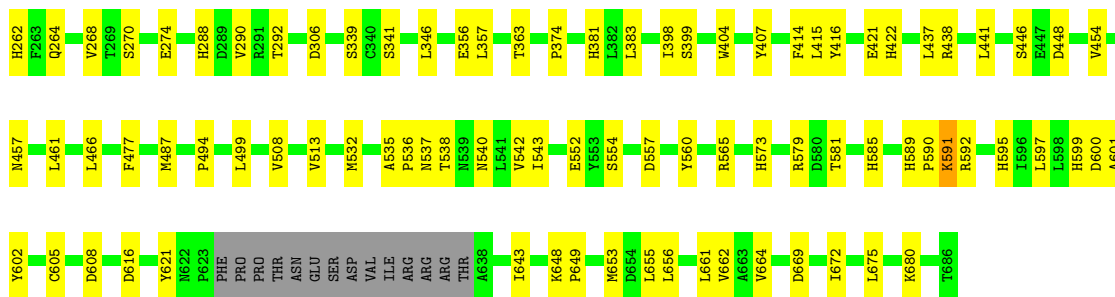


• Molecule 19: WD repeat-containing protein 43

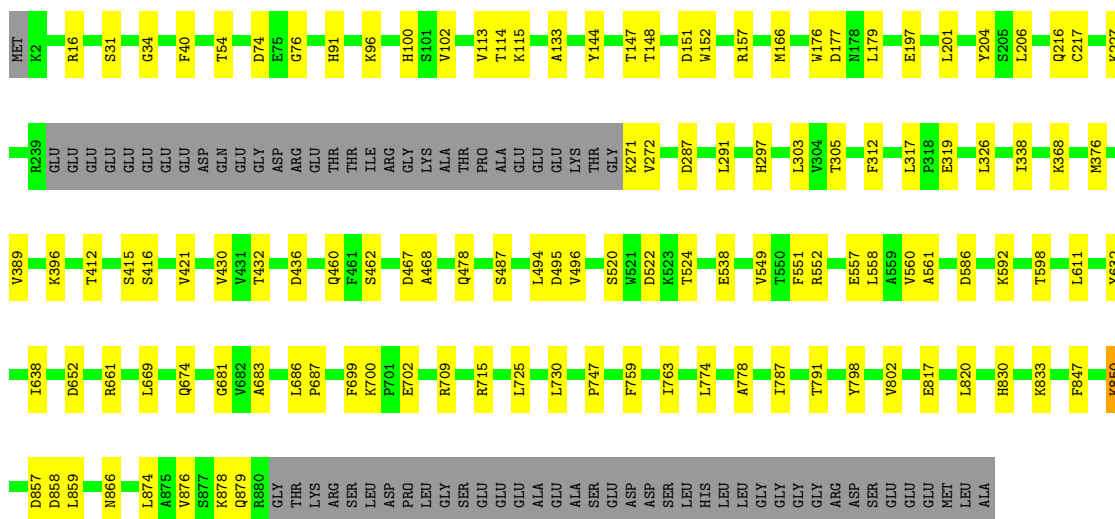
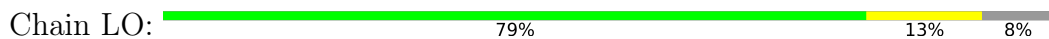


• Molecule 20: U3 small nucleolar RNA-associated protein 4 homolog

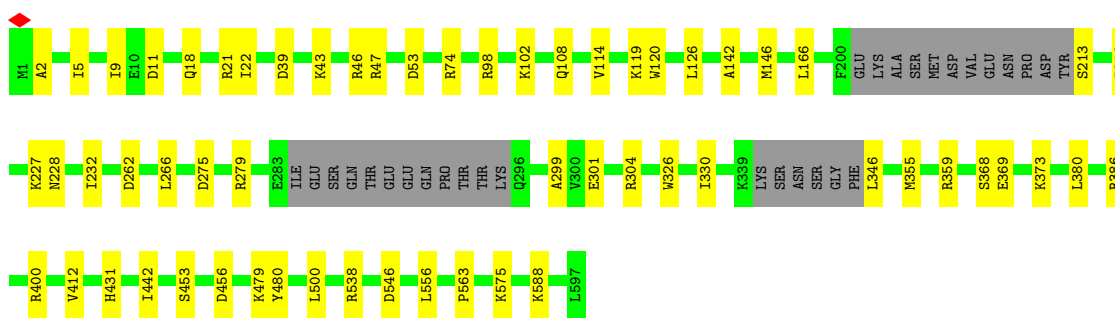
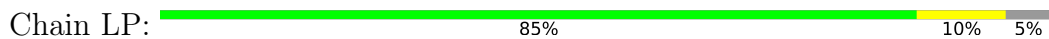




• Molecule 21: Periodic tryptophan protein 2 homolog

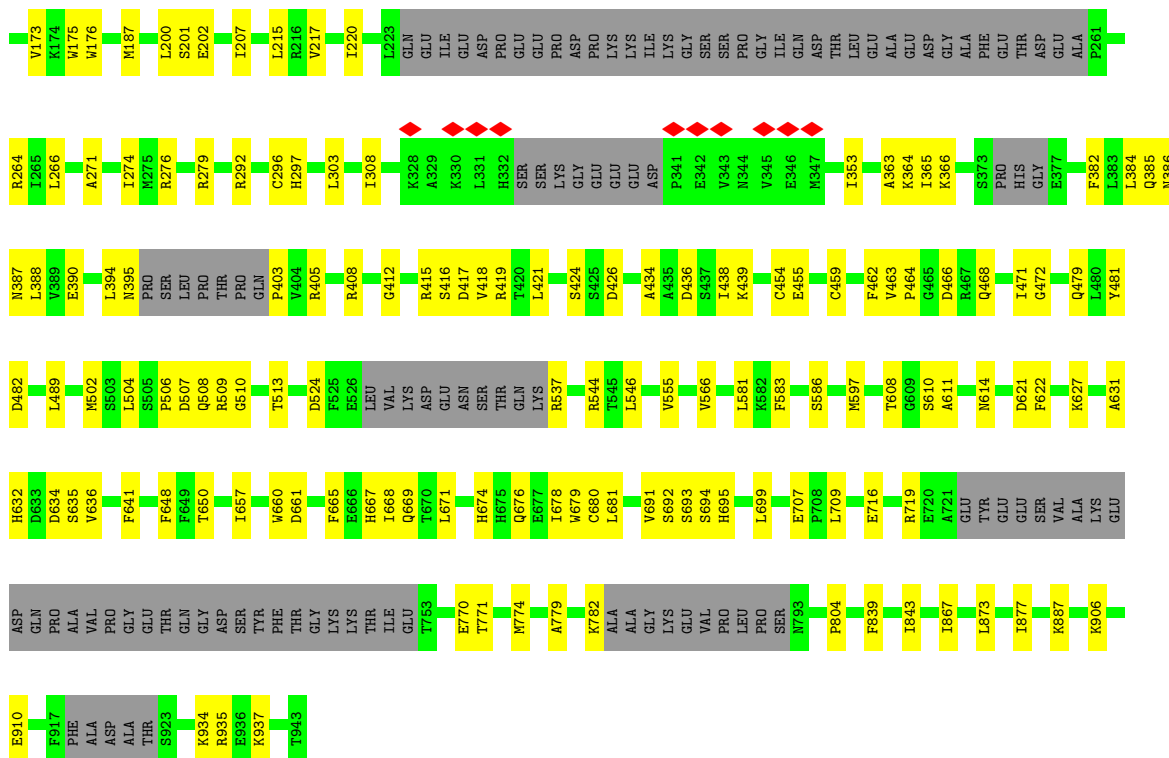


• Molecule 22: U3 small nucleolar RNA-associated protein 6 homolog

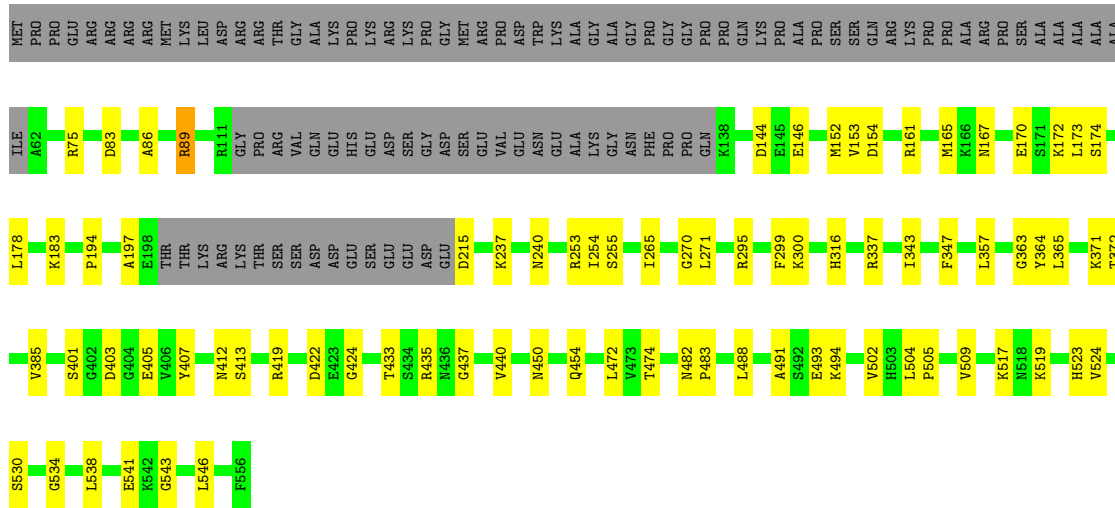


• Molecule 23: WD repeat-containing protein 3

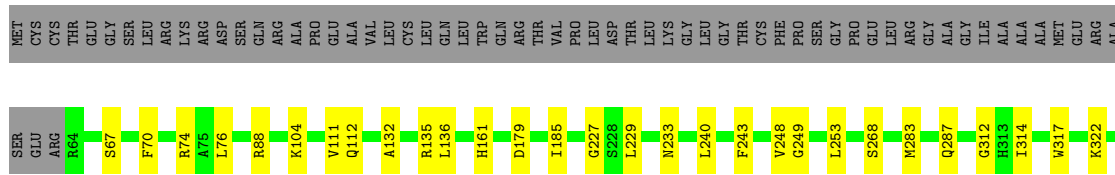
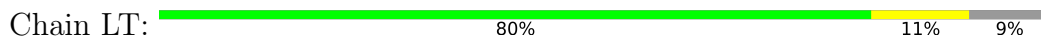


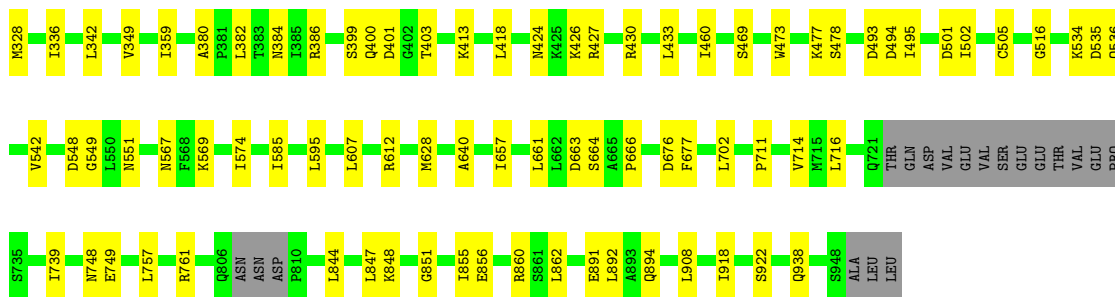


● Molecule 24: U3 small nucleolar RNA-associated protein 18 homolog



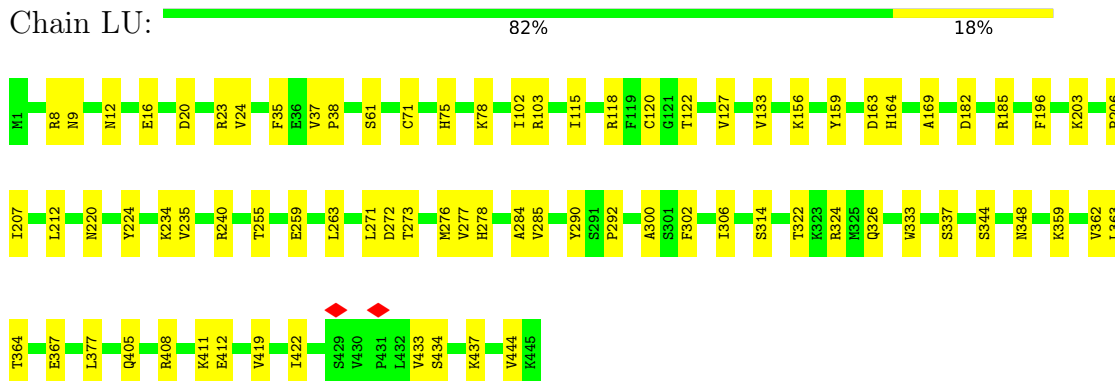
● Molecule 25: WD repeat-containing protein 36





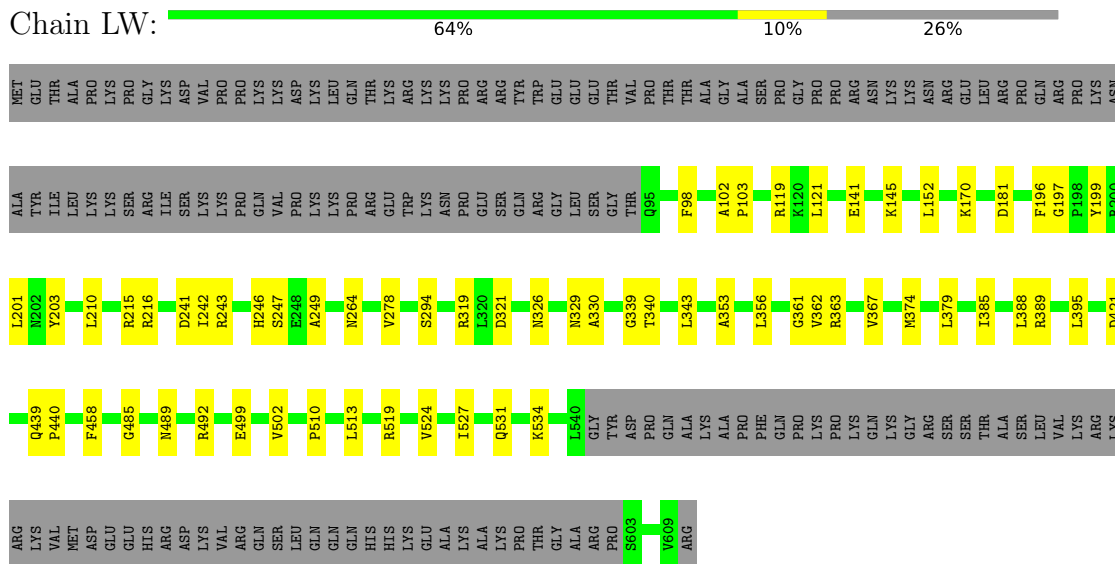
• Molecule 26: DDB1- and CUL4-associated factor 13

Chain LU:



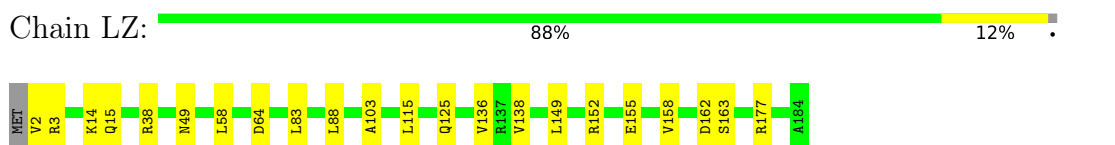
• Molecule 27: WD repeat-containing protein 46

Chain LW:



• Molecule 28: U3 small nucleolar ribonucleoprotein protein IMP3

Chain LZ:



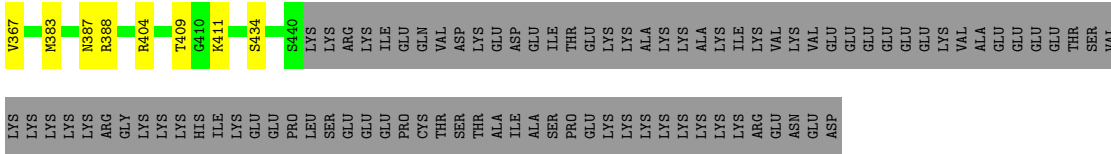
• Molecule 29: U3 small nucleolar ribonucleoprotein protein MPP10



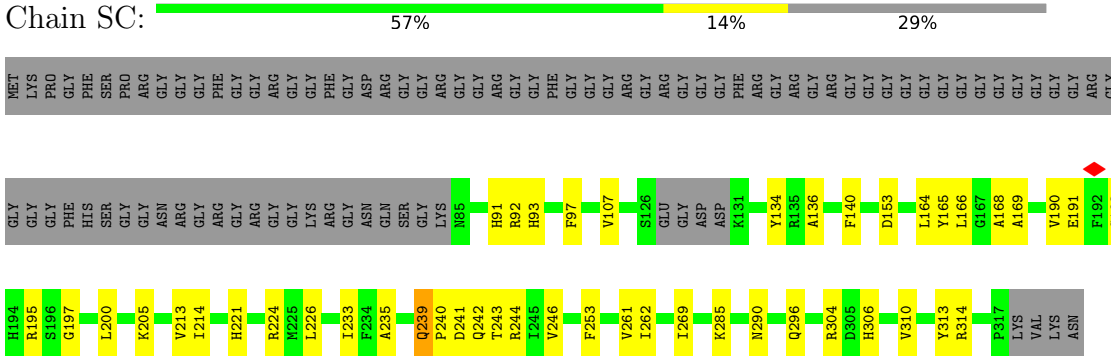
• Molecule 40: RRP12-like protein



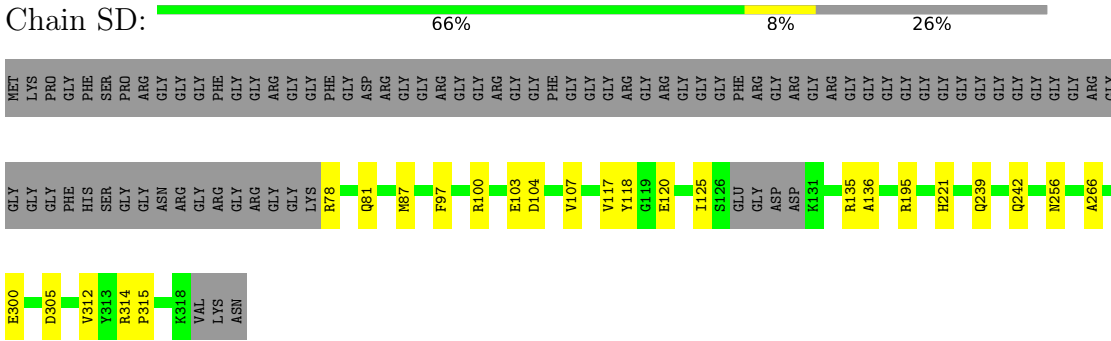
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X146	X147	X148	X149	X150	X151	X152	X153	X154	X155	X156	X157	X158	X159	X160	X161	X162	X163	X164	X165	X166	X167	X168	X169	X170	X171	X172	X173	X174	X175	X176	X177	X178	X179	X180	X181	X182	X183	X184	X185	X186	X187	X188	X189	X190	X191	X192	X193	X194	X195	X196	X197	X198	X199	X200	X201	X202	X203	X204	X205	X206	X207	X208									
X209	X210	X211	X212	X213	X214	X215	X216	X217	X218	X219	X220	X221	X222	X223	X224	X225	X226	X227	X228	X229	X230	X231	X232	X233	X234	X235	X236	X237	X238	X239	X240	X241	X242	X243	X244	X245	X246	X247	X248	X249	X250	X251	X252	X253	X254	X255	X256	X257	X258	X259	X260	X261	X262	X263	X264	X265	X266	X267	X268	X269	X270	X271	X272	X273	X274						
X275	X276	X277	X278	X279	X280	X281	X282	X283	X284	X285	X286	X287	X288	X289	X290	X291	X292	X293	X294	X295	X296	X297	X298	X299	X300	X301	X302	X303	X304	X305	X306	X307	X308	X309	X310	X311	X312	X313	X314	X315	X316	X317	X318	X319	X320	X321	X322	X323	X324	X325	X326	X327	X328	X329	X330	X331	X332	X333	X334	X335	X339										
X340	X341	X342	X343	X344	X345	X346	X347	X348	X349	X350	X351	X352	X353	X354	X355	X356	X357	X358	X359	X360	X361	X362	X363	X364	X365	X366	X367	X368	X369	X370	X371	X372	X373	X374	X375	X376	X377	X378	X379	X380	X381	X382	X383	X384	X385	X386	X387	X388	X389	X390	X391	X392	X393	X394	X395	X396	X397	X398	X399	X400	X401	X402									
X403	X404	X407	X408	X409	X410	X411	X412	X413	X414	X415	X416	X417	X418	X419	X420	X421	X422	X423	X424	X425	X426	X428	X429	X430	X431	X432	X433	X434	X435	X436	X437	X438	X439	X440	X441	X442	X443	X444	X445	X446	X447	X448	X449	X450	X451	X452	X453	X454	X455	X456	X457	X458	X459	X460	X461	X462	X463	X464	X465	X466											
X467	X468	X469	X470	X471	X472	X473	X474	X475	X476	X477	X478	X479	X480	X481	X482	X483	X484	X485	X486	X487	X488	X489	X490	X491	X492	X493	X494	X495	X496	X498	X499	X500	X501	X502	X503	X504	X505	X506	X507	X508	X509	X510	X511	X512	X513	X514	X515	X516	X517	X519	X520	X521	X522	X523	X524	X525	X526	X528	X529												
X530	X531	X532	X533	X534	X535	X536	X537	X538	X541	X542	X543	X544	X545	X546	X547	X548	X549	X550	X555	X556	X557	X558	X559	X560	X561	X562	X563	X564	X565	X566	X567	X571	X572	X573	X574	X575	X576	X577	X578	X579	X580	X581	X582	X583	X584	X585	X586	X587	X588	X589	X590	X592	X593	X594	X595	X596	X597	X598	X599												
X600	X601	X602	X603	X604	X605	X606	X607	X608	X609	X610	X611	X612	X613	X616	X617	X618	X619	X620	X621	X622	X623	X624	X625	X626	X627	X628	X629	X630	X631	X633	X634	X635	X636	X637	X638	X639	X640	X641	X642	X643	X644	X645	X646	X647	X651	X652	X653	X654	X655	X656	X657	X658	X659	X660	X661	X662	X663	X664	X665												
X666	X667	X668	X669	X670	X671	X672	X674	X675	X676	X677	X678	X679	X680	X681	X682	X683	X684	X685	X686	X687	X688	X689	X692	X693	X694	X695	X696	X697	X698	X699	X700	X701	X702	X703	X704	X705	X706	X707	X708	X709	X710	X711	X712	X713	X717	X718	X719	X720	X721	X722	X723	X724	X725	X726	X727	X728	X729	X730	X731	X732											
X733	X734	X736	X737	X738	X739	X740	X741	X742	X743	X744	X745	X746	X747	X748	X749	X750	X751	X752	X753	X754	X755	X756	X760	X761	X762	X763	X764	X765	X766	X767	X768	X769	X770	X771	X772	X773	X774	X775	X776	X777	X778	X779	X780	X784	X785	X786	X787	X788	X789	X790	X791	X792	X793	X794	X795	X796	X797	X798	X799												



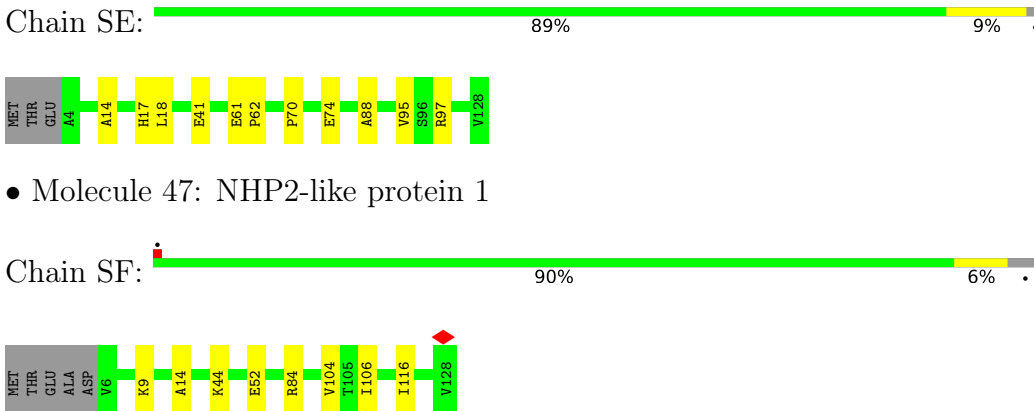
• Molecule 46: rRNA 2'-O-methyltransferase fibrillar



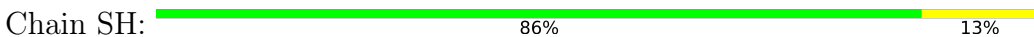
• Molecule 46: rRNA 2'-O-methyltransferase fibrillar

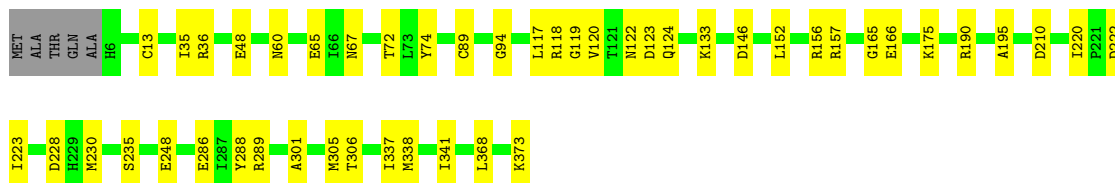


• Molecule 47: NHP2-like protein 1

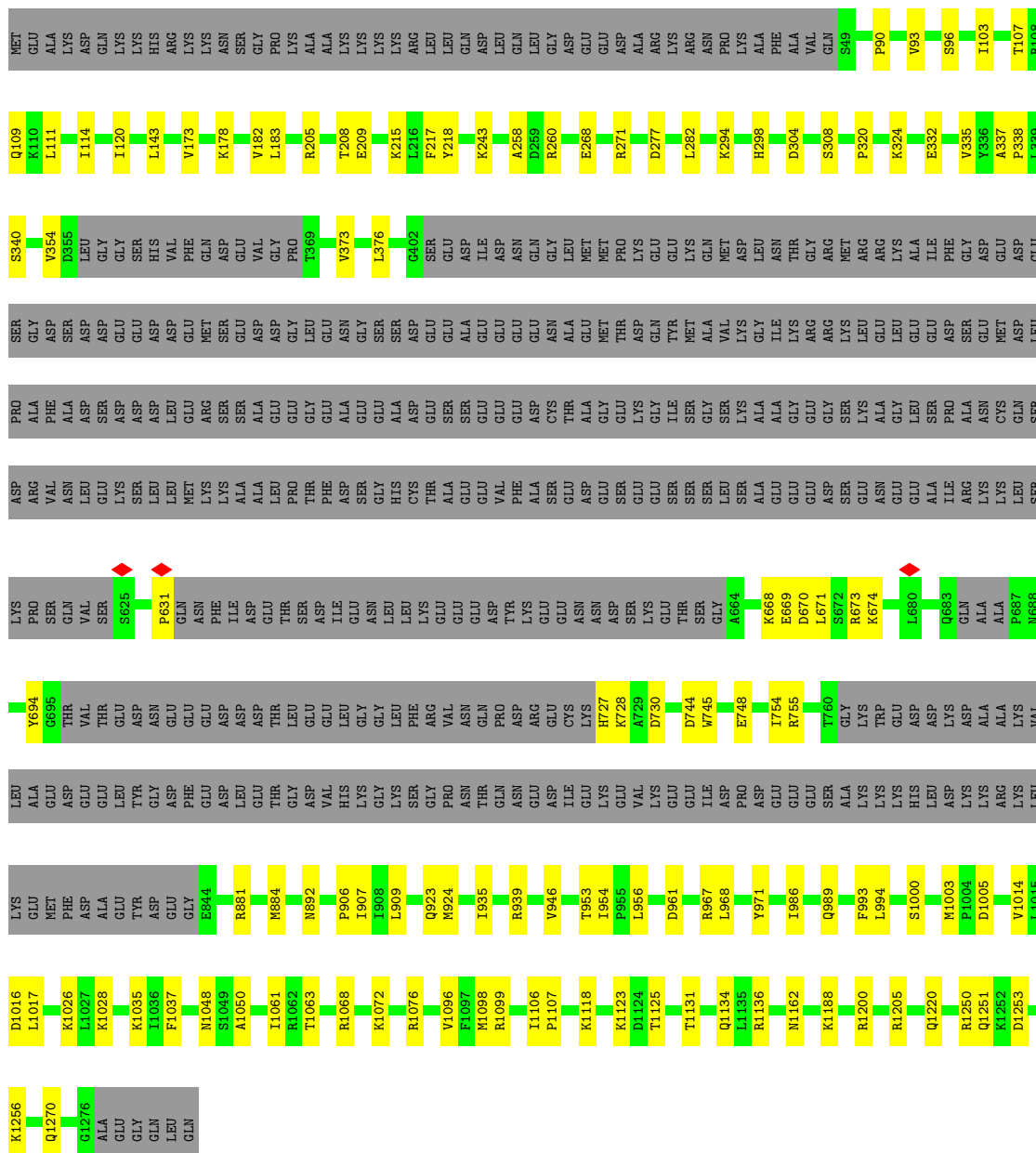


• Molecule 48: RNA 3'-terminal phosphate cyclase-like protein



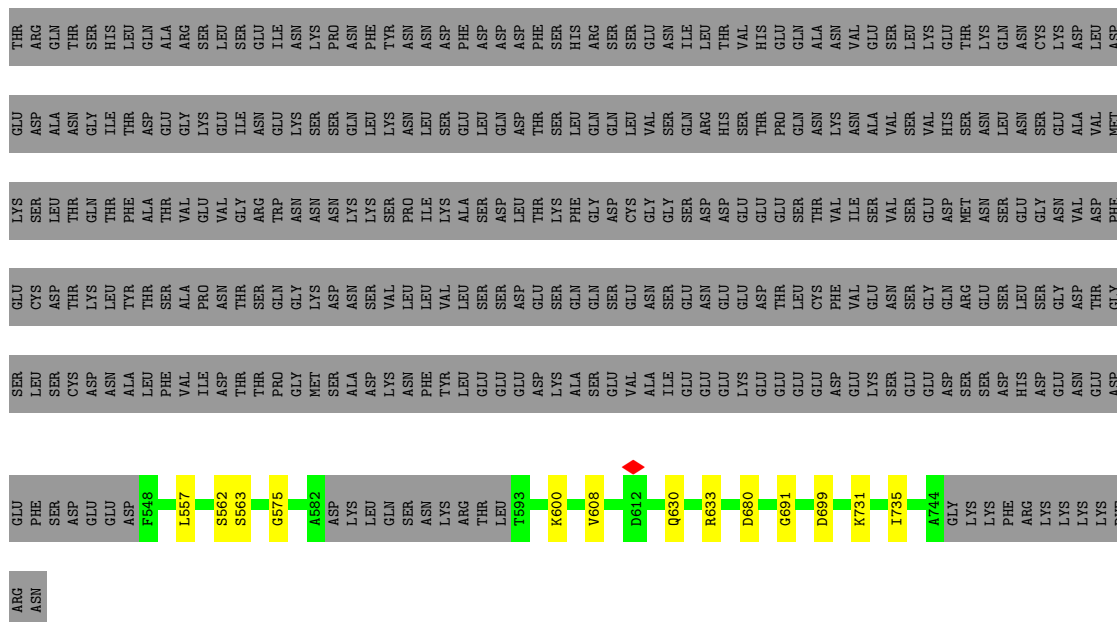


● Molecule 49: Ribosome biogenesis protein BMS1 homolog

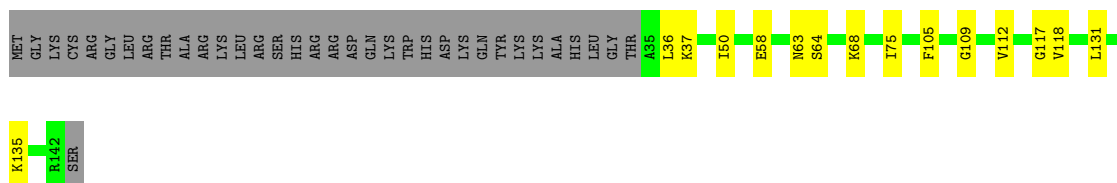


● Molecule 50: Ribosomal RNA small subunit methyltransferase NEP1

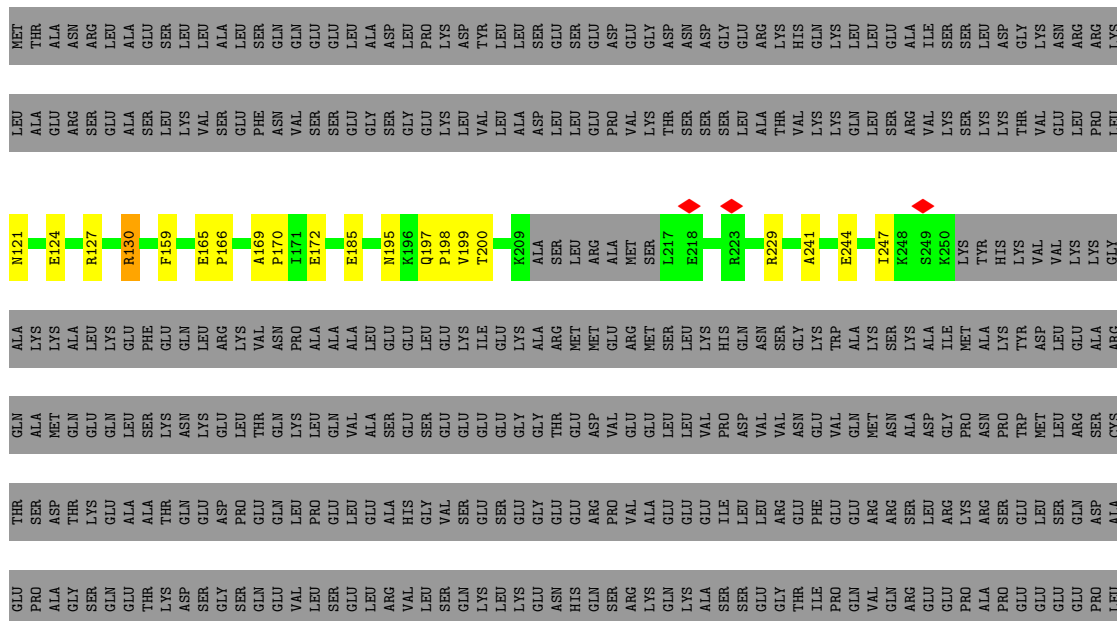


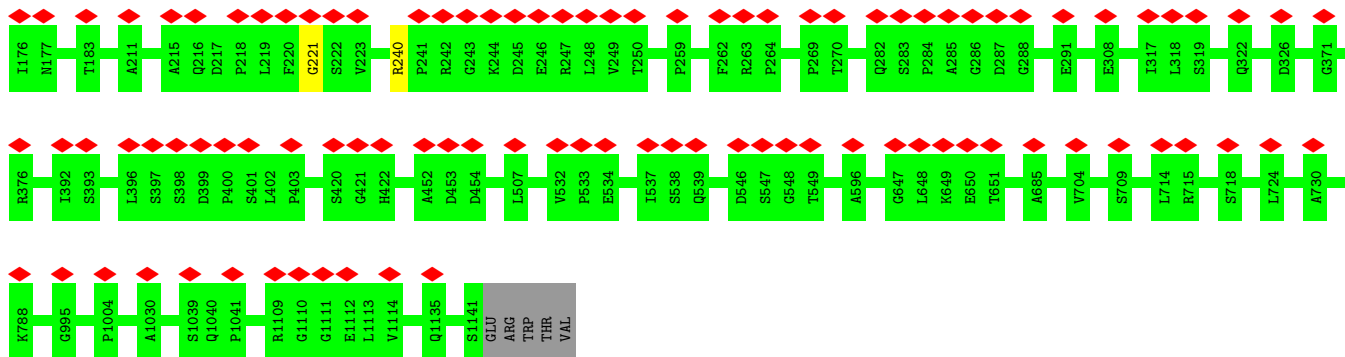


• Molecule 54: 40S ribosomal protein S23

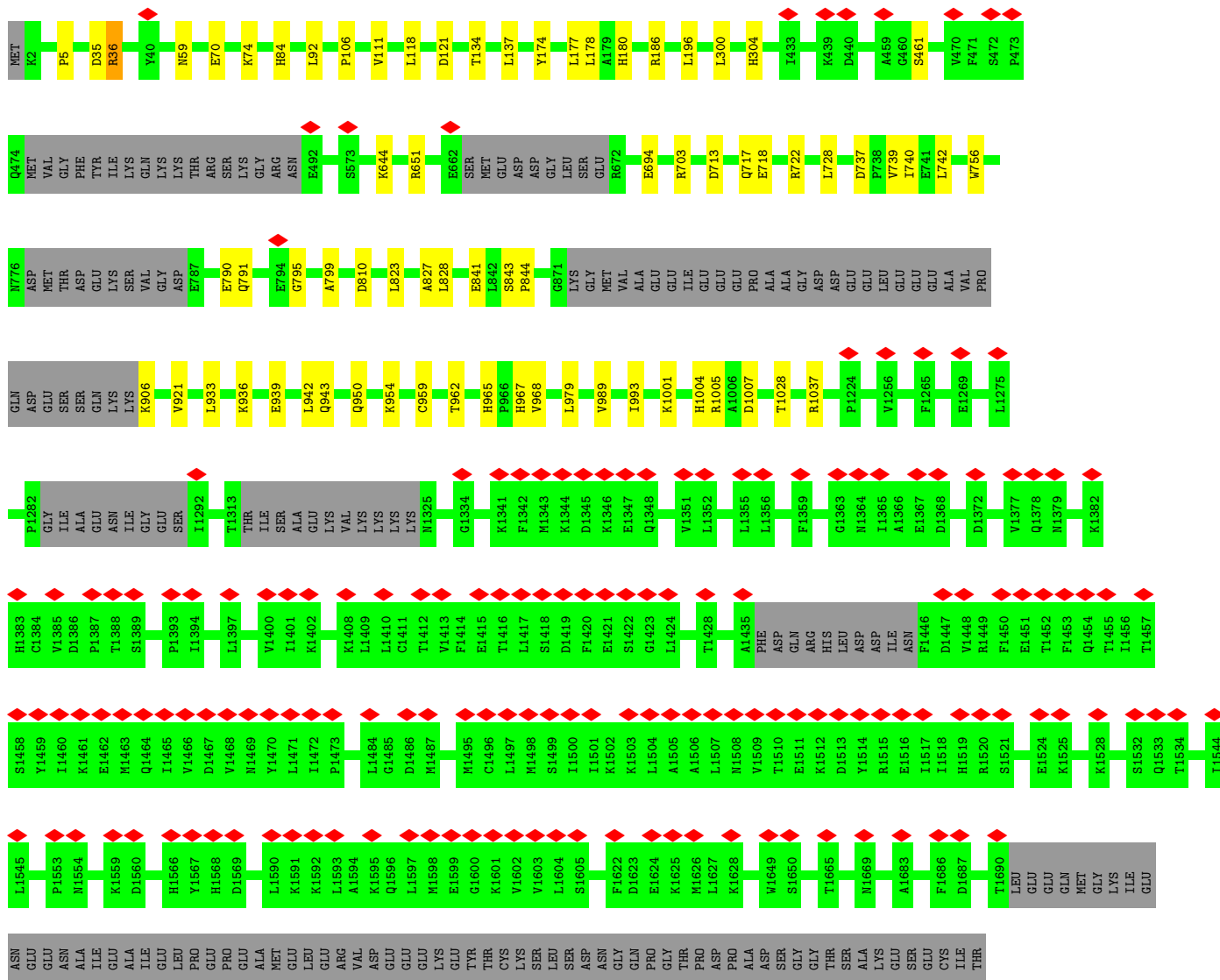


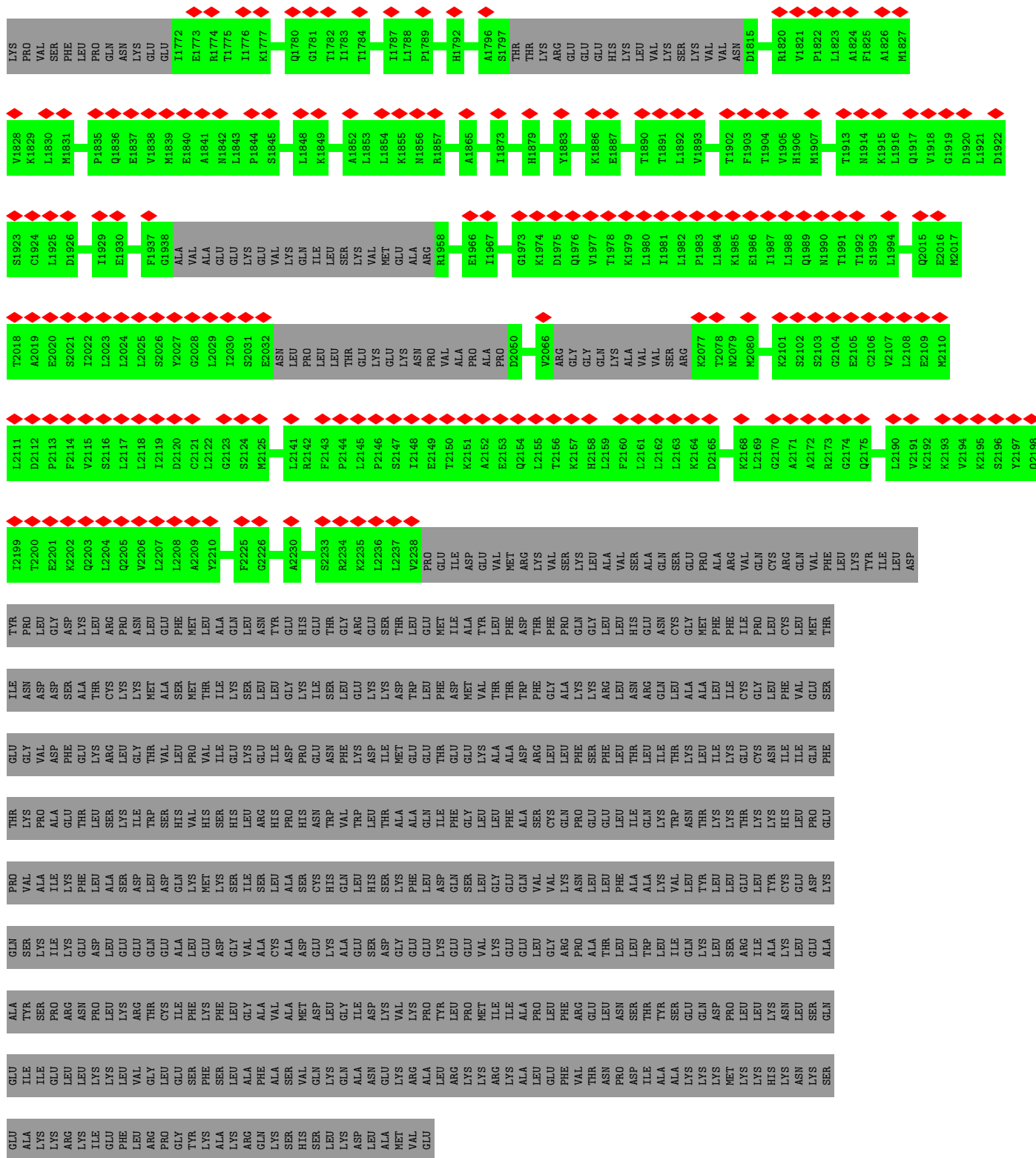
• Molecule 55: U3 small nucleolar RNA-associated protein 14 homolog A





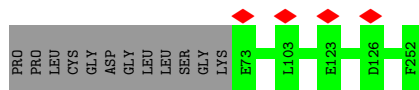
• Molecule 59: Small subunit processome component 20 homolog



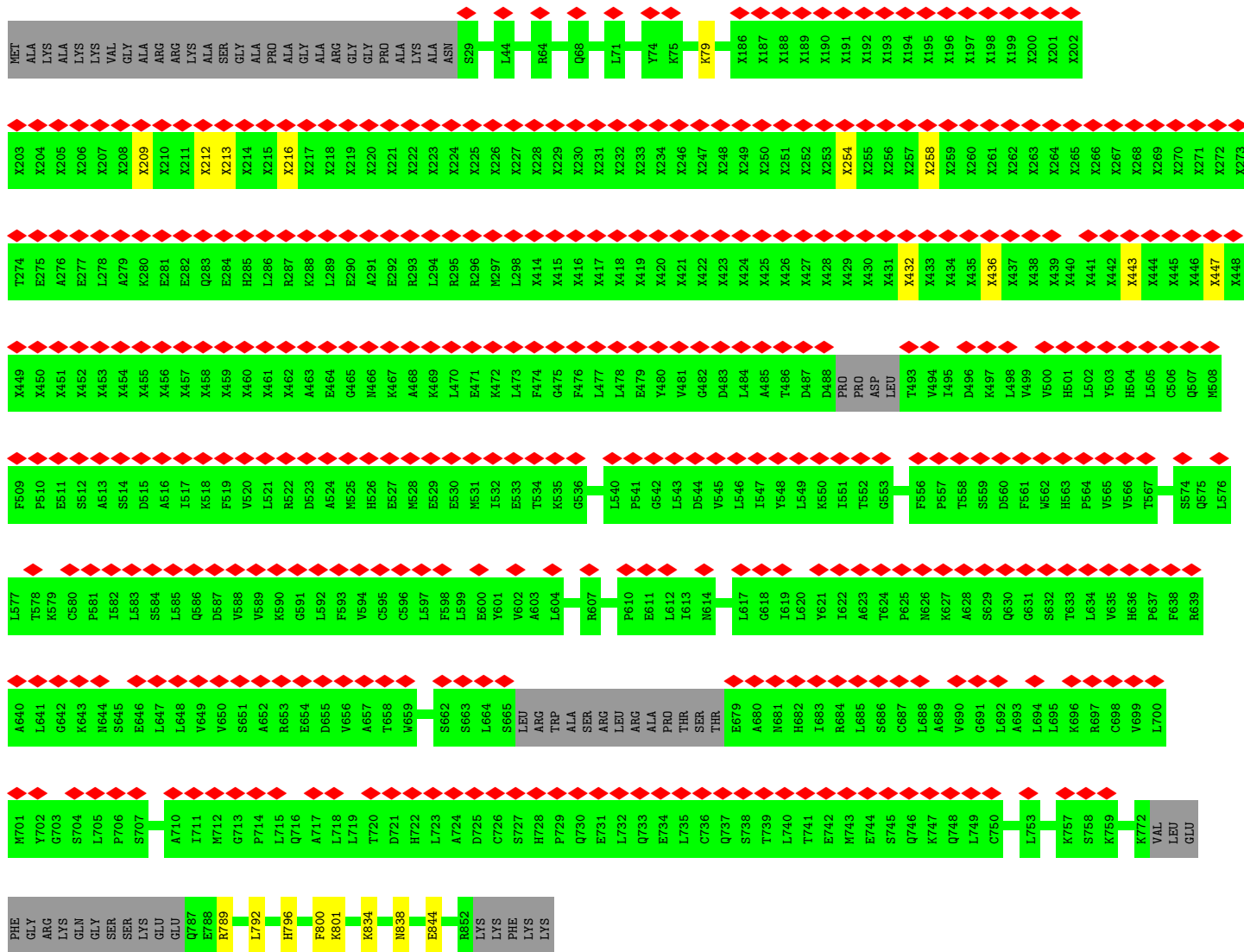
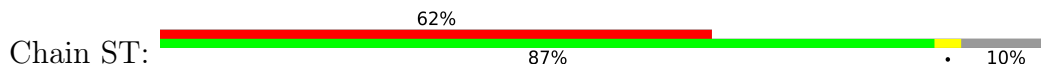


● Molecule 60: Transducin beta-like protein 3

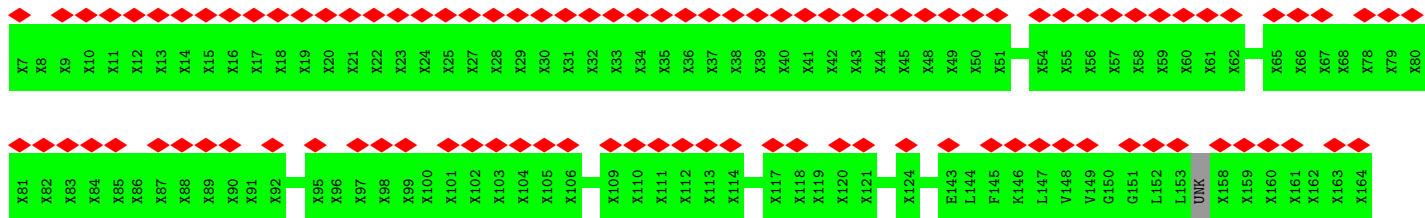
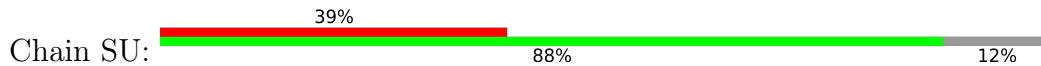


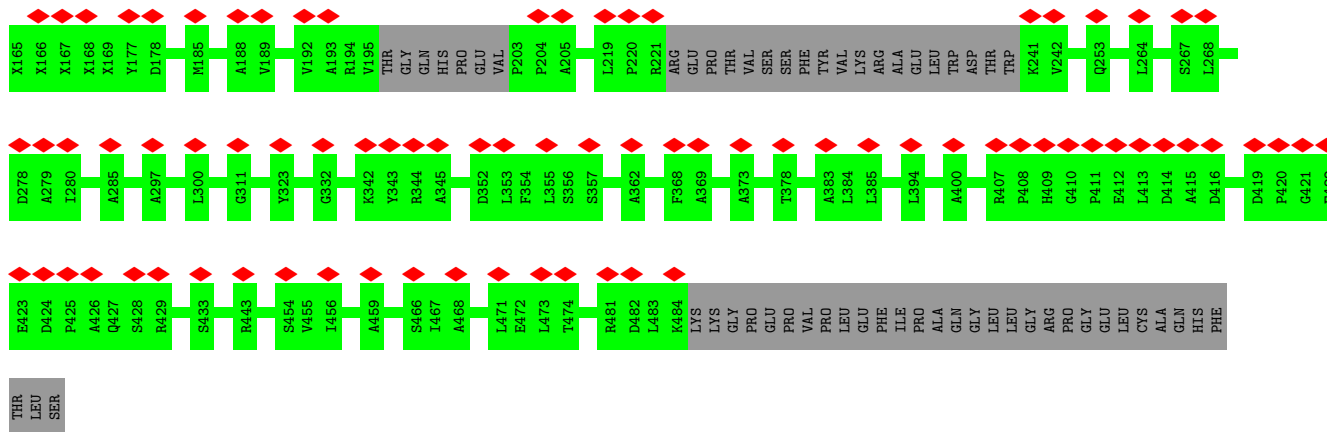


• Molecule 66: Nucleolar protein 14

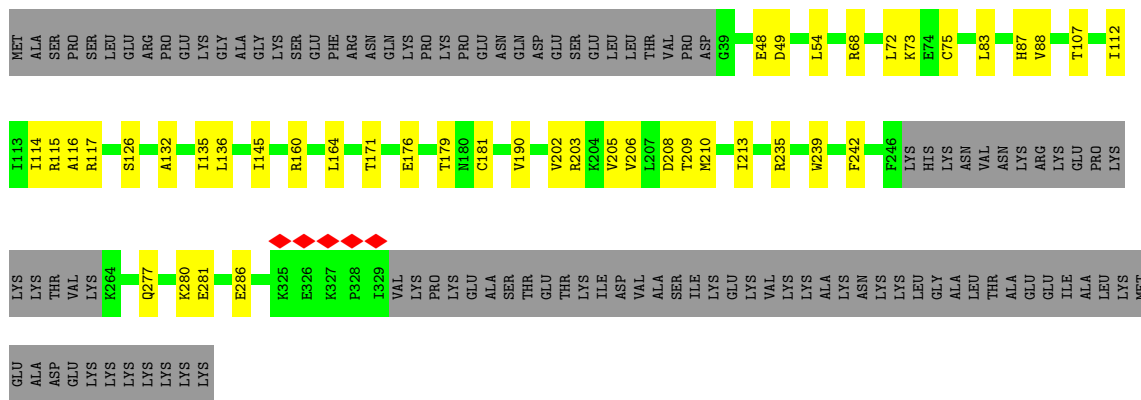


• Molecule 67: Nucleolar complex protein 4 homolog

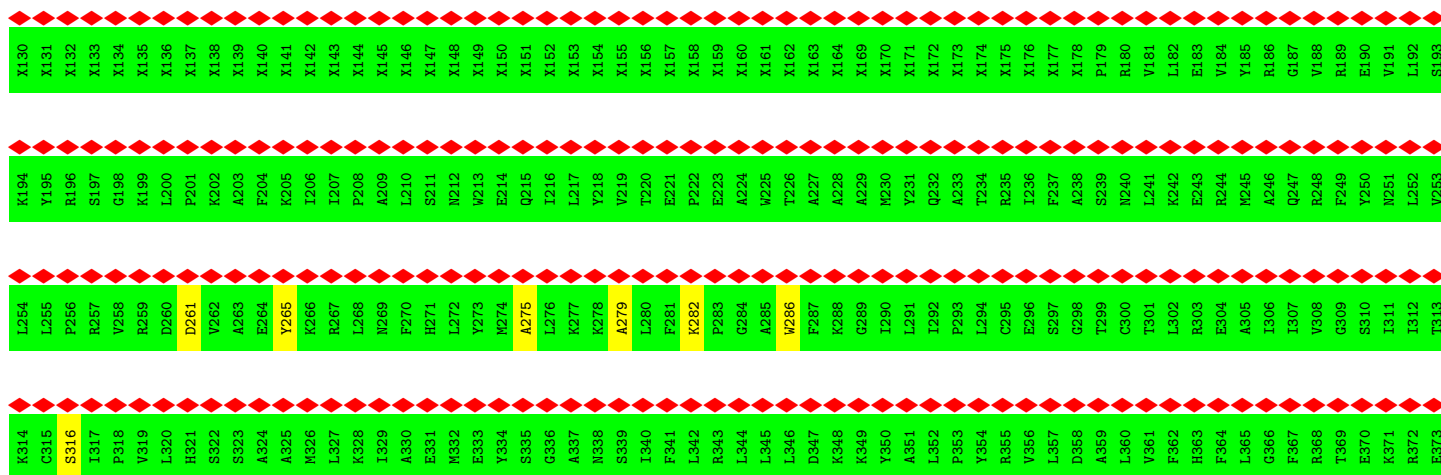
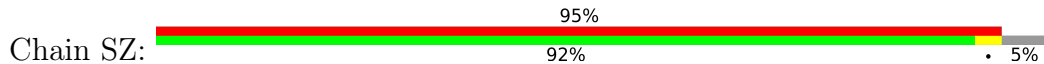




● Molecule 68: KRR1 small subunit processome component homolog



● Molecule 69: Bystin



L374	P375	V376	L377	W378	H379	Q380	C381	L382	L383	T384	L385	V386	Q387	R388	Y389	K390	A391	D392	L393	A394	T395	D396	Q397	K398	E399	A400	L401	L402	E403	L404	L405	R406	L407	Q408	P409	H410	P411	Q412	L413	S414	P415	E416	I417	R418	R419	E420	L421	Q422	S423	ALA	VAL	PRO	ARG	ASP	VAL	GLU	ASP	VAL	PRO
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

ILE	THR	VAL	GLU
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21096	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	58	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.079	Depositor
Minimum map value	-0.032	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0088	Depositor
Map size (\AA)	604.80005, 604.80005, 604.80005	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.08, 1.08, 1.08	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: MG, GTP, SAH, ATP, 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	0.20	0/5739	0.82	1/8931 (0.0%)
2	L1	0.23	0/31039	0.82	54/48327 (0.1%)
3	L2	0.24	0/5130	0.79	2/7996 (0.0%)
4	L3	0.24	0/425	0.40	0/591
5	L4	0.25	0/1944	0.53	0/2621
6	L5	0.27	0/1523	0.55	0/2048
7	L6	0.26	0/1830	0.56	0/2434
8	L7	0.26	0/1365	0.51	0/1830
9	L8	0.27	0/1500	0.58	0/2002
10	L9	0.27	0/1447	0.57	0/1930
11	LA	0.23	0/592	0.39	0/823
12	LC	0.29	0/1115	0.56	0/1494
13	LD	0.25	0/1225	0.54	0/1640
14	LF	0.26	0/868	0.52	0/1159
15	LG	0.24	0/490	0.58	0/656
16	LH	0.26	0/6127	0.51	0/8292
17	LI	0.23	0/1959	0.38	0/2719
18	LJ	0.27	0/3788	0.54	0/5128
19	LK	0.24	0/959	0.48	0/1302
19	LL	0.25	0/4072	0.51	0/5539
20	LN	0.26	0/5438	0.51	0/7377
21	LO	0.28	0/6835	0.54	1/9256 (0.0%)
22	LP	0.26	0/4806	0.47	0/6455
23	LQ	0.25	0/6548	0.53	0/8839
24	LS	0.27	0/3621	0.52	0/4876
25	LT	0.26	0/6907	0.50	0/9359
26	LU	0.26	0/3695	0.52	0/4986
27	LW	0.27	0/3594	0.54	0/4867
28	LZ	0.26	0/1560	0.56	0/2104
29	NA	0.27	0/2084	0.48	0/2789
30	NB	0.26	0/622	0.62	0/816
31	ND	0.25	0/708	0.53	0/947

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	NE	0.27	0/807	0.49	0/1069
33	NF	0.24	0/1226	0.48	0/1649
34	NG	0.24	0/873	0.51	0/1177
35	NJ	0.25	0/6652	0.51	0/9006
35	NK	0.24	0/4023	0.44	0/5594
36	NM	0.24	0/1899	0.50	0/2533
37	NN	0.24	0/346	0.57	0/462
38	NO	0.26	0/1051	0.53	0/1406
39	NQ	0.24	0/653	0.50	0/876
41	NT	0.23	0/285	0.45	0/395
42	NU	0.22	0/296	0.34	0/411
43	NW	0.27	0/2556	0.54	1/3469 (0.0%)
44	SA	0.26	0/3122	0.47	0/4208
45	SB	0.25	0/3491	0.48	1/4695 (0.0%)
46	SC	0.26	0/1818	0.52	0/2463
46	SD	0.28	0/1878	0.51	0/2540
47	SE	0.26	0/980	0.50	0/1323
47	SF	0.29	0/967	0.53	0/1305
48	SH	0.26	0/2882	0.51	0/3887
49	SI	0.27	0/6949	0.50	1/9339 (0.0%)
50	SJ	0.27	0/1007	0.47	0/1401
50	SK	0.28	0/1609	0.54	1/2181 (0.0%)
51	SL	0.27	0/1619	0.53	0/2174
52	SM	0.27	0/2420	0.56	0/3264
53	SQ	0.27	0/1561	0.49	0/2083
54	SR	0.28	0/828	0.52	0/1110
55	SS	0.28	0/1663	0.53	1/2250 (0.0%)
57	SY	0.25	0/2051	0.50	0/2723
58	NH	0.26	0/5264	0.45	0/7329
59	SP	0.24	0/11868	0.43	0/16336
60	LR	0.24	0/4340	0.49	0/5985
61	LM	0.26	0/13315	0.45	0/18214
62	N0	0.13	0/284	0.87	0/432
63	SG	0.25	0/2935	0.52	0/3981
64	NI	0.25	0/1471	0.52	0/2009
65	SW	0.24	0/889	0.44	0/1237
66	ST	0.23	0/2435	0.43	0/3343
67	SU	0.24	0/1463	0.41	0/2037
68	NY	0.27	0/2133	0.48	0/2887
69	SZ	0.23	0/1216	0.42	0/1696
All	All	0.25	0/222680	0.58	63/310612 (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
64	NI	0	1

There are no bond length outliers.

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L1	1453	C	N1-C2-O2	8.87	124.22	118.90
2	L1	1453	C	C2-N1-C1'	8.84	128.52	118.80
2	L1	1535	U	C2-N1-C1'	8.36	127.73	117.70
2	L1	1535	U	N1-C2-O2	8.18	128.52	122.80
2	L1	1742	C	C2-N1-C1'	7.78	127.36	118.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
64	NI	148	VAL	Peptide

5.2 Too-close contacts [i](#)

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	5152	0	2630	61	0
2	L1	27777	0	14063	275	0
3	L2	4589	0	2306	54	0
4	L3	571	0	220	0	0
5	L4	1902	0	1990	20	0
6	L5	1501	0	1557	21	0
7	L6	1811	0	1974	33	0
8	L7	1346	0	1410	13	0
9	L8	1474	0	1542	19	0
10	L9	1425	0	1541	20	0
11	LA	593	0	277	1	0
12	LC	1098	0	1168	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	LD	1204	0	1274	9	0
14	LF	851	0	894	5	0
15	LG	488	0	514	7	0
16	LH	5987	0	5953	84	0
17	LI	2675	0	993	3	0
18	LJ	3711	0	3758	66	0
19	LK	943	0	1023	15	0
19	LL	3982	0	4031	64	0
20	LN	5299	0	5269	75	0
21	LO	6676	0	6579	75	0
22	LP	4705	0	4720	44	0
23	LQ	6438	0	6400	108	0
24	LS	3560	0	3570	55	0
25	LT	6756	0	6768	68	0
26	LU	3611	0	3618	51	0
27	LW	3519	0	3518	46	0
28	LZ	1532	0	1553	16	0
29	NA	2055	0	2135	26	0
30	NB	617	0	685	9	0
31	ND	696	0	729	9	0
32	NE	799	0	854	9	0
33	NF	1202	0	1289	11	0
34	NG	861	0	871	10	0
35	NJ	6526	0	6599	77	0
35	NK	4030	0	1806	3	0
36	NM	1873	0	1968	23	0
37	NN	340	0	345	5	0
38	NO	1034	0	1080	14	0
39	NQ	640	0	661	5	0
40	NR	4305	0	945	3	0
41	NT	286	0	127	0	0
42	NU	297	0	133	0	0
43	NW	2498	0	2456	56	0
44	SA	3077	0	3139	34	0
45	SB	3439	0	3559	57	0
46	SC	1781	0	1803	32	0
46	SD	1841	0	1867	19	0
47	SE	968	0	1017	7	0
47	SF	955	0	1008	7	0
48	SH	2832	0	2937	32	0
49	SI	6801	0	6971	81	0
50	SJ	1008	0	440	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	SK	1579	0	1646	26	0
51	SL	1586	0	1641	21	0
52	SM	2369	0	2376	20	0
53	SQ	1533	0	1579	14	0
54	SR	816	0	871	8	0
55	SS	1626	0	1677	24	0
56	SX	885	0	192	1	0
57	SY	2024	0	2148	21	0
58	NH	5265	0	2357	1	0
59	SP	11768	0	7711	44	0
60	LR	4321	0	2717	30	0
61	LM	13156	0	10845	106	0
62	N0	264	0	134	0	0
63	SG	2878	0	2740	30	0
64	NI	1459	0	1045	8	0
65	SW	890	0	407	0	0
66	ST	3064	0	1559	11	0
67	SU	2057	0	804	0	0
68	NY	2094	0	2044	26	0
69	SZ	1442	0	604	5	0
70	L1	19	0	0	0	0
70	NH	1	0	0	0	0
70	SI	1	0	0	0	0
70	SL	1	0	0	0	0
71	NQ	1	0	0	0	0
71	NT	1	0	0	0	0
71	SL	1	0	0	0	0
72	SI	32	0	12	1	0
73	SJ	26	0	19	2	0
73	SK	26	0	19	2	0
74	NH	31	0	12	0	0
74	NK	31	0	12	0	0
All	All	223184	0	181708	1972	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 5.

The worst 5 of 1972 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)
3:L2:12:U:HO2'	52:SM:44:THR:HG1	1.17	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LN:461:LEU:HB2	20:LN:477:PHE:HB2	1.64	0.78
61:LM:843:VAL:HG22	61:LM:846:ARG:HH21	1.48	0.78
19:LL:276:THR:HB	19:LL:286:LYS:HB2	1.65	0.77
18:LJ:103:GLY:HA2	18:LJ:118:PHE:O	1.83	0.77

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	85/116 (73%)	85 (100%)	0	0	100	100
5	L4	237/263 (90%)	237 (100%)	0	0	100	100
6	L5	188/204 (92%)	183 (97%)	5 (3%)	0	100	100
7	L6	219/249 (88%)	217 (99%)	2 (1%)	0	100	100
8	L7	164/194 (84%)	162 (99%)	2 (1%)	0	100	100
9	L8	176/208 (85%)	172 (98%)	4 (2%)	0	100	100
10	L9	169/194 (87%)	168 (99%)	1 (1%)	0	100	100
11	LA	118/132 (89%)	116 (98%)	2 (2%)	0	100	100
12	LC	137/146 (94%)	134 (98%)	3 (2%)	0	100	100
13	LD	145/158 (92%)	139 (96%)	6 (4%)	0	100	100
14	LF	102/133 (77%)	101 (99%)	1 (1%)	0	100	100
15	LG	60/69 (87%)	59 (98%)	1 (2%)	0	100	100
16	LH	738/830 (89%)	721 (98%)	17 (2%)	0	100	100
17	LI	374/699 (54%)	372 (100%)	2 (0%)	0	100	100
18	LJ	465/518 (90%)	449 (97%)	16 (3%)	0	100	100
19	LK	116/677 (17%)	112 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	LL	500/677 (74%)	485 (97%)	15 (3%)	0	100	100
20	LN	667/686 (97%)	647 (97%)	19 (3%)	1 (0%)	51	84
21	LO	844/919 (92%)	825 (98%)	19 (2%)	0	100	100
22	LP	559/597 (94%)	552 (99%)	7 (1%)	0	100	100
23	LQ	810/943 (86%)	793 (98%)	17 (2%)	0	100	100
24	LS	447/556 (80%)	436 (98%)	11 (2%)	0	100	100
25	LT	863/951 (91%)	846 (98%)	17 (2%)	0	100	100
26	LU	443/445 (100%)	434 (98%)	9 (2%)	0	100	100
27	LW	449/610 (74%)	433 (96%)	16 (4%)	0	100	100
28	LZ	181/184 (98%)	179 (99%)	2 (1%)	0	100	100
29	NA	243/681 (36%)	242 (100%)	1 (0%)	0	100	100
30	NB	71/479 (15%)	69 (97%)	2 (3%)	0	100	100
31	ND	82/257 (32%)	81 (99%)	1 (1%)	0	100	100
32	NE	94/293 (32%)	94 (100%)	0	0	100	100
33	NF	147/151 (97%)	143 (97%)	4 (3%)	0	100	100
34	NG	114/151 (76%)	111 (97%)	3 (3%)	0	100	100
35	NJ	809/1025 (79%)	790 (98%)	19 (2%)	0	100	100
35	NK	801/1025 (78%)	775 (97%)	26 (3%)	0	100	100
36	NM	229/264 (87%)	224 (98%)	5 (2%)	0	100	100
37	NN	40/560 (7%)	39 (98%)	1 (2%)	0	100	100
38	NO	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
39	NQ	80/84 (95%)	77 (96%)	3 (4%)	0	100	100
41	NT	56/156 (36%)	56 (100%)	0	0	100	100
42	NU	58/135 (43%)	58 (100%)	0	0	100	100
43	NW	305/688 (44%)	292 (96%)	13 (4%)	0	100	100
44	SA	390/594 (66%)	388 (100%)	2 (0%)	0	100	100
45	SB	438/529 (83%)	432 (99%)	6 (1%)	0	100	100
46	SC	225/321 (70%)	219 (97%)	6 (3%)	0	100	100
46	SD	233/321 (73%)	228 (98%)	5 (2%)	0	100	100
47	SE	123/128 (96%)	122 (99%)	1 (1%)	0	100	100
47	SF	121/128 (94%)	118 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	SH	366/373 (98%)	362 (99%)	4 (1%)	0	100	100
49	SI	830/1282 (65%)	811 (98%)	19 (2%)	0	100	100
50	SJ	202/244 (83%)	195 (96%)	7 (4%)	0	100	100
50	SK	202/244 (83%)	200 (99%)	2 (1%)	0	100	100
51	SL	190/198 (96%)	184 (97%)	6 (3%)	0	100	100
52	SM	288/291 (99%)	279 (97%)	9 (3%)	0	100	100
53	SQ	183/756 (24%)	180 (98%)	3 (2%)	0	100	100
54	SR	106/143 (74%)	104 (98%)	2 (2%)	0	100	100
55	SS	191/771 (25%)	186 (97%)	5 (3%)	0	100	100
57	SY	232/253 (92%)	232 (100%)	0	0	100	100
58	NH	1064/1146 (93%)	1043 (98%)	21 (2%)	0	100	100
59	SP	1967/2785 (71%)	1940 (99%)	27 (1%)	0	100	100
60	LR	769/808 (95%)	749 (97%)	20 (3%)	0	100	100
61	LM	1977/2144 (92%)	1933 (98%)	44 (2%)	0	100	100
63	SG	383/475 (81%)	376 (98%)	7 (2%)	0	100	100
64	NI	232/280 (83%)	229 (99%)	3 (1%)	0	100	100
65	SW	178/252 (71%)	175 (98%)	3 (2%)	0	100	100
66	ST	432/632 (68%)	424 (98%)	8 (2%)	0	100	100
67	SU	287/472 (61%)	285 (99%)	2 (1%)	0	100	100
68	NY	270/381 (71%)	269 (100%)	1 (0%)	0	100	100
69	SZ	244/304 (80%)	237 (97%)	7 (3%)	0	100	100
All	All	24635/33692 (73%)	24132 (98%)	502 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	LN	175	SER

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	
5	L4	207/225 (92%)	207 (100%)	0	100	100
6	L5	160/170 (94%)	160 (100%)	0	100	100
7	L6	195/218 (89%)	195 (100%)	0	100	100
8	L7	149/174 (86%)	148 (99%)	1 (1%)	84	90
9	L8	155/180 (86%)	153 (99%)	2 (1%)	69	81
10	L9	152/168 (90%)	151 (99%)	1 (1%)	84	90
12	LC	114/121 (94%)	114 (100%)	0	100	100
13	LD	133/142 (94%)	132 (99%)	1 (1%)	81	89
14	LF	92/115 (80%)	92 (100%)	0	100	100
15	LG	55/62 (89%)	54 (98%)	1 (2%)	59	77
16	LH	670/748 (90%)	667 (100%)	3 (0%)	91	94
18	LJ	412/456 (90%)	412 (100%)	0	100	100
19	LK	112/594 (19%)	112 (100%)	0	100	100
19	LL	456/594 (77%)	454 (100%)	2 (0%)	91	94
20	LN	582/597 (98%)	580 (100%)	2 (0%)	92	95
21	LO	726/783 (93%)	725 (100%)	1 (0%)	93	97
22	LP	499/527 (95%)	498 (100%)	1 (0%)	93	96
23	LQ	690/828 (83%)	688 (100%)	2 (0%)	92	95
24	LS	393/476 (83%)	392 (100%)	1 (0%)	92	95
25	LT	744/823 (90%)	743 (100%)	1 (0%)	93	97
26	LU	399/399 (100%)	399 (100%)	0	100	100
27	LW	373/512 (73%)	373 (100%)	0	100	100
28	LZ	166/167 (99%)	166 (100%)	0	100	100
29	NA	229/626 (37%)	229 (100%)	0	100	100
30	NB	63/413 (15%)	63 (100%)	0	100	100
31	ND	72/222 (32%)	72 (100%)	0	100	100
32	NE	86/253 (34%)	85 (99%)	1 (1%)	71	83
33	NF	130/131 (99%)	130 (100%)	0	100	100
34	NG	92/119 (77%)	91 (99%)	1 (1%)	73	84
35	NJ	707/899 (79%)	707 (100%)	0	100	100
36	NM	207/231 (90%)	207 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	NN	37/484 (8%)	37 (100%)	0	100	100
38	NO	112/113 (99%)	112 (100%)	0	100	100
39	NQ	74/76 (97%)	74 (100%)	0	100	100
43	NW	282/635 (44%)	281 (100%)	1 (0%)	91	94
44	SA	334/511 (65%)	334 (100%)	0	100	100
45	SB	372/455 (82%)	372 (100%)	0	100	100
46	SC	192/234 (82%)	190 (99%)	2 (1%)	76	86
46	SD	198/234 (85%)	198 (100%)	0	100	100
47	SE	108/111 (97%)	108 (100%)	0	100	100
47	SF	107/111 (96%)	107 (100%)	0	100	100
48	SH	315/318 (99%)	315 (100%)	0	100	100
49	SI	738/1119 (66%)	738 (100%)	0	100	100
50	SK	181/209 (87%)	181 (100%)	0	100	100
51	SL	177/182 (97%)	177 (100%)	0	100	100
52	SM	253/254 (100%)	253 (100%)	0	100	100
53	SQ	165/676 (24%)	165 (100%)	0	100	100
54	SR	85/115 (74%)	84 (99%)	1 (1%)	71	83
55	SS	177/686 (26%)	175 (99%)	2 (1%)	73	84
57	SY	219/232 (94%)	219 (100%)	0	100	100
59	SP	504/2522 (20%)	503 (100%)	1 (0%)	93	96
60	LR	133/672 (20%)	133 (100%)	0	100	100
61	LM	977/1943 (50%)	975 (100%)	2 (0%)	93	96
63	SG	286/382 (75%)	284 (99%)	2 (1%)	84	90
64	NI	76/246 (31%)	76 (100%)	0	100	100
66	ST	59/439 (13%)	58 (98%)	1 (2%)	60	78
68	NY	211/340 (62%)	211 (100%)	0	100	100
All	All	15592/25272 (62%)	15559 (100%)	33 (0%)	93	96

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
61	LM	84	LYS
61	LM	673	ASN

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Mol	Chain	Res	Type
66	ST	789	ARG
20	LN	591	LYS
20	LN	438	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
34	NG	113	GLN
43	NW	313	HIS
61	LM	705	HIS
43	NW	299	ASN
46	SD	256	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L0	234/3617 (6%)	101 (43%)	6 (2%)
2	L1	1275/1872 (68%)	334 (26%)	21 (1%)
3	L2	214/217 (98%)	74 (34%)	4 (1%)
62	N0	20/22 (90%)	4 (20%)	0
All	All	1743/5728 (30%)	513 (29%)	31 (1%)

5 of 513 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L0	434	C
1	L0	438	G
1	L0	439	U
1	L0	442	U
1	L0	445	C

5 of 31 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	L1	589	G
3	L2	14	C
2	L1	1393	G
3	L2	152	A
2	L1	1765	C

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 30 ligands modelled in this entry, 25 are monoatomic - leaving 5 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
74	ATP	NK	1101	-	26,33,33	0.59	0	31,52,52	0.74	2 (6%)
73	SAH	SJ	301	-	24,28,28	1.20	3 (12%)	25,40,40	1.70	5 (20%)
73	SAH	SK	301	-	24,28,28	1.17	3 (12%)	25,40,40	1.68	5 (20%)
74	ATP	NH	3000	70	26,33,33	0.59	0	31,52,52	0.82	2 (6%)
72	GTP	SI	2001	70	26,34,34	1.14	2 (7%)	32,54,54	1.57	7 (21%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
74	ATP	NK	1101	-	-	6/18/38/38	0/3/3/3
73	SAH	SJ	301	-	-	1/11/31/31	0/3/3/3
73	SAH	SK	301	-	-	5/11/31/31	0/3/3/3
74	ATP	NH	3000	70	-	7/18/38/38	0/3/3/3
72	GTP	SI	2001	70	-	7/18/38/38	0/3/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
72	SI	2001	GTP	C5-C6	-4.03	1.39	1.47
73	SJ	301	SAH	C2-N3	3.84	1.38	1.32
73	SK	301	SAH	C2-N3	3.82	1.38	1.32
73	SJ	301	SAH	C2-N1	2.54	1.38	1.33
72	SI	2001	GTP	C2-N3	2.18	1.38	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
73	SK	301	SAH	N3-C2-N1	-5.63	119.88	128.68
73	SJ	301	SAH	N3-C2-N1	-5.30	120.39	128.68
72	SI	2001	GTP	PB-O3B-PG	-3.74	120.00	132.83
73	SJ	301	SAH	C5'-SD-CG	-3.31	92.34	102.27
72	SI	2001	GTP	C5-C6-N1	3.23	119.66	113.95

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
72	SI	2001	GTP	C5'-O5'-PA-O1A
73	SK	301	SAH	O-C-CA-N
73	SK	301	SAH	CA-CB-CG-SD
74	NH	3000	ATP	C5'-O5'-PA-O1A
74	NH	3000	ATP	C5'-O5'-PA-O3A

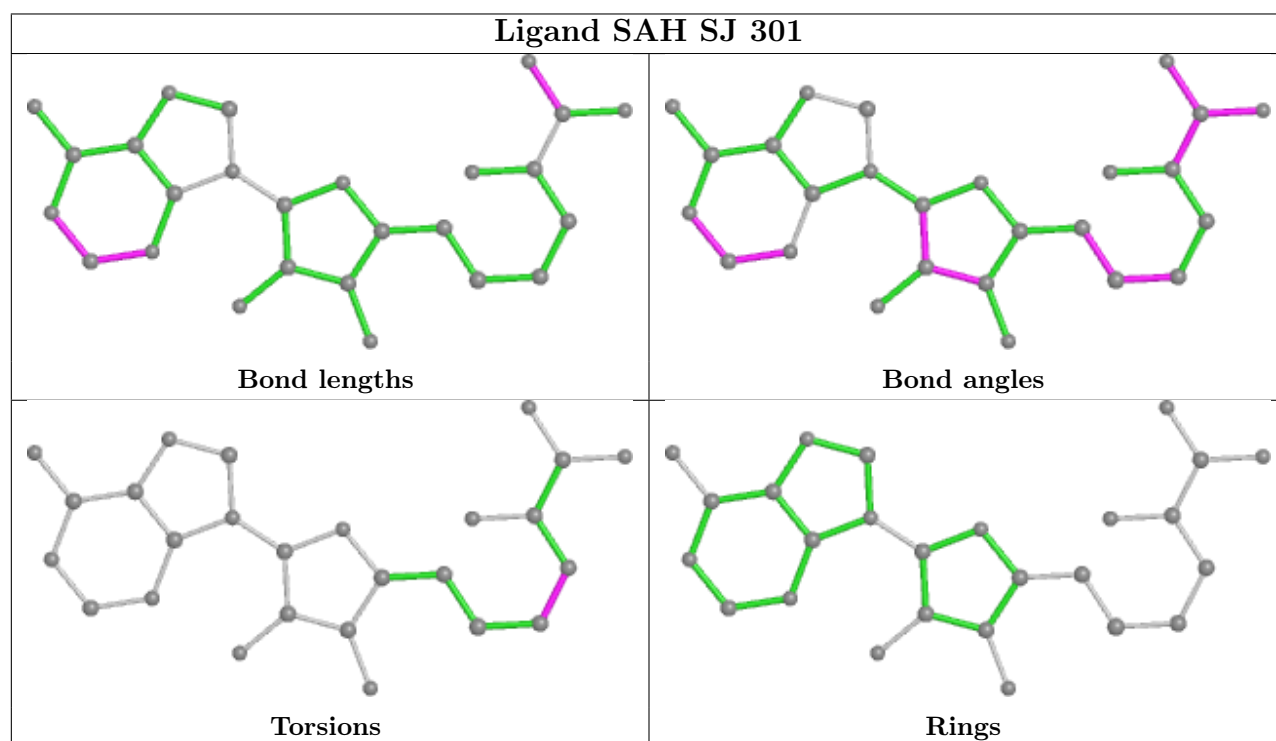
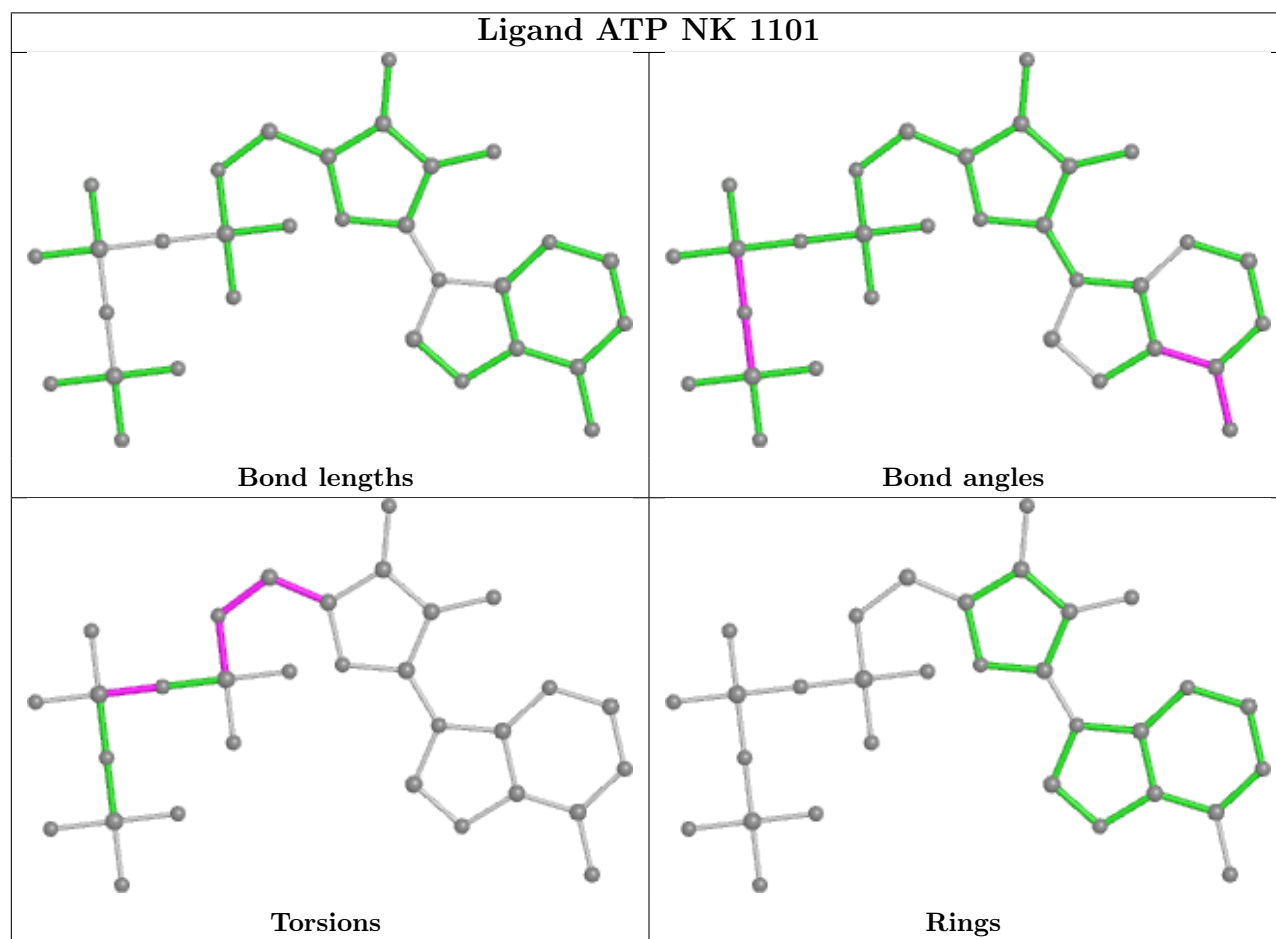
There are no ring outliers.

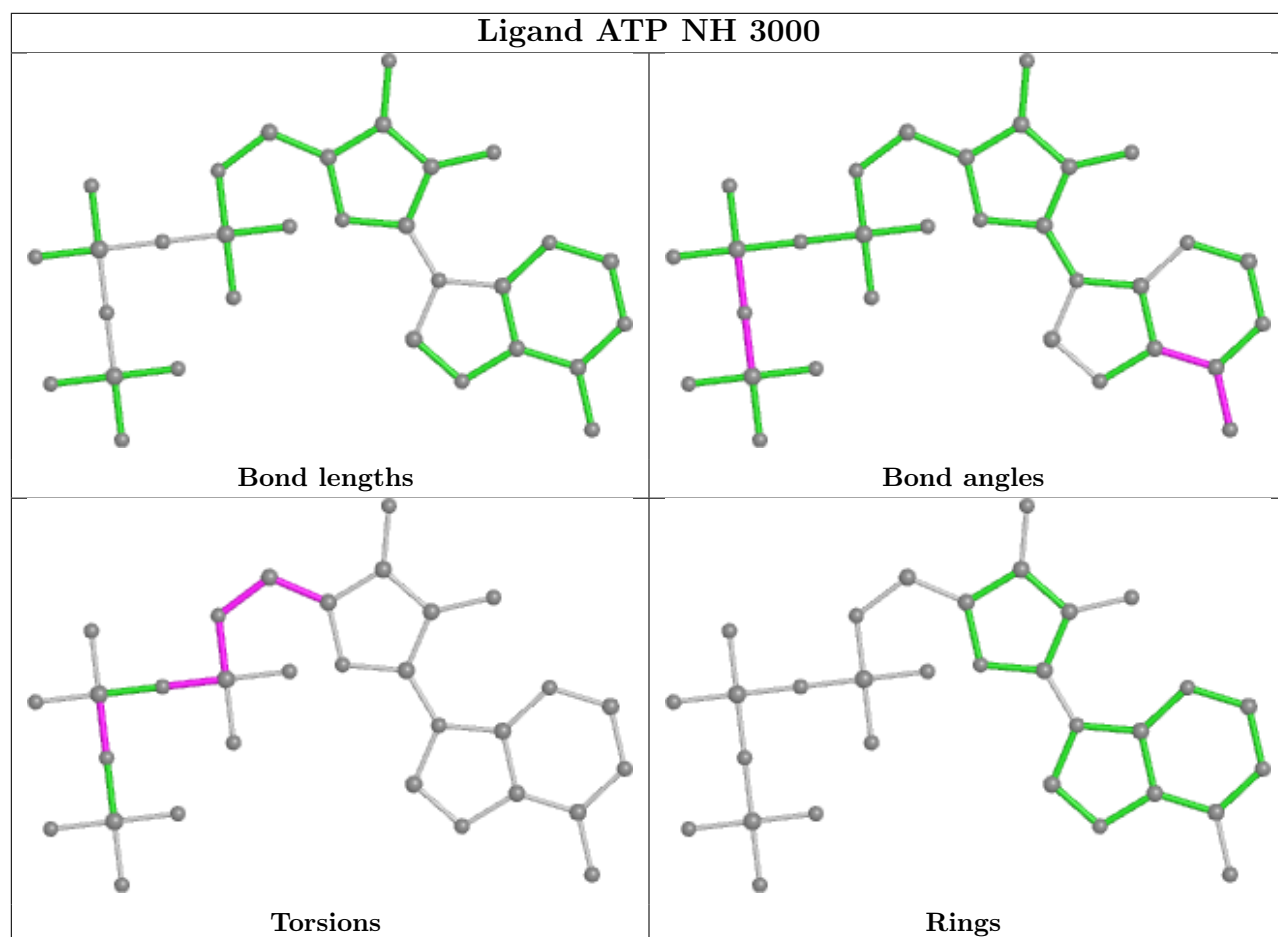
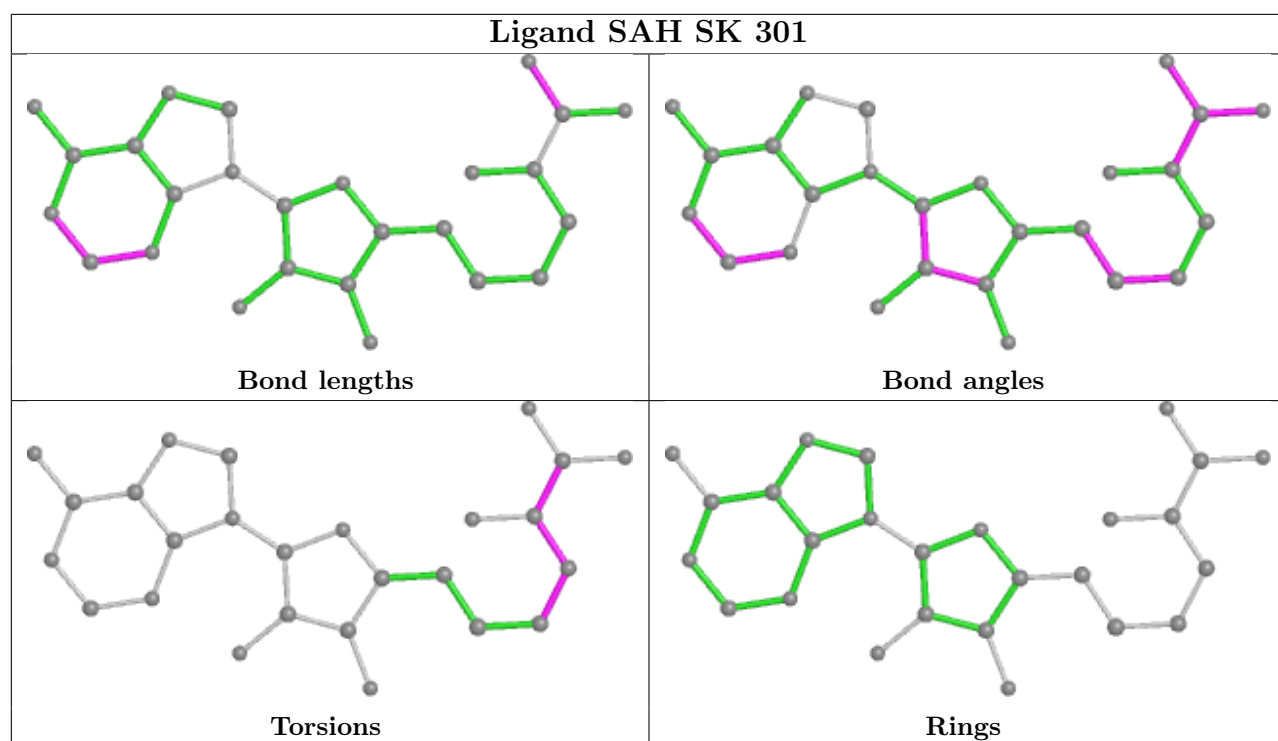
3 monomers are involved in 5 short contacts:

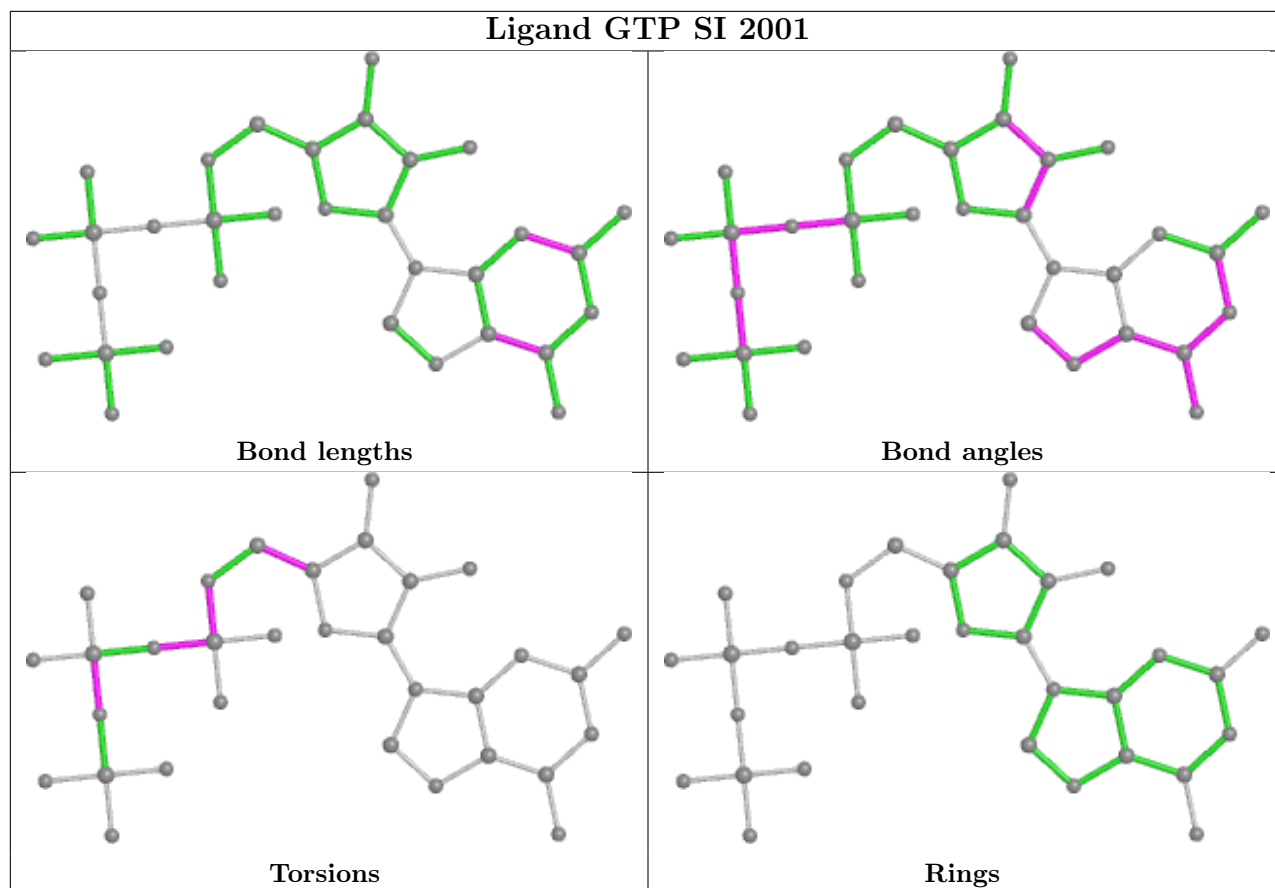
Mol	Chain	Res	Type	Clashes	Symm-Clashes
73	SJ	301	SAH	2	0
73	SK	301	SAH	2	0
72	SI	2001	GTP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [\(i\)](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
40	NR	41
56	SX	6
17	LI	5
67	SU	5
66	ST	3
62	N0	1
69	SZ	1

The worst 5 of 62 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	SX	726:UNK	C	1200:UNK	N	185.33
1	ST	298:LEU	C	414:UNK	N	53.15
1	SX	1269:UNK	C	1298:UNK	N	38.21
1	ST	86:LYS	C	186:UNK	N	37.03
1	SX	1427:UNK	C	1449:UNK	N	35.78

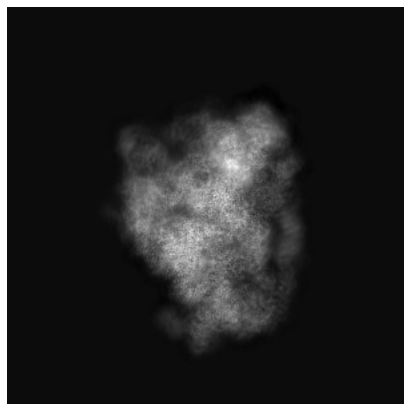
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23937. These allow visual inspection of the internal detail of the map and identification of artifacts.

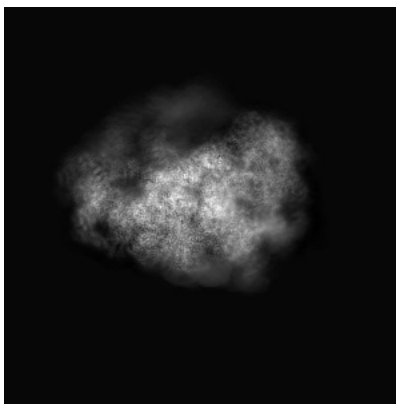
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

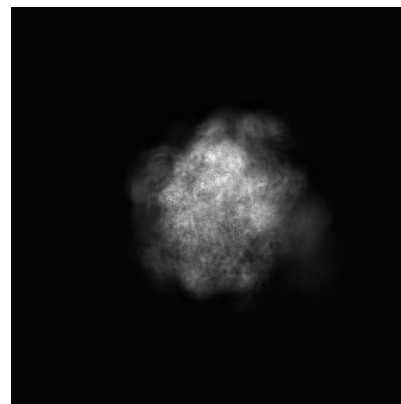
6.1.1 Primary map



X

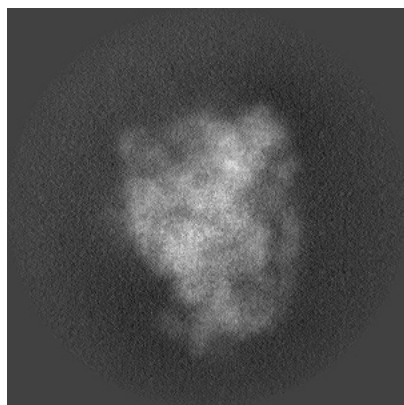


Y

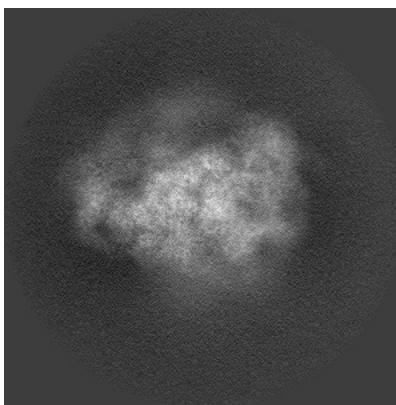


Z

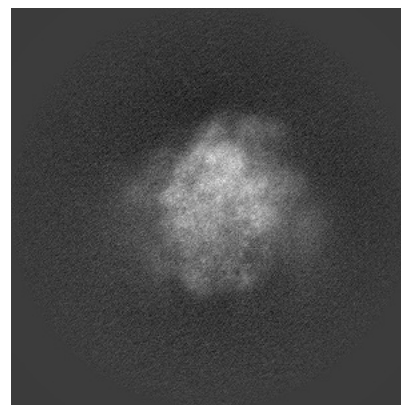
6.1.2 Raw map



X



Y

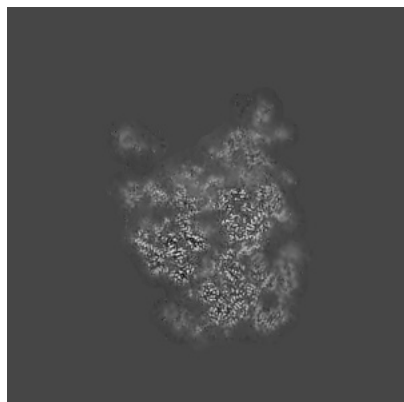


Z

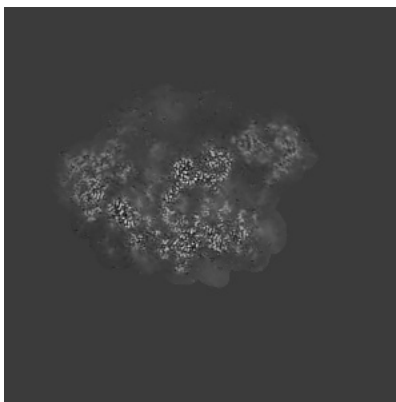
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

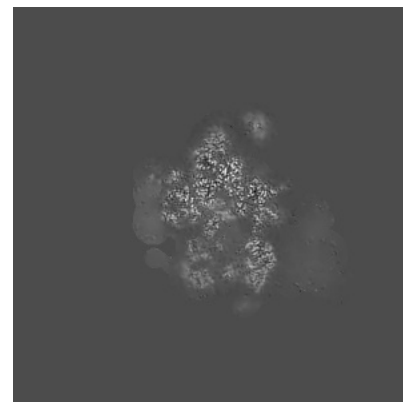
6.2.1 Primary map



X Index: 280

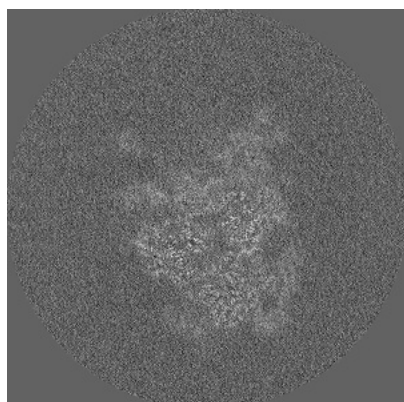


Y Index: 280

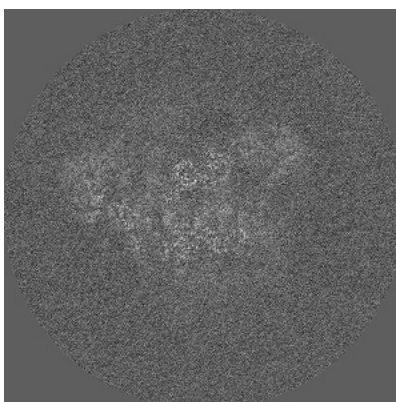


Z Index: 280

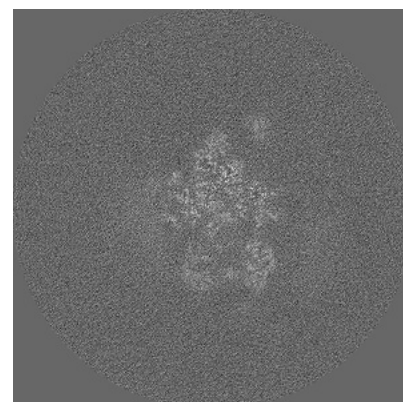
6.2.2 Raw map



X Index: 280



Y Index: 280

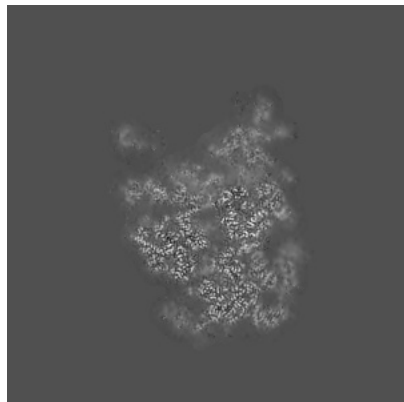


Z Index: 280

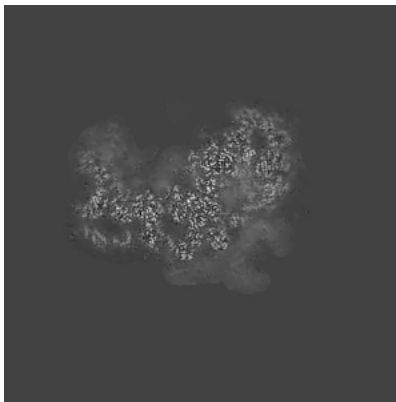
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

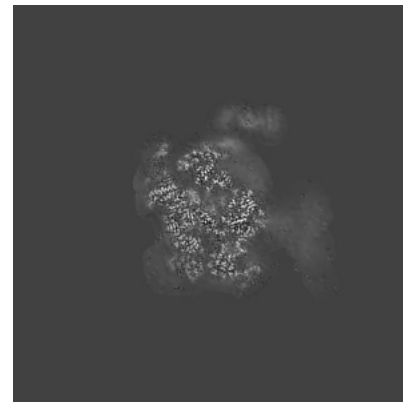
6.3.1 Primary map



X Index: 281

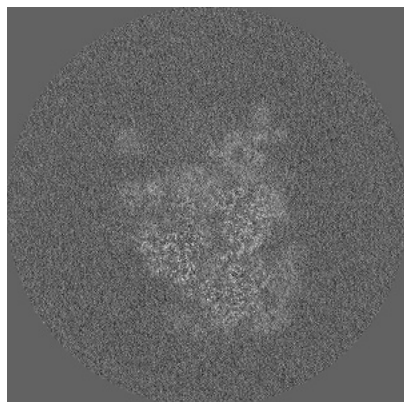


Y Index: 310

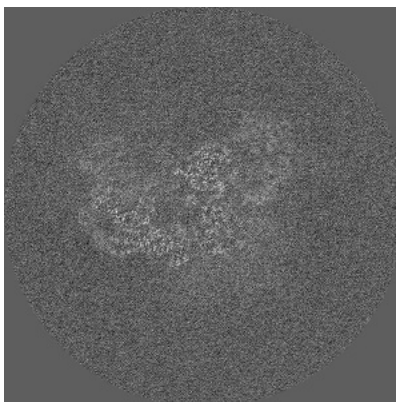


Z Index: 244

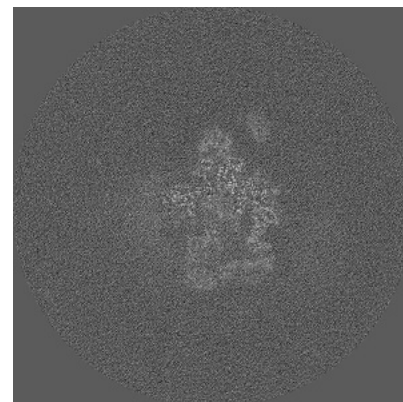
6.3.2 Raw map



X Index: 278



Y Index: 298



Z Index: 285

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



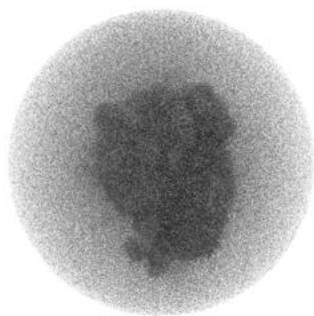
Y



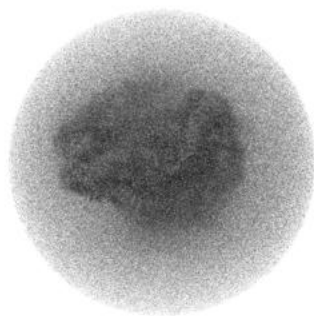
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0088. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

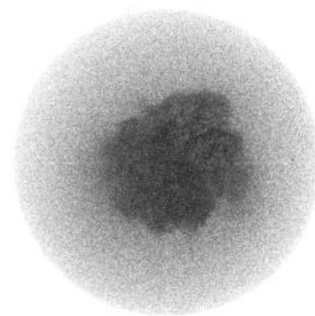
6.4.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

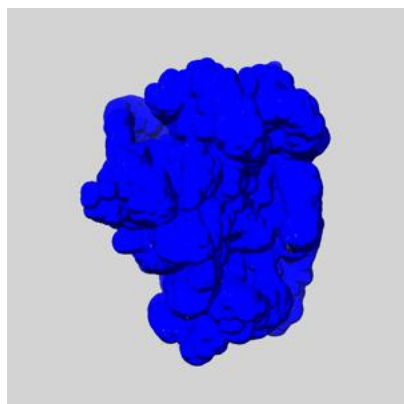
6.5 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

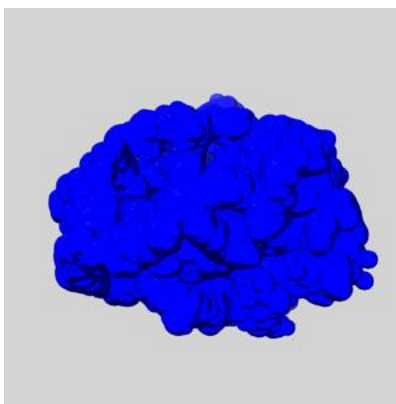
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

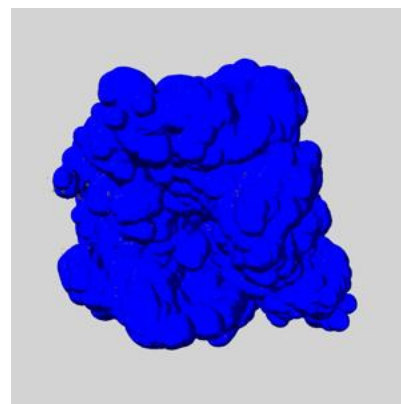
6.5.1 emd_23937_msk_1.map [i](#)



X



Y

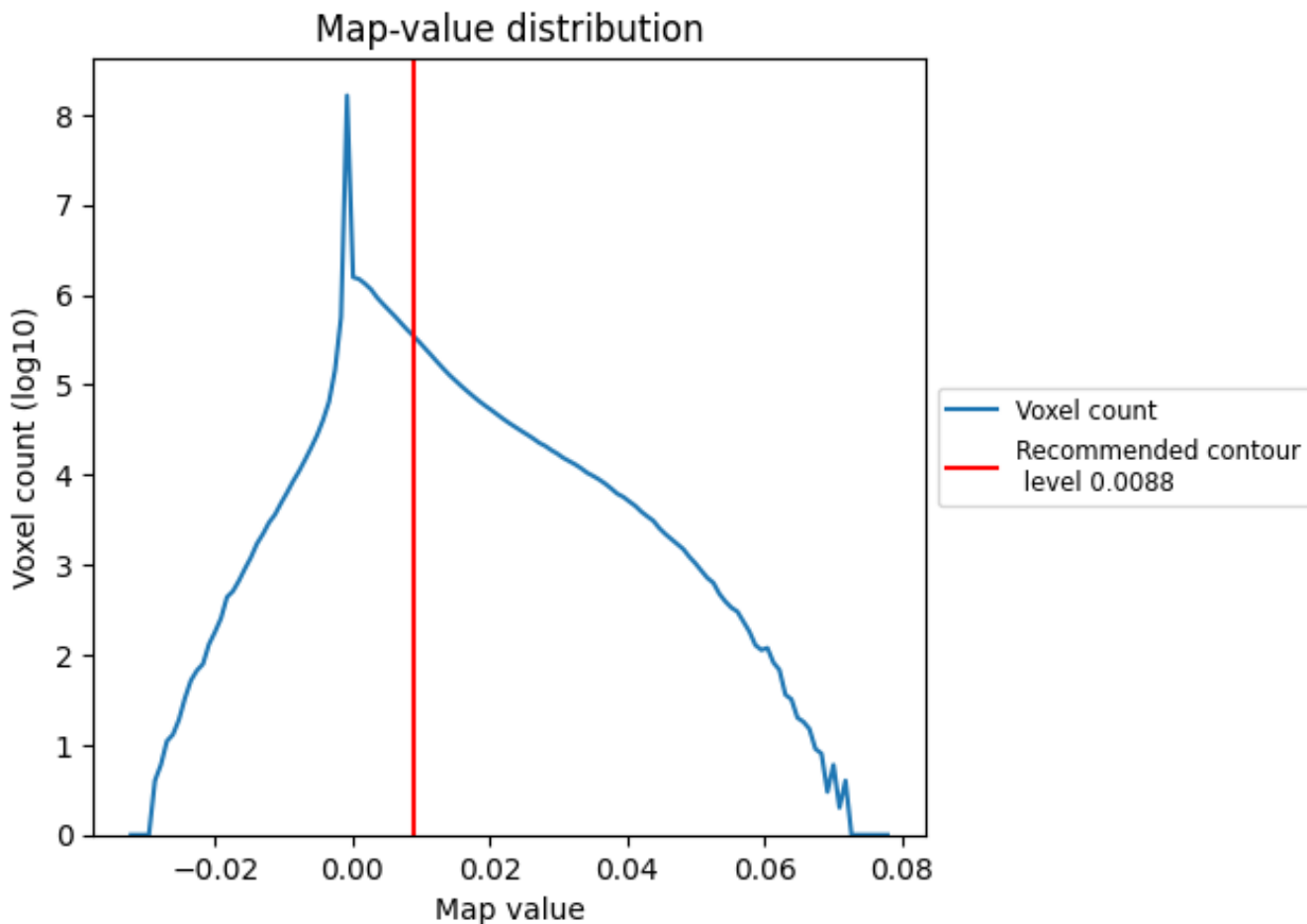


Z

7 Map analysis [i](#)

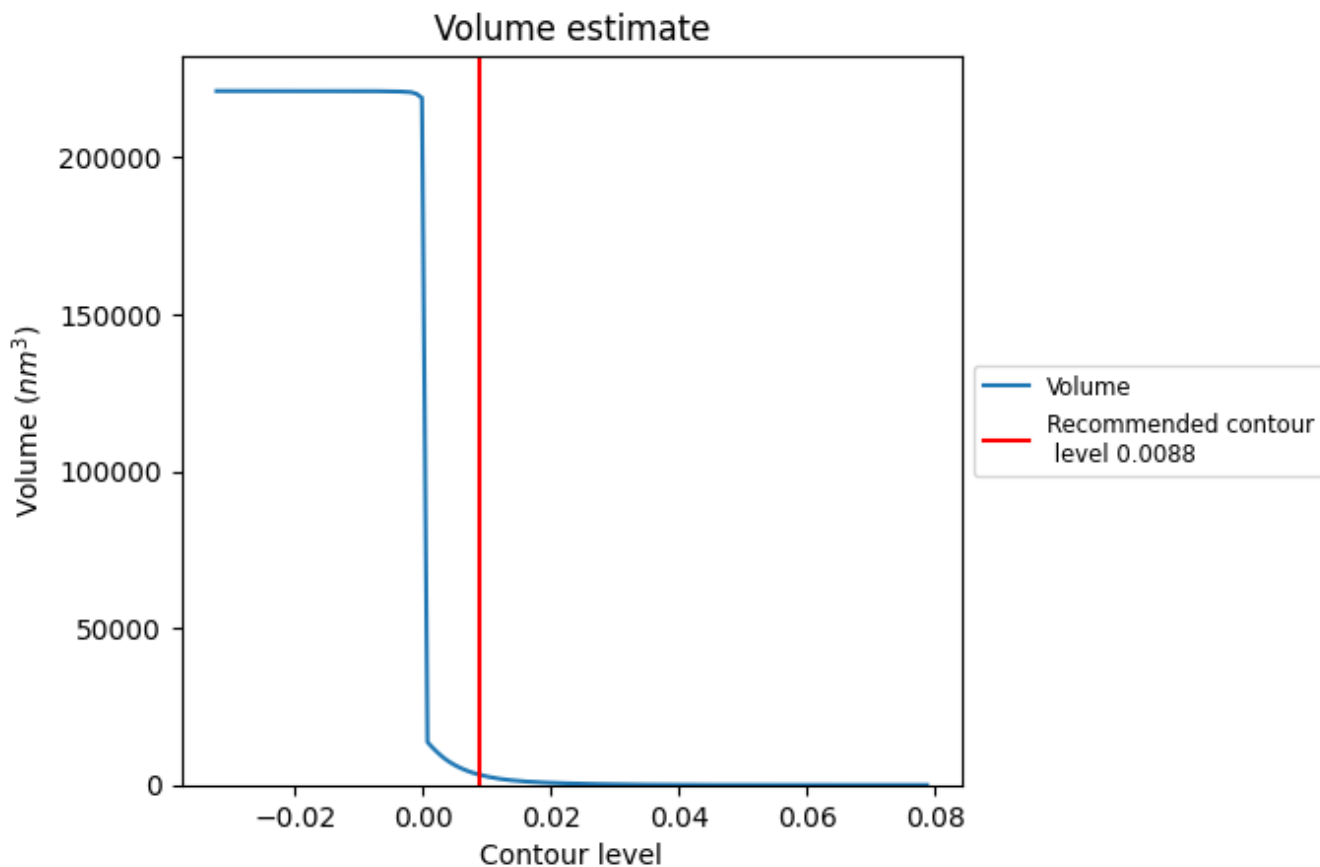
This section contains the results of statistical analysis of the map.

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.

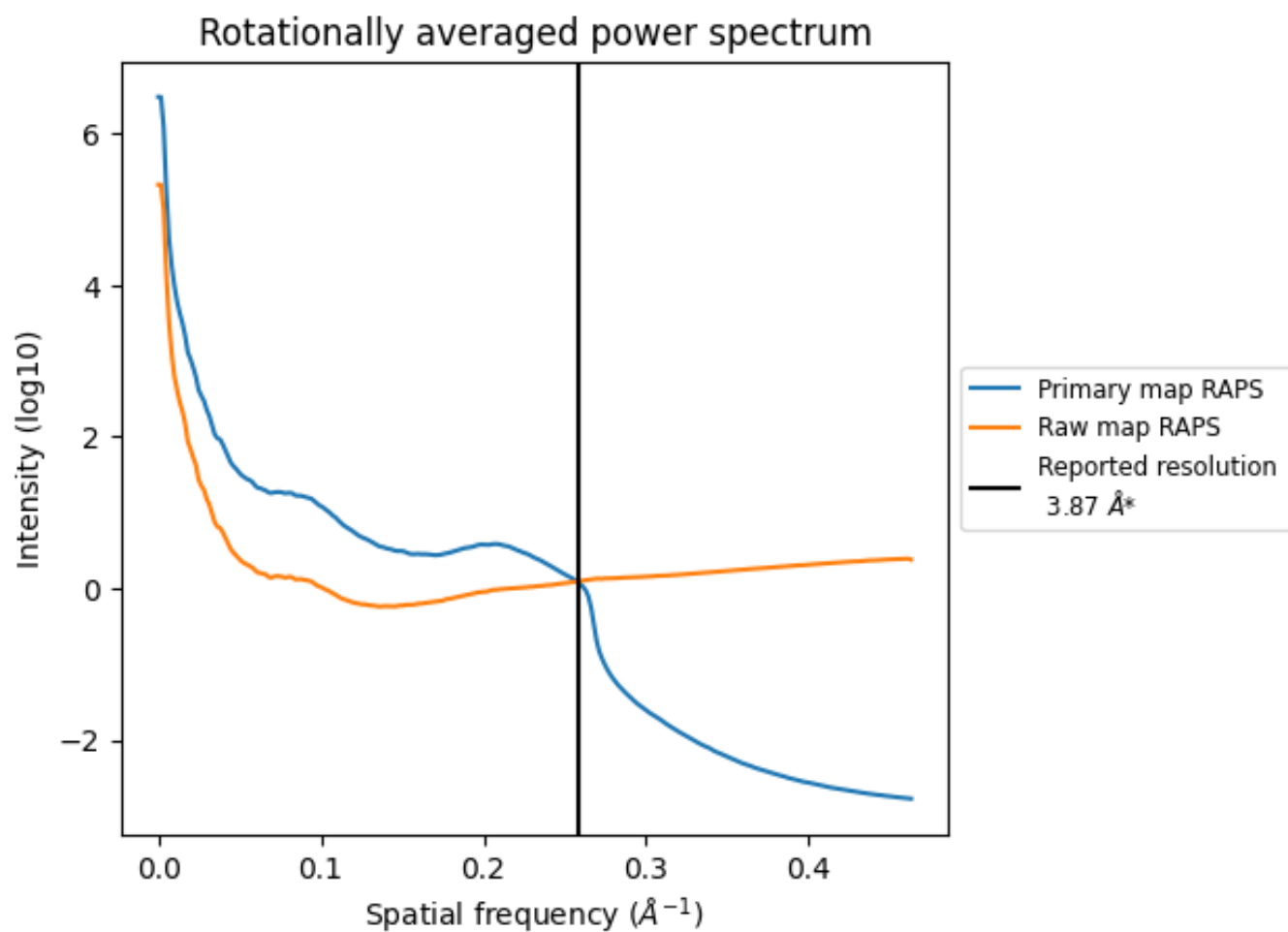
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 3275 nm^3 ; this corresponds to an approximate mass of 2958 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

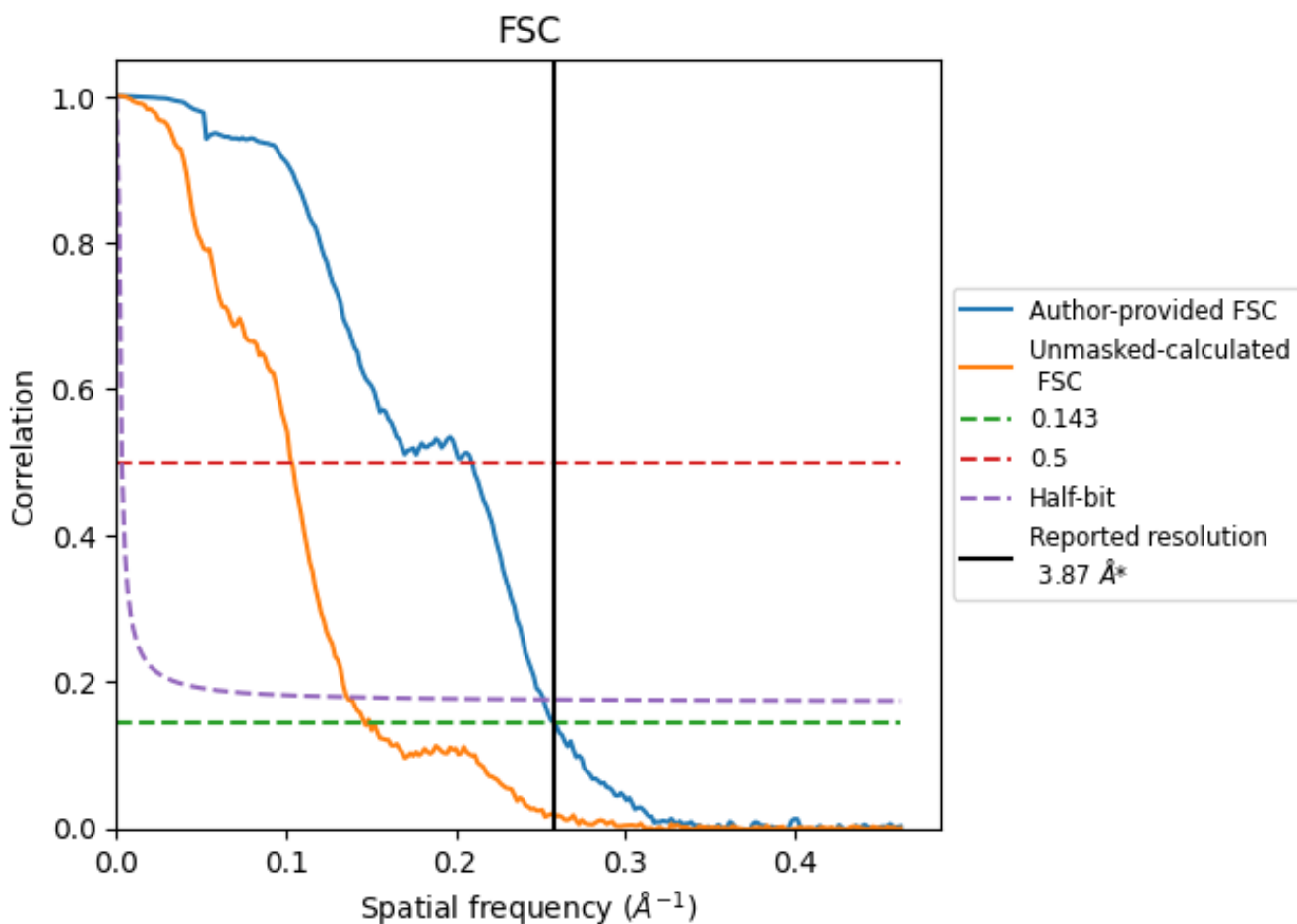


*Reported resolution corresponds to spatial frequency of 0.258 Å⁻¹

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 0.258 Å⁻¹

8.2 Resolution estimates [i](#)

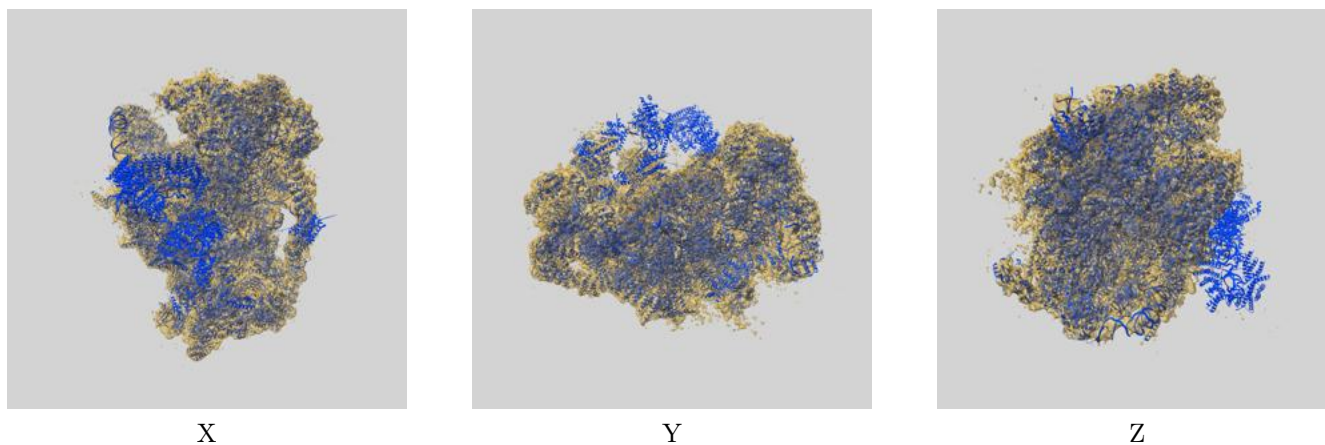
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.87	-	-
Author-provided FSC curve	3.87	4.77	3.97
Unmasked-calculated*	6.83	9.67	7.34

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.83 differs from the reported value 3.87 by more than 10 %

9 Map-model fit [i](#)

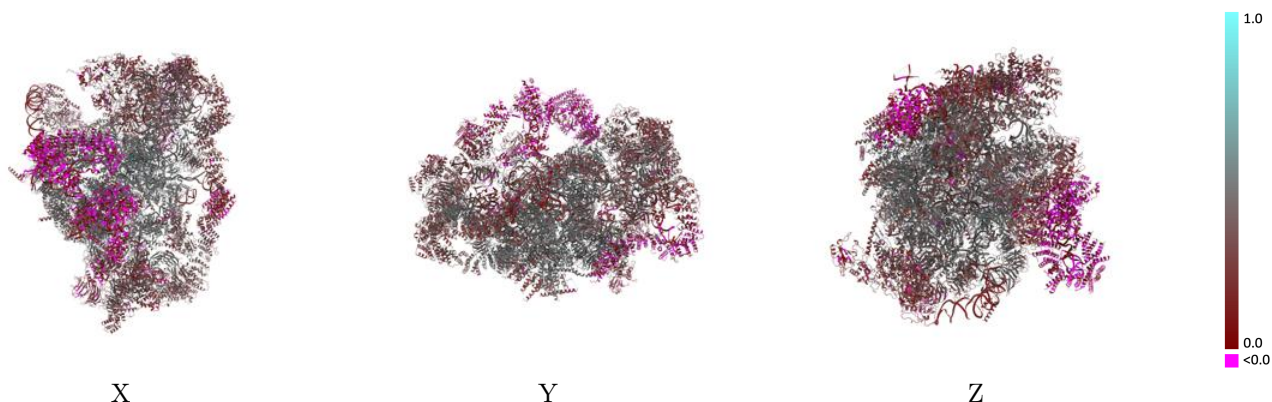
This section contains information regarding the fit between EMDB map EMD-23937 and PDB model 7MQ9. Per-residue inclusion information can be found in section 3 on page 19.

9.1 Map-model overlay [i](#)



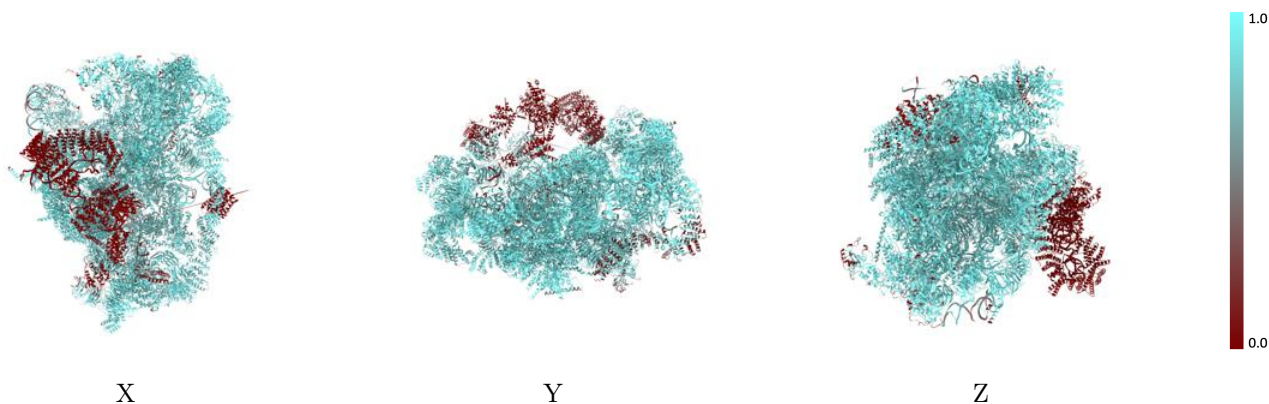
The images above show the 3D surface view of the map at the recommended contour level 0.0088 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



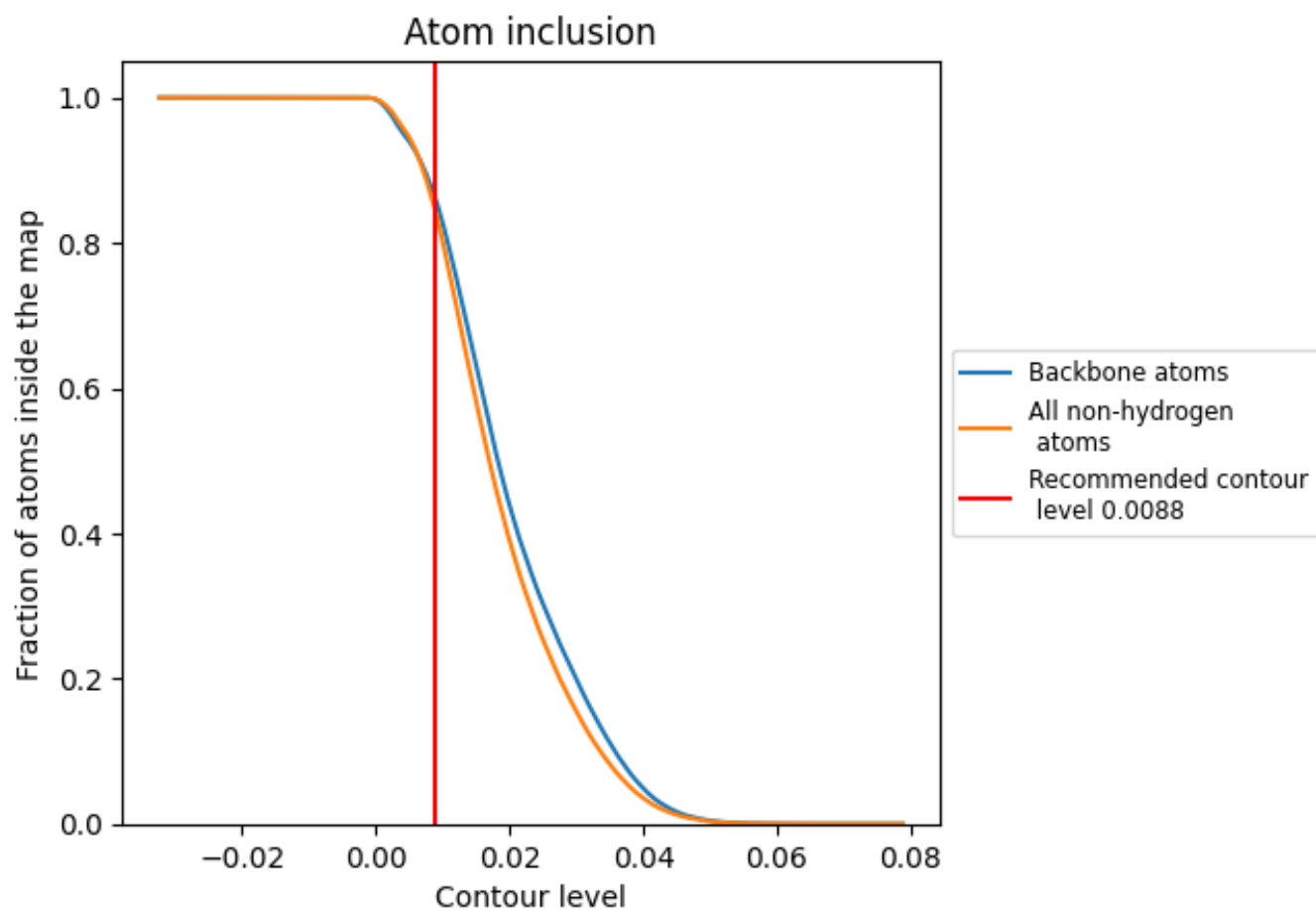
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0088).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 85% 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 (0.0088) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8484	 0.3570
L0	 0.7814	 0.3070
L1	 0.8022	 0.3010
L2	 0.9305	 0.3620
L3	 0.0543	 0.0690
L4	 0.9618	 0.4020
L5	 0.9616	 0.4680
L6	 0.9006	 0.3800
L7	 0.8445	 0.3190
L8	 0.9422	 0.3350
L9	 0.9752	 0.4920
LA	 0.0000	 0.0350
LC	 0.9671	 0.4890
LD	 0.8486	 0.2650
LF	 0.9710	 0.4790
LG	 0.9638	 0.4600
LH	 0.9374	 0.4120
LI	 0.7723	 0.2440
LJ	 0.9200	 0.3950
LK	 0.7908	 0.2460
LL	 0.9254	 0.4090
LM	 0.8783	 0.3190
LN	 0.9415	 0.4040
LO	 0.9584	 0.4870
LP	 0.9321	 0.4120
LQ	 0.9328	 0.4070
LR	 0.9678	 0.3720
LS	 0.9510	 0.4730
LT	 0.9504	 0.4740
LU	 0.9552	 0.4700
LW	 0.9430	 0.4660
LZ	 0.9620	 0.4890
N0	 0.8447	 0.3530
NA	 0.9347	 0.4610
NB	 0.9863	 0.5220



Continued on next page...

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Chain	Atom inclusion	Q-score
ND	 0.8497	 0.3200
NE	 0.9109	 0.3650
NF	 0.9400	 0.4260
NG	 0.9573	 0.4040
NH	 0.8267	 0.2540
NI	 0.6592	 0.2380
NJ	 0.8670	 0.3300
NK	 0.8966	 0.2710
NM	 0.8995	 0.3880
NN	 0.8278	 0.2710
NO	 0.9485	 0.4490
NQ	 0.9603	 0.4610
NR	 0.0002	 0.0250
NT	 0.0000	 0.0080
NU	 0.0000	 0.0840
NW	 0.9186	 0.3650
NY	 0.8968	 0.3690
SA	 0.9493	 0.4350
SB	 0.9130	 0.4100
SC	 0.8957	 0.2880
SD	 0.9789	 0.5160
SE	 0.9717	 0.4910
SF	 0.9649	 0.4780
SG	 0.9358	 0.3800
SH	 0.9593	 0.4780
SI	 0.9545	 0.4650
SJ	 0.7988	 0.2380
SK	 0.8230	 0.3470
SL	 0.9702	 0.4910
SM	 0.9655	 0.4940
SP	 0.7961	 0.2360
SQ	 0.9286	 0.4500
SR	 0.9676	 0.4990
SS	 0.8887	 0.4050
ST	 0.3477	 0.1920
SU	 0.5124	 0.2310
SW	 0.9169	 0.3890
SX	 0.2249	 0.1000
SY	 0.9217	 0.3800
SZ	 0.0062	 0.0400