wwPDB EM Validation Summary Report (i)

Mar 25, 2026 – 08:29 PM UTC

PDB ID	:	7MQ9 / pdb_00007mq9
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	:	6ZOJ, 6G18, 5FAI, 2IPX, 6G4S, 4JXM, 6ZQD, 5WLC, 2OZB

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

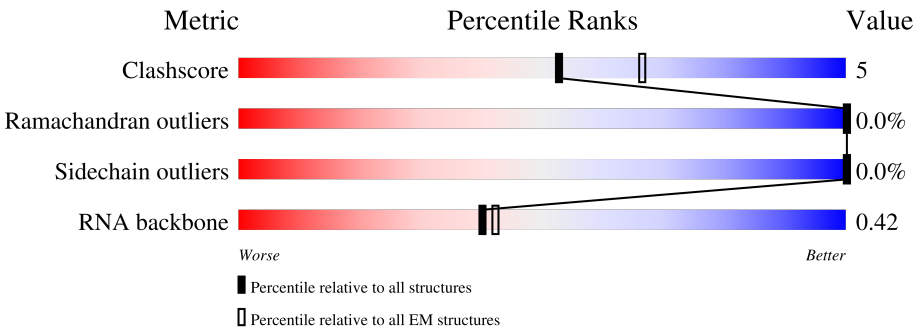
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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

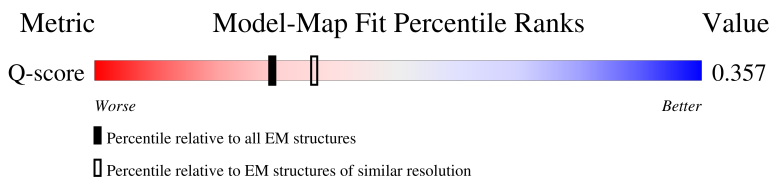
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.87 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)	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	8831 (3.37 - 4.37)

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

Mol	Chain	Length	Quality of chain
1	L0	3617	93%
2	L1	1872	12%, 36%, 29%, 31%
3	L2	217	43%, 47%, 8%

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Mol	Chain	Length	Quality of chain
4	L3	116	96% / 99%
5	L4	263	78% / 13% / 9%
6	L5	204	78% / 15% / 7%
7	L6	249	69% / 20% / 10%
8	L7	194	75% / 12% / 13%
9	L8	208	72% / 14% / 13%
10	L9	194	74% / 14% / 12%
11	LA	132	91% / 89% / 9%
12	LC	146	84% / 12% / 5%
13	LD	158	7% / 84% / 9% / 7%
14	LF	133	71% / 8% / 22%
15	LG	69	75% / 13% / 10%
16	LH	830	74% / 15% / 10%
17	LI	699	15% / 76% / 23%
18	LJ	518	72% / 18% / 9%
19	LK	677	14% / 83%
19	LL	677	60% / 15% / 25%
20	LN	686	80% / 18%
21	LO	919	79% / 13% / 8%
22	LP	597	85% / 10% / 5%
23	LQ	943	70% / 18% / 12%
24	LS	556	67% / 15% / 19%
25	LT	951	80% / 11% / 9%
26	LU	445	81% / 19%
27	LW	610	64% / 10% / 26%

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Mol	Chain	Length	Quality of chain
28	LZ	184	88% 12%
29	NA	681	31% 5% 63%
30	NB	479	13% 85%
31	ND	257	30% 67%
32	NE	293	30% 66%
33	NF	151	89% 10%
34	NG	151	64% 13% 23%
35	NJ	1025	68% 13% 19%
35	NK	1025	5% 79% 20%
36	NM	264	74% 14% 12%
37	NN	560	6% 92%
38	NO	130	86% 13%
39	NQ	84	90% 7%
40	NR	861	100% 99%
41	NT	156	37% 37% 63%
42	NU	135	44% 44% 56%
43	NW	688	34% 12% 55%
44	SA	594	58% 8% 33%
45	SB	529	67% 16% 17%
46	SC	321	57% 14% 29%
46	SD	321	65% 8% 26%
47	SE	128	89% 9%
47	SF	128	90% 6%
48	SH	373	85% 14%
49	SI	1282	56% 10% 34%

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Mol	Chain	Length	Quality of chain
50	SJ	244	9% 84% 16%
50	SK	244	66% 17% 16%
51	SL	198	81% 16%
52	SM	291	90% 10%
53	SQ	756	23% 75%
54	SR	143	64% 12% 24%
55	SS	771	22% 74%
56	SX	177	80% 99%
57	SY	253	83% 11% 6%
58	NH	1146	11% 93% 7%
59	SP	2785	13% 69% 28%
60	LR	808	91% 5%
61	LM	2144	84% 9% 6%
62	N0	22	5% 82% 18%
63	SG	475	71% 11% 18%
64	NI	280	24% 79% 5% 16%
65	SW	252	71% 29%
66	ST	632	62% 87% 10%
67	SU	472	39% 88% 12%
68	NY	381	61% 11% 28%
69	SZ	304	95% 92% 5%

2 Entry composition (i)

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
			Total	C	N	O	S		
14	LF	104	851	543	158	145	5	0	0

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

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

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

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

- Molecule 17 is a protein called Nucleolar protein 11.

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
35	NJ	827	6526	4187	1126	1178	35	0	0
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
			Total	C	N	O	S		
36	NM	233	1873	1186	339	334	14	0	0

- Molecule 37 is a protein called Protein AATF.

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

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

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

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

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

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

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

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

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

- 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 fibrillarin.

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
			Total	C	N	O			
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

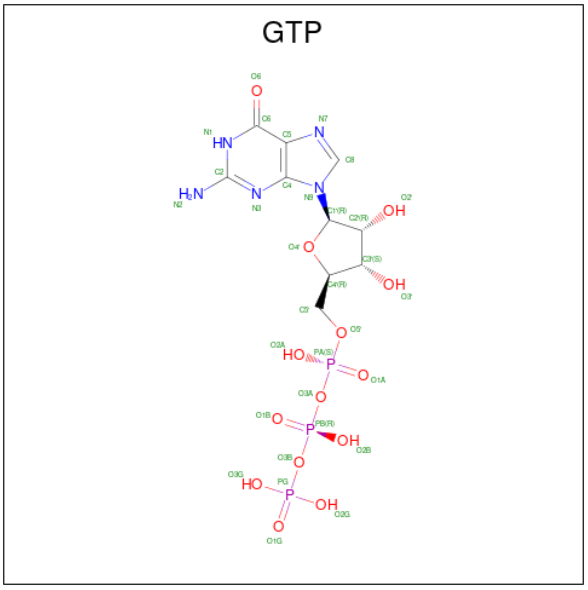
- Molecule 70 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 71 is ZINC ION (CCD ID: ZN) (formula: Zn).

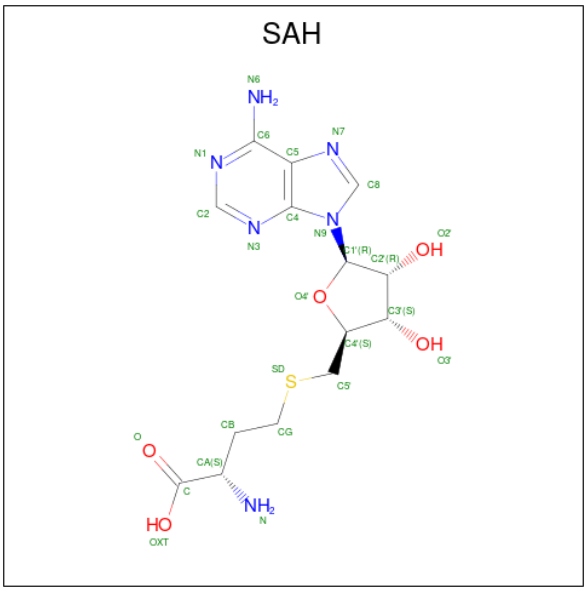
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
71	NQ	1	1	1	0
			Total	Zn	
71	NT	1	1	1	0
			Total	Zn	
71	SL	1	1	1	0

- Molecule 72 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



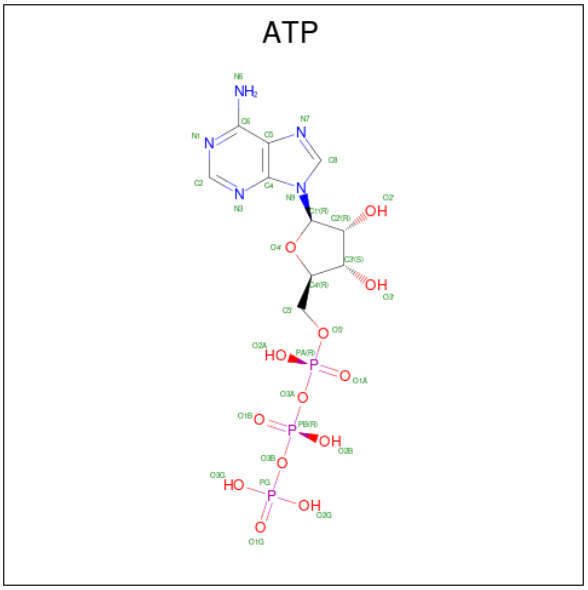
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
72	SI	1	32	10	5	14	3	0

- Molecule 73 is S-ADENOSYL-L-HOMOCYSTEINE (CCD ID: SAH) (formula: $C_{14}H_{20}N_6O_5S$).



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

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



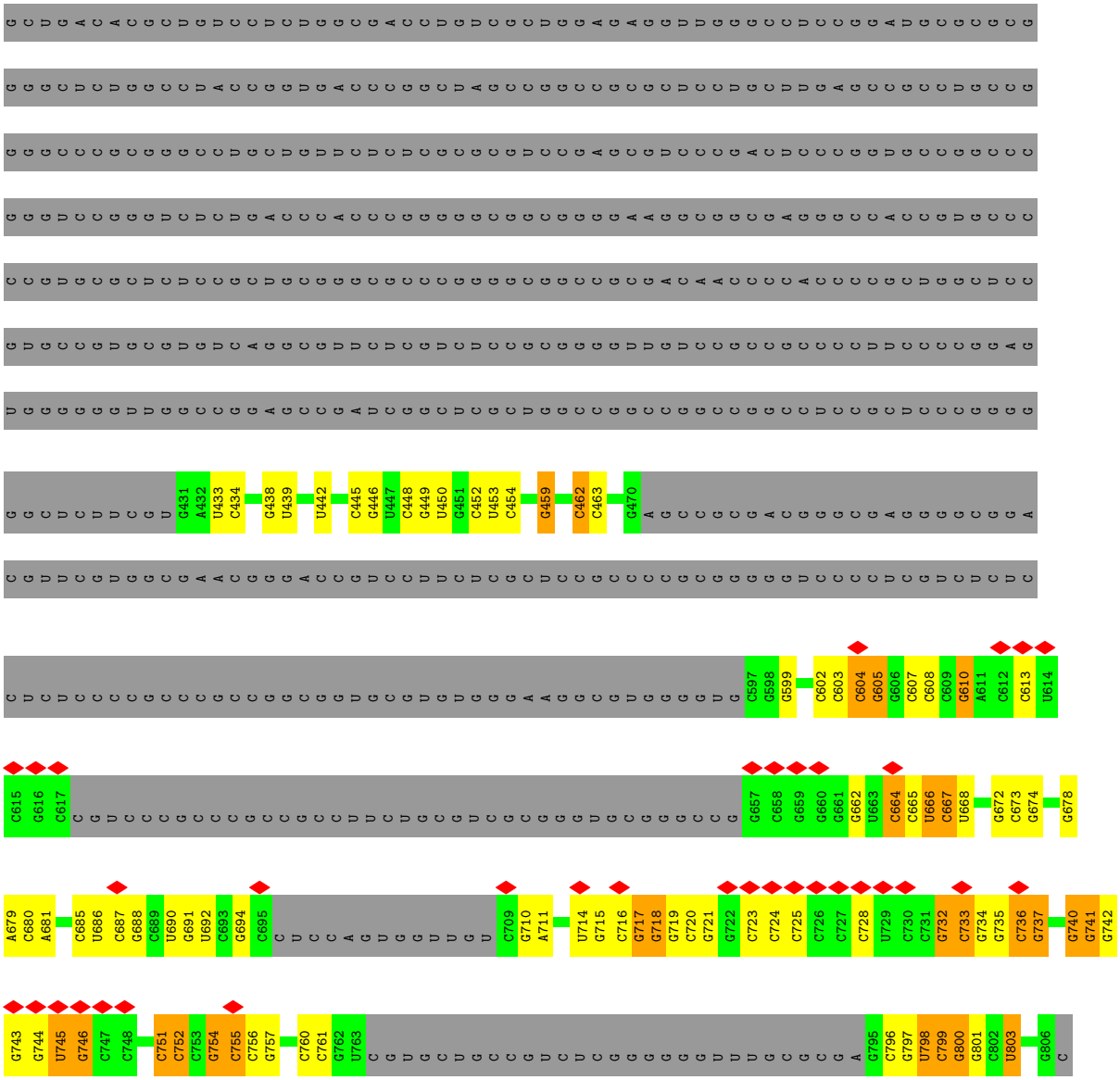
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
74	NH	1	31	10	5	13	3	0
			Total	C	N	O	P	
74	NK	1	31	10	5	13	3	0

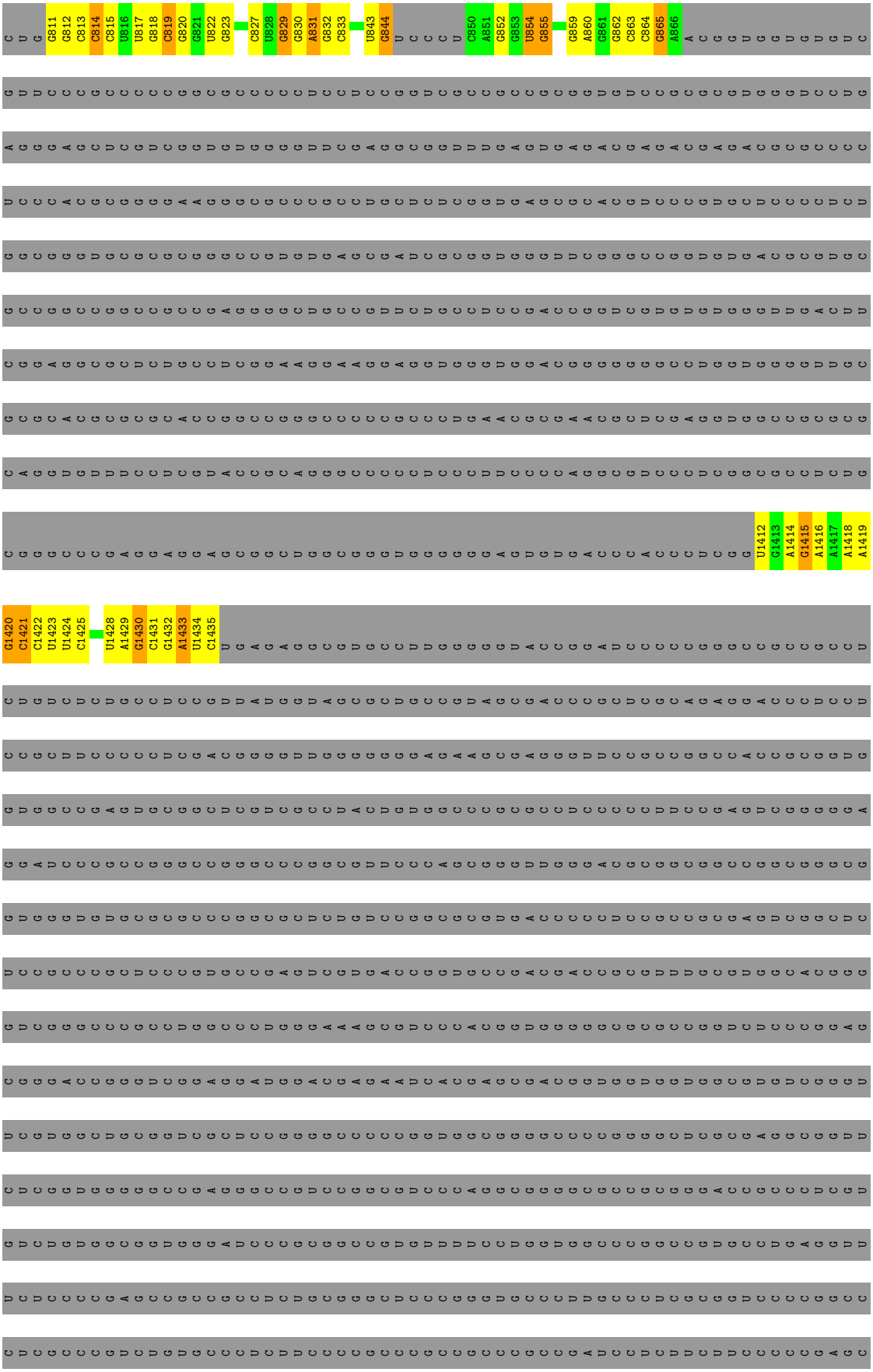
3 Residue-property plots (i)

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

- Molecule 1: 5'ETS rRNA

Chain L0: 93%




G811
G812
G813
C814
C815
U816
U817
G818
C819
G820
G821
U822
G823
C827
U828
G829
G830
A831
G832
C833
U843
G844
C850
A851
G852
G853
U854
G855
G859
A860
G861
G862
C863
C864
G865
A866
U1412
G1413
A1414
G1415
A1416
A1417
A1418
A1419
G1420
C1421
C1422
U1423
U1424
C1425
U1428
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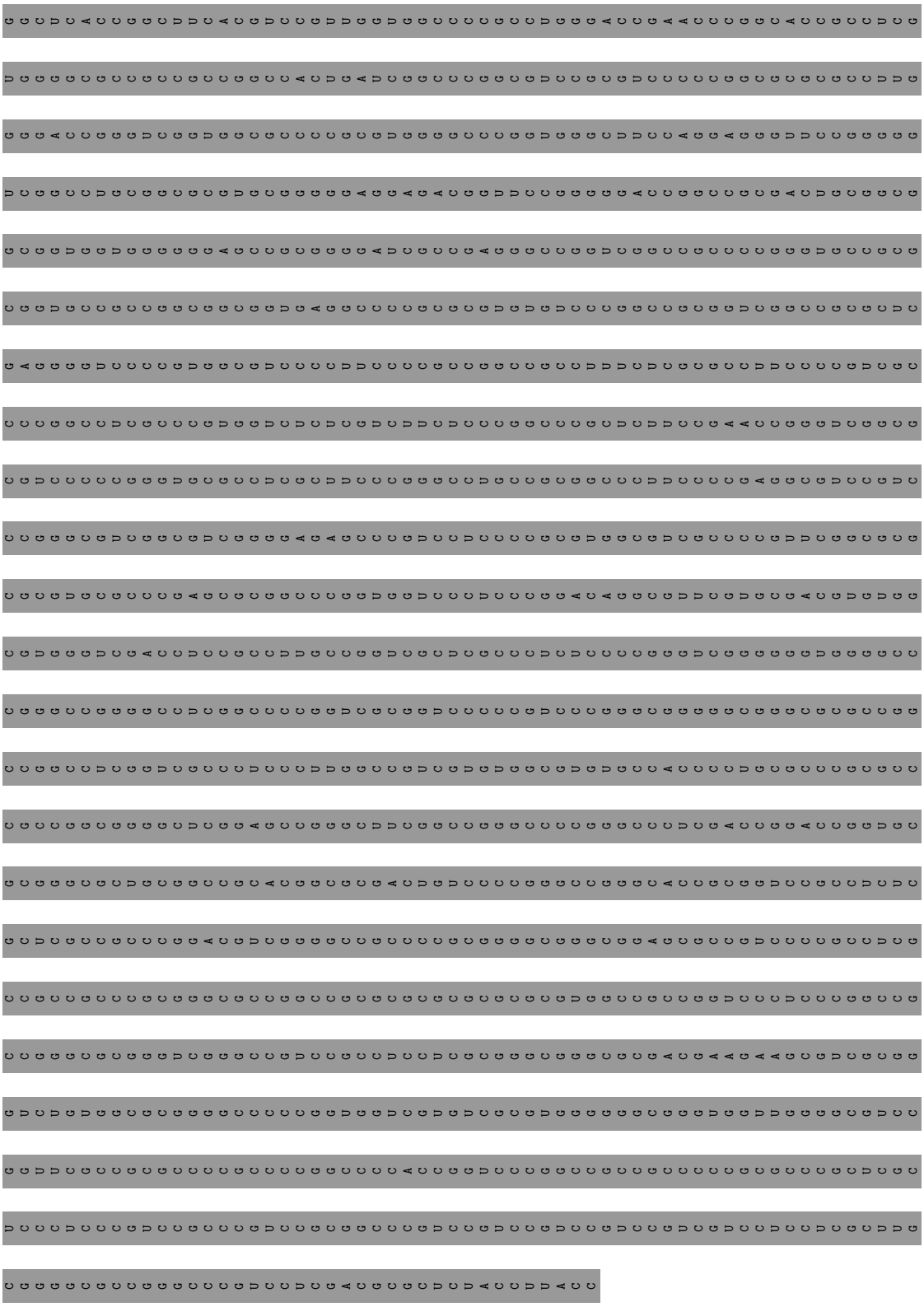
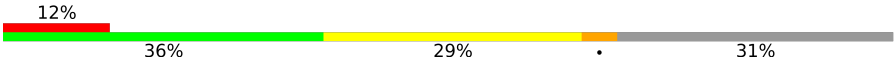
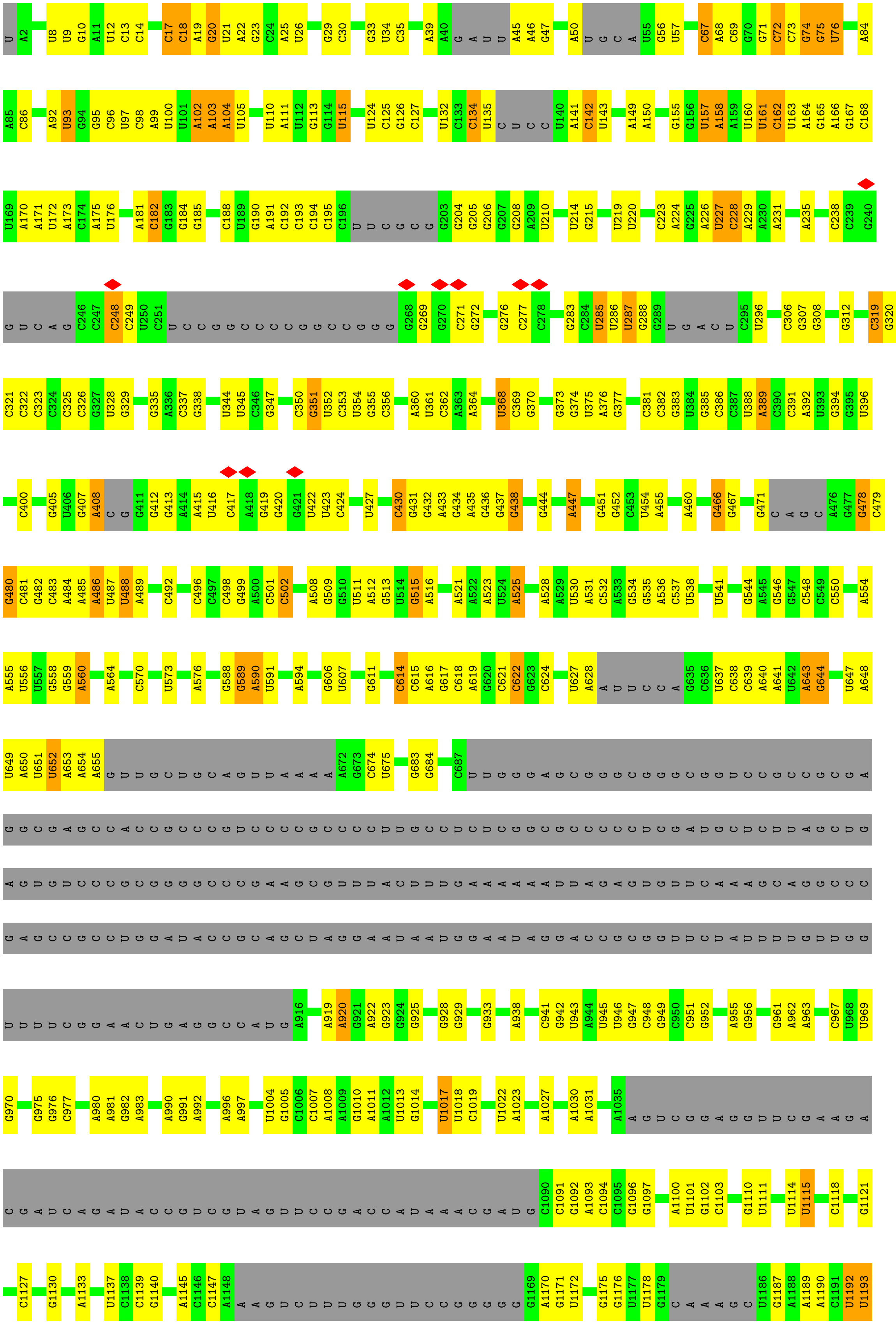
G1430
C1431
G1432
A1433
U1434
C1435



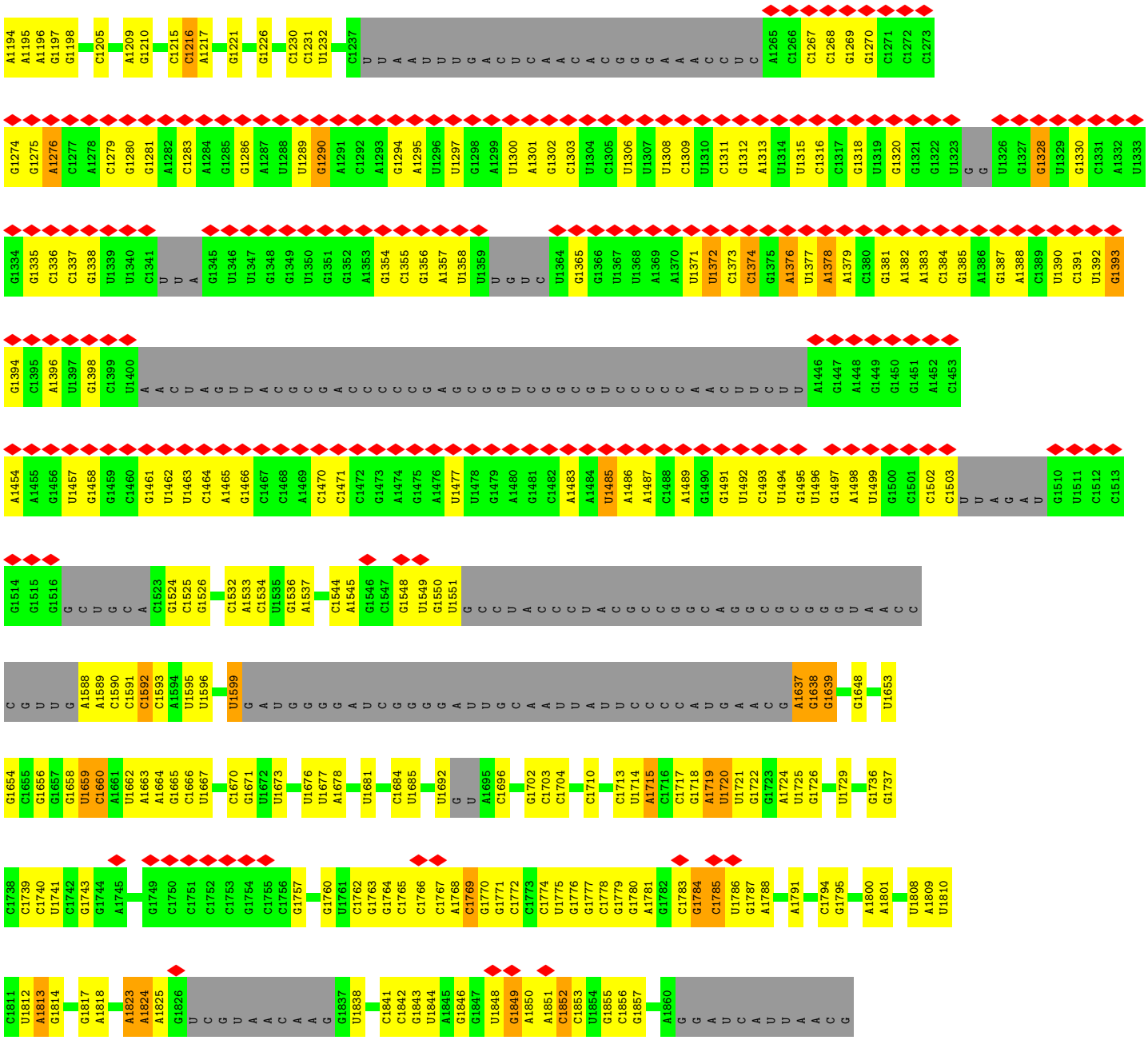
- Molecule 2: 18S rRNA

Chain L1:



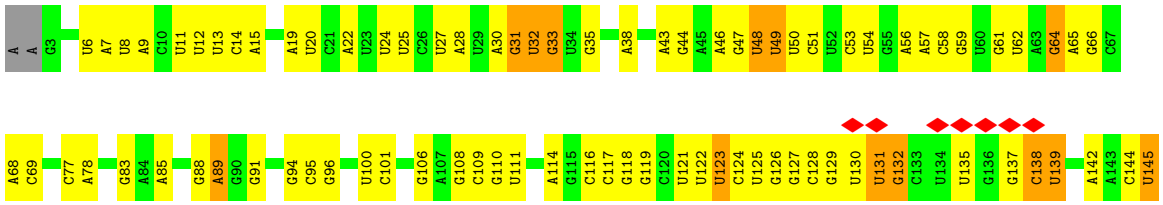


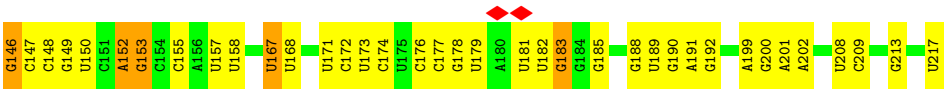
U A2 U8 U9 G10 A11 U12 C13 C14 C17 C18 A19 G20 U21 A22 G23 C24 A25 U26 G29 C30 G33 U34 C35 A39 A40 G A U U A45 A46 G47 A50 U G C A U55 G56 U57 C67 A68 C69 G70 G71 C72 C73 G74 G75 U76 A84
A85 C86 A92 U93 G94 G95 C96 U97 C98 A99 U100 U101 A102 A103 A104 U105 U110 A111 U112 G113 G114 U115 U124 C125 G126 C127 U132 C133 C134 U135 C U C C U140 A141 C142 U143 A149 A150 G155 G156 U157 A158 A159 U160 U161 C162 U163 A164 G165 A166 G167 C168
U169 A170 A171 U172 A173 C174 A175 U176 A181 C182 G183 G184 G185 C188 U189 G190 A191 C192 C193 C194 C195 C196 U U C G C G G203 G204 G205 G206 G207 G208 A209 U210 U214 G215 U219 U220 C223 A224 G225 A226 U227 C228 A229 A230 A231 A235 C238 C239 G240
G U C A G C246 C247 C248 C249 U250 C251 U C C G G C C C C G G C C G G G G268 G269 G270 C271 G272 G276 C277 C278 G283 C284 U285 U286 U287 G288 G289 U G A C U C295 U296 C306 G307 G308 G312 C319 G320
C321 C322 C323 C324 C325 C326 G327 U328 G329 G335 A336 C337 G338 U344 U345 C346 G347 C350 G351 U352 C353 U354 G355 C356 A360 U361 C362 A363 A364 U368 C369 G370 G373 G374 U375 A376 G377 C381 C382 G383 U384 G385 C386 C387 U388 A389 C390 C391 A392 U393 G394 G395 U396
C400 G405 U406 G407 A408 C G G411 G412 G413 A414 A415 U416 C417 A418 G419 G420 G421 U422 U423 C424 U427 C430 G431 G432 A433 G434 A435 G436 G437 G438 G444 A447 G451 G452 C453 U454 A455 A460 G466 G467 G471 C A G C A476 G477 G478 C479
G480 C481 G482 C483 A484 A485 A486 U487 U488 A489 C492 C496 C497 C498 G499 A500 C501 C502 A508 G509 G510 U511 A512 G513 U514 G515 A516 A521 A522 A523 U524 A525 A528 A529 U530 A531 C532 A533 G534 G535 A536 C537 U538 U541 G544 A545 G546 G547 C548 C549 C550 A554
A555 U556 U557 G558 G559 A560 A564 C570 U573 A576 G588 G589 A590 U591 A594 G606 U607 G611 C614 C615 A616 G617 C618 A619 G620 C621 C622 G623 C624 U627 A628 A U U C C A G635 C636 U637 C638 C639 A640 A641 U642 A643 G644 U647 A648
U649 A650 U651 U652 A653 A654 A655 G U U G C U G C A G U U A A A A672 G673 C674 U675 G683 G684 C687 U U G G G A G C G G G C G G G C G G U C C G C C G C G A
G G C G A G C C A C C G C C C G U C C C C G C C C U U G C C U C U C G G C G C C C C U C G A U G C U C U U A G C U G
A G U G U C C C G C G G G G C C C G A A G C G U U U A C U U U G A A A A A U U A G A G U G U U C A A A G C A G G C C C
G A G C C G C C U G G A U A C C G C A G C U A G G A A U A A U G G A A U A G G A C C G C G G U U C U A U U U U G U U G G
U U U U C G G A A C U G A G G C C A U G A916 A919 A920 G921 A922 G923 G924 G925 G928 G929 G933 A938 C941 G942 U943 A944 U945 U946 G947 C948 G949 C950 C951 G952 A955 G956 G961 A962 A963 C967 U968 U969
G970 G975 G976 C977 A980 A981 G982 A983 A990 G991 A992 A996 A997 U1004 G1005 C1006 C1007 A1008 A1009 G1010 A1011 A1012 U1013 G1014 U1017 U1018 C1019 U1022 A1023 A1027 A1030 A1031 A1035 A G U C G G A G G U U C G A A G A
C G A U C A G A U A C C G U C G U A G U U C C G A C C A U A A A C G A U G C1090 C1091 G1092 A1093 C1094 C1095 G1096 G1097 A1100 U1101 G1102 C1103 G1110 U1111 U1114 U1115 C1118 G1121
C1127 G1130 A1133 U1137 C1138 C1139 G1140 A1145 C1146 C1147 A1148 A A G U C U U U G G G U U C C G G G G G G1169 A1170 G1171 U1172 G1175 G1176 U1177 U1178 G1179 C A A A G C U1186 G1187 A1188 A1189 A1190 C1191 U1192 U1193



- Molecule 3: U3 snoRNA

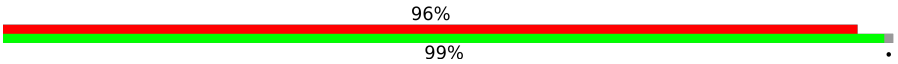
Chain L2:





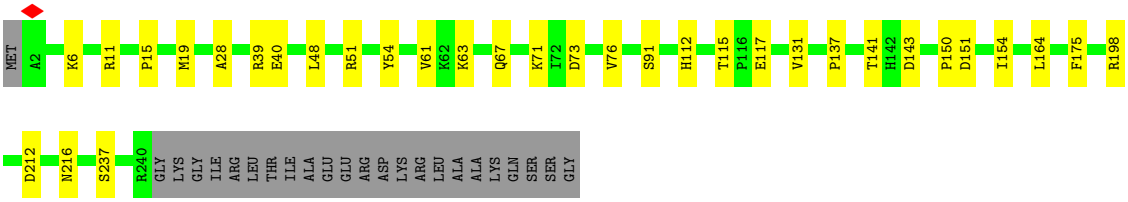
• Molecule 4: 40S ribosomal protein S18

Chain L3:



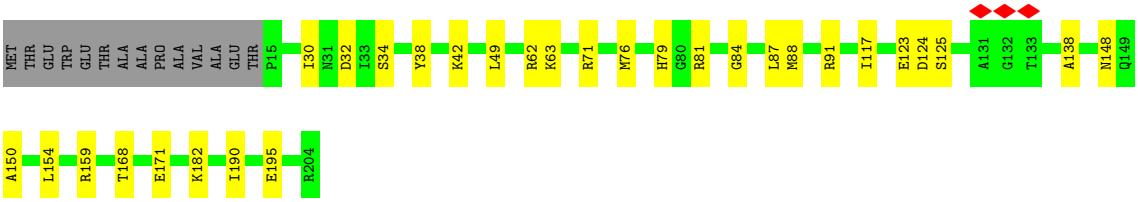
• Molecule 5: 40S ribosomal protein S4 X isoform

Chain L4:



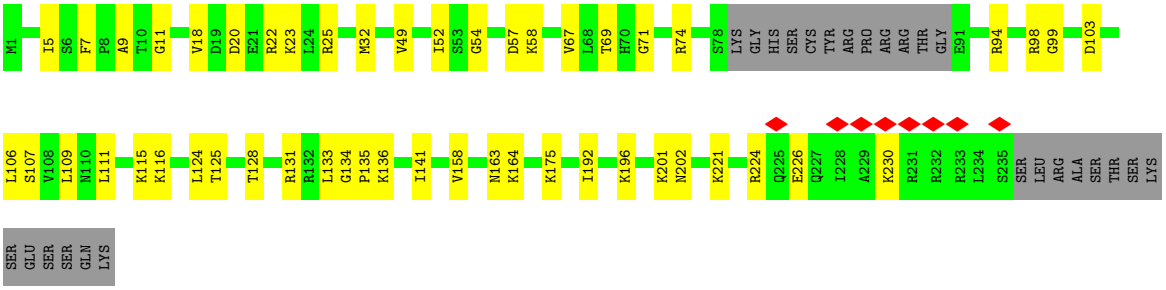
• Molecule 6: 40S ribosomal protein S5

Chain L5:



• Molecule 7: 40S ribosomal protein S6

Chain L6:



• Molecule 8: 40S ribosomal protein S7

Chain L7: 75% 12% 13%

MET PHE SER SER SER ALA LYS I8 V9 K10 P11 L30 N33 S34 L43 I51 E52 V53 R57 V64 F72 Q76 V77 R78 R81 F94 I100 LEU PRO LYS PRO THR ARG LYS SER ARG THR LYS ASN LYS GLN LYS ARG PRO ARG S119 I129

L133 E138 R145 L153 Q163 V170 K179 F187 Q193 LEU

- Molecule 9: 40S ribosomal protein S8

Chain L8: 72% 14% 13%

MET G2 R11 G15 Y21 H22 K23 R42 I43 Y55 R56 A57 L58 R59 V62 G63 N64 W67 C71 K75 D80 V81 N87 N88 E89 K98 D105 S106 K124 K125 GLY ALA LYS LEU THR PRO GLU GLU GLU GLU ILE LEU ASN LYS LYS ARG

SER LYS LYS ILE GLN LYS LYS TYR ASP E151 L162 A176 G183 R184 E191 K201 R205 K206 GLY LYS

- Molecule 10: 40S ribosomal protein S9

Chain L9: 74% 14% 12%

MET PRO VAL ALA ARG SER TRP VAL CYS ARG K11 T12 Y13 R17 K22 K40 R41 R45 R54 R58 T62 L78 M92 E107 Q113 V114 L119 A126 R127 R131 R136 V137 R138 K139 V149 D152 S153 D158 F159 K180 G181

GLN GLY GLY ALA GLY ALA GLY ASP ASP GLU GLU GLU ASP

- Molecule 11: 40S ribosomal protein S12

Chain LA: 91% 89% 9%

MET ALA GLU GLU GLY ILE ALA ALA GLY GLY V11 M12 D13 V14 N15 T16 A17 L18 Q19 E20 V21 L22 K23 T24 A25 L26 I27 H28 D29 G30 L31 A32 R33 G34 I35 R36 E37 A38 A39 K40 A41 L42 D43 K44 R45 Q46 A47 H48 L49 C50 V51 L52 A53 S54 N55 C56 D57 E58 P59 M60

Y61 V62 K63 L64 V65 E66 A67 L68 C69 A70 E71 H72 Q73 I74 N75 L76 I77 K78 V79 D80 D81 N82 K83 K84 L85 G86 E87 W88 V89 G90 L91 C92 K93 I94 D95 R96 E97 G98 K99 P100 R101 K102 V103 V104 G105 C106 S107 C108 V109 V110 V111 K112 D113 Y114 G115 K116 E117 S118 Q119 A120

K121 D122 V123 I124 E125 E126 Y127 F128 K129 C130 LYS LYS

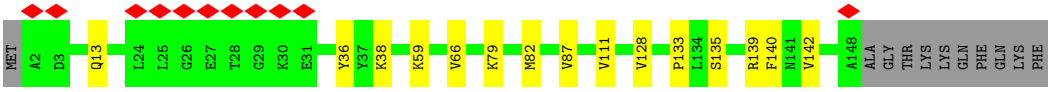
- Molecule 12: 40S ribosomal protein S16

Chain LC: 84% 12% 5%

MET PRO SER LYS G5 Q11 V12 A23 P44 K50 R62 F63 R69 I81 Y82 R85 K90 A91 L92 Y96 Q97 K98 K105 K143 SER TYR ARG

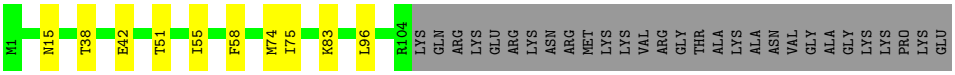
• Molecule 13: 40S ribosomal protein S11

Chain LD:



• Molecule 14: 40S ribosomal protein S24

Chain LF:

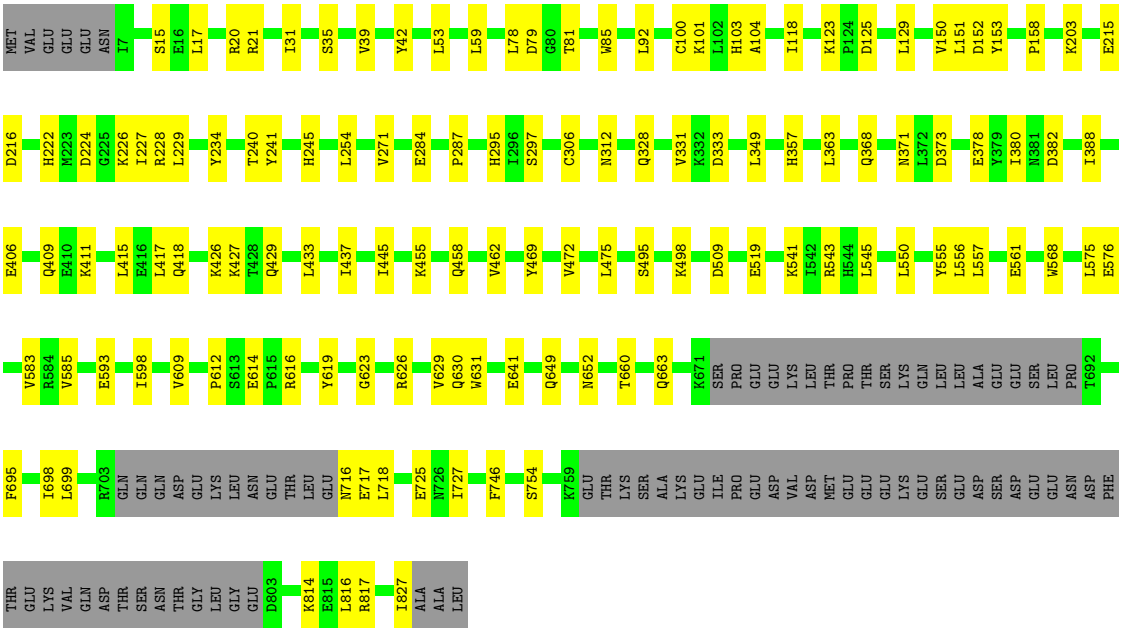


• Molecule 15: 40S ribosomal protein S28

Chain LG:

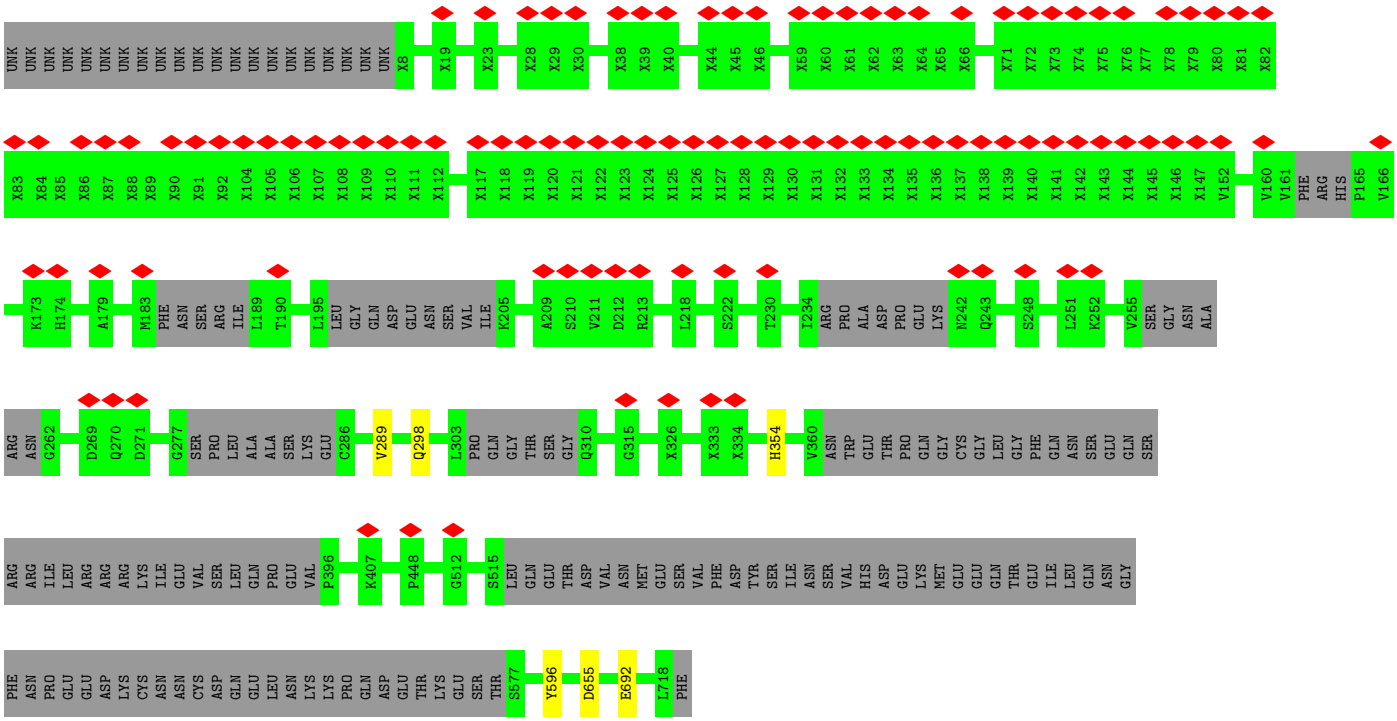
• Molecule 16: WD repeat-containing protein 75

Chain LH:



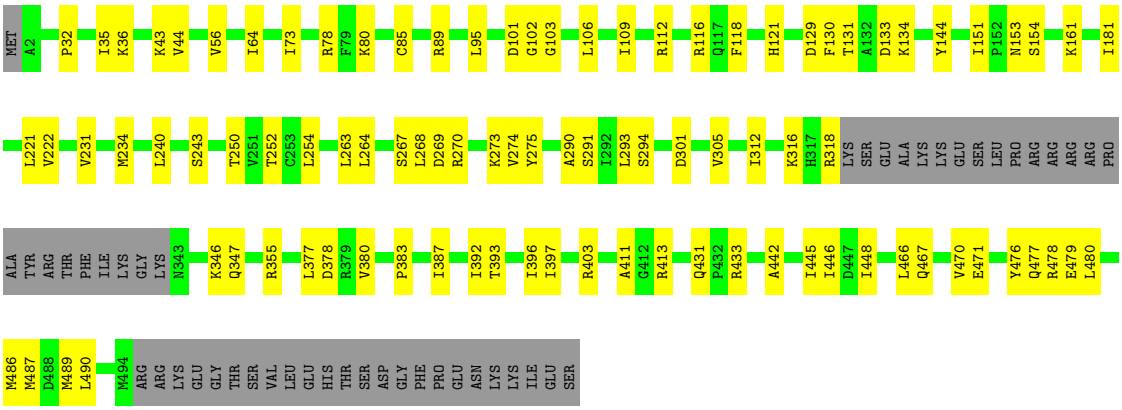
• Molecule 17: Nucleolar protein 11

Chain LI:



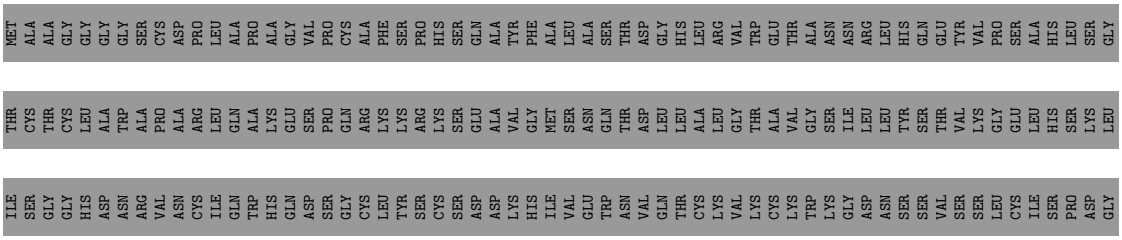
- Molecule 18: U3 small nucleolar RNA-associated protein 15 homolog

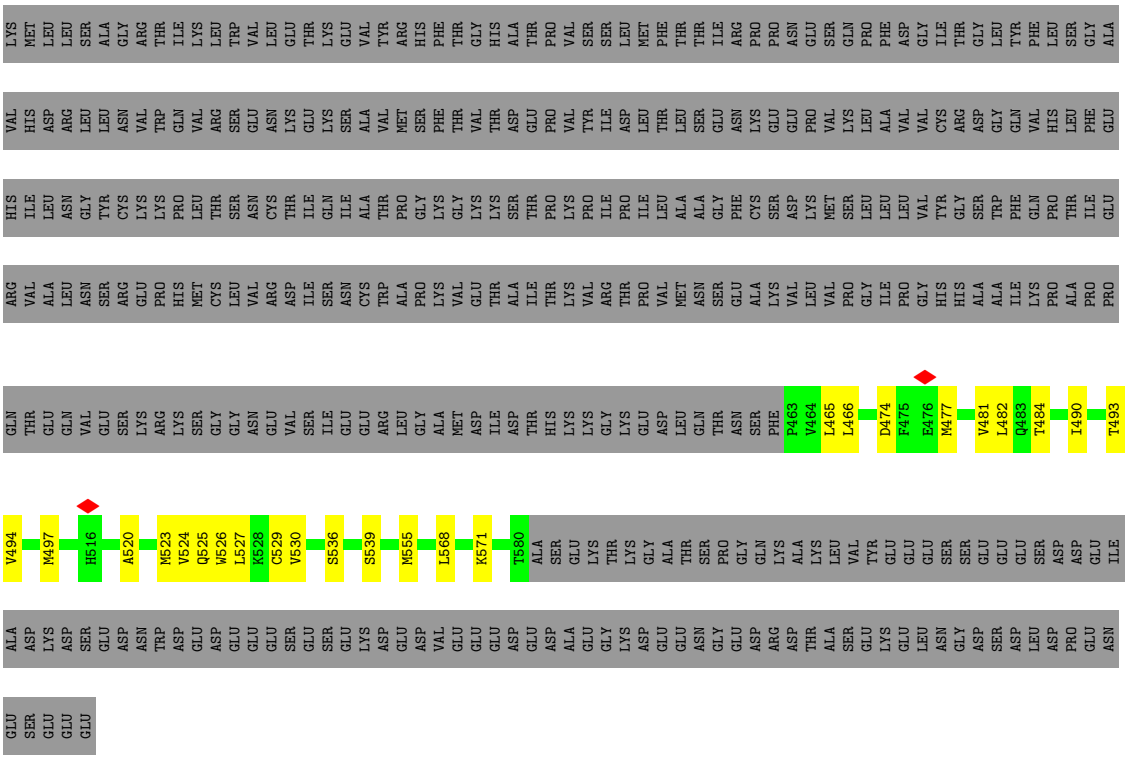
Chain LJ: 72% 18% 9%



- Molecule 19: WD repeat-containing protein 43

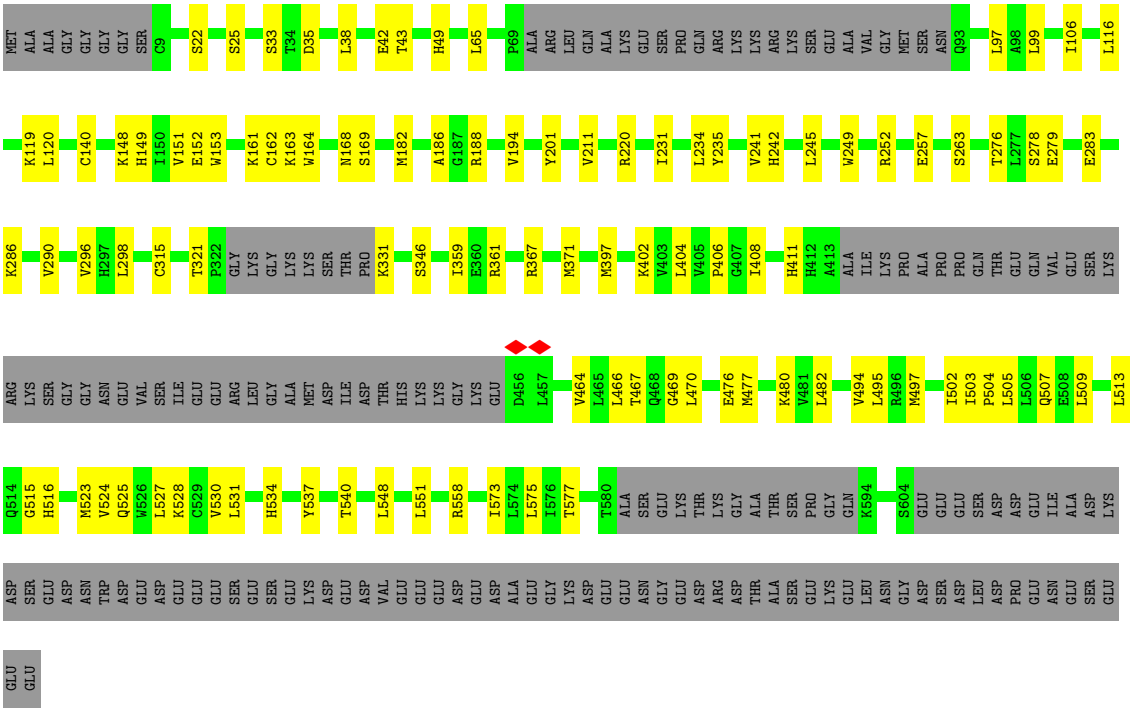
Chain LK: 14% • 83%





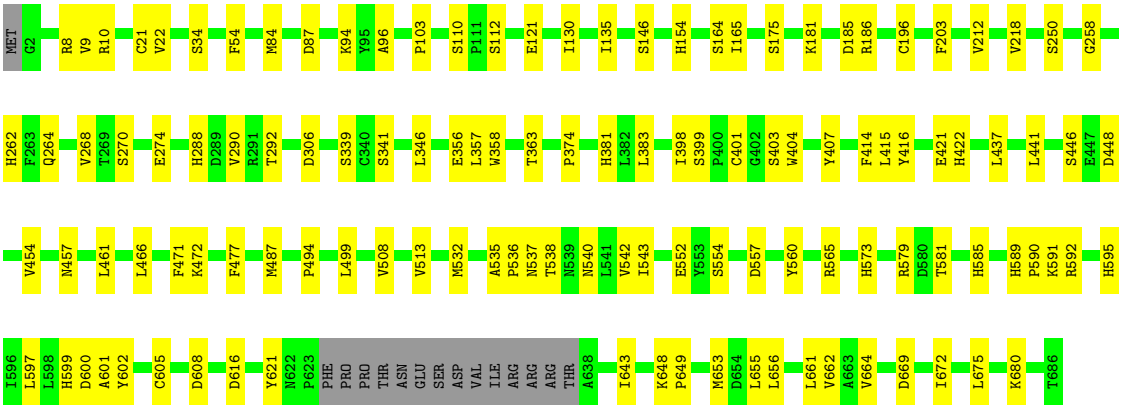
• Molecule 19: WD repeat-containing protein 43

Chain LL:



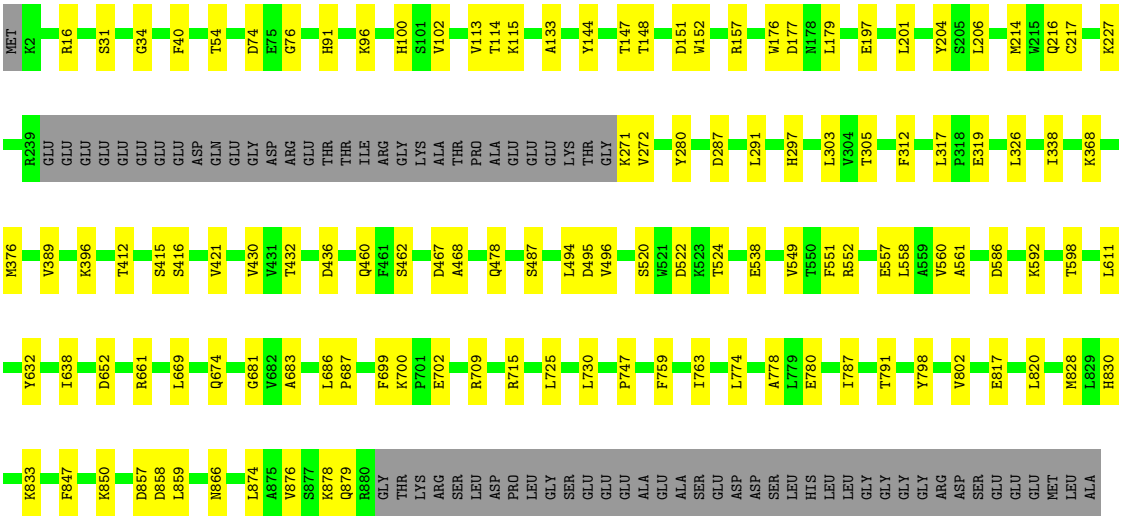
• Molecule 20: U3 small nucleolar RNA-associated protein 4 homolog

Chain LN:



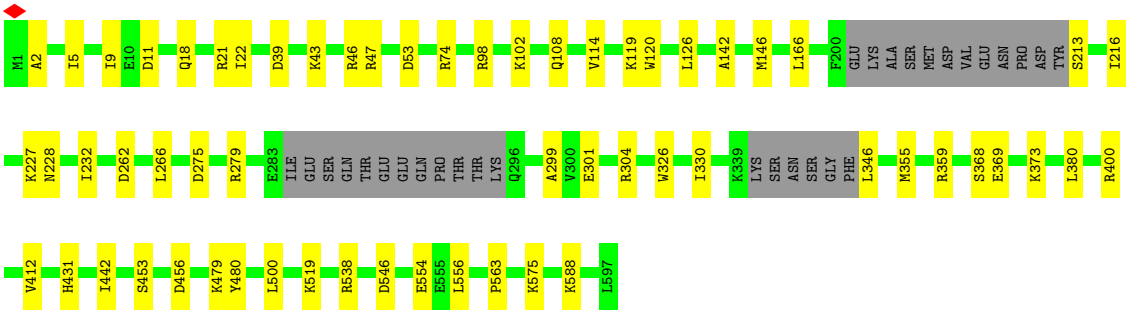
• Molecule 21: Periodic tryptophan protein 2 homolog

Chain LO:



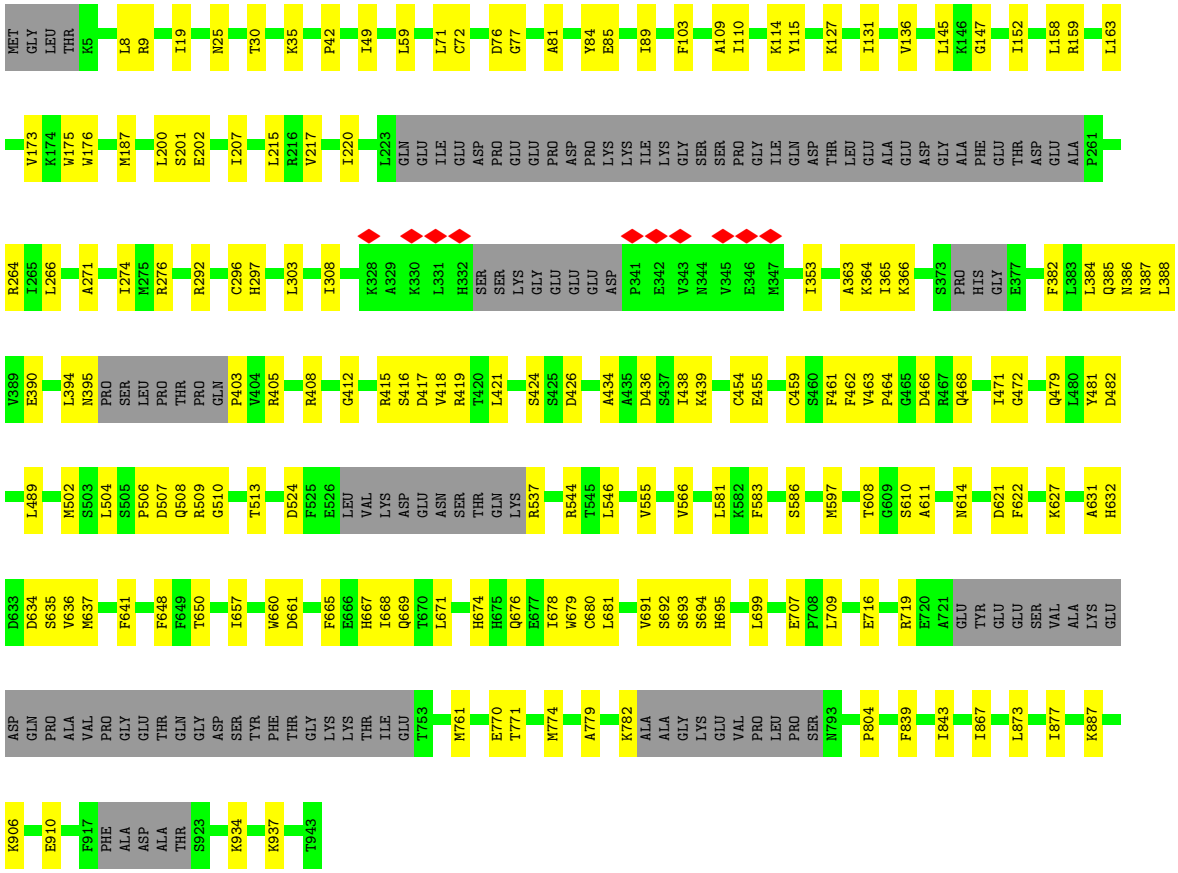
• Molecule 22: U3 small nucleolar RNA-associated protein 6 homolog

Chain LP:



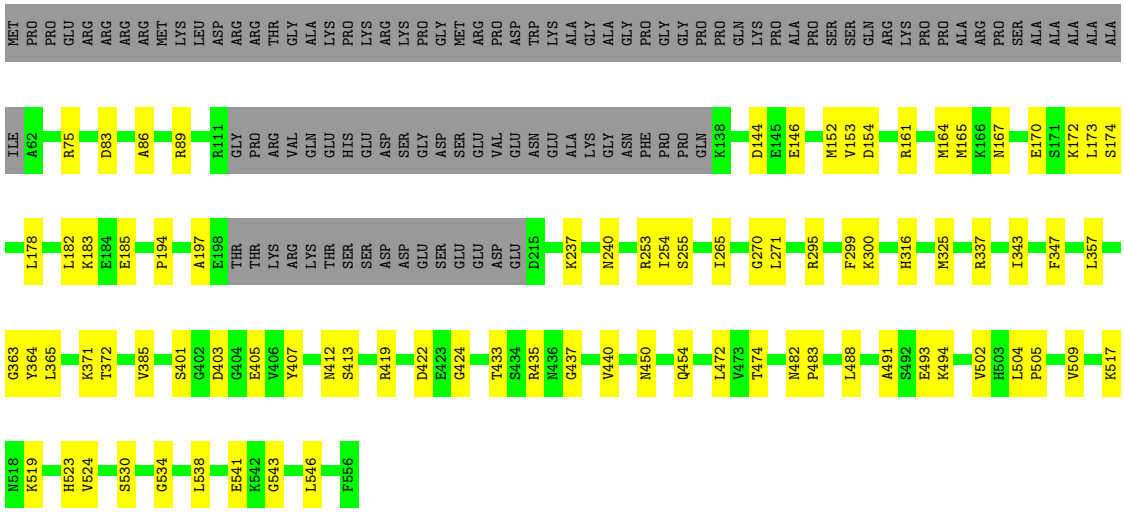
• Molecule 23: WD repeat-containing protein 3

Chain LQ:



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

Chain LS:



- Molecule 25: WD repeat-containing protein 36

Chain LT:

SER GLU ARG R64 S67 F70 R74 A75 L76 R88 K104 V111 Q112 A132 R135 L136 H161 D179 I185 G227 S228 L229 N233 L240 F243 V248 G249 L253 S268 M283 Q287 G312 H313 I314 W317 K322

M328 I336 L342 V349 I359 A380 P381 L382 T383 N384 I385 R386 S399 Q400 D401 G402 T403 K413 L418 N424 K425 K426 R427 R430 L433 I460 S469 W473 K477 S478 D493 D494 I495 D501 I502 C505 G516 K534 D535 Q536

V542 D548 G549 L550 N551 N567 F568 K569 I574 I585 L595 L607 M628 L637 A640 I657 L661 L662 D663 S664 A665 P666 D676 F677 L702 P711 V714 M715 L716 Q721 THR GLN ASP VAL GLU VAL SER GLU GLU THR VAL GLU PRO

S735 I739 E740 Y741 N748 E749 L757 R761 Q806 ASN ASN ASP P810 L844 L847 K848 G851 I855 E856 R860 S861 L862 E891 L892 A893 Q894 L908 I918 S922 Q938 S948 ALA LEU LEU

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

Chain LU: 81% 19%

M1 R8 N9 N12 E16 D20 R23 V24 F35 E36 V37 P38 S61 C71 H75 K78 L83 I102 R103 I115 R118 F119 C120 G121 T122 V127 V133 M138 K156 Y159 D163 H164 A169 D182 R185 F196

K203 P206 I207 L212 N220 L223 Y224 K234 V235 R240 T255 E259 L263 M268 L271 D272 T273 M276 V277 H278 A284 V285 Y290 S291 P292 A300 S301 F302 I306 T322 K323 R324 M325 Q326 W333 S337 S344 N348

K359 V362 L363 T364 E367 L377 Q405 R408 I409 M410 K411 E412 V419 I422 S429 V430 P431 L432 V433 S434 K437 V444 K445

- Molecule 27: WD repeat-containing protein 46

Chain LW: 64% 10% 26%

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

ALA TYR ILE LEU LYS LYS SER ARG ILE SER LYS LYS PRO GLN VAL PRO LYS LYS PRO ARG GLU TRP LYS ASN PRO GLU SER GLN ARG GLY LEU SER GLY THR Q95 F98 A102 P103 R119 K120 L121 E141 K145 L152 K170 D181 F196 G197 P198 Y199 R200

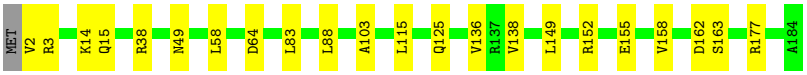
L201 N202 Y203 L210 R215 R216 D241 I242 R243 H246 S247 E248 A249 N264 V278 S294 R319 L320 D321 N326 N329 A330 G339 T340 L343 A353 L356 G361 V362 R363 V367 M374 L379 I385 L388 R389 L395 D421

Q439 P440 F458 G485 N489 R492 E499 V502 P510 L513 R519 V524 I527 Q531 K534 L540 GLY TYR ASP PRO GLN ALA LYS ALA PRO PHE GLN PRO LYS PRO LYS GLN LYS GLY ARG SER SER THR ALA SER LEU VAL LYS ARG LYS

ARG LYS VAL MET ASP GLU GLU HIS ARG ASP LYS VAL ARG GLN SER LEU GLN GLN GLN HIS HIS LYS GLU ALA LYS ALA LYS PRO THR GLY ALA ARG PRO S603 V609 ARG

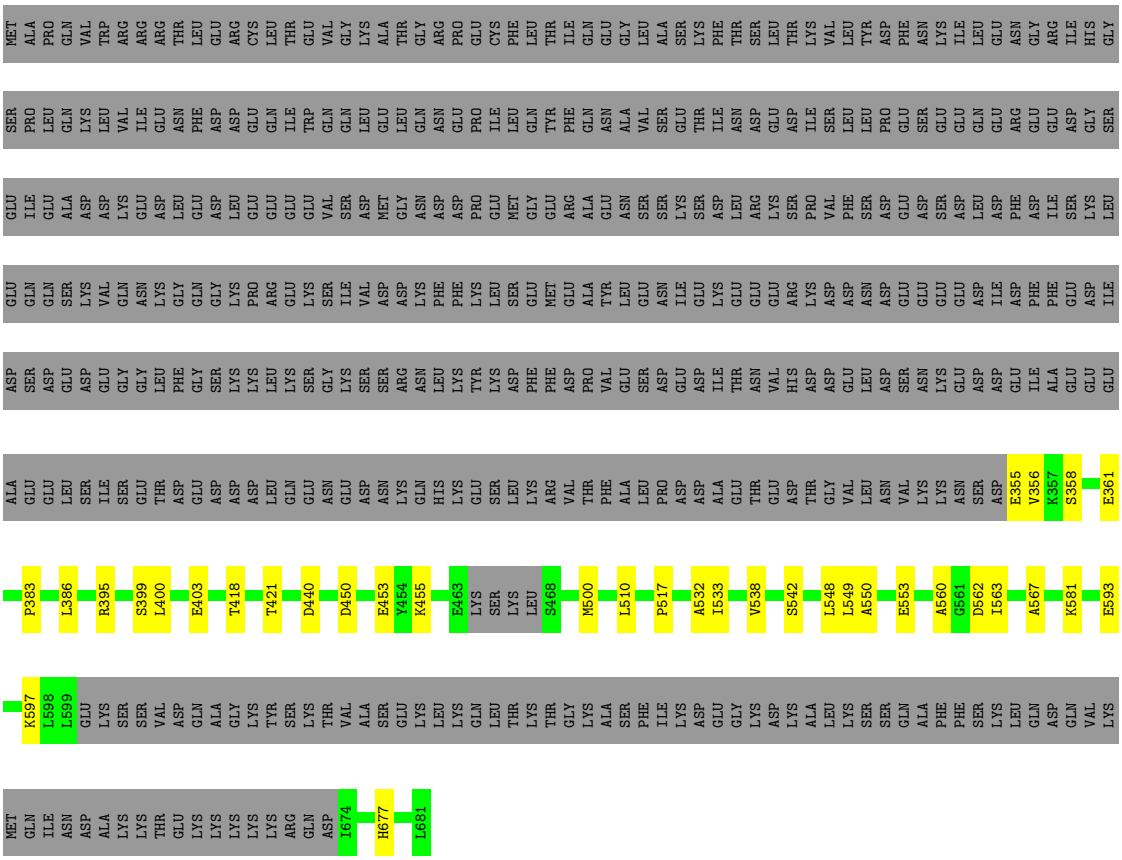
- Molecule 28: U3 small nucleolar ribonucleoprotein protein IMP3

Chain LZ: 88% 12%



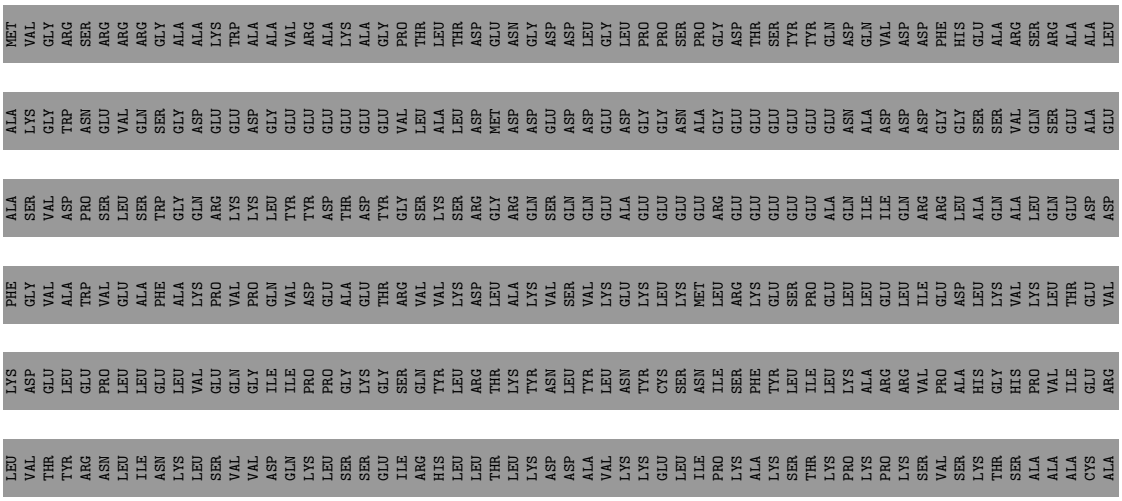
• Molecule 29: U3 small nucleolar ribonucleoprotein protein MPP10

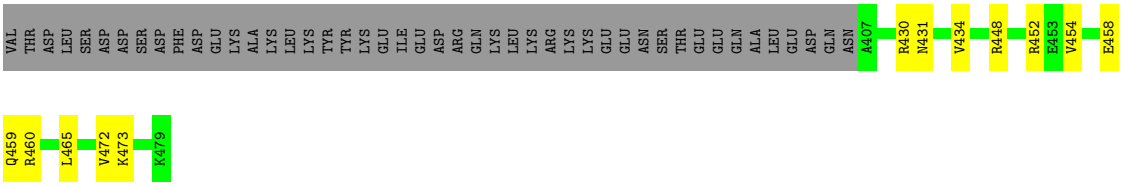
Chain NA: 31% 5% 63%



• Molecule 30: Something about silencing protein 10

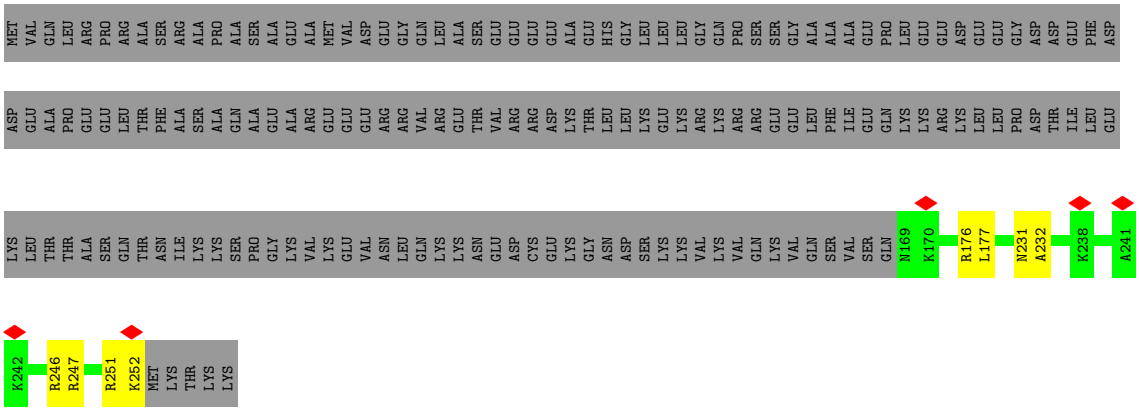
Chain NB: 13% • 85%





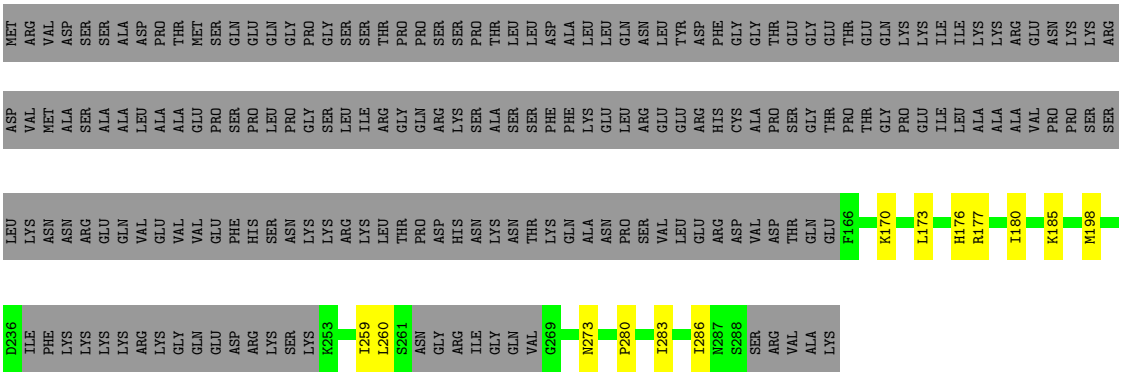
• Molecule 31: Nucleolar protein 7

Chain ND:



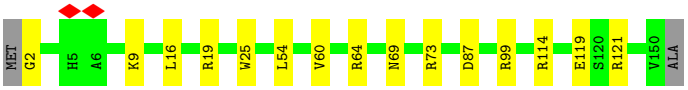
• Molecule 32: Uncharacterized protein C1orf131

Chain NE:



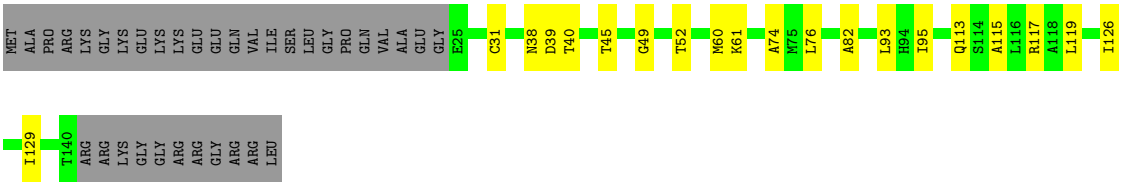
• Molecule 33: 40S ribosomal protein S13

Chain NF:



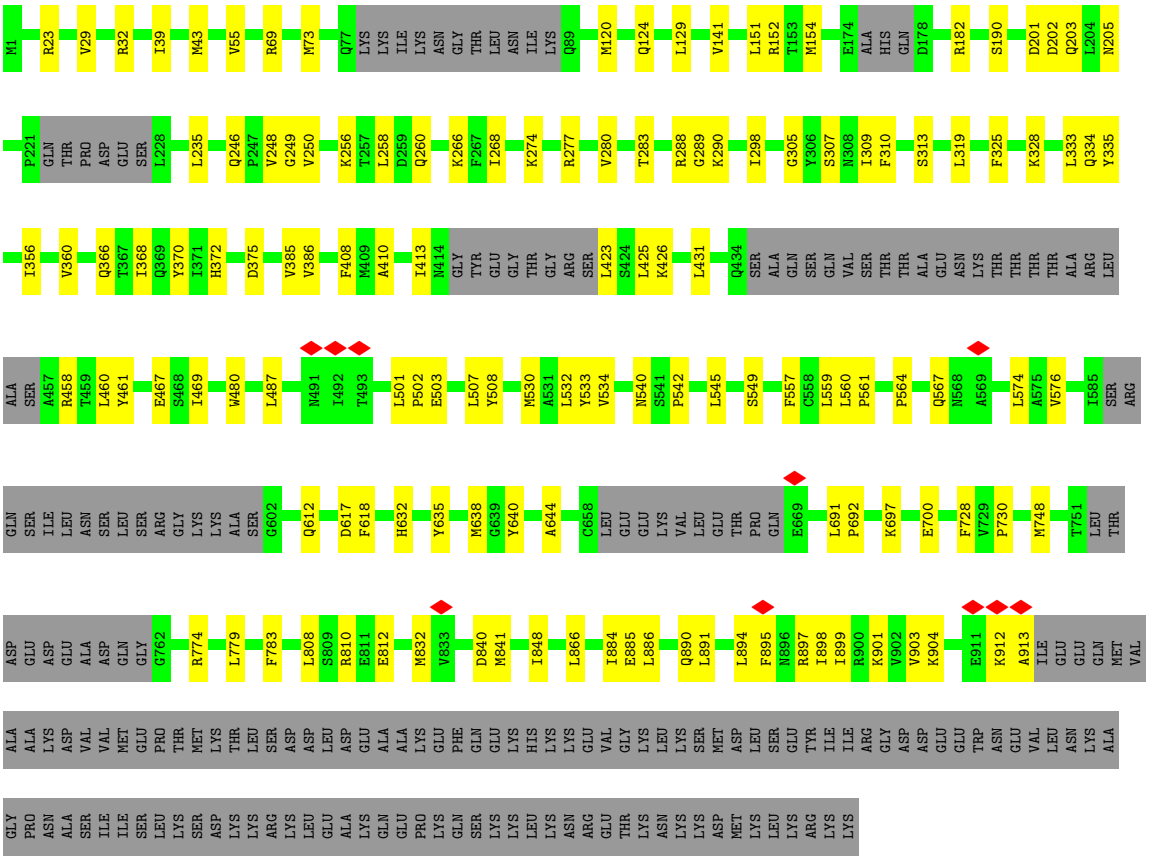
• Molecule 34: 40S ribosomal protein S14

Chain NG:



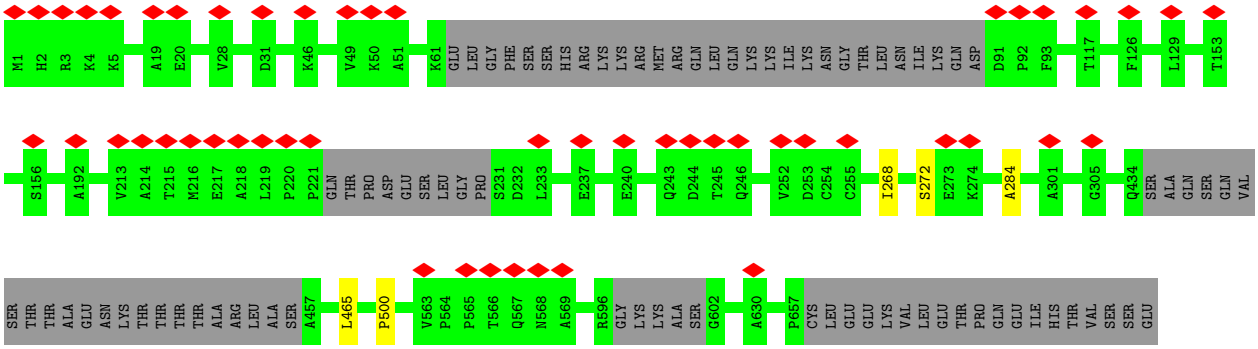
- Molecule 35: RNA cytidine acetyltransferase

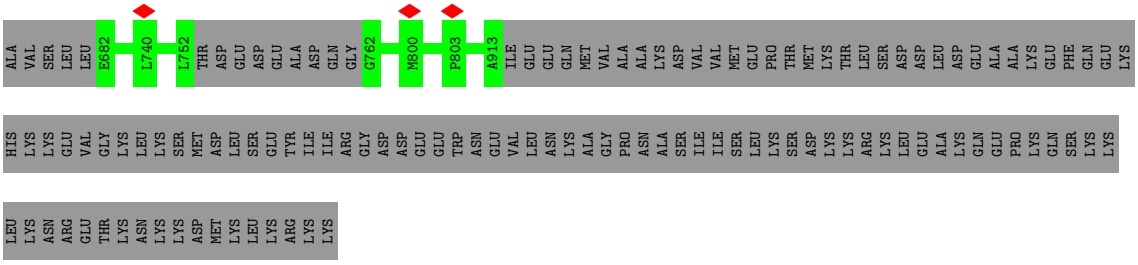
Chain NJ:



- Molecule 35: RNA cytidine acetyltransferase

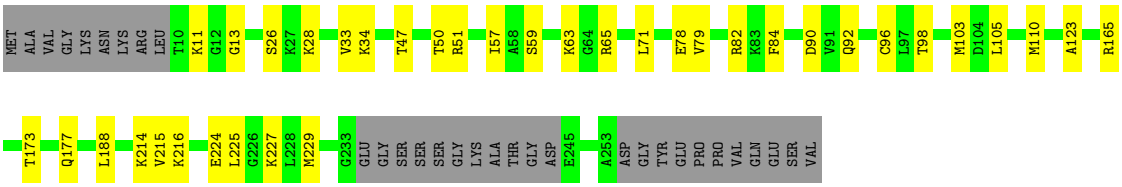
Chain NK:





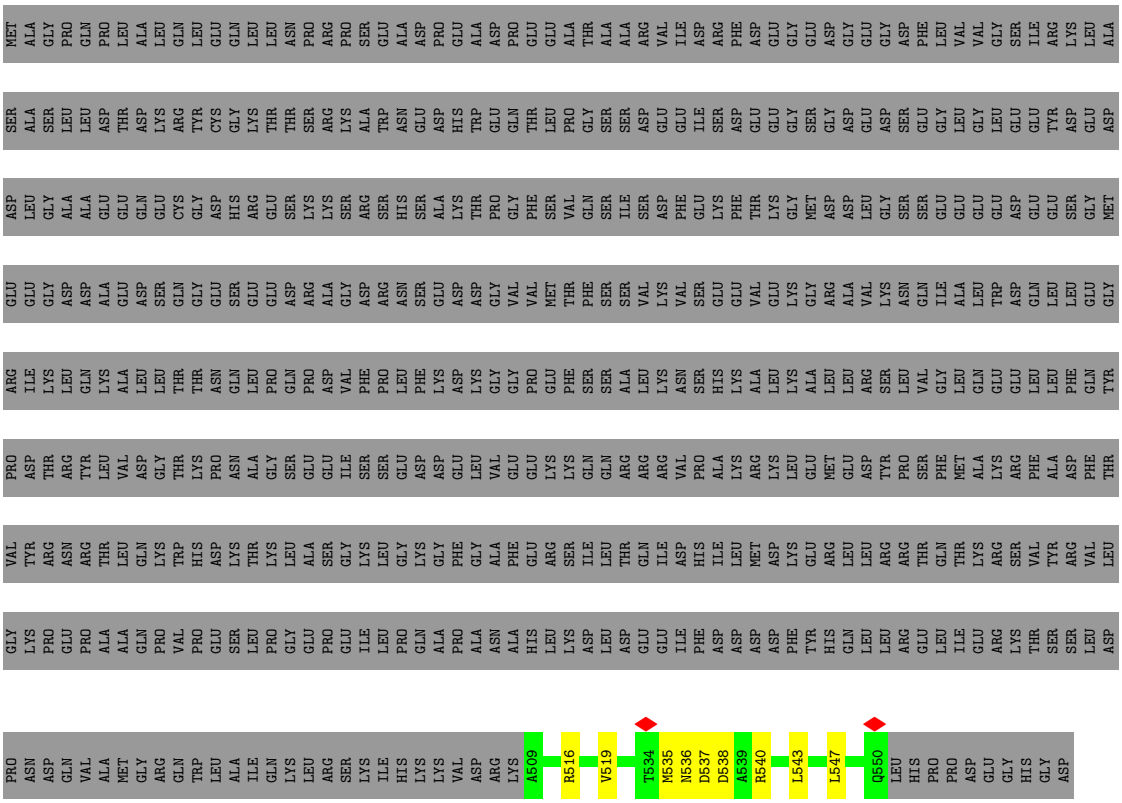
- Molecule 36: 40S ribosomal protein S3a

Chain NM:



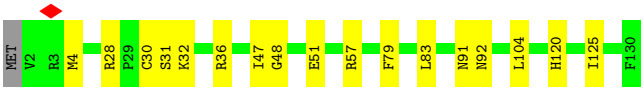
- Molecule 37: Protein AATF

Chain NN:



- Molecule 38: 40S ribosomal protein S15a

Chain NO:

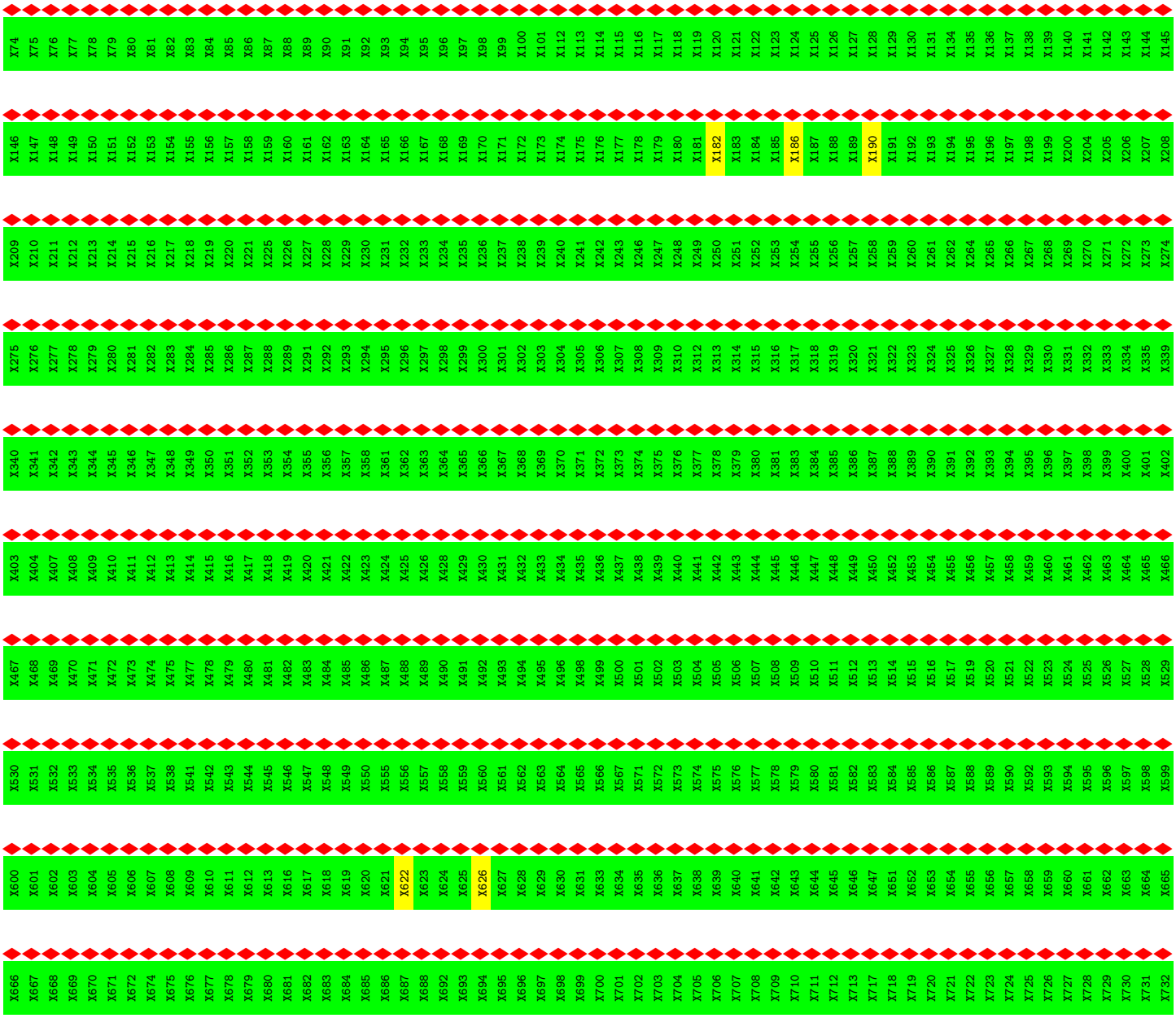


- Molecule 39: 40S ribosomal protein S27

Chain NQ:

- Molecule 40: RRP12-like protein

Chain NR:



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

X800 X801 X802 X803 X807 X808 X809 X810 X811 X812 X813 X814 X815 X816 X817 X818 X819 X820 X821 X822 X823 X824 X828 X829 X830 X831 X832 X833 X834 X835 X836 X837 X838 X839 X840 X841 X842 X843 X844 X845 X846 X850 X851 X852 X853 X854 X855 X856 X857 X858 X859 X860 X861 X862 X863 X864 X865 X866 X867 X868

X869 X870 X874 X875 X876 X877 X878 X879 X880 X881 X882 X883 X884 X885 X886 X887 X888 X889 X890 X891 X892 X893 X894 X898 X899 X900 X901 X902 X903 X904 X905 X906 X907 X908 X909 X910 X911 X912 X913 X914 X915 X919 X920 X921 X922 X923 X924 X925 X926 X927 X928 X929 X930 X931 X932 X933 X934 X936 X937 X938

X939 X940 X941 X942 X943 X944 X945 X946 X947 X948 X949 X950 X951 X952 X953 X957 X958 X959 X960 X961 X962 X963 X964 X965 X966 X967 X968 X969 X970 X971 X972 X973 X974 X975 X976 X980 X981 X982 X983 X984 X985 X986 X987 X988 X989 X990 X991 X992 X993 X994 X995 X999 X1000 X1001 X1002 X1003 X1004 X1005 X1006 X1007

X1008 X1010 X1011 X1012 X1013 X1014 X1015 X1016 X1017 X1018 X1019 X1020 X1021 X1022 X1023 X1024 X1025 X1026 X1027 X1028 X1029

- Molecule 41: Ubiquitin-40S ribosomal protein S27a

Chain NT: 37% 37% 63%

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

ILE GLN LYS GLU SER THR LEU HIS LEU VAL LEU ARG LEU ARG GLY GLY ALA LYS LYS ARG LYS LYS LYS SER TYR THR THR PRO LYS LYS ASN K92 H93 K94 R95 K96 K97 V98 K99 L100 A101 V102 L103 K104 Y105 Y106 K107 V108 D109 E110 N111 G112 K113 I114 S115 R116 L117 R118 R119 E120

C121 P122 S123 D124 E125 C126 G127 A128 G129 V130 F131 M132 A133 S134 H135 F136 D137 R138 H139 Y140 C141 G142 K143 C144 C145 L146 T147 Y148 C149 PHE ASN LYS PRO GLU ASP LYS

- Molecule 42: 40S ribosomal protein S17

Chain NU: 44% 44% 56%

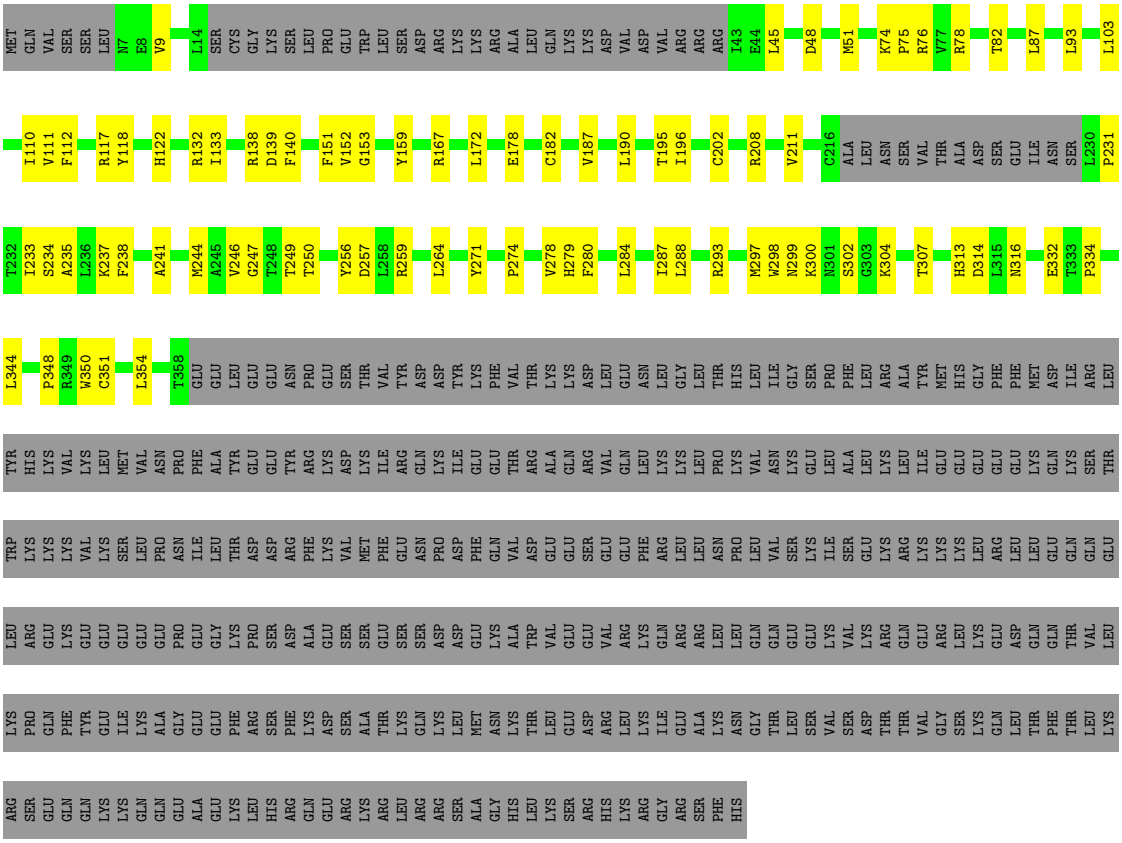
MET GLY ARG VAL R5 T6 K7 T8 V9 K10 K11 A12 A13 R14 V15 I16 I17 E18 K19 Y20 Y21 T22 R23 L24 G25 N26 D27 F28 H29 T30 N31 K32 R33 V34 C35 E36 E37 I38 A39 I40 I41 P42 S43 K44 K45 L46 R47 N48 K49 I50 A51 G52 Y53 V54 T55 H56 L57 M58 K59 R60

I61 Q62 R63 G64 PRO VAL ARG GLY ILE SER ILE LYS LEU GLN GLU GLU GLU GLU ARG GLU ARG ARG ASP ASN TYR VAL PRO GLU VAL SER ALA LEU ASP GLN GLU ILE ILE GLU VAL ASP PRO ASP THR LYS GLU MET LEU LYS LEU LEU ASP PHE GLY SER LEU SER ASN LEU GLN VAL THR

GLN PRO THR VAL GLY MET ASN PHE LYS THR PRO ARG GLY PRO VAL

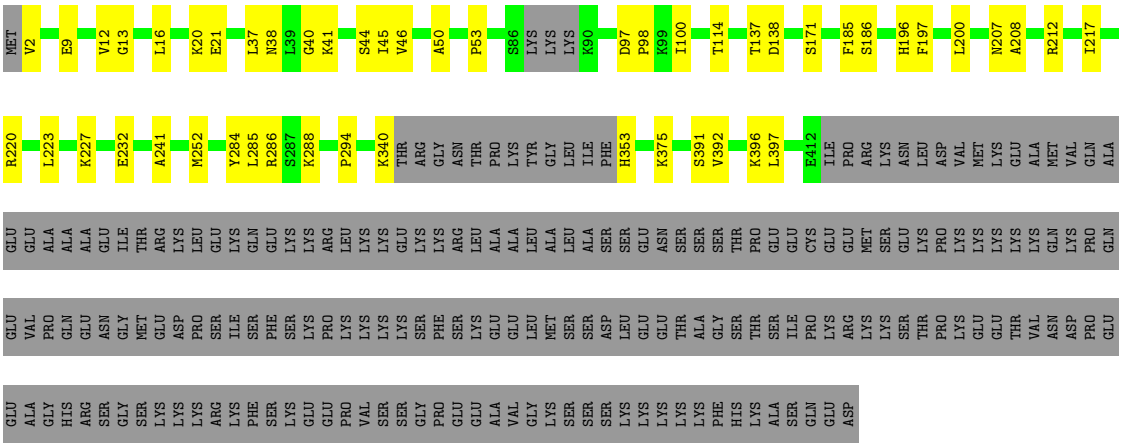
- Molecule 43: Nucleolar protein 10

Chain NW: 34% 12% 55%



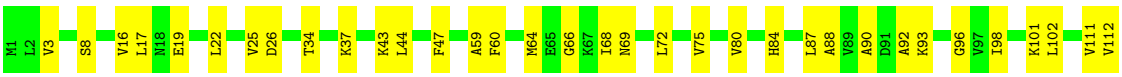
- Molecule 44: Nucleolar protein 56

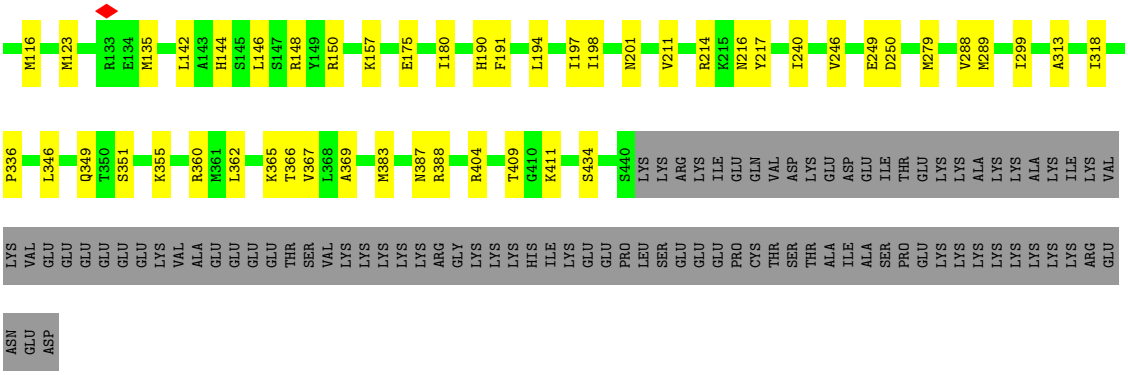
Chain SA:



- Molecule 45: Nucleolar protein 58

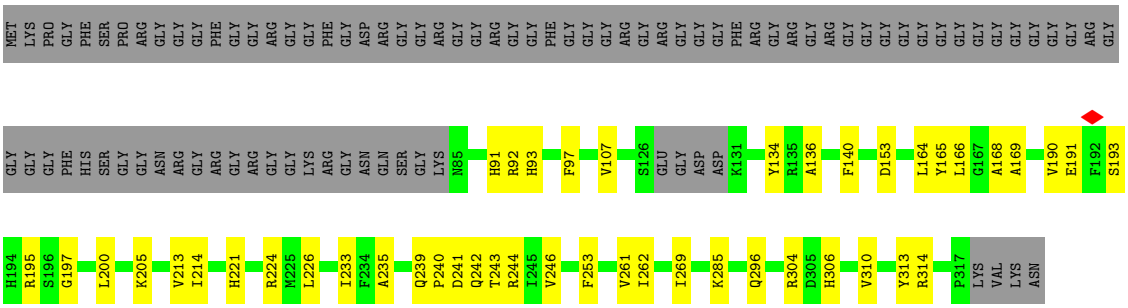
Chain SB:





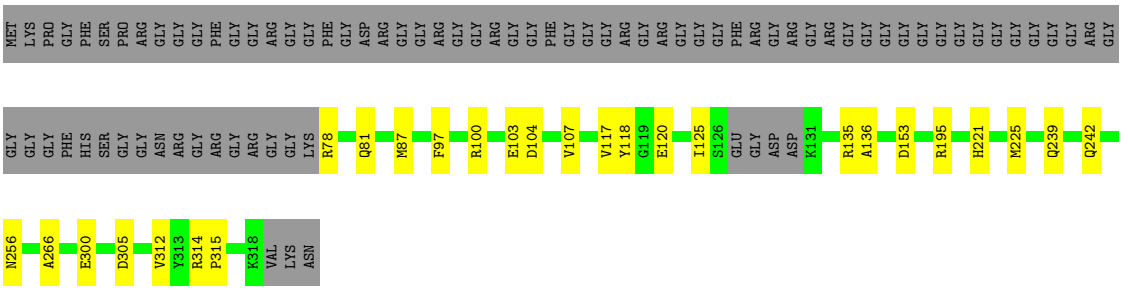
- Molecule 46: rRNA 2'-O-methyltransferase fibrillarin

Chain SC:



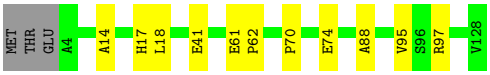
- Molecule 46: rRNA 2'-O-methyltransferase fibrillarin

Chain SD:



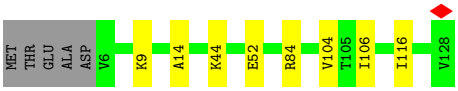
- Molecule 47: NHP2-like protein 1

Chain SE:



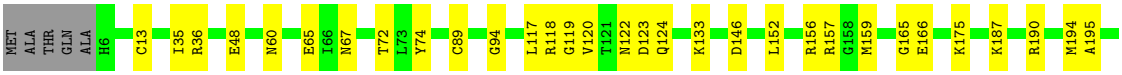
- Molecule 47: NHP2-like protein 1

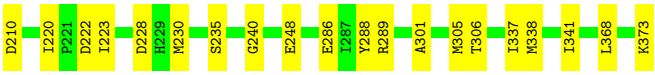
Chain SF:



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

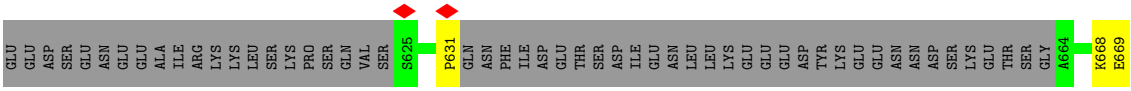
Chain SH:

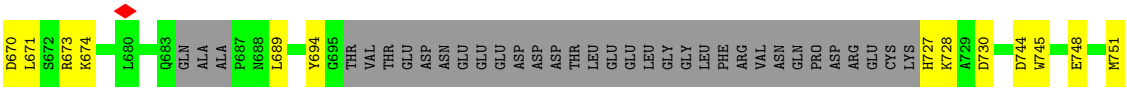


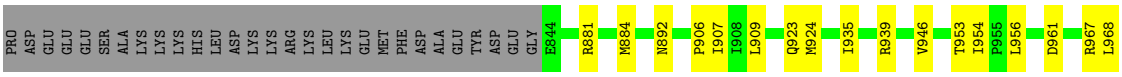


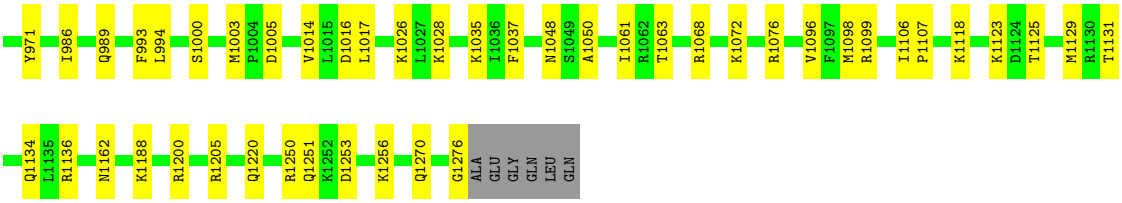
• Molecule 49: Ribosome biogenesis protein BMS1 homolog

Chain SI:



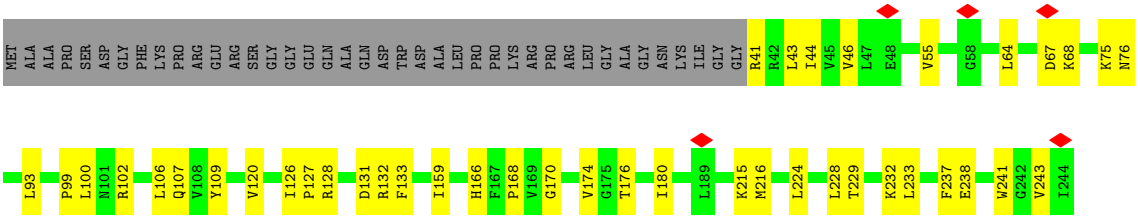






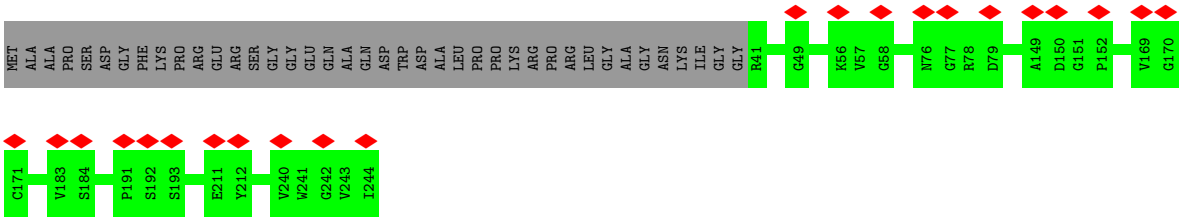
• Molecule 50: Ribosomal RNA small subunit methyltransferase NEP1

Chain SK:



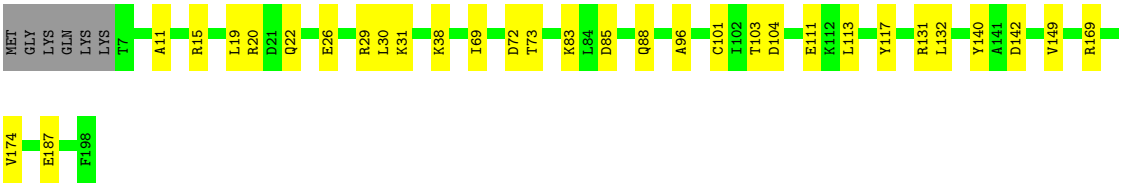
• Molecule 50: Ribosomal RNA small subunit methyltransferase NEP1

Chain SJ:



• Molecule 51: rRNA-processing protein FCF1 homolog

Chain SL:

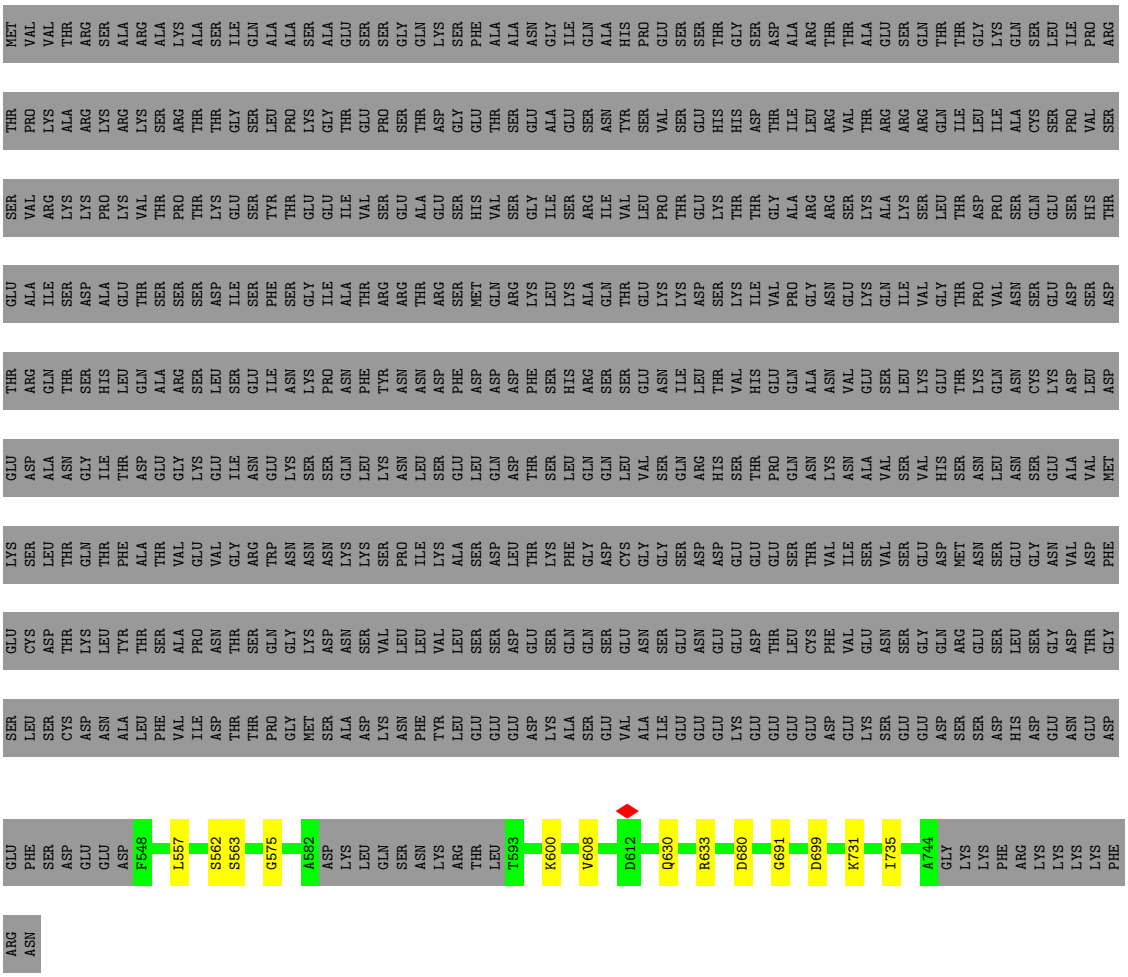


• Molecule 52: U3 small nucleolar ribonucleoprotein protein IMP4

Chain SM:

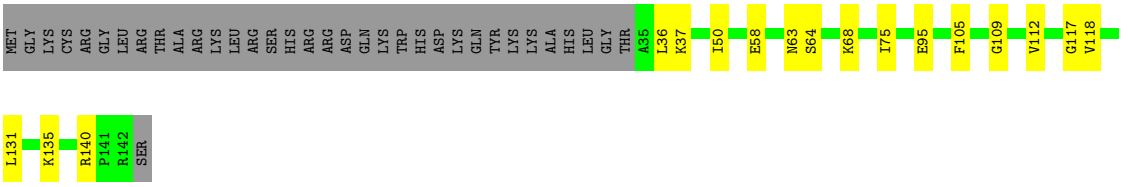
• Molecule 53: Deoxynucleotidyltransferase terminal-interacting protein 2

Chain SQ:



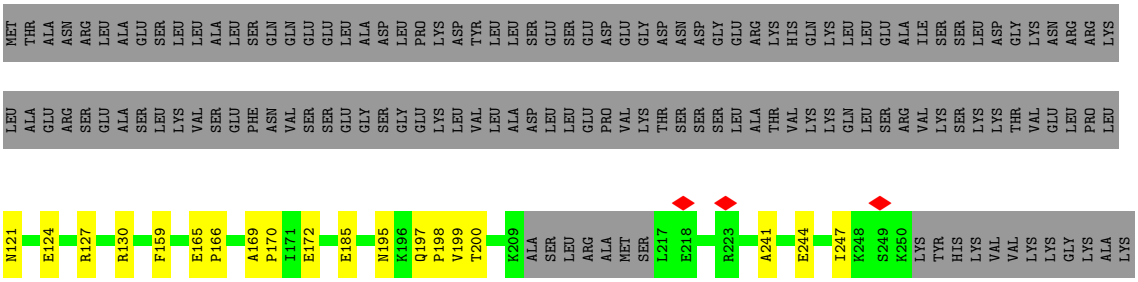
- Molecule 54: 40S ribosomal protein S23

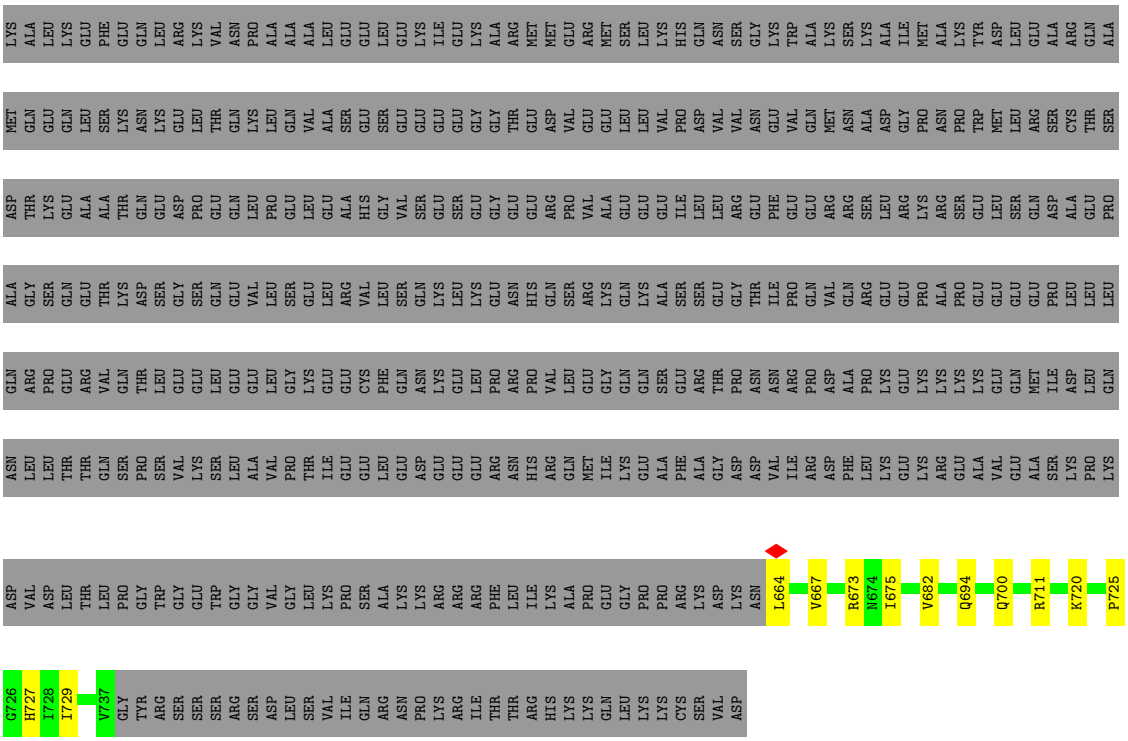
Chain SR:



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

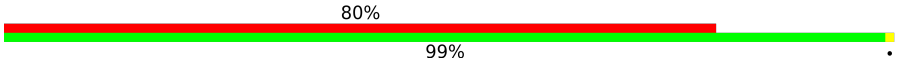
Chain SS:

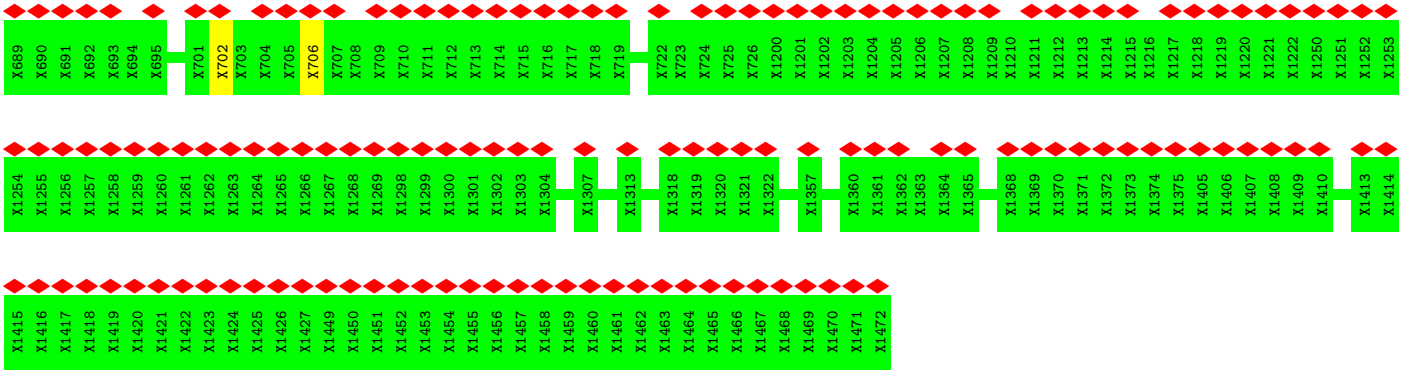




• Molecule 56: Unassigned peptides

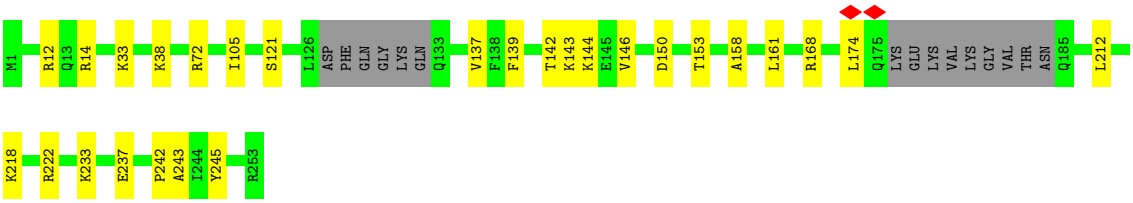
Chain SX:





• Molecule 57: Probable U3 small nucleolar RNA-associated protein 11

Chain SY:



• Molecule 58: Nucleolar protein 6

Chain NH: 11% 93% 7%

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

TYR LYS GLU PRO THR ASN GLU GLU LEU ASN ARG LEU ARG GLU THR E76 I77 L78 F79 H80 L97 S98 E99 K100 A107 F108 L109 N113 V116 V117 R118 V119 P120 S121 V122 P123 E124 D129 Q130 A131 W132 A135 G136 P140 P145 Y146 A147 V148 A158 Q159 V160

D175 I176 N177 T183 A211 A215 Q216 D217 P218 L219 F220 G221 S222 V223 R240 P241 R242 G243 K244 D245 E246 R247 L248 V249 T250 P259 F262 R263 P264 P269 T270 Q282 S283 P284 A285 G286 D287 G288 E291 E308 I317 L318 S319 Q322 D326

G371 R376 I392 S393 L396 S397 S398 D399 P400 S401 L402 P403 S420 G421 H422 A452 D453 D454 L507 V532 P533 E534 I537 S538 Q539 D546 S547 G548 T549 A596 G647 L648 K649 E650 T651 A685 V704 S709 L714 R715 S718 L724

A730 K788 G995 P1004 A1030 S1039 Q1040 P1041 R1109 G1110 G1111 E1112 L1113 V1114 Q1135 S1141 GLU ARG TRP THR VAL

- Molecule 59: Small subunit processome component 20 homolog

Chain SP: 13% 69% 28%

MET K2 P5 D35 R36 V40 N59 E70 K74 H84 L92 P106 V111 L118 D121 P127 T134 L137 M173 Y174 L177 L178 A179 H180 R186 L196 L300 H304 I433 K439 D440 A459 G460 S461 V470

F471 S472 P473 Q474 MET VAL GLY PHE TYR ILE LYS GLN LYS LYS THR ARG SER LYS GLY ARG ASN E492 S573 K644 R651 E662 SER MET GLU ASP ASP GLY LEU SER GLU R672 E694 R703 D713 Q717 E718 R722 L728 D737 P738 V739 I740 E741 L742

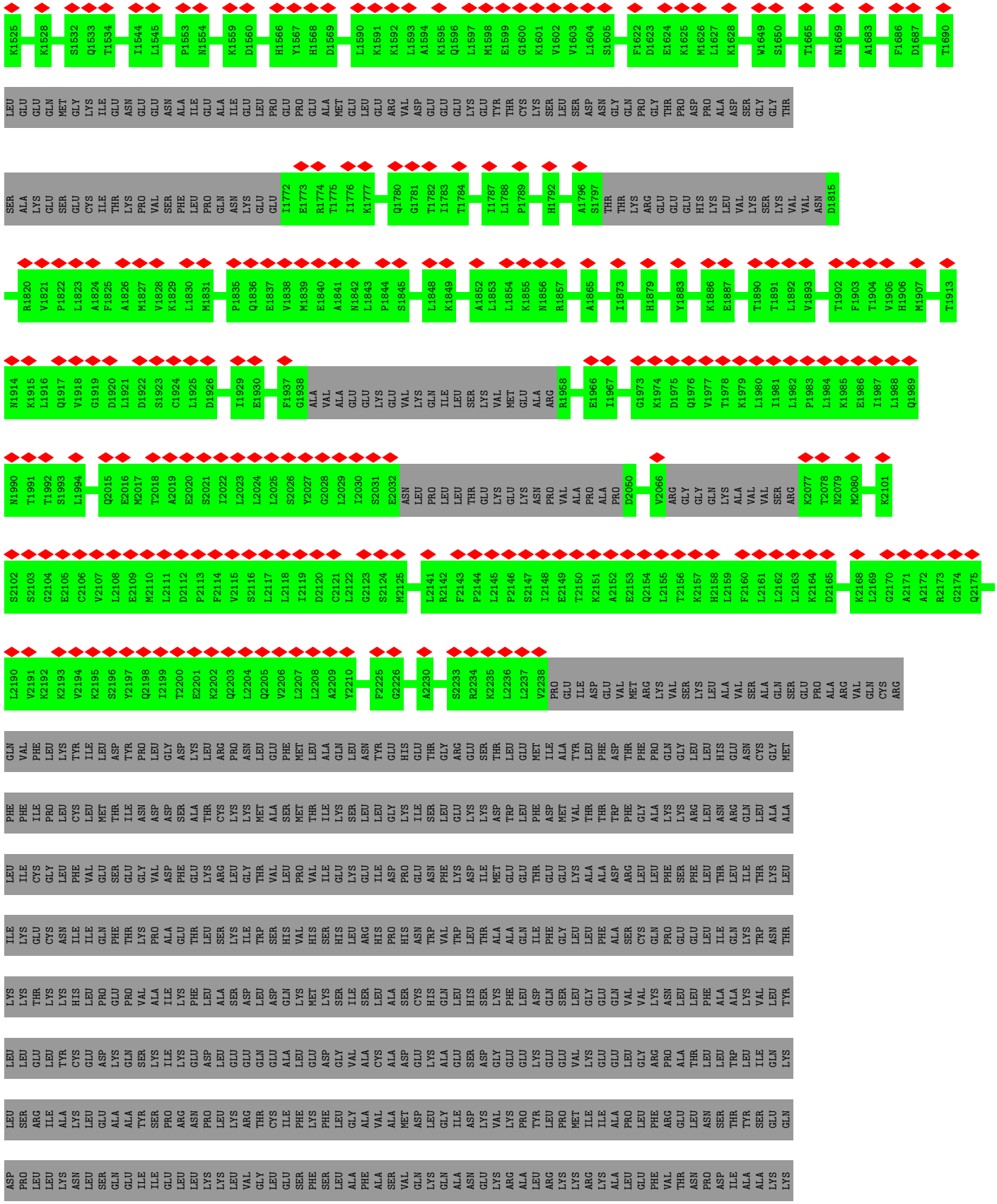
W756 N776 ASP ASP MET THR ASP GLU LYS SER VAL GLY ASP E787 E790 Q791 E794 G795 A799 D810 L823 A827 L828 E841 L842 S843 P844 G871 LYS GLY MET VAL ALA GLU GLU ILE GLU GLU GLU PRO ALA ALA GLY ASP ASP GLU GLU LEU GLU GLU GLU

ALA VAL PRO GLN ASP GLU SER SER GLN LYS LYS K906 Q920 V921 K924 L933 K936 E939 L942 Q943 Q950 K954 C959 T962 H965 P966 H967 V968 L979 V989 I993 K1001 H1004 R1005 A1006 D1007 T1028 R1037 M1038 S1100

P1224 V1256 F1265 E1269 L1275 P1282 GLY ILE ALA GLU ASN ILE GLY GLU SER I1292 T1313 THR ILE SER ALA GLU LYS VAL LYS LYS LYS LYS N1325 G1334 K1341 F1342 M1343 K1344 D1345 K1346 E1347 Q1348 V1351 L1352 L1355 L1356 F1359 G1363 N1364 I1365 A1366 E1367

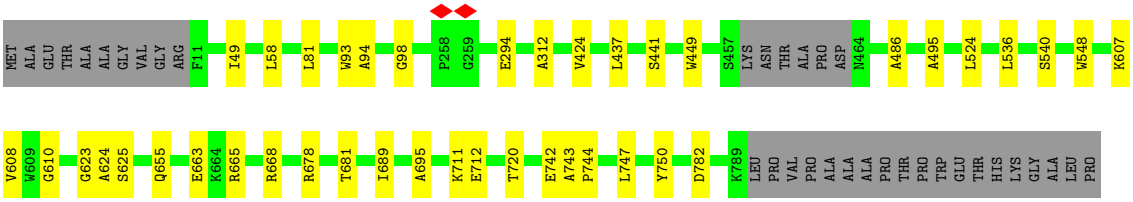
D1368 D1372 V1377 Q1378 N1379 K1382 H1383 C1384 V1385 D1386 P1387 T1388 S1389 P1393 I1394 L1397 V1400 I1401 K1402 K1408 L1409 L1410 C1411 T1412 V1413 F1414 E1415 T1416 L1417 S1418 D1419 F1420 E1421 S1422 G1423 L1424 T1428 A1435 PHE ASP GLN ARG HIS LEU ASP ASP ILE ASN F1446 D1447 V1448

R1449 F1450 E1451 T1452 F1453 Q1454 T1455 I1456 T1457 S1458 Y1459 I1460 K1461 E1462 M1463 Q1464 I1465 V1466 D1467 V1468 M1469 Y1470 L1471 I1472 P1473 L1484 G1485 D1486 M1487 M1495 C1496 L1497 M1498 S1499 I1500 I1501 K1502 K1503 L1504 A1505 A1506 L1507 N1508 V1509 T1510 E1511 K1512 D1513 Y1514 R1515 E1516 I1517 I1518 H1519 R1520 S1521 E1524


K1525 K1528 S1532 Q1533 T1534 I1544 L1545 P1553 N1554 K1559 D1560 H1566 Y1567 H1568 D1569 L1590 K1591 K1592 L1593 A1594 K1595 Q1596 L1597 M1598 E1599 G1600 K1601 V1602 V1603 L1604 S1605 F1622 D1623 E1624 K1625 M1626 L1627 K1628 W1649 S1650 T1665 N1669 A1683 F1686 D1687 T1690
LEU GLU GLU GLN MET GLY LYS LYS ILE GLU ASN GLU GLU ASN ALA ILE GLU ALA ILE GLU LEU PRO GLU PRO GLU ALA MET GLU LEU GLU ARG VAL ASP GLU GLU GLU LYS GLU TYR THR CYS LYS SER LEU SER ASP ASN GLY GLN PRO GLY THR PRO ASP PRO ALA ASP SER GLY GLY THR
SER ALA LYS GLU SER GLU CYS ILE THR LYS PRO VAL SER PHE LEU PRO GLN ASN LYS GLU GLU I1772 E1773 R1774 T1775 I1776 K1777 Q1780 G1781 T1782 I1783 T1784 I1787 L1788 P1789 H1792 A1796 S1797 THR THR LYS ARG GLU GLU GLU HIS LYS LEU VAL LYS SER LYS VAL VAL ASN D1815
R1820 V1821 P1822 L1823 A1824 F1825 A1826 M1827 V1828 K1829 L1830 M1831 P1835 Q1836 E1837 V1838 M1839 E1840 A1841 N1842 L1843 P1844 S1845 L1848 K1849 A1852 L1853 L1854 K1855 N1856 R1857 A1865 I1873 H1879 Y1883 K1886 E1887 T1890 T1891 L1892 V1893 T1902 F1903 T1904 V1905 H1906 M1907 T1913
N1914 K1915 L1916 Q1917 V1918 G1919 D1920 L1921 D1922 S1923 C1924 L1925 D1926 I1929 E1930 F1937 G1938 ALA VAL ALA GLU GLU LYS GLU VAL LYS GLN ILE LEU SER LYS VAL MET GLU ALA ARG R1958 E1966 I1967 G1973 K1974 D1975 Q1976 V1977 T1978 K1979 L1980 I1981 L1982 P1983 L1984 K1985 E1986 I1987 L1988 Q1989
N1990 T1991 T1992 S1993 L1994 Q2015 E2016 M2017 T2018 A2019 E2020 S2021 I2022 L2023 L2024 L2025 S2026 V2027 G2028 L2029 I2030 S2031 E2032 ASN LEU PRO LEU LEU THR GLU LYS GLU LYS ASN PRO VAL ALA PRO ALA PRO D2050 V2066 ARG GLY GLY GLN LYS ALA VAL VAL SER ARG K2077 T2078 N2079 M2080 K2101
S2102 S2103 G2104 E2105 C2106 V2107 L2108 E2109 M2110 L2111 D2112 P2113 F2114 V2115 S2116 L2117 L2118 I2119 D2120 C2121 L2122 G2123 S2124 M2125 L2141 R2142 F2143 P2144 L2145 P2146 S2147 I2148 E2149 T2150 K2151 A2152 E2153 Q2154 L2155 T2156 K2157 H2158 L2159 F2160 L2161 L2162 L2163 K2164 D2165 K2168 L2169 G2170 A2171 A2172 R2173 G2174 Q2175
L2190 V2191 K2192 K2193 V2194 K2195 S2196 Y2197 Q2198 I2199 T2200 E2201 K2202 Q2203 L2204 Q2205 V2206 L2207 L2208 A2209 Y2210 F2225 G2226 A2230 S2233 R2234 K2235 L2236 L2237 V2238 PRO GLU ILE ASP GLU VAL MET ARG LYS VAL SER LYS LEU ALA VAL SER ALA GLN SER GLU PRO ALA ARG VAL GLN CYS ARG
GLN VAL PHE LEU LYS TYR ILE LEU ASP TYR PRO LEU GLY ASP LYS LEU ARG PRO ASN LEU GLU PHE MET LEU ALA GLN LEU ASN TYR GLU HIS GLU THR GLY ARG GLU SER THR LEU GLU MET ILE ALA TYR LEU PHE ASP THR PHE PRO GLN GLY LEU LEU HIS GLU ASN CYS GLY MET
PHE PHE ILE PRO LEU CYS LEU MET THR ILE LYS ASN ASP ASP SER ALA THR CYS LYS LYS MET ALA SER MET THR ILE LYS SER LEU LEU GLY LYS ILE SER LEU GLU LYS LYS ASP TRP LEU PHE ASP MET VAL THR THR TRP PHE GLY ALA LYS LYS ARG LEU ASN ARG GLN LEU ALA ALA
LEU ILE CYS GLY LEU PHE VAL GLU SER GLU GLY VAL ASP PHE GLU LYS ARG LEU GLY THR VAL LEU PRO VAL ILE GLU LYS GLU ILE ASP PRO GLU ASN PHE LYS ASP ILE MET GLU GLU THR GLU GLU LYS ALA ALA ASP ARG LEU LEU PHE SER PHE LEU THR LEU ILE THR LYS LEU
ILE LYS GLU CYS ASN ILE ILE GLN PHE THR LYS PRO ALA GLU THR LEU SER LYS ILE TRP SER HIS VAL HIS SER HIS LEU ARG HIS PRO HIS ASN TRP VAL TRP LEU THR ALA ALA GLN ILE PHE GLY LEU LEU PHE ALA SER CYS GLN PRO GLU GLU LEU ILE GLN LYS TRP ASN THR
LYS LYS THR LYS LYS HIS LEU PRO GLU PRO VAL ALA ILE LYS PHE LEU ALA SER ASP LEU ASP GLN LYS MET LYS SER ILE SER LEU ALA ALA SER CYS HIS GLN LEU HIS SER LYS PHE LEU ASP GLN SER LEU GLY GLU GLN VAL VAL LYS ASN LEU LEU PHE ALA ALA LYS VAL LEU TYR
LEU LEU GLU LEU TYR CYS GLU ASP LYS GLN SER LYS ILE LYS GLU ASP LEU GLU GLU GLN GLU ALA LEU GLU ASP GLY VAL ALA CYS ALA ALA ASP GLU LYS ALA GLU SER ASP GLY GLU GLU LYS GLU GLU VAL LYS GLU GLU GLU LEU GLY ARG PRO ALA THR LEU LEU TRP LEU ILE GLN LYS
LEU SER ARG ILE ALA LYS LEU GLU ALA ALA TYR SER PRO ARG ASN PRO LEU LYS ARG THR CYS ILE PHE LYS PHE LEU GLY ALA ALA VAL ALA MET ASP LEU GLY ILE ASP LYS VAL LYS PRO TYR LEU PRO MET ILE ILE ALA PRO LEU PHE ARG GLU LEU ASN SER THR TYR SER GLU GLN
ASP PRO LEU LEU LYS ASN LEU SER GLN GLU ILE ILE GLU LEU VAL GLY LYS LEU GLU SER PHE SER LEU ALA PHE ALA SER VAL GLN LYS GLN ALA ASN GLU LYS ARG ALA LEU ARG LYS LYS ARG LYS ALA LEU GLU PHE VAL THR ASN PRO ASP ILE ALA ALA LYS LYS

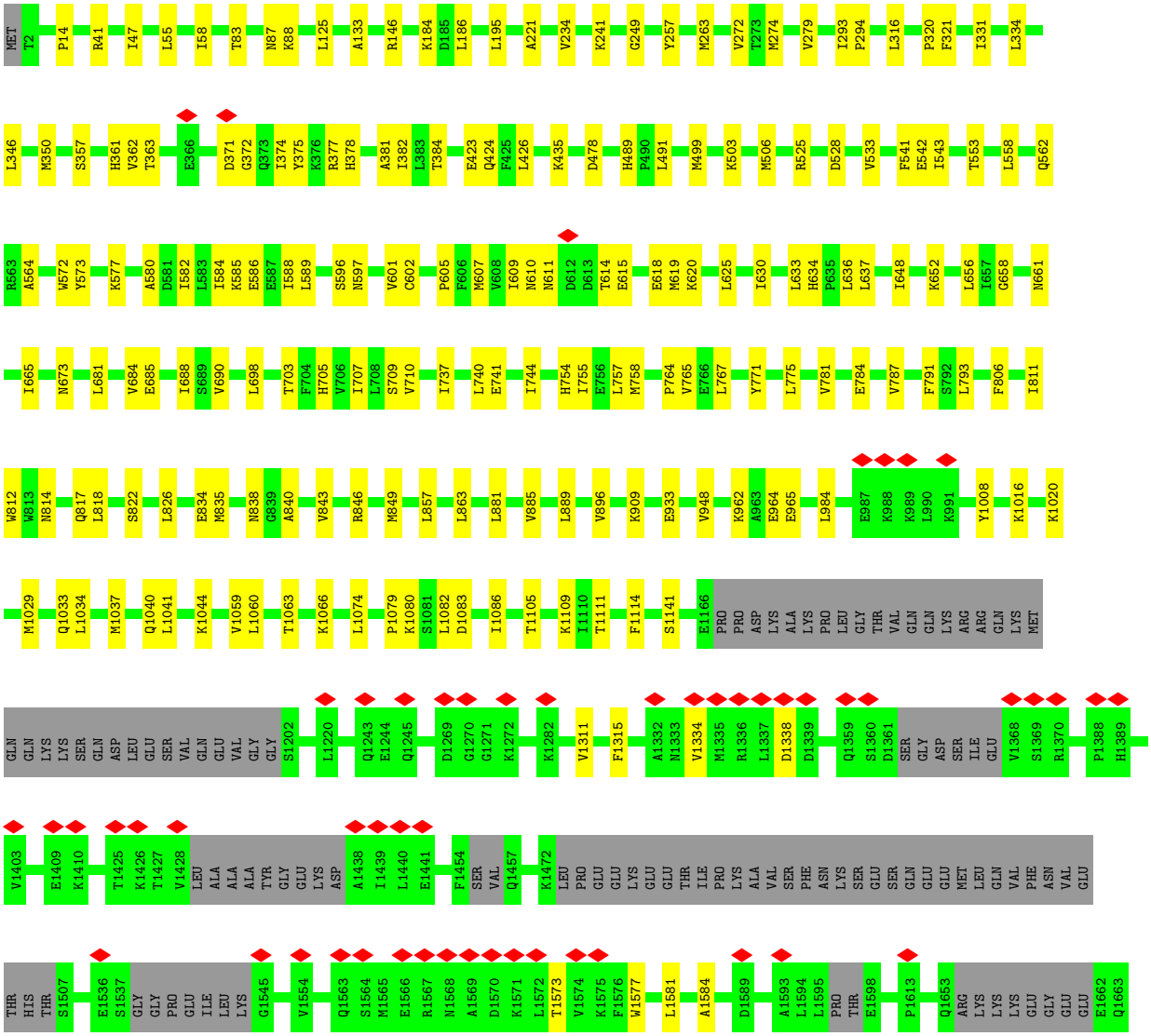
- Molecule 60: Transducin beta-like protein 3

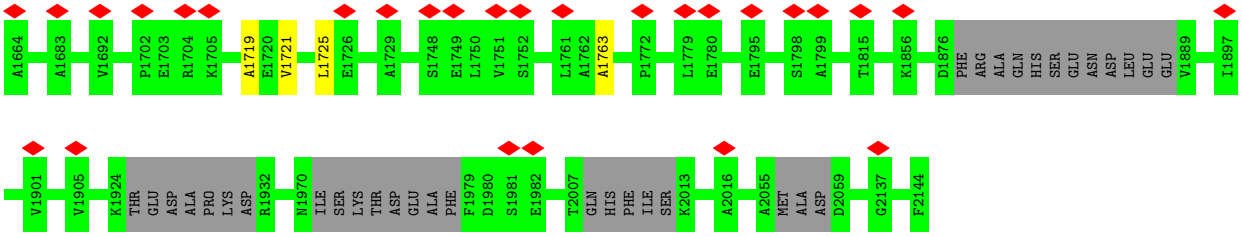
Chain LR:



- Molecule 61: HEAT repeat-containing protein 1

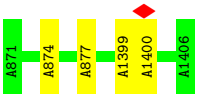
Chain LM:





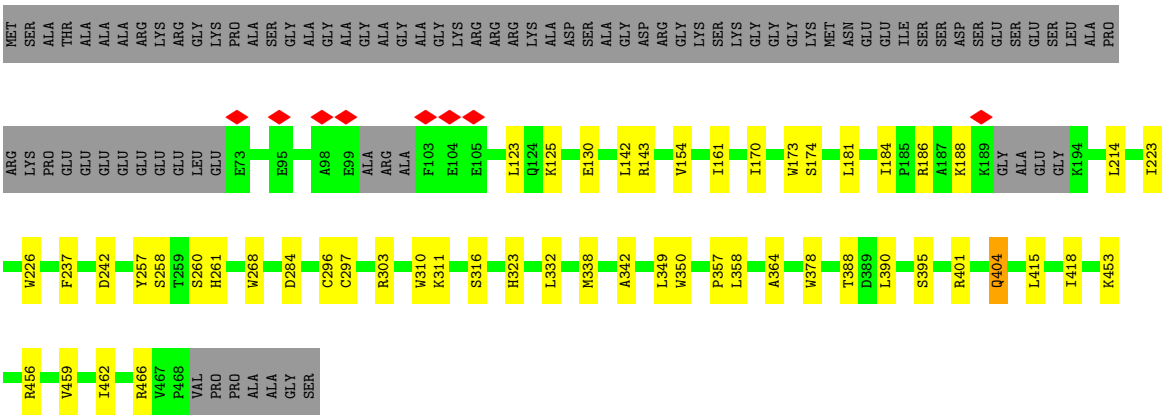
• Molecule 62: 5' ETS rRNA

Chain N0:



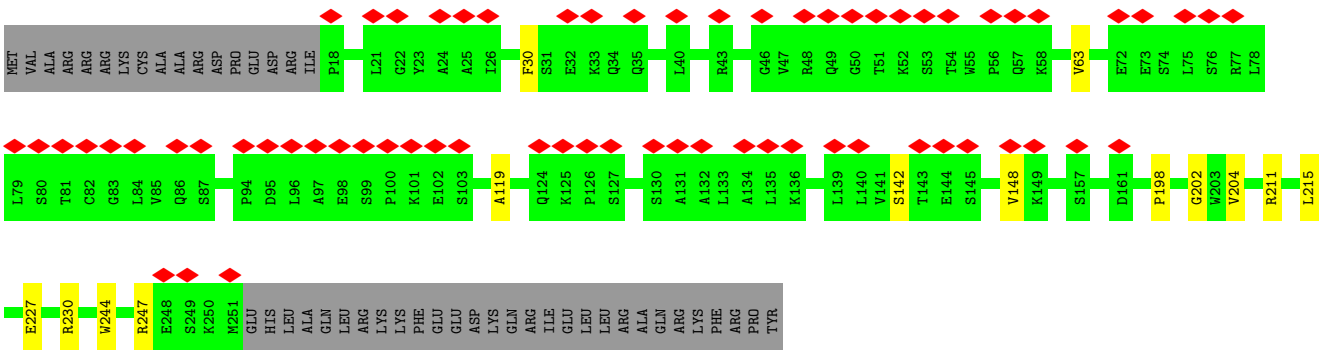
• Molecule 63: U3 small nucleolar RNA-interacting protein 2

Chain SG:



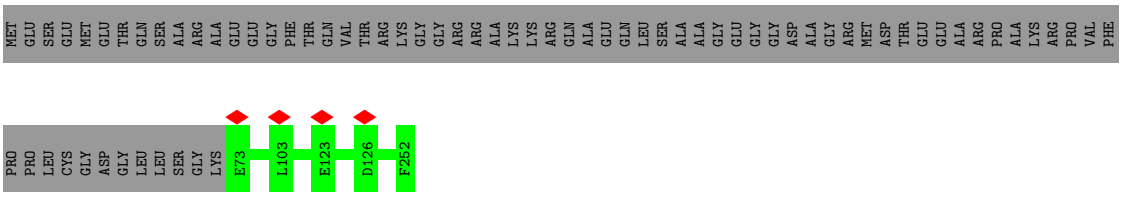
• Molecule 64: Ribosomal RNA-processing protein 7 homolog A

Chain NI:



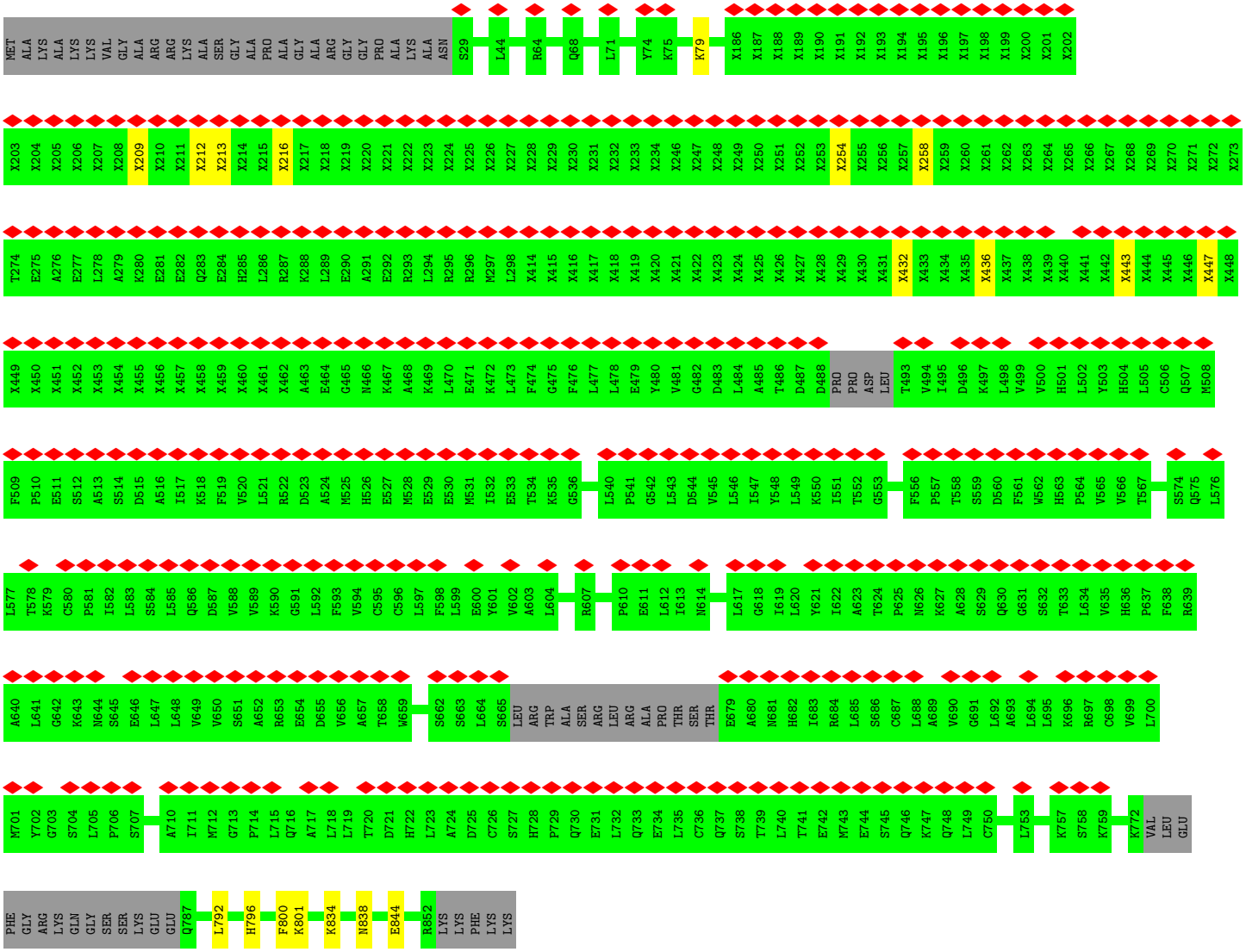
• Molecule 65: RNA-binding protein PNO1

Chain SW:



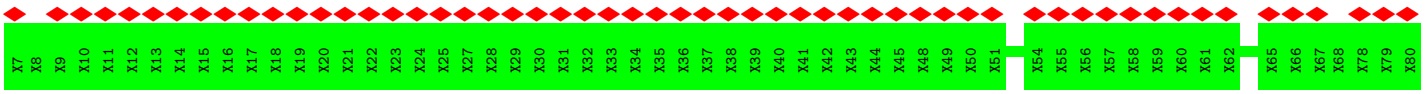
• Molecule 66: Nucleolar protein 14

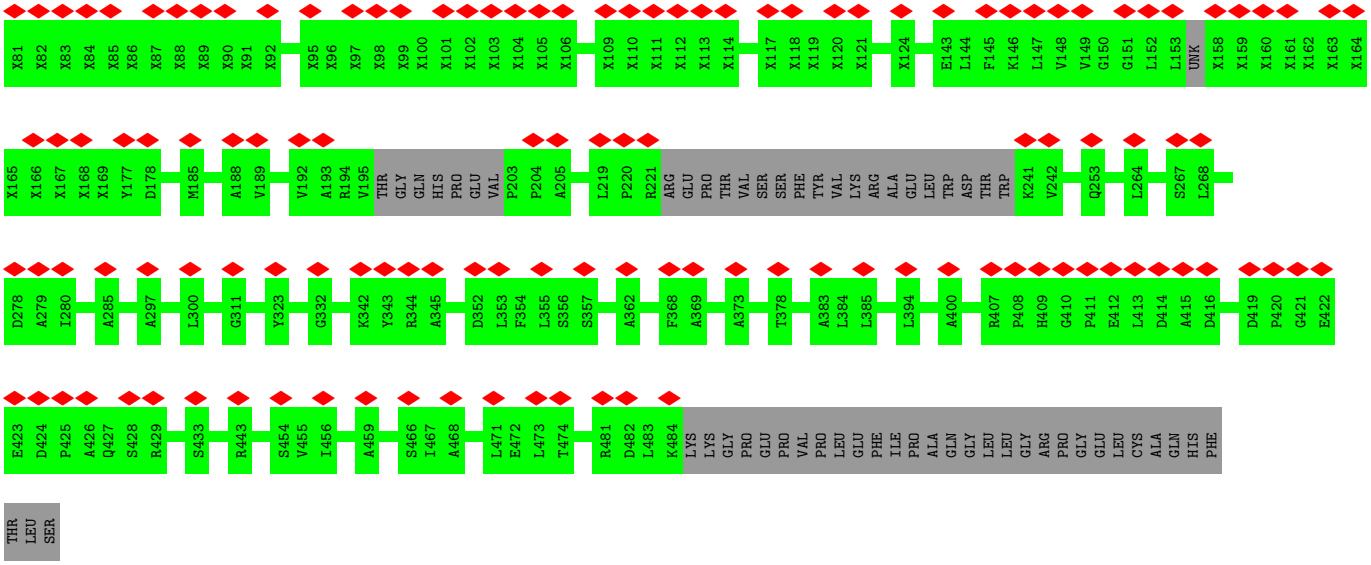
Chain ST:



• Molecule 67: Nucleolar complex protein 4 homolog

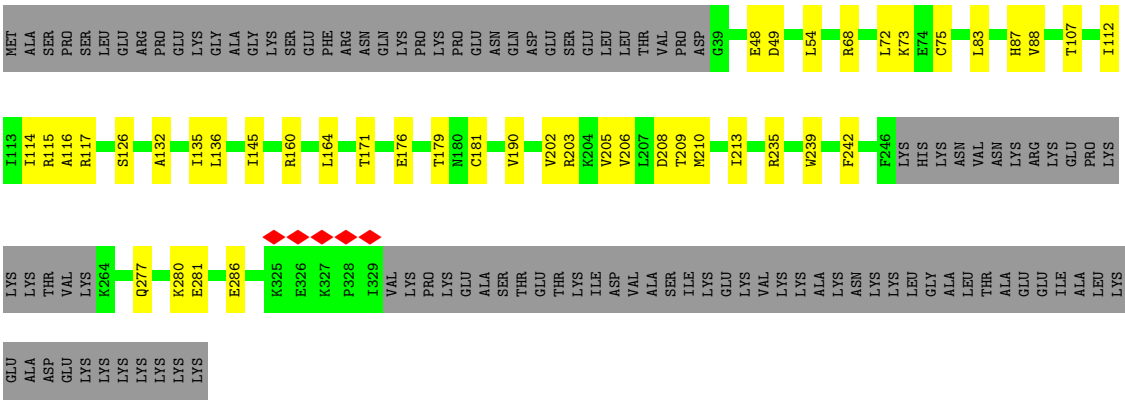
Chain SU:





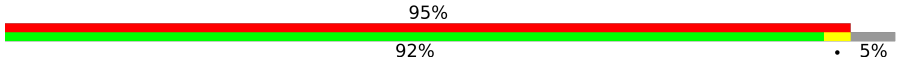
- Molecule 68: KRR1 small subunit processome component homolog

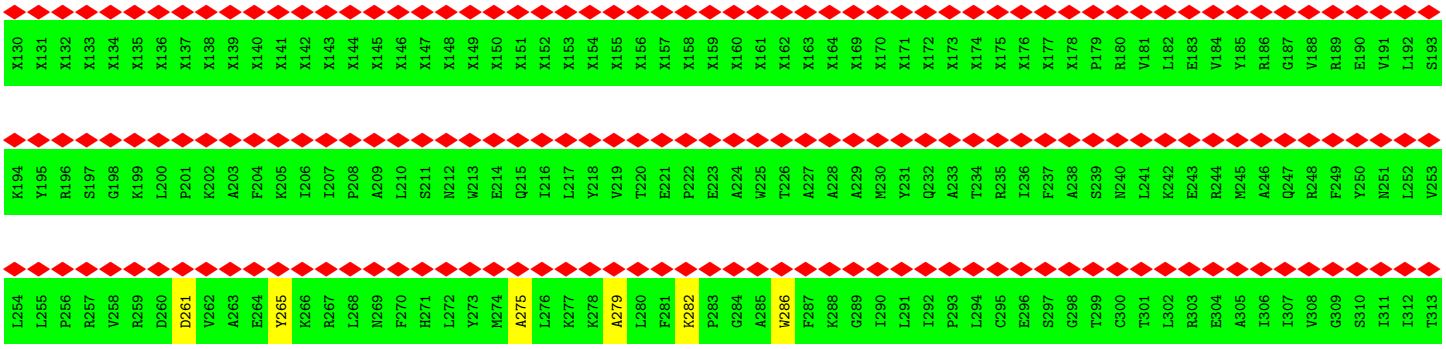
Chain NY:



- Molecule 69: Bystin

Chain SZ:





K314 C315 S316 I317 P318 V319 L320 H321 S322 S323 A324 A325 M326 L327 K328 I329 A330 E331 M332 E333 Y334 S335 G336 A337 N338 S339 I340 F341 L342 R343 L344 L345 L346 D347 K348 K349 Y350 A351 L352 P353 Y354 R355 V356 L357 D358 A359 L360 V361 F362 H363 F364 L365 G366 F367 R368 T369 E370 K371 R372 E373

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

4 Experimental information (i)

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 ($e^-/Å^2$)	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 (Å)	604.80005, 604.80005, 604.80005	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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: ATP, GTP, SAH, MG, 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	0.11	0/5739	0.31	0/8931
2	L1	0.12	0/31039	0.30	0/48327
3	L2	0.12	0/5130	0.29	0/7996
4	L3	0.09	0/425	0.27	0/591
5	L4	0.12	0/1944	0.31	0/2621
6	L5	0.15	0/1523	0.33	0/2048
7	L6	0.15	0/1830	0.34	0/2434
8	L7	0.14	0/1365	0.35	0/1830
9	L8	0.14	0/1500	0.35	0/2002
10	L9	0.15	0/1447	0.32	0/1930
11	LA	0.10	0/592	0.31	0/823
12	LC	0.17	0/1115	0.37	0/1494
13	LD	0.11	0/1225	0.31	0/1640
14	LF	0.13	0/868	0.32	0/1159
15	LG	0.13	0/490	0.29	0/656
16	LH	0.14	0/6127	0.37	0/8292
17	LI	0.09	0/1959	0.25	0/2719
18	LJ	0.15	0/3788	0.41	0/5128
19	LK	0.14	0/959	0.40	0/1302
19	LL	0.15	0/4072	0.39	0/5539
20	LN	0.14	0/5438	0.37	0/7377
21	LO	0.17	0/6835	0.40	0/9256
22	LP	0.13	0/4806	0.32	0/6455
23	LQ	0.13	0/6548	0.36	0/8839
24	LS	0.15	0/3621	0.34	0/4876
25	LT	0.14	0/6907	0.34	0/9359
26	LU	0.15	0/3695	0.35	0/4986
27	LW	0.15	0/3594	0.35	0/4867
28	LZ	0.15	0/1560	0.35	0/2104
29	NA	0.15	0/2084	0.33	0/2789
30	NB	0.14	0/622	0.30	0/816
31	ND	0.12	0/708	0.30	0/947

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	NE	0.14	0/807	0.36	0/1069
33	NF	0.09	0/1226	0.25	0/1649
34	NG	0.10	0/873	0.30	0/1177
35	NJ	0.15	0/6652	0.38	0/9006
35	NK	0.16	0/4023	0.40	0/5594
36	NM	0.11	0/1899	0.30	0/2533
37	NN	0.12	0/346	0.36	0/462
38	NO	0.15	0/1051	0.36	0/1406
39	NQ	0.12	0/653	0.31	0/876
41	NT	0.08	0/285	0.26	0/395
42	NU	0.08	0/296	0.22	0/411
43	NW	0.17	0/2556	0.44	0/3469
44	SA	0.14	0/3122	0.31	0/4208
45	SB	0.14	0/3491	0.33	0/4695
46	SC	0.14	0/1818	0.35	0/2463
46	SD	0.16	0/1878	0.32	0/2540
47	SE	0.14	0/980	0.34	0/1323
47	SF	0.18	0/967	0.38	0/1305
48	SH	0.14	0/2882	0.33	0/3887
49	SI	0.15	0/6949	0.34	1/9339 (0.0%)
50	SJ	0.22	0/1007	0.45	0/1401
50	SK	0.16	0/1609	0.39	1/2181 (0.0%)
51	SL	0.15	0/1619	0.35	0/2174
52	SM	0.15	0/2420	0.34	0/3264
53	SQ	0.15	0/1561	0.31	0/2083
54	SR	0.16	0/828	0.40	0/1110
55	SS	0.18	0/1663	0.41	2/2250 (0.1%)
57	SY	0.13	0/2051	0.30	0/2723
58	NH	0.16	1/5264 (0.0%)	0.36	0/7329
59	SP	0.13	0/11868	0.33	0/16336
60	LR	0.13	0/4340	0.35	0/5985
61	LM	0.18	0/13315	0.40	0/18214
62	N0	0.10	0/284	0.21	0/432
63	SG	0.14	0/2935	0.35	0/3981
64	NI	0.15	0/1471	0.41	0/2009
65	SW	0.17	0/889	0.37	0/1237
66	ST	0.14	0/2435	0.33	0/3343
67	SU	0.13	0/1463	0.36	0/2037
68	NY	0.14	0/2133	0.33	0/2887
69	SZ	0.15	0/1216	0.40	0/1696
All	All	0.14	1/222680 (0.0%)	0.34	4/310612 (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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	NH	118	ARG	CA-CB	5.82	1.61	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
49	SI	631	PRO	N-CA-CB	6.74	110.41	103.00
55	SS	198	PRO	N-CD-CG	-6.31	93.73	103.20
50	SK	168	PRO	CA-N-CD	-5.47	104.34	112.00
55	SS	198	PRO	CA-N-CD	-5.25	104.65	112.00

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	60	0
2	L1	27777	0	14063	274	0
3	L2	4589	0	2306	55	0
4	L3	571	0	220	0	0
5	L4	1902	0	1990	20	0
6	L5	1501	0	1557	24	0
7	L6	1811	0	1974	34	0
8	L7	1346	0	1410	14	0
9	L8	1474	0	1542	20	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	L9	1425	0	1541	20	0
11	LA	593	0	277	1	0
12	LC	1098	0	1168	11	0
13	LD	1204	0	1274	11	0
14	LF	851	0	894	6	0
15	LG	488	0	514	8	0
16	LH	5987	0	5953	84	0
17	LI	2675	0	993	5	0
18	LJ	3711	0	3758	71	0
19	LK	943	0	1023	18	0
19	LL	3982	0	4031	68	0
20	LN	5299	0	5269	77	0
21	LO	6676	0	6579	78	0
22	LP	4705	0	4720	45	0
23	LQ	6438	0	6400	113	0
24	LS	3560	0	3570	58	0
25	LT	6756	0	6768	71	0
26	LU	3611	0	3618	54	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	10	0
31	ND	696	0	729	9	0
32	NE	799	0	854	10	0
33	NF	1202	0	1289	12	0
34	NG	861	0	871	11	0
35	NJ	6526	0	6599	82	0
35	NK	4030	0	1806	3	0
36	NM	1873	0	1968	24	0
37	NN	340	0	345	6	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	58	0
44	SA	3077	0	3139	35	0
45	SB	3439	0	3559	63	0
46	SC	1781	0	1803	32	0
46	SD	1841	0	1867	21	0
47	SE	968	0	1017	7	0
47	SF	955	0	1008	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	SH	2832	0	2937	35	0
49	SI	6801	0	6971	89	0
50	SJ	1008	0	440	0	0
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	10	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	47	0
60	LR	4321	0	2717	29	0
61	LM	13156	0	10845	118	0
62	N0	264	0	134	0	0
63	SG	2878	0	2740	32	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	2052	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 2052 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	1.23	0.85
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:182:MET:HE1	19:LL:231:ILE:HB	1.66	0.78
19:LL:276:THR:HB	19:LL:286:LYS:HB2	1.65	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%)	48	80
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%)	76	78
9	L8	155/180 (86%)	155 (100%)	0	100	100
10	L9	152/168 (90%)	152 (100%)	0	100	100
12	LC	114/121 (94%)	114 (100%)	0	100	100
13	LD	133/142 (94%)	133 (100%)	0	100	100
14	LF	92/115 (80%)	92 (100%)	0	100	100
15	LG	55/62 (89%)	54 (98%)	1 (2%)	51	67
16	LH	670/748 (90%)	669 (100%)	1 (0%)	88	89
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%)	456 (100%)	0	100	100
20	LN	582/597 (98%)	582 (100%)	0	100	100
21	LO	726/783 (93%)	726 (100%)	0	100	100
22	LP	499/527 (95%)	499 (100%)	0	100	100
23	LQ	690/828 (83%)	690 (100%)	0	100	100
24	LS	393/476 (83%)	393 (100%)	0	100	100
25	LT	744/823 (90%)	744 (100%)	0	100	100
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%)	63	72
33	NF	130/131 (99%)	130 (100%)	0	100	100
34	NG	92/119 (77%)	91 (99%)	1 (1%)	65	73
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%)	282 (100%)	0	100	100
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%)	192 (100%)	0	100	100
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%)	85 (100%)	0	100	100
55	SS	177/686 (26%)	177 (100%)	0	100	100
57	SY	219/232 (94%)	219 (100%)	0	100	100
59	SP	504/2522 (20%)	504 (100%)	0	100	100
60	LR	133/672 (20%)	133 (100%)	0	100	100
61	LM	977/1943 (50%)	977 (100%)	0	100	100
63	SG	286/382 (75%)	285 (100%)	1 (0%)	86	85
64	NI	76/246 (31%)	76 (100%)	0	100	100
66	ST	59/439 (13%)	59 (100%)	0	100	100
68	NY	211/340 (62%)	211 (100%)	0	100	100
All	All	15592/25272 (62%)	15586 (100%)	6 (0%)	100	100

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	NE	273	ASN
34	NG	38	ASN

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Mol	Chain	Res	Type
63	SG	404	GLN
15	LG	29	GLN
8	L7	163	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 153 such sidechains are listed below:

Mol	Chain	Res	Type
49	SI	370	HIS
61	LM	705	HIS
49	SI	974	GLN
57	SY	21	GLN
66	ST	843	GLN

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 oligosaccharides 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	$\#\|Z\| > 2$
72	GTP	SI	2001	70	33,34,34	0.94	1 (3%)	50,54,54	1.61	9 (18%)
74	ATP	NH	3000	70	32,33,33	0.28	0	48,52,52	0.38	0
73	SAH	SK	301	-	27,28,28	1.06	4 (14%)	36,40,40	2.00	9 (25%)
74	ATP	NK	1101	-	32,33,33	0.25	0	48,52,52	0.30	0
73	SAH	SJ	301	-	27,28,28	1.09	4 (14%)	36,40,40	2.00	9 (25%)

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
72	GTP	SI	2001	70	-	7/22/38/38	0/3/3/3
74	ATP	NH	3000	70	-	7/22/38/38	0/3/3/3
73	SAH	SK	301	-	-	5/15/31/31	0/3/3/3
74	ATP	NK	1101	-	-	8/22/38/38	0/3/3/3
73	SAH	SJ	301	-	-	1/15/31/31	0/3/3/3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
73	SJ	301	SAH	C2-N1	2.64	1.38	1.33
73	SJ	301	SAH	C2-N3	2.45	1.38	1.33
73	SK	301	SAH	C2-N3	2.43	1.38	1.33
73	SK	301	SAH	C2-N1	2.22	1.37	1.33
73	SK	301	SAH	OXT-C	-2.21	1.23	1.30

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
73	SK	301	SAH	N3-C2-N1	-5.75	119.88	128.58
73	SJ	301	SAH	N3-C2-N1	-5.41	120.39	128.58
72	SI	2001	GTP	C5-C4-N3	-5.30	119.95	128.39
72	SI	2001	GTP	C2-N3-C4	4.72	120.42	112.30
73	SJ	301	SAH	C5-C4-N3	-4.55	120.45	126.72

There are no chirality outliers.

5 of 28 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
74	NH	3000	ATP	C5'-O5'-PA-O1A
74	NH	3000	ATP	C5'-O5'-PA-O3A
74	NK	1101	ATP	C5'-O5'-PA-O1A

There are no ring outliers.

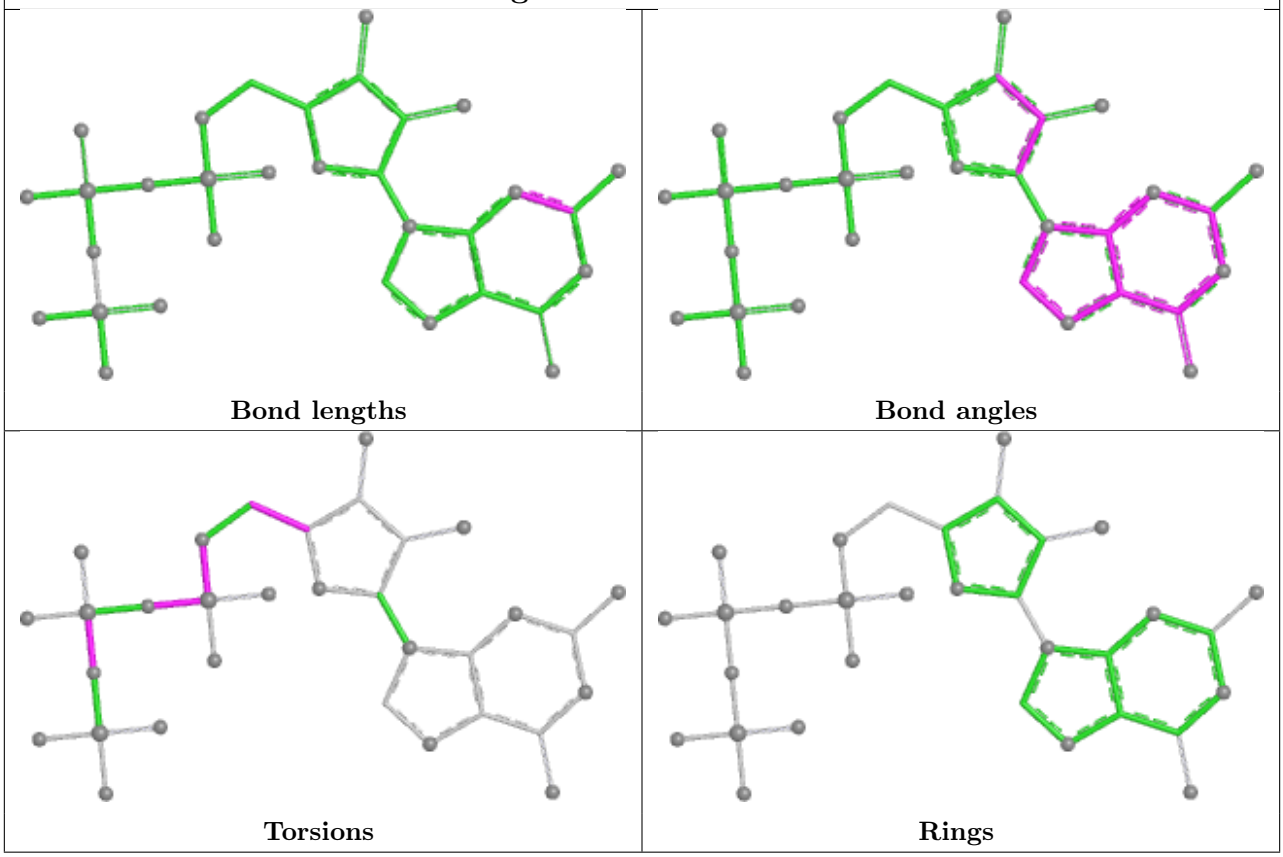
3 monomers are involved in 5 short contacts:

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

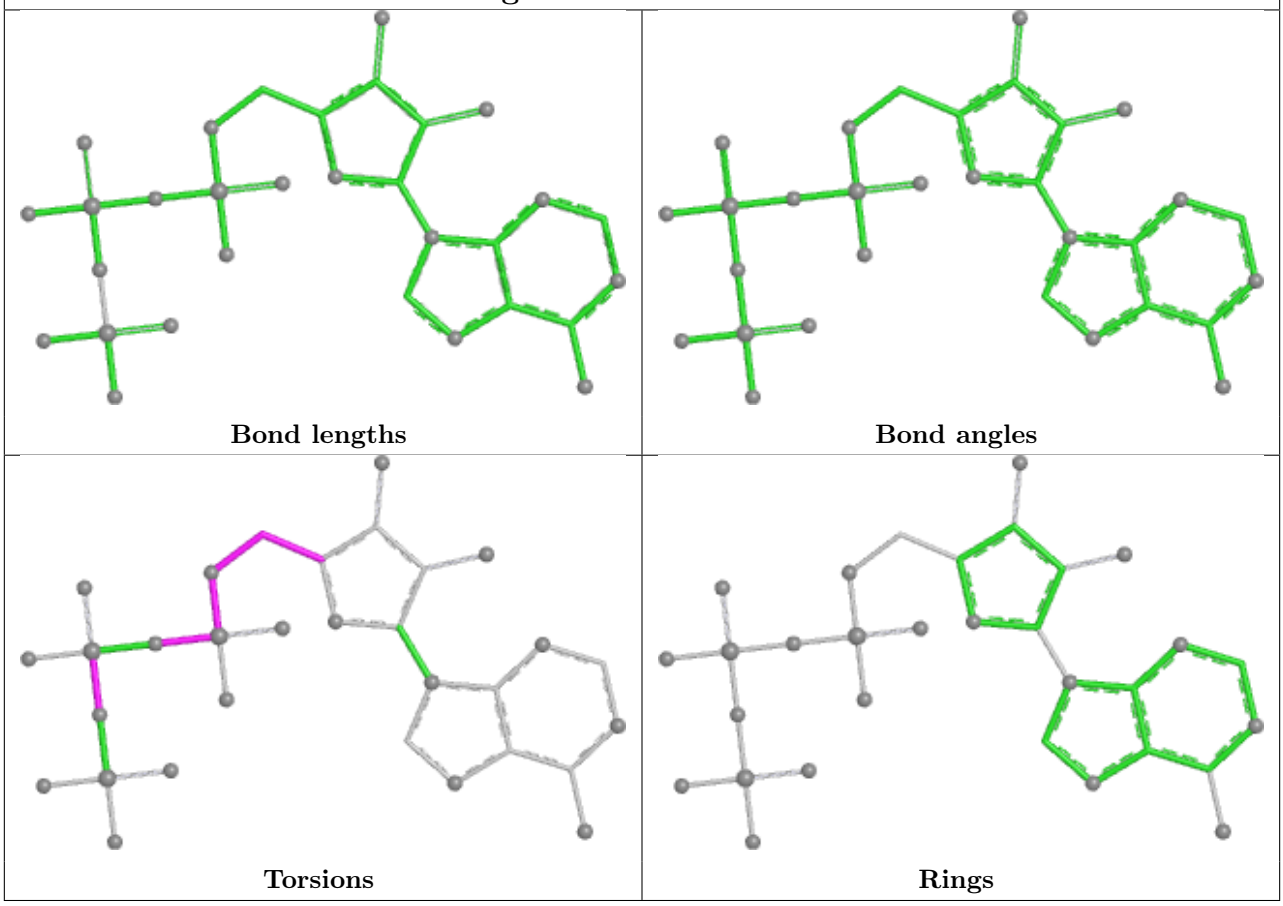
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.

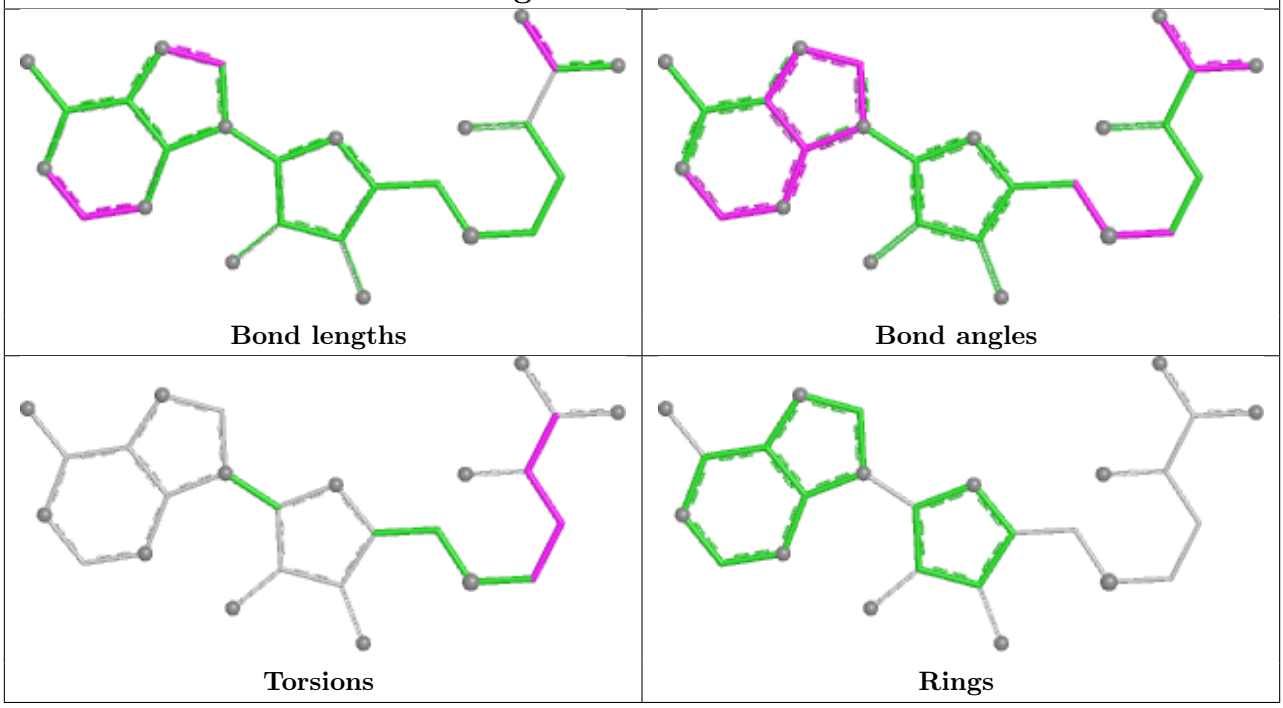
Ligand GTP SI 2001



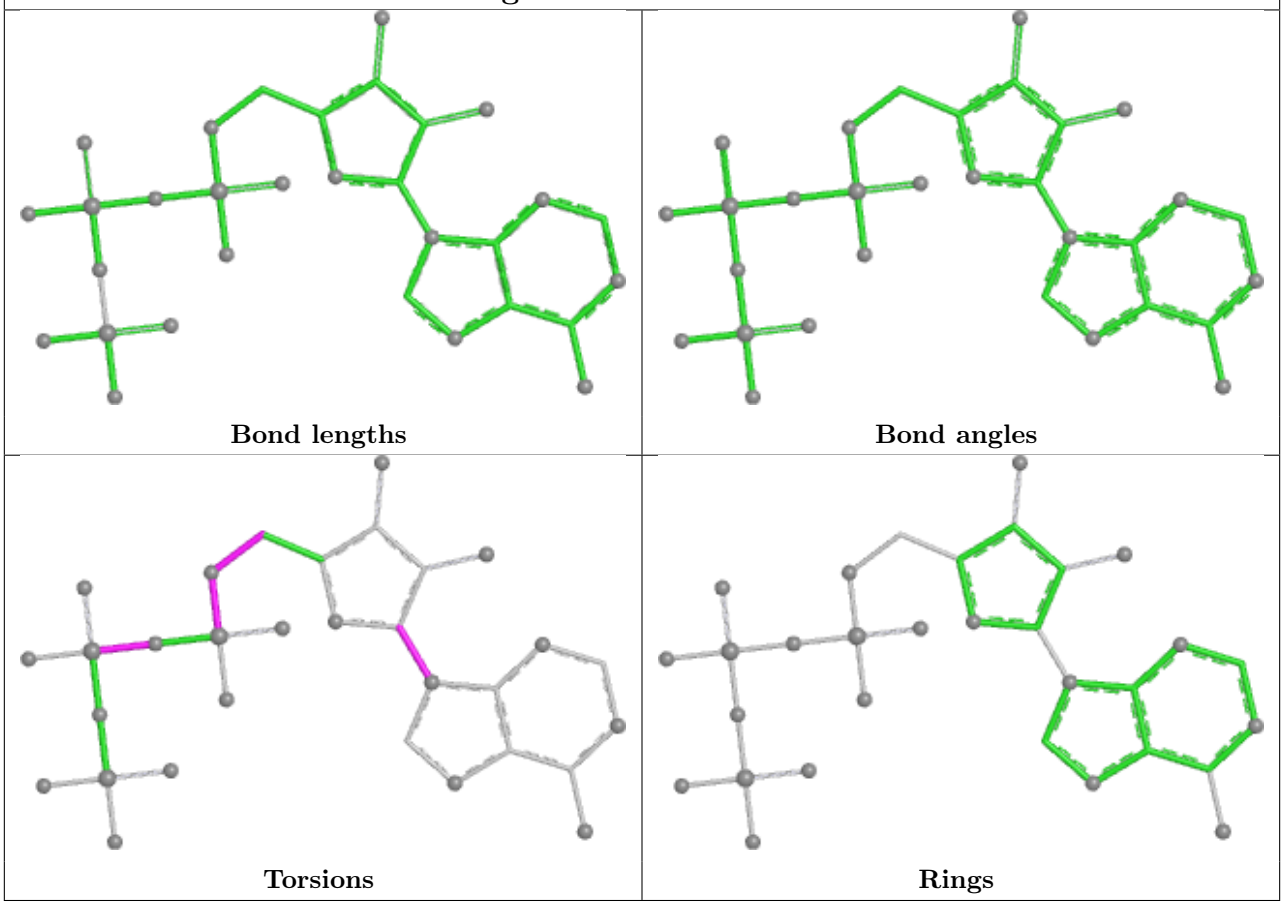
Ligand ATP NH 3000



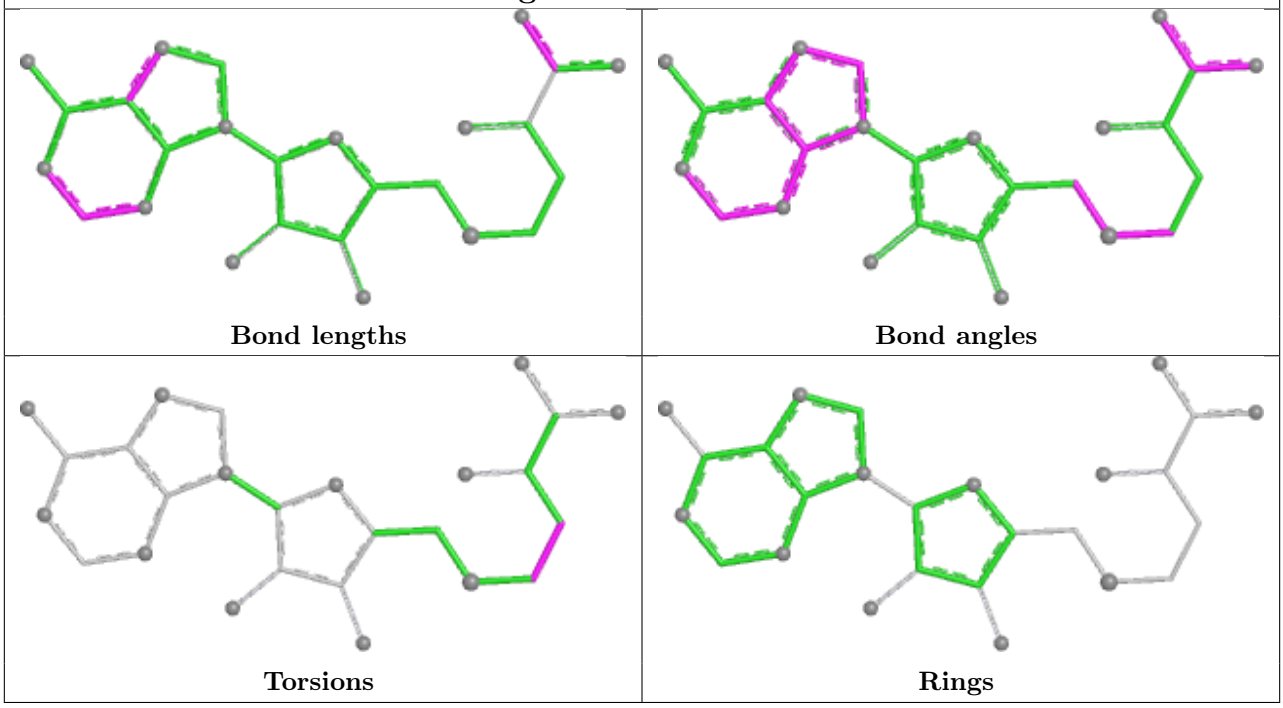
Ligand SAH SK 301



Ligand ATP NK 1101



Ligand SAH SJ 301



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

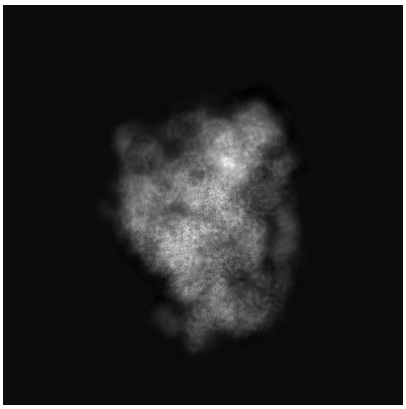
6 Map visualisation (i)

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.

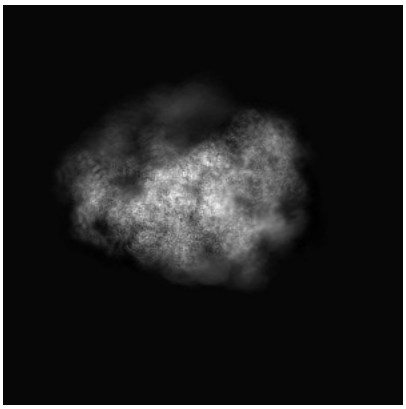
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

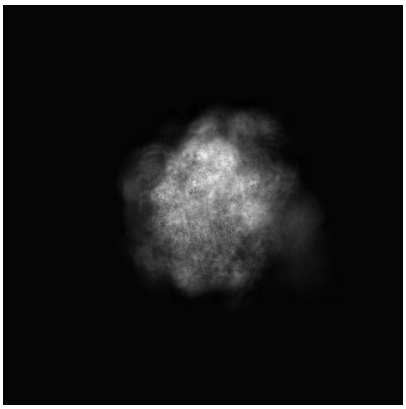
6.1.1 Primary map



X

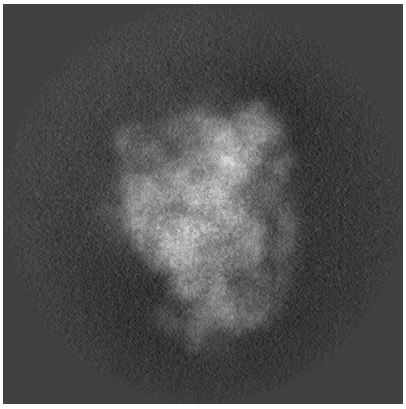


Y

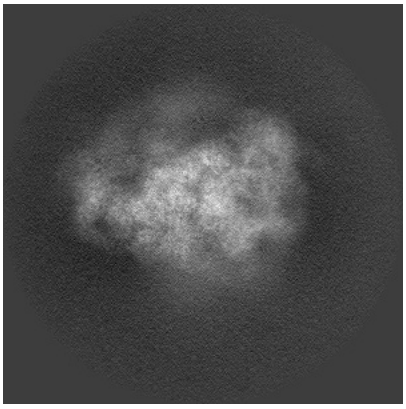


Z

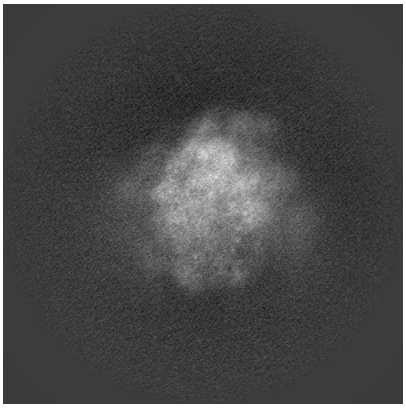
6.1.2 Raw map



X



Y

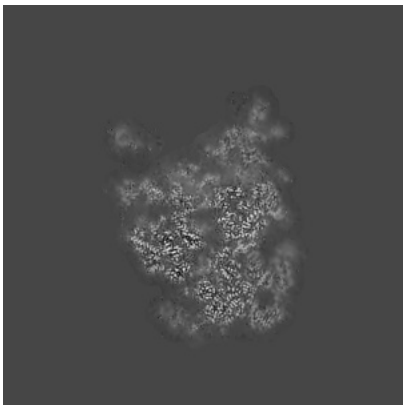


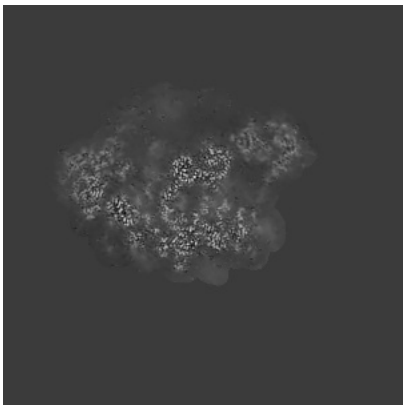
Z

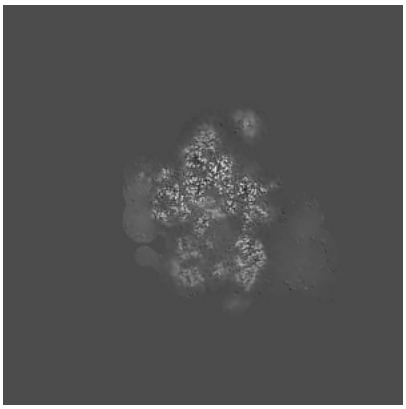
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

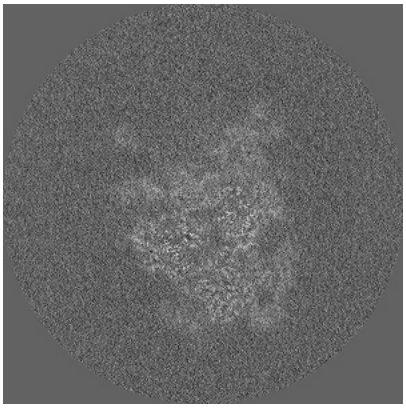
6.2.1 Primary map

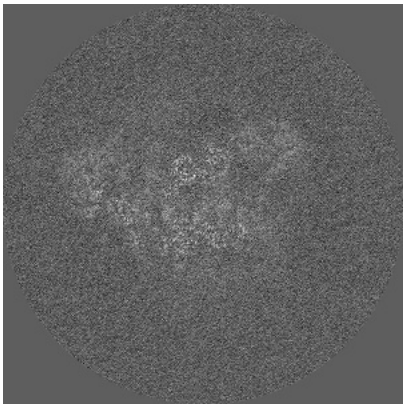

X Index: 280

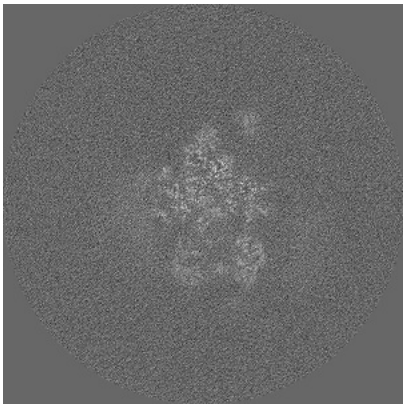

Y Index: 280


Z Index: 280

6.2.2 Raw map


X Index: 280

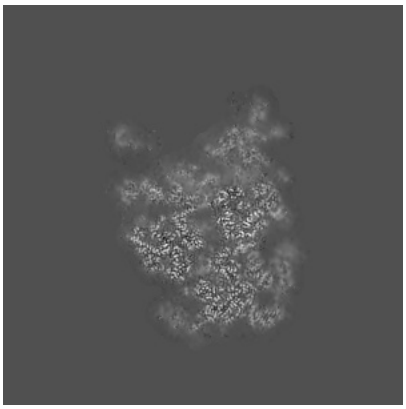

Y Index: 280


Z Index: 280

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

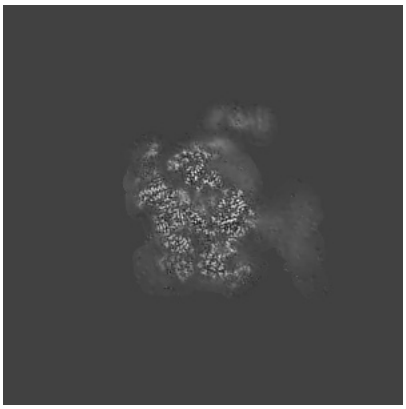
6.3 Largest variance slices (i)

6.3.1 Primary map



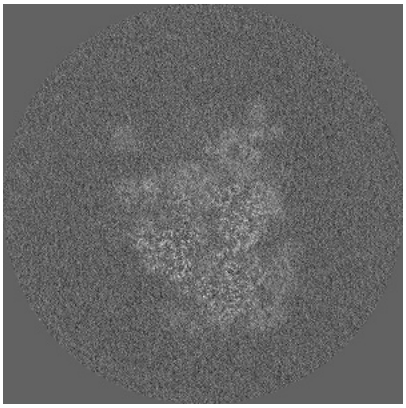
X Index: 281

Y Index: 310

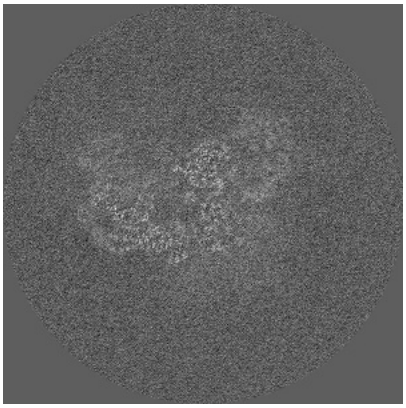


Z Index: 244

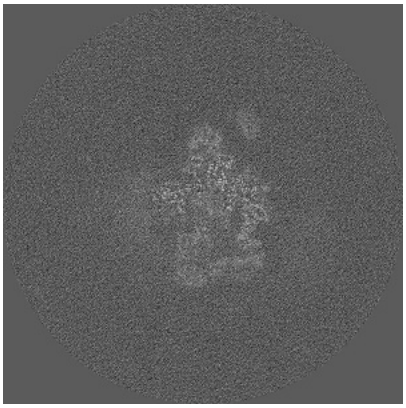
6.3.2 Raw map



X Index: 278



Y Index: 298

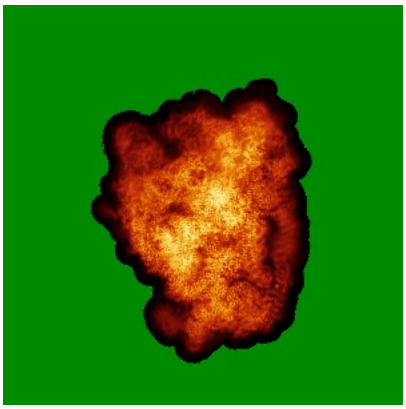


Z Index: 285

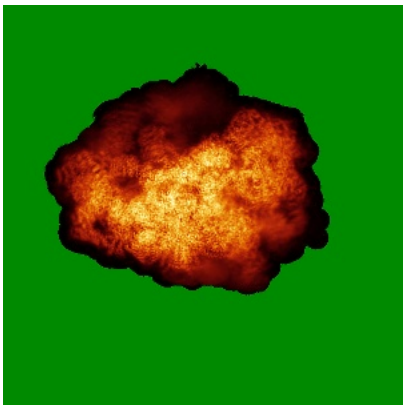
The images above show the largest variance slices of the map in three orthogonal directions.

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

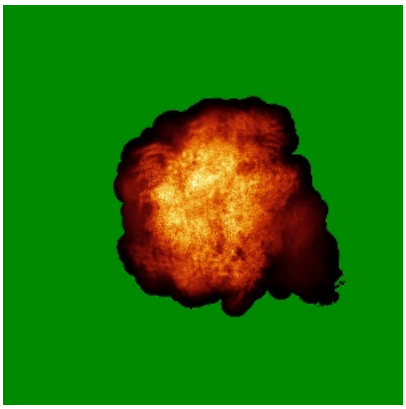
6.4.1 Primary map



X

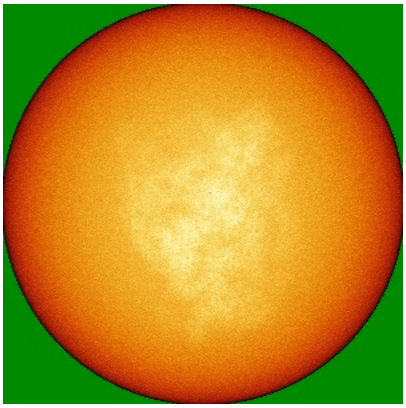


Y

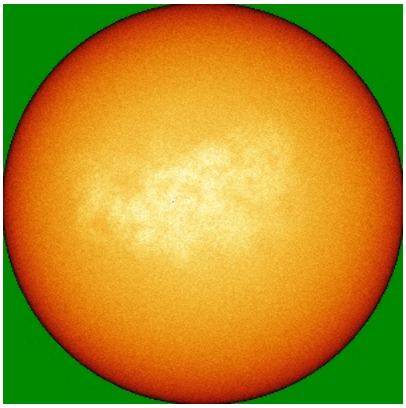


Z

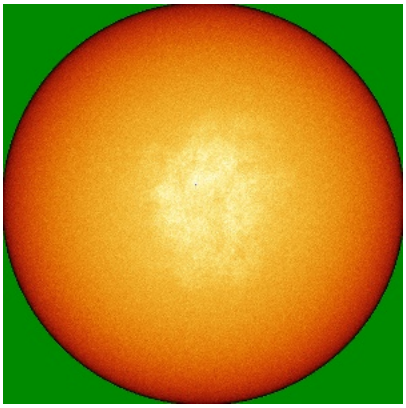
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map

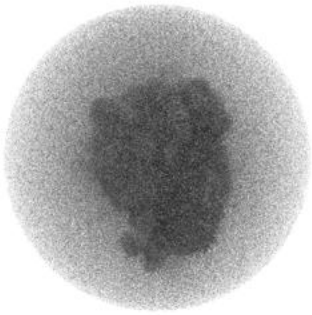
X

Y

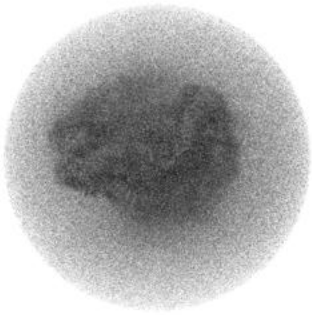
Z

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

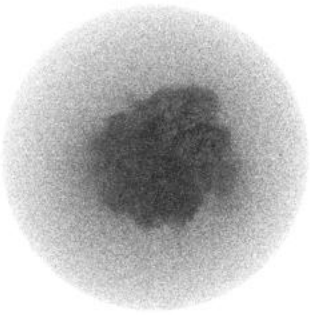
6.5.2 Raw map



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.

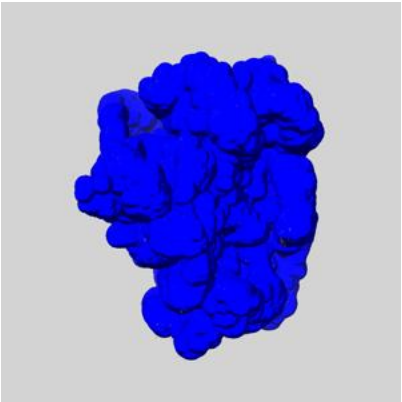
6.6 Mask visualisation (i)

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

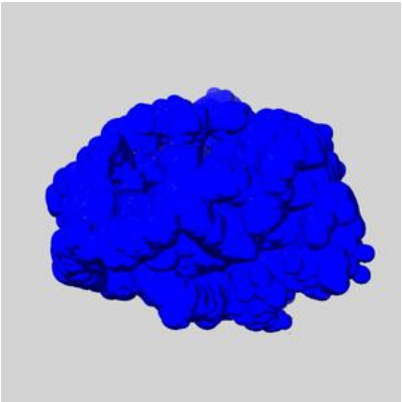
A mask typically either:

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

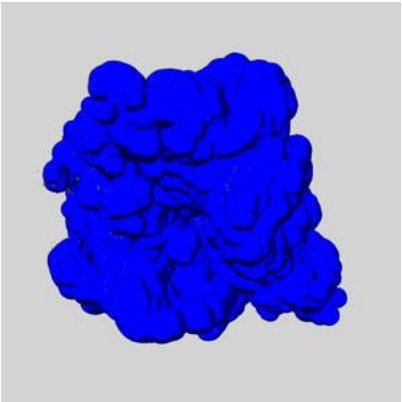
6.6.1 emd_23937_msk_1.map (i)



X



Y

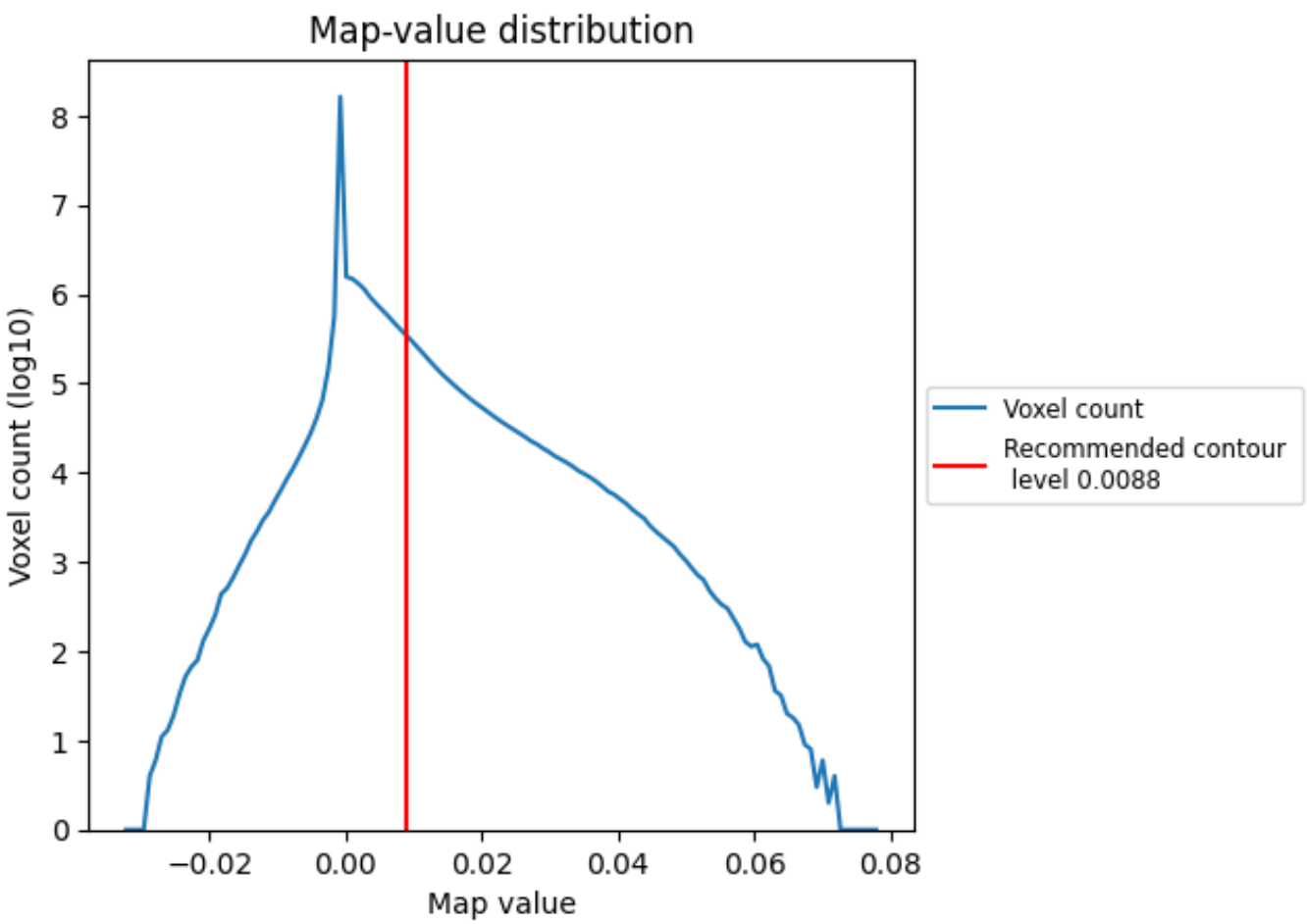


Z

7 Map analysis (i)

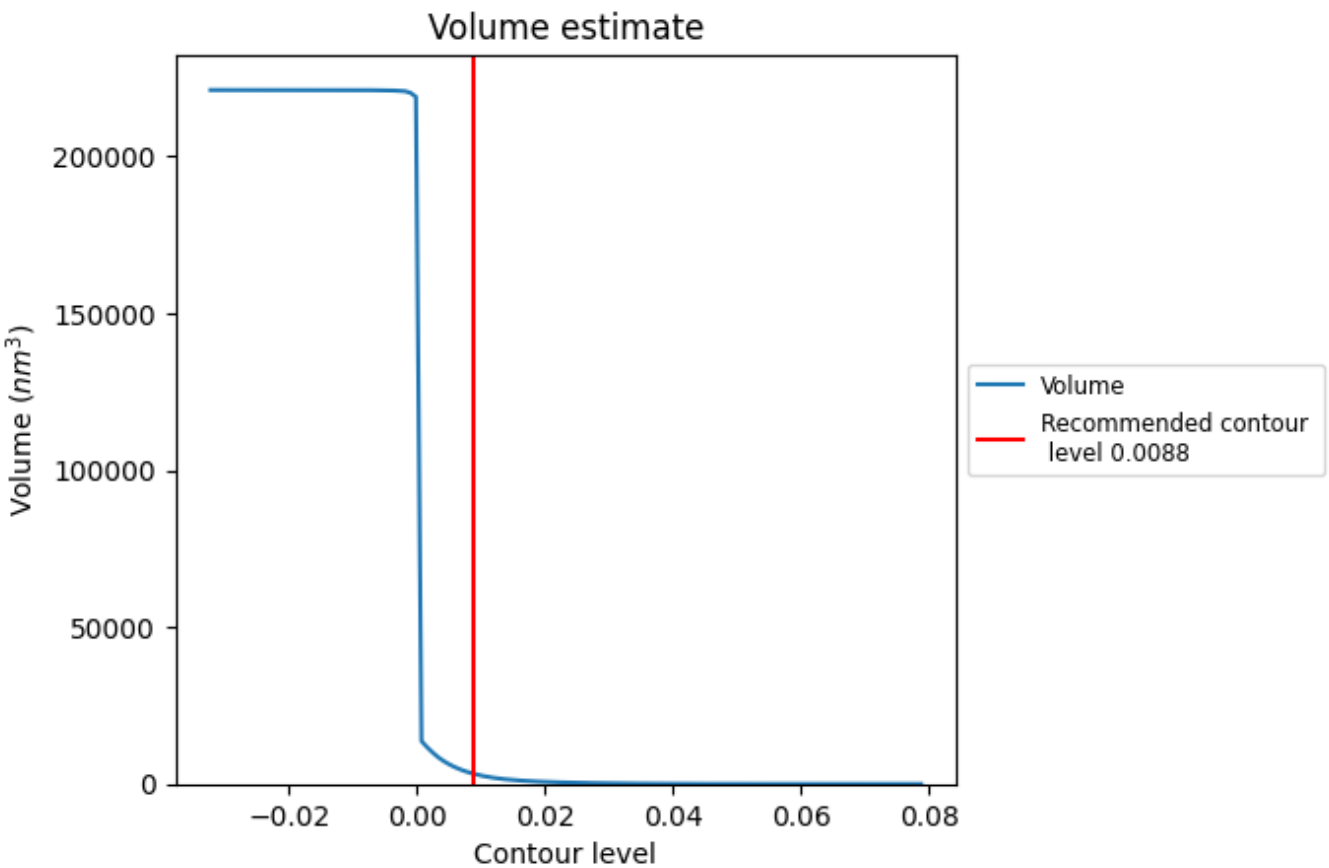
This section contains the results of statistical analysis of the map.

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.

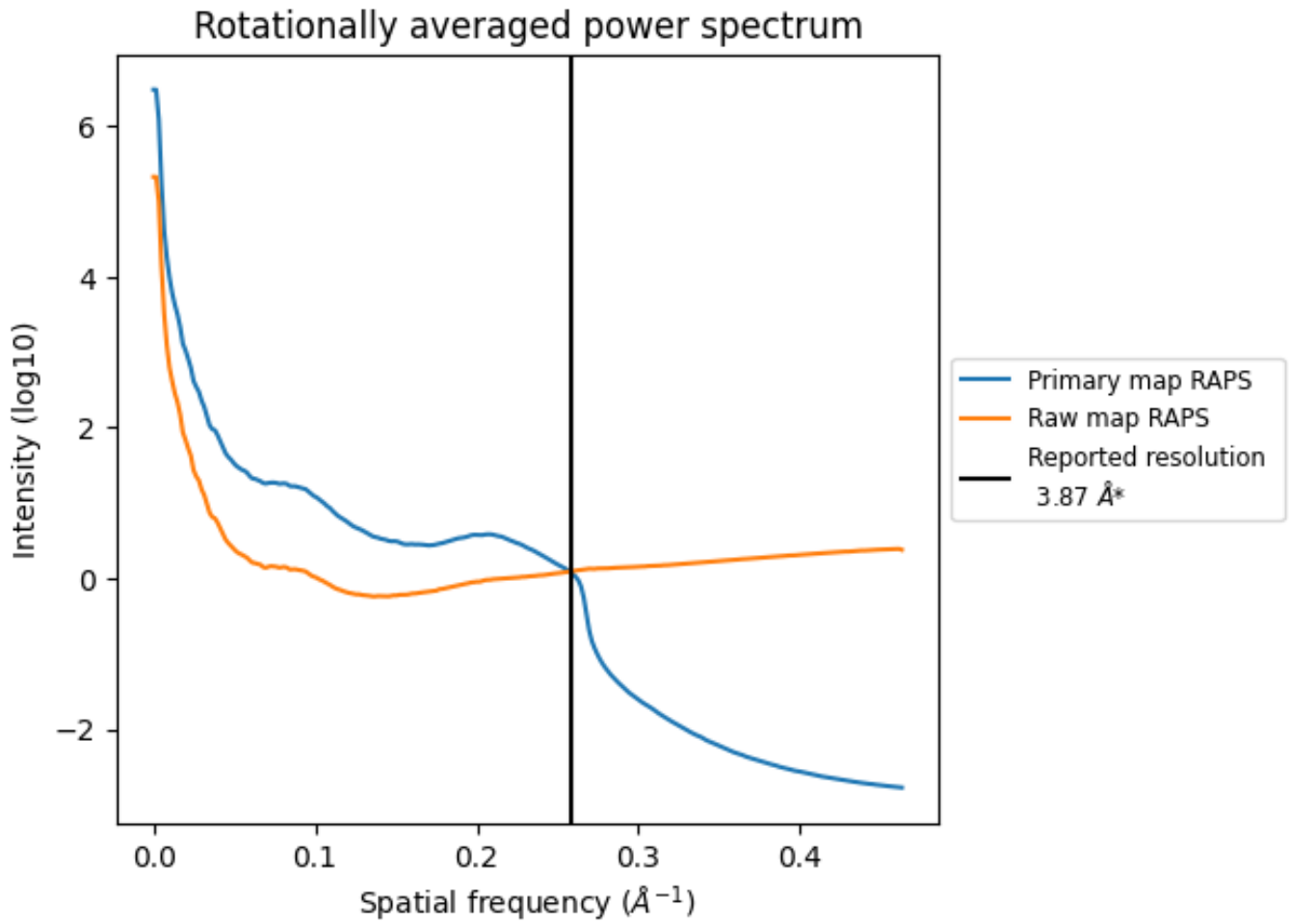
7.2 Volume estimate (i)



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)

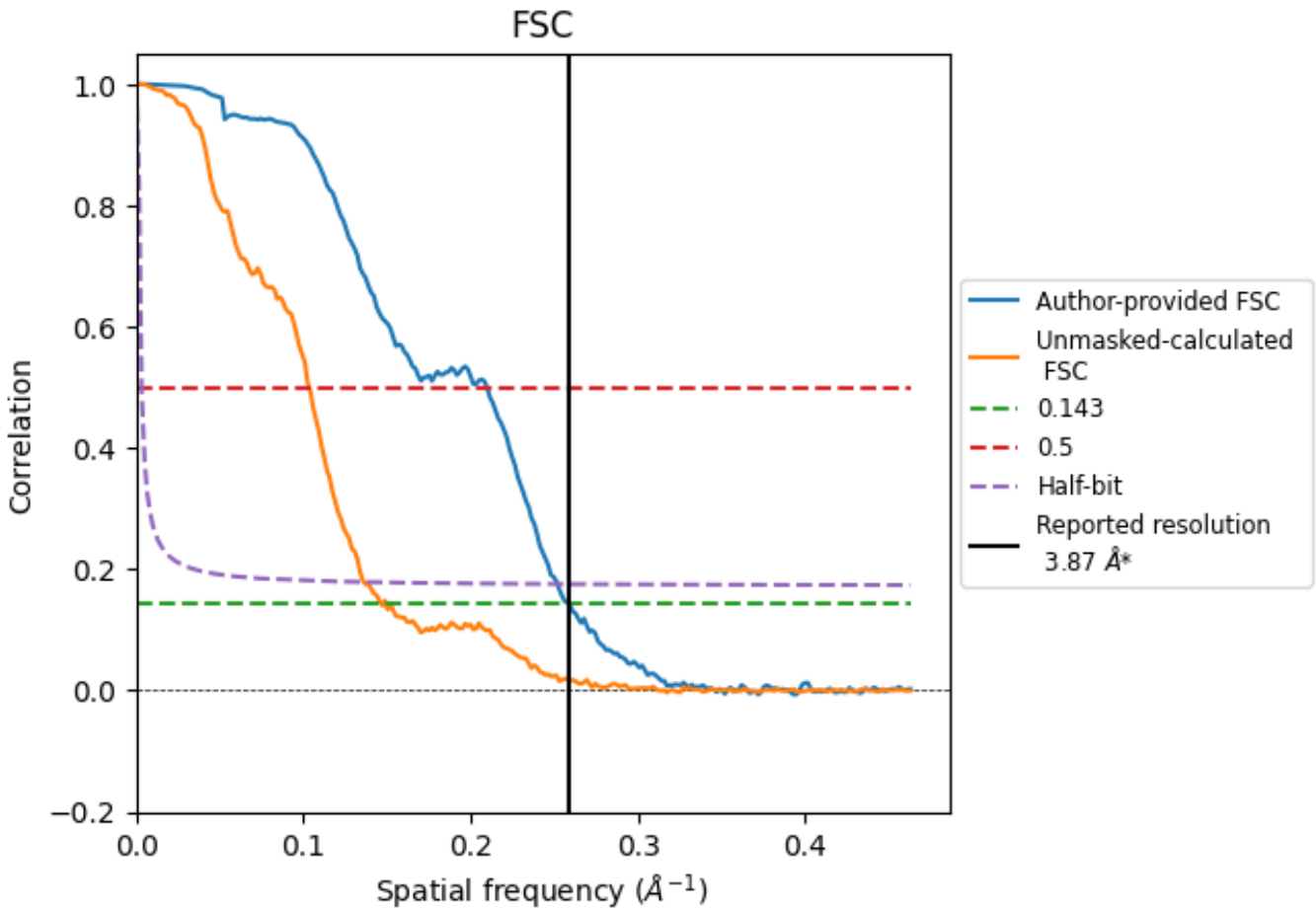


*Reported resolution corresponds to spatial frequency of 0.258 Å^{-1}

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)

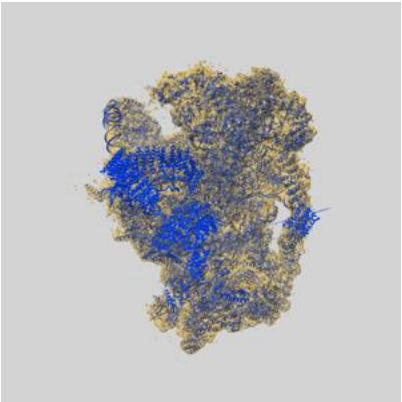
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.87	-	-
Author-provided FSC curve	3.87	4.77	3.97
Unmasked-calculated*	6.83	9.67	7.34

*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 %

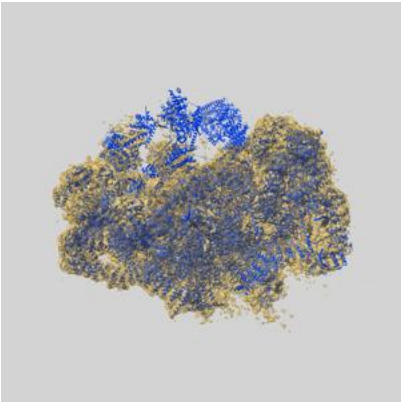
9 Map-model fit (i)

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 18.

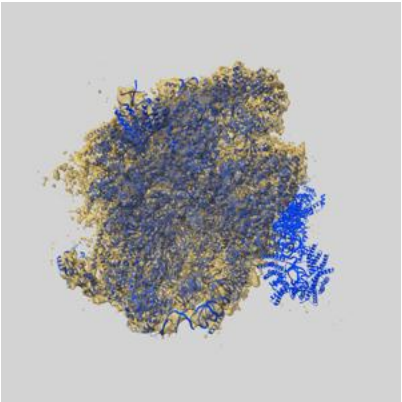
9.1 Map-model overlay (i)



X



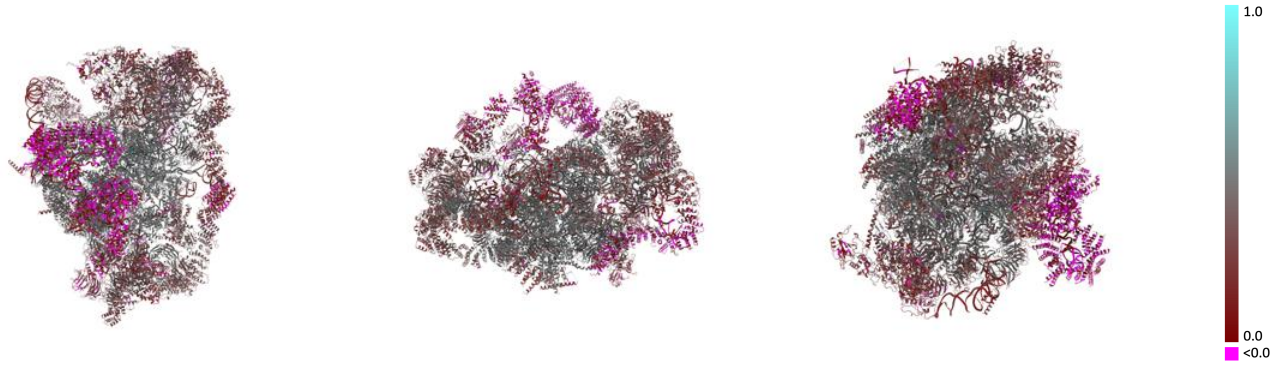
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0088 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.

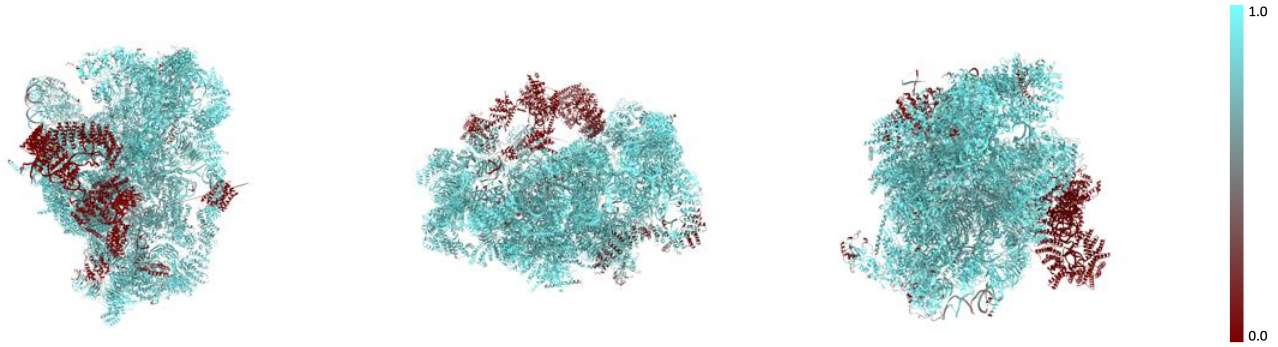
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

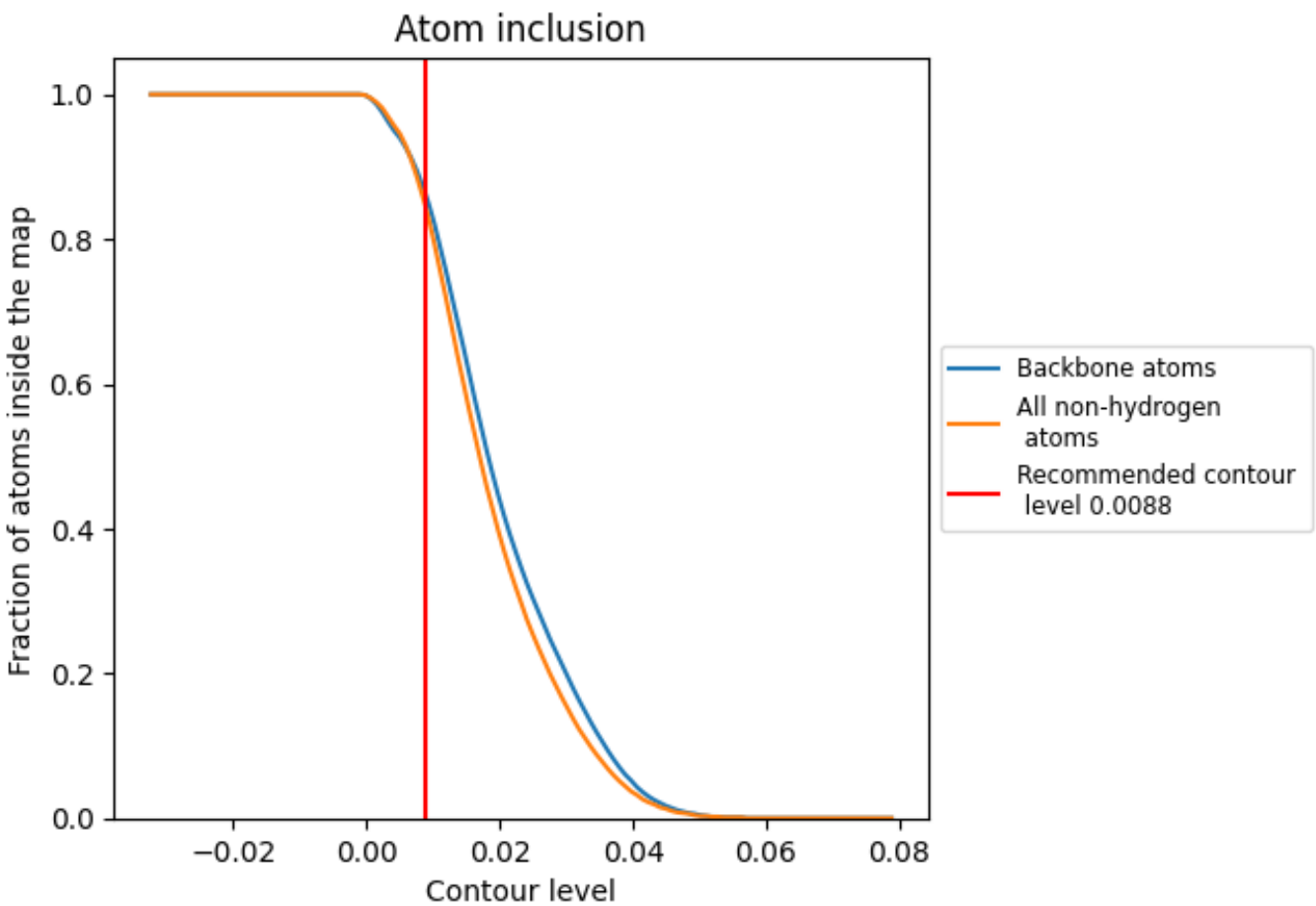
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0088).

9.4 Atom inclusion (i)



At the recommended contour level, 86% of all backbone atoms, 85% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.0088) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8480	0.3570
L0	0.7810	0.3070
L1	0.8020	0.3010
L2	0.9300	0.3620
L3	0.0540	0.0690
L4	0.9620	0.4020
L5	0.9620	0.4680
L6	0.9010	0.3800
L7	0.8450	0.3190
L8	0.9420	0.3350
L9	0.9750	0.4920
LA	0.0000	0.0350
LC	0.9670	0.4890
LD	0.8490	0.2650
LF	0.9710	0.4790
LG	0.9640	0.4600
LH	0.9370	0.4120
LI	0.7720	0.2440
LJ	0.9200	0.3950
LK	0.7910	0.2460
LL	0.9250	0.4090
LM	0.8780	0.3190
LN	0.9420	0.4040
LO	0.9580	0.4870
LP	0.9320	0.4120
LQ	0.9330	0.4070
LR	0.9680	0.3720
LS	0.9510	0.4730
LT	0.9500	0.4740
LU	0.9550	0.4700
LW	0.9430	0.4660
LZ	0.9620	0.4890
N0	0.8450	0.3530
NA	0.9350	0.4610
NB	0.9860	0.5220

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
ND	0.8500	0.3200
NE	0.9110	0.3650
NF	0.9400	0.4260
NG	0.9570	0.4040
NH	0.8270	0.2540
NI	0.6590	0.2380
NJ	0.8670	0.3300
NK	0.8970	0.2710
NM	0.8990	0.3880
NN	0.8280	0.2710
NO	0.9490	0.4490
NQ	0.9600	0.4610
NR	0.0000	0.0250
NT	0.0000	0.0080
NU	0.0000	0.0840
NW	0.9190	0.3650
NY	0.8970	0.3690
SA	0.9490	0.4350
SB	0.9130	0.4100
SC	0.8960	0.2880
SD	0.9790	0.5160
SE	0.9720	0.4910
SF	0.9650	0.4780
SG	0.9360	0.3800
SH	0.9590	0.4780
SI	0.9550	0.4650
SJ	0.7990	0.2380
SK	0.8230	0.3470
SL	0.9700	0.4910
SM	0.9660	0.4940
SP	0.7960	0.2360
SQ	0.9290	0.4500
SR	0.9680	0.4990
SS	0.8890	0.4050
ST	0.3480	0.1920
SU	0.5120	0.2310
SW	0.9170	0.3890
SX	0.2250	0.1000
SY	0.9220	0.3800
SZ	0.0060	0.0400