



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 02:02 PM UTC

PDB ID : 6LQP / pdb_00006lqp
EMDB ID : EMD-0949
Title : Cryo-EM structure of 90S small subunit preribosomes in transition states (State A)
Authors : Du, Y.; Ye, K.
Deposited on : 2020-01-14
Resolution : 3.20 Å(reported)
Based on initial model : 6KE6

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

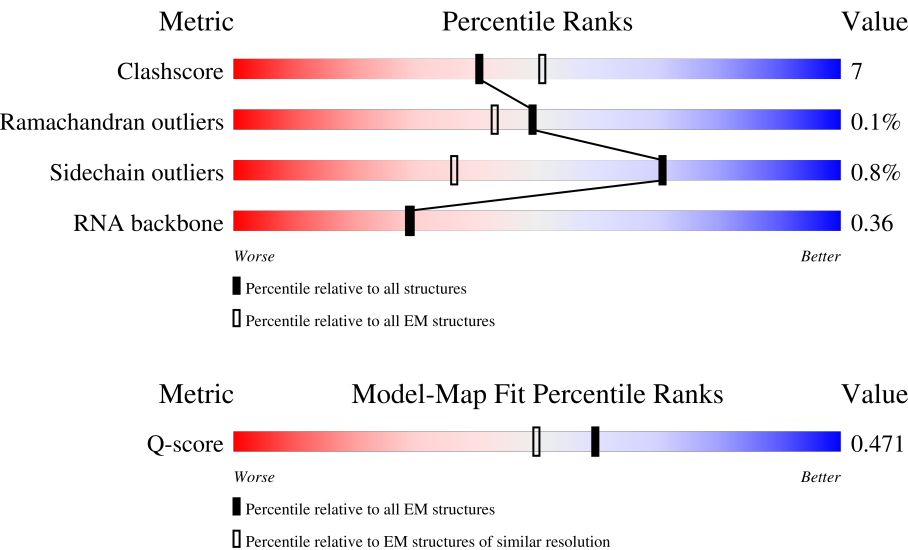
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMD 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 3.20 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.



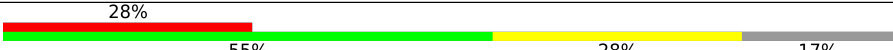
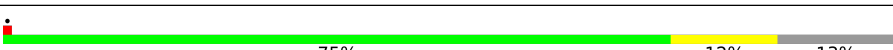
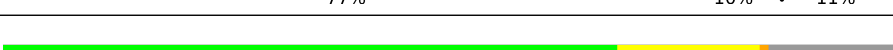
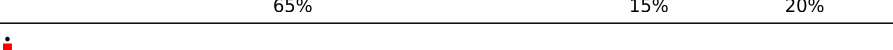
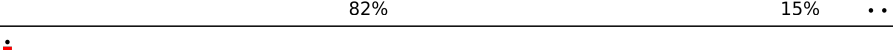
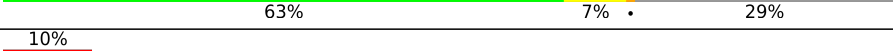
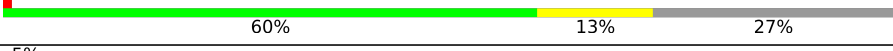
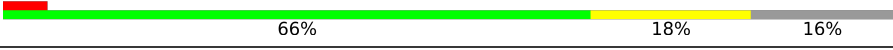
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	3A	333	
2	5A	700	
3	SA	1808	

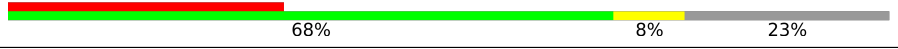
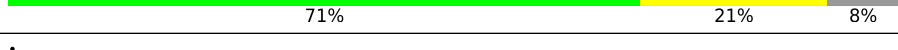
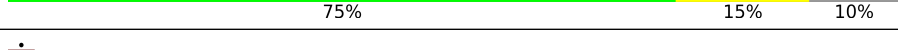
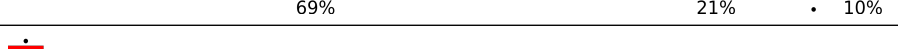
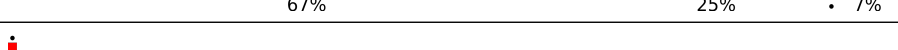
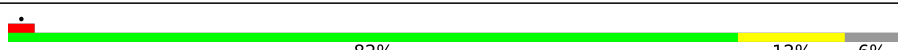
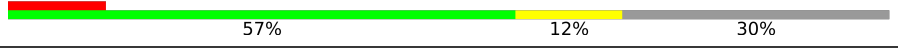
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	SC	255	
5	SF	261	
6	SG	225	
7	SH	236	
8	SI	190	
9	SJ	200	
10	SK	197	
11	SM	156	
12	SN	143	
13	SO	151	
14	SP	137	
15	SR	143	
16	ST	146	
17	SX	130	
18	SY	145	
19	SZ	135	
20	Sc	82	
21	Sd	67	
22	3B	327	
22	3C	327	
23	3D	504	
24	3E	511	
25	3F	573	
26	3G	126	
26	3H	126	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
27	A4	776	
28	A5	643	
29	A8	713	
30	A9	575	
31	AE	1769	
32	AF	513	
33	AG	896	
34	B1	923	
35	B2	943	
36	B3	817	
37	B8	594	
38	BE	939	
39	B6	440	
40	5B	214	
41	5C	554	
42	5D	250	
43	5E	593	
44	5F	183	
45	5G	290	
46	5H	610	
47	5I	489	
48	5J	217	
49	5K	189	
50	RA	707	
51	RB	357	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
52	RC	316	
53	RE	1237	
54	RF	297	
55	RG	252	
55	RH	252	
56	RI	274	
57	RJ	1183	
58	RK	367	
59	RL	1056	
59	RM	1056	
60	RN	810	
61	RO	552	
62	RP	2493	
63	RQ	899	
64	RS	483	
65	RT	326	
66	RV	346	
67	RW	206	
68	RY	534	
69	X1	347	

2 Entry composition

There are 72 unique types of molecules in this entry. The entry contains 232186 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 U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3A	175	Total	C	N	O	P	0	0
			3711	1661	648	1227	175		

- Molecule 2 is a RNA chain called 5' ETS.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5A	523	Total	C	N	O	P	0	0
			11163	4988	1984	3668	523		

- Molecule 3 is a RNA chain called 18S pre-rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SA	1325	Total	C	N	O	P	0	0
			28258	12629	5035	9269	1325		

- Molecule 4 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SC	230	Total	C	N	O	S	0	0
			1830	1156	335	335	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SF	229	Total	C	N	O	S	0	0
			1815	1161	331	320	3		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SH	167	Total	C	N	O	S	0	0
			1327	834	256	235	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SI	165	Total	C	N	O		0	0
			1321	853	226	242			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SJ	166	Total	C	N	O	S	0	0
			1324	824	262	236	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SK	171	Total	C	N	O	S	0	0
			1388	879	268	240	1		

- Molecule 11 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SM	123	Total	C	N	O	S	0	0
			997	641	189	164	3		

- Molecule 12 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SN	119	Total	C	N	O	S	0	0
			865	545	151	167	2		

- Molecule 13 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SO	134	Total	C	N	O	S	0	0
			1087	698	202	186	1		

- Molecule 14 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SP	118	Total	C	N	O	S	0	0
			868	536	164	165	3		

- Molecule 15 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SR	125	Total	C	N	O		0	0
			973	625	174	174			

- Molecule 16 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	ST	117	Total	C	N	O	S	0	0
			964	610	184	168	2		

- Molecule 17 is a protein called 40S ribosomal protein S22-B.

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

- Molecule 18 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SY	103	Total	C	N	O	S	0	0
			786	503	144	137	2		

- Molecule 19 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SZ	102	Total	C	N	O		0	0
			809	517	148	144			

- Molecule 20 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Sc	80	Total	C	N	O	S	0	0
			603	377	109	112	5		

- Molecule 21 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 22 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	3B	240	Total	C	N	O	S	0	0
			1865	1184	333	338	10		
22	3C	225	Total	C	N	O	S	0	0
			1763	1120	316	317	10		

- Molecule 23 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	3D	369	Total	C	N	O	S	0	0
			2848	1811	489	540	8		

- Molecule 24 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	3E	431	Total	C	N	O	S	0	0
			3028	1888	543	588	9		

- Molecule 25 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	3F	454	Total	C	N	O	S	0	0
			3643	2315	638	680	10		

- Molecule 26 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	3G	121	Total	C	N	O	S	0	0
			916	583	158	171	4		
26	3H	121	Total	C	N	O	S	0	0
			916	583	158	171	4		

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A4	662	Total	C	N	O	S	0	0
			5226	3309	910	986	21		

- Molecule 28 is a protein called U3 small nucleolar RNA-associated protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	A5	514	Total	C	N	O	S	0	0
			3976	2520	688	755	13		

- Molecule 29 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	A8	548	Total	C	N	O	S	0	0
			3307	2054	608	642	3		

- Molecule 30 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	A9	128	Total	C	N	O	S	0	0
			939	594	173	170	2		

- Molecule 31 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AE	1534	Total	C	N	O	S	0	0
			9955	6242	1771	1923	19		

- Molecule 32 is a protein called U3 small nucleolar RNA-associated protein 15.

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

- Molecule 33 is a protein called NET1-associated nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AG	826	Total	C	N	O	S	0	0
			6570	4181	1111	1259	19		

- Molecule 34 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B1	834	Total	C	N	O	S	0	0
			6635	4223	1140	1253	19		

- Molecule 35 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	B2	851	Total	C	N	O	S	0	0
			6723	4294	1133	1269	27		

- Molecule 36 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	B3	757	Total	C	N	O	S	0	0
			5919	3769	993	1130	27		

- Molecule 37 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	B8	477	Total	C	N	O	S	0	0
			3764	2387	662	705	10		

- Molecule 38 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BE	865	Total	C	N	O	S	0	0
			6810	4322	1175	1292	21		

- Molecule 39 is a protein called U3 small nucleolar RNA-associated protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	B6	374	Total	C	N	O	S	0	0
			2800	1782	501	505	12		

- Molecule 40 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	5B	60	Total	C	N	O	0	0
			495	310	101	84		

- Molecule 41 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	5C	535	Total	C	N	O	S	0	0
			4237	2656	762	807	12		

- Molecule 42 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	5D	235	Total	C	N	O	S	0	0
			1972	1226	380	359	7		

- Molecule 43 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	5E	204	Total	C	N	O	S	0	0
			1647	1021	294	328	4		

- Molecule 44 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	5F	182	Total	C	N	O	S	0	0
			1530	967	287	269	7		

- Molecule 45 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5G	282	Total	C	N	O	S	0	0
			2296	1441	430	418	7		

- Molecule 46 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	5H	136	Total	C	N	O		0	0
			1065	658	211	196			

- Molecule 47 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	5I	461	Total	C	N	O	S	0	0
			3765	2354	686	709	16		

- Molecule 48 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5J	151	Total	C	N	O	S	0	0
			1280	807	240	228	5		

- Molecule 49 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	5K	175	Total	C	N	O	S	0	0
			1403	896	256	241	10		

- Molecule 50 is a protein called Ribosome biogenesis protein ENP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	RA	338	Total	C	N	O	S	0	0
			2709	1713	463	524	9		

- Molecule 51 is a protein called U3 small nucleolar ribonucleoprotein protein LCP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	RB	134	Total	C	N	O	S	0	0
			1108	664	227	214	3		

- Molecule 52 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	RC	278	Total	C	N	O	S	0	0
			2207	1408	391	395	13		

- Molecule 53 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	RE	1079	Total	C	N	O	S	0	0
			8716	5666	1437	1589	24		

- Molecule 54 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	RF	241	Total	C	N	O	S	0	0
			1963	1253	335	367	8		

- Molecule 55 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	RG	216	Total	C	N	O	S	0	0
			1701	1079	296	315	11		
55	RH	230	Total	C	N	O	S	0	0
			1799	1142	313	333	11		

- Molecule 56 is a protein called Ribosome biogenesis protein UTP30.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	RI	252	Total	C	N	O	S	0	0
			2045	1309	362	366	8		

- Molecule 57 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	RJ	796	Total	C	N	O	S	0	0
			6379	4086	1136	1128	29		

- Molecule 58 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 59 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	RL	805	Total	C	N	O	S	0	0
			4539	2760	885	887	7		
59	RM	766	Total	C	N	O		0	0
			3779	2247	766	766			

- Molecule 60 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	RN	607	Total	C	N	O	S	0	0
			4529	2861	820	837	11		

- Molecule 61 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	RO	525	Total	C	N	O	S	0	0
			3766	2412	646	696	12		

- Molecule 62 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	RP	2109	Total	C	N	O	S	0	0
			12176	7486	2292	2382	16		

- Molecule 63 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	RQ	226	Total	C	N	O	S	0	0
			1651	1023	313	313	2		

- Molecule 64 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	RS	251	Total	C	N	O	S	0	0
			2051	1340	349	359	3		

- Molecule 65 is a protein called Pno1.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	RT	171	Total	C	N	O	S	0	0
			1357	864	249	240	4		

- Molecule 66 is a protein called Protein FAF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	RV	190	Total	C	N	O	S	0	0
			1448	891	290	264	3		

- Molecule 67 is a protein called Regulator of rDNA transcription protein 14.

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

- Molecule 68 is a protein called Protein BFR2.

Mol	Chain	Residues	Atoms				AltConf	Trace
68	RY	37	Total	C	N	O	0	0
			299	191	48	60		

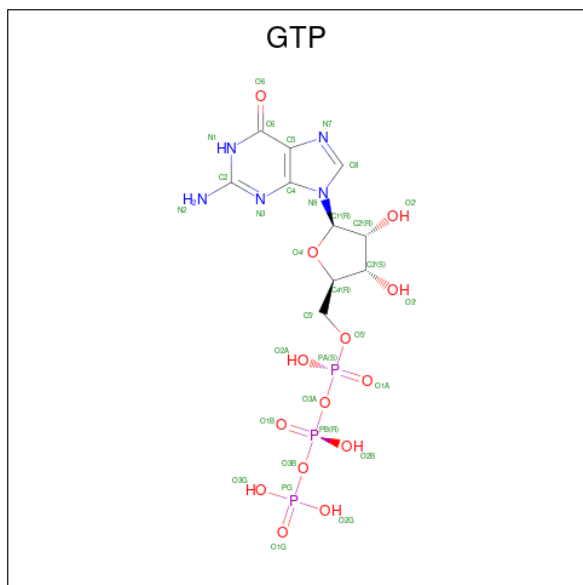
- Molecule 69 is a protein called Unassigned helices.

Mol	Chain	Residues	Atoms				AltConf	Trace
69	X1	61	Total	C	N	O	0	0
			305	183	61	61		

- Molecule 70 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
70	Sc	1	Total	Zn	0
			1	1	
70	5K	1	Total	Zn	0
			1	1	

- Molecule 71 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

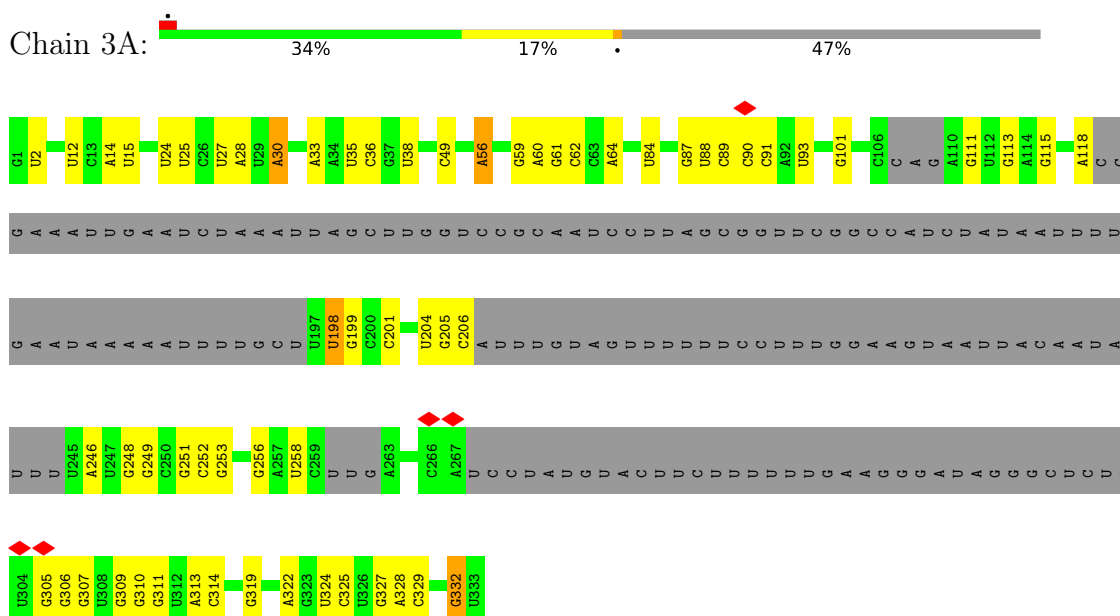
- Molecule 72 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
72	RJ	1	Total	Mg	0
			1	1	

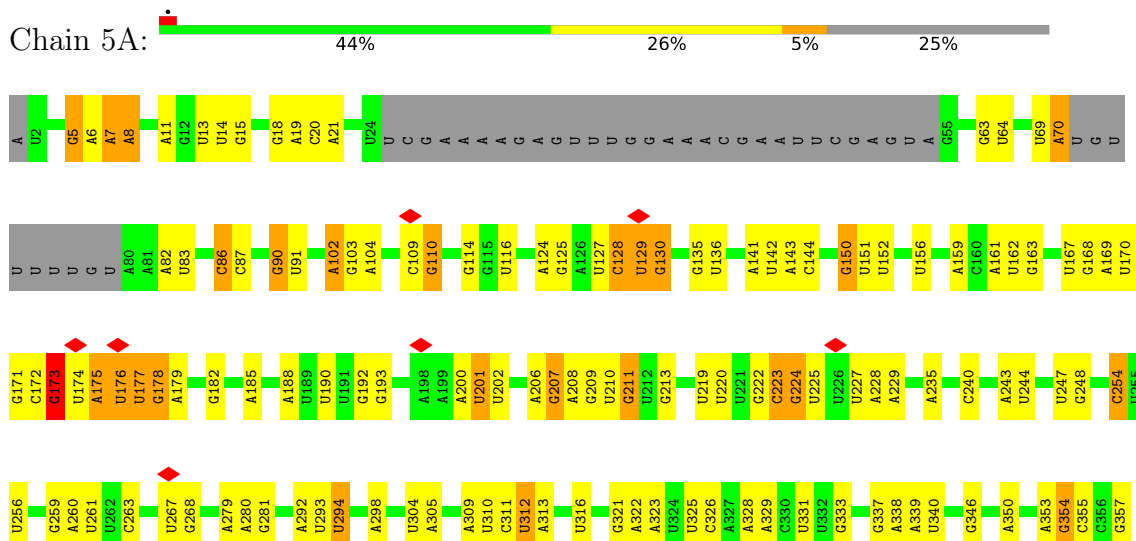
3 Residue-property plots [i](#)

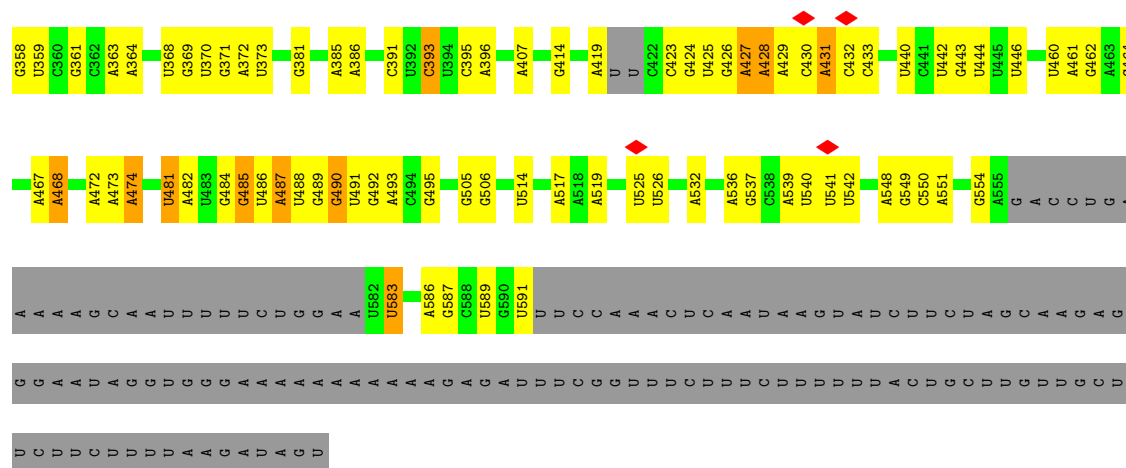
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: U3 snoRNA

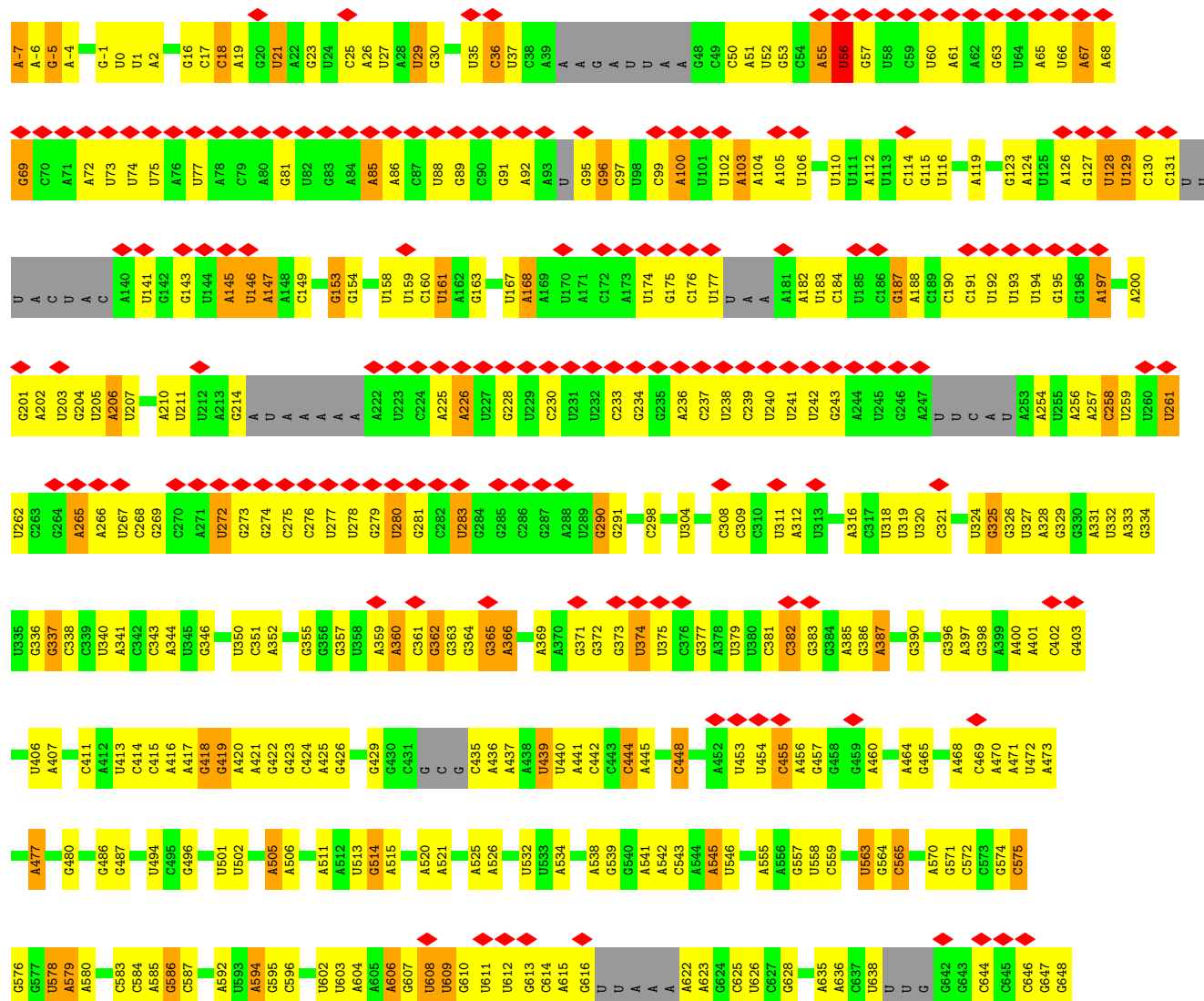


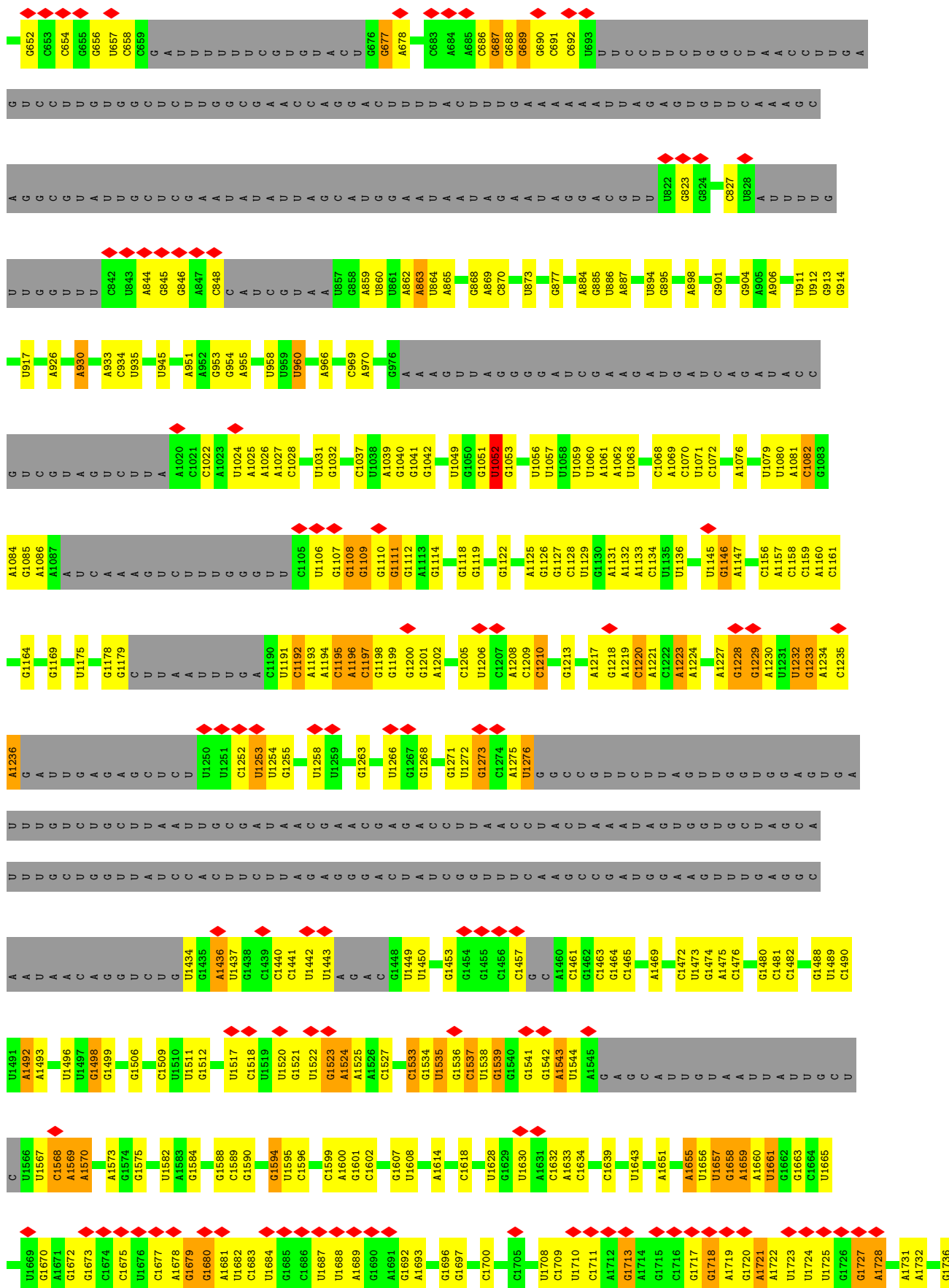
• Molecule 2: 5' ETS

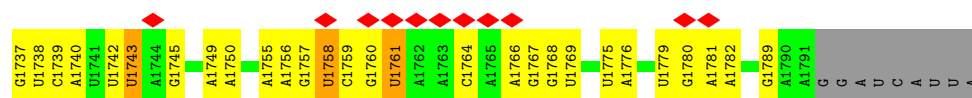




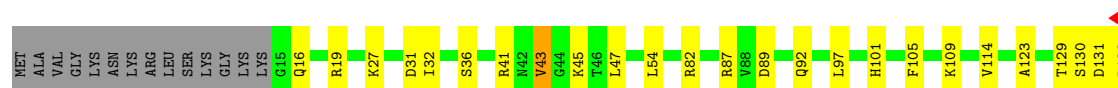
• Molecule 3: 18S pre-rRNA



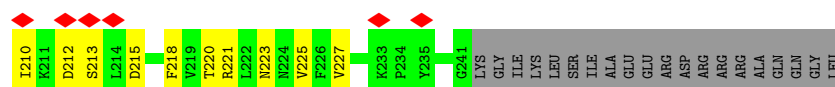
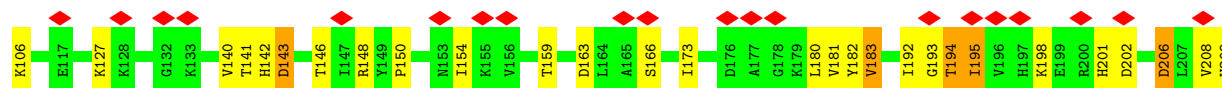




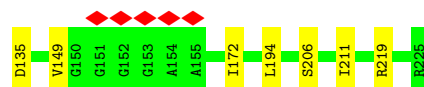
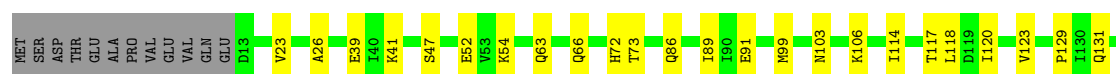
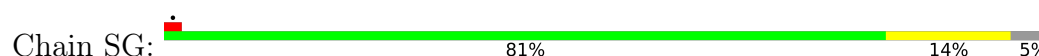
- Molecule 4: 40S ribosomal protein S1-A



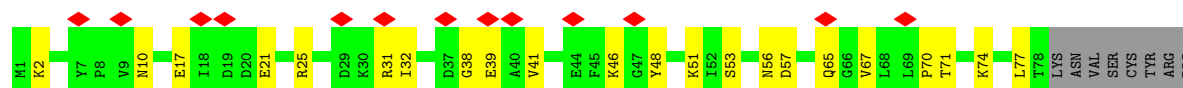
- Molecule 5: 40S ribosomal protein S4-A

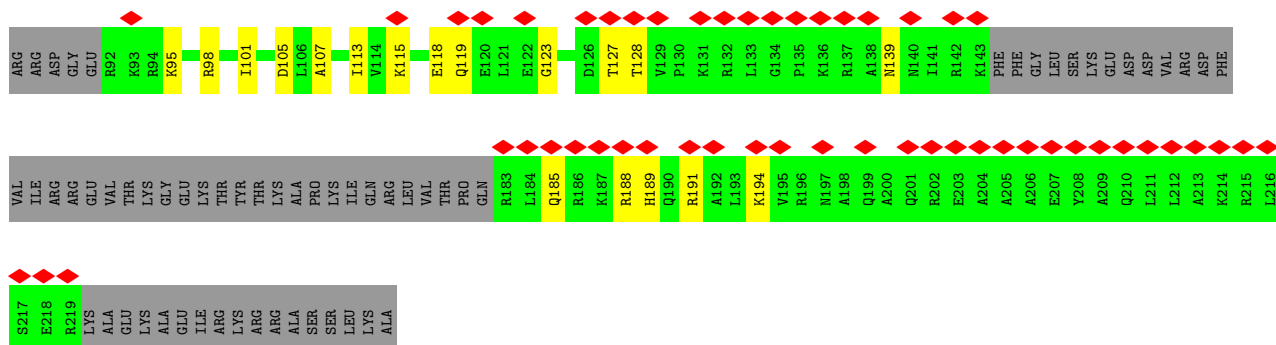


- Molecule 6: 40S ribosomal protein S5

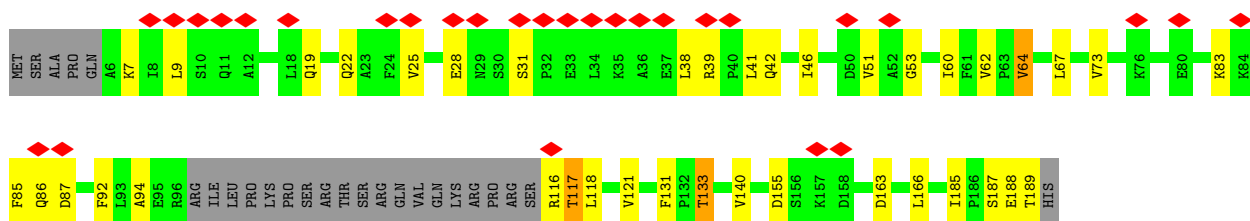


- Molecule 7: 40S ribosomal protein S6-A

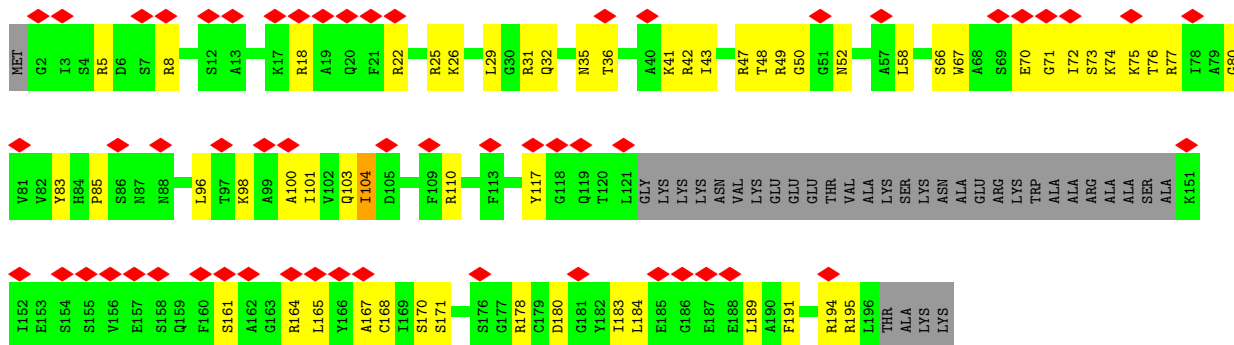




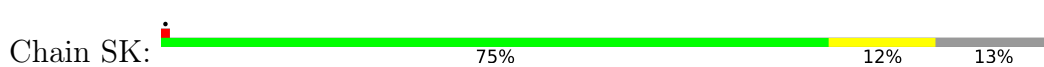
• Molecule 8: 40S ribosomal protein S7-A



• Molecule 9: 40S ribosomal protein S8-A



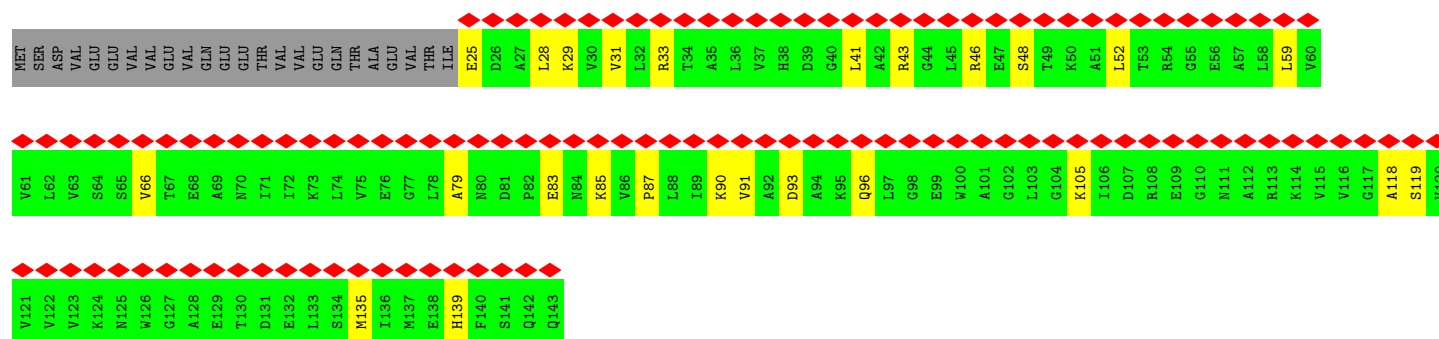
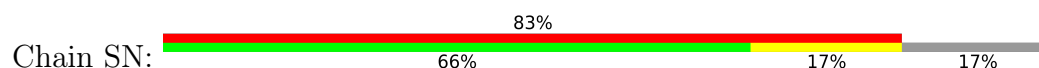
• Molecule 10: 40S ribosomal protein S9-A



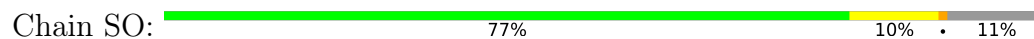
• Molecule 11: 40S ribosomal protein S11-A



- Molecule 12: 40S ribosomal protein S12



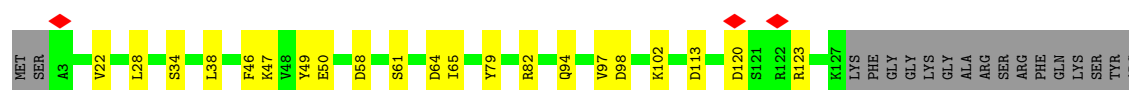
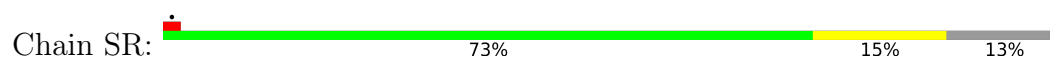
- Molecule 13: 40S ribosomal protein S13



- Molecule 14: 40S ribosomal protein S14-A

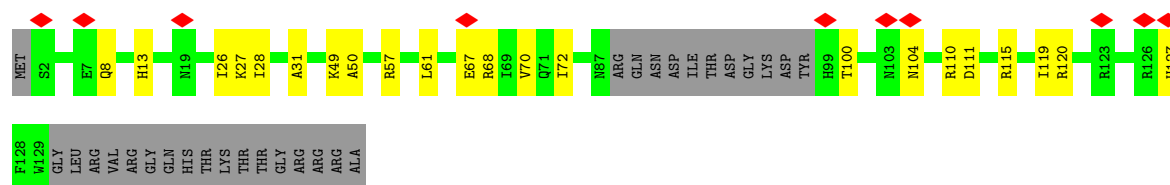


- Molecule 15: 40S ribosomal protein S16-A



- Molecule 16: 40S ribosomal protein S18-A





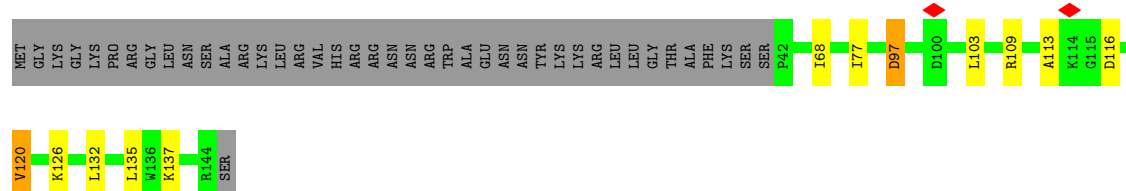
- Molecule 17: 40S ribosomal protein S22-B

Chain SX: 82% 15% ..



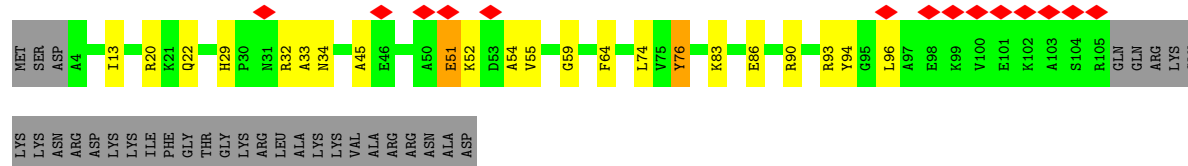
- Molecule 18: 40S ribosomal protein S23-A

Chain SY: 63% 7% 29%



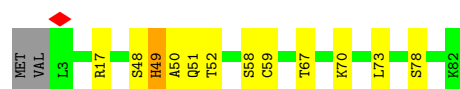
- Molecule 19: 40S ribosomal protein S24-A

Chain SZ: 10% 59% 15% 24%



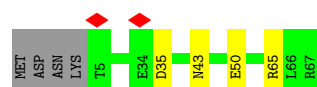
- Molecule 20: 40S ribosomal protein S27-A

Chain Sc: 83% 13% ..

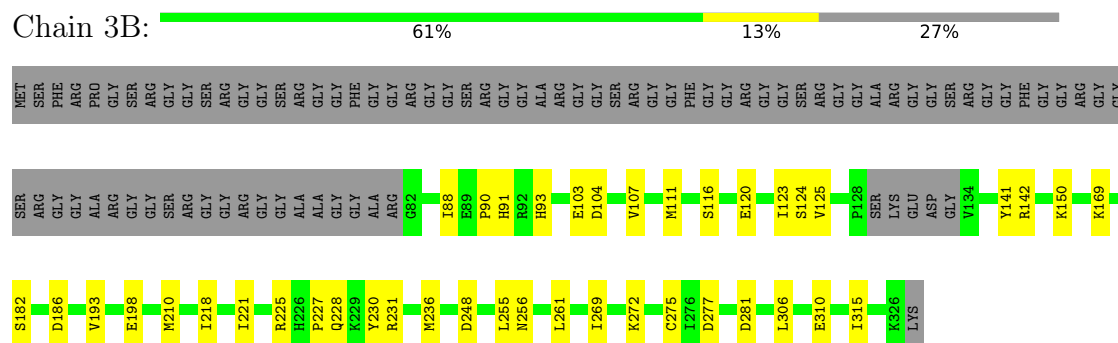


- Molecule 21: 40S ribosomal protein S28-A

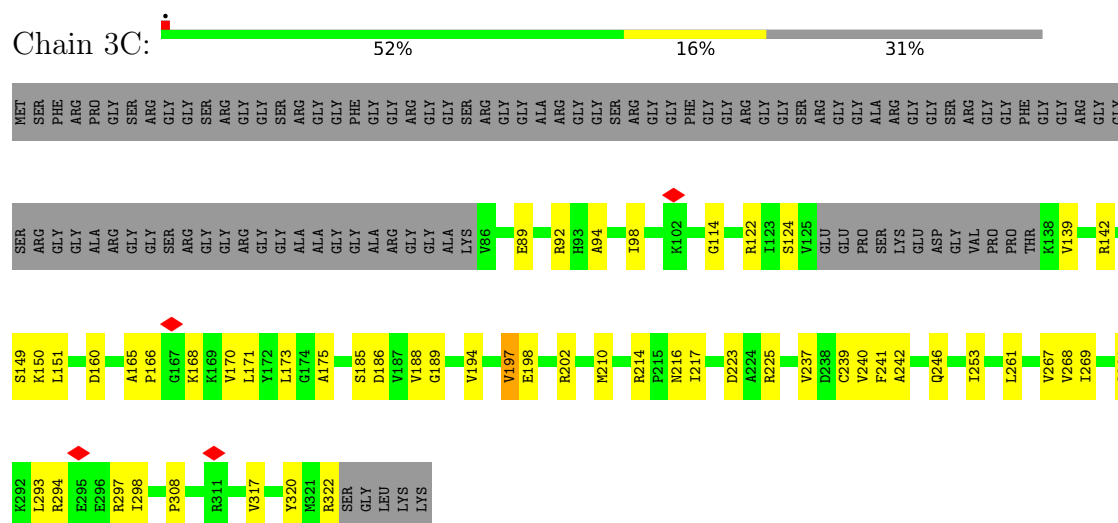
Chain Sd: 88% 6% 6%



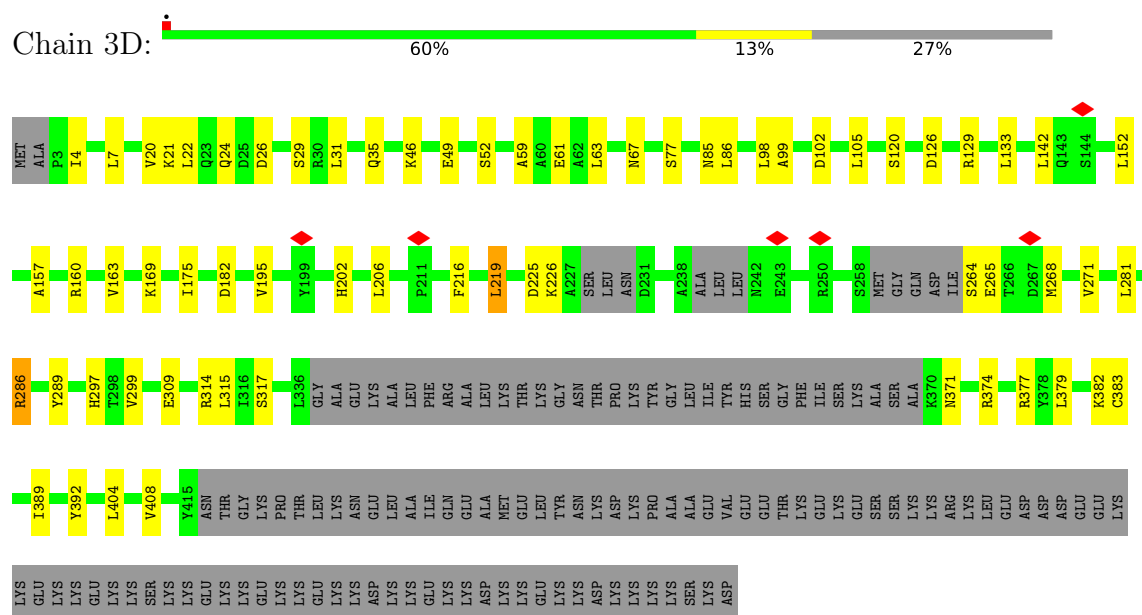
- Molecule 22: rRNA 2'-O-methyltransferase fibrillar



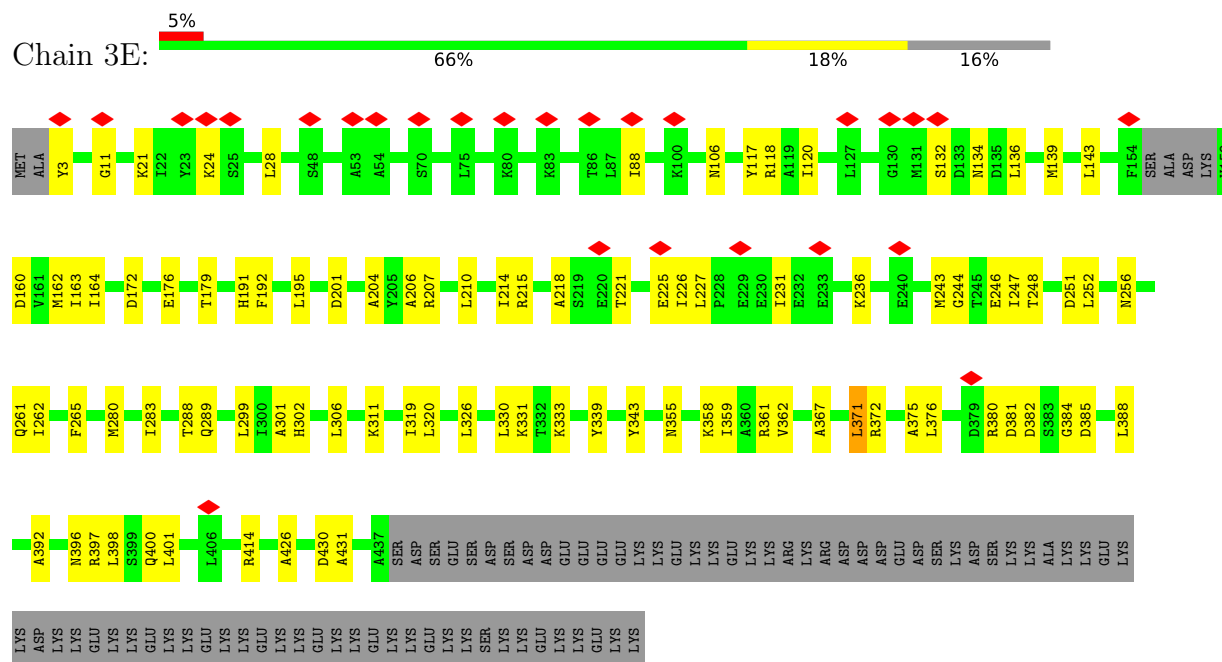
- Molecule 22: rRNA 2'-O-methyltransferase fibrillar



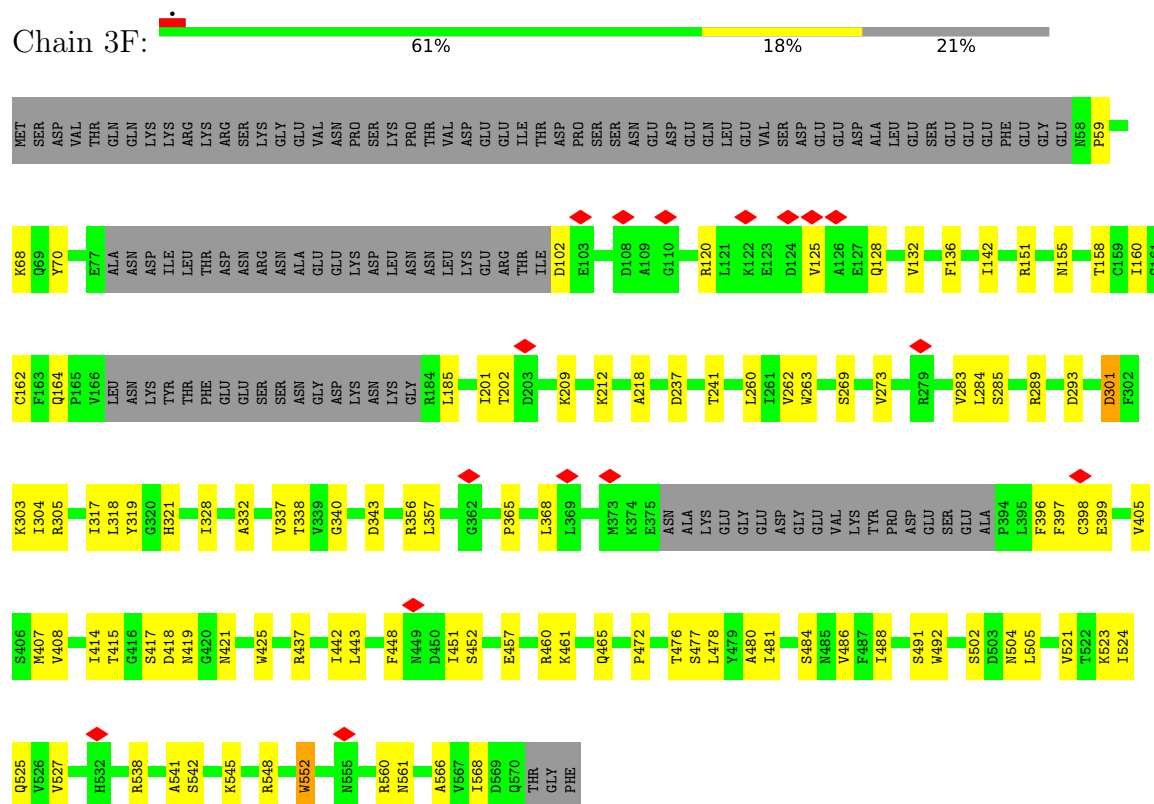
- Molecule 23: Nucleolar protein 56



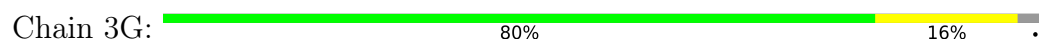
- Molecule 24: Nucleolar protein 58



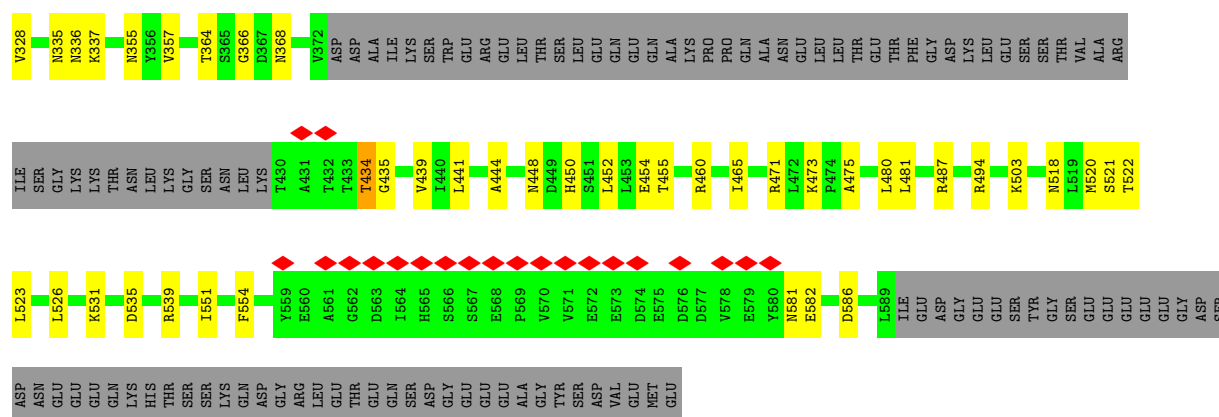
- Molecule 25: Ribosomal RNA-processing protein 9



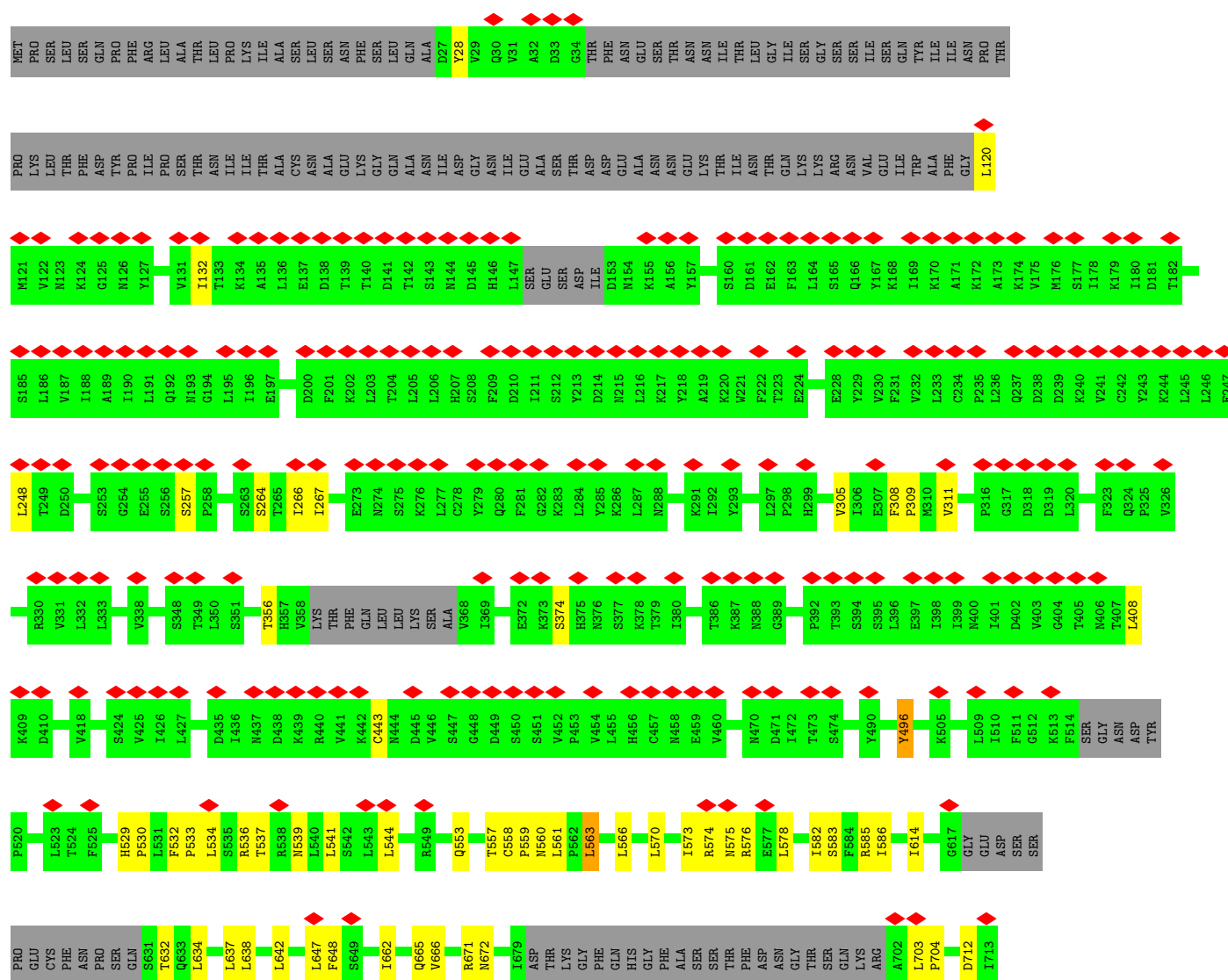
- Molecule 26: 13 kDa ribonucleoprotein-associated protein





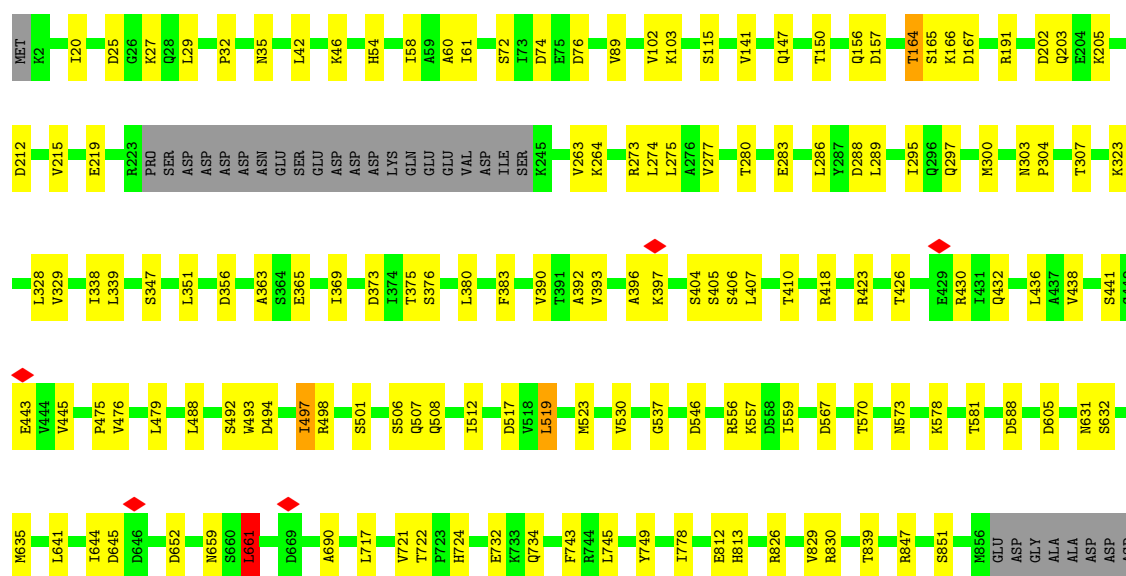


• Molecule 29: U3 small nucleolar RNA-associated protein 8

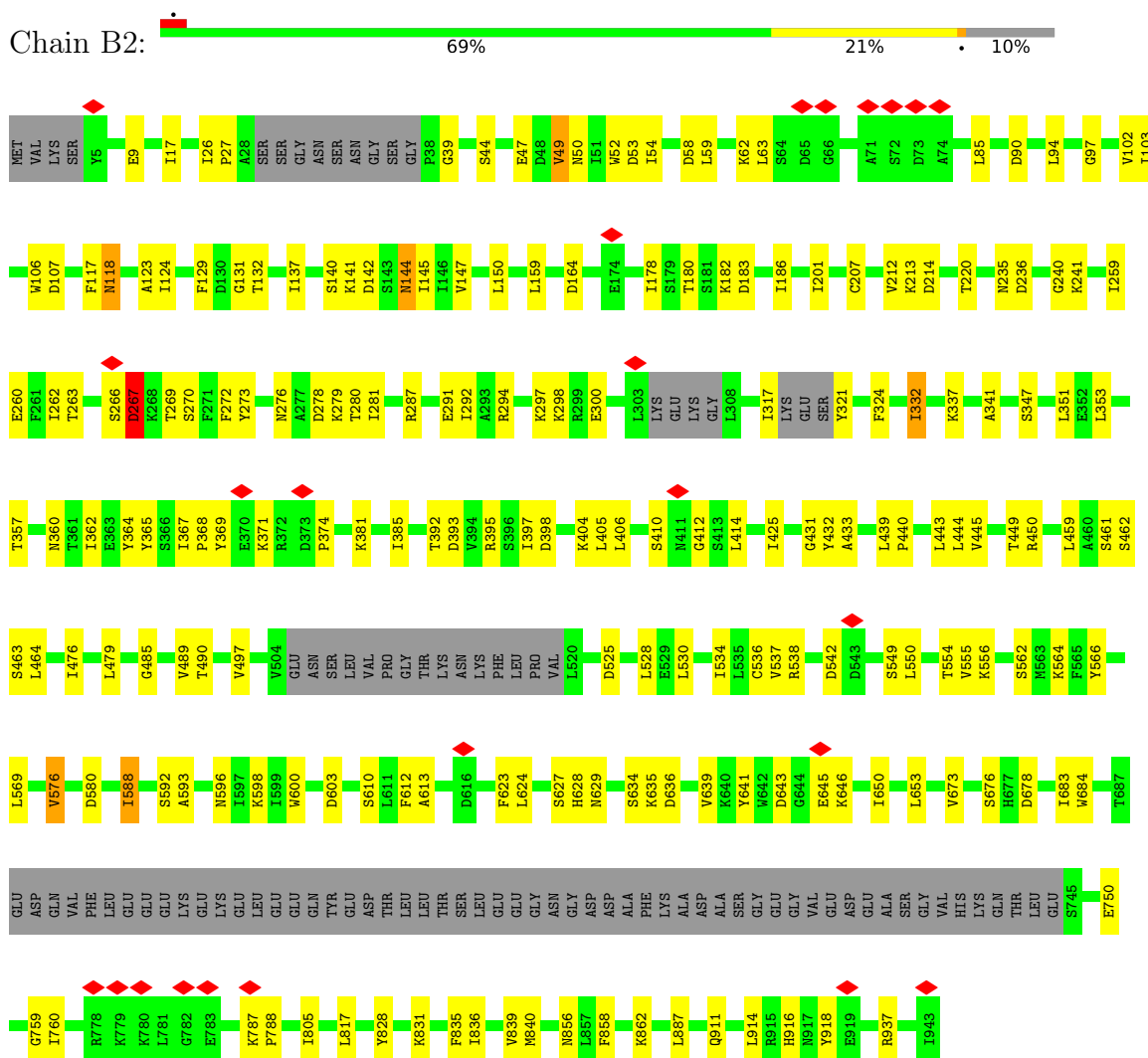


• Molecule 30: U3 small nucleolar RNA-associated protein 9

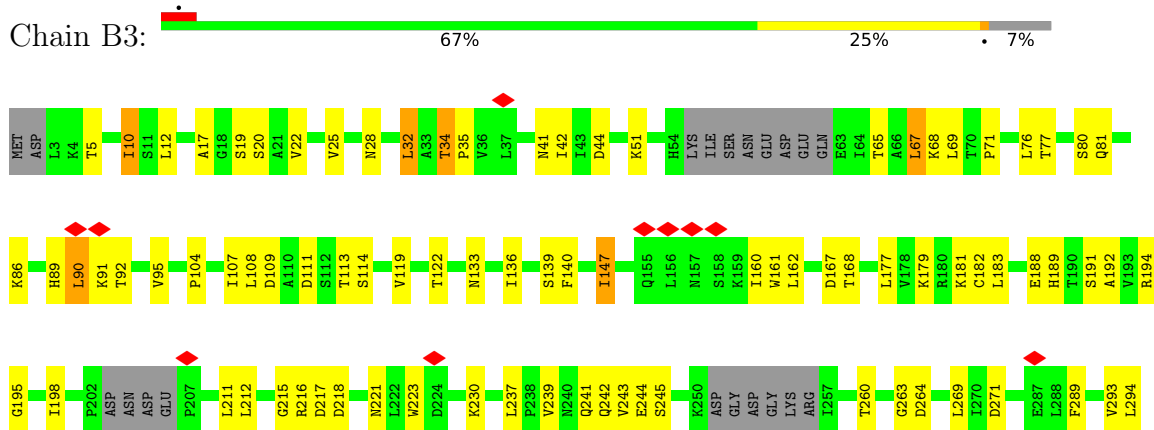


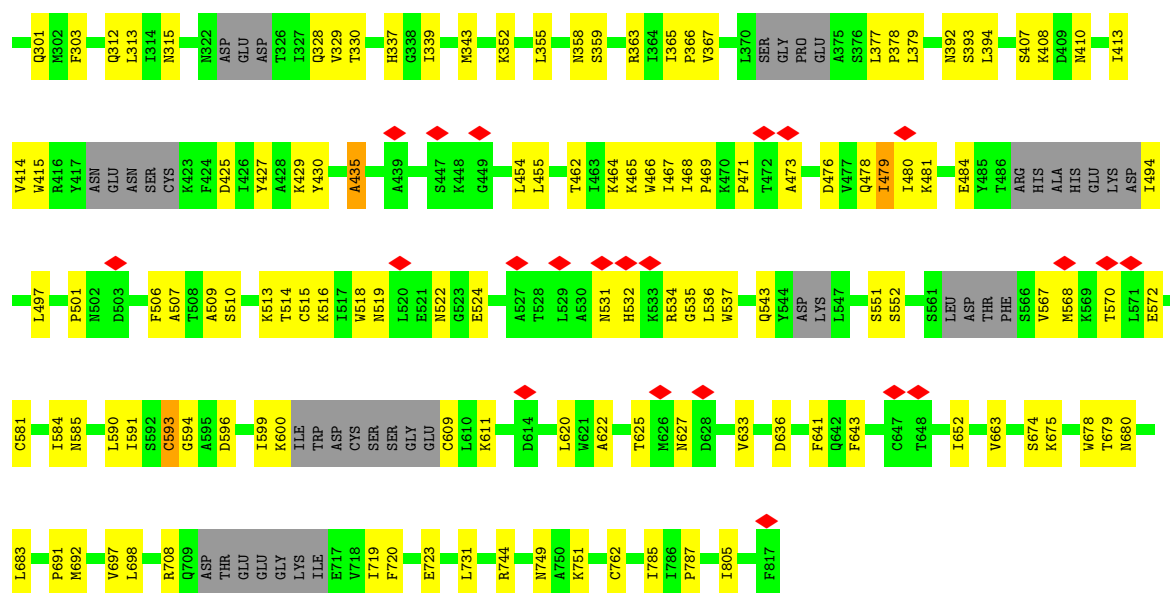


Chain B2:

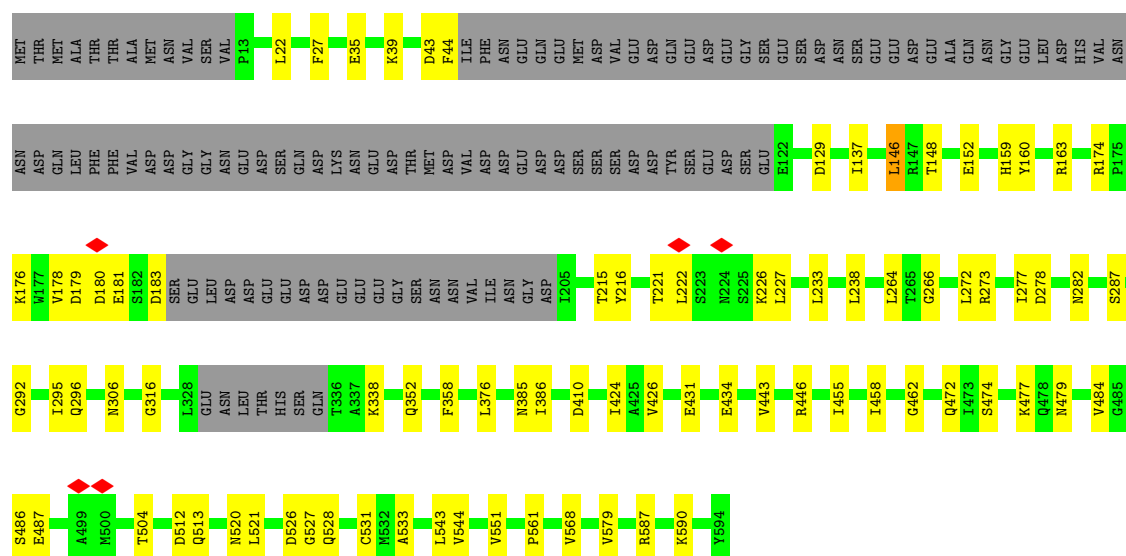


Chain B3:

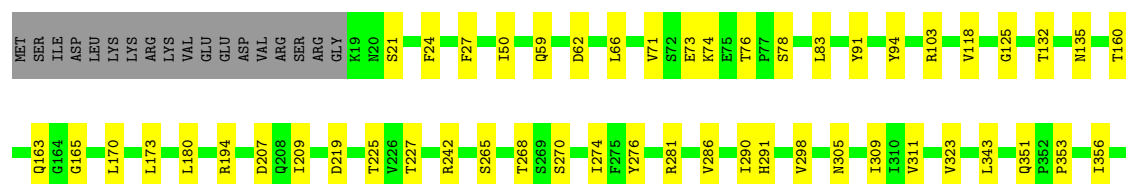
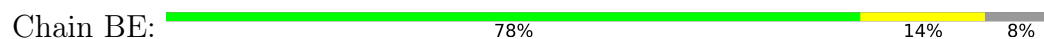


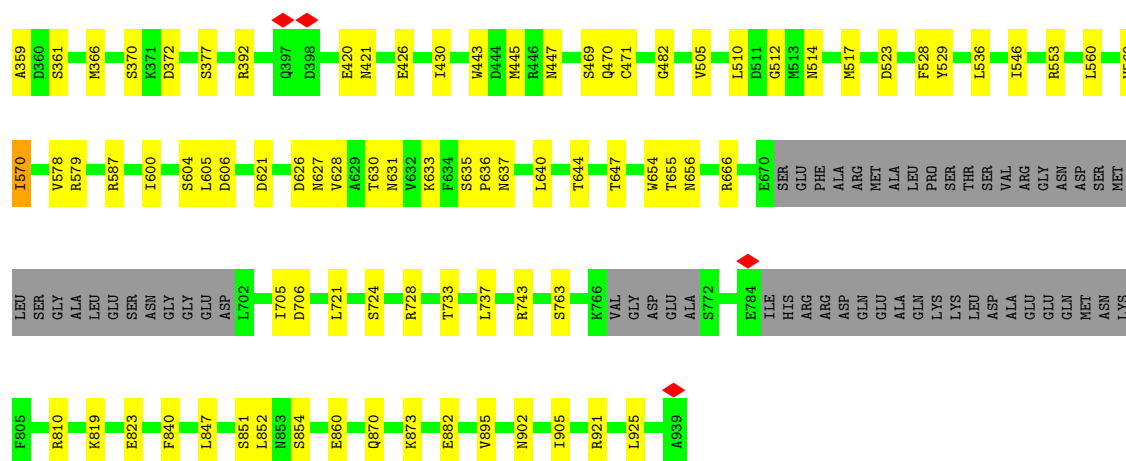


• Molecule 37: U3 small nucleolar RNA-associated protein 18

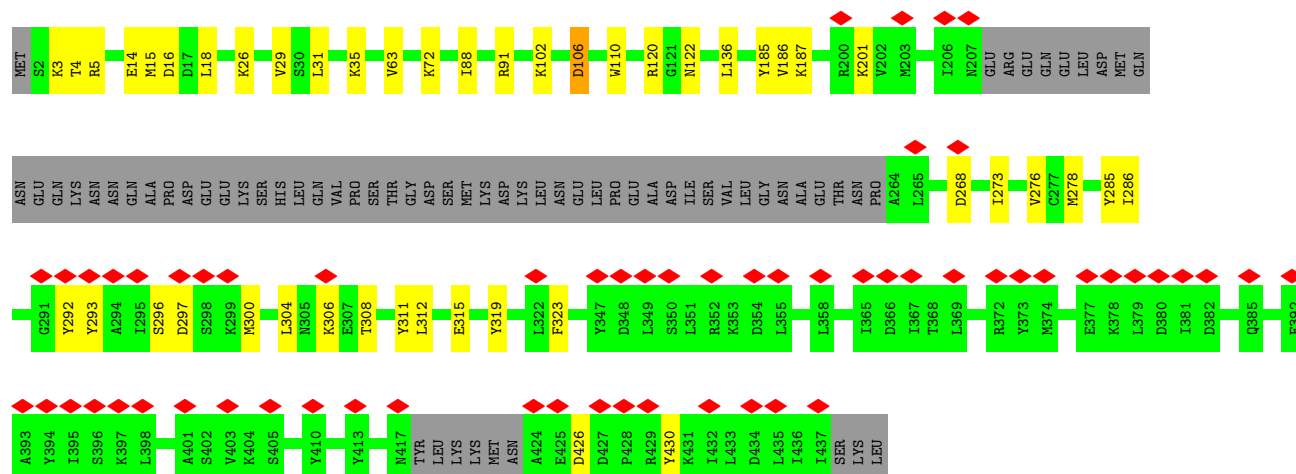
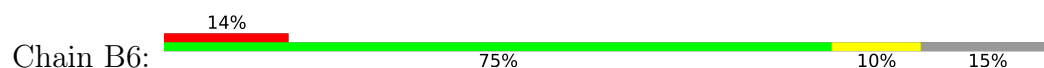


• Molecule 38: U3 small nucleolar RNA-associated protein 21

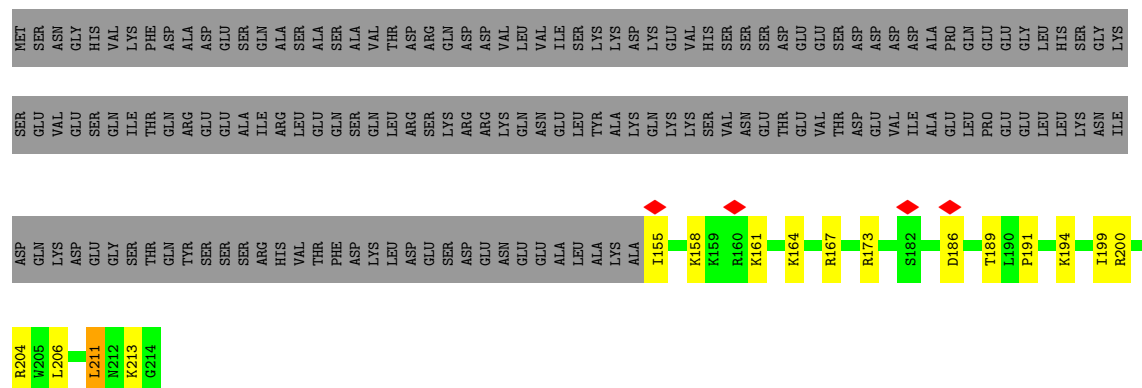




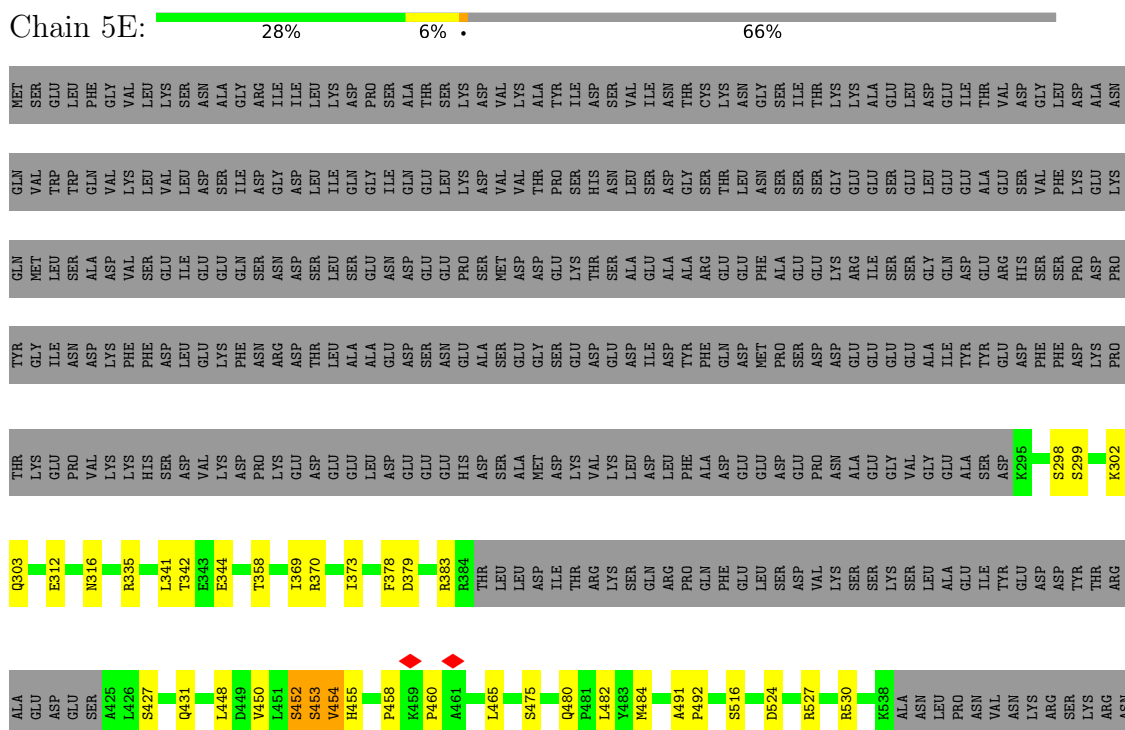
- Molecule 39: U3 small nucleolar RNA-associated protein 6

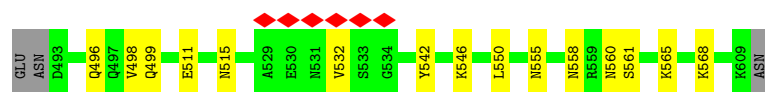


- Molecule 40: Bud site selection protein 21



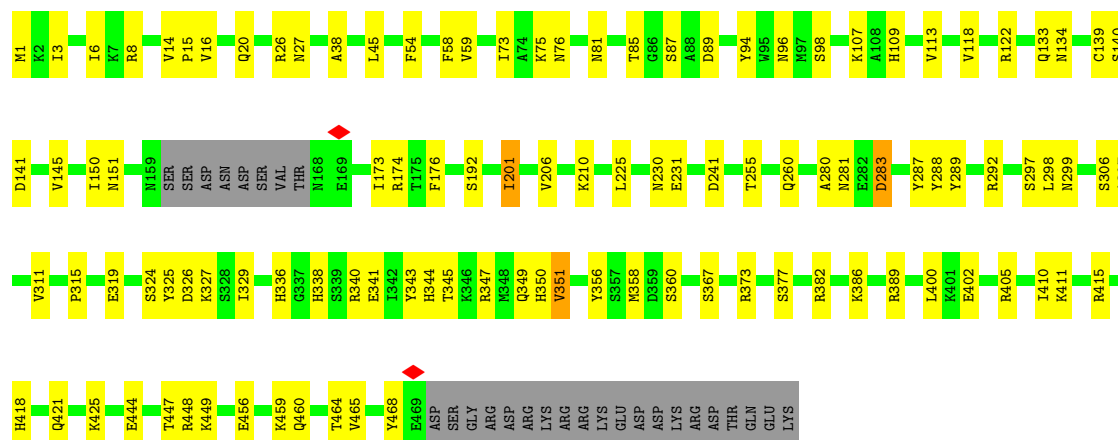
- Molecule 41: U3 small nucleolar RNA-associated protein 7





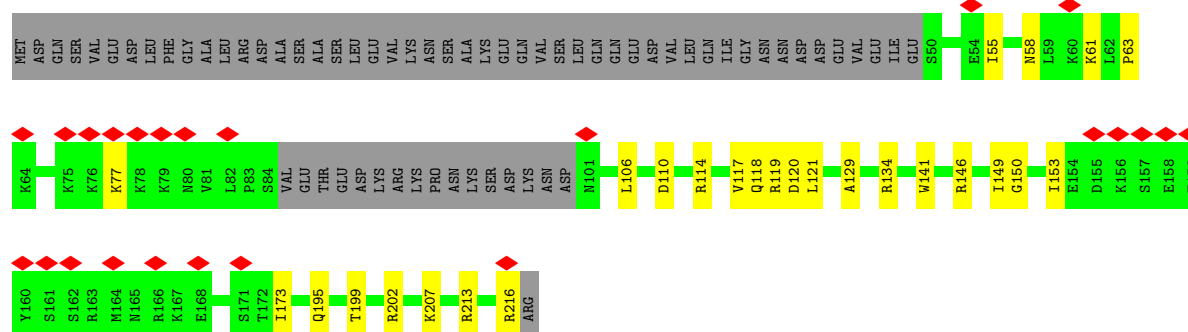
• Molecule 47: Protein SOF1

Chain 5I: 72% 22% 6%



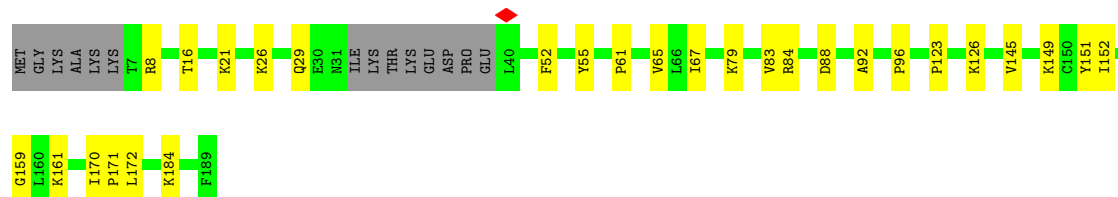
• Molecule 48: rRNA-processing protein FCF2

Chain 5J: 11% 57% 12% 30%



• Molecule 49: rRNA-processing protein FCF1

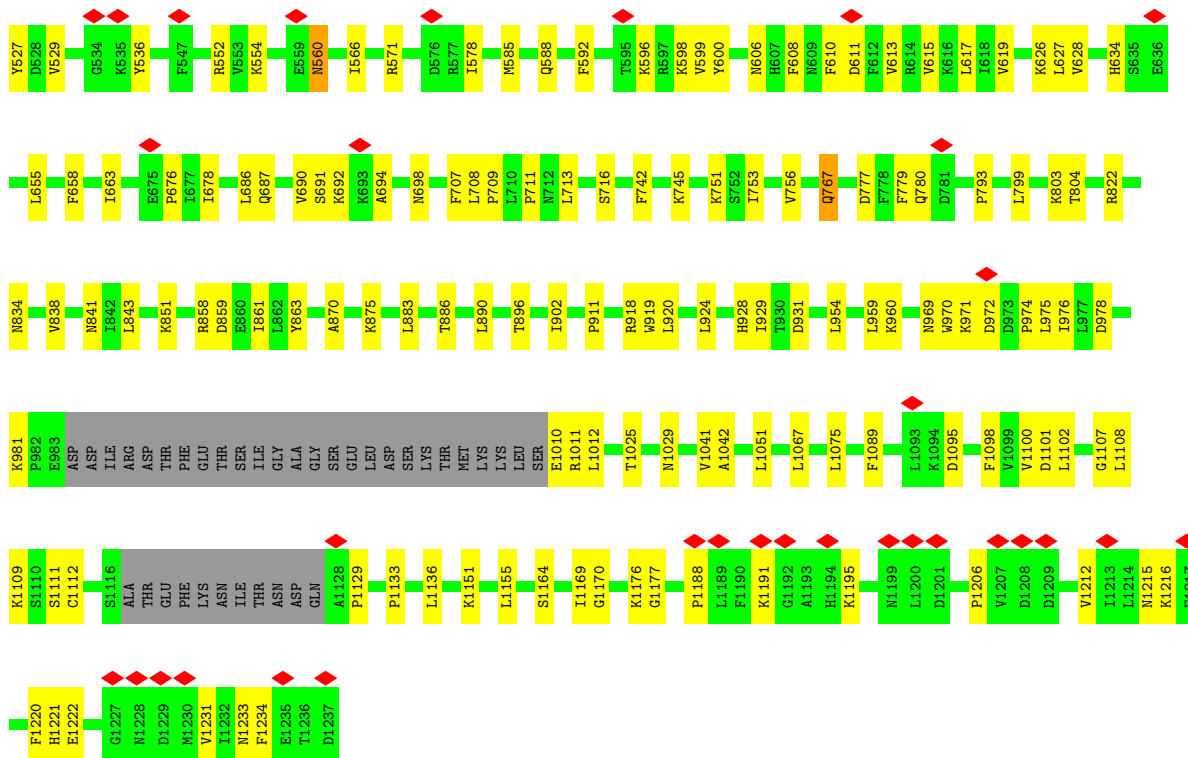
Chain 5K: 78% 15% 7%



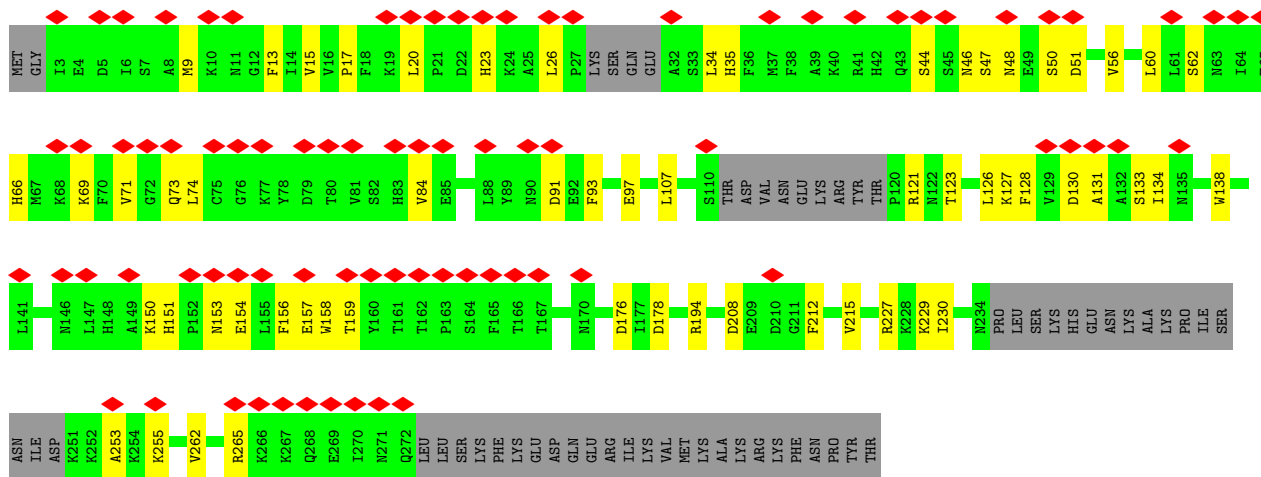
• Molecule 50: Ribosome biogenesis protein ENP2

Chain RA: 12% 35% 12% 52%

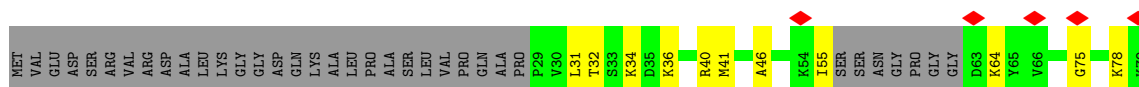


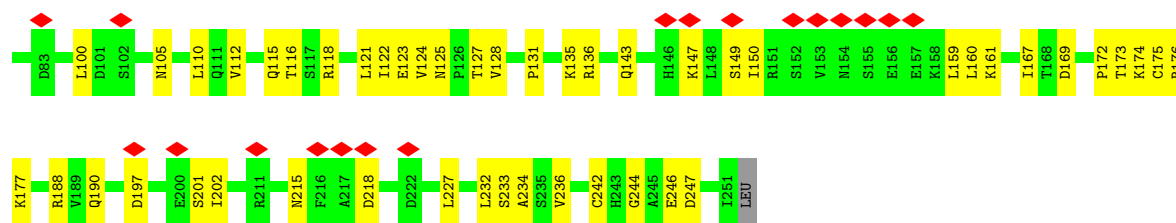


- Molecule 54: Ribosomal RNA-processing protein 7

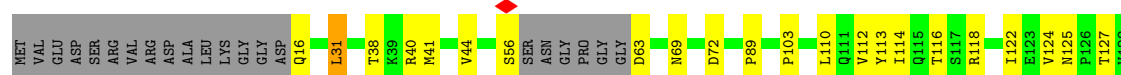
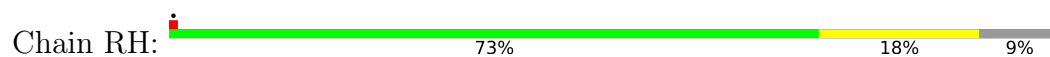


- Molecule 55: Ribosomal RNA small subunit methyltransferase NEP1

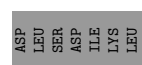




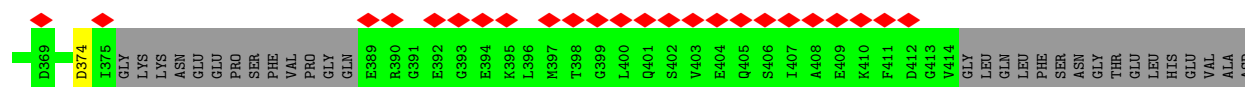
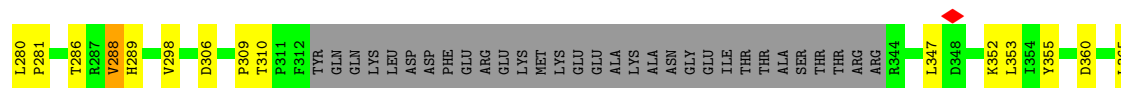
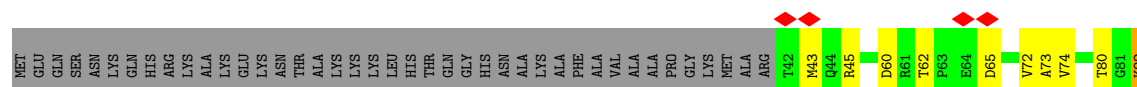
- Molecule 55: Ribosomal RNA small subunit methyltransferase NEP1



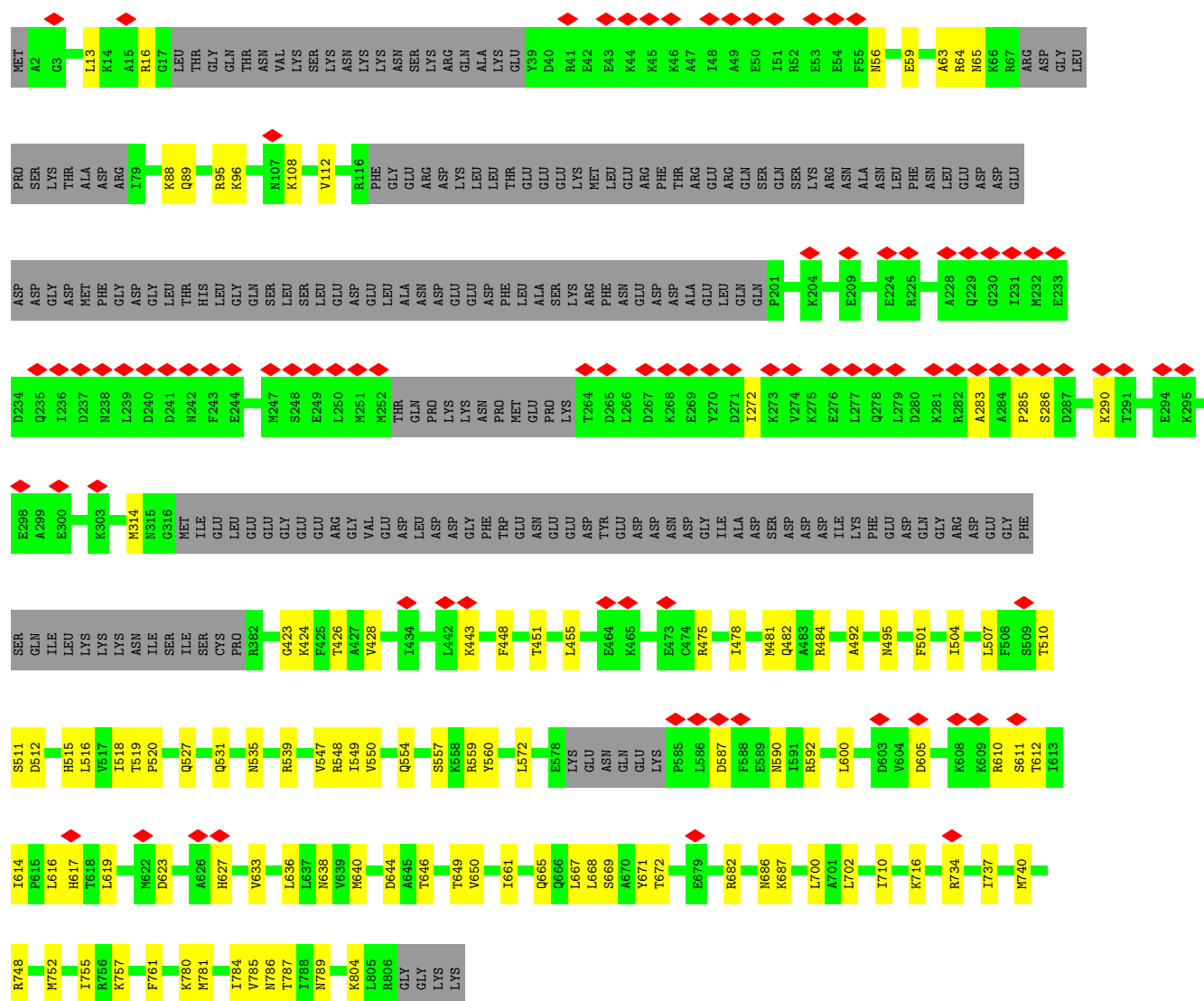
- Molecule 56: Ribosome biogenesis protein UTP30



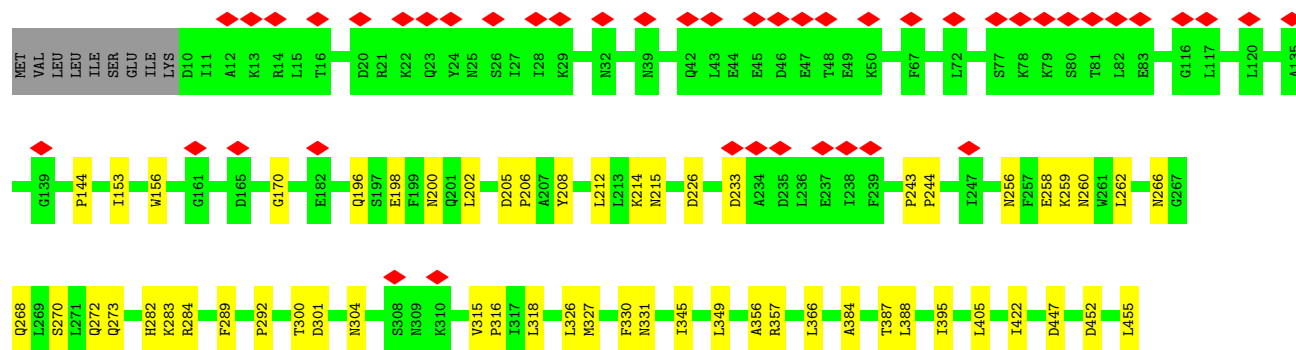
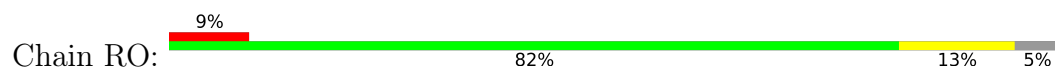
- Molecule 57: Ribosome biogenesis protein BMS1

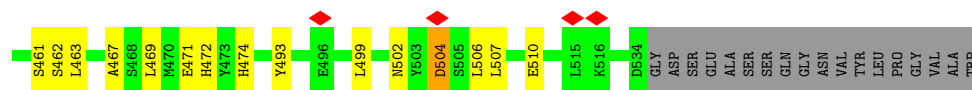


- Molecule 60: Nucleolar complex protein 14

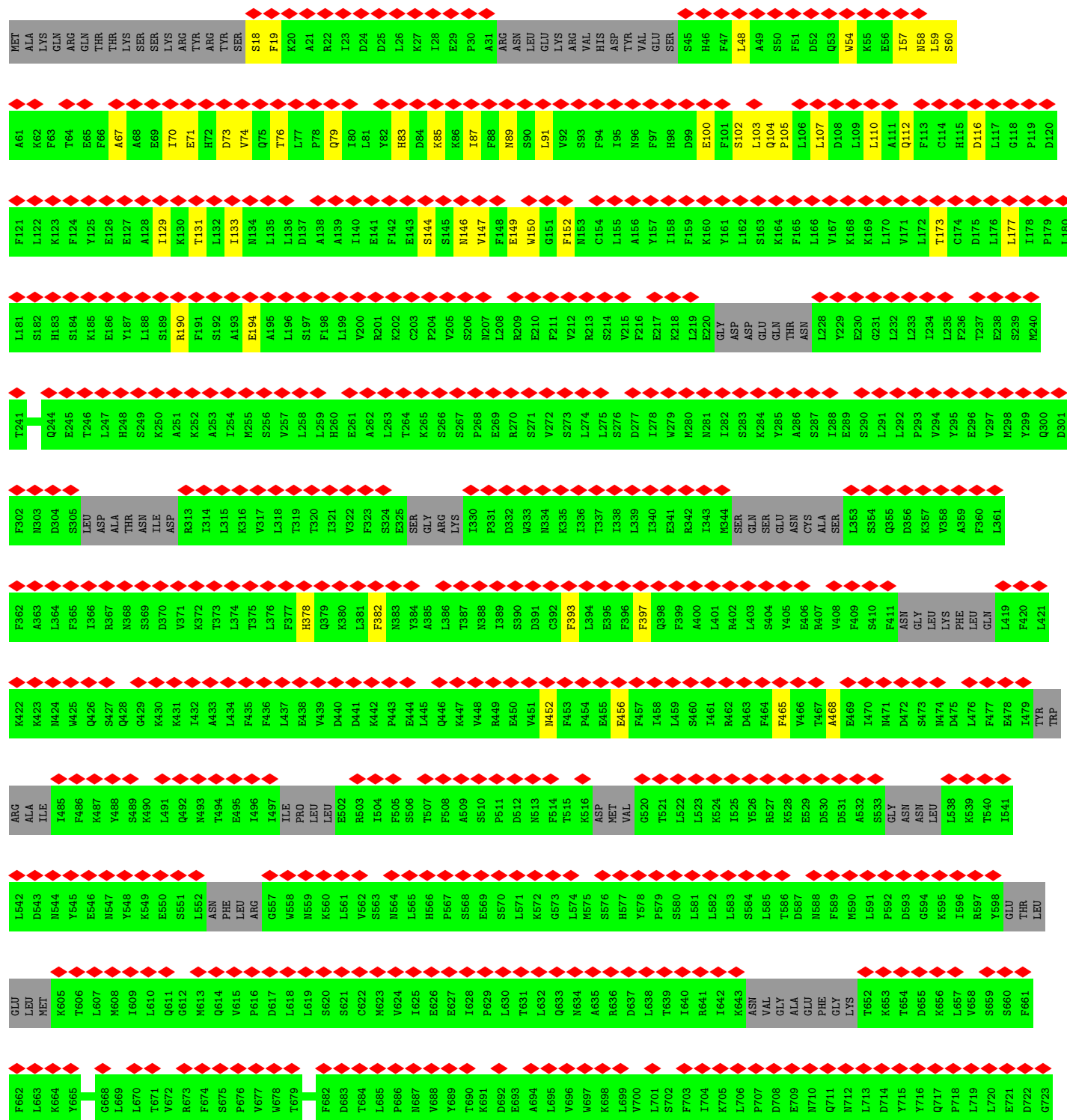
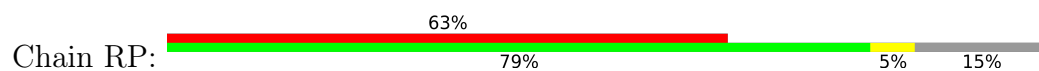


- Molecule 61: Nucleolar complex protein 4

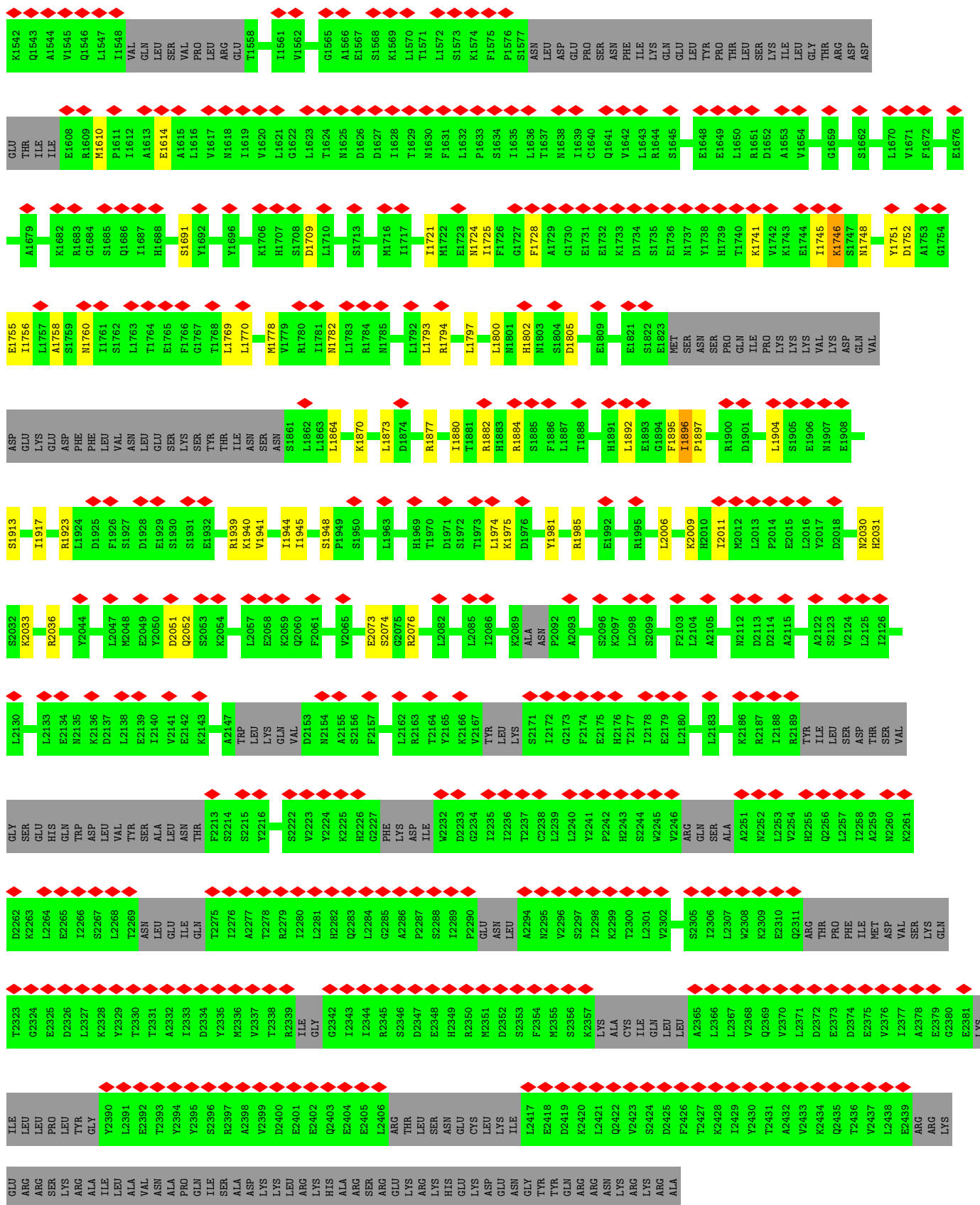




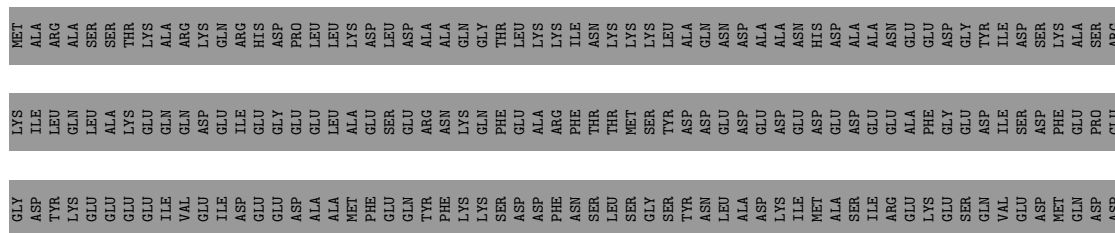
- Molecule 62: U3 small nucleolar RNA-associated protein 20

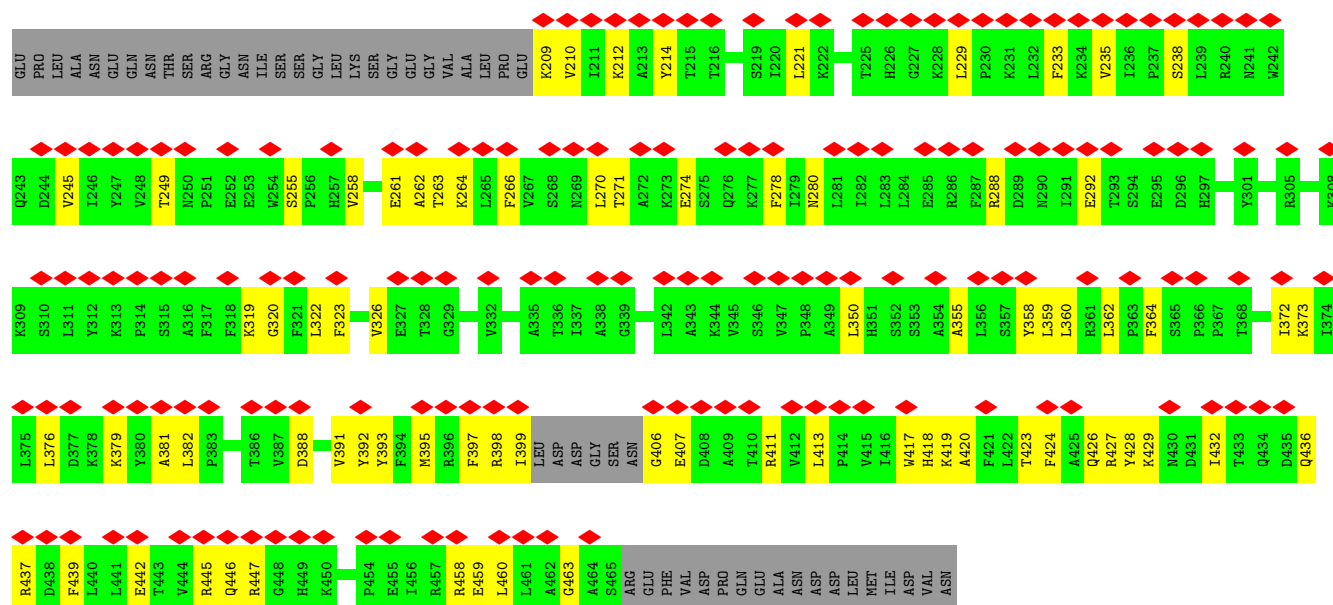


I1481	S1482	H1483	Y1484	L1485	I1486	P1487	N1488	I1489	E1490	H1491	Y1492	V1493	F1494	S1495	D1496	D1497	E1498	R1499	Y1500	R1501	N1502	I1503	G1504	N1505	E1506	T1507	Q1508	I1509	A1510	PHE	PHE	THR	THR	ASN	VAL	ASN	ASN	HIS	ILE	GLN	LEU	HIS	R1461	R1462	Q1463	R1464	A1465	I1466	K1467	R1468	L1469	G1470	E1471	H1472	A1473	S1532	M1533	L1534	K1535	T1536	P1537	M1538	N1539	Q1540	M1541							
V1420	L1421	S1422	Y1423	M1424	V1425	K1426	N1427	T1428	K1429	V1430	F1431	T1432	D1433	F1434	E1435	D1436											I1439	L1440	L1441	Y1442	N1443	G1444	D1445	E1446	T1447	A1448	D1449	PHE	PHE	THR	THR	ASN	VAL	ASN	ASN	HIS	ILE	GLN	LEU	HIS	R1461	R1462	Q1463	R1464	A1465	I1466	K1467	R1468	L1469	G1470	E1471	H1472	A1473	S1532	M1533	L1534	K1535	T1536	P1537	M1538	N1479	S1480
GLU	LEU	ALA	LEU	ARG	THR	ASN	ALA	SER	HIS	ILE	ALA	MET	LYS	PHE	ILE	D1376	F1377	I1378	N1379	E1380	K1381	P1382	M1383	L1384	M1385	E1386	A1387	S1388	K1389	S1390	I1391	S1392	M1393	L1394	K1395	D1396	I1397	L1398	L1399	P1400	N1401	I1402	R1403	I1404	G1405	L1406	R1407	D1408	S1409	L1410	E1411	E1412	V1413	GLN	SER	GLU	TYR	VAL	SER													
D1239	T1240	Q1241	K1242	L1243	L1244	K1245	I1246	L1247	K1248	L1249	I1250	V1251	F1252	M1253	Y1254	M1255	C1256	S1257	W1258	D1259	S1260	I1261	E1262	E1263	L1264	Y1265	T1266	I1267	M1268	S1269	S1270	L1271	F1272	K1273	T1274	F1275	D1276	E1277	R1278	N1279	L1280	R1281	V1282	S1283	L1284	T1285	E1286	L1287	L1288	I1289	E1290	R1293	K1294	V1295	P1296	E1297	L1298	F1299														
L1179	K1180	I1181	L1182	P1183	S1184	L1185	Y1186	V1187	K1188	L1189	S1190	D1191	S1192	M1193	S1194	I1195	S1196	T1197	F1198	L1199	M1200	L1201	L1202	V1203	S1204	I1205	T1206	E1207	M1208	G1209	F1210	I1211	Q1212	D1213	D1214	H1215	V1216	R1217	S1218	R1219	L1220	I1221	S1222	S1223	L1224	I1225	S1226	I1227	L1228	K1229	G1230	K1231	L1232	K1233	K1234	L1235	Q1236	E1237	N1238													
Y1119	Q1120	F1121	L1122	Y1123	Y1124	D1125	E1126	F1127	A1128	T1129	A1130	T1131	A1132	L1133	M1134	D1135	T1136	I1137	S1138	M1139	Q1140	H1141	V1142	K1143	E1144	A1145	V1146	I1147	G1148	P1149	I1150	I1151	E1152	A1153	A1154	D1155	S1156	I1157	I1158	R1159	N1160	P1161	V1162	N1163	D1164	D1165	H1166	Y1167	V1168	D1169	W1170	A1171	T1172	L1173	L1174	C1175	T1176	C1178														
R1055	Q1056	Q1057	G1058	L1059	K1060	C1061	L1062	S1063	S1064	V1065	F1066	V1069	G1070	N1071	T1072	F1073	D1074	W1075	S1076	T1077	S1078	D1081	A1084	V1087	K1088	P1089	R1090	I1091	S1092	H1093	F1094	S1095	D1096	E1097	N1098	L1099	Q1100	Q1101	P1102	S1103	S1104	L1105	L1106	R1107	F1109	Y1110	Y1111	W1112	A1113	H1114	N1115	P1116	S1117	L1118																		
G979	N980	S981	H982	Q983	L984	N985	S986	S987	K988	A989	T990	L991	R995	T998	G999	F1000	V1001	N1002	I1003	V1004	N1005	S1006	T1007	V1010	V1022	L1023	Q1024	P1025	S1029	I1030	A1031	M1032	A1033	Y1034	Y1035	V1036	L1037	D1038	T1039	N955	I961	F964	S969	E970	R971	L972	D973	Y974	N975	Y976	F977	F978																				
G909	S910	Q911	S912	I913	K914	A915	E916	D917	E918	K919	V920	V921	N922	P923	Y924	R927	I928	G931	R932	A933	Q934	V935	P936	P937	T938	S939	G940	Q941	K942	R943	S944	R945	K946	I947	A948	V949	I950	S951	V952	L953	P954	N955	I961	F964	S969	E970	R971	L972	D973	Y974	N975	Y976	F977	F978																		
E949	L950	H951	D952	H953	L954	M955	V956	L957	L958	G959	S960	R961	N962	T963	D964	V965	Q966	K967	L968	A969	L970	D971	A972	L973	L974	A975	R976	K977	N978	P979	T980	L981	N982	K983	Y984	R985	D986	N987	L988	K989	N990	L991	L992	D993	D994	T995	L996	F997	K998	D999	E900	I901	T902	T903	F904	L905	T906	E907	N908													
V788	A789	E790	N791	H792	F793	D794	V795	I796	A797	P798	F799	V800	L736	D738	T739	I740	K805	T806	Y807	K808	D809	E810	E811	D812	M813	E814	N815	E816	K877	V818	I819	T820	N821	S822	E825	V826	D827	R828	N829	V830	F831	L832	L833	T834	L835	S836	K837	F838	N839	I840	I841	K842	N843	Y844	S845	S846	A847	T848														
A724	A725	A726	A727	A728	A729	A730	A731	A732	A733	A734	A735	A736	A737	A738	A739	A740	F743	S744	H745	I746	I747	S748	T752	Q753	N754	T755	S756	I757	I758	S759	T760	T761	I762	E763	R764	R765	R766	N767	Y770	P771	I772	L773	I774	R775	N776	Q777	A778	L779	K780	N781	M782	L783	I785	F786	Q787																	

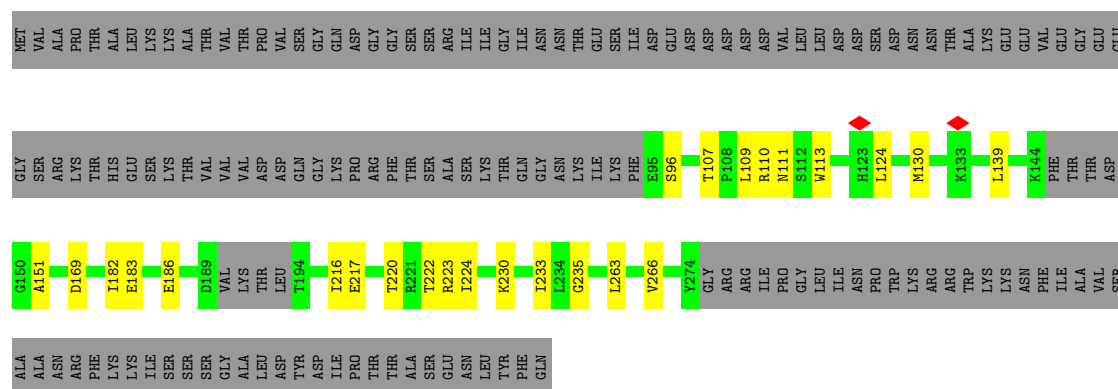


• Molecule 63: U3 small nucleolar RNA-associated protein 14

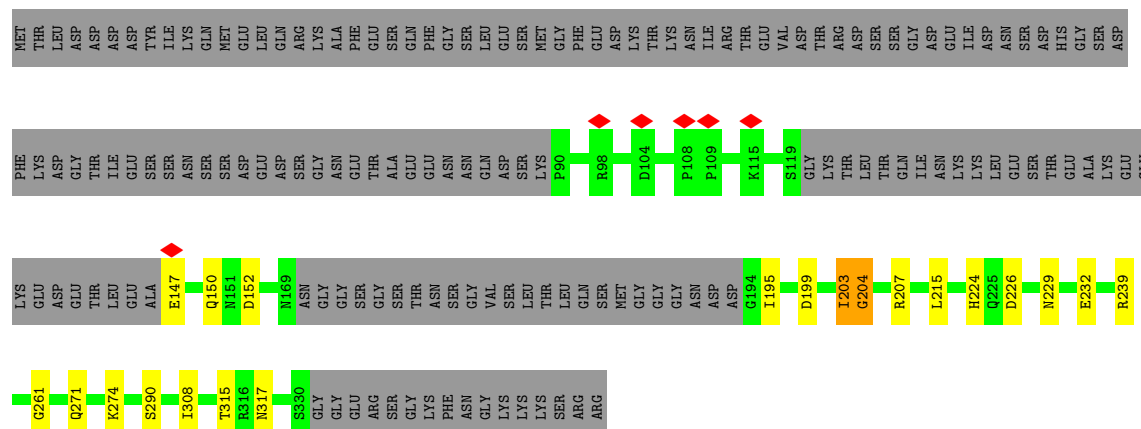




• Molecule 65: Pno1

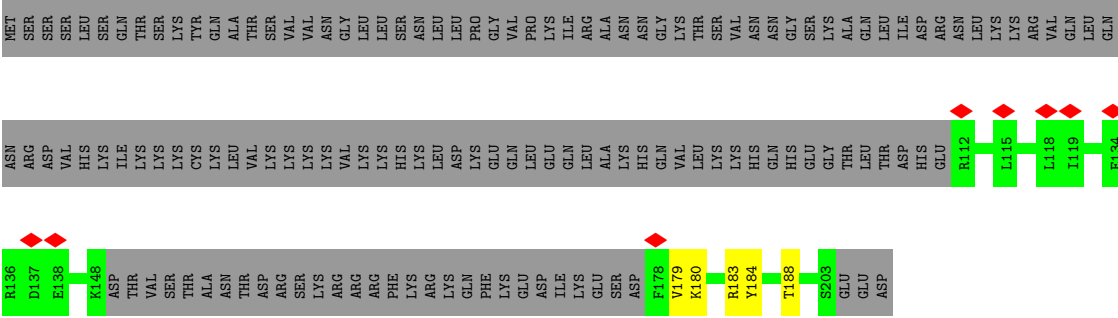


• Molecule 66: Protein FAF1



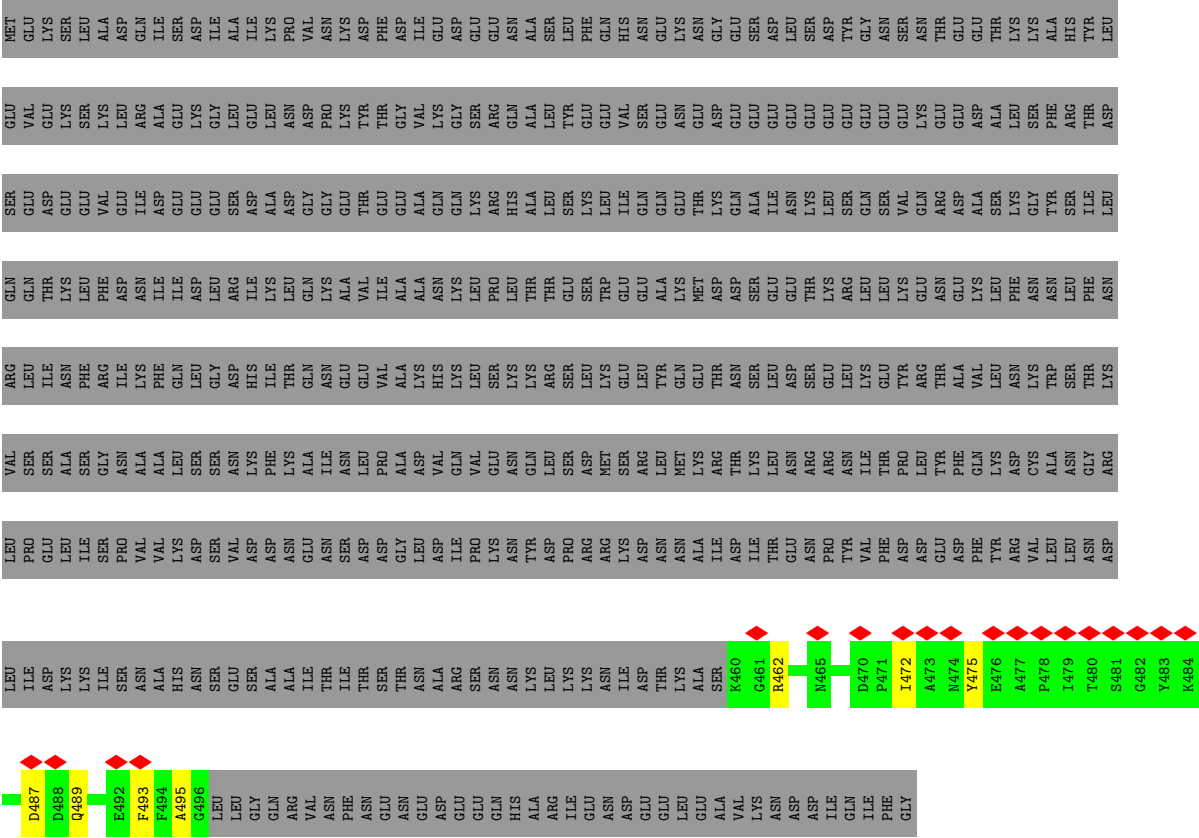
• Molecule 67: Regulator of rDNA transcription protein 14

Chain RW: 28% 69%



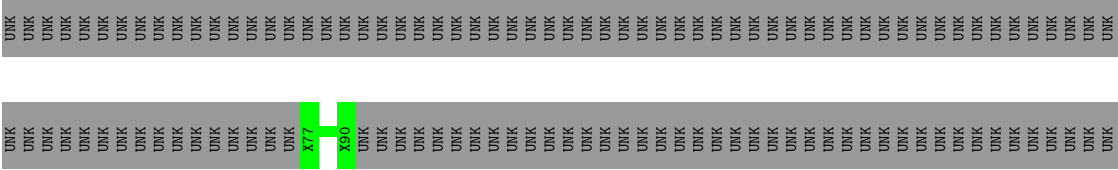
• Molecule 68: Protein BFR2

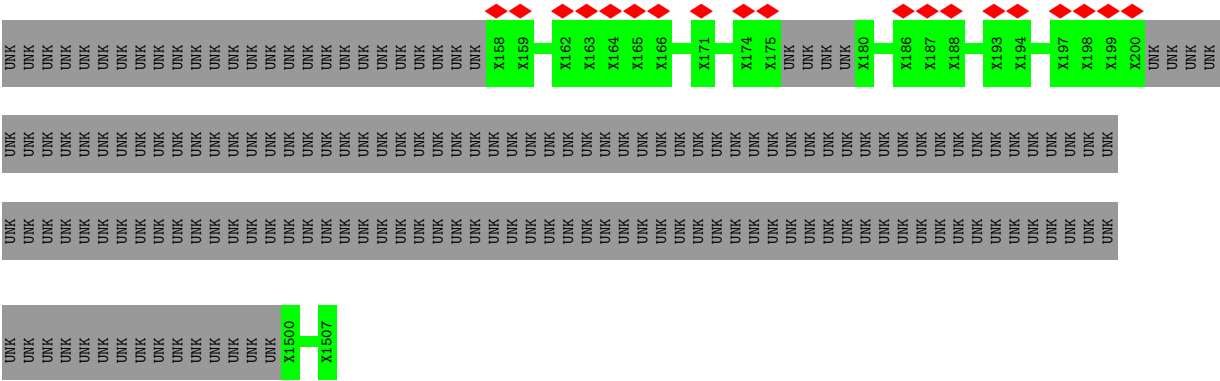
Chain RY: 6% 93%



• Molecule 69: Unassigned helices

Chain X1: 5% 18% 82%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	71230	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.246	Depositor
Minimum map value	-0.115	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	597.632, 597.632, 597.632	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.334, 1.334, 1.334	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, 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	3A	0.45	0/4141	0.48	0/6433
2	5A	0.41	0/12485	0.47	2/19449 (0.0%)
3	SA	0.35	0/31590	0.46	5/49182 (0.0%)
4	SC	0.44	0/1856	0.77	3/2490 (0.1%)
5	SF	0.29	0/1854	0.66	0/2504
6	SG	0.49	0/1690	0.67	2/2285 (0.1%)
7	SH	0.24	0/1341	0.61	1/1789 (0.1%)
8	SI	0.32	0/1341	0.69	2/1806 (0.1%)
9	SJ	0.26	0/1347	0.60	0/1801
10	SK	0.44	0/1410	0.63	0/1888
11	SM	0.26	0/1020	0.64	0/1374
12	SN	0.29	0/873	0.78	0/1185
13	SO	0.39	0/1109	0.63	0/1495
14	SP	0.46	0/879	0.79	0/1186
15	SR	0.52	0/990	0.77	3/1335 (0.2%)
16	ST	0.30	0/980	0.65	0/1319
17	SX	0.46	0/1020	0.63	0/1371
18	SY	0.48	0/798	0.65	0/1065
19	SZ	0.36	0/822	0.73	0/1103
20	Sc	0.40	0/613	0.63	0/828
21	Sd	0.50	0/499	0.72	2/670 (0.3%)
22	3B	0.51	0/1901	0.66	1/2567 (0.0%)
22	3C	0.37	0/1796	0.66	0/2424
23	3D	0.40	0/2891	0.62	0/3895
24	3E	0.38	0/3059	0.62	0/4153
25	3F	0.36	0/3715	0.64	0/5001
26	3G	0.51	0/928	0.72	1/1262 (0.1%)
26	3H	0.45	0/928	0.70	0/1262
27	A4	0.43	0/5321	0.66	0/7207
28	A5	0.44	0/4044	0.65	0/5493
29	A8	0.23	0/3328	0.62	0/4565
30	A9	0.28	0/951	0.60	0/1287

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	AE	0.32	1/10049 (0.0%)	0.56	1/13737 (0.0%)
32	AF	0.48	0/3993	0.68	0/5413
33	AG	0.42	0/6699	0.64	3/9077 (0.0%)
34	B1	0.58	0/6780	0.69	0/9175
35	B2	0.39	0/6853	0.68	2/9256 (0.0%)
36	B3	0.35	0/6014	0.70	2/8137 (0.0%)
37	B8	0.55	0/3848	0.63	0/5218
38	BE	0.53	0/6948	0.64	2/9391 (0.0%)
39	B6	0.37	0/2849	0.60	0/3853
40	5B	0.31	0/499	0.62	0/659
41	5C	0.55	0/4321	0.66	2/5832 (0.0%)
42	5D	0.46	0/1998	0.70	0/2644
43	5E	0.44	0/1665	0.66	2/2233 (0.1%)
44	5F	0.64	0/1559	0.72	1/2097 (0.0%)
45	5G	0.52	0/2337	0.67	2/3148 (0.1%)
46	5H	0.40	0/1074	0.57	0/1422
47	5I	0.56	0/3844	0.68	0/5174
48	5J	0.36	0/1302	0.58	0/1728
49	5K	0.51	0/1426	0.66	0/1917
50	RA	0.27	0/2769	0.66	2/3753 (0.1%)
51	RB	0.37	0/1121	0.79	0/1487
52	RC	0.40	0/2245	0.60	0/3021
53	RE	0.30	0/8924	0.60	1/12070 (0.0%)
54	RF	0.28	0/2004	0.66	1/2697 (0.0%)
55	RG	0.32	0/1727	0.70	0/2329
55	RH	0.37	0/1828	0.59	0/2470
56	RI	0.41	0/2080	0.65	0/2797
57	RJ	0.44	0/6514	0.61	0/8768
58	RK	0.39	0/2832	0.64	0/3825
59	RL	0.21	0/4549	0.51	1/6241 (0.0%)
59	RM	0.15	0/3765	0.44	1/5218 (0.0%)
60	RN	0.30	0/4591	0.63	1/6187 (0.0%)
61	RO	0.32	0/3849	0.63	0/5261
62	RP	0.21	0/12230	0.54	4/16819 (0.0%)
63	RQ	0.41	0/1678	0.63	1/2282 (0.0%)
64	RS	0.30	0/2104	0.70	0/2854
65	RT	0.38	0/1379	0.68	0/1853
66	RV	0.43	0/1456	0.60	1/1937 (0.1%)
67	RW	0.26	0/385	0.49	0/529
68	RY	0.23	0/307	0.53	0/415
All	All	0.39	1/239915 (0.0%)	0.60	52/334598 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	SC	0	1
5	SF	0	2
8	SI	0	3
9	SJ	0	1
11	SM	0	1
13	SO	0	1
14	SP	0	1
16	ST	0	1
19	SZ	0	1
20	Sc	0	1
23	3D	0	3
24	3E	0	1
25	3F	0	1
26	3G	0	2
26	3H	0	1
27	A4	0	1
28	A5	0	1
29	A8	0	4
33	AG	0	2
34	B1	0	3
35	B2	0	9
36	B3	0	11
38	BE	0	1
41	5C	0	2
42	5D	0	1
43	5E	0	1
44	5F	0	1
45	5G	0	1
47	5I	0	2
50	RA	0	2
51	RB	0	1
53	RE	0	1
54	RF	0	1
57	RJ	0	2
58	RK	0	1
59	RL	0	1
59	RM	0	1
60	RN	0	1
61	RO	0	1
62	RP	0	3

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
63	RQ	0	1
66	RV	0	2
All	All	0	79

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	AE	564	VAL	C-N	5.39	1.40	1.34

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	B2	267	ASP	CA-C-N	6.86	134.65	121.54
35	B2	267	ASP	C-N-CA	6.86	134.65	121.54
2	5A	312	U	P-O3'-C3'	6.82	130.43	120.20
62	RP	2033	LYS	CA-C-N	6.64	134.22	121.54
62	RP	2033	LYS	C-N-CA	6.64	134.22	121.54

There are no chirality outliers.

5 of 79 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	SC	238	GLU	Peptide
5	SF	193	GLY	Peptide
5	SF	195	ILE	Peptide
8	SI	31	SER	Peptide
8	SI	64	VAL	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3A	3711	0	1882	22	0
2	5A	11163	0	5611	84	0
3	SA	28258	0	14249	250	0
4	SC	1830	0	1914	33	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	SF	1815	0	1870	45	0
6	SG	1669	0	1724	18	0
7	SH	1327	0	1403	30	0
8	SI	1321	0	1387	23	0
9	SJ	1324	0	1344	48	0
10	SK	1388	0	1467	32	0
11	SM	997	0	1048	34	0
12	SN	865	0	874	16	0
13	SO	1087	0	1152	13	0
14	SP	868	0	894	14	0
15	SR	973	0	1029	14	0
16	ST	964	0	991	16	0
17	SX	1003	0	1040	16	0
18	SY	786	0	843	8	0
19	SZ	809	0	842	15	0
20	Sc	603	0	623	9	0
21	Sd	497	0	535	3	0
22	3B	1865	0	1910	30	0
22	3C	1763	0	1805	34	0
23	3D	2848	0	2815	46	0
24	3E	3028	0	2813	62	0
25	3F	3643	0	3654	79	0
26	3G	916	0	964	11	0
26	3H	916	0	964	26	0
27	A4	5226	0	5199	96	0
28	A5	3976	0	3919	58	0
29	A8	3307	0	2316	39	0
30	A9	939	0	898	19	0
31	AE	9955	0	7968	103	0
32	AF	3911	0	3906	73	0
33	AG	6570	0	6473	127	0
34	B1	6635	0	6525	103	0
35	B2	6723	0	6698	121	0
36	B3	5919	0	6007	127	0
37	B8	3764	0	3757	59	0
38	BE	6810	0	6787	86	0
39	B6	2800	0	2517	35	0
40	5B	495	0	561	14	0
41	5C	4237	0	4239	85	0
42	5D	1972	0	2054	28	0
43	5E	1647	0	1678	33	0
44	5F	1530	0	1572	30	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	5G	2296	0	2325	42	0
46	5H	1065	0	1097	17	0
47	5I	3765	0	3714	73	0
48	5J	1280	0	1331	23	0
49	5K	1403	0	1484	20	0
50	RA	2709	0	2622	66	0
51	RB	1108	0	1087	27	0
52	RC	2207	0	2229	29	0
53	RE	8716	0	8828	168	0
54	RF	1963	0	1942	43	0
55	RG	1701	0	1767	40	0
55	RH	1799	0	1872	32	0
56	RI	2045	0	2162	38	0
57	RJ	6379	0	6506	111	0
58	RK	2781	0	2878	51	0
59	RL	4539	0	2874	29	0
59	RM	3779	0	1650	8	0
60	RN	4529	0	4262	71	0
61	RO	3766	0	3269	47	0
62	RP	12176	0	7751	76	0
63	RQ	1651	0	1450	28	0
64	RS	2051	0	2096	54	0
65	RT	1357	0	1426	15	0
66	RV	1448	0	1435	16	0
67	RW	381	0	255	4	0
68	RY	299	0	275	6	0
69	X1	305	0	73	0	0
70	5K	1	0	0	0	0
70	Sc	1	0	0	0	0
71	RJ	32	0	12	2	0
72	RJ	1	0	0	0	0
All	All	232186	0	199393	2963	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 7.

The worst 5 of 2963 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)
29:A8:264:SER:O	29:A8:267:ILE:HA	1.61	1.01
35:B2:17:ILE:HG22	35:B2:52:TRP:CZ2	1.94	1.01

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:RN:527:GLN:O	60:RN:531:GLN:HB2	1.60	1.01
63:RQ:298:TRP:NE1	63:RQ:899:LYS:HG3	1.76	1.00
3:SA:36:C:H42	3:SA:472:U:H3	1.00	0.99

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	SC	228/255 (89%)	196 (86%)	32 (14%)	0	100	100
5	SF	227/261 (87%)	197 (87%)	29 (13%)	1 (0%)	30	62
6	SG	211/225 (94%)	195 (92%)	16 (8%)	0	100	100
7	SH	161/236 (68%)	143 (89%)	18 (11%)	0	100	100
8	SI	161/190 (85%)	143 (89%)	18 (11%)	0	100	100
9	SJ	162/200 (81%)	140 (86%)	22 (14%)	0	100	100
10	SK	169/197 (86%)	163 (96%)	6 (4%)	0	100	100
11	SM	119/156 (76%)	103 (87%)	16 (13%)	0	100	100
12	SN	117/143 (82%)	89 (76%)	28 (24%)	0	100	100
13	SO	132/151 (87%)	123 (93%)	9 (7%)	0	100	100
14	SP	116/137 (85%)	99 (85%)	16 (14%)	1 (1%)	14	47
15	SR	123/143 (86%)	112 (91%)	11 (9%)	0	100	100
16	ST	113/146 (77%)	103 (91%)	10 (9%)	0	100	100
17	SX	125/130 (96%)	119 (95%)	6 (5%)	0	100	100
18	SY	101/145 (70%)	90 (89%)	11 (11%)	0	100	100
19	SZ	100/135 (74%)	87 (87%)	12 (12%)	1 (1%)	12	45
20	Sc	78/82 (95%)	69 (88%)	9 (12%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	Sd	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
22	3B	236/327 (72%)	222 (94%)	14 (6%)	0	100	100
22	3C	221/327 (68%)	207 (94%)	14 (6%)	0	100	100
23	3D	359/504 (71%)	346 (96%)	13 (4%)	0	100	100
24	3E	427/511 (84%)	387 (91%)	40 (9%)	0	100	100
25	3F	446/573 (78%)	403 (90%)	42 (9%)	1 (0%)	43	73
26	3G	119/126 (94%)	107 (90%)	11 (9%)	1 (1%)	16	50
26	3H	119/126 (94%)	111 (93%)	8 (7%)	0	100	100
27	A4	648/776 (84%)	590 (91%)	58 (9%)	0	100	100
28	A5	504/643 (78%)	465 (92%)	39 (8%)	0	100	100
29	A8	534/713 (75%)	398 (74%)	134 (25%)	2 (0%)	30	62
30	A9	126/575 (22%)	115 (91%)	11 (9%)	0	100	100
31	AE	1496/1769 (85%)	1367 (91%)	129 (9%)	0	100	100
32	AF	489/513 (95%)	442 (90%)	47 (10%)	0	100	100
33	AG	812/896 (91%)	731 (90%)	80 (10%)	1 (0%)	48	79
34	B1	830/923 (90%)	767 (92%)	63 (8%)	0	100	100
35	B2	839/943 (89%)	749 (89%)	88 (10%)	2 (0%)	43	73
36	B3	733/817 (90%)	606 (83%)	125 (17%)	2 (0%)	36	68
37	B8	469/594 (79%)	439 (94%)	30 (6%)	0	100	100
38	BE	857/939 (91%)	803 (94%)	54 (6%)	0	100	100
39	B6	368/440 (84%)	341 (93%)	27 (7%)	0	100	100
40	5B	58/214 (27%)	55 (95%)	3 (5%)	0	100	100
41	5C	531/554 (96%)	487 (92%)	43 (8%)	1 (0%)	43	73
42	5D	231/250 (92%)	204 (88%)	27 (12%)	0	100	100
43	5E	200/593 (34%)	183 (92%)	16 (8%)	1 (0%)	24	59
44	5F	180/183 (98%)	172 (96%)	8 (4%)	0	100	100
45	5G	278/290 (96%)	256 (92%)	22 (8%)	0	100	100
46	5H	132/610 (22%)	123 (93%)	9 (7%)	0	100	100
47	5I	457/489 (94%)	421 (92%)	36 (8%)	0	100	100
48	5J	147/217 (68%)	136 (92%)	11 (8%)	0	100	100
49	5K	171/189 (90%)	166 (97%)	5 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	RA	332/707 (47%)	276 (83%)	56 (17%)	0	100	100
51	RB	132/357 (37%)	117 (89%)	14 (11%)	1 (1%)	16	50
52	RC	276/316 (87%)	259 (94%)	17 (6%)	0	100	100
53	RE	1067/1237 (86%)	999 (94%)	68 (6%)	0	100	100
54	RF	233/297 (78%)	203 (87%)	30 (13%)	0	100	100
55	RG	212/252 (84%)	182 (86%)	30 (14%)	0	100	100
55	RH	226/252 (90%)	219 (97%)	7 (3%)	0	100	100
56	RI	250/274 (91%)	233 (93%)	17 (7%)	0	100	100
57	RJ	784/1183 (66%)	721 (92%)	62 (8%)	1 (0%)	48	79
58	RK	358/367 (98%)	341 (95%)	17 (5%)	0	100	100
59	RL	781/1056 (74%)	664 (85%)	115 (15%)	2 (0%)	36	68
59	RM	738/1056 (70%)	625 (85%)	109 (15%)	4 (0%)	24	59
60	RN	593/810 (73%)	545 (92%)	47 (8%)	1 (0%)	43	73
61	RO	523/552 (95%)	455 (87%)	68 (13%)	0	100	100
62	RP	2043/2493 (82%)	1815 (89%)	227 (11%)	1 (0%)	100	100
63	RQ	220/899 (24%)	199 (90%)	21 (10%)	0	100	100
64	RS	247/483 (51%)	225 (91%)	22 (9%)	0	100	100
65	RT	165/326 (51%)	150 (91%)	15 (9%)	0	100	100
66	RV	184/346 (53%)	165 (90%)	19 (10%)	0	100	100
67	RW	59/206 (29%)	54 (92%)	5 (8%)	0	100	100
68	RY	35/534 (7%)	29 (83%)	6 (17%)	0	100	100
All	All	24979/33626 (74%)	22503 (90%)	2452 (10%)	24 (0%)	49	79

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
43	5E	454	VAL
59	RL	744	PRO
59	RM	744	PRO
59	RM	905	PRO
19	SZ	51	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	SC	203/224 (91%)	201 (99%)	2 (1%)	68	80
5	SF	196/222 (88%)	193 (98%)	3 (2%)	57	76
6	SG	180/191 (94%)	179 (99%)	1 (1%)	78	84
7	SH	139/201 (69%)	136 (98%)	3 (2%)	45	71
8	SI	146/170 (86%)	143 (98%)	3 (2%)	47	71
9	SJ	136/161 (84%)	134 (98%)	2 (2%)	57	76
10	SK	147/166 (89%)	147 (100%)	0	100	100
11	SM	110/137 (80%)	108 (98%)	2 (2%)	51	74
12	SN	88/119 (74%)	87 (99%)	1 (1%)	65	79
13	SO	117/128 (91%)	116 (99%)	1 (1%)	70	81
14	SP	90/105 (86%)	89 (99%)	1 (1%)	65	79
15	SR	105/119 (88%)	105 (100%)	0	100	100
16	ST	105/129 (81%)	105 (100%)	0	100	100
17	SX	108/111 (97%)	106 (98%)	2 (2%)	50	73
18	SY	85/120 (71%)	83 (98%)	2 (2%)	43	70
19	SZ	85/113 (75%)	85 (100%)	0	100	100
20	Sc	69/71 (97%)	69 (100%)	0	100	100
21	Sd	56/60 (93%)	56 (100%)	0	100	100
22	3B	201/240 (84%)	201 (100%)	0	100	100
22	3C	190/240 (79%)	188 (99%)	2 (1%)	65	79
23	3D	296/435 (68%)	295 (100%)	1 (0%)	86	88
24	3E	262/433 (60%)	261 (100%)	1 (0%)	84	86
25	3F	396/503 (79%)	392 (99%)	4 (1%)	68	80
26	3G	100/104 (96%)	100 (100%)	0	100	100
26	3H	100/104 (96%)	100 (100%)	0	100	100
27	A4	591/713 (83%)	584 (99%)	7 (1%)	63	79

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	A5	433/574 (75%)	429 (99%)	4 (1%)	70	81
29	A8	174/657 (26%)	173 (99%)	1 (1%)	78	84
30	A9	89/533 (17%)	89 (100%)	0	100	100
31	AE	708/1633 (43%)	705 (100%)	3 (0%)	84	86
32	AF	437/454 (96%)	431 (99%)	6 (1%)	59	77
33	AG	750/826 (91%)	739 (98%)	11 (2%)	57	76
34	B1	730/812 (90%)	720 (99%)	10 (1%)	59	77
35	B2	736/832 (88%)	729 (99%)	7 (1%)	68	80
36	B3	665/719 (92%)	656 (99%)	9 (1%)	59	77
37	B8	421/529 (80%)	417 (99%)	4 (1%)	68	80
38	BE	757/819 (92%)	752 (99%)	5 (1%)	76	83
39	B6	251/414 (61%)	249 (99%)	2 (1%)	73	82
40	5B	57/196 (29%)	56 (98%)	1 (2%)	51	74
41	5C	465/480 (97%)	463 (100%)	2 (0%)	84	86
42	5D	221/234 (94%)	221 (100%)	0	100	100
43	5E	185/535 (35%)	185 (100%)	0	100	100
44	5F	171/172 (99%)	168 (98%)	3 (2%)	51	74
45	5G	251/258 (97%)	246 (98%)	5 (2%)	48	72
46	5H	107/538 (20%)	107 (100%)	0	100	100
47	5I	416/443 (94%)	412 (99%)	4 (1%)	68	80
48	5J	140/200 (70%)	140 (100%)	0	100	100
49	5K	157/169 (93%)	157 (100%)	0	100	100
50	RA	303/636 (48%)	299 (99%)	4 (1%)	61	78
51	RB	117/315 (37%)	116 (99%)	1 (1%)	70	81
52	RC	231/289 (80%)	230 (100%)	1 (0%)	84	86
53	RE	984/1125 (88%)	977 (99%)	7 (1%)	76	83
54	RF	221/274 (81%)	221 (100%)	0	100	100
55	RG	195/222 (88%)	193 (99%)	2 (1%)	68	80
55	RH	206/222 (93%)	205 (100%)	1 (0%)	81	85
56	RI	235/256 (92%)	234 (100%)	1 (0%)	84	86
57	RJ	683/1039 (66%)	678 (99%)	5 (1%)	76	83

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	RK	307/312 (98%)	304 (99%)	3 (1%)	68	80
59	RL	164/934 (18%)	164 (100%)	0	100	100
60	RN	422/732 (58%)	422 (100%)	0	100	100
61	RO	329/506 (65%)	326 (99%)	3 (1%)	70	81
62	RP	499/2307 (22%)	496 (99%)	3 (1%)	78	84
63	RQ	148/808 (18%)	145 (98%)	3 (2%)	48	72
64	RS	225/424 (53%)	224 (100%)	1 (0%)	84	86
65	RT	148/282 (52%)	148 (100%)	0	100	100
66	RV	141/304 (46%)	141 (100%)	0	100	100
67	RW	22/192 (12%)	21 (96%)	1 (4%)	24	58
68	RY	31/482 (6%)	31 (100%)	0	100	100
All	All	18233/29007 (63%)	18082 (99%)	151 (1%)	70	82

5 of 151 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
50	RA	76	THR
62	RP	131	THR
51	RB	338	THR
55	RH	31	LEU
67	RW	179	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 436 such sidechains are listed below:

Mol	Chain	Res	Type
38	BE	447	ASN
46	5H	560	ASN
61	RO	249	ASN
38	BE	826	GLN
41	5C	394	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	169/333 (50%)	44 (26%)	2 (1%)
2	5A	518/700 (74%)	161 (31%)	11 (2%)

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	SA	1305/1808 (72%)	499 (38%)	19 (1%)
All	All	1992/2841 (70%)	704 (35%)	32 (1%)

5 of 704 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3A	2	U
1	3A	14	A
1	3A	15	U
1	3A	24	U
1	3A	25	U

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	SA	1197	C
3	SA	1521	G
2	5A	536	A
2	5A	492	G
3	SA	1594	G

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 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 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
71	GTP	RJ	1201	72	33,34,34	0.56	0	50,54,54	0.72	1 (2%)

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
71	GTP	RJ	1201	72	-	3/22/38/38	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
71	RJ	1201	GTP	C4'-O4'-C1'	-2.15	104.72	109.47

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
71	RJ	1201	GTP	O4'-C4'-C5'-O5'
71	RJ	1201	GTP	C3'-C4'-C5'-O5'
71	RJ	1201	GTP	C4'-C5'-O5'-PA

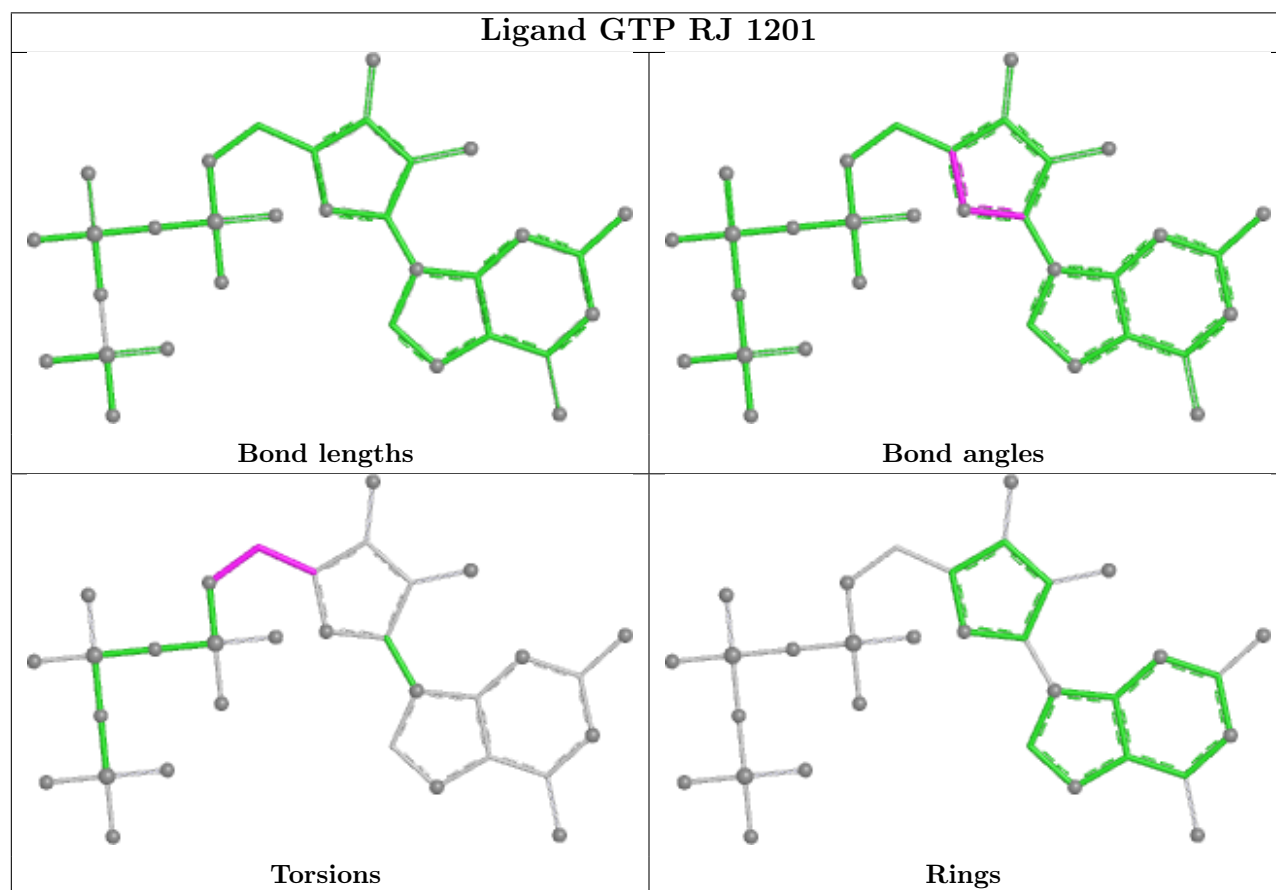
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
71	RJ	1201	GTP	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 than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

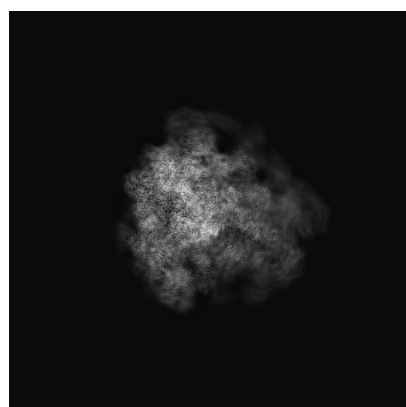
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0949. These allow visual inspection of the internal detail of the map and identification of artifacts.

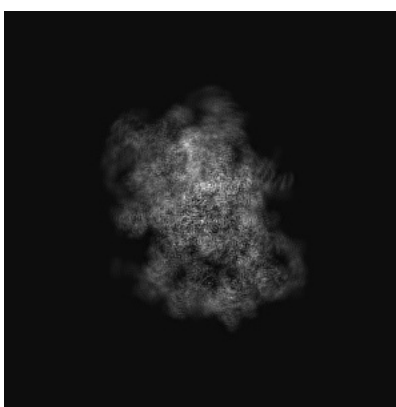
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

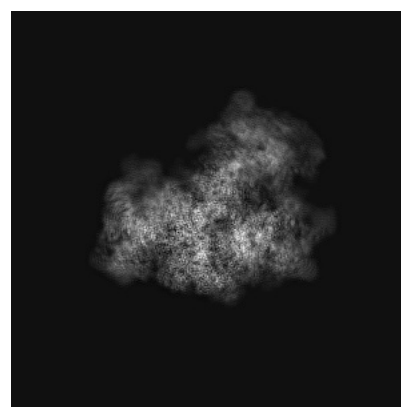
6.1.1 Primary map



X



Y

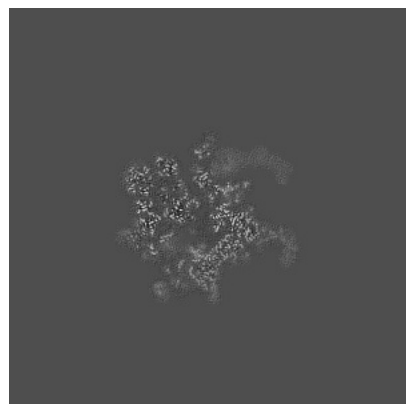


Z

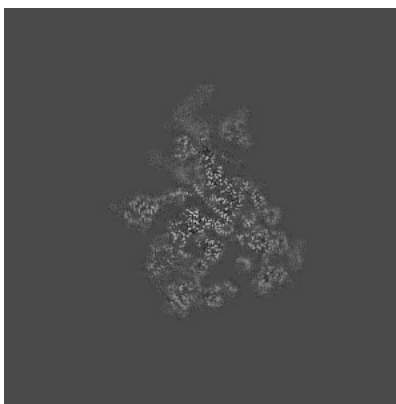
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

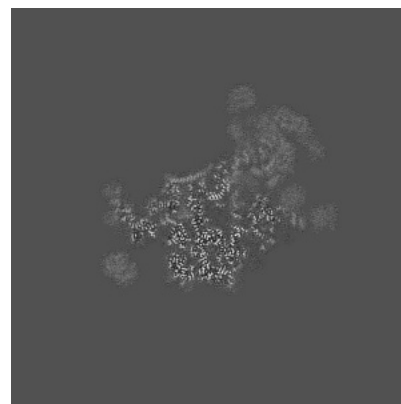
6.2.1 Primary map



X Index: 224



Y Index: 224

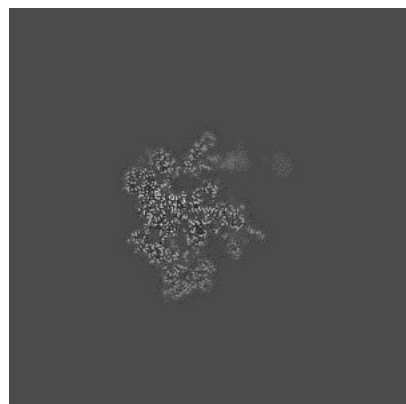


Z Index: 224

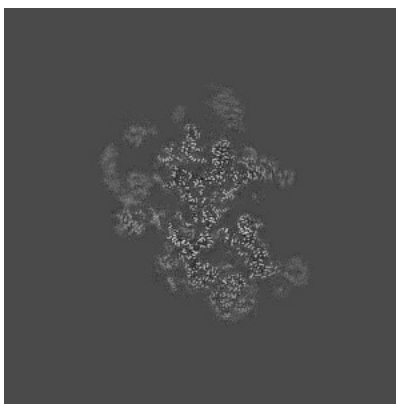
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

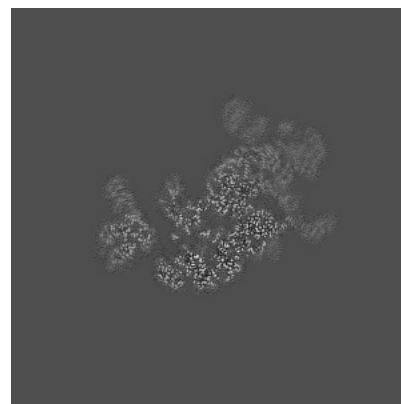
6.3.1 Primary map



X Index: 212



Y Index: 196

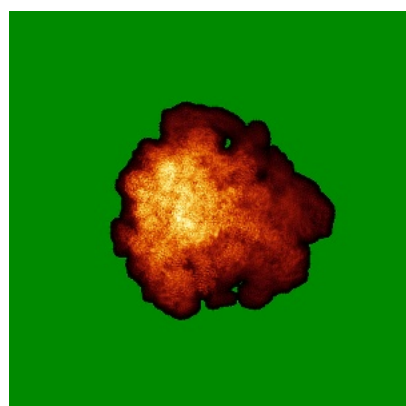


Z Index: 242

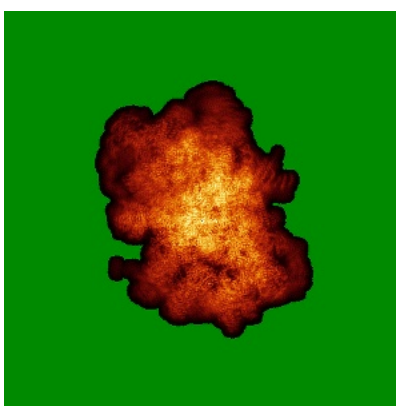
The images above show the largest variance slices of the map in three orthogonal directions.

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

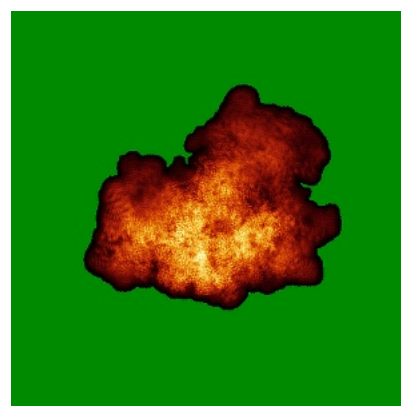
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

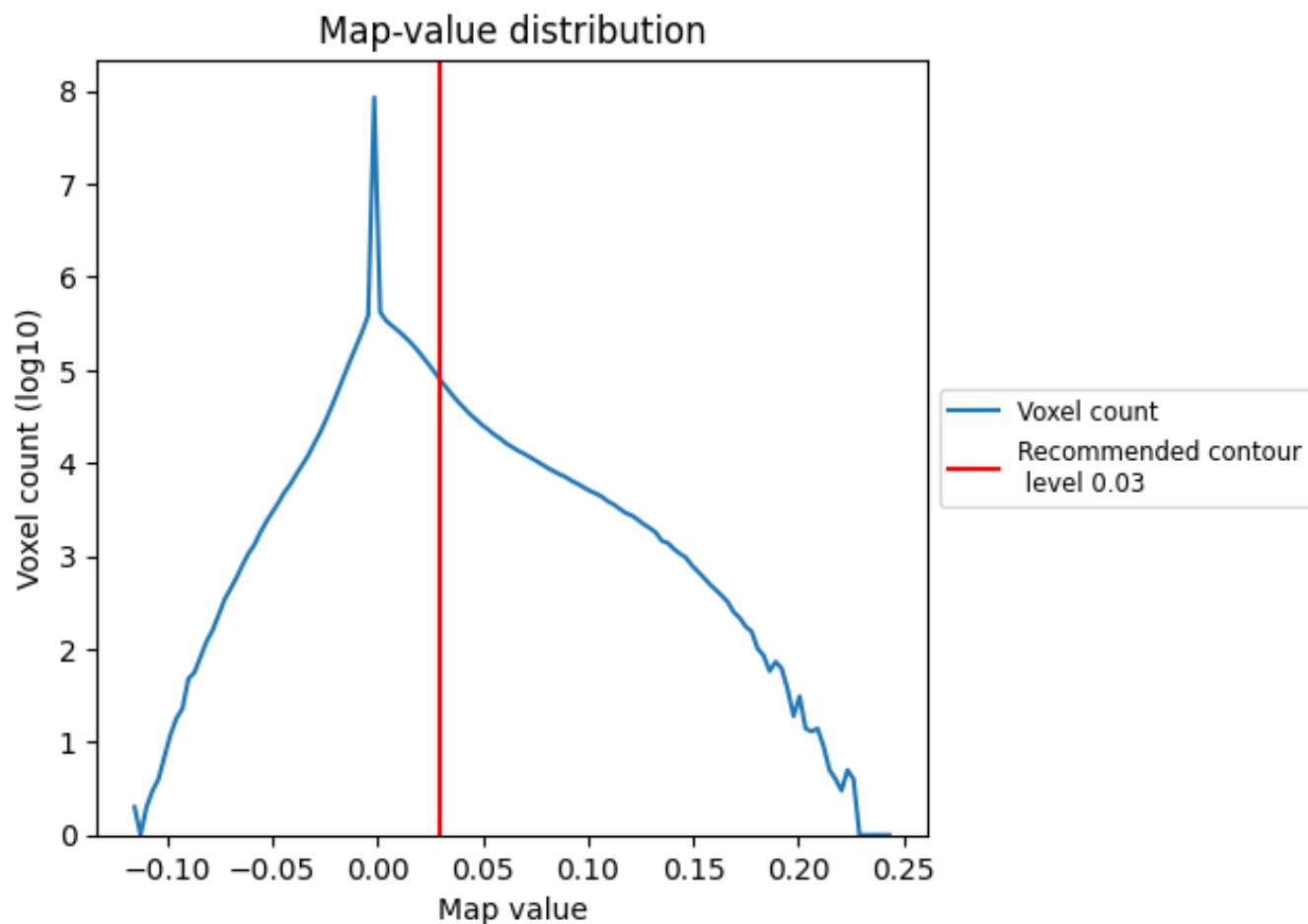
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

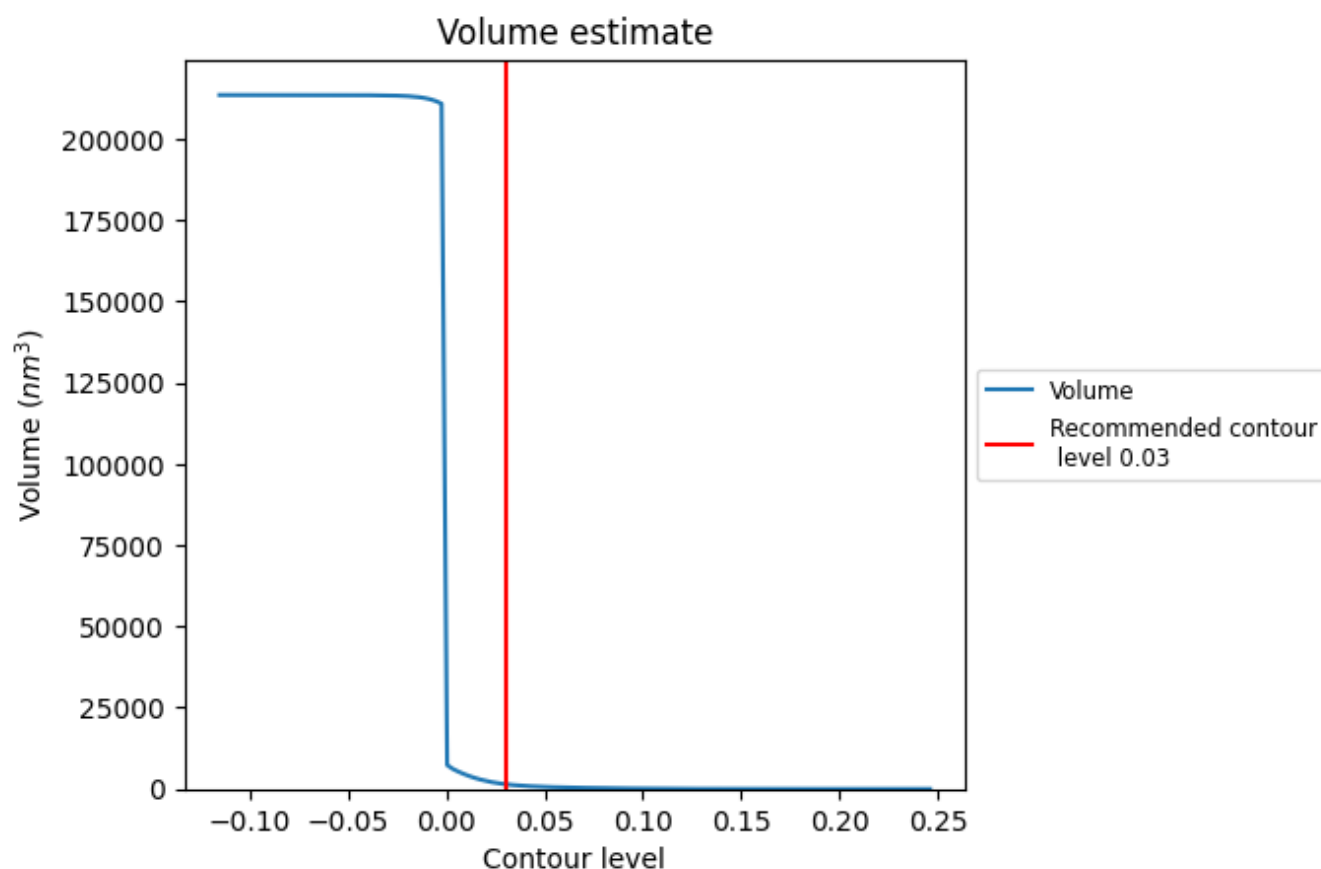
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

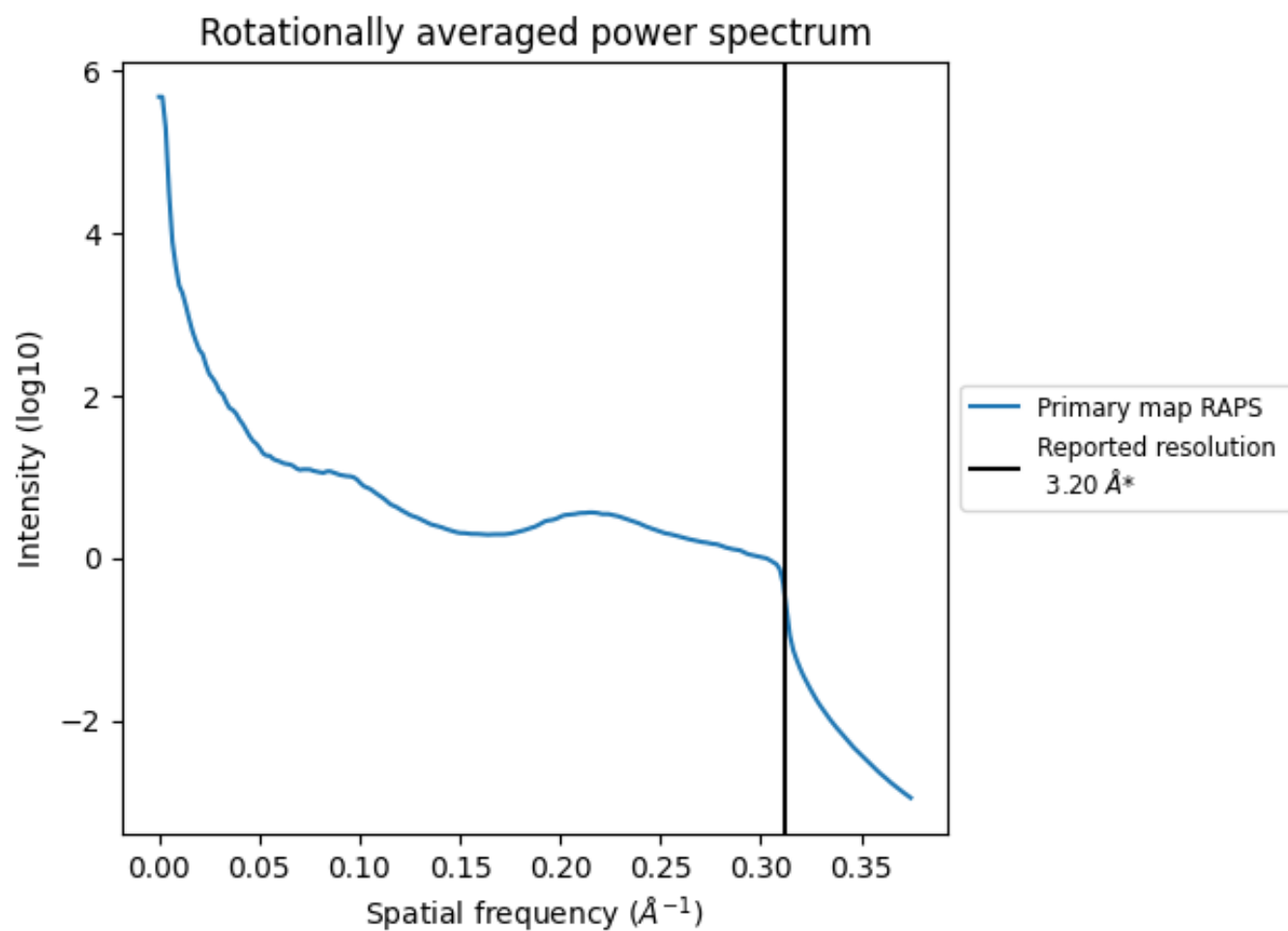
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1466 nm³; this corresponds to an approximate mass of 1324 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

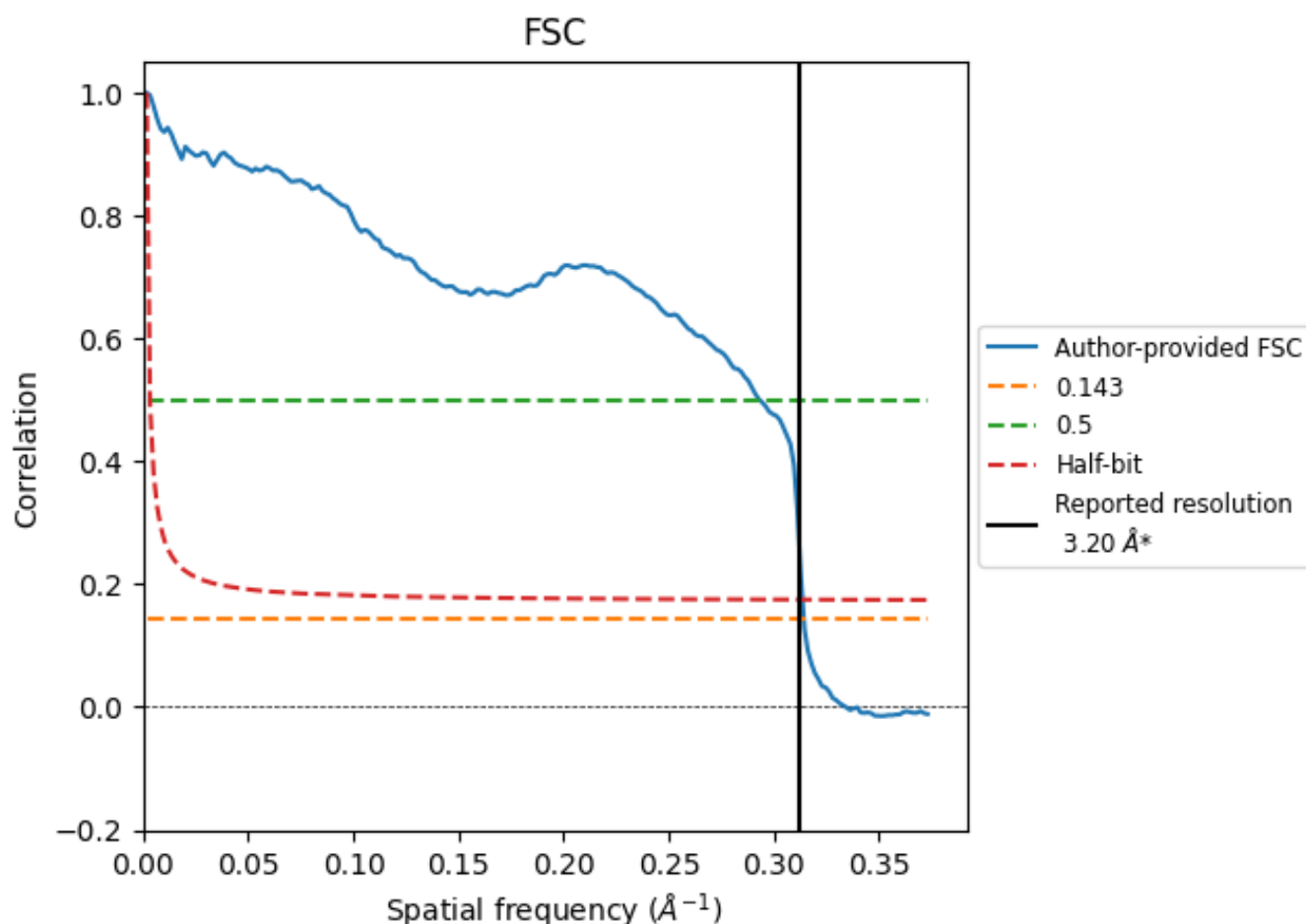


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

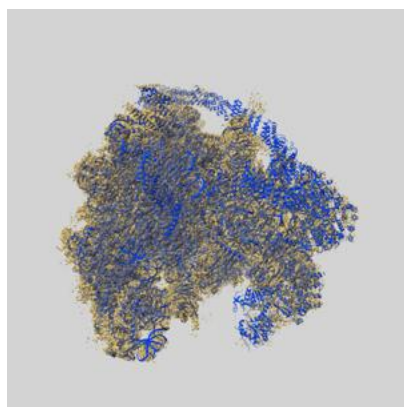
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.18	3.41	3.19
Unmasked-calculated*	-	-	-

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

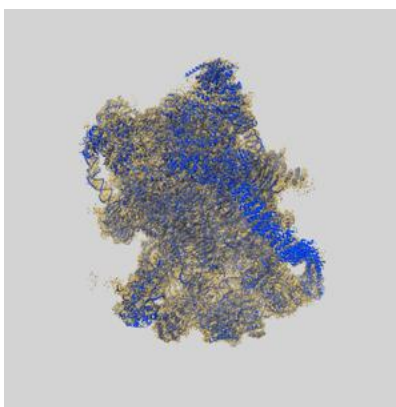
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0949 and PDB model 6LQP. Per-residue inclusion information can be found in section 3 on page 17.

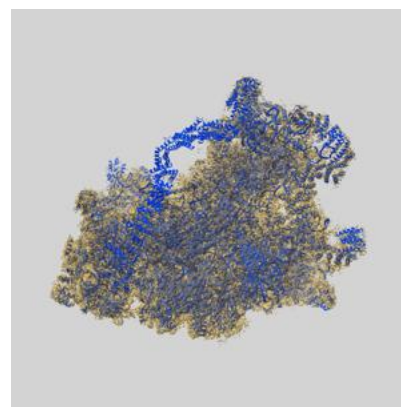
9.1 Map-model overlay [i](#)



X



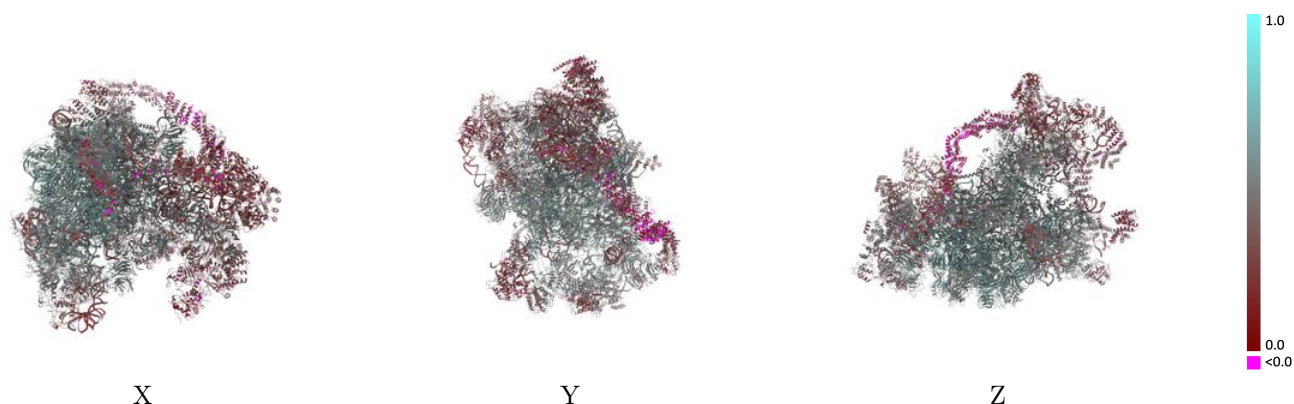
Y



Z

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

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

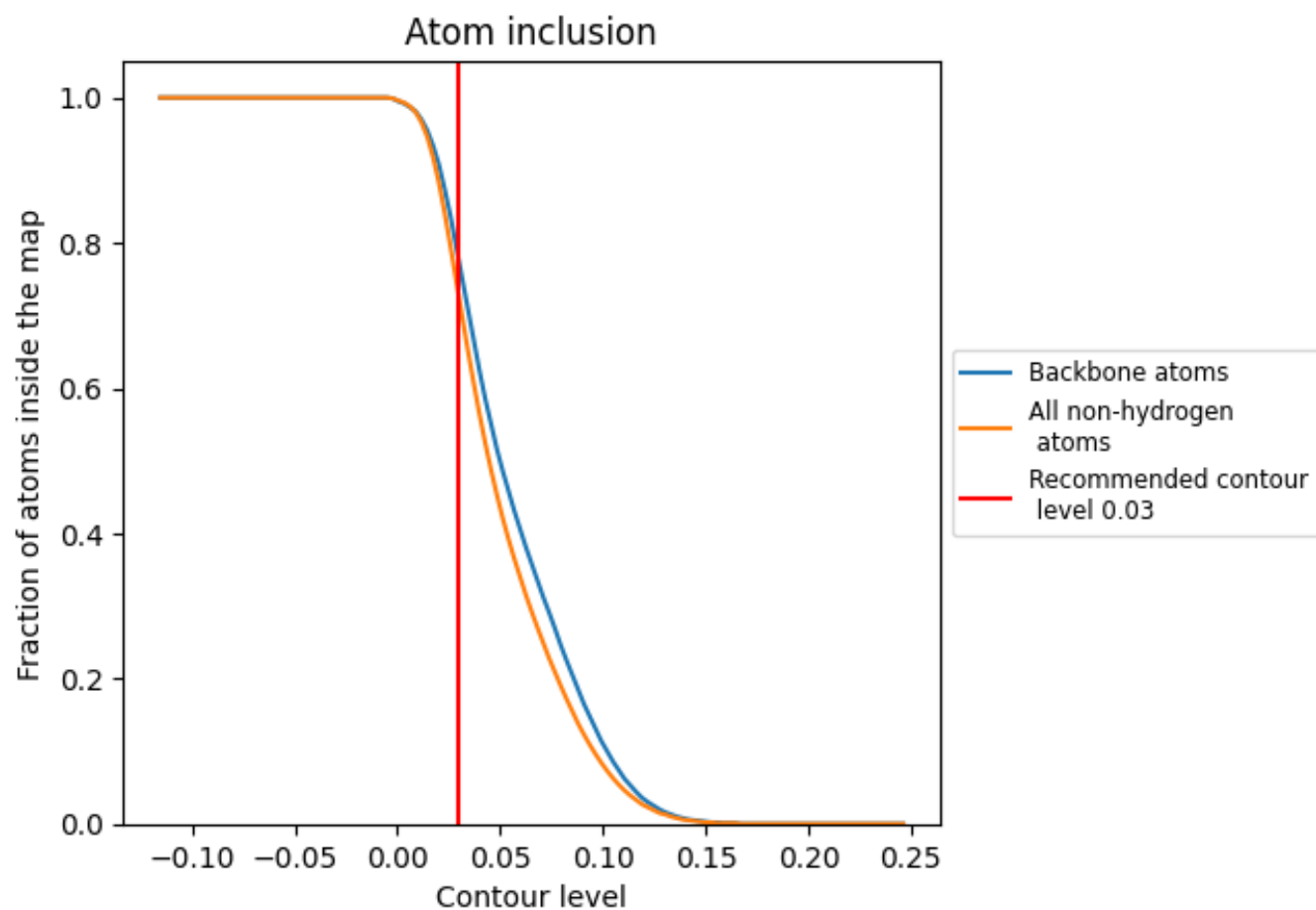


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 72% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

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

Chain	Atom inclusion	Q-score
All	 0.7240	 0.4710
3A	 0.9050	 0.5090
3B	 0.8850	 0.5680
3C	 0.7980	 0.5000
3D	 0.8130	 0.5140
3E	 0.7920	 0.4870
3F	 0.7810	 0.4970
3G	 0.8710	 0.5540
3H	 0.8270	 0.5340
5A	 0.8940	 0.4880
5B	 0.7230	 0.4830
5C	 0.8960	 0.5750
5D	 0.8260	 0.5310
5E	 0.8190	 0.5440
5F	 0.9230	 0.5830
5G	 0.8720	 0.5680
5H	 0.8170	 0.5270
5I	 0.8990	 0.5770
5J	 0.7060	 0.5110
5K	 0.8810	 0.5670
A4	 0.8400	 0.5160
A5	 0.8530	 0.5350
A8	 0.5490	 0.3710
A9	 0.7580	 0.4200
AE	 0.3280	 0.3250
AF	 0.8920	 0.5540
AG	 0.8330	 0.5210
B1	 0.9100	 0.5770
B2	 0.8170	 0.5040
B3	 0.7660	 0.4720
B6	 0.7450	 0.4690
B8	 0.8980	 0.5670
BE	 0.9110	 0.5760
RA	 0.5410	 0.4120
RB	 0.6400	 0.4590



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
RC	 0.7470	 0.5120
RE	 0.6650	 0.4410
RF	 0.5400	 0.4040
RG	 0.6890	 0.4530
RH	 0.8230	 0.5330
RI	 0.8460	 0.5290
RJ	 0.8370	 0.5370
RK	 0.8320	 0.5310
RL	 0.5790	 0.4100
RM	 0.2390	 0.3000
RN	 0.6800	 0.4410
RO	 0.7590	 0.4580
RP	 0.3010	 0.3170
RQ	 0.7450	 0.5040
RS	 0.3360	 0.2730
RT	 0.8270	 0.5200
RV	 0.8290	 0.5350
RW	 0.7040	 0.4960
RY	 0.4400	 0.3860
SA	 0.7270	 0.4210
SC	 0.8170	 0.5370
SF	 0.6230	 0.4190
SG	 0.8590	 0.5590
SH	 0.4570	 0.4220
SI	 0.6410	 0.4510
SJ	 0.5160	 0.3740
SK	 0.8580	 0.5550
SM	 0.4930	 0.3660
SN	 0.0400	 0.2760
SO	 0.8530	 0.5380
SP	 0.8680	 0.5470
SR	 0.8980	 0.5690
ST	 0.6950	 0.4700
SX	 0.8400	 0.5470
SY	 0.8750	 0.5630
SZ	 0.6750	 0.4650
Sc	 0.8620	 0.5520
Sd	 0.8600	 0.5610
X1	 0.6560	 0.4480