



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:42 AM UTC

PDB ID : 6LQT / pdb_00006lqt
EMDB ID : EMD-0953
Title : Cryo-EM structure of 90S small subunit preribosomes in transition states (State E)
Authors : Du, Y.; Ye, K.
Deposited on : 2020-01-14
Resolution : 4.90 Å(reported)
Based on initial model : 6LQS

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:

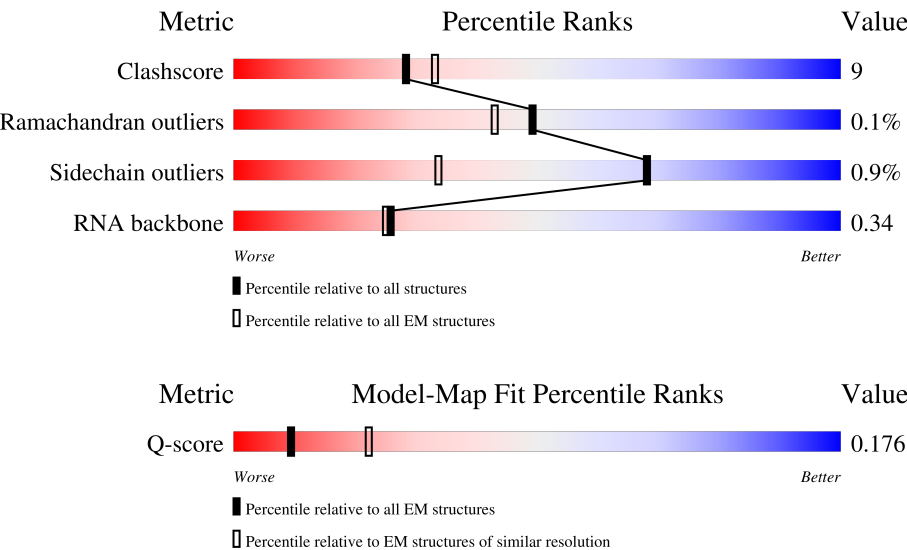
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the 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 4.90 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.



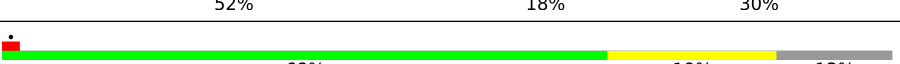
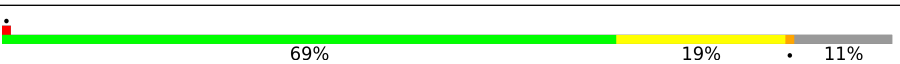
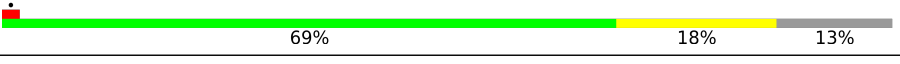
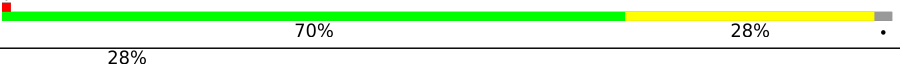
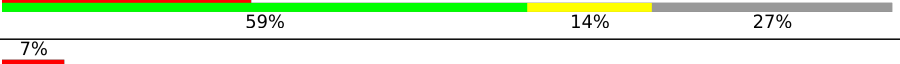
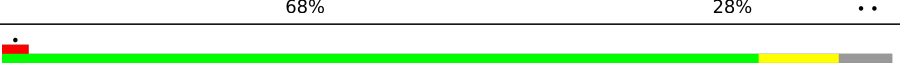
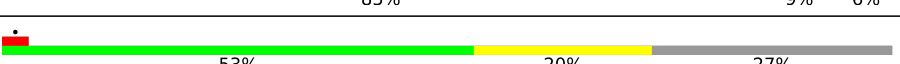
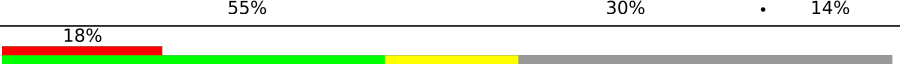
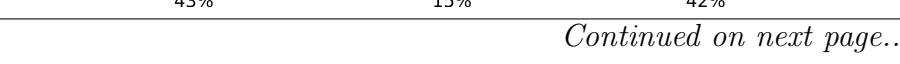
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1274 (4.40 - 5.40)

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	1809	

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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	SO	151	
13	SP	137	
14	SR	143	
15	SX	130	
16	SY	145	
17	SZ	135	
18	Sc	82	
19	Sd	67	
20	3B	327	
20	3C	327	
21	3D	504	
22	3E	511	
23	3F	572	
24	3G	126	
24	3H	126	
25	A4	776	
26	A5	643	

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Mol	Chain	Length	Quality of chain
27	A9	575	
28	AE	1769	
29	AF	513	
30	AG	896	
31	B1	923	
32	B2	943	
33	B3	817	
34	B8	594	
35	BE	939	
36	B6	440	
37	5C	554	
38	5D	250	
39	5E	593	
40	5F	183	
41	5G	290	
42	5H	610	
43	5I	489	
44	5J	217	
45	5K	189	
46	RD	1729	
47	RE	1237	
48	RF	297	
49	RH	252	
50	RJ	1183	
51	RK	367	

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Mol	Chain	Length	Quality of chain
52	RN	810	6% 93% 6%
53	RP	2493	34% 81% 6% 13%
54	RQ	899	5% 22% 75%
55	RT	326	12% 41% 11% 48%
56	X1	347	11% 22% 77%

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 175869 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	194	Total	C	N	O	P	0	0
			4114	1841	716	1363	194		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5A	152	Total	C	N	O	P	0	0
			3260	1455	593	1060	152		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SA	1155	Total	C	N	O	P	0	0
			24609	11001	4356	8097	1155		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SC	232	Total	C	N	O	S	0	0
			1848	1168	339	337	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SF	250	Total	C	N	O	S	0	0
			1930	1232	354	341	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	182	Total	C	N	O	S	0	0
			1457	917	273	266	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SI	164	Total	C	N	O		0	0
			1310	847	222	241			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SJ	140	Total	C	N	O	S	0	0
			1104	689	211	202	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	137	Total	C	N	O	S	0	0
			1113	715	212	183	3		

- Molecule 12 is a protein called 40S ribosomal protein S13.

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

- Molecule 13 is a protein called 40S ribosomal protein S14-A.

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

- Molecule 14 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 15 is a protein called 40S ribosomal protein S22-B.

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

- Molecule 16 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SY	106	Total	C	N	O	S	0	0
			807	515	148	142	2		

- Molecule 17 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	SZ	123	Total	C	N	O	0	0
			986	626	188	172		

- Molecule 18 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 19 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 20 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	3B	240	Total	C	N	O	S	0	0
			1865	1184	333	338	10		
20	3C	225	Total	C	N	O	S	0	0
			1763	1120	316	317	10		

- Molecule 21 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	3D	378	Total	C	N	O	S	0	0
			2974	1886	511	568	9		

- Molecule 22 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	3E	432	Total	C	N	O	S	0	0
			3041	1895	545	592	9		

- Molecule 23 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	3F	437	Total	C	N	O	S	0	0
			3498	2227	609	652	10		

- Molecule 24 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	3G	121	Total	C	N	O	S	0	0
			916	583	158	171	4		
24	3H	121	Total	C	N	O	S	0	0
			916	583	158	171	4		

- Molecule 25 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A4	664	Total	C	N	O	S	0	0
			5243	3320	912	990	21		

- Molecule 26 is a protein called U3 small nucleolar RNA-associated protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	A5	372	Total	C	N	O	S	0	0
			2943	1869	494	569	11		

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A9	37	Total	C	N	O	S	0	0
			299	186	60	51	2		

- Molecule 28 is a protein called U3 small nucleolar RNA-associated protein 10.

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

- Molecule 29 is a protein called U3 small nucleolar RNA-associated protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AF	479	Total	C	N	O	S	0	0
			3807	2395	685	715	12		

- Molecule 30 is a protein called NET1-associated nuclear protein 1.

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

- Molecule 31 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	B1	806	Total	C	N	O	S	0	0
			6427	4104	1099	1205	19		

- Molecule 32 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B2	825	Total	C	N	O	S	0	0
			6502	4156	1096	1223	27		

- Molecule 33 is a protein called U3 small nucleolar RNA-associated protein 13.

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

- Molecule 34 is a protein called U3 small nucleolar RNA-associated protein 18.

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

- Molecule 35 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BE	823	Total	C	N	O	S	0	0
			6475	4107	1119	1228	21		

- Molecule 36 is a protein called U3 small nucleolar RNA-associated protein 6.

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

- Molecule 37 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	5C	458	Total	C	N	O	S	0	0
			3612	2276	636	689	11		

- Molecule 38 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	5D	70	Total	C	N	O	S	0	0
			609	377	126	105	1		

- Molecule 39 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	5E	193	Total	C	N	O	S	0	0
			1564	970	280	310	4		

- Molecule 40 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	5F	182	Total	C	N	O	S	0	0
			1530	967	287	269	7		

- Molecule 41 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	5G	216	Total	C	N	O	S	0	0
			1732	1093	321	312	6		

- Molecule 42 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	5H	74	Total	C	N	O	0	0
			596	373	122	101		

- Molecule 43 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	5I	460	Total	C	N	O	S	0	0
			3756	2349	685	706	16		

- Molecule 44 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	5J	134	Total	C	N	O	S	0	0
			1127	712	205	207	3		

- Molecule 45 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5K	166	Total	C	N	O	S	0	0
			1323	849	238	226	10		

- Molecule 46 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	RD	316	Total	C	N	O	S	0	0
			2413	1541	415	452	5		

- Molecule 47 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	RE	1090	Total	C	N	O	S	0	0
			8805	5720	1452	1609	24		

- Molecule 48 is a protein called Ribosomal RNA-processing protein 7.

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

- Molecule 49 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	RH	219	Total	C	N	O	S	0	0
			1719	1090	299	319	11		

- Molecule 50 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	RJ	731	Total	C	N	O	S	0	0
			5935	3812	1051	1046	26		

- Molecule 51 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 52 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	RN	53	Total	C	N	O	S	0	0
			450	273	88	88	1		

- Molecule 53 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	RP	2180	Total	C	N	O	S	0	0
			12716	7827	2389	2484	16		

- Molecule 54 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	RQ	226	Total	C	N	O	S	0	0
			1655	1026	314	313	2		

- Molecule 55 is a protein called Pno1.

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

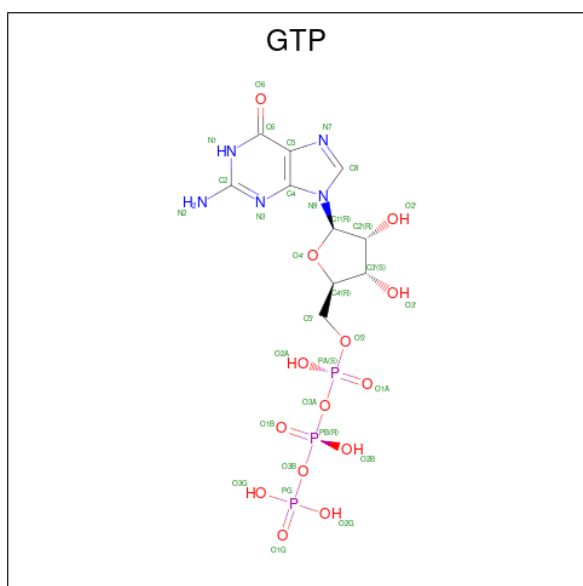
- Molecule 56 is a protein called Unassigned helices.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	X1	80	Total	C	N	O	0	0
			400	240	80	80		

- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
57	Sc	1	Total	Zn	0
			1	1	
57	5K	1	Total	Zn	0
			1	1	

- Molecule 58 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



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

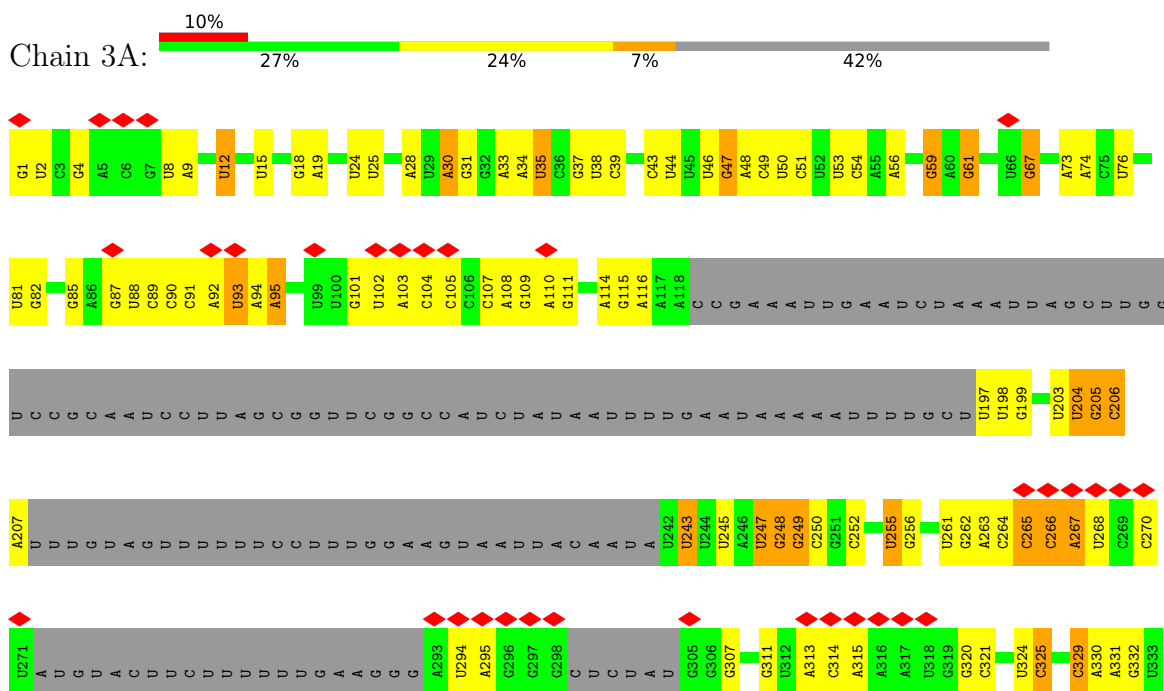
- Molecule 59 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

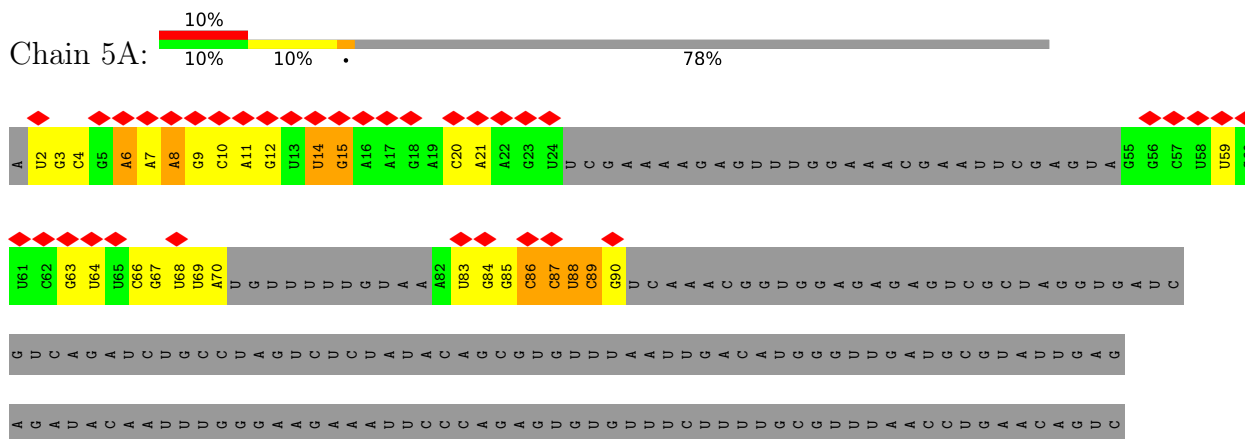
3 Residue-property plots

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

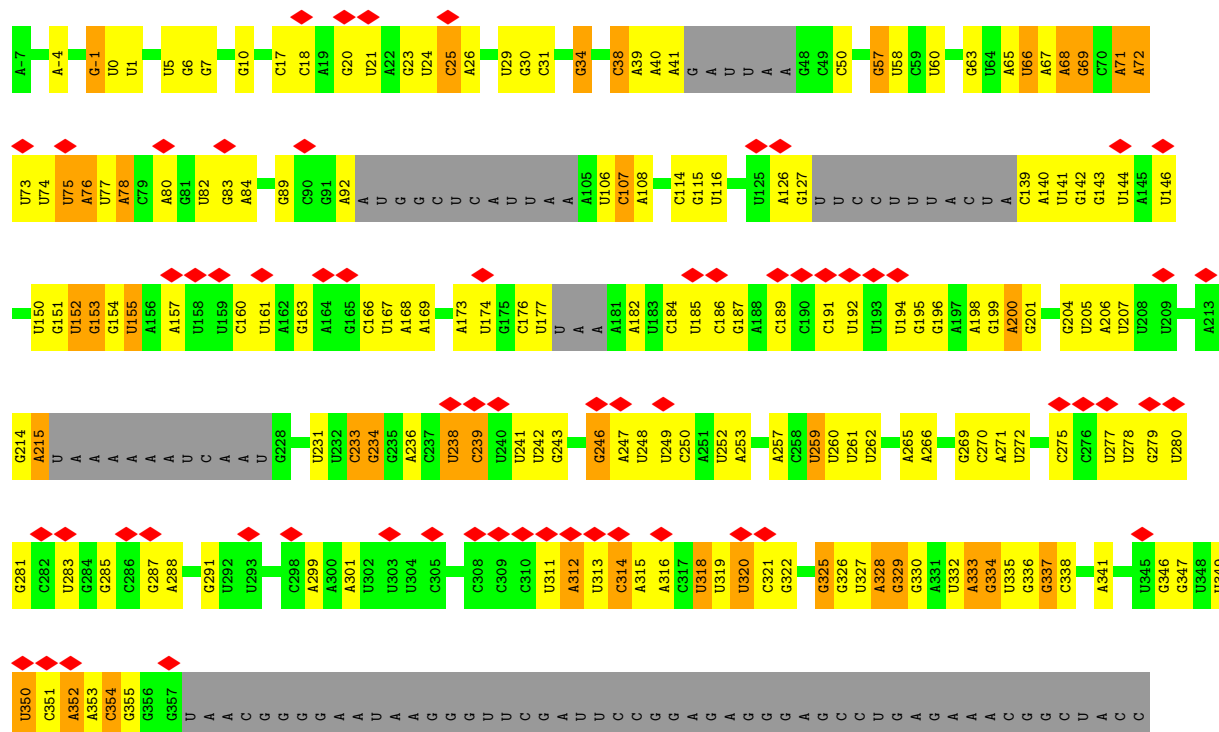
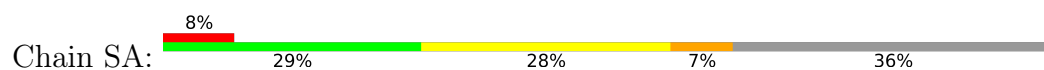
• Molecule 1: U3 snoRNA



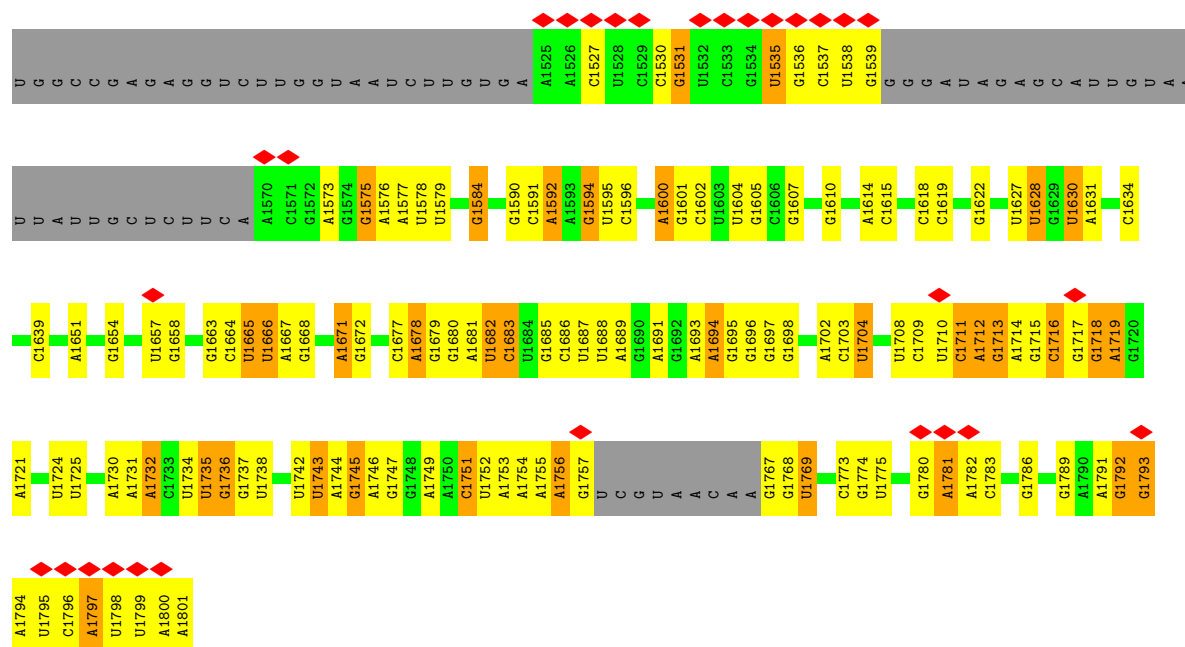
• Molecule 2: 5' ETS



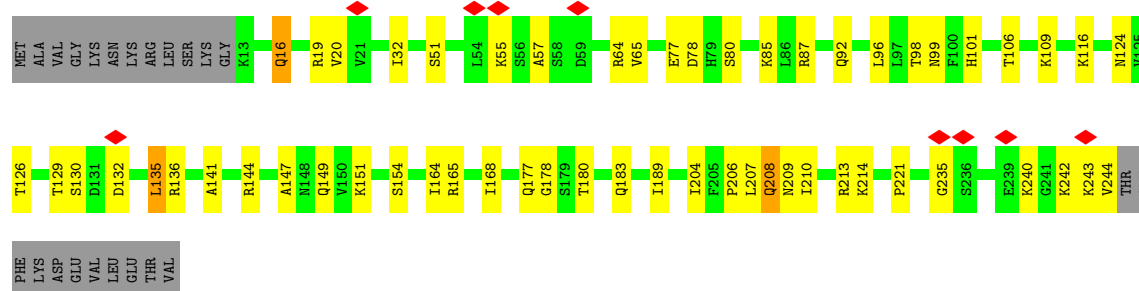
- Molecule 3: 18S pre-rRNA



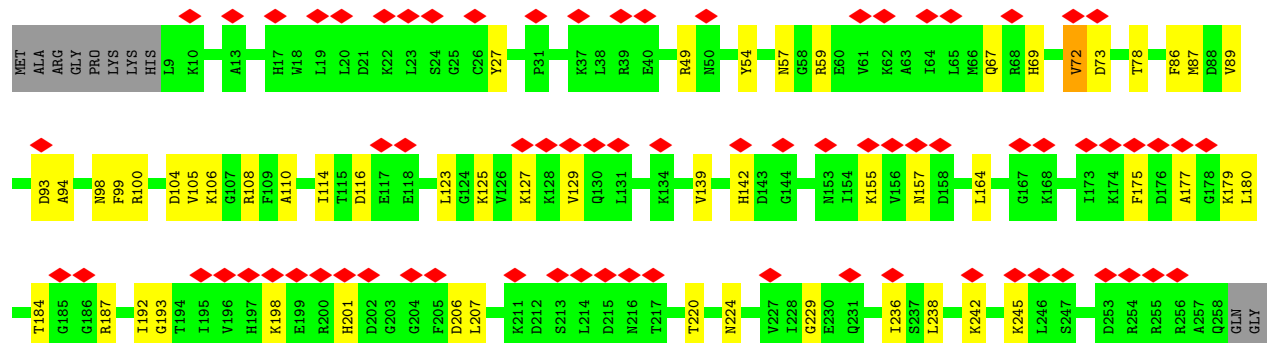
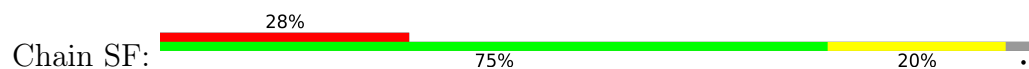




- Molecule 4: 40S ribosomal protein S1-A

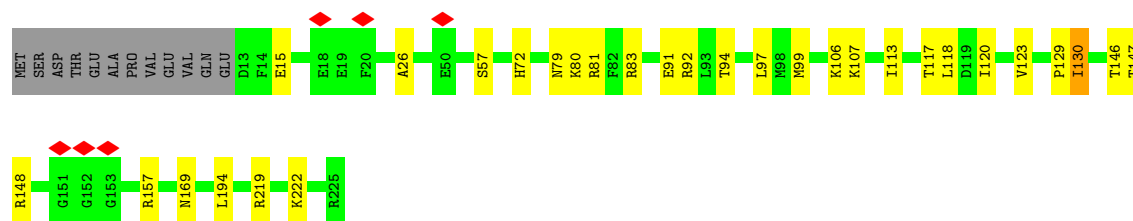


- Molecule 5: 40S ribosomal protein S4-A



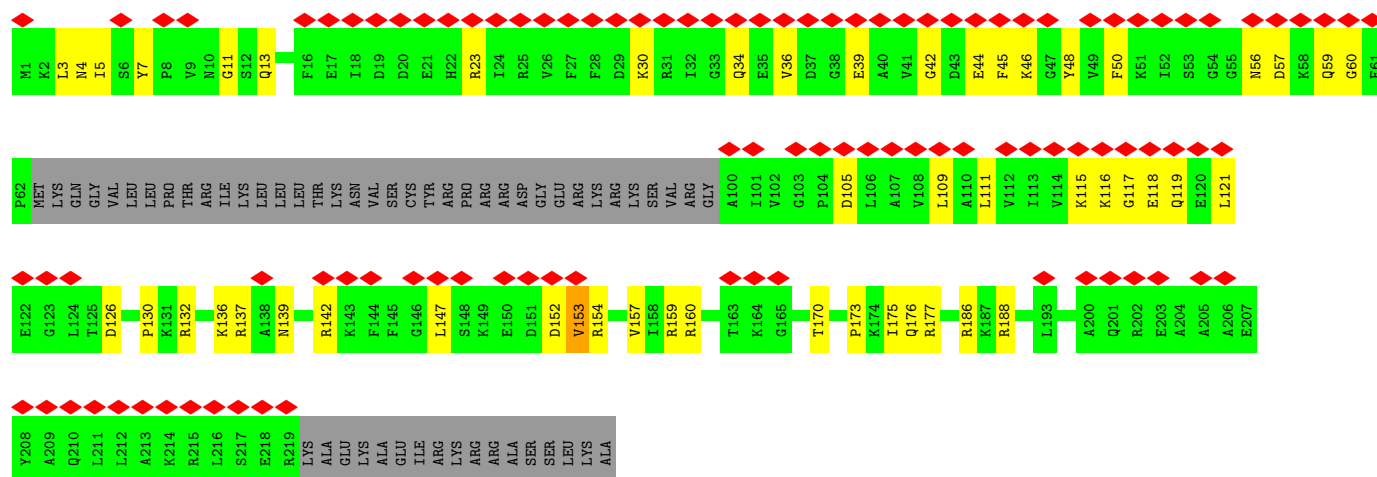
- Molecule 6: 40S ribosomal protein S5

Chain SG: 



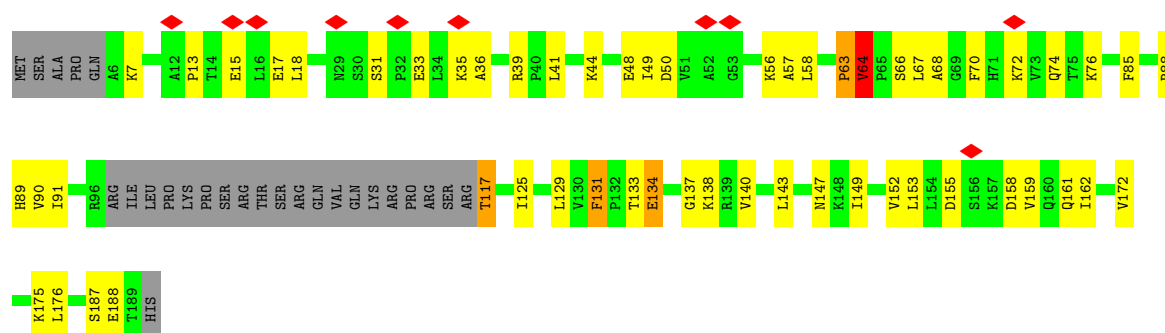
• Molecule 7: 40S ribosomal protein S6-A

Chain SH: 



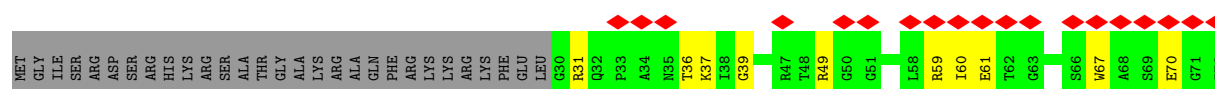
• Molecule 8: 40S ribosomal protein S7-A

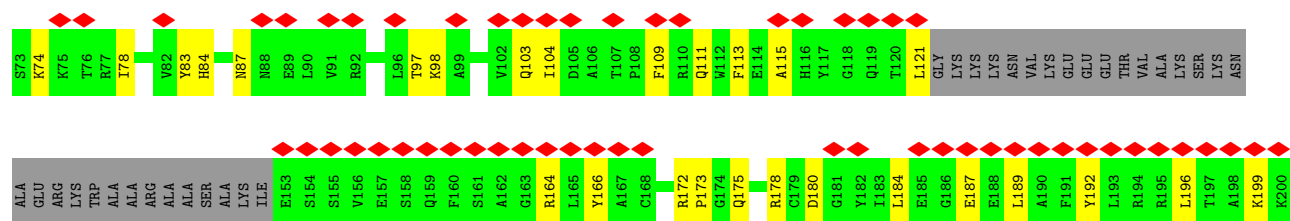
Chain SI: 



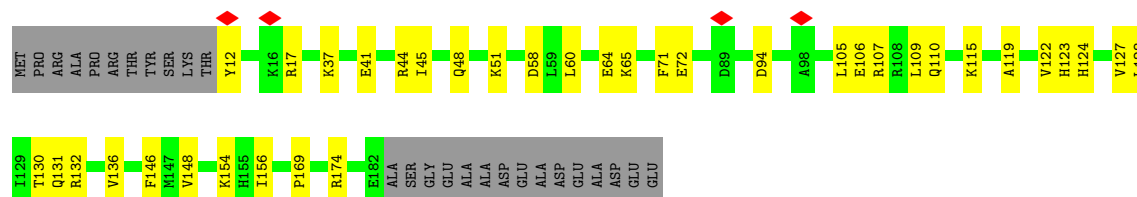
• Molecule 9: 40S ribosomal protein S8-A

Chain SJ: 

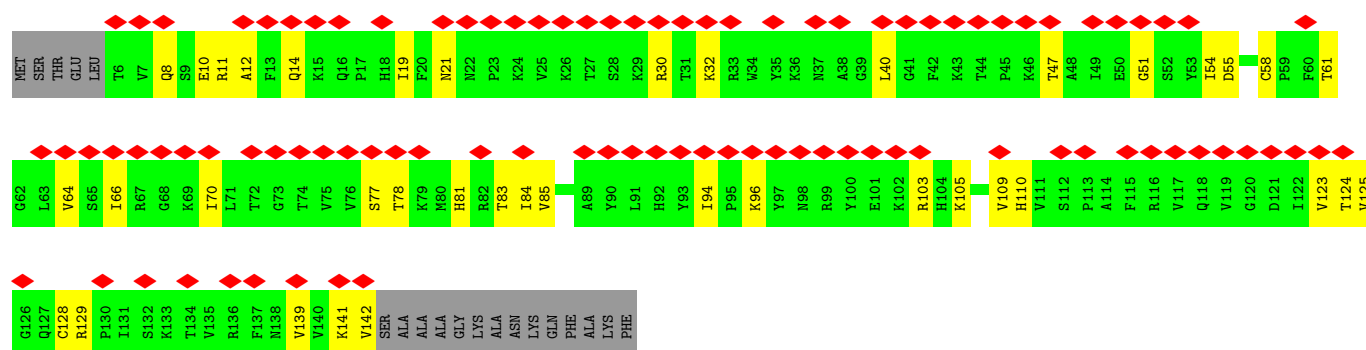




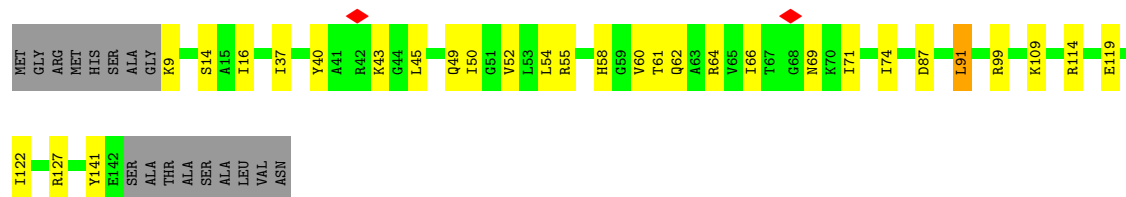
• Molecule 10: 40S ribosomal protein S9-A



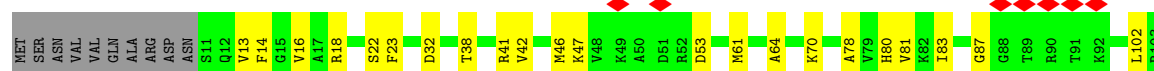
• Molecule 11: 40S ribosomal protein S11-A

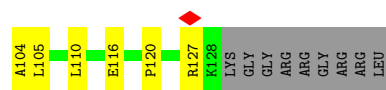


• Molecule 12: 40S ribosomal protein S13

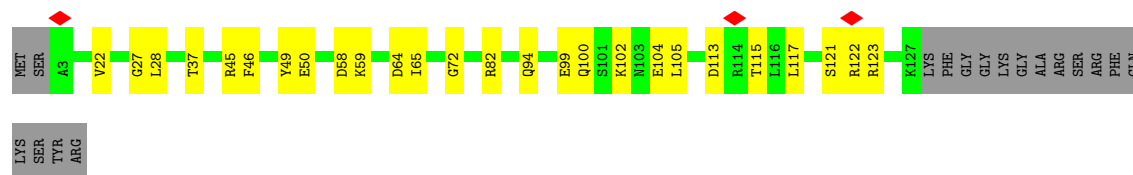


• Molecule 13: 40S ribosomal protein S14-A

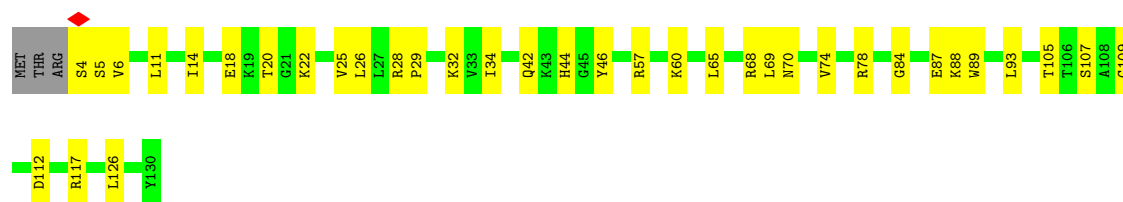




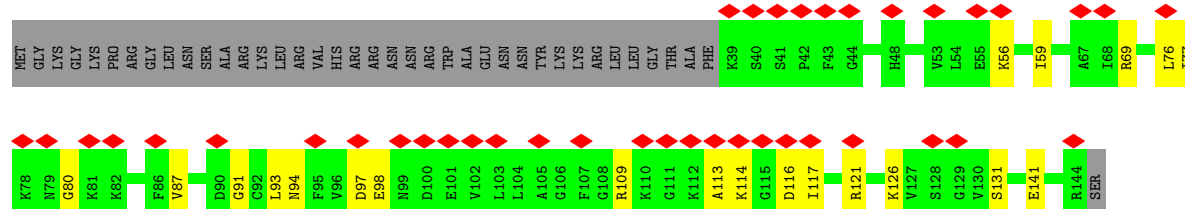
- Molecule 14: 40S ribosomal protein S16-A



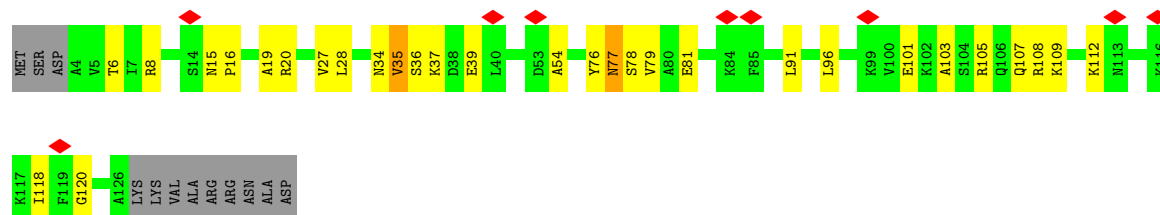
- Molecule 15: 40S ribosomal protein S22-B



- Molecule 16: 40S ribosomal protein S23-A



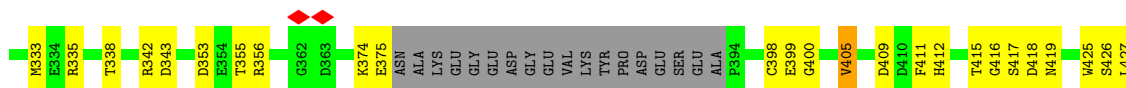
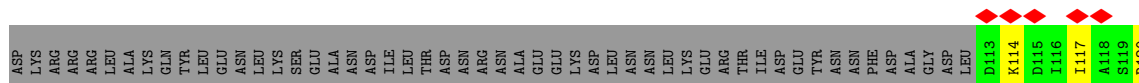
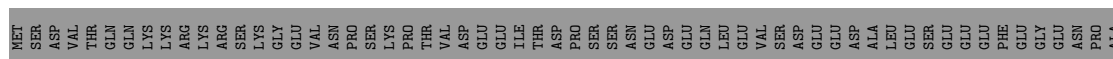
- Molecule 17: 40S ribosomal protein S24-A



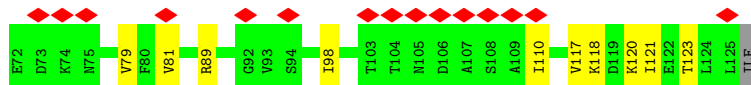
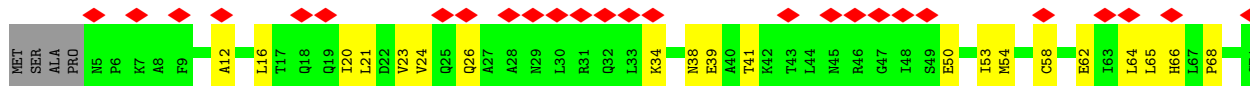
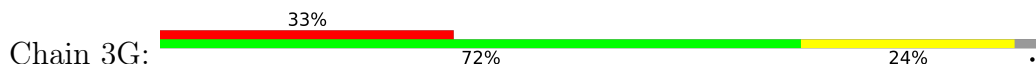
- Molecule 18: 40S ribosomal protein S27-A



- Molecule 23: Ribosomal RNA-processing protein 9

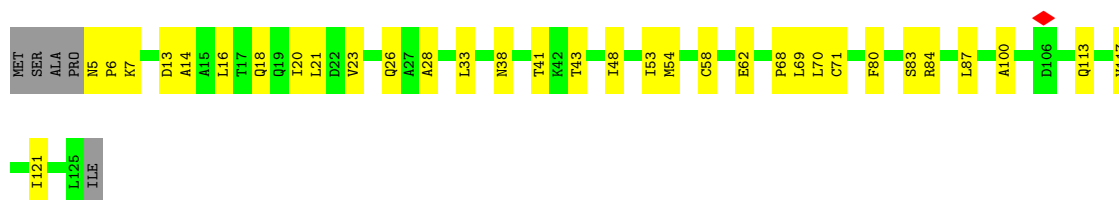


- Molecule 24: 13 kDa ribonucleoprotein-associated protein

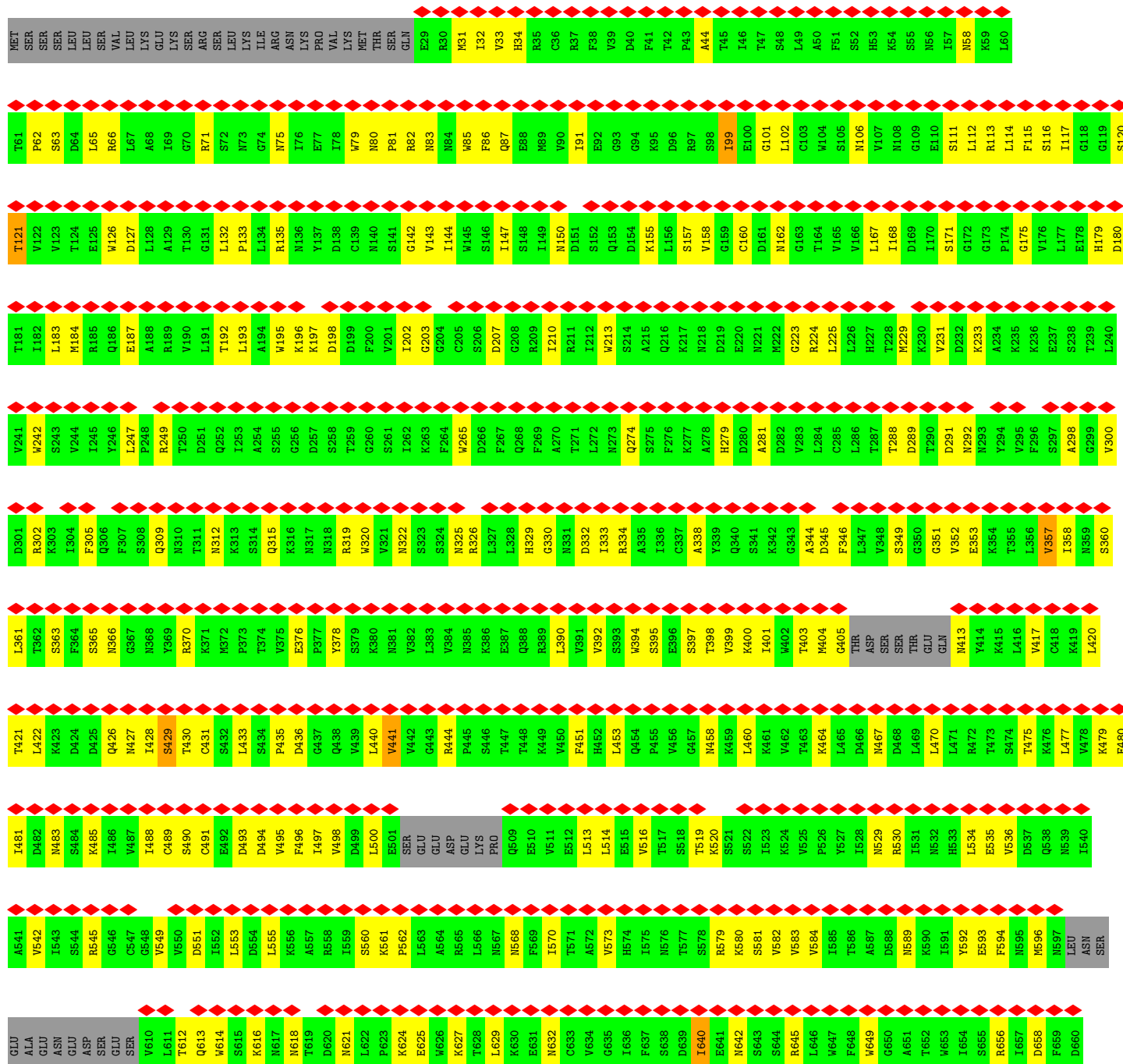
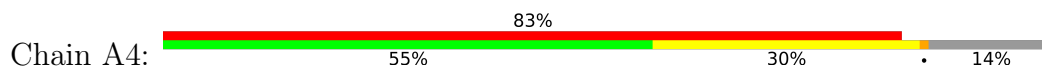


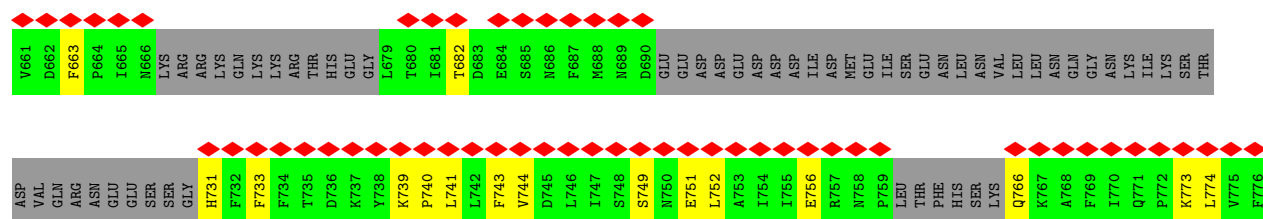
- Molecule 24: 13 kDa ribonucleoprotein-associated protein



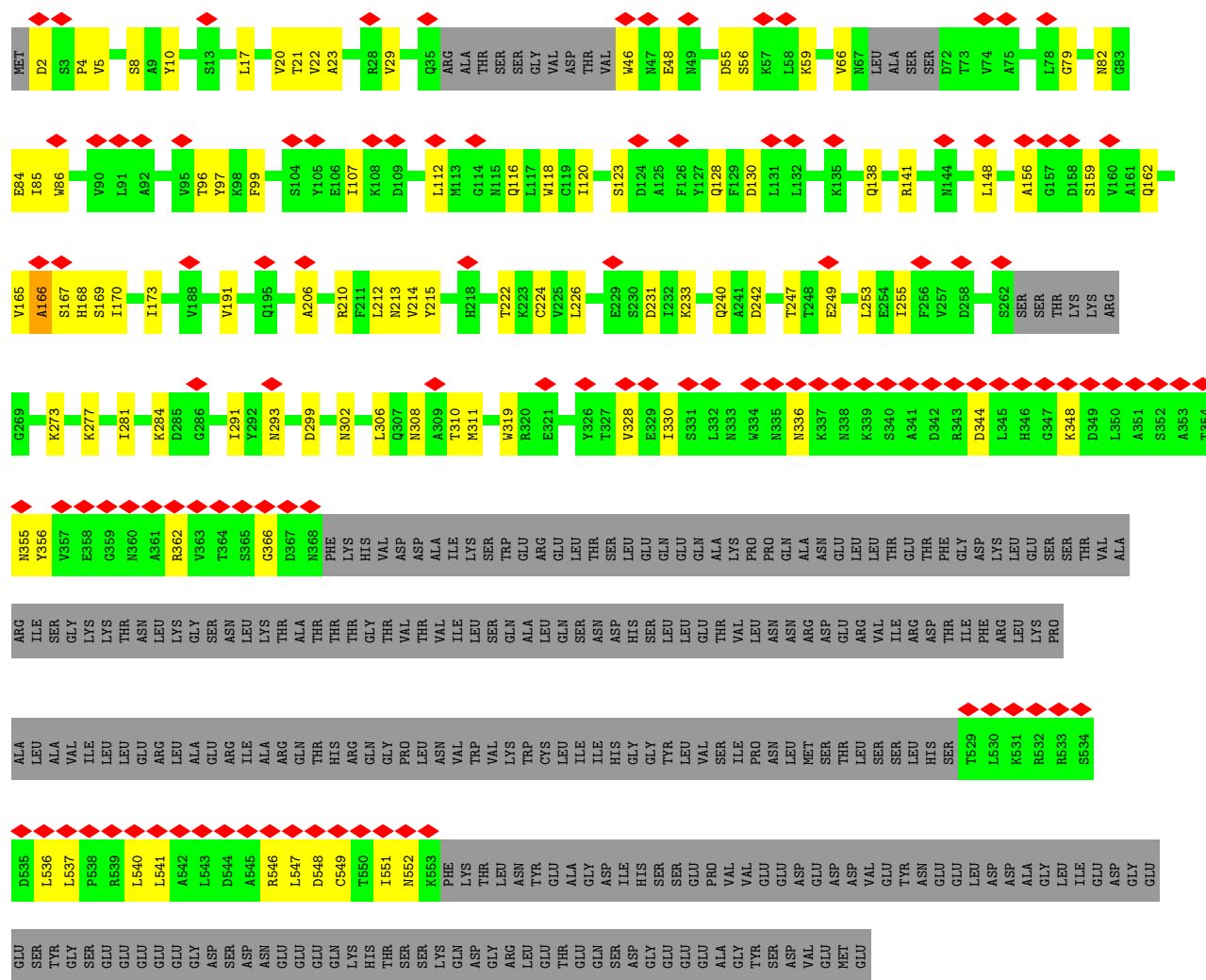


• Molecule 25: U3 small nucleolar RNA-associated protein 4

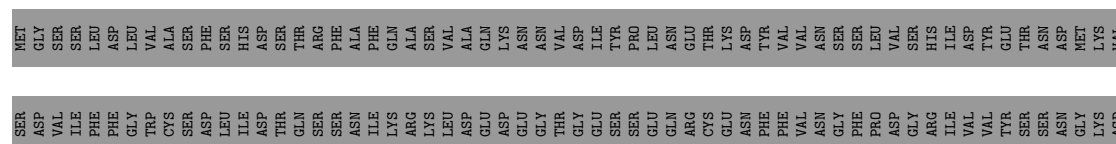




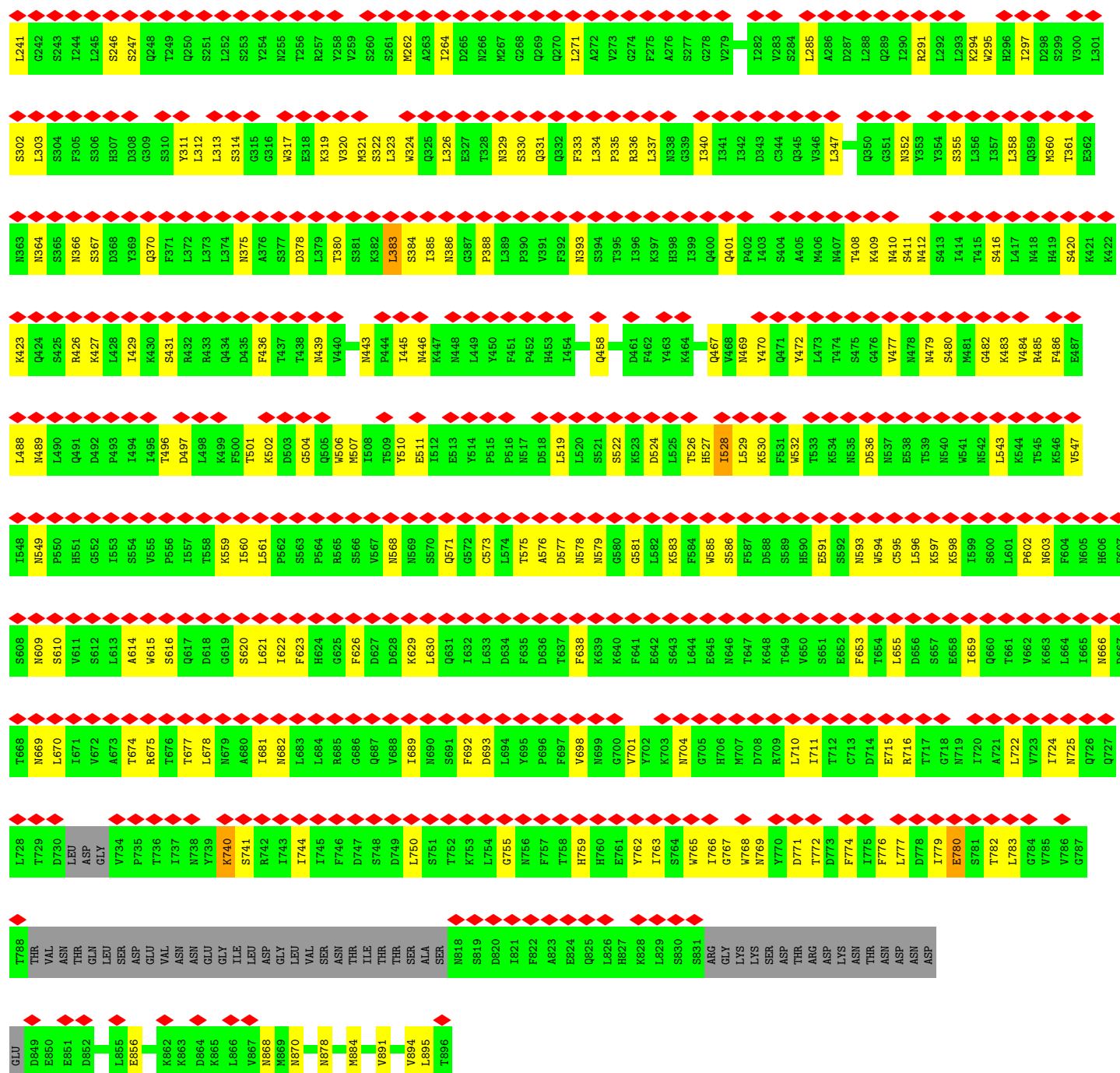
• Molecule 26: U3 small nucleolar RNA-associated protein 5



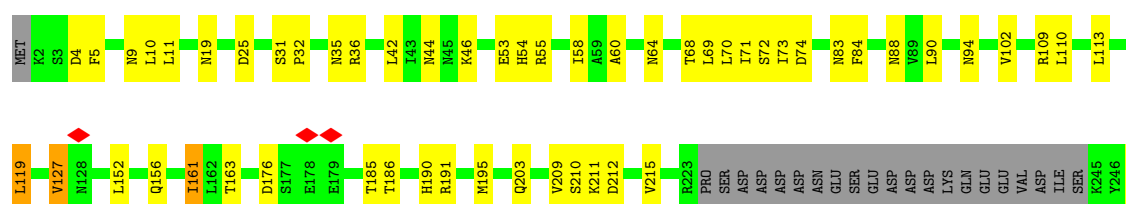
• Molecule 27: U3 small nucleolar RNA-associated protein 9



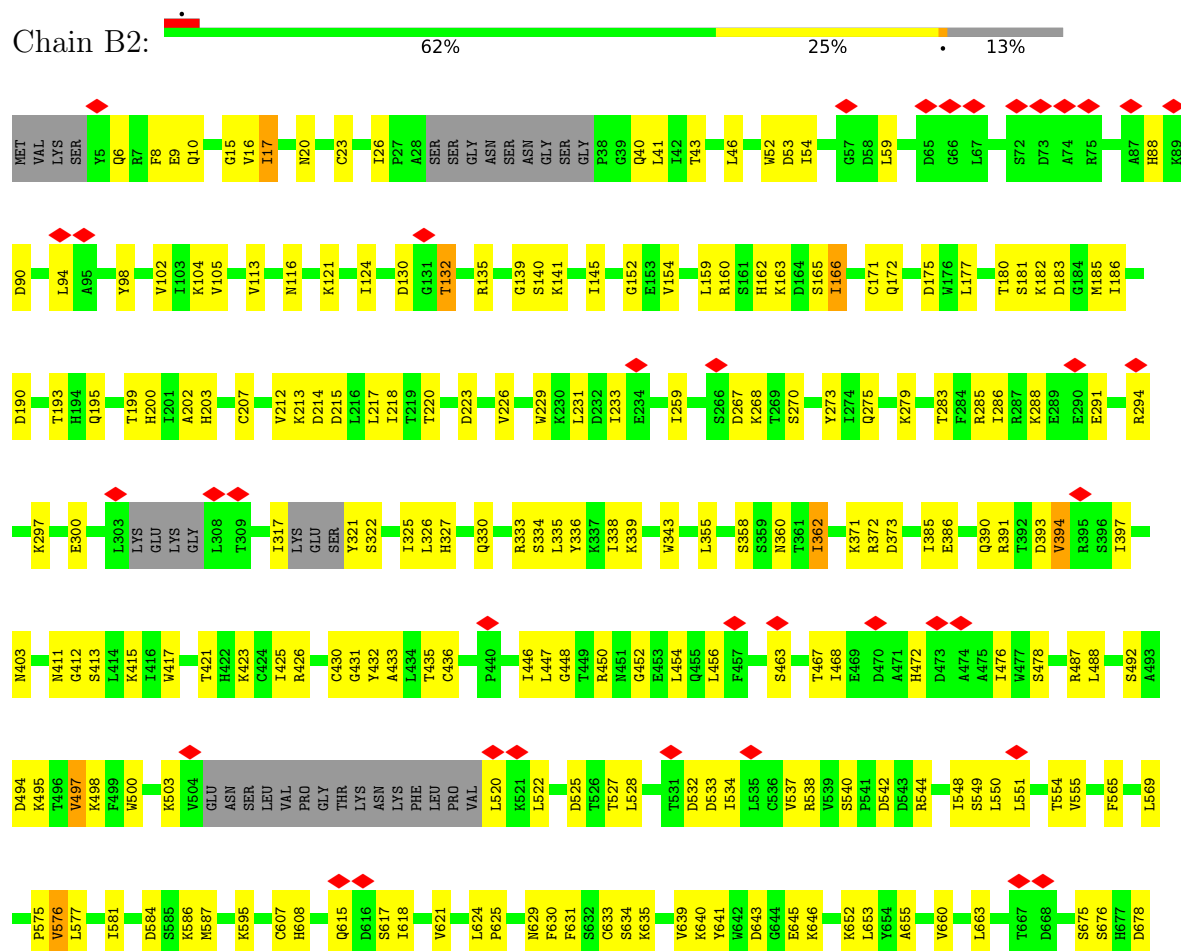


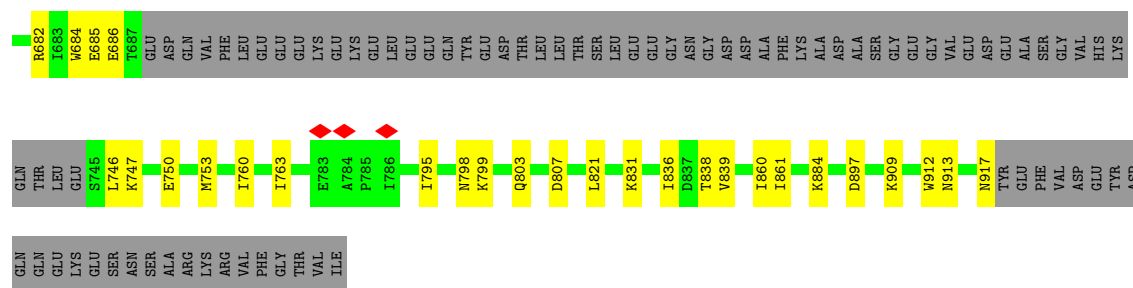


Molecule 31: Periodic tryptophan protein 2

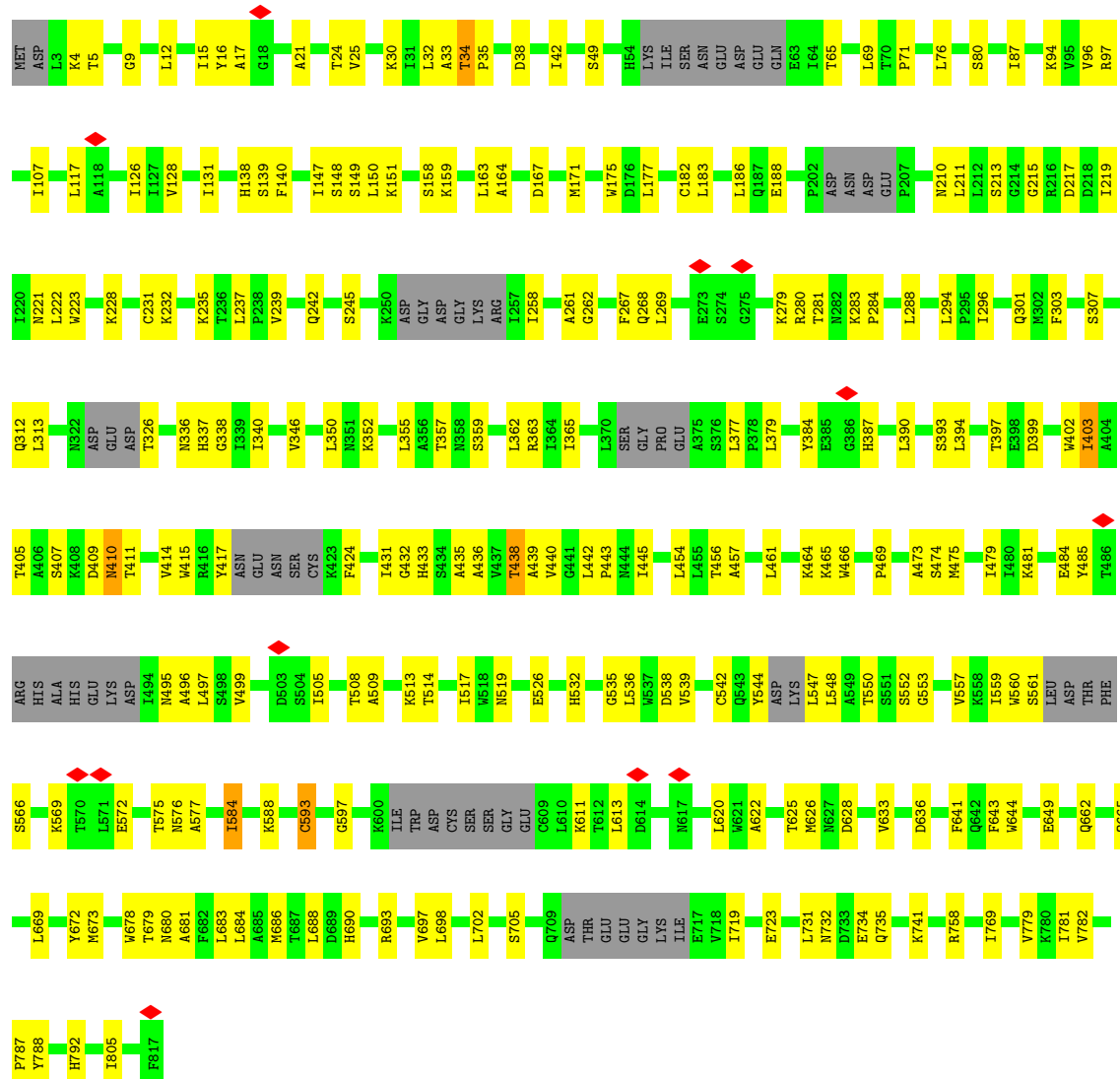


- Molecule 32: U3 small nucleolar RNA-associated protein 12



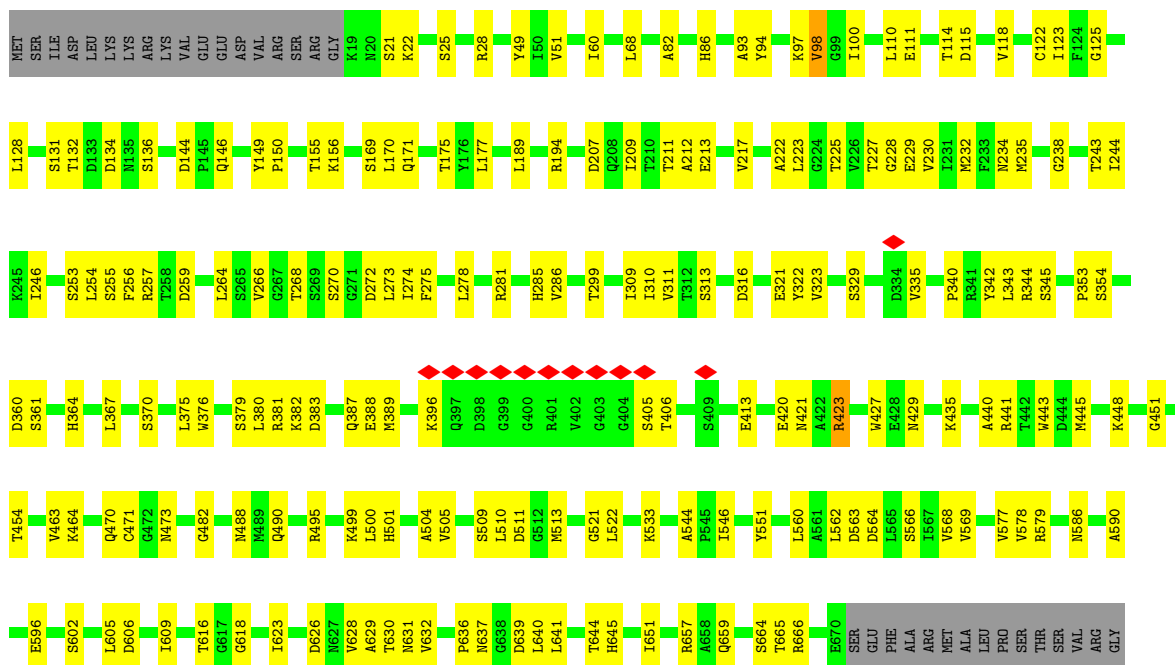


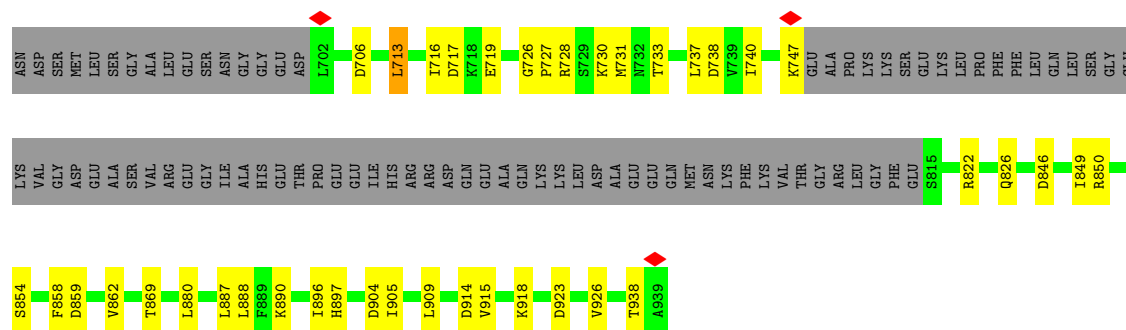
• Molecule 33: U3 small nucleolar RNA-associated protein 13



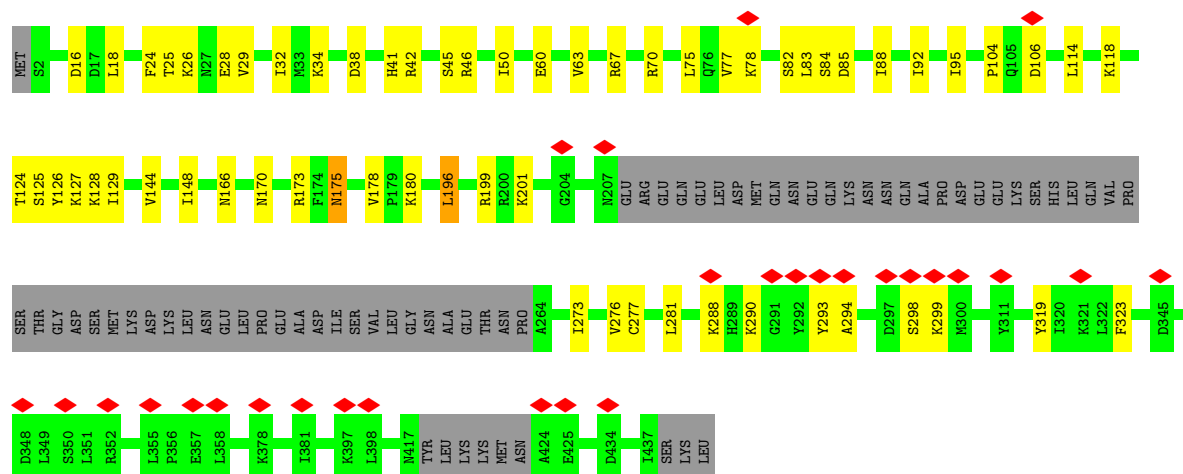
• Molecule 34: U3 small nucleolar RNA-associated protein 18



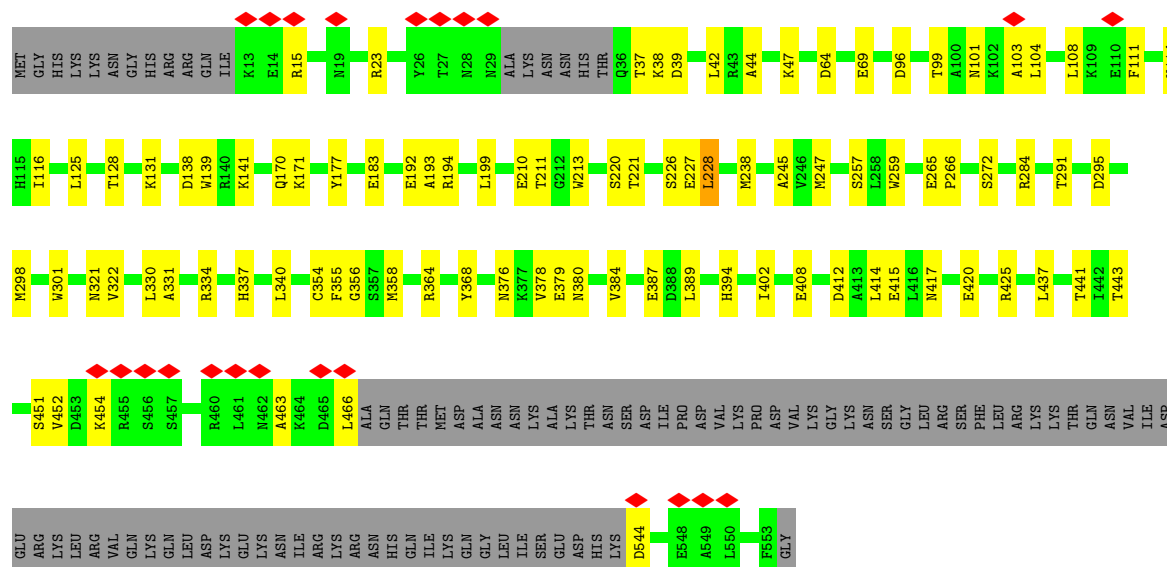


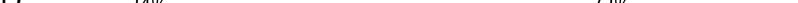


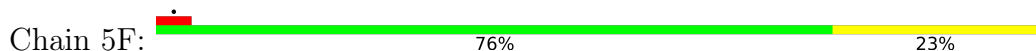
• Molecule 36: U3 small nucleolar RNA-associated protein 6

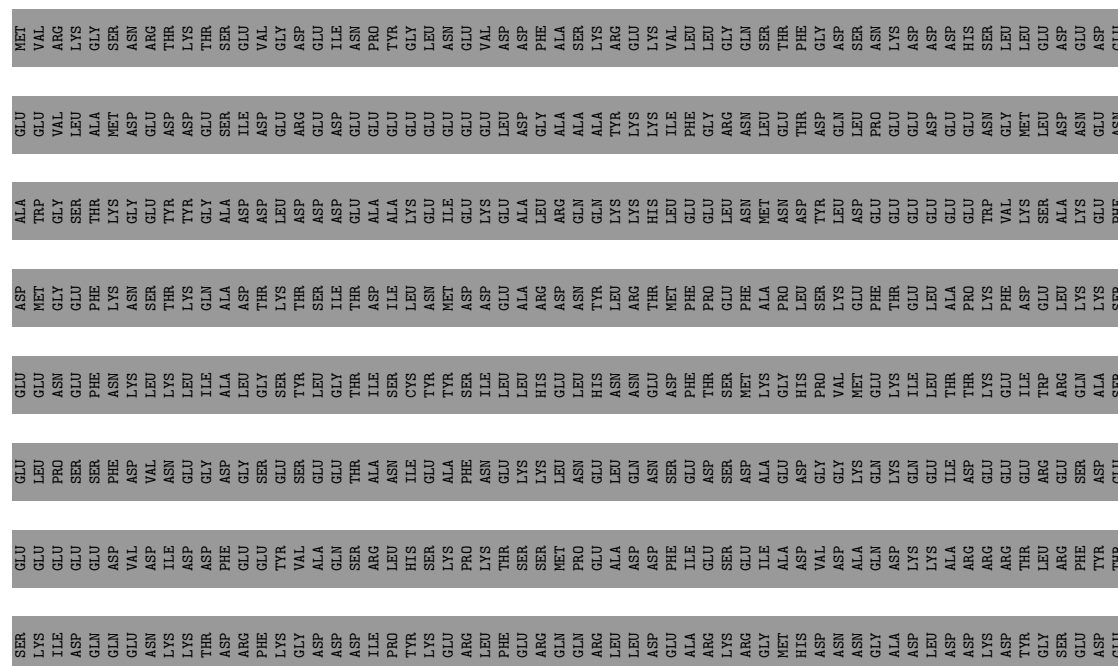


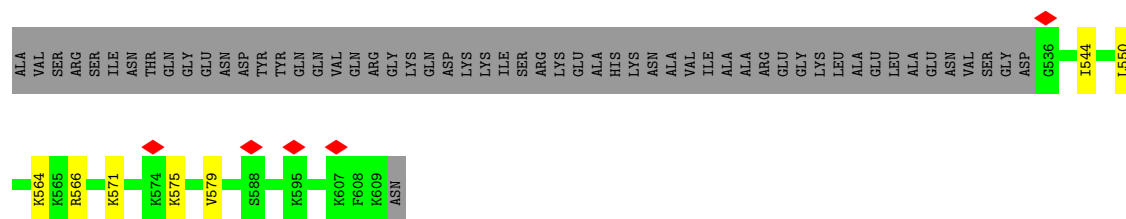
• Molecule 37: U3 small nucleolar RNA-associated protein 7



- Chain 5D: 

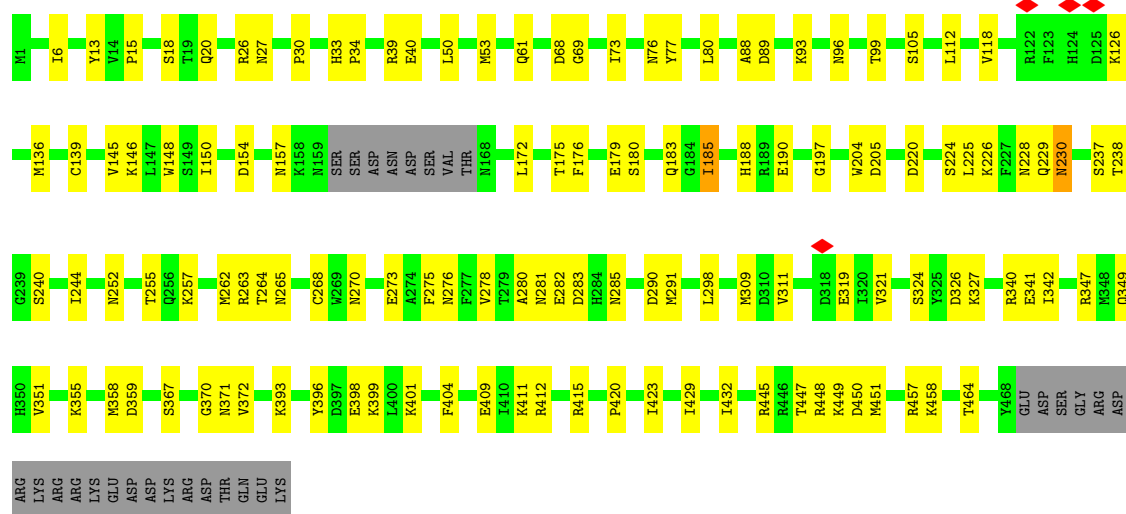






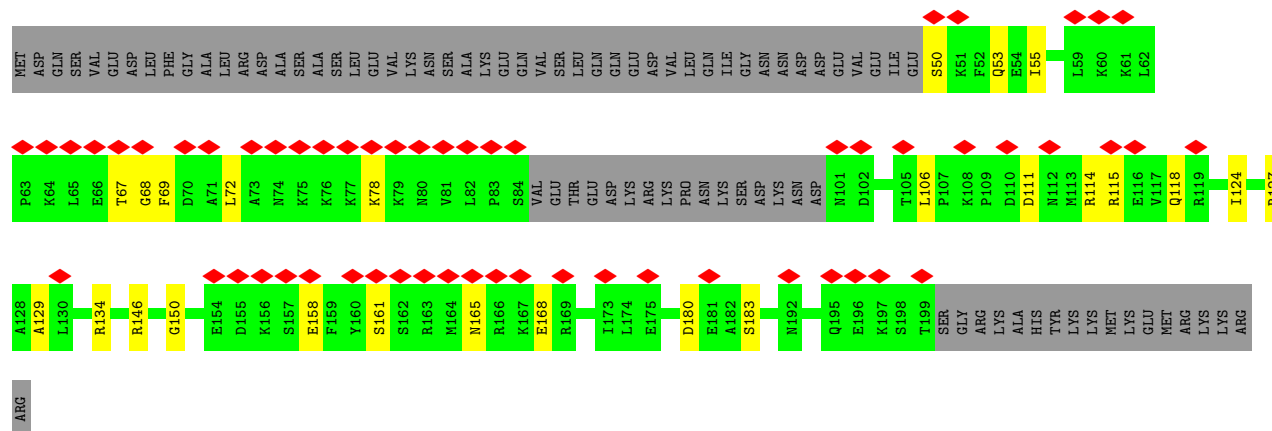
• Molecule 43: Protein SOF1

Chain 5I: 68% 25% 6%



• Molecule 44: rRNA-processing protein FCF2

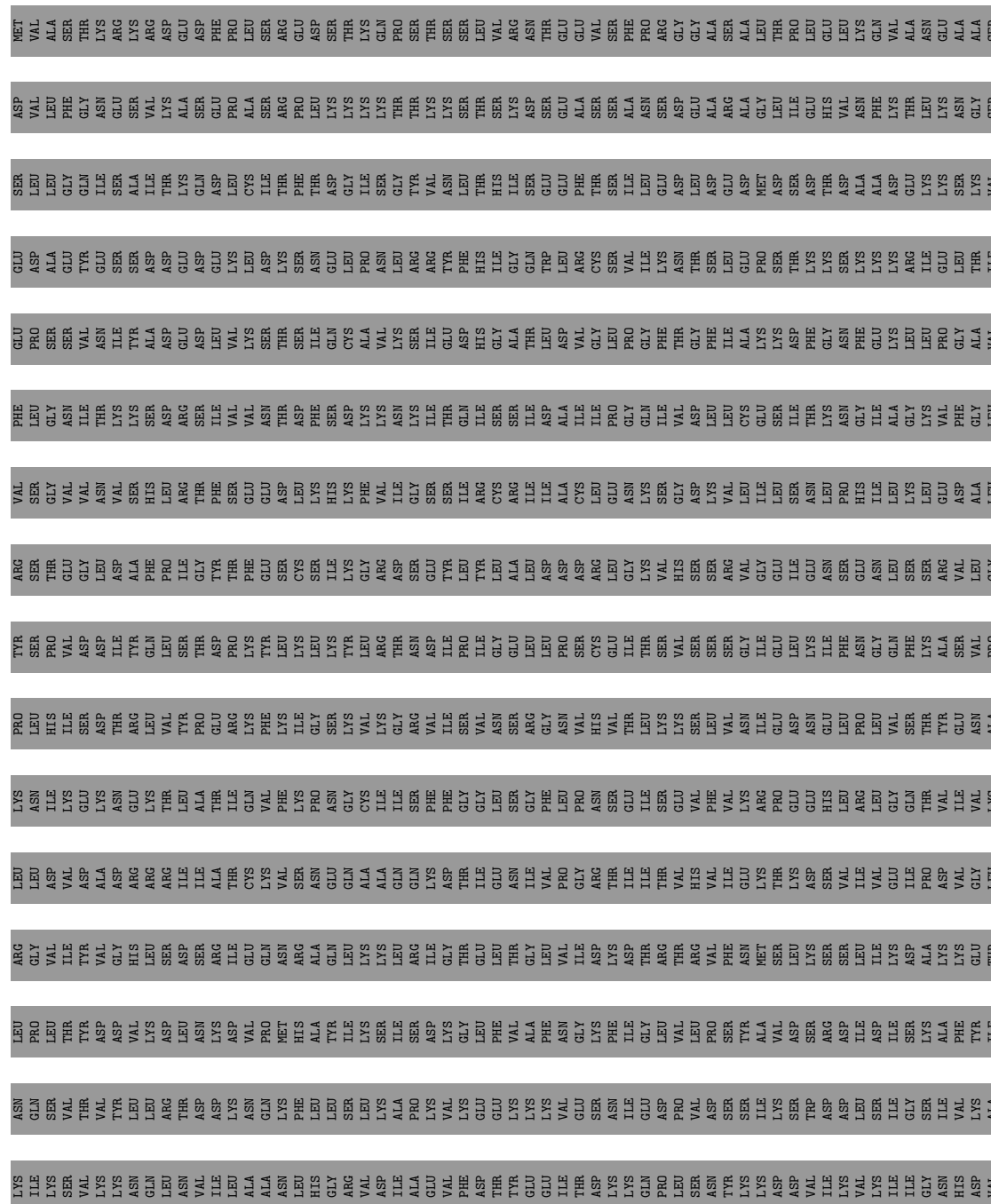
Chain 5J: 26% 50% 12% 38%

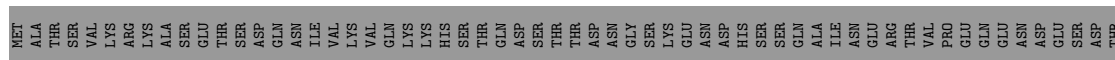


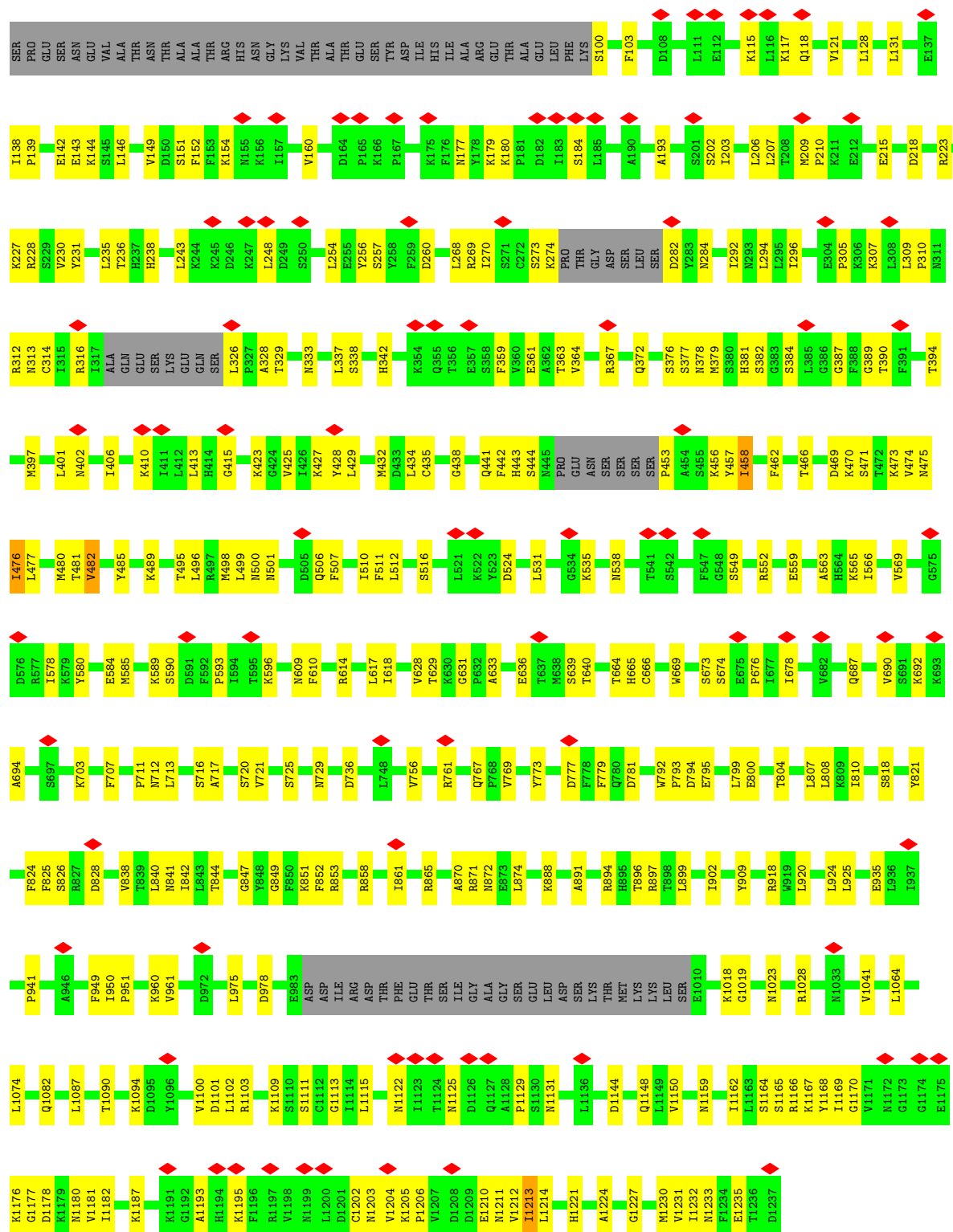
• Molecule 45: rRNA-processing protein FCF1

Chain 5K: 72% 16% 12%



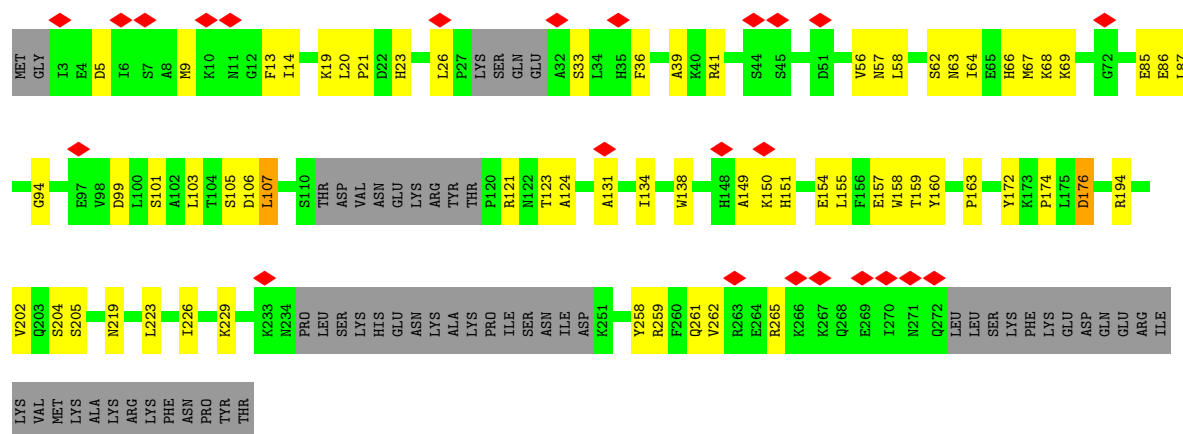




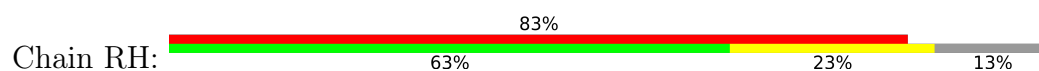


• Molecule 48: Ribosomal RNA-processing protein 7

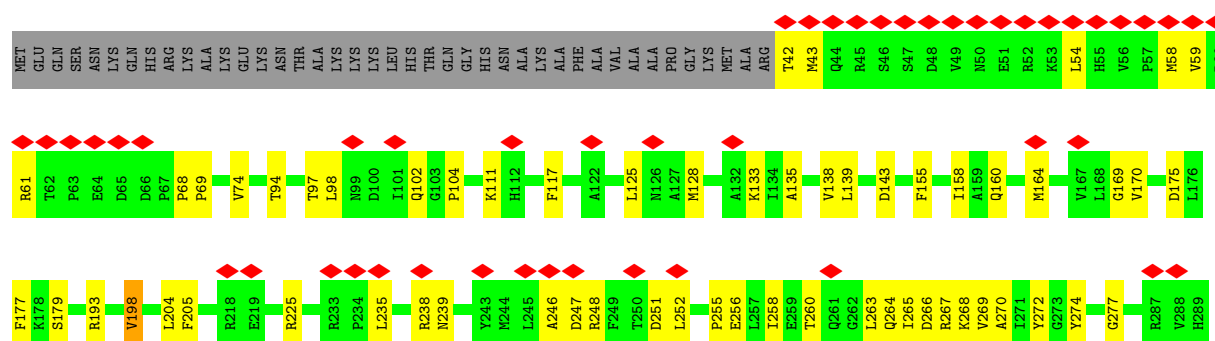


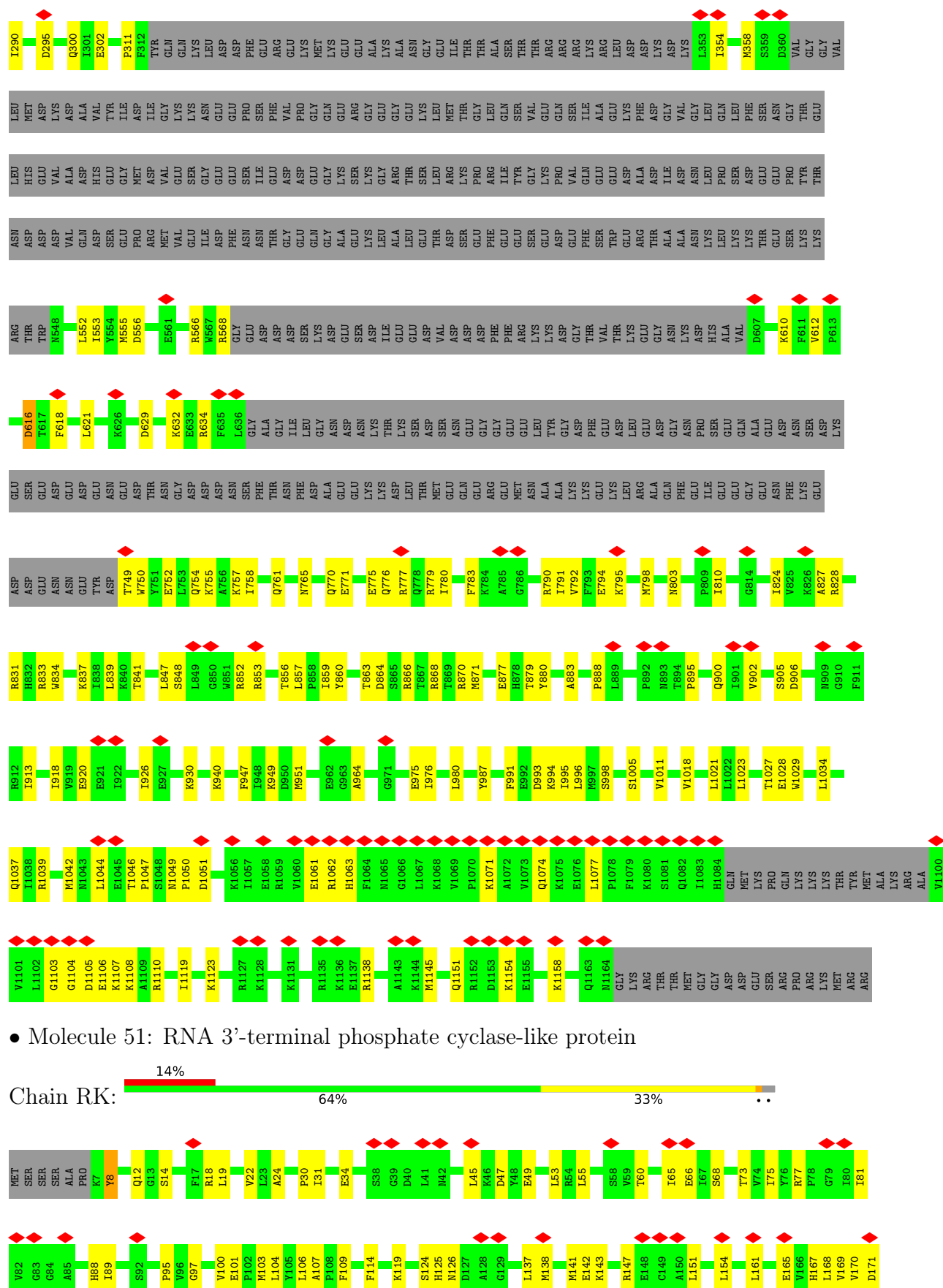


• Molecule 49: Ribosomal RNA small subunit methyltransferase NEP1

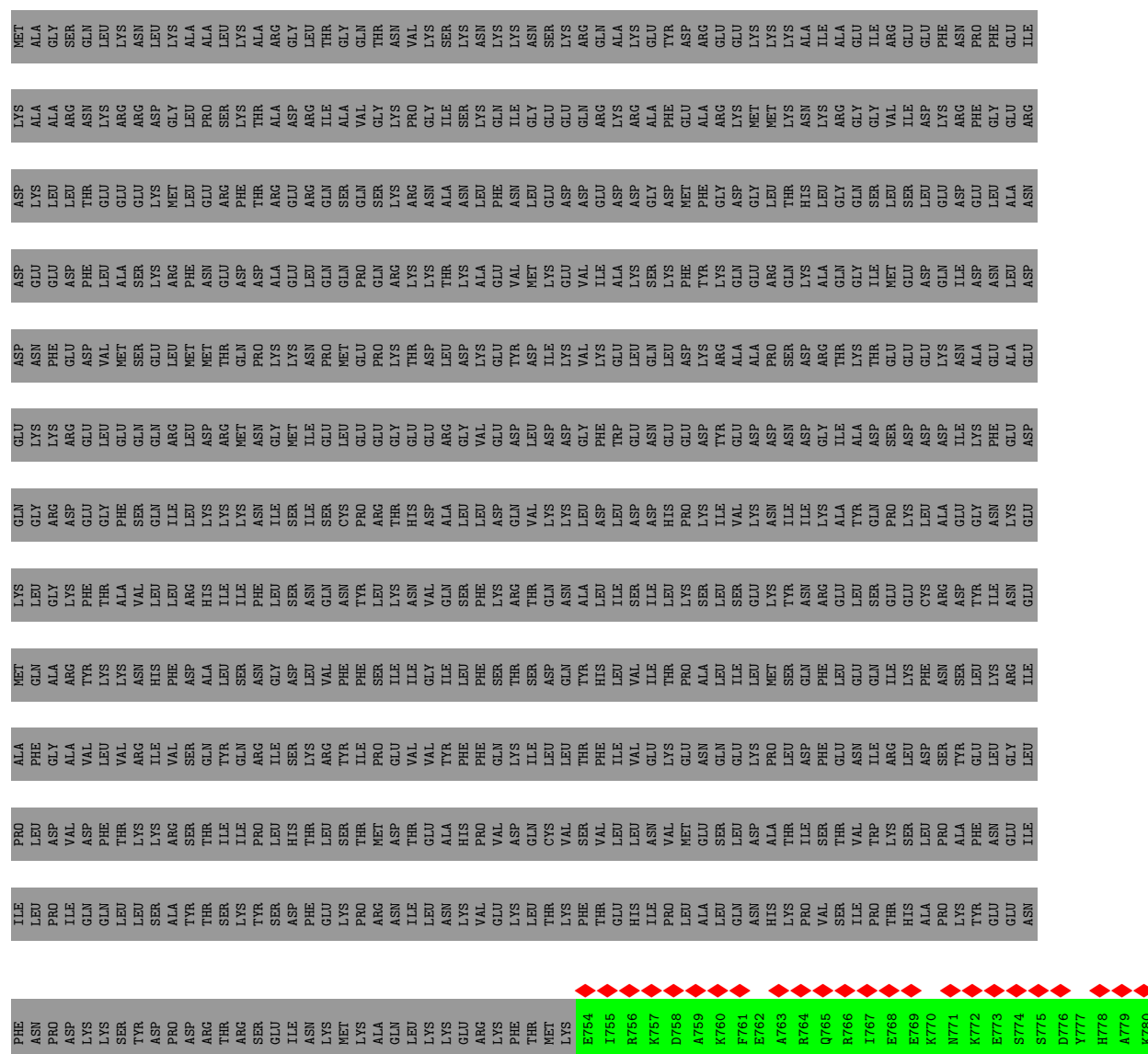


• Molecule 50: Ribosome biogenesis protein BMS1



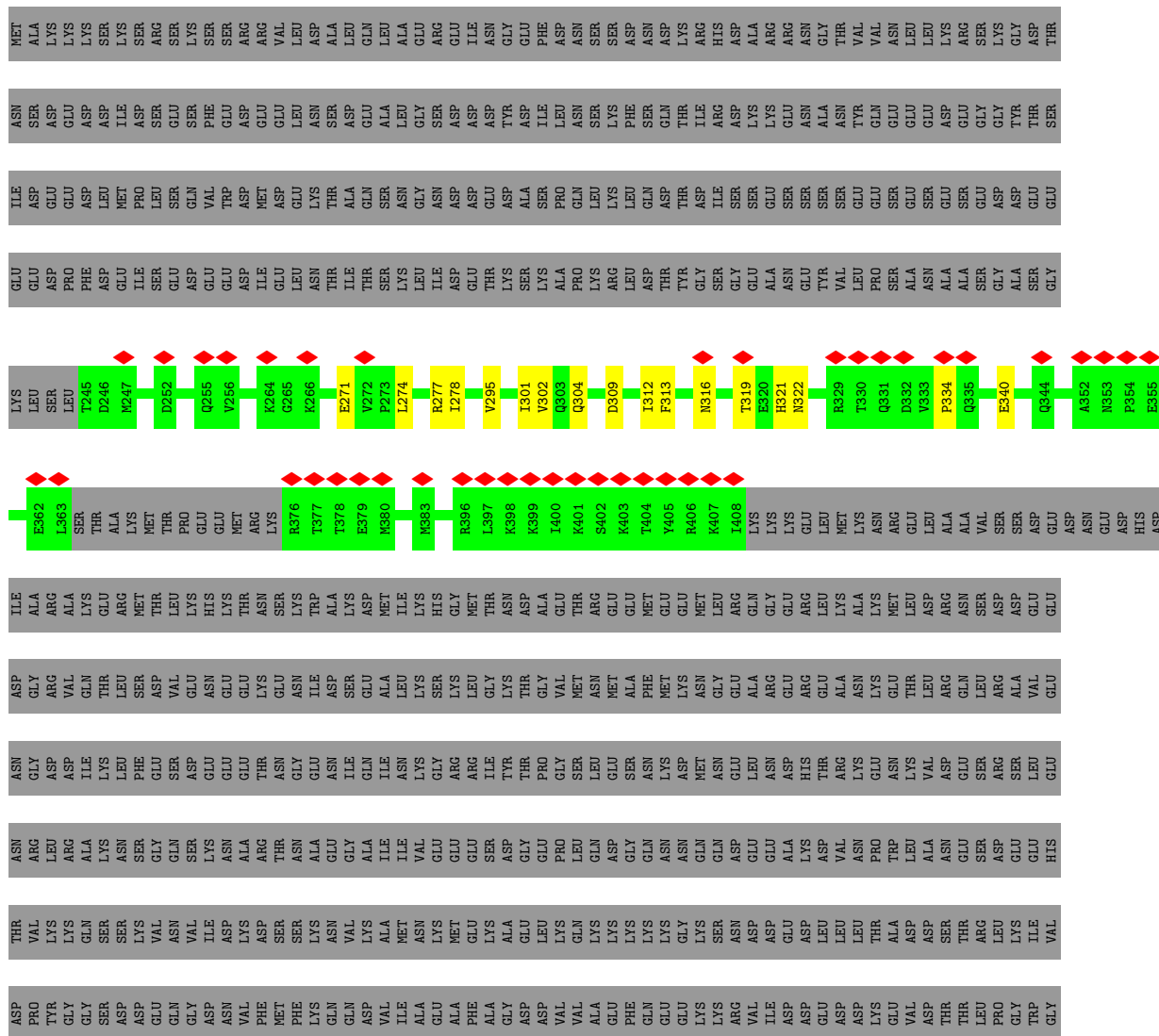


- Molecule 52: Nucleolar complex protein 14

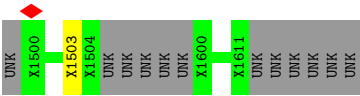












4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	14475	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	0.086	Depositor
Minimum map value	-0.035	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.018	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	0.35	0/4592	0.49	1/7138 (0.0%)
2	5A	0.27	0/3643	0.46	1/5663 (0.0%)
3	SA	0.33	0/27506	0.47	4/42818 (0.0%)
4	SC	0.43	0/1874	0.81	3/2512 (0.1%)
5	SF	0.36	0/1969	0.78	3/2661 (0.1%)
6	SG	0.41	0/1690	0.67	0/2285
7	SH	0.24	0/1477	0.59	0/1977
8	SI	0.36	0/1330	0.77	5/1792 (0.3%)
9	SJ	0.25	0/1124	0.66	0/1510
10	SK	0.48	0/1410	0.69	0/1888
11	SM	0.25	0/1139	0.60	0/1535
12	SO	0.41	0/1109	0.72	0/1495
13	SP	0.37	0/879	0.68	1/1186 (0.1%)
14	SR	0.48	0/990	0.77	0/1335
15	SX	0.45	0/1020	0.70	0/1371
16	SY	0.38	0/819	0.69	0/1093
17	SZ	0.43	0/1000	0.72	0/1334
18	Sc	0.43	0/613	0.77	0/828
19	Sd	0.47	0/499	0.80	0/670
20	3B	0.50	0/1901	0.71	0/2567
20	3C	0.31	0/1796	0.69	0/2424
21	3D	0.41	0/3020	0.67	0/4066
22	3E	0.35	0/3072	0.62	0/4169
23	3F	0.46	0/3569	0.73	0/4806
24	3G	0.37	0/928	0.75	0/1262
24	3H	0.51	0/928	0.74	0/1262
25	A4	0.32	0/5338	0.69	3/7230 (0.0%)
26	A5	0.44	0/2995	0.65	0/4060
27	A9	0.28	0/301	0.68	0/398
28	AE	0.41	0/3500	0.65	0/4736
29	AF	0.26	0/3885	0.63	2/5261 (0.0%)
30	AG	0.28	0/6699	0.63	1/9077 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
31	B1	0.51	0/6570	0.70	2/8892 (0.0%)
32	B2	0.38	0/6628	0.70	2/8954 (0.0%)
33	B3	0.34	0/6014	0.77	2/8137 (0.0%)
34	B8	0.40	0/3848	0.66	2/5218 (0.0%)
35	BE	0.51	0/6606	0.71	0/8935
36	B6	0.38	0/2849	0.64	0/3853
37	5C	0.50	0/3690	0.68	0/4991
38	5D	0.31	0/621	0.58	0/823
39	5E	0.35	0/1580	0.72	0/2115
40	5F	0.47	0/1559	0.72	0/2097
41	5G	0.47	0/1768	0.72	0/2392
42	5H	0.41	0/601	0.69	0/789
43	5I	0.59	0/3835	0.75	0/5162
44	5J	0.32	0/1147	0.60	0/1531
45	5K	0.47	0/1346	0.66	0/1812
46	RD	0.25	0/2454	0.63	1/3310 (0.0%)
47	RE	0.31	0/9015	0.65	0/12195
48	RF	0.29	0/2004	0.67	0/2697
49	RH	0.24	0/1746	0.62	1/2357 (0.0%)
50	RJ	0.40	0/6067	0.66	3/8170 (0.0%)
51	RK	0.35	0/2832	0.66	0/3825
52	RN	0.25	0/454	0.61	0/600
53	RP	0.25	0/12777	0.58	6/17558 (0.0%)
54	RQ	0.39	0/1682	0.68	1/2286 (0.0%)
55	RT	0.29	0/1379	0.67	0/1853
All	All	0.37	0/181687	0.64	44/252961 (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	4
7	SH	0	1
8	SI	0	4
12	SO	0	1
18	Sc	0	2
19	Sd	0	1
20	3C	0	1
23	3F	0	1
26	A5	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
29	AF	0	1
30	AG	0	5
31	B1	0	1
32	B2	0	2
33	B3	0	5
39	5E	0	1
43	5I	0	3
47	RE	0	3
48	RF	0	3
49	RH	0	1
50	RJ	0	1
51	RK	0	1
53	RP	0	11
54	RQ	0	2
55	RT	0	1
All	All	0	57

There are no bond length outliers.

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	B3	584	ILE	CA-C-N	6.54	134.03	121.54
33	B3	584	ILE	C-N-CA	6.54	134.03	121.54
46	RD	1187	VAL	N-CA-C	-6.43	106.54	111.62
25	A4	480	PHE	N-CA-C	6.27	118.25	110.91
5	SF	193	GLY	N-CA-C	5.92	127.21	113.18

There are no chirality outliers.

5 of 57 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	SC	135	LEU	Peptide
4	SC	16	GLN	Peptide
4	SC	177	GLN	Peptide
4	SC	208	GLN	Peptide
7	SH	152	ASP	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	4114	0	2083	42	0
2	5A	3260	0	1643	36	0
3	SA	24609	0	12403	302	0
4	SC	1848	0	1940	40	0
5	SF	1930	0	1950	32	0
6	SG	1669	0	1724	25	0
7	SH	1457	0	1504	39	0
8	SI	1310	0	1374	36	0
9	SJ	1104	0	1107	28	0
10	SK	1388	0	1467	28	0
11	SM	1113	0	1181	28	0
12	SO	1087	0	1152	27	0
13	SP	868	0	894	20	0
14	SR	973	0	1029	20	0
15	SX	1003	0	1040	25	0
16	SY	807	0	865	16	0
17	SZ	986	0	1042	19	0
18	Sc	603	0	621	14	0
19	Sd	497	0	535	5	0
20	3B	1865	0	1910	46	0
20	3C	1763	0	1805	47	0
21	3D	2974	0	3001	57	0
22	3E	3041	0	2831	72	0
23	3F	3498	0	3515	80	0
24	3G	916	0	964	17	0
24	3H	916	0	964	24	0
25	A4	5243	0	5216	183	0
26	A5	2943	0	2928	61	0
27	A9	299	0	328	7	0
28	AE	3443	0	3564	61	0
29	AF	3807	0	3791	91	0
30	AG	6570	0	6473	188	0
31	B1	6427	0	6329	131	0
32	B2	6502	0	6493	154	0
33	B3	5919	0	6007	151	0
34	B8	3764	0	3757	82	0
35	BE	6475	0	6453	160	0
36	B6	2800	0	2517	43	0
37	5C	3612	0	3578	69	0
38	5D	609	0	616	8	0
39	5E	1564	0	1592	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
40	5F	1530	0	1572	31	0
41	5G	1732	0	1744	36	0
42	5H	596	0	661	8	0
43	5I	3756	0	3708	92	0
44	5J	1127	0	1150	17	0
45	5K	1323	0	1401	20	0
46	RD	2413	0	2264	29	0
47	RE	8805	0	8911	200	0
48	RF	1963	0	1942	43	0
49	RH	1719	0	1783	40	0
50	RJ	5935	0	6100	136	0
51	RK	2781	0	2878	79	0
52	RN	450	0	447	3	0
53	RP	12716	0	8235	94	0
54	RQ	1655	0	1461	22	0
55	RT	1357	0	1426	22	0
56	X1	400	0	99	3	0
57	5K	1	0	0	0	0
57	Sc	1	0	0	0	0
58	RJ	32	0	12	0	0
59	RJ	1	0	0	0	0
All	All	175869	0	155980	3094	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 9.

The worst 5 of 3094 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)
25:A4:741:LEU:HD11	25:A4:744:VAL:CG2	1.48	1.42
25:A4:740:PRO:O	25:A4:756:GLU:HG2	1.44	1.16
25:A4:741:LEU:HD11	25:A4:744:VAL:HG21	1.16	1.13
25:A4:741:LEU:HD21	25:A4:744:VAL:HG23	1.39	1.04
25:A4:741:LEU:CD1	25:A4:744:VAL:CG2	2.39	1.00

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	230/255 (90%)	190 (83%)	39 (17%)	1 (0%)	30	67
5	SF	248/261 (95%)	211 (85%)	37 (15%)	0	100	100
6	SG	211/225 (94%)	194 (92%)	17 (8%)	0	100	100
7	SH	178/236 (75%)	158 (89%)	17 (10%)	3 (2%)	7	35
8	SI	160/190 (84%)	136 (85%)	24 (15%)	0	100	100
9	SJ	136/200 (68%)	113 (83%)	23 (17%)	0	100	100
10	SK	169/197 (86%)	155 (92%)	14 (8%)	0	100	100
11	SM	135/156 (86%)	119 (88%)	16 (12%)	0	100	100
12	SO	132/151 (87%)	119 (90%)	13 (10%)	0	100	100
13	SP	116/137 (85%)	103 (89%)	13 (11%)	0	100	100
14	SR	123/143 (86%)	110 (89%)	13 (11%)	0	100	100
15	SX	125/130 (96%)	114 (91%)	11 (9%)	0	100	100
16	SY	104/145 (72%)	91 (88%)	13 (12%)	0	100	100
17	SZ	121/135 (90%)	104 (86%)	17 (14%)	0	100	100
18	Sc	78/82 (95%)	66 (85%)	12 (15%)	0	100	100
19	Sd	61/67 (91%)	56 (92%)	5 (8%)	0	100	100
20	3B	236/327 (72%)	222 (94%)	14 (6%)	0	100	100
20	3C	221/327 (68%)	204 (92%)	17 (8%)	0	100	100
21	3D	372/504 (74%)	343 (92%)	29 (8%)	0	100	100
22	3E	428/511 (84%)	389 (91%)	39 (9%)	0	100	100
23	3F	431/572 (75%)	365 (85%)	65 (15%)	1 (0%)	43	77
24	3G	119/126 (94%)	109 (92%)	10 (8%)	0	100	100
24	3H	119/126 (94%)	112 (94%)	6 (5%)	1 (1%)	16	52
25	A4	650/776 (84%)	583 (90%)	67 (10%)	0	100	100
26	A5	362/643 (56%)	333 (92%)	29 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	A9	35/575 (6%)	34 (97%)	1 (3%)	0	100	100
28	AE	429/1769 (24%)	410 (96%)	19 (4%)	0	100	100
29	AF	473/513 (92%)	427 (90%)	46 (10%)	0	100	100
30	AG	812/896 (91%)	694 (86%)	118 (14%)	0	100	100
31	B1	800/923 (87%)	720 (90%)	80 (10%)	0	100	100
32	B2	813/943 (86%)	731 (90%)	82 (10%)	0	100	100
33	B3	733/817 (90%)	608 (83%)	123 (17%)	2 (0%)	36	71
34	B8	469/594 (79%)	423 (90%)	45 (10%)	1 (0%)	43	77
35	BE	817/939 (87%)	746 (91%)	71 (9%)	0	100	100
36	B6	368/440 (84%)	343 (93%)	25 (7%)	0	100	100
37	5C	452/554 (82%)	400 (88%)	52 (12%)	0	100	100
38	5D	68/250 (27%)	57 (84%)	10 (15%)	1 (2%)	8	38
39	5E	187/593 (32%)	173 (92%)	14 (8%)	0	100	100
40	5F	180/183 (98%)	165 (92%)	15 (8%)	0	100	100
41	5G	214/290 (74%)	196 (92%)	18 (8%)	0	100	100
42	5H	72/610 (12%)	63 (88%)	9 (12%)	0	100	100
43	5I	456/489 (93%)	422 (92%)	33 (7%)	1 (0%)	43	77
44	5J	130/217 (60%)	121 (93%)	9 (7%)	0	100	100
45	5K	162/189 (86%)	149 (92%)	13 (8%)	0	100	100
46	RD	310/1729 (18%)	278 (90%)	32 (10%)	0	100	100
47	RE	1080/1237 (87%)	996 (92%)	84 (8%)	0	100	100
48	RF	233/297 (78%)	203 (87%)	30 (13%)	0	100	100
49	RH	215/252 (85%)	198 (92%)	17 (8%)	0	100	100
50	RJ	719/1183 (61%)	649 (90%)	69 (10%)	1 (0%)	48	83
51	RK	358/367 (98%)	335 (94%)	23 (6%)	0	100	100
52	RN	51/810 (6%)	51 (100%)	0	0	100	100
53	RP	2112/2493 (85%)	1903 (90%)	203 (10%)	6 (0%)	36	71
54	RQ	220/899 (24%)	197 (90%)	23 (10%)	0	100	100
55	RT	165/326 (51%)	152 (92%)	13 (8%)	0	100	100
All	All	18398/27999 (66%)	16543 (90%)	1837 (10%)	18 (0%)	49	83

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
34	B8	226	LYS
24	3H	6	PRO
53	RP	37	ARG
53	RP	1004	VAL
4	SC	213	ARG

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	205/224 (92%)	205 (100%)	0	100	100
5	SF	199/222 (90%)	196 (98%)	3 (2%)	57	71
6	SG	180/191 (94%)	179 (99%)	1 (1%)	78	81
7	SH	153/201 (76%)	153 (100%)	0	100	100
8	SI	145/170 (85%)	143 (99%)	2 (1%)	59	72
9	SJ	114/161 (71%)	114 (100%)	0	100	100
10	SK	147/166 (89%)	146 (99%)	1 (1%)	76	79
11	SM	124/137 (90%)	124 (100%)	0	100	100
12	SO	117/128 (91%)	115 (98%)	2 (2%)	53	68
13	SP	90/105 (86%)	89 (99%)	1 (1%)	65	74
14	SR	105/119 (88%)	105 (100%)	0	100	100
15	SX	108/111 (97%)	108 (100%)	0	100	100
16	SY	88/120 (73%)	86 (98%)	2 (2%)	44	63
17	SZ	103/113 (91%)	101 (98%)	2 (2%)	50	66
18	Sc	69/71 (97%)	65 (94%)	4 (6%)	18	40
19	Sd	56/60 (93%)	56 (100%)	0	100	100
20	3B	201/240 (84%)	199 (99%)	2 (1%)	68	76
20	3C	190/240 (79%)	186 (98%)	4 (2%)	47	65
21	3D	322/435 (74%)	321 (100%)	1 (0%)	86	84
22	3E	265/433 (61%)	264 (100%)	1 (0%)	84	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	3F	382/502 (76%)	372 (97%)	10 (3%)	40	61
24	3G	100/104 (96%)	98 (98%)	2 (2%)	48	66
24	3H	100/104 (96%)	100 (100%)	0	100	100
25	A4	593/713 (83%)	585 (99%)	8 (1%)	61	72
26	A5	334/574 (58%)	332 (99%)	2 (1%)	78	81
27	A9	34/533 (6%)	34 (100%)	0	100	100
28	AE	391/1633 (24%)	390 (100%)	1 (0%)	86	84
29	AF	424/454 (93%)	421 (99%)	3 (1%)	76	79
30	AG	750/826 (91%)	747 (100%)	3 (0%)	84	83
31	B1	707/812 (87%)	699 (99%)	8 (1%)	65	74
32	B2	712/832 (86%)	702 (99%)	10 (1%)	59	72
33	B3	665/719 (92%)	659 (99%)	6 (1%)	70	77
34	B8	421/529 (80%)	413 (98%)	8 (2%)	50	66
35	BE	721/819 (88%)	713 (99%)	8 (1%)	65	74
36	B6	251/414 (61%)	248 (99%)	3 (1%)	63	74
37	5C	394/480 (82%)	391 (99%)	3 (1%)	73	78
38	5D	65/234 (28%)	65 (100%)	0	100	100
39	5E	175/535 (33%)	174 (99%)	1 (1%)	78	81
40	5F	171/172 (99%)	171 (100%)	0	100	100
41	5G	191/258 (74%)	189 (99%)	2 (1%)	68	76
42	5H	63/538 (12%)	63 (100%)	0	100	100
43	5I	415/443 (94%)	410 (99%)	5 (1%)	63	74
44	5J	124/200 (62%)	123 (99%)	1 (1%)	73	78
45	5K	148/169 (88%)	148 (100%)	0	100	100
46	RD	226/1544 (15%)	225 (100%)	1 (0%)	84	83
47	RE	994/1125 (88%)	987 (99%)	7 (1%)	76	79
48	RF	221/274 (81%)	219 (99%)	2 (1%)	70	77
49	RH	197/222 (89%)	197 (100%)	0	100	100
50	RJ	649/1039 (62%)	643 (99%)	6 (1%)	70	77
51	RK	307/312 (98%)	302 (98%)	5 (2%)	55	69
52	RN	47/732 (6%)	47 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	RP	550/2307 (24%)	546 (99%)	4 (1%)	76	79
54	RQ	149/808 (18%)	149 (100%)	0	100	100
55	RT	148/282 (52%)	147 (99%)	1 (1%)	76	79
All	All	14800/24889 (60%)	14664 (99%)	136 (1%)	68	77

5 of 136 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	RE	531	LEU
48	RF	176	ASP
51	RK	354	ILE
28	AE	87	THR
26	A5	240	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 285 such sidechains are listed below:

Mol	Chain	Res	Type
47	RE	313	ASN
47	RE	588	GLN
50	RJ	300	GLN
30	AG	370	GLN
30	AG	113	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	189/333 (56%)	77 (40%)	3 (1%)
2	5A	144/700 (20%)	62 (43%)	2 (1%)
3	SA	1137/1809 (62%)	413 (36%)	20 (1%)
All	All	1470/2842 (51%)	552 (37%)	25 (1%)

5 of 552 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3A	4	G
1	3A	12	U
1	3A	15	U
1	3A	24	U
1	3A	25	U

5 of 25 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	SA	579	A
3	SA	685	A
3	SA	1754	A
3	SA	637	C
3	SA	773	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 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	$\# Z > 2$
58	GTP	RJ	1201	59	33,34,34	0.85	1 (3%)	50,54,54	1.63	9 (18%)

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
58	GTP	RJ	1201	59	-	1/22/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	RJ	1201	GTP	C2-N3	2.01	1.38	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	RJ	1201	GTP	C5-C4-N3	-5.13	120.23	128.39
58	RJ	1201	GTP	C2-N3-C4	4.71	120.41	112.30
58	RJ	1201	GTP	C2-N1-C6	-3.20	119.31	125.11
58	RJ	1201	GTP	N9-C4-N3	3.14	132.23	125.95
58	RJ	1201	GTP	N9-C8-N7	-2.91	108.00	113.40

There are no chirality outliers.

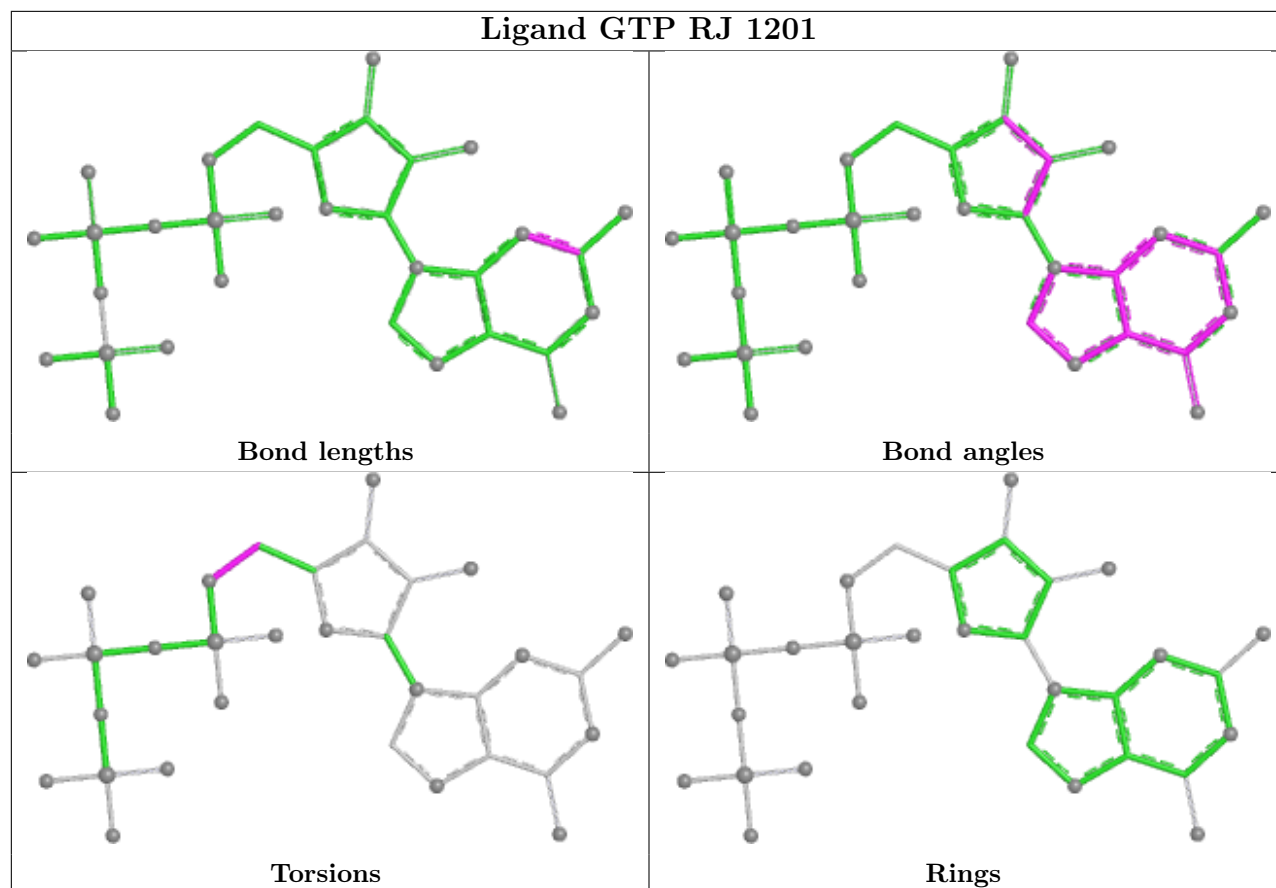
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	RJ	1201	GTP	C4'-C5'-O5'-PA

There are no ring outliers.

No monomer is involved in short contacts.

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.

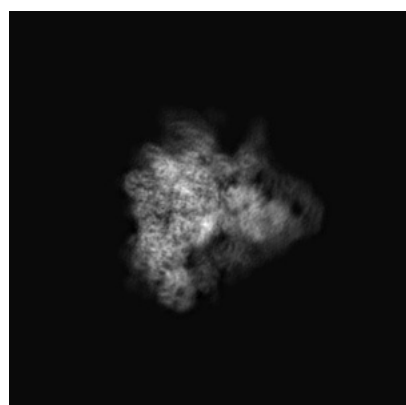
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0953. These allow visual inspection of the internal detail of the map and identification of artifacts.

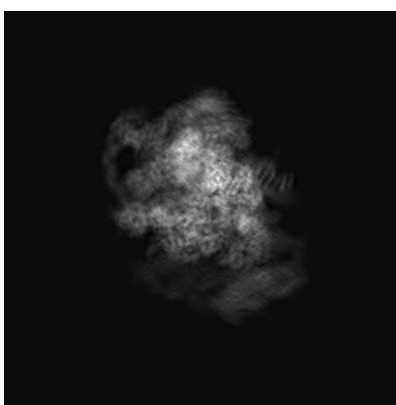
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

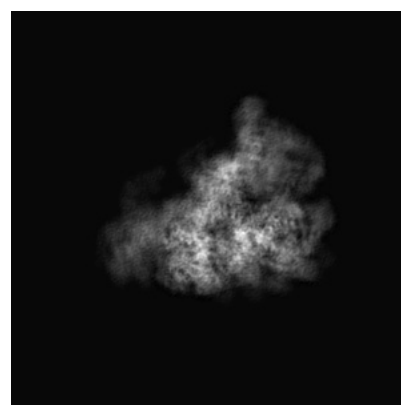
6.1.1 Primary map



X



Y

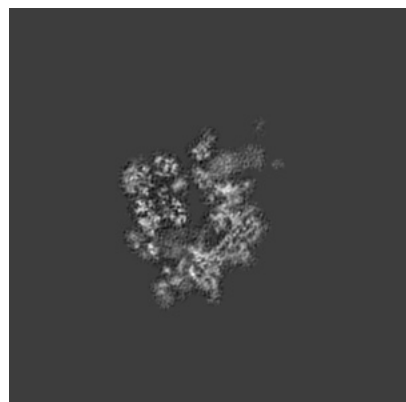


Z

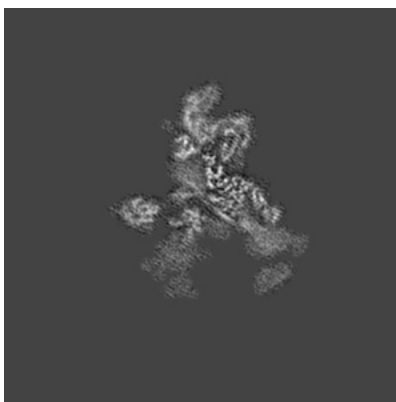
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 224



Y Index: 224

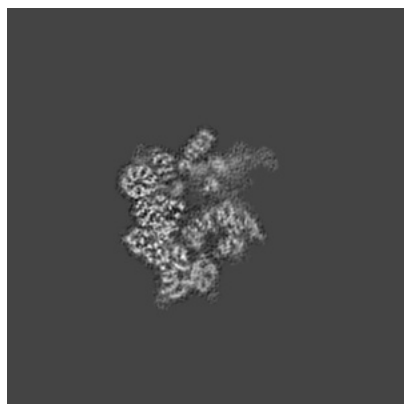


Z Index: 224

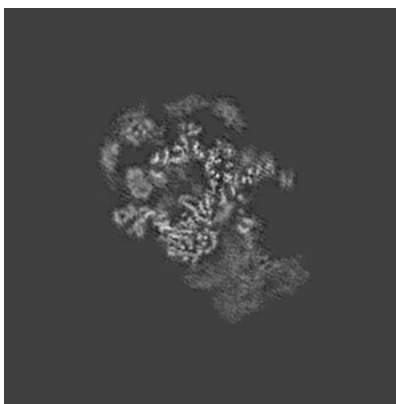
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

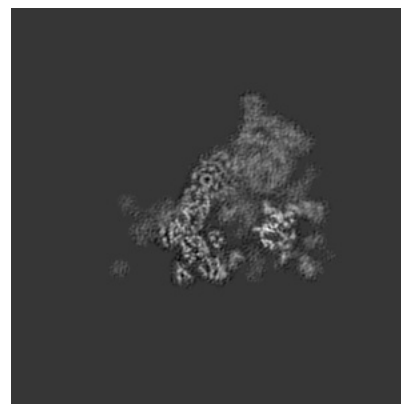
6.3.1 Primary map



X Index: 215



Y Index: 190

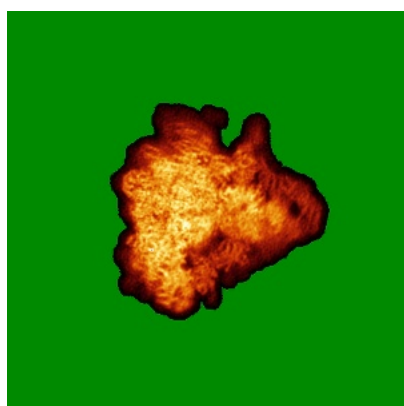


Z Index: 208

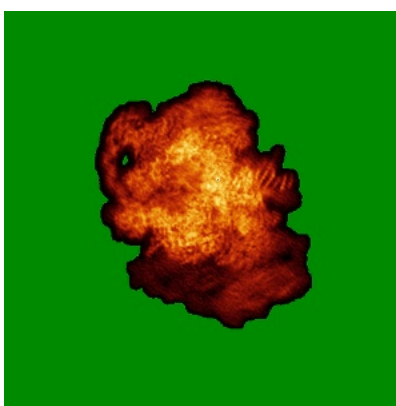
The images above show the largest variance slices of the map in three orthogonal directions.

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

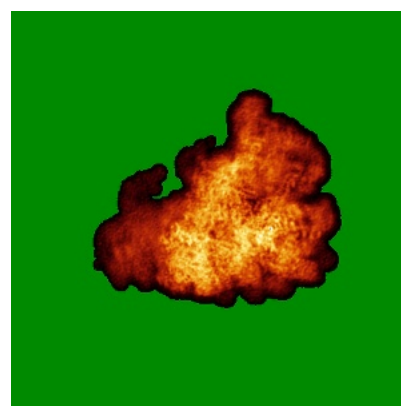
6.4.1 Primary map



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

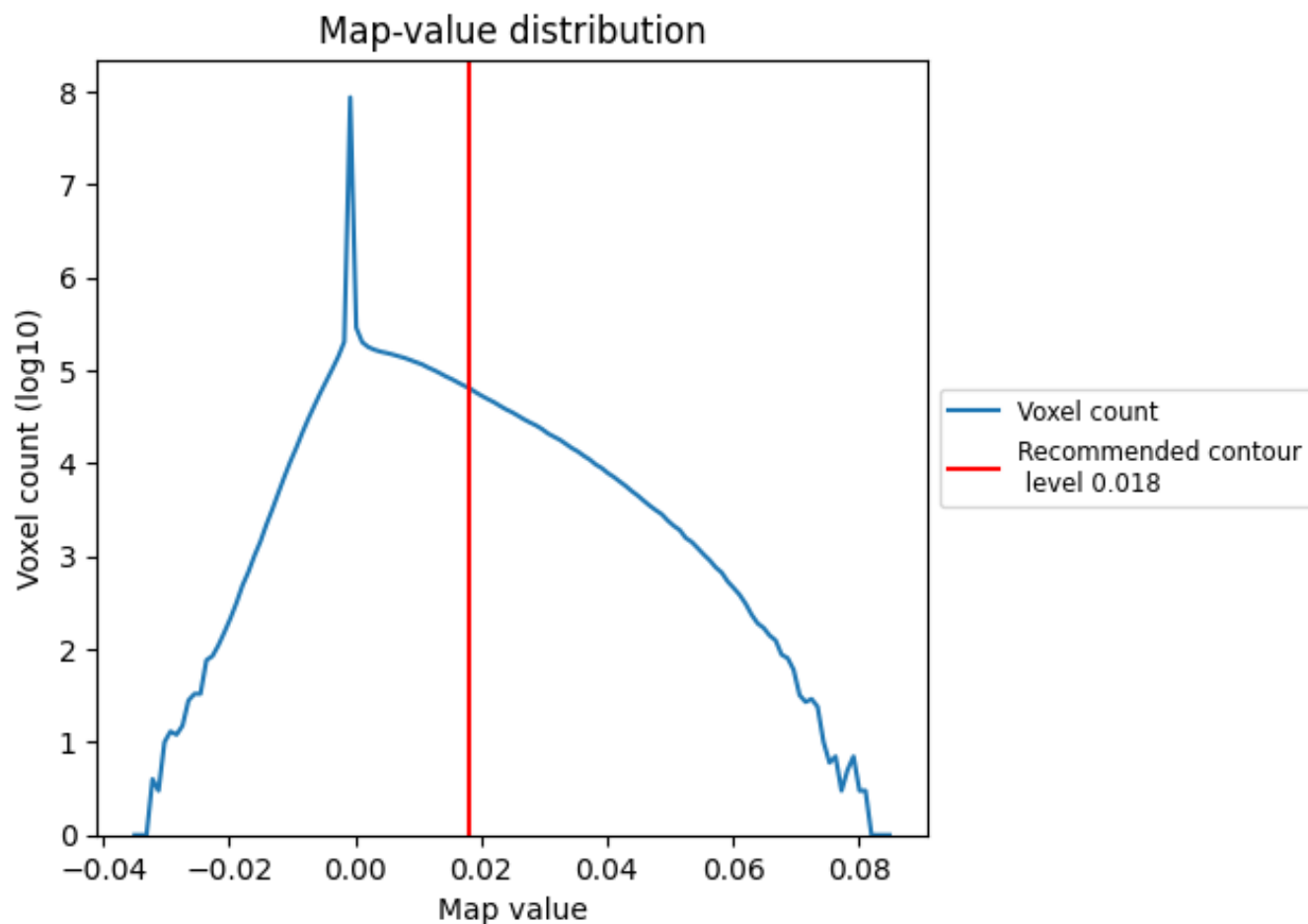
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

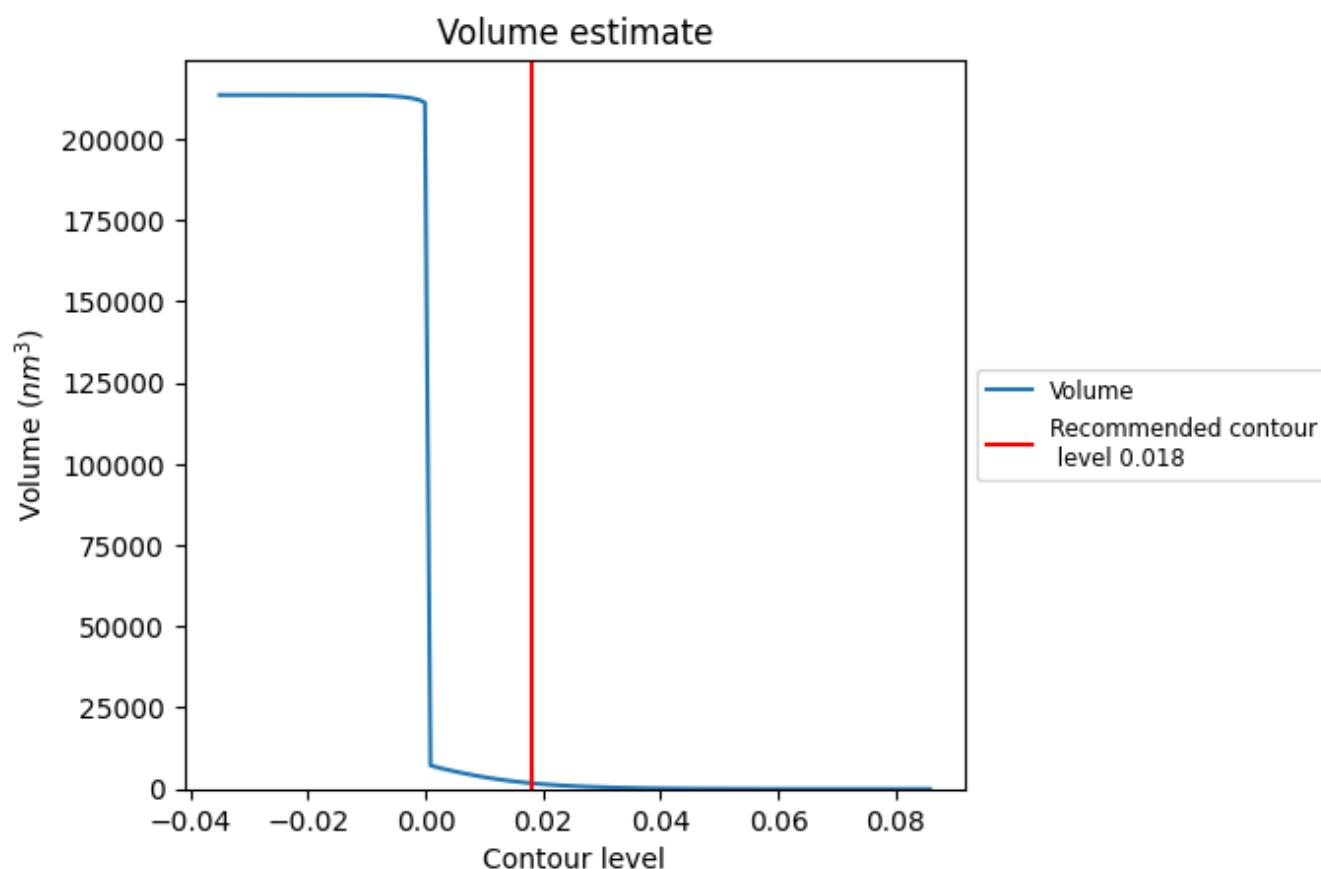
This section contains the results of statistical analysis of the map.

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.

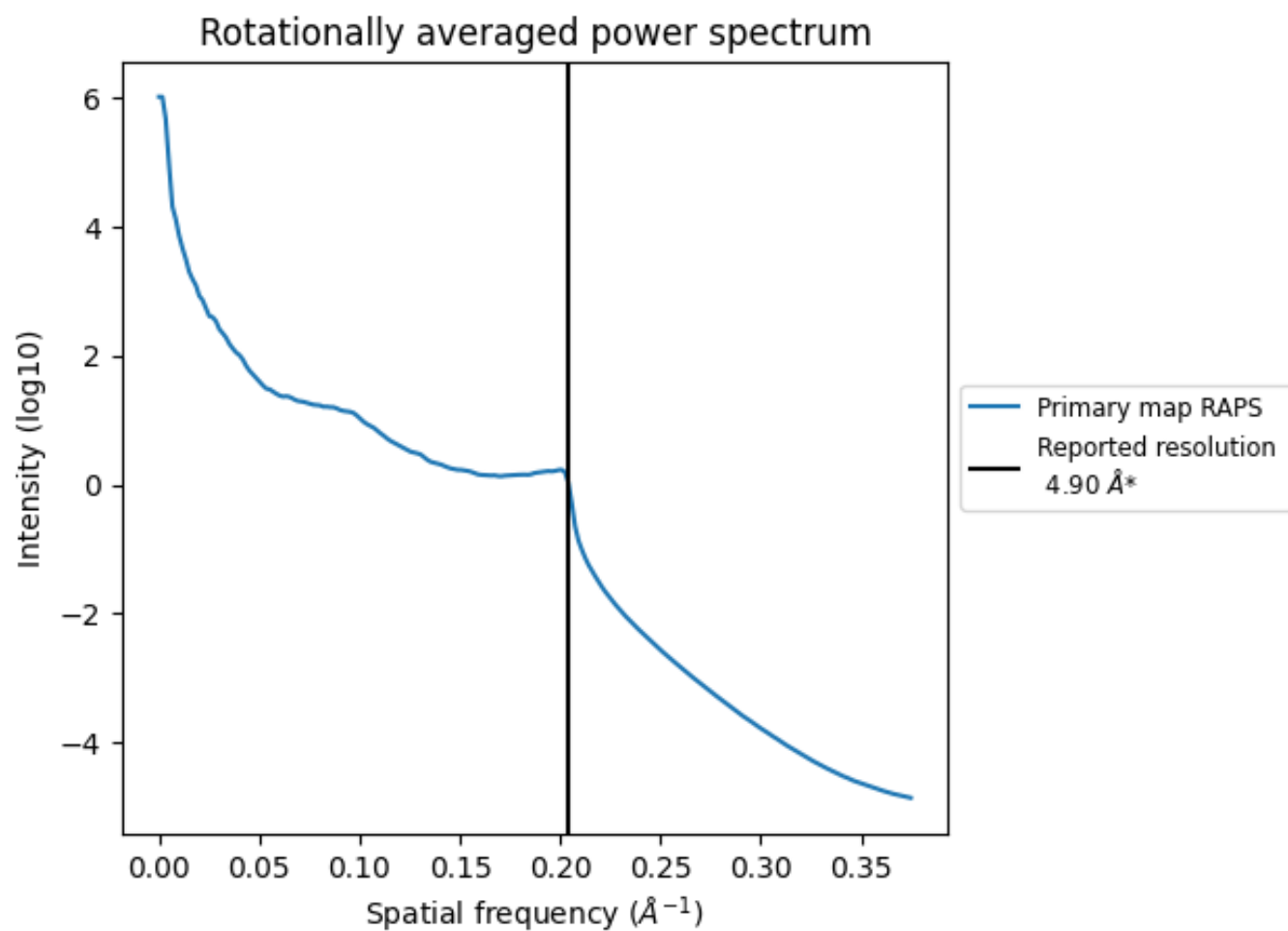
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1775 nm^3 ; this corresponds to an approximate mass of 1603 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 0.204 Å⁻¹

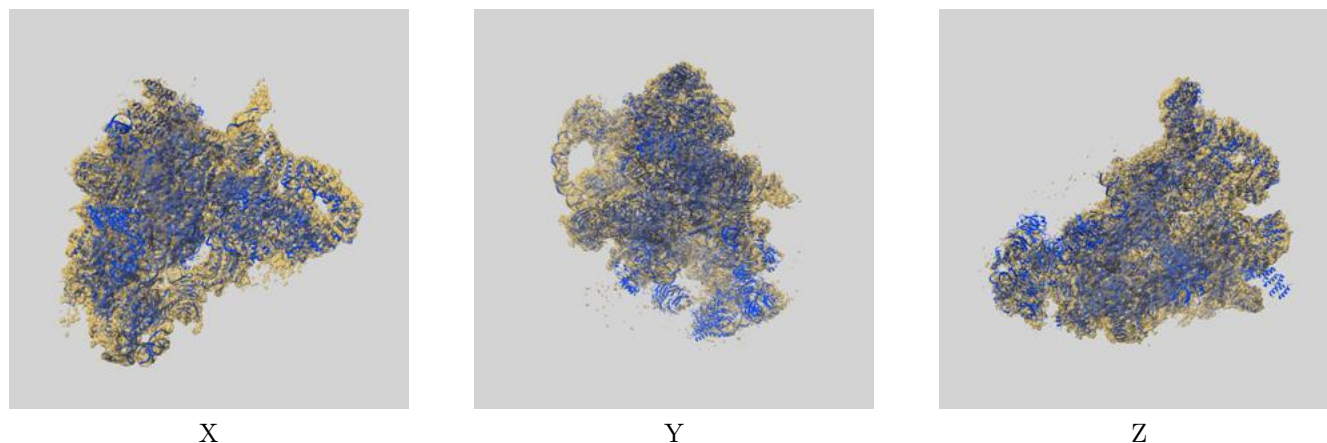
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

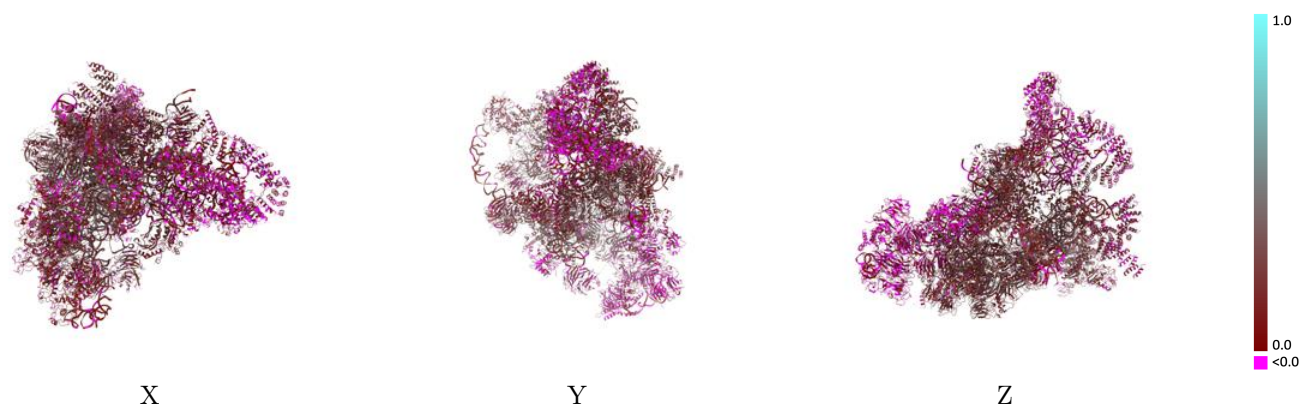
This section contains information regarding the fit between EMDB map EMD-0953 and PDB model 6LQT. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



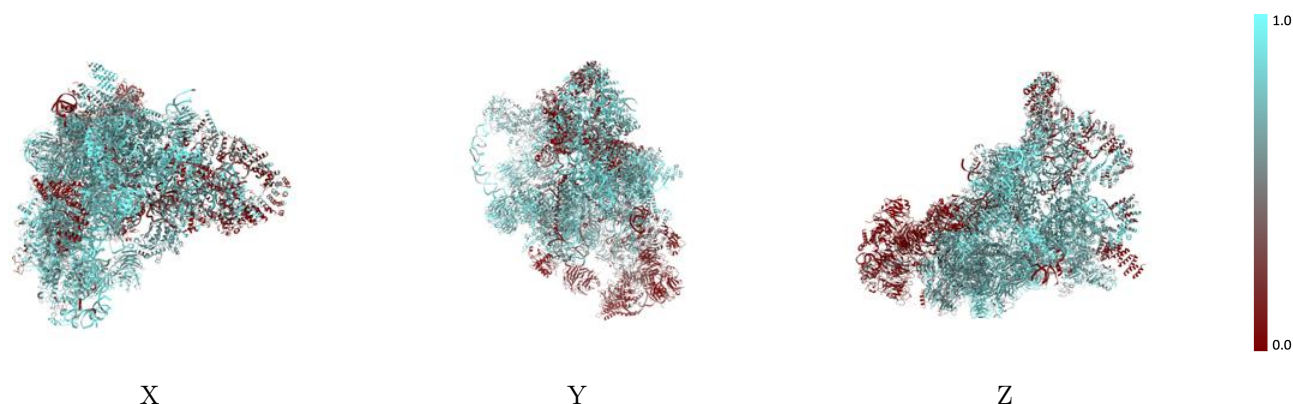
The images above show the 3D surface view of the map at the recommended contour level 0.018 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



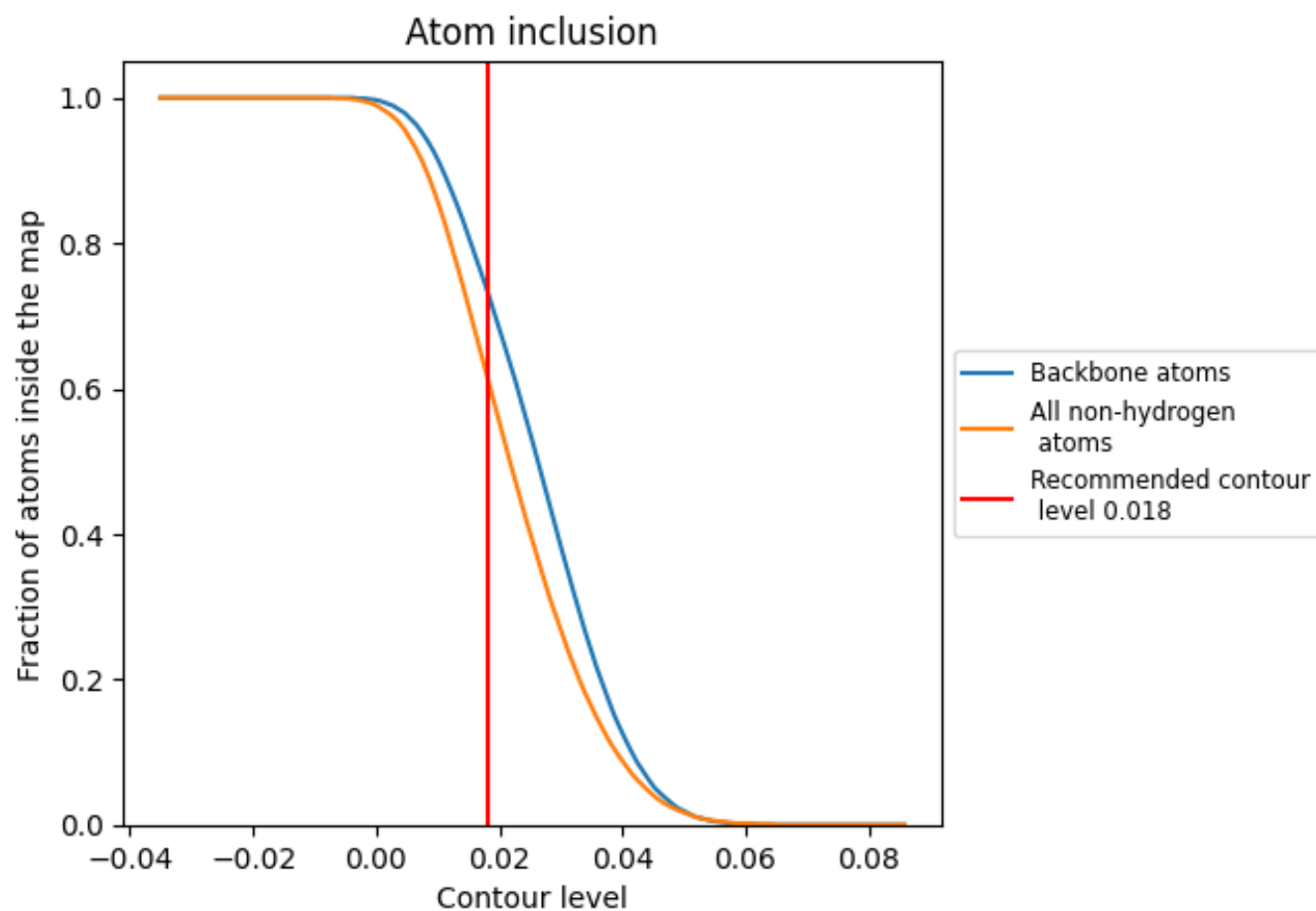
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.018).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 62% 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 (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6170	 0.1760
3A	 0.7220	 0.1730
3B	 0.7350	 0.2510
3C	 0.2290	 0.0270
3D	 0.7200	 0.2100
3E	 0.5210	 0.1280
3F	 0.7380	 0.1990
3G	 0.5690	 0.0750
3H	 0.7190	 0.2500
5A	 0.4470	 0.1260
5C	 0.7510	 0.2720
5D	 0.4040	 0.1920
5E	 0.6550	 0.2140
5F	 0.7150	 0.2580
5G	 0.5840	 0.2170
5H	 0.7250	 0.2260
5I	 0.7840	 0.2810
5J	 0.4590	 0.1630
5K	 0.7250	 0.2770
A4	 0.0530	 0.0370
A5	 0.5280	 0.1980
A9	 0.0340	 -0.0100
AE	 0.6560	 0.2260
AF	 0.0570	 0.0650
AG	 0.1490	 0.0500
B1	 0.7890	 0.2790
B2	 0.7740	 0.1980
B3	 0.8130	 0.1990
B6	 0.7470	 0.2190
B8	 0.6200	 0.1640
BE	 0.7970	 0.2680
RD	 0.1150	 0.0930
RE	 0.7000	 0.1860
RF	 0.6930	 0.1820
RH	 0.0450	 0.0060



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Chain	Atom inclusion	Q-score
RJ	 0.6150	 0.1880
RK	 0.6710	 0.1890
RN	 0.1260	 0.1140
RP	 0.5610	 0.1180
RQ	 0.6330	 0.2320
RT	 0.5970	 0.1850
SA	 0.7860	 0.1830
SC	 0.7430	 0.2580
SF	 0.5820	 0.0960
SG	 0.7470	 0.2420
SH	 0.3820	 0.0560
SI	 0.6830	 0.2190
SJ	 0.4120	 0.0390
SK	 0.7420	 0.2280
SM	 0.2760	 0.0230
SO	 0.7900	 0.2440
SP	 0.7420	 0.2350
SR	 0.7600	 0.2490
SX	 0.7770	 0.2820
SY	 0.4970	 0.1920
SZ	 0.7190	 0.1340
Sc	 0.7700	 0.2800
Sd	 0.7710	 0.2780
X1	 0.5020	 0.1910