



wwPDB EM Validation Summary Report ⓘ

May 20, 2024 – 01:21 AM JST

PDB ID : 7D5T
EMDB ID : EMD-30585
Title : Cryo-EM structure of 90S preribosome with inactive Utp24 (state F1)
Authors : Du, Y.; Zhang, J.; An, W.; Ye, K.
Deposited on : 2020-09-28
Resolution : 6.00 Å(reported)
Based on initial model : 7D4I

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.dev92
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

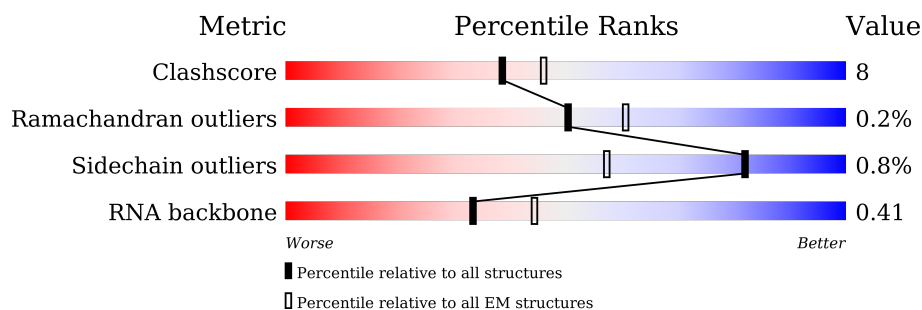
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



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

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

Mol	Chain	Length	Quality of chain
1	3A	333	
2	5A	700	
3	SA	1812	
4	SC	255	
5	SF	261	
6	SG	225	
7	SH	236	

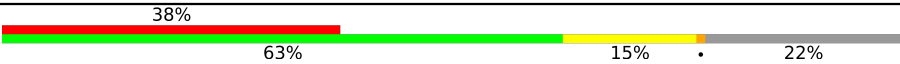

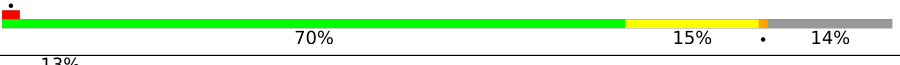
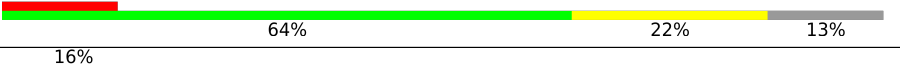

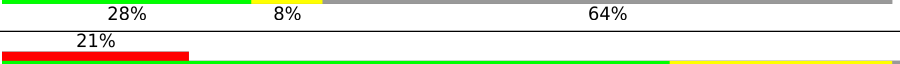
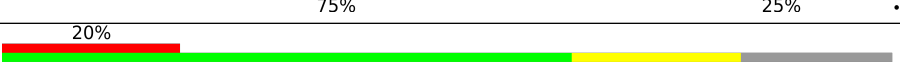

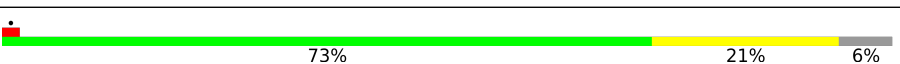

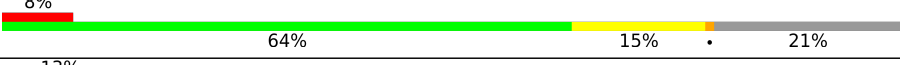



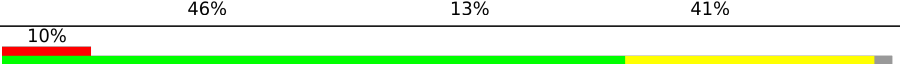
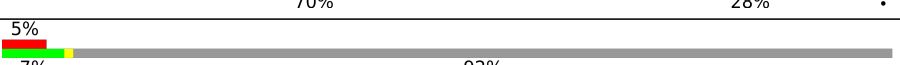
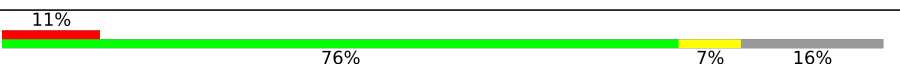






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Mol	Chain	Length	Quality of chain
8	SI	190	
9	SJ	200	
10	SK	197	
11	SM	156	
12	SO	151	
13	SP	137	
14	SR	143	
15	SX	130	
16	SY	145	
17	SZ	135	
18	Sc	82	
19	Sd	67	
20	3B	327	
20	3C	327	
21	3D	504	
22	3E	511	
23	3F	573	
24	3G	126	
24	3H	126	
25	A5	643	
26	AE	1769	
27	AG	896	
28	B1	900	
29	B2	943	
30	B3	817	

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Mol	Chain	Length	Quality of chain
31	B8	594	
32	BE	939	
33	B6	440	
34	5C	554	
35	5D	250	
36	5E	593	
37	5F	183	
38	5G	290	
39	5H	610	
40	5I	489	
41	5J	217	
42	5K	189	
43	RD	1729	
44	RE	1237	
45	RF	297	
46	RJ	1183	
47	RK	367	
48	RN	810	
49	RP	2493	
50	RQ	899	
51	RT	326	
52	RZ	1267	
53	X1	300	

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 163485 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	167	Total	C	N	O	P	0	0
			3534	1581	606	1180	167		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5A	43	Total	C	N	O	P	0	0
			926	413	173	297	43		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SA	1189	Total	C	N	O	P	0	0
			25332	11327	4490	8326	1189		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SC	242	Total	C	N	O	S	0	0
			1923	1214	356	349	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SF	247	Total	C	N	O	S	0	0
			1915	1223	351	338	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
			1456	916	273	266	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SI	165	Total	C	N	O	S	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	148	Total	C	N	O	S	0	0
			1181	739	228	212	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SK	174	Total	C	N	O	S	0	0
			1410	892	272	245	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	116	Total	C	N	O	S	0	0
			848	524	158	163	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	104	Total	C	N	O	S	0	0
			792	506	145	139	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	242	Total	C	N	O	S	0	0
			1878	1190	338	340	10		
20	3C	224	Total	C	N	O	S	0	0
			1754	1114	314	316	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	277	Total	C	N	O	S	0	0
			2130	1335	374	414	7		

- 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 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A5	309	Total	C	N	O	S	0	0
			2452	1573	397	472	10		

- Molecule 26 is a protein called U3 small nucleolar RNA-associated protein 10.

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

- Molecule 27 is a protein called NET1-associated nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AG	48	Total	C	N	O	S	0	0
			394	248	62	80	4		

- Molecule 28 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	B1	791	Total	C	N	O	S	0	0
			6316	4037	1082	1179	18		

- Molecule 29 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	B2	824	Total	C	N	O	S	0	0
			6497	4153	1095	1222	27		

- Molecule 30 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	B3	757	Total	C	N	O	S	0	0
			5906	3763	993	1123	27		

- Molecule 31 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	B8	463	Total	C	N	O	S	0	0
			3648	2314	640	684	10		

- Molecule 32 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BE	890	Total	C	N	O	S	0	0
			6876	4356	1191	1308	21		

- Molecule 33 is a protein called U3 small nucleolar RNA-associated protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	B6	377	Total	C	N	O	S	0	0
			3077	1984	529	549	15		

- Molecule 34 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	5C	482	Total	C	N	O	S	0	0
			3825	2409	684	721	11		

- Molecule 35 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	5D	68	Total	C	N	O	S	0	0
			589	365	120	103	1		

- Molecule 36 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	5E	213	Total	C	N	O	S	0	0
			1728	1072	304	348	4		

- Molecule 37 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	5F	182	Total	C	N	O	S	0	0
			1530	967	287	269	7		

- Molecule 38 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	5G	241	Total	C	N	O	S	0	0
			1956	1228	368	353	7		

- Molecule 39 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	5H	74	Total	C	N	O		0	0
			596	373	122	101			

- Molecule 40 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	5I	461	Total	C	N	O	S	0	0
			3765	2354	686	709	16		

- Molecule 41 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	5J	134	Total	C	N	O	S	0	0
			1127	712	205	207	3		

- Molecule 42 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	5K	150	Total	C	N	O	S	0	0
			1190	765	212	203	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5K	138	ASN	ASP	conflict	UNP Q05498

- Molecule 43 is a protein called rRNA biogenesis protein RRP5.

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

- Molecule 44 is a protein called U3 small nucleolar RNA-associated protein 22.

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

- Molecule 45 is a protein called Ribosomal RNA-processing protein 7.

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

- Molecule 46 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	RJ	702	Total	C	N	O	S	0	0
			5709	3669	1008	1006	26		

- Molecule 47 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 48 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	RN	61	Total	C	N	O	S	0	0
			523	320	102	99	2		

- Molecule 49 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	RP	2084	Total	C	N	O	S	0	0
			12263	7556	2298	2392	17		

- Molecule 50 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	RQ	339	Total	C	N	O	S	0	0
			2411	1487	456	466	2		

- Molecule 51 is a protein called Pno1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	RT	213	Total	C	N	O	S	0	0
			1652	1051	300	297	4		

- Molecule 52 is a protein called Probable ATP-dependent RNA helicase DHR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	RZ	838	Total	C	N	O	S	1	0
			6598	4212	1145	1206	35		

- Molecule 53 is a protein called Unassigned peptides 1.

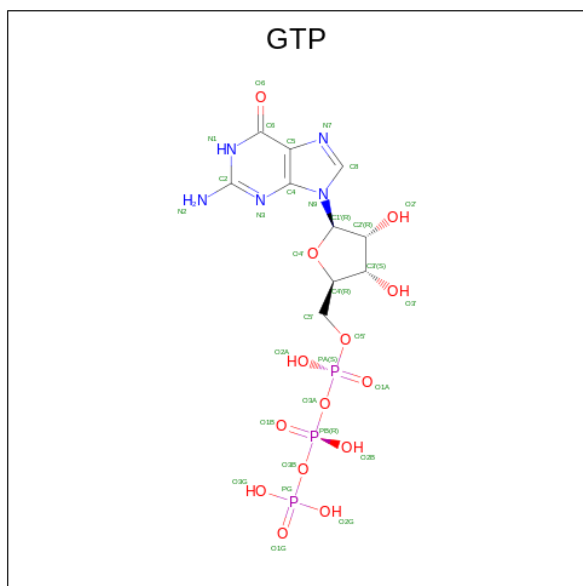
Mol	Chain	Residues	Atoms				AltConf	Trace
53	X1	151	Total	C	N	O	0	0
			755	453	151	151		

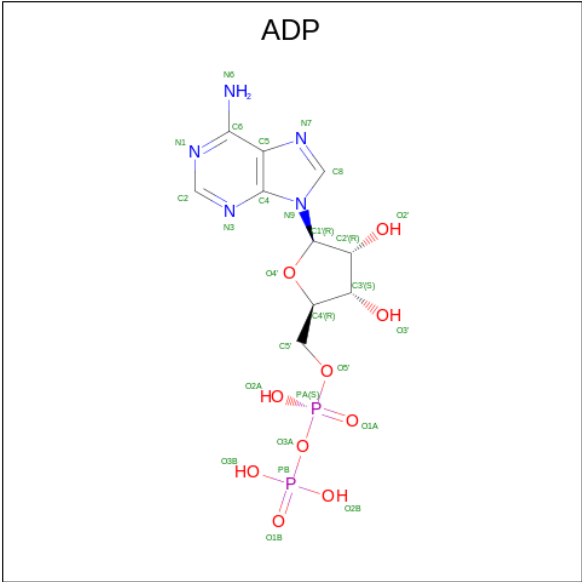
- Molecule 54 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
54	Sc	1	Total	Zn	0
			1	1	
54	5K	1	Total	Zn	0
			1	1	

- Molecule 55 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula:

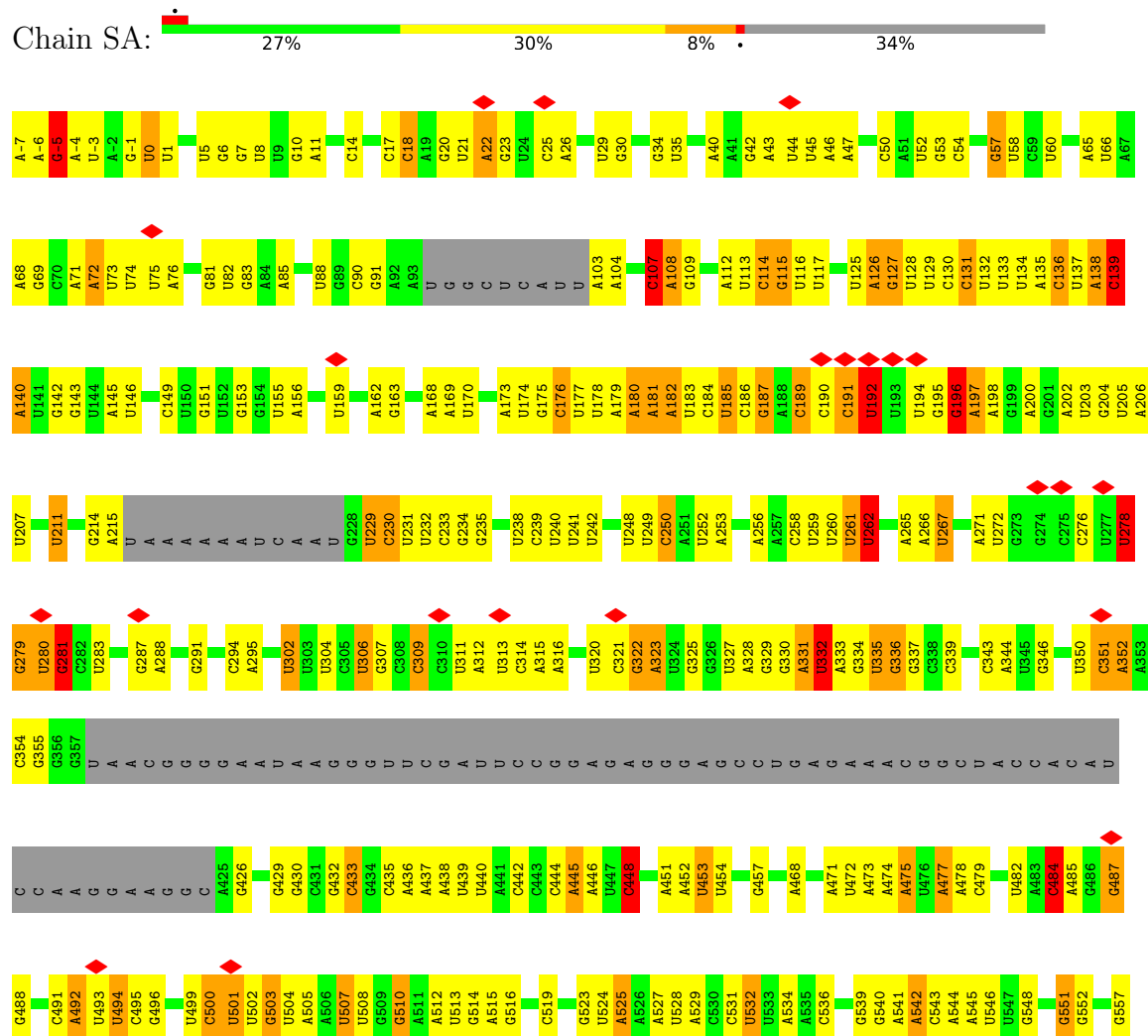
C₁₀H₁₆N₅O₁₄P₃).

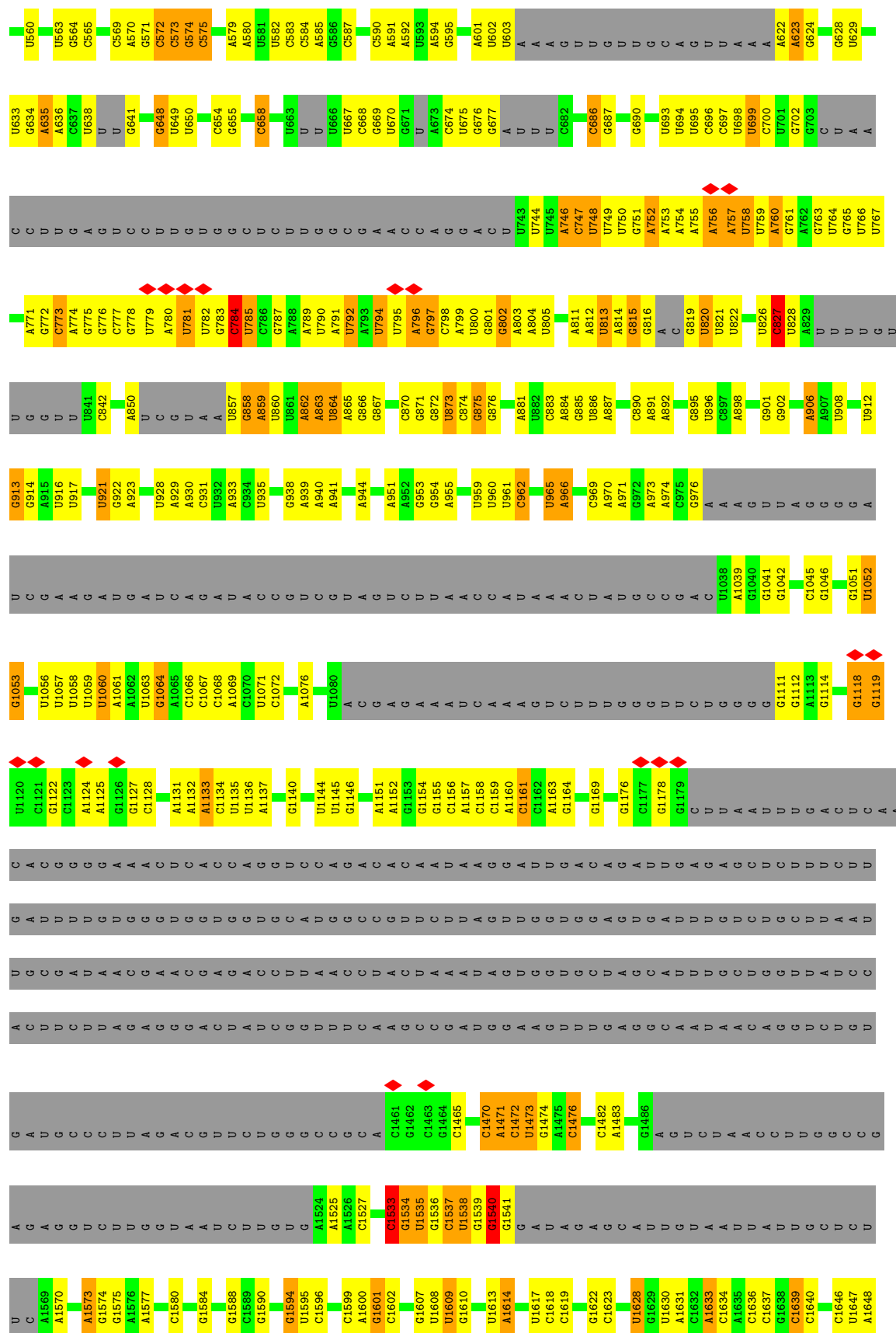




Mol	Chain	Residues	Atoms					AltConf
57	RZ	1	Total	C	N	O	P	0
			27	10	5	10	2	

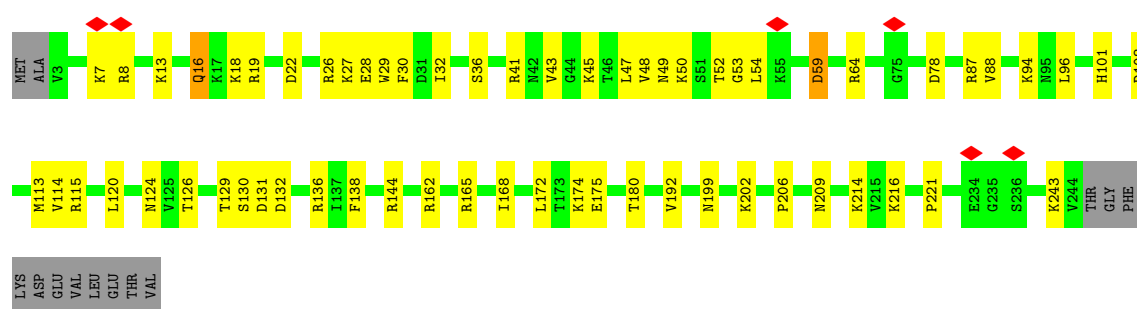
- Molecule 3: 18S rRNA



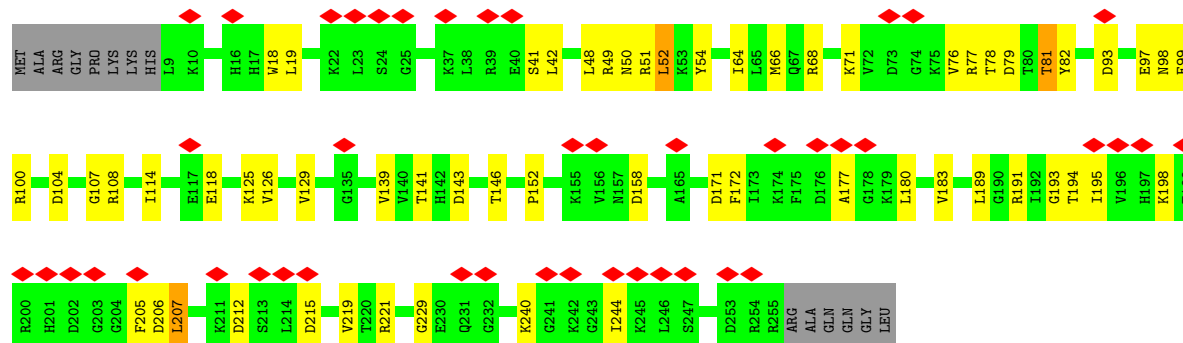
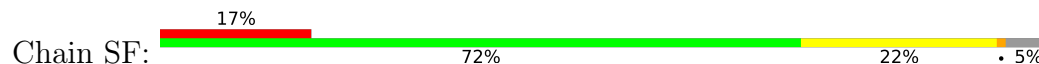




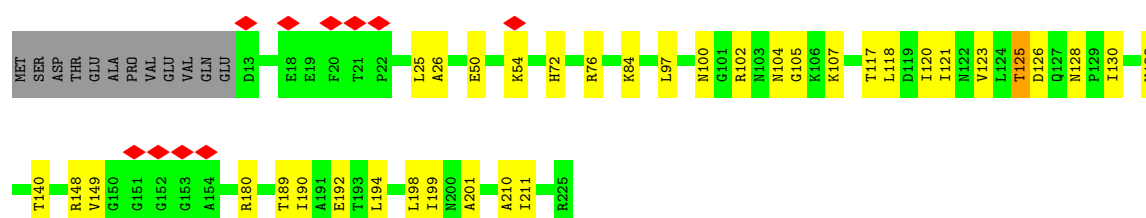
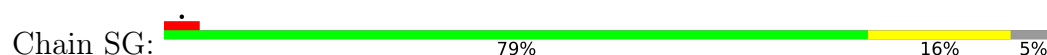
• Molecule 4: 40S ribosomal protein S1-A



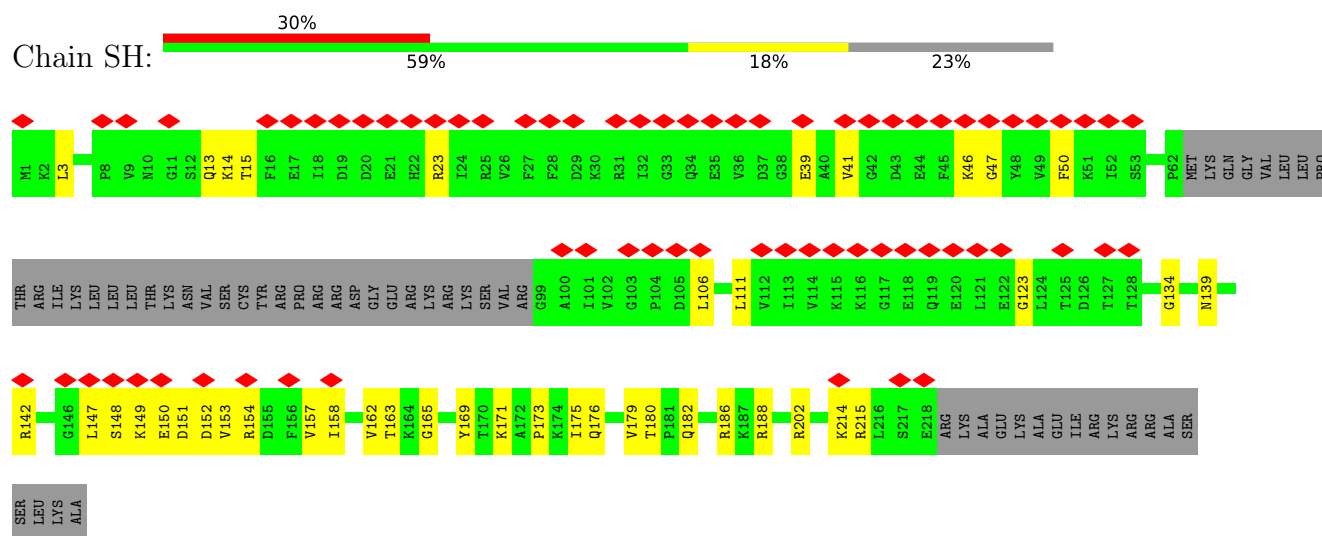
• Molecule 5: 40S ribosomal protein S4-A



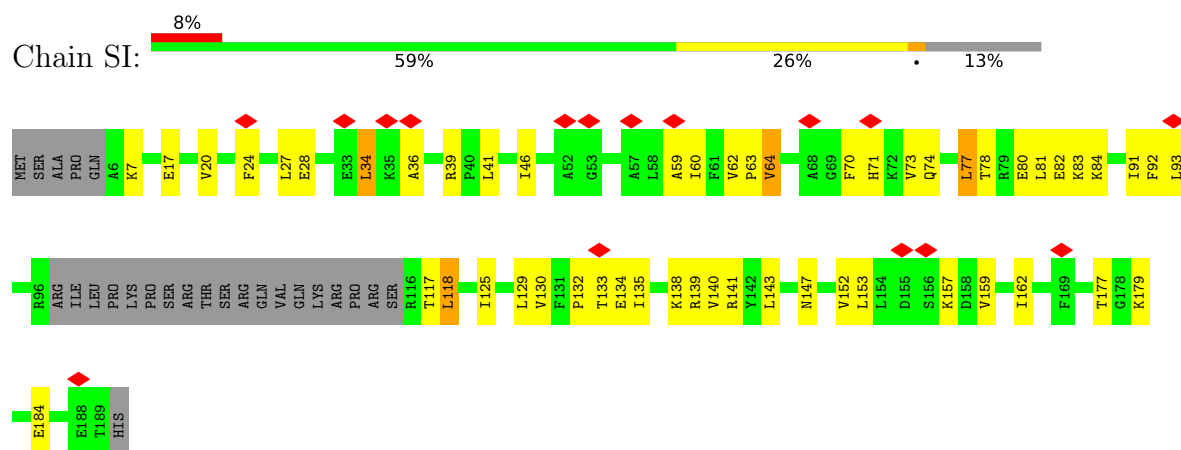
• Molecule 6: 40S ribosomal protein S5



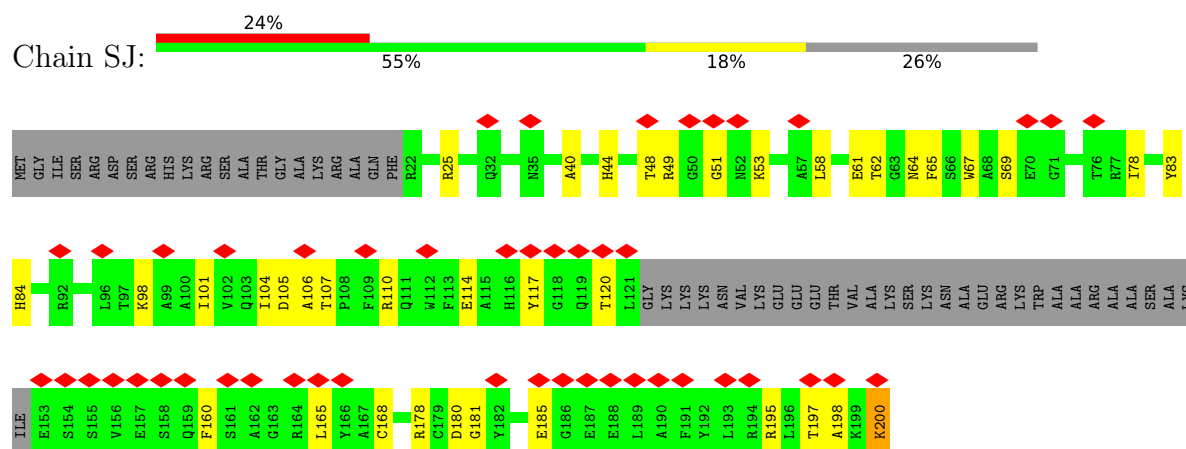
- Molecule 7: 40S ribosomal protein S6-A



- Molecule 8: 40S ribosomal protein S7-A

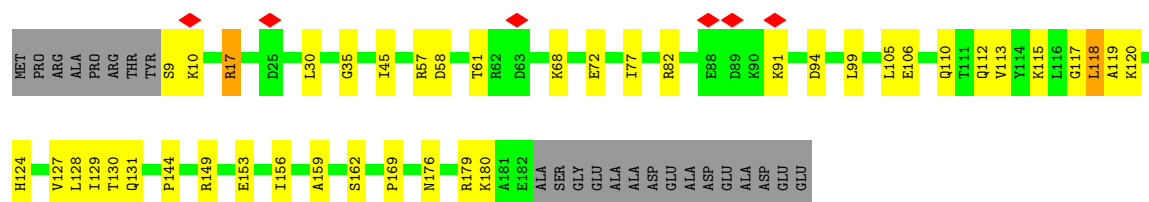


- Molecule 9: 40S ribosomal protein S8-A



- Molecule 10: 40S ribosomal protein S9-A





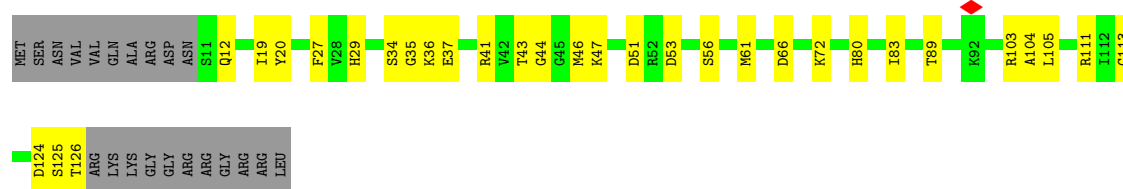
• Molecule 11: 40S ribosomal protein S11-A



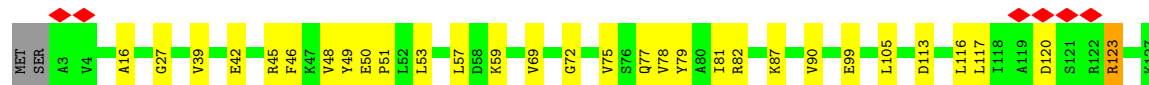
• Molecule 12: 40S ribosomal protein S13



• Molecule 13: 40S ribosomal protein S14-A




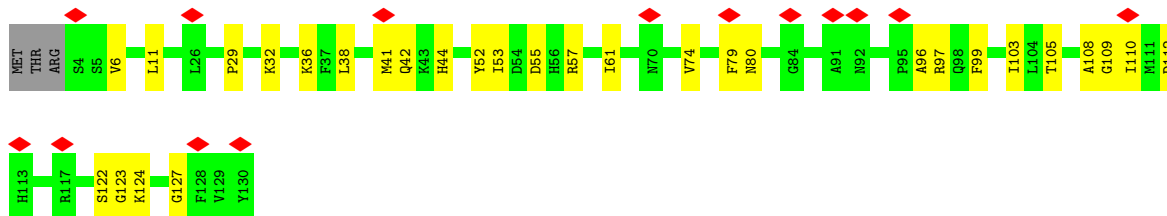
• Molecule 14: 40S ribosomal protein S16-A



LYS
PHE
GLY
GLY
LYS
GLY
ALA
ARG
SER
ARG
PHE
GLN
LYS
SER
TYR
ARG

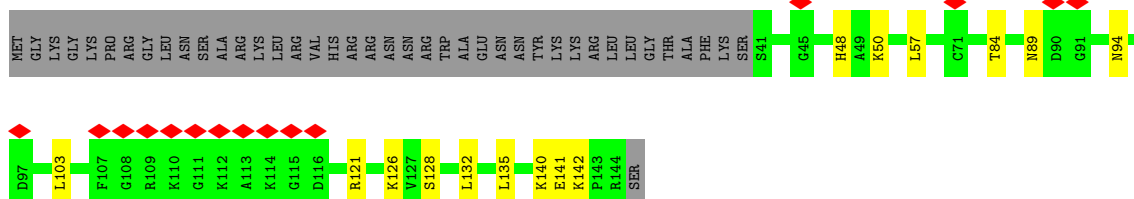
• Molecule 15: 40S ribosomal protein S22-B

Chain SX: 



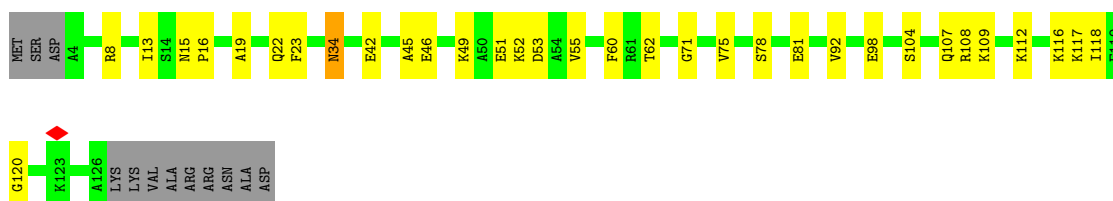
• Molecule 16: 40S ribosomal protein S23-A

Chain SY: 



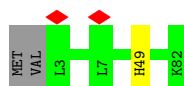
• Molecule 17: 40S ribosomal protein S24-A

Chain SZ: 



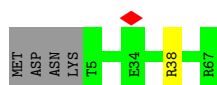
• Molecule 18: 40S ribosomal protein S27-A

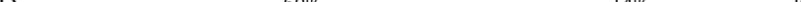
Chain Sc: 



• Molecule 19: 40S ribosomal protein S28-A

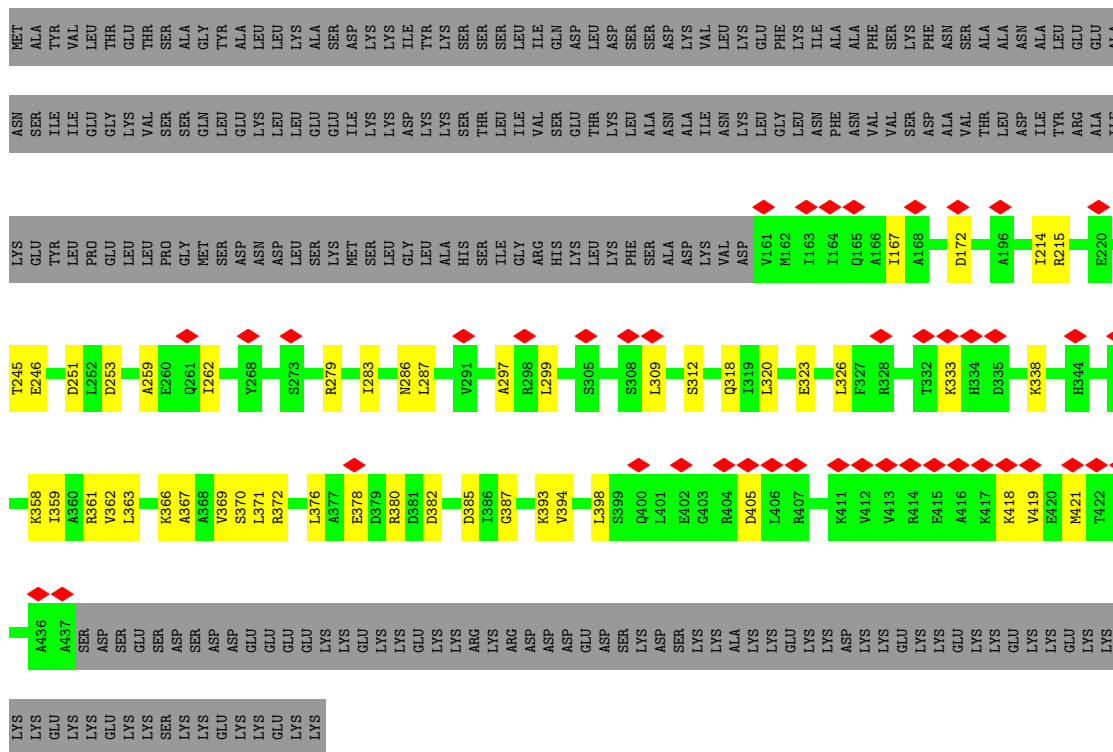
Chain Sd: 



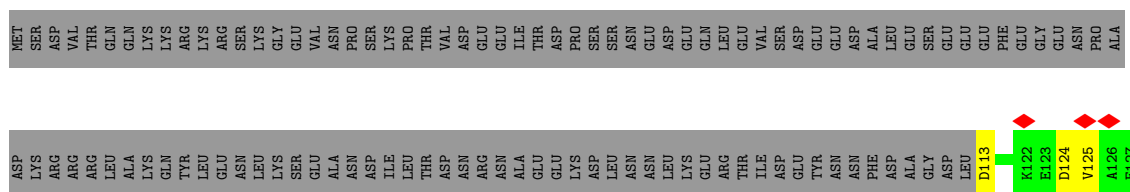
Chain 3B: 

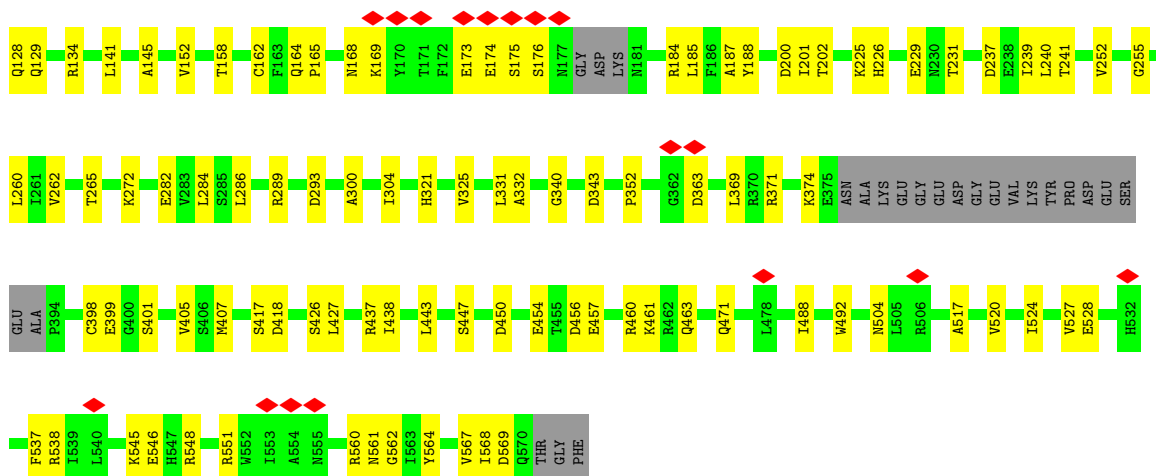


- Molecule 22: Nucleolar protein 58

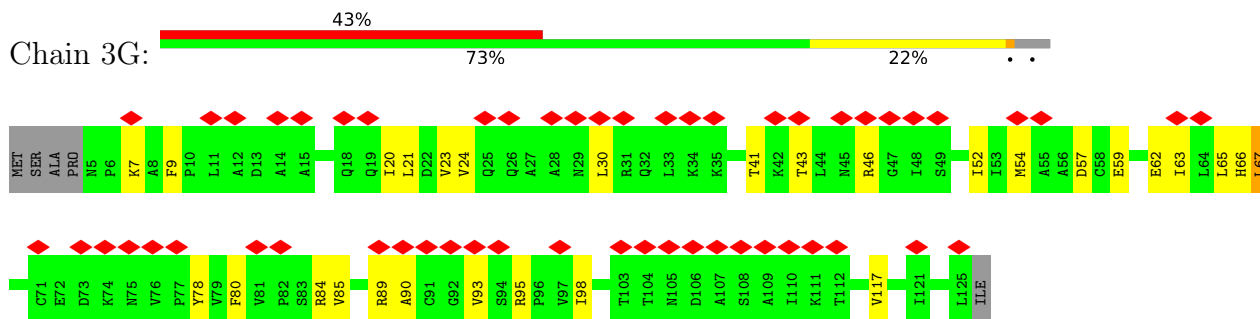


- Molecule 23: Ribosomal RNA-processing protein 9

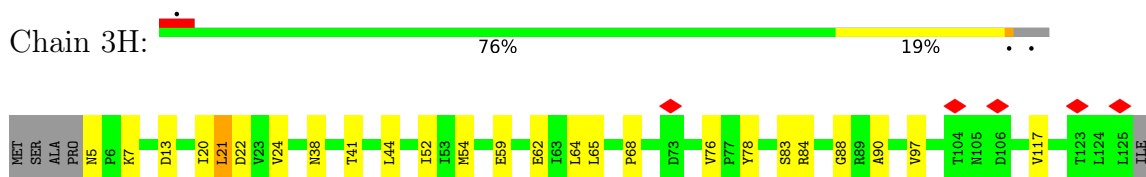




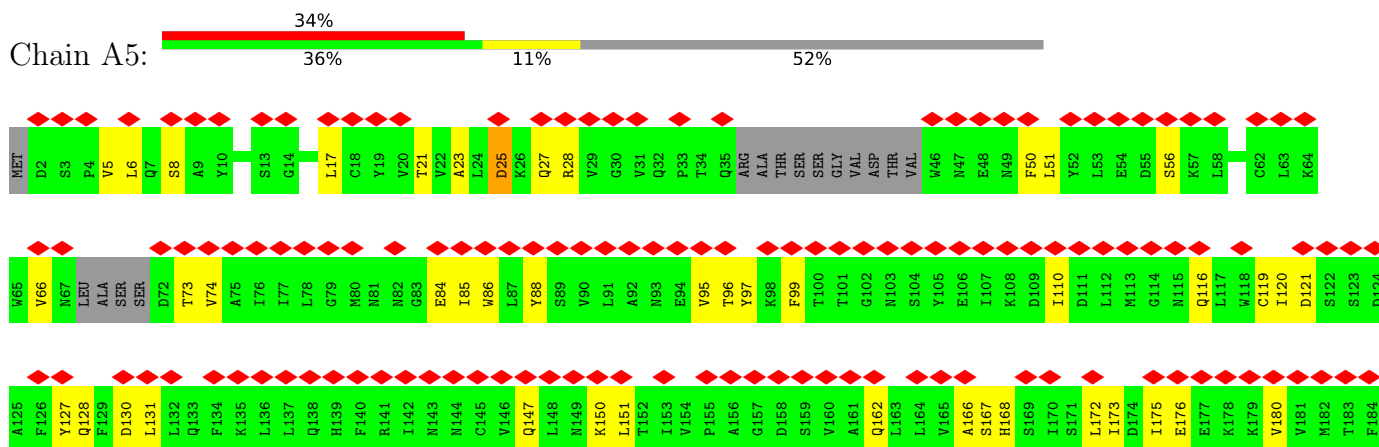
- Molecule 24: 13 kDa ribonucleoprotein-associated protein



- Molecule 24: 13 kDa ribonucleoprotein-associated protein

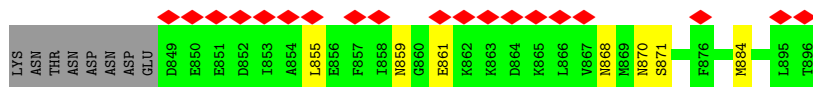


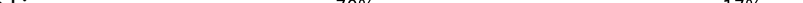
- Molecule 25: U3 small nucleolar RNA-associated protein 5

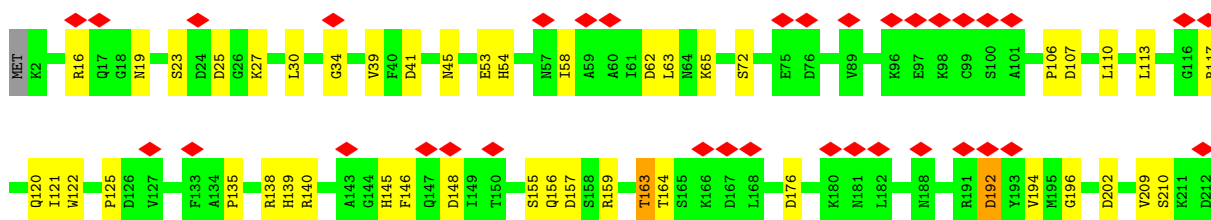


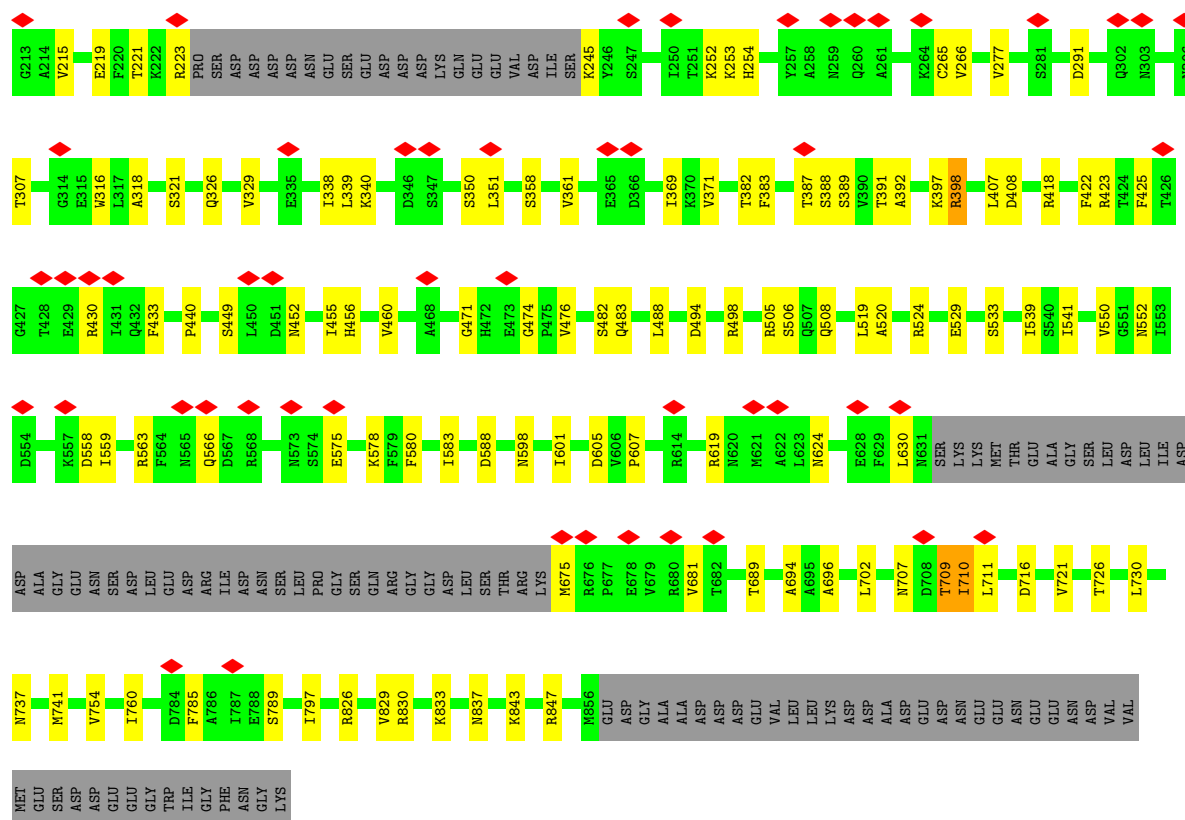


- Molecule 27: NET1-associated nuclear protein 1

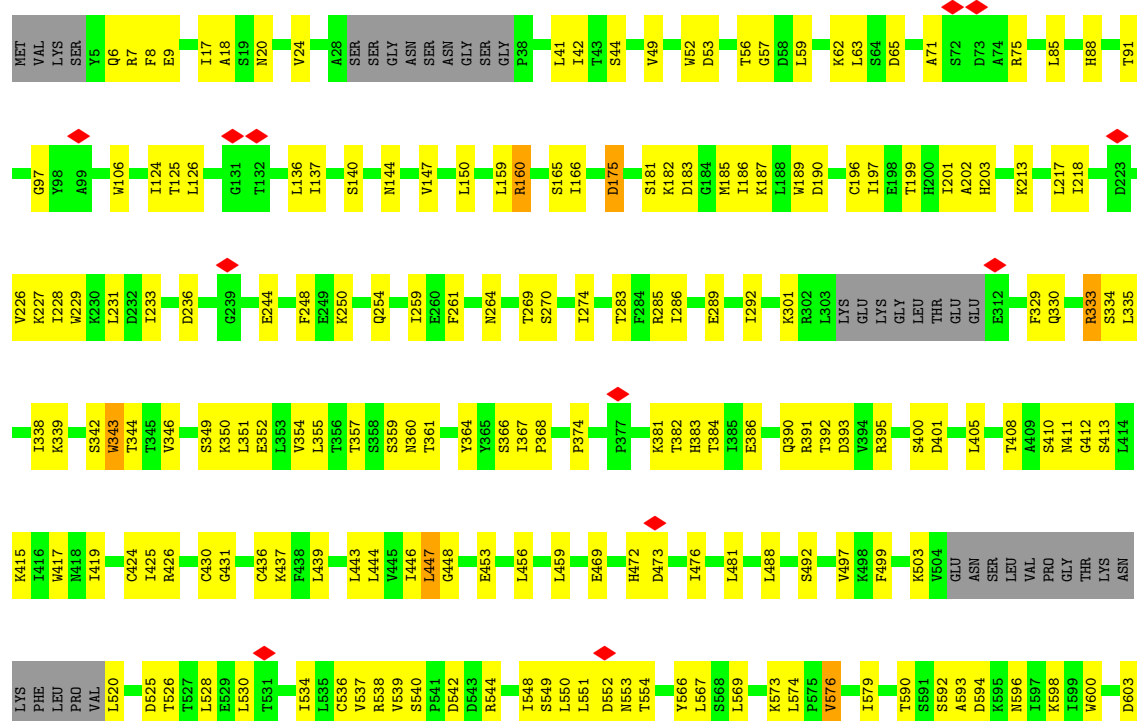
[illegible]

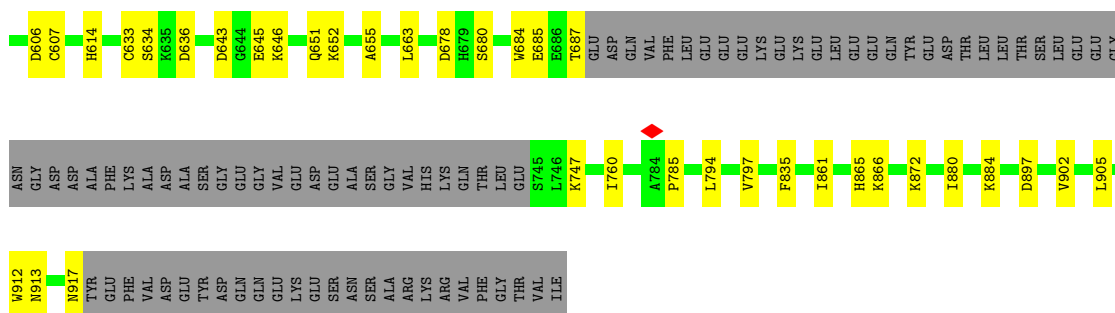
Chain B1: 



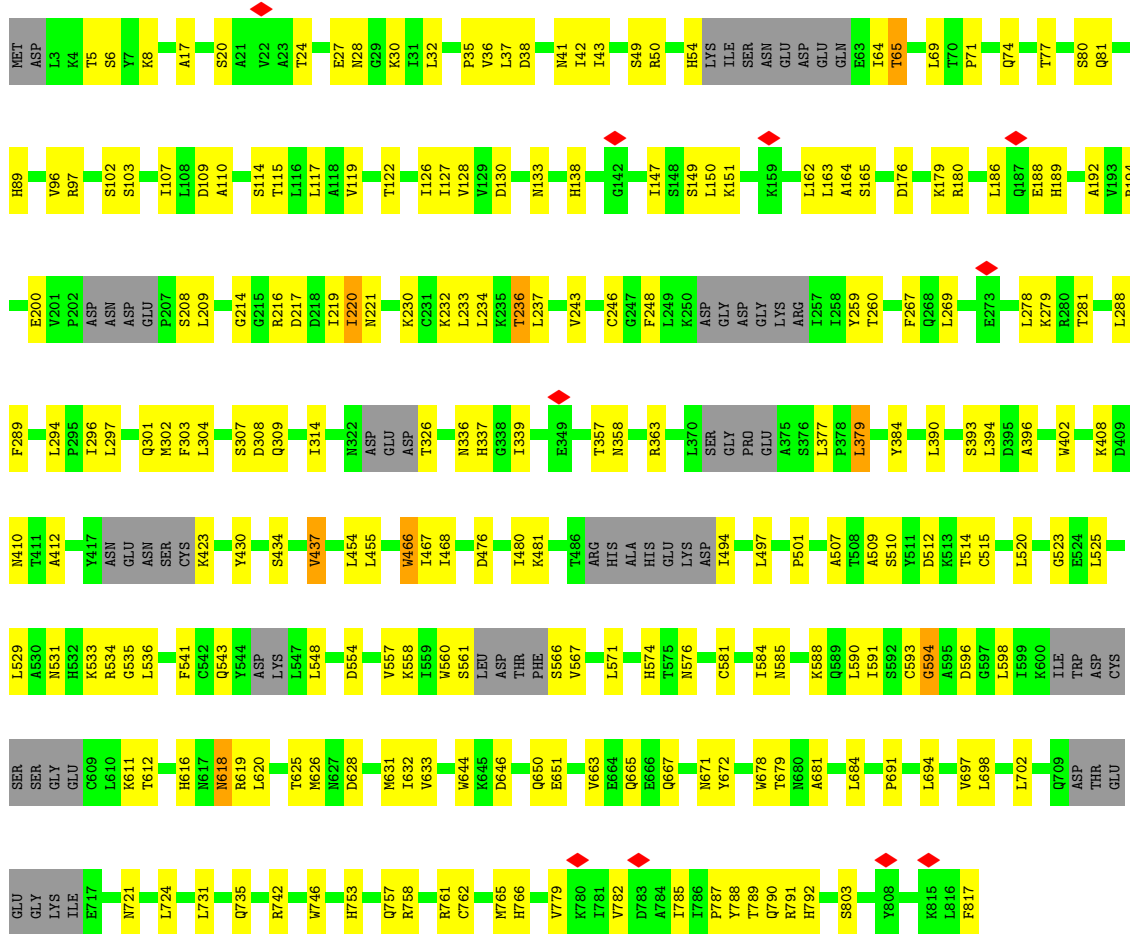


• Molecule 29: U3 small nucleolar RNA-associated protein 12

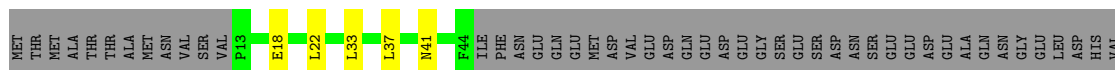
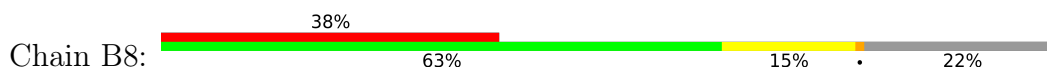


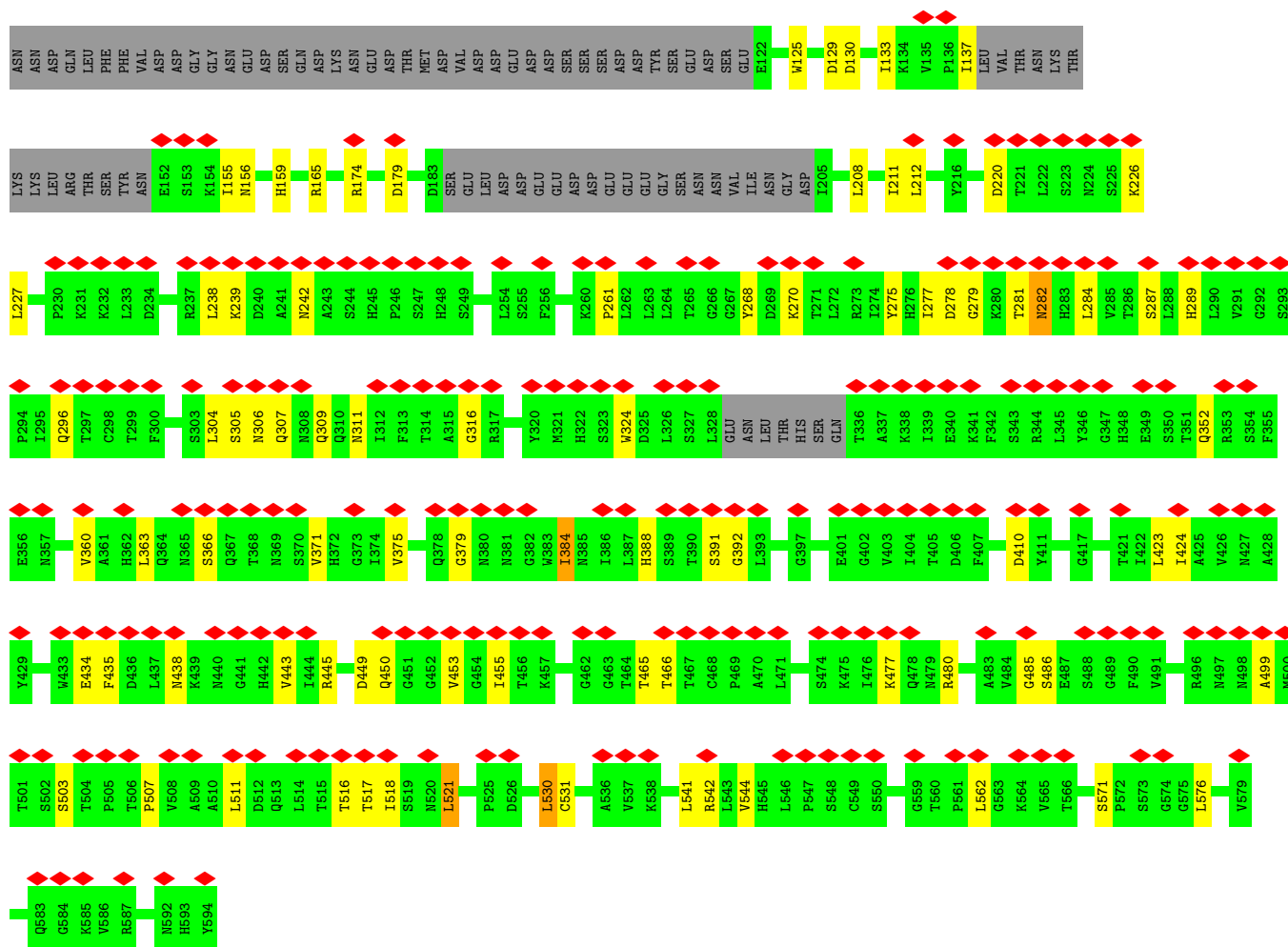


- Molecule 30: U3 small nucleolar RNA-associated protein 13

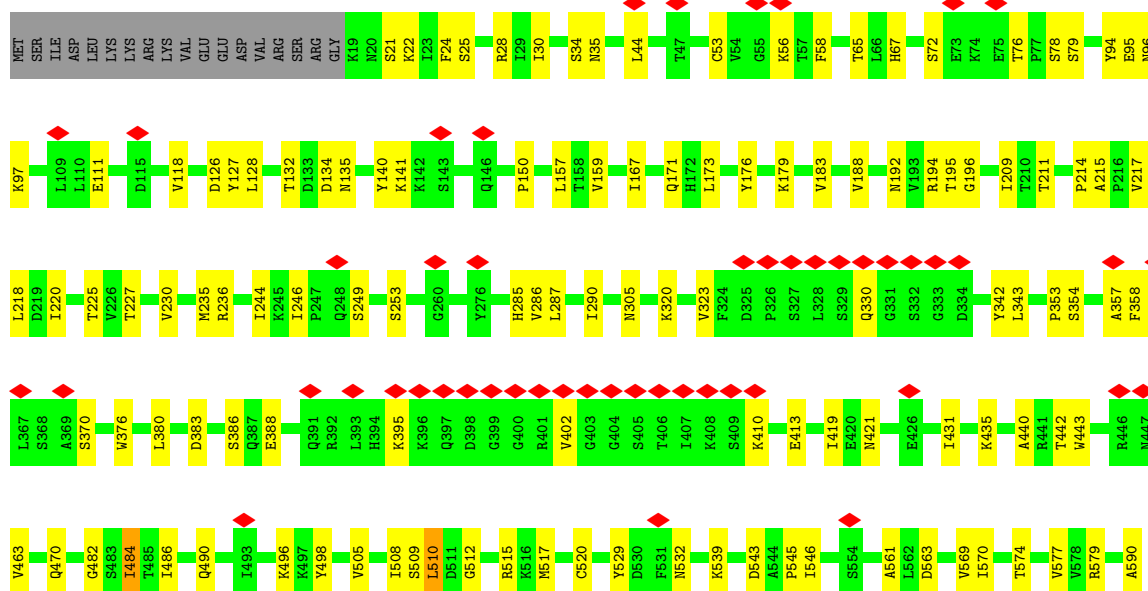
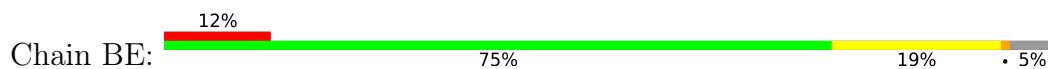


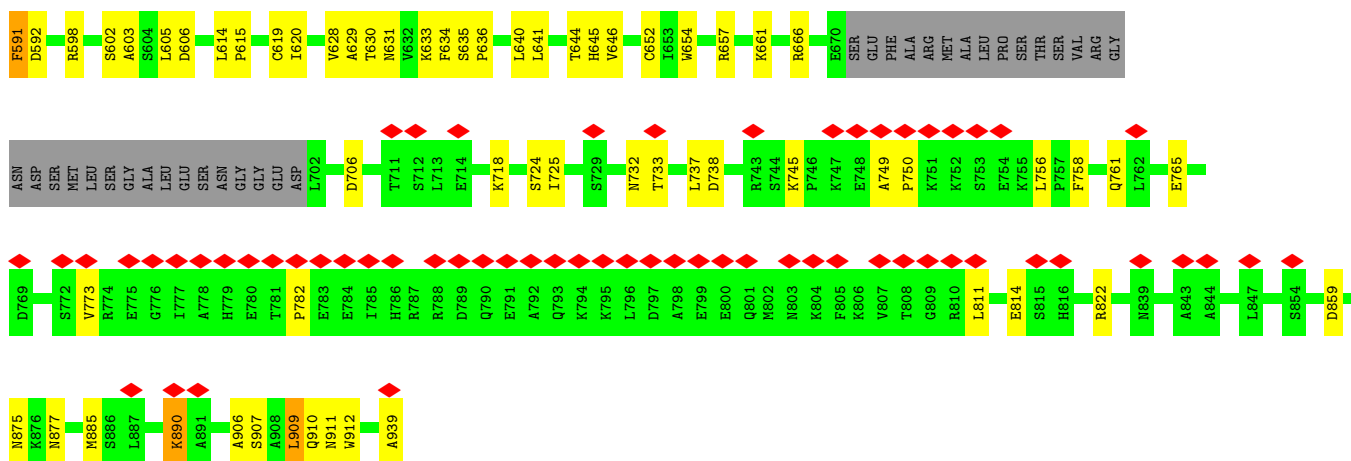
- Molecule 31: U3 small nucleolar RNA-associated protein 18



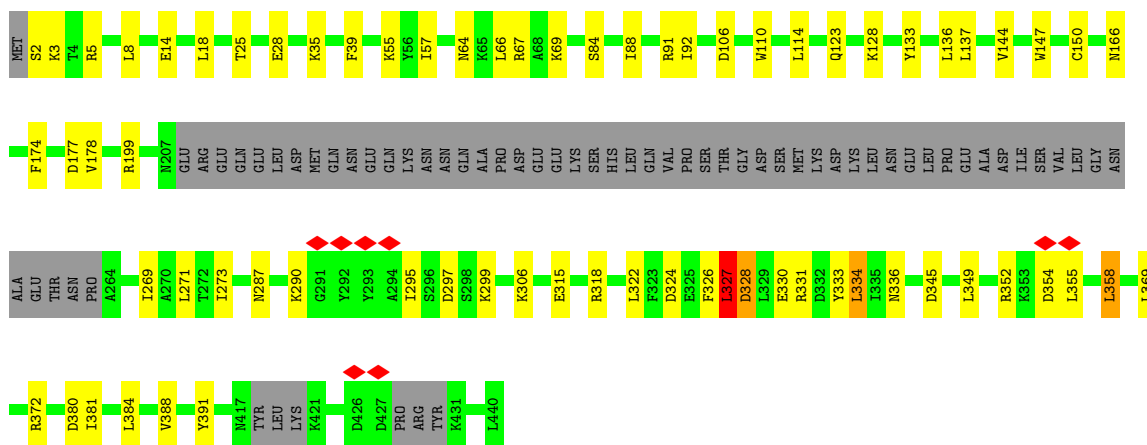


• Molecule 32: U3 small nucleolar RNA-associated protein 21

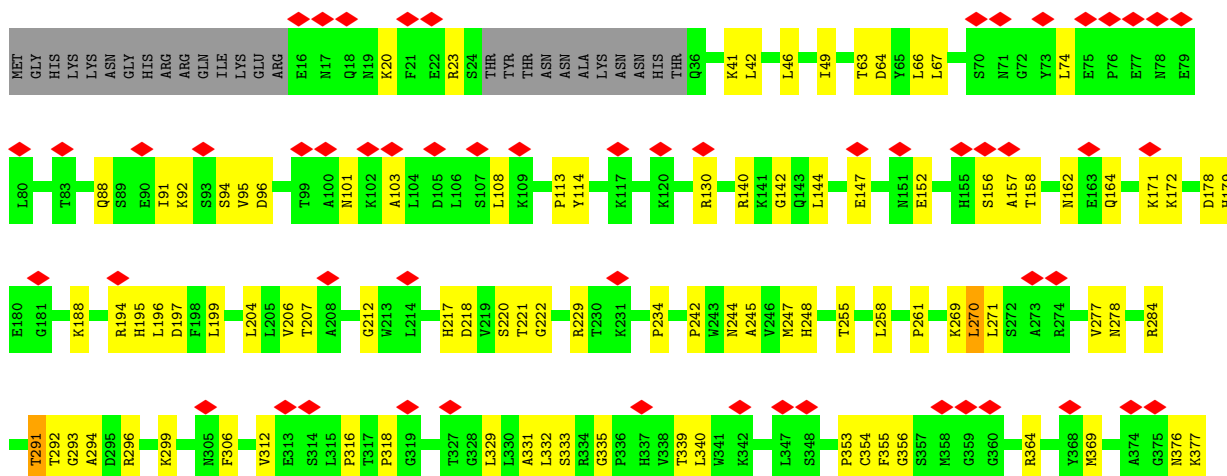




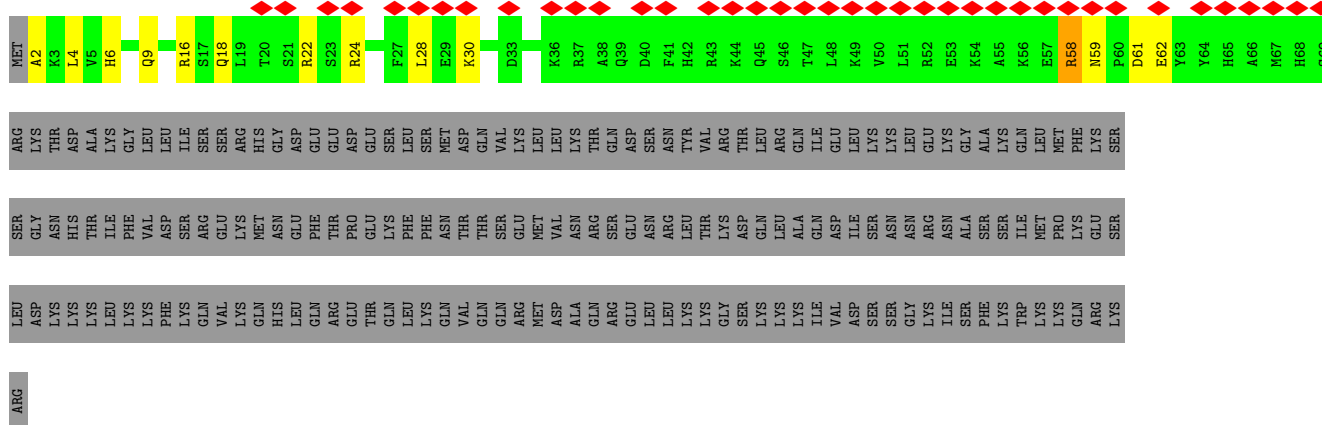
• Molecule 33: U3 small nucleolar RNA-associated protein 6



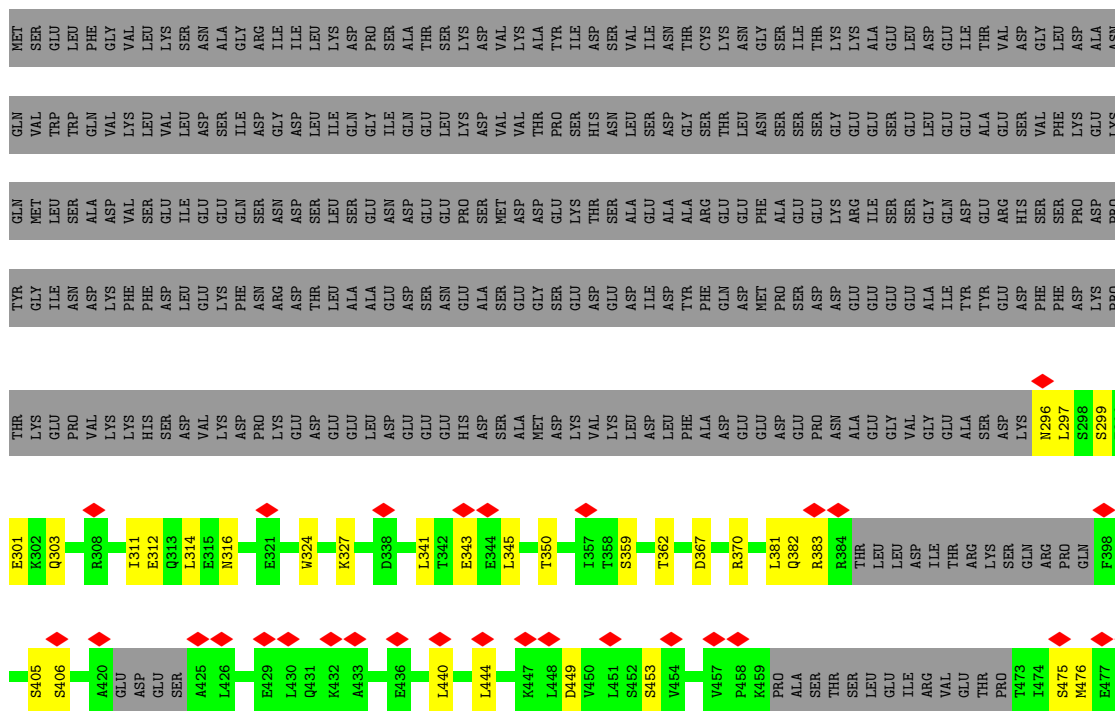
• Molecule 34: U3 small nucleolar RNA-associated protein 7

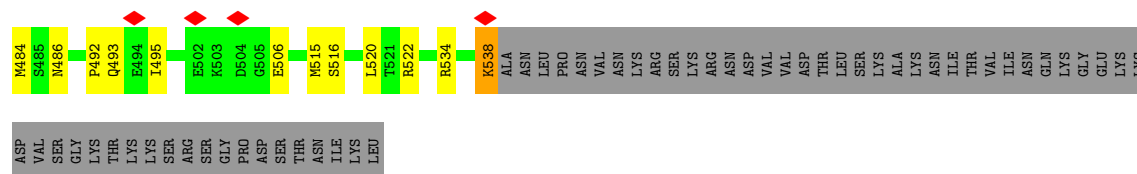


- Molecule 35: U3 small nucleolar RNA-associated protein 11

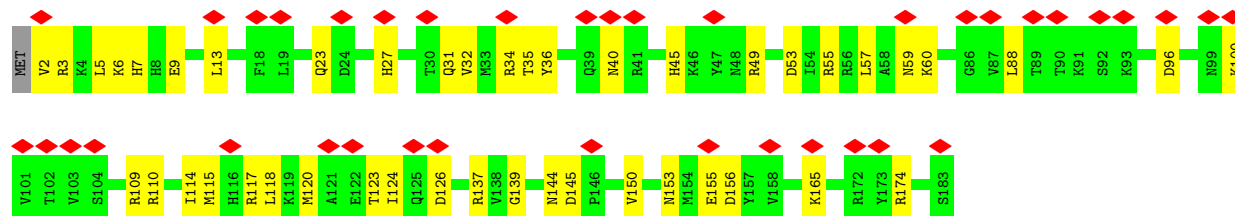
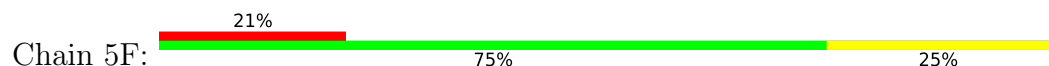


- Molecule 36: U3 small nucleolar RNA-associated protein MPP10

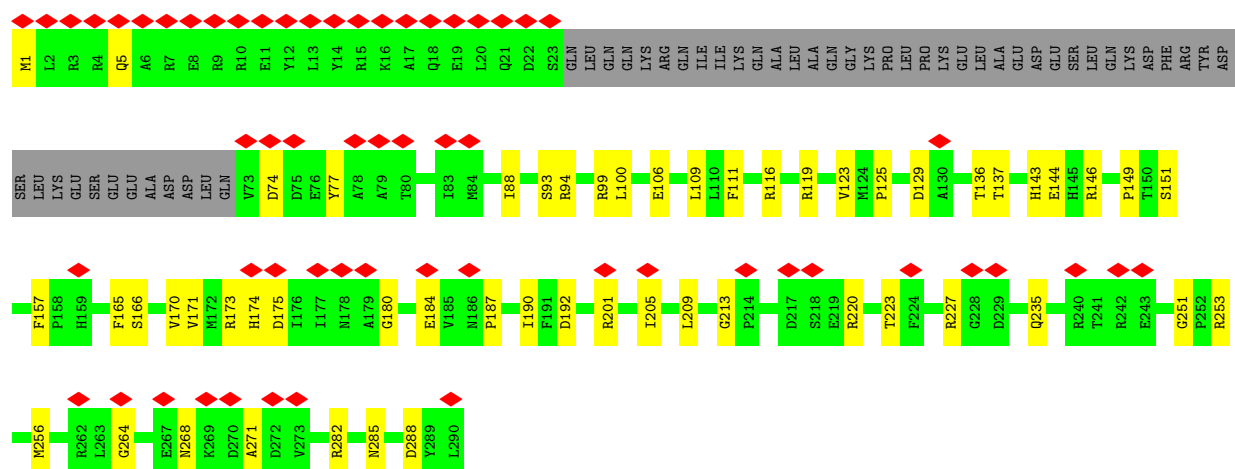




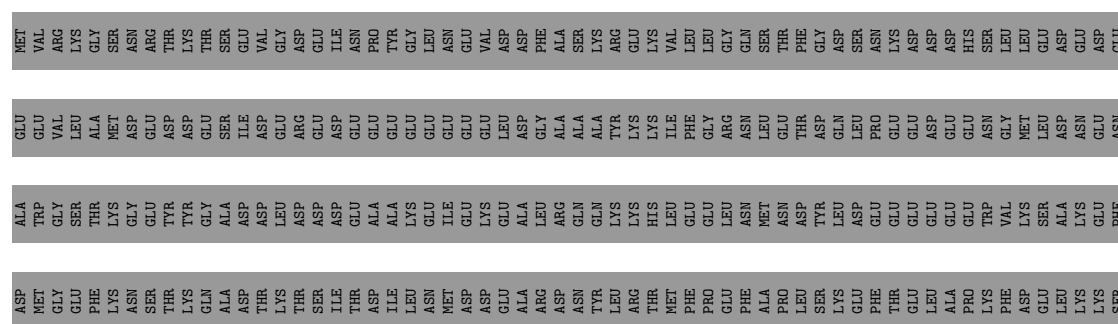
- Molecule 37: U3 small nucleolar ribonucleoprotein protein IMP3



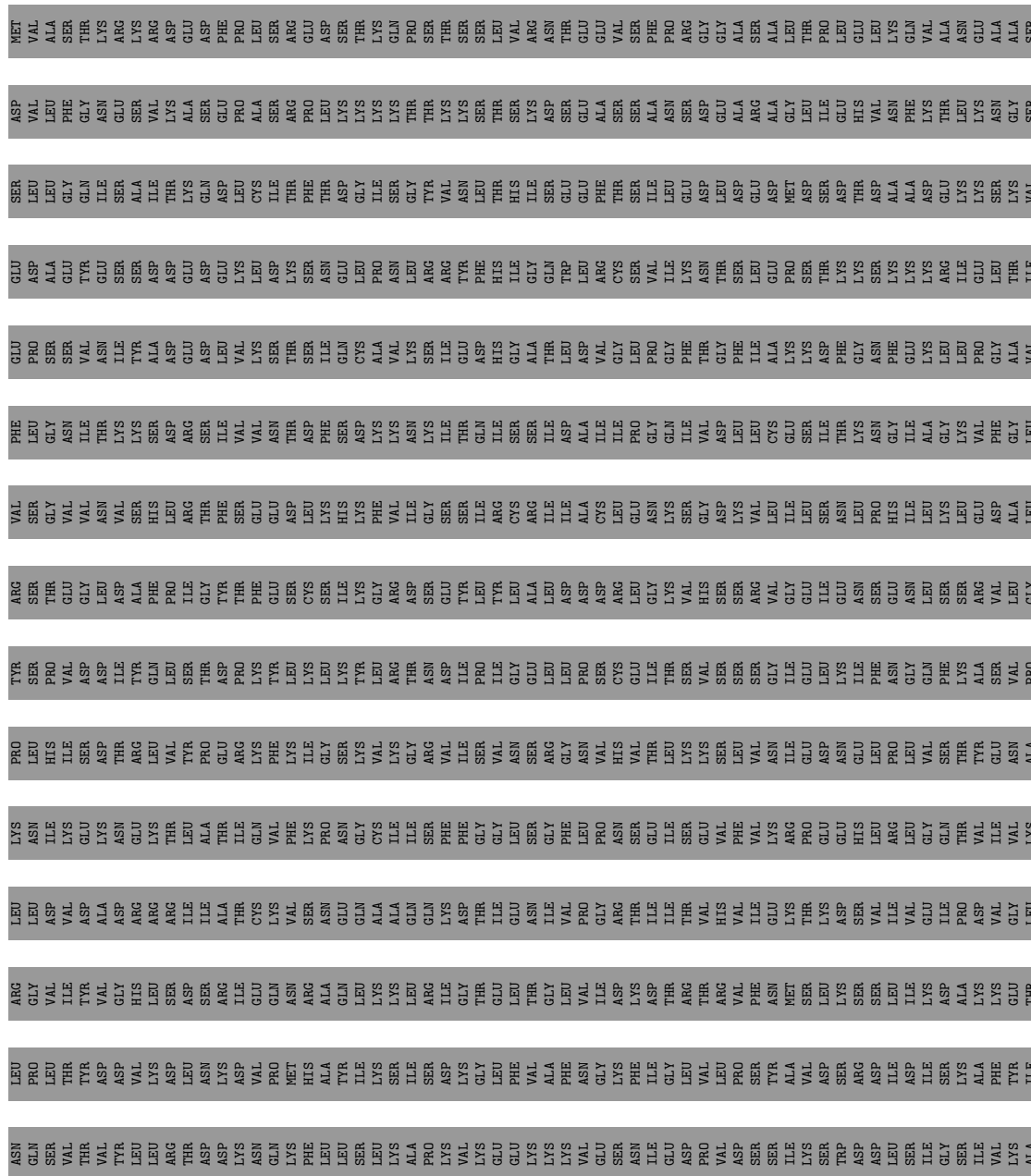
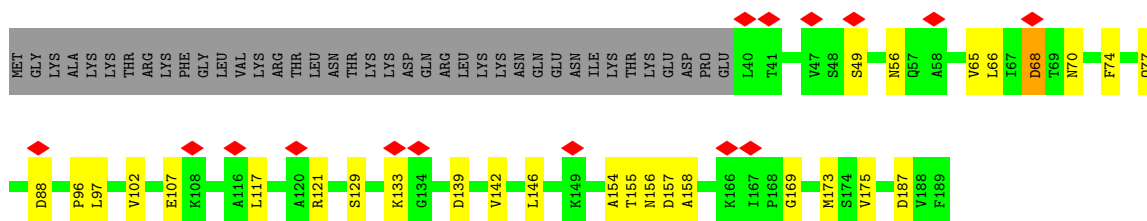
- Molecule 38: U3 small nucleolar ribonucleoprotein protein IMP4



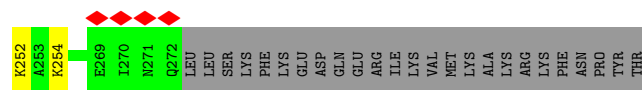
- Molecule 39: Something about silencing protein 10



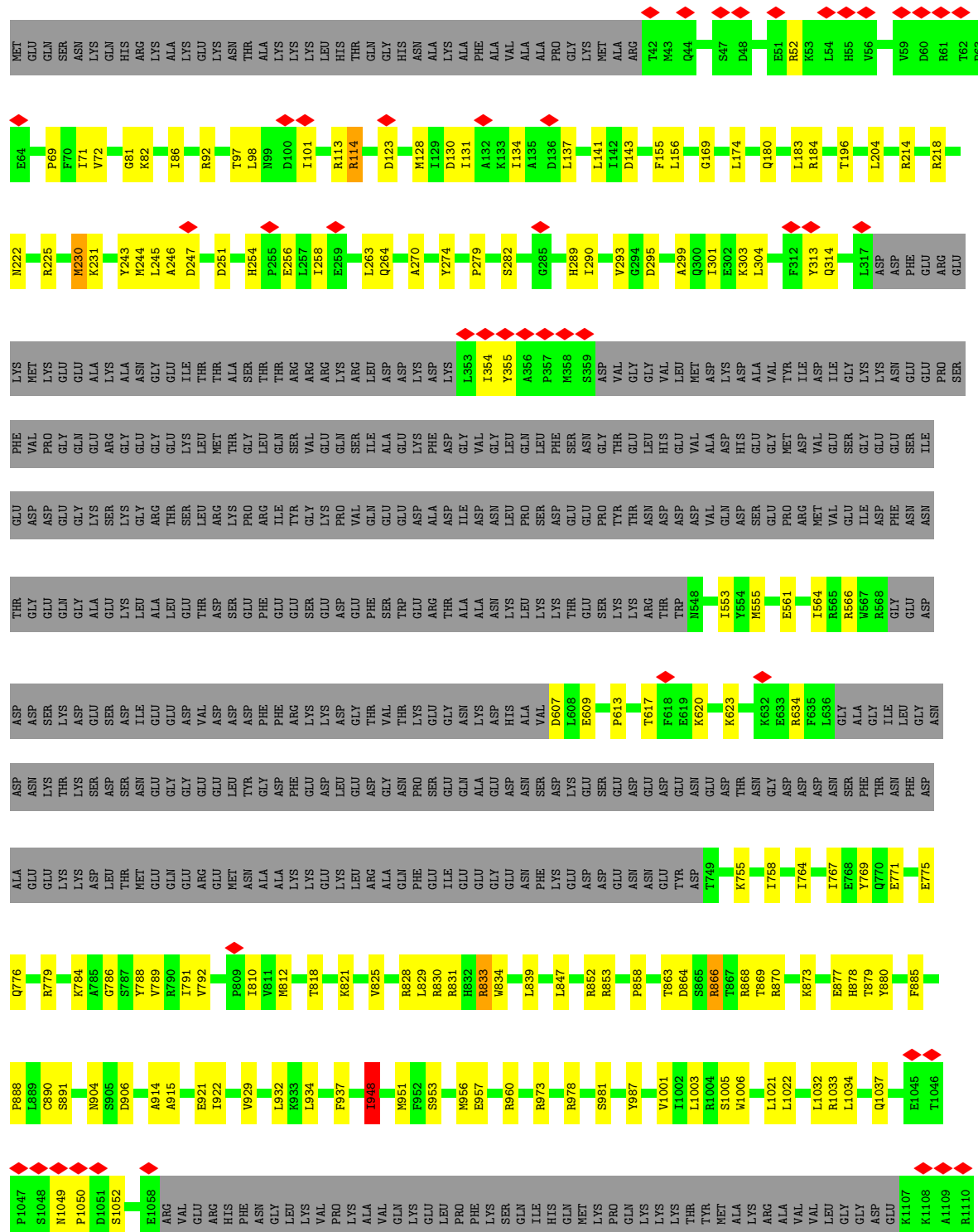


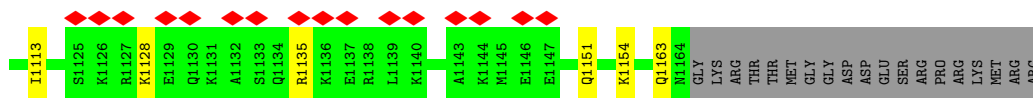




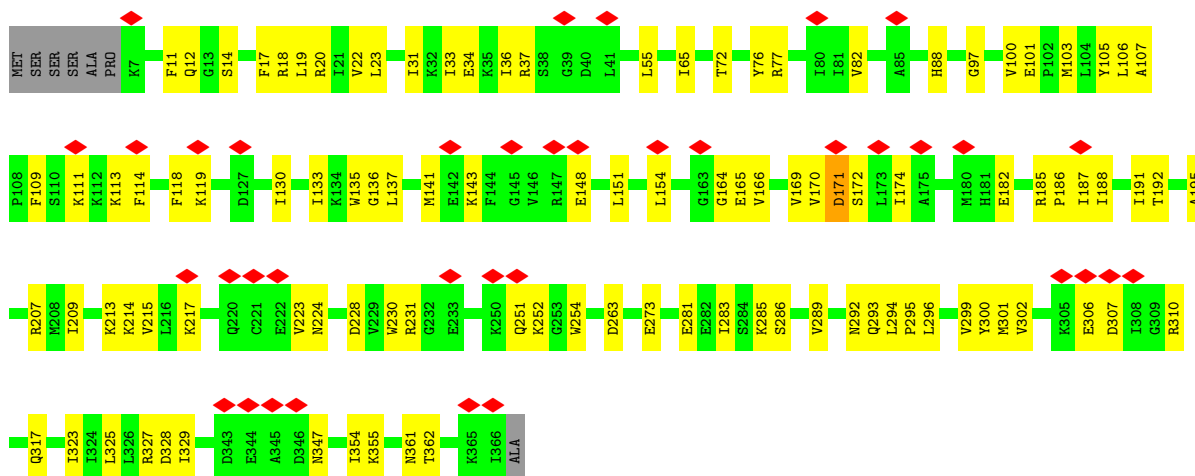


• Molecule 46: Ribosome biogenesis protein BMS1

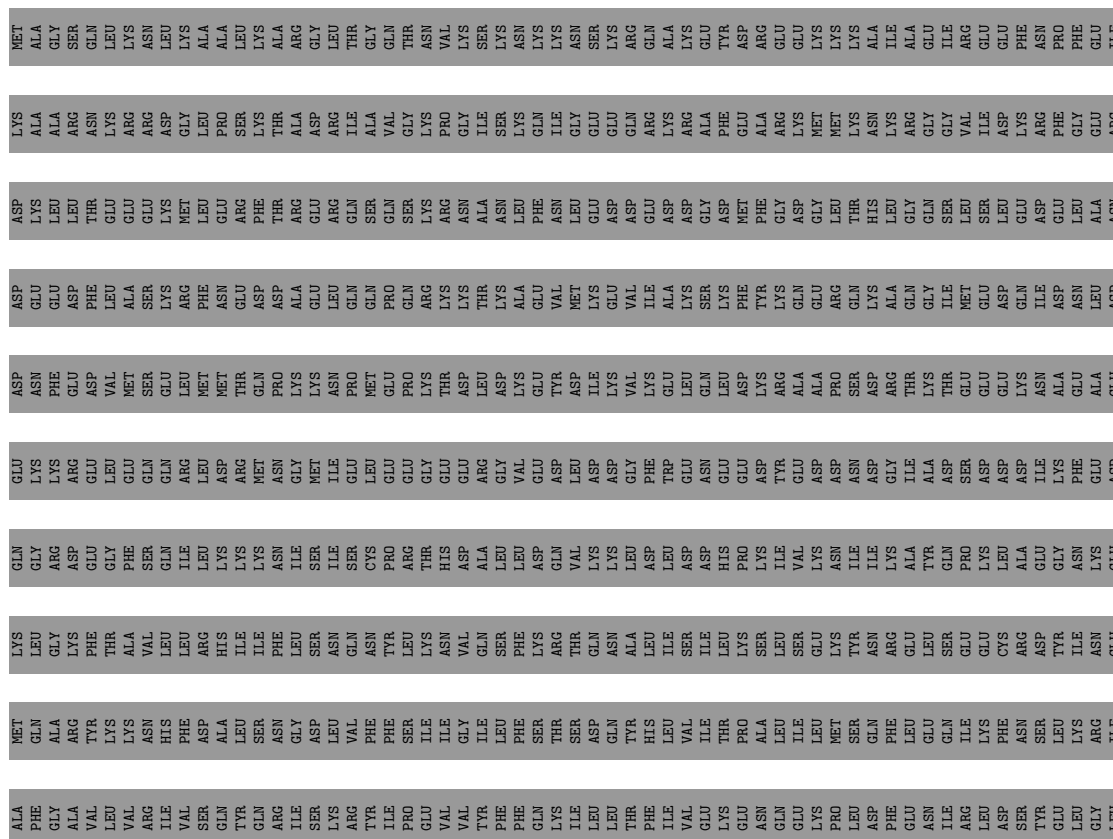




• Molecule 47: RNA 3'-terminal phosphate cyclase-like protein



• Molecule 48: Nucleolar complex protein 14



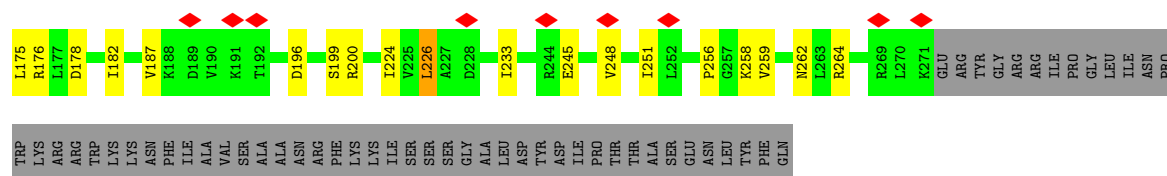
- Molecule 49: U3 small nucleolar RNA-associated protein 20



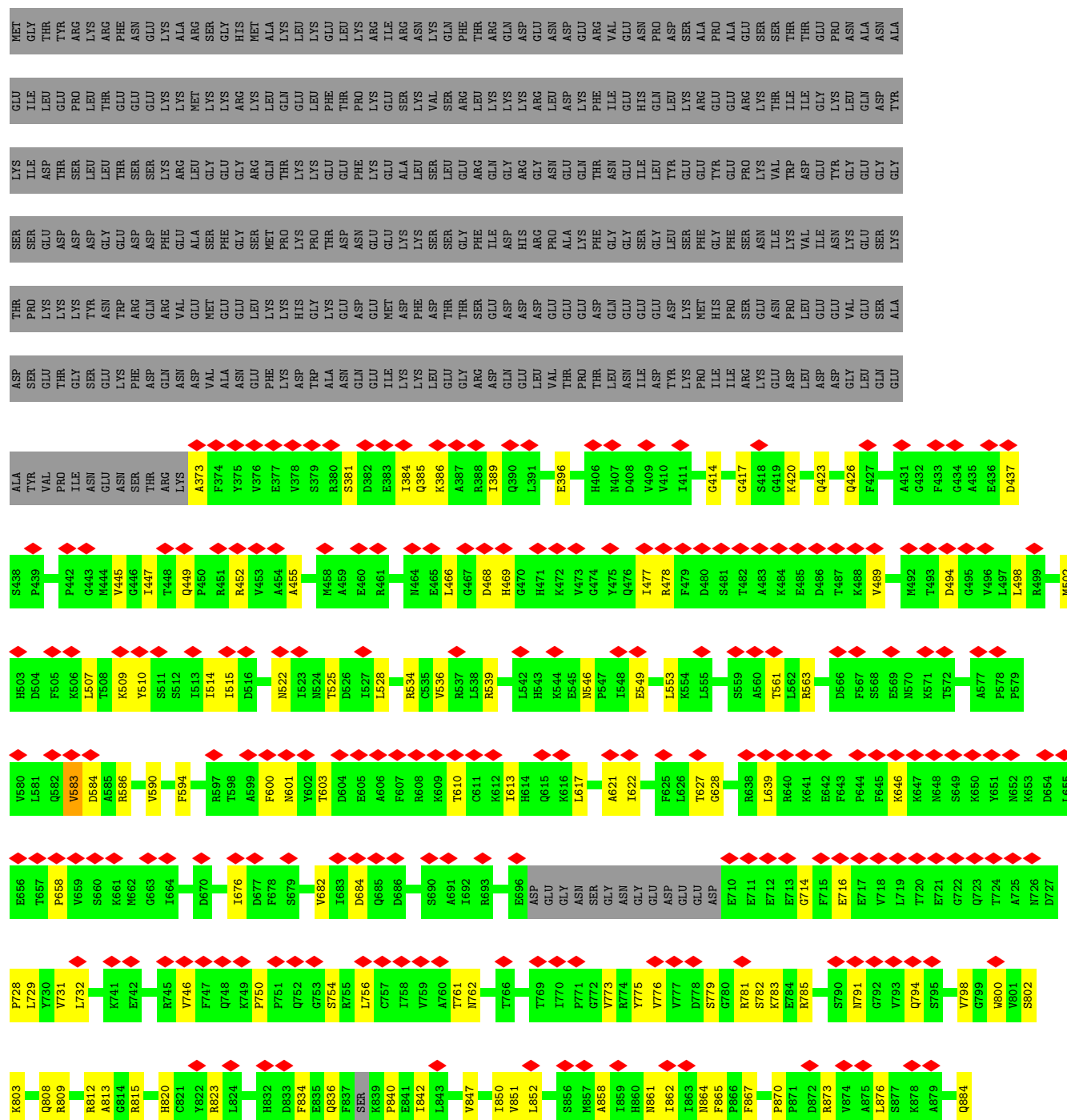
- Molecule 50: U3 small nucleolar RNA-associated protein 14

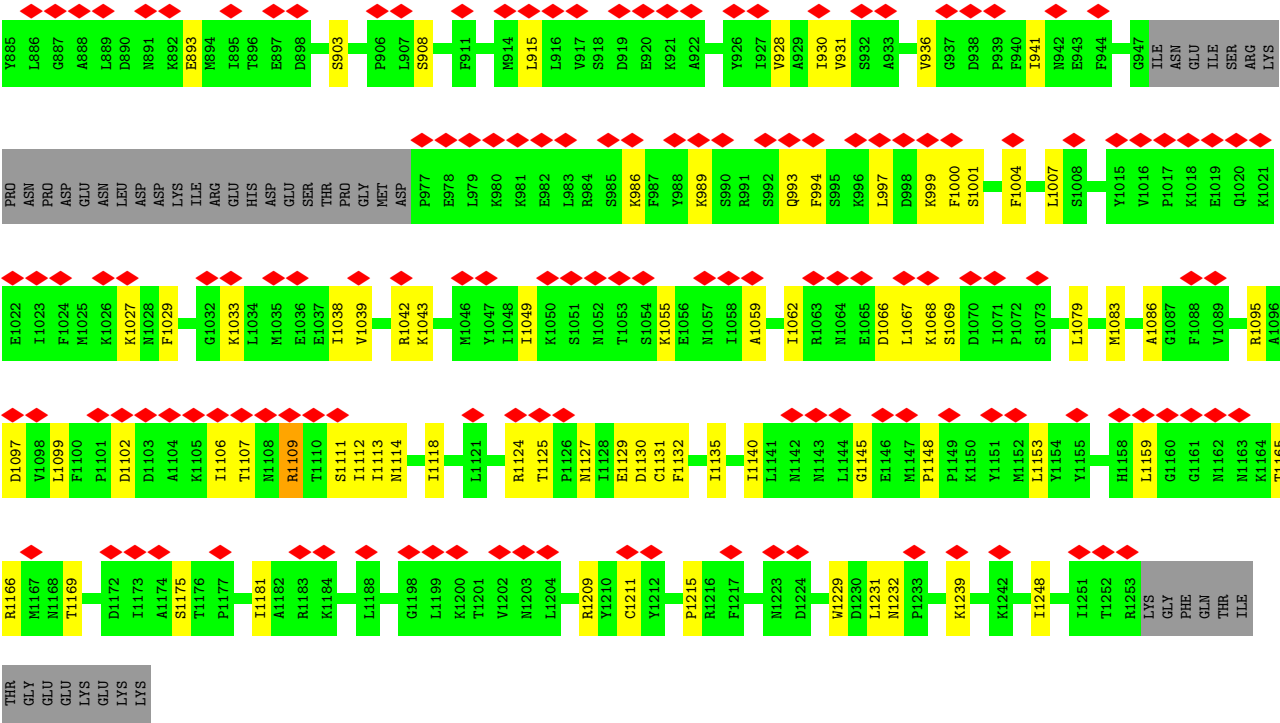




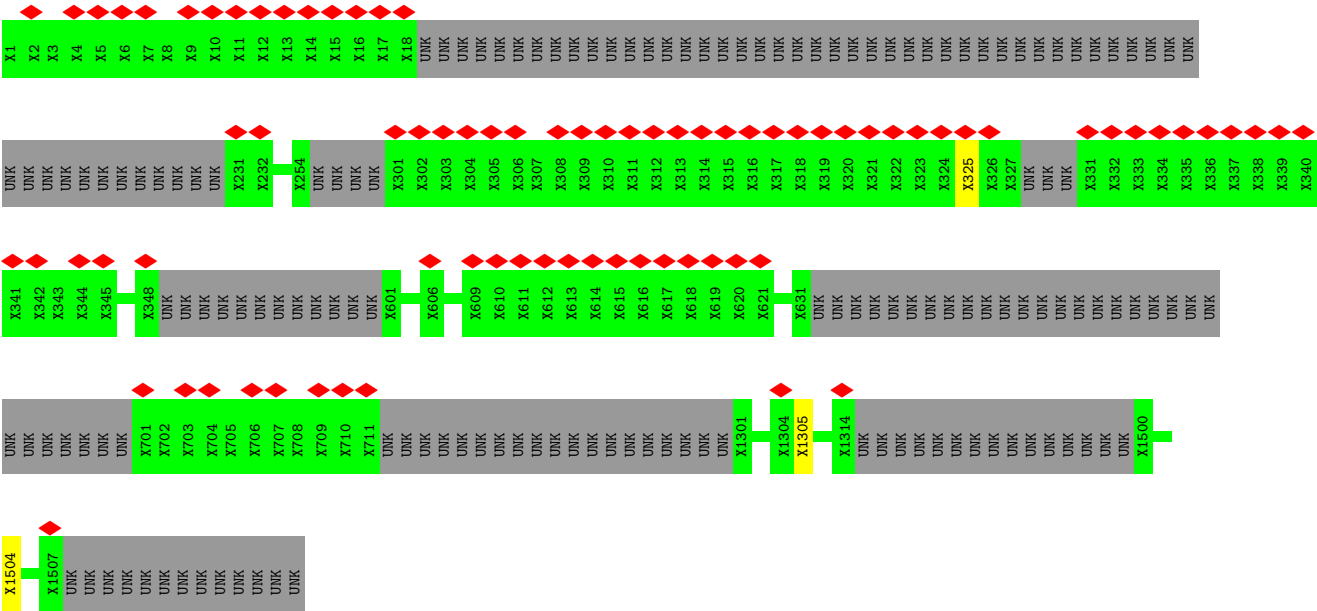


● Molecule 52: Probable ATP-dependent RNA helicase DHR1





• Molecule 53: Unassigned peptides 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	62400	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	0.051	Depositor
Minimum map value	-0.014	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	531.19995, 531.19995, 531.19995	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3279998, 1.3279998, 1.3279998	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, ADP, 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	0.66	0/3940	1.21	37/6120 (0.6%)
2	5A	0.42	0/1035	1.22	7/1608 (0.4%)
3	SA	0.58	0/28317	1.18	194/44080 (0.4%)
4	SC	0.39	0/1949	0.66	2/2609 (0.1%)
5	SF	0.37	0/1954	0.65	1/2640 (0.0%)
6	SG	0.38	0/1690	0.61	0/2285
7	SH	0.29	0/1476	0.56	1/1975 (0.1%)
8	SI	0.36	0/1341	0.76	3/1806 (0.2%)
9	SJ	0.30	0/1202	0.58	0/1610
10	SK	0.41	0/1432	0.65	2/1917 (0.1%)
11	SM	0.29	0/1139	0.52	0/1535
12	SO	0.37	0/1109	0.57	0/1495
13	SP	0.37	0/859	0.63	0/1161
14	SR	0.46	0/990	0.63	0/1335
15	SX	0.39	0/1020	0.64	0/1371
16	SY	0.40	0/804	0.57	0/1074
17	SZ	0.44	0/1000	0.66	0/1334
18	Sc	0.38	0/613	0.62	0/828
19	Sd	0.41	0/499	0.60	0/670
20	3B	0.50	0/1914	0.66	1/2582 (0.0%)
20	3C	0.41	0/1787	0.66	2/2413 (0.1%)
21	3D	0.41	0/3020	0.60	2/4066 (0.0%)
22	3E	0.40	0/2155	0.62	1/2910 (0.0%)
23	3F	0.45	0/3569	0.62	0/4806
24	3G	0.42	0/928	0.74	2/1262 (0.2%)
24	3H	0.46	0/928	0.74	2/1262 (0.2%)
25	A5	0.41	0/2500	0.64	2/3393 (0.1%)
26	AE	0.39	0/3500	0.59	1/4736 (0.0%)
27	AG	0.37	0/398	0.53	0/532
28	B1	0.43	0/6459	0.63	0/8744
29	B2	0.38	0/6624	0.65	3/8950 (0.0%)
30	B3	0.37	0/6001	0.66	3/8120 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	B8	0.44	0/3730	0.63	3/5058 (0.1%)
32	BE	0.42	0/7012	0.63	5/9493 (0.1%)
33	B6	0.40	0/3138	0.60	2/4226 (0.0%)
34	5C	0.40	0/3902	0.61	3/5265 (0.1%)
35	5D	0.36	0/601	0.55	0/798
36	5E	0.34	0/1745	0.62	1/2335 (0.0%)
37	5F	0.37	0/1559	0.60	0/2097
38	5G	0.42	0/1993	0.65	2/2689 (0.1%)
39	5H	0.42	0/601	0.58	0/789
40	5I	0.49	0/3844	0.61	0/5174
41	5J	0.37	0/1147	0.56	0/1531
42	5K	0.44	0/1213	0.63	1/1638 (0.1%)
43	RD	0.30	0/2454	0.56	3/3310 (0.1%)
44	RE	0.34	0/9015	0.58	4/12195 (0.0%)
45	RF	0.32	0/2004	0.62	0/2697
46	RJ	0.41	0/5836	0.60	1/7859 (0.0%)
47	RK	0.38	0/2832	0.61	0/3825
48	RN	0.33	0/528	0.53	0/695
49	RP	0.31	0/12292	0.58	48/16822 (0.3%)
50	RQ	0.35	0/2446	0.61	3/3323 (0.1%)
51	RT	0.34	0/1679	0.63	1/2261 (0.0%)
52	RZ	0.31	0/6730	0.58	1/9088 (0.0%)
All	All	0.43	0/168453	0.78	344/234397 (0.1%)

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	2
5	SF	0	1
7	SH	0	2
8	SI	0	2
14	SR	0	1
15	SX	0	1
17	SZ	0	1
18	Sc	0	1
23	3F	0	3
24	3G	0	2
24	3H	0	1
25	A5	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
28	B1	0	2
29	B2	0	2
30	B3	0	7
32	BE	0	3
33	B6	0	2
39	5H	0	1
40	5I	0	2
42	5K	0	1
44	RE	0	2
45	RF	0	1
46	RJ	0	1
49	RP	0	9
50	RQ	0	1
52	RZ	0	2
All	All	0	54

There are no bond length outliers.

The worst 5 of 344 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5A	494	C	C2-N1-C1'	14.08	134.28	118.80
3	SA	185	U	C2-N1-C1'	10.48	130.27	117.70
3	SA	185	U	N1-C2-O2	10.12	129.88	122.80
3	SA	1473	U	C2-N1-C1'	10.10	129.82	117.70
3	SA	1473	U	N1-C2-O2	9.84	129.69	122.80

There are no chirality outliers.

5 of 54 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	SC	16	GLN	Peptide
4	SC	18	LYS	Peptide
5	SF	207	LEU	Peptide
7	SH	147	LEU	Peptide
7	SH	152	ASP	Peptide

5.2 Too-close contacts [i](#)

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

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3A	3534	0	1792	32	0
2	5A	926	0	468	8	0
3	SA	25332	0	12769	275	0
4	SC	1923	0	2029	41	0
5	SF	1915	0	1941	38	0
6	SG	1669	0	1724	25	0
7	SH	1456	0	1505	24	0
8	SI	1321	0	1387	34	0
9	SJ	1181	0	1198	22	0
10	SK	1410	0	1492	28	0
11	SM	1113	0	1181	24	0
12	SO	1087	0	1152	22	0
13	SP	848	0	868	21	0
14	SR	973	0	1029	21	0
15	SX	1003	0	1040	21	0
16	SY	792	0	847	14	0
17	SZ	986	0	1042	23	0
18	Sc	603	0	621	0	0
19	Sd	497	0	535	0	0
20	3B	1878	0	1923	28	0
20	3C	1754	0	1792	35	0
21	3D	2974	0	3001	55	0
22	3E	2130	0	2187	33	0
23	3F	3498	0	3515	67	0
24	3G	916	0	964	15	0
24	3H	916	0	964	18	0
25	A5	2452	0	2435	48	0
26	AE	3443	0	3564	57	0
27	AG	394	0	380	6	0
28	B1	6316	0	6218	109	0
29	B2	6497	0	6492	147	0
30	B3	5906	0	5983	150	0
31	B8	3648	0	3626	64	0
32	BE	6876	0	6734	115	0
33	B6	3077	0	3022	46	0
34	5C	3825	0	3829	87	0
35	5D	589	0	590	13	0
36	5E	1728	0	1739	35	0
37	5F	1530	0	1572	33	0
38	5G	1956	0	1971	36	0
39	5H	596	0	661	17	0
40	5I	3765	0	3714	74	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
41	5J	1127	0	1150	11	0
42	5K	1190	0	1252	22	0
43	RD	2413	0	2264	33	0
44	RE	8805	0	8911	157	0
45	RF	1963	0	1942	35	0
46	RJ	5709	0	5870	111	0
47	RK	2781	0	2878	68	0
48	RN	523	0	530	7	0
49	RP	12263	0	8039	80	0
50	RQ	2411	0	2092	44	0
51	RT	1652	0	1706	32	0
52	RZ	6598	0	6631	112	0
53	X1	755	0	179	3	0
54	5K	1	0	0	0	0
54	Sc	1	0	0	0	0
55	RJ	32	0	12	0	0
56	RJ	1	0	0	0	0
57	RZ	27	0	12	1	0
All	All	163485	0	144964	2382	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 2382 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:1663:G:H1	3:SA:1738:U:H3	0.94	0.93
47:RK:213:LYS:O	47:RK:217:LYS:HB3	1.71	0.91
3:SA:174:U:H3	3:SA:266:A:H62	0.92	0.90
3:SA:1697:G:H1	3:SA:1704:U:H3	1.08	0.90
45:RF:101:SER:O	45:RF:105:SER:HB3	1.73	0.88

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	240/255 (94%)	210 (88%)	30 (12%)	0	100	100
5	SF	245/261 (94%)	198 (81%)	47 (19%)	0	100	100
6	SG	211/225 (94%)	194 (92%)	17 (8%)	0	100	100
7	SH	178/236 (75%)	159 (89%)	15 (8%)	4 (2%)	6	35
8	SI	161/190 (85%)	137 (85%)	24 (15%)	0	100	100
9	SJ	144/200 (72%)	126 (88%)	18 (12%)	0	100	100
10	SK	172/197 (87%)	154 (90%)	17 (10%)	1 (1%)	25	66
11	SM	135/156 (86%)	117 (87%)	18 (13%)	0	100	100
12	SO	132/151 (87%)	123 (93%)	9 (7%)	0	100	100
13	SP	114/137 (83%)	96 (84%)	18 (16%)	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	102/145 (70%)	88 (86%)	14 (14%)	0	100	100
17	SZ	121/135 (90%)	106 (88%)	15 (12%)	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	238/327 (73%)	215 (90%)	23 (10%)	0	100	100
20	3C	220/327 (67%)	200 (91%)	20 (9%)	0	100	100
21	3D	372/504 (74%)	342 (92%)	30 (8%)	0	100	100
22	3E	275/511 (54%)	262 (95%)	13 (5%)	0	100	100
23	3F	431/573 (75%)	394 (91%)	37 (9%)	0	100	100
24	3G	119/126 (94%)	114 (96%)	5 (4%)	0	100	100
24	3H	119/126 (94%)	110 (92%)	9 (8%)	0	100	100
25	A5	301/643 (47%)	269 (89%)	32 (11%)	0	100	100
26	AE	429/1769 (24%)	408 (95%)	21 (5%)	0	100	100
27	AG	46/896 (5%)	43 (94%)	3 (6%)	0	100	100
28	B1	785/900 (87%)	709 (90%)	75 (10%)	1 (0%)	51	85
29	B2	814/943 (86%)	716 (88%)	98 (12%)	0	100	100
30	B3	733/817 (90%)	585 (80%)	147 (20%)	1 (0%)	51	85
31	B8	453/594 (76%)	397 (88%)	56 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	BE	886/939 (94%)	804 (91%)	81 (9%)	1 (0%)	51	85
33	B6	369/440 (84%)	341 (92%)	26 (7%)	2 (0%)	29	69
34	5C	474/554 (86%)	424 (90%)	50 (10%)	0	100	100
35	5D	66/250 (26%)	56 (85%)	10 (15%)	0	100	100
36	5E	205/593 (35%)	187 (91%)	18 (9%)	0	100	100
37	5F	180/183 (98%)	169 (94%)	11 (6%)	0	100	100
38	5G	237/290 (82%)	215 (91%)	22 (9%)	0	100	100
39	5H	72/610 (12%)	67 (93%)	5 (7%)	0	100	100
40	5I	457/489 (94%)	413 (90%)	44 (10%)	0	100	100
41	5J	130/217 (60%)	117 (90%)	13 (10%)	0	100	100
42	5K	148/189 (78%)	134 (90%)	14 (10%)	0	100	100
43	RD	310/1729 (18%)	281 (91%)	25 (8%)	4 (1%)	12	48
44	RE	1080/1237 (87%)	998 (92%)	81 (8%)	1 (0%)	51	85
45	RF	233/297 (78%)	205 (88%)	26 (11%)	2 (1%)	17	56
46	RJ	690/1183 (58%)	636 (92%)	54 (8%)	0	100	100
47	RK	358/367 (98%)	332 (93%)	26 (7%)	0	100	100
48	RN	59/810 (7%)	59 (100%)	0	0	100	100
49	RP	1948/2493 (78%)	1778 (91%)	156 (8%)	14 (1%)	22	62
50	RQ	333/899 (37%)	289 (87%)	41 (12%)	3 (1%)	17	56
51	RT	207/326 (64%)	188 (91%)	19 (9%)	0	100	100
52	RZ	831/1267 (66%)	737 (89%)	91 (11%)	3 (0%)	34	72
All	All	16950/27128 (62%)	15248 (90%)	1665 (10%)	37 (0%)	50	81

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
43	RD	1223	PRO
49	RP	707	PRO
49	RP	718	PRO
49	RP	922	MET
49	RP	923	PRO

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	213/224 (95%)	210 (99%)	3 (1%)	67	80
5	SF	199/222 (90%)	197 (99%)	2 (1%)	76	86
6	SG	180/191 (94%)	178 (99%)	2 (1%)	73	84
7	SH	153/201 (76%)	151 (99%)	2 (1%)	69	82
8	SI	146/170 (86%)	144 (99%)	2 (1%)	67	80
9	SJ	122/161 (76%)	118 (97%)	4 (3%)	38	61
10	SK	150/166 (90%)	149 (99%)	1 (1%)	84	90
11	SM	124/137 (90%)	124 (100%)	0	100	100
12	SO	117/128 (91%)	117 (100%)	0	100	100
13	SP	88/105 (84%)	86 (98%)	2 (2%)	50	71
14	SR	105/119 (88%)	105 (100%)	0	100	100
15	SX	108/111 (97%)	107 (99%)	1 (1%)	78	88
16	SY	86/120 (72%)	86 (100%)	0	100	100
17	SZ	103/113 (91%)	103 (100%)	0	100	100
18	Sc	69/71 (97%)	69 (100%)	0	100	100
19	Sd	56/60 (93%)	55 (98%)	1 (2%)	59	77
20	3B	201/240 (84%)	199 (99%)	2 (1%)	76	86
20	3C	189/240 (79%)	188 (100%)	1 (0%)	88	93
21	3D	322/435 (74%)	320 (99%)	2 (1%)	86	92
22	3E	222/433 (51%)	221 (100%)	1 (0%)	88	93
23	3F	382/503 (76%)	379 (99%)	3 (1%)	81	89
24	3G	100/104 (96%)	99 (99%)	1 (1%)	76	86
24	3H	100/104 (96%)	100 (100%)	0	100	100
25	A5	280/574 (49%)	278 (99%)	2 (1%)	84	90
26	AE	391/1633 (24%)	385 (98%)	6 (2%)	65	80
27	AG	46/826 (6%)	46 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	B1	694/789 (88%)	691 (100%)	3 (0%)	91	94
29	B2	712/832 (86%)	705 (99%)	7 (1%)	76	86
30	B3	659/719 (92%)	655 (99%)	4 (1%)	86	92
31	B8	407/529 (77%)	403 (99%)	4 (1%)	76	86
32	BE	741/819 (90%)	737 (100%)	4 (0%)	88	93
33	B6	323/414 (78%)	319 (99%)	4 (1%)	71	84
34	5C	418/480 (87%)	416 (100%)	2 (0%)	88	93
35	5D	63/234 (27%)	62 (98%)	1 (2%)	62	79
36	5E	193/535 (36%)	192 (100%)	1 (0%)	88	93
37	5F	171/172 (99%)	168 (98%)	3 (2%)	59	77
38	5G	214/258 (83%)	213 (100%)	1 (0%)	88	93
39	5H	63/538 (12%)	63 (100%)	0	100	100
40	5I	416/443 (94%)	413 (99%)	3 (1%)	84	90
41	5J	124/200 (62%)	123 (99%)	1 (1%)	81	89
42	5K	133/169 (79%)	133 (100%)	0	100	100
43	RD	226/1544 (15%)	222 (98%)	4 (2%)	59	77
44	RE	994/1125 (88%)	987 (99%)	7 (1%)	84	90
45	RF	221/274 (81%)	220 (100%)	1 (0%)	88	93
46	RJ	624/1039 (60%)	612 (98%)	12 (2%)	57	75
47	RK	307/312 (98%)	304 (99%)	3 (1%)	76	86
48	RN	55/732 (8%)	55 (100%)	0	100	100
49	RP	556/2307 (24%)	550 (99%)	6 (1%)	73	84
50	RQ	206/808 (26%)	204 (99%)	2 (1%)	76	86
51	RT	178/282 (63%)	178 (100%)	0	100	100
52	RZ	717/1140 (63%)	712 (99%)	5 (1%)	84	90
All	All	13667/24085 (57%)	13551 (99%)	116 (1%)	82	89

5 of 116 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	BE	484	ILE
50	RQ	808	PHE
38	5G	116	ARG

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Mol	Chain	Res	Type
50	RQ	728	ARG
46	RJ	1033	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 187 such sidechains are listed below:

Mol	Chain	Res	Type
34	5C	424	GLN
41	5J	195	GLN
37	5F	59	ASN
40	5I	109	HIS
44	RE	333	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	161/333 (48%)	69 (42%)	4 (2%)
2	5A	40/700 (5%)	13 (32%)	0
3	SA	1170/1812 (64%)	440 (37%)	18 (1%)
All	All	1371/2845 (48%)	522 (38%)	22 (1%)

5 of 522 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3A	3	C
1	3A	4	G
1	3A	23	U
1	3A	24	U
1	3A	25	U

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	SA	773	C
3	SA	1063	U
3	SA	1052	U
3	SA	1533	C
3	SA	136	C

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 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$
55	GTP	RJ	1201	56	26,34,34	1.20	1 (3%)	32,54,54	1.70	7 (21%)
57	ADP	RZ	1301	-	24,29,29	0.96	1 (4%)	29,45,45	1.37	4 (13%)

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
55	GTP	RJ	1201	56	-	5/18/38/38	0/3/3/3
57	ADP	RZ	1301	-	-	4/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	RJ	1201	GTP	C5-C6	-4.23	1.38	1.47
57	RZ	1301	ADP	C5-C4	2.45	1.47	1.40

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	RJ	1201	GTP	PA-O3A-PB	-4.49	117.41	132.83
55	RJ	1201	GTP	PB-O3B-PG	-4.12	118.69	132.83
57	RZ	1301	ADP	N3-C2-N1	-3.40	123.36	128.68
55	RJ	1201	GTP	C5-C6-N1	3.36	119.88	113.95
55	RJ	1201	GTP	C8-N7-C5	3.10	108.89	102.99

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

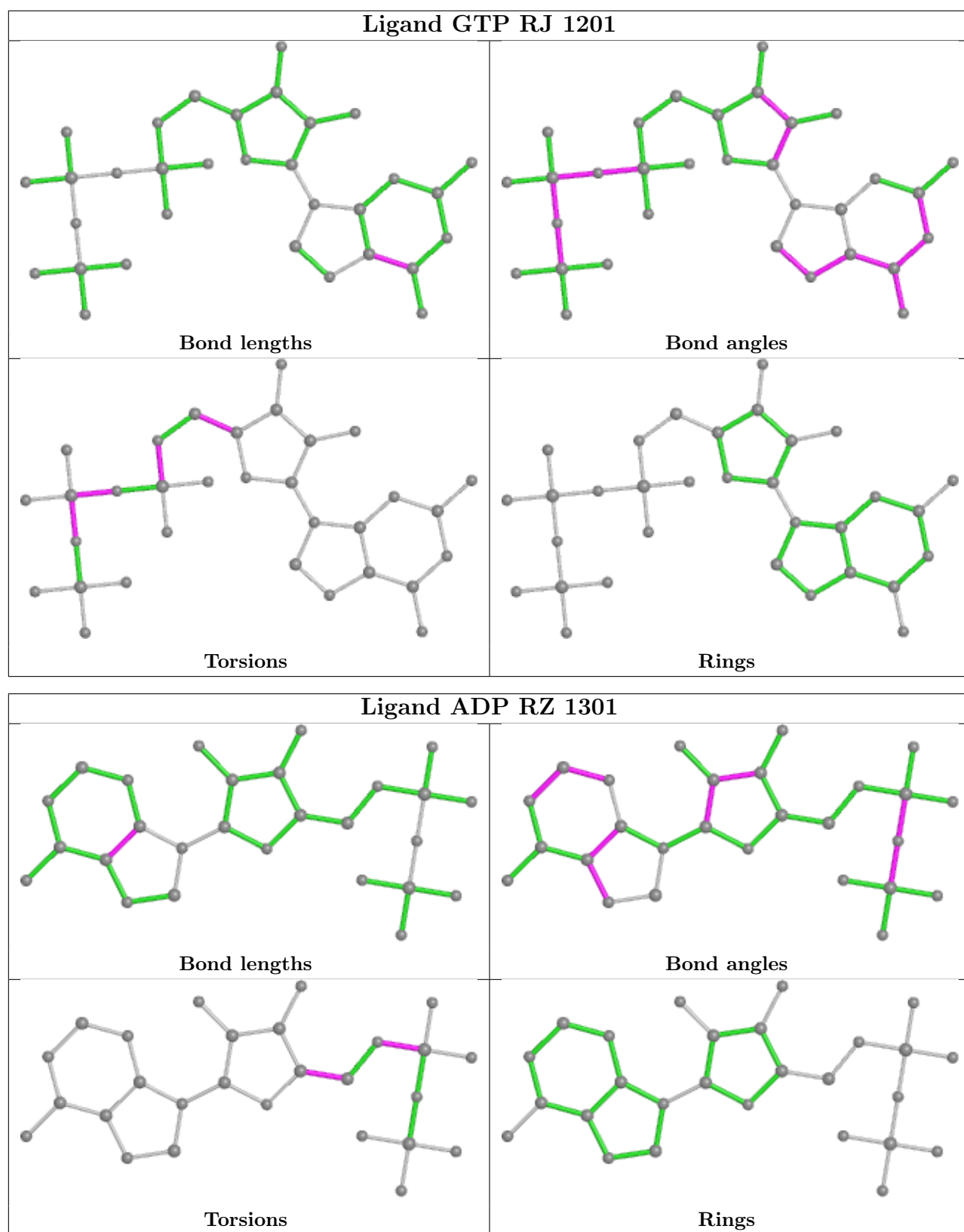
Mol	Chain	Res	Type	Atoms
57	RZ	1301	ADP	C5'-O5'-PA-O2A
57	RZ	1301	ADP	C5'-O5'-PA-O3A
55	RJ	1201	GTP	O4'-C4'-C5'-O5'
55	RJ	1201	GTP	C3'-C4'-C5'-O5'
55	RJ	1201	GTP	PA-O3A-PB-O2B

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	RZ	1301	ADP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

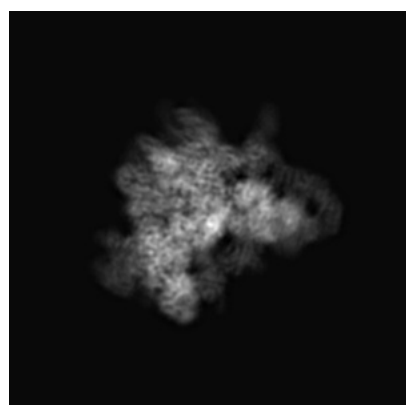
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30585. These allow visual inspection of the internal detail of the map and identification of artifacts.

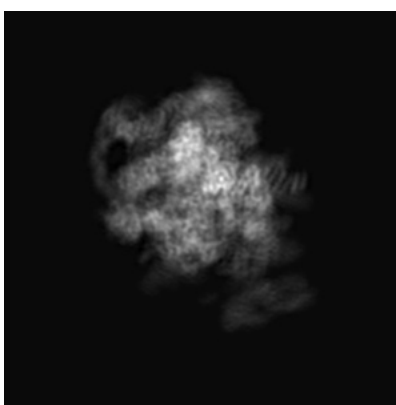
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

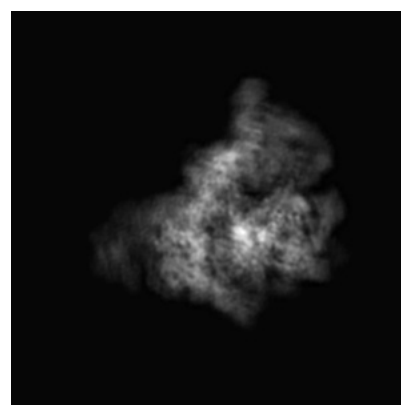
6.1.1 Primary map



X



Y

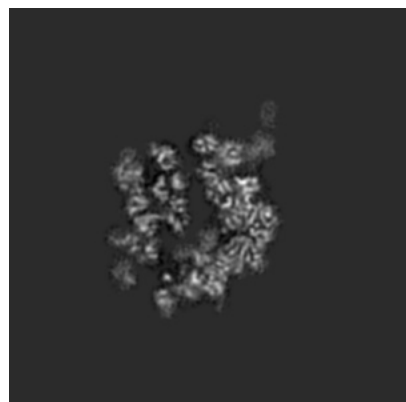


Z

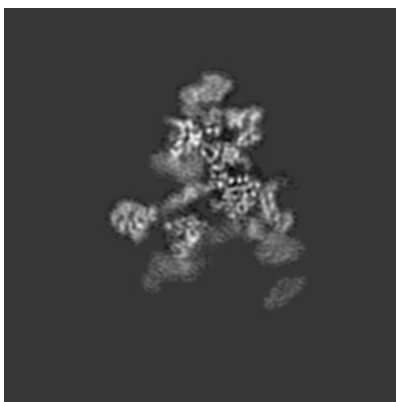
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

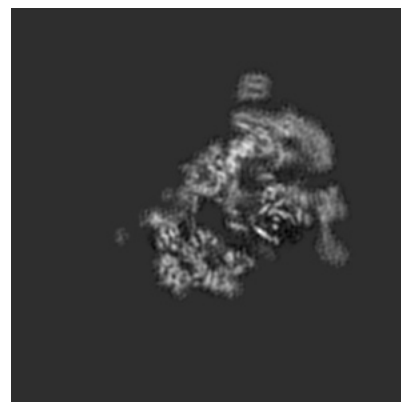
6.2.1 Primary map



X Index: 200



Y Index: 200

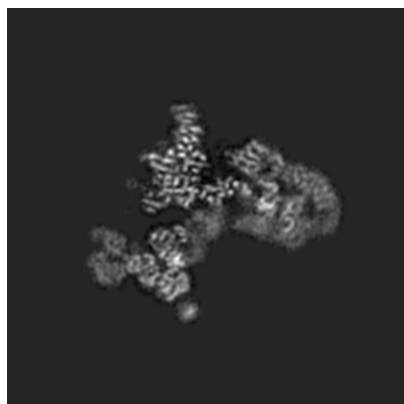


Z Index: 200

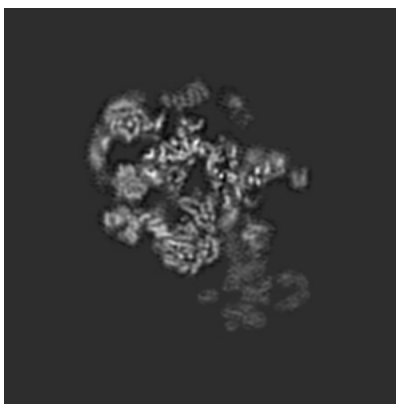
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

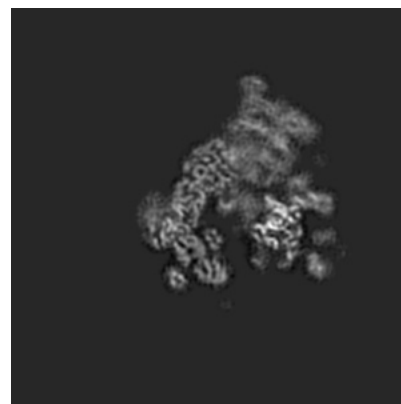
6.3.1 Primary map



X Index: 233



Y Index: 170

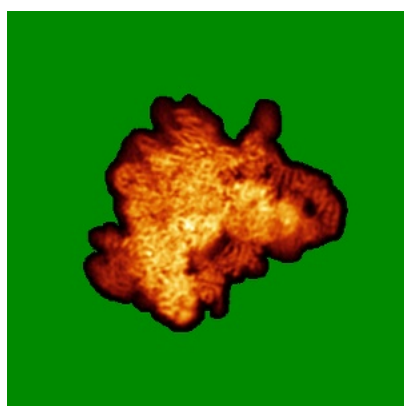


Z Index: 186

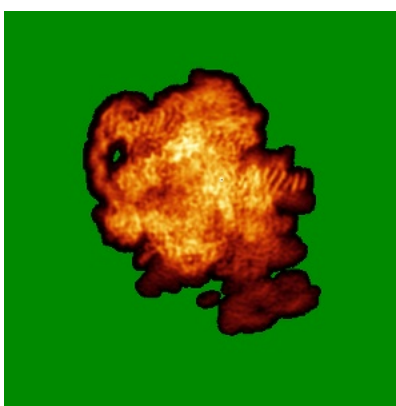
The images above show the largest variance slices of the map in three orthogonal directions.

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

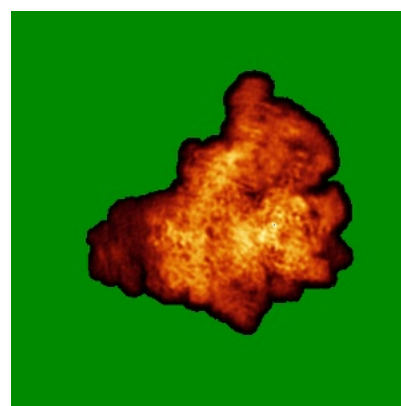
6.4.1 Primary map



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

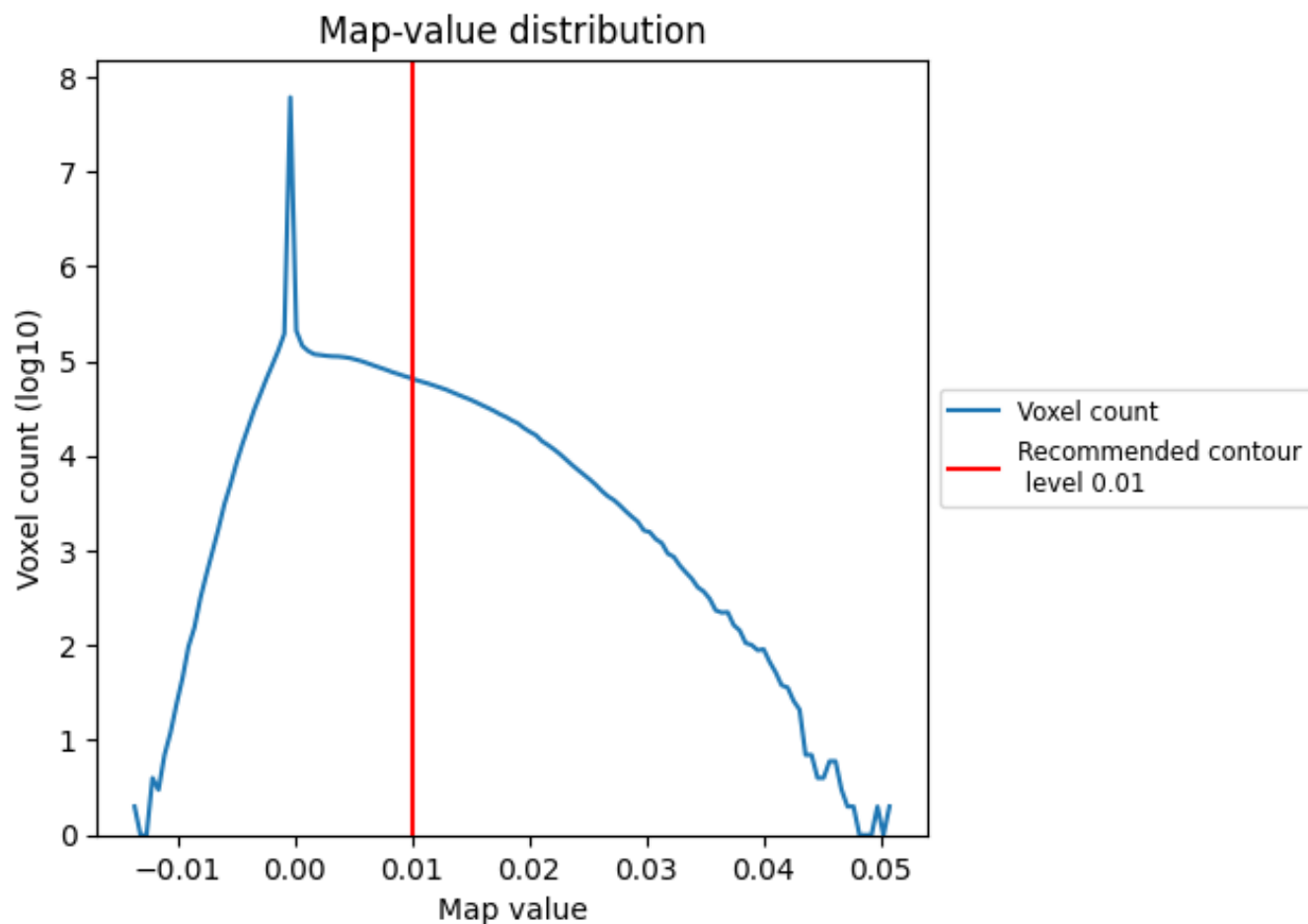
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

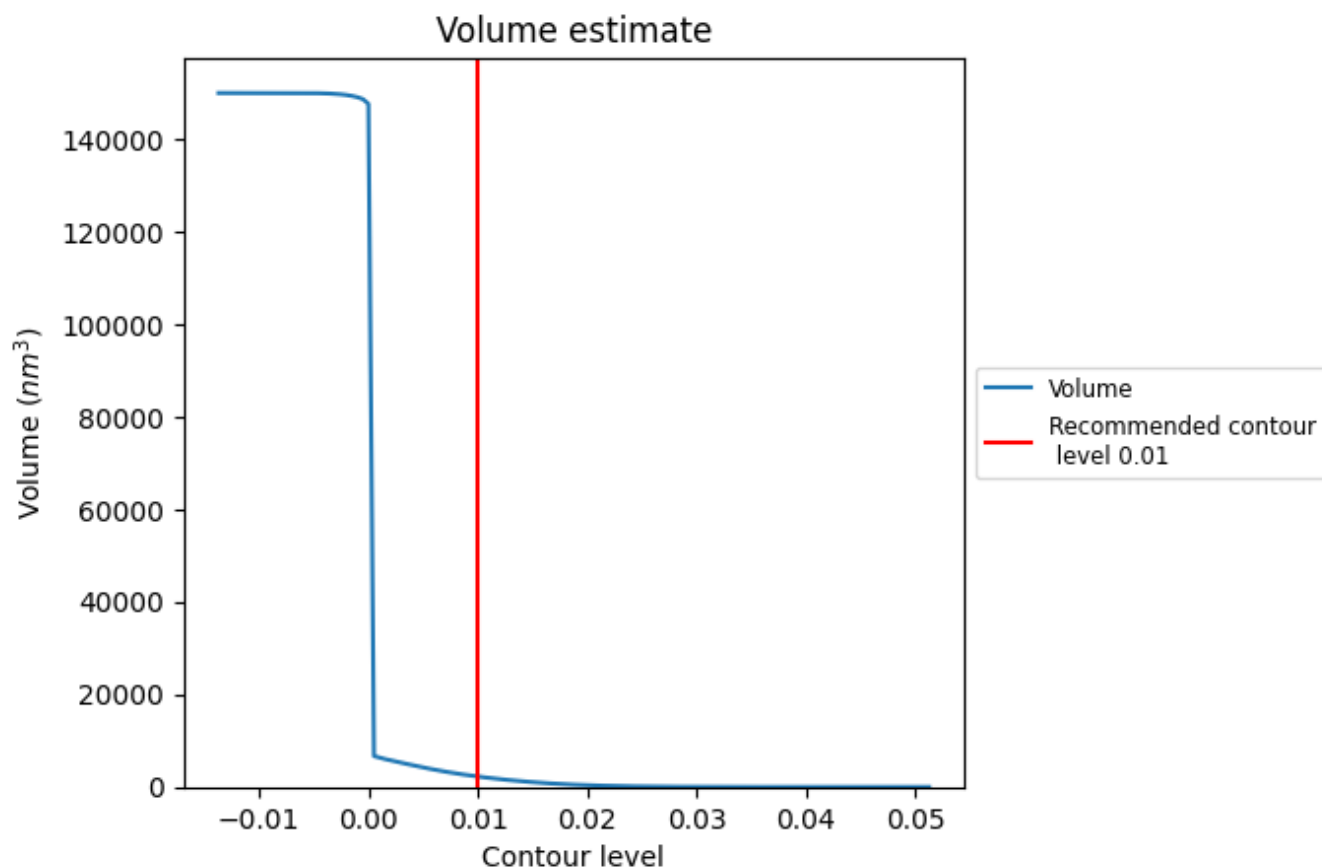
This section contains the results of statistical analysis of the map.

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.

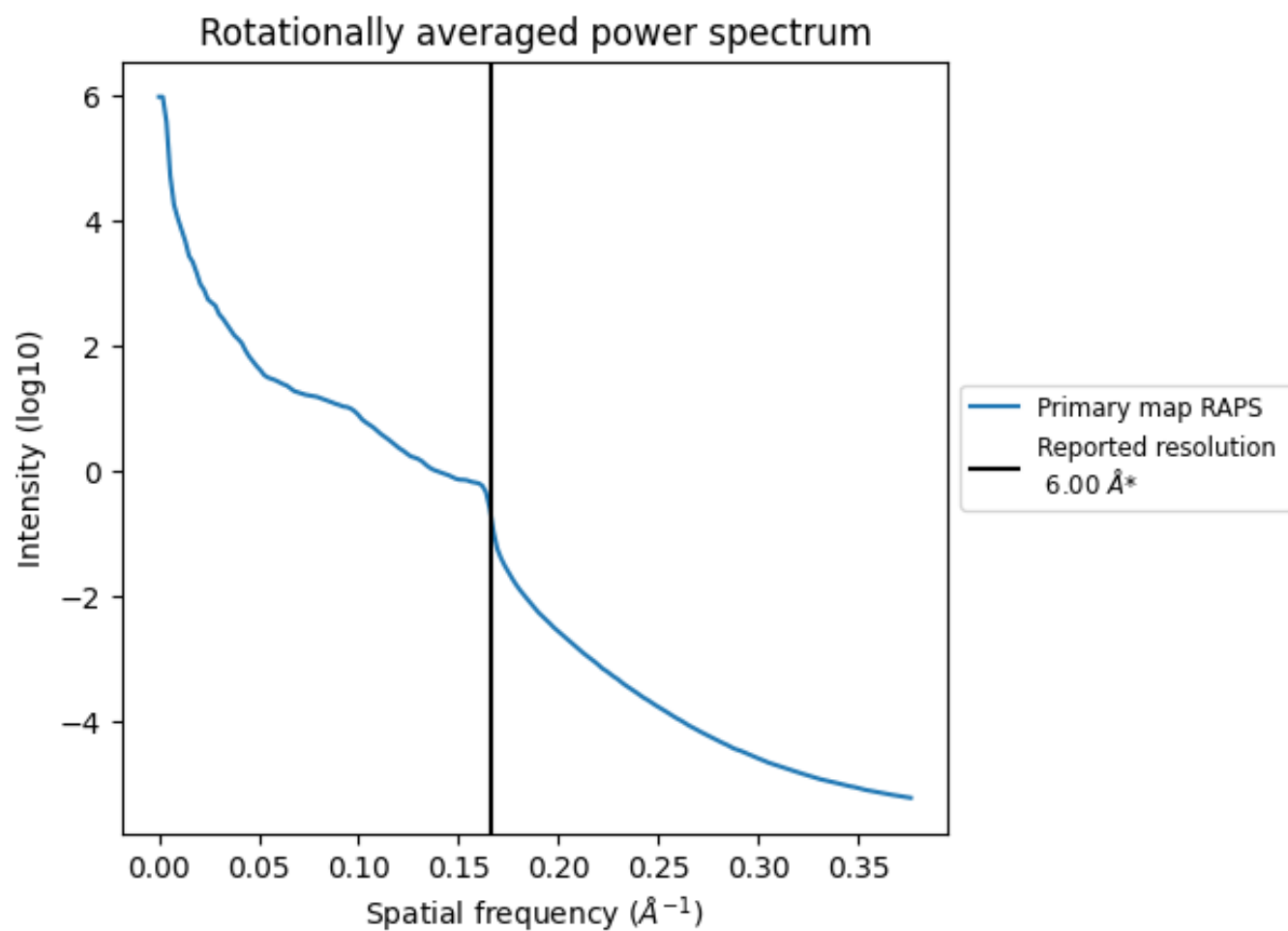
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2254 nm^3 ; this corresponds to an approximate mass of 2036 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 0.167 Å⁻¹

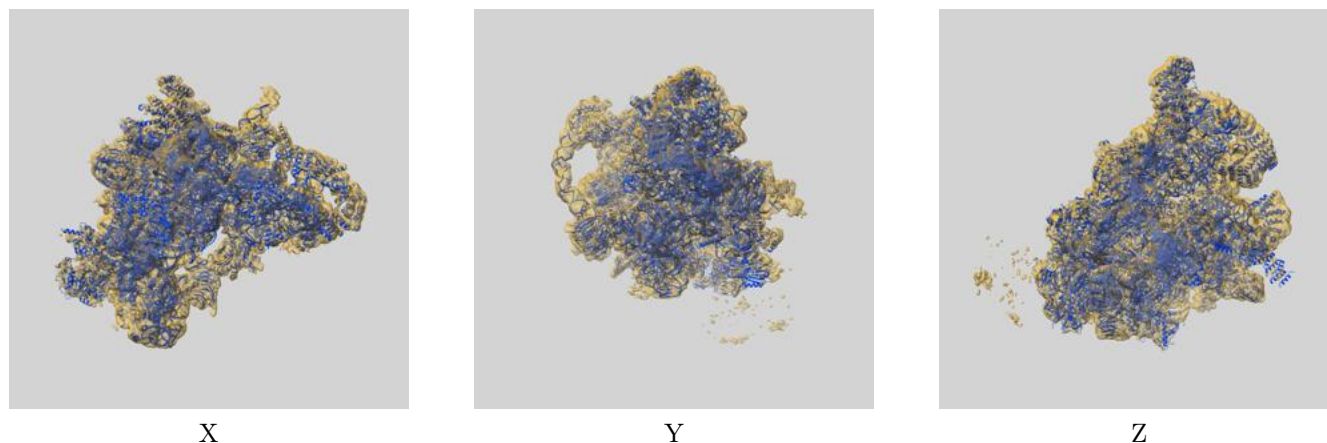
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

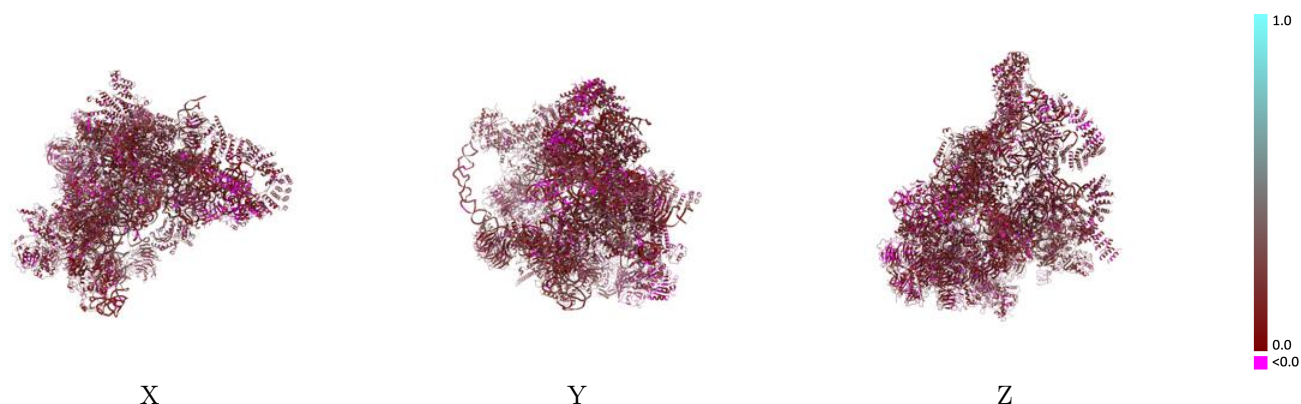
This section contains information regarding the fit between EMDB map EMD-30585 and PDB model 7D5T. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



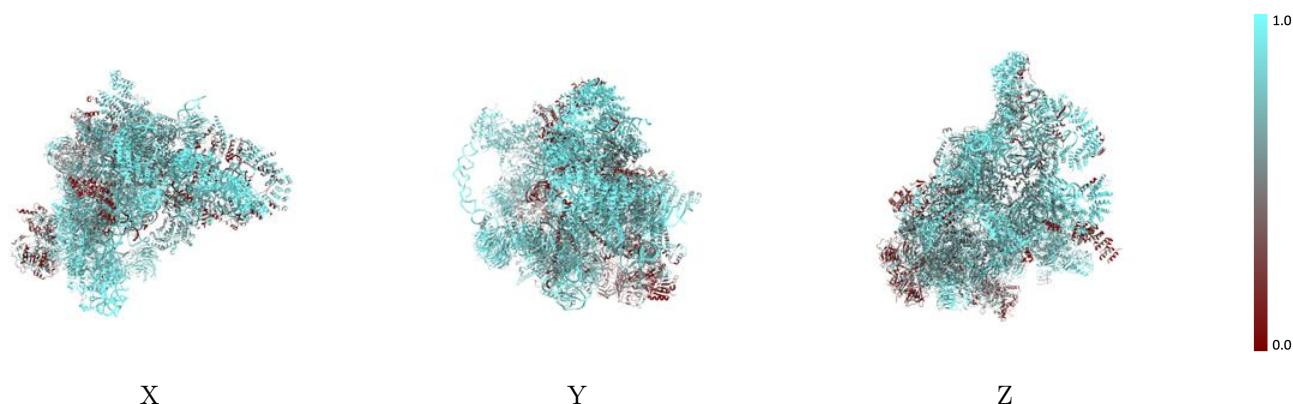
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



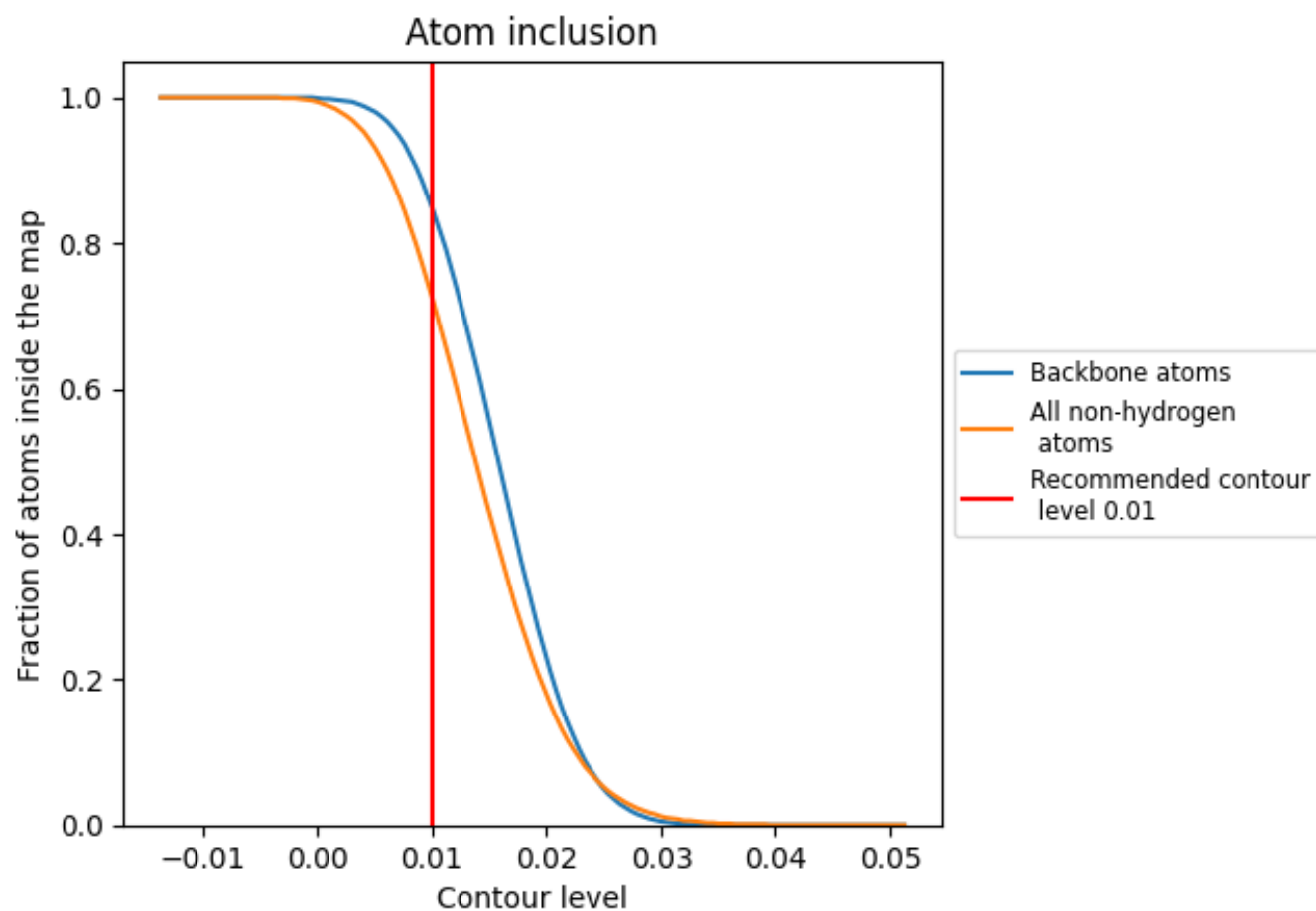
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 85% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7250	 0.1560
3A	 0.7930	 0.1610
3B	 0.6770	 0.1630
3C	 0.2000	 0.0500
3D	 0.7370	 0.1490
3E	 0.6750	 0.1330
3F	 0.7960	 0.1600
3G	 0.4540	 0.0900
3H	 0.6880	 0.1680
5A	 0.7340	 0.1360
5C	 0.6900	 0.1380
5D	 0.3410	 0.1110
5E	 0.6460	 0.1620
5F	 0.5990	 0.1360
5G	 0.5880	 0.1350
5H	 0.7530	 0.1780
5I	 0.7610	 0.1590
5J	 0.4380	 0.1360
5K	 0.6790	 0.1710
A5	 0.2450	 0.1490
AE	 0.5750	 0.1560
AG	 0.4540	 0.1530
B1	 0.7400	 0.1430
B2	 0.8700	 0.1600
B3	 0.8760	 0.1580
B6	 0.8120	 0.1460
B8	 0.4320	 0.1260
BE	 0.7600	 0.1520
RD	 0.2370	 0.1250
RE	 0.8600	 0.1660
RF	 0.8400	 0.1640
RJ	 0.7390	 0.1570
RK	 0.7040	 0.1640
RN	 0.2980	 0.1270
RP	 0.8010	 0.1550



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Chain	Atom inclusion	Q-score
RQ	 0.6120	 0.1680
RT	 0.6770	 0.1700
RZ	 0.4480	 0.1420
SA	 0.8900	 0.1880
SC	 0.7740	 0.1630
SF	 0.7130	 0.1400
SG	 0.7580	 0.1730
SH	 0.5270	 0.0990
SI	 0.7200	 0.1450
SJ	 0.6040	 0.0750
SK	 0.7280	 0.1590
SM	 0.3400	 0.0870
SO	 0.8440	 0.1660
SP	 0.8360	 0.1690
SR	 0.7740	 0.1600
SX	 0.6710	 0.1500
SY	 0.6180	 0.1690
SZ	 0.8560	 0.1480
Sc	 0.7980	 0.1870
Sd	 0.8110	 0.1780
X1	 0.4580	 0.1770