



wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 09:40 AM UTC

PDB ID : 7D4I / pdb_00007d4i
EMDB ID : EMD-30574
Title : Cryo-EM structure of 90S small ribosomal precursors complex with the DEAH-box RNA helicase Dhr1 (State F)
Authors : Du, Y.; Zhang, J.; An, W.; Ye, K.
Deposited on : 2020-09-24
Resolution : 4.00 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

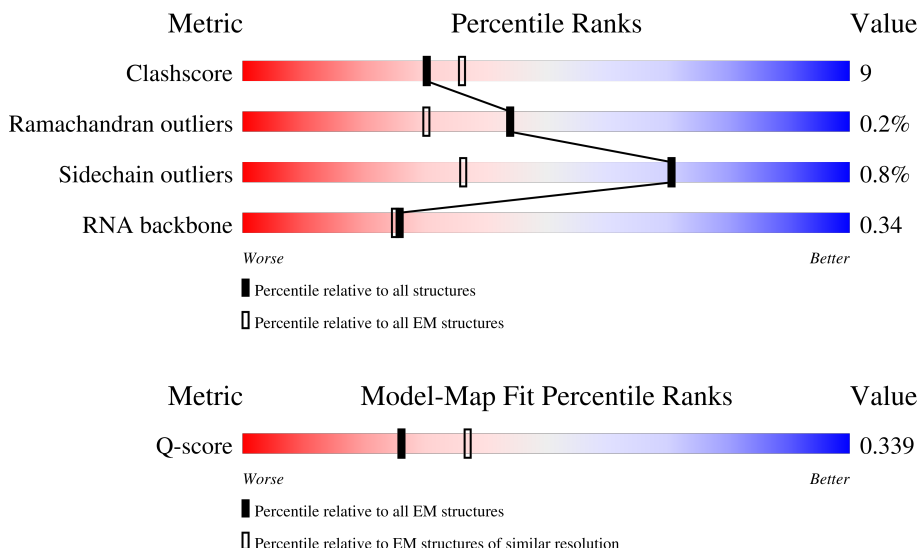
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 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)	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	7587 (3.50 - 4.50)

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	

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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	ST	146	
16	SU	144	
17	SX	130	
18	SY	145	
19	SZ	135	
20	Sc	82	
21	Sd	67	
22	3B	327	
22	3C	327	
23	3D	504	
24	3E	511	
25	3F	573	
26	3G	126	
26	3H	126	

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Mol	Chain	Length	Quality of chain
27	A4	776	
28	A5	643	
29	A8	713	
30	A9	575	
31	AE	1769	
32	AF	513	
33	AG	896	
34	B1	900	
35	B2	943	
36	B3	817	
37	B8	594	
38	BE	939	
39	B6	440	
40	5B	214	
41	5C	554	
42	5D	250	
43	5E	593	
44	5F	183	
45	5G	290	
46	5H	610	
47	5I	489	
48	5J	217	
49	5K	189	
50	RD	1729	
51	RE	1237	

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Mol	Chain	Length	Quality of chain
52	RF	297	
53	RG	252	
53	RH	252	
54	RJ	1183	
55	RK	367	
56	RN	810	
57	RO	552	
58	RP	2493	
59	RQ	899	
60	RS	480	
61	RT	326	
62	RW	206	
63	RZ	1267	
64	X1	611	
65	X2	694	
66	R5	305	
67	R1	246	
68	R3	394	
69	R6	223	
70	R2	265	
71	M3	250	
72	R0	240	
73	r4	359	
74	C4	292	
75	R4	1001	

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Mol	Chain	Length	Quality of chain
76	r6	733	
77	R7	184	
78	M4	1073	
79	M6	186	

2 Entry composition

There are 83 unique types of molecules in this entry. The entry contains 253642 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	216	Total	C	N	O	P	0	0
			4570	2044	784	1526	216		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5A	118	Total	C	N	O	P	0	0
			2536	1131	467	820	118		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SA	1337	Total	C	N	O	P	0	0
			28478	12732	5036	9373	1337		

- 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		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 S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	ST	111	Total	C	N	O	S	0	0
			902	568	171	161	2		

- Molecule 16 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SU	138	Total	C	N	O	S	0	0
			1075	673	203	197	2		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SY	104	Total	C	N	O	S	0	0
			792	506	145	139	2		

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	3B	242	Total	C	N	O	S	0	0
			1878	1190	338	340	10		
22	3C	224	Total	C	N	O	S	0	0
			1754	1114	314	316	10		

- Molecule 23 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	3D	378	Total	C	N	O	S	0	0
			2974	1886	511	568	9		

- Molecule 24 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	3E	435	Total	C	N	O	S	0	0
			3056	1904	548	595	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	3F	437	Total	C	N	O	S	0	0
			3498	2227	609	652	10		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A4	657	Total	C	N	O	S	0	0
			5187	3286	902	978	21		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	A5	511	Total	C	N	O	S	0	0
			3953	2507	682	751	13		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AE	1552	Total	C	N	O	S	0	0
			10262	6453	1810	1979	20		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AF	487	Total	C	N	O	S	0	0
			3860	2431	692	725	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AG	825	Total	C	N	O	S	0	0
			6565	4178	1110	1258	19		

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
40	5B	58	Total	C	N	O	0	0
			482	302	98	82		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	5C	482	Total	C	N	O	S	0	0
			3825	2409	684	721	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	5D	209	Total	C	N	O	S	0	0
			1778	1111	344	317	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	5E	213	Total	C	N	O	S	0	0
			1728	1072	304	348	4		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5G	241	Total	C	N	O	S	0	0
			1956	1228	368	353	7		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
46	5H	95	Total	C	N	O	0	0
			700	435	143	122		

- Molecule 47 is a protein called Protein SOF1.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5J	134	Total	C	N	O	S	0	0
			1127	712	205	207	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
49	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	variant	UNP Q05498

- Molecule 50 is a protein called rRNA biogenesis protein RRP5.

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

- Molecule 51 is a protein called U3 small nucleolar RNA-associated protein 22.

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

- Molecule 52 is a protein called Ribosomal RNA-processing protein 7.

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

- Molecule 53 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

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

- Molecule 54 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	RJ	738	Total	C	N	O	S	0	0
			5994	3851	1063	1054	26		

- Molecule 55 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 56 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	RN	584	Total	C	N	O	S	0	0
			4459	2819	800	827	13		

- Molecule 57 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	RO	520	Total	C	N	O	S	0	0
			3741	2397	641	691	12		

- Molecule 58 is a protein called U3 small nucleolar RNA-associated protein 20.

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

- Molecule 59 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	RQ	339	Total	C	N	O	S	0	0
			2408	1484	456	466	2		

- Molecule 60 is a protein called Essential nuclear protein 1.

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

- Molecule 61 is a protein called Pno1.

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

- Molecule 62 is a protein called Regulator of rDNA transcription protein 14.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	RW	153	Total	C	N	O	0	0
			762	456	153	153		

- Molecule 63 is a protein called Probable ATP-dependent RNA helicase DHR1.

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

- Molecule 64 is a protein called Unassigned peptides 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
64	X1	221	Total	C	N	O	0	0
			1105	663	221	221		

- Molecule 65 is a protein called Unassigned peptides 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
65	X2	141	Total	C	N	O	0	0
			705	423	141	141		

- Molecule 66 is a protein called Exosome complex component RRP45.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	R5	299	Total	C	N	O	S	0	0
			2304	1444	393	451	16		

- Molecule 67 is a protein called Exosome complex component SKI6.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	R1	244	Total	C	N	O	S	0	0
			1886	1177	335	366	8		

- Molecule 68 is a protein called Exosome complex component RRP43.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	R3	339	Total	C	N	O	S	1	0
			2588	1640	441	497	10		

- Molecule 69 is a protein called Exosome complex component RRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	R6	223	Total	C	N	O	S	1	0
			1701	1072	285	334	10		

- Molecule 70 is a protein called Exosome complex component RRP42.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	R2	265	Total	C	N	O	S	1	0
			2035	1299	334	397	5		

- Molecule 71 is a protein called Exosome complex component MTR3.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	M3	215	Total	C	N	O	S	0	0
			1639	1024	273	332	10		

- Molecule 72 is a protein called Exosome complex component RRP40.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	R0	237	Total	C	N	O	S	0	0
			1792	1143	295	344	10		

- Molecule 73 is a protein called Exosome complex component RRP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	r4	293	Total	C	N	O	S	0	0
			2236	1393	403	428	12		

- Molecule 74 is a protein called Exosome complex component CSL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	C4	222	Total	C	N	O	S	0	0
			1653	1034	287	325	7		

- Molecule 75 is a protein called Exosome complex exonuclease DIS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	R4	948	Total	C	N	O	S	0	0
			7430	4693	1308	1394	35		

- Molecule 76 is a protein called Exosome complex exonuclease RRP6.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	r6	414	Total	C	N	O	S	0	0
			2517	1544	469	498	6		

- Molecule 77 is a protein called Exosome complex protein LRP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	R7	113	Total	C	N	O	S	0	0
			894	565	151	174	4		

- Molecule 78 is a protein called ATP-dependent RNA helicase DOB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	M4	978	Total	C	N	O	S	0	0
			7626	4871	1294	1419	42		

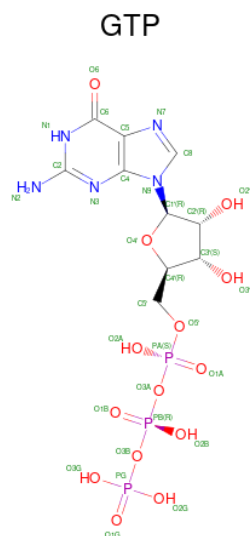
- Molecule 79 is a protein called M-phase phosphoprotein 6 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
79	M6	40	Total	C	N	O	0	0
			275	170	51	54		

- Molecule 80 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
80	Sc	1	Total	Zn	0
			1	1	
80	5K	1	Total	Zn	0
			1	1	

- Molecule 81 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

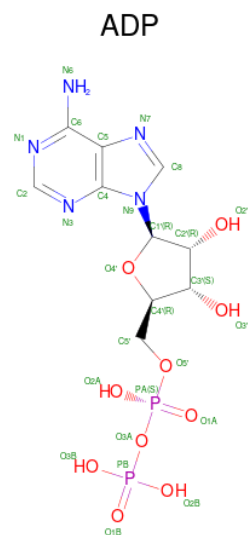


Mol	Chain	Residues	Atoms					AltConf
81	RJ	1	Total 32	C 10	N 5	O 14	P 3	0

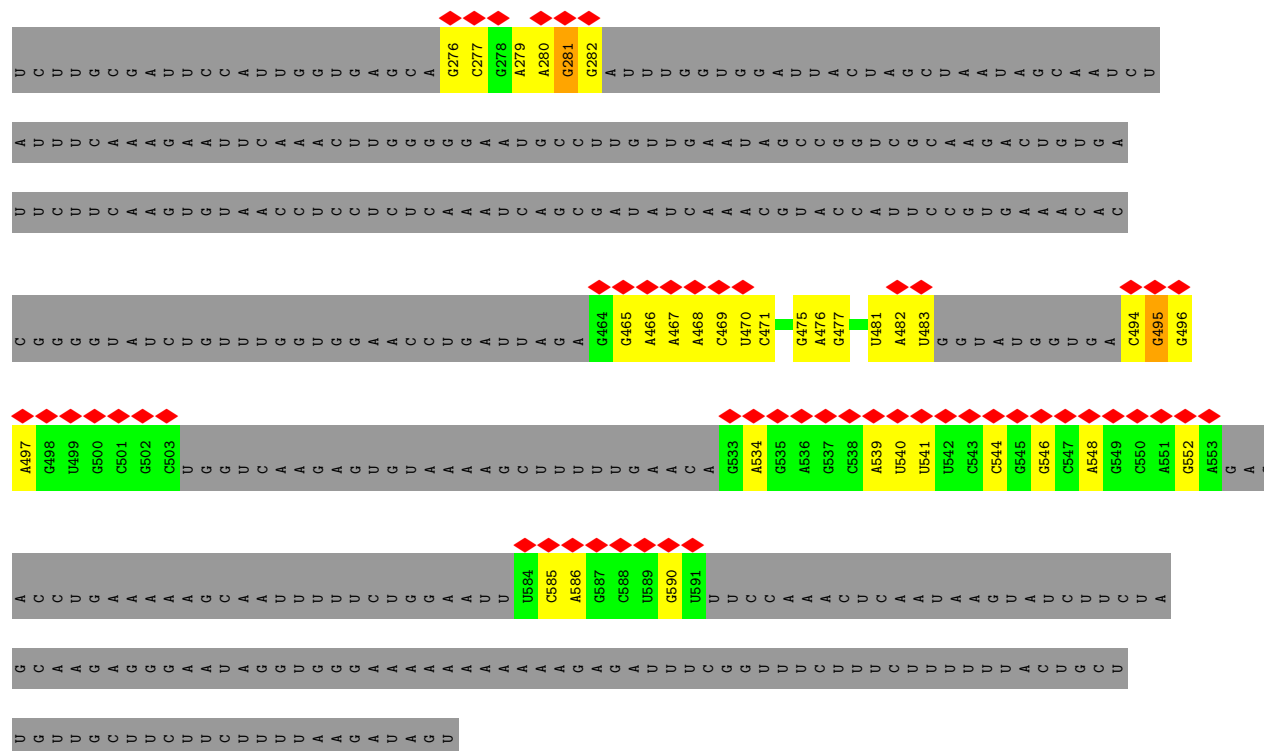
- Molecule 82 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

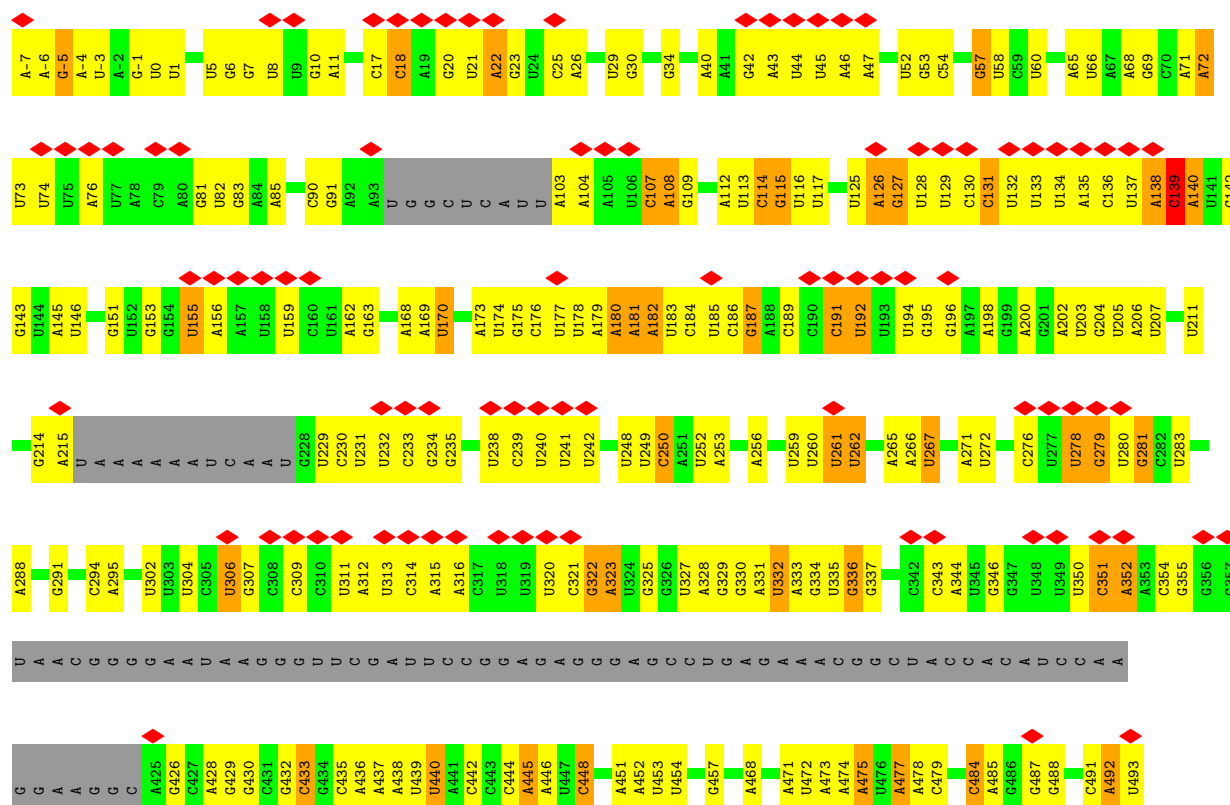
- Molecule 83 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



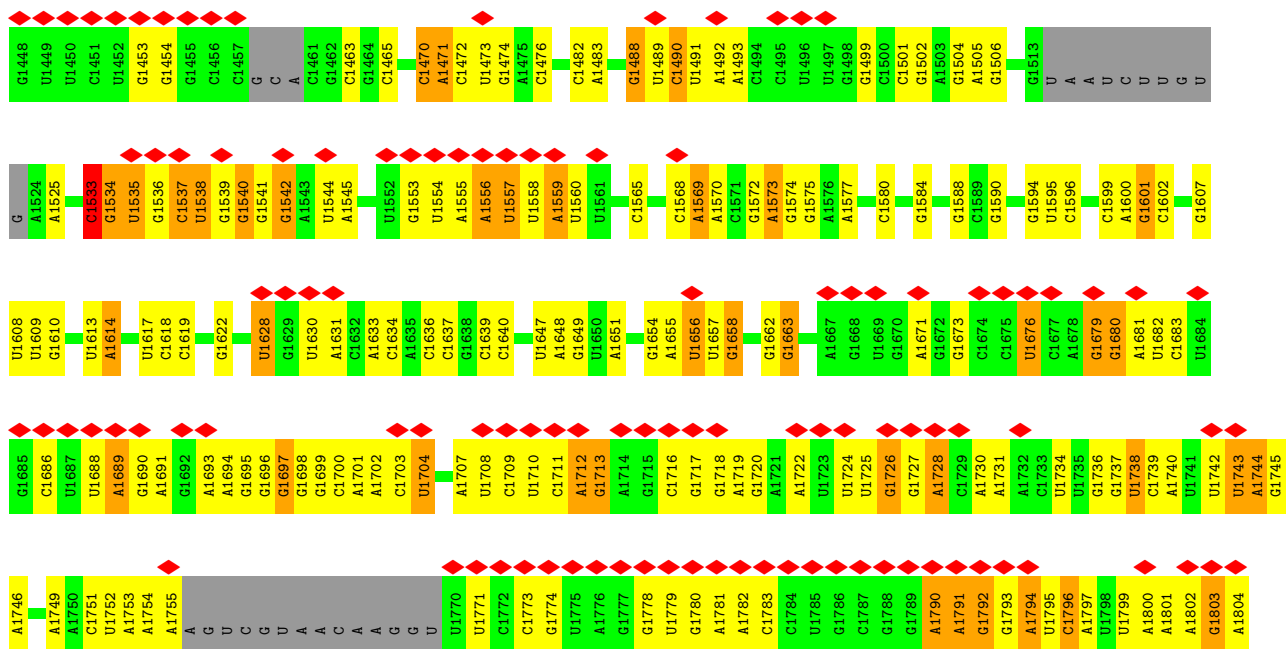
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
83	RZ	1	27	10	5	10	2	0



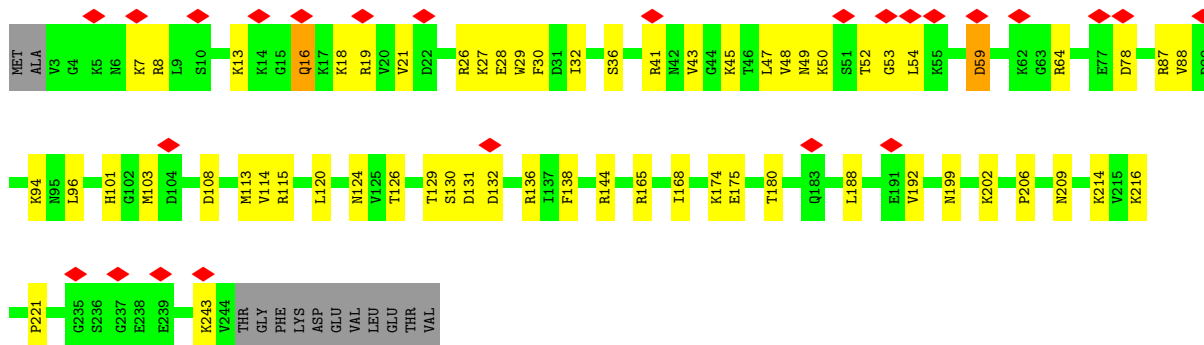
● Molecule 3: 18S rRNA



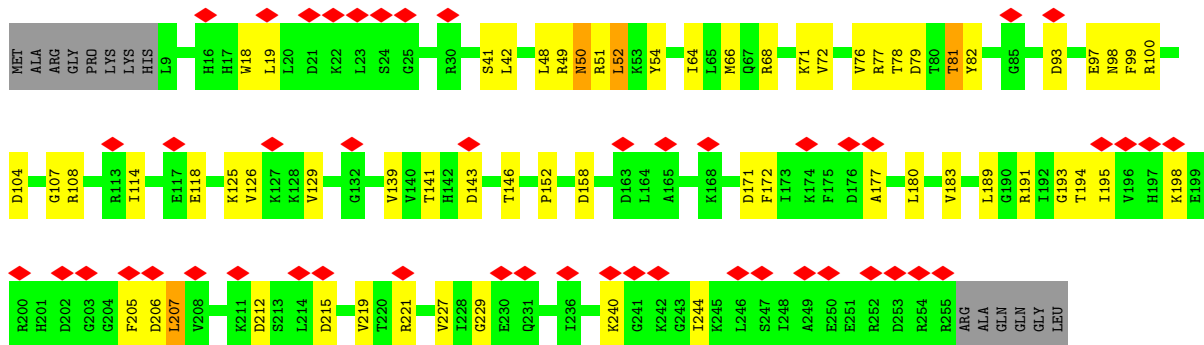




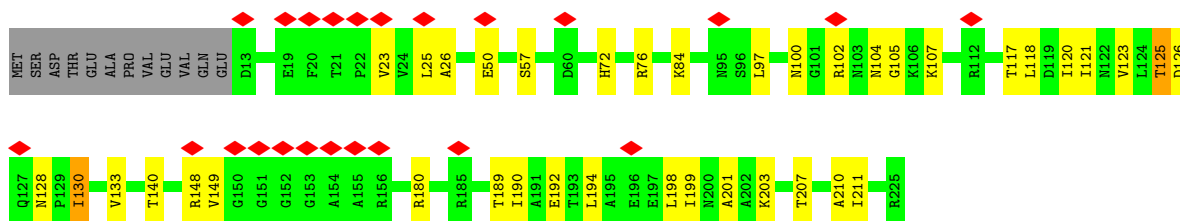
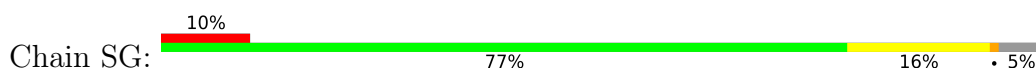
• Molecule 4: 40S ribosomal protein S1-A



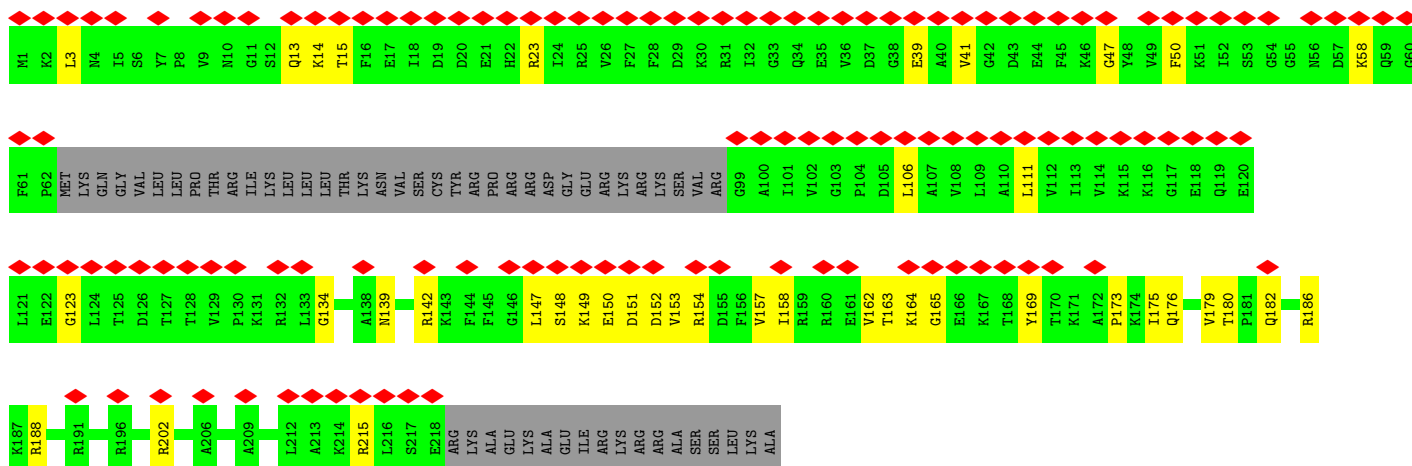
• Molecule 5: 40S ribosomal protein S4-A



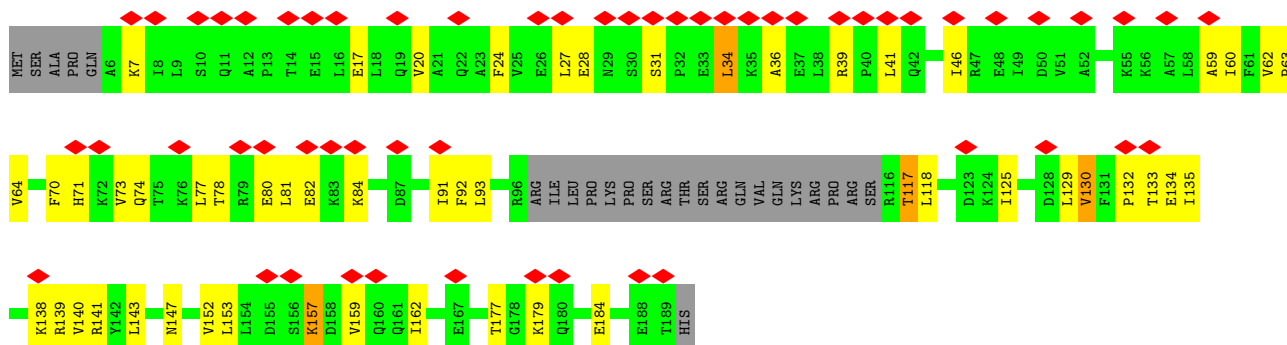
• Molecule 6: 40S ribosomal protein S5



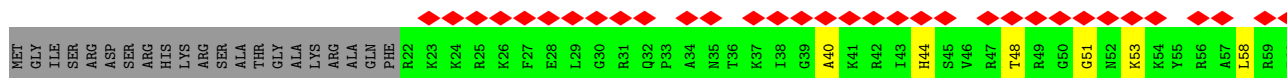
• Molecule 7: 40S ribosomal protein S6-A

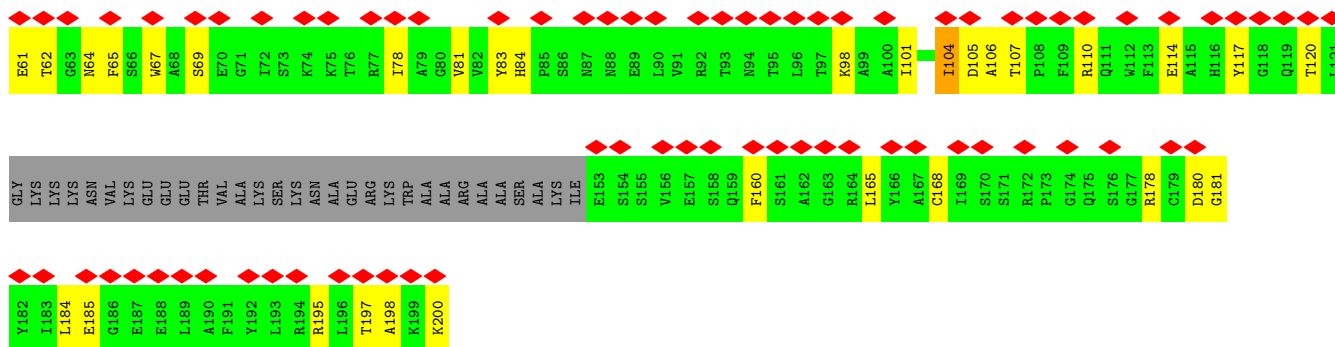


• Molecule 8: 40S ribosomal protein S7-A

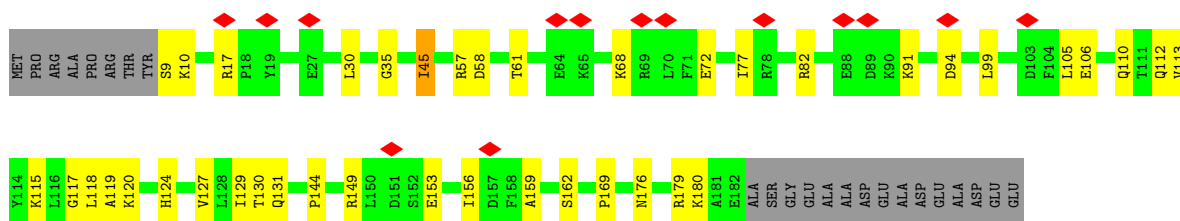


• Molecule 9: 40S ribosomal protein S8-A

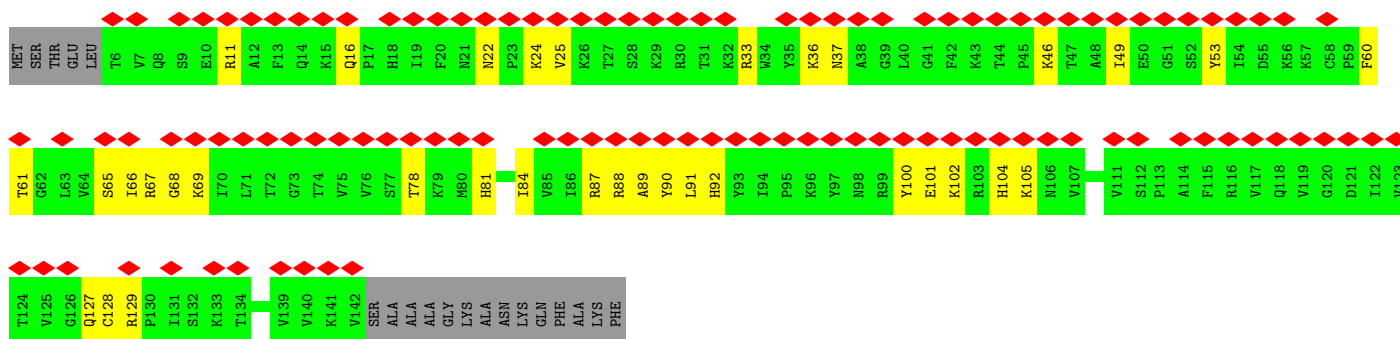
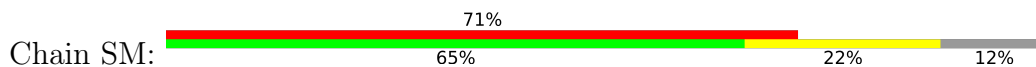




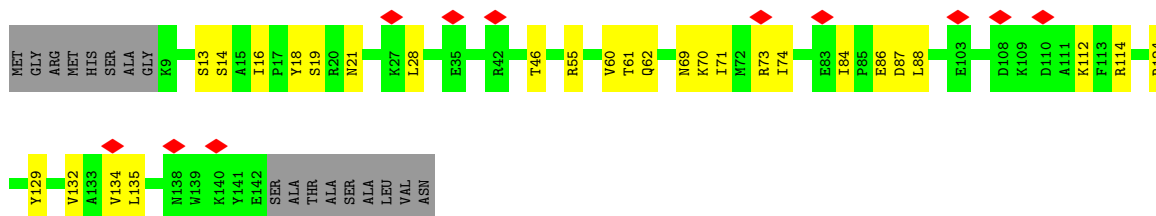
- Molecule 10: 40S ribosomal protein S9-A



- Molecule 11: 40S ribosomal protein S11-A



- Molecule 12: 40S ribosomal protein S13



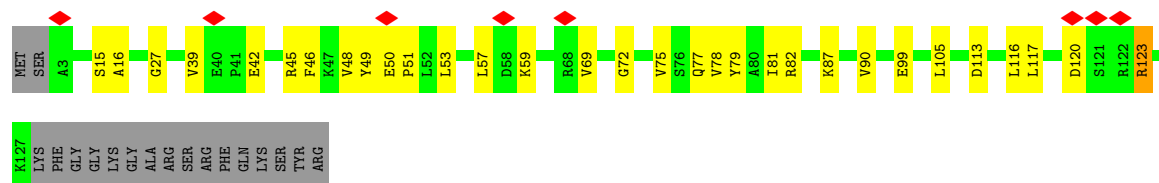
- Molecule 13: 40S ribosomal protein S14-A

Chain SP: 



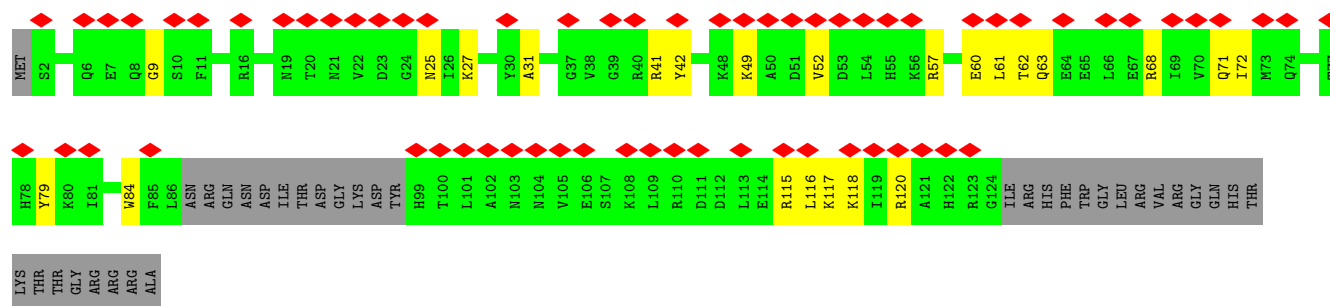
- Molecule 14: 40S ribosomal protein S16-A

Chain SR: 



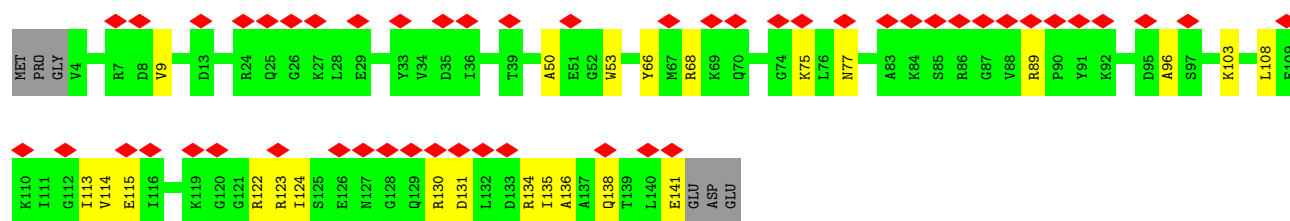
- Molecule 15: 40S ribosomal protein S18-A

Chain ST: 



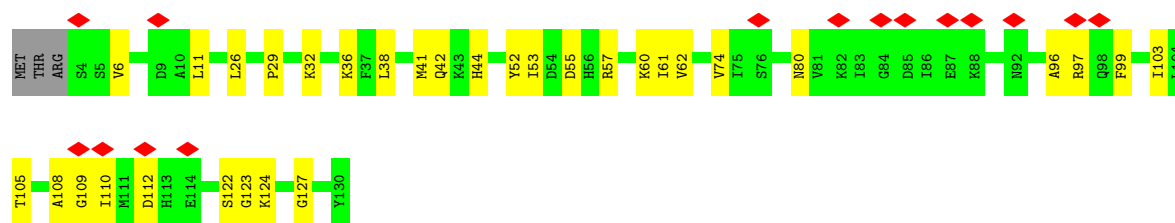
- Molecule 16: 40S ribosomal protein S19-A

Chain SU: 

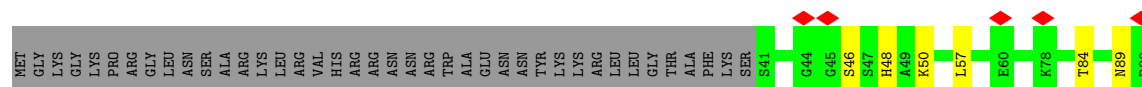


- Molecule 17: 40S ribosomal protein S22-B

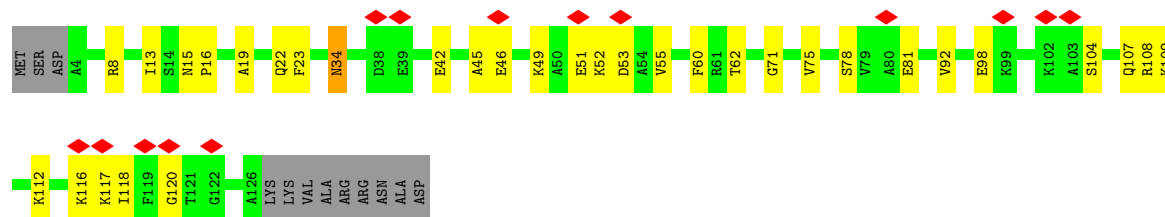
Chain SX: 



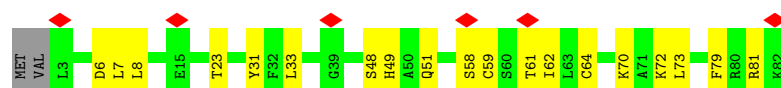
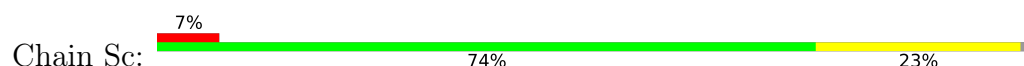
- Molecule 18: 40S ribosomal protein S23-A



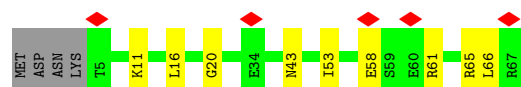
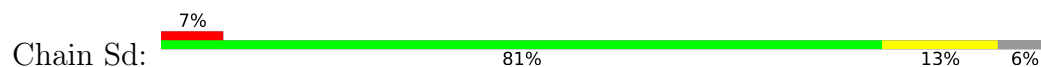
- Molecule 19: 40S ribosomal protein S24-A



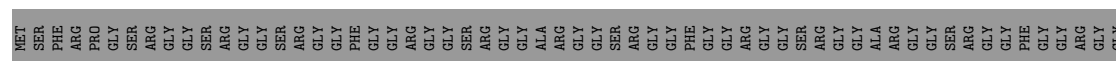
- Molecule 20: 40S ribosomal protein S27-A



- Molecule 21: 40S ribosomal protein S28-A



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

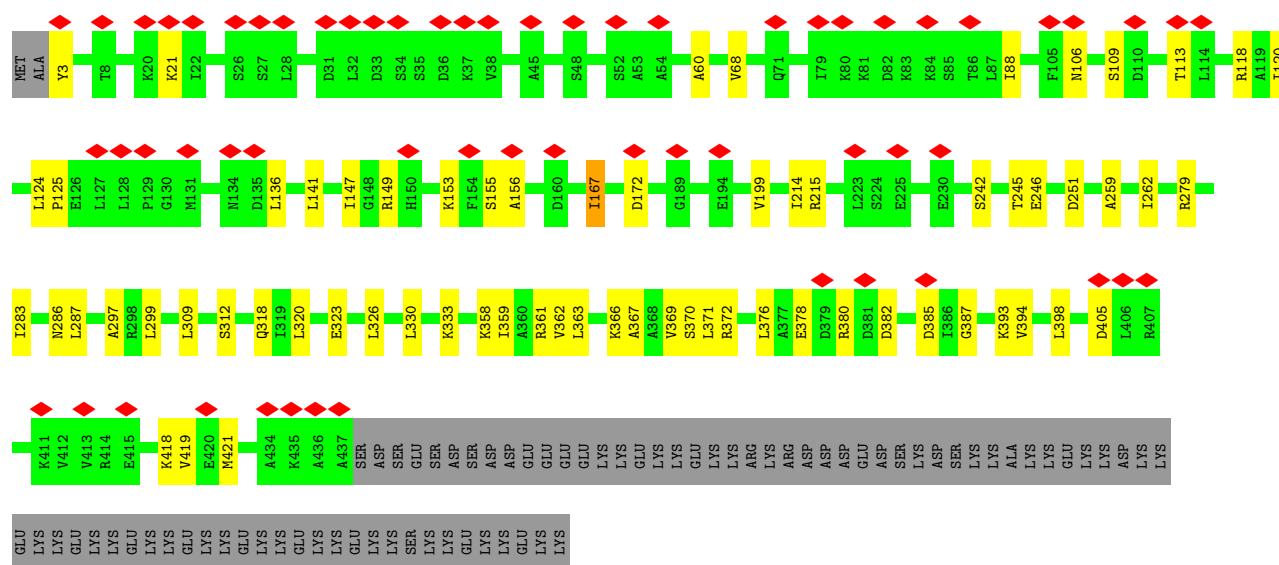




LYS
LYS
SER
LYS
ASP

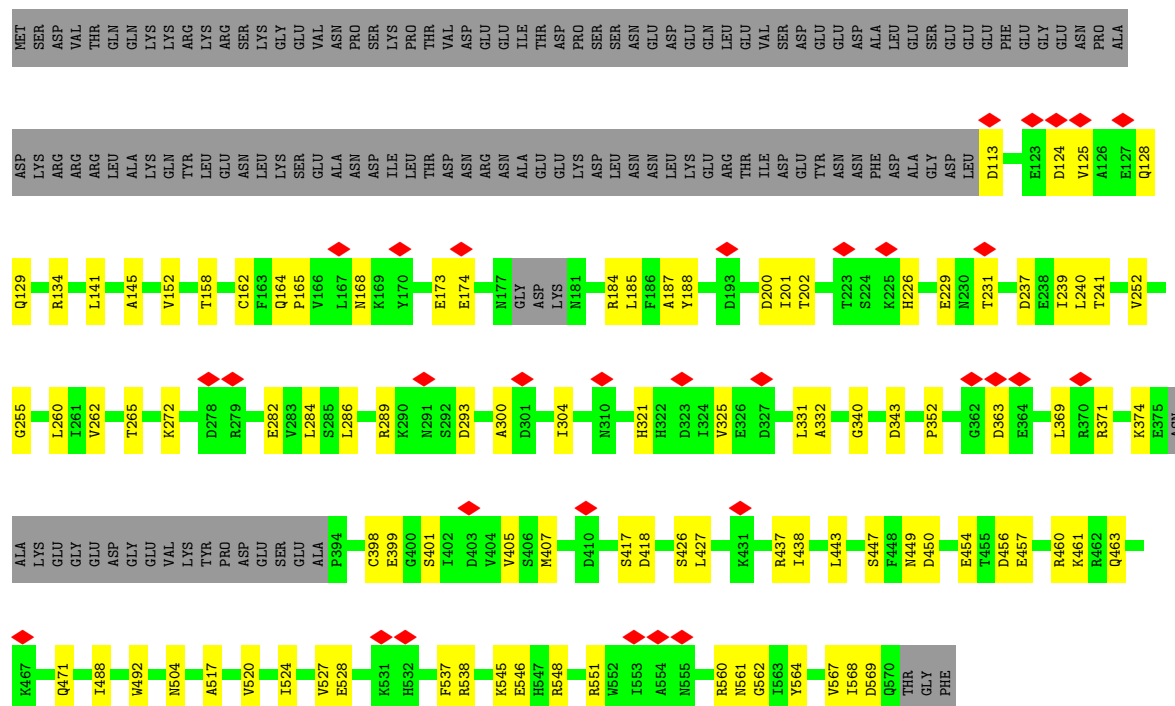
• Molecule 24: Nucleolar protein 58

Chain 3E: 

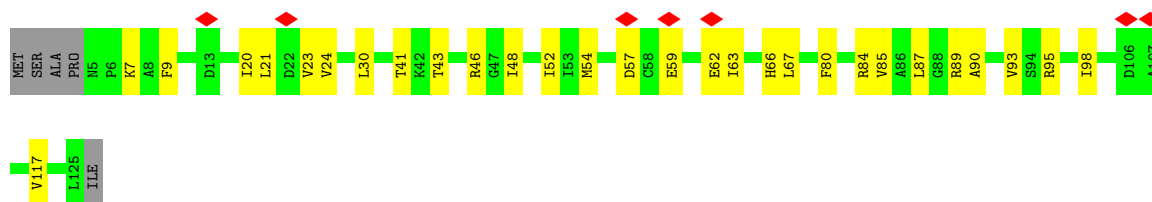
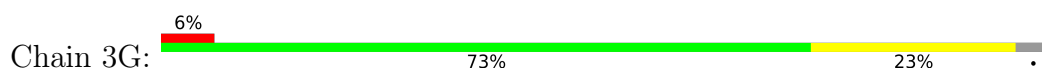


• Molecule 25: Ribosomal RNA-processing protein 9

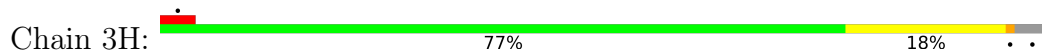
Chain 3F: 



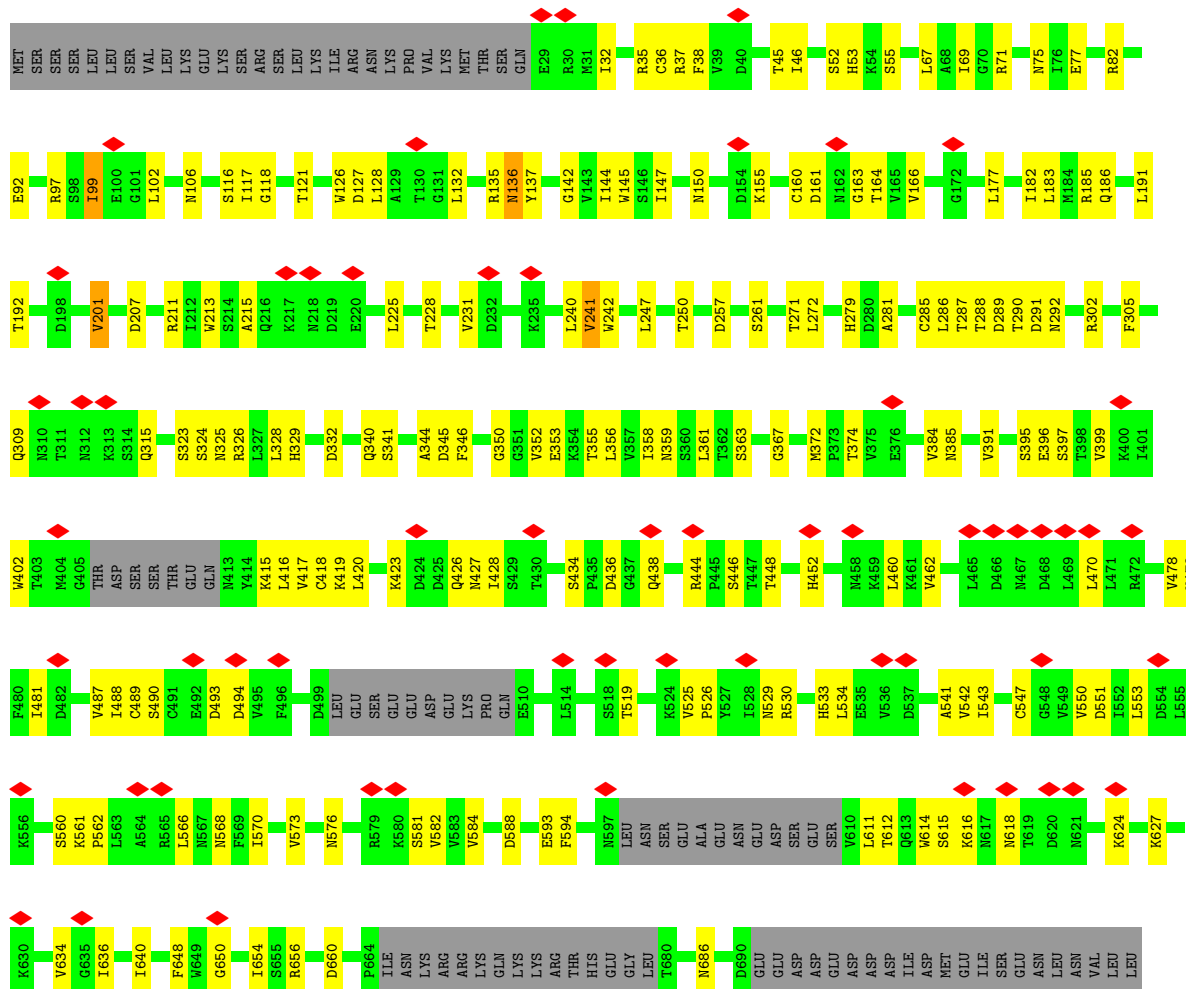
• Molecule 26: 13 kDa ribonucleoprotein-associated protein



- Molecule 26: 13 kDa ribonucleoprotein-associated protein

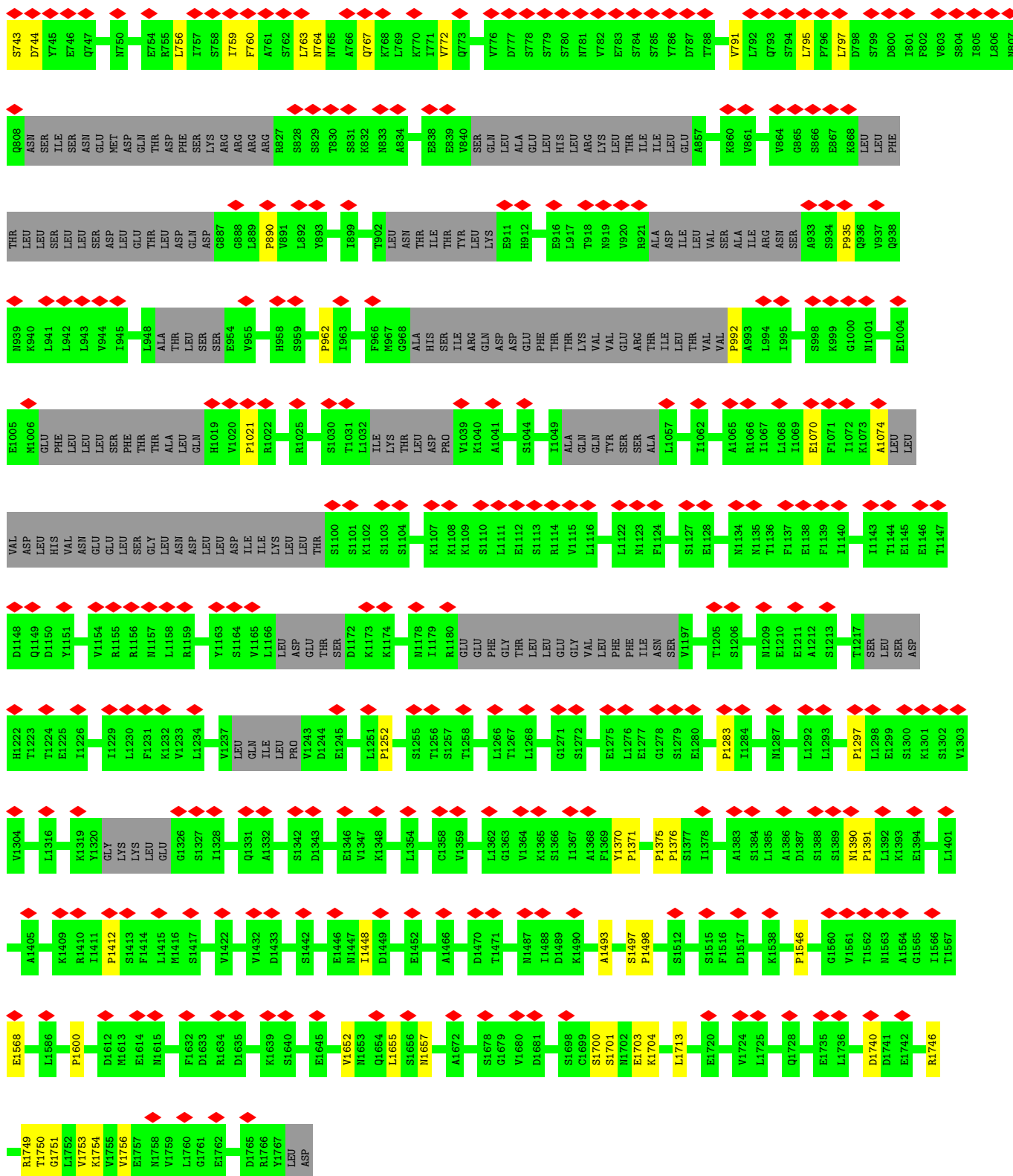


- Molecule 27: U3 small nucleolar RNA-associated protein 4

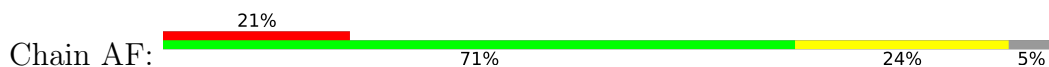


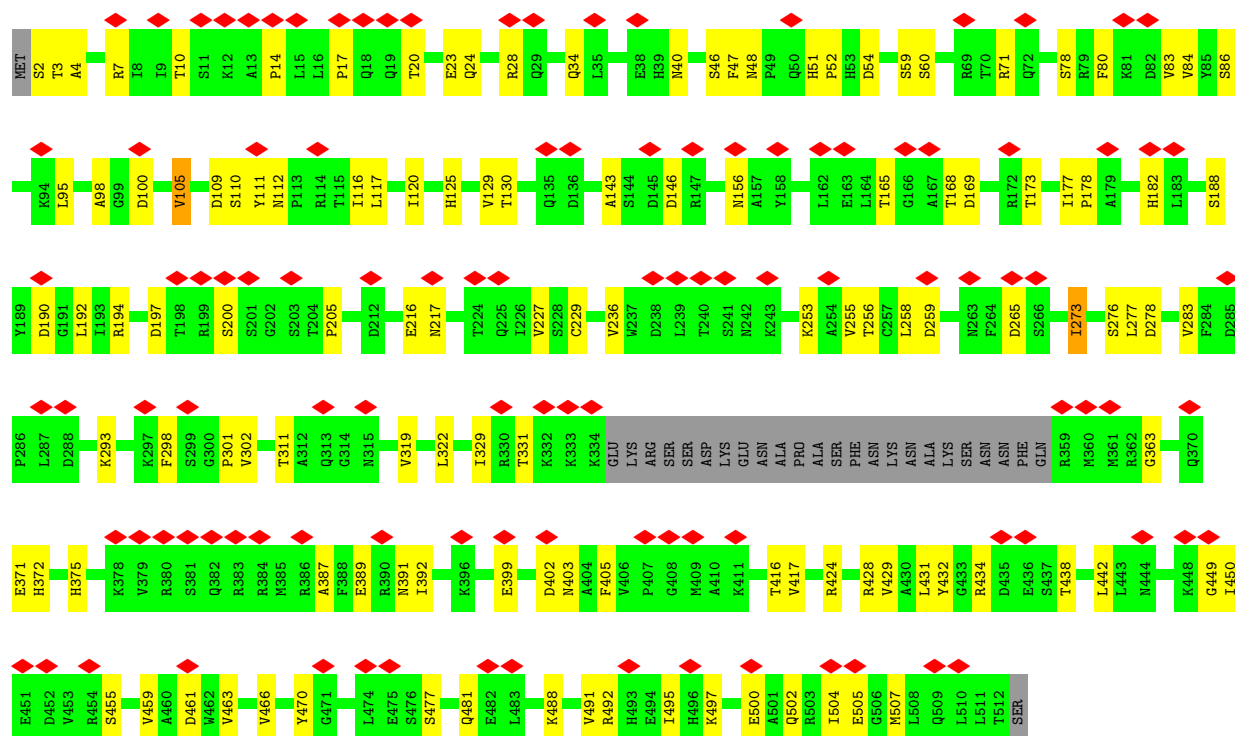






- Molecule 32: U3 small nucleolar RNA-associated protein 15

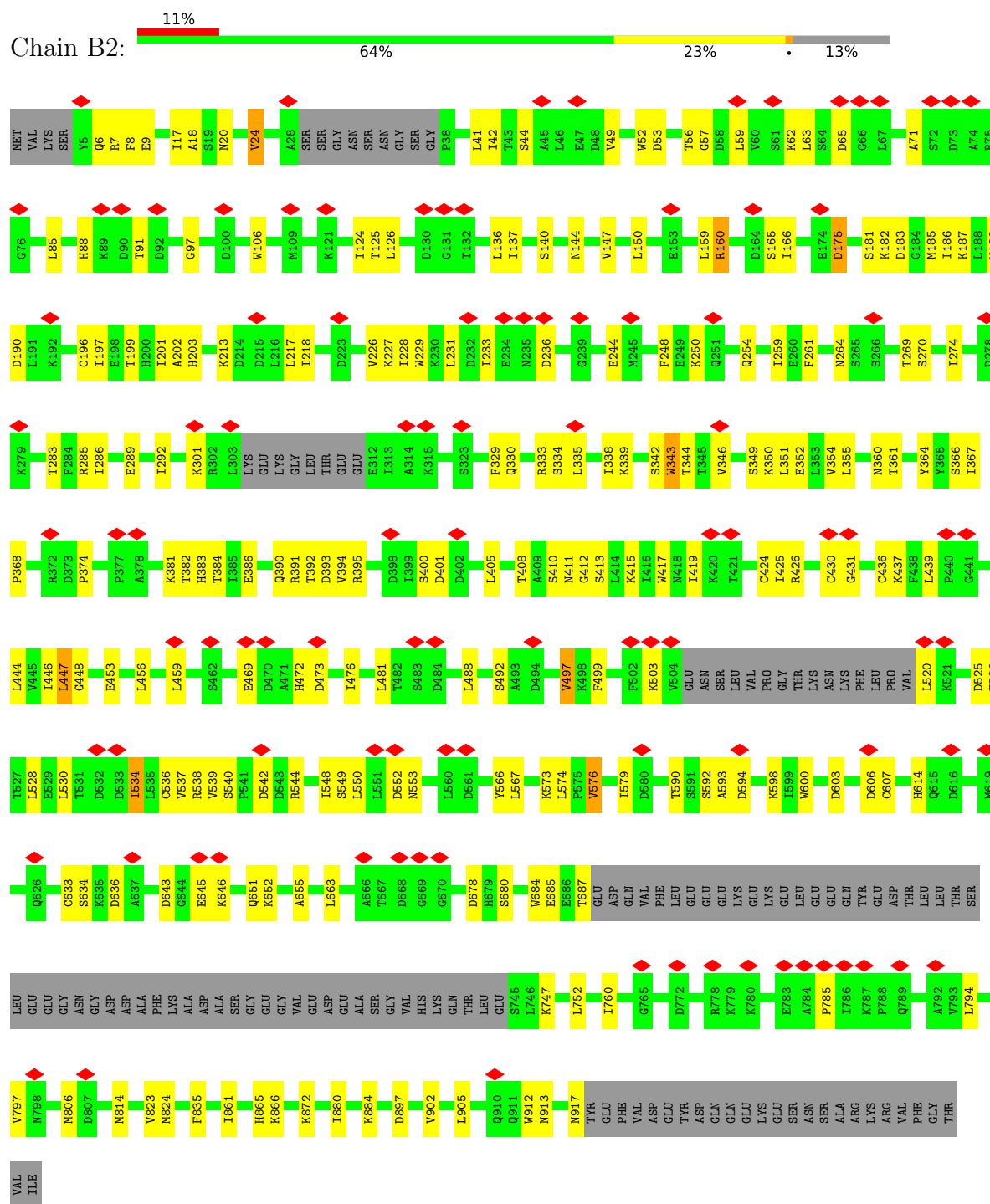




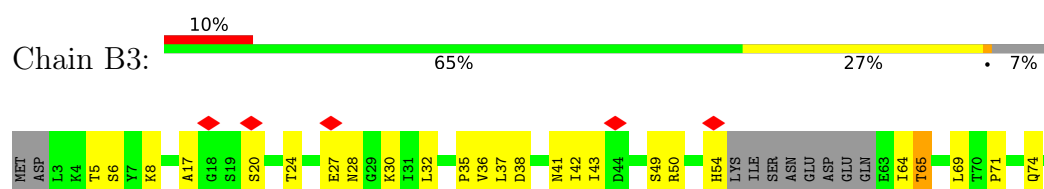
• Molecule 33: NET1-associated nuclear protein 1



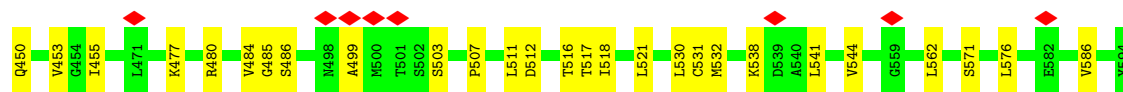
• Molecule 35: U3 small nucleolar RNA-associated protein 12



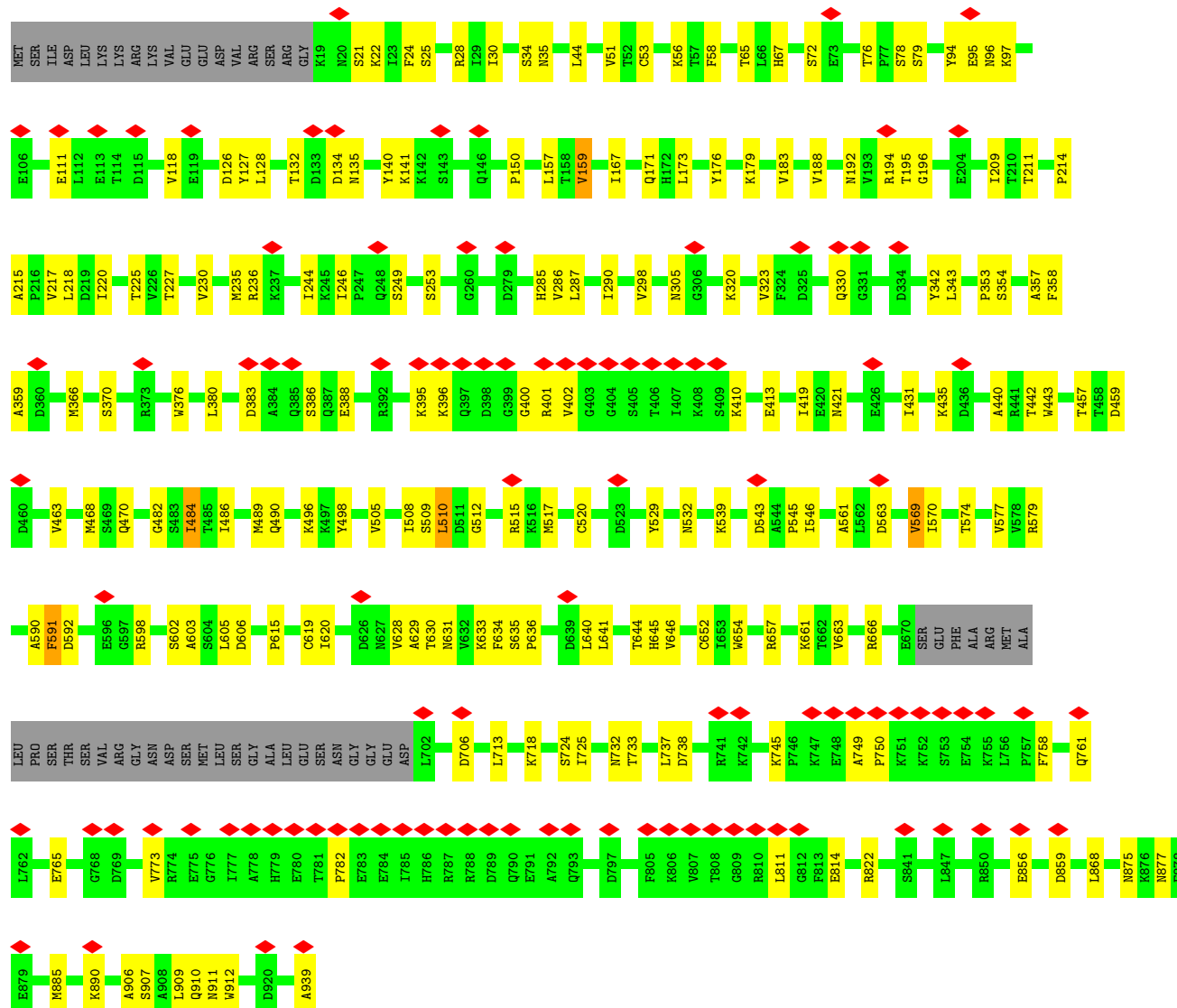
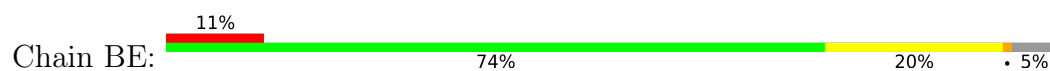
• Molecule 36: U3 small nucleolar RNA-associated protein 13



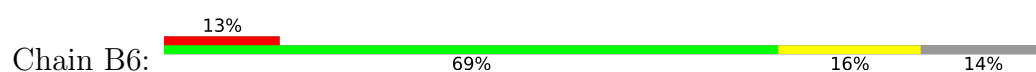


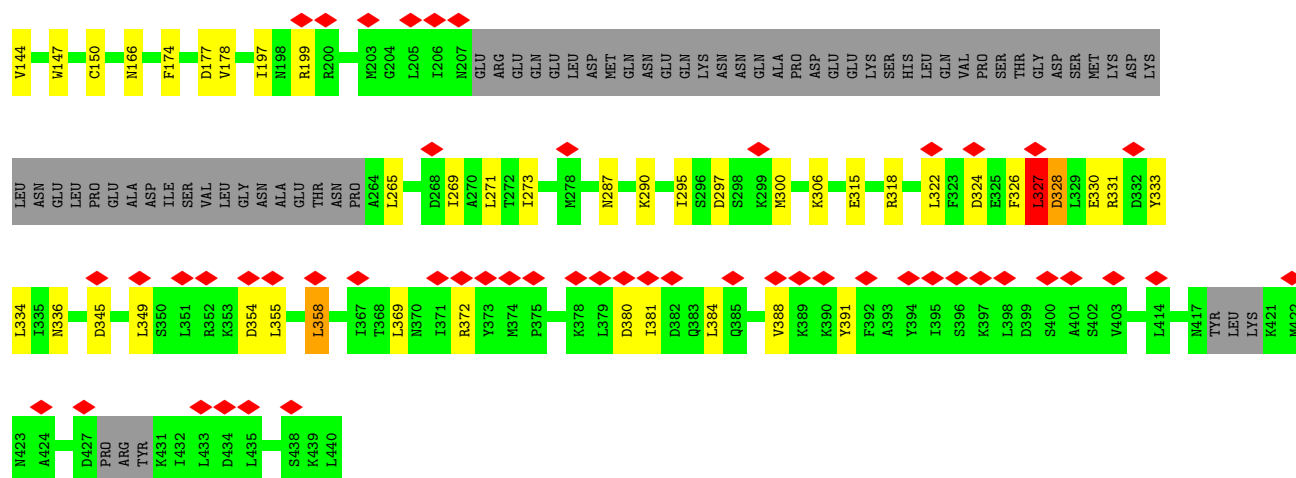


- Molecule 38: U3 small nucleolar RNA-associated protein 21

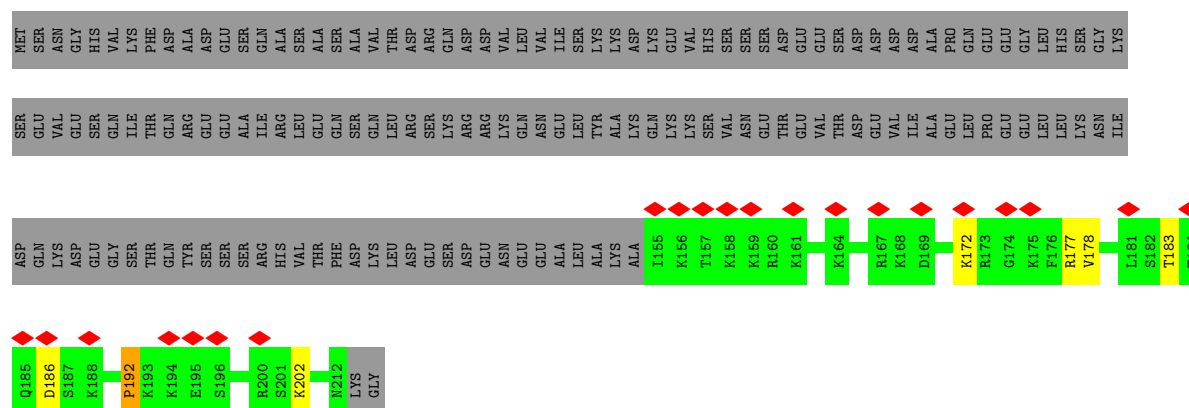


- Molecule 39: U3 small nucleolar RNA-associated protein 6

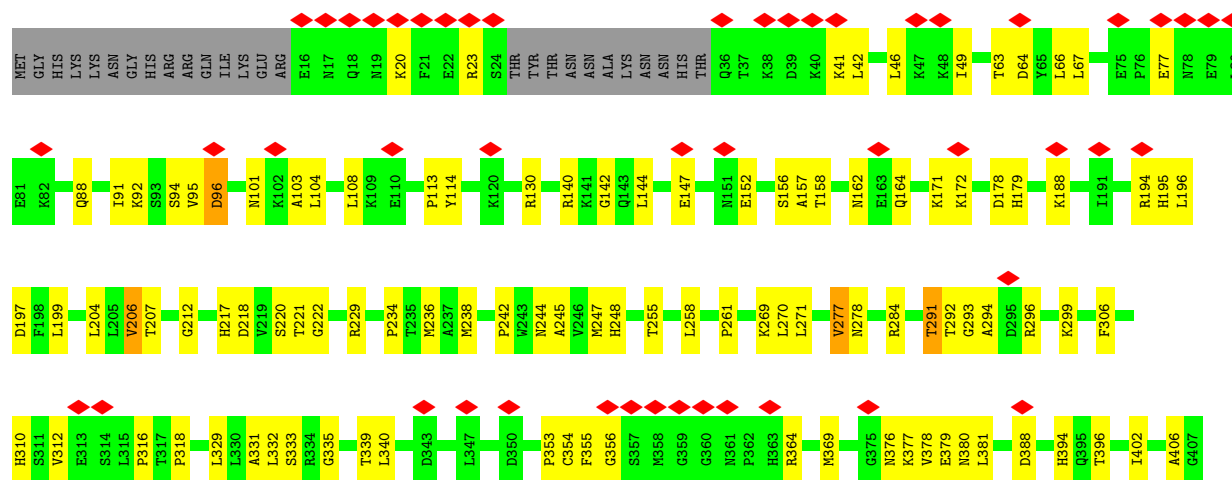


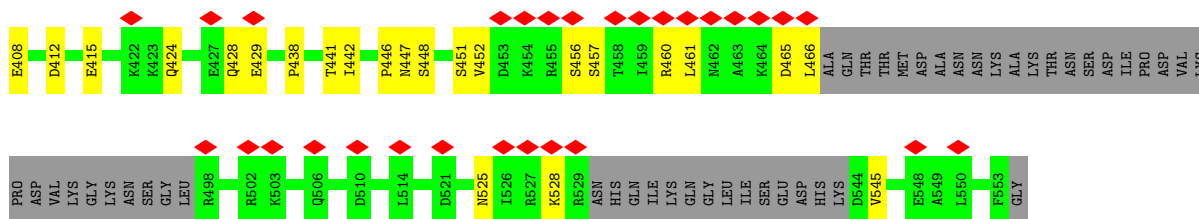


• Molecule 40: Bud site selection protein 21

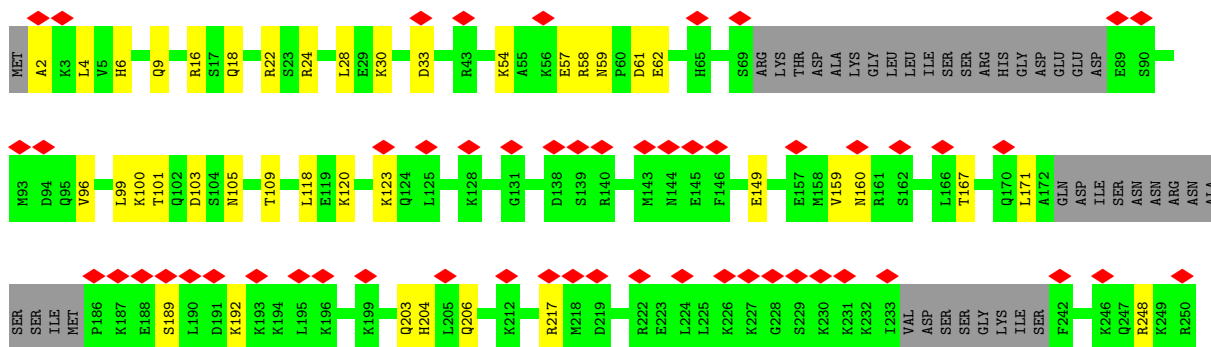


• Molecule 41: U3 small nucleolar RNA-associated protein 7

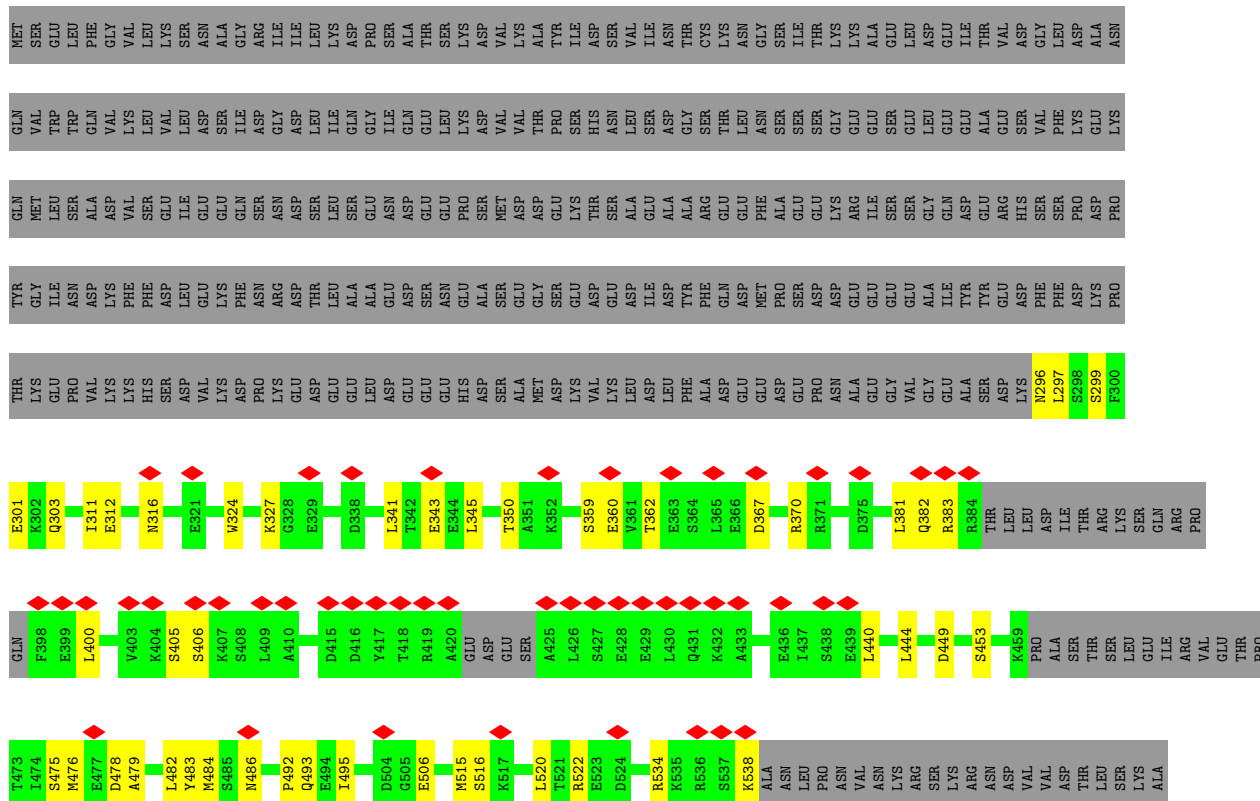


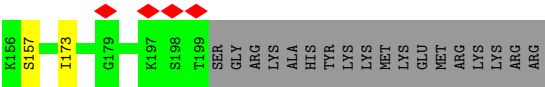


• Molecule 42: U3 small nucleolar RNA-associated protein 11

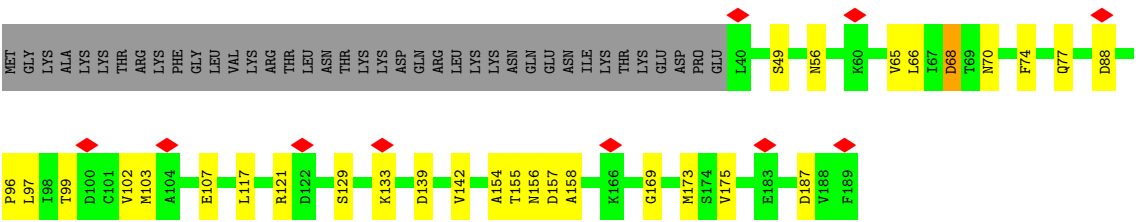


• Molecule 43: U3 small nucleolar RNA-associated protein MPP10

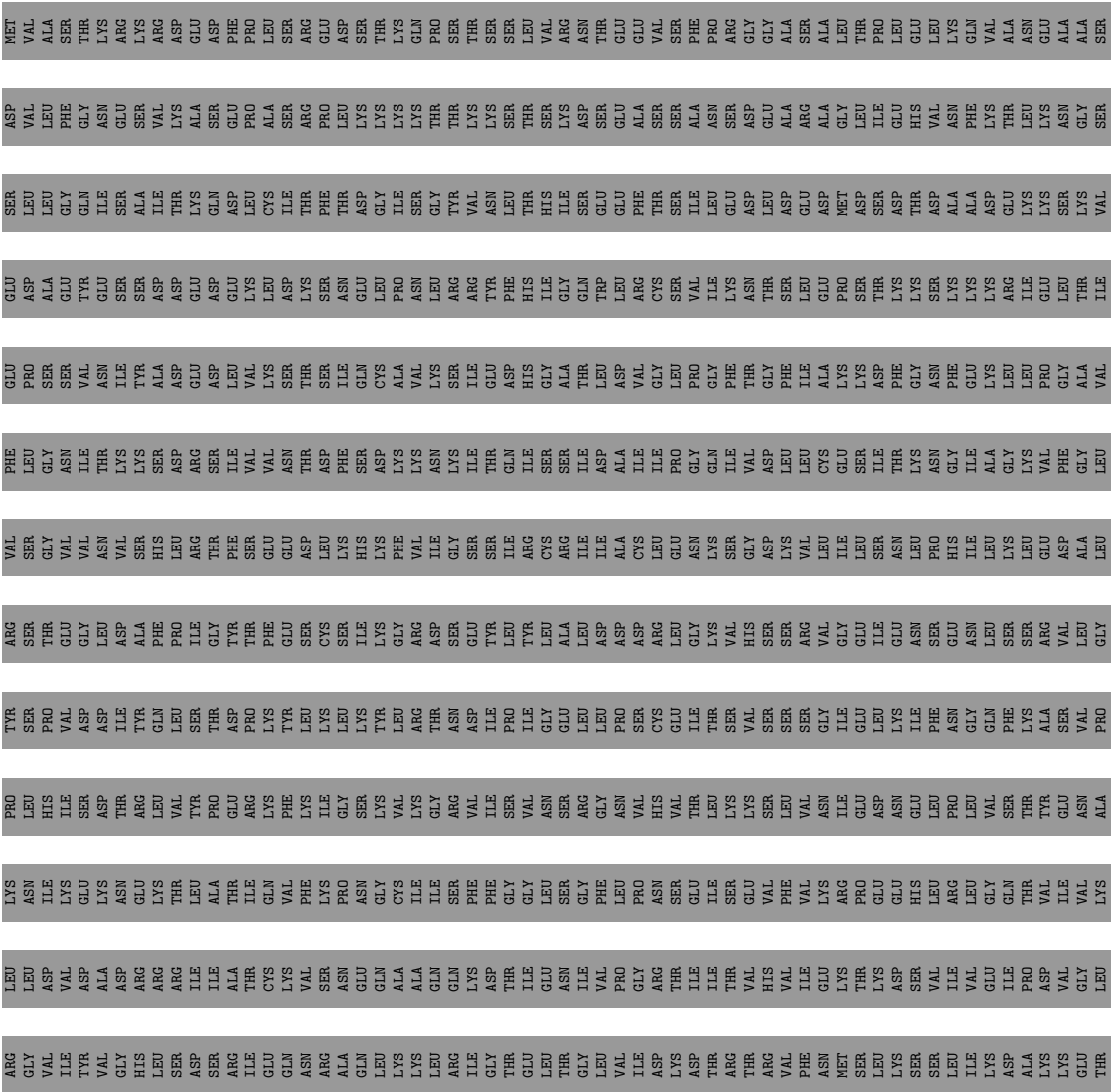




• Molecule 49: rRNA-processing protein FCF1

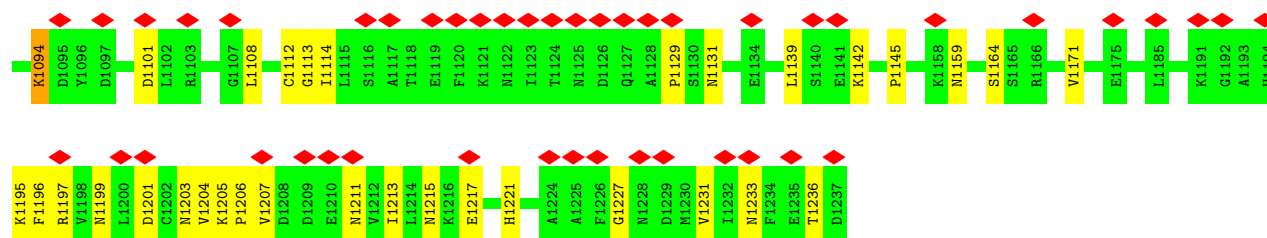


• Molecule 50: rRNA biogenesis protein RRP5

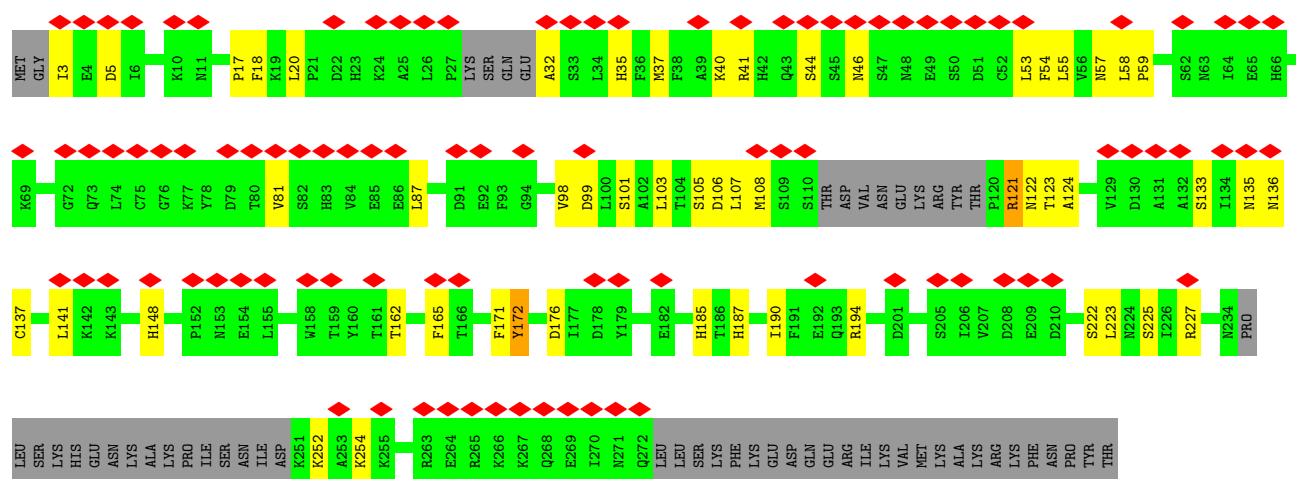


- Molecule 51: U3 small nucleolar RNA-associated protein 22

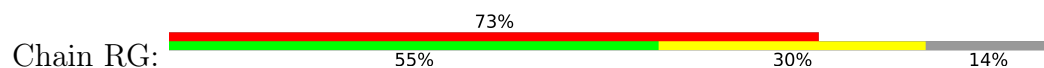




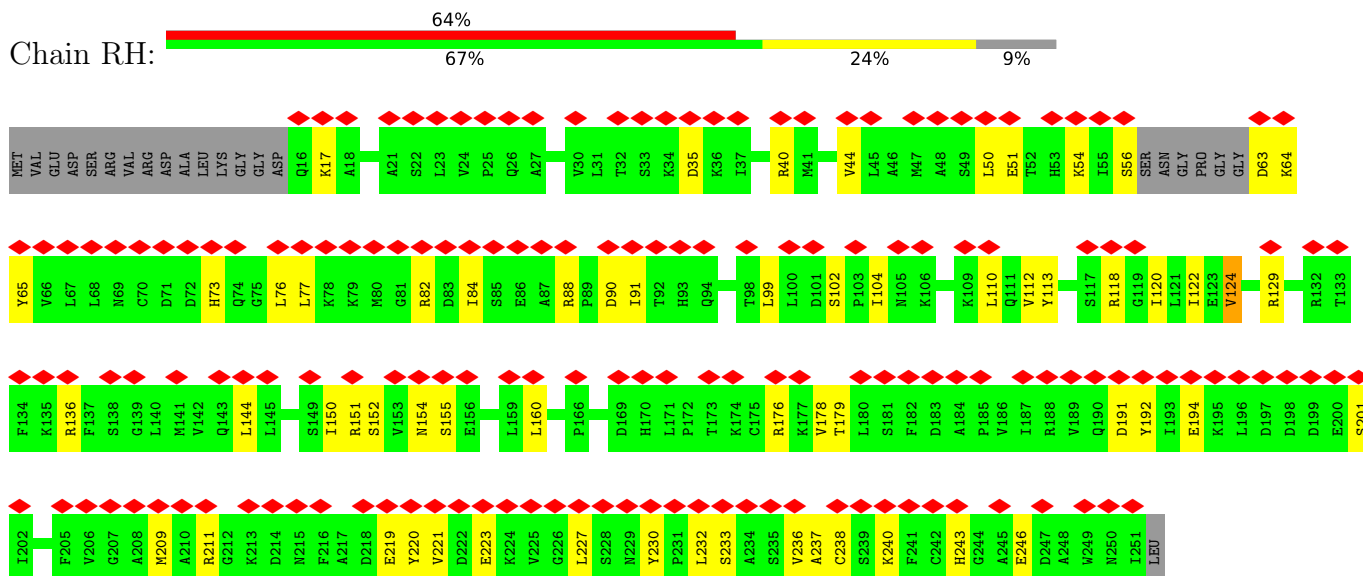
• Molecule 52: Ribosomal RNA-processing protein 7



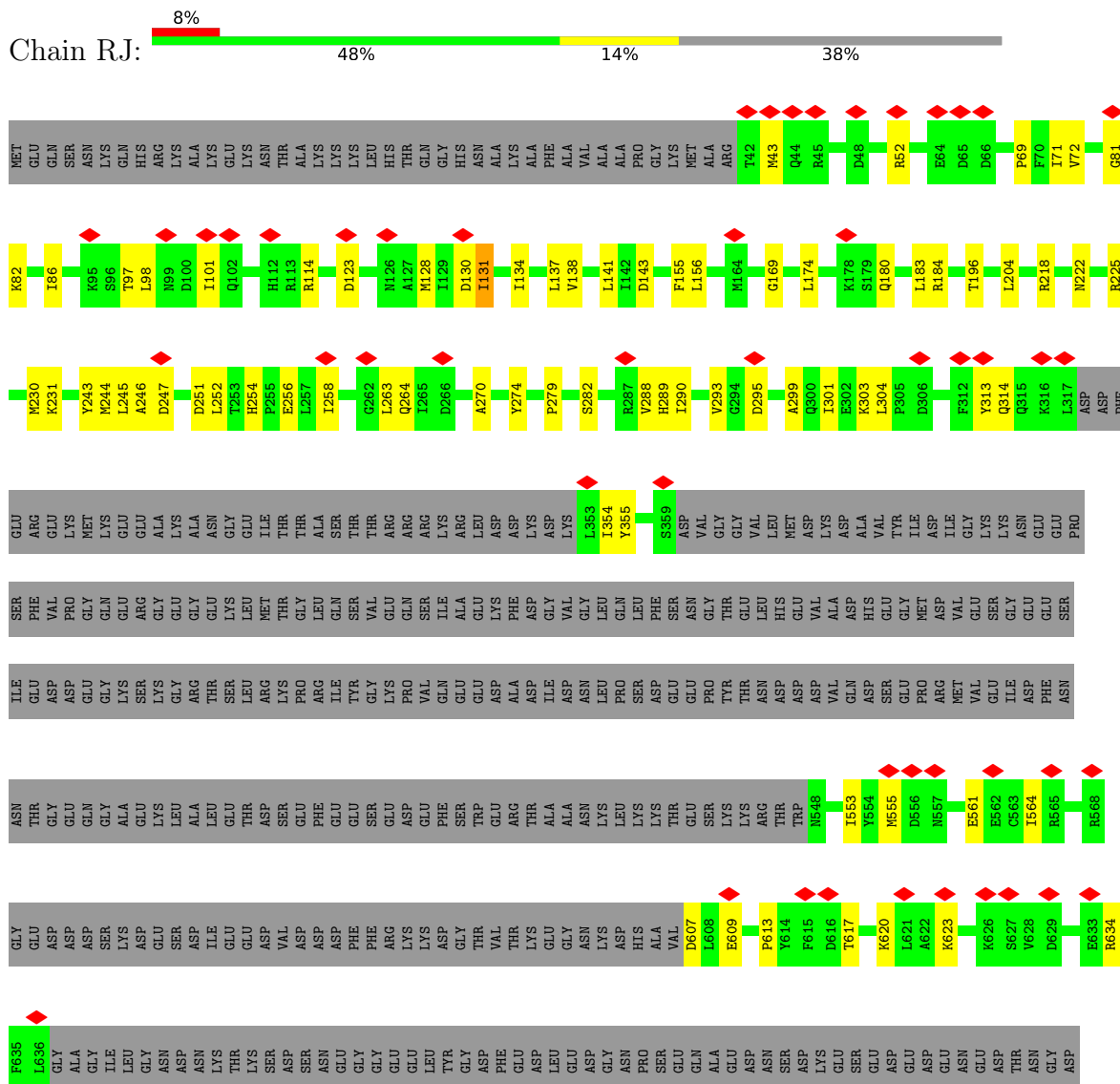
• Molecule 53: Ribosomal RNA small subunit methyltransferase NEP1

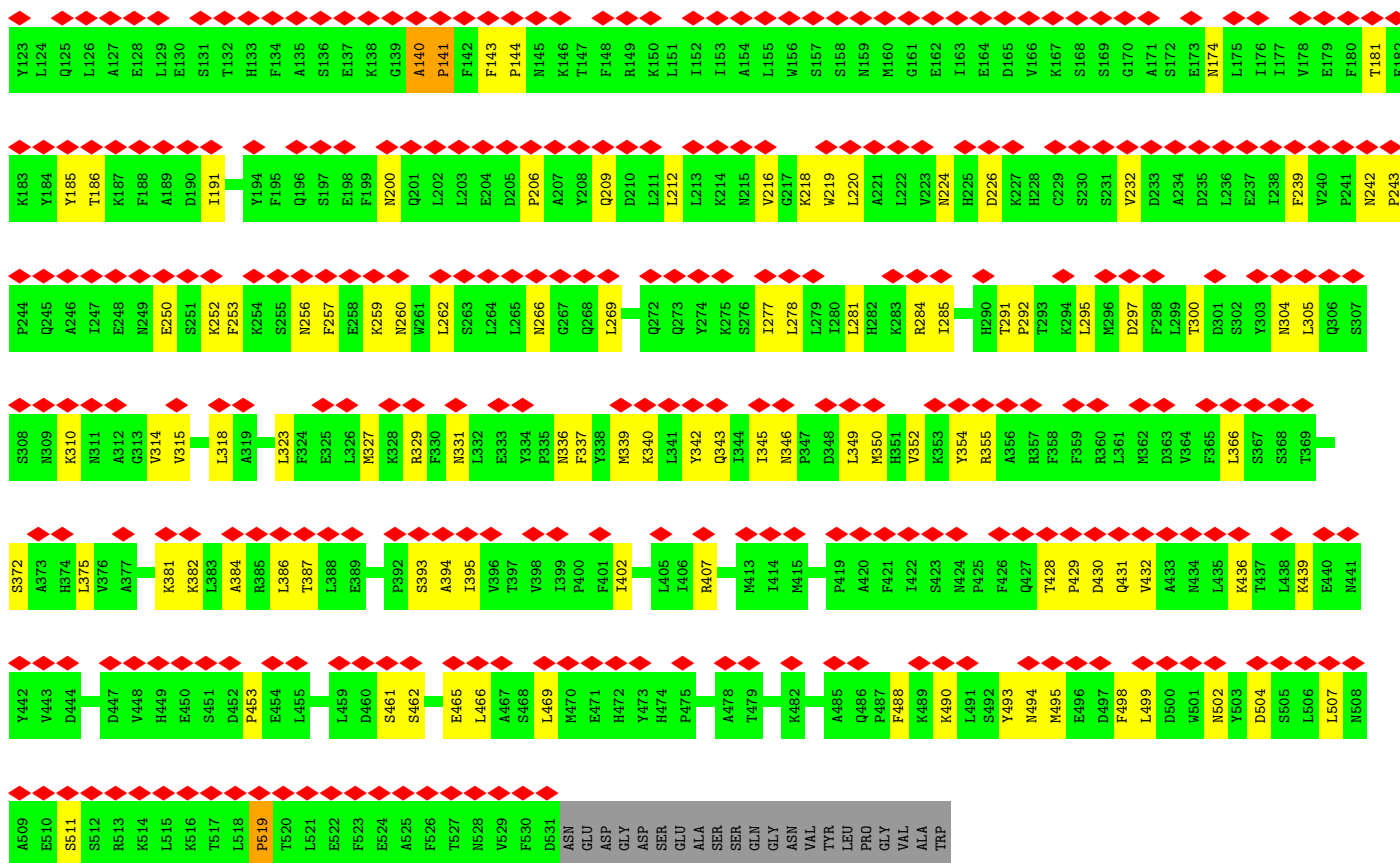


• Molecule 53: Ribosomal RNA small subunit methyltransferase NEP1

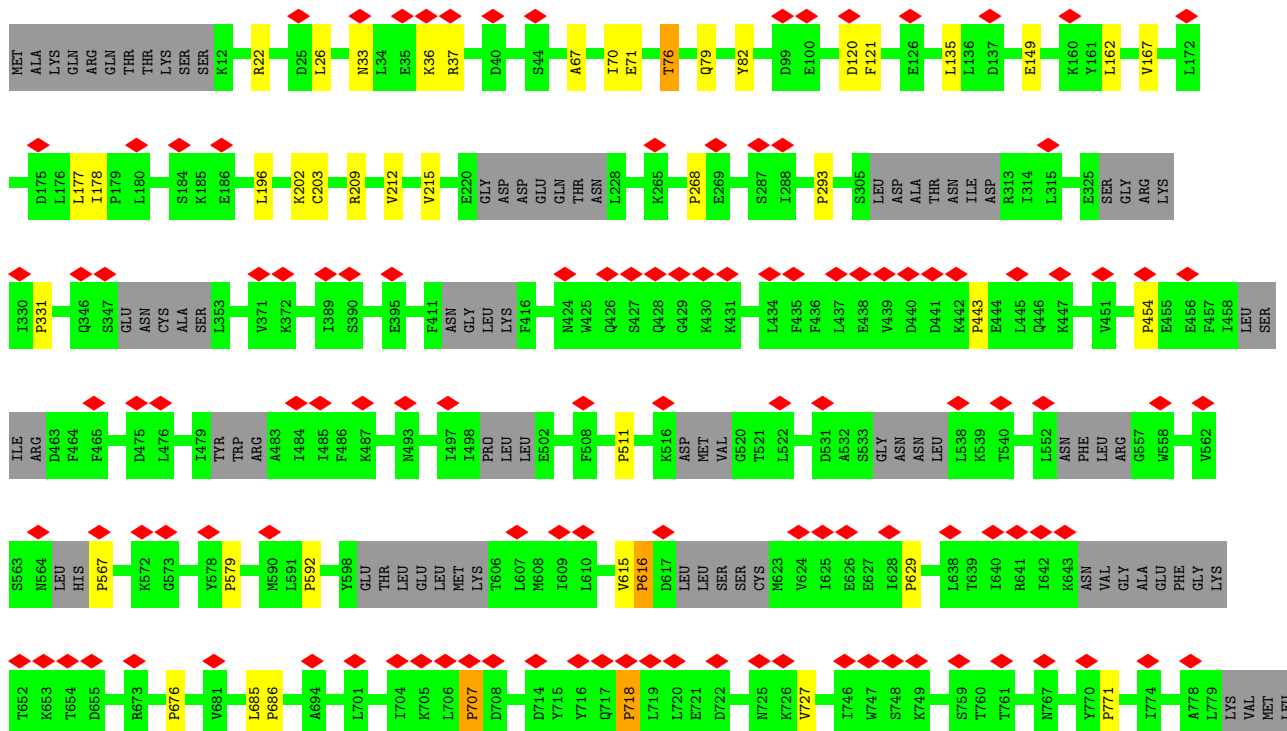
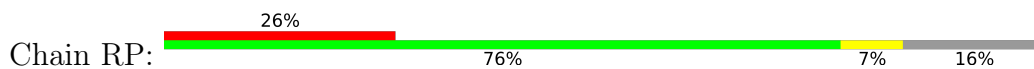


- Molecule 54: Ribosome biogenesis protein BMS1

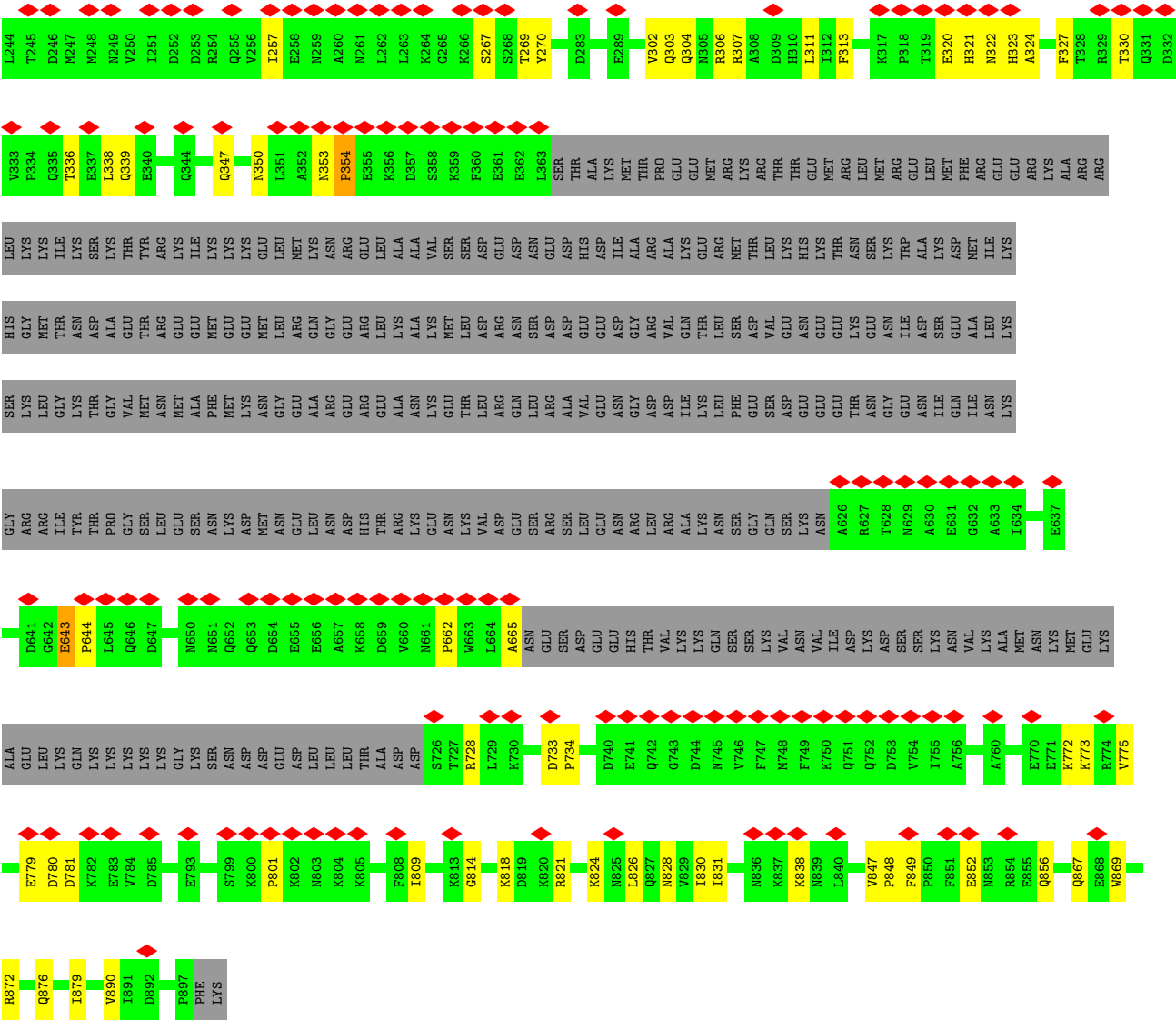




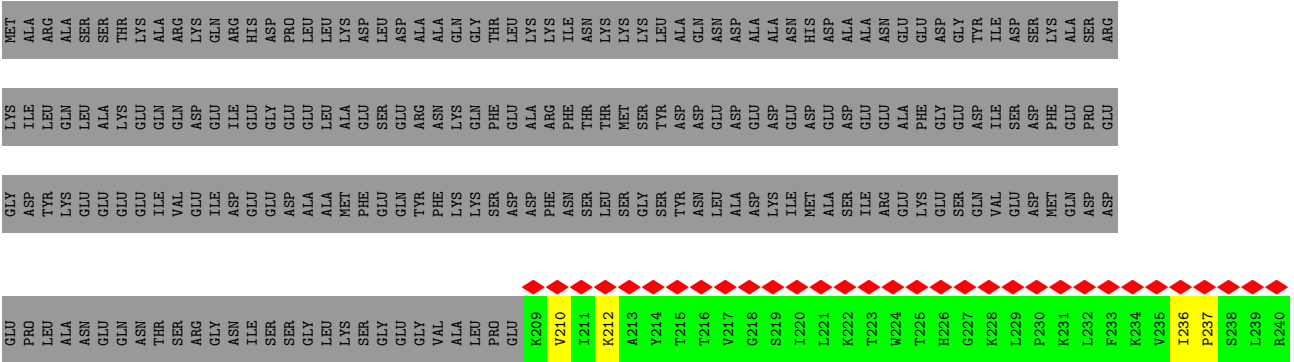
• Molecule 58: U3 small nucleolar RNA-associated protein 20

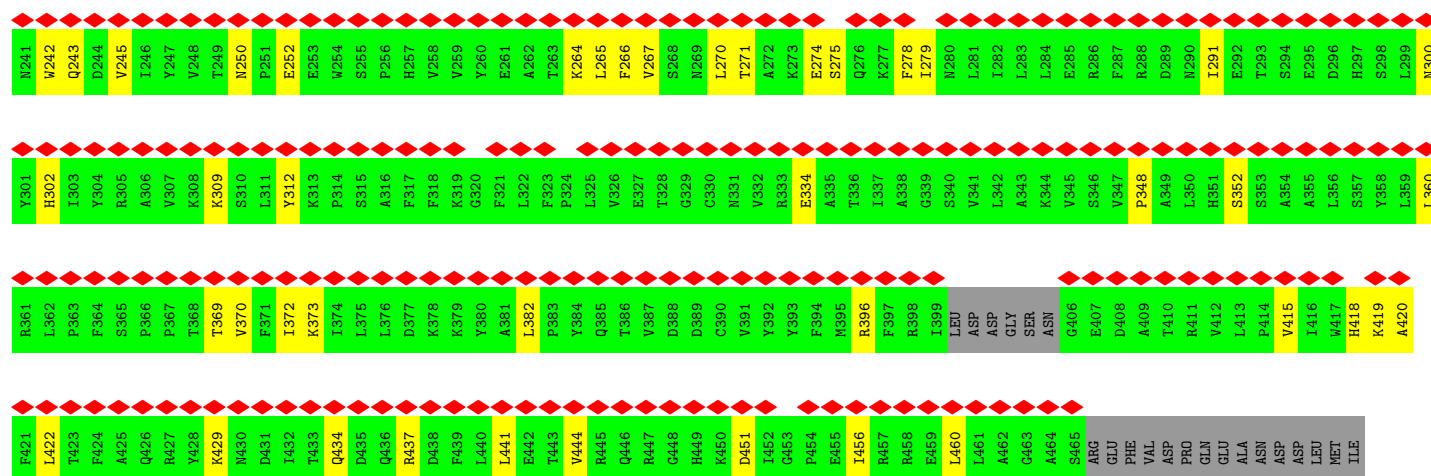




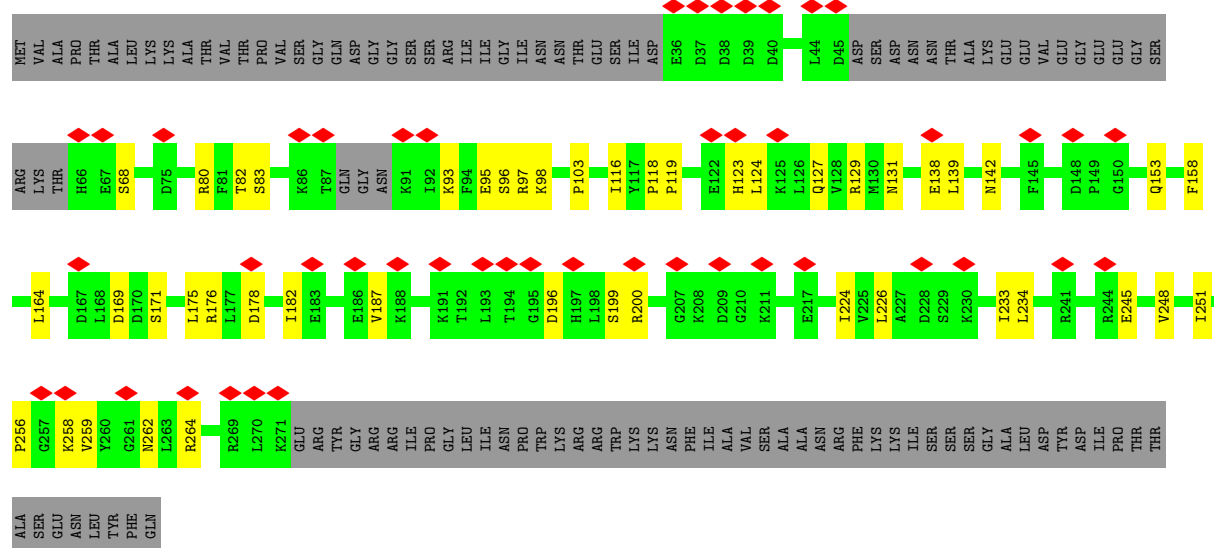


● Molecule 60: Essential nuclear protein 1

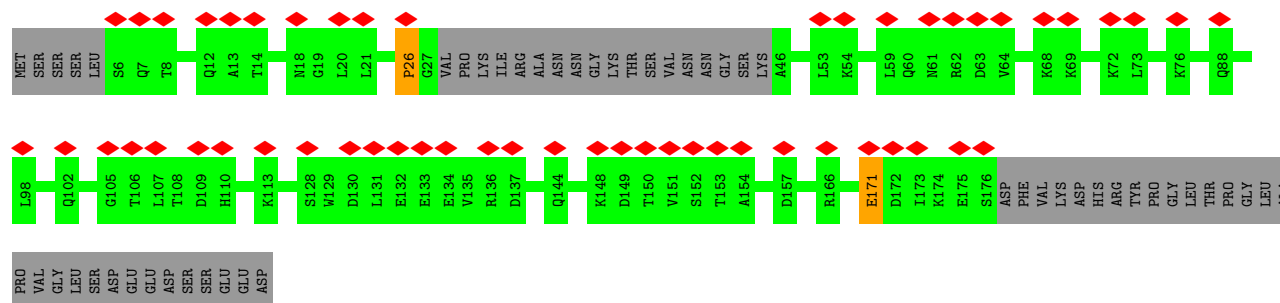
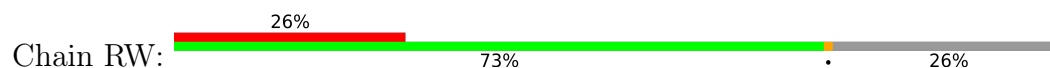




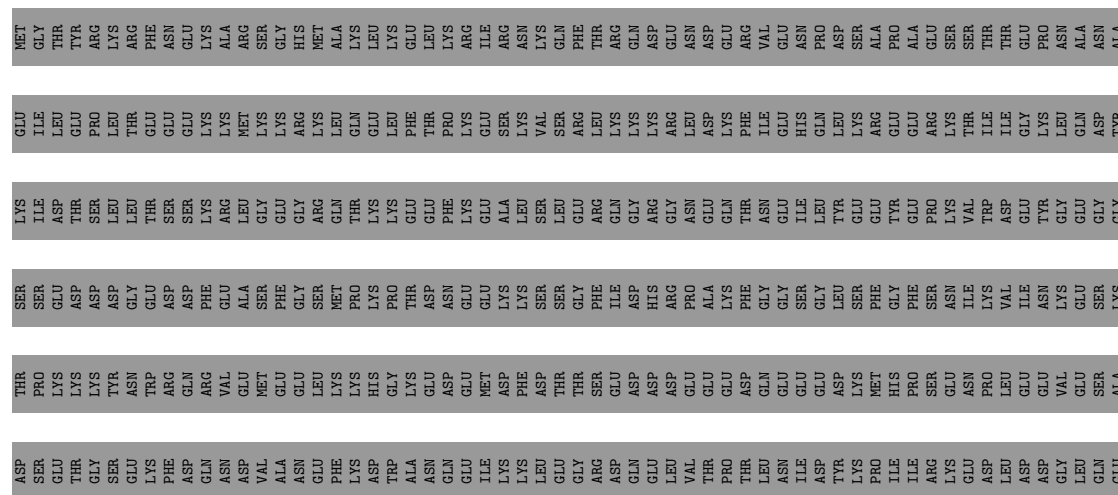
• Molecule 61: Pno1

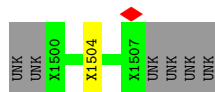


• Molecule 62: Regulator of rDNA transcription protein 14

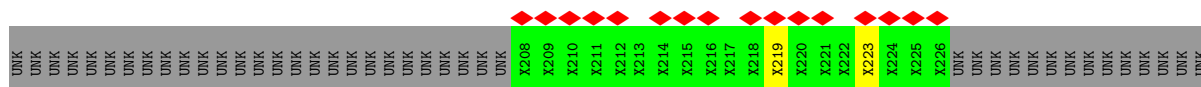
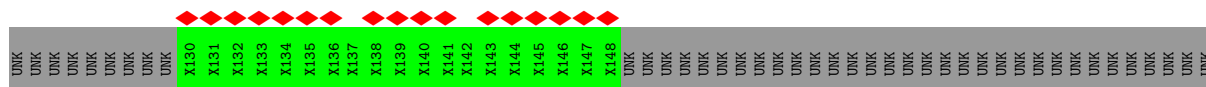
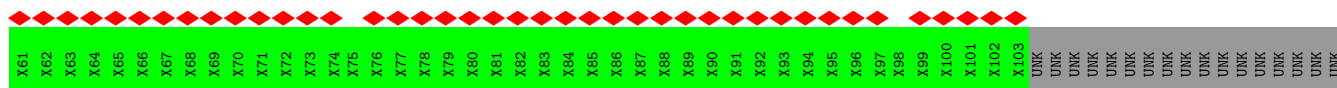


• Molecule 63: Probable ATP-dependent RNA helicase DHR1

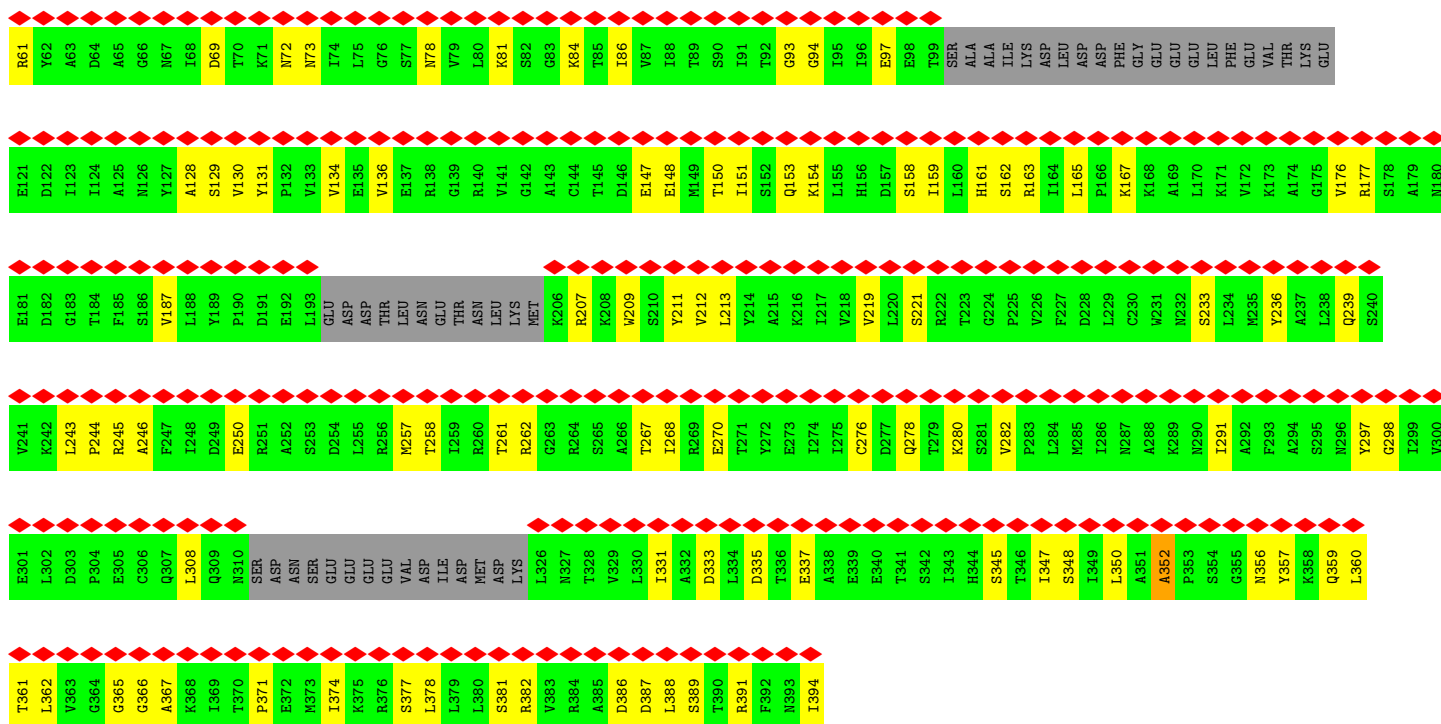




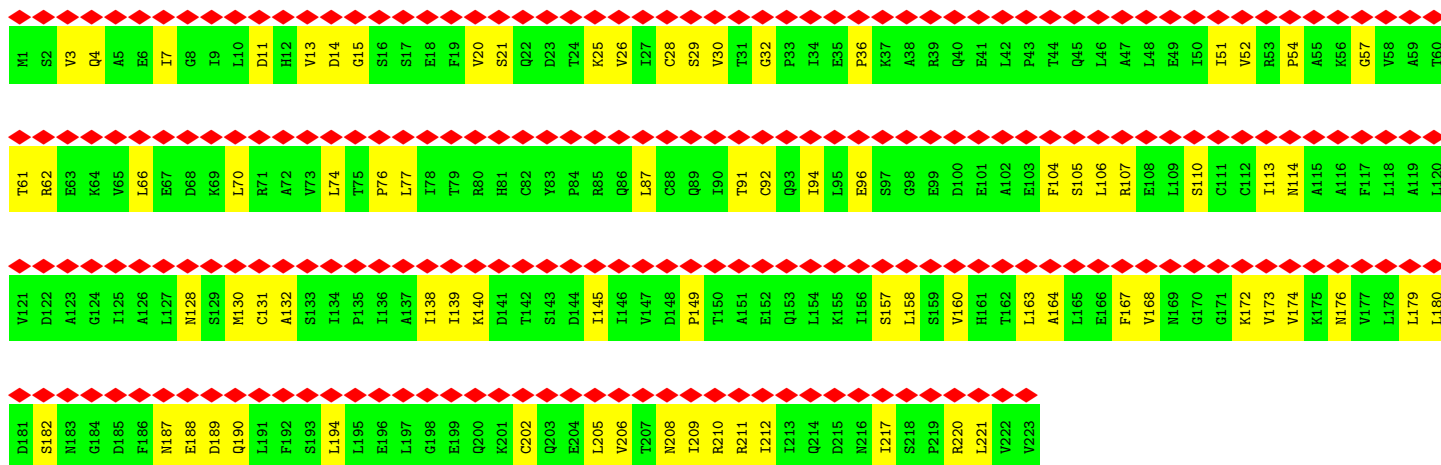
Chain X2:



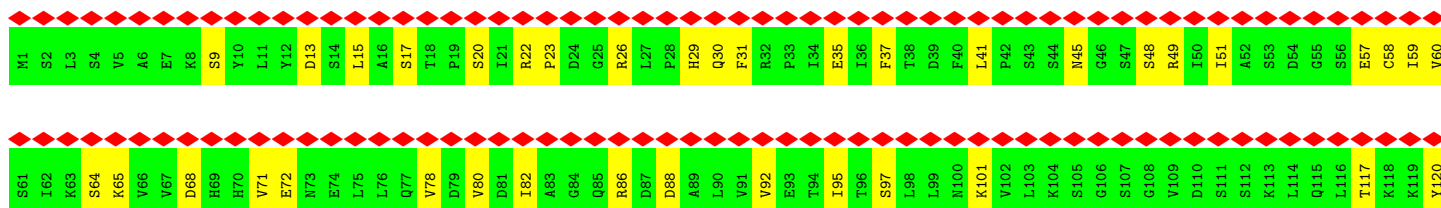
Chain R5: 98% 67% 31%



• Molecule 69: Exosome complex component RRP46

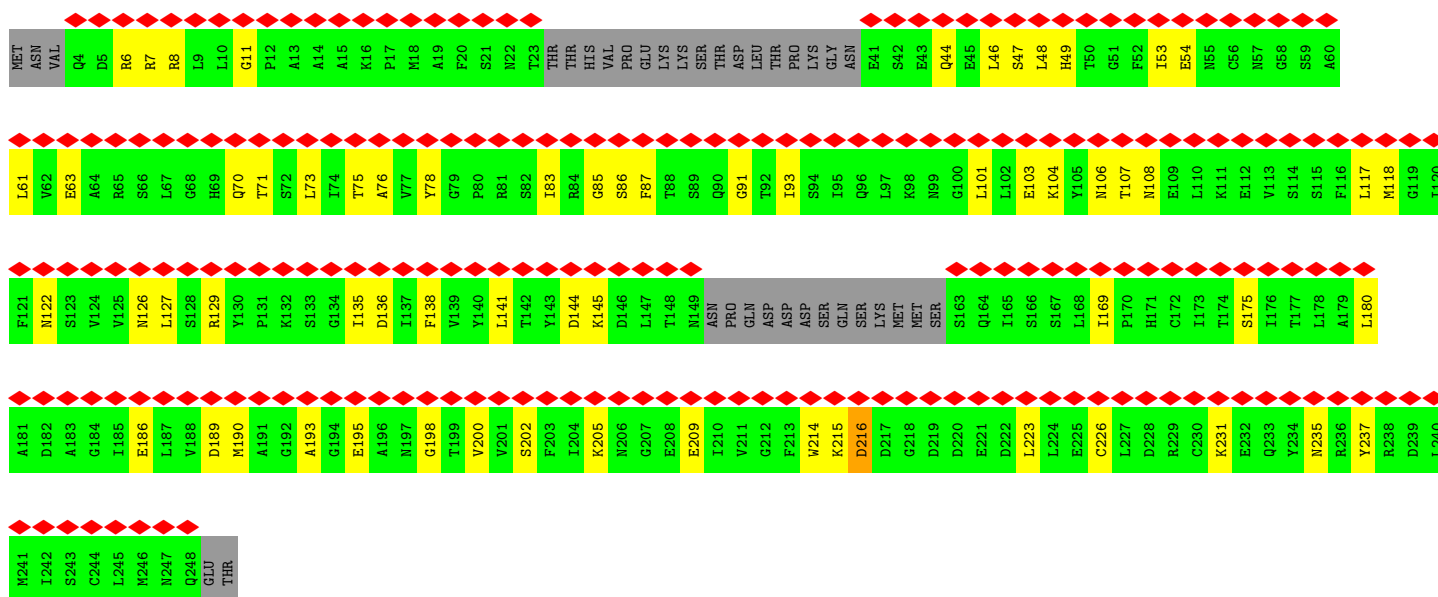


• Molecule 70: Exosome complex component RRP42

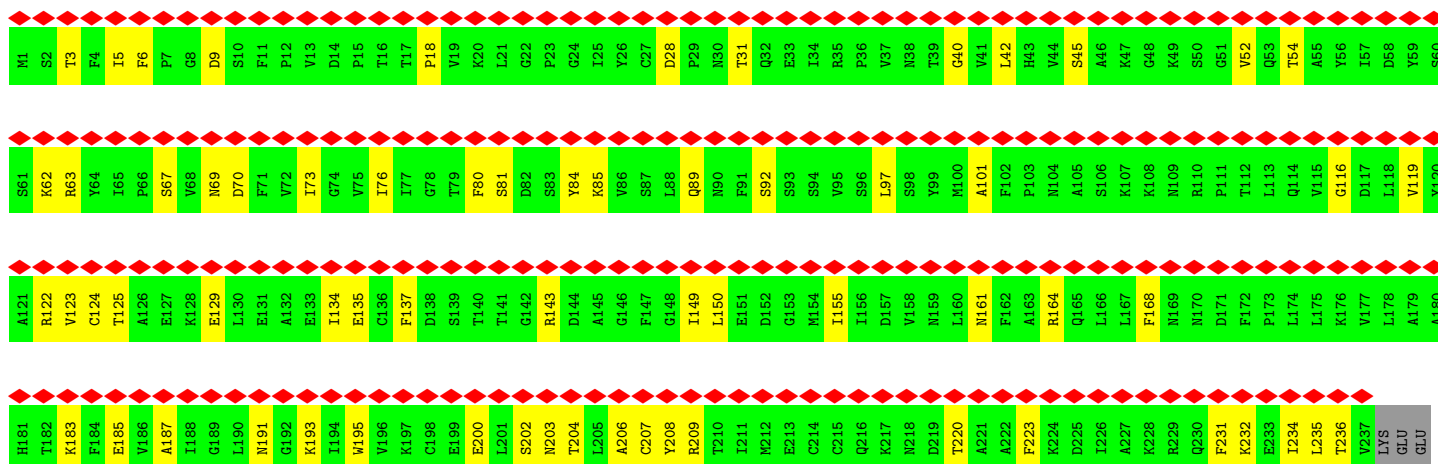
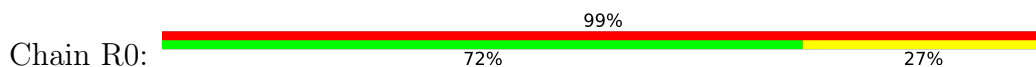




• Molecule 71: Exosome complex component MTR3

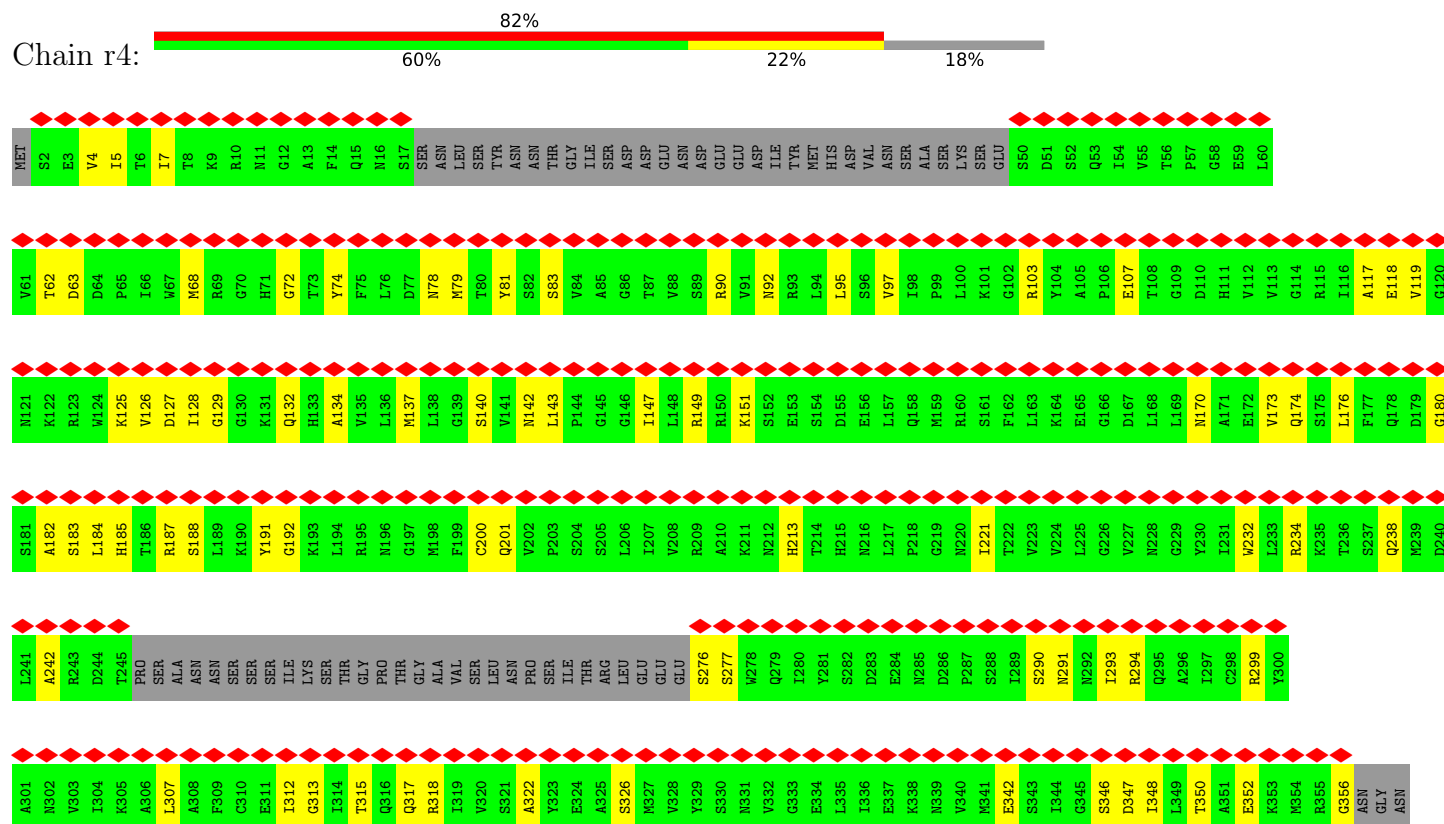


• Molecule 72: Exosome complex component RRP40

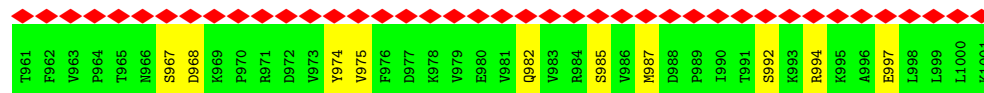
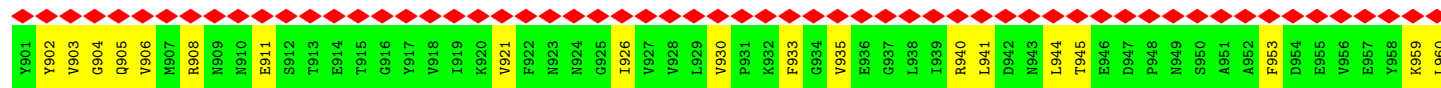
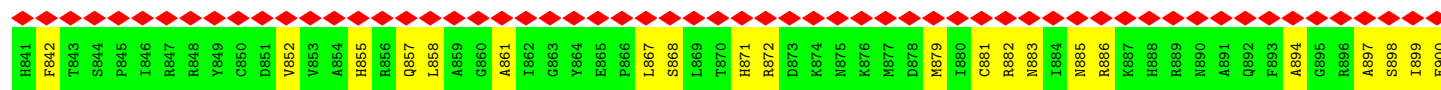


- Molecule 73: Exosome complex component RRP4

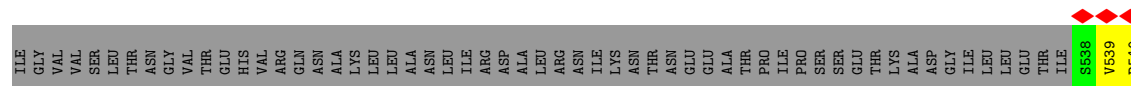
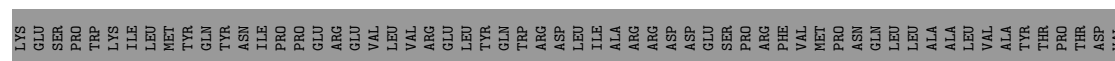
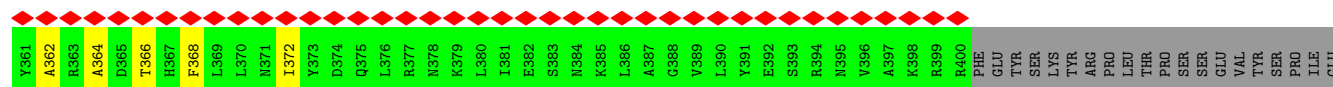
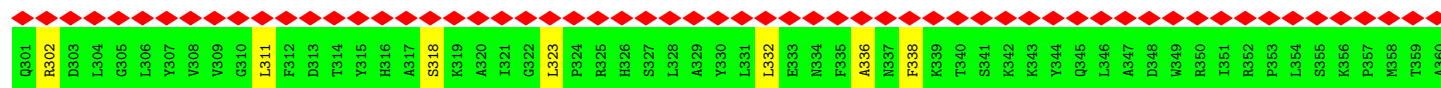
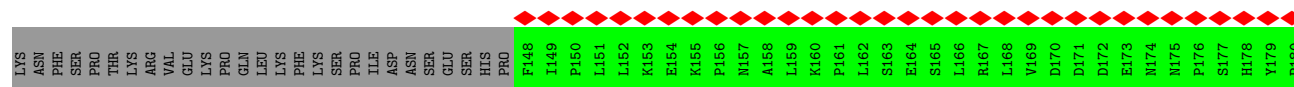
Chain r4:



781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860
L721	A722	T723	N724	S725	L726	V727	E728	G729	T730	M731	L732	L733	L734	N735	I736	S737	L738	A739	R740	K741	I742	Y743	D744	A745	F746	P747	Q748	T749	A750	M751	L752	R753	A754	H755	A756	A757	N758	P759	S760	T761	N762	F763	E764	T765	L766	N767	E768	T769	L770	N771	T772	R773	K774	N775	M776	S777	T778	S779	L780																				
E61	D62	A63	G64	N65	E66	L67	P68	K69	F70	L71	L72	S73	D74	S75	P76	L77	E78	L79	S80	A81	P82	I83	G84	H85	R86	Y87	V88	H89	L90	D91	T92	N93	A94	H95	L96	Q97	A98	I99	D100	L101	L102	E103	N104	P105	N106	C107	F108	D109	D110	V111	I112	P113	Q115	T116	L117	D119	E120																						
V121	R122	M123	K124	S125	Y126	P127	V128	I129	T130	R131	L132	L133	T134	L135	C136	D137	D138	S139	D140	D141	H142	K143	R144	F145	I146	V147	H149	N150	E151	F152	S153	E154	H155	T156	F157	V158	E159	R160	L161	P162	M163	T165	I166	M167	D168	R169	N170	D171	R172	A173	I174	R175	T177	C178	Q179	W180																							
Y181	S182	E183	H184	L185	K186	P187	Y188	D189	I190	N191	V192	L193	L194	V195	T196	D197	R198	R199	L200	D201	R202	E203	A204	A205	T206	K207	E208	V209	E210	S211	N212	I213	I214	T215	K216	S217	L218	V219	Q220	T221	I222	E223	L224	L225	P226	N227	A228	D229	D230	I231	R232	D233	S234	I235	T236	Q237	MET	ASP	SER																				
PHE	ASP	LYS	ASP	LEU	GLU	ARG	ASP	T249	F250	S251	D252	F253	T254	F255	P256	E257	Y258	Y259	S260	T261	A262	R263	V264	M265	G266	G267	L268	K269	N270	G271	V272	L273	Y274	Q275	G276	N277	I278	Q279	L280	V281	A282	S283	G284	E285	S286	G287	S288	G289	V290	ASP	ASN	L292	P293	R294	F295	S296	P298	L300																					
I301	V302	G303	Q304	K305	N306	L307	N308	R309	A310	F311	N312	G313	D314	Q315	V316	I317	V318	E319	L320	L321	P322	Q323	S324	G325	W326	K327	A328	P329	SER	SER	ILE	VAL	LEU	ASP	SER	GLU	PHE	ASP	VAL	ASN	ASP	ASN	ASP	PRO	ASP	ILE	GLU	ALA	GLY	ASP	ASP	ASP	ASN	GLU	SER	SER																							
ASN	THR	V364	I365	S366	D367	K368	Q369	R370	R371	L372	L373	A374	K375	D376	A377	M378	I379	A380	Q381	R382	S383	K384	K385	I386	Q387	P388	T389	A390	K391	V392	V393	Y394	I395	Q396	R397	R398	S399	W400	R401	Q402	Y403	V404	G405	Q406	L407	A408	P409	S410	S411	V412	D413	Q414	S416	S417	S418	T419	Q420																						
M421	V422	F423	V424	I425	L426	M427	D428	K429	C430	L431	P432	K433	V434	R435	I436	R437	L438	R439	R440	A441	A442	E443	L444	L445	D446	K447	R448	I449	V450	I451	S452	L453	D454	S455	W456	P457	L458	T459	H460	K461	Y462	P463	L464	Q465	H466	F467	V468	R469	L470	L471	Q472	I473	E475	S476	A477	Q478	A479	E480																					
T481	E482	A483	L484	L485	L486	E487	H488	D489	V490	E491	Y492	R493	A494	P495	F496	S496	K497	K498	V499	L500	E501	C502	L503	P504	A505	E506	G507	H508	D509	W510	K511	A512	P513	T514	K515	L516	D517	K518	P519	E520	A521	V522	S523	K524	D525	P526	L527	L528	T529	K530	R531	K532	D533	L534	R535	D536	K537	L538	I539	C540																			
S541	I542	D543	P544	P545	G546	C547	V548	D549	I550	D551	D552	A553	L554	H555	A556	K557	K558	L559	P560	N561	G562	N563	V564	E565	V566	G567	V568	H569	I570	A571	D572	V573	T574	H575	F576	V577	K578	P579	G580	T581	M582	L583	D584	A585	E586	G587	S588	A589	R590	G591	T592	S593	V594	Y595	L596	V597	D598	K599	R600																				
I601	D602	M603	L604	P605	M606	L607	L608	G609	T610	D611	L612	C613	S614	L615	K616	P617	Y618	V619	D620	R621	F622	A623	F624	S625	V626	I627	W628	E629	L630	D631	S632	S633	A634	M635	I636	V637	N638	V639	N640	F641	M642	K643	S644	V645	L646	R647	S648	R649	E650	A651	F652	S653	Y654	E655	Q656	A657	Q658	L659	R660																				
I661	D662	D663	K664	Q665	Q666	M667	D668	E669	L670	T671	M672	G673	M674	R675	A676	L677	L678	K679	L680	S681	V682	K683	L684	K685	Q686	K687	B688	L689	E690	A691	G692	A693	L694	M695	L696	A697	S698	P699	E700	V701	K702	V703	H704	M705	L706	S707	E708	T709	S710	D711	P712	N713	L714	E715	E716	I717	K718	K719	L720																				
L721	A722	T723	N724	S725	L726	V727	E728	G729	T730	M731	L732	L733	L734	N735	I736	S737	L738	A739	R740	K741	I742	Y743	D744	A745	F746	P747	Q748	T749	A750	M751	L752	R753	A754	H755	A756	A757	N758	P759	S760	T761	N762	F763	E764	T765	L766	N767	E768	T769	L770	N771	T772	R773	K774	N775	M776	S777	T778	S779	L780																				



● Molecule 76: Exosome complex exonuclease RRP6





E1021	E961	I901	T841	I781	V721	R661	P601	S841	P481	E421	S361
G1022	P962	E902	N842	R782	V722	Q662	E602	G542	P482	L422	ASN
S1023	L963	L903	S843	A783	V723	V663	F603	R543	L483	A423	GLN
L1024	K964	K904	N844	S784	N724	V664	M604	A544	K484	L424	ILE
I1025	G965	G905	R845	Q785	T725	T665	L605	G545	E485	K425	GLY
R1026	M966	R906	L846	G786	M726	H666	E606	R546	M426	M426	ASP
M1027	R967	V907	E847	K787	Y727	P667	H607	R547	S427	S427	PRO
F1028	E968	A908	E848	E788	I728	A668	S608	G548	K428	K428	ASN
K1029	I969	C909	L849	T789	D729	N669	F609	L549	L429	L429	THR
A1030	A970	E910	Y850	V790	S730	A670	F610	D550	L430	L430	ASP
L1031	A971	I911	G851	G791	P731	L671	Q611	D551	F431	F431	SER
E1032	K972	S912	K852	K792	V732	S672	F612	R552	M432	M432	ARG
L1033	I973	S913	S853	S793	M733	F673	Q613	G553	S433	S433	LYS
A1034	A974	G914	S854	L794	L734	L674	N614	I554	D434	D434	LYS
V1035	K975	D915	R855	R795	L735	Q675	V615	V555	D435	D435	GLY
K1036	I976	E916	K856	E796	K736	P676	I616	I556	E436	E436	GLN
L1037	M977	L917	H857	V797	F737	G677	S617	M557	K437	K437	THR
E1038	K978	N918	D858	N798	F738	R678	V618	M558	E438	E438	LYS
V1039	D979	L919	L859	R799	M739	L679	P619	I559	A439	A439	GLY
D1040	S980	T920	H860	R800	P740	V680	V620	D560	L440	L440	SER
V1041	K981	E921	E861	F801	T741	E681	M621	E561	T441	T441	ALA
M1042	I982	L922	D862	P802	L742	I682	E522	K562	K442	K442	LYS
M1043	E983	I923	K863	D803	F743	S683	K623	M563	I443	I443	ASP
T1044	V984	F924	K864	G804	E744	V684	K624	E564	F444	F444	ALA
I1045	N985	N925	Q865	I805	G745	N685	L625	P665	N445	N445	LYS
G1046	E986	G926	L866	P806	I746	G686	A626	Q566	N446	N446	D392
M1047	K987	N927	K867	V807	R747	K687	E527	V567	A447	A447	D393
S1048	D988	F928	R868	L808	F748	D688	L628	A568	I448	I448	I394
L1049	Y989	N929	K869	D809	A749	N689	K629	K569	A449	A449	Y395
L1050	V990	E930	T870	P810	E750	G690	K630	G570	L450	L450	K396
K1051	E991	L931	S871	V811	E751	G691	D631	M571	L451	L451	I397
S1052	S992	K932	E872	K812	G752	N692	F632	V572	P452	P452	V398
K1053	P993	P933	S873	N813	E753	G693	D633	K573	E453	E453	K399
M1054	R994	E934	K874	M814	K754	A694	G634	G574	T454	T454	M400
E1055	H995	Q935	A875	K815	S755	V695	I635	Q575	D455	D455	I401
A1056	E996	A936	V876	I816	I756	V696	E636	A576	R456	R456	W402
V1057	L997	A937	L877	E817	C757	D697	V637	D577	E457	E457	K403
L1058	M998	F938	K878	D818	A758	F698	E638	R578	L458	L458	K404
K1059	E999	L939	L879	E819	V759	A699	D639	L579	P459	P459	K405
V1060	V1000	L940	D880	D820	I760	K700	E640	D580	Q460	Q460	Y406
I1061	V1001	S941	D881	F821	F761	R701	E641	S881	I461	I461	N407
H1062	Y1002	C942	L882	L822	I762	I702	N642	A582	K462	K462	P408
R1063	E1003	F943	K883	K623	T763	N703	V643	F583	H463	H463	V409
D1064	V1004	A944	R884	L824	L764	K704	K644	H584	I464	I464	I410
I1065	C1005	F945	R885	N825	D765	R705	E645	L585	L465	L465	V411
V1066	R1006	D946	K886	K826	S766	N706	Y646	G586	P466	P466	F412
G1007	G1007	E947	R887	K827	I767	P707	H647	Y887	L467	L467	S413
A1008	A1008	R948	V888	I828	K768	S708	E648	N588	L468	L468	F414
T1009	C949	C949	L889	D829	S769	A709	I649	M589	R469	R469	S415
F1010	K950	K950	R890	V830	I770	V710	E650	I590	R470	R470	K416
T1011	E951	E951	R891	L831	G771	Y711	Q651	L591	G471	G471	R417
Q1012	A952	A952	L892	N832	N772	T712	A652	N592	I472	I472	D418
I1013	P953	P953	G893	T833	L773	D713	I653	L593	G473	G473	C419
C1014	R954	R954	F894	K834	R774	H714	K654	M594	I474	I474	E420
K1015	L955	L955	C895	L835	L775	E715	G655	R595	H475	H475	
M1016	K956	K956	T896	S836	Y776	S716	Y656	V596	H476	H476	
T1017	P957	P957	R897	S837	M777	T717	E657	E597	S477	S477	
D1018	E958	E958	N898	N838	P778	I718	R658	G598	G478	G478	
V1019	L959	L959	D899	P839	K779	V719	D659	I599	L479	L479	
L1073	A960	A960	I900	L840	D780	N720	V660	S600	M480	M480	

• Molecule 79: M-phase phosphoprotein 6 homolog



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	219545	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	0.120	Depositor
Minimum map value	-0.072	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.025	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: ADP, 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	0.30	0/5088	0.46	1/7888 (0.0%)
2	5A	0.22	0/2833	0.41	1/4401 (0.0%)
3	SA	0.27	0/31829	0.46	5/49545 (0.0%)
4	SC	0.35	0/1949	0.71	1/2609 (0.0%)
5	SF	0.32	0/1954	0.69	3/2640 (0.1%)
6	SG	0.34	0/1690	0.65	0/2285
7	SH	0.22	0/1476	0.58	0/1975
8	SI	0.29	0/1341	0.78	5/1806 (0.3%)
9	SJ	0.23	0/1202	0.64	0/1610
10	SK	0.37	0/1432	0.68	0/1917
11	SM	0.23	0/1139	0.56	1/1535 (0.1%)
12	SO	0.32	0/1109	0.60	0/1495
13	SP	0.31	0/859	0.64	0/1161
14	SR	0.39	0/990	0.70	0/1335
15	ST	0.24	0/914	0.63	0/1229
16	SU	0.27	0/1092	0.55	0/1466
17	SX	0.34	0/1020	0.66	0/1371
18	SY	0.35	0/804	0.63	0/1074
19	SZ	0.38	0/1000	0.68	0/1334
20	Sc	0.34	0/613	0.64	0/828
21	Sd	0.35	0/499	0.64	0/670
22	3B	0.42	0/1914	0.65	0/2582
22	3C	0.35	0/1787	0.68	1/2413 (0.0%)
23	3D	0.35	0/3020	0.60	0/4066
24	3E	0.32	0/3088	0.61	0/4193
25	3F	0.38	0/3569	0.64	0/4806
26	3G	0.38	0/928	0.72	0/1262
26	3H	0.41	0/928	0.74	1/1262 (0.1%)
27	A4	0.35	0/5282	0.64	0/7154
28	A5	0.31	0/4021	0.64	1/5462 (0.0%)
29	A8	0.19	0/3328	0.55	0/4565
30	A9	0.26	0/951	0.67	1/1287 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	AE	0.29	0/10367	0.63	20/14163 (0.1%)
32	AF	0.27	0/3941	0.57	0/5344
33	AG	0.29	0/6694	0.59	1/9070 (0.0%)
34	B1	0.37	0/6459	0.64	1/8744 (0.0%)
35	B2	0.32	0/6624	0.65	1/8950 (0.0%)
36	B3	0.31	0/6001	0.68	0/8120
37	B8	0.40	0/3730	0.64	0/5058
38	BE	0.36	0/7012	0.64	3/9493 (0.0%)
39	B6	0.32	0/3138	0.61	0/4226
40	5B	0.28	0/486	0.70	0/643
41	5C	0.34	0/3902	0.59	0/5265
42	5D	0.28	0/1801	0.59	0/2379
43	5E	0.28	0/1745	0.63	0/2335
44	5F	0.31	0/1559	0.59	0/2097
45	5G	0.36	0/1993	0.67	0/2689
46	5H	0.36	0/704	0.65	3/931 (0.3%)
47	5I	0.43	0/3844	0.64	0/5174
48	5J	0.30	0/1147	0.59	0/1531
49	5K	0.40	0/1213	0.66	0/1638
50	RD	0.23	0/2454	0.59	2/3310 (0.1%)
51	RE	0.26	0/9015	0.57	3/12195 (0.0%)
52	RF	0.24	0/2004	0.63	2/2697 (0.1%)
53	RG	0.21	0/1727	0.58	0/2329
53	RH	0.23	0/1828	0.56	0/2470
54	RJ	0.33	0/6126	0.60	1/8247 (0.0%)
55	RK	0.31	0/2832	0.62	0/3825
56	RN	0.25	0/4521	0.62	3/6083 (0.0%)
57	RO	0.23	0/3824	0.64	8/5226 (0.2%)
58	RP	0.27	0/12292	0.67	49/16822 (0.3%)
59	RQ	0.30	0/2443	0.68	5/3317 (0.2%)
60	RS	0.24	0/2104	0.61	0/2854
61	RT	0.34	1/1679 (0.1%)	0.66	0/2261
62	RW	0.31	0/760	0.57	2/1059 (0.2%)
63	RZ	0.26	0/6730	0.59	3/9088 (0.0%)
66	R5	0.58	1/2340 (0.0%)	0.74	0/3161
67	R1	0.58	0/1910	0.76	0/2579
68	R3	0.51	0/2628	0.77	0/3569
69	R6	0.56	0/1722	0.77	0/2339
70	R2	0.51	0/2077	0.75	0/2828
71	M3	0.54	0/1661	0.75	0/2243
72	R0	0.54	0/1828	0.79	2/2486 (0.1%)
73	r4	0.53	0/2269	0.77	0/3066
74	C4	0.47	0/1676	0.77	0/2277

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	R4	0.38	0/7575	0.69	1/10290 (0.0%)
76	r6	0.35	0/2540	0.66	0/3497
77	R7	0.37	0/903	0.70	0/1210
78	M4	0.48	0/7772	0.77	4/10521 (0.0%)
79	M6	0.45	0/277	0.94	1/371 (0.3%)
All	All	0.34	2/259526 (0.0%)	0.62	136/359296 (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	2
5	SF	0	1
7	SH	0	2
8	SI	0	2
14	SR	0	1
17	SX	0	1
19	SZ	0	1
20	Sc	0	1
25	3F	0	3
26	3G	0	2
26	3H	0	1
27	A4	0	1
28	A5	0	2
29	A8	0	2
33	AG	0	4
34	B1	0	2
35	B2	0	2
36	B3	0	7
38	BE	0	3
39	B6	0	2
40	5B	0	1
46	5H	0	1
47	5I	0	2
49	5K	0	1
51	RE	0	2
52	RF	0	1
54	RJ	0	1
56	RN	0	1
57	RO	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
58	RP	0	9
59	RQ	0	1
62	RW	0	1
63	RZ	0	2
67	R1	0	1
68	R3	0	3
69	R6	0	1
70	R2	0	1
71	M3	0	2
73	r4	0	1
74	C4	0	1
75	R4	0	1
78	M4	0	3
All	All	0	81

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
66	R5	250	LYS	CA-CB	-7.15	1.43	1.53
61	RT	118	PRO	C-N	5.86	1.38	1.33

The worst 5 of 136 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	RP	1582	PRO	N-CA-CB	10.72	109.99	102.81
31	AE	1371	PRO	N-CA-CB	10.65	109.95	102.81
50	RD	1205	PRO	N-CA-CB	10.62	110.34	103.23
58	RP	579	PRO	N-CA-CB	10.34	109.74	102.81
57	RO	314	VAL	CA-C-N	8.93	125.86	120.24

There are no chirality outliers.

5 of 81 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 ⓘ

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	4570	0	2326	35	0
2	5A	2536	0	1281	29	0
3	SA	28478	0	14356	317	0
4	SC	1923	0	2029	43	0
5	SF	1915	0	1941	38	0
6	SG	1669	0	1724	27	0
7	SH	1456	0	1505	26	0
8	SI	1321	0	1387	34	0
9	SJ	1181	0	1198	23	0
10	SK	1410	0	1492	28	0
11	SM	1113	0	1181	25	0
12	SO	1087	0	1152	23	0
13	SP	848	0	868	21	0
14	SR	973	0	1029	23	0
15	ST	902	0	935	18	0
16	SU	1075	0	1097	14	0
17	SX	1003	0	1040	24	0
18	SY	792	0	847	16	0
19	SZ	986	0	1042	23	0
20	Sc	603	0	621	16	0
21	Sd	497	0	535	7	0
22	3B	1878	0	1923	31	0
22	3C	1754	0	1792	41	0
23	3D	2974	0	3001	57	0
24	3E	3056	0	2841	45	0
25	3F	3498	0	3515	68	0
26	3G	916	0	964	14	0
26	3H	916	0	964	18	0
27	A4	5187	0	5164	133	0
28	A5	3953	0	3894	79	0
29	A8	3307	0	2316	33	0
30	A9	939	0	898	14	0
31	AE	10262	0	8429	130	0
32	AF	3860	0	3859	81	0
33	AG	6565	0	6468	167	0
34	B1	6316	0	6218	114	0
35	B2	6497	0	6492	147	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	B3	5906	0	5983	150	0
37	B8	3648	0	3626	74	0
38	BE	6876	0	6734	122	0
39	B6	3077	0	3022	47	0
40	5B	482	0	545	6	0
41	5C	3825	0	3829	90	0
42	5D	1778	0	1857	27	0
43	5E	1728	0	1739	36	0
44	5F	1530	0	1572	38	0
45	5G	1956	0	1971	37	0
46	5H	700	0	702	21	0
47	5I	3765	0	3714	75	0
48	5J	1127	0	1150	11	0
49	5K	1190	0	1252	23	0
50	RD	2413	0	2264	36	0
51	RE	8805	0	8911	160	0
52	RF	1963	0	1942	37	0
53	RG	1701	0	1767	49	0
53	RH	1799	0	1872	44	0
54	RJ	5994	0	6175	124	0
55	RK	2781	0	2878	71	0
56	RN	4459	0	4265	72	0
57	RO	3741	0	3259	64	0
58	RP	12263	0	8039	84	0
59	RQ	2408	0	2106	46	0
60	RS	2051	0	2096	28	0
61	RT	1652	0	1706	31	0
62	RW	762	0	318	0	0
63	RZ	6598	0	6631	114	0
64	X1	1105	0	260	6	0
65	X2	705	0	166	2	0
66	R5	2304	0	2265	62	0
67	R1	1886	0	1904	62	0
68	R3	2588	0	2607	79	0
69	R6	1701	0	1755	49	0
70	R2	2035	0	2051	58	0
71	M3	1639	0	1592	47	0
72	R0	1792	0	1747	43	0
73	r4	2236	0	2215	52	0
74	C4	1653	0	1616	43	0
75	R4	7430	0	7346	216	0
76	r6	2517	0	1819	64	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
77	R7	894	0	917	27	0
78	M4	7626	0	7521	247	0
79	M6	275	0	254	6	0
80	5K	1	0	0	0	0
80	Sc	1	0	0	0	0
81	RJ	32	0	12	0	0
82	RJ	1	0	0	0	0
83	RZ	27	0	12	1	0
All	All	253642	0	226308	4274	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 4274 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)
56:RN:323:GLY:O	56:RN:327:GLY:HA3	1.30	1.30
31:AE:791:VAL:O	31:AE:795:LEU:HB2	1.64	0.96
3:SA:1663:G:H1	3:SA:1738:U:H3	0.94	0.93
55:RK:213:LYS:O	55:RK:217:LYS:HB3	1.71	0.91
3:SA:174:U:H3	3:SA:266:A:H62	0.92	0.90

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	SC	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	SH	178/236 (75%)	159 (89%)	15 (8%)	4 (2%)	5	31
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%)	21	57
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	ST	107/146 (73%)	91 (85%)	16 (15%)	0	100	100
16	SU	136/144 (94%)	123 (90%)	13 (10%)	0	100	100
17	SX	125/130 (96%)	114 (91%)	11 (9%)	0	100	100
18	SY	102/145 (70%)	88 (86%)	14 (14%)	0	100	100
19	SZ	121/135 (90%)	106 (88%)	15 (12%)	0	100	100
20	Sc	78/82 (95%)	66 (85%)	12 (15%)	0	100	100
21	Sd	61/67 (91%)	56 (92%)	5 (8%)	0	100	100
22	3B	238/327 (73%)	215 (90%)	23 (10%)	0	100	100
22	3C	220/327 (67%)	200 (91%)	20 (9%)	0	100	100
23	3D	372/504 (74%)	342 (92%)	30 (8%)	0	100	100
24	3E	433/511 (85%)	392 (90%)	40 (9%)	1 (0%)	43	75
25	3F	431/573 (75%)	394 (91%)	37 (9%)	0	100	100
26	3G	119/126 (94%)	114 (96%)	5 (4%)	0	100	100
26	3H	119/126 (94%)	110 (92%)	9 (8%)	0	100	100
27	A4	643/776 (83%)	568 (88%)	75 (12%)	0	100	100
28	A5	501/643 (78%)	447 (89%)	52 (10%)	2 (0%)	30	65
29	A8	534/713 (75%)	407 (76%)	127 (24%)	0	100	100
30	A9	126/575 (22%)	111 (88%)	15 (12%)	0	100	100
31	AE	1516/1769 (86%)	1374 (91%)	138 (9%)	4 (0%)	36	70
32	AF	483/513 (94%)	440 (91%)	43 (9%)	0	100	100
33	AG	811/896 (90%)	726 (90%)	84 (10%)	1 (0%)	48	81
34	B1	785/900 (87%)	709 (90%)	75 (10%)	1 (0%)	48	81
35	B2	814/943 (86%)	716 (88%)	98 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	B3	733/817 (90%)	585 (80%)	147 (20%)	1 (0%)	48	81
37	B8	453/594 (76%)	397 (88%)	56 (12%)	0	100	100
38	BE	886/939 (94%)	804 (91%)	81 (9%)	1 (0%)	48	81
39	B6	369/440 (84%)	341 (92%)	26 (7%)	2 (0%)	24	60
40	5B	56/214 (26%)	51 (91%)	5 (9%)	0	100	100
41	5C	474/554 (86%)	424 (90%)	50 (10%)	0	100	100
42	5D	201/250 (80%)	175 (87%)	26 (13%)	0	100	100
43	5E	205/593 (35%)	187 (91%)	18 (9%)	0	100	100
44	5F	180/183 (98%)	169 (94%)	11 (6%)	0	100	100
45	5G	237/290 (82%)	215 (91%)	22 (9%)	0	100	100
46	5H	91/610 (15%)	81 (89%)	9 (10%)	1 (1%)	11	44
47	5I	457/489 (94%)	413 (90%)	44 (10%)	0	100	100
48	5J	130/217 (60%)	117 (90%)	13 (10%)	0	100	100
49	5K	148/189 (78%)	134 (90%)	14 (10%)	0	100	100
50	RD	310/1729 (18%)	281 (91%)	25 (8%)	4 (1%)	9	41
51	RE	1080/1237 (87%)	998 (92%)	81 (8%)	1 (0%)	48	81
52	RF	233/297 (78%)	205 (88%)	26 (11%)	2 (1%)	14	48
53	RG	212/252 (84%)	191 (90%)	21 (10%)	0	100	100
53	RH	226/252 (90%)	207 (92%)	19 (8%)	0	100	100
54	RJ	726/1183 (61%)	670 (92%)	56 (8%)	0	100	100
55	RK	358/367 (98%)	332 (93%)	26 (7%)	0	100	100
56	RN	568/810 (70%)	513 (90%)	55 (10%)	0	100	100
57	RO	518/552 (94%)	462 (89%)	50 (10%)	6 (1%)	10	42
58	RP	1948/2493 (78%)	1778 (91%)	156 (8%)	14 (1%)	18	54
59	RQ	333/899 (37%)	287 (86%)	42 (13%)	4 (1%)	10	42
60	RS	247/480 (52%)	224 (91%)	23 (9%)	0	100	100
61	RT	207/326 (64%)	188 (91%)	19 (9%)	0	100	100
62	RW	149/206 (72%)	135 (91%)	13 (9%)	1 (1%)	18	54
63	RZ	831/1267 (66%)	737 (89%)	91 (11%)	3 (0%)	30	65
66	R5	297/305 (97%)	275 (93%)	22 (7%)	0	100	100
67	R1	242/246 (98%)	224 (93%)	18 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	R3	332/394 (84%)	304 (92%)	27 (8%)	1 (0%)	36	70
69	R6	222/223 (100%)	209 (94%)	13 (6%)	0	100	100
70	R2	264/265 (100%)	250 (95%)	14 (5%)	0	100	100
71	M3	209/250 (84%)	192 (92%)	17 (8%)	0	100	100
72	R0	235/240 (98%)	216 (92%)	19 (8%)	0	100	100
73	r4	287/359 (80%)	263 (92%)	24 (8%)	0	100	100
74	C4	214/292 (73%)	198 (92%)	16 (8%)	0	100	100
75	R4	942/1001 (94%)	875 (93%)	67 (7%)	0	100	100
76	r6	404/733 (55%)	367 (91%)	37 (9%)	0	100	100
77	R7	111/184 (60%)	108 (97%)	3 (3%)	0	100	100
78	M4	972/1073 (91%)	908 (93%)	64 (7%)	0	100	100
79	M6	36/186 (19%)	32 (89%)	4 (11%)	0	100	100
All	All	28063/37702 (74%)	25255 (90%)	2753 (10%)	55 (0%)	44	75

5 of 55 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
28	A5	569	PRO
50	RD	1223	PRO
57	RO	141	PRO
57	RO	519	PRO
58	RP	707	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%)	211 (99%)	2 (1%)	70	76
5	SF	199/222 (90%)	195 (98%)	4 (2%)	48	66
6	SG	180/191 (94%)	176 (98%)	4 (2%)	45	65
7	SH	153/201 (76%)	153 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	SI	146/170 (86%)	144 (99%)	2 (1%)	59	71
9	SJ	122/161 (76%)	118 (97%)	4 (3%)	33	56
10	SK	150/166 (90%)	149 (99%)	1 (1%)	76	79
11	SM	124/137 (90%)	124 (100%)	0	100	100
12	SO	117/128 (91%)	116 (99%)	1 (1%)	70	76
13	SP	88/105 (84%)	85 (97%)	3 (3%)	32	55
14	SR	105/119 (88%)	105 (100%)	0	100	100
15	ST	99/129 (77%)	99 (100%)	0	100	100
16	SU	111/116 (96%)	110 (99%)	1 (1%)	70	76
17	SX	108/111 (97%)	108 (100%)	0	100	100
18	SY	86/120 (72%)	86 (100%)	0	100	100
19	SZ	103/113 (91%)	103 (100%)	0	100	100
20	Sc	69/71 (97%)	69 (100%)	0	100	100
21	Sd	56/60 (93%)	56 (100%)	0	100	100
22	3B	201/240 (84%)	199 (99%)	2 (1%)	68	76
22	3C	189/240 (79%)	189 (100%)	0	100	100
23	3D	322/435 (74%)	321 (100%)	1 (0%)	86	85
24	3E	265/433 (61%)	262 (99%)	3 (1%)	65	74
25	3F	382/503 (76%)	381 (100%)	1 (0%)	86	85
26	3G	100/104 (96%)	97 (97%)	3 (3%)	36	57
26	3H	100/104 (96%)	100 (100%)	0	100	100
27	A4	587/713 (82%)	578 (98%)	9 (2%)	57	70
28	A5	431/574 (75%)	429 (100%)	2 (0%)	81	82
29	A8	174/657 (26%)	172 (99%)	2 (1%)	65	74
30	A9	89/533 (17%)	88 (99%)	1 (1%)	65	74
31	AE	770/1633 (47%)	765 (99%)	5 (1%)	78	81
32	AF	431/454 (95%)	426 (99%)	5 (1%)	63	73
33	AG	750/826 (91%)	747 (100%)	3 (0%)	84	84
34	B1	694/789 (88%)	688 (99%)	6 (1%)	70	76
35	B2	712/832 (86%)	703 (99%)	9 (1%)	61	72
36	B3	659/719 (92%)	652 (99%)	7 (1%)	65	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	B8	407/529 (77%)	402 (99%)	5 (1%)	63	73
38	BE	741/819 (90%)	732 (99%)	9 (1%)	63	73
39	B6	323/414 (78%)	317 (98%)	6 (2%)	50	67
40	5B	56/196 (29%)	55 (98%)	1 (2%)	51	68
41	5C	418/480 (87%)	411 (98%)	7 (2%)	53	68
42	5D	198/234 (85%)	198 (100%)	0	100	100
43	5E	193/535 (36%)	193 (100%)	0	100	100
44	5F	171/172 (99%)	166 (97%)	5 (3%)	37	58
45	5G	214/258 (83%)	213 (100%)	1 (0%)	81	82
46	5H	63/538 (12%)	63 (100%)	0	100	100
47	5I	416/443 (94%)	410 (99%)	6 (1%)	59	71
48	5J	124/200 (62%)	123 (99%)	1 (1%)	73	77
49	5K	133/169 (79%)	132 (99%)	1 (1%)	73	77
50	RD	226/1544 (15%)	225 (100%)	1 (0%)	84	84
51	RE	994/1125 (88%)	988 (99%)	6 (1%)	78	81
52	RF	221/274 (81%)	221 (100%)	0	100	100
53	RG	195/222 (88%)	192 (98%)	3 (2%)	57	70
53	RH	206/222 (93%)	205 (100%)	1 (0%)	81	82
54	RJ	654/1039 (63%)	646 (99%)	8 (1%)	63	73
55	RK	307/312 (98%)	304 (99%)	3 (1%)	68	76
56	RN	435/732 (59%)	435 (100%)	0	100	100
57	RO	329/506 (65%)	327 (99%)	2 (1%)	78	81
58	RP	556/2307 (24%)	553 (100%)	3 (0%)	81	82
59	RQ	206/808 (26%)	206 (100%)	0	100	100
60	RS	225/421 (53%)	225 (100%)	0	100	100
61	RT	178/282 (63%)	177 (99%)	1 (1%)	78	81
63	RZ	717/1140 (63%)	714 (100%)	3 (0%)	84	84
66	R5	255/266 (96%)	252 (99%)	3 (1%)	63	73
67	R1	210/218 (96%)	209 (100%)	1 (0%)	81	82
68	R3	282/349 (81%)	282 (100%)	0	100	100
69	R6	196/197 (100%)	196 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	R2	237/240 (99%)	237 (100%)	0	100	100
71	M3	181/219 (83%)	180 (99%)	1 (1%)	78	81
72	R0	194/209 (93%)	194 (100%)	0	100	100
73	r4	243/311 (78%)	241 (99%)	2 (1%)	73	77
74	C4	174/240 (72%)	174 (100%)	0	100	100
75	R4	812/901 (90%)	812 (100%)	0	100	100
76	r6	150/671 (22%)	150 (100%)	0	100	100
77	R7	99/168 (59%)	97 (98%)	2 (2%)	48	66
78	M4	810/953 (85%)	809 (100%)	1 (0%)	88	89
79	M6	25/168 (15%)	25 (100%)	0	100	100
All	All	21859/33364 (66%)	21695 (99%)	164 (1%)	70	77

5 of 164 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	5I	62	LEU
55	RK	171	ASP
47	5I	279	THR
53	RG	95	CYS
61	RT	234	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 398 such sidechains are listed below:

Mol	Chain	Res	Type
46	5H	573	GLN
53	RG	105	ASN
47	5I	134	ASN
51	RE	261	ASN
56	RN	467	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	203/333 (60%)	78 (38%)	4 (1%)
2	5A	110/700 (15%)	42 (38%)	0
3	SA	1315/1812 (72%)	510 (38%)	20 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	1628/2845 (57%)	630 (38%)	24 (1%)

5 of 630 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 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	SA	773	C
3	SA	1063	U
3	SA	1052	U
3	SA	1490	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 oligosaccharides 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
81	GTP	RJ	1201	82	33,34,34	0.87	0	50,54,54	1.57	8 (16%)
83	ADP	RZ	1301	-	28,29,29	1.43	5 (17%)	43,45,45	1.84	10 (23%)

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
81	GTP	RJ	1201	82	-	5/22/38/38	0/3/3/3
83	ADP	RZ	1301	-	-	4/16/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	RZ	1301	ADP	C5-C4	4.66	1.47	1.39
83	RZ	1301	ADP	C5-C6	2.83	1.48	1.41
83	RZ	1301	ADP	C8-N7	2.36	1.36	1.31
83	RZ	1301	ADP	C5-N7	-2.23	1.35	1.39
83	RZ	1301	ADP	PA-O3A	2.17	1.61	1.59

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	RZ	1301	ADP	C5-C4-N3	-5.89	118.61	126.72
81	RJ	1201	GTP	C5-C4-N3	-4.86	120.66	128.39
83	RZ	1301	ADP	N3-C4-N9	4.59	134.97	127.17
81	RJ	1201	GTP	C2-N3-C4	4.52	120.08	112.30
83	RZ	1301	ADP	C2-N3-C4	3.85	121.24	111.83

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

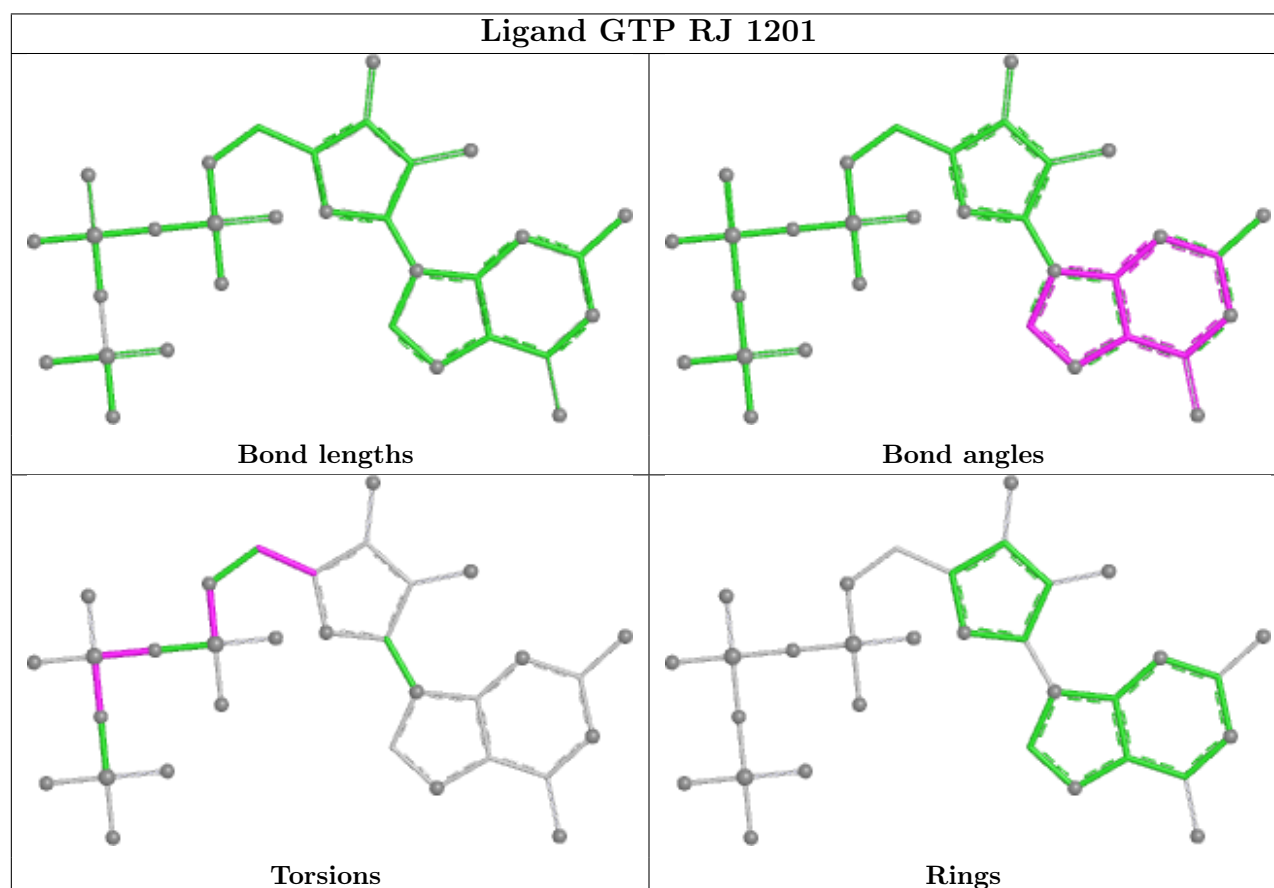
Mol	Chain	Res	Type	Atoms
83	RZ	1301	ADP	C5'-O5'-PA-O2A
83	RZ	1301	ADP	C5'-O5'-PA-O3A
81	RJ	1201	GTP	O4'-C4'-C5'-O5'
81	RJ	1201	GTP	C3'-C4'-C5'-O5'
81	RJ	1201	GTP	PA-O3A-PB-O2B

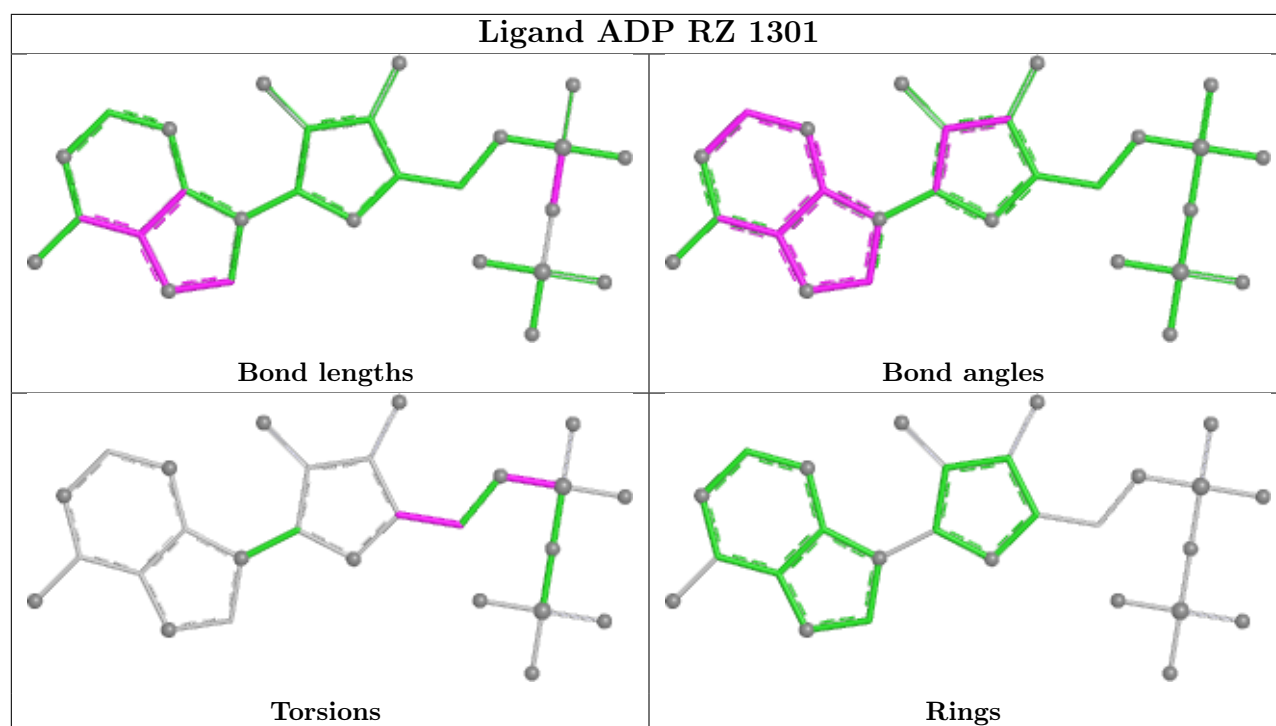
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
83	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 [i](#)

There are no chain breaks in this entry.

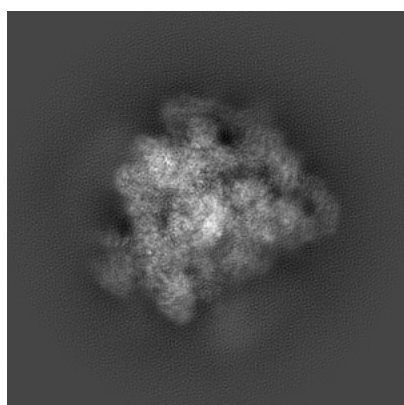
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30574. These allow visual inspection of the internal detail of the map and identification of artifacts.

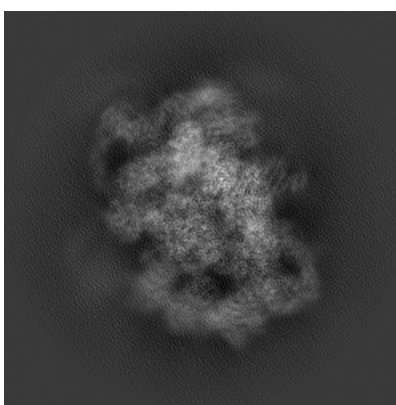
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

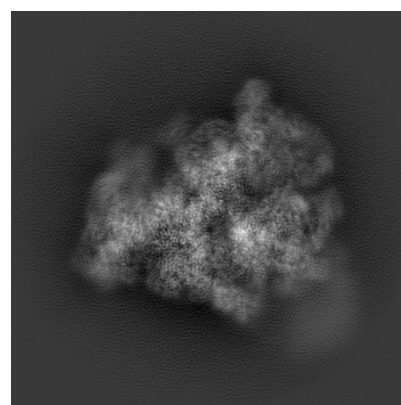
6.1.1 Primary map



X



Y

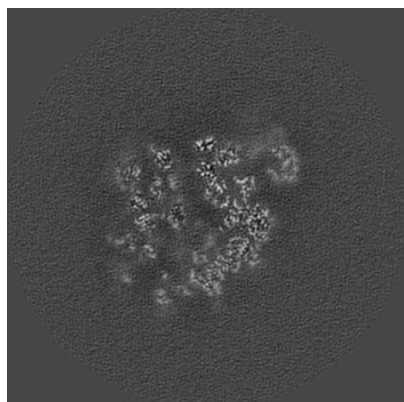


Z

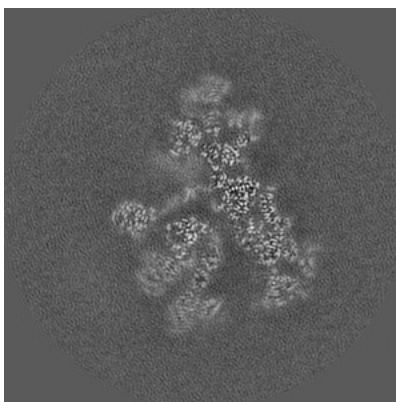
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

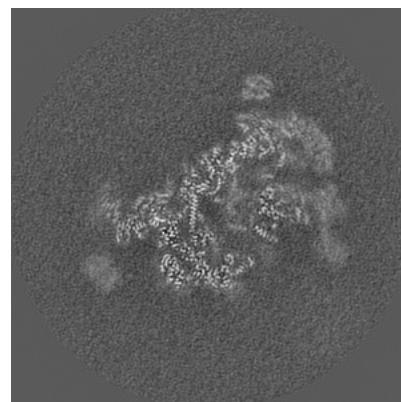
6.2.1 Primary map



X Index: 200



Y Index: 200

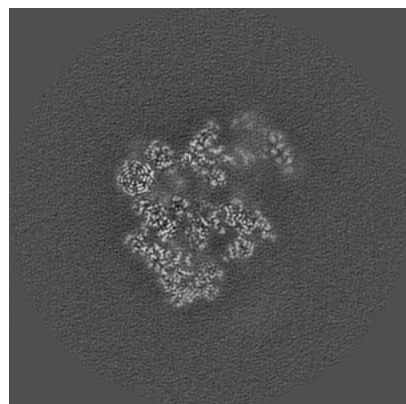


Z Index: 200

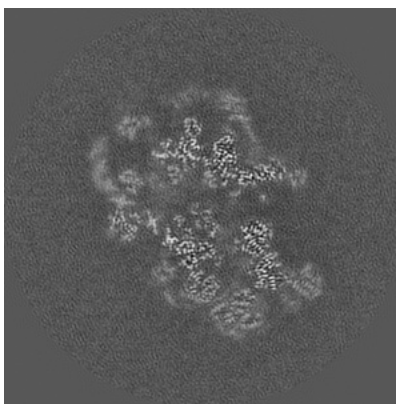
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

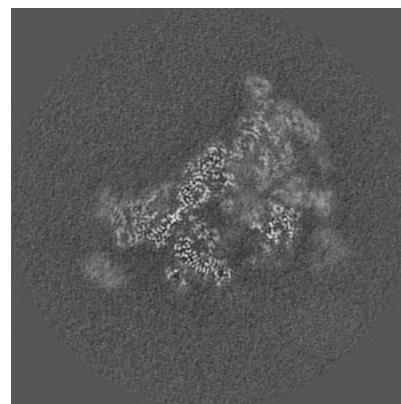
6.3.1 Primary map



X Index: 186



Y Index: 178

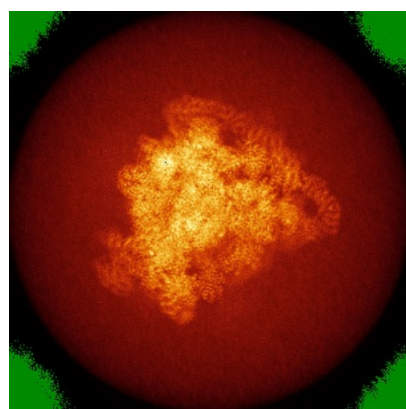


Z Index: 192

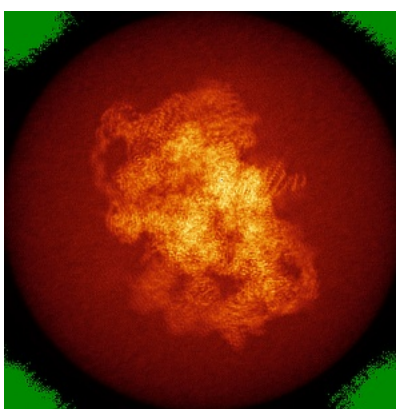
The images above show the largest variance slices of the map in three orthogonal directions.

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

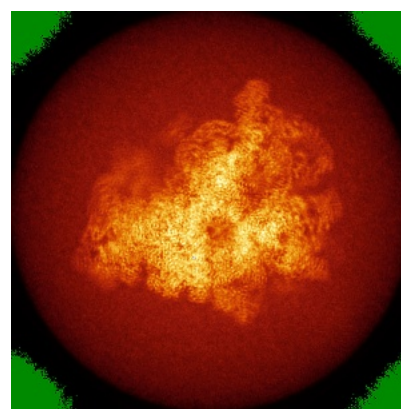
6.4.1 Primary map



X



Y

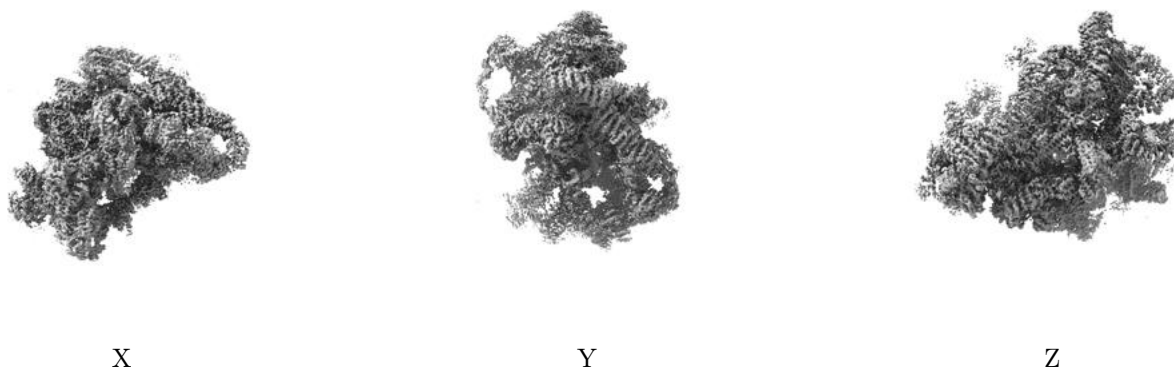


Z

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

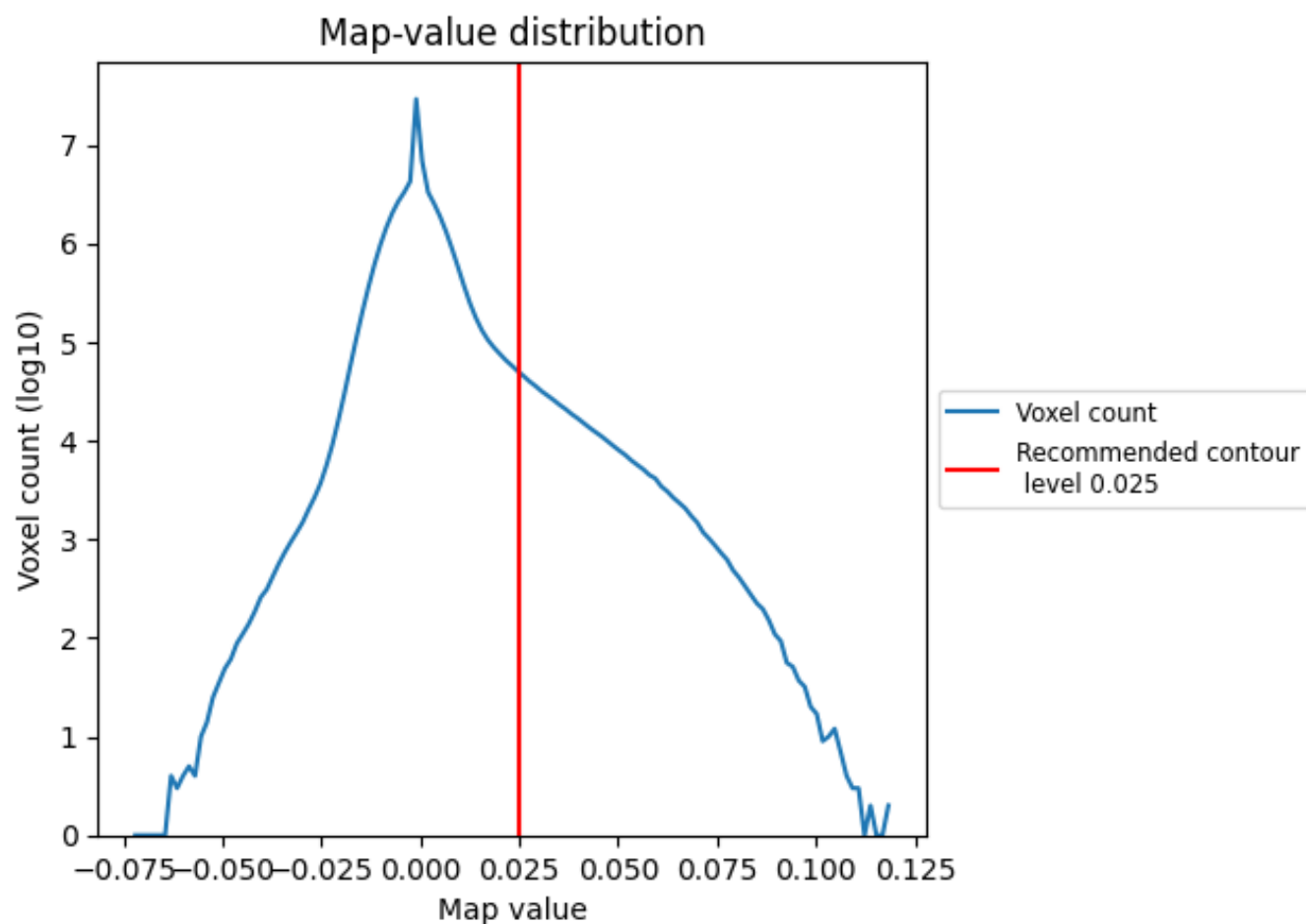
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

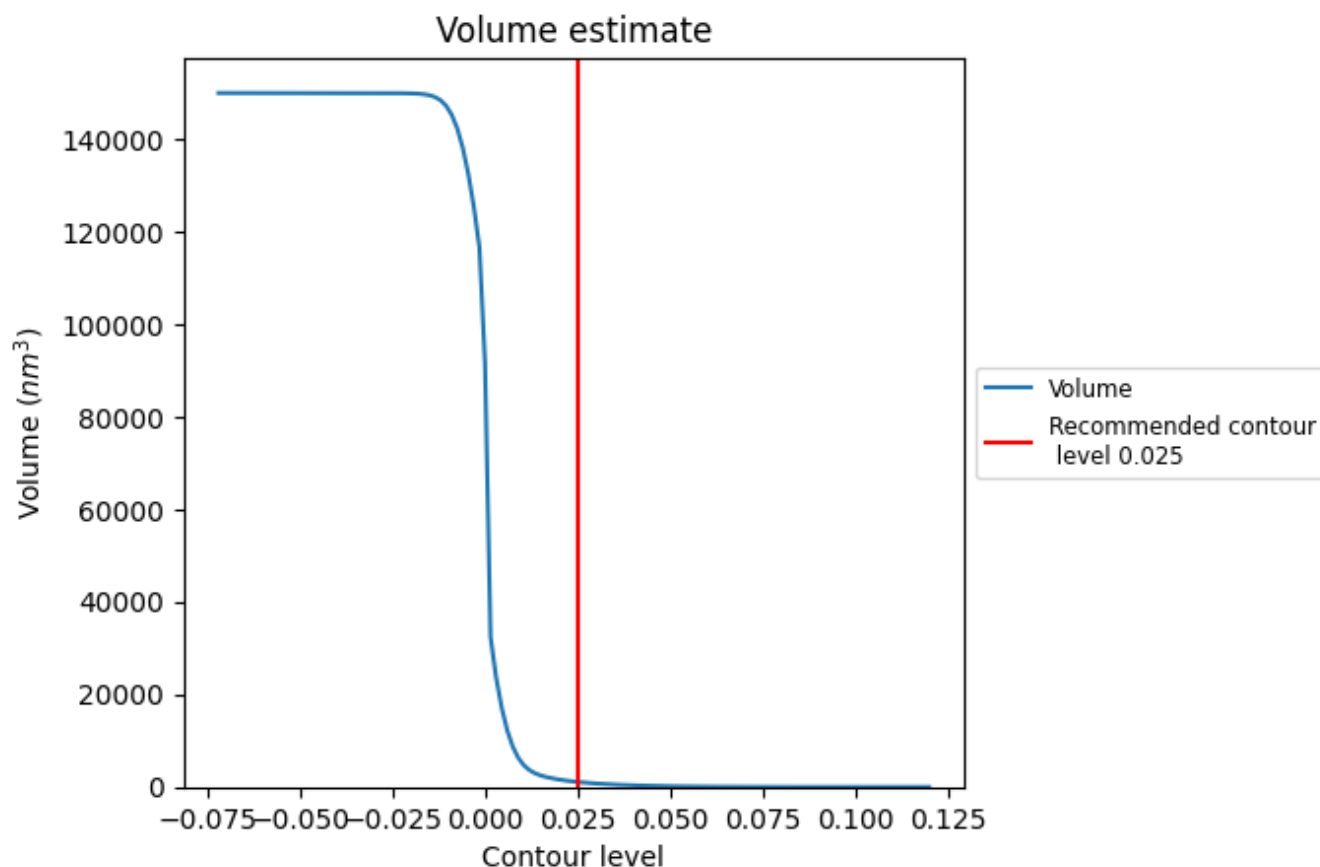
This section contains the results of statistical analysis of the map.

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.

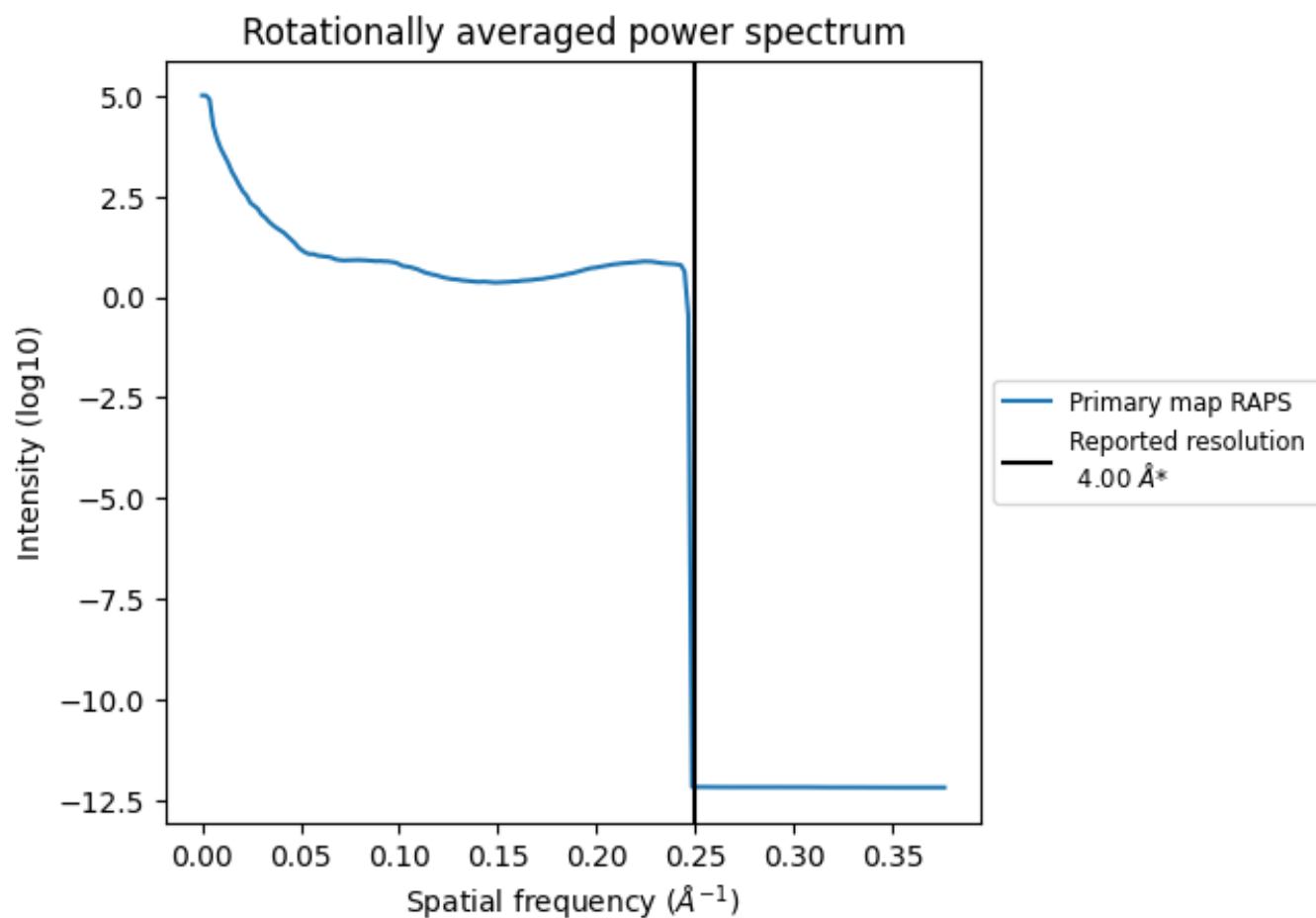
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1074 nm³; this corresponds to an approximate mass of 970 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 0.250 $\text{\AA}^{-1}$

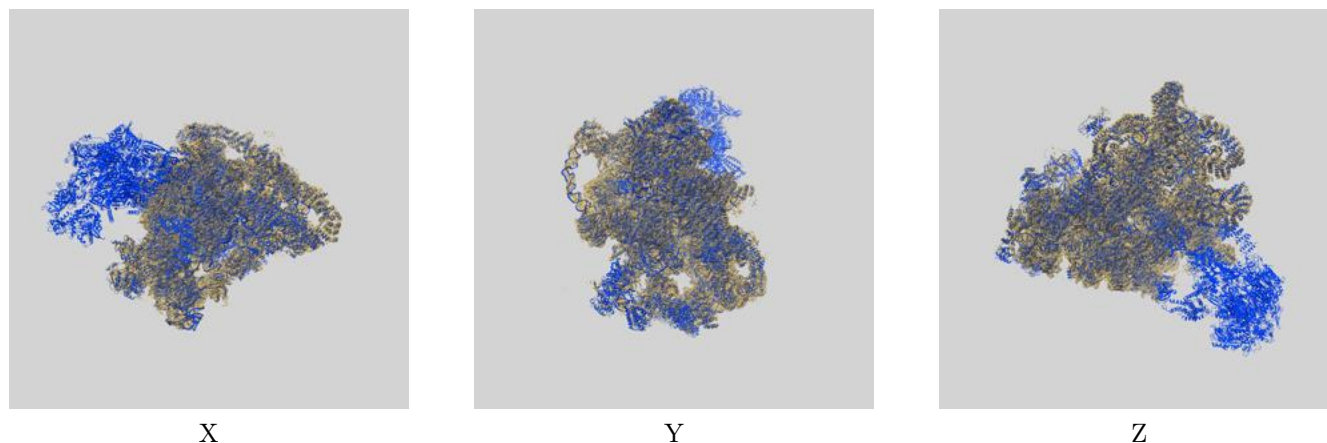
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

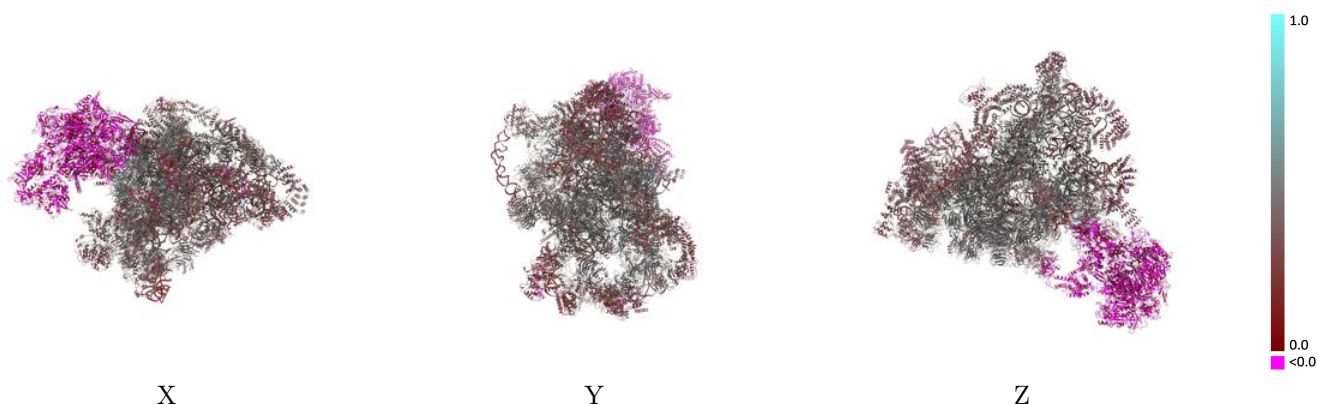
This section contains information regarding the fit between EMDB map EMD-30574 and PDB model 7D4I. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



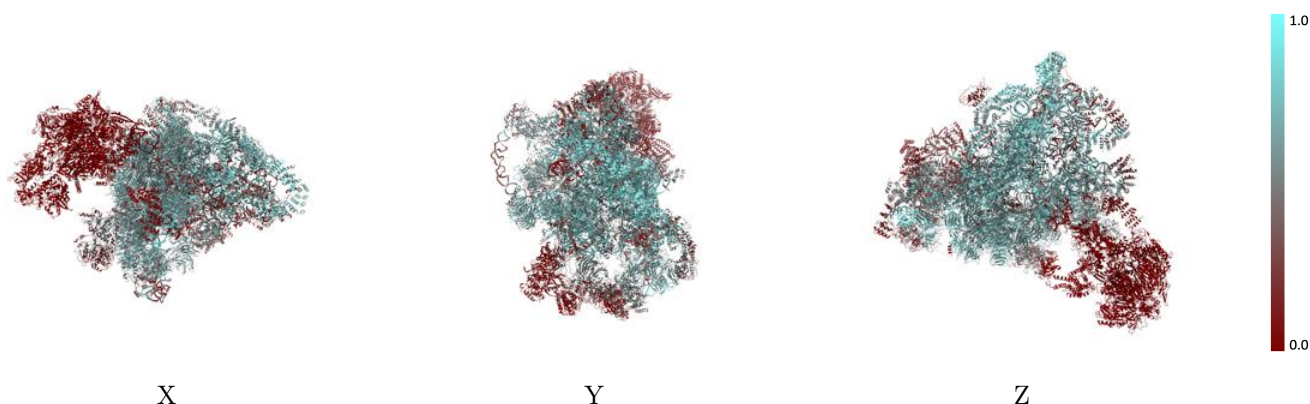
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



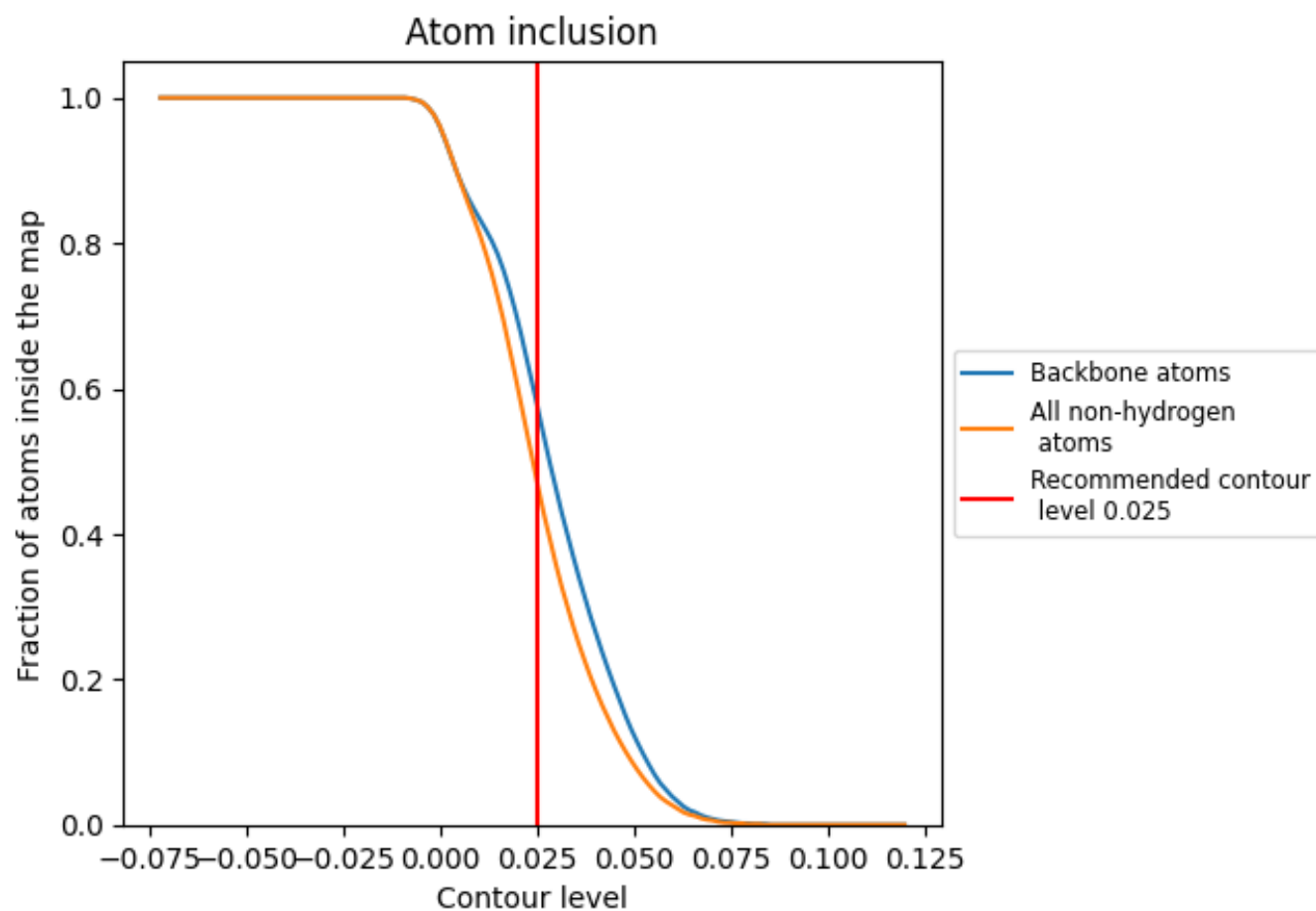
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).

9.4 Atom inclusion [i](#)



At the recommended contour level, 58% of all backbone atoms, 47% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4720	 0.3390
3A	 0.6880	 0.3800
3B	 0.7030	 0.4820
3C	 0.6510	 0.4460
3D	 0.6820	 0.4450
3E	 0.6470	 0.4270
3F	 0.6890	 0.4600
3G	 0.6460	 0.4550
3H	 0.6860	 0.4620
5A	 0.4290	 0.2980
5B	 0.4730	 0.4040
5C	 0.6100	 0.4530
5D	 0.5590	 0.4350
5E	 0.5350	 0.4230
5F	 0.4980	 0.4190
5G	 0.6040	 0.4540
5H	 0.6420	 0.4620
5I	 0.7000	 0.4760
5J	 0.5670	 0.4540
5K	 0.6690	 0.4760
A4	 0.6530	 0.4270
A5	 0.5790	 0.4240
A8	 0.1930	 0.3060
A9	 0.4450	 0.3310
AE	 0.5490	 0.3640
AF	 0.5390	 0.4190
AG	 0.5810	 0.4120
B1	 0.6430	 0.4640
B2	 0.6440	 0.4170
B3	 0.6320	 0.4210
B6	 0.6330	 0.4130
B8	 0.6830	 0.4570
BE	 0.6630	 0.4540
C4	 0.0000	 0.0140
M3	 0.0000	 0.0020



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Chain	Atom inclusion	Q-score
M4	0.0000	0.0070
M6	0.0000	-0.0180
R0	0.0000	0.0240
R1	0.0000	-0.0040
R2	0.0000	-0.0020
R3	0.0000	-0.0050
R4	0.0000	-0.0040
R5	0.0000	-0.0020
R6	0.0000	0.0200
R7	0.0000	-0.0180
RD	0.0440	0.2830
RE	0.5240	0.3780
RF	0.4600	0.3590
RG	0.1550	0.3120
RH	0.2780	0.3730
RJ	0.6410	0.4430
RK	0.6320	0.4350
RN	0.1620	0.3150
RO	0.2540	0.3260
RP	0.5770	0.3540
RQ	0.4820	0.4150
RS	0.0670	0.2420
RT	0.5490	0.4390
RW	0.5620	0.3770
RZ	0.3570	0.3490
SA	0.6220	0.3510
SC	0.6420	0.4550
SF	0.5580	0.4330
SG	0.6220	0.4540
SH	0.2820	0.3650
SI	0.4950	0.3850
SJ	0.2730	0.3480
SK	0.6780	0.4600
SM	0.1890	0.3280
SO	0.6660	0.4340
SP	0.6450	0.4560
SR	0.6690	0.4730
ST	0.3580	0.3880
SU	0.4630	0.4250
SX	0.6490	0.4510
SY	0.6180	0.4530
SZ	0.6590	0.4520

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Chain	Atom inclusion	Q-score
Sc	 0.6710	 0.4620
Sd	 0.6620	 0.4830
X1	 0.4410	 0.3940
X2	 0.1570	 0.3330
r4	 0.0000	 0.0010
r6	 0.0000	 0.0010