



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 09:58 PM UTC

PDB ID : 7AJT / pdb_00007ajt
EMDB ID : EMD-11807
Title : Cryo-EM structure of the 90S-exosome super-complex (state Pre-A1-exosome)
Authors : Cheng, J.; Lau, B.; Flemming, D.; Venuta, G.L.; Berninghausen, O.; Beckmann, R.; Hurt, E.
Deposited on : 2020-09-29
Resolution : 4.60 Å(reported)

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

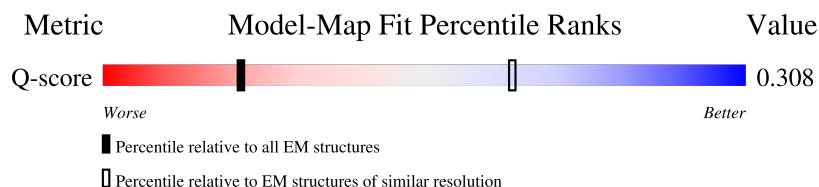
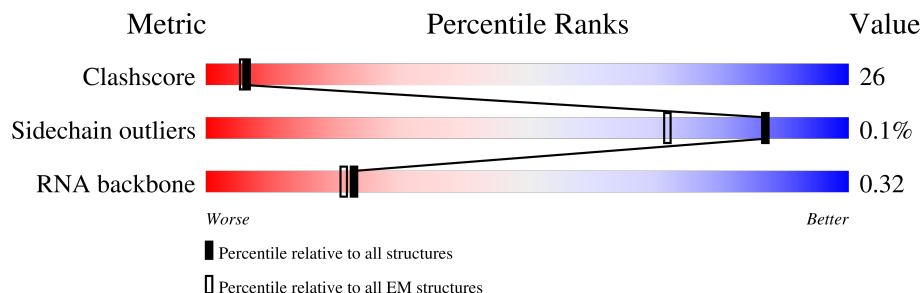
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.60 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	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	2407 (4.10 - 5.10)

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	CA	327	
1	CB	327	
2	DA	255	
3	JA	1056	

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Mol	Chain	Length	Quality of chain
3	JB	1056	
4	UA	923	
5	UB	810	
6	UC	610	
7	UD	776	
8	UE	643	
9	UF	440	
10	UG	554	
11	UH	713	
12	UI	575	
13	UJ	1769	
14	UK	250	
15	UL	943	
16	UM	817	
17	UN	899	
18	UO	513	
19	UP	214	
20	UQ	896	
21	UR	594	
22	US	552	
23	UT	2493	
24	UU	939	
25	UV	1237	
26	UX	189	
27	UZ	274	

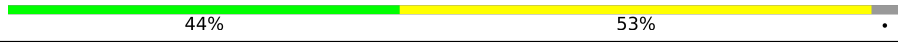
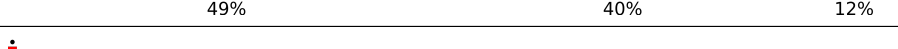
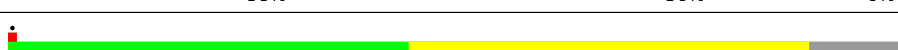
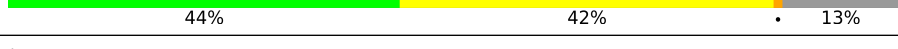
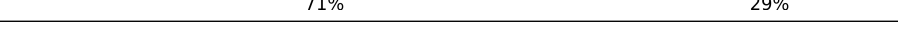
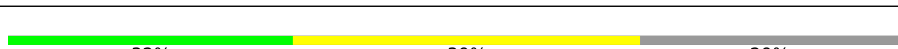
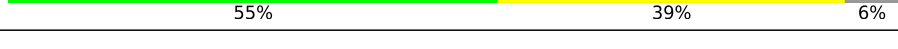
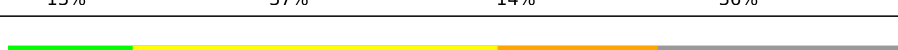
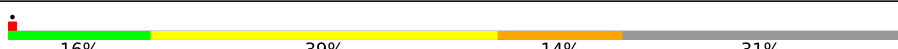
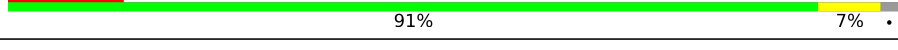
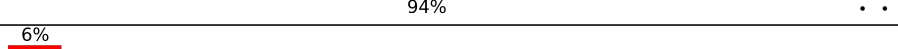
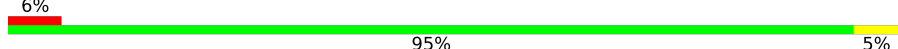
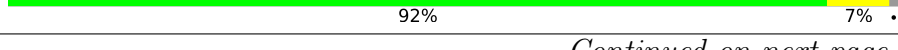
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Mol	Chain	Length	Quality of chain
28	CD	504	
29	CE	511	
30	CF	126	
30	CG	126	
31	CH	573	
32	CI	183	
33	CJ	290	
34	CK	593	
35	CL	1183	
36	CM	367	
37	CN	297	
38	JC	707	
39	JF	252	
39	JG	252	
40	JH	483	
41	JI	1729	
42	JJ	274	
43	JK	534	
44	JM	217	
45	JN	346	
46	JO	316	
47	JP	489	
48	JQ	206	
49	DE	261	
50	DF	225	

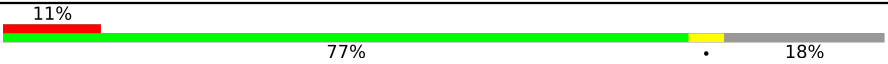
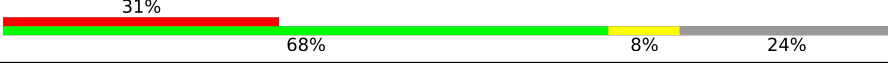
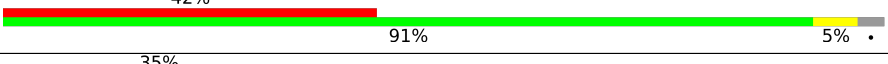
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Mol	Chain	Length	Quality of chain
51	DG	236	
52	DH	190	
53	DI	200	
54	DJ	197	
55	DL	156	
56	DN	151	
57	DO	137	
58	DQ	143	
59	DS	146	
60	DW	130	
61	DX	145	
62	DY	135	
63	Db	82	
64	Dc	67	
65	D2	700	
66	D3	1808	
67	D4	333	
68	EA	22	
69	EB	305	
70	EC	246	
71	ED	394	
72	EE	223	
73	EF	267	
74	EG	250	
75	EH	240	

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Mol	Chain	Length	Quality of chain
76	EI	359	
77	EJ	292	
78	EK	1001	
79	EN	1073	

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 256149 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 protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CA	242	Total	C	N	O	S	0	0
			1881	1193	338	340	10		
1	CB	228	Total	C	N	O	S	0	0
			1782	1131	320	321	10		

- Molecule 2 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	DA	240	Total	C	N	O	S	0	0
			1912	1209	354	345	4		

- Molecule 3 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	JA	812	Total	C	N	O	S	0	0
			5916	3745	1044	1102	25		
3	JB	835	Total	C	N	O		0	0
			4132	2462	835	835			

- Molecule 4 is a protein called Periodic tryptophan protein 2.

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

- Molecule 5 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	UB	507	Total	C	N	O	S	0	0
			3734	2367	663	695	9		

- Molecule 6 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	UC	128	Total	C	N	O	0	0
			1026	633	204	189		

- Molecule 7 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	UD	675	Total	C	N	O	S	0	0
			5361	3395	929	1015	22		

- Molecule 8 is a protein called U3 small nucleolar RNA-associated protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	UE	475	Total	C	N	O	S	0	0
			3772	2400	649	710	13		

- Molecule 9 is a protein called U3 small nucleolar RNA-associated protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	UF	293	Total	C	N	O	S	0	0
			2487	1605	435	434	13		

- Molecule 10 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	UG	533	Total	C	N	O	S	0	0
			4218	2646	758	802	12		

- Molecule 11 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	UH	442	Total	C	N	O	S	0	0
			2701	1680	494	524	3		

- Molecule 12 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	UI	104	Total	C	N	O	S	0	0
			860	556	152	150	2		

- Molecule 13 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	UJ	1116	Total	C	N	O	S	0	0
			8961	5802	1468	1666	25		

- Molecule 14 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	UK	242	Total	C	N	O	S	0	0
			2021	1254	389	371	7		

- Molecule 15 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	UL	842	Total	C	N	O	S	0	0
			6726	4303	1129	1267	27		

- Molecule 16 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	UM	762	Total	C	N	O	S	0	0
			5969	3785	1007	1149	28		

- Molecule 17 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	UN	147	Total	C	N	O	S	0	0
			1227	765	233	227	2		

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

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

- Molecule 19 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	UP	60	Total	C	N	O	0	0
			495	310	101	84		

- Molecule 20 is a protein called NET1-associated nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	UQ	832	Total	C	N	O	S	0	0
			6662	4236	1124	1283	19		

- Molecule 21 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	UR	482	Total	C	N	O	S	0	0
			3799	2405	669	715	10		

- Molecule 22 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	US	494	Total	C	N	O	S	0	0
			3622	2326	617	667	12		

- Molecule 23 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	UT	2255	Total	C	N	O	S	0	0
			17290	11076	2927	3235	52		

- Molecule 24 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	UU	848	Total	C	N	O	S	0	0
			6678	4241	1149	1267	21		

- Molecule 25 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	UV	1081	Total	C	N	O	S	0	0
			8736	5681	1440	1591	24		

- Molecule 26 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	UX	174	Total	C	N	O	S	0	0
			1395	890	255	240	10		

- Molecule 27 is a protein called Ribosome biogenesis protein UTP30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	UZ	247	Total	C	N	O	S	0	0
			2006	1284	356	358	8		

- Molecule 28 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	CD	380	Total	C	N	O	S	0	0
			2994	1898	513	574	9		

- Molecule 29 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	CE	435	Total	C	N	O	S	0	0
			3325	2093	571	653	8		

- Molecule 30 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	CF	123	Total	C	N	O	S	0	0
			931	594	160	173	4		
30	CG	123	Total	C	N	O	S	0	0
			928	591	160	173	4		

- Molecule 31 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	CH	465	Total	C	N	O	S	0	0
			3725	2365	653	697	10		

- Molecule 32 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	CI	182	Total	C	N	O	S	0	0
			1530	967	287	269	7		

- Molecule 33 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	CJ	282	Total	C	N	O	S	0	0
			2296	1441	430	418	7		

- Molecule 34 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	CK	207	Total	C	N	O	S	0	0
			1667	1034	297	332	4		

- Molecule 35 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	CL	781	Total	C	N	O	S	0	0
			6332	4063	1122	1117	30		

- Molecule 36 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 37 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	CN	232	Total	C	N	O	S	0	0
			1893	1213	322	351	7		

- Molecule 38 is a protein called Ribosome biogenesis protein ENP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	JC	354	Total	C	N	O	S	0	0
			2845	1795	489	552	9		

- Molecule 39 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	JF	216	Total	C	N	O	S	0	0
			1701	1079	296	315	11		
39	JG	230	Total	C	N	O	S	0	0
			1799	1142	313	333	11		

- Molecule 40 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	JH	261	Total	C	N	O		0	0
			1295	773	261	261			

- Molecule 41 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	Jl	265	Total	C	N	O	0	0
			1314	784	265	265		

- Molecule 42 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	JJ	182	Total	C	N	O	S	0	0
			1442	923	259	256	4		

- Molecule 43 is a protein called Protein BFR2.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	JK	42	Total	C	N	O	0	0
			334	213	54	67		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
44	JM	135	Total	C	N	O	S	0	0
			1137	721	211	201	4		

- Molecule 45 is a protein called Protein FAF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	JN	186	Total	C	N	O	S	0	0
			1428	879	287	259	3		

- Molecule 46 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	JO	230	Total	C	N	O	S	0	0
			1876	1203	330	332	11		

- Molecule 47 is a protein called Protein SOF1.

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

- Molecule 48 is a protein called Regulator of rDNA transcription protein 14.

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

- Molecule 49 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	DE	245	Total	C	N	O	S	0	0
			1944	1245	360	336	3		

- Molecule 50 is a protein called 40S ribosomal protein S5.

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

- Molecule 51 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	DG	218	Total	C	N	O	S	0	0
			1755	1102	337	313	3		

- Molecule 52 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	DH	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 53 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	DI	177	Total	C	N	O	S	0	0
			1399	869	279	249	2		

- Molecule 54 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	DJ	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 55 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	DL	140	Total	C	N	O	S	0	0
			1129	724	215	187	3		

- Molecule 56 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	DN	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 57 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	DO	120	Total	C	N	O	S	0	0
			881	544	167	167	3		

- Molecule 58 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
58	DQ	125	Total	C	N	O	0	0
			973	625	174	174		

- Molecule 59 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	DS	104	Total	C	N	O	0	0
			516	308	104	104		

- Molecule 60 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	DW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 61 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 62 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	DY	134	Total	C	N	O		
			1073	676	208	189	0	0

- Molecule 63 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Db	81	Total	C	N	O	S		
			610	382	110	113	5	0	0

- Molecule 64 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 65 is a RNA chain called 5'ETS RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	D2	446	Total	C	N	O	P		
			9508	4250	1682	3130	446	0	0

- Molecule 66 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	D3	1327	Total	C	N	O	P		
			28287	12644	5022	9294	1327	0	0

- Molecule 67 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	D4	230	Total	C	N	O	P		
			4869	2180	841	1618	230	0	0

- Molecule 68 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	EA	22	Total	C	N	O	P		
			366	161	43	140	22	0	0

- Molecule 69 is a protein called Exosome complex component RRP45.

Mol	Chain	Residues	Atoms				AltConf	Trace
69	EB	299	Total	C	N	O	0	0
			1475	877	299	299		

- Molecule 70 is a protein called Exosome complex component SKI6.

Mol	Chain	Residues	Atoms				AltConf	Trace
70	EC	244	Total	C	N	O	0	0
			1204	716	244	244		

- Molecule 71 is a protein called Exosome complex component RRP43.

Mol	Chain	Residues	Atoms				AltConf	Trace
71	ED	317	Total	C	N	O	1	0
			1571	937	317	317		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
ED	363	MET	VAL	conflict	UNP P25359

- Molecule 72 is a protein called Exosome complex component RRP46.

Mol	Chain	Residues	Atoms				AltConf	Trace
72	EE	223	Total	C	N	O	1	0
			1107	661	223	223		

- Molecule 73 is a protein called Exosome complex component RRP42.

Mol	Chain	Residues	Atoms				AltConf	Trace
73	EF	267	Total	C	N	O	1	0
			1326	792	267	267		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EF	-1	GLY	-	expression tag	UNP Q12277
EF	0	HIS	-	expression tag	UNP Q12277
EF	138	ILE	VAL	conflict	UNP Q12277

- Molecule 74 is a protein called Exosome complex component MTR3.

Mol	Chain	Residues	Atoms				AltConf	Trace
74	EG	215	Total	C	N	O	0	0
			1058	628	215	215		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EG	75	SER	THR	conflict	UNP P48240

- Molecule 75 is a protein called Exosome complex component RRP40.

Mol	Chain	Residues	Atoms				AltConf	Trace
75	EH	237	Total	C	N	O	0	0
			1170	696	237	237		

- Molecule 76 is a protein called Exosome complex component RRP4.

Mol	Chain	Residues	Atoms				AltConf	Trace
76	EI	293	Total	C	N	O	0	0
			1440	854	293	293		

- Molecule 77 is a protein called Exosome complex component CSL4.

Mol	Chain	Residues	Atoms				AltConf	Trace
77	EJ	222	Total	C	N	O	0	0
			1091	647	222	222		

- Molecule 78 is a protein called Exosome complex exonuclease DIS3.

Mol	Chain	Residues	Atoms				AltConf	Trace
78	EK	970	Total	C	N	O	1	0
			4818	2878	970	970		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EK	171	ASN	ASP	conflict	UNP Q08162
EK	551	ASN	ASP	conflict	UNP Q08162

- Molecule 79 is a protein called ATP-dependent RNA helicase DOB1.

Mol	Chain	Residues	Atoms				AltConf	Trace
79	EN	964	Total	C	N	O	0	0
			4767	2842	964	961		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EN	80	MET	VAL	conflict	UNP P47047

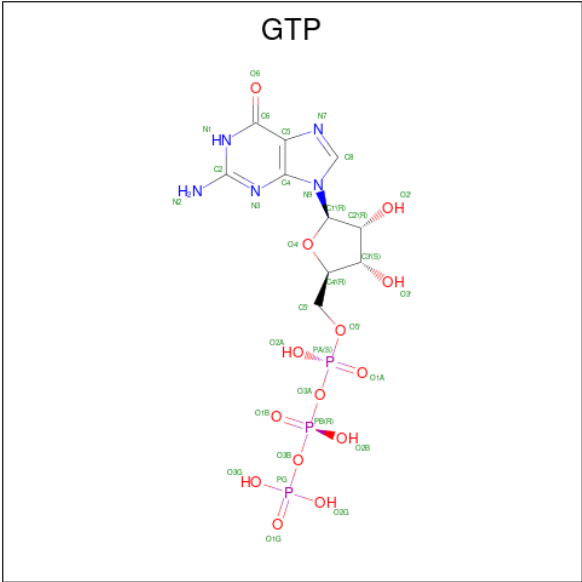
- Molecule 80 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
80	UX	1	Total	Zn	0
			1	1	
80	Db	1	Total	Zn	0
			1	1	
80	EK	1	Total	Zn	0
			1	1	

- Molecule 81 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
81	UX	1	Total	Mg	0
			1	1	
81	CL	1	Total	Mg	0
			1	1	
81	EK	1	Total	Mg	0
			1	1	

- Molecule 82 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

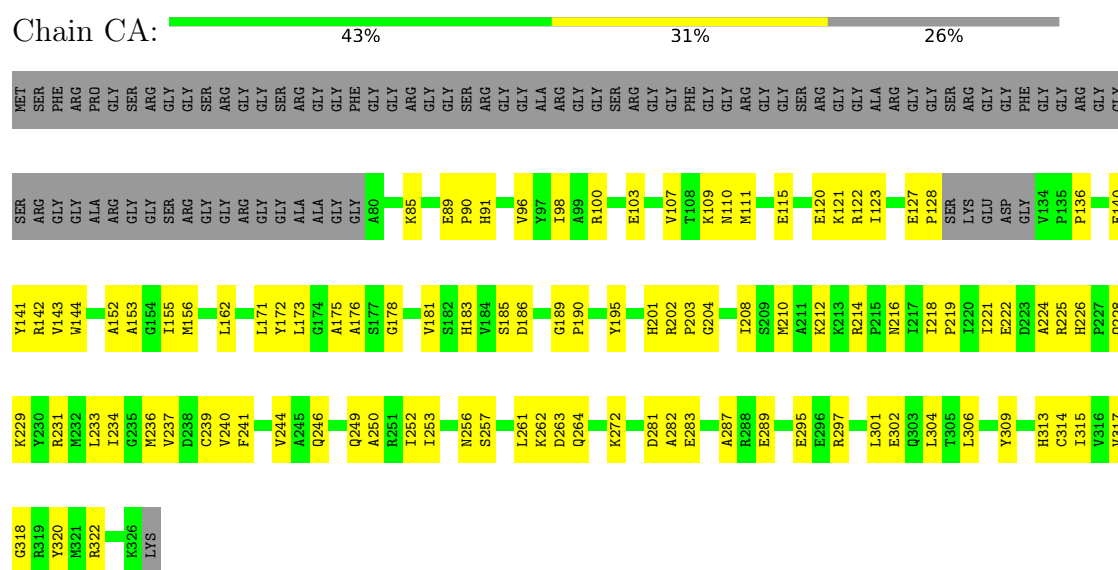


Mol	Chain	Residues	Atoms					AltConf
82	CL	1	Total	C	N	O	P	0
			32	10	5	14	3	

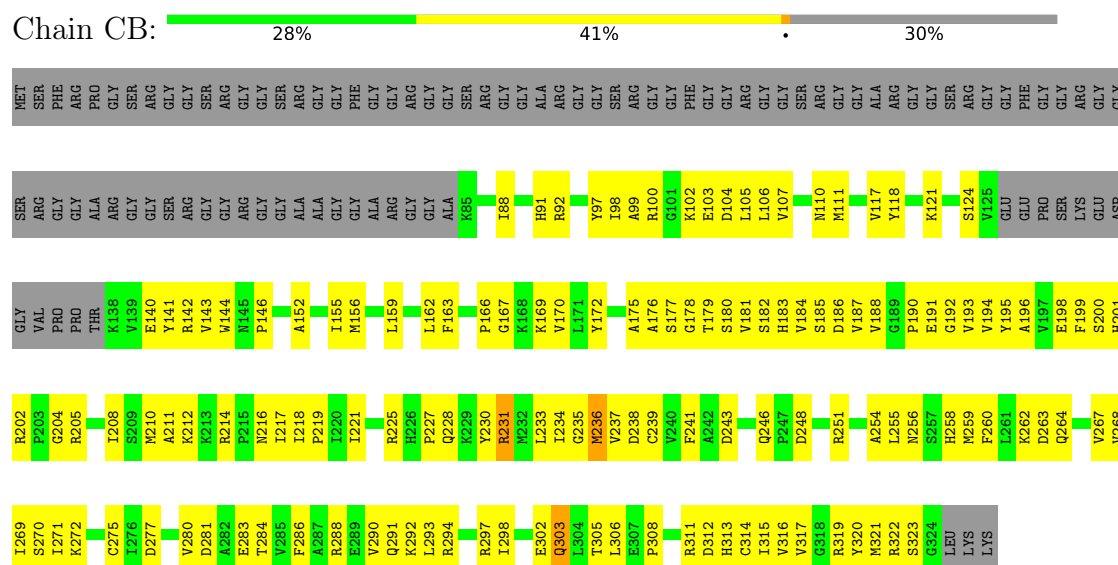
3 Residue-property plots

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

• Molecule 1: rRNA 2'-O-methyltransferase fibrillarin

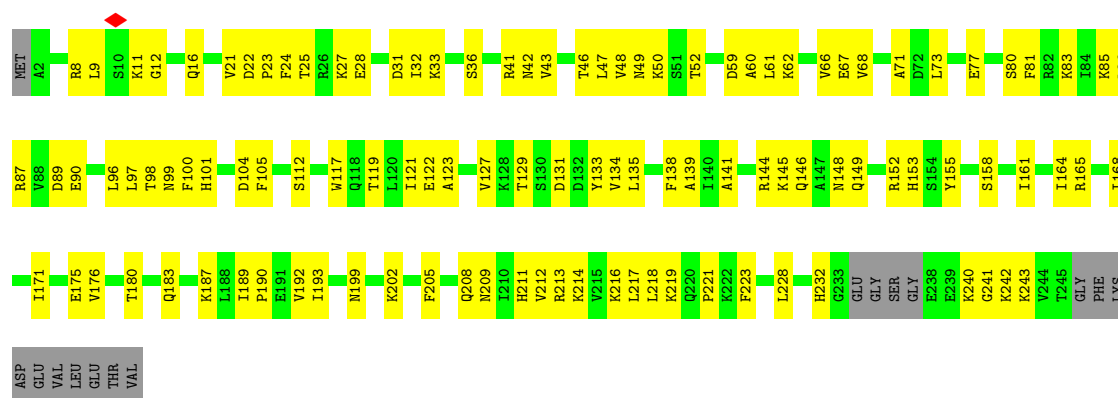


• Molecule 1: rRNA 2'-O-methyltransferase fibrillarin



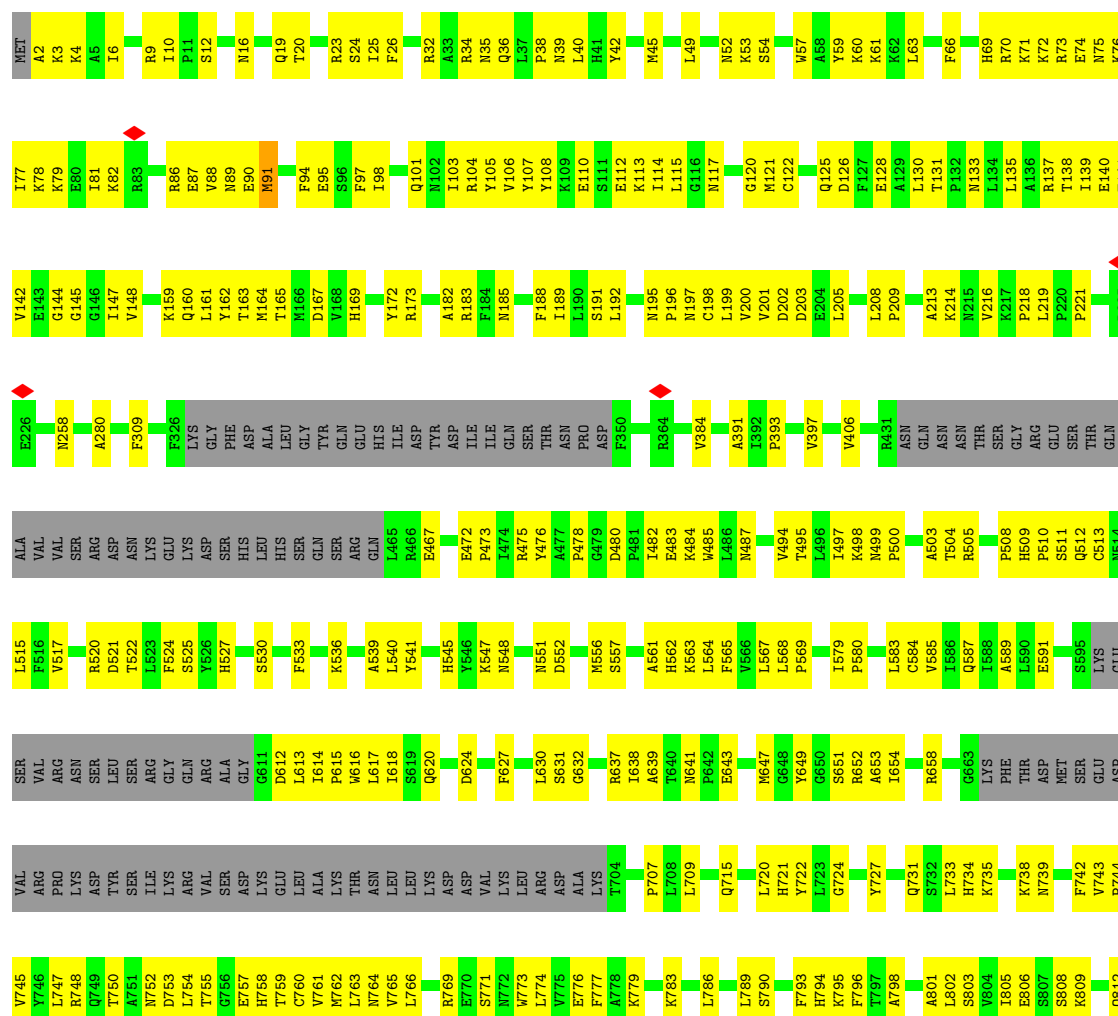
• Molecule 2: 40S ribosomal protein S1-A

Chain DA:  51% 43% 6%

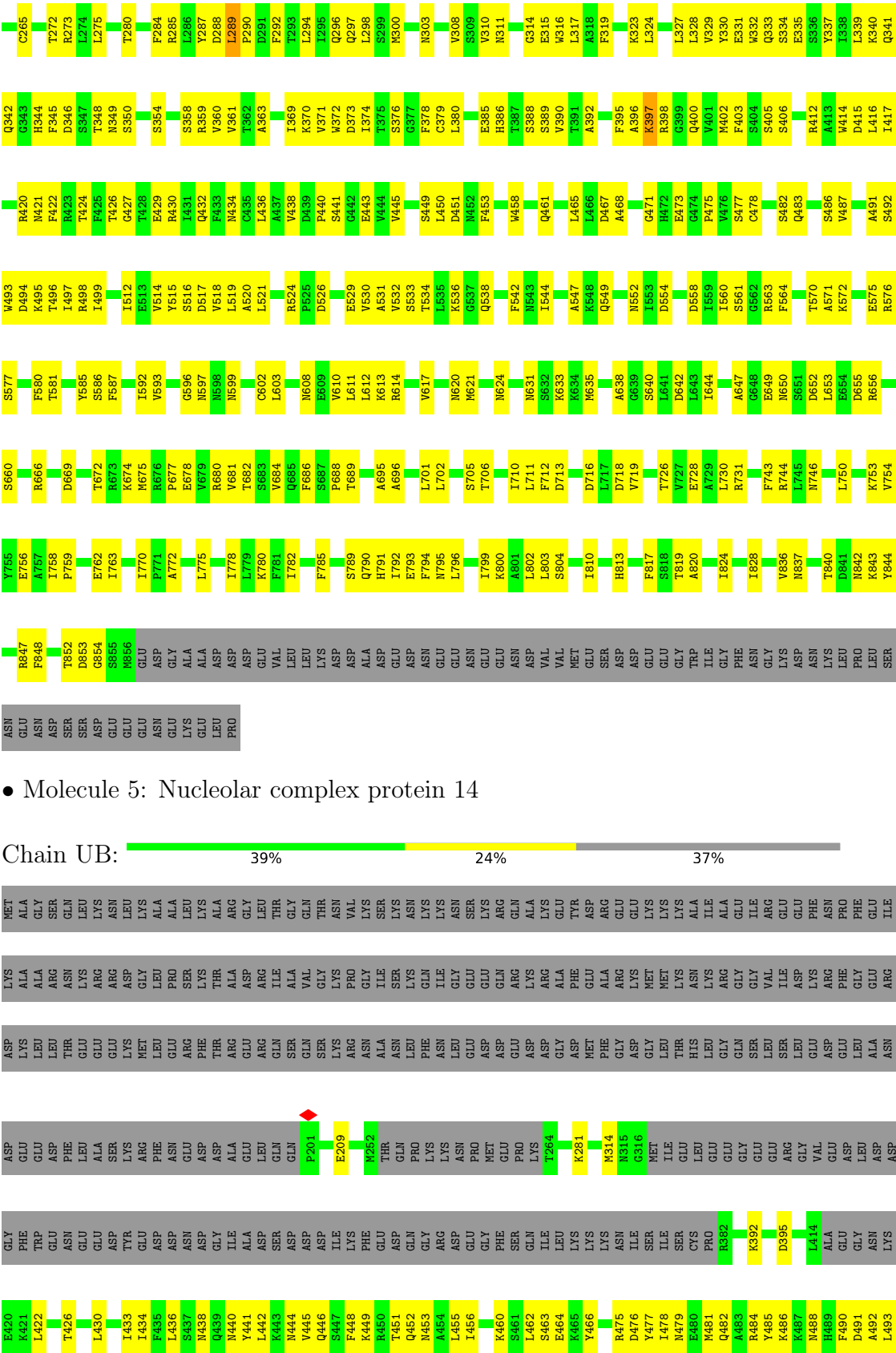


• Molecule 3: RNA cytidine acetyltransferase

Chain JA:  44% 32% 23%





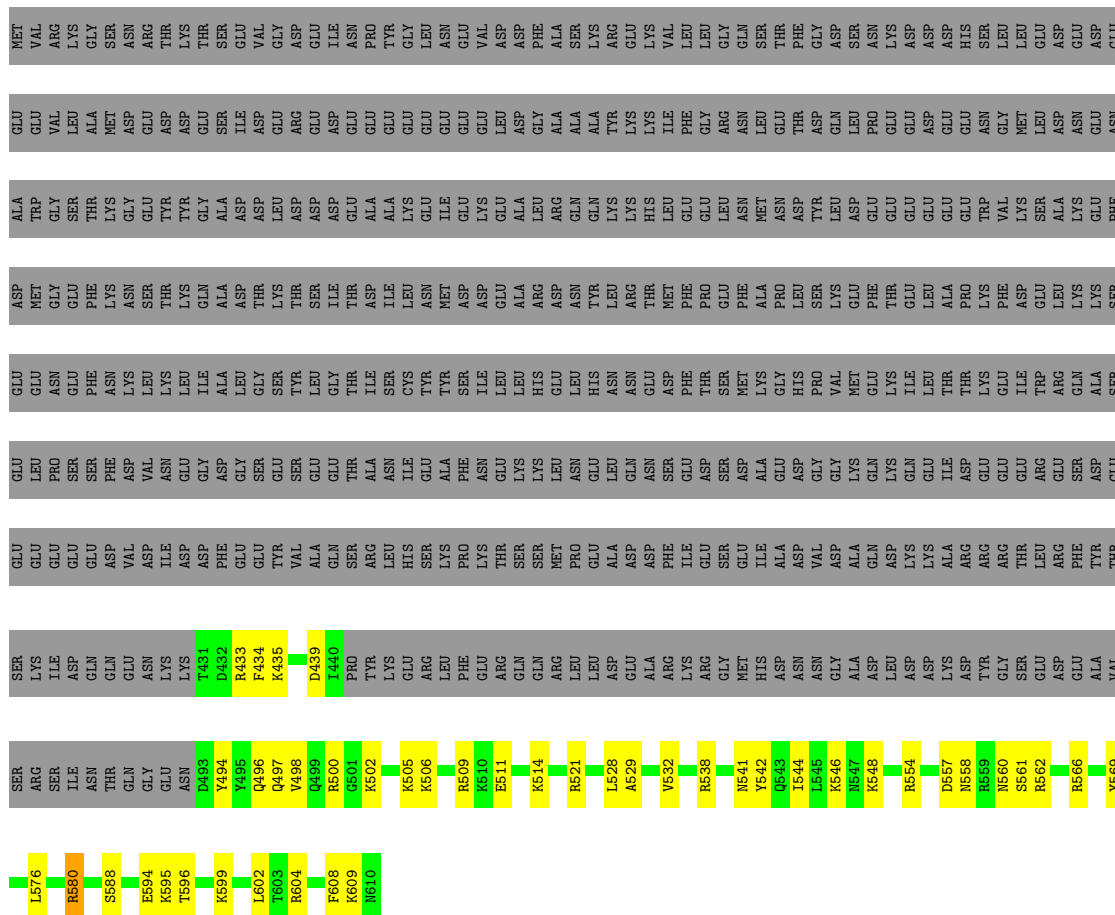


● Molecule 5: Nucleolar complex protein 14

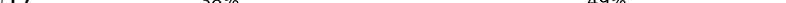
Chain UB: 39% 24% 37%

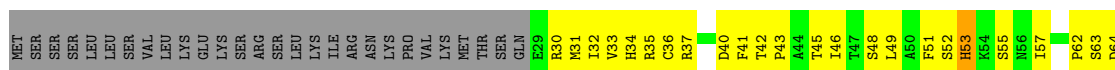
- Molecule 6: Something about silencing protein 10

Chain UC:



- Molecule 7: U3 small nucleolar RNA-associated protein 4

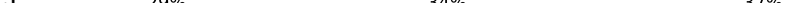
Chain UD: 

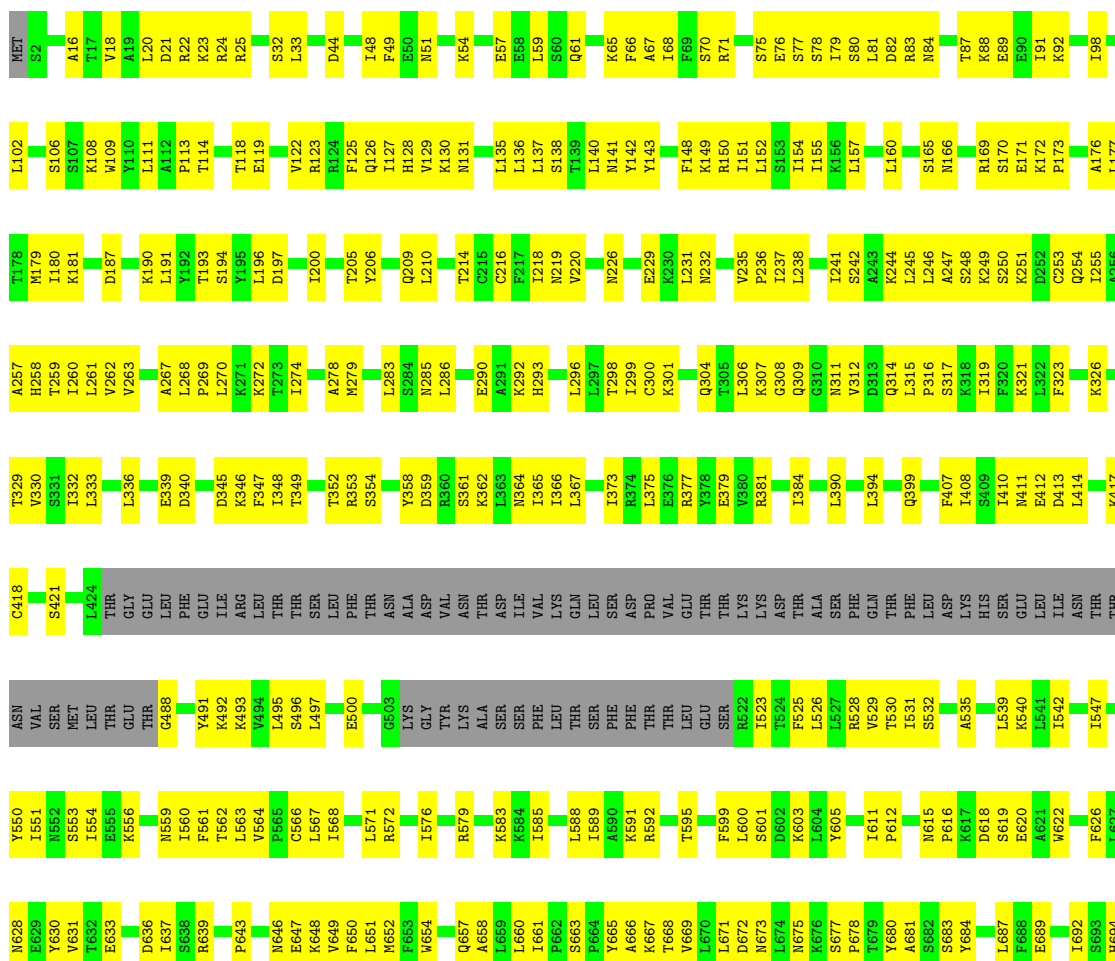




LEU	GLU	L492	L421	GLN	THR	ASP	HIS
	PRO	L493	T422	PRO	PRO	LEU	GLN
	ASN	P494	K423	GLU	ILE	LYS	ASN
	ASP	V495	I424	VAL	GLN	GLU	GLY
	SER	L496	N425	ASN	SER	ASP	THR
	ILE	L497	T426	HIS	LYS	SER	LEU
	VAL	G498	V427	GLU	GLN	LYS	LEU
	TYR	L499	ASP	LYS	GLN	LEU	VAL
	ALA	Q500	H429	LYS	VAL	ILE	CYS
	ASN	G501	L430	GLU	LEU	GLN	ILE
GLY	GLY	R502	S431	THR	ILE	TRP	THR
	GLU	L503	K432	GLU	SER	SER	THR
	SER	E504		THR	THR	PRO	LYS
	ASP	M505	L435	LYS	VAL	VAL	GLN
	GLU	L506	T436	ILE	ASN	GLN	MET
	PHE	R507	I437	ASN	VAL	VAL	VAL
	VAL	R508	S438	LYS	ASN	LYS	TYR
	ASP	Q509	K439	LYS	GLU	THR	ILE
	ALA	A510		VAL	PRO	LEU	VAL
	ALA	A511	T442	SER	ASN	LYS	ASP
SER	GLU	L512	P445	LYS	PHE	THR	PRO
	TYR	R513	W446	SER	GLU	LEU	SER
	LYS	E514	W447	GLN	ILE	ASP	LYS
	ASP	P515	S448	VAL	SER	LEU	ARG
	LEU		E449	GLU	LEU	ILE	PRO
	ALA	ALA	N450	ILE	LYS	MET	SER
	GLN	LEU	L451	ALA	GLU	ALA	THR
	SER	SER	L452	ASN	ILE	LEU	LYS
	MET	MET	P453	ILE	GLU	THR	TYR
	GLN	GLN	L454	SER	THR	THR	SER
GLU	GLU	L455	W455	LEU	GLN	ASP	PHE
	GLY	L456	L461	SER	GLY	GLY	GLU
	GLU	GLU	K457	HIS	TYR	ILE	ILE
	ASP	ASP	W458	LEU	ILE	ILE	SER
	ASP	L459		GLU	THR	ASN	ASP
	GLU	L460	L460	ALA	ILE	ASN	ALA
	ILE	ILE	T461	ASN	ASN	TYR	VAL
	GLU	GLU	L462	SER	LYS	ALA	ALA
	VAL	VAL	K463	THR	ASN	ILE	CYS
	ILE	ILE		GLU	GLU	GLY	GLU
GLU	GLU	E466		ILE	LYS	GLU	PHE
	HIS			LEU	ASN	ALA	SER
	SER	K473		ASP	ASN	ASP	SER
	ASN	H474	L474	ASP	ALA	LYS	ASP
	VAL	T475		LEU	ASP	VAL	GLY
	ILE	ILE		MET	GLU	CYS	LYS
	SER	SER	N478	SER	ALA	SER	TYR
	ASN	ASN	C479	GLY	ASP	ILE	LEU
	PRO	PRO		GLN	VAL	VAL	LEU
	LEU	LEU	L482	LYS	LYS	VAL	ILE
GLN	GLN	K483	T412	LYS	ASN	ALA	ILE
	ASP	S484	E413	LEU	GLU	ASN	ASN
	GLN	A485	P414	GLU	ASP	ASP	ASN
	ALA	L486	R487	GLU	LEU	GLU	GLU
	SER	R487	I416	LYS	ILE	ILE	GLU
	PRO	S488	K417	GLU	GLU	ILE	ILE
	VAL	S489	K418	GLU	GLU	ILE	ILE
	GLU	E490	F419	GLU	ASP	ALA	ALA
	LYS	E491	T420	ALA	PHE	THR	THR

- Molecule 13: U3 small nucleolar RNA-associated protein 10

Chain UJ:  29% 34% 37%

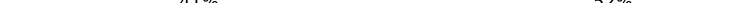


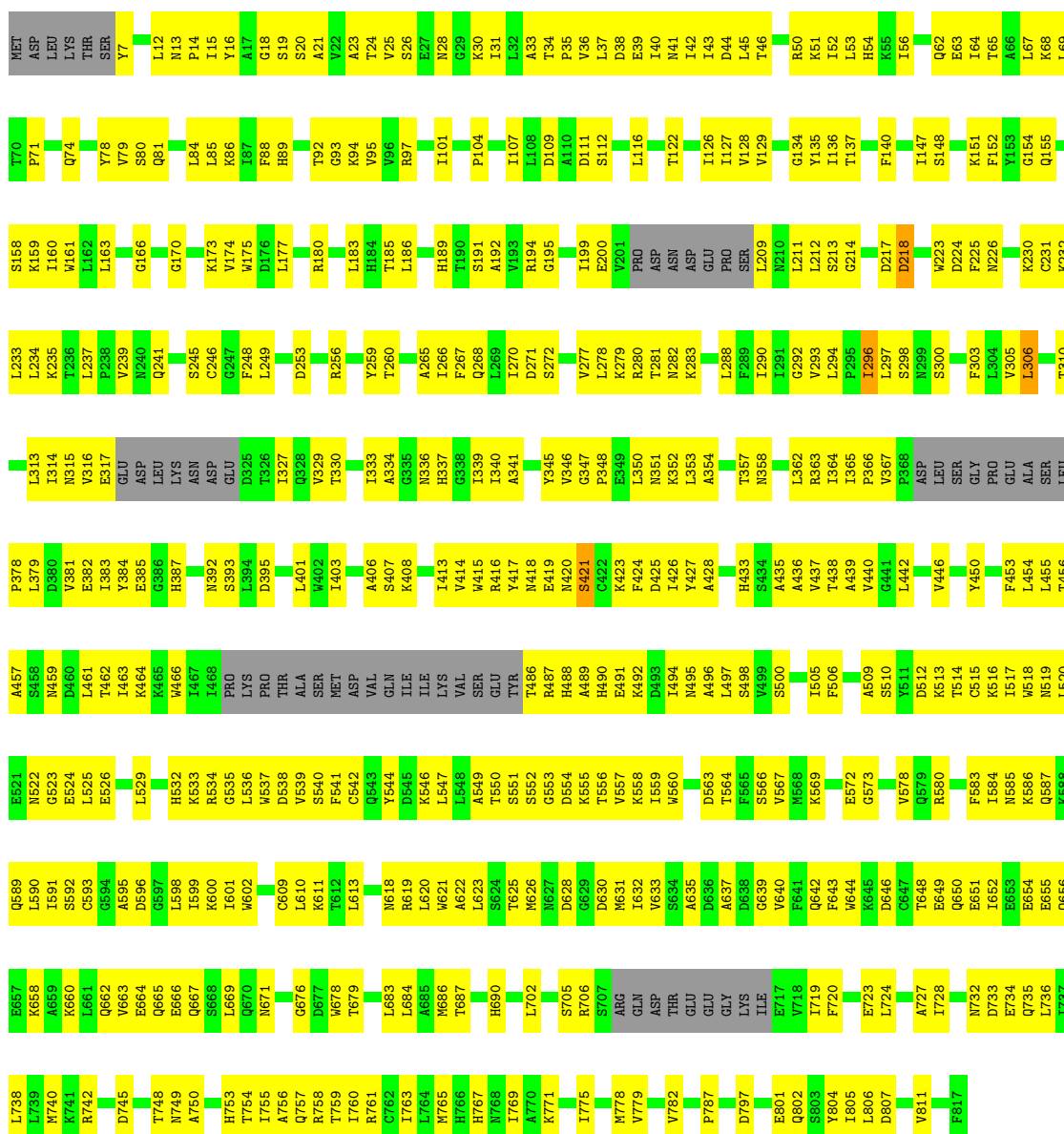


- Chain UK: 41% 56%



- Molecule 16: U3 small nucleolar RNA-associated protein 13

Chain UM: 

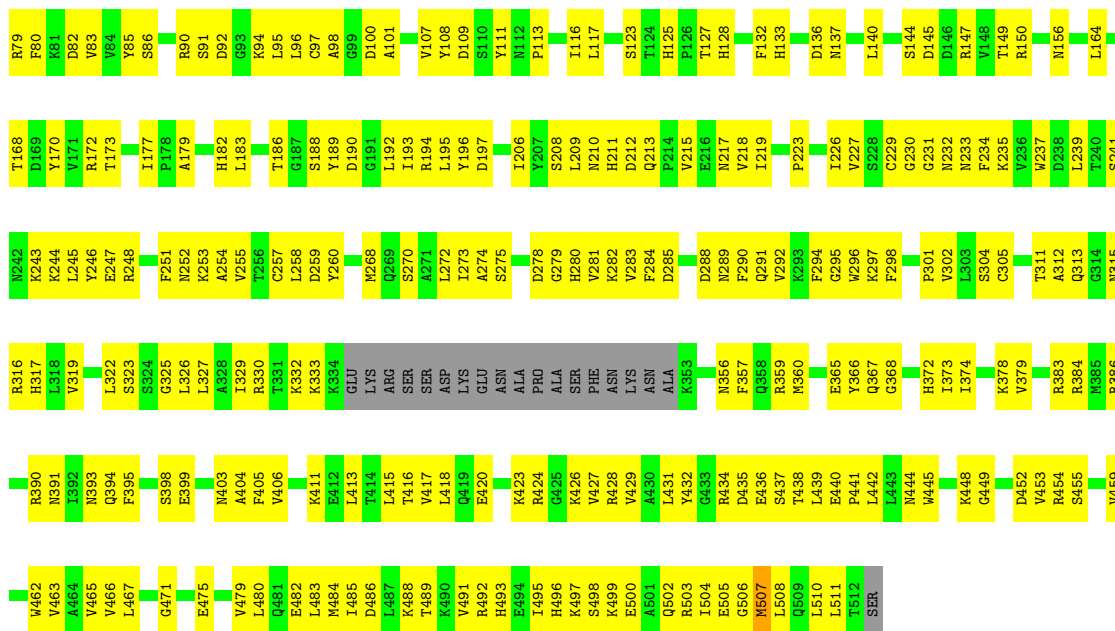


- Molecule 17: U3 small nucleolar RNA-associated protein 14

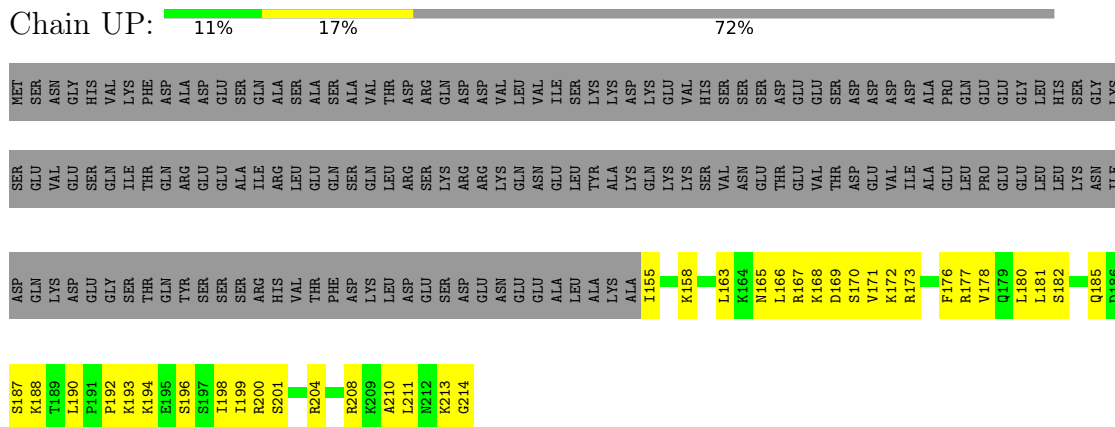
[illegible]

- Chain UO:

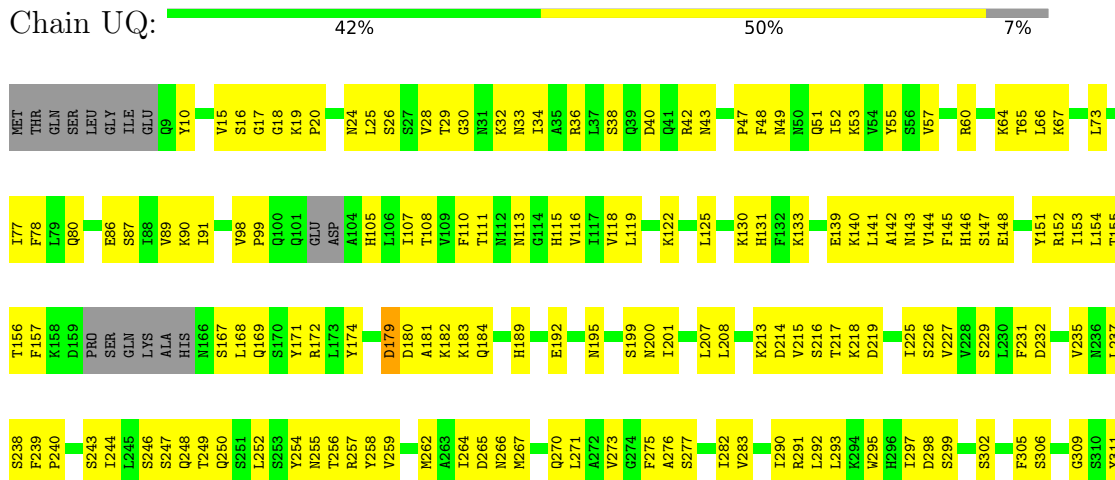
Met	S2	A4	R5	P6	R7	I8	I9	T10	S11	K12	L16	P17	T21	P22	E23	R25	R28	Q29	Y30	T31	S32	A33	Q34	L35	N40	S41	V42	T43	H44	F47	H51	P52	H53	D54	F55	A56	V57	T58	R62	V63	Q64	I65	F66	S67	I74	K75	T76	F77	S78
-----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



- Molecule 19: Bud site selection protein 21



- Molecule 20: NET1-associated nuclear protein 1

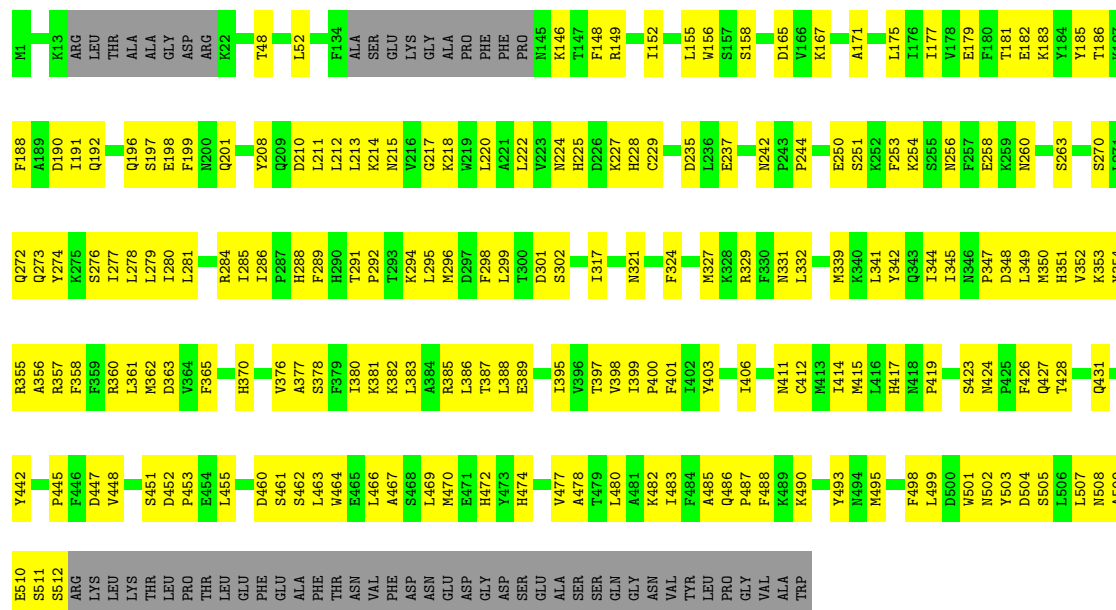






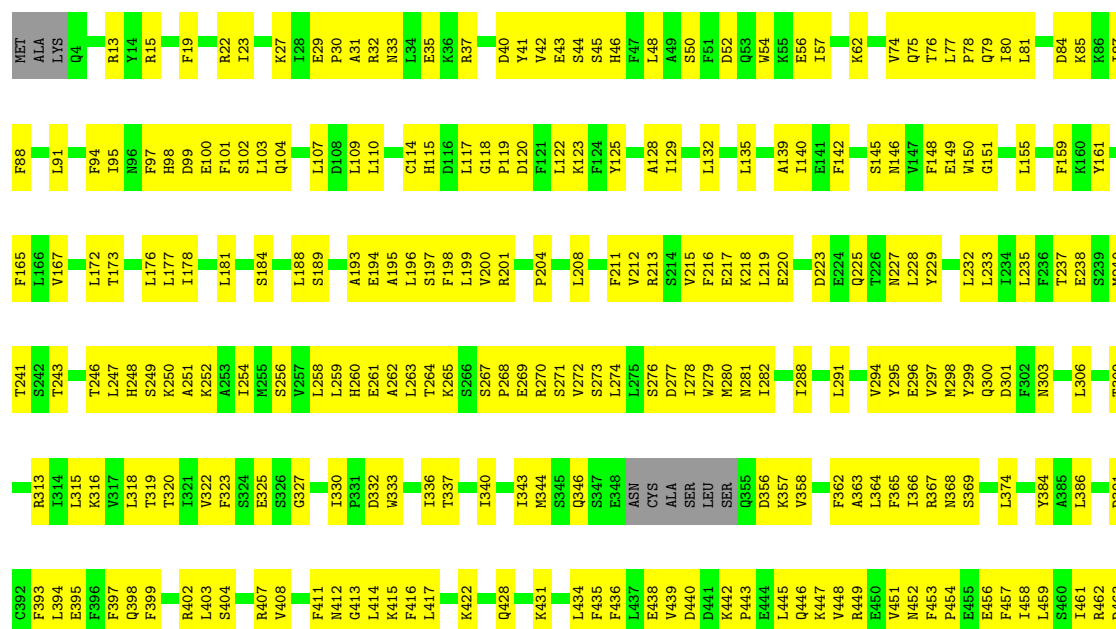
• Molecule 22: Nucleolar complex protein 4

Chain US: 56% 34% 11%



• Molecule 23: U3 small nucleolar RNA-associated protein 20

Chain UT: 49% 42% 10%



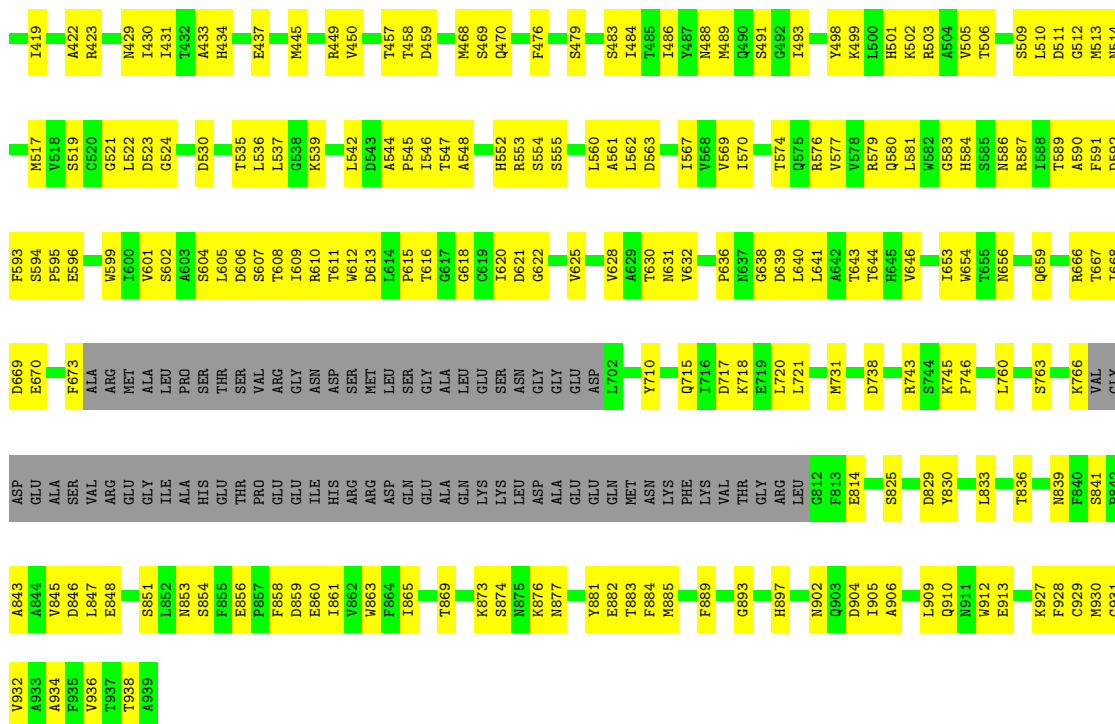


ARG	LYS	GLU	ARG	ARG	ARG	ARG	LYS	ARG	ALA	ILE	LEU	ALA	VAL	VAL	ALA	LEU	GLU	THR	TYR	SER	ALA	LYS	ARG	ALA	VAL	ASP	GLU	GLU	GLN	ILE	GLY	GLU	GLN	GLY	TYR	GLN	VAL	GLN	ARG	ARG	ASN	GLY	TYR	GLN	VAL	VAL	LYS	GLN	THR	HIS	ARG	GLU	ARG			
L1590	L1591	P1592	L1661	S1662	S1663	L1664	L1665	G1666	A1667	E1668	Y1669	L1670	D1602	D1603	I1606	I1607	E1608	R1609	M1610	P1611	L1612	A1613	E1614	L1615	L1616	V1617	V1620	L1621	G1622	M1625	D1626	F1631	L1632	P1633	S1634	I1635	L1636	I1639	C1640	L1643	R1644	S1645	K1646	S1647	E1648	R1651	D1652	V1653	R1654	R1655	V1656	T1657	L1658	G1659	K1660	
L1725	F1726	G1727	F1728	L1729	G1730	A1731	E1732	K1733	E1736	N1737	Y1738	H1739	K1740	V1742	K1743	E1744	L1745	S1747	L1748	K1749	S1750	Y1751	E1755	A1758	S1759	N1760	I1761	L1763	F1766	S1771	P1772	V1773	K1774	L1775	L1776	L1777	M1778	V1779	R1780	I1781	L1789	L1792	V1795	G1799	L1800	N1801	E1802	H1802								
M1803	S1804	D1805	L1810	L1811	H1816	Q1817	L1818	S1825	ASN	SER	PRO	GLN	ILE	PRO	PRO	LYS	LYS	VAL	LYS	ASP	GLN	VAL	E1841	D1844	F1845	F1846	L1847	E1851	S1852	K1853	T1856	I1857	M1860	L1863	K1870	F1871	A1872	L1875	L1876	N1877	V1878	L1879	L1880	L1887	T1888	V1889	S1890	Q1957								
H1891	L1892	E1893	L1894	F1895	L1896	P1897	F1898	L1899	R1900	S1902	L1903	E1906	M1907	V1910	V1911	L1912	S1913	T1914	L1915	R1916	L1917	L1918	I1919	I1922	R1923	L1924	D1925	F1926	S1927	D1928	L1929	S1930	S1931	E1932	I1933	F1934	K1935	N1936	C1937	A1938	R1939	K1940	V1941	L1942	N1943	I1944	I1945	S1948	P1949	S1950	T1951	S1952	Q1957			
M1958	F1966	I1967	R1968	L1969	T1970	K1975	L1979	L1983	V1986	L1987	P1988	D1989	L1990	N1991	E1992	S1994	R1995	Q1996	G1997	L1998	A1999	F2000	N2001	F2002	L2003	K2004	A2005	L2006	V2007	S2008	K2009	L2149	L1938	L1939	L1936	L1937	N2154	S2171	ILE	GLY	PHE	E2175	T2195	SER	VAL	GLY	SER	GLU	HIS	Q2202						
T2220	GLU	SER	VAL	TYR	LYS	HIS	G2227	Y2241	PRO	H2243	K2261	ASP	LEU	THR	LYS	LEU	GLU	ILE	SER	THR	N2270	F2287	SER	ILE	PRO	E2291	K2312	THR	PRO	PHE	ILE	ASP	VAL	SER	LYS	GLN	THR	GLY	GLU	ASP	ASP	THR	THR	ALA	S2346	ASP	GLU	HIS	ARG	MET						
ASP	S2353	Q2369	Y2370	LEU	ASP	E2373	E2379	E2381	Y2390	LEU	GLU	THR	TYR	SER	ARG	ALA	VAL	ASP	GLU	GLU	E2404	T2408	N2411	L2414	K2415	L2416	L2417	GLU	ASP	LYS	LEU	GLN	VAL	SER	ASN	GLY	TYR	GLN	GLN	ARG	ARG	VAL	VAL	GLN	THR	ALA	VAL	GLN	THR	VAL	LEU	GLU	ARG			
ARG	GLU	ARG	ARG	SER	ARG	ALA	LEU	ALA	ASN	ALA	PRO	GLN	ILE	SER	ALA	LYS	LYS	VAL	LEU	ARG	LYS	HIS	ALA	ARG	ARG	ARG	GLY	ARG	GLY	TYR	GLN	GLY	TYR	GLN	GLN	ARG	ARG	ASN	GLY	TYR	GLN	GLN	ARG	ARG	VAL	VAL	GLN	THR	ALA	VAL	GLN	THR	VAL	LEU	GLU	ARG

• Molecule 24: U3 small nucleolar RNA-associated protein 21

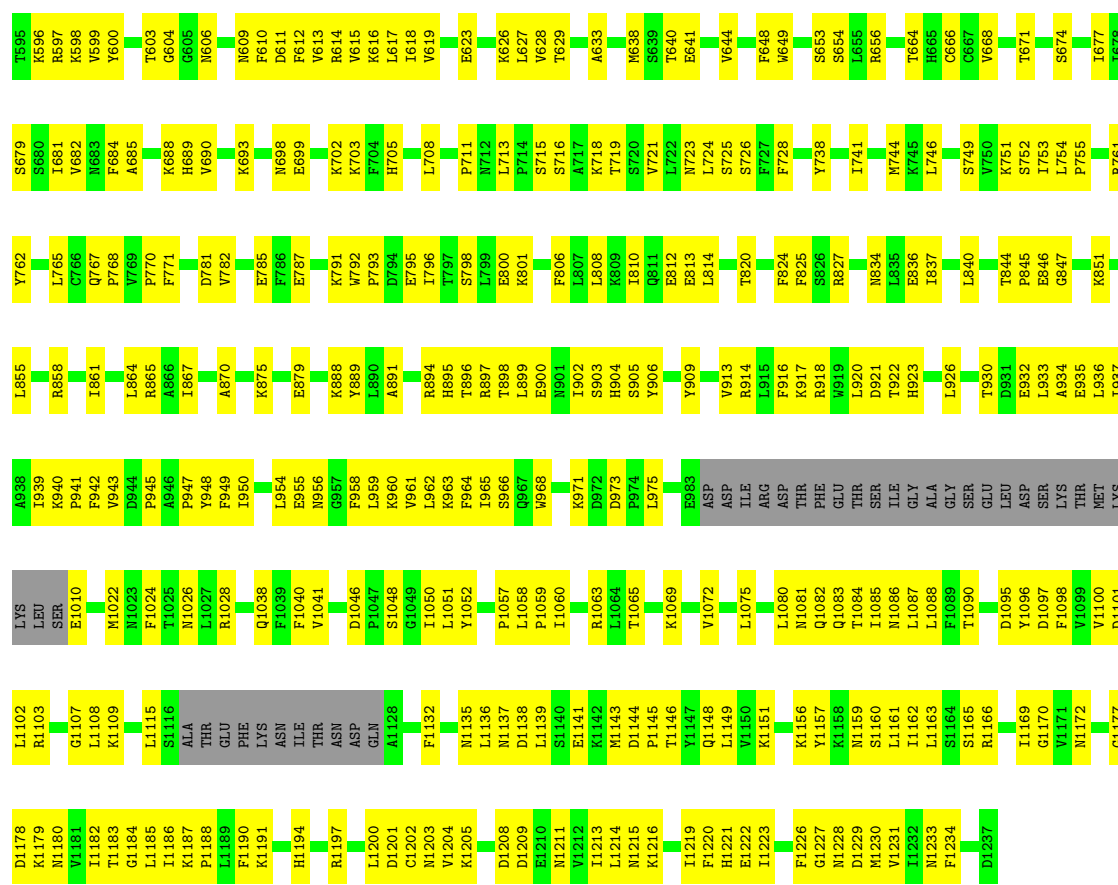
Chain UU:  49% 41% 10%

MET	SER	ILE	ASP	LEU	LYS	ARG	LYS	ARG	LYS	VAL	GLU	GLU	ASP	VAL	ARG	SER	ARG	GLY	K19	N20	S21	K22	I23	F24	S25	R28	I29	I30	N35	F39	G42	G45	Y49	I50	V51	T52	C53	V54	G55	K56	T57	F58	Q59	I60	Y61	A63	D62	L66	H67	L68	L69	F70
T76	P77	S78	S79	I80	L83	S84	A85	H86	F87	H88	Y89	V90	Y91	A93	E95	K97	Y101	E106	L109	L110	D115	A116	N117	V118	E119	H120	L121	C122	I123	F124	G125	D126	Y127	L128	C53	S131	T132	D133	D134	N135	Q59	Y140	K141	K142	S143	E229	P145	Q146	D147	P150		
Y154	V159	G165	E166	V167	H168	S169	L170	L173	A174	T175	Y176	K179	V183	T184	K185	S186	N187	V188	L189	L190	F191	M192	V193	R194	F200	D207	S202	F205	P206	D207	Q208	I209	V217	L218	D219	I220	I221	A222	L223	G224	T225	V226	T227	G228	E229	V230	I231	M232	F233	N234		
M235	R242	T243	I244	K245	L246	P247	Q248	R249	G250	I251	S252	S253	L254	S255	F256	S261	S262	H263	L264	G267	T268	D272	L273	I274	D277	L278	D279	R280	R281	L283	H284	V286	L287	K288	N289	R292	T302	Q307	P308	I309	I310	V311	T312	S313	P412	E413	I414	Y322	A416			
F324	D325	P326	S327	L328	S332	G333	D334	V335	V336	V337	Q338	P339	Y342	L343	R344	S345	R346	P353	S361	H364	F365	M366	L367	S370	K371	D372	R373	S374	L375	W376	S377	F378	S379	L380	R381	K382	D383	S386	Q387	E388	M389	R392	R401	F411	P412	E413	I414	Y415				

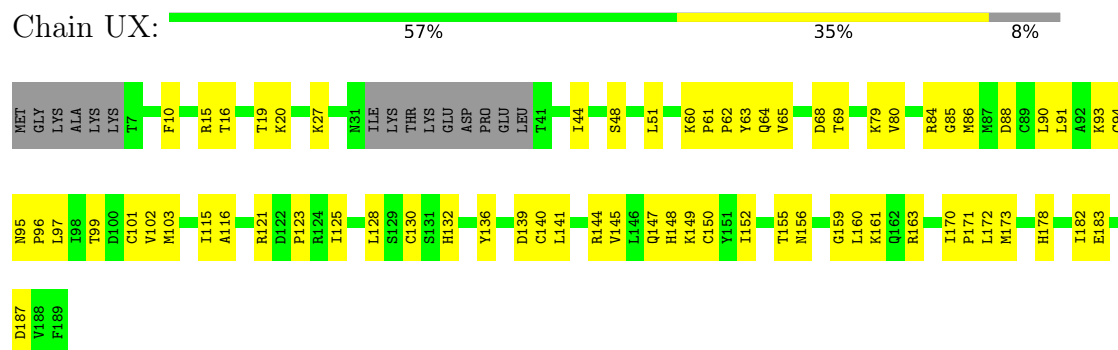


- Molecule 25: U3 small nucleolar RNA-associated protein 22



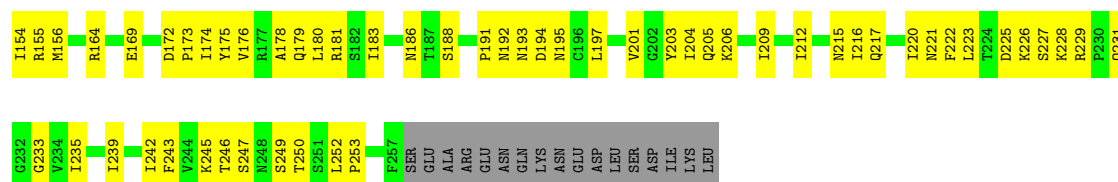


• Molecule 26: rRNA-processing protein FCF1



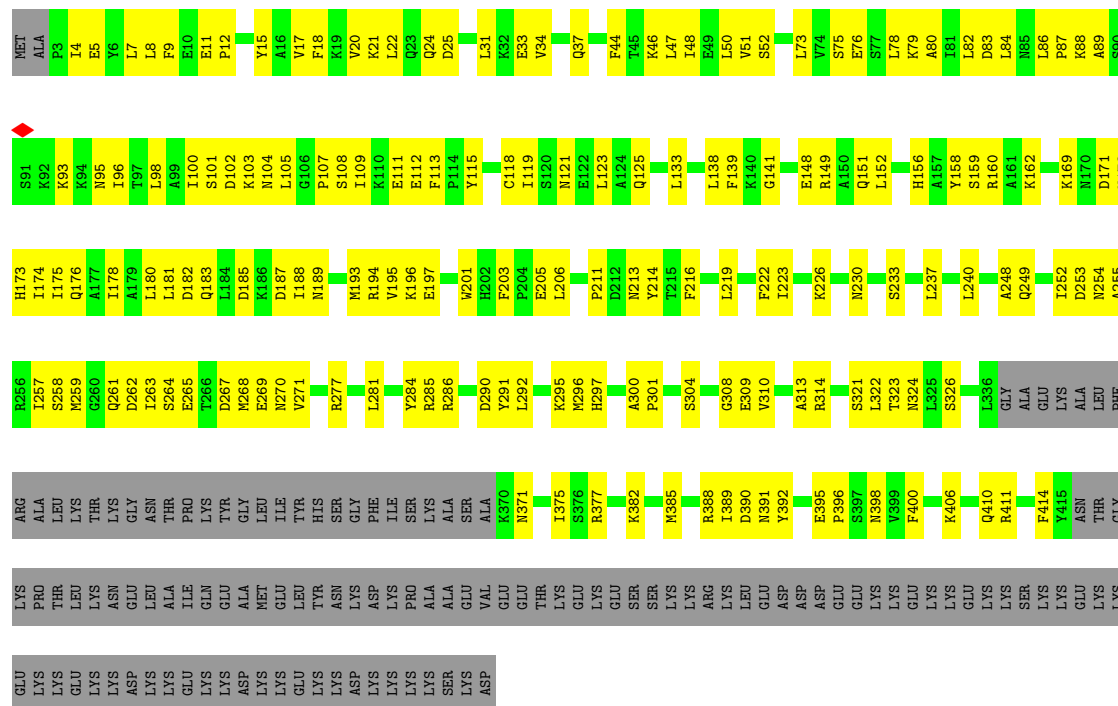
• Molecule 27: Ribosome biogenesis protein UTP30





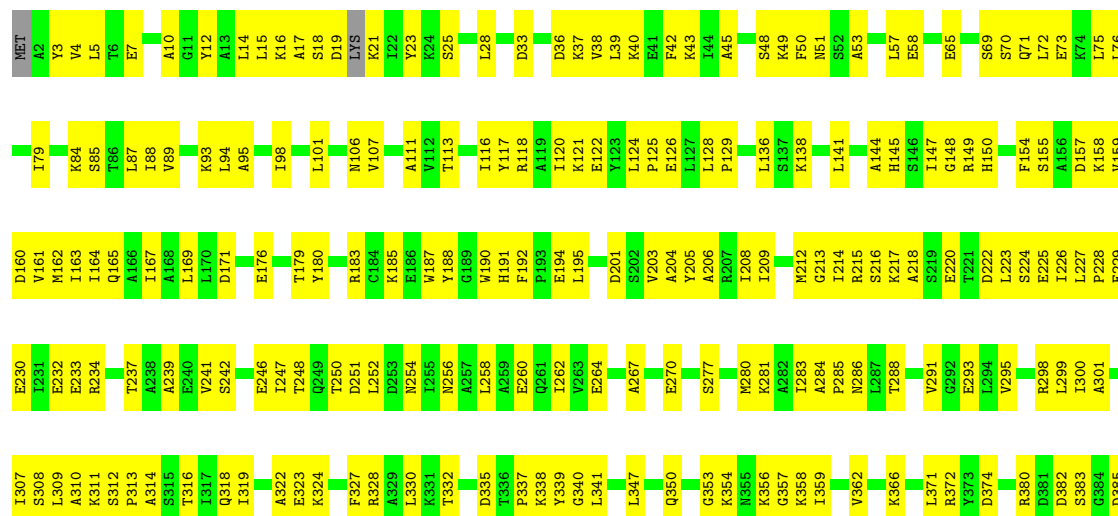
• Molecule 28: Nucleolar protein 56

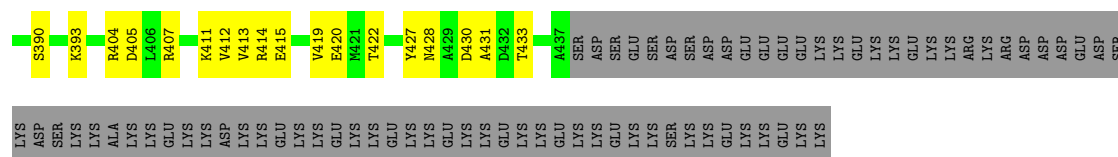
Chain CD: 41% 34% 25%



• Molecule 29: Nucleolar protein 58

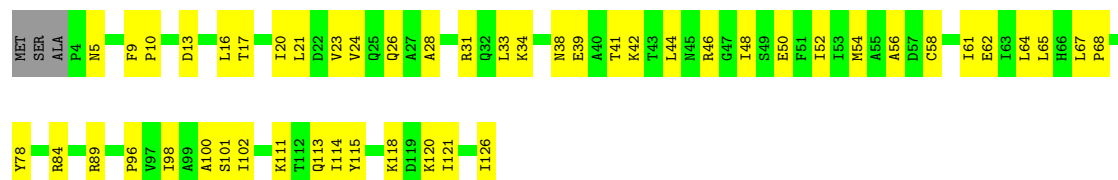
Chain CE: 42% 43% 15%





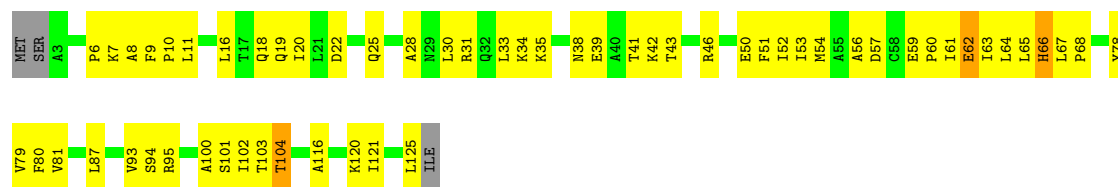
- Molecule 30: 13 kDa ribonucleoprotein-associated protein

Chain CF: 59% 39% .



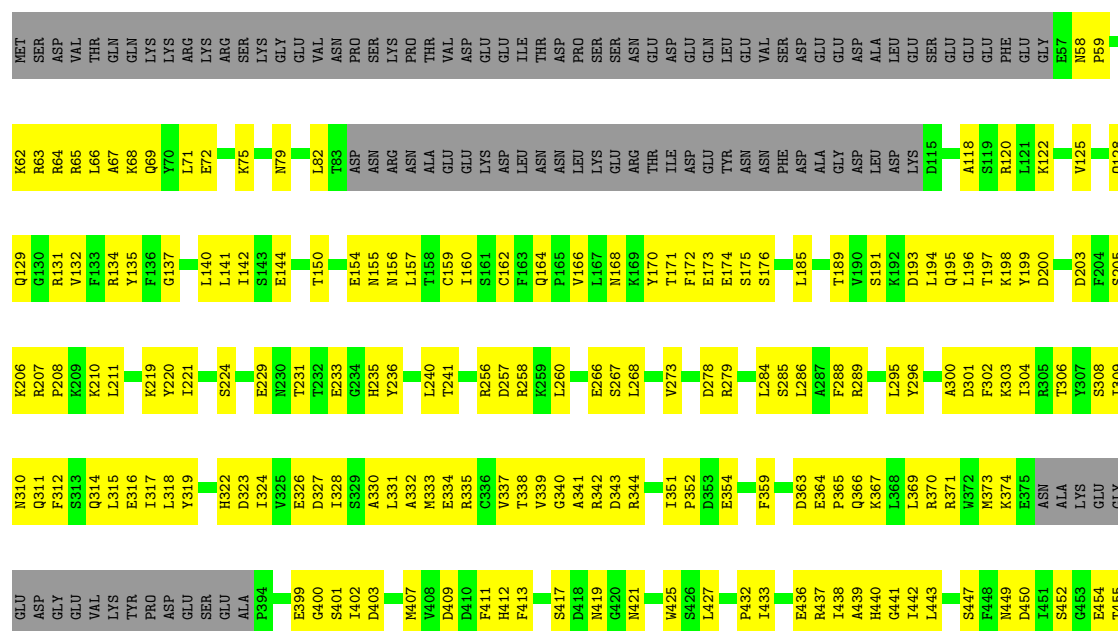
- Molecule 30: 13 kDa ribonucleoprotein-associated protein

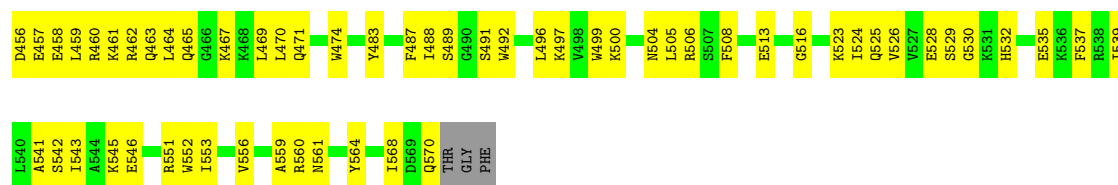
Chain CG: 52% 44% . .



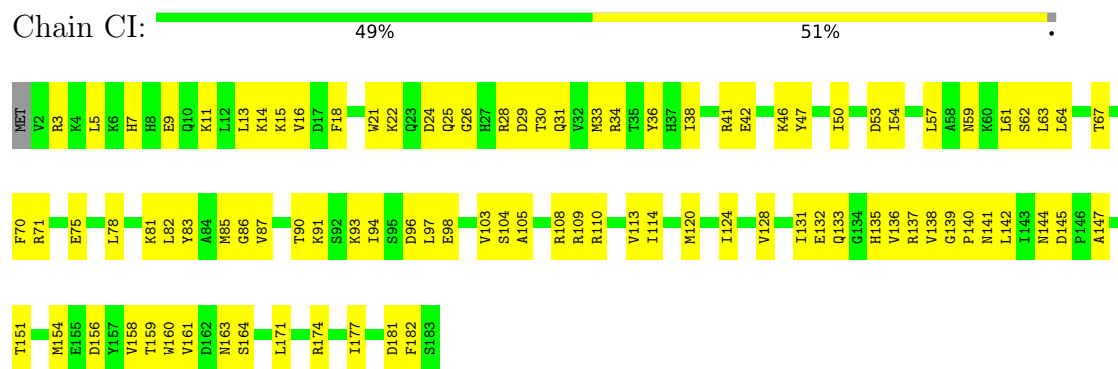
- Molecule 31: Ribosomal RNA-processing protein 9

Chain CH: 40% 41% 19%

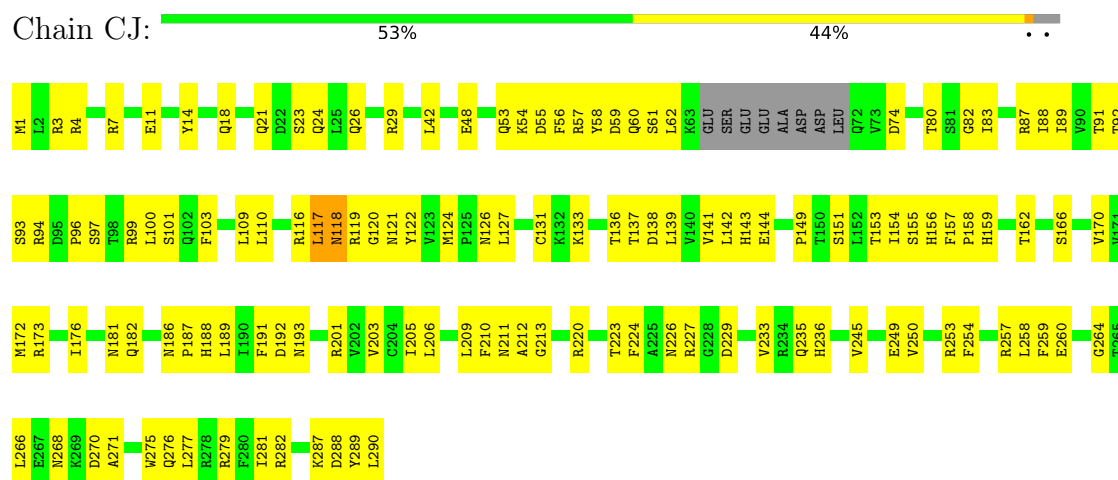




• Molecule 32: U3 small nucleolar ribonucleoprotein protein IMP3



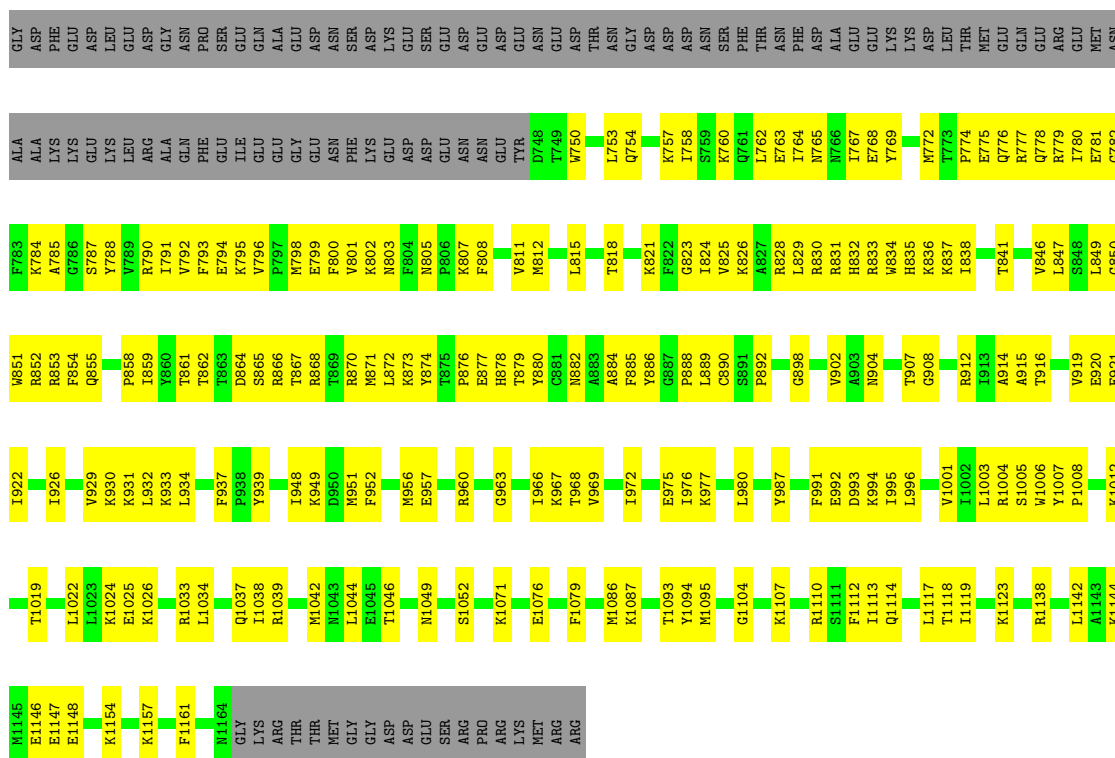
• Molecule 33: U3 small nucleolar ribonucleoprotein protein IMP4



• Molecule 34: U3 small nucleolar RNA-associated protein MPP10

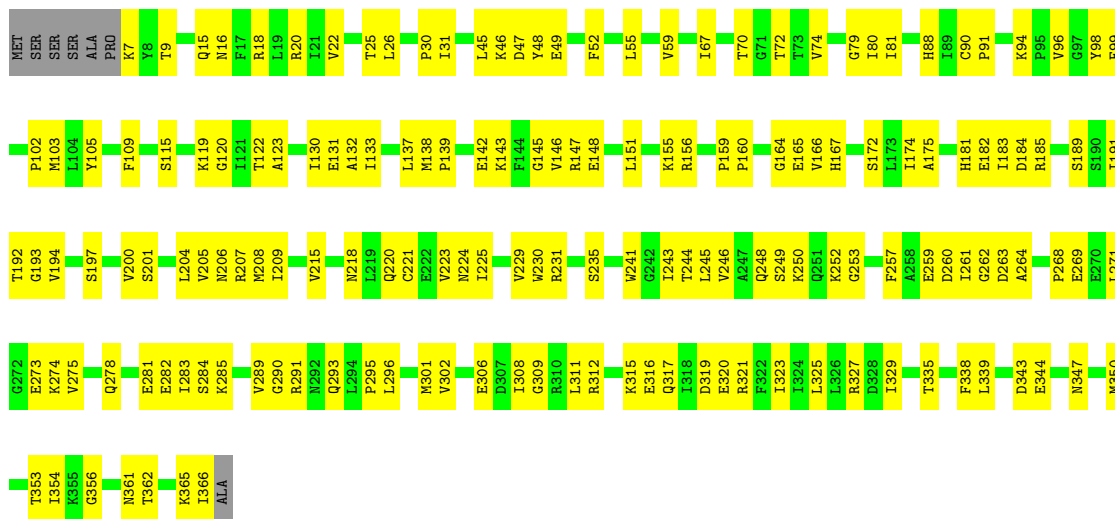






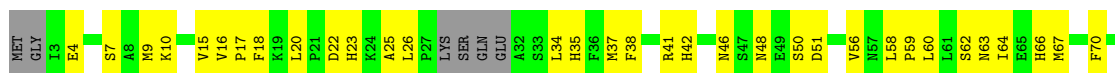
• Molecule 36: RNA 3'-terminal phosphate cyclase-like protein

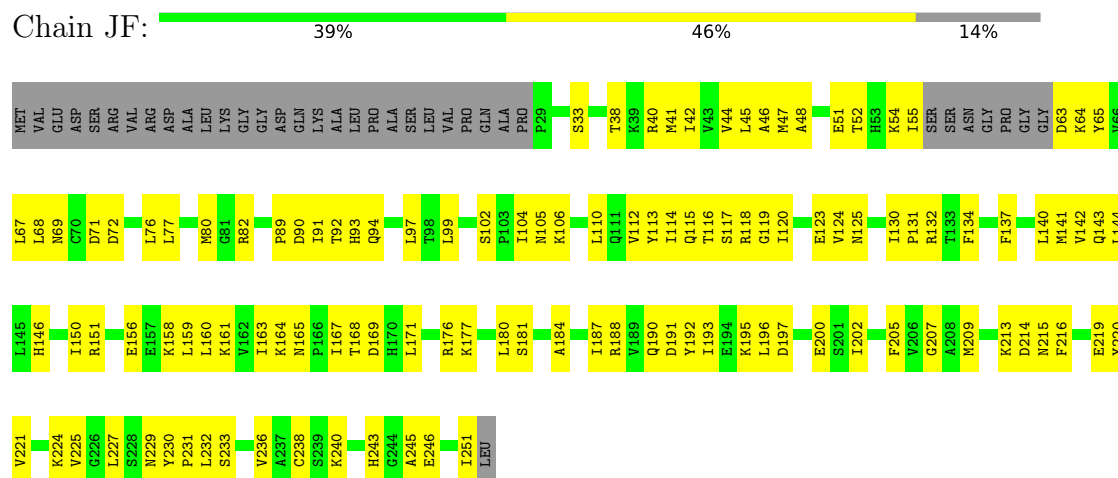
Chain CM: 54% 44%



• Molecule 37: Ribosomal RNA-processing protein 7

Chain CN: 40% 38% 22%

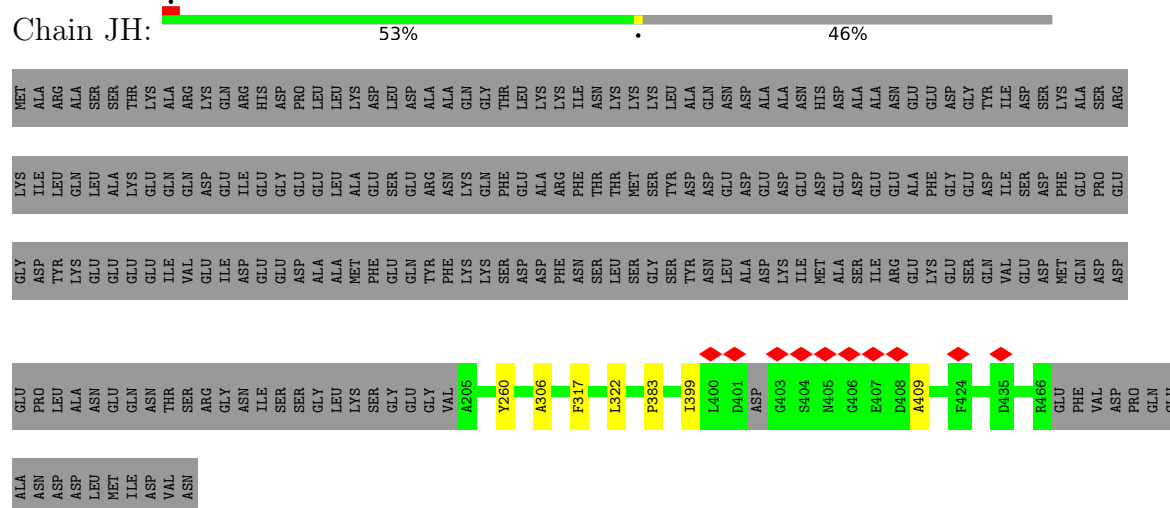




- Molecule 39: Ribosomal RNA small subunit methyltransferase NEP1



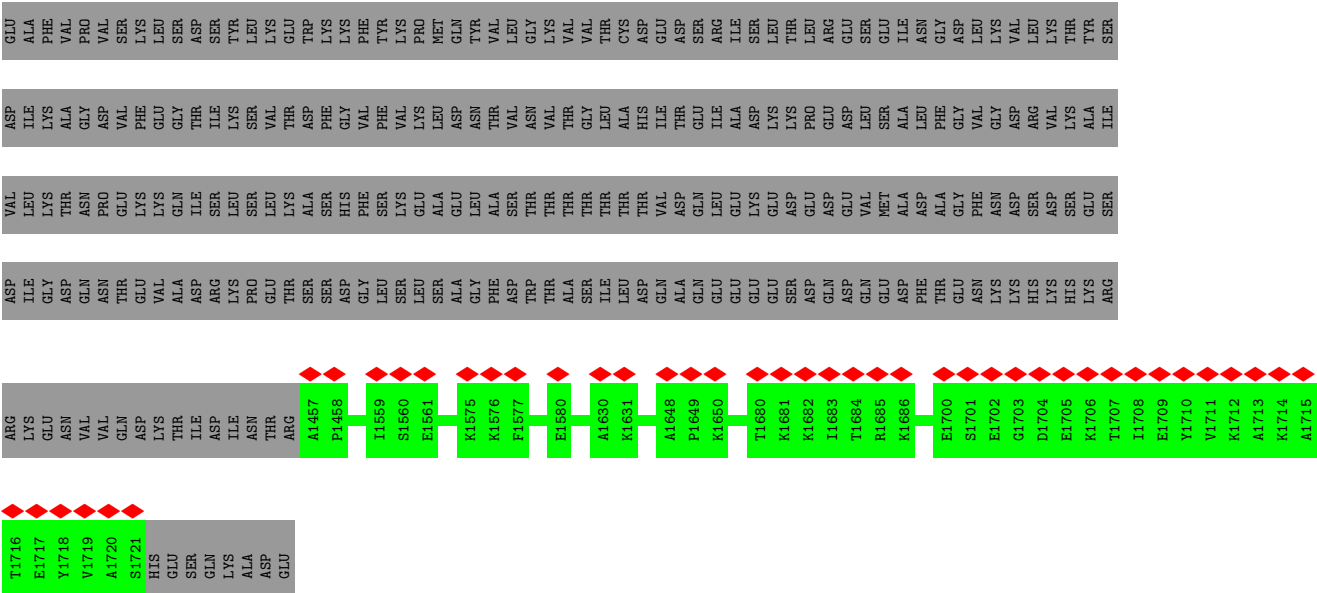
- Molecule 40: Essential nuclear protein 1



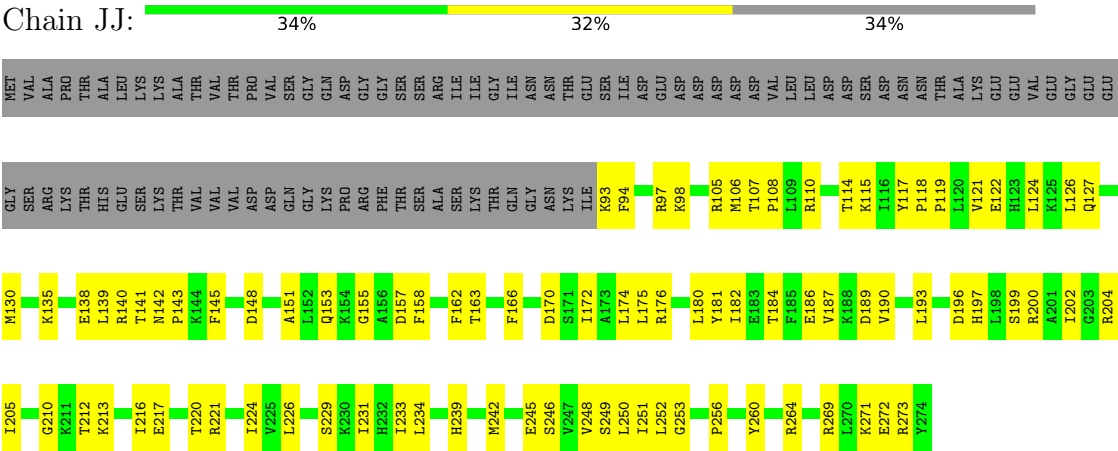
- Molecule 41: rRNA biogenesis protein RRP5



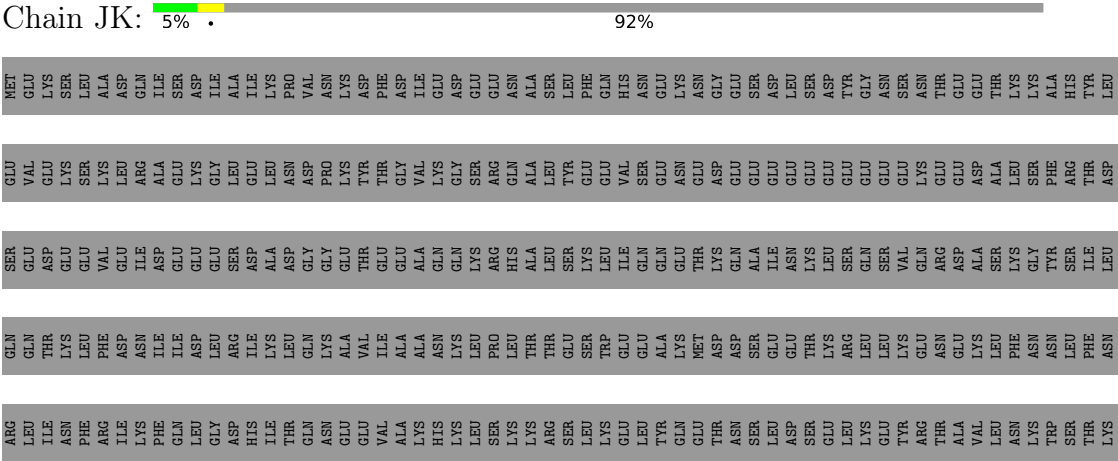




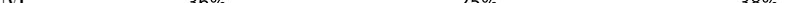
• Molecule 42: Pre-rRNA-processing protein PNO1

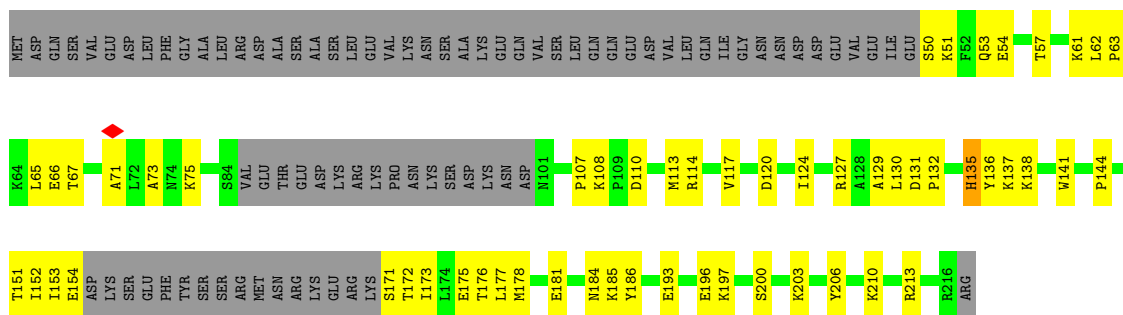


• Molecule 43: Protein BFR2

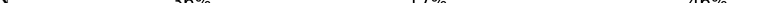


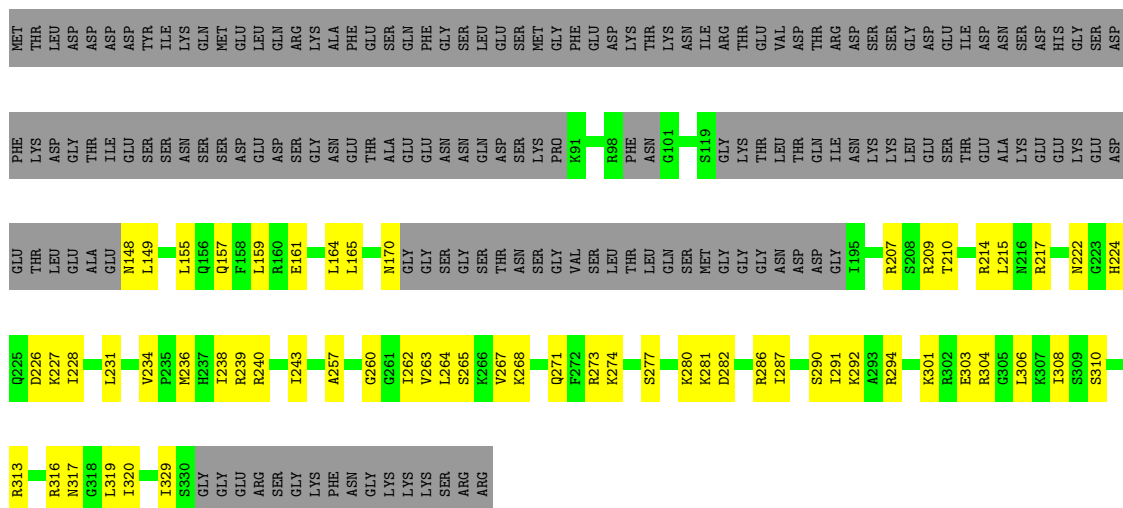
- Molecule 44: rRNA-processing protein FCF2

Chain JM: 

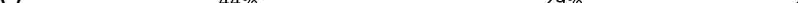


- Molecule 45: Protein FAF1

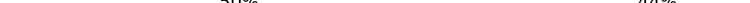
Chain JN: 

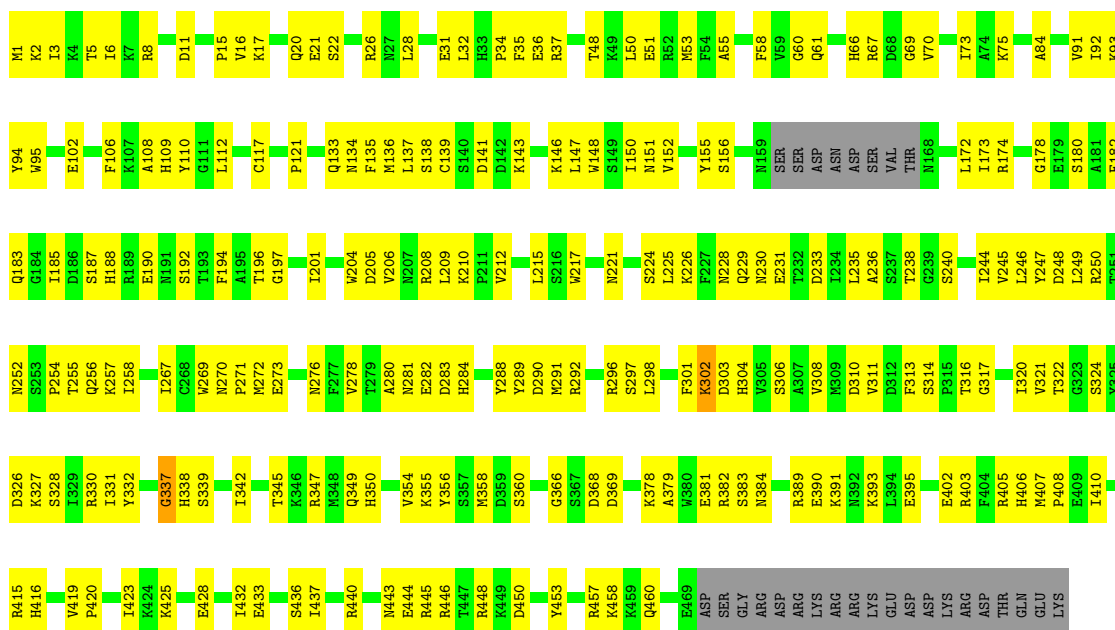


- Molecule 46: KRR1 small subunit processome component

Chain JO: 

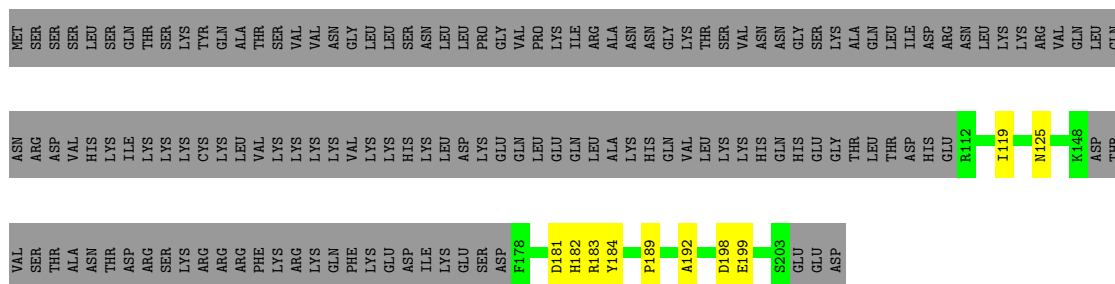
- Molecule 47: Protein SOF1

Chain JP:  50% 44% 6%

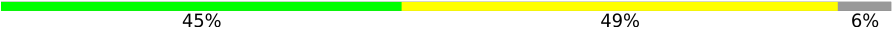


- Molecule 48: Regulator of rDNA transcription protein 14

Chain IQ: 26% 5% 69%

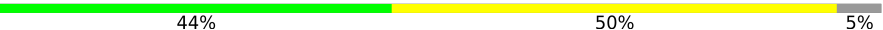


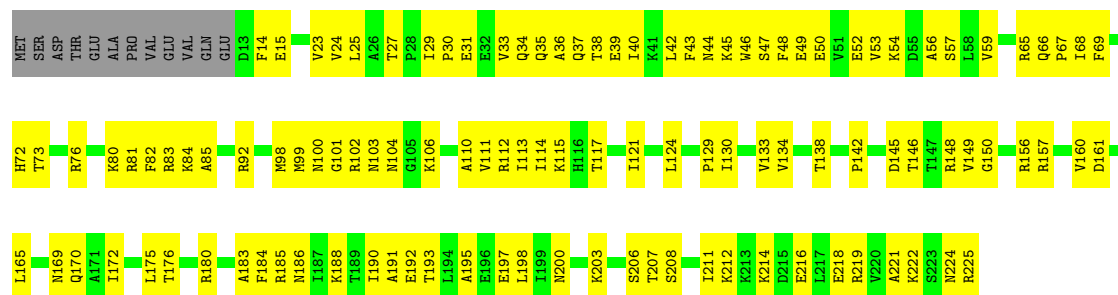
- Molecule 49: 40S ribosomal protein S4-A

Chain DE:  45% 49% 6%



- Molecule 50: 40S ribosomal protein S5

Chain DF:  44% 50% 5%



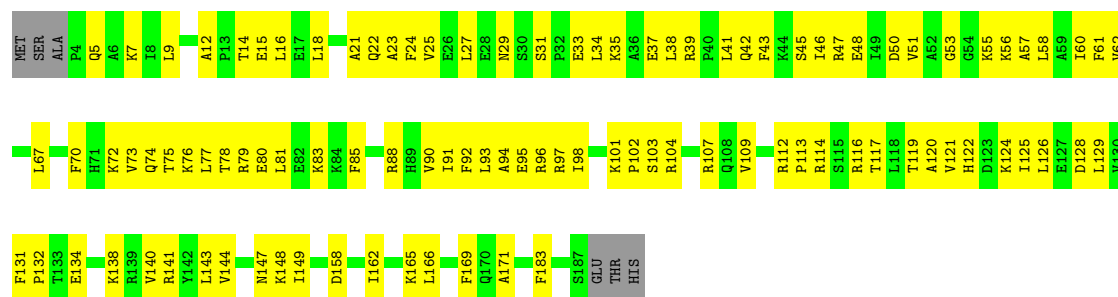
- Molecule 51: 40S ribosomal protein S6-A

Chain DG:  43% 49% 8%

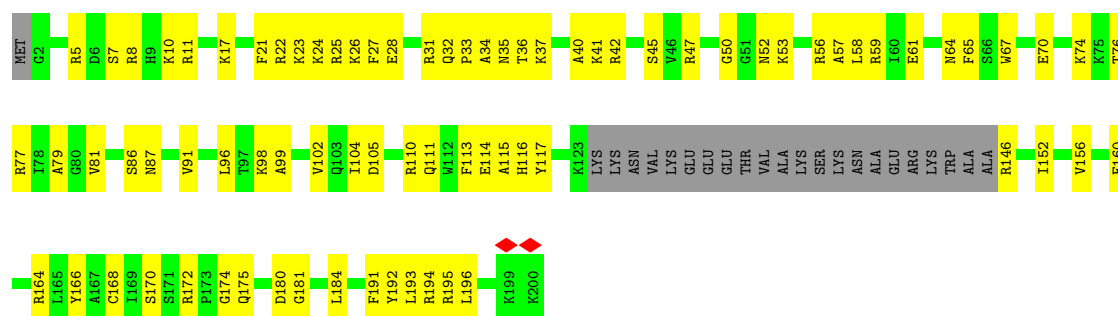


- Molecule 52: 40S ribosomal protein S7-A

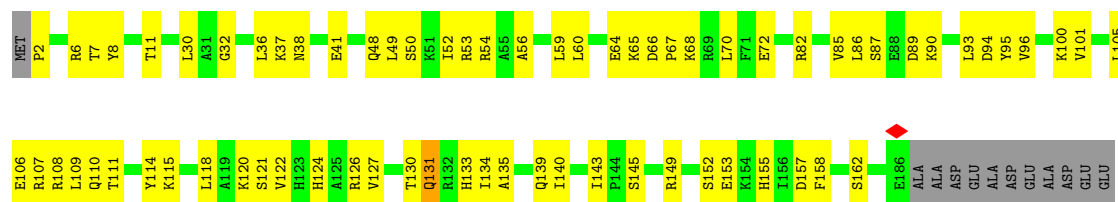
Chain DH:  44% 53% 3%



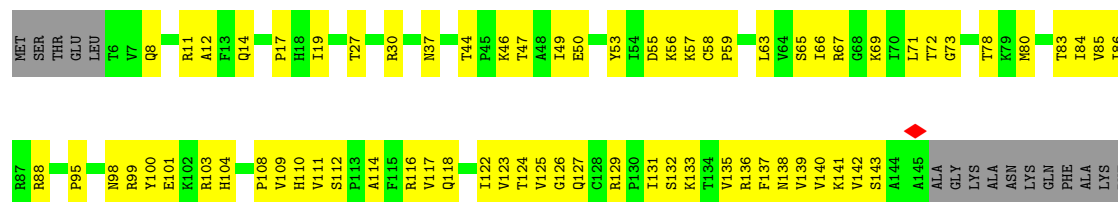
• Molecule 53: 40S ribosomal protein S8-A



• Molecule 54: 40S ribosomal protein S9-A

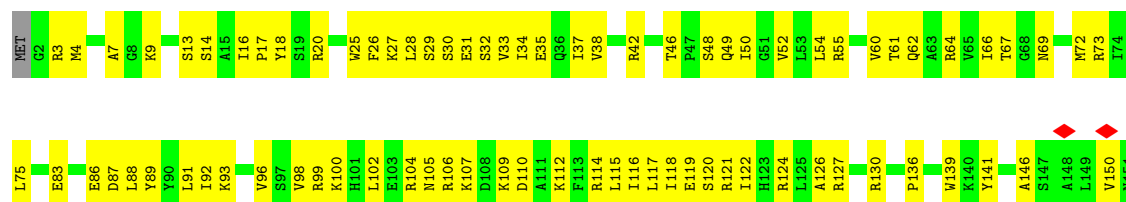


• Molecule 55: 40S ribosomal protein S11-A

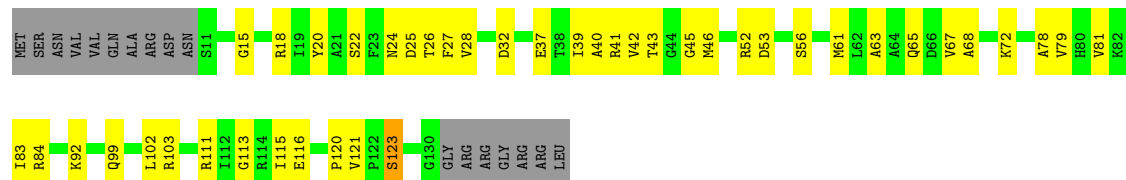


• Molecule 56: 40S ribosomal protein S13

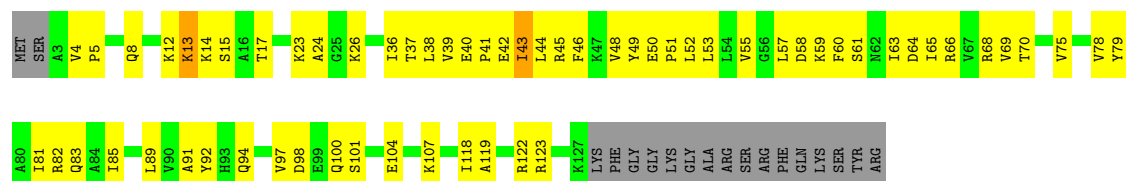




• Molecule 57: 40S ribosomal protein S14-A



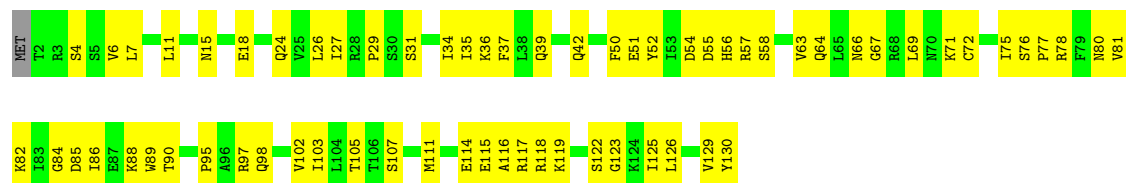
• Molecule 58: 40S ribosomal protein S16-A



• Molecule 59: 40S ribosomal protein S18-A



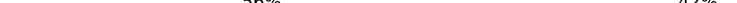
• Molecule 60: 40S ribosomal protein S22-A



• Molecule 61: 40S ribosomal protein S23-A

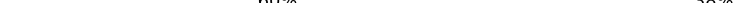


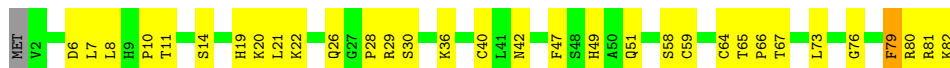
- Molecule 62: 40S ribosomal protein S24-A

Chain DY:  56% 42%

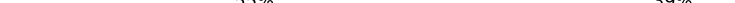


- Molecule 63: 40S ribosomal protein S27-A

Chain Db:  60% 38% ..



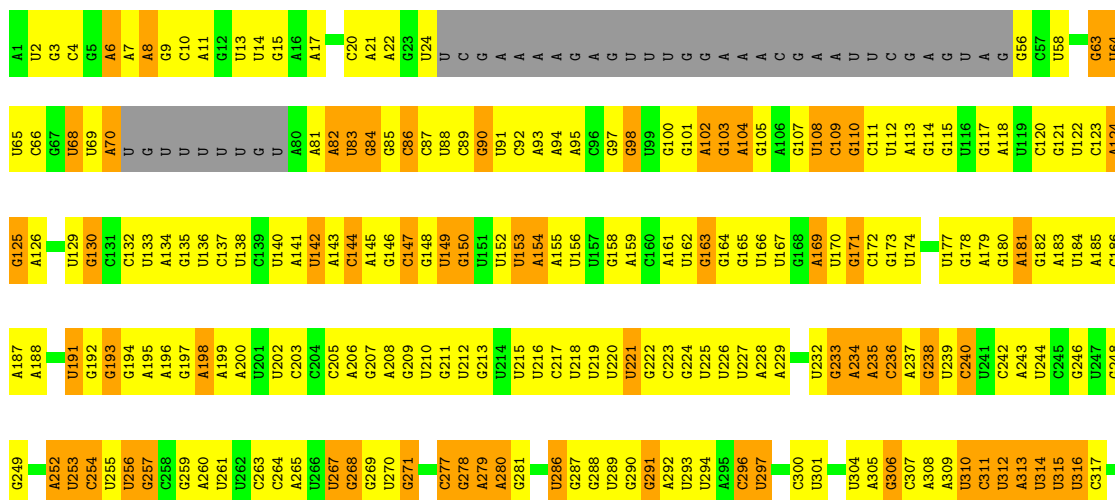
- Molecule 64: 40S ribosomal protein S28-A

Chain Dc:  55% 39% 6%

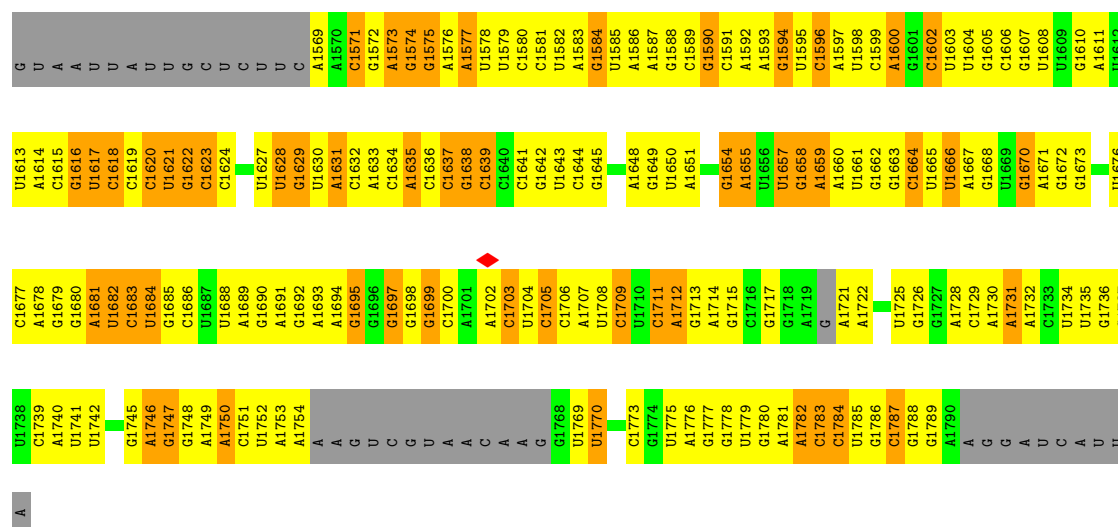


- Molecule 65: 5'ETS RNA

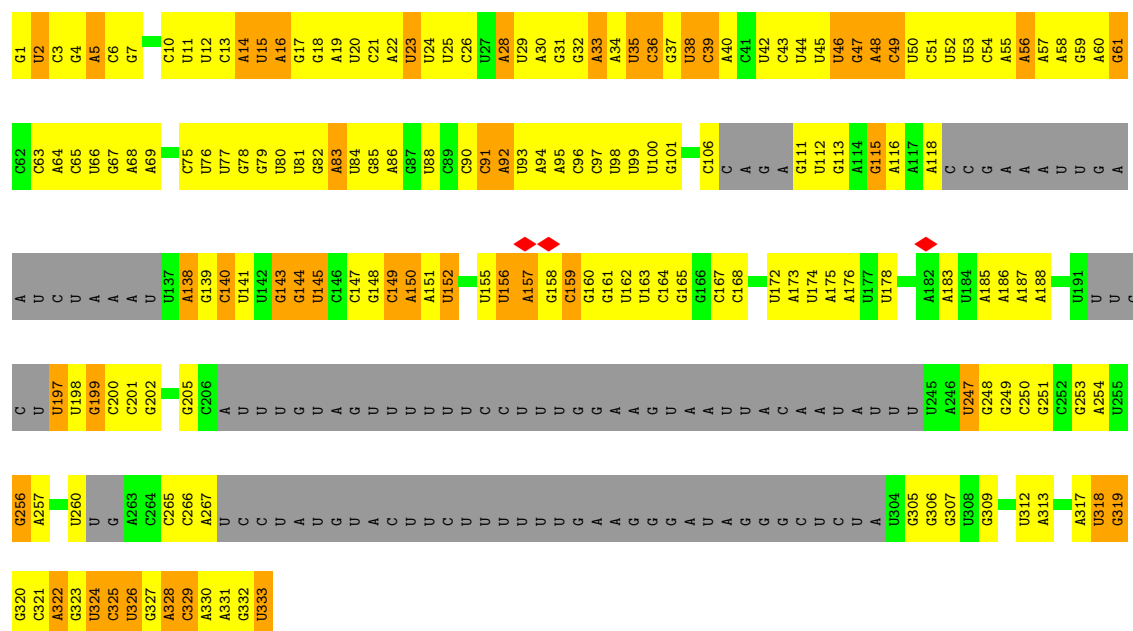
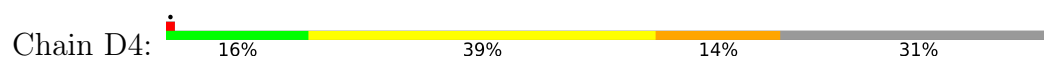
Chain D2:



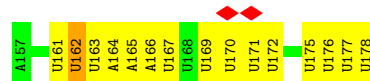




• Molecule 67: U3 snoRNA

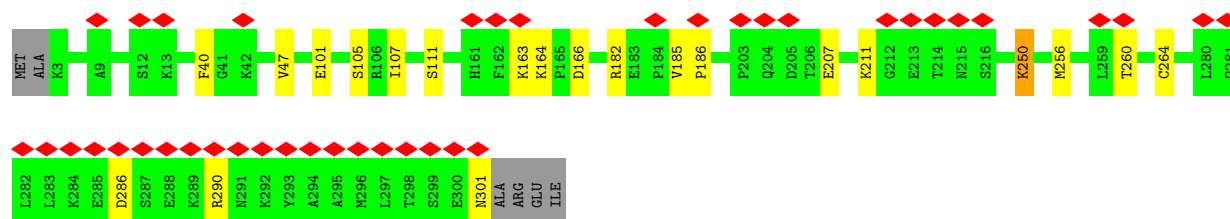


• Molecule 68: RNA



• Molecule 69: Exosome complex component RRP45

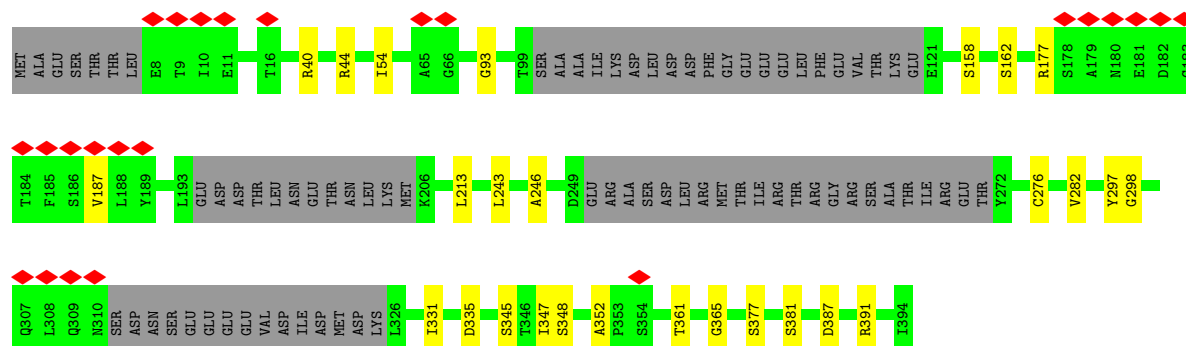
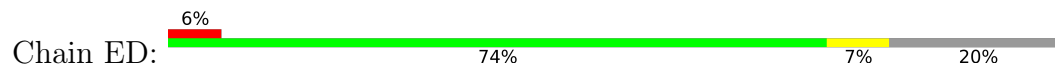




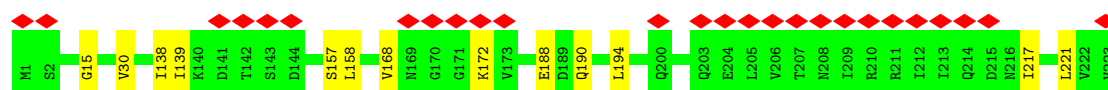
- Molecule 70: Exosome complex component SKI6



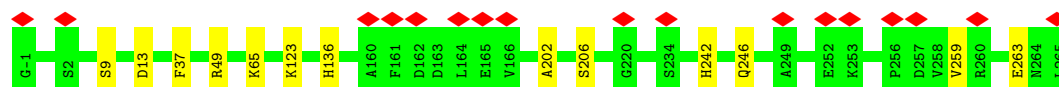
- Molecule 71: Exosome complex component RRP43



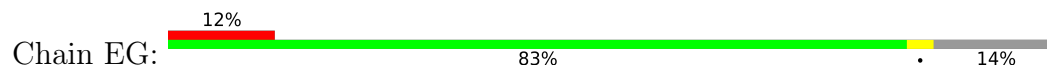
- Molecule 72: Exosome complex component RRP46

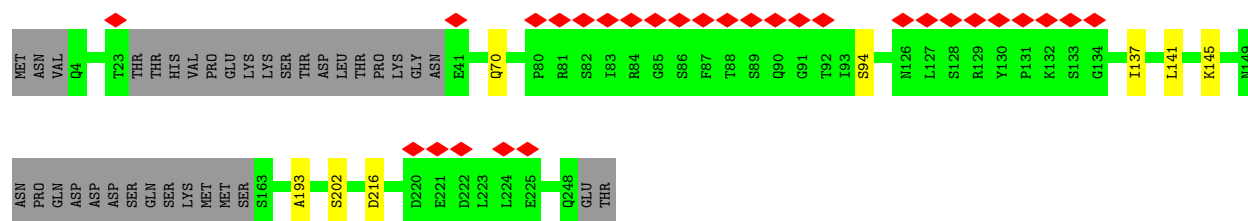


- Molecule 73: Exosome complex component RRP42

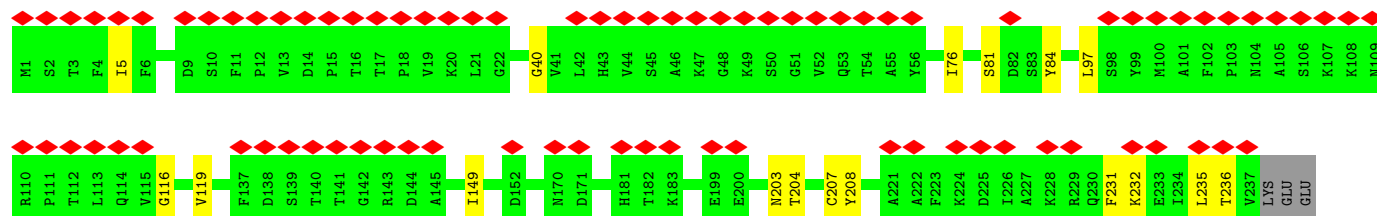


- Molecule 74: Exosome complex component MTR3

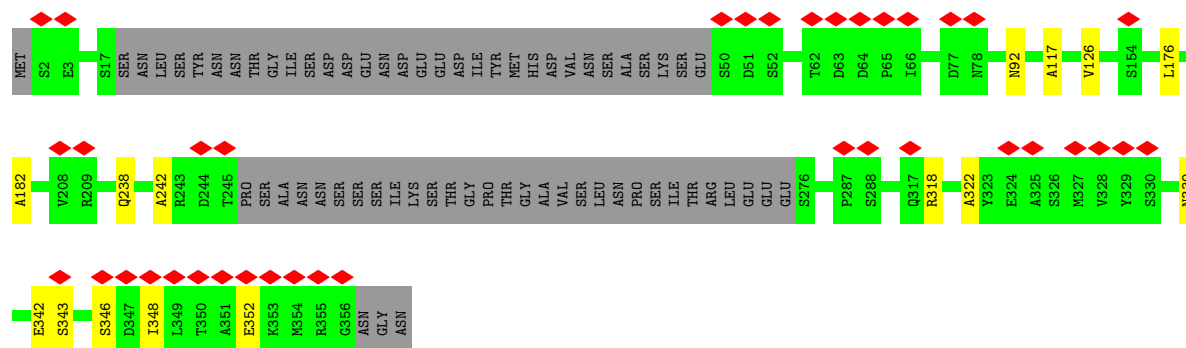
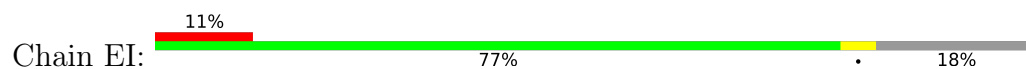




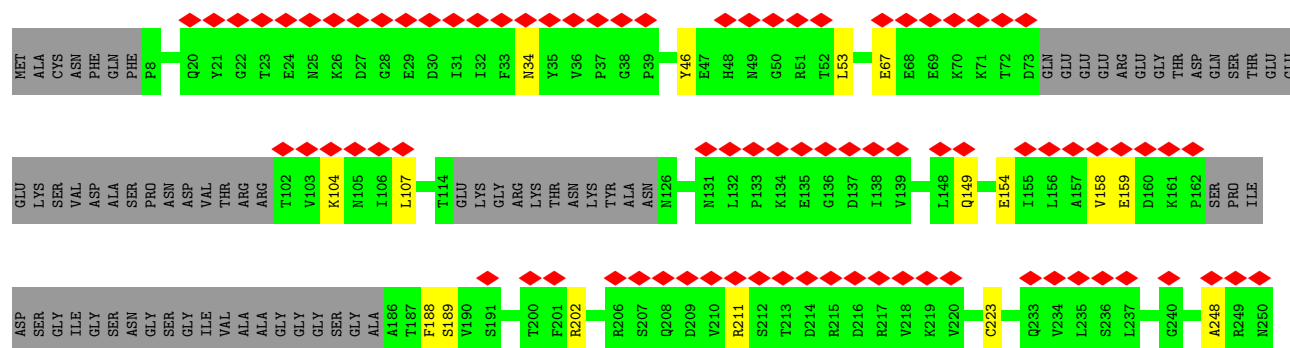
• Molecule 75: Exosome complex component RRP40

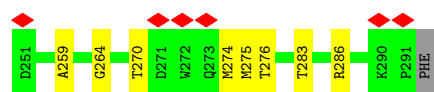


• Molecule 76: Exosome complex component RRP4

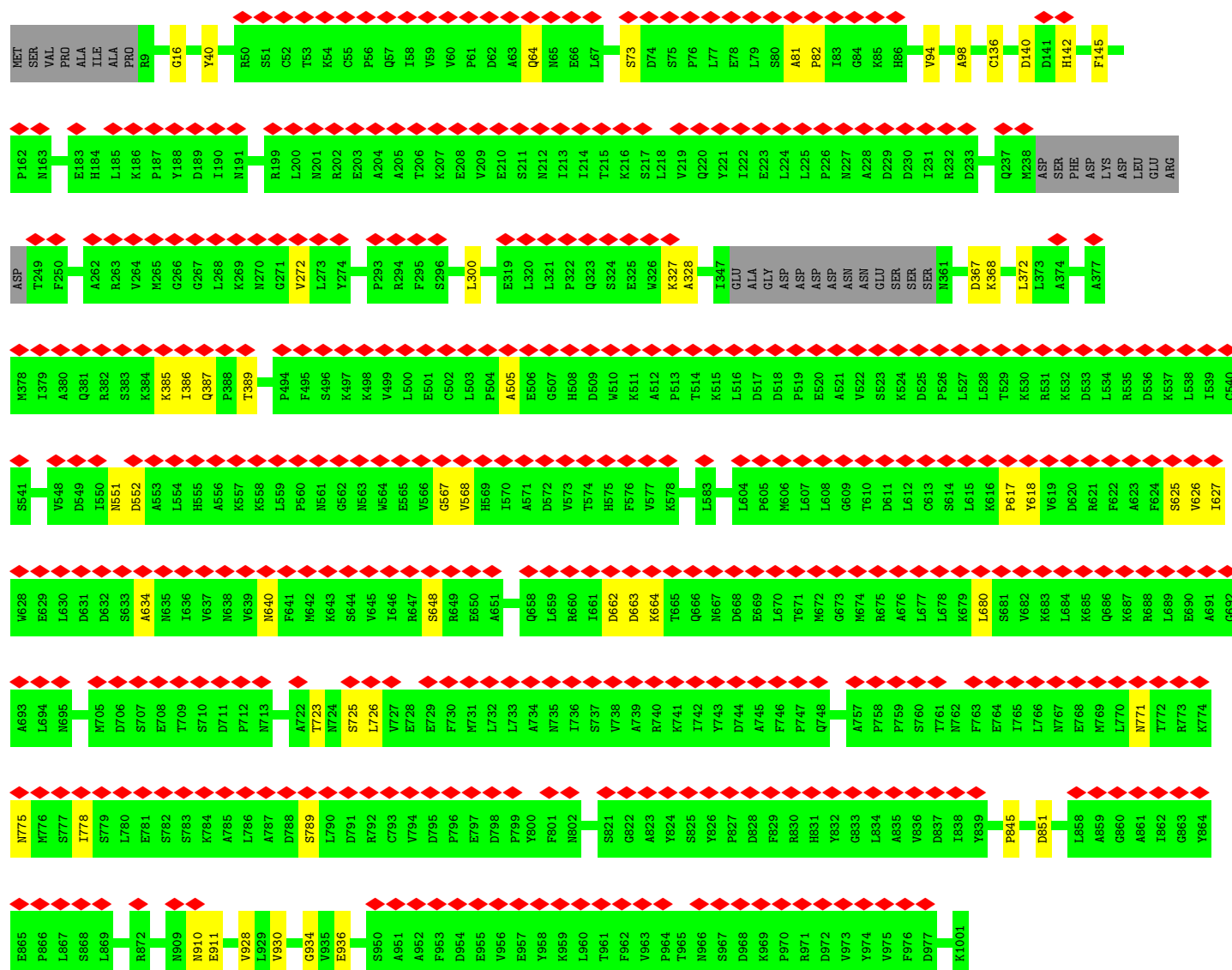
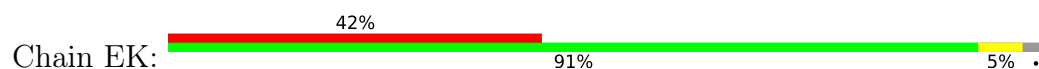


• Molecule 77: Exosome complex component CSL4

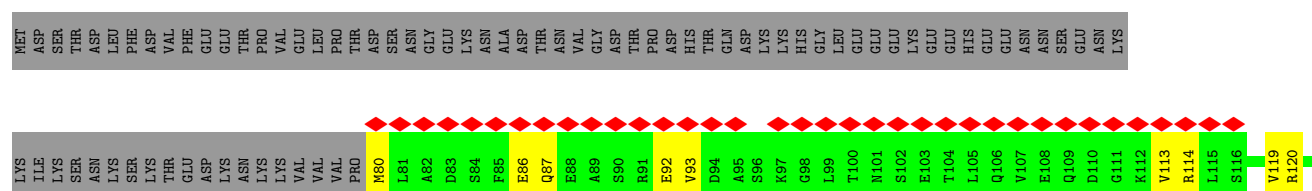
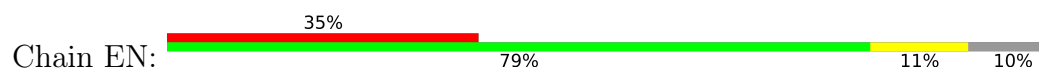




• Molecule 78: Exosome complex exonuclease DIS3



• Molecule 79: ATP-dependent RNA helicase DOB1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6024	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 ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.259	Depositor
Minimum map value	-0.204	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	571.86, 571.86, 571.86	wwPDB
Map dimensions	540, 540, 540	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, MG, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	CA	0.59	0/1917	0.75	0/2588
1	CB	0.35	0/1815	0.68	2/2448 (0.1%)
2	DA	0.40	0/1937	0.66	0/2593
3	JA	0.19	0/6021	0.50	2/8176 (0.0%)
3	JB	0.14	0/4128	0.40	0/5747
4	UA	0.48	0/6780	0.72	4/9175 (0.0%)
5	UB	0.24	0/3787	0.52	0/5126
6	UC	0.48	0/1034	0.75	0/1365
7	UD	0.33	0/5461	0.62	0/7395
8	UE	0.32	0/3840	0.61	0/5208
9	UF	0.37	0/2538	0.61	0/3405
10	UG	0.57	0/4302	0.78	0/5805
11	UH	0.21	0/2716	0.56	0/3721
12	UI	0.24	0/875	0.59	0/1176
13	UJ	0.30	0/9111	0.54	1/12323 (0.0%)
14	UK	0.48	0/2047	0.78	2/2711 (0.1%)
15	UL	0.29	0/6857	0.58	0/9253
16	UM	0.27	0/6070	0.57	3/8216 (0.0%)
17	UN	0.48	0/1252	0.75	0/1688
18	UO	0.35	0/3993	0.63	1/5413 (0.0%)
19	UP	0.30	0/499	0.58	0/659
20	UQ	0.32	0/6794	0.59	1/9203 (0.0%)
21	UR	0.48	0/3883	0.70	2/5265 (0.0%)
22	US	0.28	0/3703	0.56	0/5053
23	UT	0.20	0/17584	0.50	2/23824 (0.0%)
24	UU	0.40	0/6815	0.62	2/9213 (0.0%)
25	UV	0.23	0/8945	0.47	0/12097
26	UX	0.61	0/1418	0.78	0/1906
27	UZ	0.31	0/2041	0.58	0/2745
28	CD	0.40	0/3041	0.61	0/4098
29	CE	0.35	0/3362	0.63	0/4533
30	CF	0.45	0/944	0.71	1/1284 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	CG	0.50	0/941	0.85	3/1281 (0.2%)
31	CH	0.32	0/3798	0.61	0/5113
32	CI	0.71	0/1559	0.91	0/2097
33	CJ	0.54	0/2337	0.73	2/3148 (0.1%)
34	CK	0.40	0/1685	0.66	0/2261
35	CL	0.43	0/6471	0.71	4/8708 (0.0%)
36	CM	0.28	0/2832	0.52	0/3825
37	CN	0.20	0/1934	0.46	0/2604
38	JC	0.20	0/2908	0.53	0/3938
39	JF	0.24	0/1727	0.55	0/2329
39	JG	0.32	0/1828	0.64	0/2470
40	JH	0.12	0/1293	0.35	0/1801
41	JI	0.09	0/1313	0.32	0/1830
42	JJ	0.28	0/1469	0.57	0/1980
43	JK	0.21	0/342	0.47	0/462
44	JM	0.41	0/1156	0.67	0/1536
45	JN	0.51	0/1435	0.73	0/1907
46	JO	0.42	0/1910	0.65	0/2569
47	JP	0.61	0/3844	0.86	4/5174 (0.1%)
48	JQ	0.28	0/385	0.56	0/529
49	DE	0.28	0/1985	0.55	0/2675
50	DF	0.46	0/1690	0.67	0/2285
51	DG	0.19	0/1779	0.46	0/2379
52	DH	0.30	0/1506	0.56	0/2028
53	DI	0.19	0/1422	0.47	0/1899
54	DJ	0.51	0/1519	0.76	1/2035 (0.0%)
55	DL	0.19	0/1155	0.48	0/1557
56	DN	0.36	0/1215	0.65	0/1638
57	DO	0.38	0/892	0.61	0/1202
58	DQ	0.58	0/990	0.84	1/1335 (0.1%)
59	DS	0.19	0/513	0.44	0/711
60	DW	0.53	0/1038	0.76	0/1395
61	DX	0.47	0/798	0.79	0/1065
62	DY	0.35	0/1087	0.63	1/1449 (0.1%)
63	Db	0.43	0/620	0.66	0/838
64	Dc	0.41	0/499	0.75	0/670
65	D2	0.36	0/10633	0.37	0/16564
66	D3	0.32	0/31617	0.35	0/49213
67	D4	0.36	1/5432 (0.0%)	0.34	0/8439
68	EA	0.42	0/405	0.72	0/625
69	EB	0.60	1/1474 (0.1%)	0.79	0/2050
70	EC	0.60	0/1203	0.79	0/1673
71	ED	0.54	0/1569	0.82	0/2179

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
72	EE	0.56	0/1109	0.81	0/1545
73	EF	0.52	0/1328	0.80	0/1851
74	EG	0.56	0/1055	0.80	0/1462
75	EH	0.55	0/1169	0.86	2/1626 (0.1%)
76	EI	0.54	0/1437	0.84	0/1992
77	EJ	0.48	0/1087	0.84	0/1504
78	EK	0.66	0/4818	1.10	10/6720 (0.1%)
79	EN	0.49	0/4765	0.84	4/6636 (0.1%)
All	All	0.37	2/264486 (0.0%)	0.60	55/368214 (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
2	DA	0	1
3	JA	0	1
4	UA	0	1
6	UC	0	1
9	UF	0	1
11	UH	0	3
15	UL	0	2
16	UM	0	3
20	UQ	0	1
21	UR	0	1
23	UT	0	2
30	CG	0	1
31	CH	0	1
33	CJ	0	1
34	CK	0	1
38	JC	0	1
44	JM	0	1
47	JP	0	3
56	DN	0	1
57	DO	0	1
58	DQ	0	1
63	Db	0	1
70	EC	0	1
71	ED	0	3
72	EE	0	1
73	EF	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
74	EG	0	2
76	EI	0	1
77	EJ	0	1
79	EN	0	3
All	All	0	43

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
69	EB	250	LYS	CA-CB	-7.14	1.43	1.53
67	D4	197	U	C1'-N1	5.73	1.57	1.48

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
78	EK	272	VAL	N-CA-C	9.36	120.17	110.62
23	UT	1991	ASN	CA-C-N	-8.37	109.97	121.61
23	UT	1991	ASN	C-N-CA	-8.37	109.97	121.61
58	DQ	43	ILE	N-CA-C	-7.83	104.90	113.43
62	DY	114	ARG	CB-CG-CD	7.77	129.17	111.30

There are no chirality outliers.

5 of 43 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	DA	104	ASP	Peptide
3	JA	739	ASN	Peptide
4	UA	289	LEU	Peptide
6	UC	580	ARG	Peptide
9	UF	45	SER	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	CA	1881	0	1928	101	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CB	1782	0	1826	147	0
2	DA	1912	0	2023	106	0
3	JA	5916	0	5463	316	0
3	JB	4132	0	1819	21	0
4	UA	6635	0	6525	332	0
5	UB	3734	0	3432	170	0
6	UC	1026	0	1080	61	0
7	UD	5361	0	5364	342	0
8	UE	3772	0	3806	206	0
9	UF	2487	0	2533	144	0
10	UG	4218	0	4223	232	0
11	UH	2701	0	1951	121	0
12	UI	860	0	922	83	0
13	UJ	8961	0	9273	521	0
14	UK	2021	0	2098	163	0
15	UL	6726	0	6764	389	0
16	UM	5969	0	6006	393	0
17	UN	1227	0	1223	69	0
18	UO	3911	0	3906	269	0
19	UP	495	0	561	49	0
20	UQ	6662	0	6588	406	0
21	UR	3799	0	3783	238	0
22	US	3622	0	3214	183	0
23	UT	17290	0	16616	906	0
24	UU	6678	0	6652	343	0
25	UV	8736	0	8850	452	0
26	UX	1395	0	1473	73	0
27	UZ	2006	0	2118	118	0
28	CD	2994	0	3018	160	0
29	CE	3325	0	3414	213	0
30	CF	931	0	983	45	0
30	CG	928	0	976	72	0
31	CH	3725	0	3746	213	0
32	CI	1530	0	1572	100	0
33	CJ	2296	0	2325	131	0
34	CK	1667	0	1701	102	0
35	CL	6332	0	6515	424	0
36	CM	2781	0	2878	142	0
37	CN	1893	0	1875	104	0
38	JC	2845	0	2761	231	0
39	JF	1701	0	1767	102	0
39	JG	1799	0	1872	100	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
40	JH	1295	0	570	4	0
41	JI	1314	0	610	0	0
42	JJ	1442	0	1513	67	0
43	JK	334	0	313	23	0
44	JM	1137	0	1188	55	0
45	JN	1428	0	1425	69	0
46	JO	1876	0	1968	83	0
47	JP	3765	0	3714	226	0
48	JQ	381	0	255	12	0
49	DE	1944	0	2030	118	0
50	DF	1669	0	1724	118	0
51	DG	1755	0	1846	116	0
52	DH	1481	0	1572	96	0
53	DI	1399	0	1431	92	0
54	DJ	1494	0	1573	68	0
55	DL	1129	0	1196	65	0
56	DN	1192	0	1255	85	0
57	DO	881	0	910	40	0
58	DQ	973	0	1029	71	0
59	DS	516	0	222	0	0
60	DW	1021	0	1060	71	0
61	DX	786	0	843	67	0
62	DY	1073	0	1132	65	0
63	Db	610	0	630	41	0
64	Dc	497	0	535	26	0
65	D2	9508	0	4781	392	0
66	D3	28287	0	14261	1138	0
67	D4	4869	0	2468	186	0
68	EA	366	0	184	1	0
69	EB	1475	0	658	13	0
70	EC	1204	0	530	9	0
71	ED	1571	0	699	12	0
72	EE	1107	0	499	6	0
73	EF	1326	0	580	6	0
74	EG	1058	0	478	3	0
75	EH	1170	0	528	8	0
76	EI	1440	0	648	7	0
77	EJ	1091	0	500	12	0
78	EK	4818	0	2108	31	0
79	EN	4767	0	2109	59	0
80	Db	1	0	0	0	0
80	EK	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	UX	1	0	0	0	0
81	CL	1	0	0	0	0
81	EK	1	0	0	0	0
81	UX	1	0	0	0	0
82	CL	32	0	12	2	0
All	All	256149	0	219010	11209	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 26.

The worst 5 of 11209 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)
24:UU:228:GLY:CA	24:UU:246:ILE:O	1.81	1.28
11:UH:341:LEU:HA	11:UH:358:VAL:O	1.15	1.27
4:UA:77:GLY:HA3	4:UA:95:PHE:O	1.33	1.24
24:UU:228:GLY:HA3	24:UU:246:ILE:O	1.04	1.18
16:UM:30:LYS:HA	16:UM:45:LEU:O	1.42	1.18

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CA	202/240 (84%)	202 (100%)	0	100	100
1	CB	192/240 (80%)	191 (100%)	1 (0%)	81	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	DA	212/224 (95%)	212 (100%)	0	100	100
3	JA	555/934 (59%)	555 (100%)	0	100	100
4	UA	730/812 (90%)	730 (100%)	0	100	100
5	UB	344/732 (47%)	344 (100%)	0	100	100
6	UC	107/538 (20%)	107 (100%)	0	100	100
7	UD	615/713 (86%)	613 (100%)	2 (0%)	86	84
8	UE	428/574 (75%)	428 (100%)	0	100	100
9	UF	277/414 (67%)	277 (100%)	0	100	100
10	UG	462/480 (96%)	462 (100%)	0	100	100
11	UH	152/657 (23%)	152 (100%)	0	100	100
12	UI	99/533 (19%)	99 (100%)	0	100	100
13	UJ	1031/1633 (63%)	1031 (100%)	0	100	100
14	UK	226/234 (97%)	226 (100%)	0	100	100
15	UL	747/832 (90%)	747 (100%)	0	100	100
16	UM	668/719 (93%)	668 (100%)	0	100	100
17	UN	137/808 (17%)	137 (100%)	0	100	100
18	UO	437/454 (96%)	437 (100%)	0	100	100
19	UP	57/196 (29%)	57 (100%)	0	100	100
20	UQ	769/826 (93%)	768 (100%)	1 (0%)	88	88
21	UR	425/529 (80%)	425 (100%)	0	100	100
22	US	332/506 (66%)	332 (100%)	0	100	100
23	UT	1787/2307 (78%)	1787 (100%)	0	100	100
24	UU	743/819 (91%)	743 (100%)	0	100	100
25	UV	986/1125 (88%)	986 (100%)	0	100	100
26	UX	156/169 (92%)	156 (100%)	0	100	100
27	UZ	230/256 (90%)	230 (100%)	0	100	100
28	CD	326/435 (75%)	326 (100%)	0	100	100
29	CE	353/433 (82%)	353 (100%)	0	100	100
30	CF	102/104 (98%)	102 (100%)	0	100	100
30	CG	101/104 (97%)	101 (100%)	0	100	100
31	CH	406/503 (81%)	406 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	CI	171/172 (99%)	171 (100%)	0	100	100
33	CJ	251/258 (97%)	250 (100%)	1 (0%)	84	82
34	CK	187/535 (35%)	187 (100%)	0	100	100
35	CL	690/1039 (66%)	684 (99%)	6 (1%)	70	76
36	CM	307/312 (98%)	307 (100%)	0	100	100
37	CN	212/274 (77%)	212 (100%)	0	100	100
38	JC	318/636 (50%)	318 (100%)	0	100	100
39	JF	195/222 (88%)	195 (100%)	0	100	100
39	JG	206/222 (93%)	206 (100%)	0	100	100
42	JJ	158/238 (66%)	158 (100%)	0	100	100
43	JK	35/482 (7%)	35 (100%)	0	100	100
44	JM	124/200 (62%)	124 (100%)	0	100	100
45	JN	141/304 (46%)	141 (100%)	0	100	100
46	JO	210/289 (73%)	210 (100%)	0	100	100
47	JP	416/443 (94%)	416 (100%)	0	100	100
48	JQ	22/192 (12%)	22 (100%)	0	100	100
49	DE	209/222 (94%)	209 (100%)	0	100	100
50	DF	180/191 (94%)	180 (100%)	0	100	100
51	DG	187/201 (93%)	187 (100%)	0	100	100
52	DH	165/170 (97%)	165 (100%)	0	100	100
53	DI	142/161 (88%)	142 (100%)	0	100	100
54	DJ	158/166 (95%)	158 (100%)	0	100	100
55	DL	125/137 (91%)	125 (100%)	0	100	100
56	DN	127/128 (99%)	127 (100%)	0	100	100
57	DO	91/105 (87%)	91 (100%)	0	100	100
58	DQ	105/119 (88%)	105 (100%)	0	100	100
60	DW	110/111 (99%)	110 (100%)	0	100	100
61	DX	85/120 (71%)	85 (100%)	0	100	100
62	DY	112/113 (99%)	112 (100%)	0	100	100
63	Db	70/71 (99%)	70 (100%)	0	100	100
64	Dc	56/60 (93%)	56 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	19959/27976 (71%)	19948 (100%)	11 (0%)	87 88

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	CL	173	HIS
35	CL	175	ASP
35	CL	215	TYR
35	CL	208	SER
33	CJ	118	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 254 such sidechains are listed below:

Mol	Chain	Res	Type
20	UQ	606	HIS
44	JM	205	HIS
23	UT	1241	GLN
42	JJ	197	HIS
52	DH	5	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
65	D2	443/700 (63%)	140 (31%)	4 (0%)
66	D3	1303/1808 (72%)	498 (38%)	26 (1%)
67	D4	223/333 (66%)	72 (32%)	4 (1%)
68	EA	21/22 (95%)	15 (71%)	0
All	All	1990/2863 (69%)	725 (36%)	34 (1%)

5 of 725 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
65	D2	6	A
65	D2	8	A
65	D2	14	U
65	D2	15	G
65	D2	17	A

5 of 34 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
66	D3	1638	G
66	D3	1657	U
67	D4	157	A
66	D3	500	C
66	D3	417	A

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 7 ligands modelled in this entry, 6 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
82	GTP	CL	2001	81	33,34,34	1.15	3 (9%)	50,54,54	1.71	7 (14%)

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
82	GTP	CL	2001	81	-	7/22/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	CL	2001	GTP	C5-C4	3.06	1.47	1.38
82	CL	2001	GTP	C6-N1	-2.50	1.34	1.38
82	CL	2001	GTP	C5-N7	-2.05	1.35	1.39

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	CL	2001	GTP	C5-C4-N3	-5.90	119.00	128.39
82	CL	2001	GTP	C2-N3-C4	4.91	120.76	112.30
82	CL	2001	GTP	N9-C4-N3	4.42	134.78	125.95
82	CL	2001	GTP	C6-C5-N7	3.39	136.47	130.29
82	CL	2001	GTP	C4-C5-N7	-2.58	106.59	110.67

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

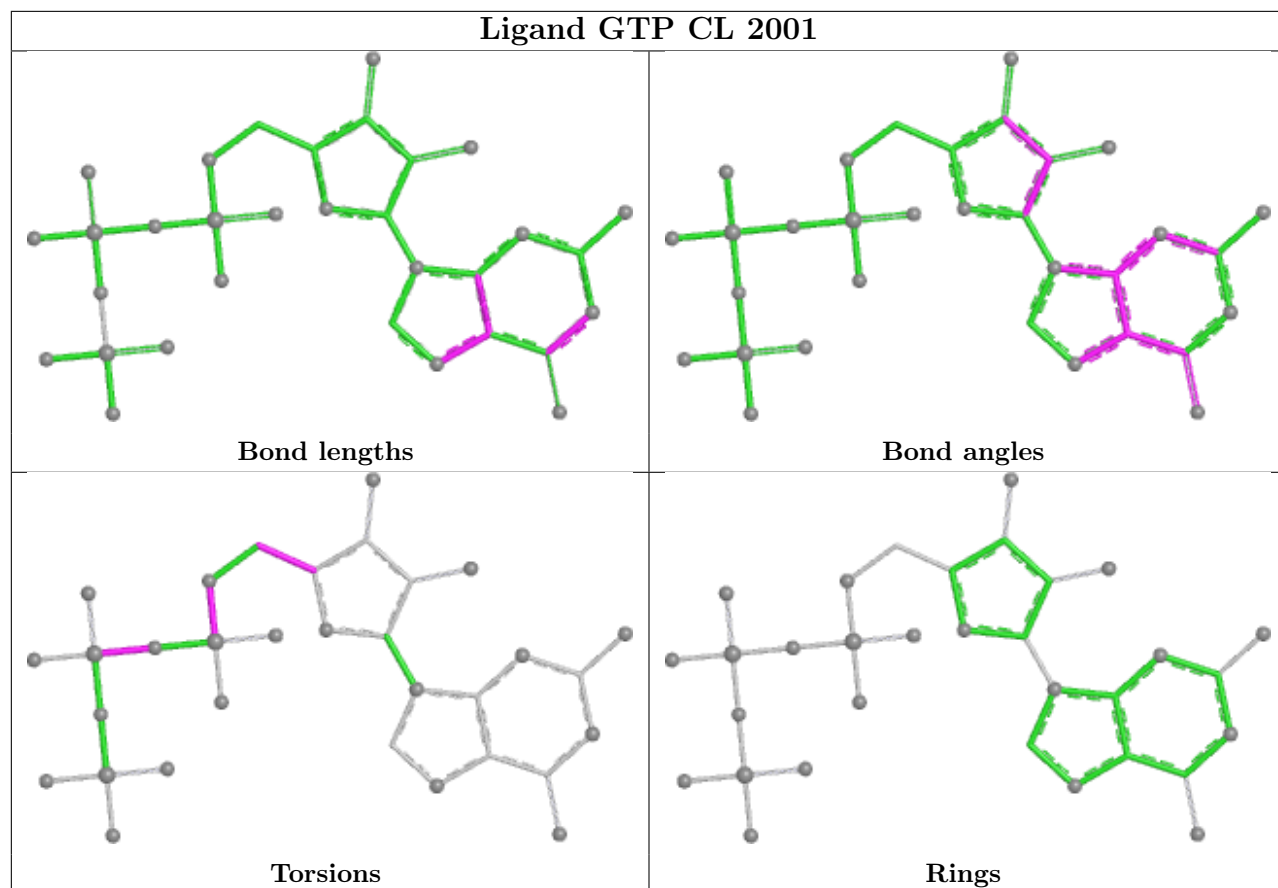
Mol	Chain	Res	Type	Atoms
82	CL	2001	GTP	C5'-O5'-PA-O3A
82	CL	2001	GTP	C5'-O5'-PA-O1A
82	CL	2001	GTP	C3'-C4'-C5'-O5'
82	CL	2001	GTP	O4'-C4'-C5'-O5'
82	CL	2001	GTP	C5'-O5'-PA-O2A

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
82	CL	2001	GTP	2	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

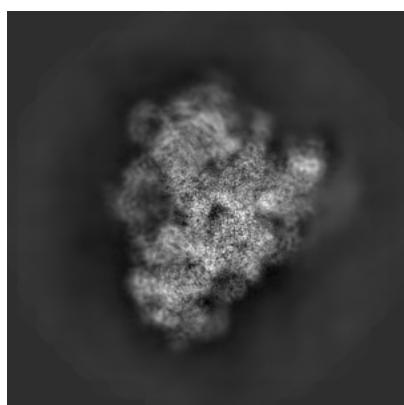
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11807. These allow visual inspection of the internal detail of the map and identification of artifacts.

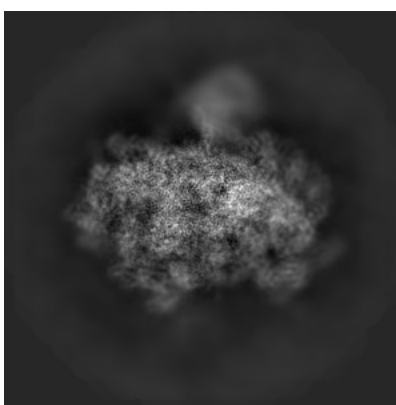
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

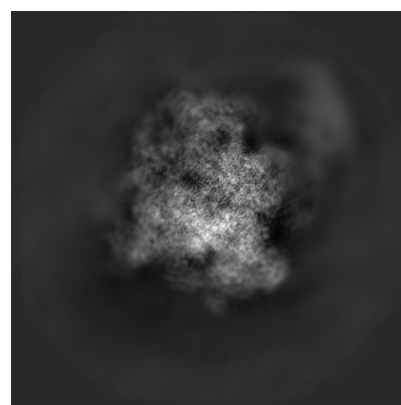
6.1.1 Primary map



X



Y

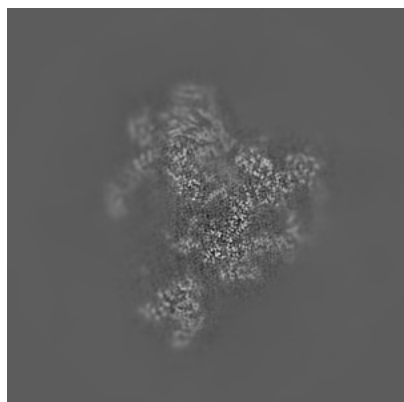


Z

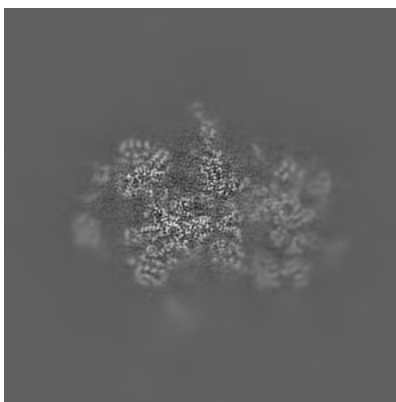
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

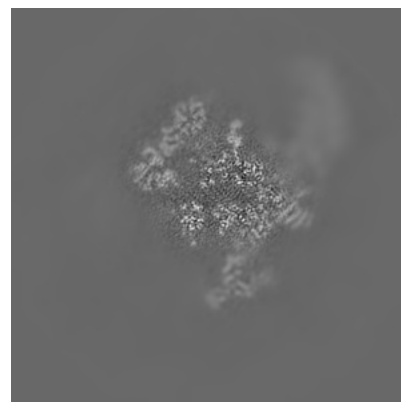
6.2.1 Primary map



X Index: 270



Y Index: 270

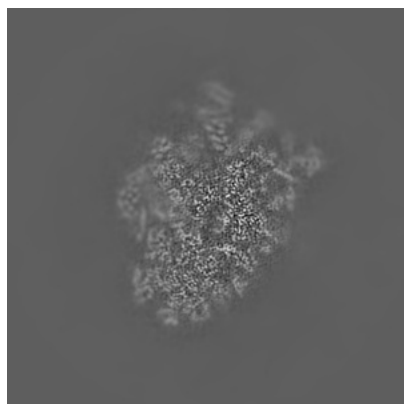


Z Index: 270

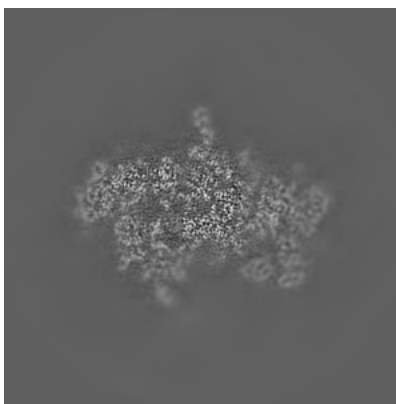
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

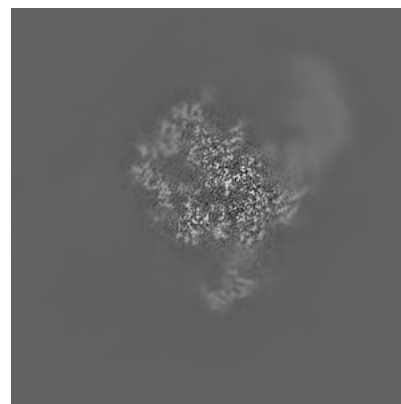
6.3.1 Primary map



X Index: 310



Y Index: 252

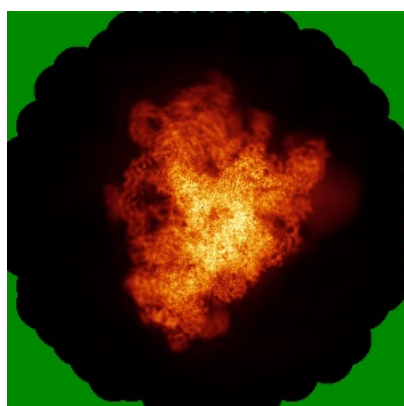


Z Index: 279

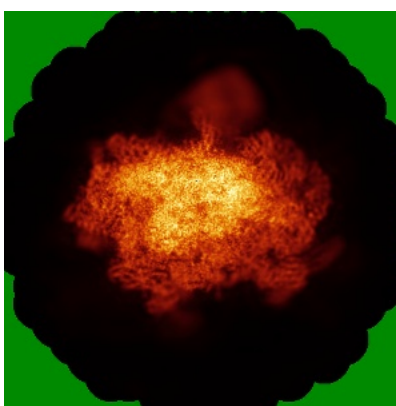
The images above show the largest variance slices of the map in three orthogonal directions.

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

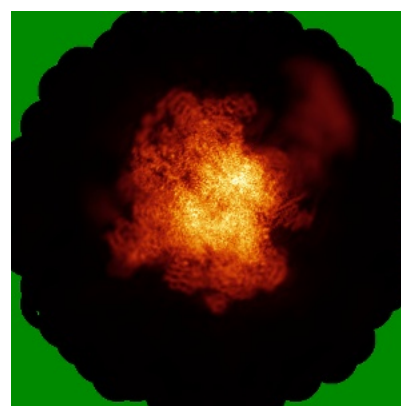
6.4.1 Primary map



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

This section was not generated.

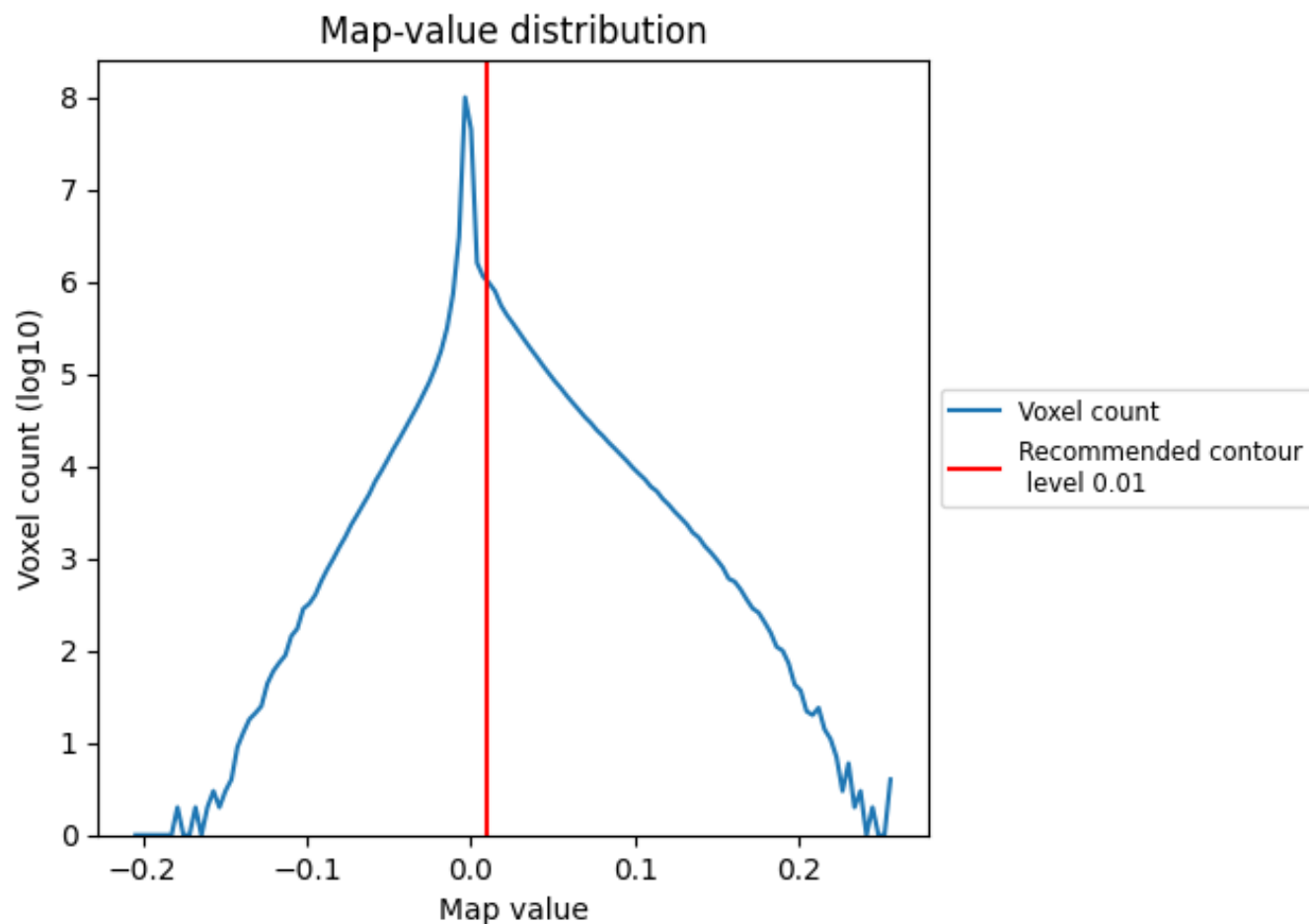
6.6 Mask visualisation

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

7 Map analysis [i](#)

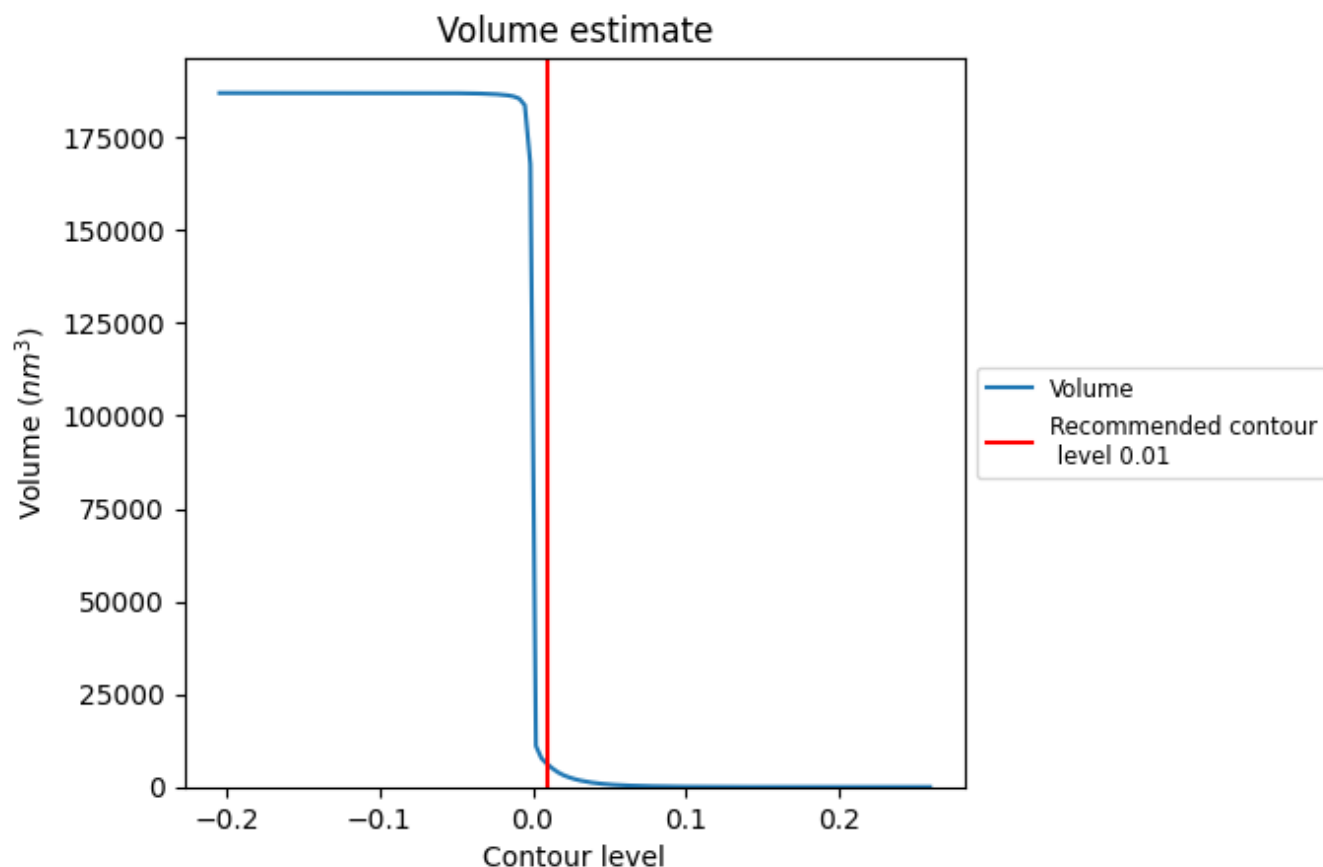
This section contains the results of statistical analysis of the map.

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.

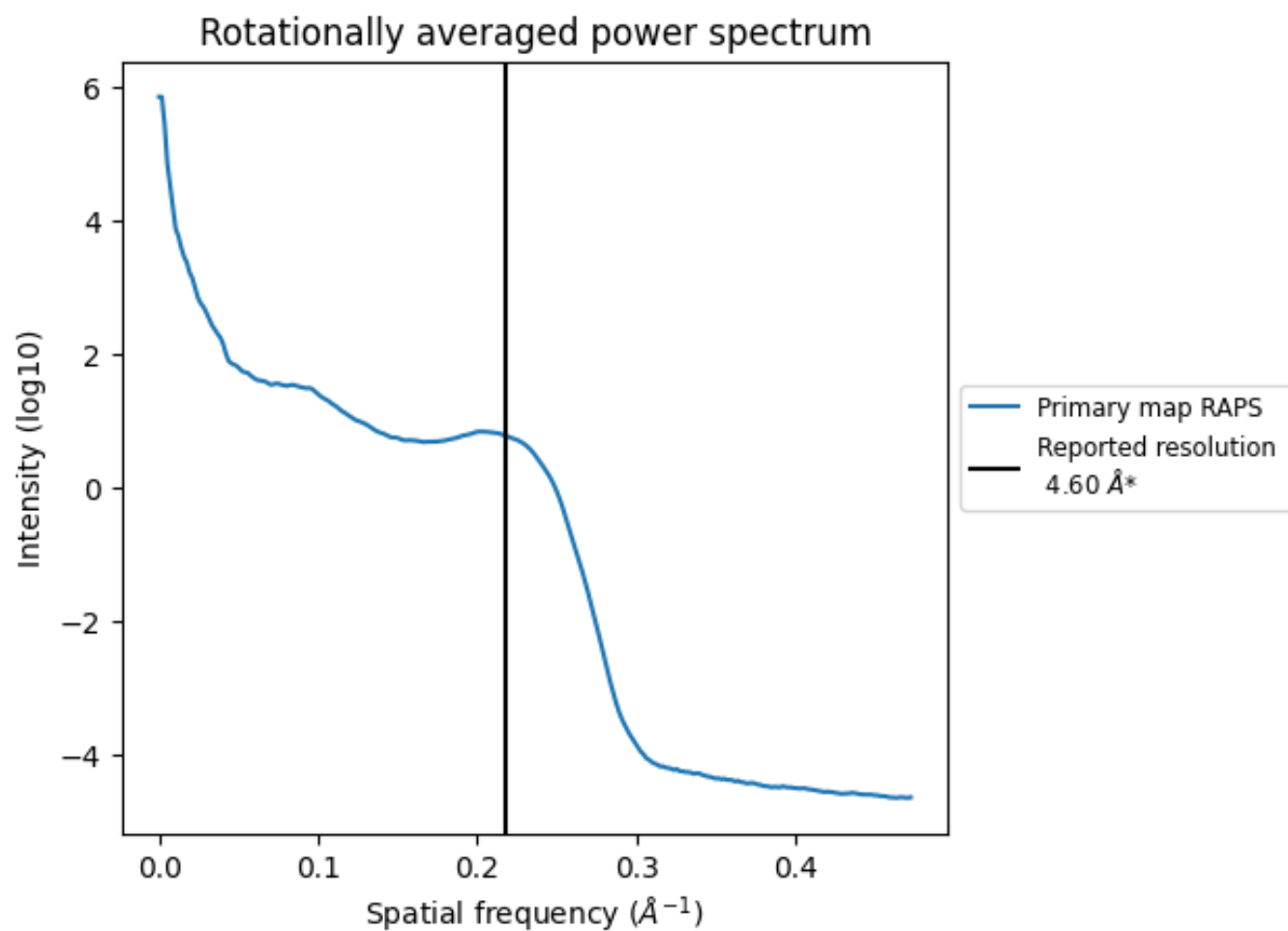
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5975 nm³; this corresponds to an approximate mass of 5397 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 ⓘ

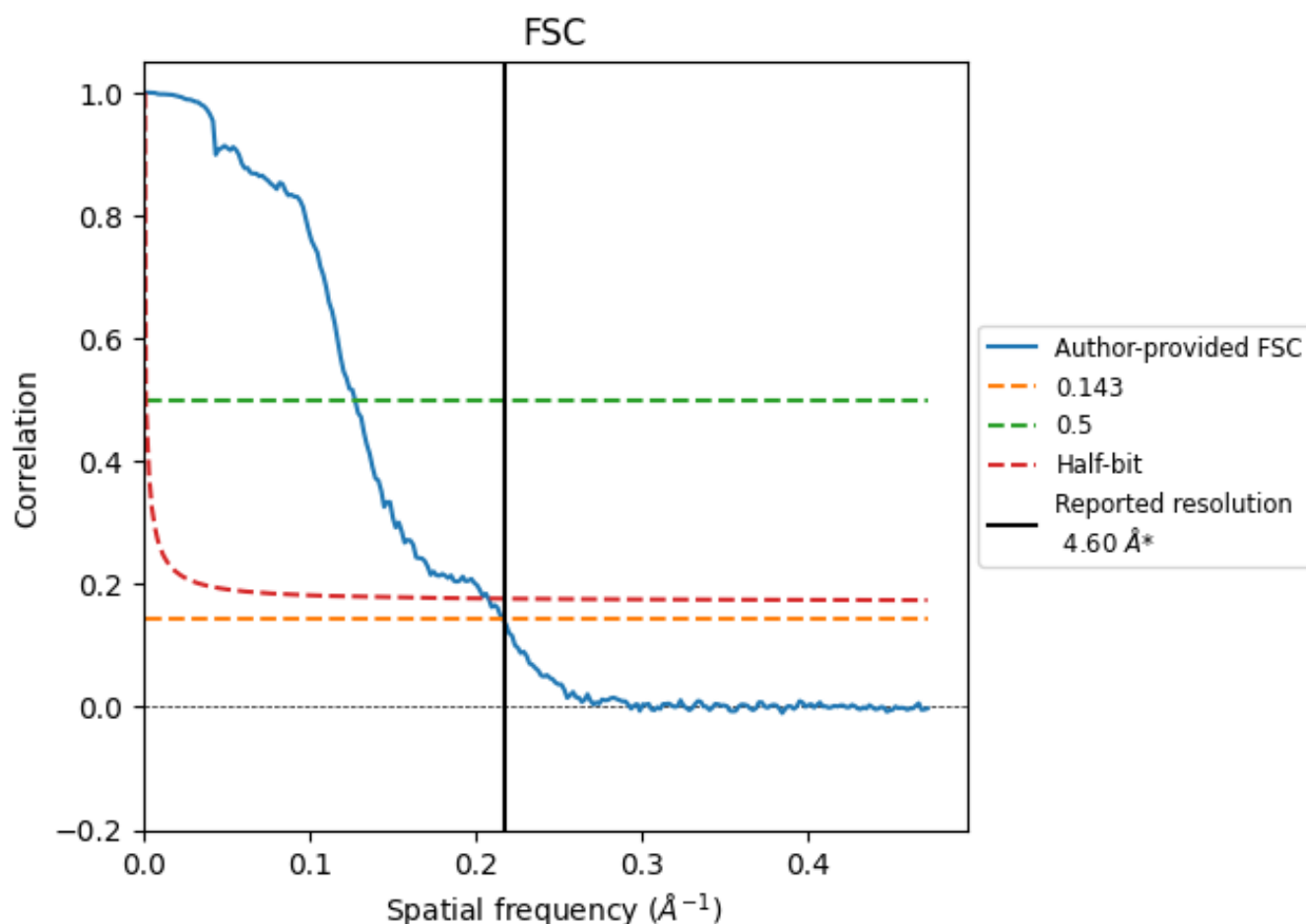


*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.217 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	4.62	7.84	4.81
Unmasked-calculated*	-	-	-

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

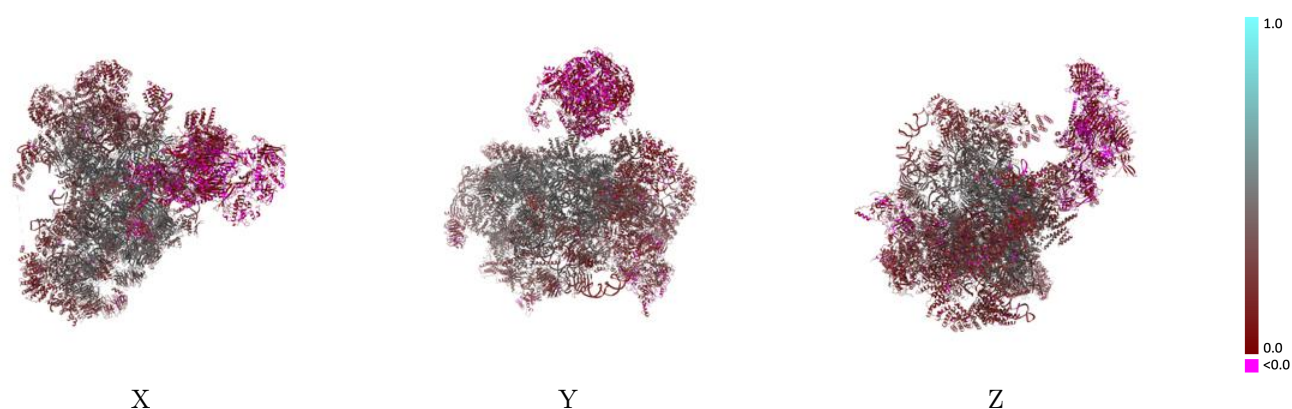
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11807 and PDB model 7AJT. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)

This section was not generated.

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

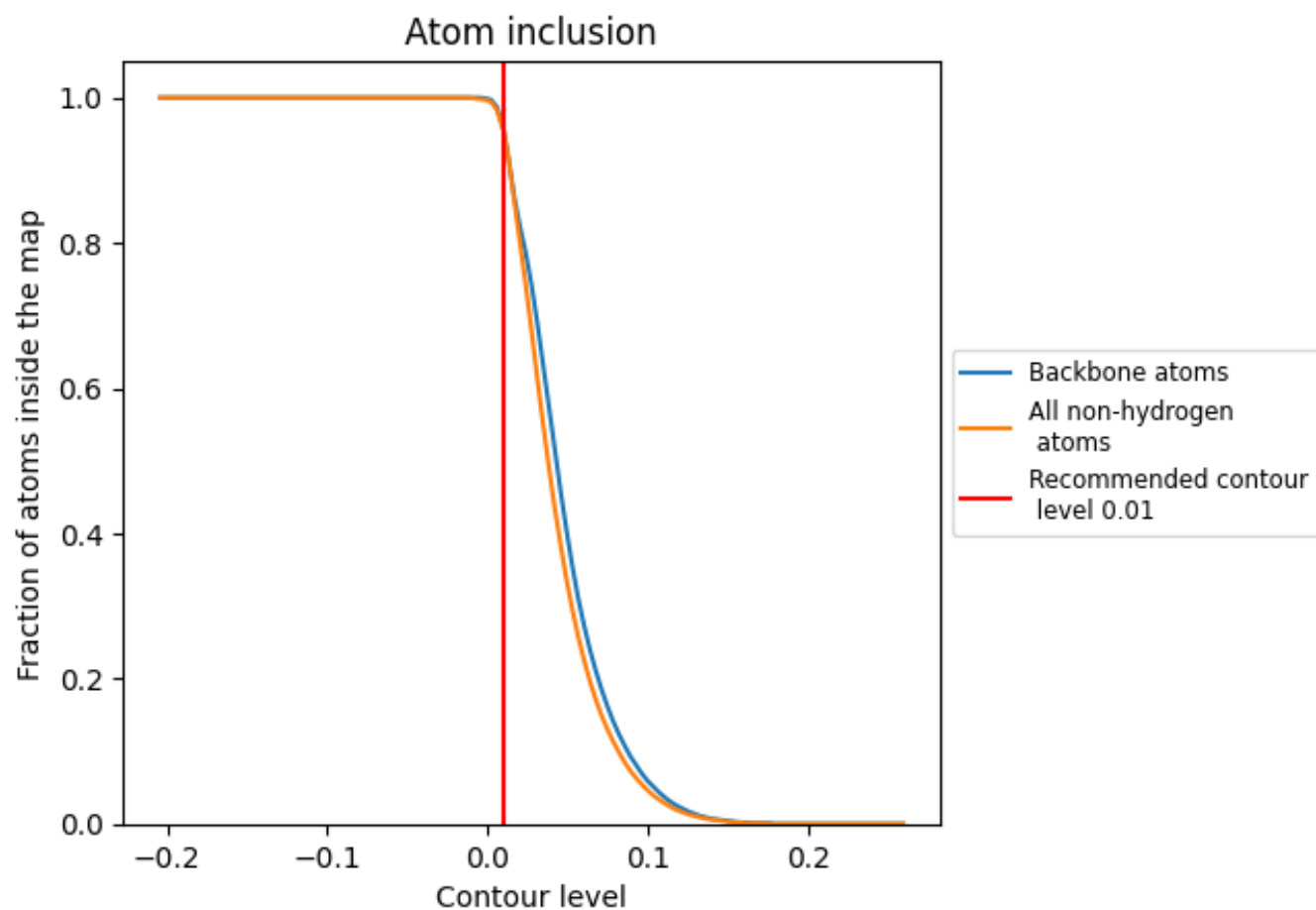


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 95% 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	 0.9540	 0.3080
CA	 0.9740	 0.4780
CB	 0.9640	 0.3520
CD	 0.9760	 0.3780
CE	 0.9710	 0.3380
CF	 0.9680	 0.4410
CG	 0.9650	 0.4290
CH	 0.9840	 0.3800
CI	 0.9820	 0.5020
CJ	 0.9740	 0.4640
CK	 0.9710	 0.4120
CL	 0.9710	 0.3950
CM	 0.9760	 0.3510
CN	 0.9730	 0.2290
D2	 0.9950	 0.3830
D3	 0.9840	 0.3300
D4	 0.9740	 0.3570
DA	 0.9670	 0.4030
DE	 0.9630	 0.3290
DF	 0.9820	 0.4290
DG	 0.9620	 0.2000
DH	 0.9530	 0.3050
DI	 0.9680	 0.2110
DJ	 0.9580	 0.4480
DL	 0.9580	 0.2070
DN	 0.9630	 0.3770
DO	 0.9740	 0.4170
DQ	 0.9730	 0.4730
DS	 0.9860	 0.3270
DW	 0.9700	 0.4610
DX	 0.9760	 0.4450
DY	 0.9710	 0.3820
Db	 0.9850	 0.4420
Dc	 0.9750	 0.4500
EA	 0.9180	 0.0410



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Chain	Atom inclusion	Q-score
EB	 0.8550	 0.0250
EC	 0.9640	 0.0340
ED	 0.9200	 0.0480
EE	 0.8910	 0.0310
EF	 0.9320	 0.0460
EG	 0.8690	 0.0230
EH	 0.6400	 0.0500
EI	 0.8720	 0.0500
EJ	 0.5890	 0.0360
EK	 0.5680	 0.0340
EN	 0.6120	 0.0570
JA	 0.9600	 0.1970
JB	 0.9280	 0.1730
JC	 0.9340	 0.1790
JF	 0.9800	 0.2710
JG	 0.9620	 0.3670
JH	 0.9510	 0.1210
JI	 0.8140	 0.1750
JJ	 0.9710	 0.2930
JK	 0.9360	 0.1590
JM	 0.9720	 0.4140
JN	 0.9730	 0.4460
JO	 0.9720	 0.4170
JP	 0.9740	 0.4840
JQ	 0.9890	 0.3430
UA	 0.9810	 0.4650
UB	 0.9860	 0.2670
UC	 0.9710	 0.4160
UD	 0.9820	 0.3340
UE	 0.9780	 0.3730
UF	 0.9790	 0.3530
UG	 0.9810	 0.4670
UH	 0.9890	 0.1870
UI	 0.9780	 0.2160
UJ	 0.9700	 0.2600
UK	 0.9740	 0.4070
UL	 0.9820	 0.3270
UM	 0.9740	 0.2870
UN	 0.9590	 0.4230
UO	 0.9760	 0.3790
UP	 0.9770	 0.3200
UQ	 0.9820	 0.3440

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Chain	Atom inclusion	Q-score
UR	 0.9830	 0.4350
US	 0.9810	 0.2890
UT	 0.9750	 0.2090
UU	 0.9790	 0.4300
UV	 0.9750	 0.2370
UX	 0.9730	 0.4970
UZ	 0.9820	 0.3500