



wwPDB EM Validation Summary Report ⓘ

Oct 28, 2024 – 08:43 am GMT

PDB ID : 7AJT
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.dev113
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

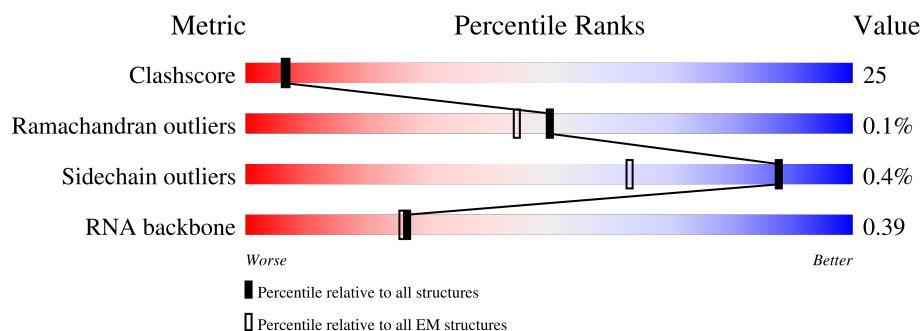
1 Overall quality at a glance

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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	43% 30% 26%
1	CB	327	28% 41% 30%
2	DA	255	50% 44% 6%
3	JA	1056	45% 32% 23%
3	JB	1056	5% 75% 21%
4	UA	923	48% 42% 10%
5	UB	810	38% 24% 37%


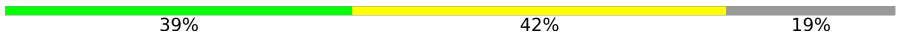



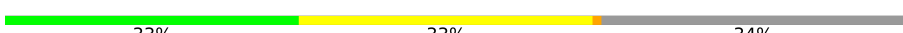










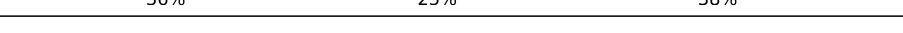








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Mol	Chain	Length	Quality of chain
6	UC	610	
7	UD	776	
8	UE	643	
9	UF	440	
10	UG	554	
11	UH	713	
12	UI	575	
13	UJ	1769	
14	UK	250	
15	UL	943	
16	UM	817	
17	UN	899	
18	UO	513	
19	UP	214	
20	UQ	896	
21	UR	594	
22	US	552	
23	UT	2493	
24	UU	939	
25	UV	1237	
26	UX	189	
27	UZ	274	
28	CD	504	
29	CE	511	
30	CF	126	





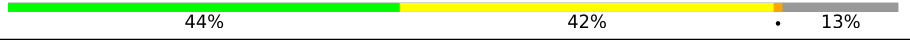


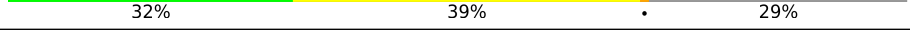
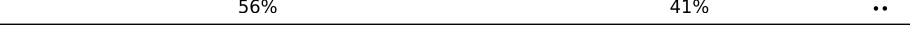
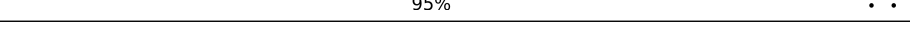
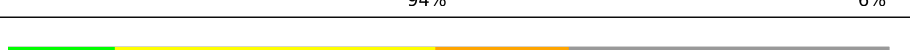
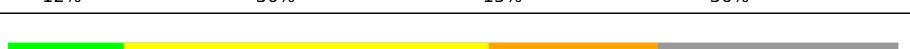
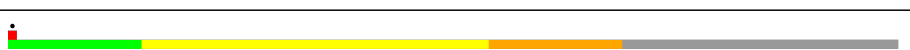
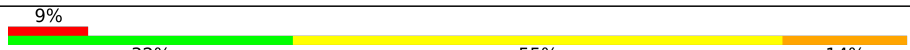
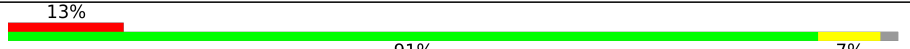
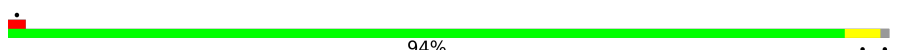

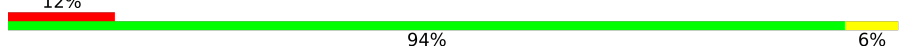
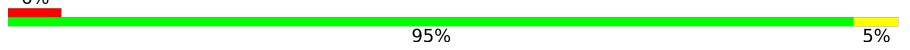

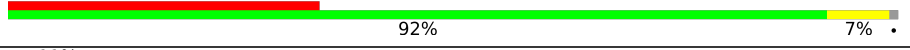
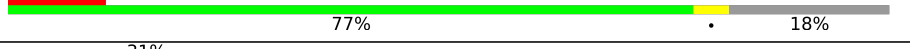

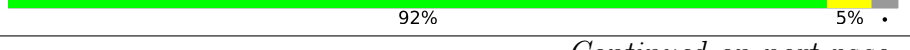

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Mol	Chain	Length	Quality of chain
30	CG	126	
31	CH	573	
32	CI	183	
33	CJ	290	
34	CK	593	
35	CL	1183	
36	CM	367	
37	CN	297	
38	JC	707	
39	JF	252	
39	JG	252	
40	JH	483	
41	JI	1729	
42	JJ	274	
43	JK	534	
44	JM	217	
45	JN	346	
46	JO	316	
47	JP	489	
48	JQ	206	
49	DE	261	
50	DF	225	
51	DG	236	
52	DH	190	
53	DI	200	

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

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Mol	Chain	Length	Quality of chain
79	EN	1073	<div><div></div><div>35%</div><div></div><div>79%</div><div></div><div>10%</div><div></div><div>10%</div></div>

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	JI	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		
			973	625	174	174	0	0

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

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

- 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	0	0
			1073	676	208	189		

- 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	0	0
			610	382	110	113	5		

- 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	0	0
			497	306	99	91	1		

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

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

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

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

- Molecule 67 is a RNA chain called U3 snoRNA.

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

- Molecule 68 is a RNA chain called RNA.

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

- 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 (three-letter code: 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 (three-letter code: MG) (formula: Mg).

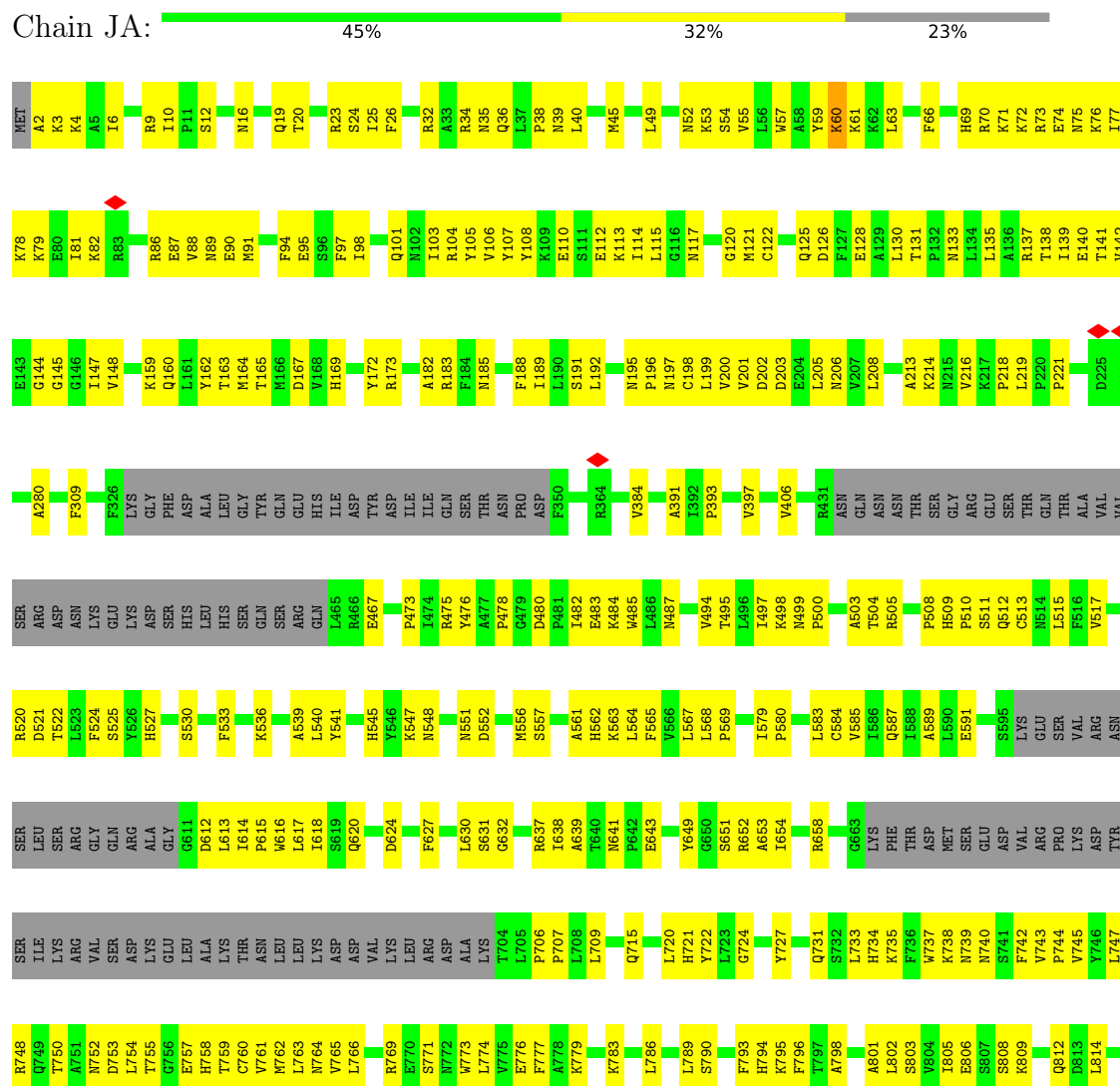
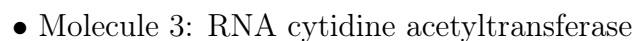
Mol	Chain	Residues	Atoms		AltConf
81	UX	1	Total	Mg	0
			1	1	
81	CL	1	Total	Mg	0
			1	1	
81	EK	1	Total	Mg	0
			1	1	

- Molecule 82 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



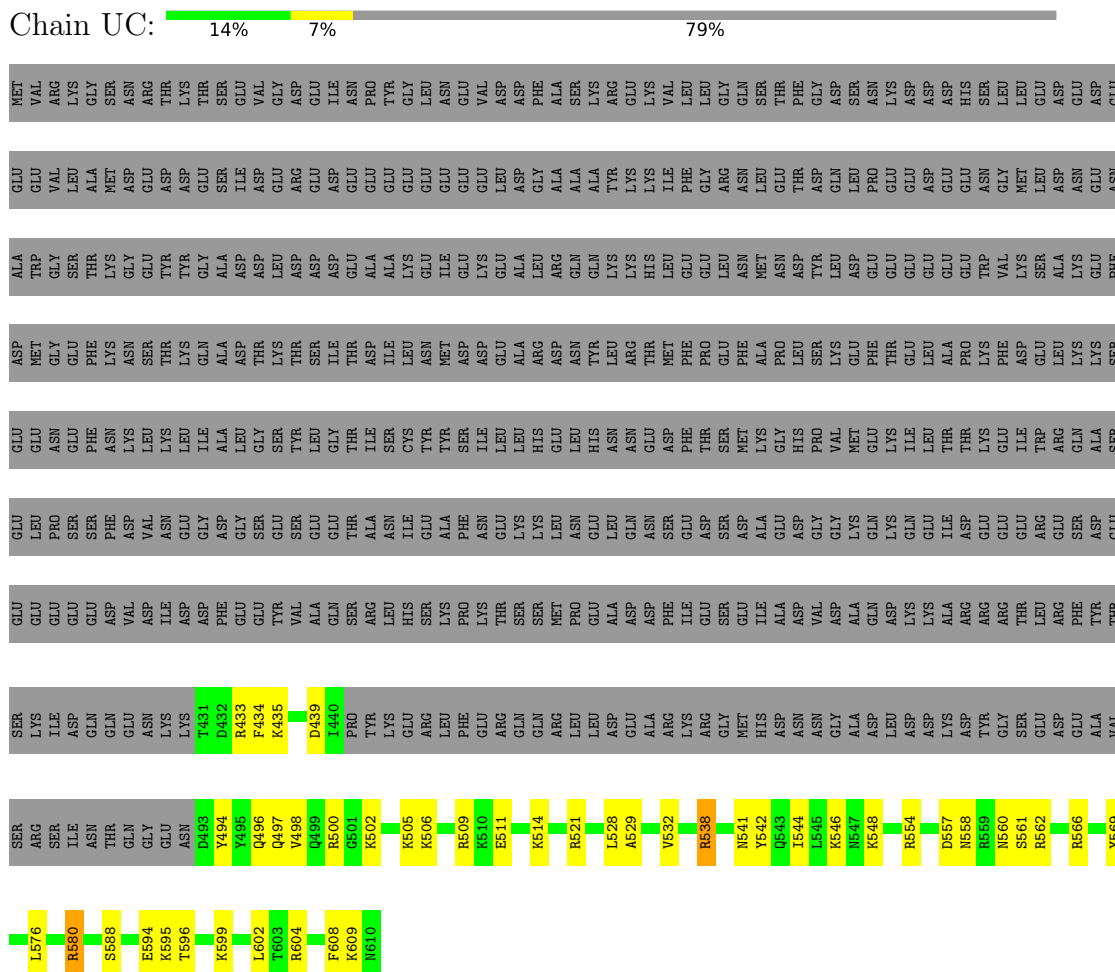
Mol	Chain	Residues	Atoms					AltConf
82	CL	1	Total	C	N	O	P	0
			32	10	5	14	3	

Chain DA:



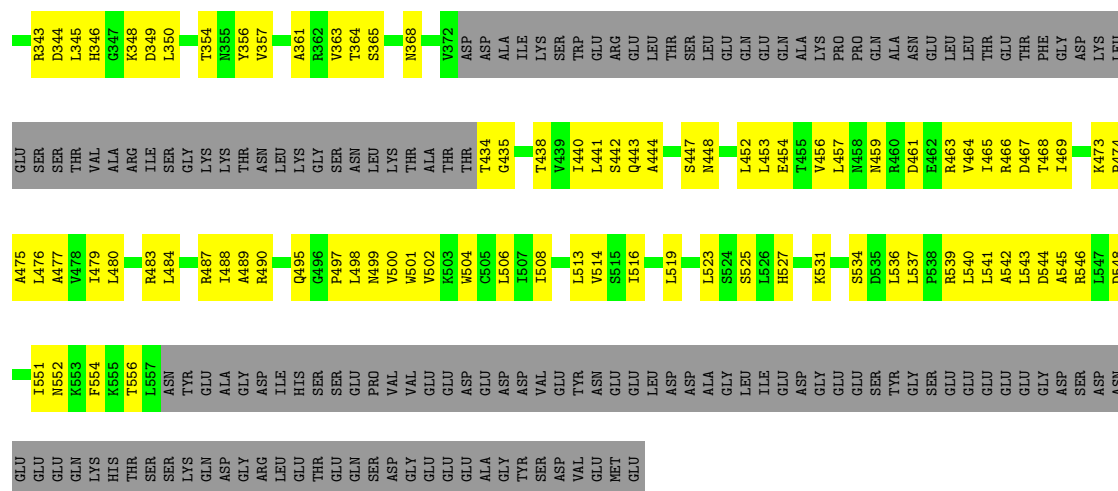


- Molecule 6: Something about silencing protein 10



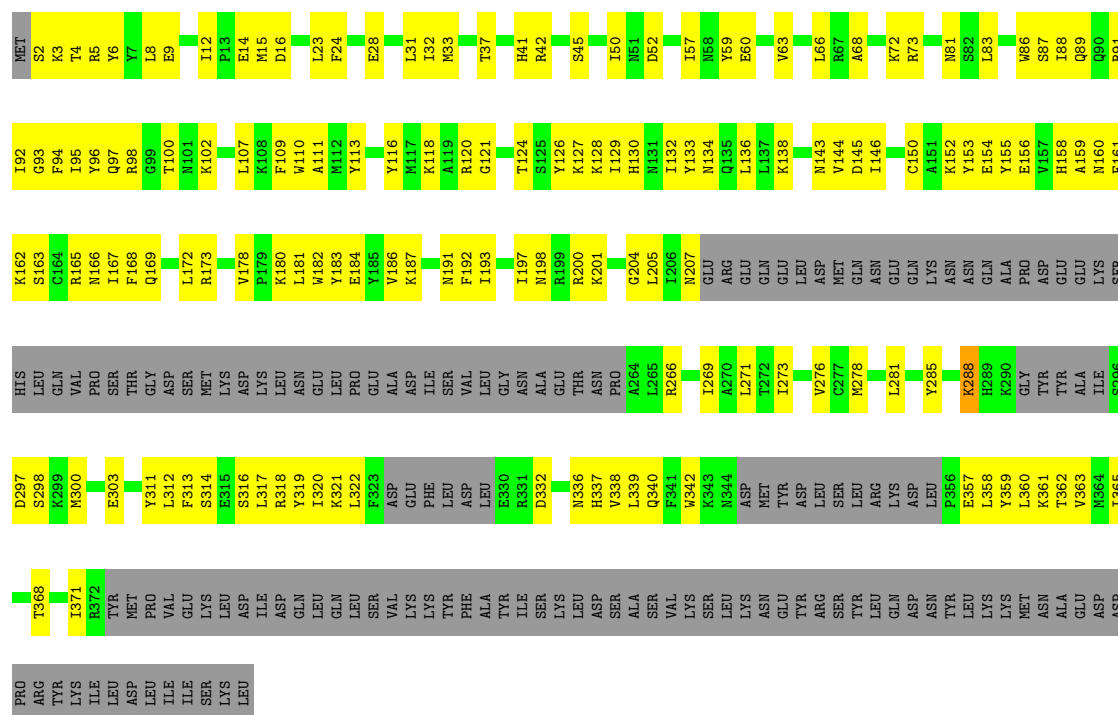
- Molecule 7: U3 small nucleolar RNA-associated protein 4





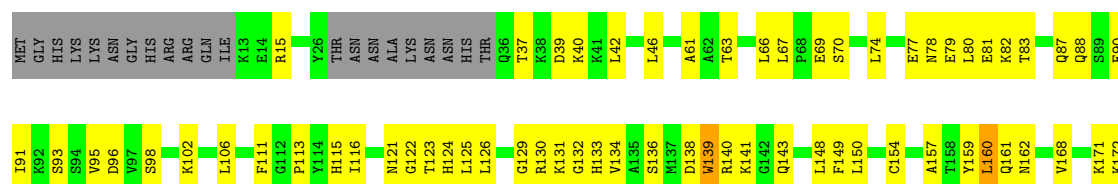
• Molecule 9: U3 small nucleolar RNA-associated protein 6

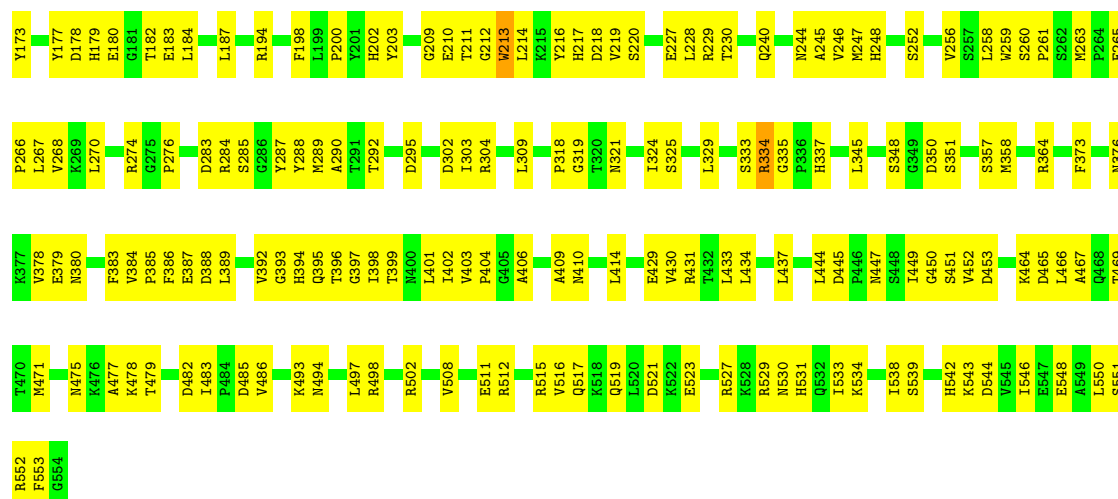
Chain UF: 33% 34% 33%



• Molecule 10: U3 small nucleolar RNA-associated protein 7

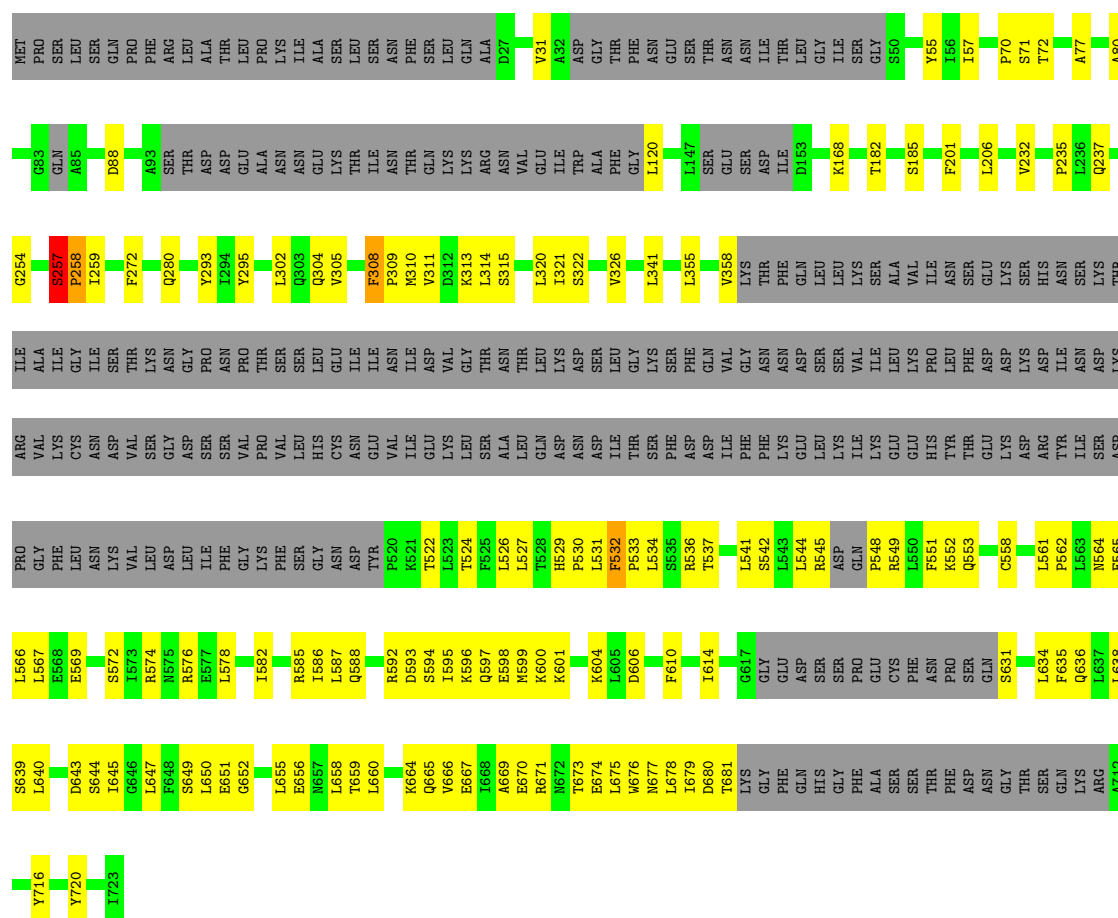
Chain UG: 55% 41% 4%





- Molecule 11: U3 small nucleolar RNA-associated protein 8

Chain UH: 43% 18% 38%

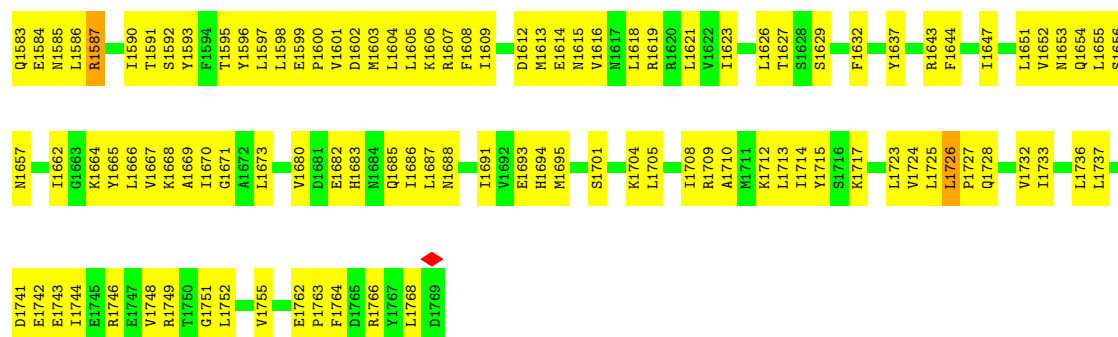


- Molecule 12: U3 small nucleolar RNA-associated protein 9

Chain UI: 5% 13% 82%







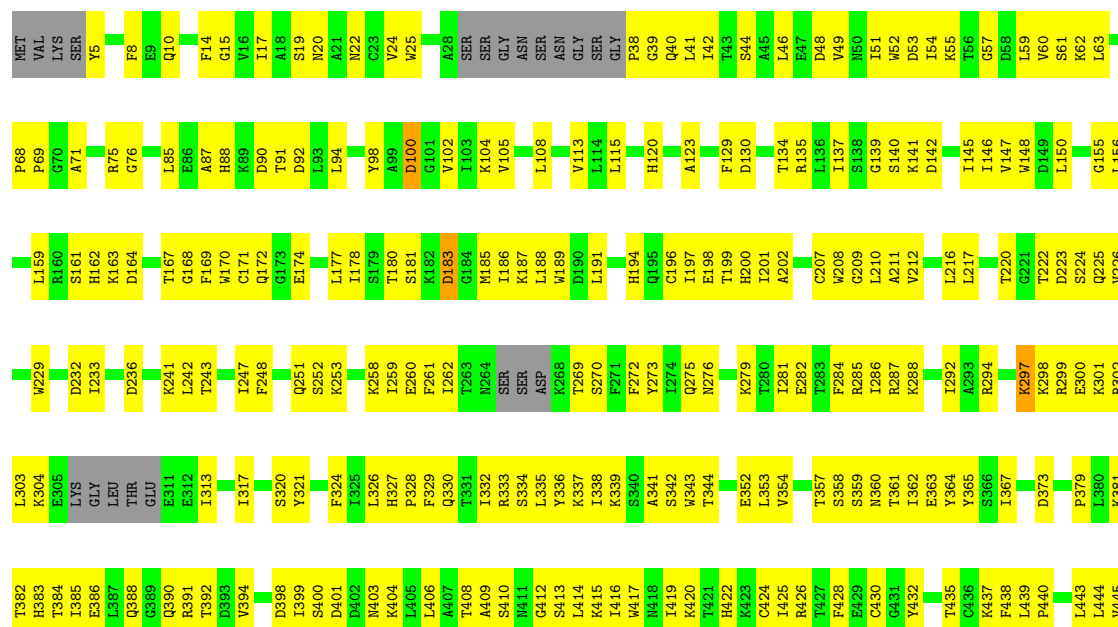
• Molecule 14: U3 small nucleolar RNA-associated protein 11

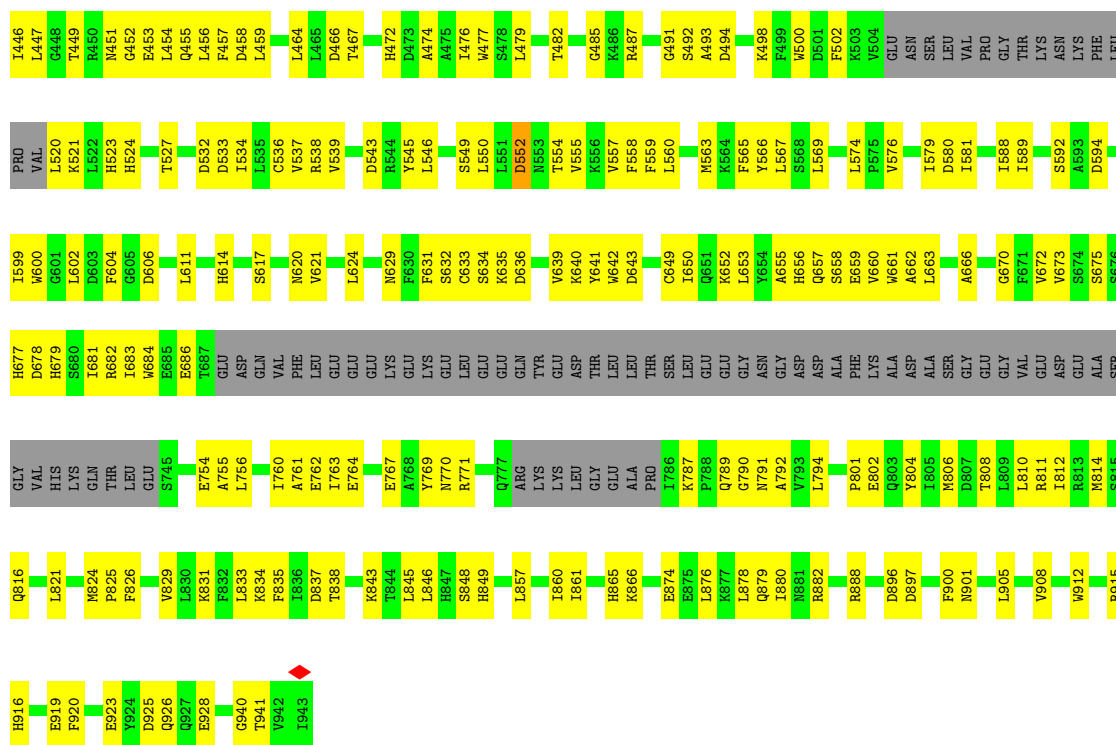
Chain UK: 41% 55%



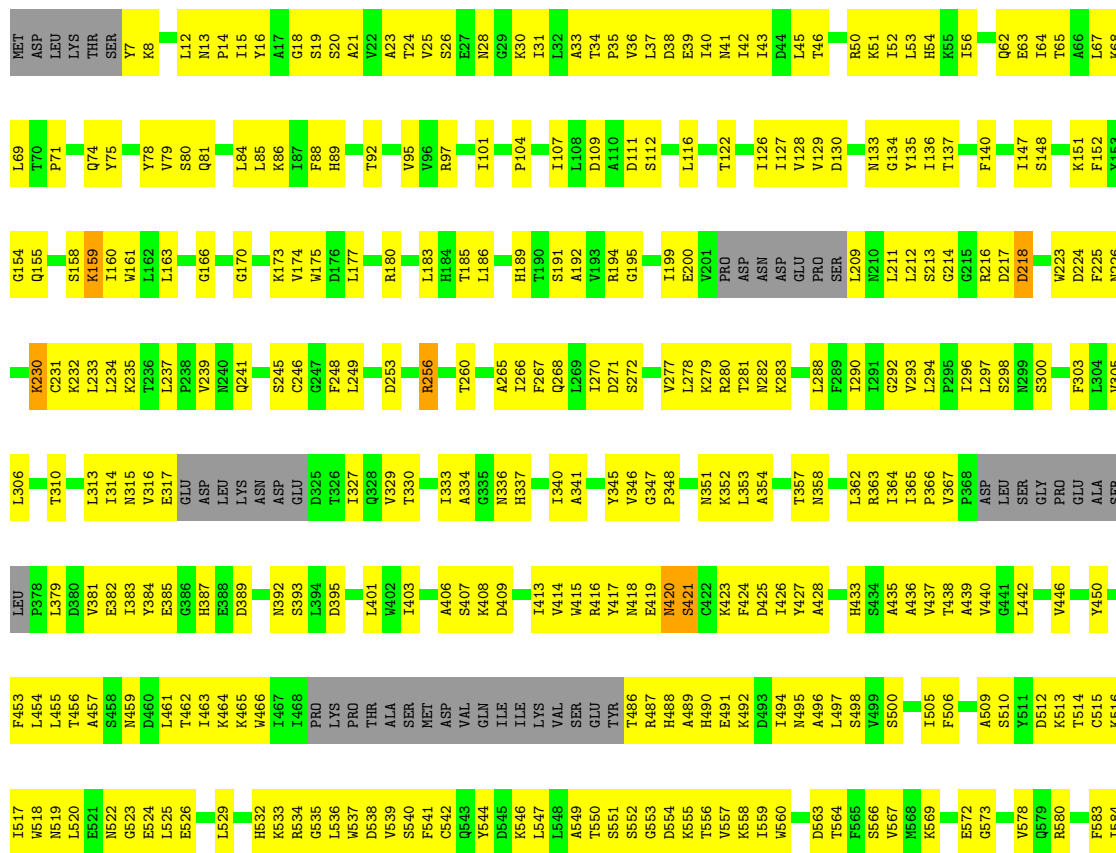
• Molecule 15: U3 small nucleolar RNA-associated protein 12

Chain UL: 44% 45% 11%





Chain UM: 41% 51% 7%

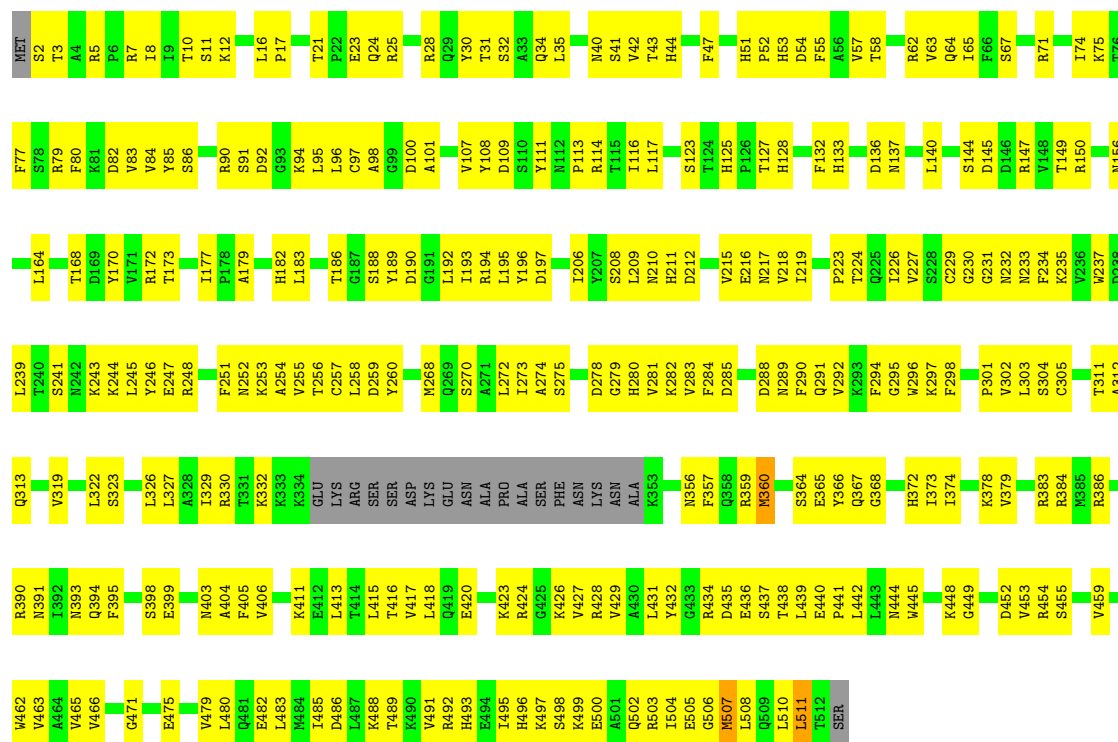






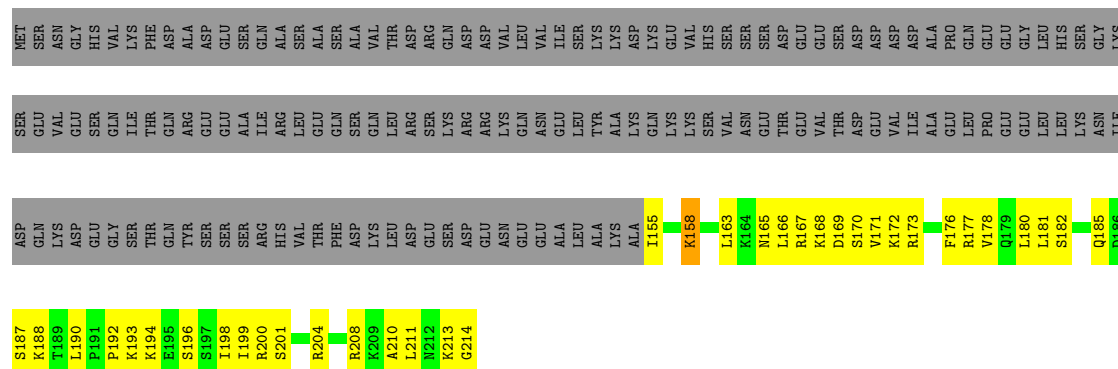
- Molecule 18: U3 small nucleolar RNA-associated protein 15

Chain UO: 42% 53% ..



- Molecule 19: Bud site selection protein 21

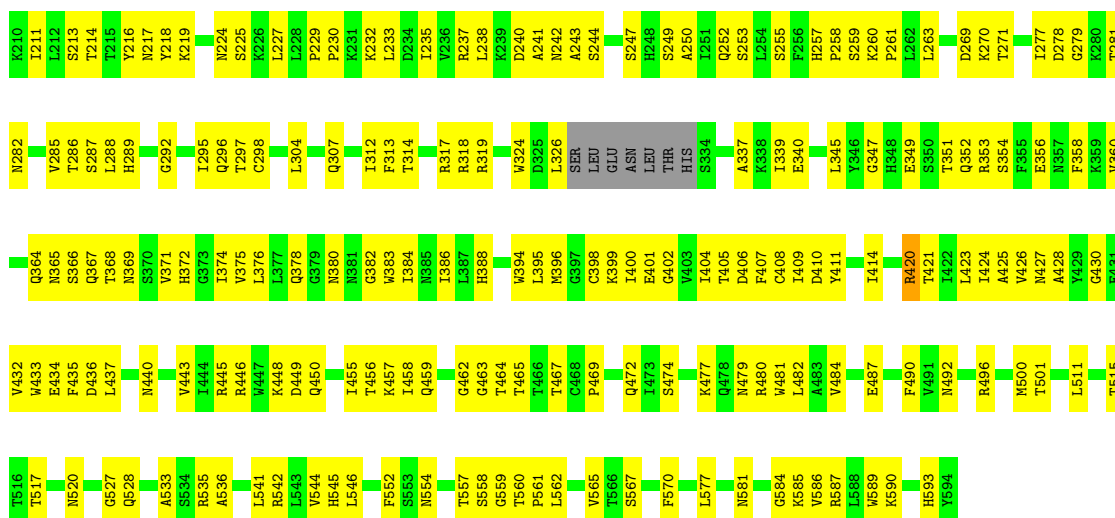
Chain UP: 11% 16% 72%



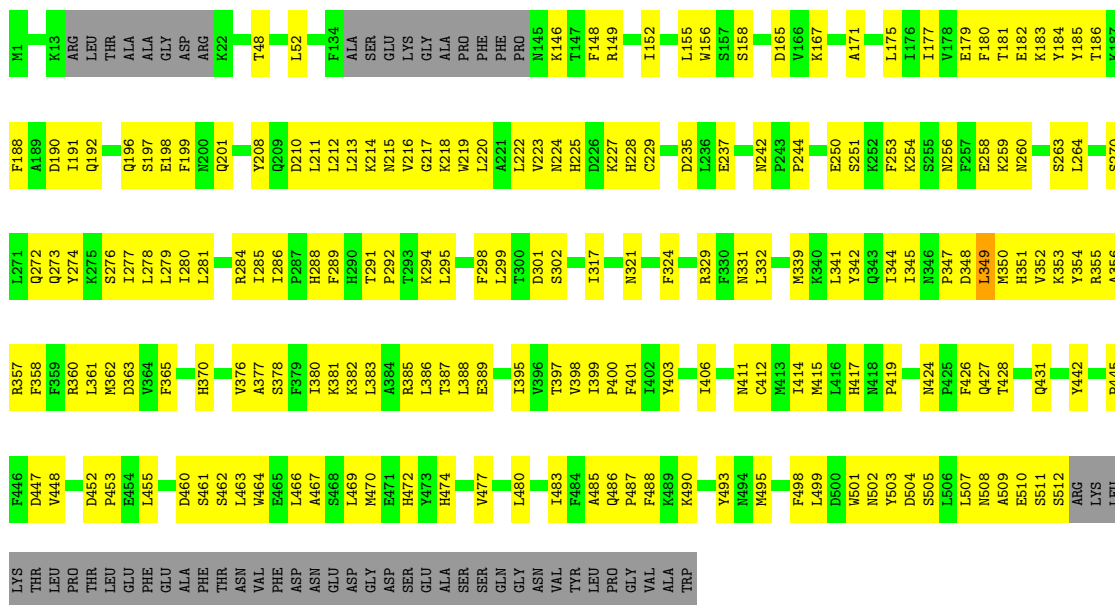
- Molecule 20: NET1-associated nuclear protein 1

Chain UQ: 43% 49% 7%

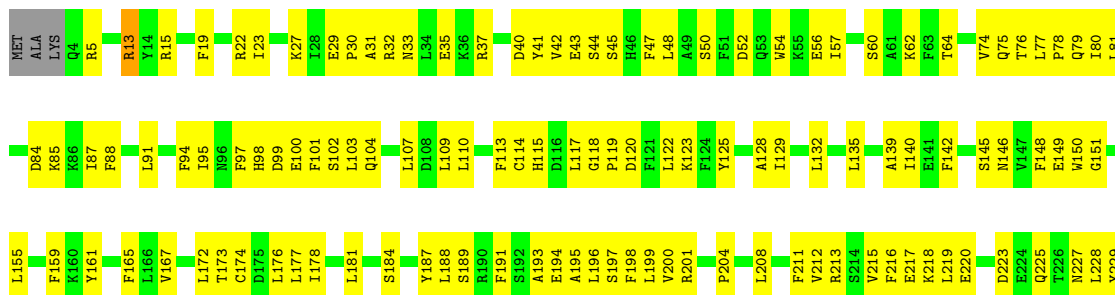




- Molecule 22: Nucleolar complex protein 4



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



F1288	V1216	D1125	L1054	L972	I901	V830	W754	W678	K605	I525	E456	S369	M298	L232
I1289	R1217	E1126	R1055	D973	T902	F831	N755	V681	T606	Y526	F457	S374	Y299	L233
G1292	S1218	F1127	Q1056	Y974	T903	L832	S756	F682	L607	R527	I458	L374	Q300	I234
V1295	R1219	A1130	Q1057	F977	L905	F838	I758	D683	L610	GLU	S460	L386	N303	L235
P1296	L1220	G1058	G1058	F978	T906	K839	S759	N687	P616	ASP	I461	D391	L306	P236
E1297	I1221	L1059	L1059	G979	S910	N840	I760	V688	D617	ASP	R462	C392	T237	E238
L1298	L1224	K1060	K1060	N980	S914	I841	S761	V689	S620	ALA	R463	T309	L306	T241
I1301	I1227	S1063	S1063	H982	K914	Y844	E763	T690	S621	GLY	F464	L309	L306	T242
V1305	L1228	H1141	H1141	S986	D917	Y845	R764	D692	S622	N535	F465	L309	L306	T243
L1308	Q1236	K1143	V1065	S987	K918	E849	P771	L895	K623	N536	A468	L309	L306	T244
N1309	E1237	K1144	V1066	K988	K919	L850	I772	V696	M623	L537	D472	L309	L306	T245
L1312	M1238	A1145	E1067	K989	V920	H851	I773	V697	V624	L538	L476	L309	L306	T246
S1313	M1239	V1146	F1068	T990	W921	L852	L773	L625	M624	L539	L476	L309	L306	T247
S1314	T1240	G1148	V1069	T991	N922	H853	L774	K698	E626	T540	L476	L309	L306	T248
R1315	T1241	P1149	T1072	K992	P923	L854	R775	L699	I541	L542	L476	L309	L306	T249
M1316	Q1242	I1150	F1073	T993	Y924	M855	W776	V700	T631	I479	L479	L309	L306	T250
D1320	K1243	I1151	D1074	I994	V925	M856	Q777	L701	L632	W480	S404	L309	L306	T251
S1326	I1244	A1154	S1078	R995	L926	L857	W781	S702	K633	W481	Y405	L309	L306	T252
K1329	K1245	D1155	M1079	R996	R927	L858	W782	F703	N634	R482	E406	L309	L306	T253
I1332	K1246	S1156	M1079	M997	T928	C859	W783	L704	A635	A483	R407	L309	L306	T254
E1333	I1247	I1157	I1082	G998	F929	S860	S784	K705	R636	I484	V408	L309	L306	T255
D1334	K1248	N1163	V1083	F1000	F930	R861	L785	P707	D637	I485	F411	L309	L306	T256
G1335	L1249	H1166	V1087	V1001	Q934	M862	W786	D708	L638	I486	N412	L309	L306	T257
N1336	I1250	H1167	K1088	N1002	V935	T863	Q787	L719	R641	I488	G413	L309	L306	T258
E1337	N1253	D1169	P1089	I1003	P936	V865	E790	Q711	I642	I489	L414	L309	L306	T259
L1338	K1254	C1178	K1090	N1004	R937	Q866	L791	D714	K643	I490	K415	L309	L306	T260
S1340	I1255	I1181	I1091	N1005	S939	K867	E790	W715	G557	I491	K416	L309	L306	T261
E1341	N1256	L1185	F1094	S1006	T938	L868	D795	Y715	W558	I492	L417	L309	L306	T262
L1342	K1257	Y1186	D1095	L1007	G940	A869	I796	L718	N589	I493	K422	L309	L306	T263
E1343	I1258	Y1187	D1096	L1008	Q941	L870	A797	W719	K560	I494	K422	L309	L306	T264
G1344	S1269	K1188	D1097	V1010	R943	L873	F798	L719	L561	I495	Q428	L309	L306	T265
L1345	L1270	L1189	E1097	L1011	S944	L874	F799	G723	V562	I497	K431	L309	L306	T266
P1346	L1271	SER	S1103	R1012	R945	A875	Y801	A724	L565	I498	K431	L309	L306	T267
L1347	F1272	D1191	S1104	R1013	K946	T876	M802	N725	R566	I499	K431	L309	L306	T268
L1348	K1273	L1190	L1105	N1014	T947	R377	D803	K726	P567	L500	L434	L309	L306	T269
F1349	F1275	L1191	R1107	F1015	A948	N878	F804	L727	D655	L501	F435	L309	L306	T270
F1350	D1276	W1200	L1023	P1016	V949	N878	LYS	L728	K572	E502	F436	L309	L306	T271
F1351	E1277	L1201	L1024	Q1024	K957	L889	THR	W729	L657	R503	L437	L309	L306	T272
L1352	R1278	L1202	I1027	K958	R958	N890	THR	D730	V658	F508	F438	L309	L306	T273
N1355	L1279	Y1203	Y1028	P959	S951	L891	LYS	D730	V658	A509	F439	L309	L306	T274
N1356	L1280	S1204	Y1028	Y960	S951	L891	LYS	D730	V658	S510	D440	L309	L306	T275
K1358	R1281	L1205	A1033	Y961	P954	L892	ASP	S732	S639	P511	D441	L309	L306	T276
A1362	V1282	T1206	A1033	Y961	P954	L892	GLU	S732	S639	P511	D441	L309	L306	T277
L1363	E1207	Q1120	Y1034	Y961	P954	L892	GLU	S732	S639	P511	D441	L309	L306	T278
L1364	F1121	Q1120	Y1034	Y961	P954	L892	GLU	S732	S639	P511	D441	L309	L306	T279
T1365	F1122	Q1120	Y1034	Y961	P954	L892	GLU	S732	S639	P511	D441	L309	L306	T280
	F1123	Q1120	Y1034	Y961	P954	L892	GLU	S732	S639	P511	D441	L309	L306	T281
	E1286	Y1123	Y1036	Y961	P954	L892	GLU	S732	S639	P511	D441	L309	L306	T282
	L1287	Y1124	E1040	Y971	R971	E900	GLU	S751	V677	M604	K524	L309	L306	T283

THR	LYS	ILE	TYR	THR	THR	ALA	VAL	LYS	GLN	LYS	ARG	LYS	GLU	VAL	GLU	GLU	ASP	VAL	ARG	ARG	LYS	GLU	ARG	GLY	ARG	ASN	LYS	ARG	ALA																											
LEU	LYS	TYR	THR	THR	ALA	VAL	LYS	GLN	LYS	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP																											
S2171	ILE	GLY	PHE	E2175	T2195	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY																												
G1937	A1938	R1939	K1940	V1941	L1942	N1943	I1944	I1945	S1948	P1949	S1950	T1951	S1952	L1887	T1888	V1889	S1890	H1891	L1892	F1896	I1967	R1968	H1969	T1970	K1975	L1979	L1983	V1986																												
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L1710	D1711	T1712	S1713	S1714	S1715	M1716	V1717	K1719	I1720	L1721	L1722	E1723	M1724	I1725	F1726	I1727	I1728	A1729	G1730	E1731	E1732	K1733	E1736	M1737	Y1738	H1739	I1740	K1741																												
K1646	S1647	E1648	D1651	D1652	A1653	V1654	V1655	V1656	L1657	L1658	G1659	K1660	I1661	S1662	I1663	I1664	G1665	A1667	E1668	L1670	V1671	F1672	V1673	L1674	K1675	E1676	L1677	M1678																												
PHE	PRO	SER	ASN	LEU	ASP	GLU	PRO	SER	N1584	K1587	Q1588	E1589	Y1591	P1592	S1595	I1597	T1600	R1601	D1602	D1603	I1606	R1609	M1610	P1611	I1612	A1613	A1615	L1616	V1617																											
N1505	N1506	T1507	Q1508	A1515	Q1516	H1517	M1518	W1520	L1521	Q1522	Y1523	L1524	L1527	I1531	S1532	M1533	T1535	K1536	K1537	M1541	Q1543	A1544	V1545	Q1546	L1547	L1548	V1549	Q1550	L1551																											
F1431	T1432	F1433	F1434	D1435	D1436	M1437	L1441	TYR	ASN	GLY	ASP	GLU	ALA	ASP	PHE	THR	ASN	VAL	ASN	ILE	Q1458	R1462	Q1463	R1464	A1465	I1466	K1467	R1468	E1471	L1476																										
N1366	A1367	S1368	H1369	I1370	L1371	M1372	K1373	F1374	D1375	L1376	L1377	T1378	N1379	E1380	K1381	P1382	N1383	L1384	N1385	E1386	K1389	S1390	L1394	I1397	L1398	L1399	P1400	A1401	I1402	T1404	G1405	L1406	R1407	D1408	N1409	L1410	E1411	S1412	V1413	Q1414	S1415	Y1416	V1417	V1418	S1419	V1420	L1421	S1422	ASP	L1423	M1424	V1425	K1426	N1427	R1501	N1502

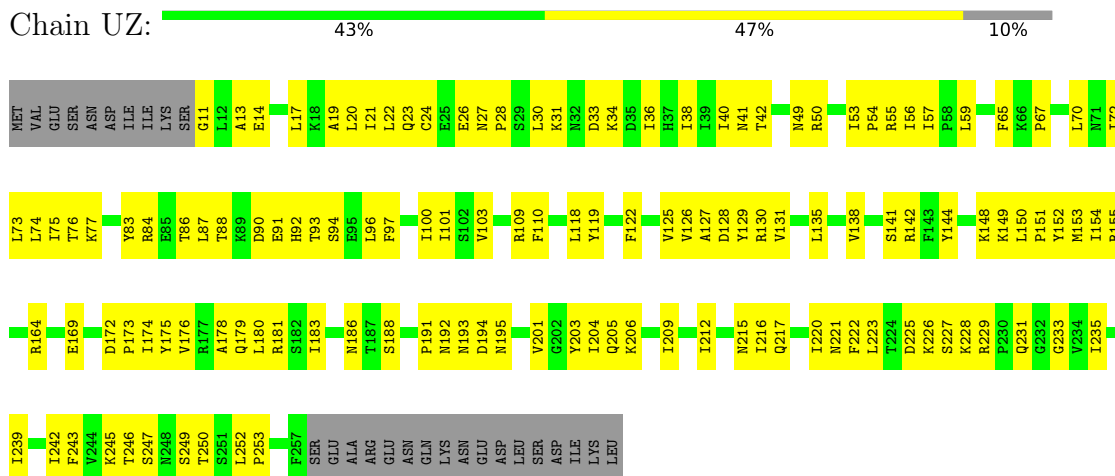
- Molecule 24: U3 small nucleolar RNA-associated protein 21

Chain UU:  50% 41% 10%

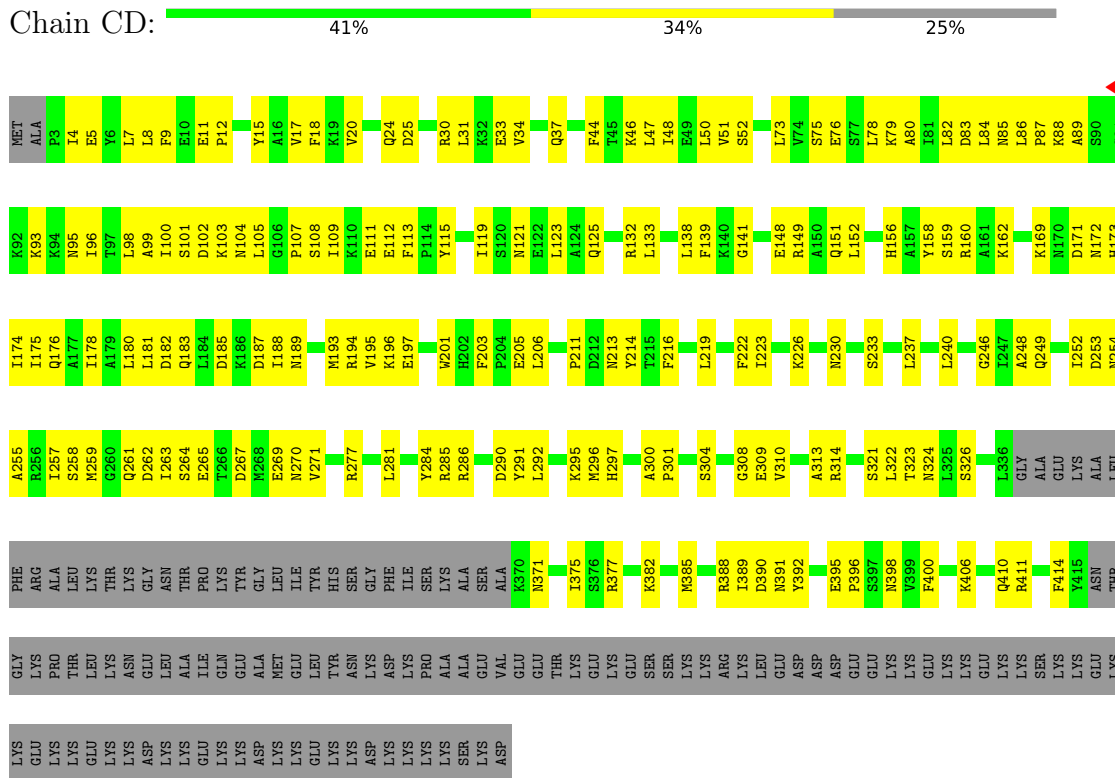
MET	SER	ILE	ASP	LEU	LYS	LYS	ARG	GLN	VAL	LYS	VAL	GLU	GLU	GLU	ASP	VAL	VAL	ARG	SER	SER	ARG	GLY	K19	R20	S21	K22	I23	F24	S25	R28	I29	I30	N35	G36	V37	P38	F39	G42	G45	Y49	I50	V51	T52	C53	G54	V54	G55	F58	G59	I60	Y61	D62	A63	L66	L69	F70
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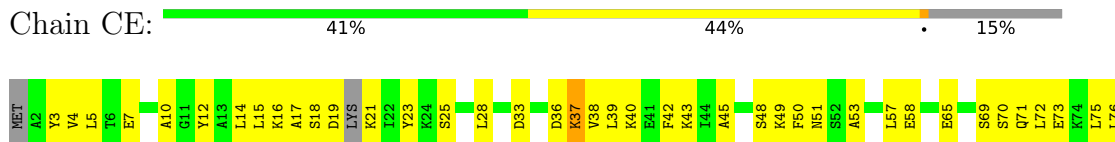
- Molecule 27: Ribosome biogenesis protein UTP30

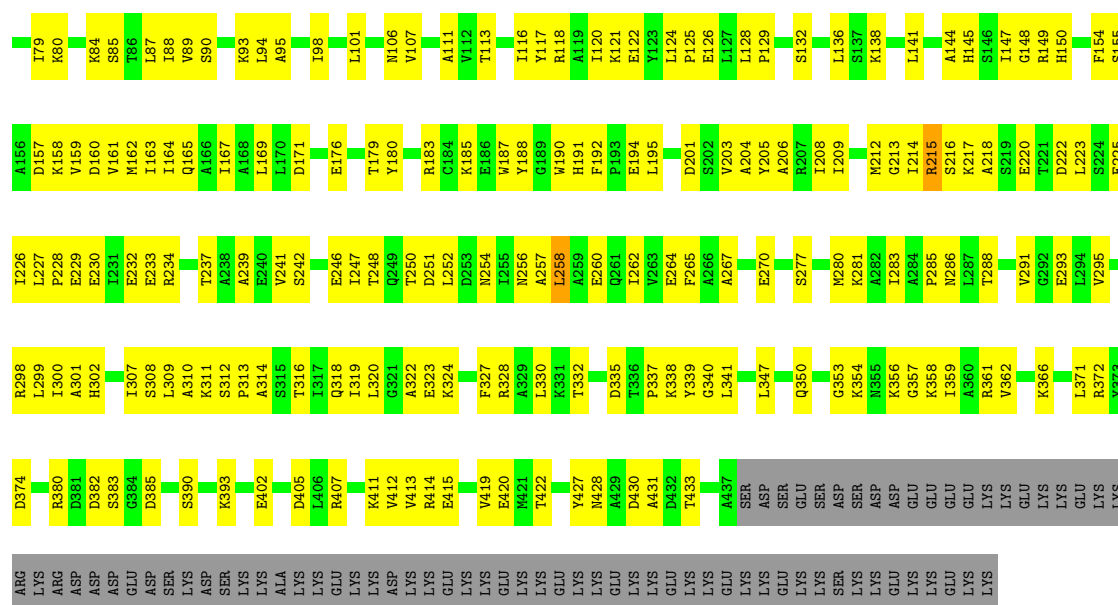


- Molecule 28: Nucleolar protein 56



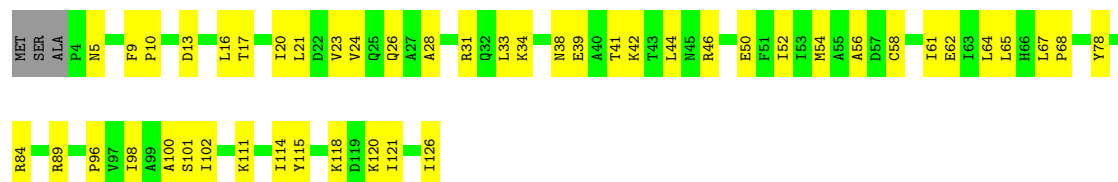
- Molecule 29: Nucleolar protein 58





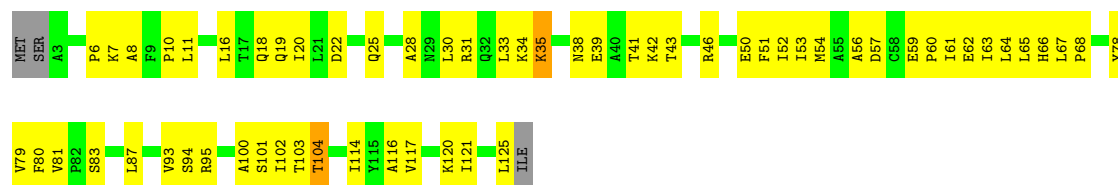
- Molecule 30: 13 kDa ribonucleoprotein-associated protein

Chain CF: 60% 37%



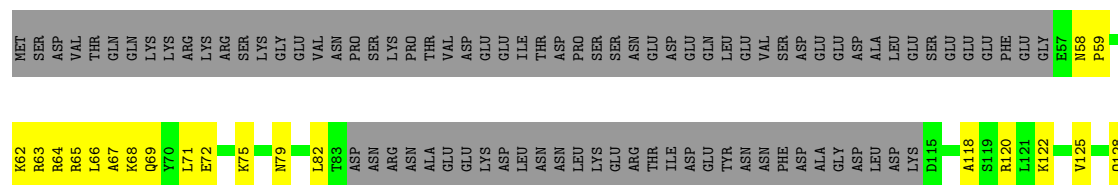
- Molecule 30: 13 kDa ribonucleoprotein-associated protein

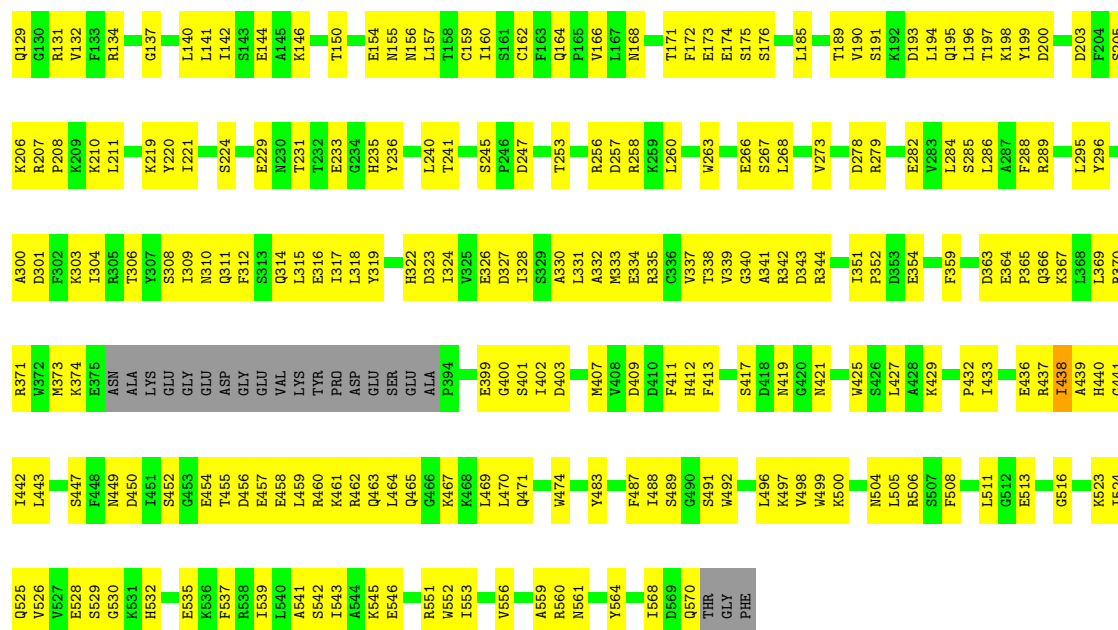
Chain CG: 50% 46%



- Molecule 31: Ribosomal RNA-processing protein 9

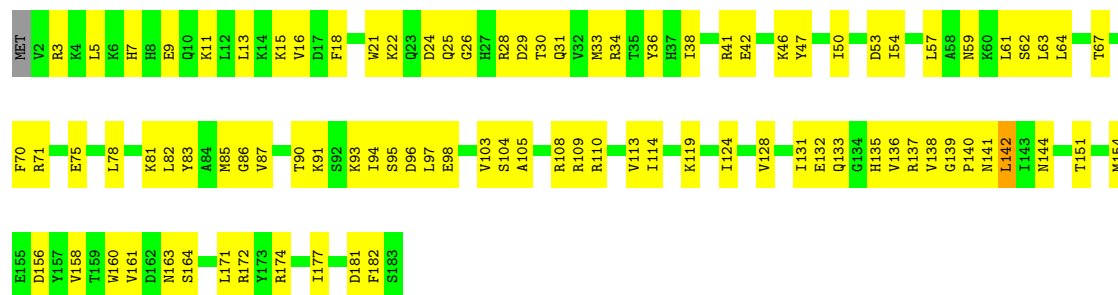
Chain CH: 39% 42% 19%





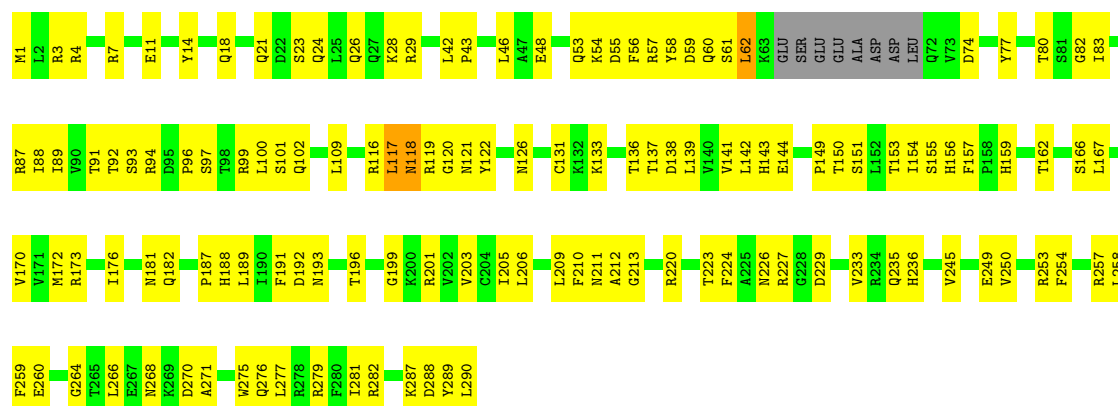
- Molecule 32: U3 small nucleolar ribonucleoprotein protein IMP3

Chain CI: 50% 49% ..



- Molecule 33: U3 small nucleolar ribonucleoprotein protein IMP4

Chain CJ: 52% 44% ..



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

Chain CK:  19% 15% 65%

MET	GLN	GLN	TYR	THR	Q304	THR	S464	RS34
SER	VAL	VAL	GLY	LYS	I306	ARG	L465	RS38
LEU	TRP	TRP	ILE	GLU	E306	LYS	E466	AS39
PHE	GLN	GLN	ASN	PRO	I307	SER	I467	ASN
GLY	VAL	VAL	ASP	VAL	R308	GLN	R468	LEU
VAL	ASP	ASP	LYS	LYS	K309	ARG	Y469	PRO
LEU	SER	SER	PHE	HIS	Q310	PRO	E470	ASN
LYS	LEU	LEU	PHE	ASP	I311	GLN	I471	ASN
ASN	VAL	VAL	LEU	VAL	E312	GLU	I473	LYS
SER	ASP	ASP	GLU	VAL	E315	SER	I474	ARG
ALA	SER	SER	LYS	LYS	N316	ASP	E477	SER
GLY	ILE	ILE	PHE	PRO	E317	VAL	D478	LYS
ARG	ASP	ASP	ASN	LYS	A318	LYS	A479	ARG
ILE	GLY	GLY	ASP	GLU	V319	SER	Q480	ASN
LEU	LEU	LEU	THR	GLU	W324	LYS	P481	ASP
LYS	ILE	ILE	LEU	GLU	S325	LYS	I482	VAL
ASP	GLN	GLN	ALA	GLU	I326	SER	Y483	VAL
PRO	GLY	GLY	ALA	LEU	K327	LEU	Y484	ASP
ASN	ILE	ILE	ALA	ASP	G328	ALA	S485	THR
ALA	GLN	GLN	ASP	GLU	E329	GLU	S488	LEU
THR	GLU	GLU	ASN	GLU	V330	ILE	L490	LYS
LYS	LEU	LEU	GLY	TYR	K331	GLY	L491	ALA
SER	ASP	ASP	ALA	ASP	A332	ASP	A491	LYS
ASP	VAL	VAL	SER	SER	R335	TYR	P492	LYS
VAL	VAL	VAL	GLU	ALA	L340	ASP	Q493	ILE
LYS	THR	THR	GLY	MET	L341	THR	E494	THR
ALA	PRO	PRO	SER	ASP	T342	ARG	I495	VAL
THR	LYS	LYS	GLY	LYS	T343	ALA	Y496	ILE
ILE	SER	SER	ASP	VAL	E343	GLU	Y497	ASN
ASP	HIS	HIS	GLU	LYS	E344	ASP	V498	GLN
ASP	ASN	ASN	GLU	LYS	F347	SER	A501	LYS
SER	LEU	LEU	ILE	ASP	D348	ALA	G505	GLU
VAL	ALA	ALA	ASP	LEU	R349	PHE	E506	LYS
ASN	GLY	GLY	TYR	LEU	T358	ALA	I507	LYS
THR	SER	SER	PHE	ALA	S359	ASP	E428	ASP
CYS	THR	THR	GLN	GLU	E360	GLU	E429	VAL
LYS	LYS	LYS	ASP	PRO	V361	ASP	K432	SER
ILE	ILE	ILE	SER	GLY	E366	PRO	A433	GLY
THR	GLY	GLY	ASP	ASN	D367	ASN	H434	LYS
LYS	GLU	GLU	ASP	ALA	E370	ALA	A442	THR
ALA	GLU	GLU	GLU	GLY	I373	GLY	N443	LYS
LEU	SER	SER	GLY	VAL	F378	VAL	L444	ARG
ASP	GLY	GLY	ALA	GLY	E381	GLY	V445	SER
GLU	ILE	ILE	ILE	GLU	R382	ALA	L448	GLY
THR	GLU	GLU	TYR	ALA	R383	TYR	D449	PRO
VAL	ALA	ALA	GLU	SER	L386	GLU	R522	ASP
SER	SER	SER	ASP	ASP	E301	ASP	E523	LYS
GLY	VAL	VAL	PHE	K295	LEU	ASP	D524	ASN
LEU	PHE	PHE	ASP	N296	ASP	LYS	R527	ILE
ASP	LYS	LYS	ASP	L297	ASP	LEU	R530	LYS
ALA	GLU	GLU	LYS	E301	ILE	ASP	A531	LEU
ASN	LYS	LYS	PRO					

• Molecule 35: Ribosome biogenesis protein BMS1

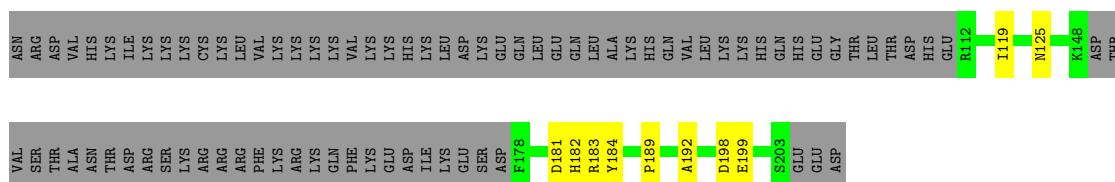
Chain CL:  33% 33% 34%

MET	R61	D124	L207	P279	L353
GLU	T62	L125	S208	L280	I354
GLN	P63	N126	G209	H289	M358
SER	E64	A127	V210	T290	S359
ASN	D65	I128	I211	A291	V364
LYS	D66	M129	N212	G292	L365
GLN	P67	K133	G213	R214	M366
HIS	P68	I134	R214	P216	D367
ARG	P69	A135	F70	P216	K368
LYS	I71	D136	I137	E219	D369
ALA	V72	V138	I220	I220	Y372
GLY	A73	L139	L221	L221	G376
LYS	V74	V75	N222	N222	LYS
ASN	V75	L140	L141	L141	ASN
THR	P78	I142	I143	I143	GLY
LYS	G79	G144	T80	G144	ASN
LYS	T80	N145	K82	K82	GLU
LYS	G81	F146	G147	G147	GLU
LEU	K82	F148	L85	L85	PRO
HIS	L86	E149	I86	I86	PHE
GLN	R87	M150	R87	R87	VAL
GLY	S88	E151	S88	S88	PRO
HIS	L89	T152	L89	L89	GLY
ASN	M153	F153	V90	V90	GLN
ALA	E154	F155	R91	R91	LYS
LYS	F155	H161	M93	M93	ALA
ALA	T94	K95	T94	T94	PHE
VAL	S96	R166	K95	K95	ALA
ALA	N99	V167	S96	S96	ALA
ALA	P36	L168	N99	N99	ALA
G37	G37	G169	D100	D100	ALA
K38	K38	V170	I101	I101	LYS
P39	P39	A171	Q102	Q102	LYS
A40	A40	T172	G103	G103	ASP
R41	R41	H173	P104	P104	VAL
T42	T42	L174	I105	I105	SER
N43	N43	D175	T106	T106	GLY
Q44	Q44	L176	V107	V107	LYS
S46	S46	F177	V108	V108	THR
S47	S47	L183	G110	G110	LYS
D48	D48	R184	K111	K111	SER
V49	V49	K187	H112	H112	ARG
N50	N50	R113	R113	R113	SER
E51	E51	L115	R115	R115	GLY
R52	R52	T116	F117	F117	PRO
K53	K53	R193	G118	G118	ASP
L54	L54	V198	E119	E119	LYS
H55	H55	Y199	C120	C120	ILE
V56	V56	F206	P121	P121	LYS
P57	P57	Y206	G277	G277	LEU
M58	M58		T278	T278	ASP
D60	D60				PHE
					LYS

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

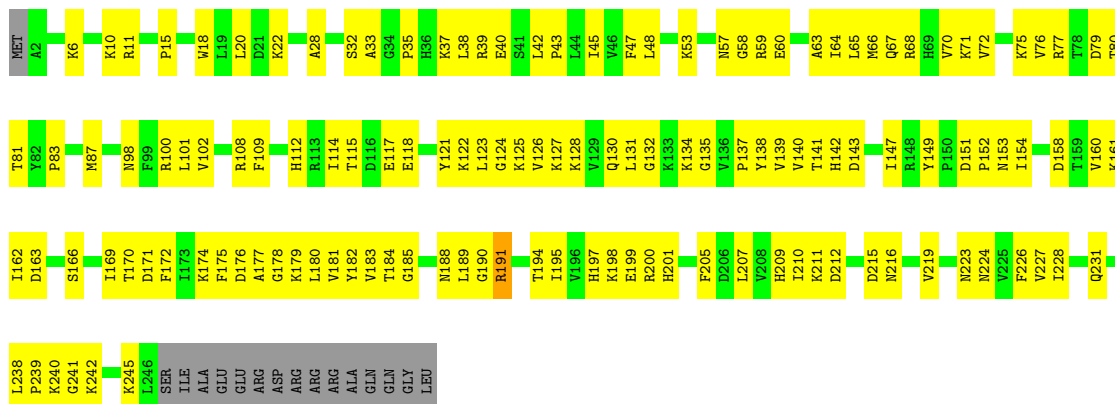






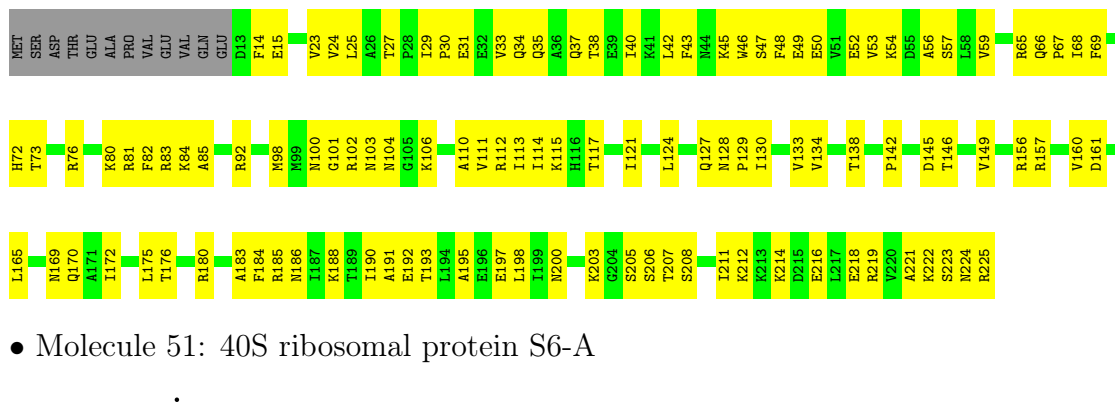
• Molecule 49: 40S ribosomal protein S4-A

Chain DE: 43% 51% 6%



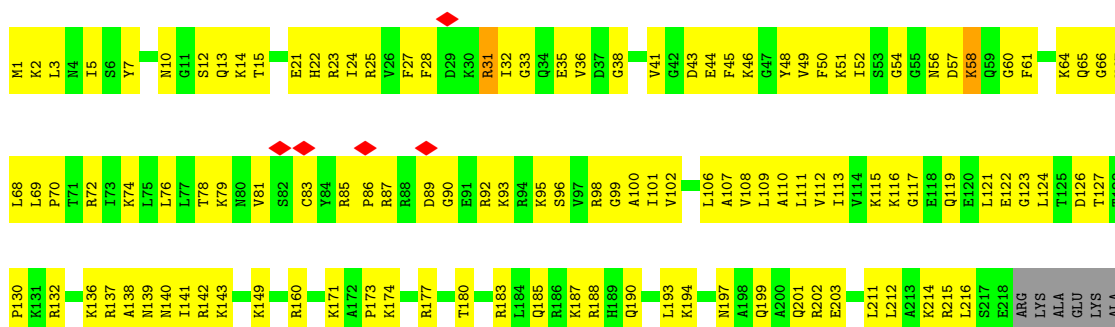
• Molecule 50: 40S ribosomal protein S5

Chain DF: 45% 49% 5%



• Molecule 51: 40S ribosomal protein S6-A

Chain DG: 42% 50% 8%



GLU
ILE
SER
ARG
LYS
LYS
ARG
ARG
ALA
SER
SER
SER
LYS
LYS
ALA

• Molecule 52: 40S ribosomal protein S7-A

Chain DH:  44% 53%

MET SER ALA P4 Q5 A6 K7 I8 L9 A12 P13 T14 E15 L16 E17 L18 A21 Q22 A23 F24 V25 E26 L27 E28 N29 S30 S31 P32 E33 L34 K35 A36 E37 L38 R39 P40 L41 Q42 F43 K44 S45 I46 R47 E48 I49 D50 V51 A52 G53 G54 K55 K56 A57 L58 A59 I60 F61 V62 L67 F70 H71 K72 V73 Q74 T75 K76 L77 K78 R79 E80 L81 E82 K83 K84 F85 R88 H89 V90 I91 F92 L93 A94 E95 S96 R97 E98 K101 P102 S103 R104 R107 Q108 V109 R112 P113 R114 S115 R116 T117 L118 T119 A120 V121 H122 G123 K124 I125 L126 A127 D128 L129 V130 F131 P132 E134 K138 R139 V140 Y142 V144 N147 K148 I149 D158 I162 K166 L166 F169 Q170 A171 F183 S187 GLU THR HIS

• Molecule 53: 40S ribosomal protein S8-A

Chain DI:  48% 40% 12%

MET G2 R5 D6 S7 R8 H9 R11 K17 F21 R22 K23 K24 R25 K26 F27 L29 L30 Q32 P33 A34 N35 T36 K37 A40 K41 R42 S45 Y46 R47 T48 G49 G50 G51 N52 K53 R56 A57 L58 R59 T60 E61 N64 F65 S66 V67 E70 K74 K75 T76 R77 I78 A79 G80 V81 S86 N87 V91 L96 T97 K98 A99 V102 Q103 D105 R110 Q111 Y112 F113 E114 H115 A116 Y117 K123 LYS ASN VAL LYS GLU GLU THR VAL ALA LYS SER LYS ASN ALA GLU ARG LYS TRP ALA ALA R146 K151 I152 V156 F160 R164 L165 Y166 C168 A169 S170 S171 R172 F173 G174 Q175 D180 G181 L184 F191 Y192 L193 R194 R195 L196 K199 K200

• Molecule 54: 40S ribosomal protein S9-A

Chain DJ:  58% 36% 6%

MET P2 R6 T7 Y8 T11 L30 A31 G32 L36 N38 E41 Q48 L49 S50 K51 Y52 R53 R54 A55 A56 L59 L60 E64 K65 D66 P67 K68 R69 L70 F71 E72 R82 V85 L86 S87 E88 D89 K90 L93 D94 Y95 Y96 K100 V101 L105 E106 R107 L108 L109 Q110 T111 Y114 K115 L118 A119 K120 S121 H124 H125 A126 R126 V127 T130 Q131 R132 H133 T134 A135 Q139 T140 I143 F144 S145 R149 S152 E153 R154 I156 D157 F158 S162 E166 ALA ALA ASP GLU ALA ALA ASP GLU ALA ASP GLU ALA ASP GLU

• Molecule 55: 40S ribosomal protein S11-A

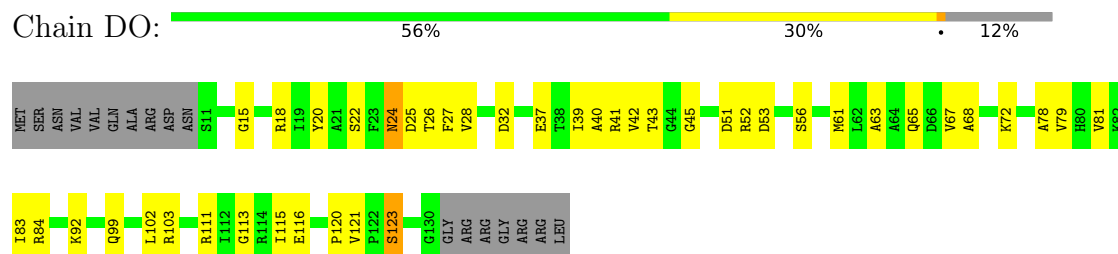
Chain DL:  46% 43% 10%

MET THR GLU LEU T6 V7 Q8 R11 A12 F13 Q14 P17 I19 T27 R30 N37 T44 P45 K46 T47 A48 E50 Y53 I54 D55 K56 K57 C58 P59 L63 V64 S65 I66 R67 G68 K69 I70 L71 T72 G73 T78 I84 V85 I86 R87 P88 P95 N98 R99 Y100 E101 K102 R103 H104 P108 P109 H110 V111 S112 P113 P114 F115 R116 V117 Q118 I122 V123 T124 V125 Q126 T127 C128 R129 E130 F131 S132 K133 T134 V135 R136 F137 N138 V139 V140 K141 V142 S143 A144 A145 ALA GLY LYS ALA ASN LYS GLN PHE ALA LYS PHE

- Molecule 56: 40S ribosomal protein S13



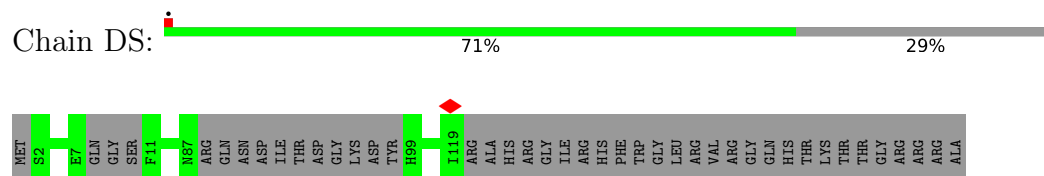
- Molecule 57: 40S ribosomal protein S14-A



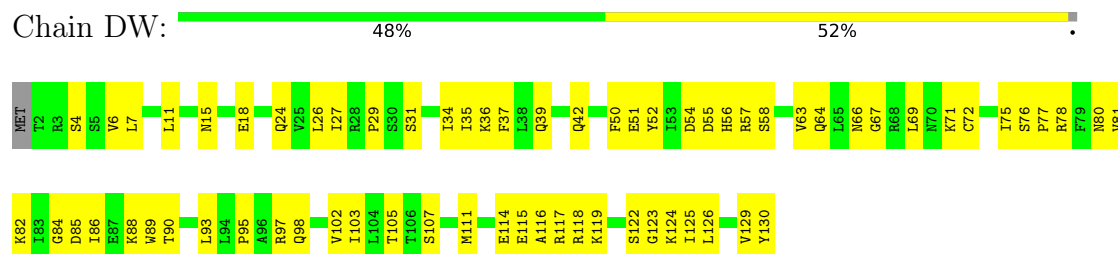
- Molecule 58: 40S ribosomal protein S16-A



- Molecule 59: 40S ribosomal protein S18-A



- Molecule 60: 40S ribosomal protein S22-A



- Molecule 61: 40S ribosomal protein S23-A

SER	A67	I68	R69	K70	V74	Q75	L76	I77	G80	A85	F86	V87	P88	N89	D90	G91	C92	L93	N94	F95	E98	N99	D100	E101	L104	R109	K112	A113	K114	I117	P118	G119	V120	R121	F122	K123	V124	V130	S131	L132	L133	A134	L135	W136	K137	E138	K139	E141	R144						
	GLY	LYS	GLY	LYS	PRO	ARG	GLY	LEU	ASN	SER	ALA	ARG	LYS	LEU	ARG	VAL	HIS	ARG	ASN	ASN	ARG	TRP	ALA	GLU	ASN	ASN	TYR	LYS	LYS	ARG	LEU	LEU	GLY	THR	ALA	PHE	LYS	SER	SER	P42	F43	G44	G45	S46	S47	H48	A49	K50	G51	I52	I59	E60	G63	P64	N65

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| A97 | E98 | K99 | V100 | E101 | K102 | A103 | S104 | Q105 | R106 | Q107 | R108 | K109 | Q110 | K111 | K112 | N113 | R114 | R124 | L125 | A126 | K127 | K128 | R131 | D135 | A97 | E98 | K99 | V100 | E101 | K102 | A103 | S104 | Q105 | R106 | Q107 | R108 | K109 | Q110 | K111 | K112 | N113 | R114 | R124 | L125 | A126 | K127 | K128 | R131 | D135 | MET | S2 | R8 | K11 | V12 | I13 | S14 | N15 | P16 | L17 | L18 | A19 | R20 | K21 | Q22 | F23 | V24 | V25 | H29 | K37 | D38 | E39 | L40 | K49 | A50 | E51 | K52 | D53 | A54 | V55 | S56 | G59 | F60 | G71 | L74 | V75 | Y76 | N77 | E81 | K84 | F85 | E86 | Y89 | A90 | L91 | V92 | R93 | L95 |
|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

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- ```

graph TD
 MET[MET] --- V2[V2]
 V2 --- L21[L21]
 L21 --- F79[F79]
 F79 --- R80[R80]
 F79 --- R81[R81]
 F79 --- K82[K82]

```

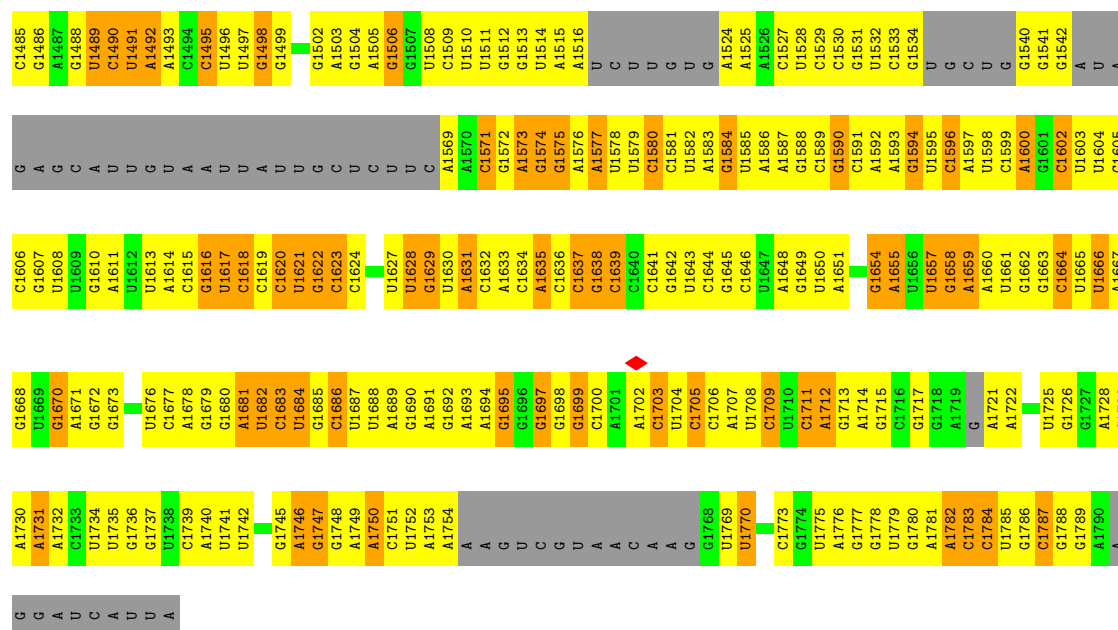
- MET  
ASP  
ASN  
LYS  
T5  
R67

- |      |      |      |     |
|------|------|------|-----|
| C186 | A124 | U64  | A1  |
| C187 | G125 | U65  | U2  |
| C188 | A126 | C56  | G3  |
|      |      | G67  | C4  |
| U191 | U129 | U68  | G5  |
| G192 | G130 | U69  | A6  |
| G193 | C131 | A70  | A7  |
| G194 | C132 | U    | A8  |
| A195 | U133 | G    | G9  |
| A196 | A134 | U    | C10 |
| G197 | G135 | U    | A11 |
| A198 | U136 | U    | G12 |
| A199 | C137 | U    | U13 |
| A200 | U138 | U    | U14 |
| U201 | C139 | G    | G15 |
| U202 | U140 | U    | A16 |
| C203 | A141 | A80  | A17 |
| C204 | U142 | A81  | G18 |
| C205 | A143 | A82  | A19 |
| A206 | C144 | U83  | C20 |
| G207 | U145 | G84  | A21 |
| A208 | G146 | G85  | A22 |
| G209 | C147 | C86  | G23 |
| U210 | G148 | C87  | U24 |
| G211 | U149 | U88  | U   |
| U212 | G150 | C89  | C   |
| G213 | U151 | G90  | G   |
| U214 | U152 | U91  | A   |
| U215 | U153 | C92  | A   |
| U216 | A154 | A93  | A   |
| C217 | U155 | A94  | A   |
| U218 | U156 | A95  | G   |
| U219 | U157 | C96  | A   |
| U220 | G158 | G97  | G   |
| U221 | A159 | G98  | U   |
| G222 | C160 | U99  | U   |
| C223 | A161 | G100 | U   |
| G224 | U162 | G101 | G   |
| U225 | C163 | A102 | G   |
| U226 | G164 | G103 | A   |
| U227 | G165 | A104 | A   |
| A228 | U166 | G105 | A   |
| A229 | U167 | A106 | A   |
|      | G168 | G107 | C   |
| U232 | A169 | U108 | C   |
| G233 | U170 | C109 | A   |
| A234 | G171 | G110 | A   |
| A235 | C172 | C111 | U   |
| C236 | G173 | U112 | C   |
| U237 | U174 | A113 | G   |
| G238 |      | G114 | A   |
| U239 | U177 | G115 | G   |
| C240 | A179 | U116 | U   |
| U241 | G180 | G117 | A   |
| C242 | A181 | A118 | G   |
| A243 | G182 | U119 | G56 |
| U244 | A183 | C120 | C57 |
| G245 | U184 | G121 | U58 |
| G246 | A185 | U122 |     |
| C247 |      | C122 | C58 |

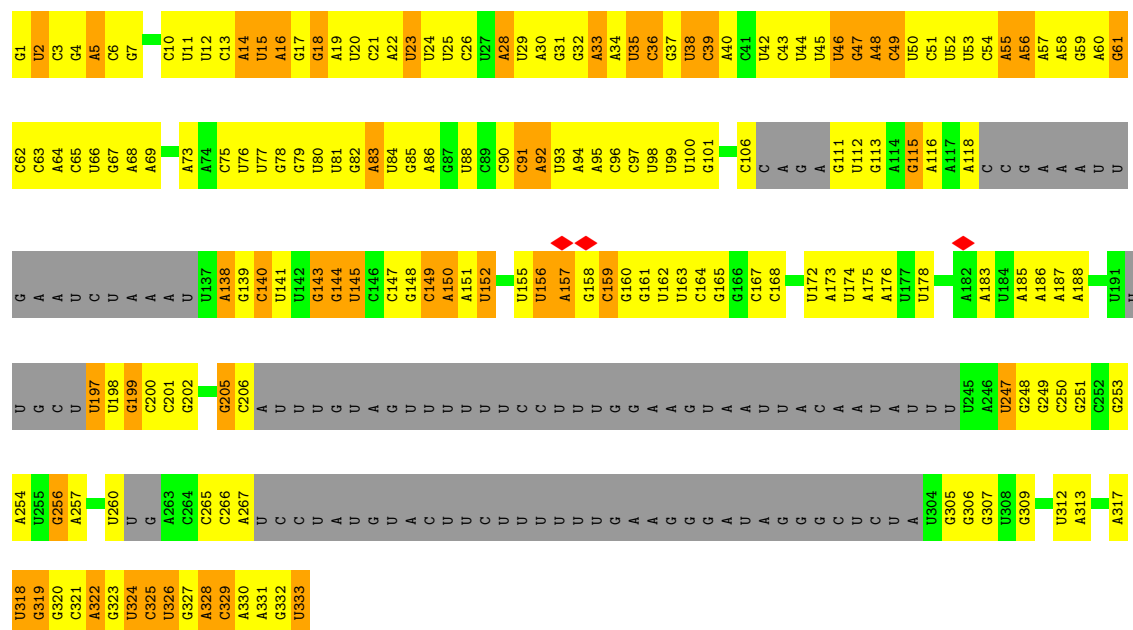




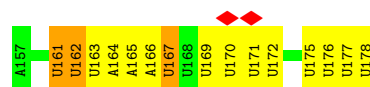




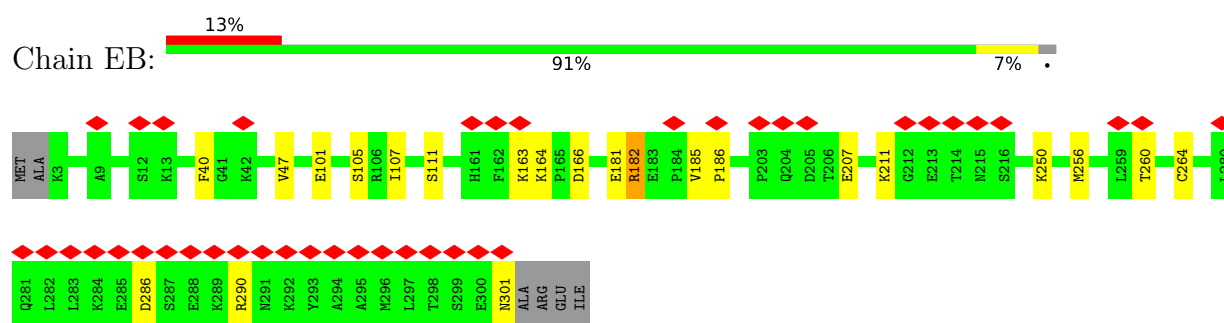
• Molecule 67: U3 snoRNA



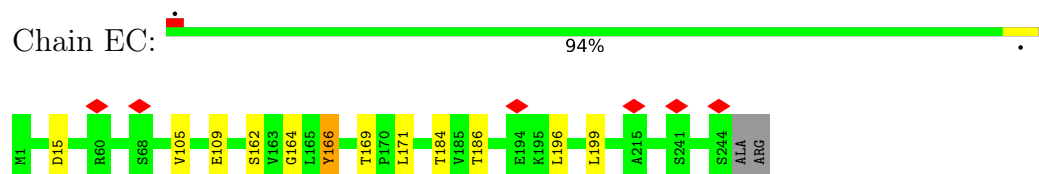
• Molecule 68: RNA



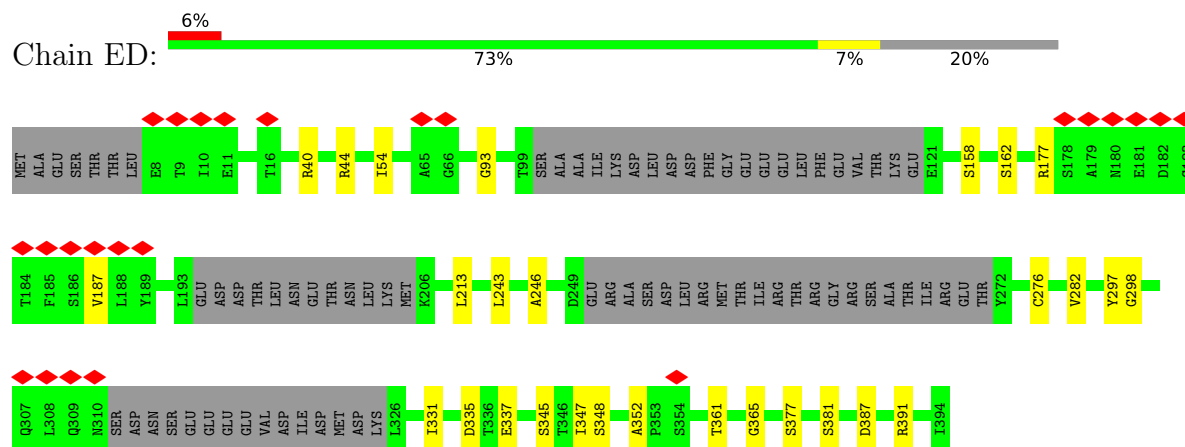
• Molecule 69: Exosome complex component RRP45



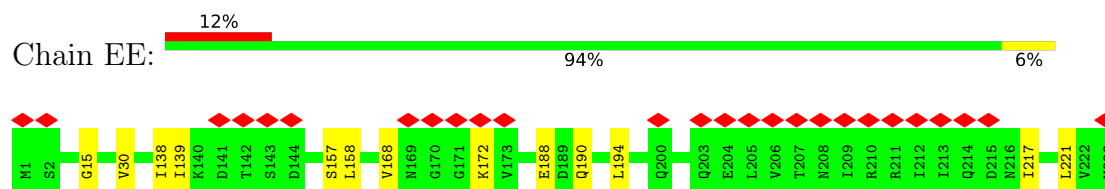
- Molecule 70: Exosome complex component SKI6



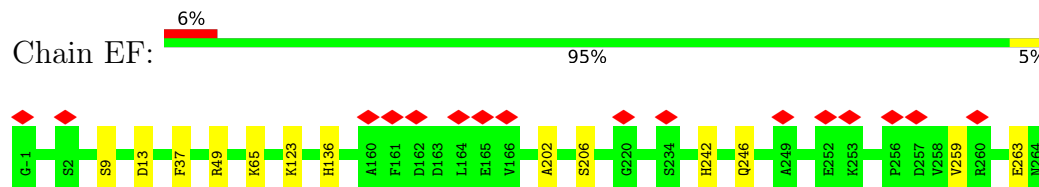
- Molecule 71: Exosome complex component RRP43



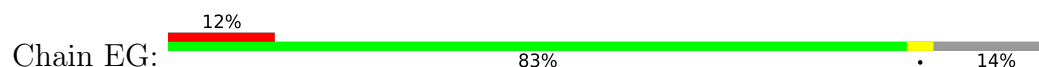
- Molecule 72: Exosome complex component RRP46

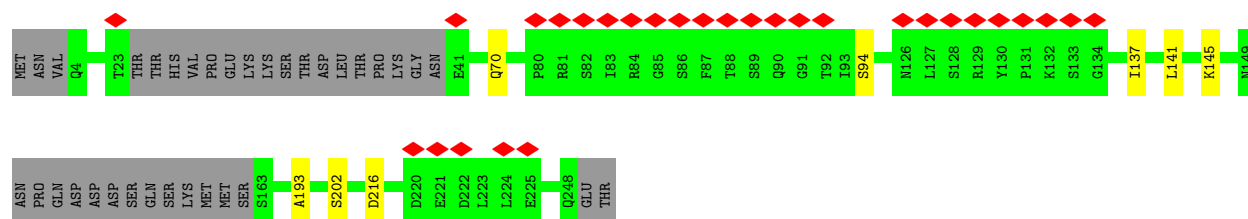


- Molecule 73: Exosome complex component RRP42

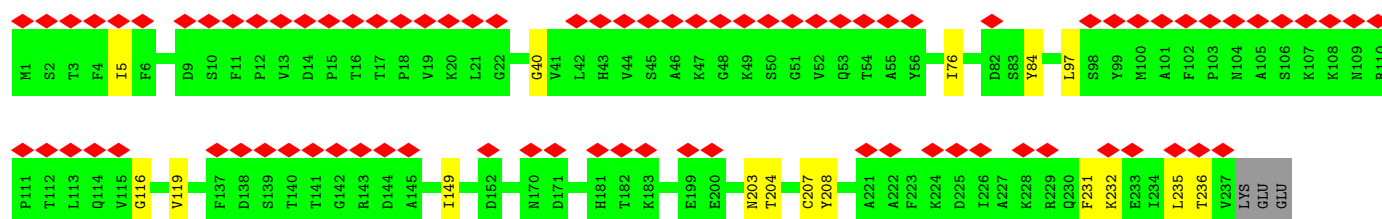
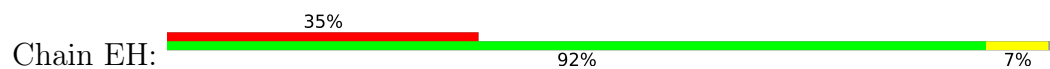


- Molecule 74: Exosome complex component MTR3

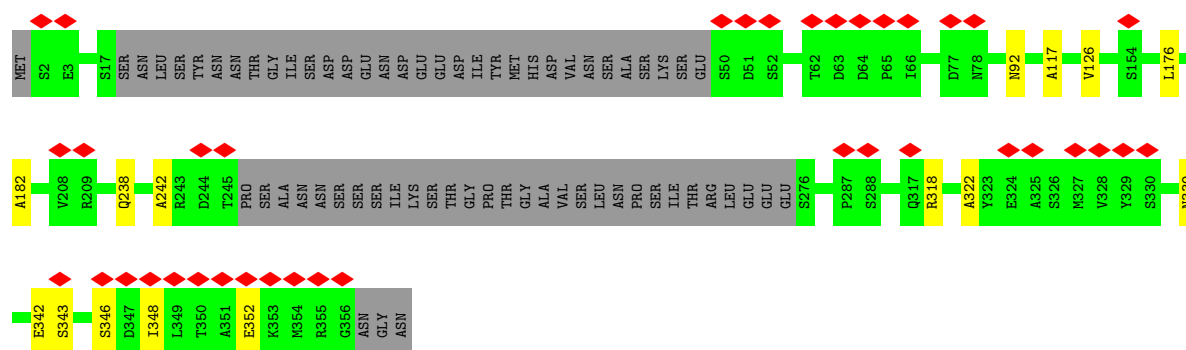
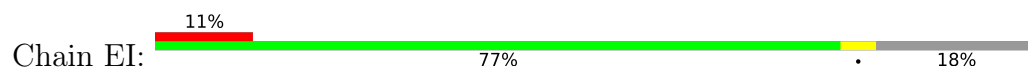




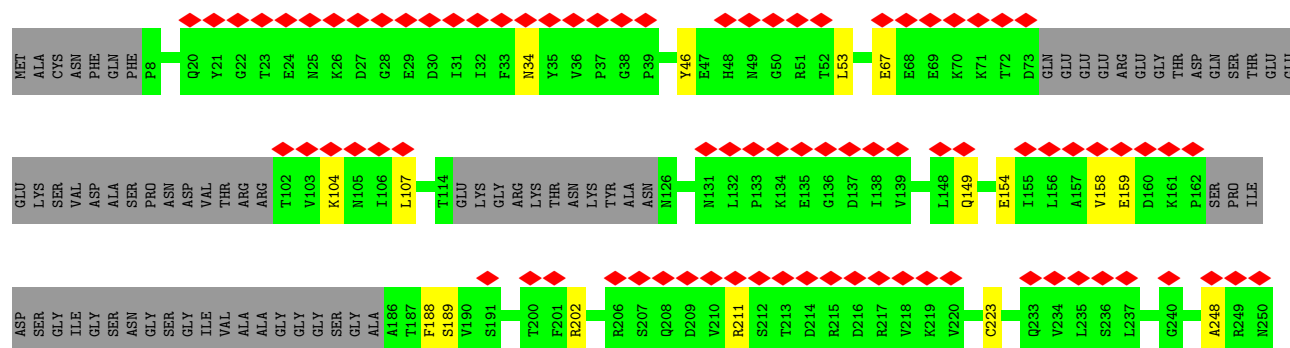
• Molecule 75: Exosome complex component RRP40

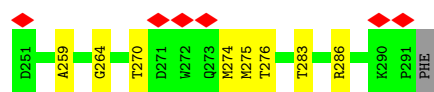


• Molecule 76: Exosome complex component RRP4

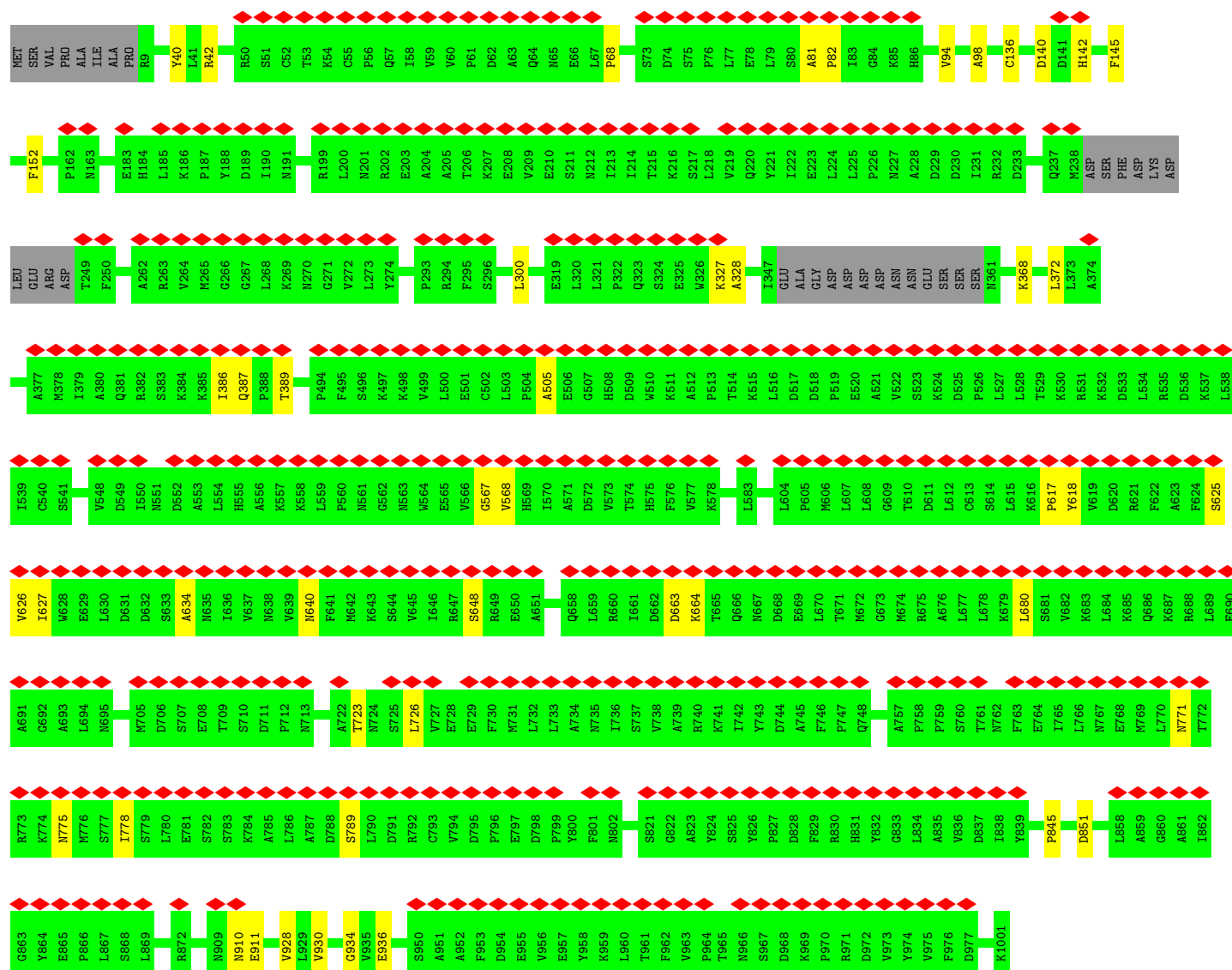
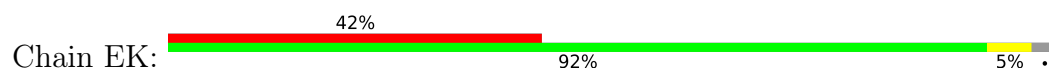


• Molecule 77: Exosome complex component CSL4

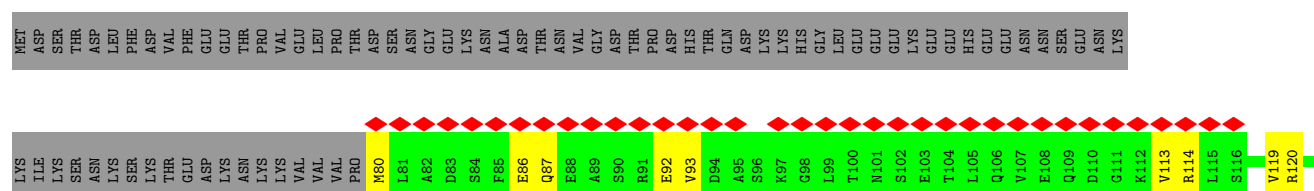
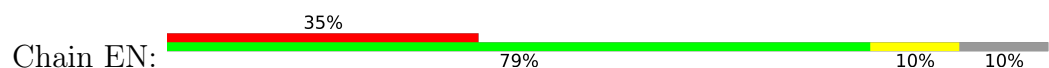


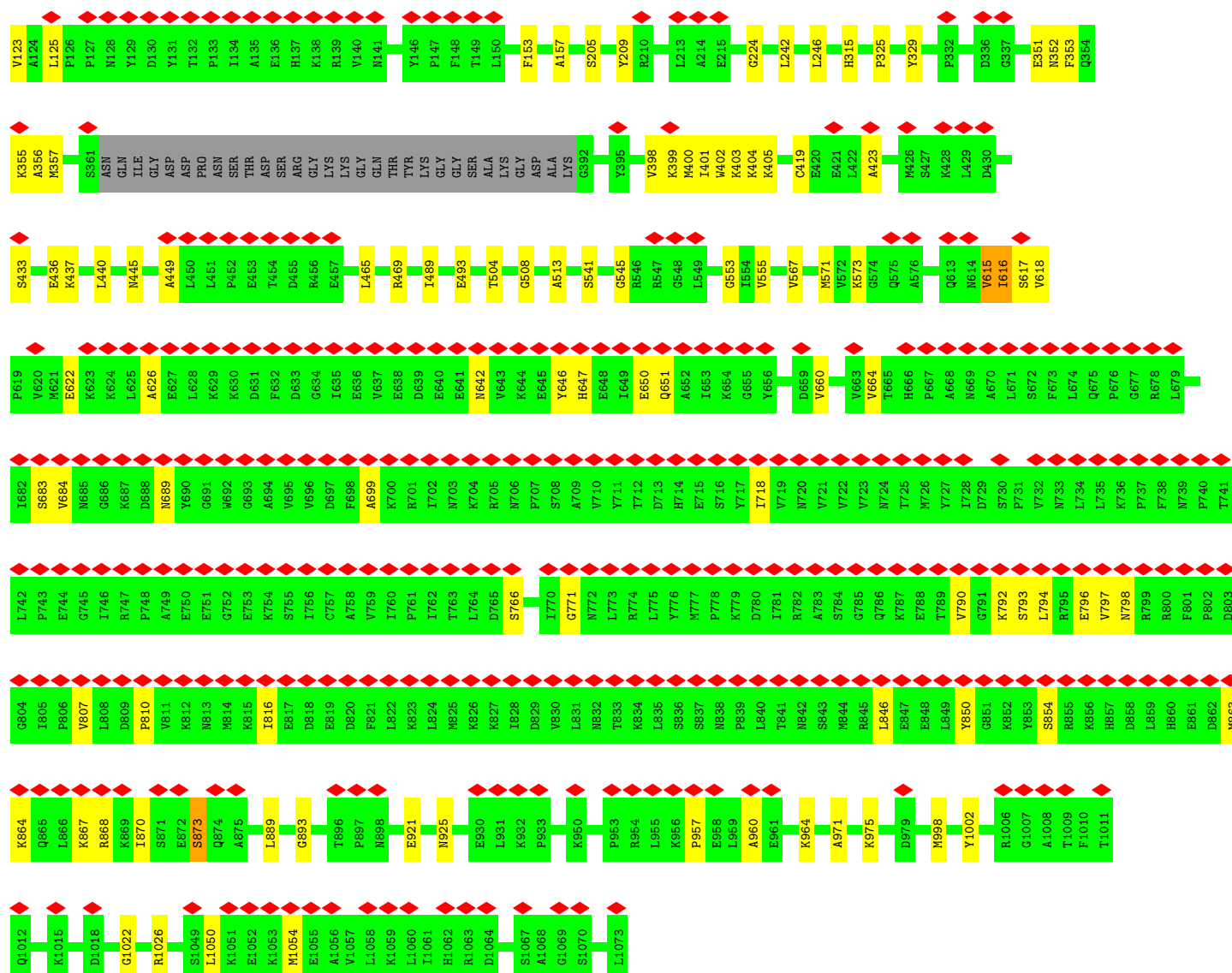


• Molecule 78: Exosome complex exonuclease DIS3



• 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: MG, GTP, 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    | 0.66         | 0/1917        | 0.66        | 1/2588 (0.0%)  |
| 1   | CB    | 0.40         | 0/1815        | 0.61        | 1/2448 (0.0%)  |
| 2   | DA    | 0.43         | 0/1937        | 0.59        | 0/2593         |
| 3   | JA    | 0.28         | 0/6021        | 0.50        | 0/8176         |
| 3   | JB    | 0.24         | 0/4128        | 0.41        | 0/5747         |
| 4   | UA    | 0.52         | 0/6780        | 0.62        | 2/9175 (0.0%)  |
| 5   | UB    | 0.31         | 0/3787        | 0.50        | 1/5126 (0.0%)  |
| 6   | UC    | 0.52         | 0/1034        | 0.63        | 1/1365 (0.1%)  |
| 7   | UD    | 0.39         | 0/5461        | 0.57        | 0/7395         |
| 8   | UE    | 0.37         | 0/3840        | 0.57        | 0/5208         |
| 9   | UF    | 0.45         | 0/2538        | 0.56        | 0/3405         |
| 10  | UG    | 0.62         | 2/4302 (0.0%) | 0.68        | 2/5805 (0.0%)  |
| 11  | UH    | 0.28         | 0/2716        | 0.51        | 0/3721         |
| 12  | UI    | 0.28         | 0/875         | 0.59        | 1/1176 (0.1%)  |
| 13  | UJ    | 0.35         | 0/9111        | 0.52        | 1/12323 (0.0%) |
| 14  | UK    | 0.51         | 0/2047        | 0.65        | 1/2711 (0.0%)  |
| 15  | UL    | 0.34         | 0/6857        | 0.56        | 1/9253 (0.0%)  |
| 16  | UM    | 0.33         | 0/6070        | 0.56        | 0/8216         |
| 17  | UN    | 0.53         | 0/1252        | 0.66        | 0/1688         |
| 18  | UO    | 0.40         | 0/3993        | 0.58        | 3/5413 (0.1%)  |
| 19  | UP    | 0.32         | 0/499         | 0.56        | 0/659          |
| 20  | UQ    | 0.37         | 0/6794        | 0.55        | 1/9203 (0.0%)  |
| 21  | UR    | 0.50         | 0/3883        | 0.61        | 0/5265         |
| 22  | US    | 0.33         | 0/3703        | 0.53        | 1/5053 (0.0%)  |
| 23  | UT    | 0.29         | 0/17584       | 0.49        | 1/23824 (0.0%) |
| 24  | UU    | 0.46         | 0/6815        | 0.58        | 1/9213 (0.0%)  |
| 25  | UV    | 0.31         | 0/8945        | 0.48        | 0/12097        |
| 26  | UX    | 0.64         | 0/1418        | 0.70        | 0/1906         |
| 27  | UZ    | 0.36         | 0/2041        | 0.54        | 0/2745         |
| 28  | CD    | 0.44         | 0/3041        | 0.57        | 0/4098         |
| 29  | CE    | 0.40         | 0/3362        | 0.59        | 1/4533 (0.0%)  |
| 30  | CF    | 0.46         | 0/944         | 0.63        | 0/1284         |



| Mol | Chain | Bond lengths |               | Bond angles |                 |
|-----|-------|--------------|---------------|-------------|-----------------|
|     |       | RMSZ         | # Z  >5       | RMSZ        | # Z  >5         |
| 30  | CG    | 0.52         | 0/941         | 0.66        | 0/1281          |
| 31  | CH    | 0.39         | 0/3798        | 0.55        | 0/5113          |
| 32  | CI    | 0.76         | 0/1559        | 0.77        | 1/2097 (0.0%)   |
| 33  | CJ    | 0.57         | 0/2337        | 0.68        | 1/3148 (0.0%)   |
| 34  | CK    | 0.44         | 0/1685        | 0.63        | 0/2261          |
| 35  | CL    | 0.47         | 0/6471        | 0.61        | 0/8708          |
| 36  | CM    | 0.34         | 0/2832        | 0.53        | 0/3825          |
| 37  | CN    | 0.30         | 0/1934        | 0.48        | 0/2604          |
| 38  | JC    | 0.29         | 0/2908        | 0.52        | 0/3938          |
| 39  | JF    | 0.31         | 0/1727        | 0.53        | 0/2329          |
| 39  | JG    | 0.37         | 0/1828        | 0.58        | 0/2470          |
| 40  | JH    | 0.23         | 0/1293        | 0.35        | 0/1801          |
| 41  | JI    | 0.23         | 0/1313        | 0.36        | 0/1830          |
| 42  | JJ    | 0.31         | 0/1469        | 0.55        | 0/1980          |
| 43  | JK    | 0.29         | 0/342         | 0.45        | 0/462           |
| 44  | JM    | 0.46         | 0/1156        | 0.59        | 0/1536          |
| 45  | JN    | 0.52         | 0/1435        | 0.63        | 1/1907 (0.1%)   |
| 46  | JO    | 0.45         | 0/1910        | 0.58        | 0/2569          |
| 47  | JP    | 0.67         | 0/3844        | 0.72        | 0/5174          |
| 48  | JQ    | 0.32         | 0/385         | 0.52        | 0/529           |
| 49  | DE    | 0.33         | 0/1985        | 0.53        | 0/2675          |
| 50  | DF    | 0.47         | 0/1690        | 0.59        | 0/2285          |
| 51  | DG    | 0.29         | 0/1779        | 0.49        | 0/2379          |
| 52  | DH    | 0.35         | 0/1506        | 0.54        | 0/2028          |
| 53  | DI    | 0.28         | 0/1422        | 0.49        | 0/1899          |
| 54  | DJ    | 0.54         | 0/1519        | 0.67        | 1/2035 (0.0%)   |
| 55  | DL    | 0.26         | 0/1155        | 0.50        | 1/1557 (0.1%)   |
| 56  | DN    | 0.41         | 0/1215        | 0.58        | 0/1638          |
| 57  | DO    | 0.41         | 0/892         | 0.56        | 0/1202          |
| 58  | DQ    | 0.67         | 0/990         | 0.70        | 1/1335 (0.1%)   |
| 59  | DS    | 0.24         | 0/513         | 0.40        | 0/711           |
| 60  | DW    | 0.56         | 0/1038        | 0.66        | 0/1395          |
| 61  | DX    | 0.51         | 0/798         | 0.65        | 0/1065          |
| 62  | DY    | 0.40         | 0/1087        | 0.60        | 1/1449 (0.1%)   |
| 63  | Db    | 0.45         | 0/620         | 0.66        | 1/838 (0.1%)    |
| 64  | Dc    | 0.45         | 0/499         | 0.68        | 0/670           |
| 65  | D2    | 0.76         | 0/10633       | 0.94        | 11/16564 (0.1%) |
| 66  | D3    | 0.67         | 0/31617       | 0.89        | 16/49213 (0.0%) |
| 67  | D4    | 0.76         | 1/5432 (0.0%) | 0.90        | 2/8439 (0.0%)   |
| 68  | EA    | 0.77         | 0/405         | 1.53        | 6/625 (1.0%)    |
| 69  | EB    | 0.47         | 0/1474        | 0.57        | 0/2050          |
| 70  | EC    | 0.47         | 0/1203        | 0.58        | 0/1673          |
| 71  | ED    | 0.43         | 0/1569        | 0.61        | 0/2179          |

| Mol | Chain | Bond lengths |                 | Bond angles |                  |
|-----|-------|--------------|-----------------|-------------|------------------|
|     |       | RMSZ         | # Z  >5         | RMSZ        | # Z  >5          |
| 72  | EE    | 0.46         | 0/1109          | 0.61        | 0/1545           |
| 73  | EF    | 0.42         | 0/1328          | 0.60        | 0/1851           |
| 74  | EG    | 0.45         | 0/1055          | 0.59        | 0/1462           |
| 75  | EH    | 0.44         | 0/1169          | 0.64        | 0/1626           |
| 76  | EI    | 0.44         | 0/1437          | 0.62        | 0/1992           |
| 77  | EJ    | 0.40         | 0/1087          | 0.62        | 0/1504           |
| 78  | EK    | 0.39         | 0/4818          | 0.57        | 0/6720           |
| 79  | EN    | 0.40         | 0/4765          | 0.58        | 0/6636           |
| All | All   | 0.48         | 3/264486 (0.0%) | 0.65        | 63/368214 (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                   |

*Continued on next page...*

*Continued from previous page...*

| 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 (3) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms  | Z     | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|--------|-------|-------------|----------|
| 10  | UG    | 139 | TRP  | CB-CG  | -5.96 | 1.39        | 1.50     |
| 67  | D4    | 197 | U    | C1'-N1 | 5.53  | 1.57        | 1.48     |
| 10  | UG    | 213 | TRP  | CB-CG  | -5.39 | 1.40        | 1.50     |

The worst 5 of 63 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms     | Z      | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-----------|--------|-------------|----------|
| 68  | EA    | 167 | U    | N1-C2-O2  | 13.96  | 132.57      | 122.80   |
| 68  | EA    | 167 | U    | N3-C2-O2  | -11.26 | 114.32      | 122.20   |
| 68  | EA    | 167 | U    | C2-N1-C1' | 11.18  | 131.12      | 117.70   |
| 24  | UU    | 143 | SER  | C-N-CA    | 10.16  | 147.09      | 121.70   |
| 68  | EA    | 167 | U    | C6-N1-C1' | -8.20  | 109.72      | 121.20   |

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.

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1   | CA    | 1881  | 0        | 1928     | 99      | 0            |
| 1   | CB    | 1782  | 0        | 1826     | 149     | 0            |
| 2   | DA    | 1912  | 0        | 2023     | 113     | 0            |
| 3   | JA    | 5916  | 0        | 5463     | 317     | 0            |
| 3   | JB    | 4132  | 0        | 1819     | 21      | 0            |
| 4   | UA    | 6635  | 0        | 6525     | 334     | 0            |
| 5   | UB    | 3734  | 0        | 3432     | 169     | 0            |
| 6   | UC    | 1026  | 0        | 1080     | 58      | 0            |
| 7   | UD    | 5361  | 0        | 5364     | 358     | 0            |
| 8   | UE    | 3772  | 0        | 3806     | 203     | 0            |
| 9   | UF    | 2487  | 0        | 2533     | 147     | 0            |
| 10  | UG    | 4218  | 0        | 4223     | 231     | 0            |
| 11  | UH    | 2701  | 0        | 1951     | 127     | 0            |
| 12  | UI    | 860   | 0        | 922      | 79      | 0            |
| 13  | UJ    | 8961  | 0        | 9273     | 525     | 0            |
| 14  | UK    | 2021  | 0        | 2098     | 165     | 0            |
| 15  | UL    | 6726  | 0        | 6764     | 390     | 0            |
| 16  | UM    | 5969  | 0        | 6006     | 388     | 0            |
| 17  | UN    | 1227  | 0        | 1223     | 68      | 0            |
| 18  | UO    | 3911  | 0        | 3906     | 273     | 0            |
| 19  | UP    | 495   | 0        | 561      | 51      | 0            |
| 20  | UQ    | 6662  | 0        | 6588     | 394     | 0            |
| 21  | UR    | 3799  | 0        | 3783     | 237     | 0            |
| 22  | US    | 3622  | 0        | 3214     | 181     | 0            |
| 23  | UT    | 17290 | 0        | 16616    | 924     | 0            |
| 24  | UU    | 6678  | 0        | 6651     | 339     | 0            |
| 25  | UV    | 8736  | 0        | 8850     | 468     | 0            |
| 26  | UX    | 1395  | 0        | 1473     | 70      | 0            |
| 27  | UZ    | 2006  | 0        | 2118     | 117     | 0            |
| 28  | CD    | 2994  | 0        | 3018     | 166     | 0            |
| 29  | CE    | 3325  | 0        | 3414     | 215     | 0            |
| 30  | CF    | 931   | 0        | 983      | 47      | 0            |
| 30  | CG    | 928   | 0        | 976      | 71      | 0            |
| 31  | CH    | 3725  | 0        | 3746     | 220     | 0            |
| 32  | CI    | 1530  | 0        | 1572     | 99      | 0            |
| 33  | CJ    | 2296  | 0        | 2325     | 133     | 0            |
| 34  | CK    | 1667  | 0        | 1701     | 98      | 0            |
| 35  | CL    | 6332  | 0        | 6515     | 416     | 0            |
| 36  | CM    | 2781  | 0        | 2878     | 140     | 0            |
| 37  | CN    | 1893  | 0        | 1875     | 100     | 0            |
| 38  | JC    | 2845  | 0        | 2761     | 234     | 0            |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 39  | JF    | 1701  | 0        | 1767     | 102     | 0            |
| 39  | JG    | 1799  | 0        | 1872     | 106     | 0            |
| 40  | JH    | 1295  | 0        | 570      | 4       | 0            |
| 41  | JI    | 1314  | 0        | 610      | 0       | 0            |
| 42  | JJ    | 1442  | 0        | 1513     | 72      | 0            |
| 43  | JK    | 334   | 0        | 313      | 24      | 0            |
| 44  | JM    | 1137  | 0        | 1188     | 52      | 0            |
| 45  | JN    | 1428  | 0        | 1425     | 67      | 0            |
| 46  | JO    | 1876  | 0        | 1968     | 76      | 0            |
| 47  | JP    | 3765  | 0        | 3714     | 232     | 0            |
| 48  | JQ    | 381   | 0        | 255      | 12      | 0            |
| 49  | DE    | 1944  | 0        | 2030     | 126     | 0            |
| 50  | DF    | 1669  | 0        | 1724     | 110     | 0            |
| 51  | DG    | 1755  | 0        | 1846     | 119     | 0            |
| 52  | DH    | 1481  | 0        | 1572     | 102     | 0            |
| 53  | DI    | 1399  | 0        | 1431     | 94      | 0            |
| 54  | DJ    | 1494  | 0        | 1573     | 69      | 0            |
| 55  | DL    | 1129  | 0        | 1196     | 65      | 0            |
| 56  | DN    | 1192  | 0        | 1255     | 79      | 0            |
| 57  | DO    | 881   | 0        | 910      | 40      | 0            |
| 58  | DQ    | 973   | 0        | 1029     | 69      | 0            |
| 59  | DS    | 516   | 0        | 222      | 0       | 0            |
| 60  | DW    | 1021  | 0        | 1060     | 73      | 0            |
| 61  | DX    | 786   | 0        | 843      | 69      | 0            |
| 62  | DY    | 1073  | 0        | 1132     | 63      | 0            |
| 63  | Db    | 610   | 0        | 630      | 0       | 0            |
| 64  | Dc    | 497   | 0        | 535      | 0       | 0            |
| 65  | D2    | 9508  | 0        | 4781     | 404     | 0            |
| 66  | D3    | 28287 | 0        | 14261    | 1182    | 0            |
| 67  | D4    | 4869  | 0        | 2468     | 191     | 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     | 32      | 0            |
| 79  | EN    | 4767  | 0        | 2109     | 59      | 0            |

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| Mol | Chain | Non-H  | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|--------|----------|----------|---------|--------------|
| 80  | Db    | 1      | 0        | 0        | 0       | 0            |
| 80  | EK    | 1      | 0        | 0        | 0       | 0            |
| 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        | 219009   | 11280   | 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 25.

The worst 5 of 11280 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](#)

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 |     |
|-----|-------|----------------|-----------|----------|----------|-------------|-----|
| 1   | CA    | 238/327 (73%)  | 207 (87%) | 31 (13%) | 0        | 100         | 100 |
| 1   | CB    | 224/327 (68%)  | 201 (90%) | 23 (10%) | 0        | 100         | 100 |
| 2   | DA    | 236/255 (92%)  | 212 (90%) | 24 (10%) | 0        | 100         | 100 |
| 3   | JA    | 802/1056 (76%) | 734 (92%) | 68 (8%)  | 0        | 100         | 100 |

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| Mol | Chain | Analysed        | Favoured   | Allowed  | Outliers | Percentiles |     |
|-----|-------|-----------------|------------|----------|----------|-------------|-----|
| 3   | JB    | 827/1056 (78%)  | 770 (93%)  | 57 (7%)  | 0        | 100         | 100 |
| 4   | UA    | 830/923 (90%)   | 733 (88%)  | 97 (12%) | 0        | 100         | 100 |
| 5   | UB    | 495/810 (61%)   | 465 (94%)  | 30 (6%)  | 0        | 100         | 100 |
| 6   | UC    | 124/610 (20%)   | 112 (90%)  | 12 (10%) | 0        | 100         | 100 |
| 7   | UD    | 663/776 (85%)   | 575 (87%)  | 88 (13%) | 0        | 100         | 100 |
| 8   | UE    | 465/643 (72%)   | 419 (90%)  | 46 (10%) | 0        | 100         | 100 |
| 9   | UF    | 283/440 (64%)   | 273 (96%)  | 10 (4%)  | 0        | 100         | 100 |
| 10  | UG    | 529/554 (96%)   | 461 (87%)  | 68 (13%) | 0        | 100         | 100 |
| 11  | UH    | 426/713 (60%)   | 375 (88%)  | 46 (11%) | 5 (1%)   | 11          | 44  |
| 12  | UI    | 100/575 (17%)   | 98 (98%)   | 2 (2%)   | 0        | 100         | 100 |
| 13  | UJ    | 1092/1769 (62%) | 1031 (94%) | 61 (6%)  | 0        | 100         | 100 |
| 14  | UK    | 238/250 (95%)   | 214 (90%)  | 24 (10%) | 0        | 100         | 100 |
| 15  | UL    | 828/943 (88%)   | 733 (88%)  | 95 (12%) | 0        | 100         | 100 |
| 16  | UM    | 750/817 (92%)   | 662 (88%)  | 87 (12%) | 1 (0%)   | 48          | 83  |
| 17  | UN    | 143/899 (16%)   | 124 (87%)  | 19 (13%) | 0        | 100         | 100 |
| 18  | UO    | 489/513 (95%)   | 432 (88%)  | 57 (12%) | 0        | 100         | 100 |
| 19  | UP    | 58/214 (27%)    | 54 (93%)   | 4 (7%)   | 0        | 100         | 100 |
| 20  | UQ    | 820/896 (92%)   | 735 (90%)  | 85 (10%) | 0        | 100         | 100 |
| 21  | UR    | 474/594 (80%)   | 424 (90%)  | 50 (10%) | 0        | 100         | 100 |
| 22  | US    | 488/552 (88%)   | 440 (90%)  | 48 (10%) | 0        | 100         | 100 |
| 23  | UT    | 2213/2493 (89%) | 2072 (94%) | 141 (6%) | 0        | 100         | 100 |
| 24  | UU    | 842/939 (90%)   | 755 (90%)  | 87 (10%) | 0        | 100         | 100 |
| 25  | UV    | 1069/1237 (86%) | 1018 (95%) | 51 (5%)  | 0        | 100         | 100 |
| 26  | UX    | 170/189 (90%)   | 150 (88%)  | 20 (12%) | 0        | 100         | 100 |
| 27  | UZ    | 245/274 (89%)   | 225 (92%)  | 20 (8%)  | 0        | 100         | 100 |
| 28  | CD    | 376/504 (75%)   | 344 (92%)  | 32 (8%)  | 0        | 100         | 100 |
| 29  | CE    | 431/511 (84%)   | 393 (91%)  | 38 (9%)  | 0        | 100         | 100 |
| 30  | CF    | 121/126 (96%)   | 109 (90%)  | 12 (10%) | 0        | 100         | 100 |
| 30  | CG    | 121/126 (96%)   | 112 (93%)  | 9 (7%)   | 0        | 100         | 100 |
| 31  | CH    | 459/573 (80%)   | 401 (87%)  | 57 (12%) | 1 (0%)   | 44          | 78  |
| 32  | CI    | 180/183 (98%)   | 157 (87%)  | 23 (13%) | 0        | 100         | 100 |

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| Mol | Chain | Analysed       | Favoured  | Allowed  | Outliers | Percentiles |     |
|-----|-------|----------------|-----------|----------|----------|-------------|-----|
| 33  | CJ    | 278/290 (96%)  | 242 (87%) | 36 (13%) | 0        | 100         | 100 |
| 34  | CK    | 203/593 (34%)  | 184 (91%) | 18 (9%)  | 1 (0%)   | 25          | 64  |
| 35  | CL    | 771/1183 (65%) | 716 (93%) | 54 (7%)  | 1 (0%)   | 48          | 83  |
| 36  | CM    | 358/367 (98%)  | 335 (94%) | 23 (6%)  | 0        | 100         | 100 |
| 37  | CN    | 224/297 (75%)  | 211 (94%) | 13 (6%)  | 0        | 100         | 100 |
| 38  | JC    | 350/707 (50%)  | 316 (90%) | 34 (10%) | 0        | 100         | 100 |
| 39  | JF    | 212/252 (84%)  | 203 (96%) | 9 (4%)   | 0        | 100         | 100 |
| 39  | JG    | 226/252 (90%)  | 217 (96%) | 9 (4%)   | 0        | 100         | 100 |
| 40  | JH    | 257/483 (53%)  | 243 (95%) | 14 (5%)  | 0        | 100         | 100 |
| 41  | JI    | 263/1729 (15%) | 257 (98%) | 6 (2%)   | 0        | 100         | 100 |
| 42  | JJ    | 180/274 (66%)  | 172 (96%) | 8 (4%)   | 0        | 100         | 100 |
| 43  | JK    | 40/534 (8%)    | 31 (78%)  | 9 (22%)  | 0        | 100         | 100 |
| 44  | JM    | 129/217 (59%)  | 121 (94%) | 8 (6%)   | 0        | 100         | 100 |
| 45  | JN    | 178/346 (51%)  | 160 (90%) | 18 (10%) | 0        | 100         | 100 |
| 46  | JO    | 226/316 (72%)  | 214 (95%) | 12 (5%)  | 0        | 100         | 100 |
| 47  | JP    | 457/489 (94%)  | 392 (86%) | 65 (14%) | 0        | 100         | 100 |
| 48  | JQ    | 59/206 (29%)   | 53 (90%)  | 6 (10%)  | 0        | 100         | 100 |
| 49  | DE    | 243/261 (93%)  | 218 (90%) | 25 (10%) | 0        | 100         | 100 |
| 50  | DF    | 211/225 (94%)  | 189 (90%) | 22 (10%) | 0        | 100         | 100 |
| 51  | DG    | 216/236 (92%)  | 203 (94%) | 13 (6%)  | 0        | 100         | 100 |
| 52  | DH    | 182/190 (96%)  | 165 (91%) | 17 (9%)  | 0        | 100         | 100 |
| 53  | DI    | 173/200 (86%)  | 160 (92%) | 13 (8%)  | 0        | 100         | 100 |
| 54  | DJ    | 183/197 (93%)  | 154 (84%) | 29 (16%) | 0        | 100         | 100 |
| 55  | DL    | 138/156 (88%)  | 124 (90%) | 14 (10%) | 0        | 100         | 100 |
| 56  | DN    | 148/151 (98%)  | 140 (95%) | 8 (5%)   | 0        | 100         | 100 |
| 57  | DO    | 118/137 (86%)  | 107 (91%) | 11 (9%)  | 0        | 100         | 100 |
| 58  | DQ    | 123/143 (86%)  | 109 (89%) | 14 (11%) | 0        | 100         | 100 |
| 59  | DS    | 98/146 (67%)   | 91 (93%)  | 7 (7%)   | 0        | 100         | 100 |
| 60  | DW    | 127/130 (98%)  | 110 (87%) | 17 (13%) | 0        | 100         | 100 |
| 61  | DX    | 101/145 (70%)  | 79 (78%)  | 21 (21%) | 1 (1%)   | 13          | 48  |
| 62  | DY    | 132/135 (98%)  | 121 (92%) | 11 (8%)  | 0        | 100         | 100 |

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| Mol | Chain | Analysed          | Favoured    | Allowed   | Outliers | Percentiles |     |
|-----|-------|-------------------|-------------|-----------|----------|-------------|-----|
| 63  | Db    | 79/82 (96%)       | 67 (85%)    | 12 (15%)  | 0        | 100         | 100 |
| 64  | Dc    | 61/67 (91%)       | 53 (87%)    | 8 (13%)   | 0        | 100         | 100 |
| 69  | EB    | 297/305 (97%)     | 274 (92%)   | 21 (7%)   | 2 (1%)   | 19          | 56  |
| 70  | EC    | 242/246 (98%)     | 225 (93%)   | 17 (7%)   | 0        | 100         | 100 |
| 71  | ED    | 308/394 (78%)     | 283 (92%)   | 24 (8%)   | 1 (0%)   | 37          | 72  |
| 72  | EE    | 222/223 (100%)    | 209 (94%)   | 13 (6%)   | 0        | 100         | 100 |
| 73  | EF    | 266/267 (100%)    | 252 (95%)   | 14 (5%)   | 0        | 100         | 100 |
| 74  | EG    | 209/250 (84%)     | 192 (92%)   | 17 (8%)   | 0        | 100         | 100 |
| 75  | EH    | 235/240 (98%)     | 216 (92%)   | 19 (8%)   | 0        | 100         | 100 |
| 76  | EI    | 287/359 (80%)     | 263 (92%)   | 24 (8%)   | 0        | 100         | 100 |
| 77  | EJ    | 214/292 (73%)     | 198 (92%)   | 16 (8%)   | 0        | 100         | 100 |
| 78  | EK    | 965/1001 (96%)    | 939 (97%)   | 25 (3%)   | 1 (0%)   | 48          | 83  |
| 79  | EN    | 960/1073 (90%)    | 890 (93%)   | 66 (7%)   | 4 (0%)   | 30          | 68  |
| All | All   | 28798/39453 (73%) | 26318 (91%) | 2462 (8%) | 18 (0%)  | 50          | 83  |

5 of 18 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 11  | UH    | 258 | PRO  |
| 31  | CH    | 438 | ILE  |
| 34  | CK    | 454 | VAL  |
| 79  | EN    | 615 | VAL  |
| 79  | EN    | 617 | SER  |

### 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 |     |
|-----|-------|---------------|------------|----------|-------------|-----|
| 1   | CA    | 202/240 (84%) | 202 (100%) | 0        | 100         | 100 |
| 1   | CB    | 192/240 (80%) | 189 (98%)  | 3 (2%)   | 58          | 74  |
| 2   | DA    | 212/224 (95%) | 212 (100%) | 0        | 100         | 100 |

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| Mol | Chain | Analysed        | Rotameric   | Outliers | Percentiles |     |
|-----|-------|-----------------|-------------|----------|-------------|-----|
| 3   | JA    | 555/934 (59%)   | 553 (100%)  | 2 (0%)   | 89          | 90  |
| 4   | UA    | 730/812 (90%)   | 728 (100%)  | 2 (0%)   | 91          | 91  |
| 5   | UB    | 344/732 (47%)   | 343 (100%)  | 1 (0%)   | 91          | 91  |
| 6   | UC    | 107/538 (20%)   | 107 (100%)  | 0        | 100         | 100 |
| 7   | UD    | 615/713 (86%)   | 612 (100%)  | 3 (0%)   | 86          | 89  |
| 8   | UE    | 428/574 (75%)   | 428 (100%)  | 0        | 100         | 100 |
| 9   | UF    | 277/414 (67%)   | 275 (99%)   | 2 (1%)   | 81          | 87  |
| 10  | UG    | 462/480 (96%)   | 461 (100%)  | 1 (0%)   | 92          | 93  |
| 11  | UH    | 152/657 (23%)   | 151 (99%)   | 1 (1%)   | 81          | 87  |
| 12  | UI    | 99/533 (19%)    | 98 (99%)    | 1 (1%)   | 73          | 81  |
| 13  | UJ    | 1031/1633 (63%) | 1025 (99%)  | 6 (1%)   | 84          | 88  |
| 14  | UK    | 226/234 (97%)   | 225 (100%)  | 1 (0%)   | 89          | 90  |
| 15  | UL    | 747/832 (90%)   | 746 (100%)  | 1 (0%)   | 92          | 94  |
| 16  | UM    | 668/719 (93%)   | 665 (100%)  | 3 (0%)   | 89          | 90  |
| 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%)    | 56 (98%)    | 1 (2%)   | 54          | 71  |
| 20  | UQ    | 769/826 (93%)   | 766 (100%)  | 3 (0%)   | 89          | 90  |
| 21  | UR    | 425/529 (80%)   | 424 (100%)  | 1 (0%)   | 92          | 93  |
| 22  | US    | 332/506 (66%)   | 332 (100%)  | 0        | 100         | 100 |
| 23  | UT    | 1787/2307 (78%) | 1780 (100%) | 7 (0%)   | 89          | 90  |
| 24  | UU    | 743/819 (91%)   | 743 (100%)  | 0        | 100         | 100 |
| 25  | UV    | 986/1125 (88%)  | 982 (100%)  | 4 (0%)   | 89          | 90  |
| 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%)   | 350 (99%)   | 3 (1%)   | 79          | 84  |
| 30  | CF    | 102/104 (98%)   | 102 (100%)  | 0        | 100         | 100 |
| 30  | CG    | 101/104 (97%)   | 100 (99%)   | 1 (1%)   | 73          | 81  |
| 31  | CH    | 406/503 (81%)   | 405 (100%)  | 1 (0%)   | 92          | 93  |
| 32  | CI    | 171/172 (99%)   | 171 (100%)  | 0        | 100         | 100 |

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| Mol | Chain | Analysed          | Rotameric    | Outliers | Percentiles |     |
|-----|-------|-------------------|--------------|----------|-------------|-----|
| 33  | CJ    | 251/258 (97%)     | 250 (100%)   | 1 (0%)   | 89          | 90  |
| 34  | CK    | 187/535 (35%)     | 186 (100%)   | 1 (0%)   | 86          | 89  |
| 35  | CL    | 690/1039 (66%)    | 679 (98%)    | 11 (2%)  | 58          | 74  |
| 36  | CM    | 307/312 (98%)     | 306 (100%)   | 1 (0%)   | 91          | 91  |
| 37  | CN    | 212/274 (77%)     | 212 (100%)   | 0        | 100         | 100 |
| 38  | JC    | 318/636 (50%)     | 316 (99%)    | 2 (1%)   | 84          | 88  |
| 39  | JF    | 195/222 (88%)     | 194 (100%)   | 1 (0%)   | 86          | 89  |
| 39  | JG    | 206/222 (93%)     | 206 (100%)   | 0        | 100         | 100 |
| 42  | JJ    | 158/238 (66%)     | 157 (99%)    | 1 (1%)   | 84          | 88  |
| 43  | JK    | 35/482 (7%)       | 35 (100%)    | 0        | 100         | 100 |
| 44  | JM    | 124/200 (62%)     | 123 (99%)    | 1 (1%)   | 79          | 84  |
| 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%)     | 415 (100%)   | 1 (0%)   | 92          | 93  |
| 48  | JQ    | 22/192 (12%)      | 22 (100%)    | 0        | 100         | 100 |
| 49  | DE    | 209/222 (94%)     | 206 (99%)    | 3 (1%)   | 62          | 75  |
| 50  | DF    | 180/191 (94%)     | 180 (100%)   | 0        | 100         | 100 |
| 51  | DG    | 187/201 (93%)     | 183 (98%)    | 4 (2%)   | 48          | 67  |
| 52  | DH    | 165/170 (97%)     | 165 (100%)   | 0        | 100         | 100 |
| 53  | DI    | 142/161 (88%)     | 139 (98%)    | 3 (2%)   | 48          | 67  |
| 54  | DJ    | 158/166 (95%)     | 158 (100%)   | 0        | 100         | 100 |
| 55  | DL    | 125/137 (91%)     | 124 (99%)    | 1 (1%)   | 79          | 84  |
| 56  | DN    | 127/128 (99%)     | 126 (99%)    | 1 (1%)   | 79          | 84  |
| 57  | DO    | 91/105 (87%)      | 90 (99%)     | 1 (1%)   | 70          | 80  |
| 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%)     | 111 (99%)    | 1 (1%)   | 75          | 83  |
| 63  | Db    | 70/71 (99%)       | 69 (99%)     | 1 (1%)   | 62          | 75  |
| 64  | Dc    | 56/60 (93%)       | 56 (100%)    | 0        | 100         | 100 |
| All | All   | 19959/27976 (71%) | 19876 (100%) | 83 (0%)  | 88          | 90  |

5 of 83 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 35  | CL    | 366 | MET  |
| 51  | DG    | 31  | ARG  |
| 35  | CL    | 624 | LYS  |
| 42  | JJ    | 144 | LYS  |
| 53  | DI    | 22  | ARG  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 161 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 28  | CD    | 287 | GLN  |
| 50  | DF    | 103 | ASN  |
| 31  | CH    | 164 | GLN  |
| 35  | CL    | 835 | HIS  |
| 53  | DI    | 87  | ASN  |

### 5.3.3 RNA [i](#)

| 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    |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 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   | 26,34,34     | 0.92 | 1 (3%)   | 32,54,54    | 1.49 | 5 (15%)  |

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   | -       | 7/18/38/38 | 0/3/3/3 |

All (1) bond length outliers are listed below:

| Mol | Chain | Res  | Type | Atoms | Z     | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|-------|-------|-------------|----------|
| 82  | CL    | 2001 | GTP  | C6-N1 | -2.49 | 1.34        | 1.37     |

All (5) bond angle outliers are listed below:

| Mol | Chain | Res  | Type | Atoms       | Z     | Observed(°) | Ideal(°) |
|-----|-------|------|------|-------------|-------|-------------|----------|
| 82  | CL    | 2001 | GTP  | PB-O3B-PG   | -3.53 | 120.73      | 132.83   |
| 82  | CL    | 2001 | GTP  | PA-O3A-PB   | -3.32 | 121.42      | 132.83   |
| 82  | CL    | 2001 | GTP  | C3'-C2'-C1' | 3.21  | 105.81      | 100.98   |
| 82  | CL    | 2001 | GTP  | C8-N7-C5    | 2.39  | 107.54      | 102.99   |
| 82  | CL    | 2001 | GTP  | C5-C6-N1    | 2.32  | 118.05      | 113.95   |

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

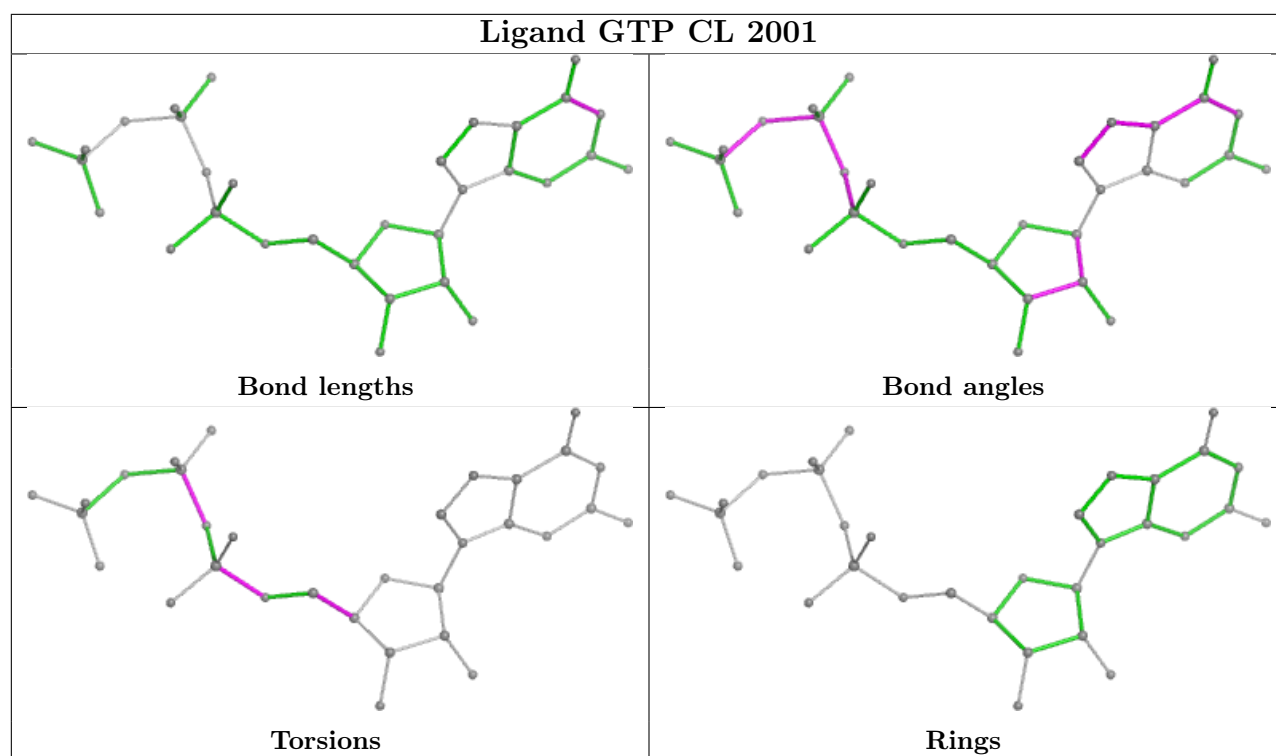
| Mol | Chain | Res  | Type | Atoms           |
|-----|-------|------|------|-----------------|
| 82  | CL    | 2001 | GTP  | C5'-O5'-PA-O1A  |
| 82  | CL    | 2001 | GTP  | C3'-C4'-C5'-O5' |
| 82  | CL    | 2001 | GTP  | O4'-C4'-C5'-O5' |
| 82  | CL    | 2001 | GTP  | C5'-O5'-PA-O3A  |
| 82  | CL  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

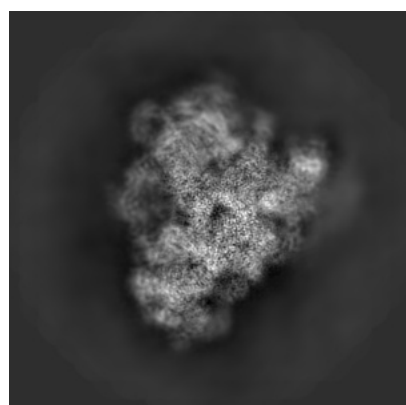
## 6 Map visualisation [i](#)

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.

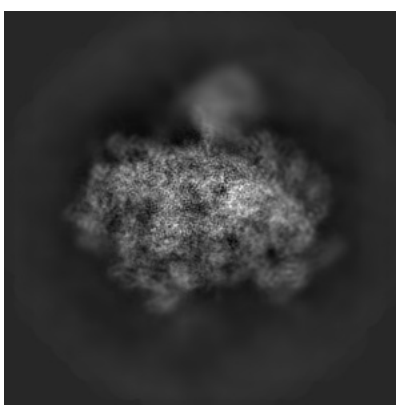
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

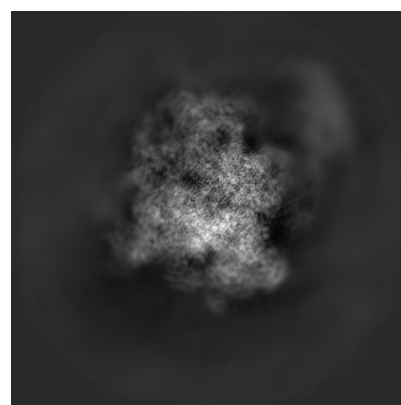
#### 6.1.1 Primary map



X



Y

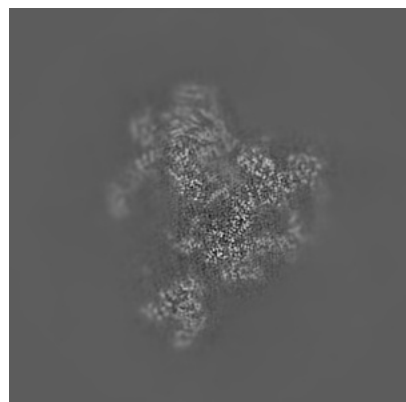


Z

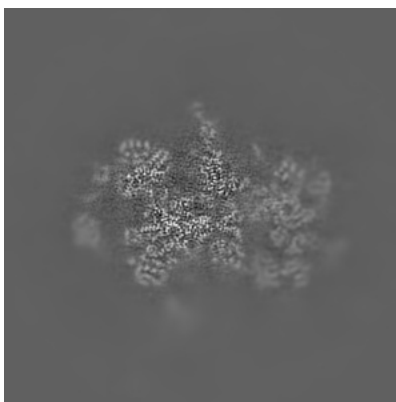
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

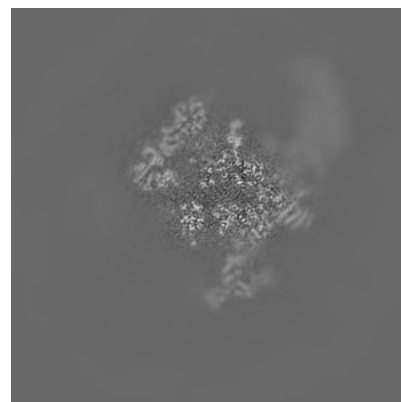
#### 6.2.1 Primary map



X Index: 270



Y Index: 270



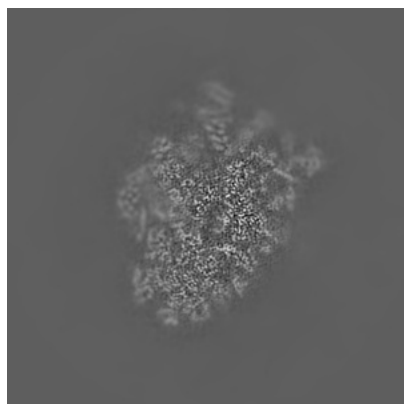
Z Index: 270



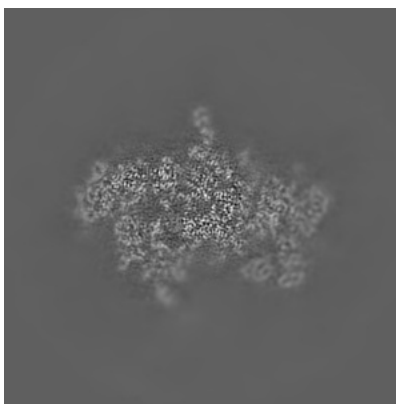
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

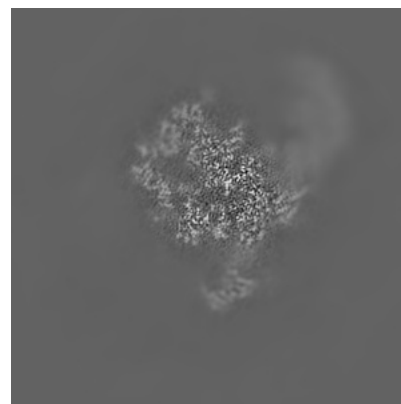
### 6.3.1 Primary map



X Index: 310



Y Index: 252

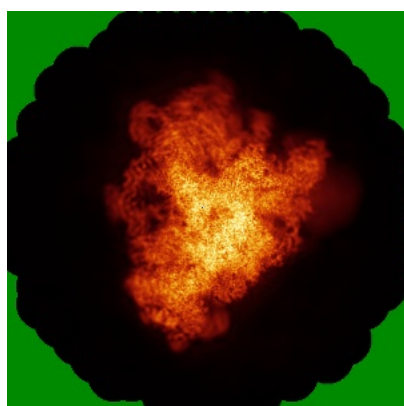


Z Index: 279

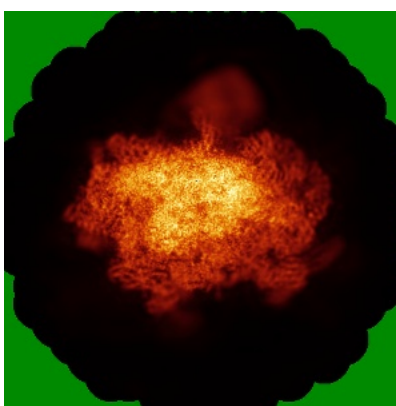
The images above show the largest variance slices of the map in three orthogonal directions.

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

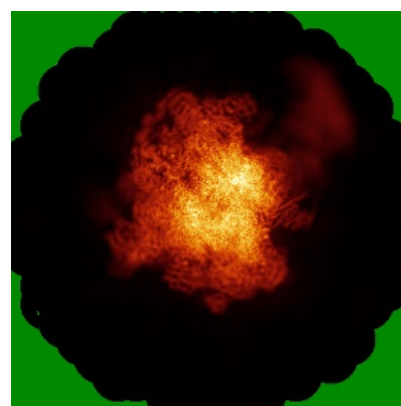
### 6.4.1 Primary map



X



Y

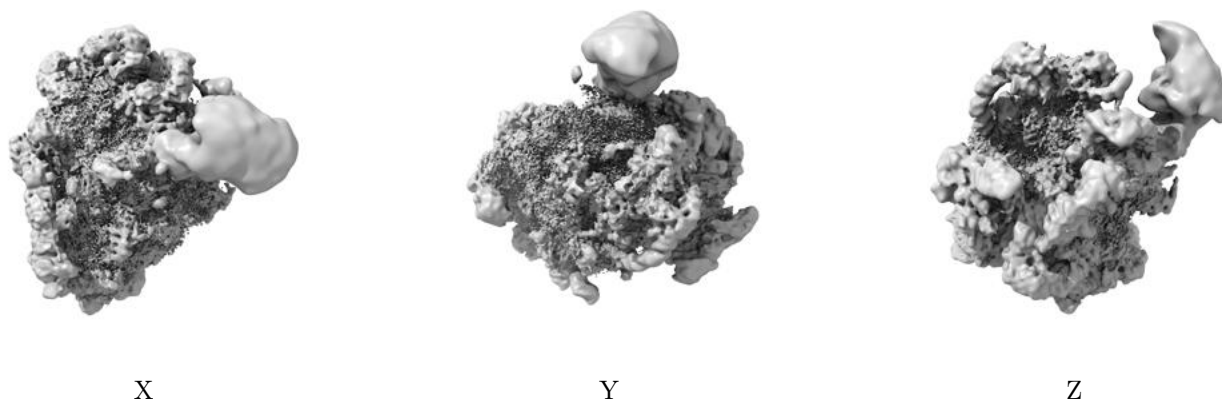


Z

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 [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

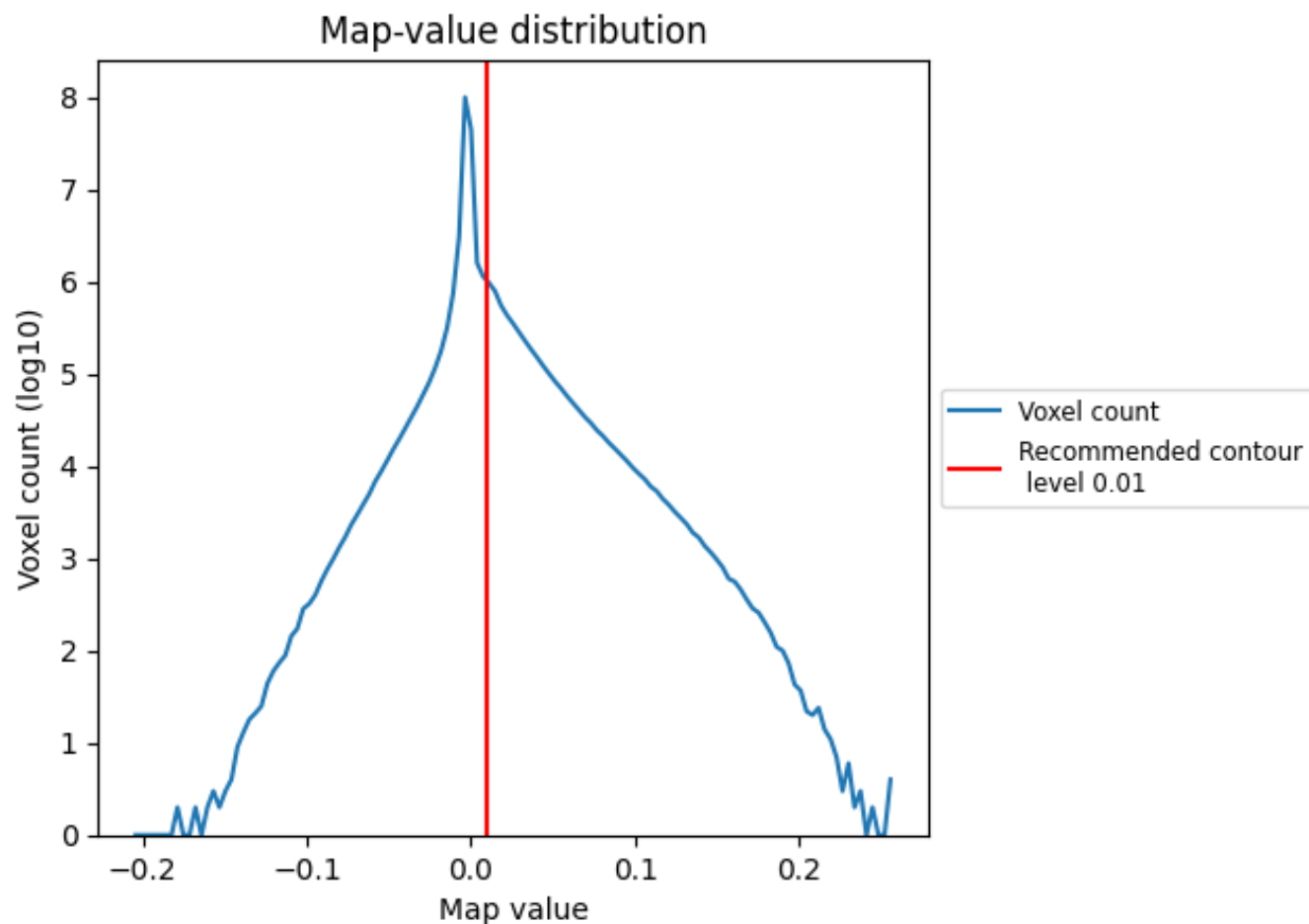
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

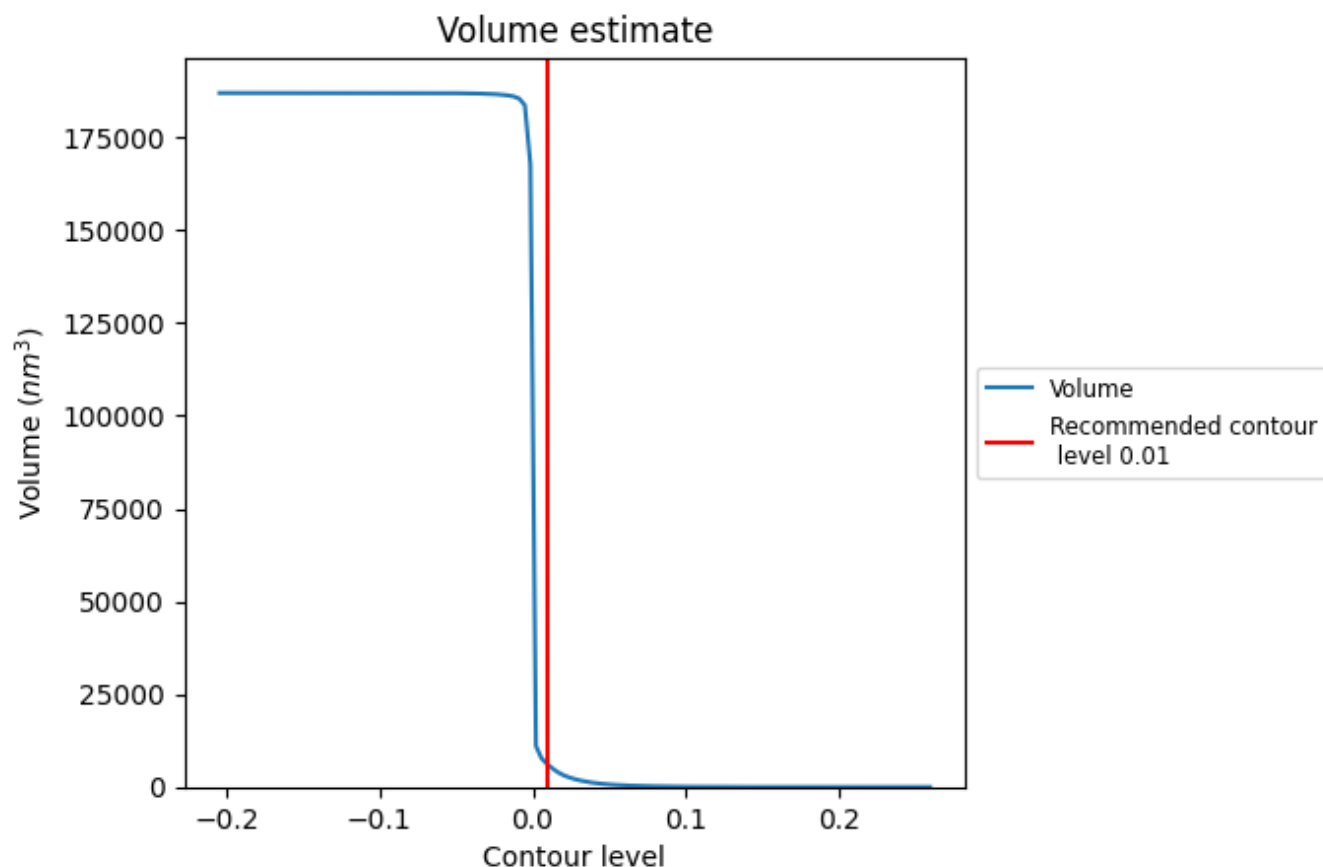
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

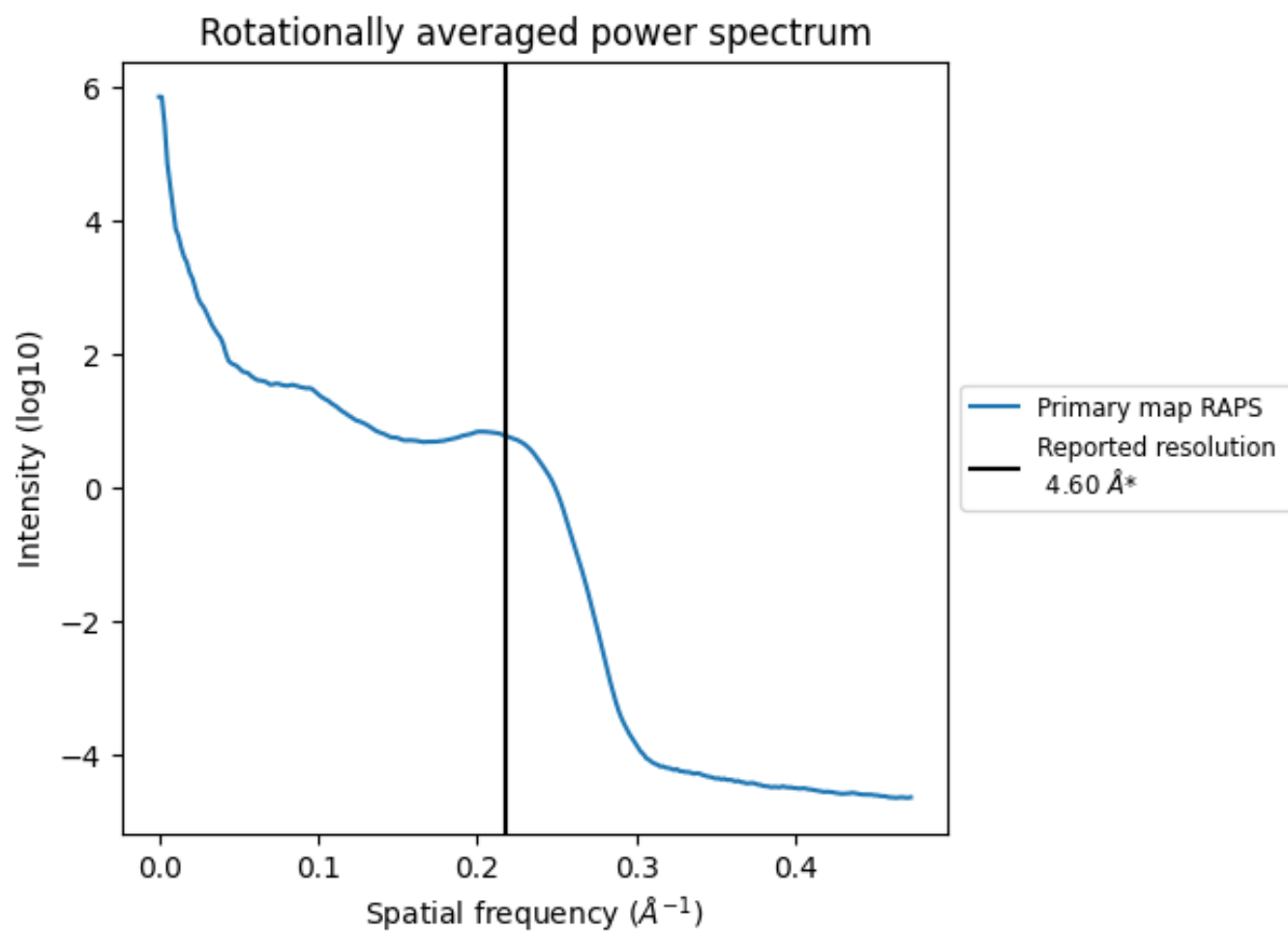
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5975  $\text{nm}^3$ ; 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 ⓘ

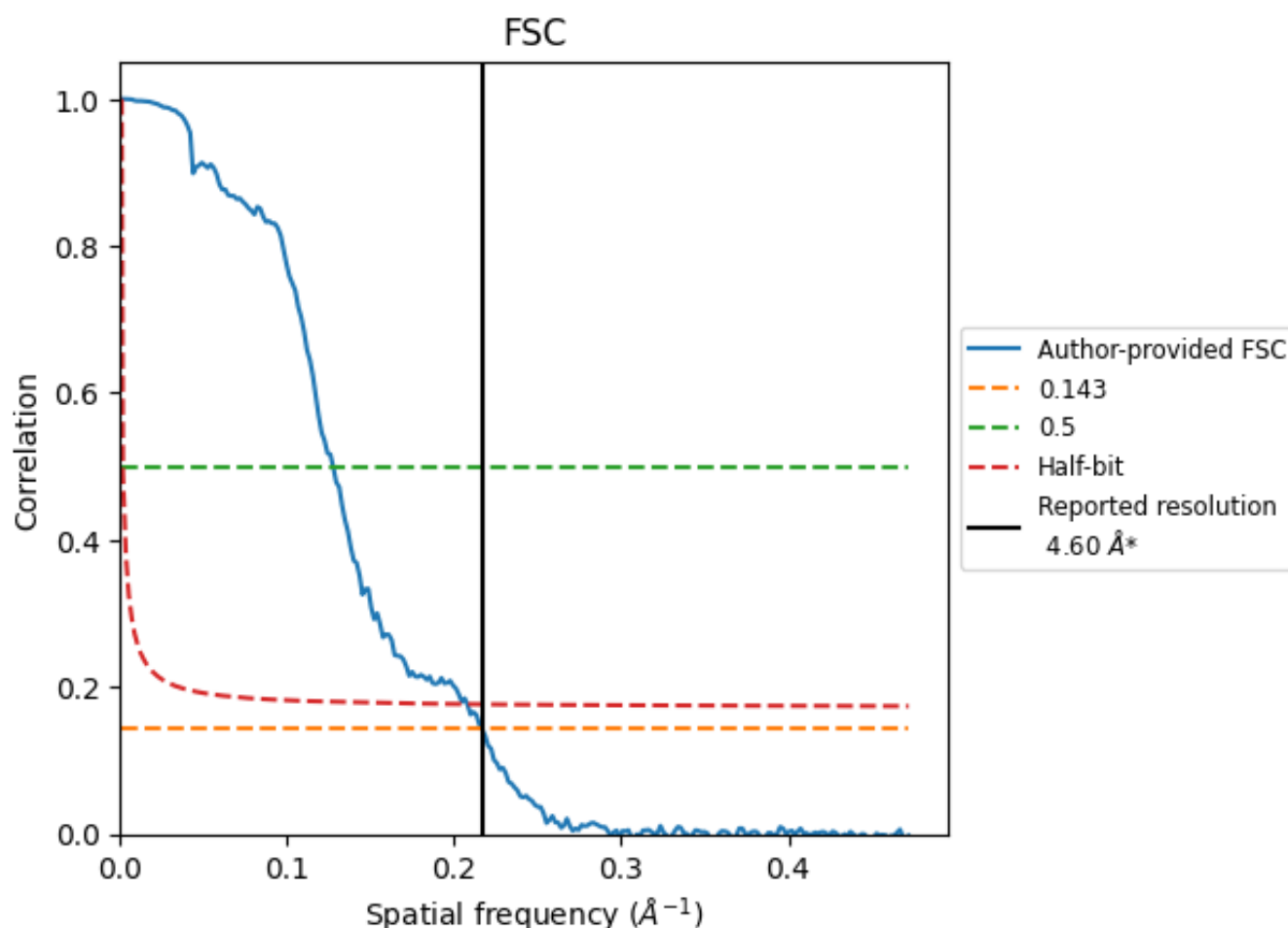


\*Reported resolution corresponds to spatial frequency of 0.217 Å<sup>-1</sup>

## 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<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

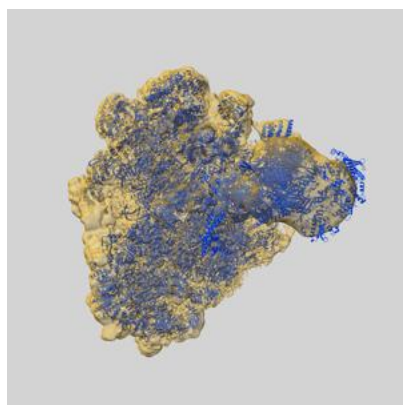
| Resolution estimate (Å)   | Estimation criterion (FSC cut-off) |      |          |
|---------------------------|------------------------------------|------|----------|
|                           | 0.143                              | 0.5  | Half-bit |
| Reported by author        | 4.60                               | -    | -        |
| 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.

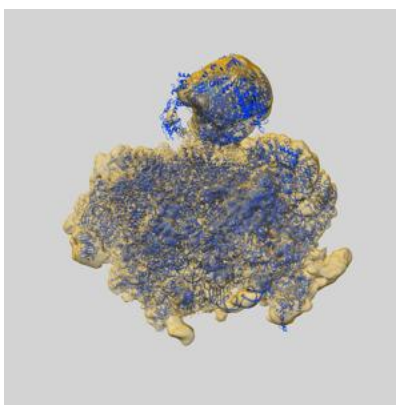
## 9 Map-model fit [i](#)

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](#).

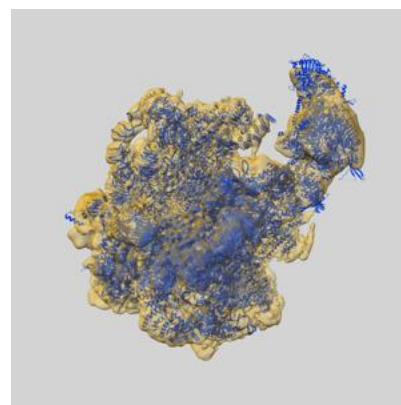
### 9.1 Map-model overlay [i](#)



X



Y

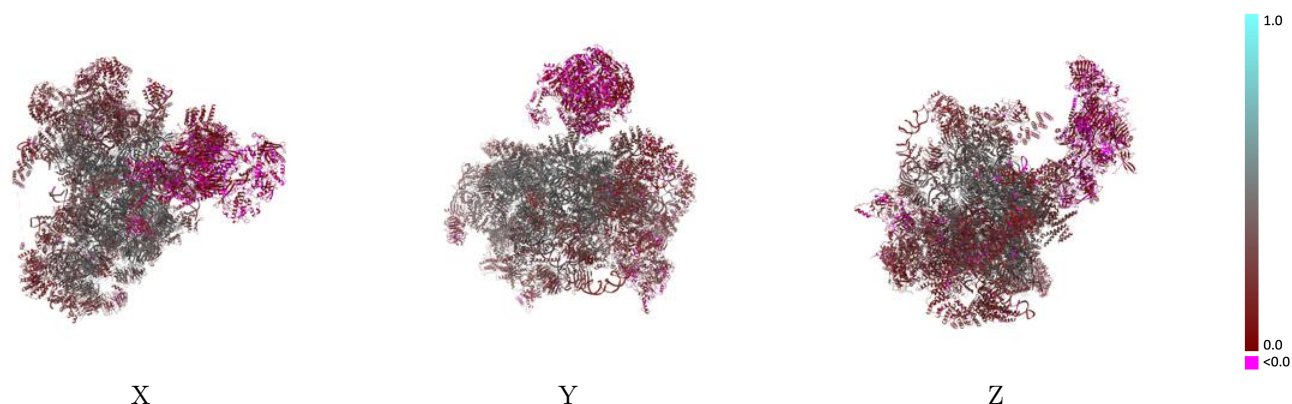


Z

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

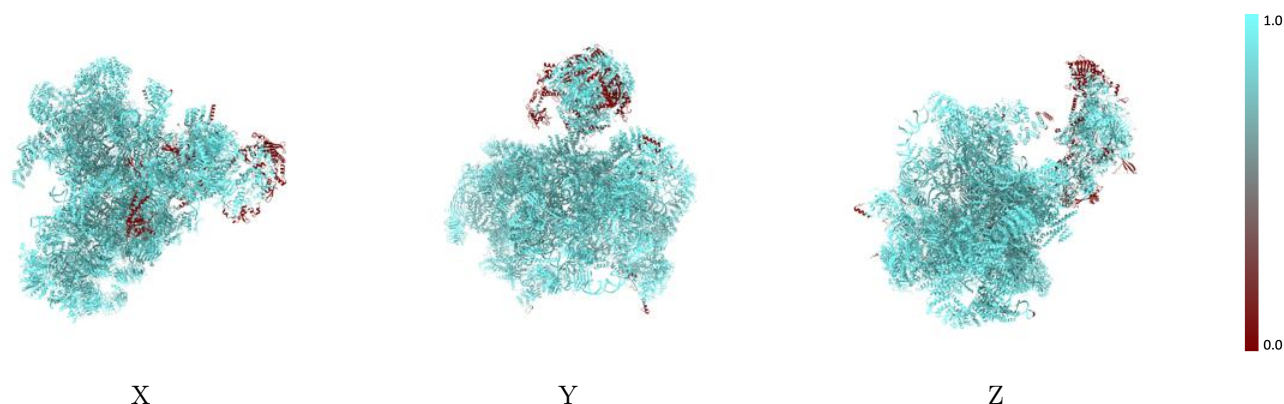


## 9.2 Q-score mapped to coordinate model [i](#)



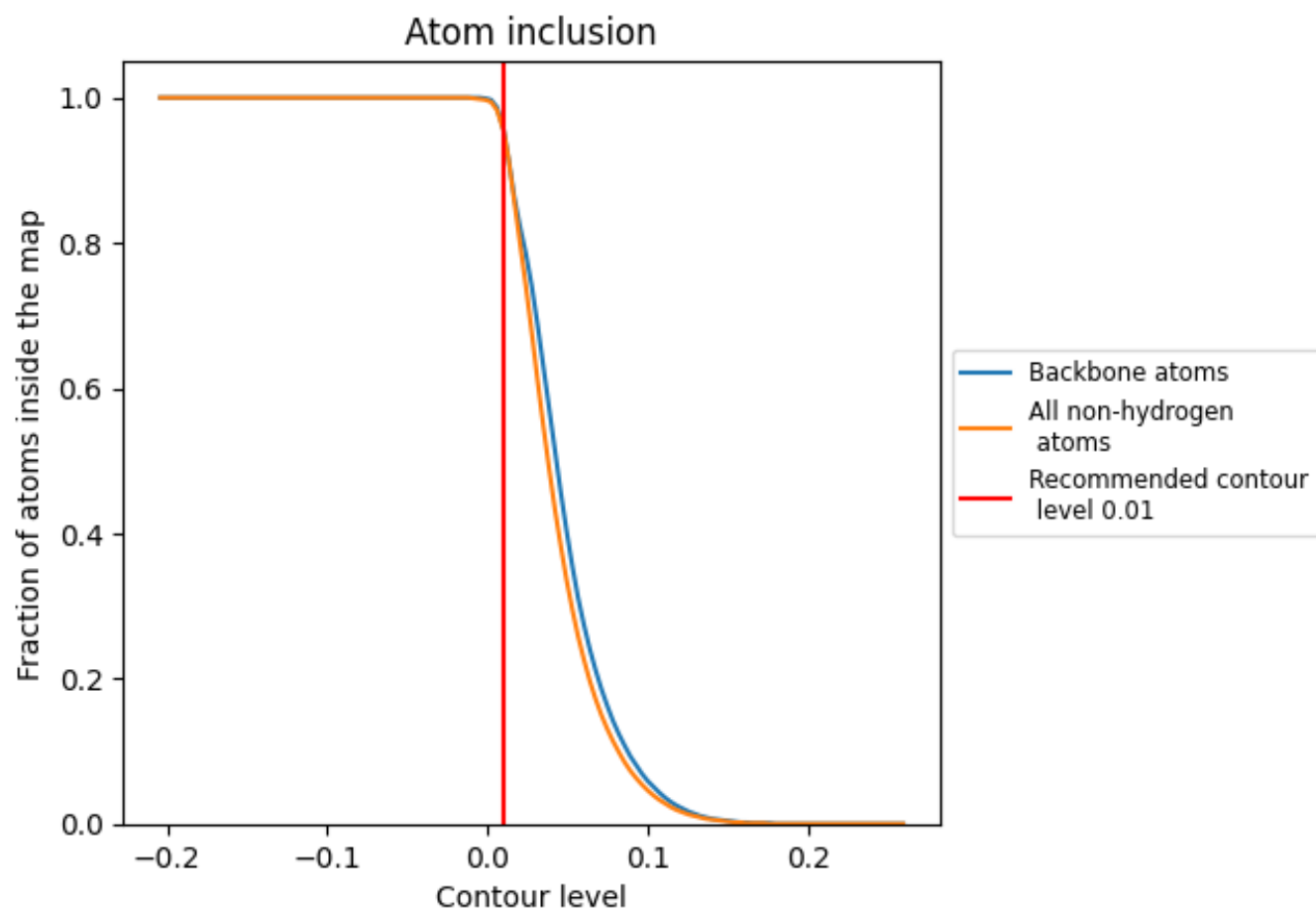
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).







































































## 9.4 Atom inclusion [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 |