



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 07:59 AM UTC

PDB ID : 9G33 / pdb_00009g33
EMDB ID : EMD-50991
Title : Stalled 90S - Utp23-Krr1-deltaC3
Authors : Thoms, M.; Berninghausen, O.; Beckmann, R.
Deposited on : 2024-07-11
Resolution : 3.05 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

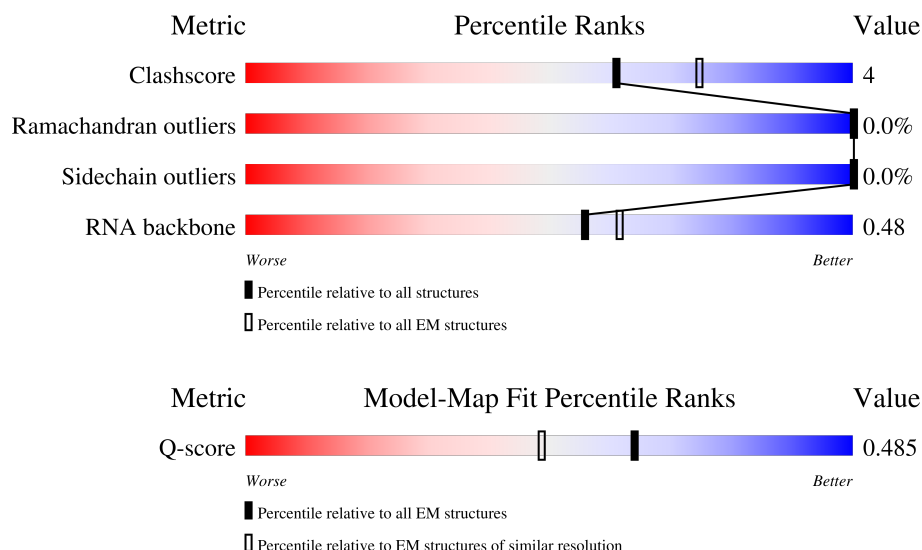
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.05 Å.

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



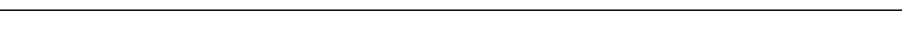
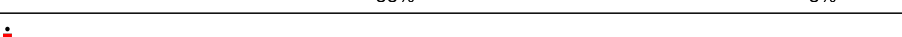
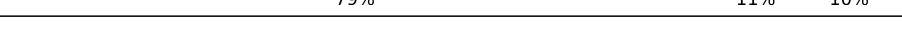
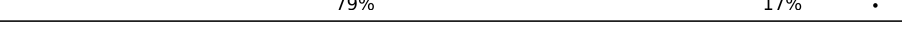
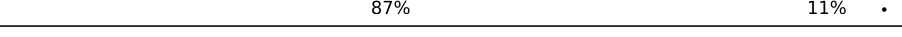
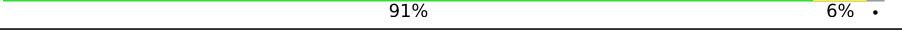
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13971 (2.55 - 3.55)

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	D3	1808	
2	D2	700	
3	D4	333	

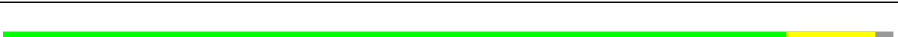
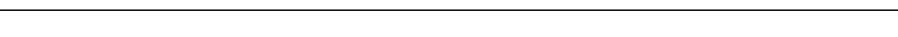
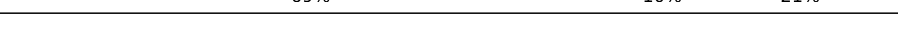
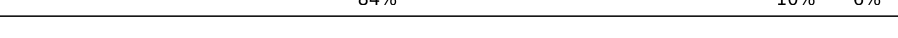
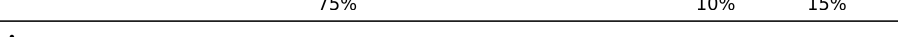
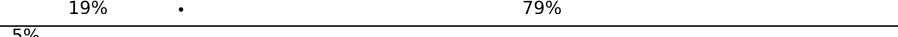
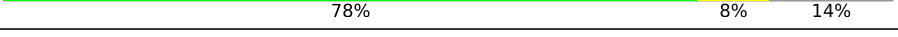
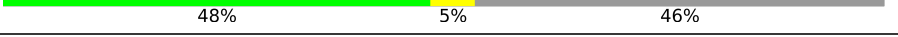
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Mol	Chain	Length	Quality of chain
4	CJ	290	
5	CK	593	
6	CL	1183	
7	DY	135	
8	UX	189	
9	JF	252	
9	JG	252	
10	CA	327	
10	CB	327	
11	UB	810	
12	UC	610	
13	UE	643	
14	UH	713	
15	UK	250	
16	UL	943	
17	UM	817	
18	UO	513	
19	UP	214	
20	US	552	
21	CF	126	
21	CG	126	
22	CI	183	
23	JE	357	
24	JH	483	
25	JJ	274	

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Mol	Chain	Length	Quality of chain
26	JK	534	
27	JM	217	
28	JQ	206	
29	DF	225	
30	DI	200	
31	DJ	197	
32	DS	146	
33	JC	707	
34	DE	261	
35	DX	145	
36	DW	130	
37	DG	236	
38	DL	156	
39	CH	573	
40	Dc	67	
41	DQ	143	
42	CE	511	
43	CD	504	
44	UN	899	
45	UF	440	
46	UG	554	
47	JN	346	
48	JO	316	
49	CM	367	
50	UZ	274	

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Mol	Chain	Length	Quality of chain
51	JP	489	 81%13%6%
52	UR	594	 73%8%19%
53	UU	939	 79%11%10%
54	UD	776	 77%11%12%
55	UQ	896	 83%10%7%
56	UA	923	 81%10%10%
57	UI	575	 22%77%
58	UJ	1769	 16%92%. .
59	DH	190	 79%11%11%
60	UT	2493	 11%90%.6%
61	JA	1056	 7%71%14%16%
61	JB	1056	 27%67%14%19%

2 Entry composition

There are 63 unique types of molecules in this entry. The entry contains 203584 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D3	886	Total	C	N	O	P	0	0
			18883	8442	3361	6194	886		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D2	519	Total	C	N	O	P	0	0
			11078	4950	1970	3639	519		

- Molecule 3 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D4	176	Total	C	N	O	P	0	0
			3731	1670	650	1235	176		

- Molecule 4 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CJ	282	Total	C	N	O	S	0	0
			2281	1432	426	416	7		

- Molecule 5 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	CK	199	Total	C	N	O	S	0	0
			1584	984	280	316	4		

- Molecule 6 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CL	818	Total	C	N	O	S	0	0
			6472	4155	1141	1147	29		

- Molecule 7 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	DY	96	Total	C	N	O	0	0
			761	487	137	137		

- Molecule 8 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	UX	174	Total	C	N	O	S	0	0
			1396	890	255	241	10		

- Molecule 9 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	JG	231	Total	C	N	O	S	0	0
			1789	1137	308	334	10		
9	JF	217	Total	C	N	O	S	0	0
			1647	1047	281	308	11		

- Molecule 10 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CA	241	Total	C	N	O	S	0	0
			1868	1185	334	339	10		
10	CB	227	Total	C	N	O	S	0	0
			1778	1129	319	320	10		

- Molecule 11 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	UB	491	Total	C	N	O	S	0	0
			3660	2331	643	675	11		

- Molecule 12 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	UC	128	Total	C	N	O	0	0
			1027	633	204	190		

- Molecule 13 is a protein called U3 small nucleolar RNA-associated protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	UE	478	Total	C	N	O	S	0	0
			3773	2401	647	712	13		

- Molecule 14 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	UH	581	Total	C	N	O	S	0	0
			3518	2204	633	678	3		

- Molecule 15 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	UK	240	Total	C	N	O	S	0	0
			1985	1233	384	361	7		

- Molecule 16 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	UL	849	Total	C	N	O	S	0	0
			6393	4104	1080	1185	24		

- Molecule 17 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	UM	160	Total	C	N	O	S	0	0
			1269	800	224	236	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	UO	494	Total	C	N	O	S	0	0
			3905	2459	700	734	12		

- Molecule 19 is a protein called U3 small nucleolar RNA-associated protein 16.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	UP	60	Total	C	N	O	0	0
			419	259	81	79		

- Molecule 20 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	US	542	Total	C	N	O	S	0	0
			3967	2581	663	711	12		

- Molecule 21 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CF	123	Total	C	N	O	S	0	0
			932	594	160	174	4		
21	CG	121	Total	C	N	O	S	0	0
			916	583	158	171	4		

- Molecule 22 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	CI	182	Total	C	N	O	S	0	0
			1531	967	287	270	7		

- Molecule 23 is a protein called U3 small nucleolar ribonucleoprotein protein LCP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	JE	136	Total	C	N	O	S	0	0
			959	580	180	197	2		

- Molecule 24 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	JH	257	Total	C	N	O		0	0
			1276	762	257	257			

- Molecule 25 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	JJ	96	Total	C	N	O		0	0
			500	300	101	99			

- Molecule 26 is a protein called Protein BFR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	JK	42	Total	C	N	O		0	0
			330	210	53	67			

- Molecule 27 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	JM	135	Total	C	N	O	S	0	0
			1100	697	200	199	4		

- Molecule 28 is a protein called Regulator of rDNA transcription protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	JQ	157	Total	C	N	O		0	0
			860	525	164	171			

- Molecule 29 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	DF	209	Total	C	N	O	S	0	0
			1638	1029	296	310	3		

- Molecule 30 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	DI	175	Total	C	N	O	S	0	0
			1350	836	264	248	2		

- Molecule 31 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	DJ	177	Total	C	N	O	S	0	0
			1406	889	270	246	1		

- Molecule 32 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	DS	104	Total	C	N	O		0	0
			526	315	105	106			

- Molecule 33 is a protein called Ribosome biogenesis protein ENP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	JC	352	Total	C	N	O	S	0	0
			2695	1704	465	517	9		

- Molecule 34 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	DE	236	Total	C	N	O	S	0	0
			1836	1178	339	316	3		

- Molecule 35 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	DX	103	Total	C	N	O	S	0	0
			774	494	141	137	2		

- Molecule 36 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	DW	127	Total	C	N	O	S	0	0
			954	612	167	172	3		

- Molecule 37 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	DG	209	Total	C	N	O	S	0	0
			1577	999	304	272	2		

- Molecule 38 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	DL	138	Total	C	N	O	S	0	0
			1052	673	195	181	3		

- Molecule 39 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	CH	452	Total	C	N	O	S	0	0
			3531	2248	616	658	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Dc	63	Total	C	N	O	S	0	0
			498	306	99	92	1		

- Molecule 41 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 42 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	CE	436	Total	C	N	O	S		
			3038	1912	541	578	7	0	0

- Molecule 43 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	CD	380	Total	C	N	O	S		
			2802	1771	489	535	7	0	0

- Molecule 44 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	UN	188	Total	C	N	O	S		
			1441	894	272	273	2	0	0

- Molecule 45 is a protein called U3 small nucleolar RNA-associated protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	UF	379	Total	C	N	O	S		
			2795	1791	500	493	11	0	0

- Molecule 46 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	UG	515	Total	C	N	O	S		
			3917	2462	706	738	11	0	0

- Molecule 47 is a protein called Protein FAF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	JN	186	Total	C	N	O	S		
			1363	844	266	250	3	0	0

- Molecule 48 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	JO	190	Total	C	N	O	S	0	0
			1483	955	260	258	10		

- Molecule 49 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	CM	363	Total	C	N	O	S	0	0
			2768	1776	469	512	11		

- Molecule 50 is a protein called Ribosome biogenesis protein UTP30.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	UZ	254	Total	C	N	O	S	0	0
			1963	1256	351	349	7		

- Molecule 51 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	JP	460	Total	C	N	O	S	0	0
			3718	2330	674	698	16		

- Molecule 52 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	UR	480	Total	C	N	O	S	0	0
			3751	2379	662	700	10		

- Molecule 53 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	UU	846	Total	C	N	O	S	0	0
			6606	4197	1139	1249	21		

- Molecule 54 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	UD	680	Total	C	N	O	S	0	0
			5176	3286	901	968	21		

- Molecule 55 is a protein called NET1-associated nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	UQ	837	Total	C	N	O	S	0	0
			6559	4181	1110	1249	19		

- Molecule 56 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	UA	834	Total	C	N	O	S	0	0
			6602	4203	1135	1246	18		

- Molecule 57 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	UI	134	Total	C	N	O	S	0	0
			959	614	171	172	2		

- Molecule 58 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	UJ	1701	Total	C	N	O	S	0	0
			10158	6323	1863	1958	14		

- Molecule 59 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	DH	170	Total	C	N	O	0	0
			1207	776	210	221		

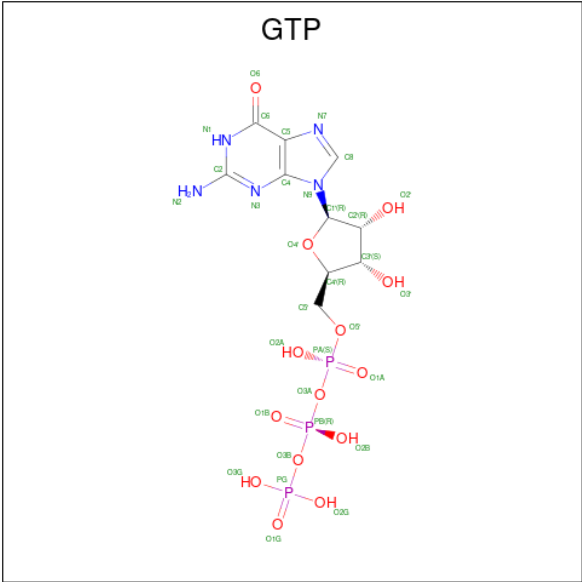
- Molecule 60 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	UT	2345	Total	C	N	O	S	0	0
			13871	8770	2561	2529	11		

- Molecule 61 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	JA	891	Total	C	N	O	S	0	0
			6631	4260	1157	1190	24		
61	JB	856	Total	C	N	O	S	0	0
			6345	4083	1094	1145	23		

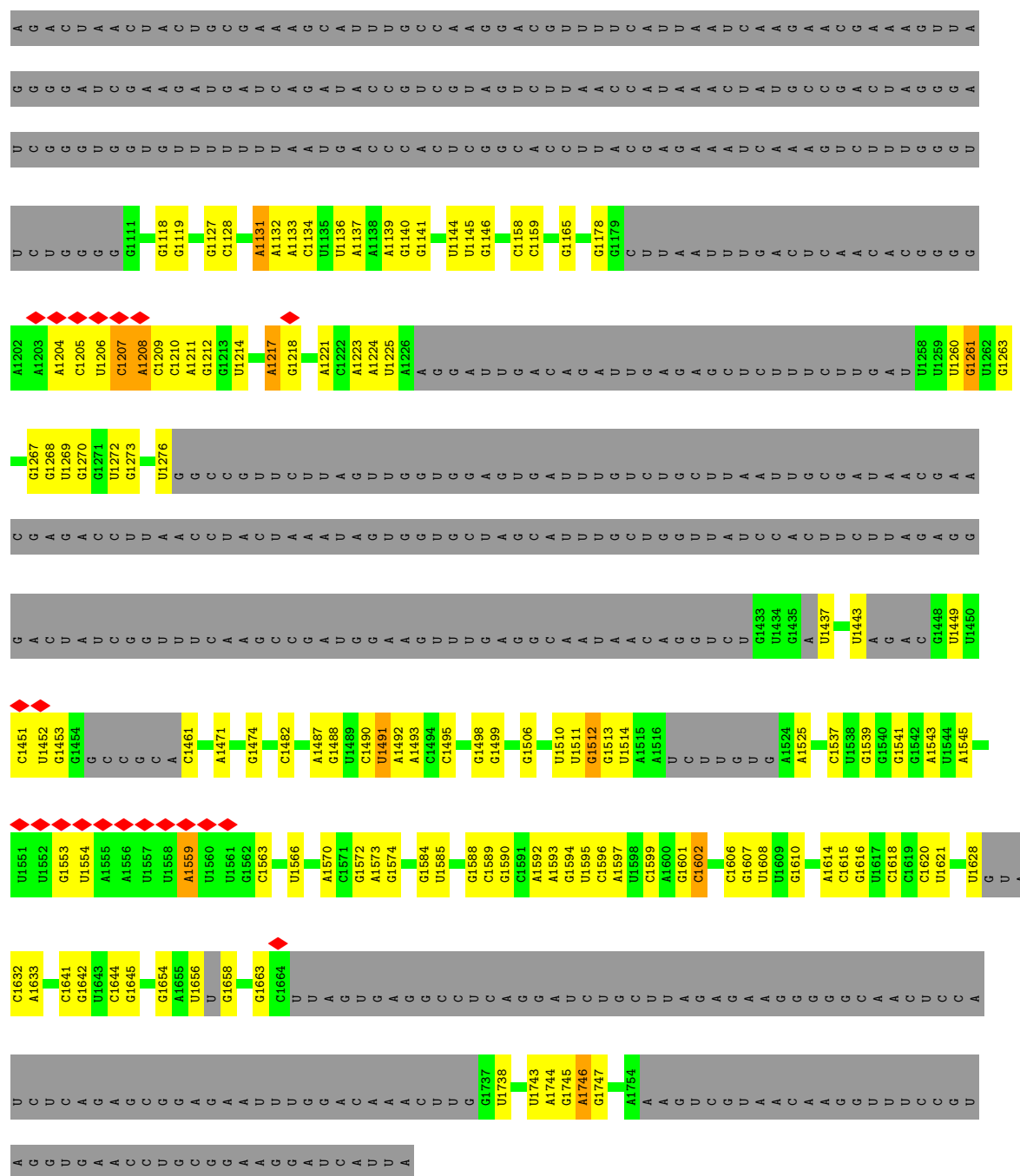
- Molecule 62 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



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

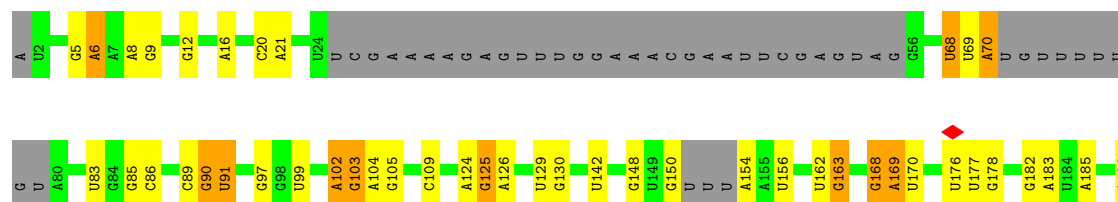
- Molecule 63 is ZINC ION (CCD ID: ZN) (formula: Zn).

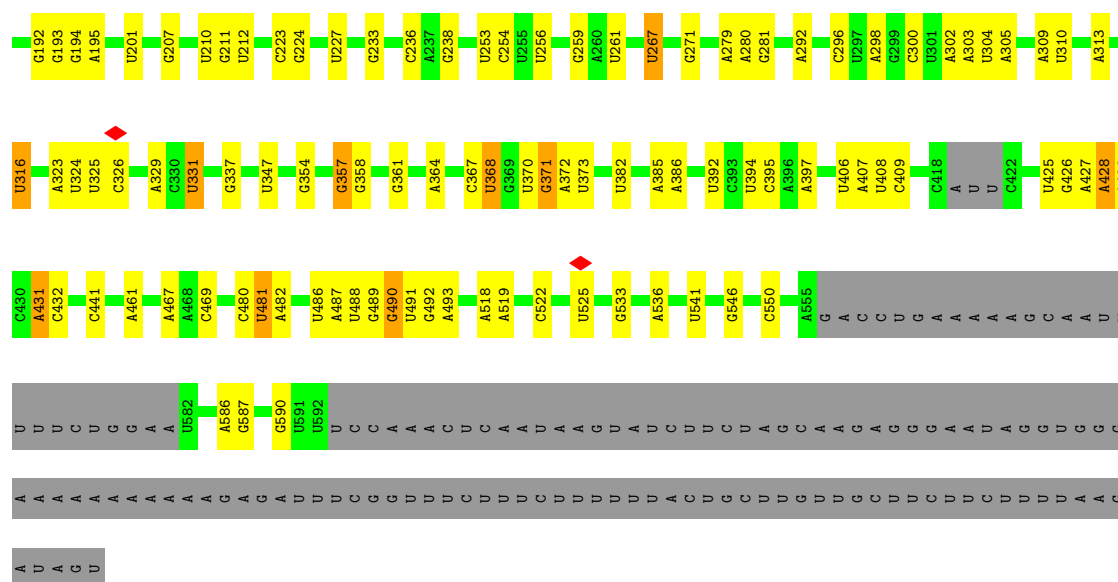
Mol	Chain	Residues	Atoms		AltConf
63	UX	1	Total	Zn	0
			1	1	



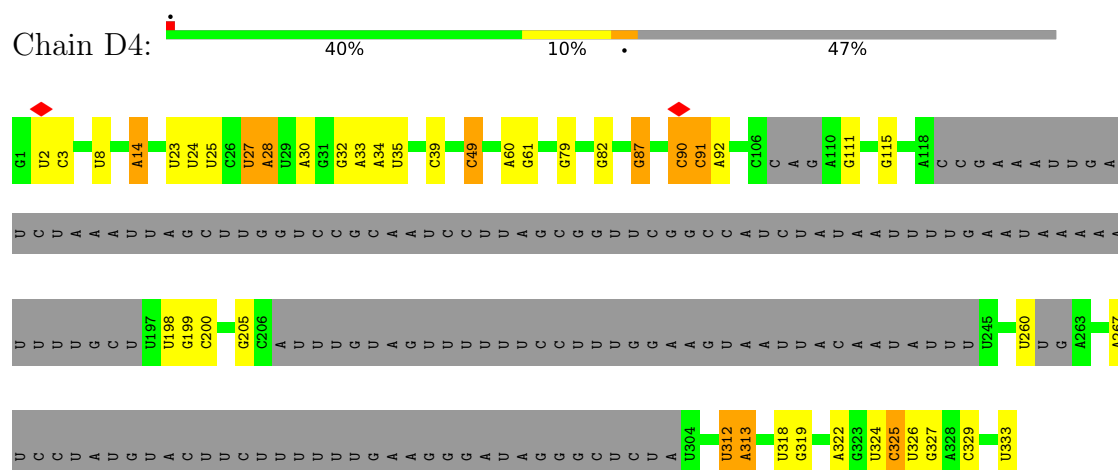
• Molecule 2: 5' ETS

Chain D2: 53% 18% 26%

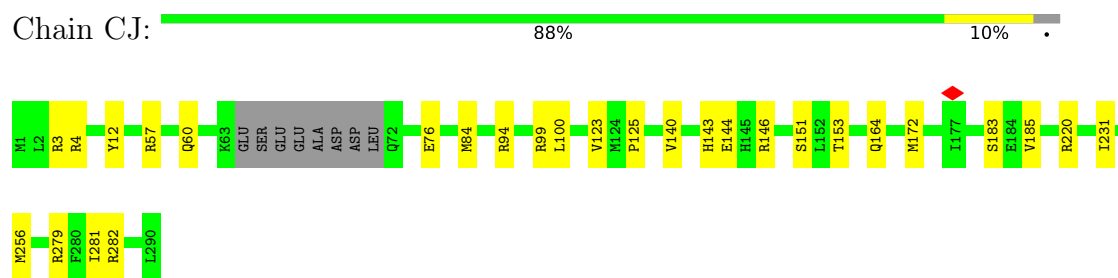




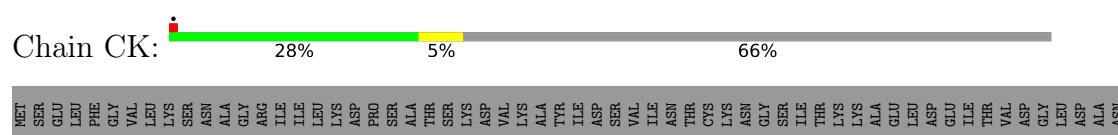
- Molecule 3: U3 snoRNA



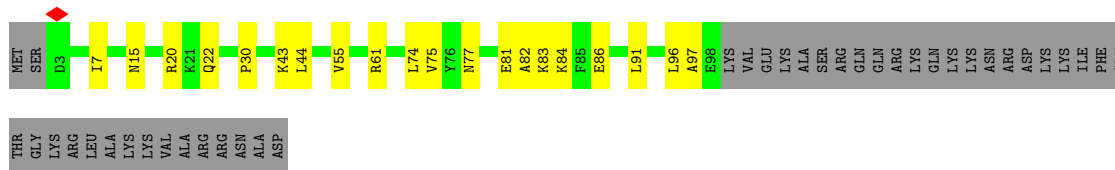
- Molecule 4: U3 small nucleolar ribonucleoprotein protein IMP4



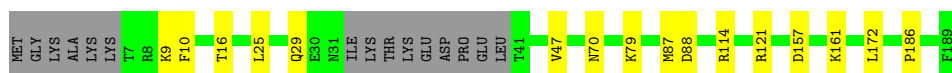
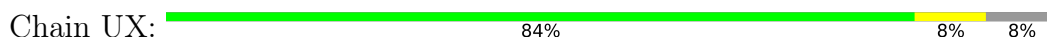
- Molecule 5: U3 small nucleolar RNA-associated protein MPP10



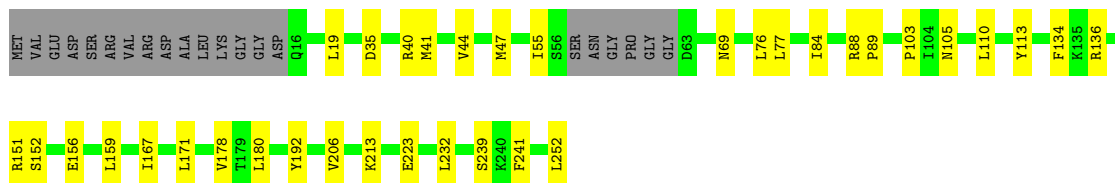
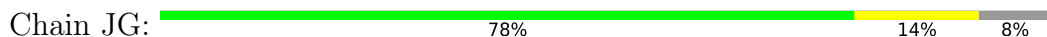
- Molecule 7: 40S ribosomal protein S24-A



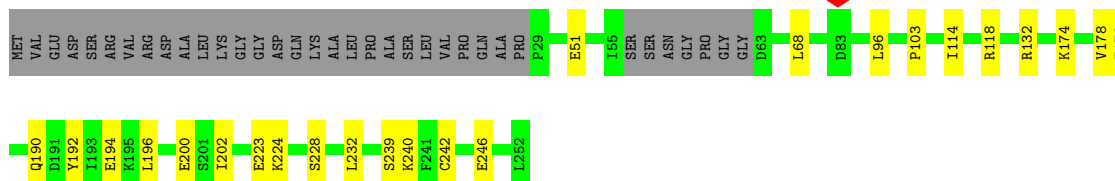
- Molecule 8: rRNA-processing protein FCF1



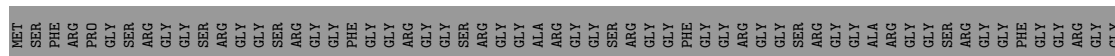
- Molecule 9: Ribosomal RNA small subunit methyltransferase NEP1

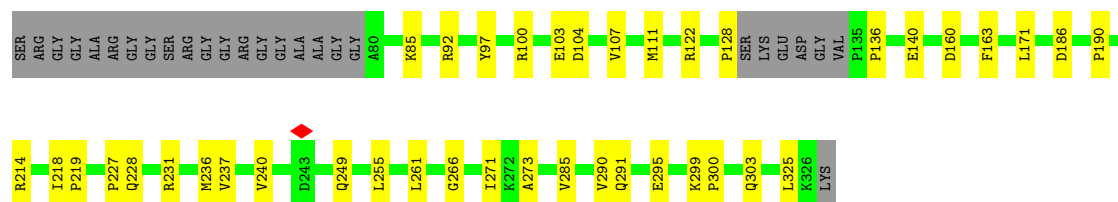


- Molecule 9: Ribosomal RNA small subunit methyltransferase NEP1



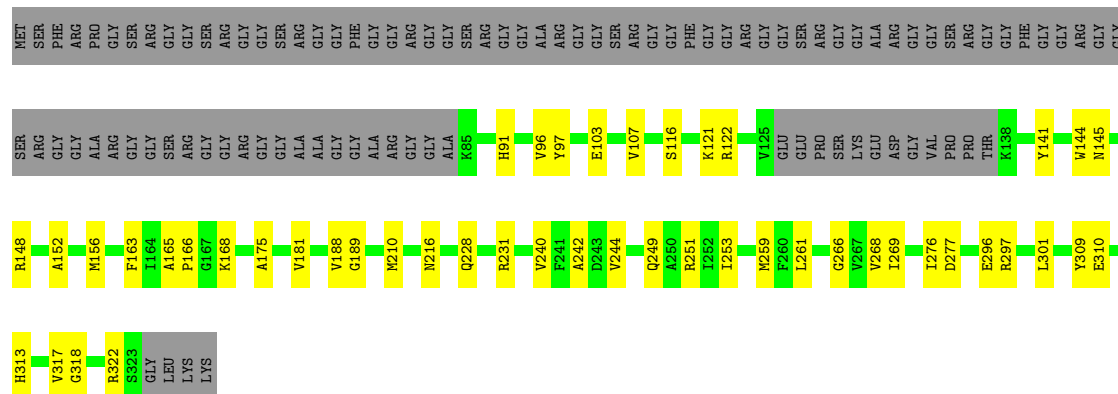
- Molecule 10: rRNA 2'-O-methyltransferase fibrillar





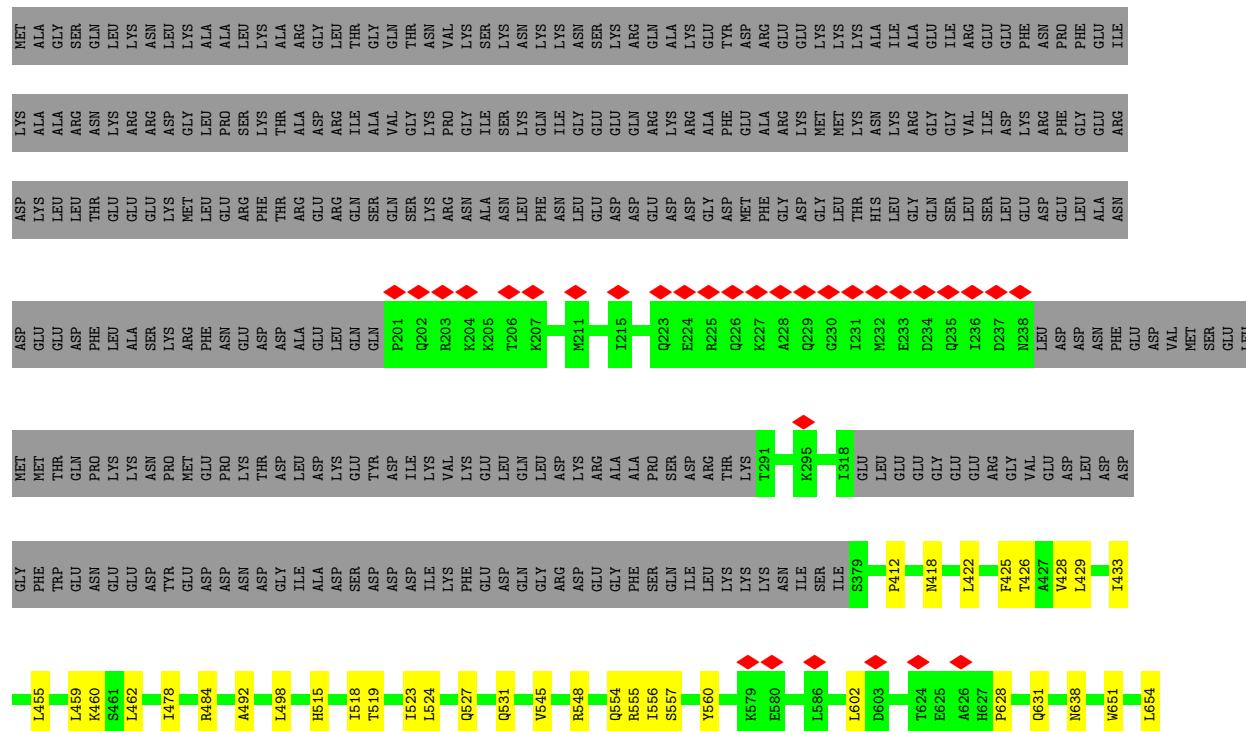
• Molecule 10: rRNA 2'-O-methyltransferase fibrillar

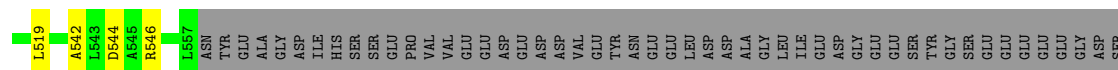
Chain CB: 55% 15% 31%



• Molecule 11: Nucleolar complex protein 14

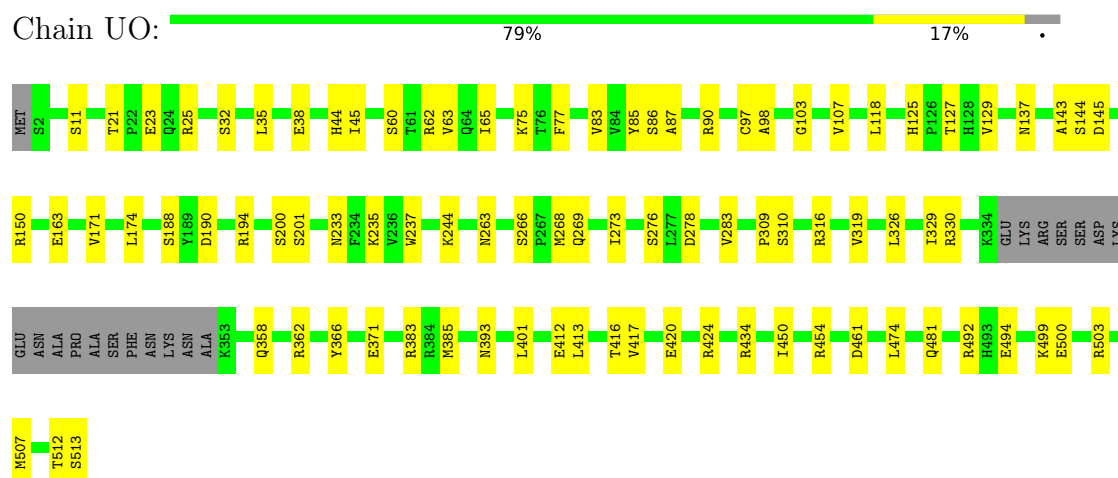
Chain UB: 55% 6% 39%



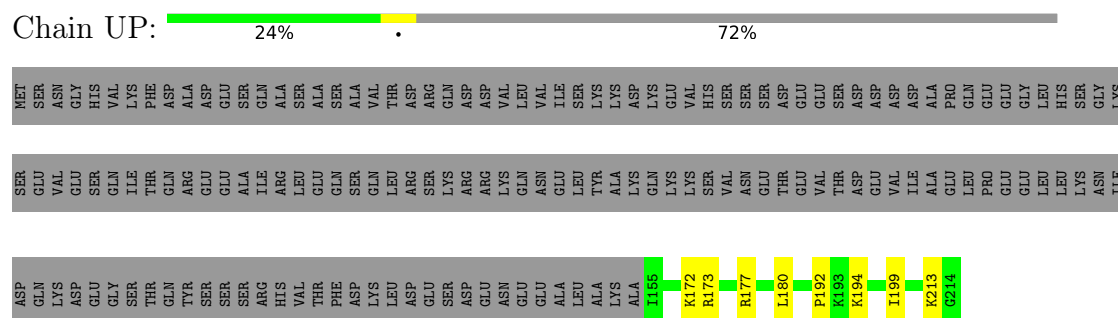




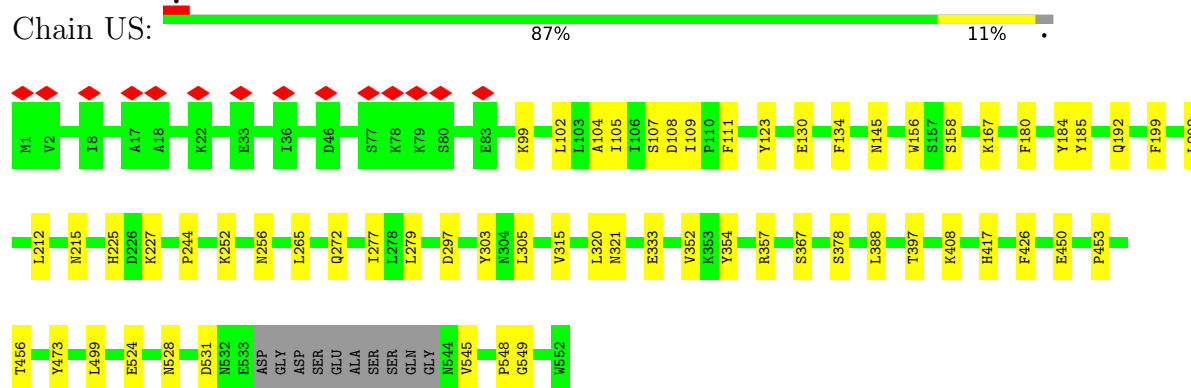
- Molecule 18: U3 small nucleolar RNA-associated protein 15



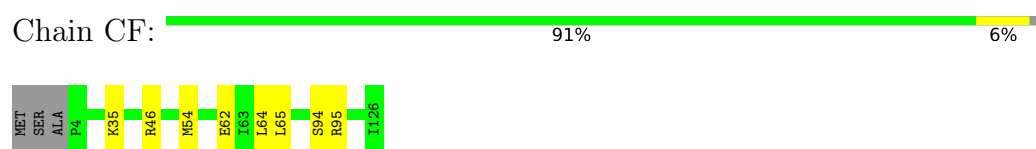
- Molecule 19: U3 small nucleolar RNA-associated protein 16



- Molecule 20: Nucleolar complex protein 4



- Molecule 21: 13 kDa ribonucleoprotein-associated protein

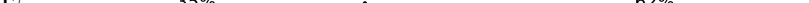


- Molecule 21: 13 kDa ribonucleoprotein-associated protein

MTT	SER	ALA	PRO	N5	P6	K7	A8	L33	K34	E39	K42	R46	M54	P60	I61	E62	I63	L64	Y78	R84	V85	P96	V97	I98	A99	A100	L125	I1E
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- Chain CI:  86% 14%

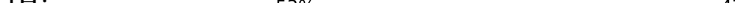
MET	V2	K22	Q23	D24	Q25	D29	K33	I50	L57	K60	L61	S62	L63	L64	P65	P66	Tl02	R108	Q125	V128	K129	E132	N153	R154	E155	D162	Y173	R174	N175	D179	S183
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- Chain JE:  35% 5% 60%

[illegible]

LEU	ASP	LYS	LEU	THR	ARG	ALA	TYR	VAL	LYS	MET	GLU	LYS	GLU	TYR	LYS	ASP	ALA	GLU	LYS	ARG	ALA	LEU	GLU	LYS	SER	THR	LEU	VAL	ASN	HIS	SER	SER	GLY	ASN	ASP	ASP	SER	ASP	GLU	GLU	ASP	GLU	ILE	ALA	TYR	PRO	ARG	ASN	THR	SER	GLY	ILE	ASN	THR	SER	GLN
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Protein	Number of Mutations
D324	10
S330	10
L334	10
T338	10
L357	10
LYS	10
LYS	10
SER	10
SER	10
ALA	10
TTR	10
ARG	10
VAL	10
GLU	10
THR	10
ALA	10
LYS	10
GLN	10
GLU	10
ASN	10
ASP	10
ASN	10
ASP	10
ASP	10
GLU	10
THR	10
GLY	10
VAL	10
THR	10
LYS	10
PRO	10
PRO	10
ILE	10
THR	10
ALA	10
VAL	10
LEU	10
PRO	10
PRO	10
PRO	10
GLN	10
T222	10
Q243	10
E251	10
S252	10
S253	10
P256	10
D257	10
G263	10
I299	10
R316	10
V319	10

- Chain JH: 

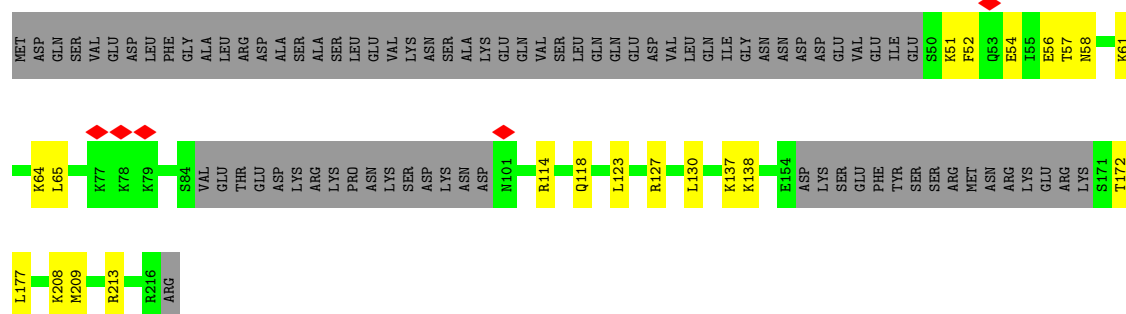
[illegible]

GLY	ASP	TYR	LYS	GLU	GLU	GLU	ILE	VAL	GLU	ILE	ASP	GLU	GLY	ALA	ALA	MET	PHE	GLU	GLN	TYR	PHE	LYS	SER	SER	ASP	ASP	PHE	ASN	SER	LEU	GLY	SER	TYR	LYS	ILE	ASP	LYS	ARG	GLU	LYS	GLU	SER	GLN	VAL	GLU	ASP	MET	GLN	ASP	SER
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

GLU	PRO	LEU	ALA	ASN	GLU	GLN	ASN	THR	SER	ARG	GLY	ASN	ILE	SER	SER	GLY	LEU	LYS	SER	GLY	GLU	GLY	VAL																																			
S255			A262		S268	N269		A272		I279		E282	T293		H297	S298		L311	Y312		E327	T328		V332	R333	E334	A335	T336		S340		A349		F364		D377		A381	L382		F397	R398	I399	L400	ASP	GLY	SER	ASN	G406	E407	D408	A409	T410	R411	V412	L413		T424

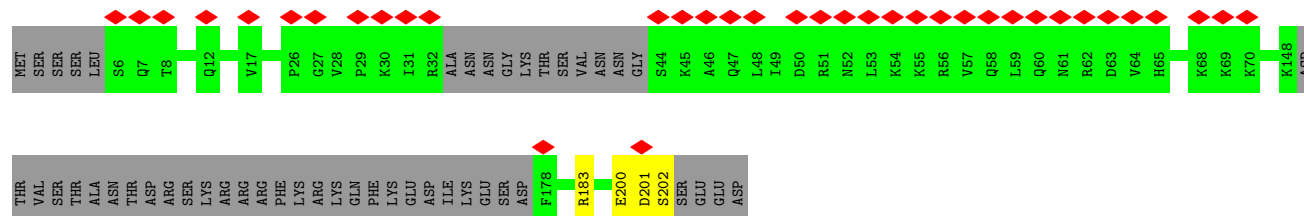
- Molecule 27: rRNA-processing protein FCF2

Chain JM:  53% 10% 38%



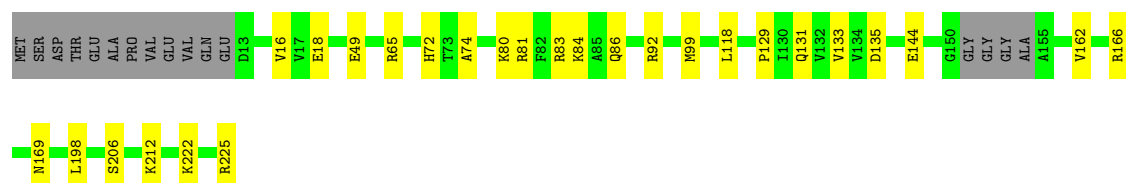
- Molecule 28: Regulator of rDNA transcription protein 14

Chain JQ:  18% 74% 24%



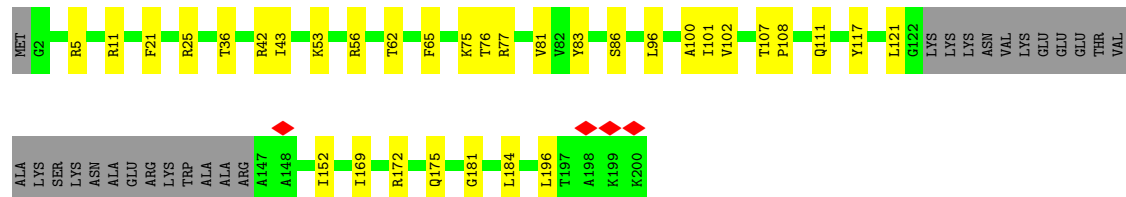
- Molecule 29: 40S ribosomal protein S5

Chain DF:  81% 12% 7%



- Molecule 30: 40S ribosomal protein S8-A

Chain DI:  71% 16% 12%

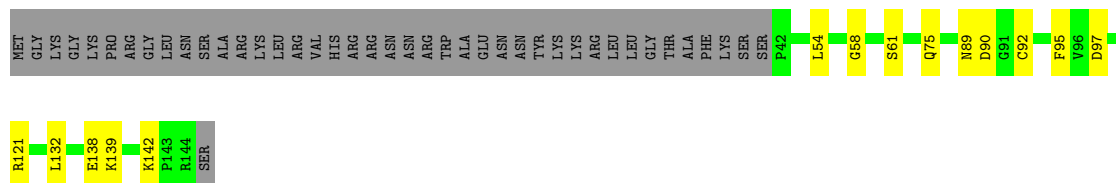


- Molecule 31: 40S ribosomal protein S9-A

Chain DJ:  82% 8% 10%

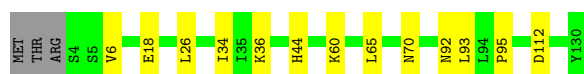
- Molecule 35: 40S ribosomal protein S23-A

Chain DX:  61% 10% 29%



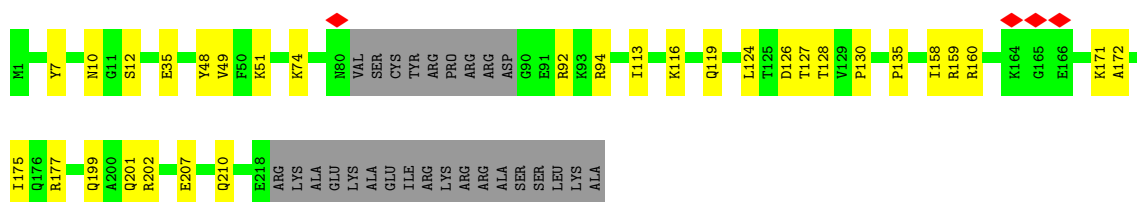
- Molecule 36: 40S ribosomal protein S22-A

Chain DW:  88% 10% .



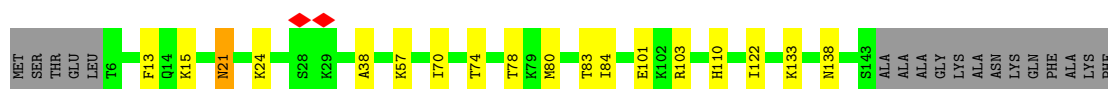
- Molecule 37: 40S ribosomal protein S6-A

Chain DG:  75% 13% 11%



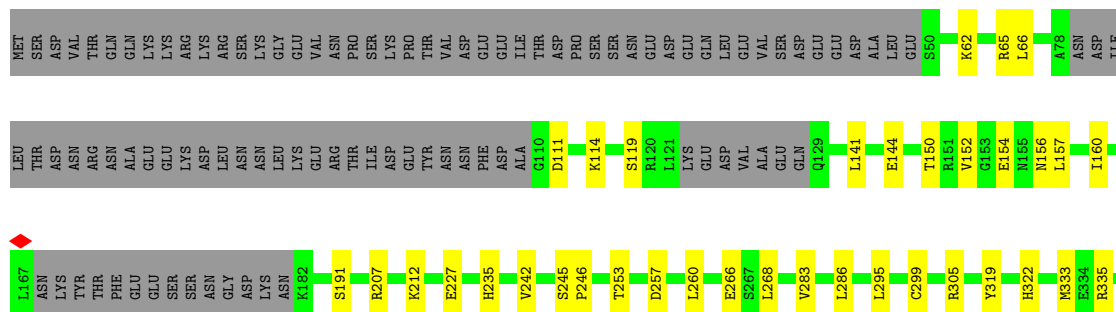
- Molecule 38: 40S ribosomal protein S11-A

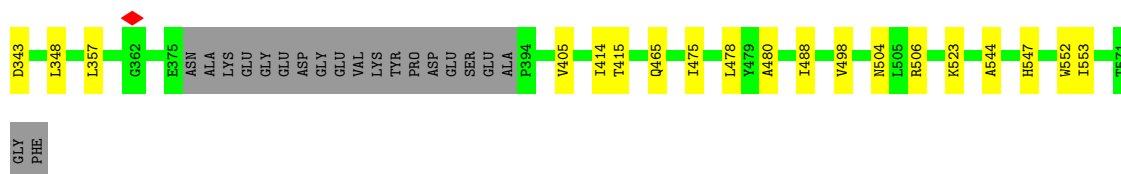
Chain DL:  77% 11% . 12%



- Molecule 39: Ribosomal RNA-processing protein 9

Chain CH:  69% 10% 21%





- Molecule 40: 40S ribosomal protein S28-A

Chain Dc: 84% 10% 6%



- Molecule 41: 40S ribosomal protein S16-A

Chain DQ: 72% 15% 13%



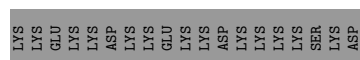
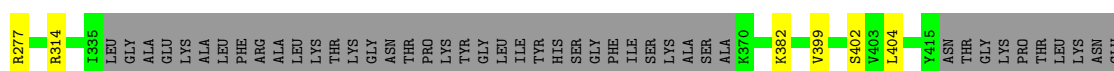
- Molecule 42: Nucleolar protein 58

Chain CE: 75% 10% 15%



- Molecule 43: Nucleolar protein 56

Chain CD: 70% 5% 25%

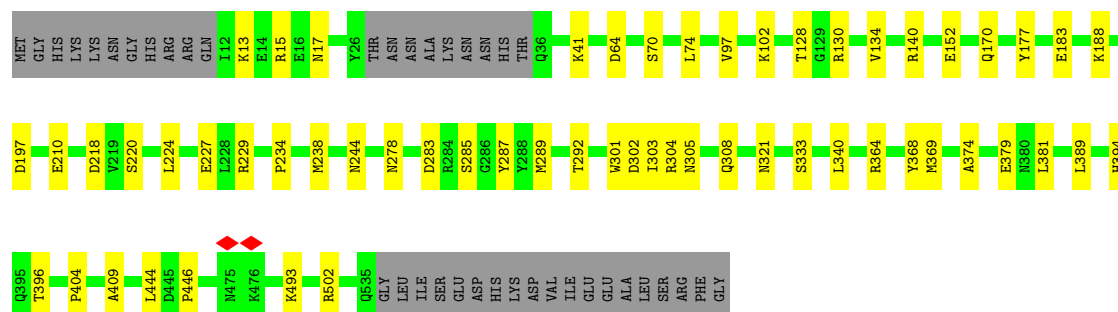


- Molecule 44: U3 small nucleolar RNA-associated protein 14

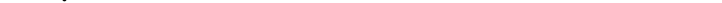


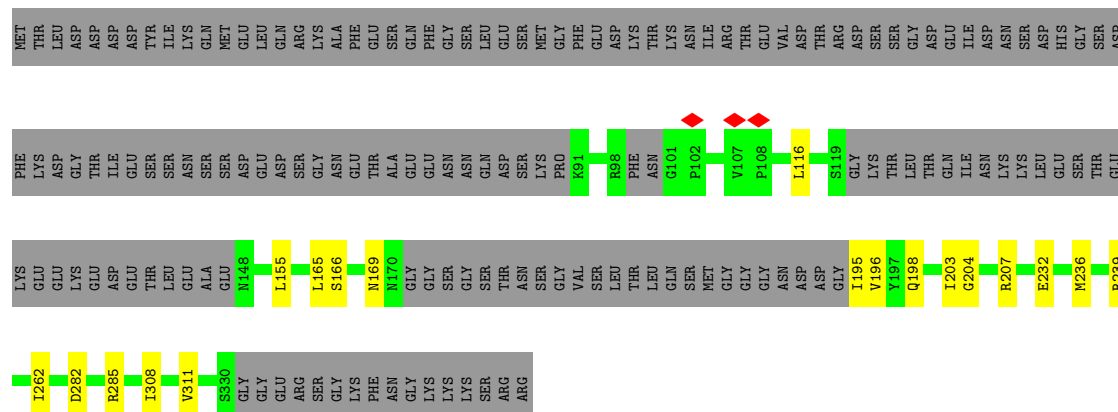
- Molecule 46: U3 small nucleolar RNA-associated protein 7

Chain UG:  82% 10% 7%



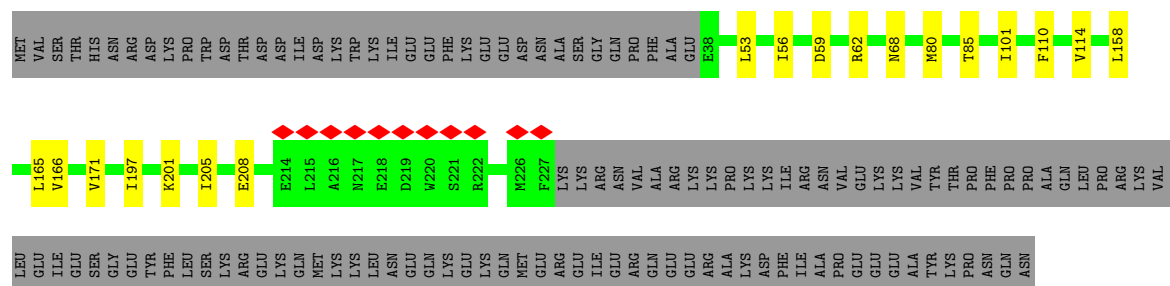
- Molecule 47: Protein FAF1

Chain JN: 



- Molecule 48: KRR1 small subunit processome component

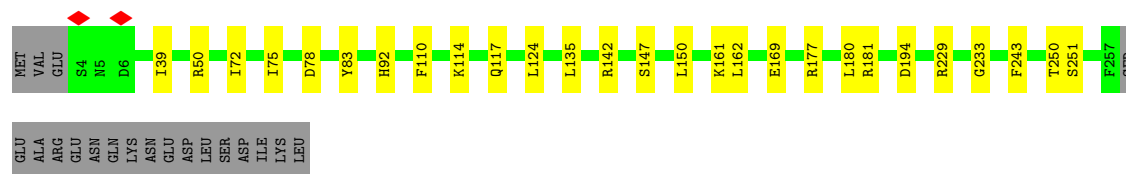
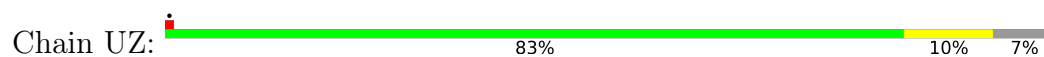
Chain JO:



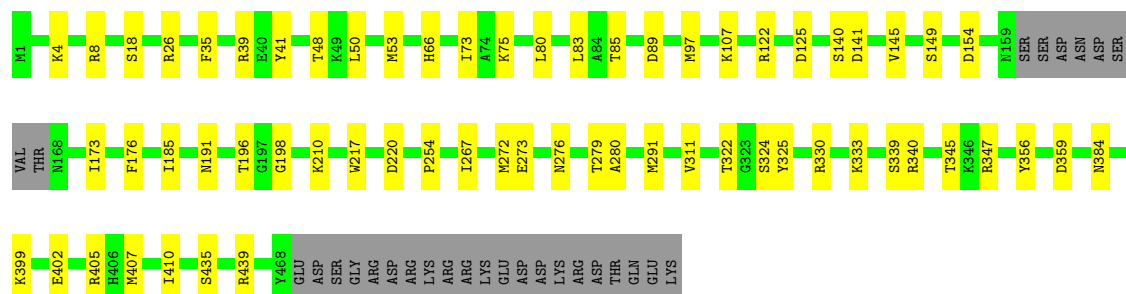
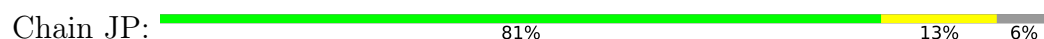
- Molecule 49: RNA 3'-terminal phosphate cyclase-like protein

Chain CM: 82% 17%

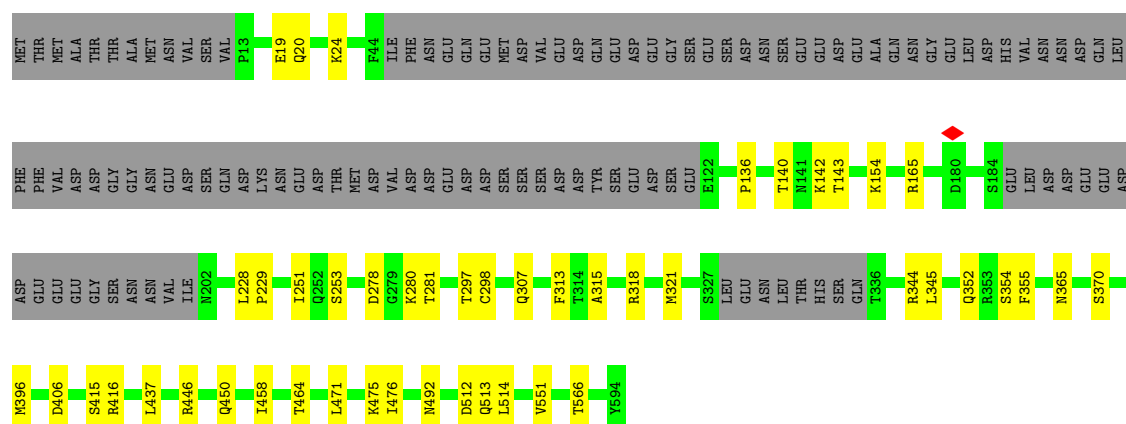
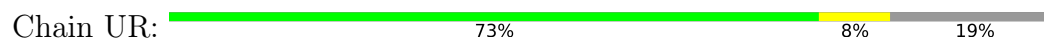
- Molecule 50: Ribosome biogenesis protein UTP30



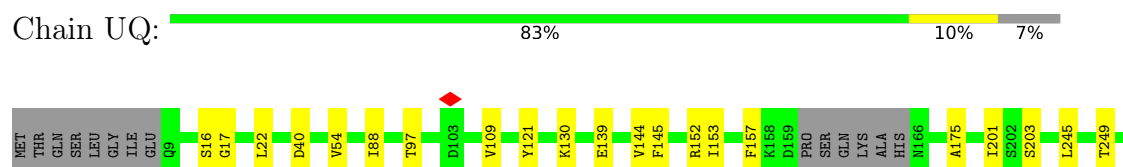
- Molecule 51: Protein SOF1

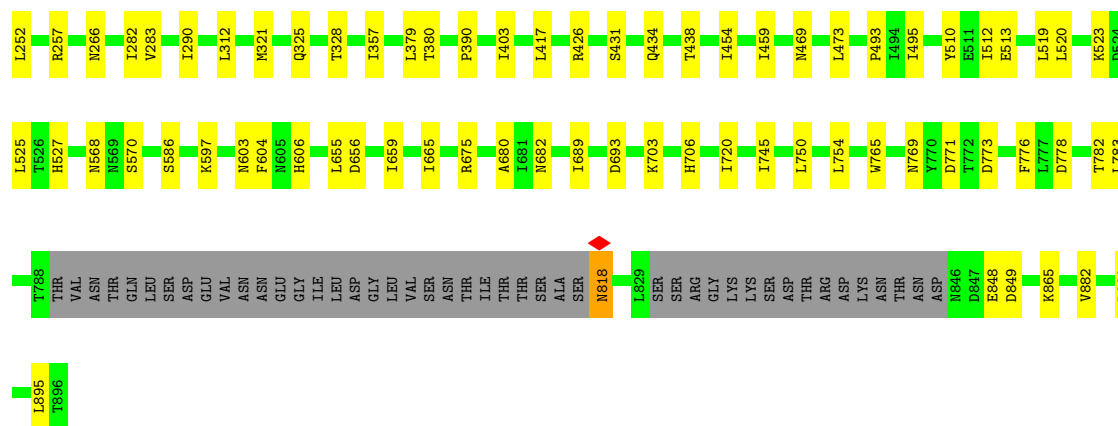


- Molecule 52: U3 small nucleolar RNA-associated protein 18



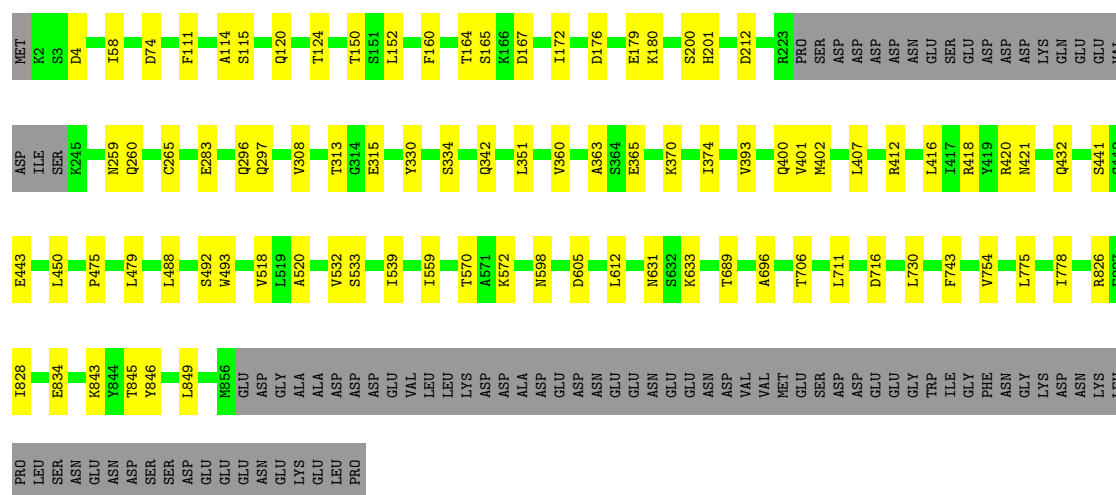
- Molecule 53: U3 small nucleolar RNA-associated protein 21





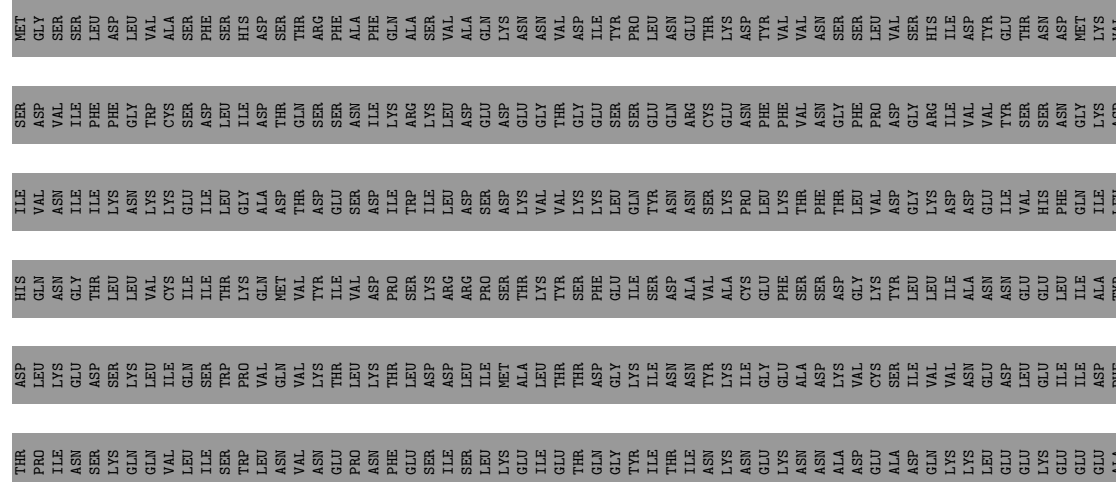
• Molecule 56: Periodic tryptophan protein 2

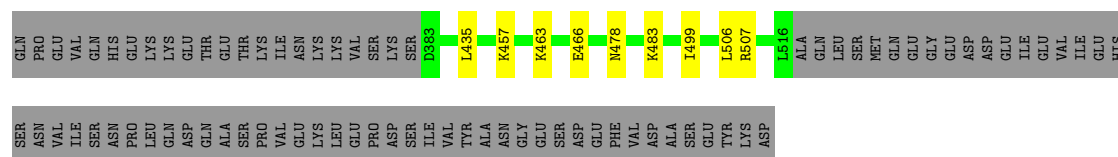
Chain UA: 81% 10% 10%



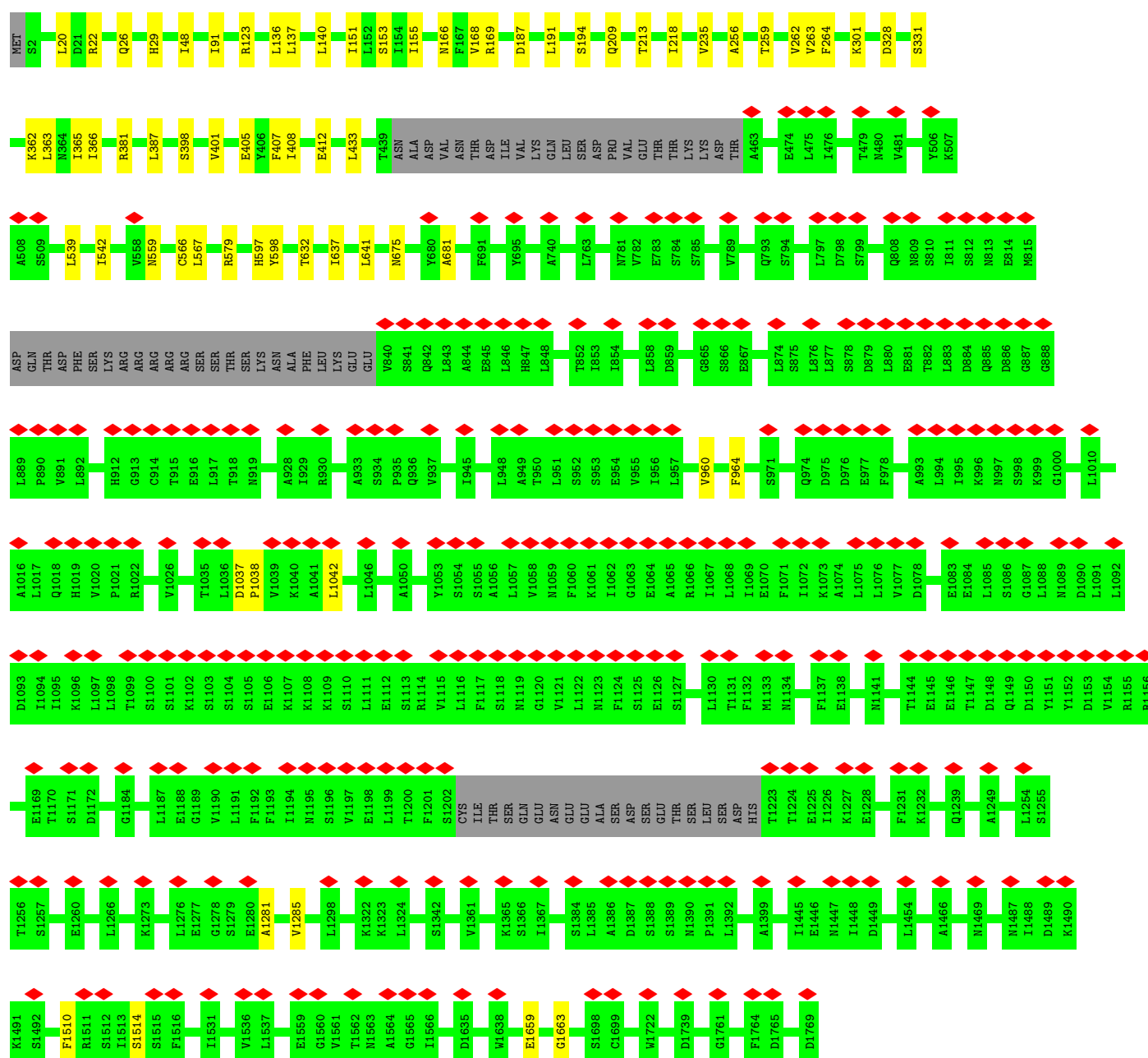
• Molecule 57: U3 small nucleolar RNA-associated protein 9

Chain UI: 22% 77%

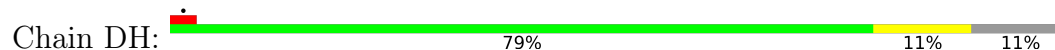


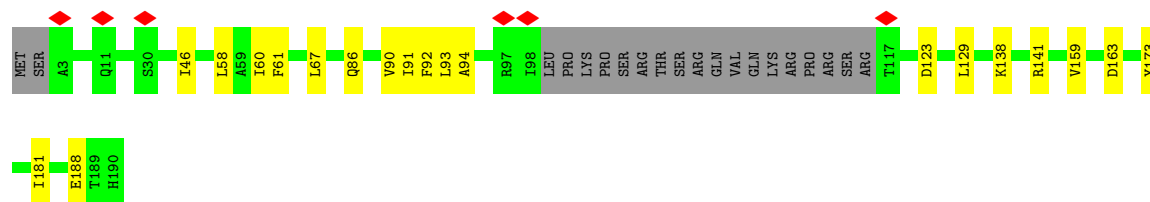


• Molecule 58: U3 small nucleolar RNA-associated protein 10

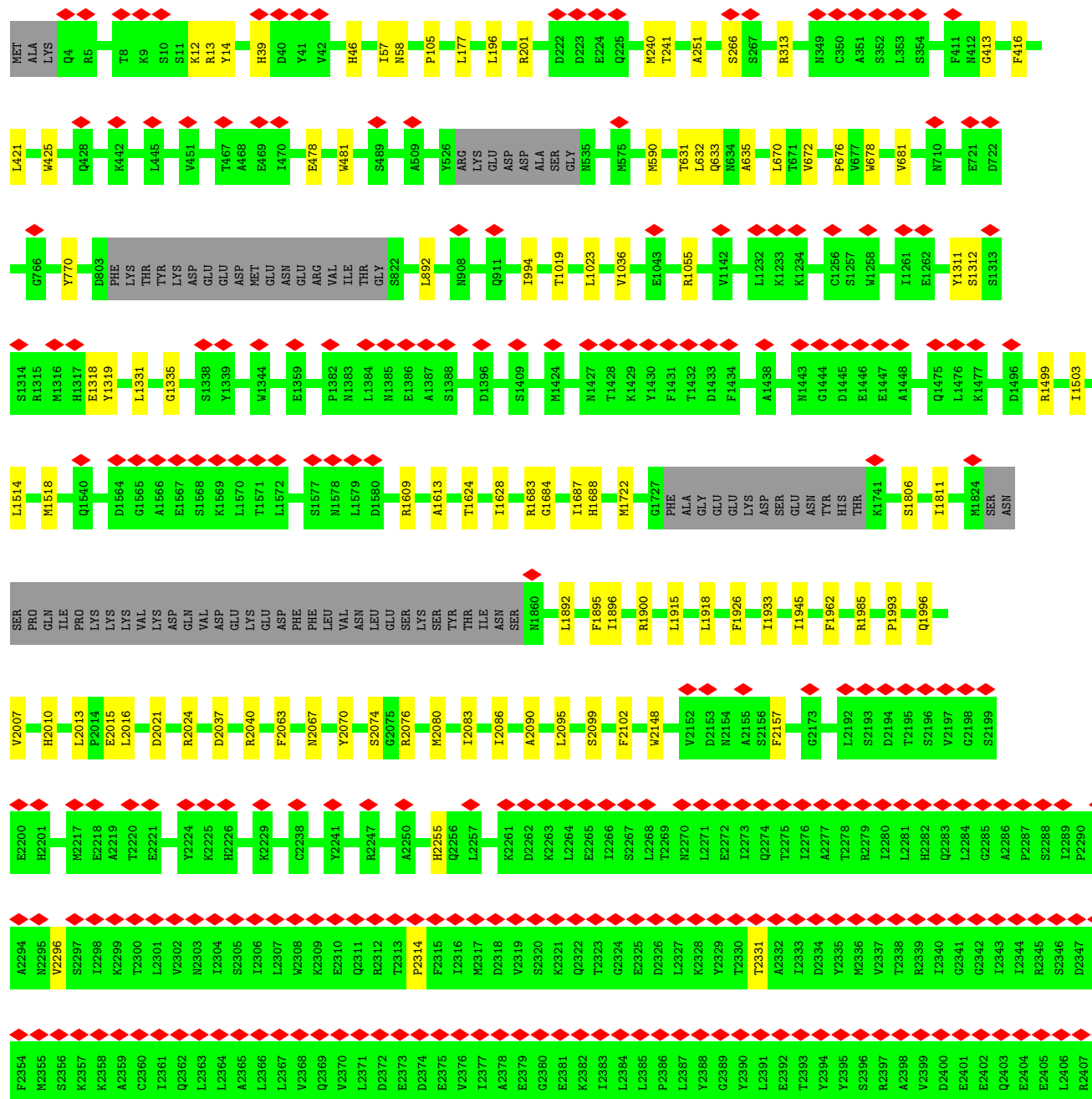
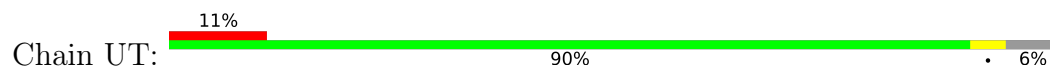


• Molecule 59: 40S ribosomal protein S7-A

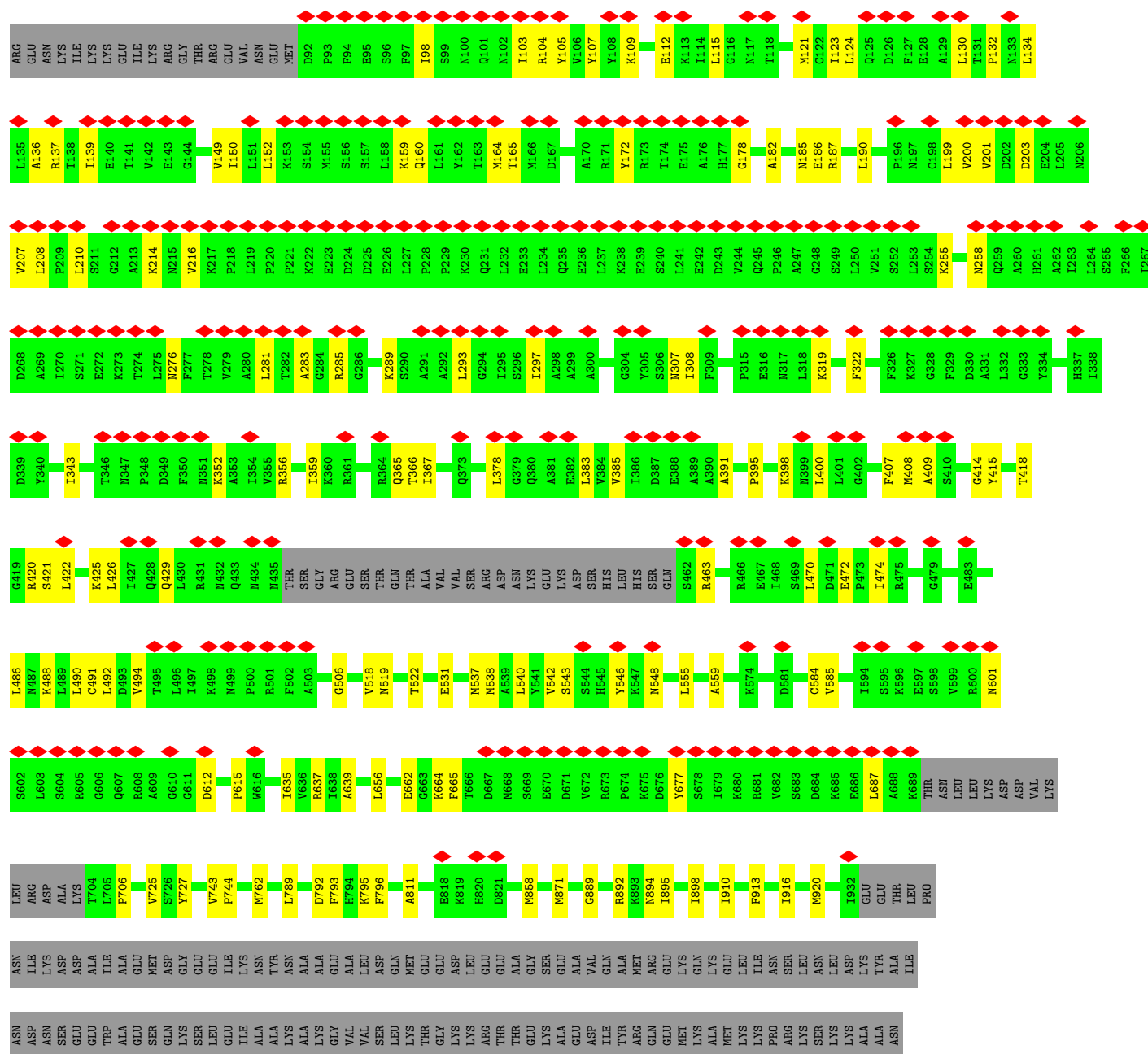




- Molecule 60: U3 small nucleolar RNA-associated protein 20







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	32278	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	46.4	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	5.585	Depositor
Minimum map value	0.000	Depositor
Average map value	0.022	Depositor
Map value standard deviation	0.132	Depositor
Recommended contour level	0.45	Depositor
Map size (Å)	522.5, 522.5, 522.5	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, 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	D3	0.21	0/21102	0.31	0/32834
2	D2	0.25	0/12389	0.27	0/19297
3	D4	0.26	0/4163	0.28	0/6467
4	CJ	0.27	0/2322	0.49	0/3128
5	CK	0.24	0/1601	0.53	2/2150 (0.1%)
6	CL	0.27	0/6612	0.48	0/8919
7	DY	0.25	0/774	0.56	2/1041 (0.2%)
8	UX	0.30	0/1419	0.48	0/1906
9	JF	0.22	0/1673	0.52	0/2268
9	JG	0.26	0/1818	0.50	0/2460
10	CA	0.30	0/1904	0.48	0/2570
10	CB	0.28	0/1811	0.56	2/2443 (0.1%)
11	UB	0.21	0/3722	0.40	0/5048
12	UC	0.26	0/1035	0.54	0/1365
13	UE	0.28	0/3841	0.50	0/5213
14	UH	0.18	0/3555	0.48	2/4897 (0.0%)
15	UK	0.27	0/2010	0.46	0/2662
16	UL	0.31	0/6526	0.55	0/8873
17	UM	0.27	0/1287	0.55	0/1739
18	UO	0.30	0/3987	0.56	0/5405
19	UP	0.26	0/423	0.45	0/571
20	US	0.23	0/4074	0.47	0/5581
21	CF	0.32	0/945	0.48	0/1284
21	CG	0.25	0/928	0.48	0/1262
22	CI	0.31	0/1560	0.51	0/2097
23	JE	0.22	0/971	0.59	2/1314 (0.2%)
24	JH	0.13	0/1274	0.32	0/1775
25	JJ	0.14	0/502	0.42	0/692
26	JK	0.25	0/338	0.53	0/458
27	JM	0.24	0/1119	0.49	0/1494
28	JQ	0.18	0/867	0.41	0/1203
29	DF	0.28	0/1658	0.55	0/2242

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	DI	0.28	0/1372	0.52	0/1839
31	DJ	0.25	0/1428	0.50	0/1916
32	DS	0.14	0/523	0.38	0/724
33	JC	0.27	0/2753	0.49	0/3742
34	DE	0.23	0/1876	0.51	0/2536
35	DX	0.28	0/786	0.52	0/1053
36	DW	0.26	0/970	0.52	0/1312
37	DG	0.24	0/1598	0.52	0/2151
38	DL	0.22	0/1077	0.43	0/1466
39	CH	0.24	0/3601	0.55	0/4862
40	Dc	0.29	0/500	0.54	0/670
41	DQ	0.32	0/990	0.55	0/1335
42	CE	0.23	0/3075	0.46	0/4186
43	CD	0.25	0/2847	0.47	0/3860
44	UN	0.26	0/1468	0.50	0/1993
45	UF	0.24	0/2852	0.46	0/3871
46	UG	0.32	0/3997	0.51	0/5413
47	JN	0.25	0/1370	0.56	0/1830
48	JO	0.23	0/1510	0.49	0/2043
49	CM	0.24	0/2820	0.49	0/3814
50	UZ	0.23	0/1998	0.52	0/2704
51	JP	0.35	1/3797 (0.0%)	0.56	0/5116
52	UR	0.34	0/3835	0.52	0/5201
53	UU	0.31	0/6743	0.54	1/9126 (0.0%)
54	UD	0.30	0/5275	0.54	0/7180
55	UQ	0.32	0/6692	0.52	0/9087
56	UA	0.33	0/6747	0.54	0/9136
57	UI	0.23	0/974	0.54	0/1329
58	UJ	0.21	0/10267	0.46	1/14176 (0.0%)
59	DH	0.22	0/1229	0.50	0/1676
60	UT	0.17	0/14115	0.40	0/19566
61	JA	0.21	0/6767	0.49	1/9207 (0.0%)
61	JB	0.18	0/6479	0.46	0/8830
All	All	0.25	1/210541 (0.0%)	0.46	13/293608 (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
9	JG	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
29	DF	0	1
50	UZ	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	JP	198	GLY	C-O	5.92	1.27	1.24

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	CK	426	LEU	CA-C-N	6.11	133.22	121.54
5	CK	426	LEU	C-N-CA	6.11	133.22	121.54
10	CB	296	GLU	CA-C-N	5.88	132.77	121.54
10	CB	296	GLU	C-N-CA	5.88	132.77	121.54
53	UU	930	MET	CB-CG-SD	-5.78	95.36	112.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
29	DF	49	GLU	Peptide
9	JG	213	LYS	Peptide
50	UZ	78	ASP	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D3	18883	0	9534	126	0
2	D2	11078	0	5570	60	0
3	D4	3731	0	1892	16	0
4	CJ	2281	0	2297	22	0
5	CK	1584	0	1589	25	0
6	CL	6472	0	6530	72	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	DY	761	0	782	15	0
8	UX	1396	0	1473	12	0
9	JF	1647	0	1643	16	0
9	JG	1789	0	1841	26	0
10	CA	1868	0	1909	27	0
10	CB	1778	0	1823	30	0
11	UB	3660	0	3404	34	0
12	UC	1027	0	1080	21	0
13	UE	3773	0	3787	33	0
14	UH	3518	0	2497	34	0
15	UK	1985	0	2051	18	0
16	UL	6393	0	6116	66	0
17	UM	1269	0	1247	13	0
18	UO	3905	0	3894	52	0
19	UP	419	0	380	6	0
20	US	3967	0	3505	39	0
21	CF	932	0	983	6	0
21	CG	916	0	964	11	0
22	CI	1531	0	1572	21	0
23	JE	959	0	787	12	0
24	JH	1276	0	561	1	0
25	JJ	500	0	275	2	0
26	JK	330	0	302	6	0
27	JM	1100	0	1099	14	0
28	JQ	860	0	469	4	0
29	DF	1638	0	1683	17	0
30	DI	1350	0	1343	25	0
31	DJ	1406	0	1465	14	0
32	DS	526	0	247	2	0
33	JC	2695	0	2512	25	0
34	DE	1836	0	1867	27	0
35	DX	774	0	810	10	0
36	DW	954	0	945	9	0
37	DG	1577	0	1597	22	0
38	DL	1052	0	1035	16	0
39	CH	3531	0	3473	37	0
40	Dc	498	0	535	5	0
41	DQ	973	0	1029	15	0
42	CE	3038	0	2817	33	0
43	CD	2802	0	2625	21	0
44	UN	1441	0	1330	13	0
45	UF	2795	0	2461	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
46	UG	3917	0	3777	42	0
47	JN	1363	0	1295	18	0
48	JO	1483	0	1522	12	0
49	CM	2768	0	2844	42	0
50	UZ	1963	0	1971	20	0
51	JP	3718	0	3645	40	0
52	UR	3751	0	3706	34	0
53	UU	6606	0	6523	69	0
54	UD	5176	0	4984	49	0
55	UQ	6559	0	6385	59	0
56	UA	6602	0	6461	56	0
57	UI	959	0	881	7	0
58	UJ	10158	0	7084	41	0
59	DH	1207	0	1092	12	0
60	UT	13871	0	8948	60	0
61	JA	6631	0	6373	85	0
61	JB	6345	0	6043	93	0
62	CL	32	0	12	0	0
63	UX	1	0	0	0	0
All	All	203584	0	173176	1597	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 4.

The worst 5 of 1597 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)
20:US:130:GLU:O	20:US:134:PHE:HB2	1.75	0.86
54:UD:614:TRP:NE1	54:UD:618:ASN:HD22	1.75	0.85
61:JA:309:PHE:HB2	61:JA:384:VAL:HG22	1.63	0.81
55:UQ:818:ASN:N	55:UQ:818:ASN:HD22	1.78	0.80
55:UQ:16:SER:O	55:UQ:783:LEU:HB2	1.83	0.78

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	CJ	278/290 (96%)	272 (98%)	6 (2%)	0	100	100
5	CK	193/593 (32%)	192 (100%)	0	1 (0%)	24	52
6	CL	806/1183 (68%)	792 (98%)	14 (2%)	0	100	100
7	DY	94/135 (70%)	91 (97%)	3 (3%)	0	100	100
8	UX	170/189 (90%)	167 (98%)	3 (2%)	0	100	100
9	JF	213/252 (84%)	209 (98%)	4 (2%)	0	100	100
9	JG	227/252 (90%)	223 (98%)	4 (2%)	0	100	100
10	CA	237/327 (72%)	230 (97%)	7 (3%)	0	100	100
10	CB	223/327 (68%)	211 (95%)	11 (5%)	1 (0%)	30	57
11	UB	483/810 (60%)	477 (99%)	6 (1%)	0	100	100
12	UC	124/610 (20%)	124 (100%)	0	0	100	100
13	UE	468/643 (73%)	453 (97%)	15 (3%)	0	100	100
14	UH	565/713 (79%)	550 (97%)	15 (3%)	0	100	100
15	UK	234/250 (94%)	226 (97%)	7 (3%)	1 (0%)	30	57
16	UL	841/943 (89%)	815 (97%)	26 (3%)	0	100	100
17	UM	156/817 (19%)	154 (99%)	2 (1%)	0	100	100
18	UO	490/513 (96%)	478 (98%)	12 (2%)	0	100	100
19	UP	58/214 (27%)	57 (98%)	1 (2%)	0	100	100
20	US	538/552 (98%)	518 (96%)	20 (4%)	0	100	100
21	CF	121/126 (96%)	119 (98%)	2 (2%)	0	100	100
21	CG	119/126 (94%)	118 (99%)	1 (1%)	0	100	100
22	CI	180/183 (98%)	178 (99%)	2 (1%)	0	100	100
23	JE	134/357 (38%)	129 (96%)	5 (4%)	0	100	100
24	JH	253/483 (52%)	249 (98%)	4 (2%)	0	100	100
25	JJ	94/274 (34%)	93 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	JK	40/534 (8%)	39 (98%)	1 (2%)	0	100	100
27	JM	129/217 (59%)	127 (98%)	2 (2%)	0	100	100
28	JQ	151/206 (73%)	148 (98%)	3 (2%)	0	100	100
29	DF	205/225 (91%)	198 (97%)	7 (3%)	0	100	100
30	DI	171/200 (86%)	168 (98%)	3 (2%)	0	100	100
31	DJ	175/197 (89%)	171 (98%)	4 (2%)	0	100	100
32	DS	98/146 (67%)	98 (100%)	0	0	100	100
33	JC	346/707 (49%)	341 (99%)	5 (1%)	0	100	100
34	DE	234/261 (90%)	230 (98%)	4 (2%)	0	100	100
35	DX	101/145 (70%)	99 (98%)	2 (2%)	0	100	100
36	DW	125/130 (96%)	124 (99%)	1 (1%)	0	100	100
37	DG	205/236 (87%)	203 (99%)	2 (1%)	0	100	100
38	DL	136/156 (87%)	132 (97%)	4 (3%)	0	100	100
39	CH	442/573 (77%)	428 (97%)	14 (3%)	0	100	100
40	Dc	61/67 (91%)	60 (98%)	1 (2%)	0	100	100
41	DQ	123/143 (86%)	120 (98%)	3 (2%)	0	100	100
42	CE	434/511 (85%)	427 (98%)	7 (2%)	0	100	100
43	CD	376/504 (75%)	369 (98%)	7 (2%)	0	100	100
44	UN	182/899 (20%)	180 (99%)	2 (1%)	0	100	100
45	UF	373/440 (85%)	370 (99%)	3 (1%)	0	100	100
46	UG	511/554 (92%)	499 (98%)	12 (2%)	0	100	100
47	JN	178/346 (51%)	169 (95%)	9 (5%)	0	100	100
48	JO	188/316 (60%)	187 (100%)	1 (0%)	0	100	100
49	CM	361/367 (98%)	354 (98%)	7 (2%)	0	100	100
50	UZ	252/274 (92%)	245 (97%)	7 (3%)	0	100	100
51	JP	456/489 (93%)	446 (98%)	10 (2%)	0	100	100
52	UR	472/594 (80%)	457 (97%)	15 (3%)	0	100	100
53	UU	840/939 (90%)	818 (97%)	22 (3%)	0	100	100
54	UD	670/776 (86%)	648 (97%)	21 (3%)	1 (0%)	48	75
55	UQ	829/896 (92%)	805 (97%)	23 (3%)	1 (0%)	48	75
56	UA	830/923 (90%)	808 (97%)	22 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	UI	132/575 (23%)	130 (98%)	2 (2%)	0	100	100
58	UJ	1693/1769 (96%)	1659 (98%)	33 (2%)	1 (0%)	48	75
59	DH	166/190 (87%)	163 (98%)	3 (2%)	0	100	100
60	UT	2335/2493 (94%)	2313 (99%)	22 (1%)	0	100	100
61	JA	885/1056 (84%)	867 (98%)	18 (2%)	0	100	100
61	JB	848/1056 (80%)	833 (98%)	15 (2%)	0	100	100
All	All	23052/31272 (74%)	22558 (98%)	488 (2%)	6 (0%)	100	100

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	CK	427	SER
10	CB	297	ARG
55	UQ	454	ILE
58	UJ	1037	ASP
15	UK	184	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	CJ	247/258 (96%)	247 (100%)	0	100	100
5	CK	174/535 (32%)	174 (100%)	0	100	100
6	CL	683/1039 (66%)	683 (100%)	0	100	100
7	DY	80/113 (71%)	80 (100%)	0	100	100
8	UX	156/169 (92%)	156 (100%)	0	100	100
9	JF	179/222 (81%)	179 (100%)	0	100	100
9	JG	202/222 (91%)	202 (100%)	0	100	100
10	CA	200/240 (83%)	200 (100%)	0	100	100
10	CB	192/240 (80%)	192 (100%)	0	100	100
11	UB	348/732 (48%)	348 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	UC	107/538 (20%)	107 (100%)	0	100	100
13	UE	425/574 (74%)	425 (100%)	0	100	100
14	UH	193/657 (29%)	193 (100%)	0	100	100
15	UK	219/234 (94%)	219 (100%)	0	100	100
16	UL	648/832 (78%)	648 (100%)	0	100	100
17	UM	135/719 (19%)	135 (100%)	0	100	100
18	UO	435/454 (96%)	435 (100%)	0	100	100
19	UP	37/196 (19%)	37 (100%)	0	100	100
20	US	357/506 (71%)	357 (100%)	0	100	100
21	CF	102/104 (98%)	102 (100%)	0	100	100
21	CG	100/104 (96%)	100 (100%)	0	100	100
22	CI	171/172 (99%)	171 (100%)	0	100	100
23	JE	80/315 (25%)	80 (100%)	0	100	100
25	JJ	7/238 (3%)	7 (100%)	0	100	100
26	JK	34/482 (7%)	34 (100%)	0	100	100
27	JM	114/200 (57%)	114 (100%)	0	100	100
28	JQ	24/192 (12%)	24 (100%)	0	100	100
29	DF	177/191 (93%)	177 (100%)	0	100	100
30	DI	134/161 (83%)	134 (100%)	0	100	100
31	DJ	146/166 (88%)	146 (100%)	0	100	100
32	DS	4/129 (3%)	4 (100%)	0	100	100
33	JC	280/636 (44%)	279 (100%)	1 (0%)	84	84
34	DE	190/222 (86%)	190 (100%)	0	100	100
35	DX	82/120 (68%)	82 (100%)	0	100	100
36	DW	96/111 (86%)	96 (100%)	0	100	100
37	DG	152/201 (76%)	152 (100%)	0	100	100
38	DL	109/137 (80%)	108 (99%)	1 (1%)	70	78
39	CH	372/503 (74%)	372 (100%)	0	100	100
40	Dc	56/60 (93%)	56 (100%)	0	100	100
41	DQ	105/119 (88%)	105 (100%)	0	100	100
42	CE	258/433 (60%)	258 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	CD	267/435 (61%)	267 (100%)	0	100	100
44	UN	143/808 (18%)	142 (99%)	1 (1%)	76	80
45	UF	240/414 (58%)	240 (100%)	0	100	100
46	UG	399/480 (83%)	399 (100%)	0	100	100
47	JN	124/304 (41%)	124 (100%)	0	100	100
48	JO	158/289 (55%)	158 (100%)	0	100	100
49	CM	300/312 (96%)	300 (100%)	0	100	100
50	UZ	208/256 (81%)	208 (100%)	0	100	100
51	JP	406/443 (92%)	406 (100%)	0	100	100
52	UR	411/529 (78%)	411 (100%)	0	100	100
53	UU	724/819 (88%)	724 (100%)	0	100	100
54	UD	554/713 (78%)	554 (100%)	0	100	100
55	UQ	732/826 (89%)	731 (100%)	1 (0%)	88	89
56	UA	721/812 (89%)	721 (100%)	0	100	100
57	UI	85/533 (16%)	85 (100%)	0	100	100
58	UJ	512/1633 (31%)	512 (100%)	0	100	100
59	DH	105/170 (62%)	105 (100%)	0	100	100
60	UT	571/2307 (25%)	571 (100%)	0	100	100
61	JA	652/934 (70%)	652 (100%)	0	100	100
61	JB	622/934 (67%)	622 (100%)	0	100	100
All	All	15744/27427 (57%)	15740 (100%)	4 (0%)	100	100

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	JC	76	THR
38	DL	21	ASN
44	UN	299	ASN
55	UQ	818	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 160 such sidechains are listed below:

Mol	Chain	Res	Type
54	UD	595	ASN

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Mol	Chain	Res	Type
60	UT	1891	HIS
55	UQ	491	GLN
57	UI	468	ASN
61	JA	380	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	D3	866/1808 (47%)	213 (24%)	17 (1%)
2	D2	513/700 (73%)	96 (18%)	3 (0%)
3	D4	170/333 (51%)	34 (20%)	1 (0%)
All	All	1549/2841 (54%)	343 (22%)	21 (1%)

5 of 343 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	D3	-1	G
1	D3	0	U
1	D3	1	U
1	D3	10	G
1	D3	17	C

5 of 21 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	D3	1594	G
2	D2	90	G
3	D4	312	U
2	D2	370	U
1	D3	1632	C

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 1 is 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
62	GTP	CL	2001	-	33,34,34	0.89	1 (3%)	50,54,54	1.61	9 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
62	GTP	CL	2001	-	-	5/22/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	CL	2001	GTP	C2-N3	2.03	1.38	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	CL	2001	GTP	C5-C4-N3	-5.06	120.33	128.39
62	CL	2001	GTP	C2-N3-C4	4.65	120.30	112.30
62	CL	2001	GTP	N9-C4-N3	3.20	132.36	125.95
62	CL	2001	GTP	C2-N1-C6	-2.92	119.81	125.11
62	CL	2001	GTP	N9-C8-N7	-2.72	108.36	113.40

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
62	CL	2001	GTP	C5'-O5'-PA-O3A
62	CL	2001	GTP	C5'-O5'-PA-O1A

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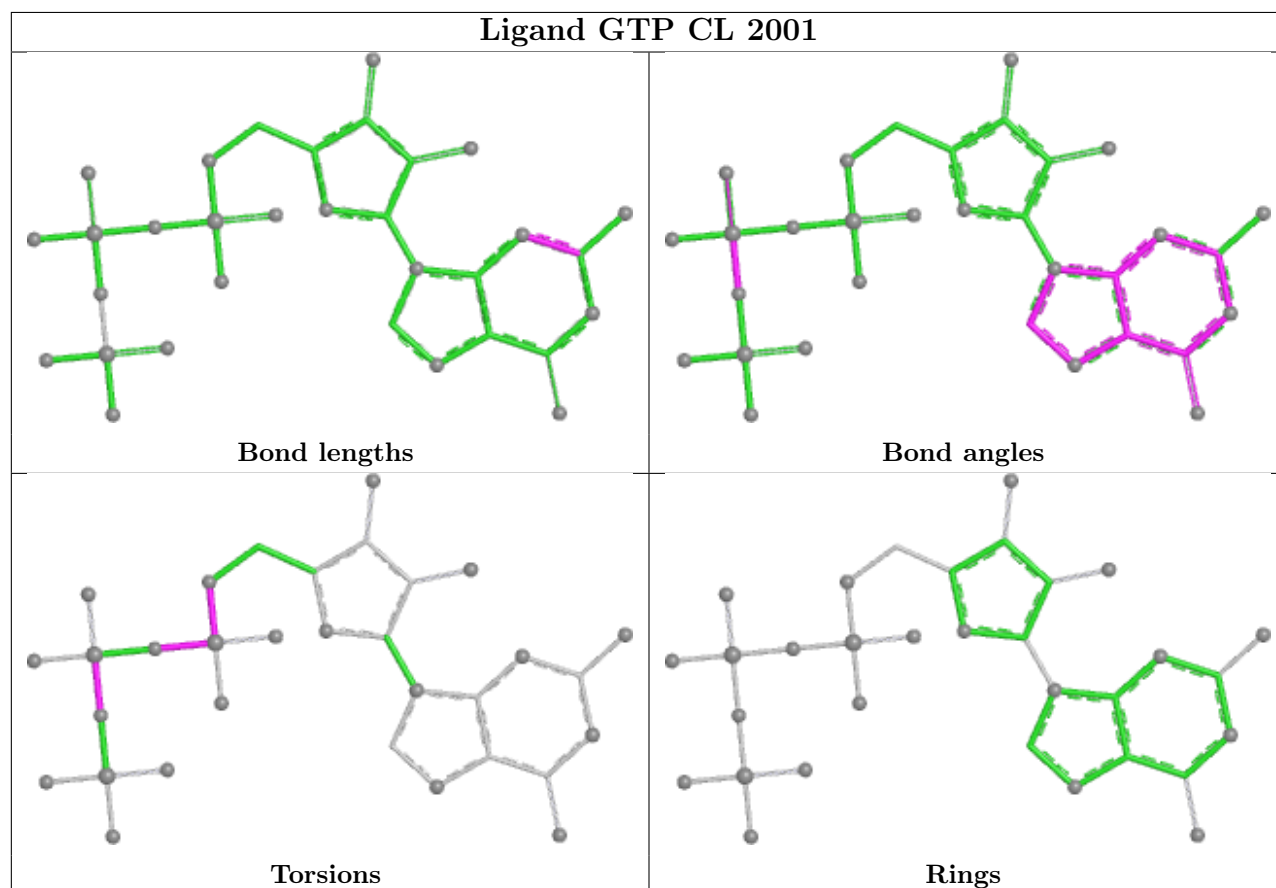
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Mol	Chain	Res	Type	Atoms
62	CL	2001	GTP	C5'-O5'-PA-O2A
62	CL	2001	GTP	PG-O3B-PB-O2B
62	CL	2001	GTP	PB-O3A-PA-O2A

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

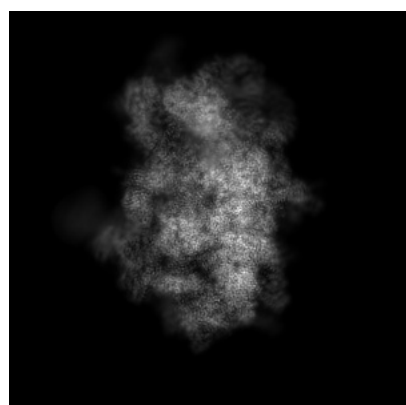
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-50991. These allow visual inspection of the internal detail of the map and identification of artifacts.

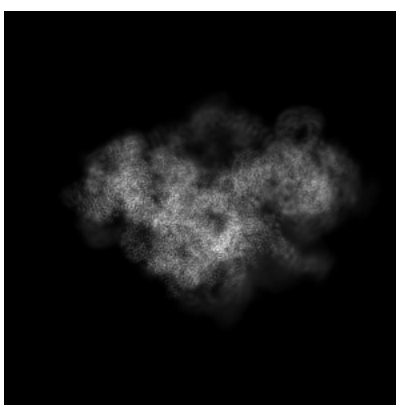
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

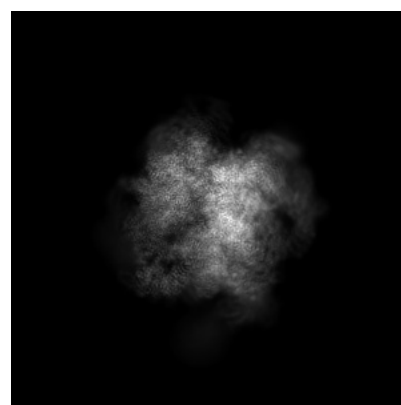
6.1.1 Primary map



X



Y

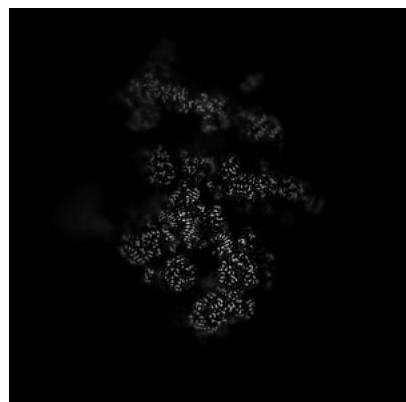


Z

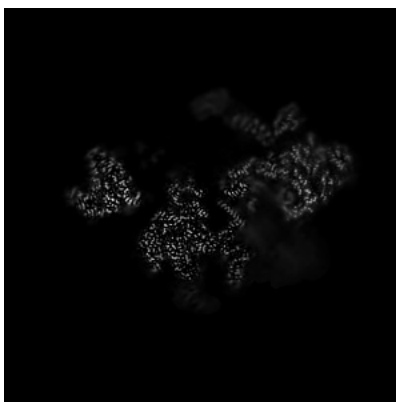
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

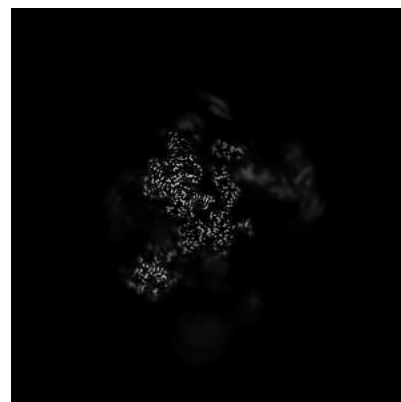
6.2.1 Primary map



X Index: 250



Y Index: 250

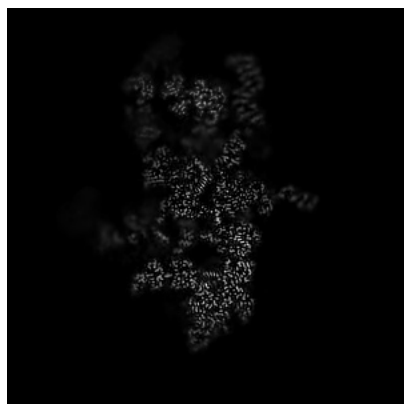


Z Index: 250

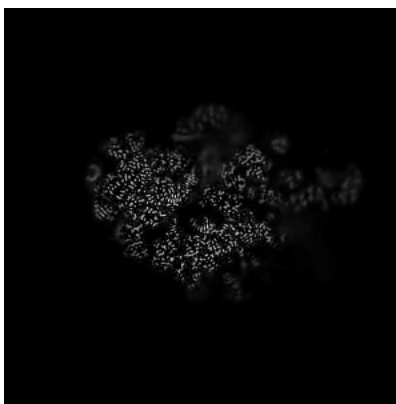
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

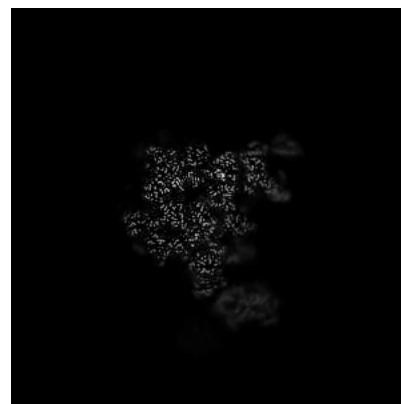
6.3.1 Primary map



X Index: 265



Y Index: 290

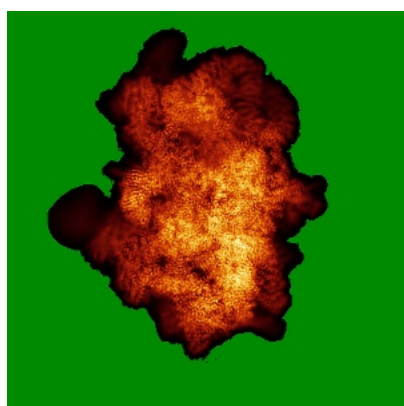


Z Index: 210

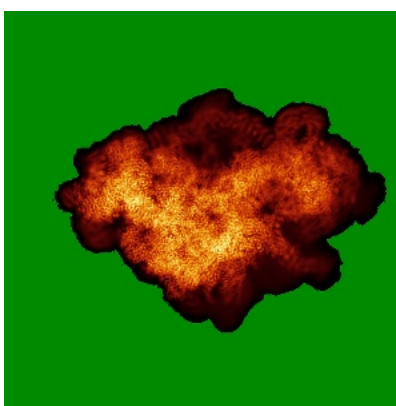
The images above show the largest variance slices of the map in three orthogonal directions.

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

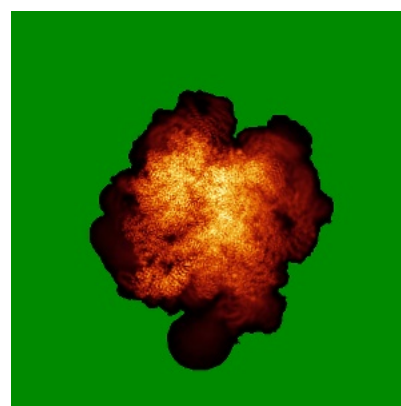
6.4.1 Primary map



X



Y

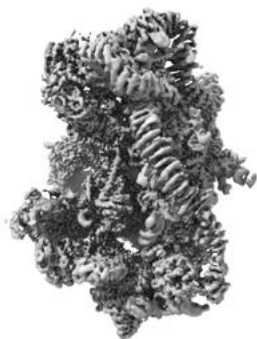


Z

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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.45. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

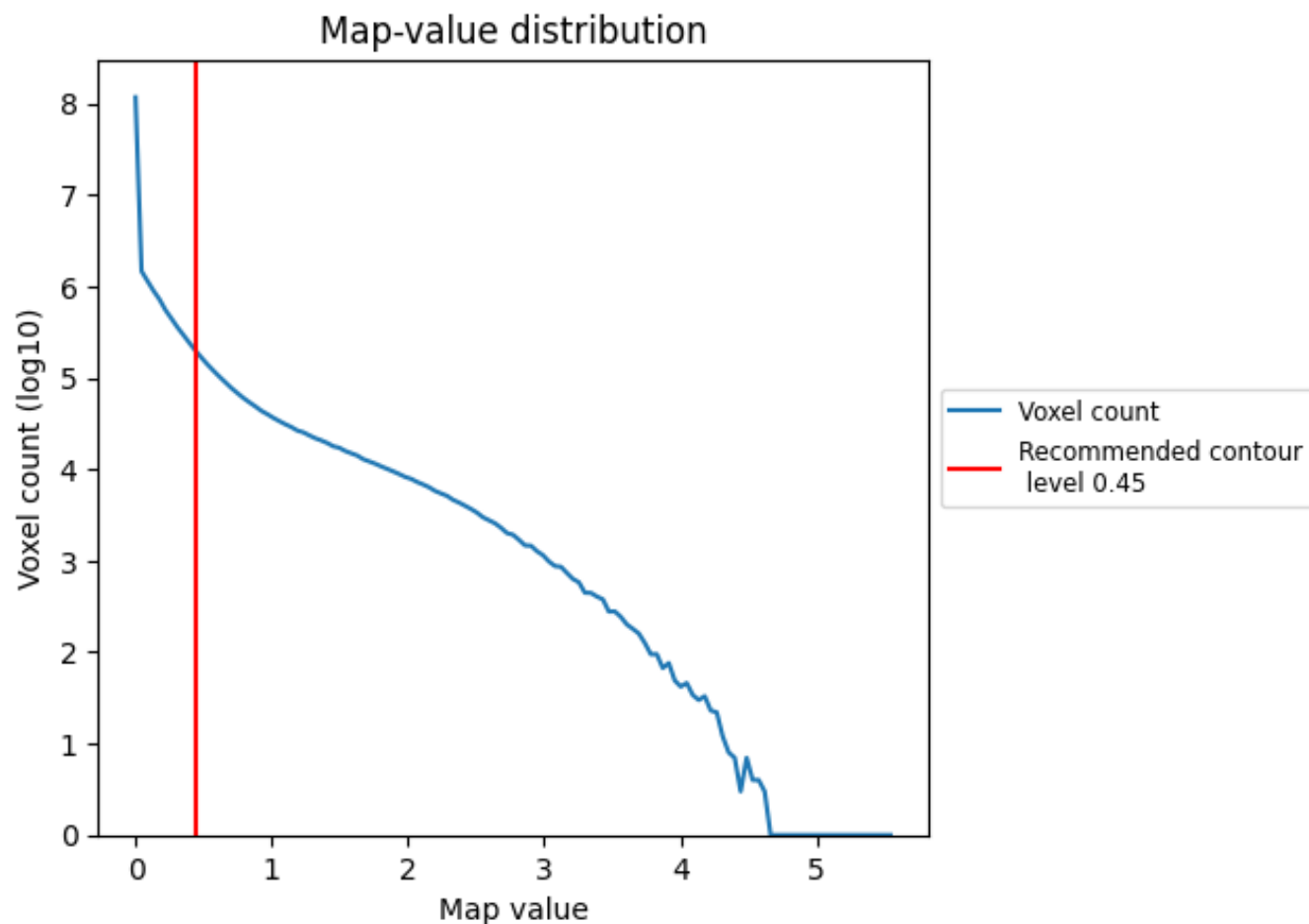
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

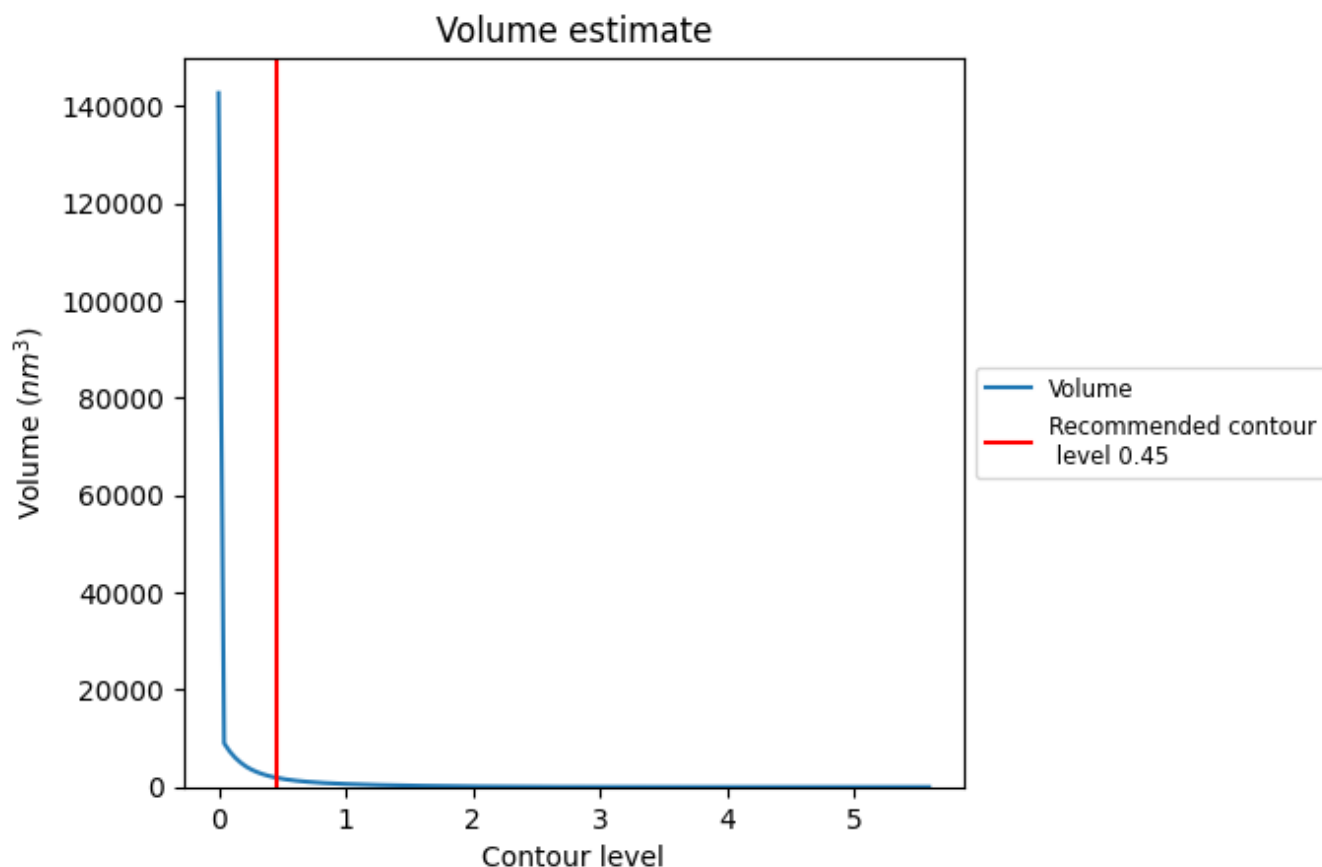
This section contains the results of statistical analysis of the map.

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.

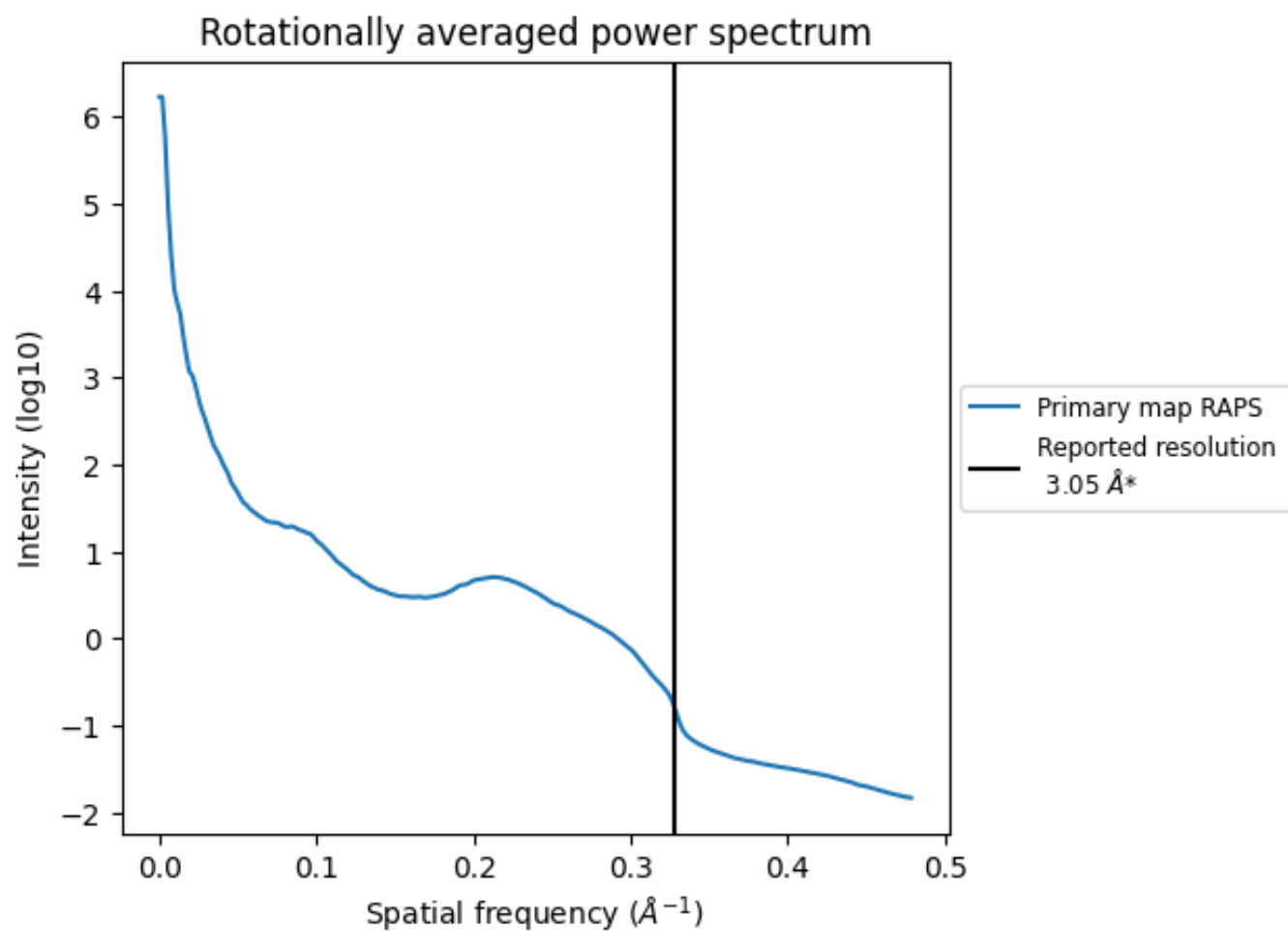
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1930 nm^3 ; this corresponds to an approximate mass of 1743 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 0.328 $\text{\AA}^{-1}$

8 Fourier-Shell correlation

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

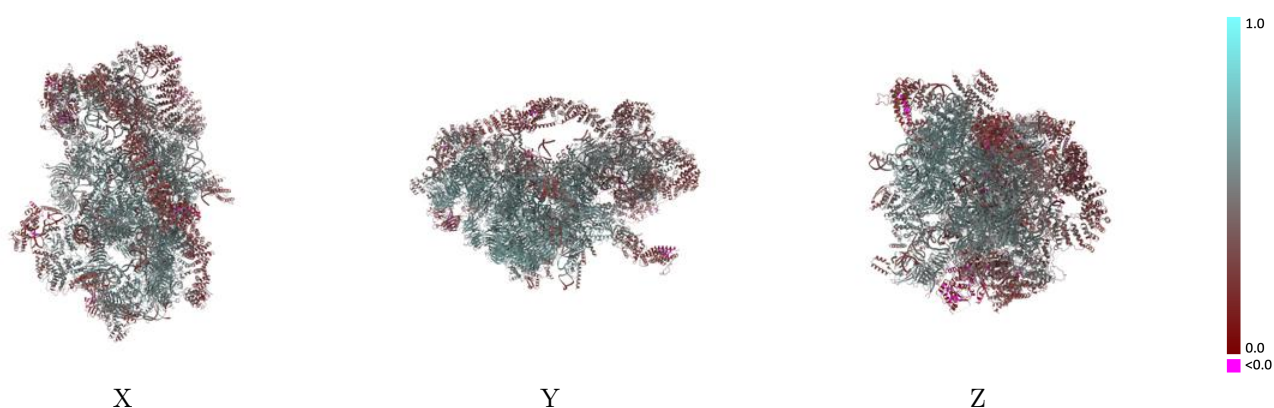
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-50991 and PDB model 9G33. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)

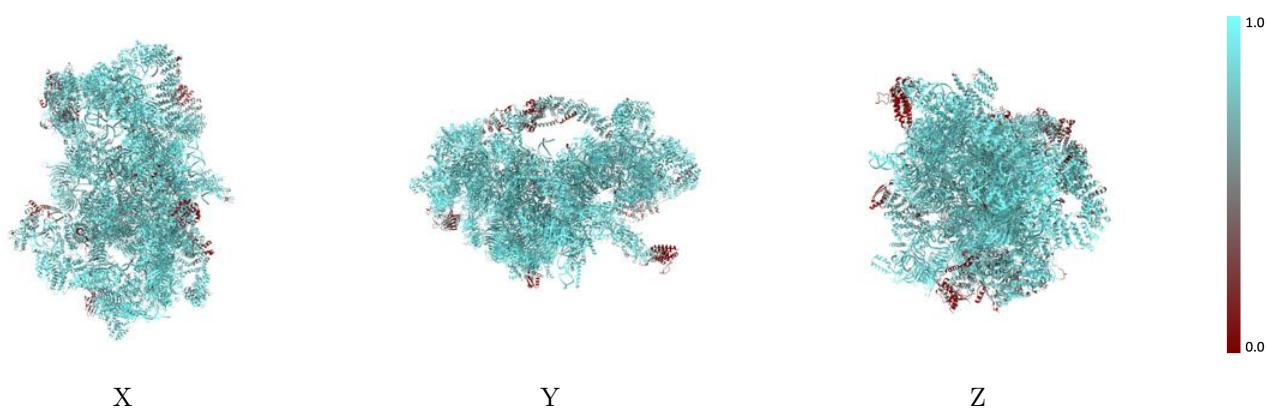
This section was not generated.

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



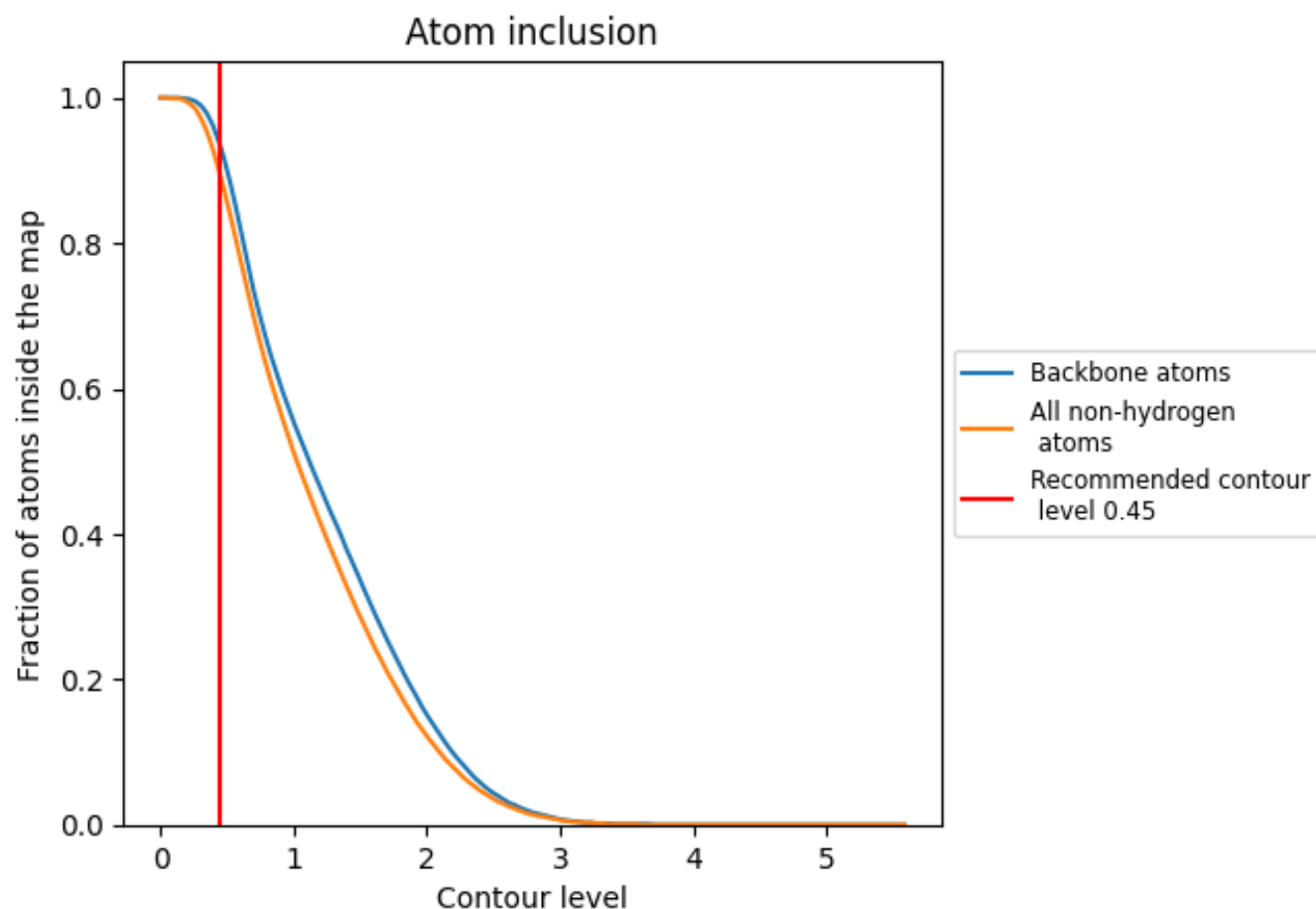
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.45).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 89% 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 (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8920	 0.4850
CA	 0.9520	 0.5910
CB	 0.9510	 0.5240
CD	 0.9090	 0.4920
CE	 0.9180	 0.4950
CF	 0.9700	 0.5890
CG	 0.9390	 0.5250
CH	 0.9230	 0.4930
CI	 0.9830	 0.6240
CJ	 0.9410	 0.5720
CK	 0.8680	 0.5210
CL	 0.9210	 0.5440
CM	 0.8940	 0.5180
D2	 0.9710	 0.5120
D3	 0.9220	 0.4450
D4	 0.9640	 0.5140
DE	 0.9170	 0.4680
DF	 0.9570	 0.5760
DG	 0.9020	 0.4660
DH	 0.8480	 0.4440
DI	 0.9380	 0.5130
DJ	 0.9430	 0.5450
DL	 0.9390	 0.4770
DQ	 0.9730	 0.6050
DS	 0.7850	 0.3810
DW	 0.9400	 0.5320
DX	 0.9480	 0.5790
DY	 0.8960	 0.4890
Dc	 0.9370	 0.5700
JA	 0.7910	 0.3960
JB	 0.5550	 0.2550
JC	 0.9300	 0.5020
JE	 0.8740	 0.4510
JF	 0.8840	 0.4790
JG	 0.9330	 0.5450



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Chain	Atom inclusion	Q-score
JH	 0.6530	 0.2360
JJ	 0.2860	 0.3190
JK	 0.8980	 0.4690
JM	 0.8630	 0.5240
JN	 0.9110	 0.5230
JO	 0.8650	 0.5030
JP	 0.9780	 0.5930
JQ	 0.7020	 0.3690
UA	 0.9640	 0.6110
UB	 0.8670	 0.4510
UC	 0.8610	 0.5040
UD	 0.9660	 0.5590
UE	 0.9460	 0.5630
UF	 0.9000	 0.4730
UG	 0.9630	 0.5980
UH	 0.6730	 0.3420
UI	 0.9090	 0.4200
UJ	 0.7650	 0.3700
UK	 0.9460	 0.5690
UL	 0.9390	 0.5010
UM	 0.9440	 0.5090
UN	 0.8980	 0.5270
UO	 0.9740	 0.5740
UP	 0.9440	 0.4920
UQ	 0.9560	 0.5620
UR	 0.9710	 0.5980
US	 0.9240	 0.4750
UT	 0.8020	 0.3350
UU	 0.9440	 0.6000
UX	 0.9690	 0.5900
UZ	 0.9030	 0.4890