



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 01:47 AM UTC

PDB ID : 8IR3 / pdb_00008ir3
EMDB ID : EMD-35673
Title : human nuclear pre-60S ribosomal particle - State B'
Authors : Zhang, Y.; Gao, N.
Deposited on : 2023-03-17
Resolution : 3.50 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:

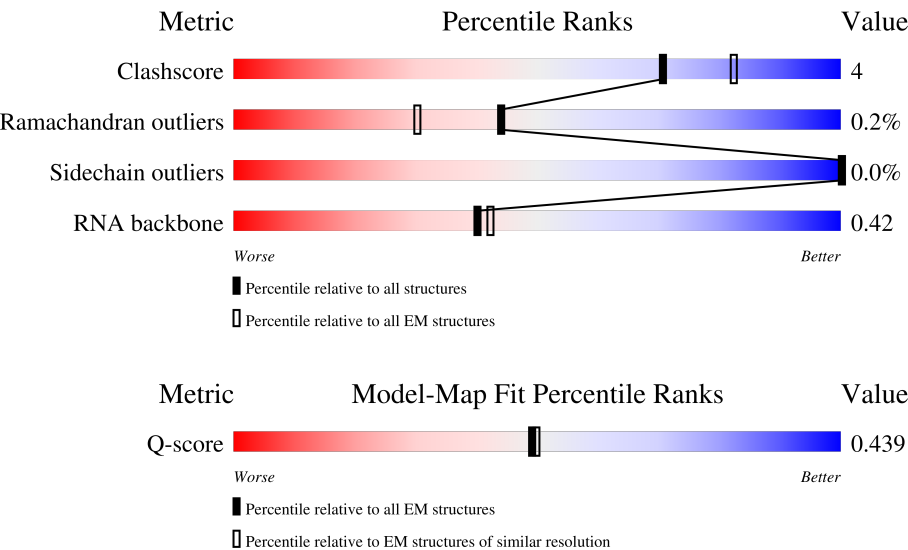
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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	13950 (3.00 - 4.00)

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	y	165	56% 91% 9%
2	4	634	23% 83% 14% ..
3	6	245	10% 87% 13%

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Mol	Chain	Length	Quality of chain
4	7	163	
5	9	134	
6	B	403	
7	D	427	
8	E	115	
9	F	117	
10	G	266	
11	H	123	
12	I	192	
13	K	105	
14	L	148	
15	M	97	
16	P	51	
17	Q	211	
18	S	215	
19	U	204	
20	V	203	
21	X	92	
22	Z	188	
23	a	196	
24	b	176	
25	c	160	
26	e	140	
27	h	145	
28	l	137	

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Mol	Chain	Length	Quality of chain
29	m	257	
30	n	110	
31	o	288	
32	p	248	
33	z	129	
34	A	178	
35	C	297	
36	J	260	
37	N	485	
38	R	365	
39	u	549	
40	v	239	
41	w	731	
42	r	360	
43	8	156	
44	2	5054	
45	d	128	
46	j	125	
47	k	135	
48	Y	184	
49	t	293	
50	s	490	
51	i	136	
52	T	306	
53	5	120	

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Mol	Chain	Length	Quality of chain
54	q	588	
55	f	478	
56	O	70	
57	3	255	
58	g	156	
59	x	60	

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 166429 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 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	y	165	Total	C	N	O	S	0	0
			1250	779	232	234	5		

- Molecule 2 is a protein called GTP-binding protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	4	620	Total	C	N	O	S	0	0
			5093	3198	935	933	27		

- Molecule 3 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	6	244	Total	C	N	O	S	0	0
			1852	1149	318	372	13		

- Molecule 4 is a protein called Probable ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	7	135	Total	C	N	O	S	0	0
			1159	737	225	187	10		

- Molecule 5 is a protein called Zinc finger protein 593.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	9	86	Total	C	N	O	S	0	0
			711	433	154	121	3		

- Molecule 6 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	402	Total	C	N	O	S	1	0
			3244	2065	609	556	14		

- Molecule 7 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	358	Total	C	N	O	S	0	0
			2853	1797	570	473	13		

- Molecule 8 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 9 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	109	Total	C	N	O	S	0	0
			868	544	179	139	6		

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	241	Total	C	N	O	S	1	0
			1935	1233	374	324	4		

- Molecule 11 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 12 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 13 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	K	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 14 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 15 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 16 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	135	Total	C	N	O	S	0	0
			1111	713	213	178	7		

- Molecule 19 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	U	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 20 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 21 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	X	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 22 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Z	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 23 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	a	148	Total	C	N	O	S	0	0
			1239	772	266	192	9		

- Molecule 24 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	b	176	Total	C	N	O	S	0	0
			1461	930	284	236	11		

- Molecule 25 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	c	119	Total	C	N	O	S	0	0
			975	619	189	164	3		

- Molecule 26 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	e	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 27 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	h	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 28 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	l	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 29 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	m	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 30 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	n	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 31 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	o	235	Total	C	N	O	S	0	0
			1897	1217	360	316	4		

- Molecule 32 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	p	225	Total	C	N	O	S	1	0
			1878	1207	361	301	9		

- Molecule 33 is a protein called Protein LLP homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	z	67	Total	C	N	O	S	0	0
			581	363	128	88	2		

- Molecule 34 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	A	165	Total	C	N	O	S	0	0
			1319	836	245	233	5		

- Molecule 35 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	C	248	Total	C	N	O	S	0	0
			2027	1289	370	354	14		

- Molecule 36 is a protein called Ribosome biogenesis protein NSA2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	J	259	Total	C	N	O	S	0	0
			2106	1339	399	359	9		

- Molecule 37 is a protein called Notchless protein homolog 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	N	472	Total	C	N	O	S	0	0
			3669	2307	660	690	12		

- Molecule 38 is a protein called Ribosome biogenesis regulatory protein homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	R	199	Total	C	N	O	S	0	0
			1636	1022	315	296	3		

- Molecule 39 is a protein called Guanine nucleotide-binding protein-like 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	u	75	Total	C	N	O	S	0	0
			639	400	138	98	3		

- Molecule 40 is a protein called mRNA turnover protein 4 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	v	206	Total	C	N	O	S	0	0
			1680	1072	293	304	11		

- Molecule 41 is a protein called G Protein Nucleolar 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	w	449	Total	C	N	O	S	0	0
			3623	2301	643	665	14		

- Molecule 42 is a protein called Coiled-coil domain-containing protein 86.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	24	Total	C	N	O	S	0	0
			217	134	45	37	1		

- Molecule 43 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	8	155	Total	C	N	O	P	0	0
			3295	1472	583	1086	154		

- Molecule 44 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	2	3541	Total	C	N	O	P	0	0
			75906	33833	13870	24663	3540		

- Molecule 45 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	d	104	Total	C	N	O	S	0	0
			850	542	149	157	2		

- Molecule 46 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	j	111	Total	C	N	O	S	0	0
			918	578	178	160	2		

- Molecule 47 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	k	129	Total	C	N	O	S	0	0
			1064	673	220	166	5		

- Molecule 48 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Y	167	Total	C	N	O	S	0	0
			1355	848	260	238	9		

- Molecule 49 is a protein called MKI67 FHA domain-interacting nucleolar phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	t	111	Total	C	N	O	S	0	0
			928	601	157	167	3		

- Molecule 50 is a protein called Ribosomal L1 domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	s	239	Total	C	N	O	S	0	0
			1924	1232	338	348	6		

- Molecule 51 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	i	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 52 is a protein called Ribosome production factor 2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	T	266	Total	C	N	O	S	0	0
			2166	1388	382	384	12		

- Molecule 53 is a RNA chain called 5S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	5	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 54 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	q	404	Total	C	N	O	S	0	0
			3317	2140	582	582	13		

- Molecule 55 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	f	258	Total	C	N	O	S	0	0
			2137	1326	427	382	2		

- Molecule 56 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	O	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 57 is a protein called 60S ribosomal protein L7-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	3	229	Total	C	N	O	S	0	0
			1892	1223	356	309	4		

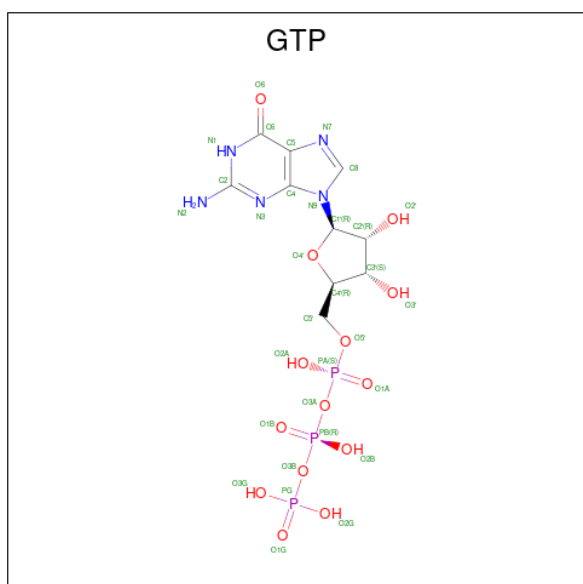
- Molecule 58 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	g	143	Total	C	N	O	S	0	0
			1156	740	220	195	1		

- Molecule 59 is a RNA chain called ITS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	x	54	Total	C	N	O	P	0	0
			648	270	1	323	54		

- Molecule 60 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

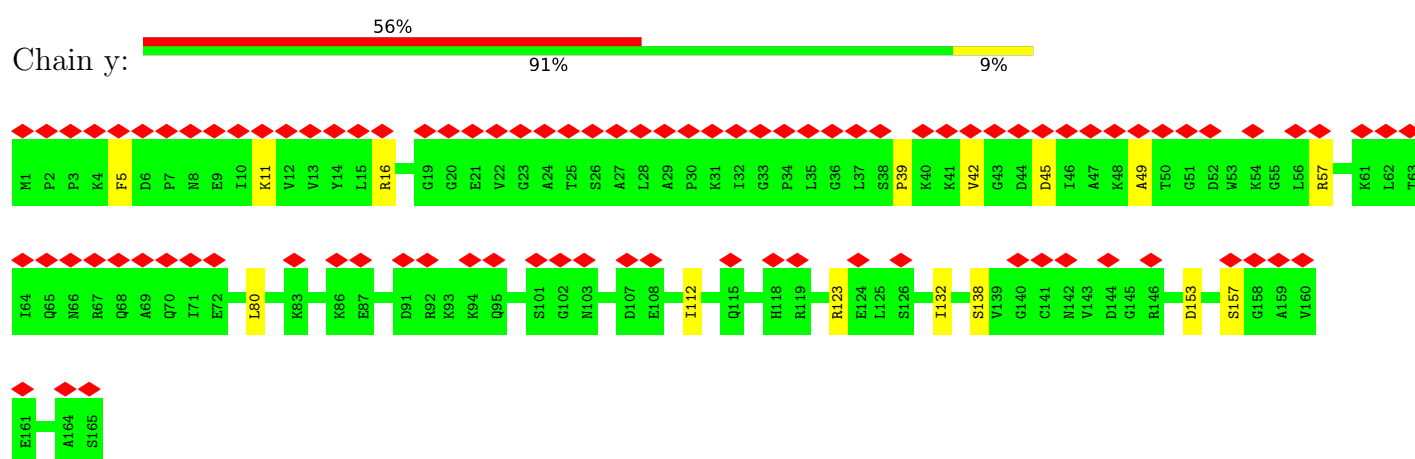
- Molecule 61 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
61	w	1	Total 1	Mg 1	0

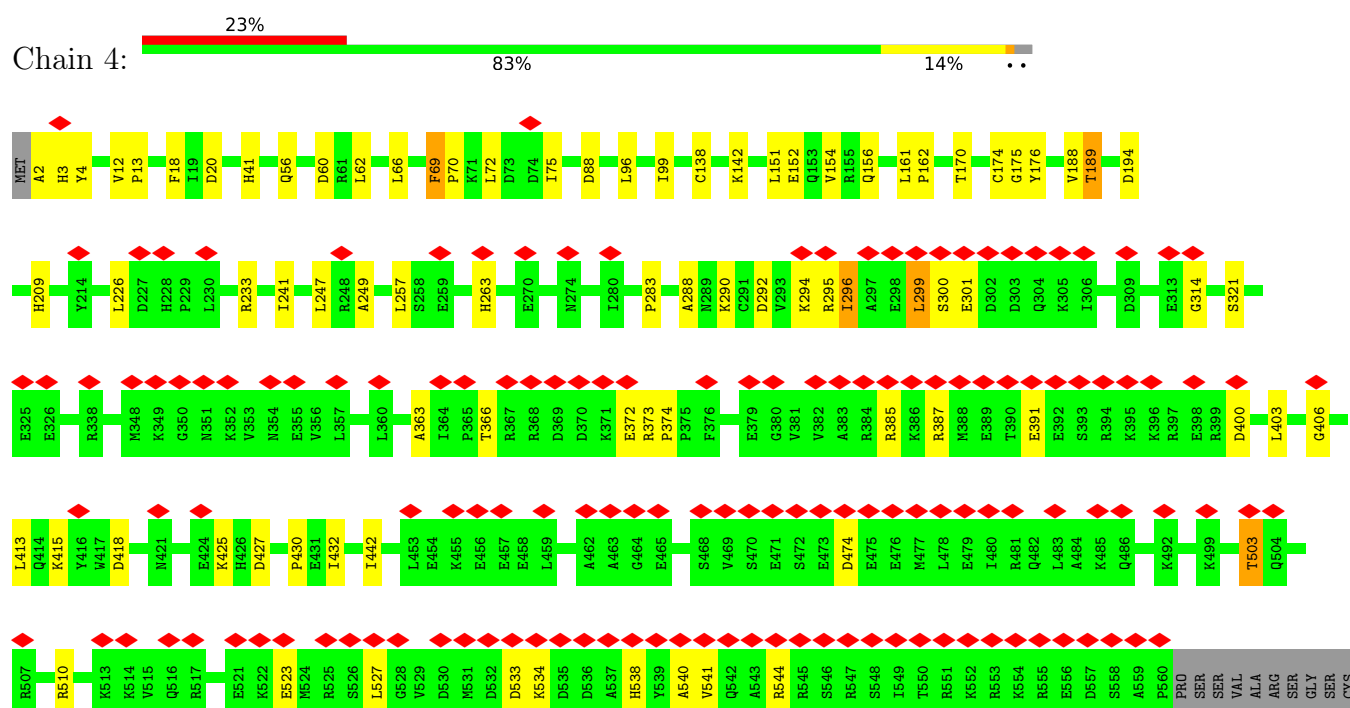
3 Residue-property plots [i](#)

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

• Molecule 1: 60S ribosomal protein L12

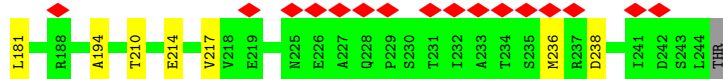
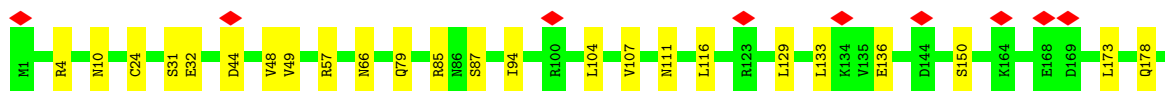
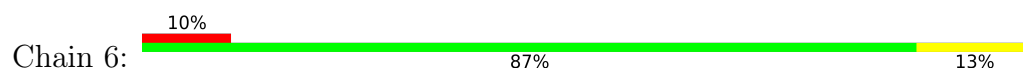


• Molecule 2: GTP-binding protein 4

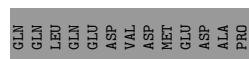
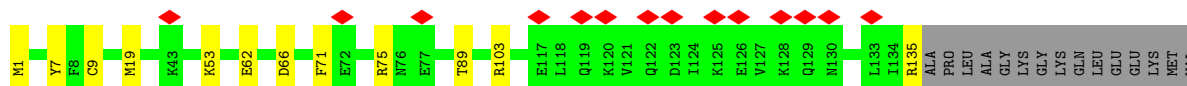
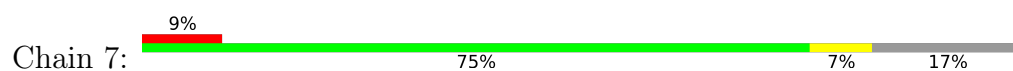




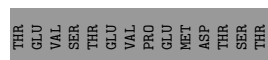
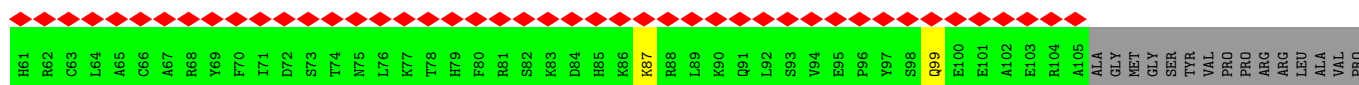
- Molecule 3: Eukaryotic translation initiation factor 6



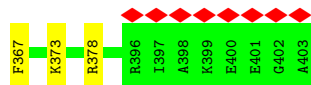
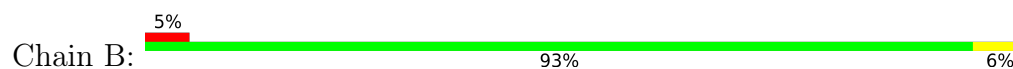
- Molecule 4: Probable ribosome biogenesis protein RLP24



- Molecule 5: Zinc finger protein 593

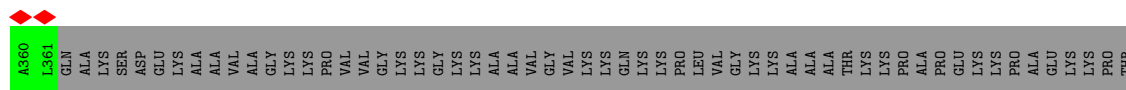


- Molecule 6: 60S ribosomal protein L3



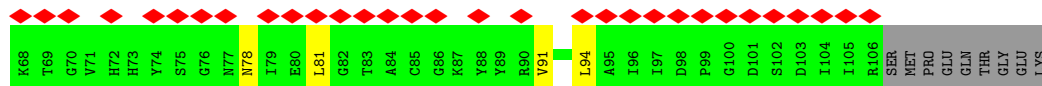
- Molecule 7: 60S ribosomal protein L4

Frequency	Percentage
Daily	78%
Weekly	5%
Monthly	16%



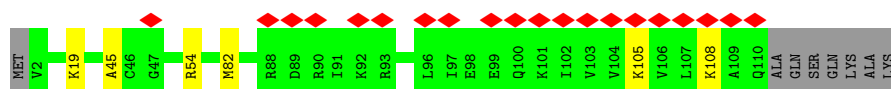
THR
GLU
GLU
LYS
LYS
PRO
ALA
ALA

Response	Percentage
U.S. is a threat to my country's security	58%
U.S. is not a threat to my country's security	74%
Don't know	11%
No answer	15%



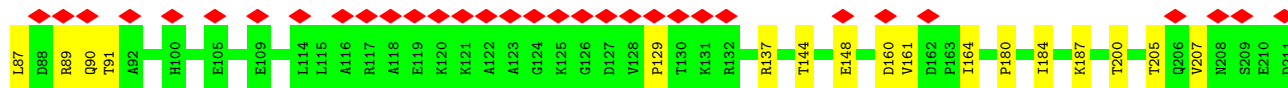
- Molecule 9: 60S ribosomal protein L34

Device Type	Percentage
Smartphone	88%
Tablet	17%
Smartwatch	5%
Wearable device	7%



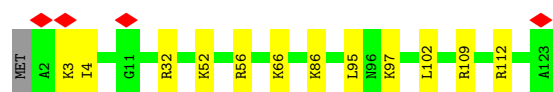
- Molecule 10: 60S ribosomal protein L7a

Responsibility	Percentage
Current government	38%
Previous government	80%
Both governments	10%
Neither government	9%

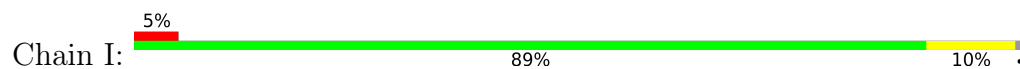


Year	Number of Publications
2012	10
2013	15
2014	18
2015	12
2016	10
2017	15
2018	18
2019	12
2020	10
2021	15
2022	18
2023	12
2024	10
2025	15
2026	18

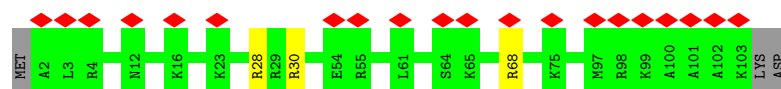
Response	Percentage
Yes	89%
No	10%



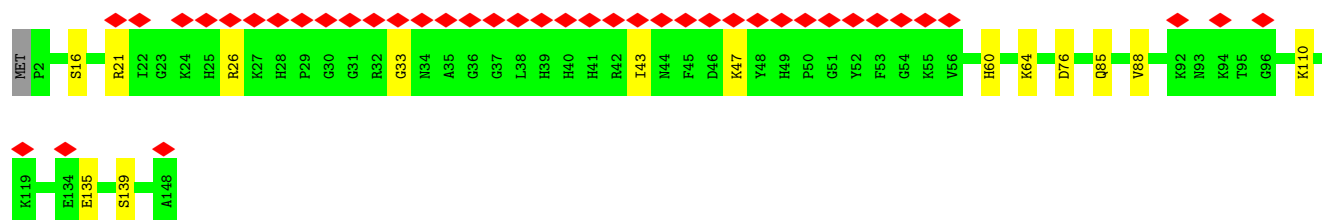
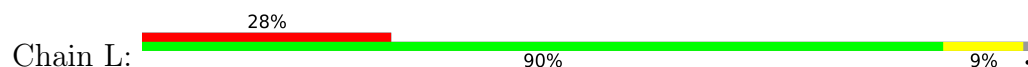
- Molecule 12: 60S ribosomal protein L9



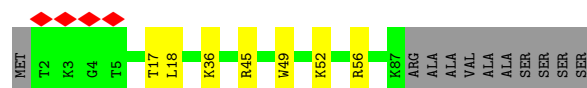
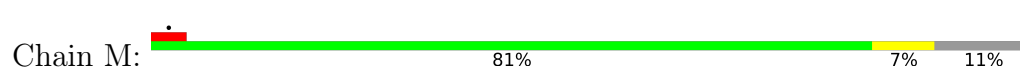
- Molecule 13: 60S ribosomal protein L36



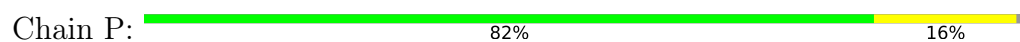
- Molecule 14: 60S ribosomal protein L27a



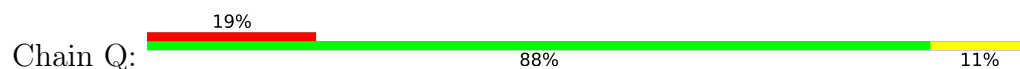
- Molecule 15: 60S ribosomal protein L37



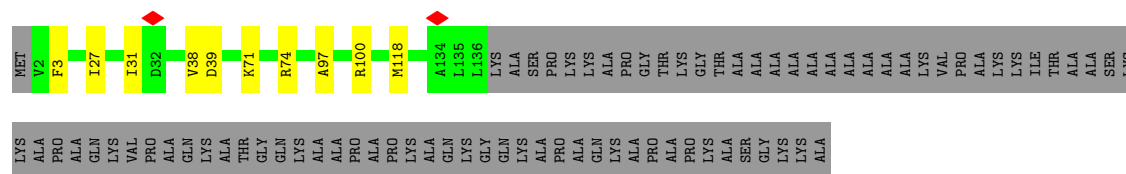
- Molecule 16: 60S ribosomal protein L39



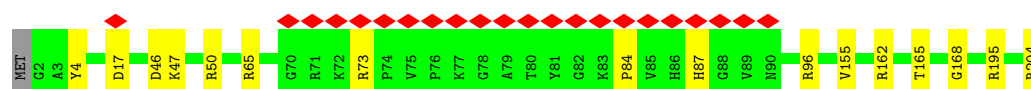
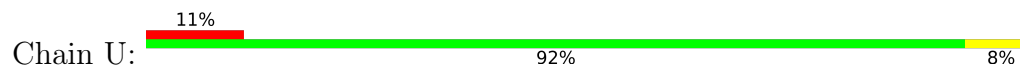
- Molecule 17: 60S ribosomal protein L13



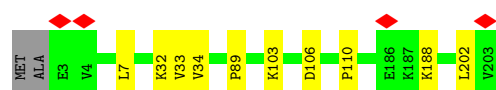
- Molecule 18: 60S ribosomal protein L14



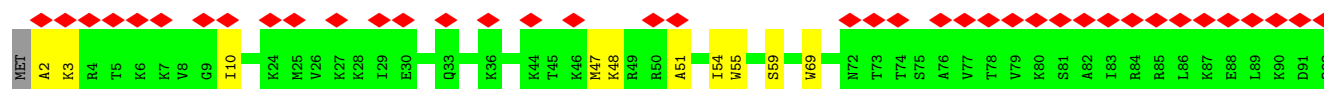
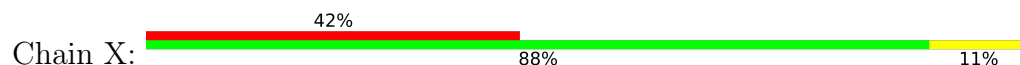
- Molecule 19: 60S ribosomal protein L15



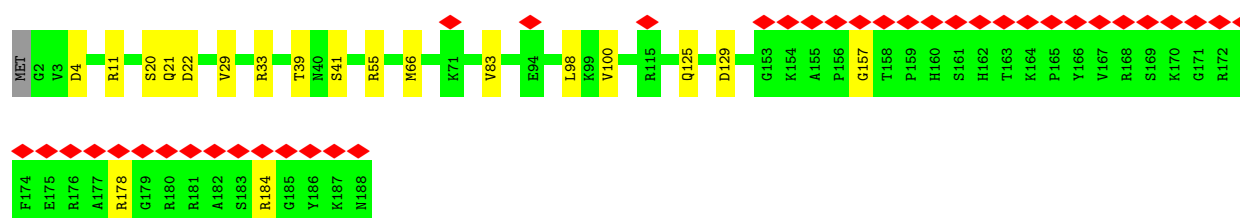
- Molecule 20: 60S ribosomal protein L13a



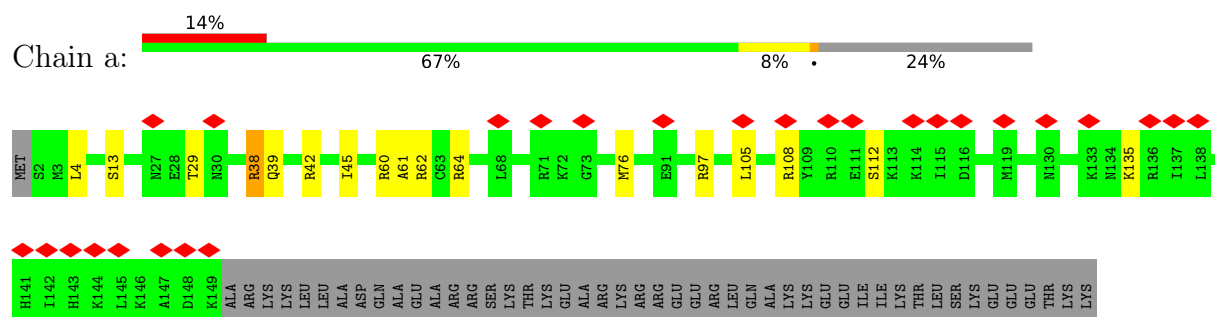
- Molecule 21: 60S ribosomal protein L37a



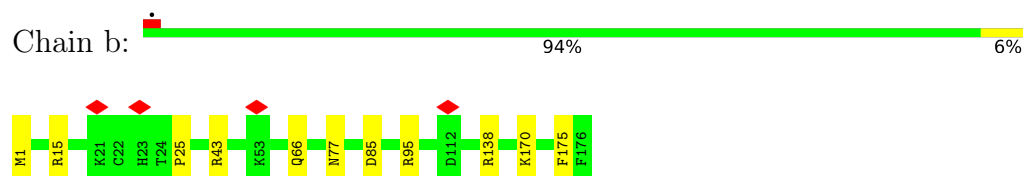
- Molecule 22: 60S ribosomal protein L18



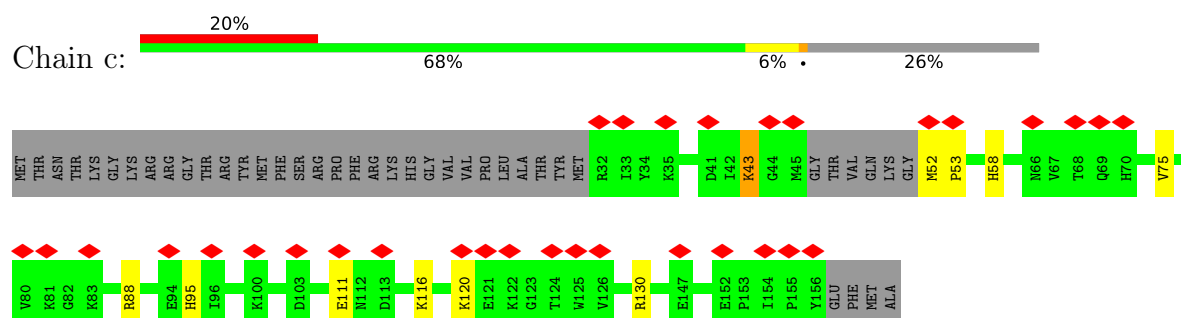
- Molecule 23: 60S ribosomal protein L19



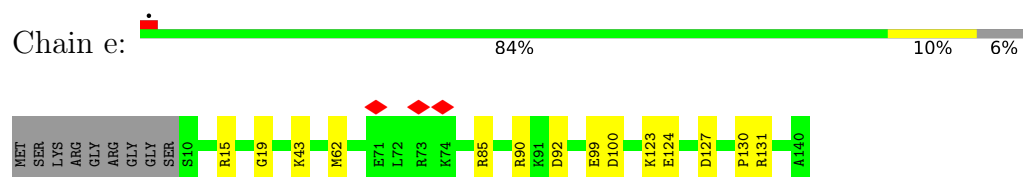
- Molecule 24: 60S ribosomal protein L18a



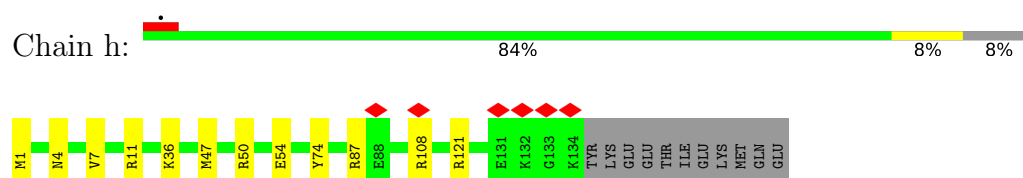
- Molecule 25: 60S ribosomal protein L21



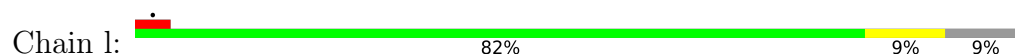
- Molecule 26: 60S ribosomal protein L23

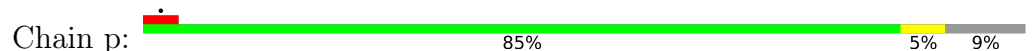


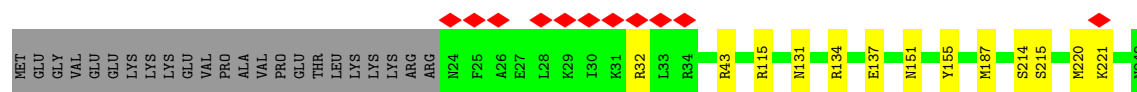
- Molecule 27: 60S ribosomal protein L26



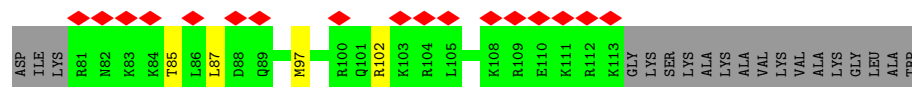
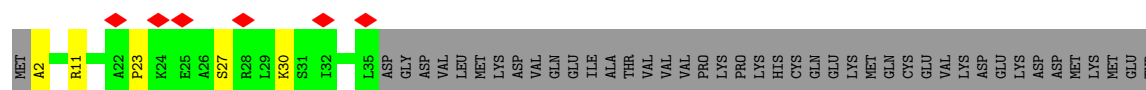
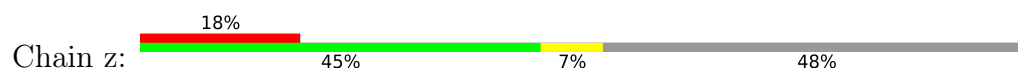
- Molecule 28: 60S ribosomal protein L28



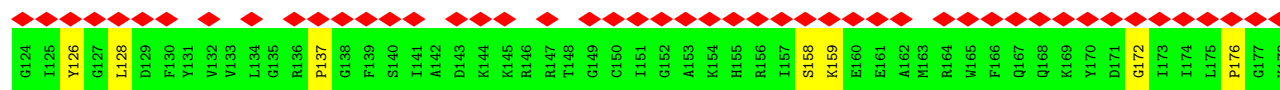
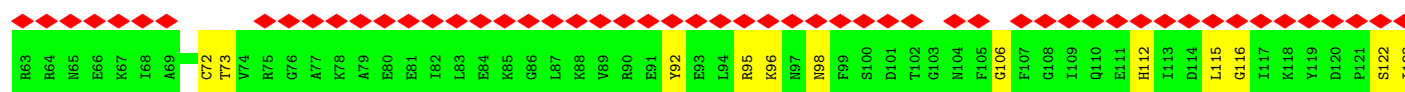
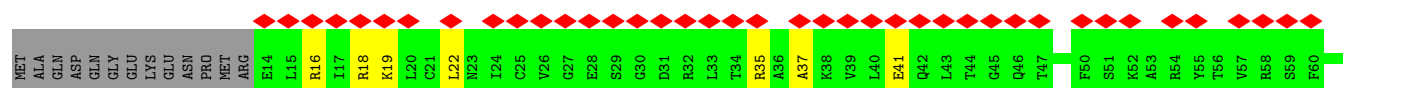
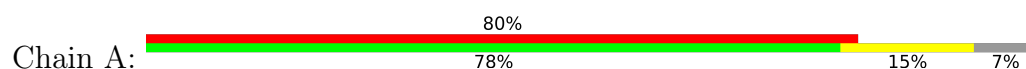




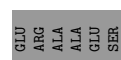
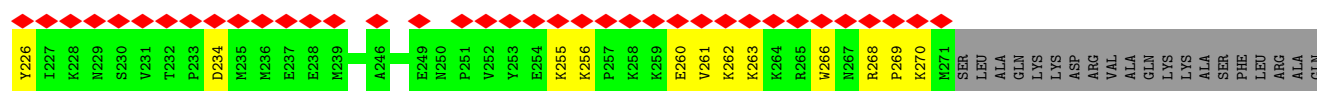
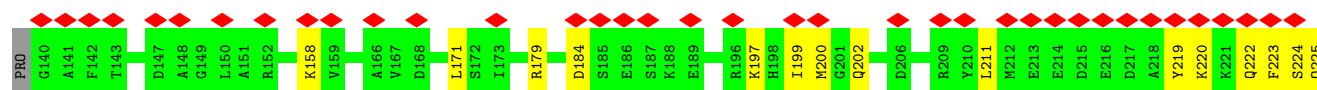
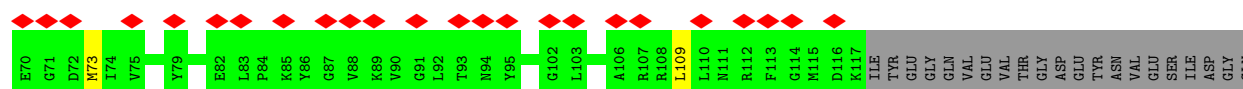
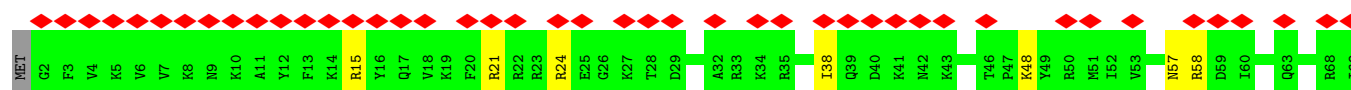
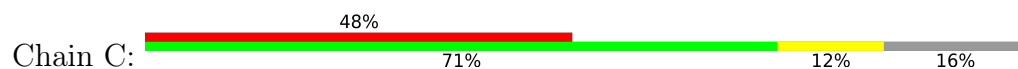
• Molecule 33: Protein LLP homolog

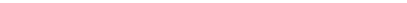


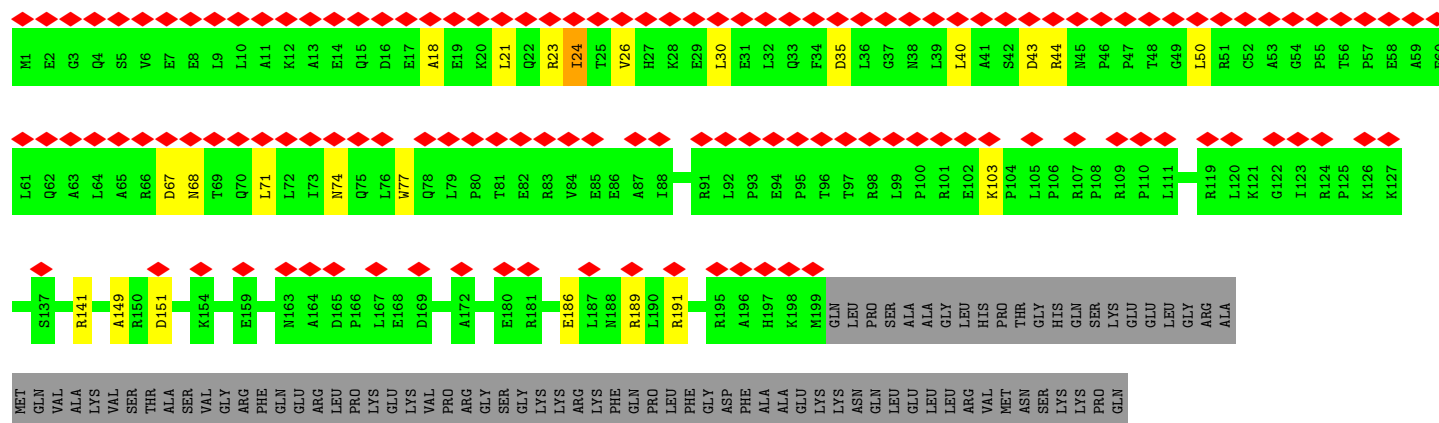
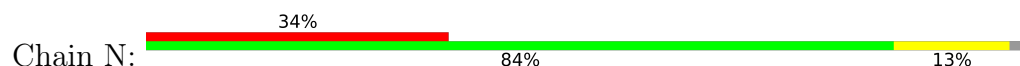
• Molecule 34: 60S ribosomal protein L11

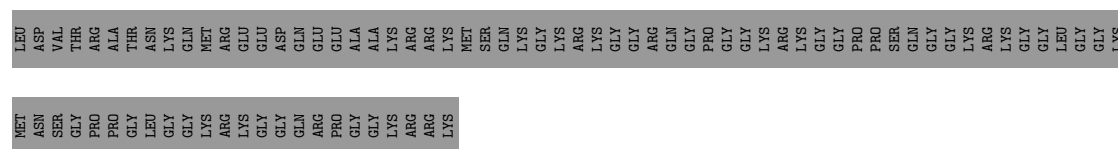


• Molecule 35: 60S ribosomal protein L5

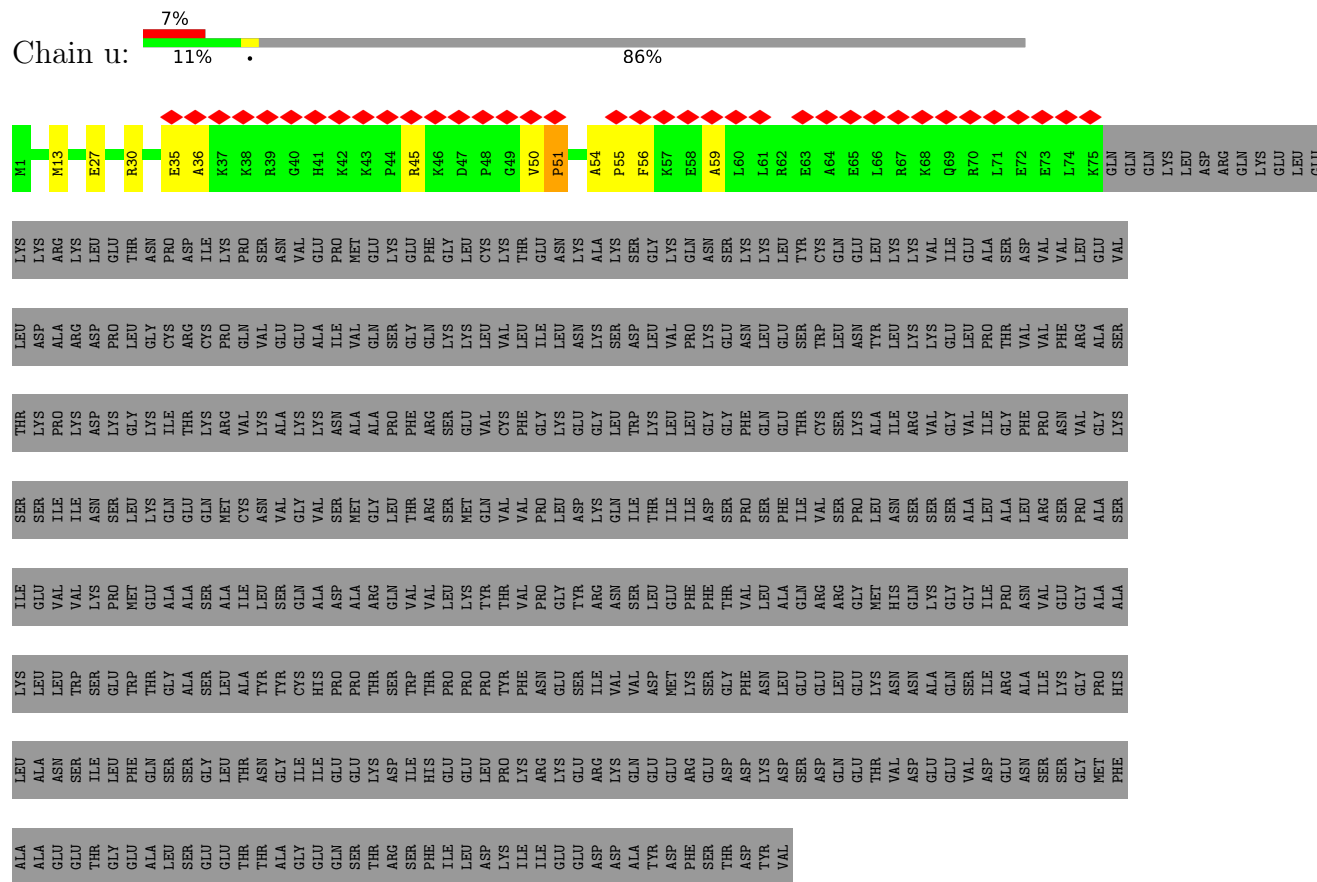


- Chain J:  8% 92% 8%

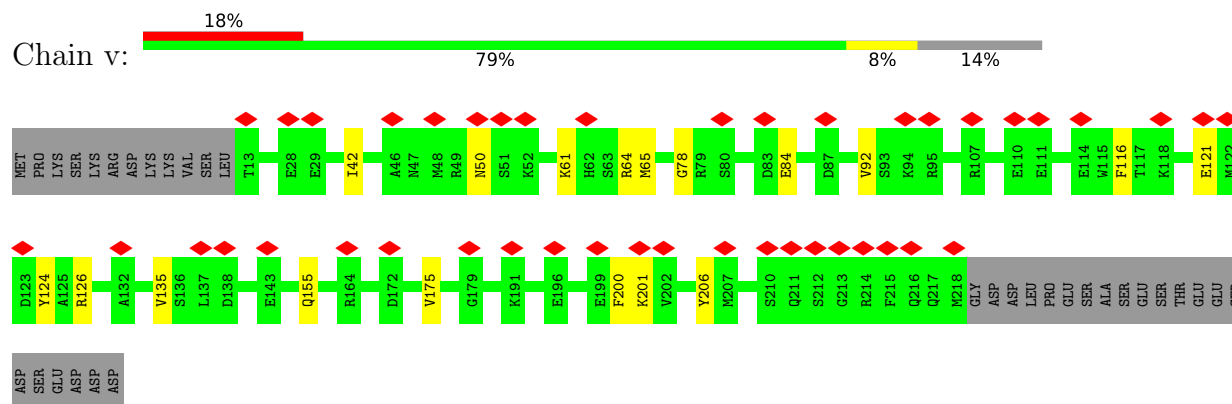




• Molecule 39: Guanine nucleotide-binding protein-like 3



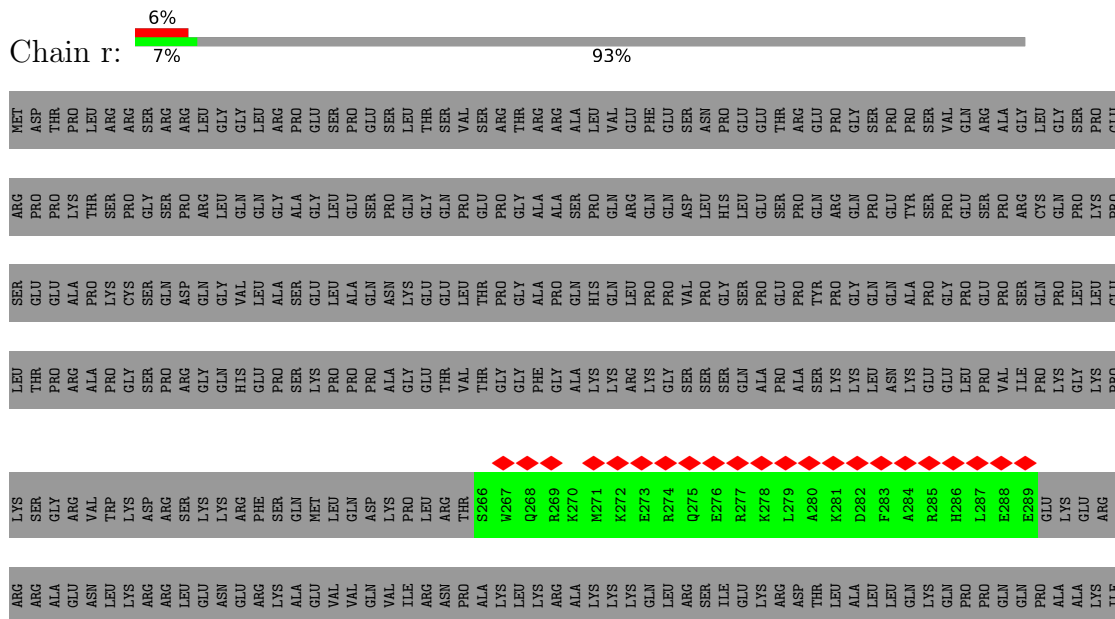
• Molecule 40: mRNA turnover protein 4 homolog



• Molecule 41: G Protein Nucleolar 2

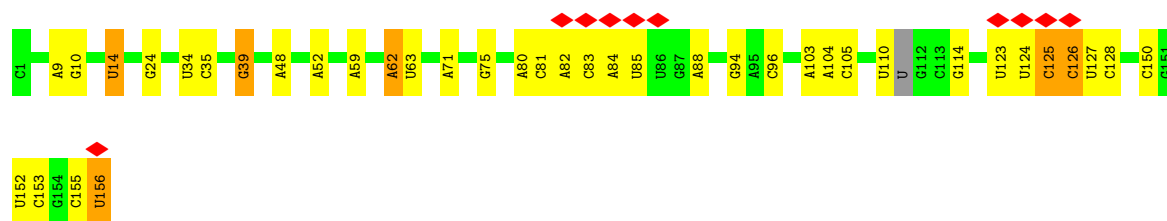


- Molecule 42: Coiled-coil domain-containing protein 86

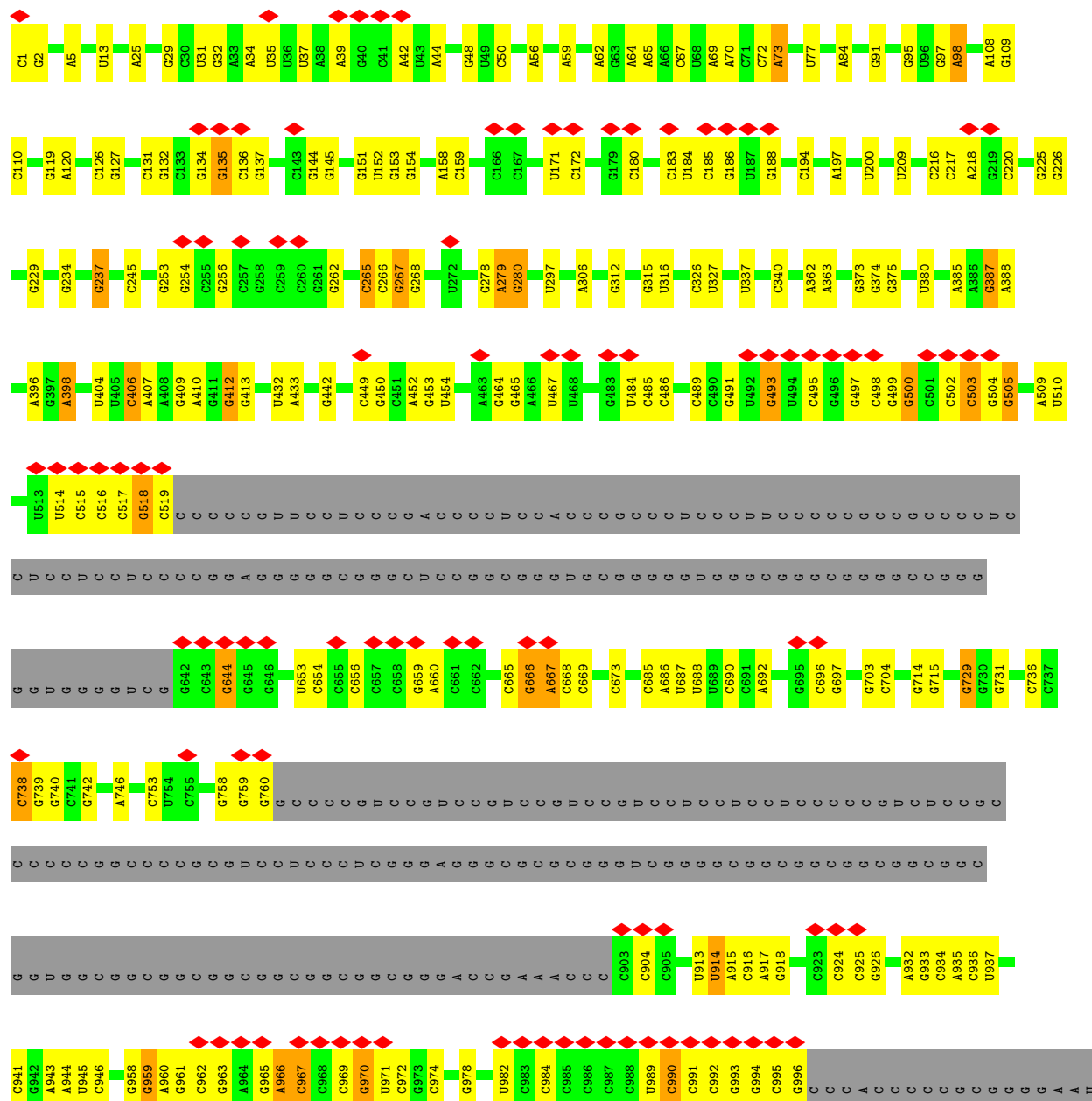


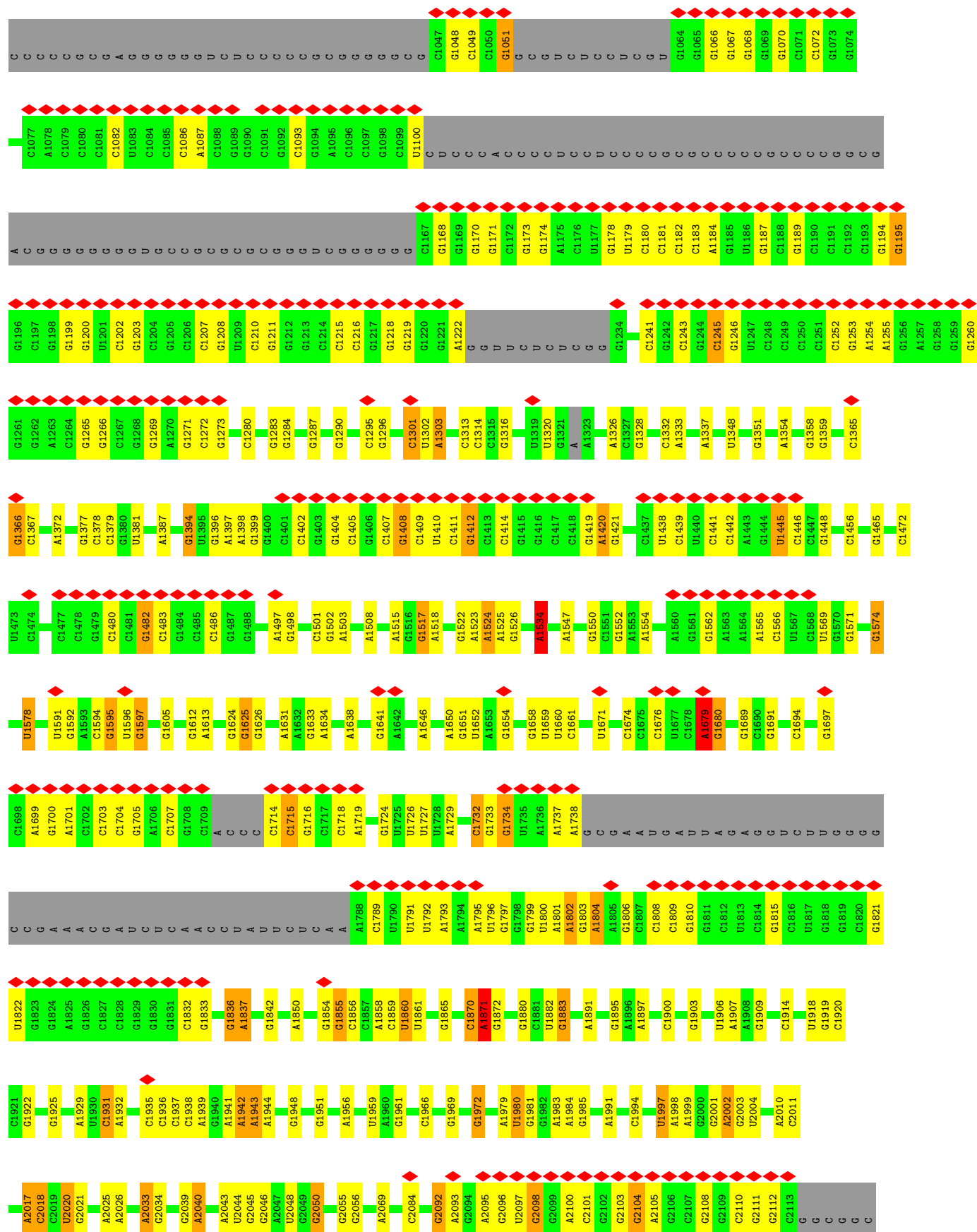
- Molecule 43: 5.8S rRNA





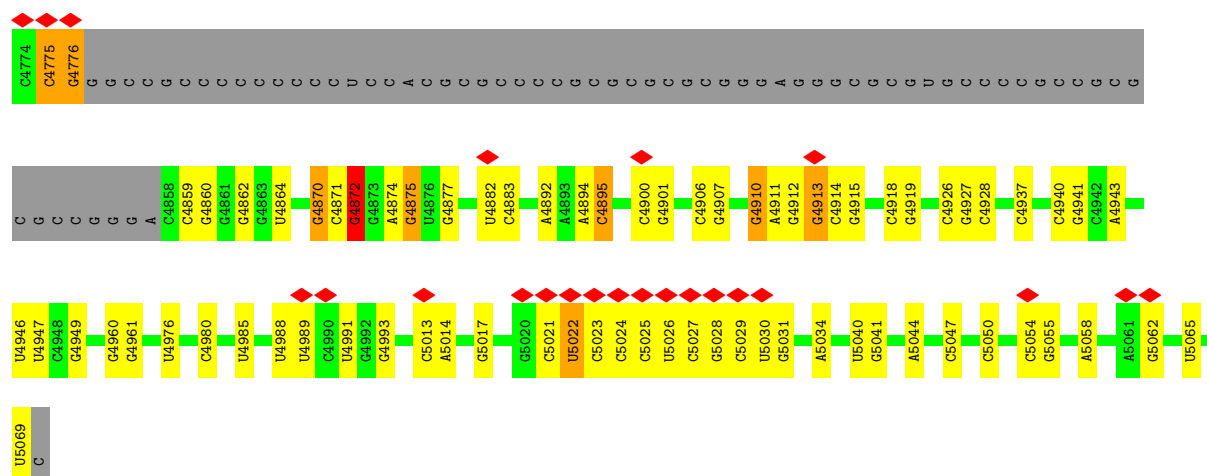
• Molecule 44: 28S rRNA



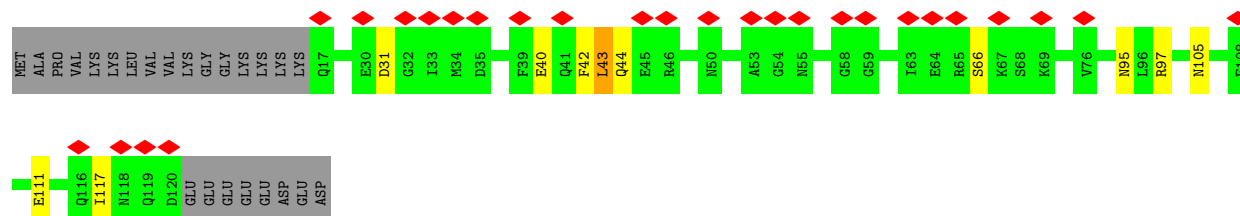




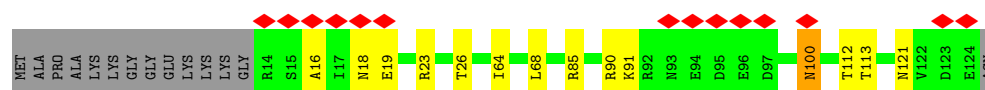
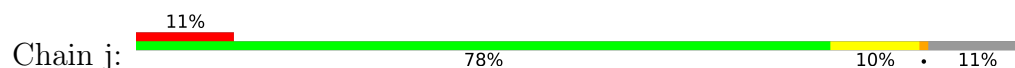
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U4846	U4532	U4437	A4348	A4273	A4205	C4133	U4066	A3845	U3773	U3713	C3615
G4852	C4536	G4440	C4349	G4274	C4206	C4134	U4067	U3851	A3774	G3714	U3616
A4556	C4537	G4446	C4350	G4275	C4207	G4135	U4068	C3855	A3775	U3715	C3617
U4557	G4538	U4448	U4354	G4276	U4208	C4136	U4069	A3856	G3776	C3716	C3618
G4559	U4539	C4447	C4355	G4277	U4209	C4137	U4070	U3859	G3777	A3717	C3619
C4545	C4540	G4448	G4356	A4279	U4210	C4138	U4071	G3859	A3718	A3719	G3626
U4548	U4449	A4280	A4369	A4281	C4211	G4139	C4072	A3865	G3779	G3720	A3630
G4549	U4450	G4282	G4370	A4282	U4212	C4140	A4073	C3866	G3780	U3721	A3635
G4550	U4451	G4283	G4371	G4283	A4213	G4141	C4074	A3867	C3781	G3722	U3641
C4453	U4452	U4284	U4372	U4285	A4214	C4142	U4075	G3868	A3782	A3723	A3635
G4454	C4453	G4454	G4373	U4290	C4215	G4143	C4076	C3869	A3783	A3724	U3641
U4555	A4464	U4291	U4374	G4291	G4216	C4144	C4080	G3875	A	G3725	U3644
U4556	U4465	A4292	C4375	A4292	G4217	C4145	U4081	A3876	A	A3726	U3644
U4557	C4466	U4296	A4376	U4296	U4218	G4146	G4082	A3877	U	G3727	U3645
A4559	G4472	U4297	G4377	U4297	A4219	G4147	U4083	C3878	C	A3728	U3646
C4560	G4475	G4297	A4378	U4298	A4220	C4148	G4084	G3880	U	U3729	C3658
A4564	G4476	U4300	A4379	U4299	C4221	C4149	G4087	C3887	C	U3730	G3659
G4569	G4477	U4301	A4380	U4299	C4222	G4150	C4092	G3897	U	C3731	A3662
U4570	G4478	U4302	A4381	U4299	C4223	G4151	C4093	C3898	C	A3732	A3663
A4571	A4479	C4303	C4386	U4300	A4224	G4152	C4094	G3899	U	U3733	G3664
U4572	U4480	C4304	C4387	U4301	G4225	C4153	C4095	C3903	C	A3734	U3669
C4483	C4483	G4305	G4393	U4302	G4226	G4154	C4096	C3904	U	G3735	C3670
U4484	A4484	G4306	A	U4303	U4227	C4155	C4097	A3905	U	A3736	C3671
U4492	U4492	U4307	U	A4307	G4228	G4156	C4098	C3906	U	G3737	C3672
U4493	G4493	C4308	A	C4308	U4229	A4157	A4099	C3909	U	C3738	C3673
G4499	U4499	G4309	A	G4309	C4230	C4158	C4100	C	A	G3739	C3674
U4500	U4500	A4310	C	A4310	C	C4162	C4101	U3914	G	G3740	U3678
U4501	G4400	A4311	U	A4311	U	U4163	C4102	U3915	U	G3742	U3679
C4502	G4401	U4312	A	G4312	G4235	G4166	C4103	G3916	C	G3743	U3680
A4503	C4402	A4313	U	A4313	G4236	G4167	C4104	C	C	G3744	C3681
C4508	U4403	C4314	U	C4314	G4237	G4168	C4105	G3922	C	U3745	C3691
U4509	U4404	G4315	G4405	G4315	G4238	G4169	A4170	A3923	C	A3746	A3692
A4510	G4405	G4316	C	G4316	C4243	C4171	G4106	C3924	C	A3747	U3693
A4511	G4411	C4319	U	C4319	A4244	U4174	G4107	U3925	C	A3748	U3695
U4512	A4414	G4328	A	G4328	G4245	C4175	C4108	C3926	U	G3749	C3696
A4513	A4415	G4329	U	G4329	G4246	C4176	C4109	U3927	C	G3750	U3697
G4518	G4418	G4330	U	G4330	G4247	C4177	C4110	A3928	A	G3751	C3698
C4519	U4419	U4334	U	U4334	A4251	C4178	U4111	G3929	U	C3752	C3699
G4520	U4420	C4335	U	C4335	A4252	G4179	C4112	U3930	C	G3753	C3700
U4521	C4421	A4336	U	A4336	G4254	G4180	U4113	C3931	C	G3754	C3701
C4522	C4422	C4337	U	C4337	A4255	G4181	C4114	U3932	A	G3755	C3702
A4523	U4423	G4338	U	G4338	C4258	G4183	U4115	C3933	U	A3756	A3702
G4524	U4424	A4339	U	A4339	G4263	G4184	C4116	G3938	C	G3757	C3703
C4528	G4425	U4340	U	U4340	G4264	G4185	U4117	G3939	C	U3758	U3704
U4529	G4426	C4341	U	C4341	U4265	U4188	C4119	A3942	U	A3759	C3705
U4634	U4427	C4342	U	C4342	G4266	U4190	U4120	A3943	C	A3760	C3706
A4635	A4428	C4343	U	C4343	A4267	G	C4121	G3944	C	C3761	U3707
U4636	C4429	U4343	U	U4343	A4268	A	C4125	U3838	U	U3762	C3708
C4771	G4430	U4343	U	U4343	C	C	C4126	C3839	C	A3763	U3709
C4772	U4530	U4343	U	U4343	U	G4196	A4127	U3840	C	U3764	G3710
C4773	U4530	U4343	U	U4343	U	G4197	A4128	C3843	C	G3765	A3711
		U4343	U	U4343	U	G4197	C4129			A3766	
		U4343	U	U4343	U	G4197	C4130			C3767	
		U4343	U	U4343	U	G4197	C4131			U3768	
		U4343	U	U4343	U	G4197	C4131			C3769	
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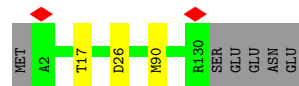
• Molecule 45: 60S ribosomal protein L22



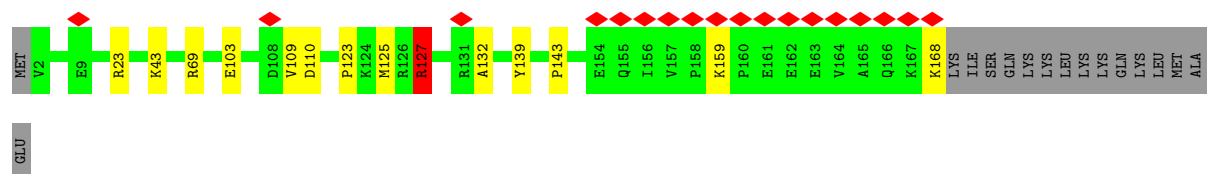
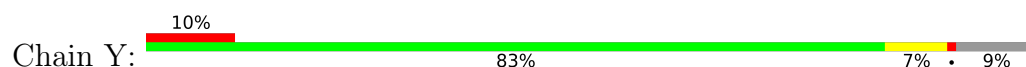
• Molecule 46: 60S ribosomal protein L31



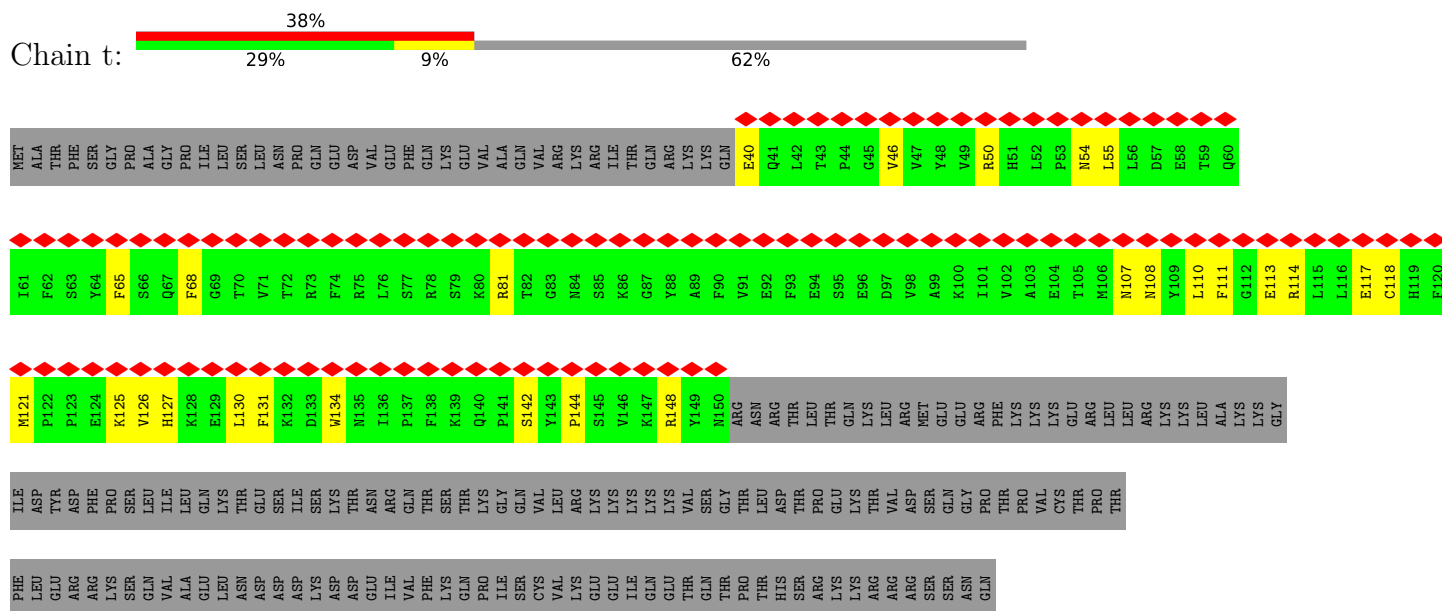
• Molecule 47: 60S ribosomal protein L32



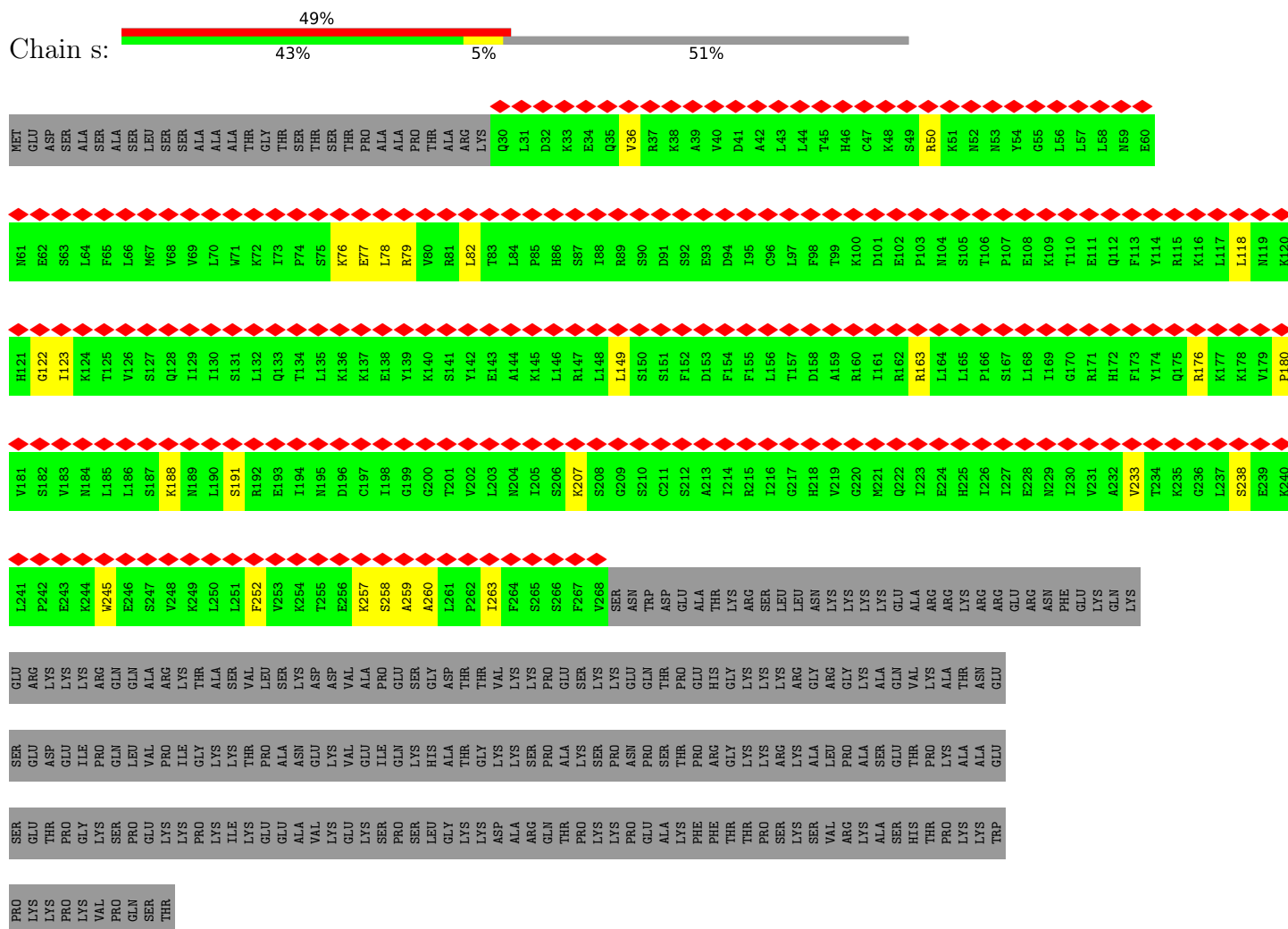
• Molecule 48: 60S ribosomal protein L17



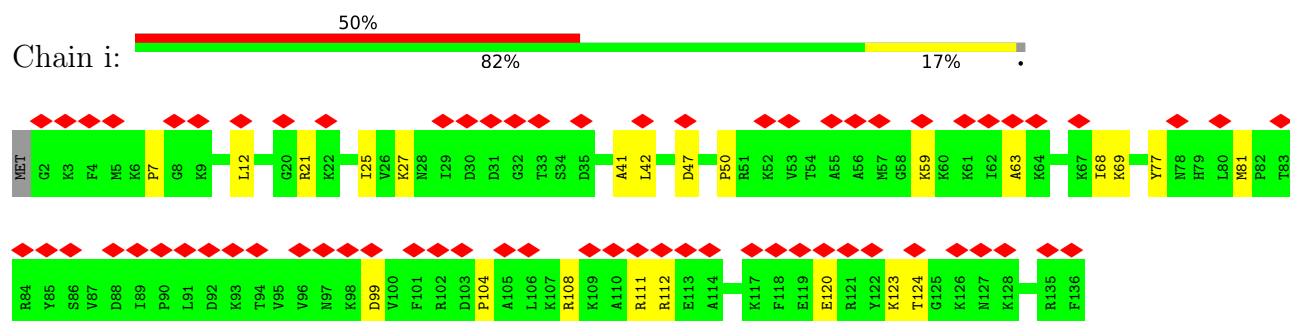
• Molecule 49: MKI67 FHA domain-interacting nucleolar phosphoprotein



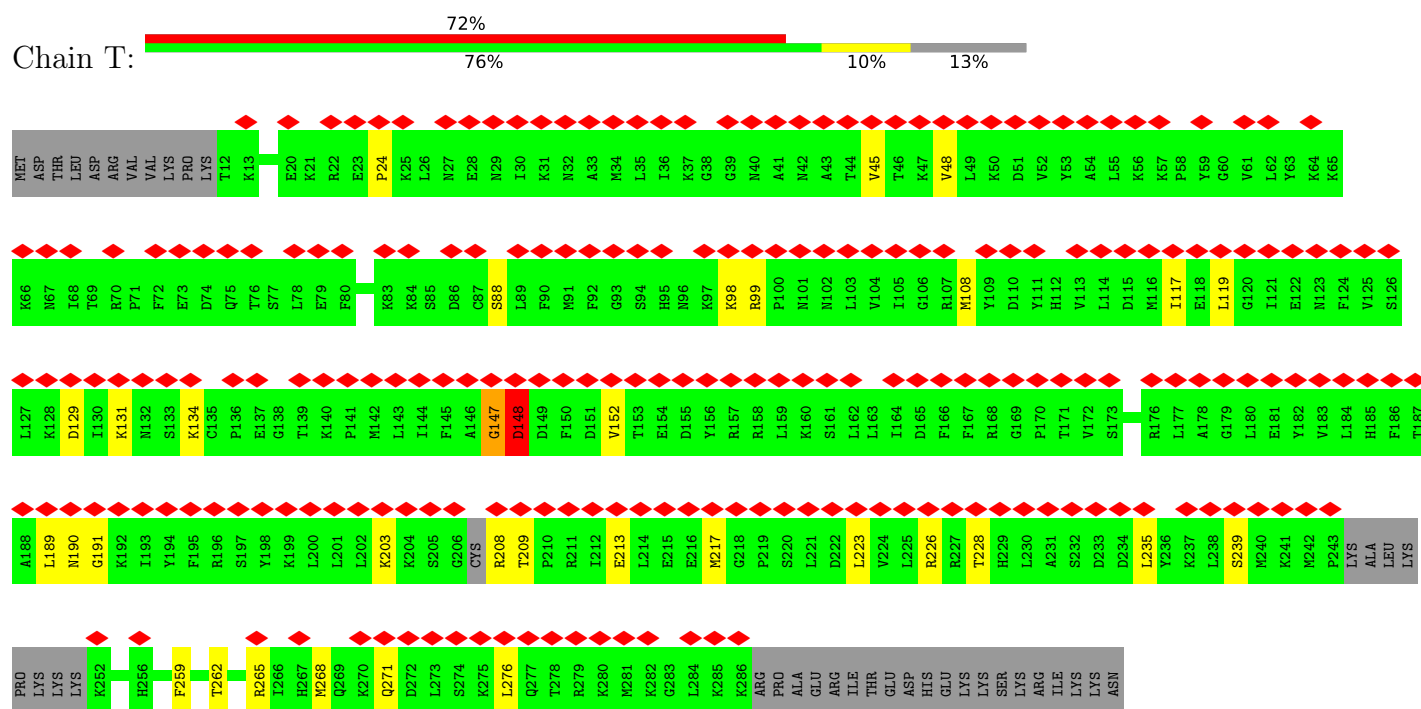
• Molecule 50: Ribosomal L1 domain-containing protein 1



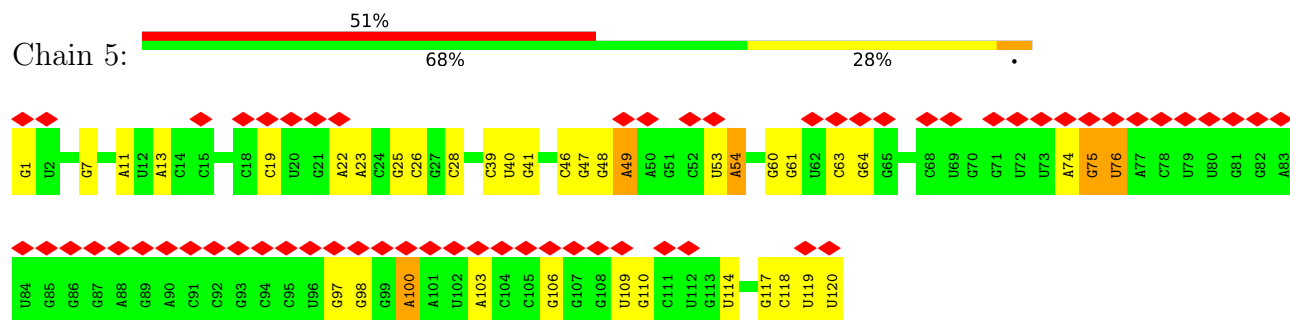
- Molecule 51: 60S ribosomal protein L27



- Molecule 52: Ribosome production factor 2 homolog

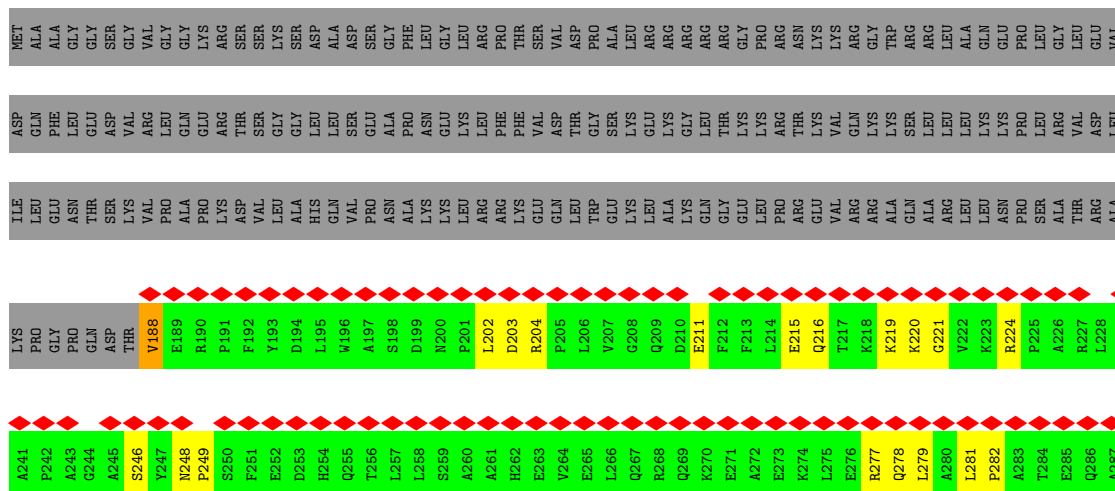
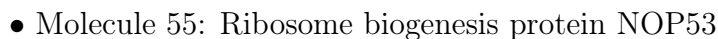


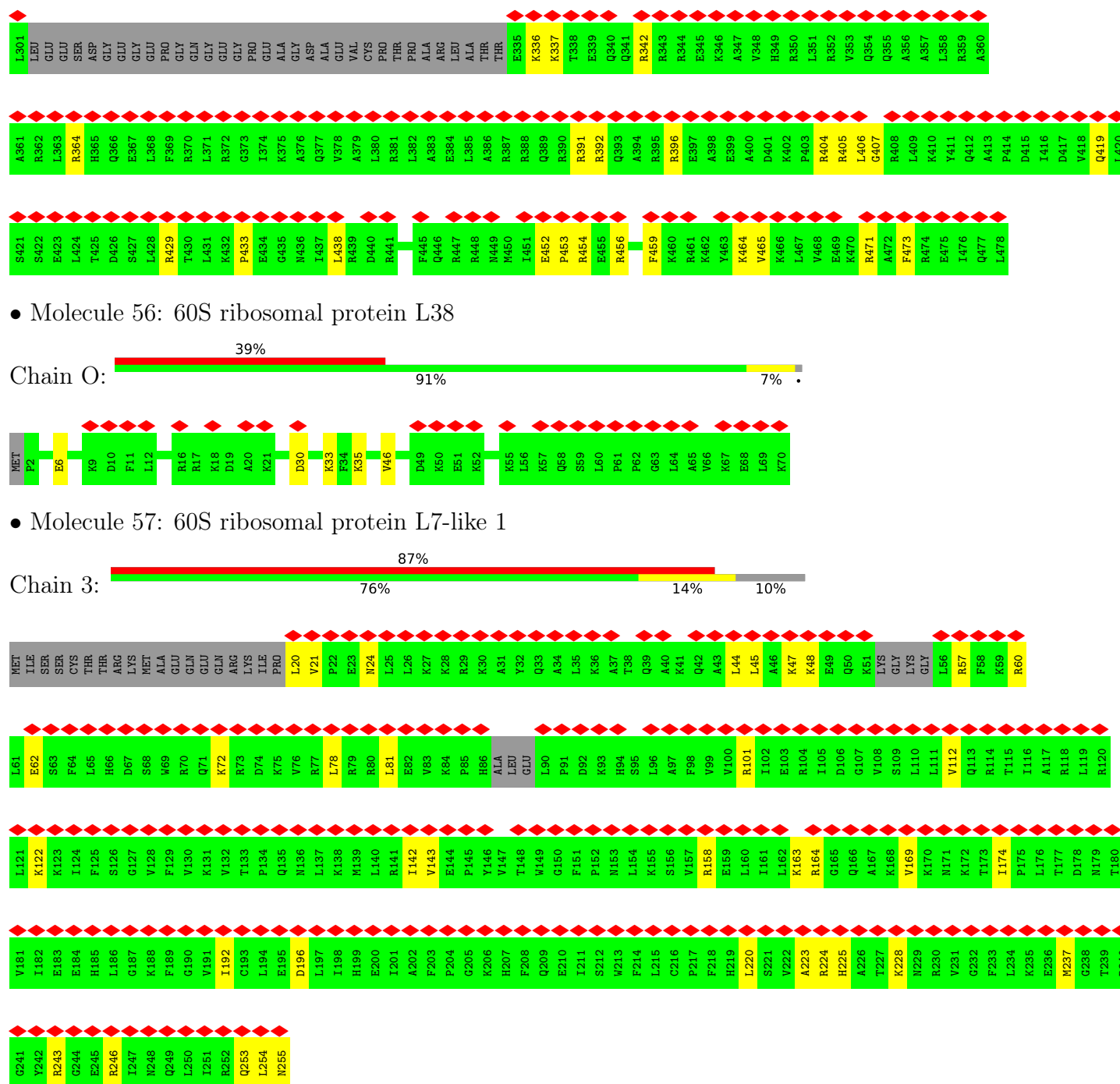
- Molecule 53: 5S RNA

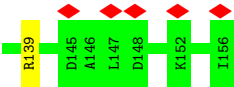


- Molecule 54: Pescadillo homolog

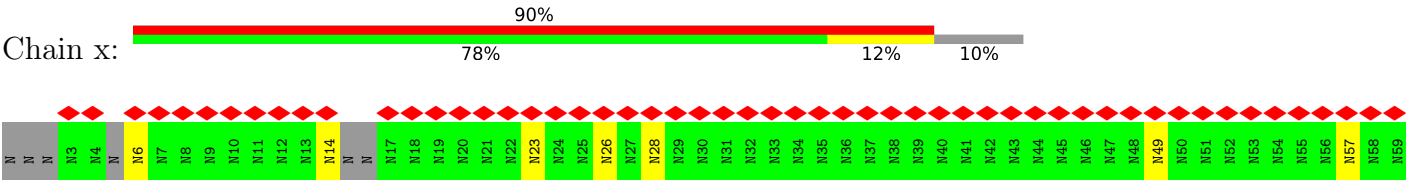








• Molecule 59: ITS2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18549	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 ($e^-/\text{\AA}^2$)	1.8	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.165	Depositor
Minimum map value	-0.056	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	548.0, 548.0, 548.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.37, 1.37, 1.37	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: PSU, UR3, B9B, B8W, A2M, E7G, 7MG, B8T, OMG, MG, B9H, OMC, I4U, B8Q, 5MU, P4U, M7A, P7G, OMU, 1MA, B8K, BGH, GTP, 2MG

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	y	0.34	0/1269	0.79	0/1712
2	4	0.38	1/5177 (0.0%)	0.91	24/6942 (0.3%)
3	6	0.34	0/1877	0.74	1/2554 (0.0%)
4	7	0.33	0/1181	0.69	2/1563 (0.1%)
5	9	0.35	0/723	0.84	3/961 (0.3%)
6	B	0.34	1/3315 (0.0%)	0.72	4/4435 (0.1%)
7	D	0.31	0/2907	0.68	3/3905 (0.1%)
8	E	0.34	0/774	0.75	2/1038 (0.2%)
9	F	0.30	0/878	0.63	0/1170
10	G	0.32	0/1971	0.75	4/2651 (0.2%)
11	H	0.31	0/1023	0.60	0/1351
12	I	0.34	0/1537	0.76	2/2066 (0.1%)
13	K	0.30	0/843	0.71	0/1115
14	L	0.27	0/1191	0.62	0/1591
15	M	0.30	0/720	0.68	0/952
16	P	0.30	0/454	0.59	0/599
17	Q	0.32	0/1732	0.67	1/2315 (0.0%)
18	S	0.34	0/1133	0.71	3/1516 (0.2%)
19	U	0.27	0/1746	0.55	0/2338
20	V	0.34	0/1682	0.62	1/2250 (0.0%)
21	X	0.29	0/718	0.72	0/953
22	Z	0.29	0/1537	0.60	1/2052 (0.0%)
23	a	0.30	0/1255	0.76	4/1662 (0.2%)
24	b	0.30	0/1501	0.64	0/2013
25	c	0.33	0/994	0.76	2/1327 (0.2%)
26	e	0.34	0/993	0.74	0/1332
27	h	0.30	0/1132	0.63	0/1504
28	l	0.29	0/1017	0.62	0/1364
29	m	0.33	1/1936 (0.1%)	0.75	0/2596
30	n	0.29	0/895	0.73	3/1198 (0.3%)
31	o	0.32	0/1935	0.73	4/2596 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	p	0.39	1/1916 (0.1%)	0.75	4/2553 (0.2%)
33	z	0.33	0/587	0.80	0/767
34	A	0.32	0/1341	0.81	0/1793
35	C	0.28	0/2068	0.72	2/2767 (0.1%)
36	J	0.30	0/2146	0.66	4/2865 (0.1%)
37	N	0.29	0/3756	0.70	4/5103 (0.1%)
38	R	0.31	0/1668	0.80	4/2255 (0.2%)
39	u	0.40	0/649	0.95	5/851 (0.6%)
40	v	0.30	0/1714	0.69	1/2300 (0.0%)
41	w	0.30	0/3699	0.69	1/4992 (0.0%)
42	r	0.24	0/220	0.72	0/288
43	8	0.30	0/3656	0.47	1/5694 (0.0%)
44	2	0.28	5/83201 (0.0%)	0.49	27/129722 (0.0%)
45	d	0.36	0/864	0.96	6/1160 (0.5%)
46	j	0.32	0/933	0.69	0/1256
47	k	0.32	0/1082	0.68	0/1443
48	Y	0.29	0/1383	0.66	1/1856 (0.1%)
49	t	0.32	0/955	0.77	3/1290 (0.2%)
50	s	0.28	0/1956	0.67	0/2631
51	i	0.32	0/1130	0.75	0/1507
52	T	0.33	0/2204	0.81	4/2944 (0.1%)
53	5	0.23	0/2858	0.41	0/4455
54	q	0.31	0/3395	0.72	1/4578 (0.0%)
55	f	0.49	1/2169 (0.0%)	0.71	5/2902 (0.2%)
56	O	0.38	0/575	0.77	0/761
57	3	0.30	0/1928	0.71	0/2584
58	g	0.39	0/1175	0.69	1/1572 (0.1%)
All	All	0.30	10/175274 (0.0%)	0.61	138/254510 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	4	0	5
6	B	0	1
7	D	0	1
17	Q	0	1
25	c	0	1
30	n	0	1
39	u	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
48	Y	0	1
49	t	0	1
52	T	0	1
55	f	0	1
All	All	0	17

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	f	188	VAL	C-N	19.48	1.55	1.33
32	p	137	GLU	C-N	8.01	1.40	1.33
44	2	4405	G	C1'-N9	-6.39	1.37	1.47
44	2	4399	U	C1'-N1	5.95	1.56	1.47
44	2	4403	U	C1'-N1	5.94	1.57	1.48

The worst 5 of 138 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	1871	A2M	OP2-P-O3'	-16.21	69.55	105.20
44	2	1871	A2M	OP1-P-O3'	14.68	137.48	105.20
44	2	1872	G	OP1-P-OP2	-13.46	79.22	119.60
55	f	188	VAL	O-C-N	-10.18	106.72	123.00
2	4	314	GLY	CA-C-N	10.15	134.90	122.42

There are no chirality outliers.

5 of 17 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	4	189	THR	Peptide
2	4	299	LEU	Peptide
2	4	300	SER	Peptide
2	4	503	THR	Peptide
2	4	69	PHE	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	y	1250	0	1305	10	0
2	4	5093	0	5239	49	0
3	6	1852	0	1828	19	0
4	7	1159	0	1224	9	0
5	9	711	0	724	5	0
6	B	3244	0	3389	16	0
7	D	2853	0	3028	18	0
8	E	764	0	804	6	0
9	F	868	0	963	5	0
10	G	1935	0	2087	30	0
11	H	1015	0	1148	11	0
12	I	1518	0	1601	10	0
13	K	832	0	917	3	0
14	L	1162	0	1213	11	0
15	M	705	0	741	5	0
16	P	444	0	483	6	0
17	Q	1701	0	1818	15	0
18	S	1111	0	1174	6	0
19	U	1701	0	1749	13	0
20	V	1650	0	1794	7	0
21	X	708	0	760	8	0
22	Z	1513	0	1628	12	0
23	a	1239	0	1363	13	0
24	b	1461	0	1502	8	0
25	c	975	0	1032	8	0
26	e	979	0	1039	12	0
27	h	1115	0	1205	10	0
28	l	1002	0	1068	9	0
29	m	1898	0	1993	18	0
30	n	876	0	912	9	0
31	o	1897	0	2046	23	0
32	p	1878	0	2009	8	0
33	z	581	0	656	6	0
34	A	1319	0	1358	15	0
35	C	2027	0	2058	53	0
36	J	2106	0	2250	14	0
37	N	3669	0	3614	34	0
38	R	1636	0	1672	16	0
39	u	639	0	718	5	0
40	v	1680	0	1698	12	0
41	w	3623	0	3697	28	0
42	r	217	0	219	0	0
43	8	3295	0	1676	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	2	75906	0	38197	381	0
45	d	850	0	868	6	0
46	j	918	0	964	8	0
47	k	1064	0	1160	3	0
48	Y	1355	0	1389	10	0
49	t	928	0	906	27	0
50	s	1924	0	2027	20	0
51	i	1107	0	1182	29	0
52	T	2166	0	2262	24	0
53	5	2558	0	1295	46	0
54	q	3317	0	3366	45	0
55	f	2137	0	2202	89	0
56	O	569	0	637	4	0
57	3	1892	0	2024	63	0
58	g	1156	0	1268	28	0
59	x	648	0	432	20	0
60	w	32	0	12	1	0
61	w	1	0	0	0	0
All	All	166429	0	129593	1000	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 1000 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)
44:2:4083:5MU:C5	44:2:4083:5MU:C4	1.79	1.62
44:2:2484:A:C5	57:3:44:LEU:HD21	1.31	1.61
44:2:2484:A:N7	57:3:44:LEU:HD21	1.36	1.40
44:2:2484:A:N1	57:3:48:LYS:CD	1.82	1.40
51:i:120:GLU:OE1	55:f:282:PRO:CG	1.72	1.38

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	y	163/165 (99%)	160 (98%)	3 (2%)	0	100	100
2	4	616/634 (97%)	555 (90%)	57 (9%)	4 (1%)	21	54
3	6	242/245 (99%)	227 (94%)	15 (6%)	0	100	100
4	7	133/163 (82%)	128 (96%)	5 (4%)	0	100	100
5	9	82/134 (61%)	71 (87%)	10 (12%)	1 (1%)	10	41
6	B	401/403 (100%)	380 (95%)	21 (5%)	0	100	100
7	D	356/427 (83%)	330 (93%)	26 (7%)	0	100	100
8	E	96/115 (84%)	92 (96%)	4 (4%)	0	100	100
9	F	107/117 (92%)	105 (98%)	2 (2%)	0	100	100
10	G	240/266 (90%)	225 (94%)	15 (6%)	0	100	100
11	H	120/123 (98%)	116 (97%)	4 (3%)	0	100	100
12	I	188/192 (98%)	176 (94%)	11 (6%)	1 (0%)	24	57
13	K	100/105 (95%)	96 (96%)	4 (4%)	0	100	100
14	L	145/148 (98%)	131 (90%)	14 (10%)	0	100	100
15	M	84/97 (87%)	74 (88%)	10 (12%)	0	100	100
16	P	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
17	Q	208/211 (99%)	198 (95%)	10 (5%)	0	100	100
18	S	133/215 (62%)	124 (93%)	9 (7%)	0	100	100
19	U	201/204 (98%)	188 (94%)	13 (6%)	0	100	100
20	V	199/203 (98%)	195 (98%)	4 (2%)	0	100	100
21	X	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
22	Z	185/188 (98%)	180 (97%)	5 (3%)	0	100	100
23	a	146/196 (74%)	141 (97%)	5 (3%)	0	100	100
24	b	174/176 (99%)	167 (96%)	7 (4%)	0	100	100
25	c	115/160 (72%)	101 (88%)	12 (10%)	2 (2%)	7	35
26	e	129/140 (92%)	116 (90%)	13 (10%)	0	100	100
27	h	132/145 (91%)	126 (96%)	6 (4%)	0	100	100
28	l	123/137 (90%)	115 (94%)	8 (6%)	0	100	100
29	m	246/257 (96%)	223 (91%)	23 (9%)	0	100	100
30	n	107/110 (97%)	100 (94%)	6 (6%)	1 (1%)	14	47

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	o	231/288 (80%)	214 (93%)	17 (7%)	0	100	100
32	p	224/248 (90%)	215 (96%)	9 (4%)	0	100	100
33	z	63/129 (49%)	61 (97%)	2 (3%)	0	100	100
34	A	163/178 (92%)	151 (93%)	12 (7%)	0	100	100
35	C	244/297 (82%)	226 (93%)	18 (7%)	0	100	100
36	J	257/260 (99%)	244 (95%)	11 (4%)	2 (1%)	16	49
37	N	470/485 (97%)	444 (94%)	23 (5%)	3 (1%)	21	54
38	R	197/365 (54%)	184 (93%)	12 (6%)	1 (0%)	24	57
39	u	73/549 (13%)	63 (86%)	8 (11%)	2 (3%)	4	27
40	v	204/239 (85%)	197 (97%)	7 (3%)	0	100	100
41	w	445/731 (61%)	424 (95%)	20 (4%)	1 (0%)	43	74
42	r	22/360 (6%)	21 (96%)	1 (4%)	0	100	100
45	d	102/128 (80%)	92 (90%)	10 (10%)	0	100	100
46	j	109/125 (87%)	103 (94%)	6 (6%)	0	100	100
47	k	127/135 (94%)	119 (94%)	8 (6%)	0	100	100
48	Y	165/184 (90%)	156 (94%)	9 (6%)	0	100	100
49	t	109/293 (37%)	103 (94%)	6 (6%)	0	100	100
50	s	237/490 (48%)	230 (97%)	7 (3%)	0	100	100
51	i	133/136 (98%)	125 (94%)	8 (6%)	0	100	100
52	T	260/306 (85%)	235 (90%)	22 (8%)	3 (1%)	10	41
54	q	398/588 (68%)	385 (97%)	13 (3%)	0	100	100
55	f	254/478 (53%)	236 (93%)	17 (7%)	1 (0%)	30	62
56	O	67/70 (96%)	62 (92%)	5 (8%)	0	100	100
57	3	223/255 (88%)	209 (94%)	13 (6%)	1 (0%)	30	62
58	g	141/156 (90%)	135 (96%)	5 (4%)	1 (1%)	18	51
All	All	10226/13292 (77%)	9605 (94%)	597 (6%)	24 (0%)	44	74

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	c	53	PRO
36	J	106	ILE
37	N	59	PRO

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Mol	Chain	Res	Type
37	N	267	ARG
38	R	24	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	
1	y	137/137 (100%)	137 (100%)	0	100	100
2	4	562/574 (98%)	562 (100%)	0	100	100
3	6	212/213 (100%)	212 (100%)	0	100	100
4	7	126/149 (85%)	126 (100%)	0	100	100
5	9	74/114 (65%)	74 (100%)	0	100	100
6	B	349/349 (100%)	349 (100%)	0	100	100
7	D	298/348 (86%)	298 (100%)	0	100	100
8	E	83/97 (86%)	83 (100%)	0	100	100
9	F	94/100 (94%)	94 (100%)	0	100	100
10	G	204/223 (92%)	202 (99%)	2 (1%)	68	75
11	H	109/110 (99%)	109 (100%)	0	100	100
12	I	169/171 (99%)	169 (100%)	0	100	100
13	K	86/89 (97%)	86 (100%)	0	100	100
14	L	120/121 (99%)	120 (100%)	0	100	100
15	M	73/80 (91%)	73 (100%)	0	100	100
16	P	47/48 (98%)	47 (100%)	0	100	100
17	Q	176/177 (99%)	176 (100%)	0	100	100
18	S	115/161 (71%)	115 (100%)	0	100	100
19	U	171/172 (99%)	171 (100%)	0	100	100
20	V	173/174 (99%)	173 (100%)	0	100	100
21	X	74/75 (99%)	74 (100%)	0	100	100
22	Z	164/165 (99%)	164 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	a	133/175 (76%)	133 (100%)	0	100	100
24	b	157/157 (100%)	156 (99%)	1 (1%)	78	79
25	c	106/140 (76%)	106 (100%)	0	100	100
26	e	101/107 (94%)	101 (100%)	0	100	100
27	h	124/135 (92%)	124 (100%)	0	100	100
28	l	109/121 (90%)	109 (100%)	0	100	100
29	m	190/199 (96%)	190 (100%)	0	100	100
30	n	88/89 (99%)	88 (100%)	0	100	100
31	o	208/252 (82%)	208 (100%)	0	100	100
32	p	195/215 (91%)	195 (100%)	0	100	100
33	z	61/115 (53%)	61 (100%)	0	100	100
34	A	138/149 (93%)	138 (100%)	0	100	100
35	C	209/250 (84%)	209 (100%)	0	100	100
36	J	227/228 (100%)	227 (100%)	0	100	100
37	N	396/404 (98%)	396 (100%)	0	100	100
38	R	173/300 (58%)	173 (100%)	0	100	100
39	u	68/485 (14%)	68 (100%)	0	100	100
40	v	182/214 (85%)	182 (100%)	0	100	100
41	w	405/654 (62%)	405 (100%)	0	100	100
42	r	22/312 (7%)	22 (100%)	0	100	100
45	d	94/115 (82%)	94 (100%)	0	100	100
46	j	101/110 (92%)	100 (99%)	1 (1%)	68	75
47	k	115/121 (95%)	115 (100%)	0	100	100
48	Y	147/163 (90%)	147 (100%)	0	100	100
49	t	103/274 (38%)	103 (100%)	0	100	100
50	s	222/437 (51%)	222 (100%)	0	100	100
51	i	117/118 (99%)	117 (100%)	0	100	100
52	T	241/279 (86%)	241 (100%)	0	100	100
54	q	359/509 (70%)	359 (100%)	0	100	100
55	f	222/402 (55%)	222 (100%)	0	100	100
56	O	64/65 (98%)	64 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	3	206/228 (90%)	206 (100%)	0	100	100
58	g	124/133 (93%)	124 (100%)	0	100	100
All	All	9023/11502 (78%)	9019 (100%)	4 (0%)	100	100

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

Mol	Chain	Res	Type
10	G	137[A]	ARG
10	G	137[B]	ARG
24	b	77	ASN
46	j	100	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 84 such sidechains are listed below:

Mol	Chain	Res	Type
33	z	92	GLN
45	d	119	GLN
34	A	155	HIS
37	N	177	ASN
49	t	119	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
43	8	153/156 (98%)	28 (18%)	2 (1%)
44	2	3524/5054 (69%)	962 (27%)	33 (0%)
53	5	119/120 (99%)	19 (15%)	0
59	x	0/60	-	-
All	All	3796/5390 (70%)	1009 (26%)	35 (0%)

5 of 1009 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
43	8	24	G
43	8	34	U
43	8	35	C
43	8	39	G
43	8	48	A

5 of 35 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
44	2	4426	C
44	2	4555	U
44	2	4634	U
44	2	2475	G
44	2	2474	G

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

65 non-standard protein/DNA/RNA residues are modelled in this entry.

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
44	7MG	2	1605	44	23,26,27	3.48	11 (47%)	27,39,42	2.05	9 (33%)
44	7MG	2	2522	44	23,26,27	3.41	10 (43%)	27,39,42	2.08	9 (33%)
44	UR3	2	4597	44	19,22,23	2.69	7 (36%)	26,32,35	2.38	5 (19%)
44	B8W	2	2380	44	23,26,27	2.83	5 (21%)	33,38,41	2.85	18 (54%)
44	OMG	2	2424	44	23,26,27	2.68	8 (34%)	32,38,41	2.92	10 (31%)
44	A2M	2	1326	44	22,25,26	3.21	10 (45%)	30,36,39	2.92	10 (33%)
44	A2M	2	2401	44	22,25,26	3.25	10 (45%)	30,36,39	2.91	11 (36%)
44	OMG	2	2364	44	23,26,27	2.60	9 (39%)	32,38,41	2.79	11 (34%)
44	OMC	2	3909	44	19,22,23	3.06	8 (42%)	25,31,34	1.99	7 (28%)
44	OMG	2	373	44	23,26,27	2.64	9 (39%)	32,38,41	2.71	14 (43%)
44	OMG	2	2050	44	23,26,27	2.62	9 (39%)	32,38,41	2.72	11 (34%)
44	OMU	2	4620	44	19,22,23	2.88	7 (36%)	25,31,34	1.79	4 (16%)
44	1MA	2	4415	44	21,25,26	3.00	4 (19%)	30,37,40	1.78	6 (20%)
44	B8K	2	4690	44	24,28,29	3.05	12 (50%)	29,42,45	2.92	11 (37%)
44	I4U	2	1659	44	20,24,25	3.43	8 (40%)	27,34,37	2.09	2 (7%)
44	OMG	2	1316	44	23,26,27	2.62	9 (39%)	32,38,41	2.80	13 (40%)
44	OMC	2	2365	44	19,22,23	2.91	8 (42%)	25,31,34	0.74	0
44	2MG	2	978	44	23,26,27	3.07	9 (39%)	33,38,41	2.12	7 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
44	B8Q	2	1456	44	18,22,23	2.96	5 (27%)	21,32,35	2.28	6 (28%)
44	OMG	2	4870	44	23,26,27	2.67	8 (34%)	32,38,41	2.95	9 (28%)
44	A2M	2	1524	44	22,25,26	3.26	9 (40%)	30,36,39	3.16	13 (43%)
44	A2M	2	1534	44	22,25,26	3.23	10 (45%)	30,36,39	3.01	10 (33%)
44	B8K	2	3897	44	24,28,29	3.15	11 (45%)	29,42,45	2.61	11 (37%)
44	OMC	2	2804	44	19,22,23	2.93	8 (42%)	25,31,34	0.79	1 (4%)
44	OMG	2	4637	44	23,26,27	2.64	8 (34%)	32,38,41	2.83	10 (31%)
44	B9B	2	1574	44	25,28,29	1.82	7 (28%)	35,40,43	5.11	13 (37%)
44	A2M	2	1871	44	22,25,26	3.29	10 (45%)	30,36,39	3.13	12 (40%)
44	A2M	2	398	44	22,25,26	3.23	10 (45%)	30,36,39	2.89	10 (33%)
44	A2M	2	2363	44	22,25,26	3.23	9 (40%)	30,36,39	2.94	11 (36%)
44	OMC	2	4536	44	19,22,23	3.00	8 (42%)	25,31,34	0.72	0
44	P7G	2	1909	44	24,28,29	3.62	11 (45%)	25,41,44	1.40	2 (8%)
44	P4U	2	1348	44	21,24,25	3.45	7 (33%)	28,33,36	1.60	4 (14%)
43	OMU	8	14	43,44	19,22,23	2.94	8 (42%)	25,31,34	1.96	6 (24%)
44	OMG	2	1625	44	23,26,27	2.75	8 (34%)	32,38,41	3.21	9 (28%)
44	OMC	2	2422	44	19,22,23	2.97	8 (42%)	25,31,34	1.27	3 (12%)
44	B9B	2	2754	44	25,28,29	1.78	6 (24%)	35,40,43	5.21	13 (37%)
44	OMG	2	2773	44	23,26,27	2.68	8 (34%)	32,38,41	2.86	9 (28%)
44	OMG	2	4494	44	23,26,27	2.68	8 (34%)	32,38,41	2.85	9 (28%)
44	OMC	2	3869	44	19,22,23	2.93	7 (36%)	25,31,34	1.18	3 (12%)
44	A2M	2	4523	44	22,25,26	3.20	10 (45%)	30,36,39	2.96	11 (36%)
44	B8W	2	4185	44	23,26,27	2.83	5 (21%)	33,38,41	2.80	15 (45%)
44	OMG	2	1522	44	23,26,27	2.65	9 (39%)	32,38,41	2.81	10 (31%)
44	P7G	2	3880	44	24,28,29	3.56	11 (45%)	25,41,44	1.24	2 (8%)
44	A2M	2	3867	44	22,25,26	3.19	10 (45%)	30,36,39	2.97	11 (36%)
44	M7A	2	4564	44	19,25,26	1.55	2 (10%)	25,37,40	4.17	6 (24%)
44	E7G	2	1797	44	24,27,28	3.68	12 (50%)	28,40,43	2.26	9 (32%)
44	OMC	2	2861	44	19,22,23	3.00	8 (42%)	25,31,34	1.28	3 (12%)
44	7MG	2	4550	44	23,26,27	3.55	10 (43%)	27,39,42	2.12	9 (33%)
44	OMC	2	3701	44	19,22,23	3.11	8 (42%)	25,31,34	0.99	1 (4%)
44	2MG	2	729	44	23,26,27	2.98	8 (34%)	33,38,41	2.30	10 (30%)
44	OMG	2	1883	44	23,26,27	2.69	8 (34%)	32,38,41	2.78	11 (34%)
44	A2M	2	3825	44	22,25,26	3.20	10 (45%)	30,36,39	2.97	10 (33%)
44	B9H	2	2786	44	21,25,26	3.14	5 (23%)	22,35,38	2.13	6 (27%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
44	B8T	2	4671	44	19,22,23	3.53	8 (42%)	25,31,34	0.96	1 (4%)
44	E7G	2	2297	44	24,27,28	3.49	11 (45%)	28,40,43	2.25	9 (32%)
44	PSU	2	4636	44	18,21,22	1.11	1 (5%)	21,30,33	1.96	4 (19%)
44	2MG	2	1517	44	23,26,27	2.99	9 (39%)	33,38,41	2.32	8 (24%)
44	B9B	2	237	44	25,28,29	1.84	6 (24%)	35,40,43	5.31	13 (37%)
44	2MG	2	4872	44	23,26,27	2.89	9 (39%)	33,38,41	2.60	13 (39%)
44	5MU	2	4083	44	19,22,23	7.35	8 (42%)	27,32,35	3.21	11 (40%)
44	B8W	2	4472	44	23,26,27	2.85	5 (21%)	33,38,41	2.83	17 (51%)
44	BGH	2	3899	44	25,29,30	4.50	17 (68%)	30,43,46	2.68	11 (36%)
44	B8T	2	4483	44	19,22,23	3.55	8 (42%)	25,31,34	1.50	5 (20%)
44	OMC	2	3887	44	19,22,23	3.00	8 (42%)	25,31,34	0.96	1 (4%)
44	OMG	2	4623	44	23,26,27	2.61	9 (39%)	32,38,41	2.77	12 (37%)

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
44	7MG	2	1605	44	-	1/7/37/38	0/3/3/3
44	7MG	2	2522	44	-	0/7/37/38	0/3/3/3
44	UR3	2	4597	44	-	0/7/25/26	0/2/2/2
44	B8W	2	2380	44	-	2/9/27/28	0/3/3/3
44	OMG	2	2424	44	-	2/9/27/28	0/3/3/3
44	A2M	2	1326	44	-	0/9/27/28	0/3/3/3
44	A2M	2	2401	44	-	0/9/27/28	0/3/3/3
44	OMG	2	2364	44	-	3/9/27/28	0/3/3/3
44	OMC	2	3909	44	-	2/9/27/28	0/2/2/2
44	OMG	2	373	44	-	1/9/27/28	0/3/3/3
44	OMG	2	2050	44	-	0/9/27/28	0/3/3/3
44	OMU	2	4620	44	-	0/9/27/28	0/2/2/2
44	1MA	2	4415	44	-	2/7/25/26	0/3/3/3
44	B8K	2	4690	44	-	0/11/41/42	0/3/3/3
44	I4U	2	1659	44	-	2/9/29/30	0/2/2/2
44	OMG	2	1316	44	-	0/9/27/28	0/3/3/3
44	OMC	2	2365	44	-	0/9/27/28	0/2/2/2
44	2MG	2	978	44	-	0/9/27/28	0/3/3/3
44	B8Q	2	1456	44	-	0/7/42/43	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
44	OMG	2	4870	44	-	3/9/27/28	0/3/3/3
44	A2M	2	1524	44	-	3/9/27/28	0/3/3/3
44	A2M	2	1534	44	-	2/9/27/28	0/3/3/3
44	B8K	2	3897	44	-	2/11/41/42	0/3/3/3
44	OMC	2	2804	44	-	0/9/27/28	0/2/2/2
44	OMG	2	4637	44	-	2/9/27/28	0/3/3/3
44	B9B	2	1574	44	-	5/11/29/30	0/3/3/3
44	A2M	2	1871	44	-	2/9/27/28	0/3/3/3
44	A2M	2	398	44	-	2/9/27/28	0/3/3/3
44	A2M	2	2363	44	-	0/9/27/28	0/3/3/3
44	OMC	2	4536	44	-	0/9/27/28	0/2/2/2
44	P7G	2	1909	44	-	4/10/40/41	0/3/3/3
44	P4U	2	1348	44	-	1/10/29/30	0/2/2/2
43	OMU	8	14	43,44	-	1/9/27/28	0/2/2/2
44	OMG	2	1625	44	-	3/9/27/28	0/3/3/3
44	OMC	2	2422	44	-	1/9/27/28	0/2/2/2
44	B9B	2	2754	44	-	3/11/29/30	0/3/3/3
44	OMG	2	2773	44	-	2/9/27/28	0/3/3/3
44	OMG	2	4494	44	-	0/9/27/28	0/3/3/3
44	OMC	2	3869	44	-	0/9/27/28	0/2/2/2
44	A2M	2	4523	44	-	0/9/27/28	0/3/3/3
44	B8W	2	4185	44	-	0/9/27/28	0/3/3/3
44	OMG	2	1522	44	-	0/9/27/28	0/3/3/3
44	P7G	2	3880	44	-	3/10/40/41	0/3/3/3
44	A2M	2	3867	44	-	2/9/27/28	0/3/3/3
44	M7A	2	4564	44	-	0/7/37/38	0/3/3/3
44	E7G	2	1797	44	-	1/9/39/40	0/3/3/3
44	OMC	2	2861	44	-	0/9/27/28	0/2/2/2
44	7MG	2	4550	44	-	2/7/37/38	0/3/3/3
44	OMC	2	3701	44	-	7/9/27/28	0/2/2/2
44	2MG	2	729	44	-	2/9/27/28	0/3/3/3
44	OMG	2	1883	44	-	2/9/27/28	0/3/3/3
44	A2M	2	3825	44	-	0/9/27/28	0/3/3/3
44	B9H	2	2786	44	-	0/12/47/48	0/2/2/2
44	B8T	2	4671	44	-	0/7/27/28	0/2/2/2
44	E7G	2	2297	44	-	1/9/39/40	0/3/3/3
44	PSU	2	4636	44	-	3/7/25/26	0/2/2/2
44	2MG	2	1517	44	-	2/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
44	B9B	2	237	44	-	4/11/29/30	0/3/3/3
44	2MG	2	4872	44	-	2/9/27/28	0/3/3/3
44	5MU	2	4083	44	-	3/7/25/26	0/2/2/2
44	B8W	2	4472	44	-	2/9/27/28	0/3/3/3
44	BGH	2	3899	44	-	0/13/43/44	0/3/3/3
44	B8T	2	4483	44	-	0/7/27/28	0/2/2/2
44	OMC	2	3887	44	-	1/9/27/28	0/2/2/2
44	OMG	2	4623	44	-	0/9/27/28	0/3/3/3

The worst 5 of 542 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	2	4083	5MU	C4-C5	21.05	1.79	1.44
44	2	4083	5MU	C6-N1	16.61	1.66	1.38
44	2	4083	5MU	C6-C5	-11.52	1.15	1.34
44	2	4083	5MU	C4-N3	-11.00	1.18	1.38
44	2	1659	I4U	C4-N3	10.77	1.45	1.31

The worst 5 of 541 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	237	B9B	O6-C6-C5	20.59	143.92	116.73
44	2	1574	B9B	O6-C6-C5	20.44	143.72	116.73
44	2	2754	B9B	O6-C6-C5	19.91	143.03	116.73
44	2	237	B9B	O6-C6-N1	-19.34	94.19	120.02
44	2	2754	B9B	O6-C6-N1	-18.81	94.90	120.02

There are no chirality outliers.

5 of 88 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
43	8	14	OMU	C1'-C2'-O2'-CM2
44	2	237	B9B	C5-C6-O6-C61
44	2	237	B9B	N1-C6-O6-C61
44	2	237	B9B	O4'-C4'-C5'-O5'
44	2	398	A2M	O4'-C4'-C5'-O5'

There are no ring outliers.

13 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
44	2	2522	7MG	1	0
44	2	2364	OMG	1	0
44	2	2050	OMG	1	0
44	2	1524	A2M	1	0
44	2	1534	A2M	1	0
44	2	1574	B9B	1	0
44	2	1871	A2M	1	0
44	2	2363	A2M	1	0
43	8	14	OMU	2	0
44	2	729	2MG	1	0
44	2	1517	2MG	1	0
44	2	4872	2MG	1	0
44	2	4083	5MU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
60	GTP	w	801	61	33,34,34	0.55	0	50,54,54	0.54	0

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
60	GTP	w	801	61	-	1/22/38/38	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

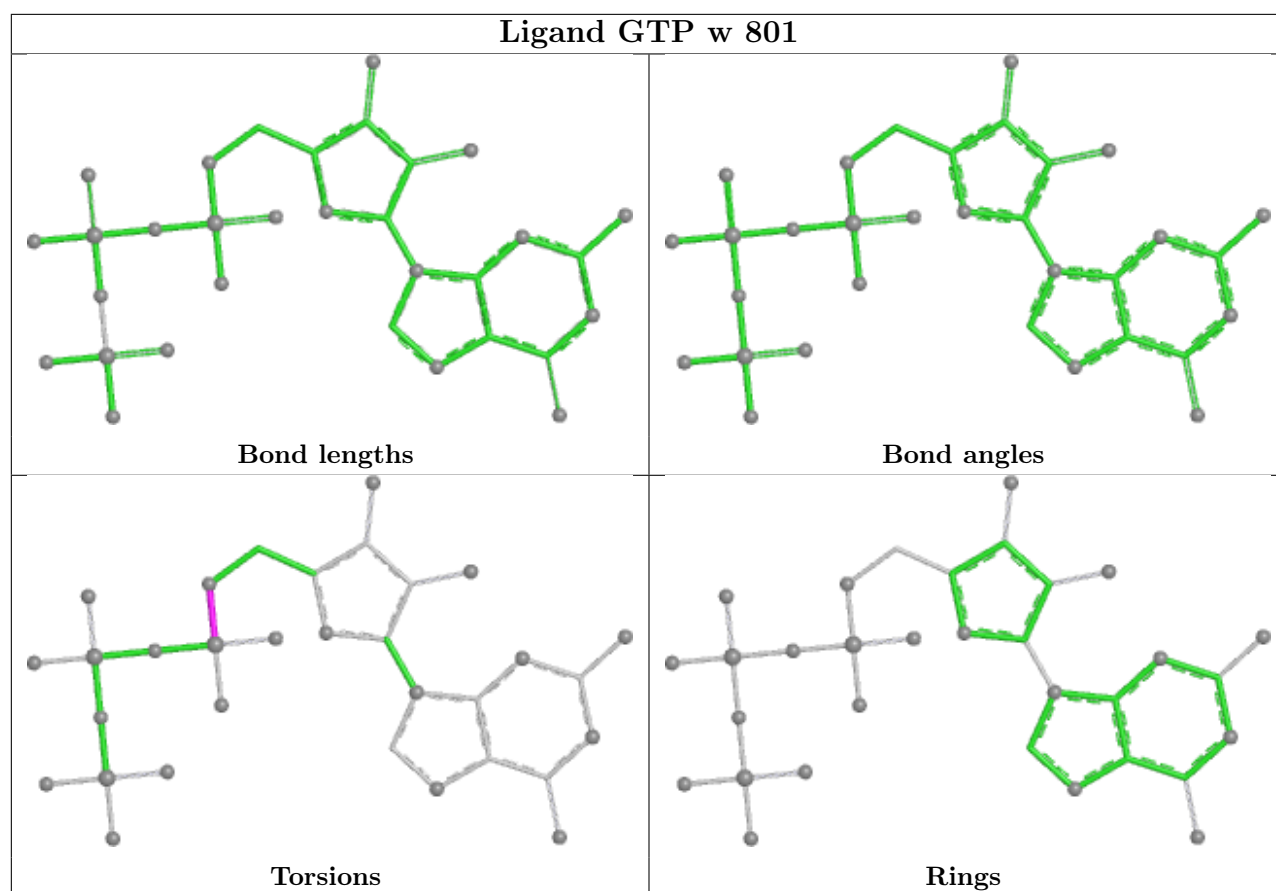
Mol	Chain	Res	Type	Atoms
60	w	801	GTP	C5'-O5'-PA-O1A

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	w	801	GTP	1	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

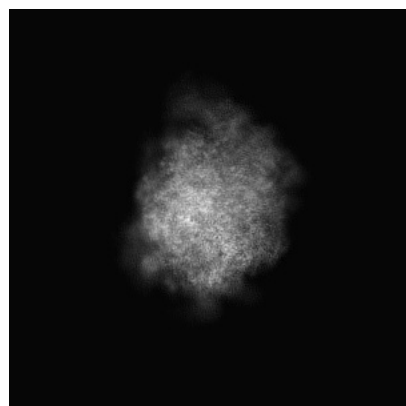
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35673. These allow visual inspection of the internal detail of the map and identification of artifacts.

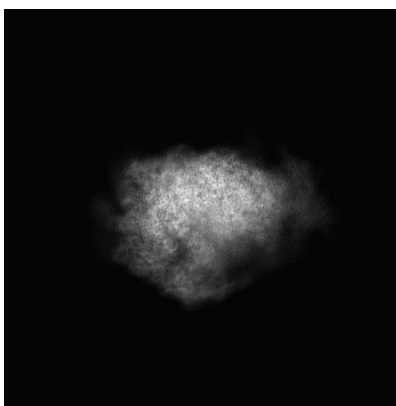
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

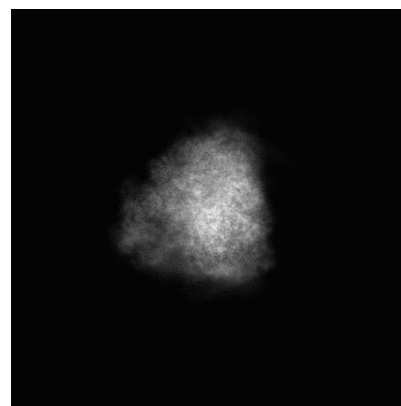
6.1.1 Primary map



X

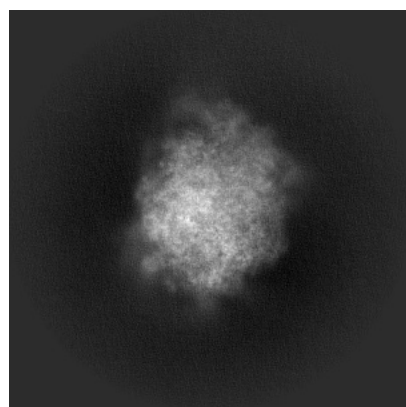


Y

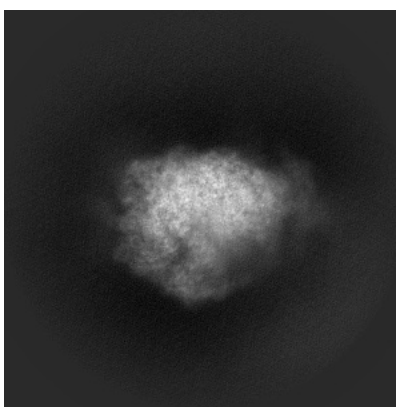


Z

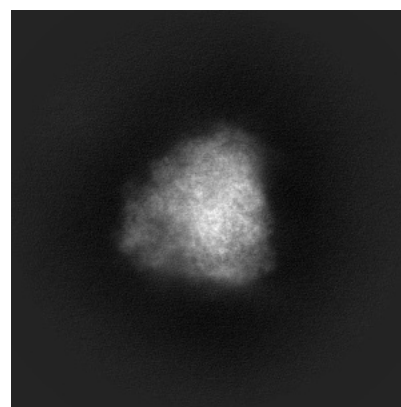
6.1.2 Raw map



X



Y

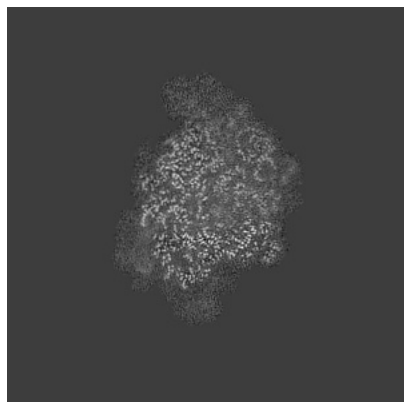


Z

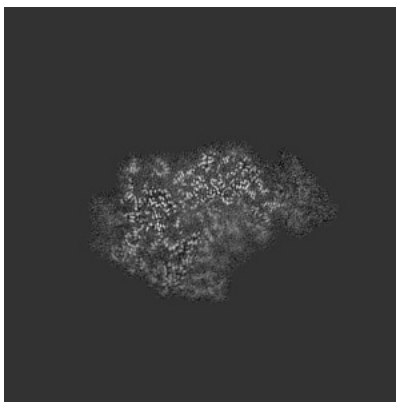
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

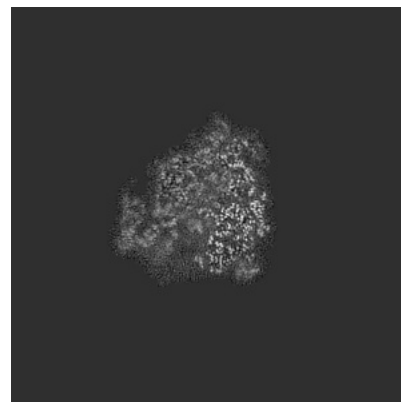
6.2.1 Primary map



X Index: 200

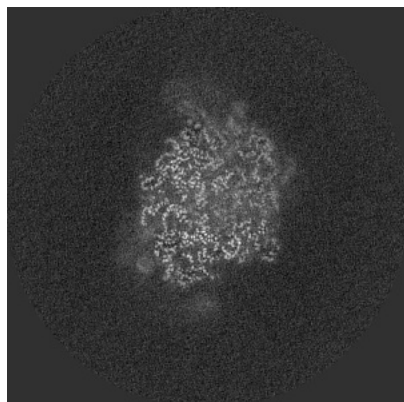


Y Index: 200

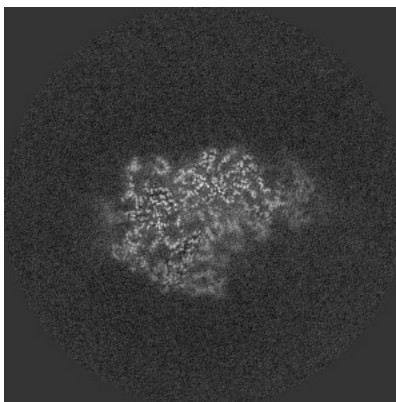


Z Index: 200

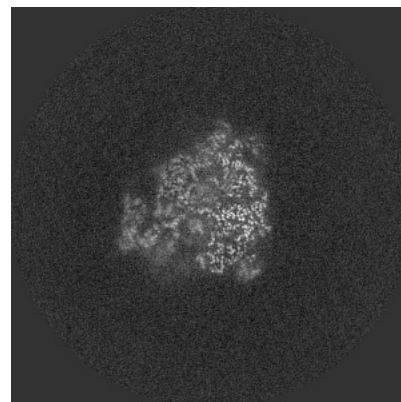
6.2.2 Raw map



X Index: 200



Y Index: 200

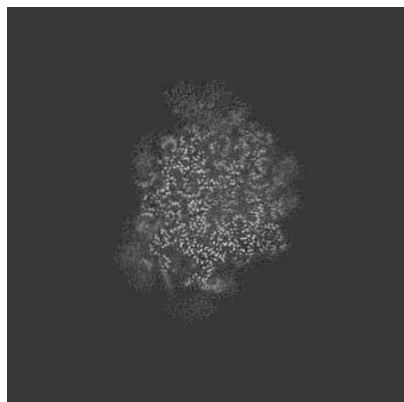


Z Index: 200

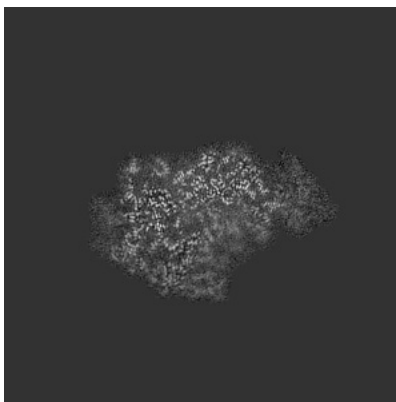
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

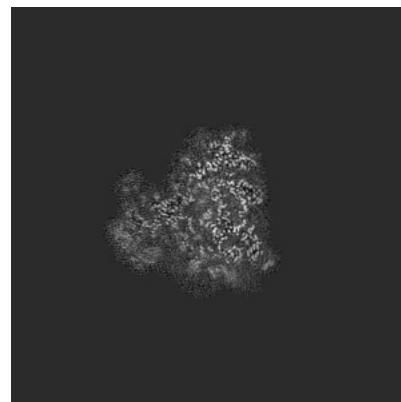
6.3.1 Primary map



X Index: 207

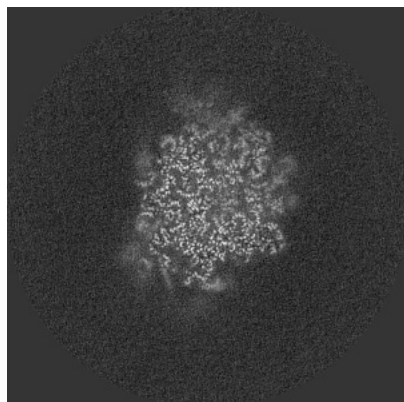


Y Index: 200

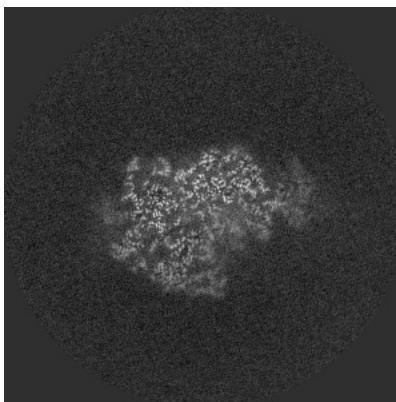


Z Index: 183

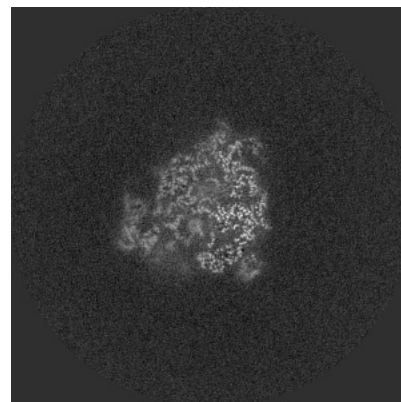
6.3.2 Raw map



X Index: 208



Y Index: 199

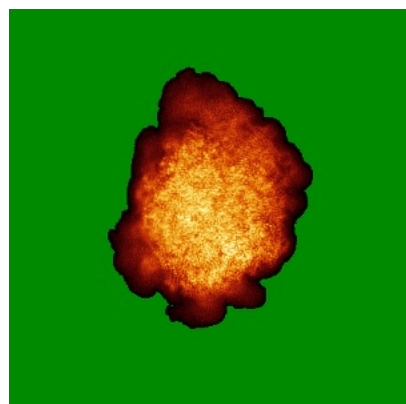


Z Index: 199

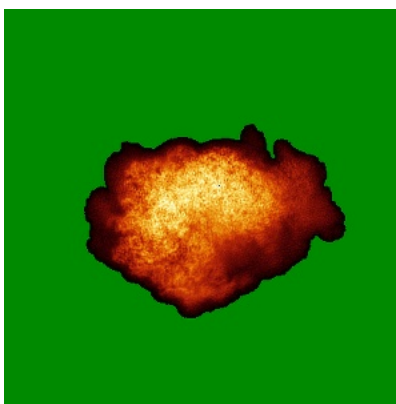
The images above show the largest variance slices of the map in three orthogonal directions.

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

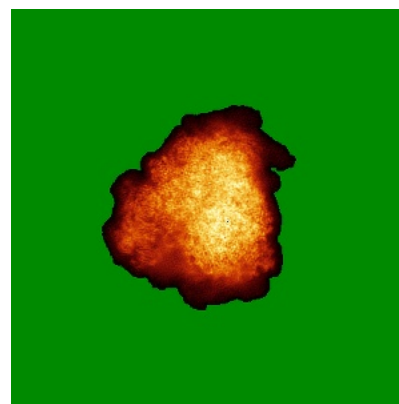
6.4.1 Primary map



X

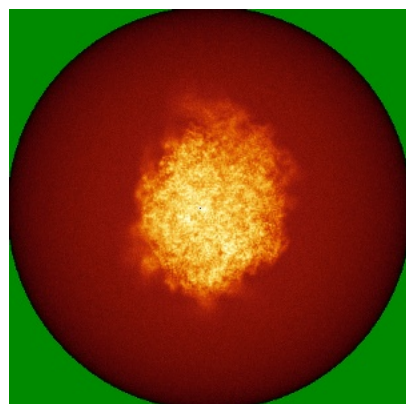


Y

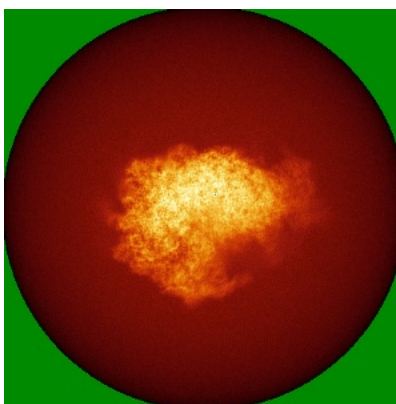


Z

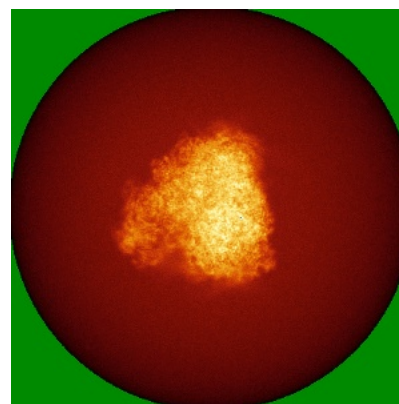
6.4.2 Raw map



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

6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

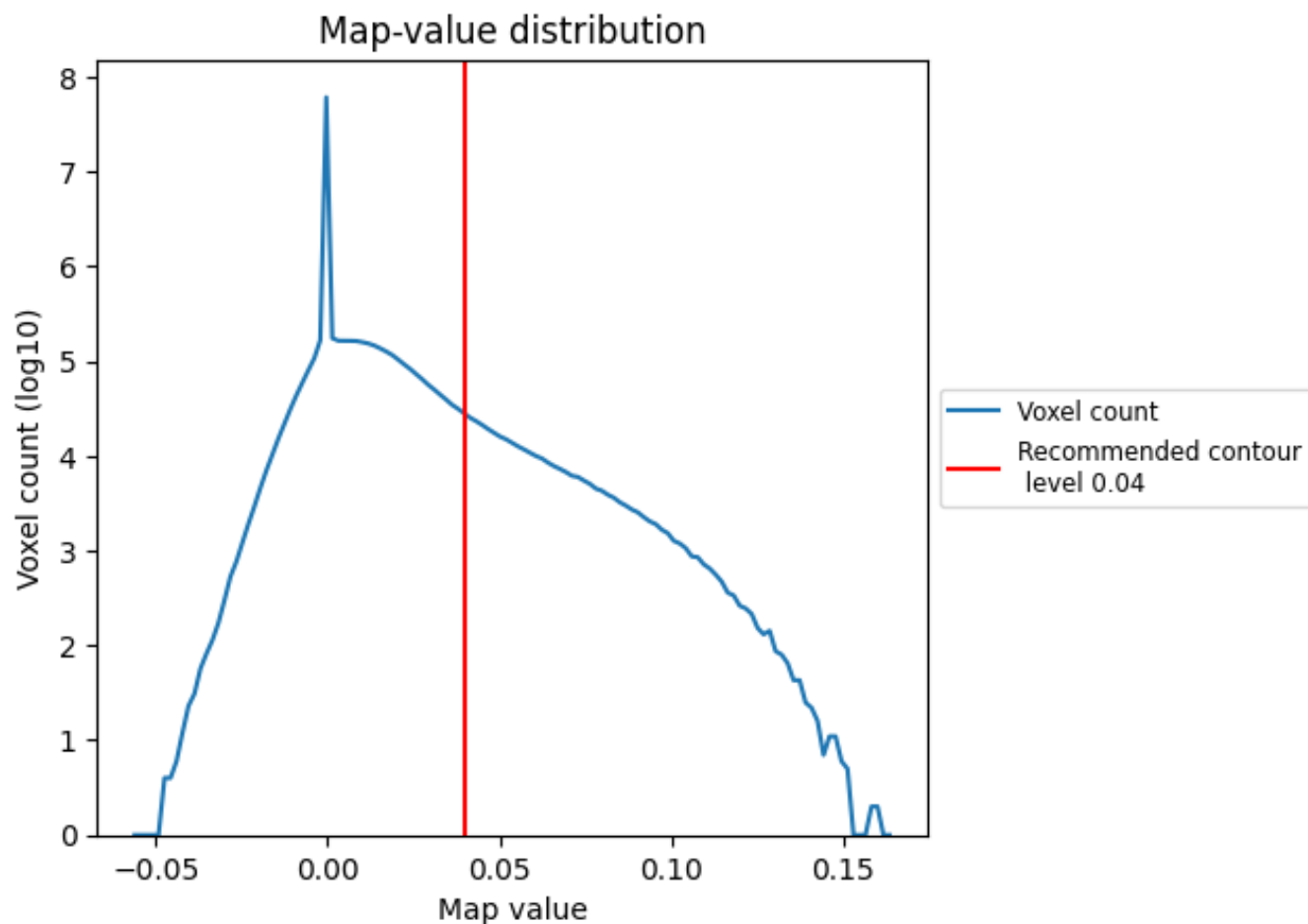
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

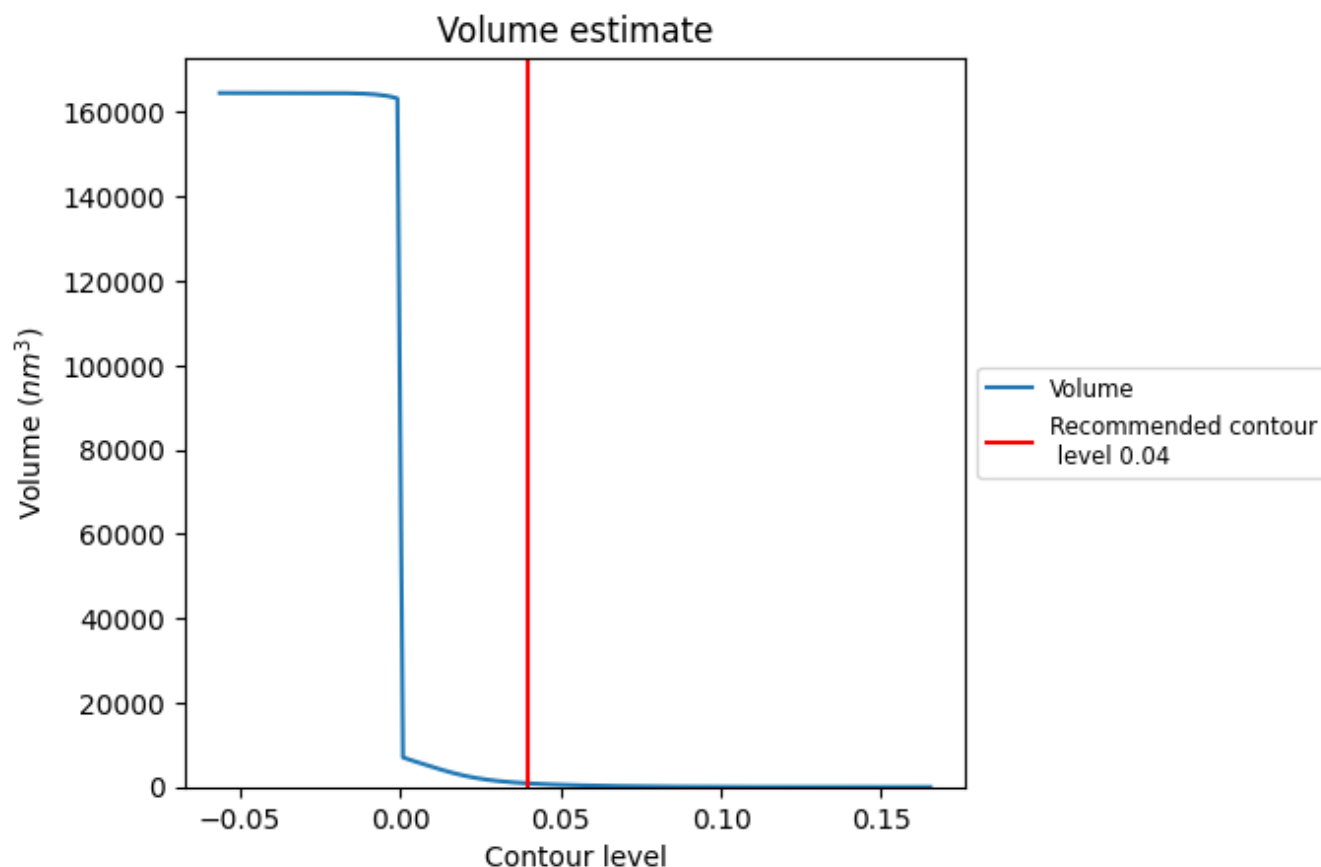
This section contains the results of statistical analysis of the map.

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.

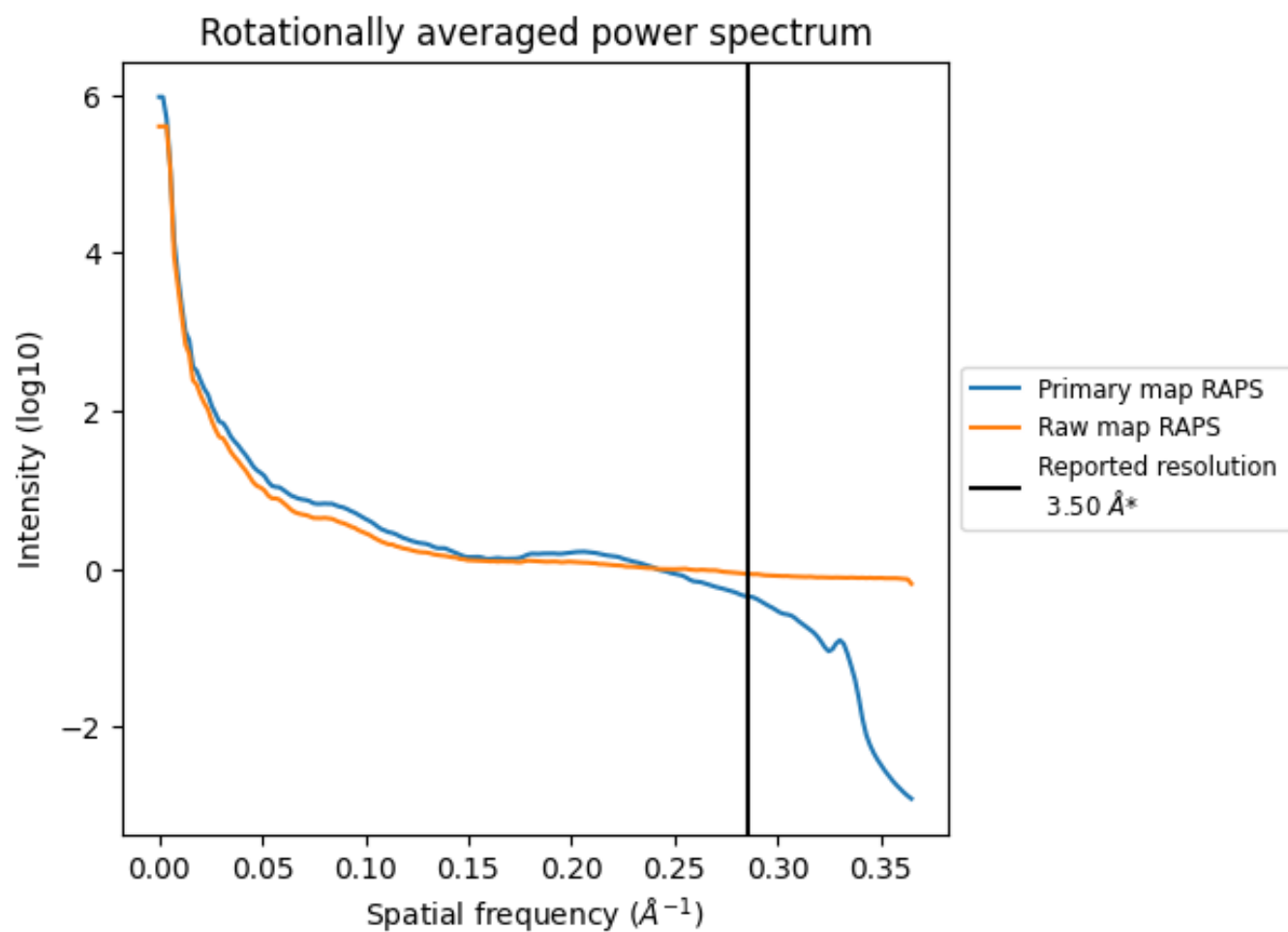
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 849 nm^3 ; this corresponds to an approximate mass of 767 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 ⓘ

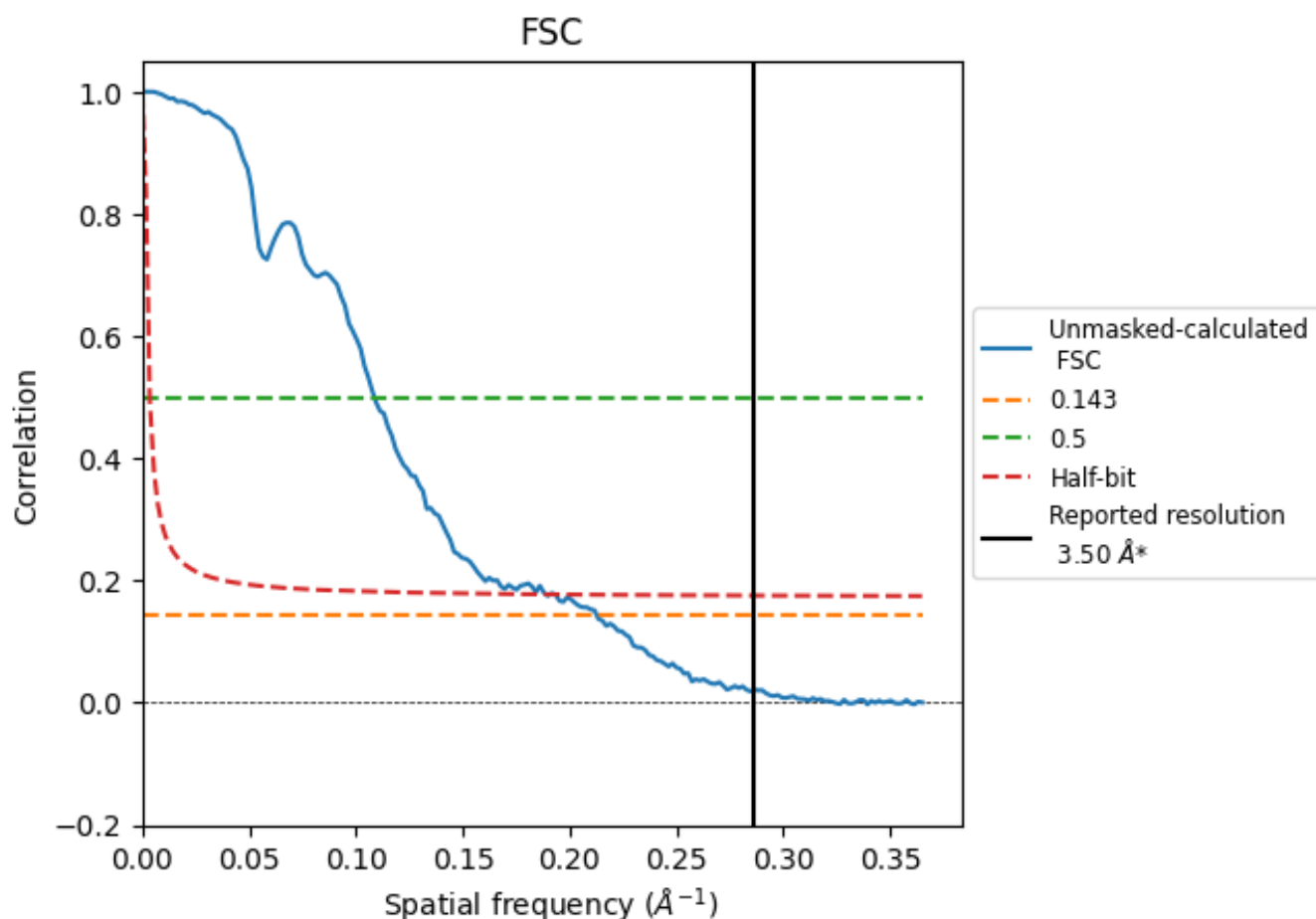


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

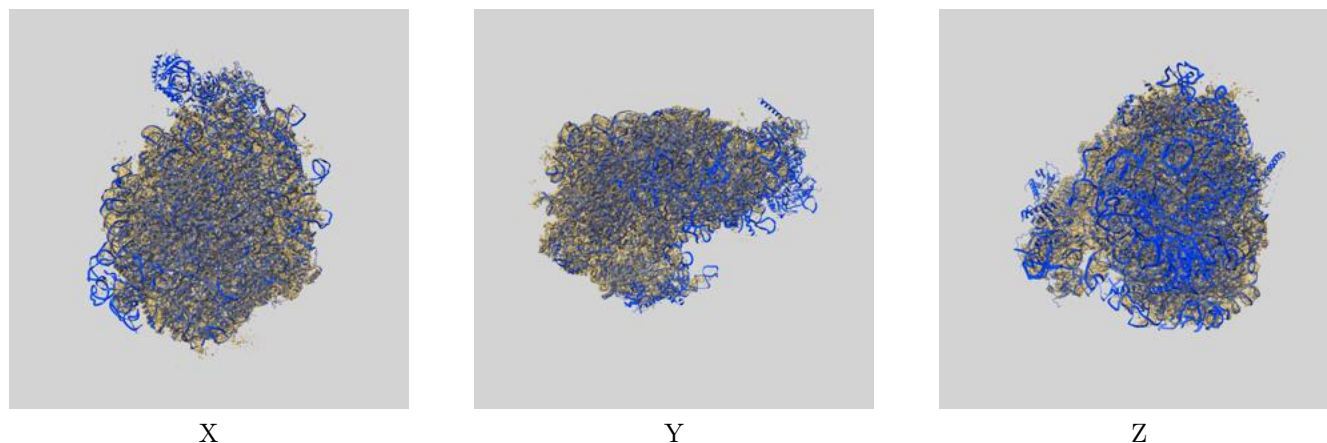
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.70	9.21	5.29

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.70 differs from the reported value 3.5 by more than 10 %

9 Map-model fit [i](#)

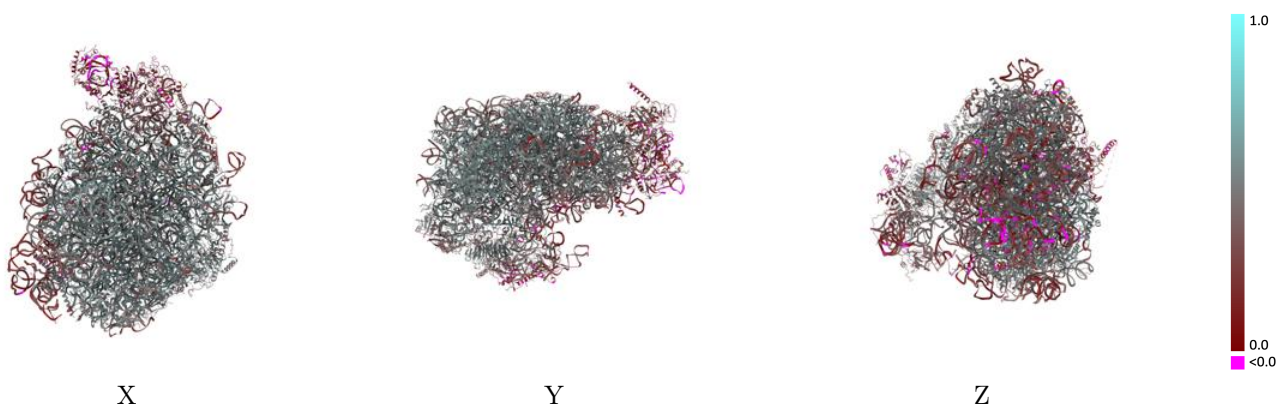
This section contains information regarding the fit between EMDB map EMD-35673 and PDB model 8IR3. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



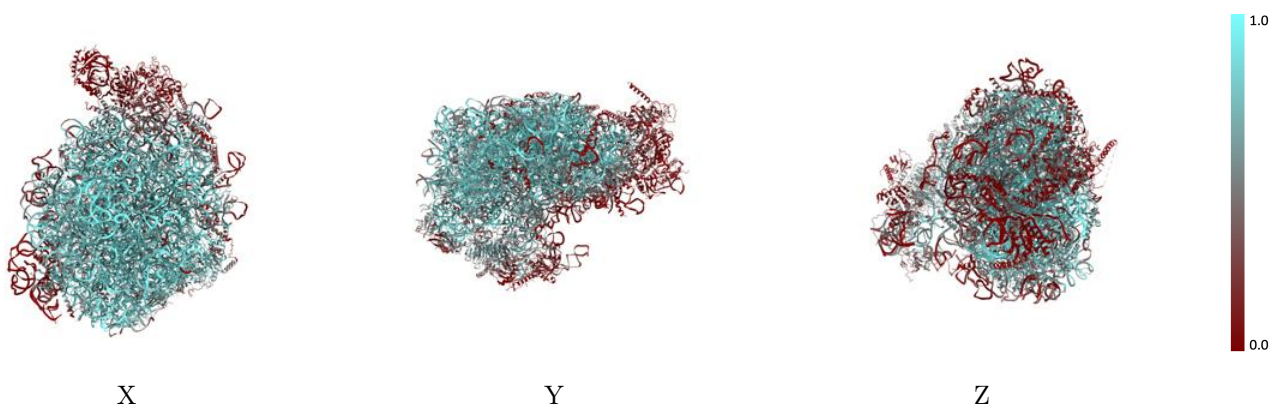
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



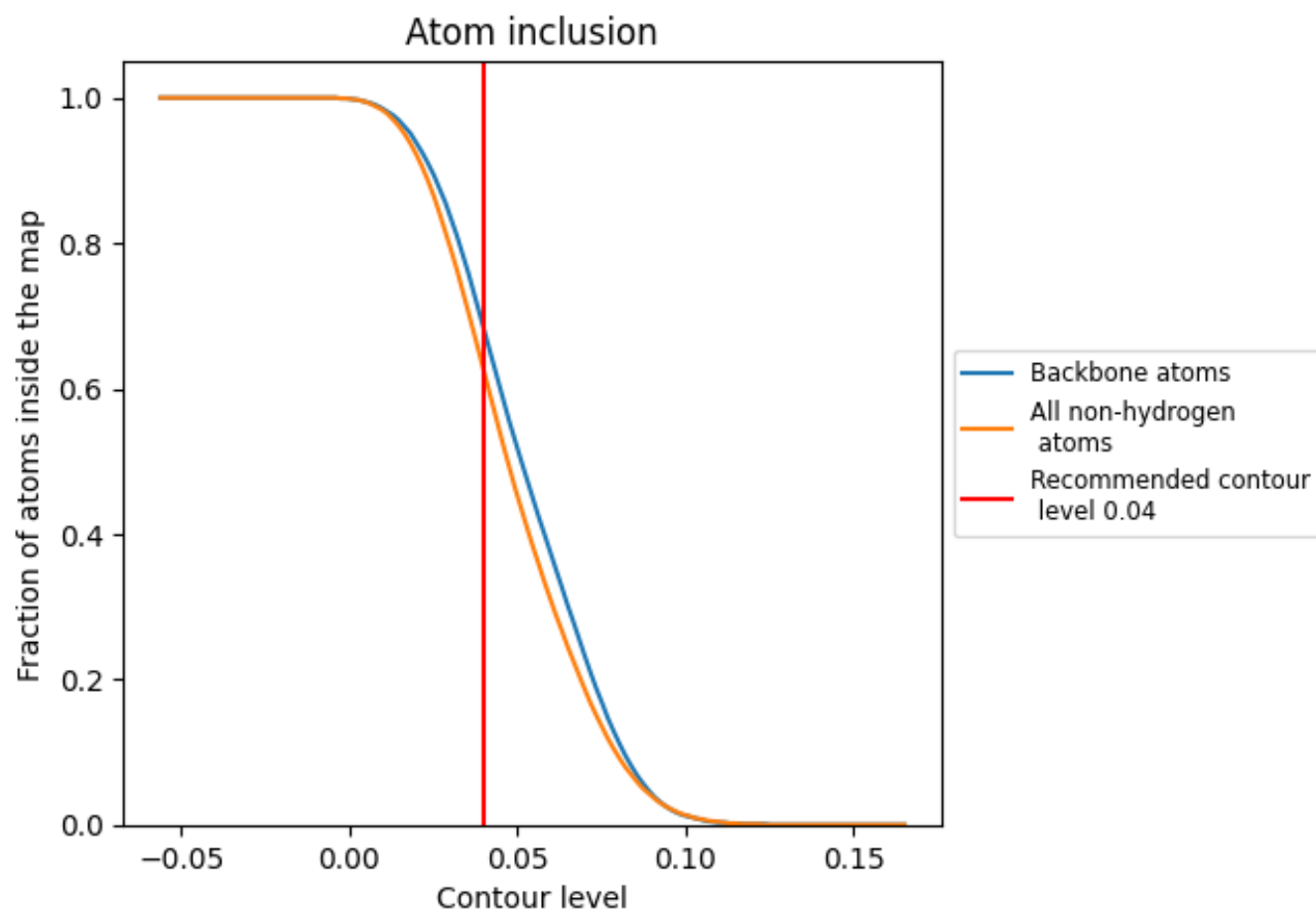
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 62% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6250	 0.4390
2	 0.7200	 0.4400
3	 0.1010	 0.2160
4	 0.5930	 0.4630
5	 0.4090	 0.2530
6	 0.6770	 0.5030
7	 0.6930	 0.5240
8	 0.8810	 0.5140
9	 0.0710	 0.3690
A	 0.1830	 0.3060
B	 0.7890	 0.5400
C	 0.3550	 0.3670
D	 0.7960	 0.5370
E	 0.2930	 0.4090
F	 0.6440	 0.5060
G	 0.4460	 0.4340
H	 0.7220	 0.5130
I	 0.7370	 0.5310
J	 0.7090	 0.5190
K	 0.6100	 0.4640
L	 0.5570	 0.4300
M	 0.8350	 0.5410
N	 0.4720	 0.4280
O	 0.4690	 0.4100
P	 0.8720	 0.5620
Q	 0.6470	 0.4770
R	 0.2940	 0.3390
S	 0.7650	 0.5260
T	 0.2110	 0.3270
U	 0.7560	 0.5130
V	 0.8290	 0.5410
X	 0.4260	 0.4480
Y	 0.7580	 0.5150
Z	 0.6440	 0.4620
a	 0.6110	 0.4990



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Chain	Atom inclusion	Q-score
b	 0.7960	 0.5330
c	 0.5210	 0.4360
d	 0.5520	 0.4790
e	 0.7750	 0.5370
f	 0.1460	 0.2800
g	 0.5800	 0.4360
h	 0.7670	 0.5400
i	 0.4100	 0.4440
j	 0.7120	 0.5120
k	 0.8150	 0.5460
l	 0.7910	 0.5380
m	 0.3340	 0.3880
n	 0.8560	 0.5570
o	 0.5640	 0.4720
p	 0.7500	 0.5110
q	 0.2440	 0.3220
r	 0.0670	 0.3300
s	 0.0030	 0.2130
t	 0.0240	 0.2500
u	 0.4720	 0.4030
v	 0.5420	 0.4680
w	 0.6060	 0.4620
x	 0.0000	 0.0260
y	 0.3440	 0.4030
z	 0.5130	 0.4610