



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:28 PM UTC

PDB ID : 3JCT / pdb_00003jct
EMDB ID : EMD-6615
Title : Cryo-em structure of eukaryotic pre-60S ribosomal subunits
Authors : Wu, S.; Kumcuoglu, B.; Yan, K.G.; Brown, H.; Zhang, Y.X.; Tan, D.; Gama-
linda, M.; Yuan, Y.; Li, Z.F.; Jakovljevic, J.; Ma, C.Y.; Lei, J.L.; Dong, M.Q.;
Woolford Jr., J.L.; Gao, N.
Deposited on : 2016-03-09
Resolution : 3.08 Å(reported)
Based on initial model : 4V88

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:

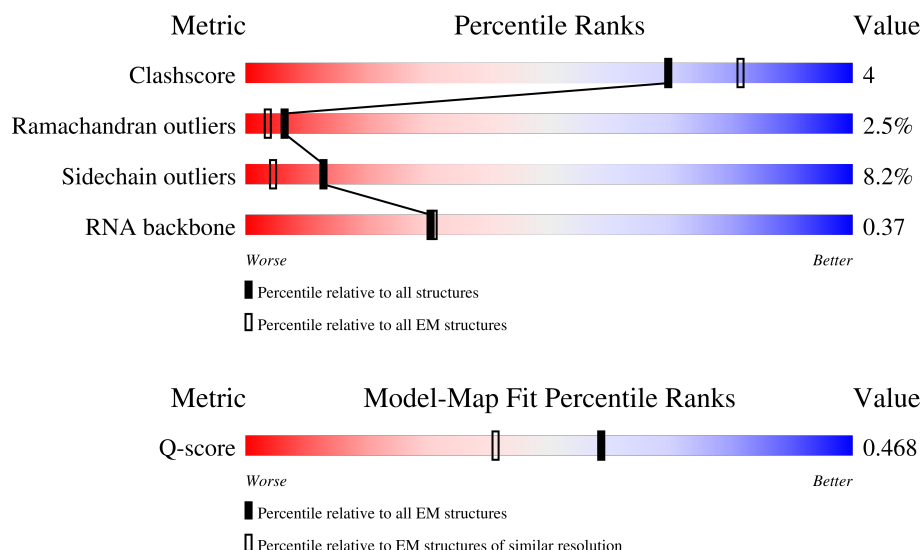
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.08 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.



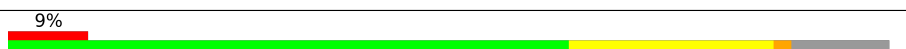
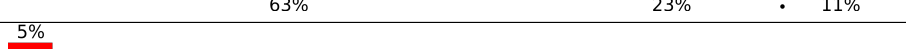
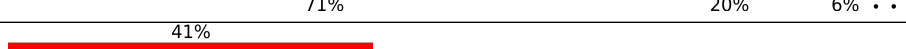
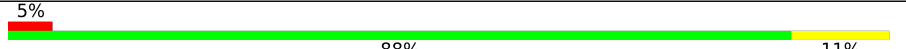
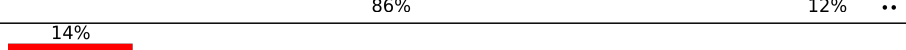
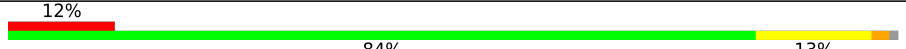
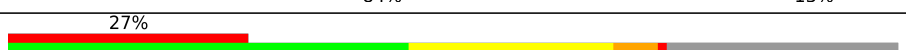
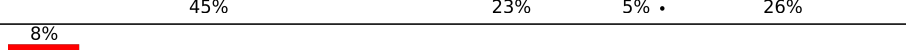
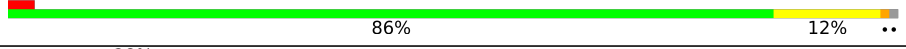
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14000 (2.58 - 3.58)

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	A	254	6% 69% 14% 16%
2	B	387	5% 56% 34% 9%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	C	362	
4	D	297	
5	E	176	
6	F	244	
7	G	256	
8	H	191	
9	I	166	
10	J	174	
11	K	376	
12	L	199	
13	M	138	
14	N	204	
15	O	199	
16	P	184	
17	Q	186	
18	R	189	
19	S	172	
20	T	160	
21	U	121	
22	V	137	
23	W	236	
24	X	142	
25	Y	127	
26	Z	136	
27	a	149	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
28	b	647	
29	c	105	
30	d	113	
31	e	130	
32	f	107	
33	g	121	
34	h	120	
35	i	100	
36	j	88	
37	k	78	
38	l	51	
39	m	486	
40	n	605	
41	o	220	
42	p	92	
43	q	455	
44	r	261	
45	s	520	
46	t	322	
47	u	199	
48	v	344	
49	w	203	
50	x	515	
51	y	245	
52	z	106	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
53	1	3396	10% 59% 26% 5% 10%
54	2	158	73% 24%
55	3	121	41% 77% 21%
56	4	593	46% 75% 12% 13%
57	5	120	54% 52% 8% 39%
58	6	232	7% 10% 13% 5% 72%

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 156562 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 L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	213	Total	C	N	O	S	0	0
			1634	1023	326	284	1		

- Molecule 2 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	386	Total	C	N	O	S	0	0
			3081	1956	584	533	8		

- Molecule 3 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	361	Total	C	N	O	S	0	0
			2749	1730	522	494	3		

- Molecule 4 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	276	Total	C	N	O	S	0	0
			2211	1397	391	421	2		

- Molecule 5 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 6 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 7 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	233	Total	C	N	O	S	0	0
			1817	1159	326	329	3		

- Molecule 8 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 9 is a protein called Bud site selection protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	131	Total	C	N	O	S	0	0
			1059	662	195	198	4		

- Molecule 10 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 11 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	256	Total	C	N	O	S	0	0
			2064	1332	342	387	3		

- Molecule 12 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	L	187	Total	C	N	O	0	0
			1499	934	307	258		

- Molecule 13 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

- Molecule 14 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 15 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 16 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	183	Total	C	N	O	S	0	0
			1442	896	287	259			

- Molecule 17 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	134	Total	C	N	O	S	0	0
			1035	659	196	179	1		

- Molecule 18 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	156	Total	C	N	O	S	0	0
			1258	781	265	212			

- Molecule 19 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 20 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	119	Total	C	N	O	S	0	0
			943	595	180	165	3		

- Molecule 21 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	106	Total	C	N	O	0	0
			844	545	138	161		

- Molecule 22 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 23 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	234	Total	C	N	O	S	0	0
			1885	1194	323	362	6		

- Molecule 24 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	141	Total	C	N	O	S	0	0
			1100	705	196	197	2		

- Molecule 25 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Y	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 26 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	Z	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 27 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	93	Total	C	N	O	S	0	0
			735	479	130	125	1		

- Molecule 28 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	642	Total	C	N	O	S	0	0
			5185	3251	938	970	26		

- Molecule 29 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 30 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	107	Total	C	N	O	S	0	0
			873	553	165	154	1		

- Molecule 31 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 32 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 33 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 34 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 35 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 36 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	j	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 37 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	k	77	Total	C	N	O	S	0	0
			612	391	115	106			

- Molecule 38 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	l	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 39 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	m	469	Total	C	N	O	S	0	0
			3774	2381	685	699	9		

- Molecule 40 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	n	371	Total	C	N	O	S	0	0
			3030	1963	523	534	10		

- Molecule 41 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	o	133	Total	C	N	O	S	0	0
			1107	716	198	189	4		

- Molecule 42 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	p	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 43 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	q	183	Total	C	N	O	S	0	0
			1514	957	268	288	1		

- Molecule 44 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	r	230	Total	C	N	O	S	0	0
			1860	1177	352	324	7		

- Molecule 45 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	s	69	Total	C	N	O	S	0	0
			573	359	113	98	3		

- Molecule 46 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	t	287	Total	C	N	O	S	0	0
			2306	1459	427	417	3		

- Molecule 47 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	u	150	Total	C	N	O	S	0	0
			1265	793	253	210	9		

- Molecule 48 is a protein called Ribosome biogenesis protein RPF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	v	287	Total	C	N	O	S	0	0
			2318	1482	408	412	16		

- Molecule 49 is a protein called Regulator of ribosome biosynthesis.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	w	182	Total	C	N	O	S	0	0
			1448	911	261	271	5		

- Molecule 50 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	x	488	Total	C	N	O	S	0	0
			3807	2398	677	711	21		

- Molecule 51 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	y	244	Total	C	N	O	S	0	0
			1849	1146	319	377	7		

- Molecule 52 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	z	55	Total	C	N	O		
			444	273	88	83	0	0

- Molecule 53 is a RNA chain called RDN25-1 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	1	3058	Total	C	N	O	P	0	0
			65427	29223	11807	21339	3058		

- Molecule 54 is a RNA chain called RDN58-1 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	2	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 55 is a RNA chain called RDN5-2 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 56 is a protein called Probable metalloprotease ARX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	4	516	Total	C	N	O	S	0	0
			3999	2530	688	766	15		

- Molecule 57 is a protein called rRNA-processing protein CGR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	5	73	Total	C	N	O	S	0	0
			645	395	133	114	3		

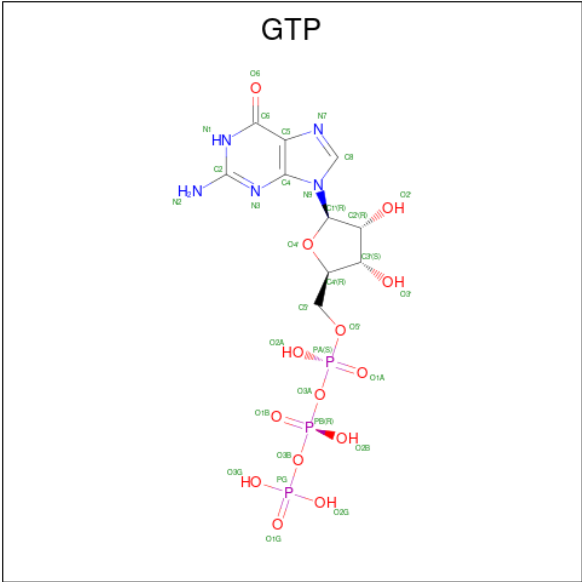
- Molecule 58 is a RNA chain called ITS2-1 miscRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	6	65	Total	C	N	O	P	0	0
			1370	614	228	463	65		

- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
59	I	1	Total	Zn	0
			1	1	
59	j	1	Total	Zn	0
			1	1	
59	p	1	Total	Zn	0
			1	1	
59	u	1	Total	Zn	0
			1	1	

- Molecule 60 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



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

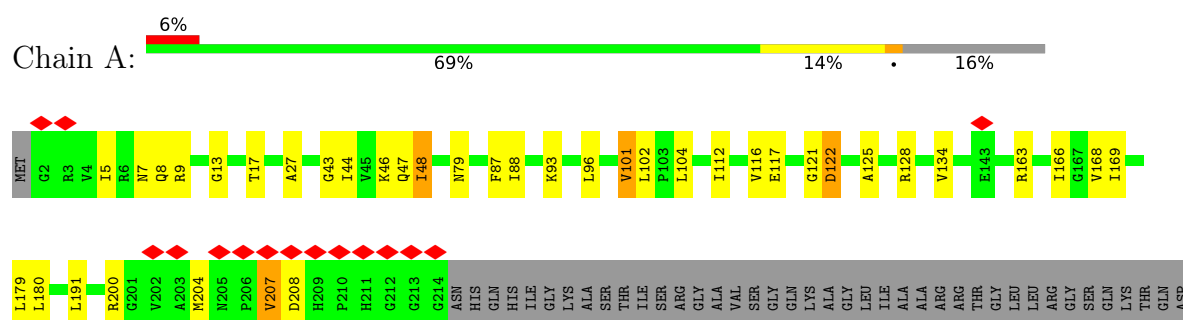
- Molecule 61 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
61	b	1	Total	Mg	0
			1	1	
61	m	1	Total	Mg	0
			1	1	

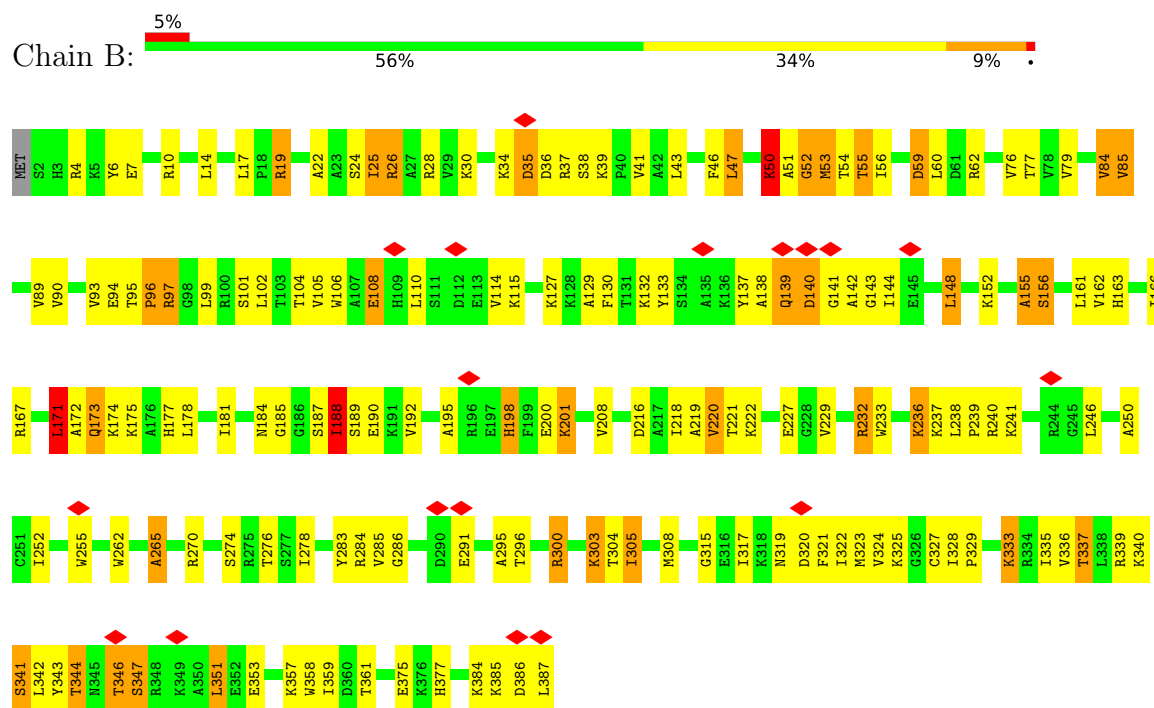
3 Residue-property plots

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

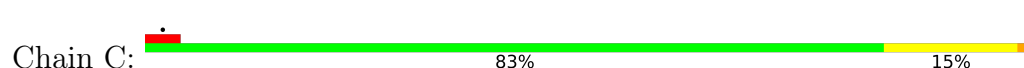
• Molecule 1: 60S ribosomal protein L2-A

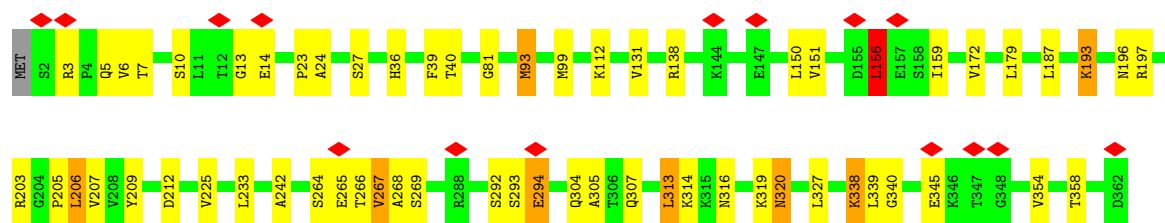


• Molecule 2: 60S ribosomal protein L3

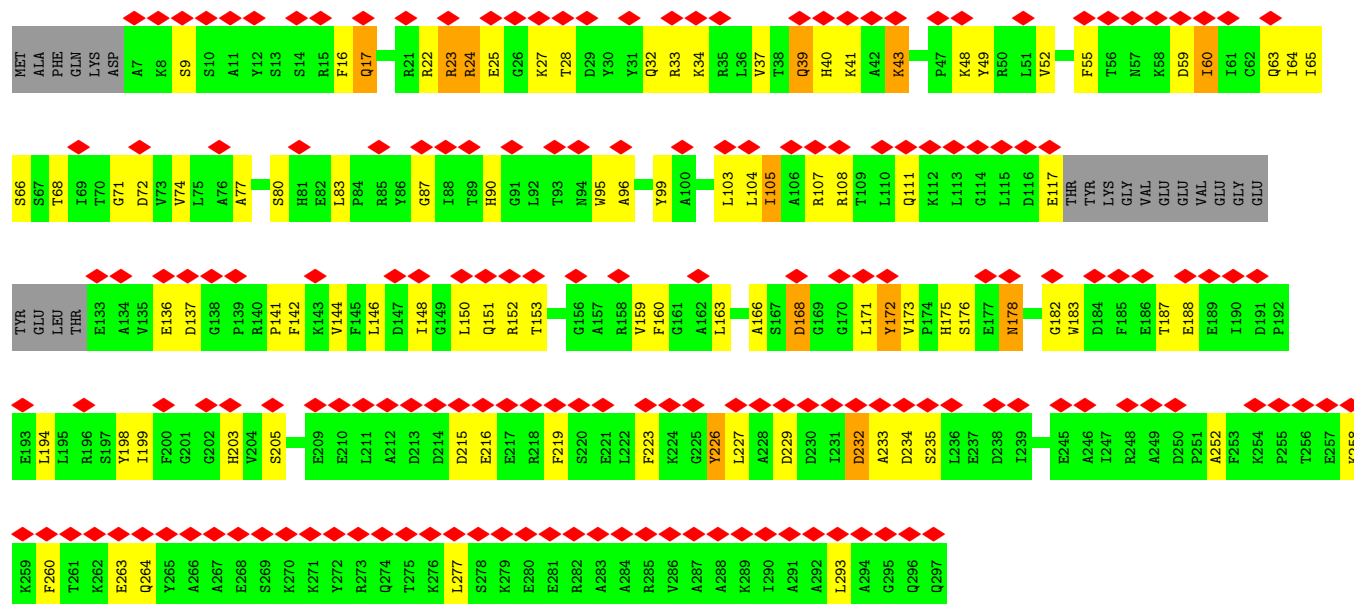


• Molecule 3: 60S ribosomal protein L4-A

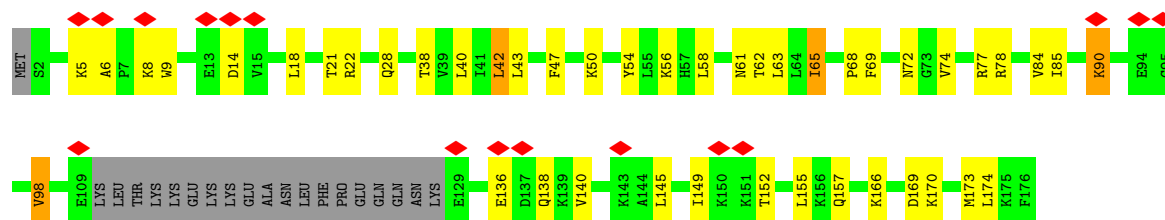




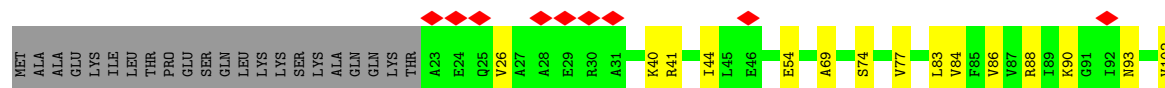
• Molecule 4: 60S ribosomal protein L5

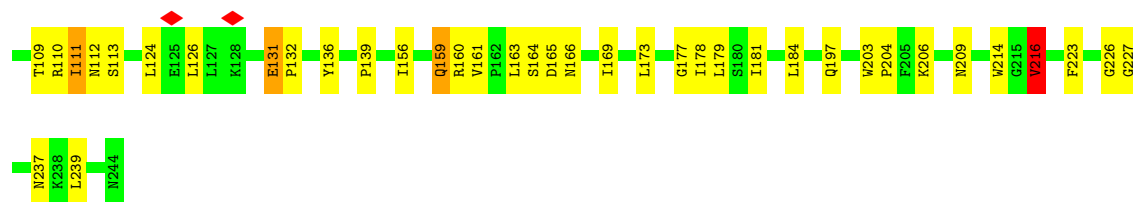


• Molecule 5: 60S ribosomal protein L6-A

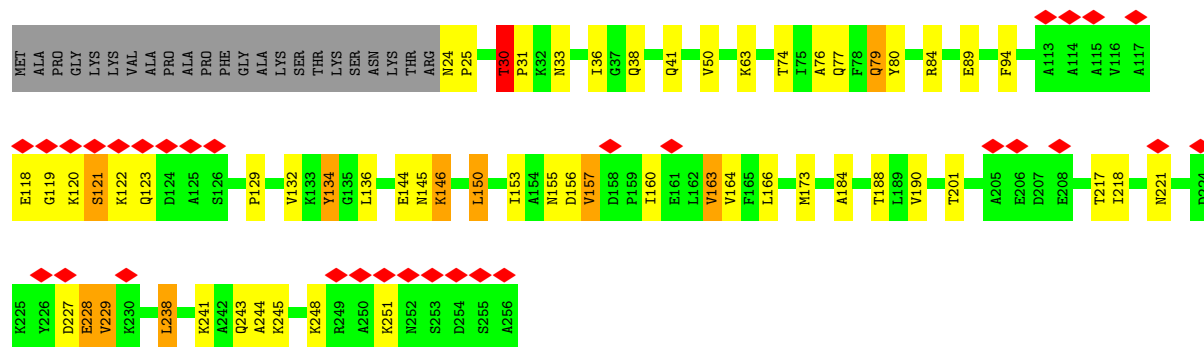


• Molecule 6: 60S ribosomal protein L7-A

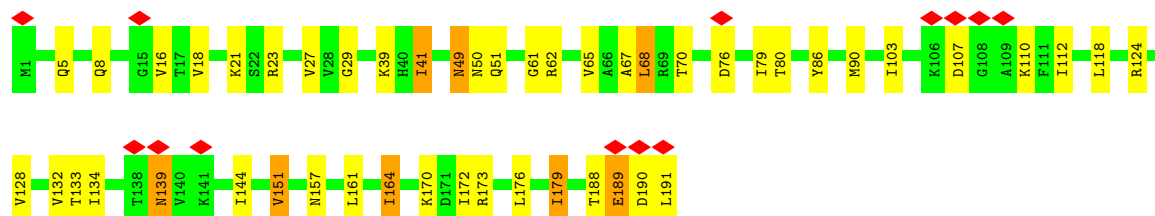




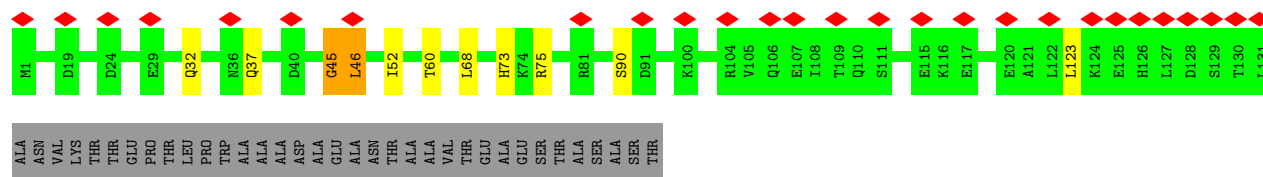
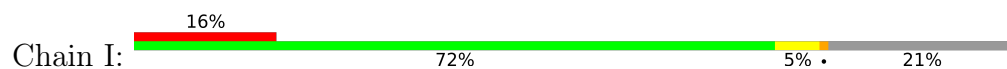
• Molecule 7: 60S ribosomal protein L8-A



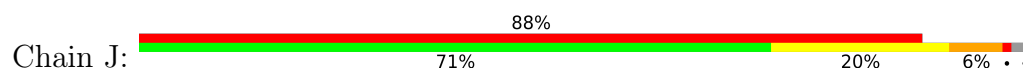
• Molecule 8: 60S ribosomal protein L9-A



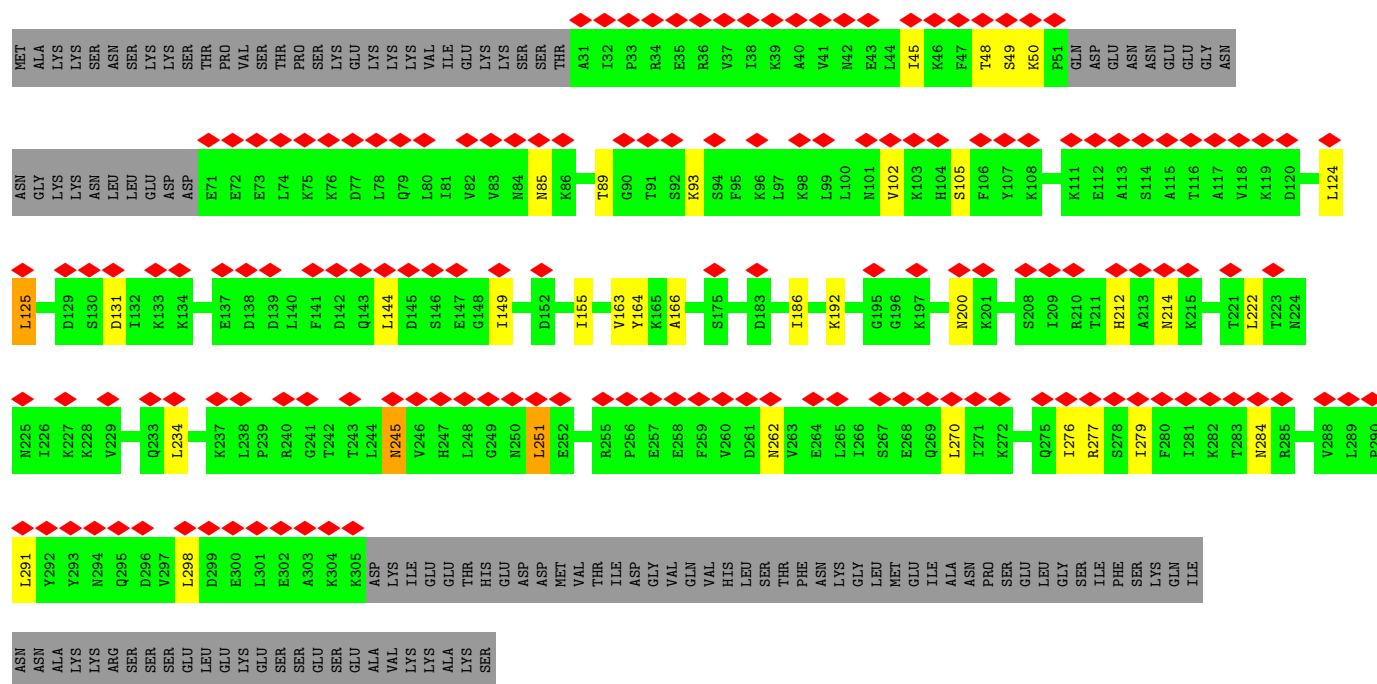
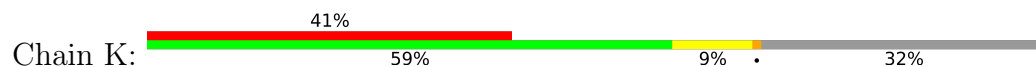
• Molecule 9: Bud site selection protein 20



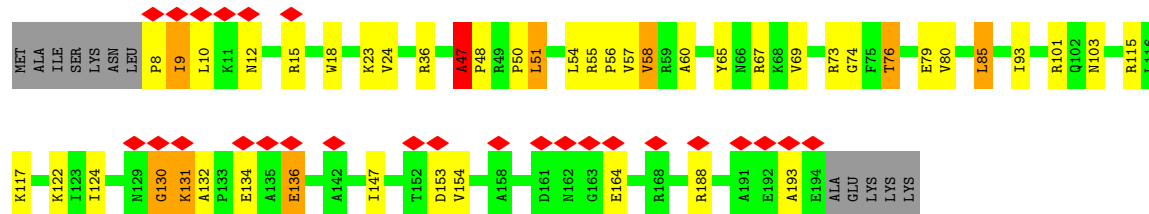
• Molecule 10: 60S ribosomal protein L11-A



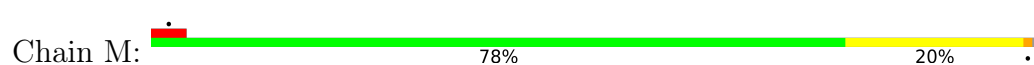
- Molecule 11: Proteasome-interacting protein CIC1



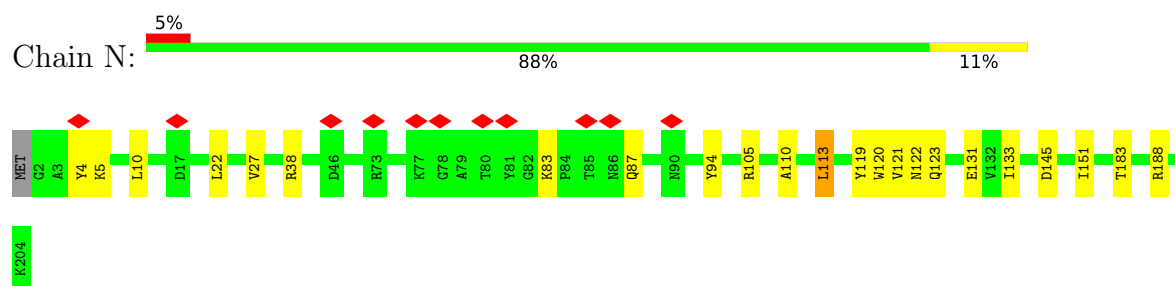
- Molecule 12: 60S ribosomal protein L13-A



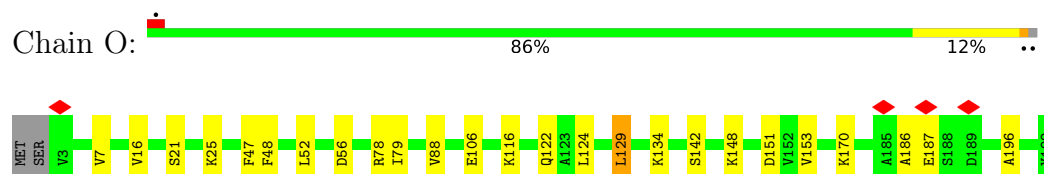
- Molecule 13: 60S ribosomal protein L14-A



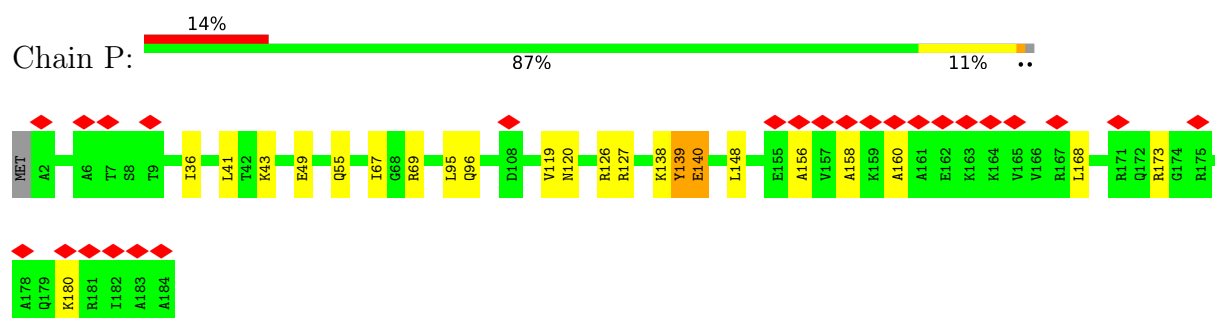
- Molecule 14: 60S ribosomal protein L15-A



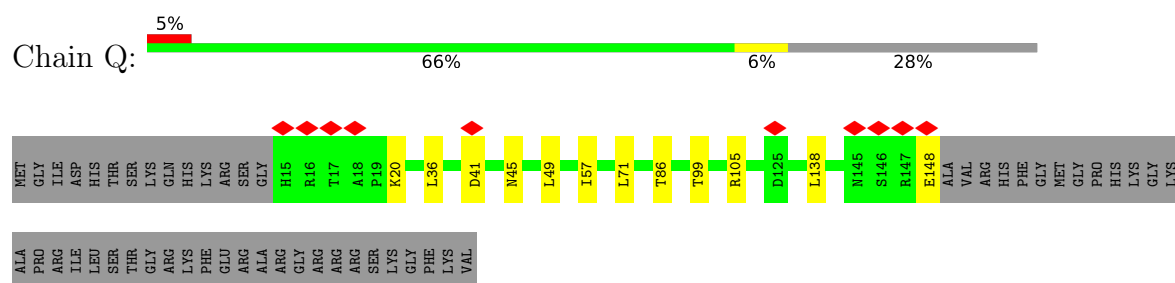
- Molecule 15: 60S ribosomal protein L16-A



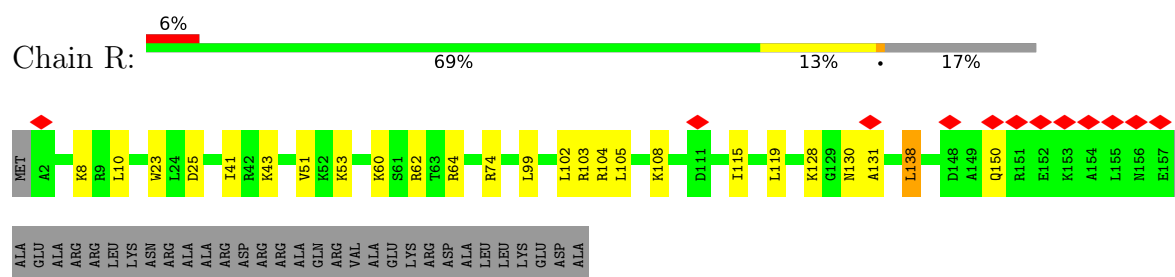
- Molecule 16: 60S ribosomal protein L17-A



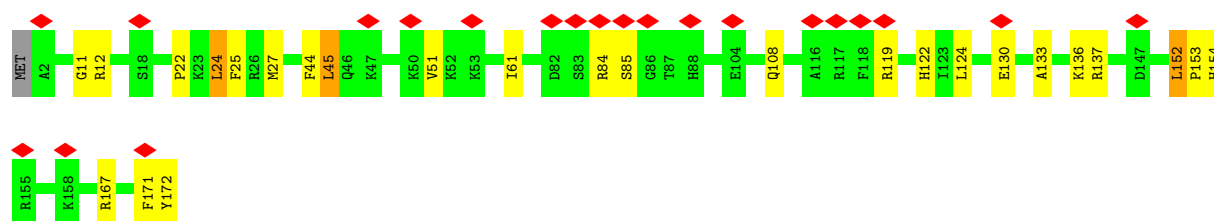
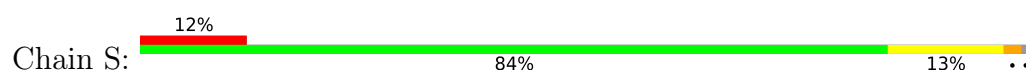
- Molecule 17: 60S ribosomal protein L18-A



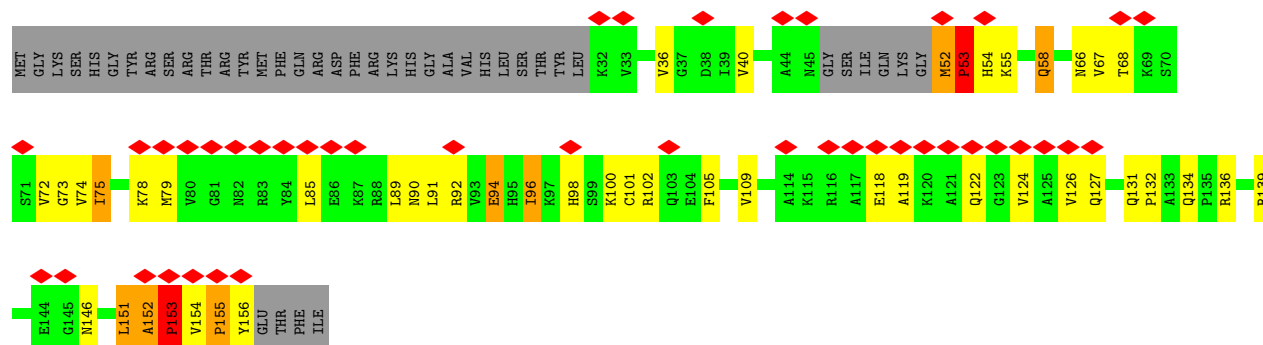
- Molecule 18: 60S ribosomal protein L19-A



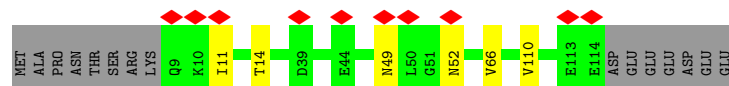
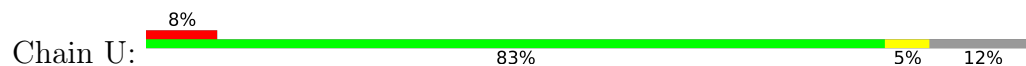
- Molecule 19: 60S ribosomal protein L20-A



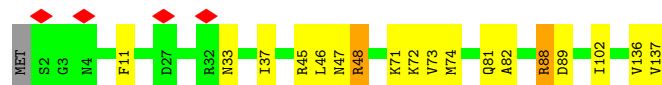
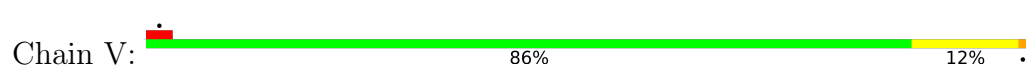
- Molecule 20: 60S ribosomal protein L21-A



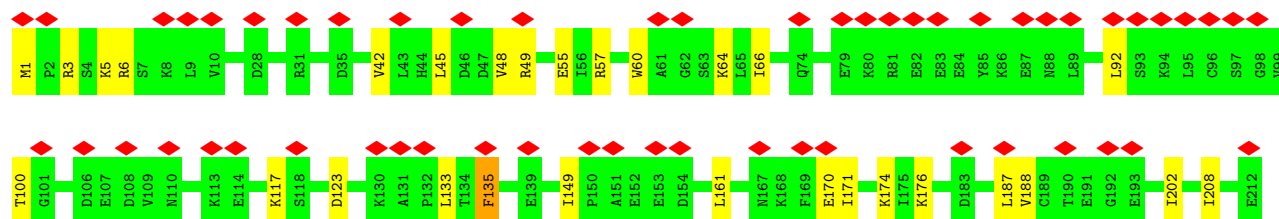
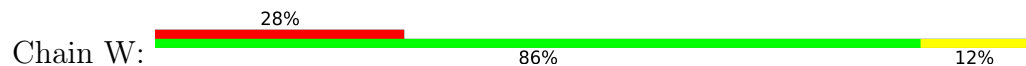
- Molecule 21: 60S ribosomal protein L22-A

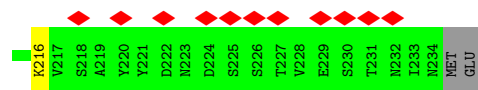


- Molecule 22: 60S ribosomal protein L23-A

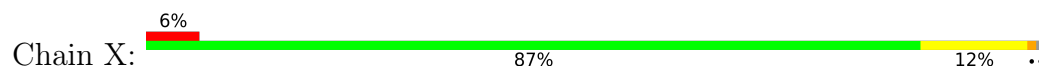


- Molecule 23: Ribosome assembly factor MRT4

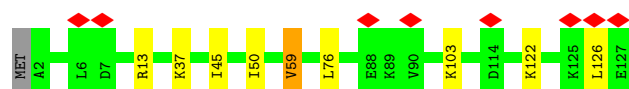




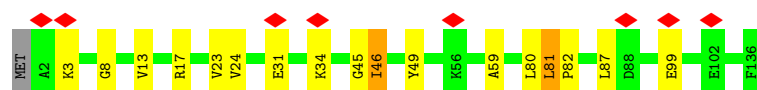
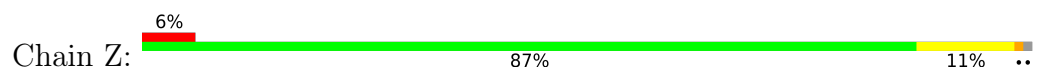
- Molecule 24: 60S ribosomal protein L25



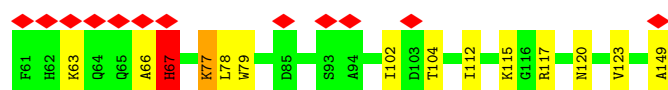
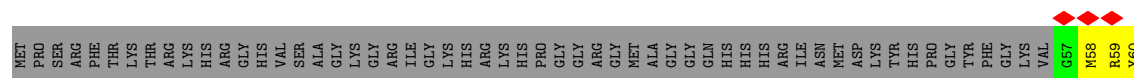
- Molecule 25: 60S ribosomal protein L26-A



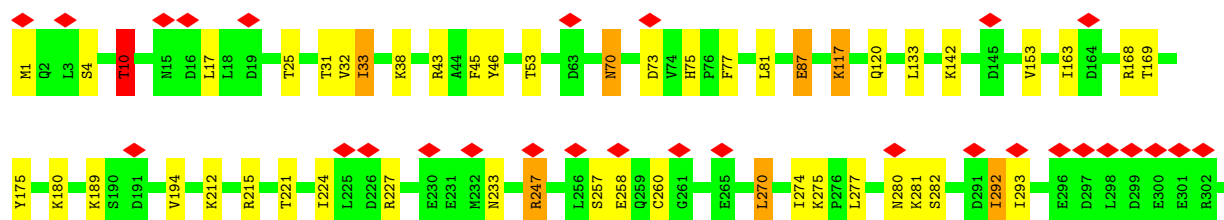
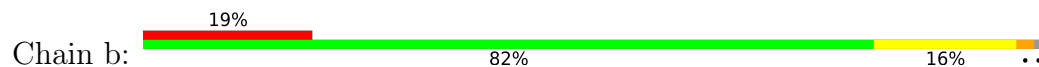
- Molecule 26: 60S ribosomal protein L27-A

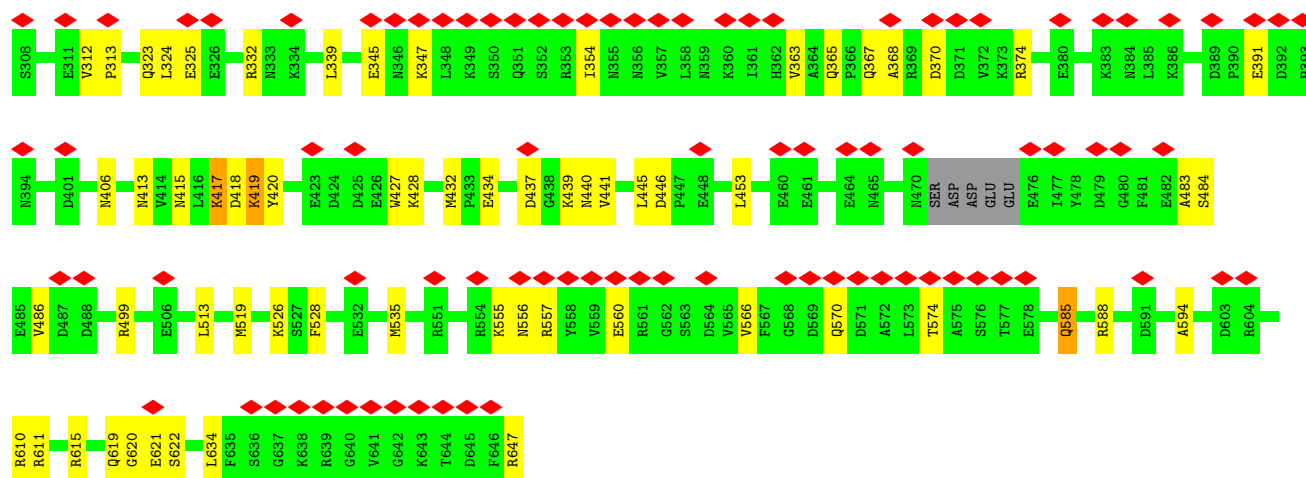


- Molecule 27: 60S ribosomal protein L28

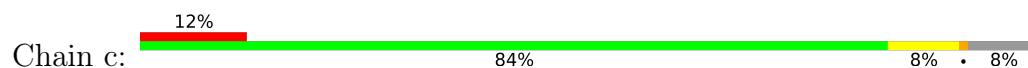


- Molecule 28: Nucleolar GTP-binding protein 1

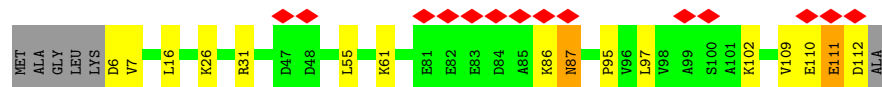
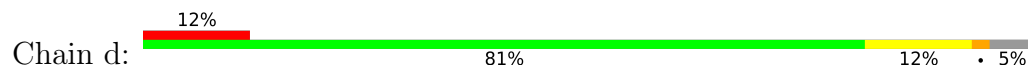




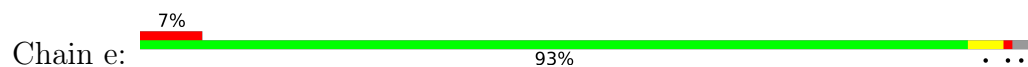
- Molecule 29: 60S ribosomal protein L30



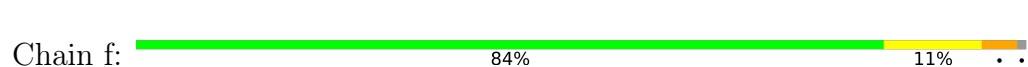
- Molecule 30: 60S ribosomal protein L31-A



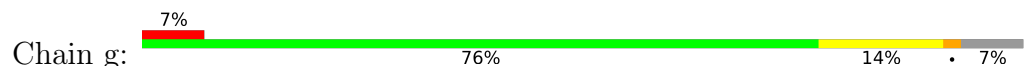
- Molecule 31: 60S ribosomal protein L32

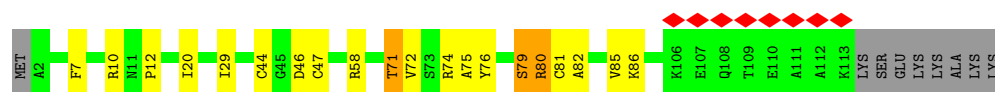


- Molecule 32: 60S ribosomal protein L33-A

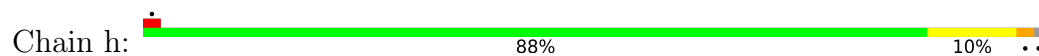


- Molecule 33: 60S ribosomal protein L34-A

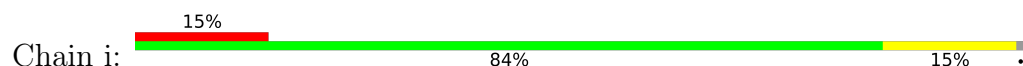




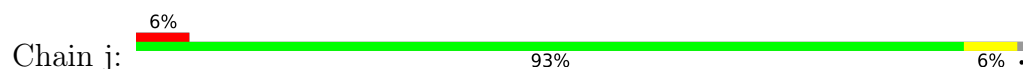
- Molecule 34: 60S ribosomal protein L35-A



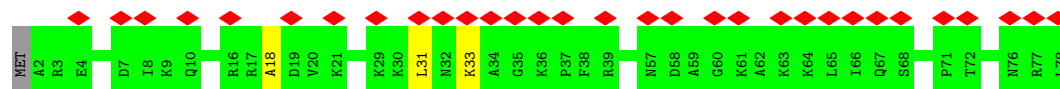
- Molecule 35: 60S ribosomal protein L36-A



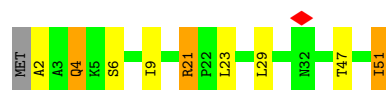
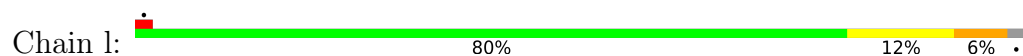
- Molecule 36: 60S ribosomal protein L37-A



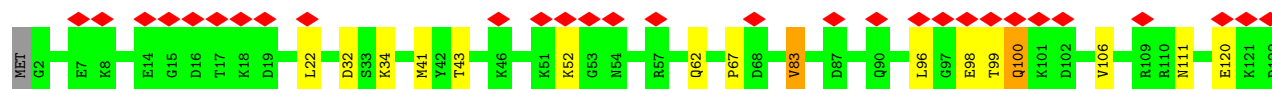
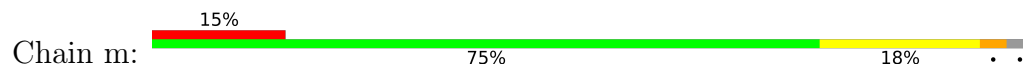
- Molecule 37: 60S ribosomal protein L38

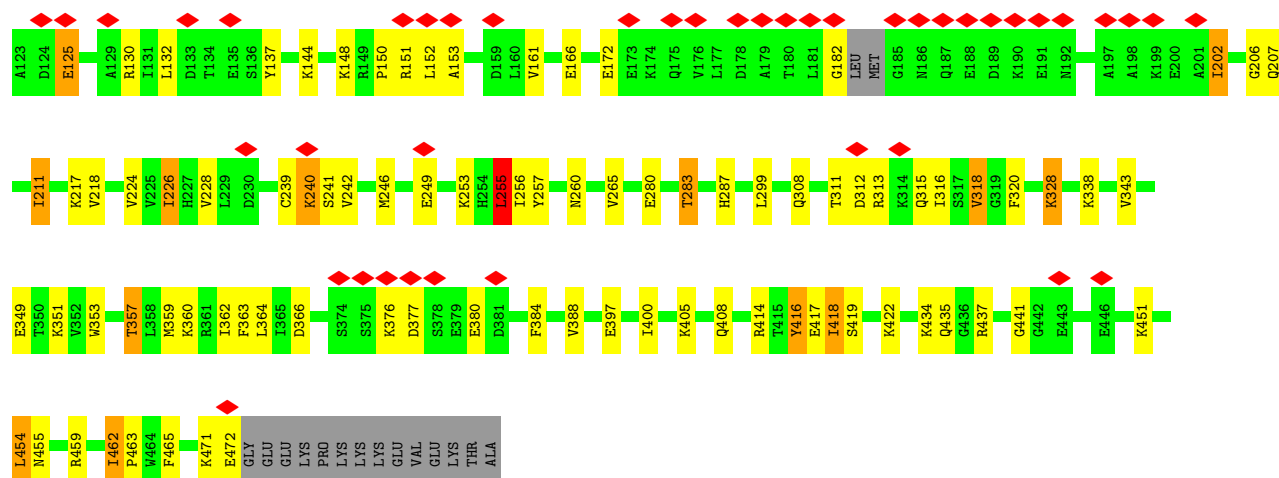


- Molecule 38: 60S ribosomal protein L39

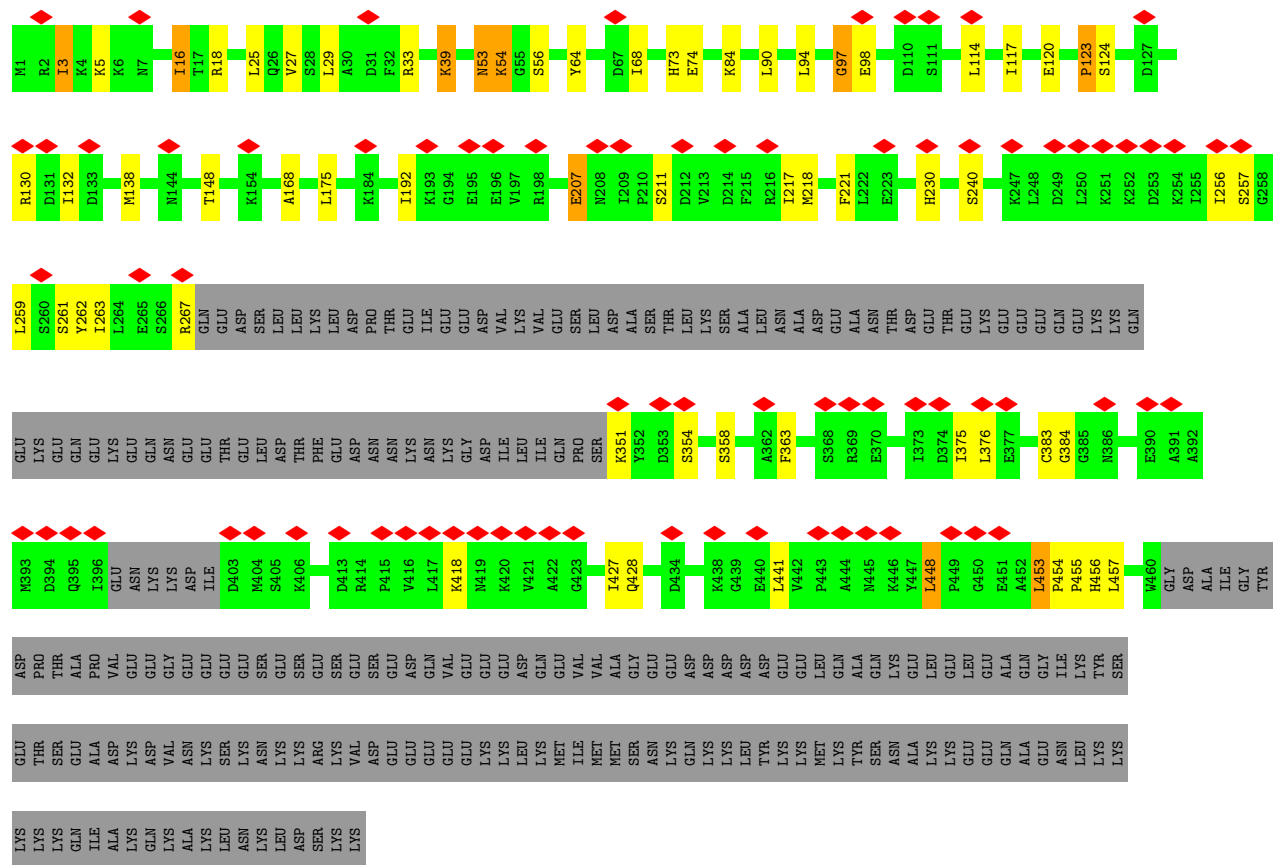


- Molecule 39: Nucleolar GTP-binding protein 2

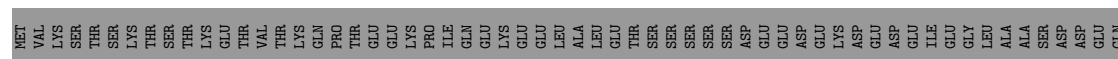


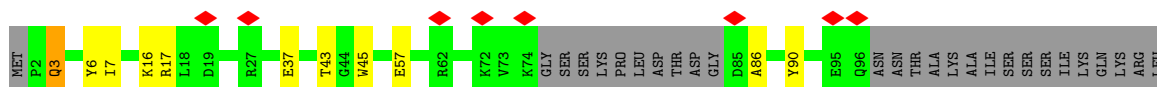


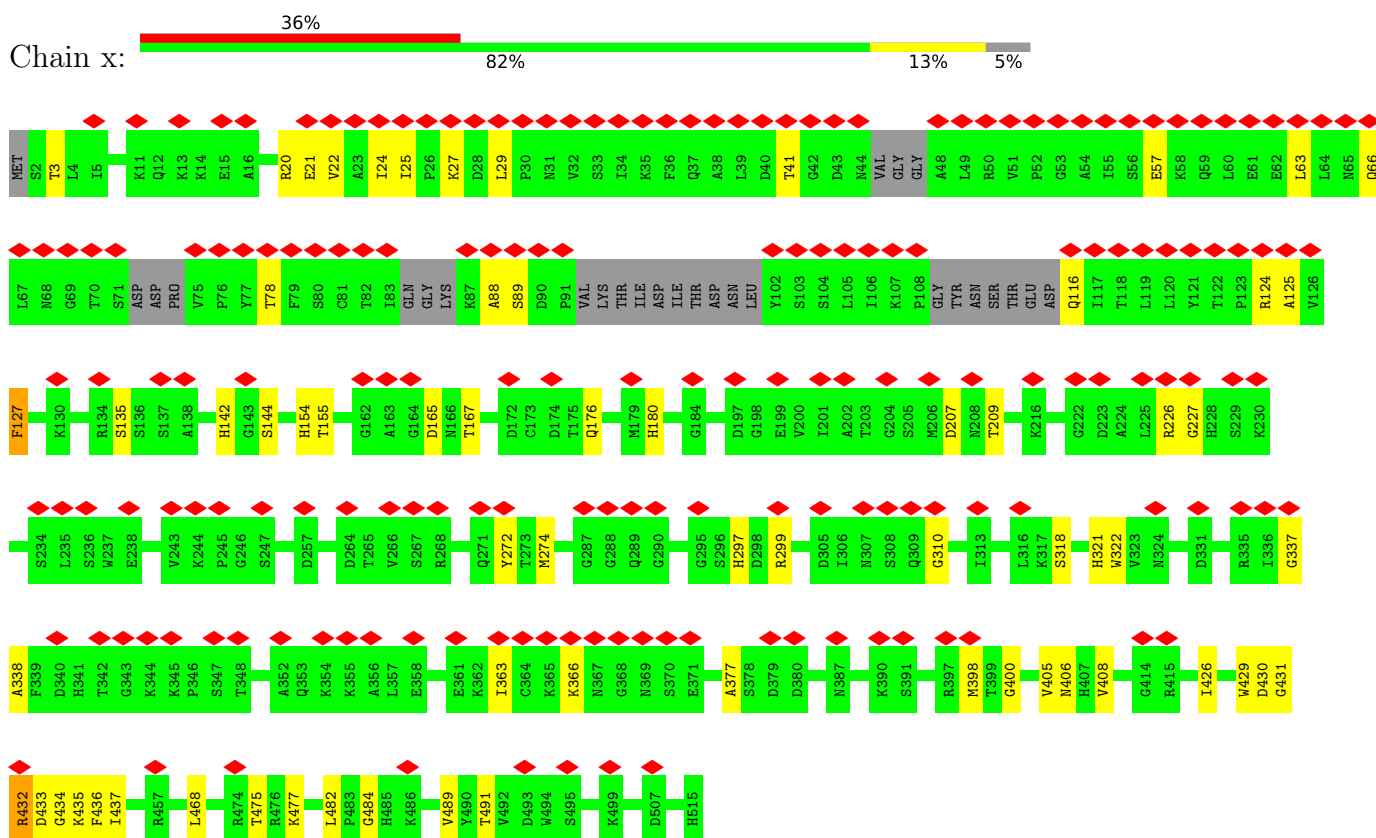
• Molecule 40: Pescadillo homolog



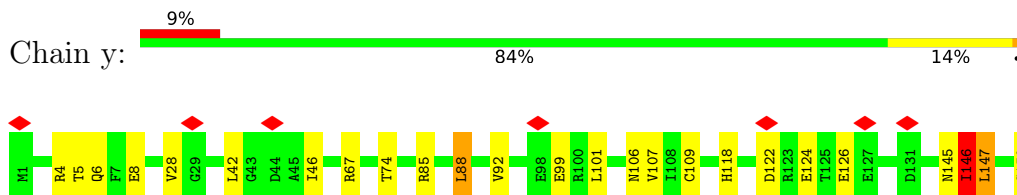
• Molecule 41: Ribosome biogenesis protein 15



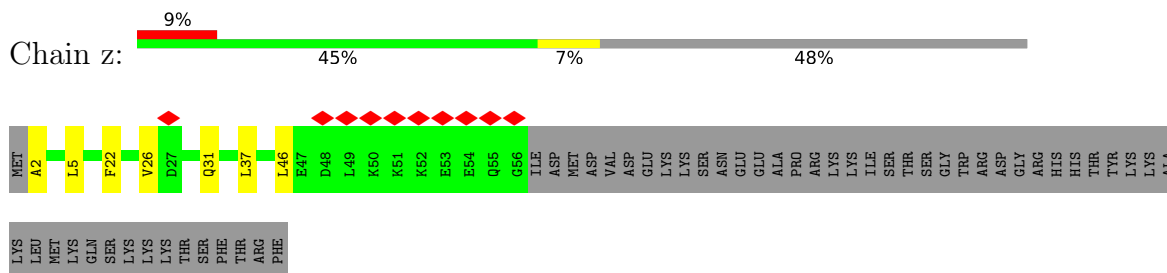




- Molecule 51: Eukaryotic translation initiation factor 6

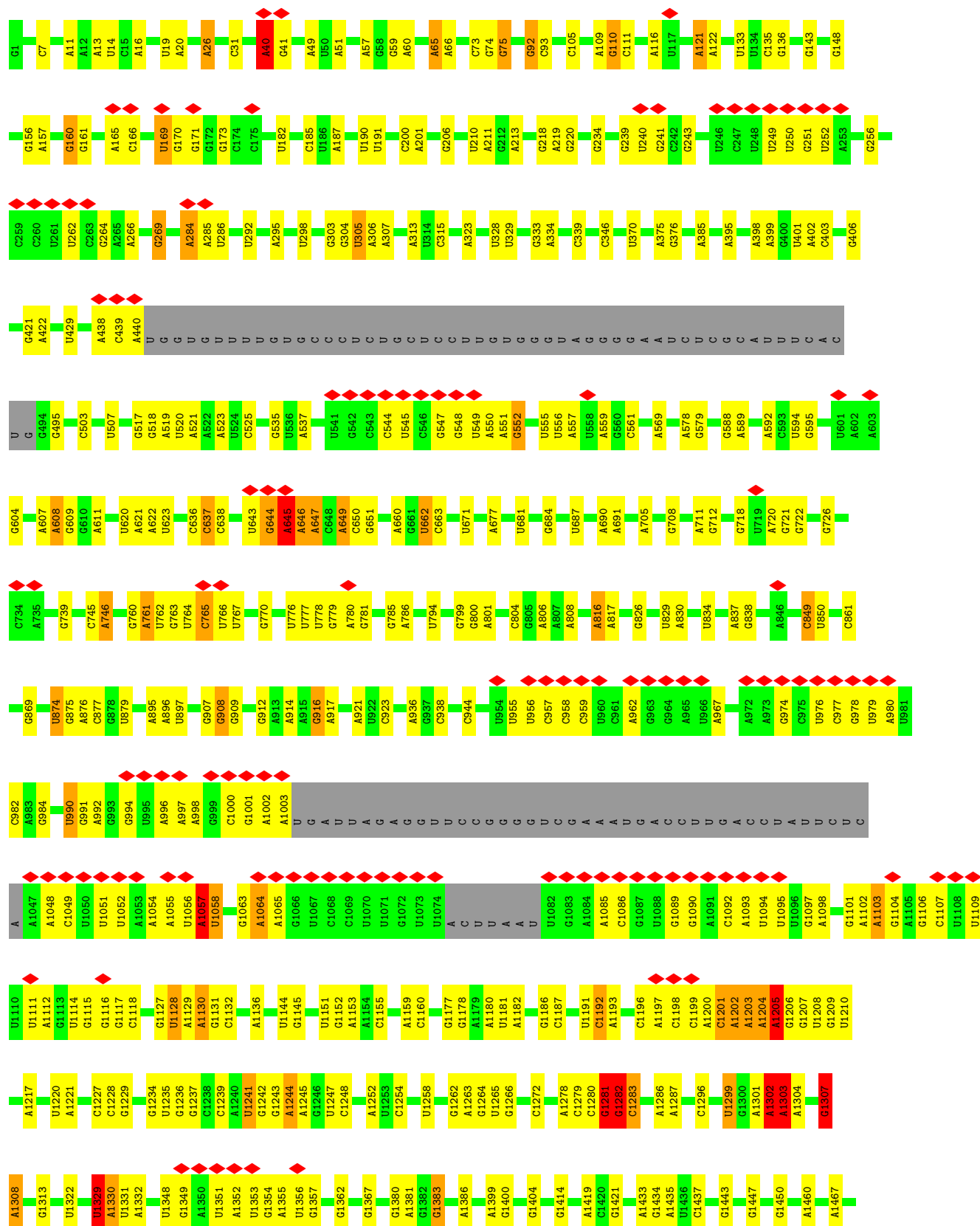


- Molecule 52: UPF0642 protein YBL028C

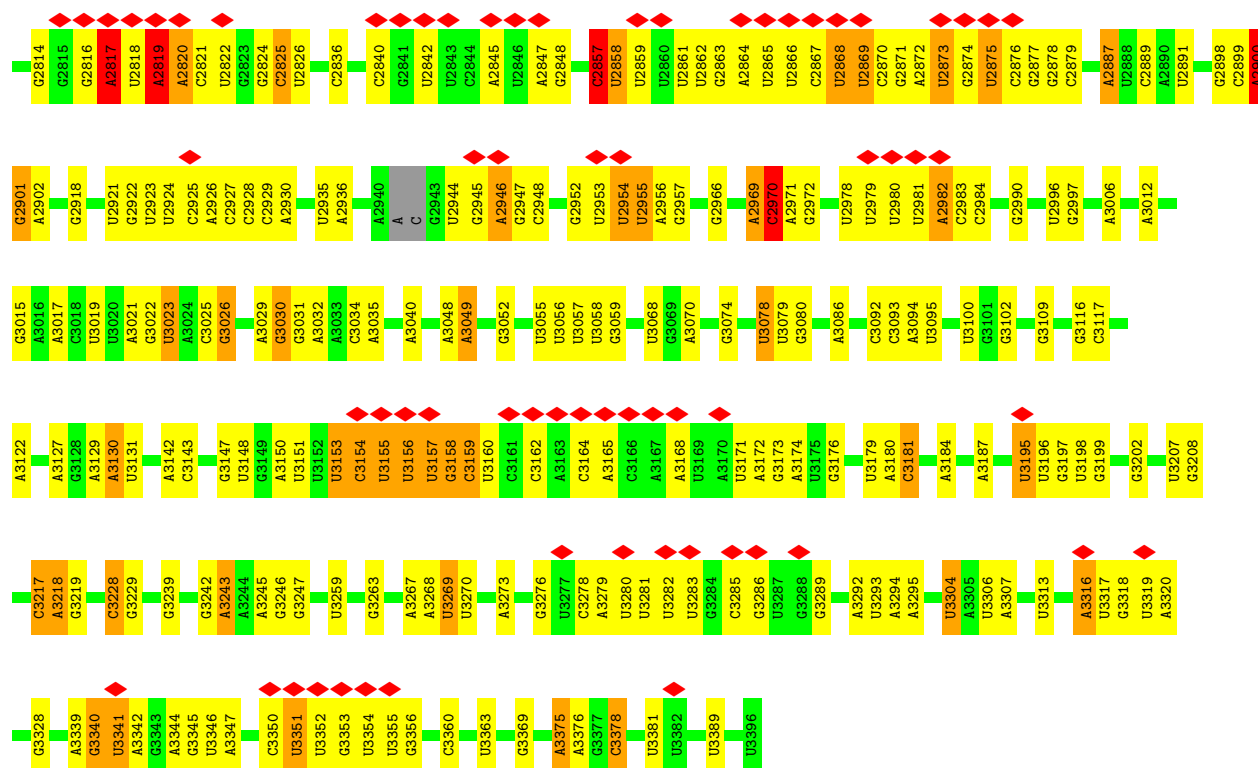


- Molecule 53: RDN25-1 rRNA



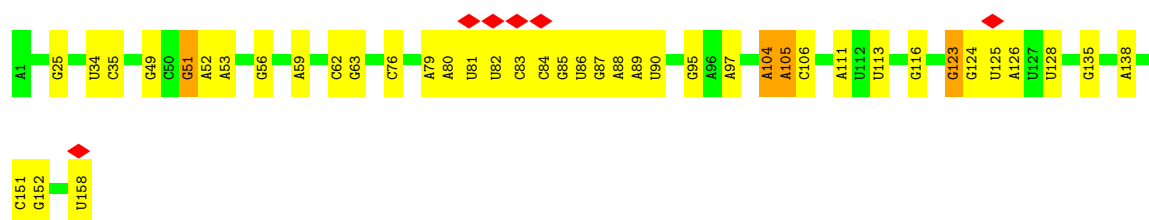






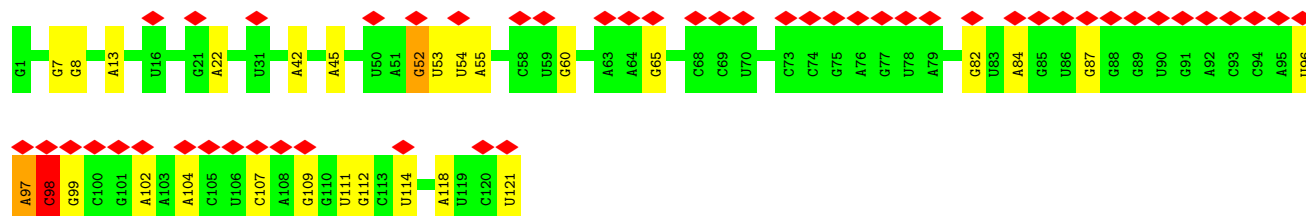
• Molecule 54: RDN58-1 rRNA

Chain 2: 73% 24% .



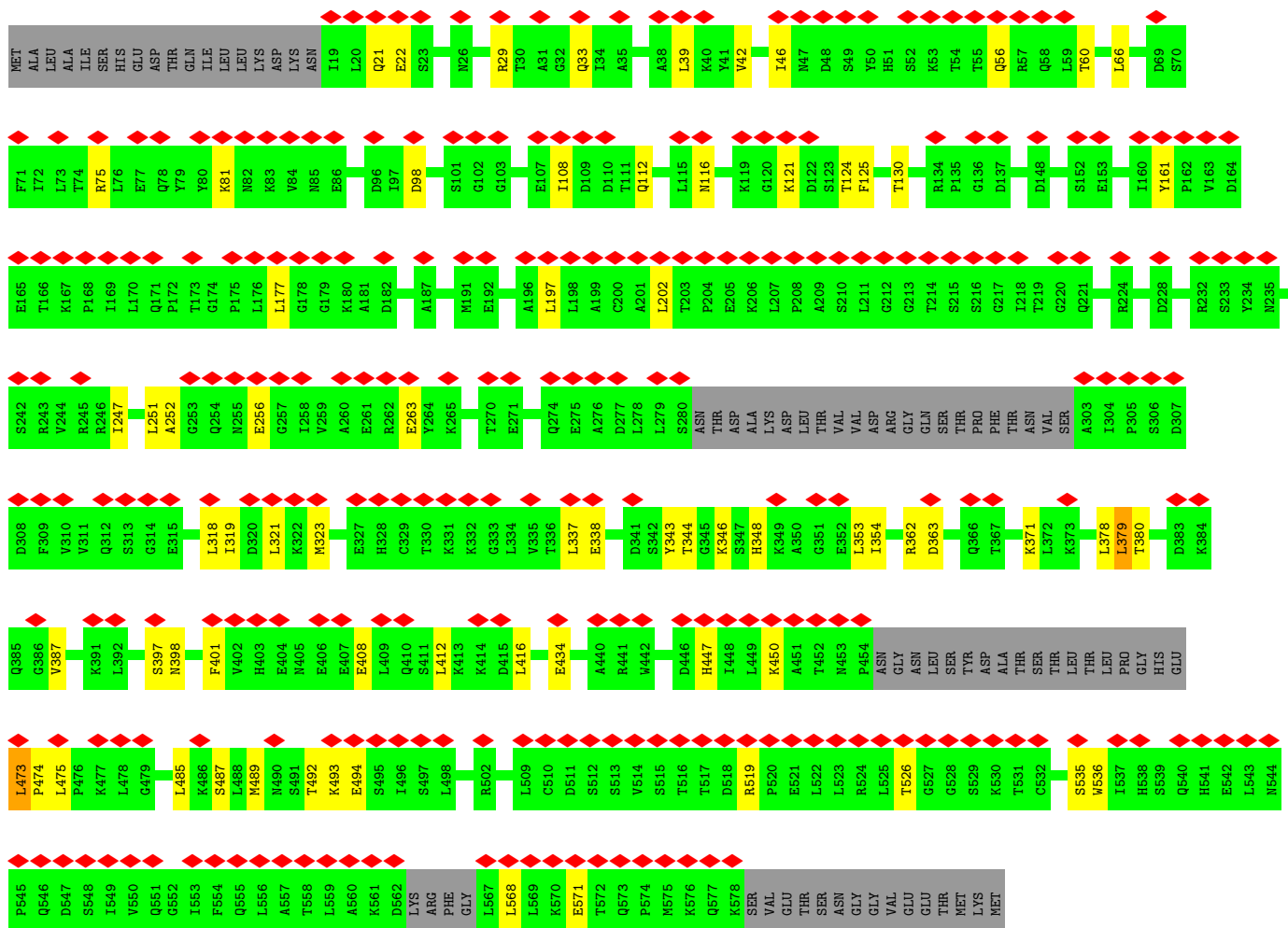
• Molecule 55: RDN5-2 rRNA

Chain 3: 41% 77% 21% ..

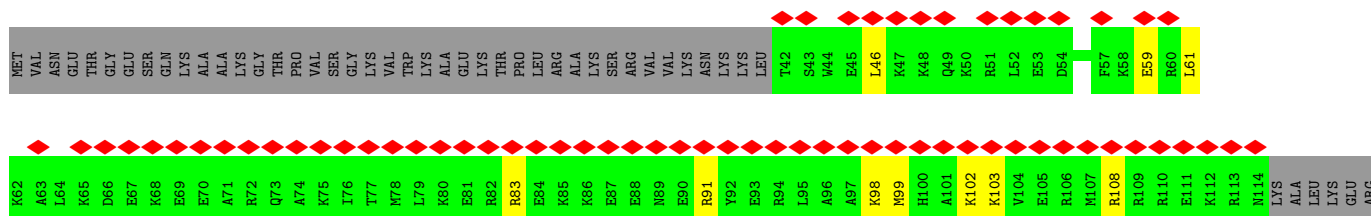


• Molecule 56: Probable metalloprotease ARX1

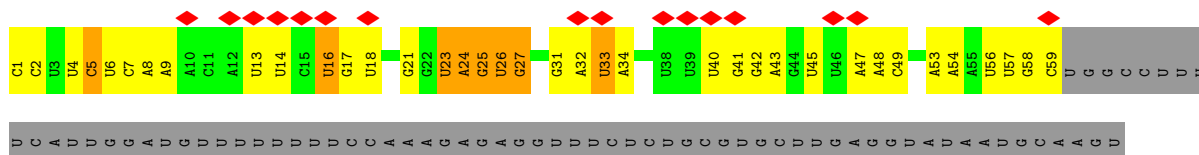
Chain 4: 46% 75% 12% 13%



• Molecule 57: rRNA-processing protein CGR1



• Molecule 58: ITS2-1 miscRNA





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	191848	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.272	Depositor
Minimum map value	-0.177	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.029	Depositor
Map size ($\text{\AA}$)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.32, 1.32, 1.32	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.56	0/1666	0.78	0/2241
2	B	0.60	0/3152	0.84	2/4239 (0.0%)
3	C	0.56	0/2801	0.84	0/3792
4	D	0.55	0/2257	0.87	0/3043
5	E	0.54	0/1260	0.80	0/1694
6	F	0.55	0/1821	0.87	2/2451 (0.1%)
7	G	0.55	0/1849	0.91	2/2495 (0.1%)
8	H	0.50	0/1539	0.76	1/2073 (0.0%)
9	I	0.54	0/1075	0.78	0/1443
10	J	0.64	0/1374	0.86	2/1842 (0.1%)
11	K	0.56	0/2098	0.77	0/2830
12	L	0.56	0/1524	0.93	2/2046 (0.1%)
13	M	0.49	0/1074	0.82	0/1446
14	N	0.54	0/1757	0.81	1/2354 (0.0%)
15	O	0.46	0/1585	0.72	0/2128
16	P	0.50	0/1465	0.80	2/1968 (0.1%)
17	Q	0.52	0/1050	0.74	0/1419
18	R	0.51	0/1275	0.84	0/1702
19	S	0.48	0/1473	0.71	0/1980
20	T	0.57	0/957	0.89	3/1285 (0.2%)
21	U	0.53	0/861	0.72	0/1167
22	V	0.50	0/1018	0.74	0/1369
23	W	0.54	0/1918	0.74	0/2586
24	X	0.50	0/1116	0.76	0/1503
25	Y	0.50	0/1004	0.72	0/1341
26	Z	0.52	0/1118	0.74	0/1497
27	a	0.53	0/751	0.77	1/1013 (0.1%)
28	b	0.54	0/5270	0.82	0/7080
29	c	0.52	0/751	0.75	0/1008
30	d	0.45	0/887	0.65	0/1191
31	e	0.50	0/1041	0.77	1/1394 (0.1%)
32	f	0.48	0/868	0.73	1/1168 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.53	0/891	0.85	1/1191 (0.1%)
34	h	0.52	0/978	0.86	0/1301
35	i	0.55	0/778	0.82	1/1034 (0.1%)
36	j	0.54	0/696	0.80	0/923
37	k	0.54	0/618	0.70	0/826
38	l	0.50	0/443	0.75	0/588
39	m	0.57	1/3848 (0.0%)	0.82	0/5181
40	n	0.56	0/3101	0.80	0/4187
41	o	0.54	0/1129	0.72	0/1502
42	p	0.52	0/701	0.80	0/934
43	q	0.57	0/1539	0.78	0/2059
44	r	0.55	0/1892	0.81	2/2528 (0.1%)
45	s	0.49	0/577	0.74	0/752
46	t	0.57	1/2333 (0.0%)	0.81	0/3128
47	u	0.52	0/1287	0.82	0/1711
48	v	0.49	0/2361	0.66	0/3153
49	w	0.52	0/1471	0.74	0/1980
50	x	0.52	0/3897	0.67	2/5282 (0.0%)
51	y	0.53	0/1872	0.79	0/2548
52	z	0.54	0/445	0.86	0/585
53	1	0.37	0/73234	0.73	91/114167 (0.1%)
54	2	0.36	0/3746	0.69	1/5832 (0.0%)
55	3	0.37	0/2883	0.65	2/4491 (0.0%)
56	4	0.57	0/4069	0.76	0/5520
57	5	0.57	0/649	0.82	0/848
58	6	0.38	0/1527	0.78	1/2371 (0.0%)
All	All	0.47	2/166620 (0.0%)	0.76	121/241410 (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	B	0	10
3	C	0	1
4	D	0	3
6	F	0	1
7	G	0	4
9	I	0	1
10	J	0	3
11	K	0	3

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
13	M	0	1
18	R	0	1
19	S	0	6
20	T	0	2
21	U	0	1
22	V	0	2
23	W	0	3
24	X	0	2
26	Z	0	2
28	b	0	18
30	d	0	3
31	e	0	1
32	f	0	1
33	g	0	1
34	h	0	2
36	j	0	1
37	k	0	2
38	l	0	1
39	m	0	16
40	n	0	18
41	o	0	4
43	q	0	8
44	r	0	6
46	t	0	7
47	u	0	3
49	w	0	9
50	x	0	8
51	y	0	3
56	4	0	11
All	All	0	169

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	m	182	GLY	C-O	6.01	1.35	1.23
46	t	322	ASN	C-O	5.78	1.35	1.23

The worst 5 of 121 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	1	1307	G	C2'-C3'-O3'	11.01	126.02	109.50
53	1	3341	U	C2'-C3'-O3'	9.52	123.78	109.50

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	e	126	LEU	N-CA-C	8.85	122.21	110.88
53	1	305	U	C2'-C3'-O3'	8.78	122.67	109.50
53	1	637	C	C4'-C3'-O3'	8.49	122.14	109.40

There are no chirality outliers.

5 of 169 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	156	SER	Peptide
2	B	220	VAL	Peptide
2	B	50	LYS	Peptide
2	B	52	GLY	Peptide
2	B	59	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	A	1634	0	1685	22	0
2	B	3081	0	3165	89	0
3	C	2749	0	2863	33	0
4	D	2211	0	2175	69	0
5	E	1239	0	1326	21	0
6	F	1784	0	1862	24	0
7	G	1817	0	1908	31	0
8	H	1518	0	1587	32	0
9	I	1059	0	1090	4	0
10	J	1353	0	1383	9	0
11	K	2064	0	2156	16	0
12	L	1499	0	1558	19	0
13	M	1059	0	1154	23	0
14	N	1720	0	1779	10	0
15	O	1555	0	1659	1	0
16	P	1442	0	1485	9	0
17	Q	1035	0	1115	4	0
18	R	1258	0	1341	10	0
19	S	1437	0	1475	10	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	T	943	0	994	33	0
21	U	844	0	855	1	0
22	V	1003	0	1048	13	0
23	W	1885	0	1921	5	0
24	X	1100	0	1187	5	0
25	Y	993	0	1081	2	0
26	Z	1092	0	1155	10	0
27	a	735	0	776	7	0
28	b	5185	0	5251	22	0
29	c	743	0	797	3	0
30	d	873	0	914	6	0
31	e	1020	0	1090	2	0
32	f	850	0	880	9	0
33	g	881	0	945	14	0
34	h	969	0	1078	1	0
35	i	771	0	849	3	0
36	j	681	0	683	0	0
37	k	612	0	682	0	0
38	l	436	0	475	5	0
39	m	3774	0	3835	21	0
40	n	3030	0	3107	11	0
41	o	1107	0	1159	0	0
42	p	694	0	734	8	0
43	q	1514	0	1570	7	0
44	r	1860	0	1965	32	0
45	s	573	0	644	1	0
46	t	2306	0	2454	8	0
47	u	1265	0	1314	7	0
48	v	2318	0	2398	6	0
49	w	1448	0	1510	8	0
50	x	3807	0	3790	31	0
51	y	1849	0	1835	22	0
52	z	444	0	478	4	0
53	1	65427	0	32875	340	0
54	2	3353	0	1695	4	0
55	3	2579	0	1303	12	0
56	4	3999	0	4088	8	0
57	5	645	0	688	0	0
58	6	1370	0	692	21	0
59	I	1	0	0	0	0
59	j	1	0	0	0	0
59	p	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	u	1	0	0	1	0
60	b	32	0	12	0	0
60	m	32	0	12	1	0
61	b	1	0	0	0	0
61	m	1	0	0	0	0
All	All	156562	0	123585	1008	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 1008 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)
53:1:2428:U:C5	53:1:2602:G:N1	1.70	1.54
53:1:2428:U:H5	53:1:2602:G:N1	0.92	1.40
50:x:366:LYS:HD2	50:x:432:ARG:NH2	1.08	1.40
50:x:366:LYS:CD	50:x:432:ARG:NH2	1.86	1.38
53:1:2255:A:N7	53:1:2261:G:N2	1.70	1.35

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	A	211/254 (83%)	205 (97%)	5 (2%)	1 (0%)	24	54
2	B	384/387 (99%)	281 (73%)	67 (17%)	36 (9%)	0	2
3	C	359/362 (99%)	330 (92%)	21 (6%)	8 (2%)	5	21
4	D	272/297 (92%)	246 (90%)	21 (8%)	5 (2%)	6	26
5	E	152/176 (86%)	145 (95%)	6 (4%)	1 (1%)	18	46

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	220/244 (90%)	207 (94%)	8 (4%)	5 (2%)	5	21
7	G	231/256 (90%)	213 (92%)	12 (5%)	6 (3%)	4	19
8	H	189/191 (99%)	181 (96%)	6 (3%)	2 (1%)	11	36
9	I	129/166 (78%)	110 (85%)	18 (14%)	1 (1%)	16	44
10	J	167/174 (96%)	137 (82%)	15 (9%)	15 (9%)	0	3
11	K	252/376 (67%)	226 (90%)	20 (8%)	6 (2%)	4	20
12	L	185/199 (93%)	170 (92%)	8 (4%)	7 (4%)	2	13
13	M	135/138 (98%)	128 (95%)	6 (4%)	1 (1%)	18	46
14	N	201/204 (98%)	190 (94%)	9 (4%)	2 (1%)	12	39
15	O	195/199 (98%)	150 (77%)	35 (18%)	10 (5%)	1	8
16	P	181/184 (98%)	169 (93%)	9 (5%)	3 (2%)	7	27
17	Q	132/186 (71%)	126 (96%)	6 (4%)	0	100	100
18	R	154/189 (82%)	149 (97%)	4 (3%)	1 (1%)	21	49
19	S	169/172 (98%)	156 (92%)	9 (5%)	4 (2%)	4	20
20	T	115/160 (72%)	102 (89%)	6 (5%)	7 (6%)	1	6
21	U	104/121 (86%)	94 (90%)	8 (8%)	2 (2%)	6	24
22	V	134/137 (98%)	126 (94%)	8 (6%)	0	100	100
23	W	232/236 (98%)	214 (92%)	17 (7%)	1 (0%)	30	58
24	X	139/142 (98%)	130 (94%)	9 (6%)	0	100	100
25	Y	124/127 (98%)	114 (92%)	10 (8%)	0	100	100
26	Z	133/136 (98%)	123 (92%)	9 (7%)	1 (1%)	16	44
27	a	91/149 (61%)	80 (88%)	9 (10%)	2 (2%)	5	21
28	b	638/647 (99%)	561 (88%)	59 (9%)	18 (3%)	4	18
29	c	95/105 (90%)	93 (98%)	1 (1%)	1 (1%)	11	36
30	d	105/113 (93%)	99 (94%)	4 (4%)	2 (2%)	6	24
31	e	125/130 (96%)	120 (96%)	5 (4%)	0	100	100
32	f	104/107 (97%)	99 (95%)	4 (4%)	1 (1%)	12	39
33	g	110/121 (91%)	107 (97%)	2 (2%)	1 (1%)	14	41
34	h	117/120 (98%)	109 (93%)	6 (5%)	2 (2%)	7	27
35	i	97/100 (97%)	87 (90%)	7 (7%)	3 (3%)	3	16
36	j	85/88 (97%)	75 (88%)	9 (11%)	1 (1%)	10	34

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	k	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
38	l	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
39	m	465/486 (96%)	399 (86%)	53 (11%)	13 (3%)	4	18
40	n	365/605 (60%)	321 (88%)	27 (7%)	17 (5%)	2	10
41	o	131/220 (60%)	116 (88%)	12 (9%)	3 (2%)	5	21
42	p	89/92 (97%)	81 (91%)	7 (8%)	1 (1%)	11	36
43	q	179/455 (39%)	155 (87%)	18 (10%)	6 (3%)	3	14
44	r	224/261 (86%)	194 (87%)	23 (10%)	7 (3%)	3	16
45	s	65/520 (12%)	59 (91%)	3 (5%)	3 (5%)	2	10
46	t	283/322 (88%)	249 (88%)	24 (8%)	10 (4%)	3	14
47	u	148/199 (74%)	134 (90%)	9 (6%)	5 (3%)	3	14
48	v	283/344 (82%)	269 (95%)	11 (4%)	3 (1%)	11	36
49	w	178/203 (88%)	152 (85%)	21 (12%)	5 (3%)	4	18
50	x	476/515 (92%)	433 (91%)	29 (6%)	14 (3%)	3	17
51	y	242/245 (99%)	222 (92%)	16 (7%)	4 (2%)	7	27
52	z	53/106 (50%)	51 (96%)	2 (4%)	0	100	100
56	4	508/593 (86%)	469 (92%)	31 (6%)	8 (2%)	7	28
57	5	71/120 (59%)	70 (99%)	1 (1%)	0	100	100
All	All	10349/12508 (83%)	9344 (90%)	750 (7%)	255 (2%)	6	19

5 of 255 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	25	ILE
2	B	34	LYS
2	B	38	SER
2	B	140	ASP
2	B	142	ALA

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	A	166/196 (85%)	156 (94%)	10 (6%)	17	45
2	B	322/323 (100%)	257 (80%)	65 (20%)	1	5
3	C	288/289 (100%)	270 (94%)	18 (6%)	16	43
4	D	227/245 (93%)	203 (89%)	24 (11%)	6	24
5	E	134/153 (88%)	122 (91%)	12 (9%)	9	31
6	F	186/205 (91%)	175 (94%)	11 (6%)	18	45
7	G	191/208 (92%)	173 (91%)	18 (9%)	8	29
8	H	171/171 (100%)	157 (92%)	14 (8%)	10	34
9	I	117/141 (83%)	112 (96%)	5 (4%)	26	55
10	J	147/150 (98%)	125 (85%)	22 (15%)	3	12
11	K	236/346 (68%)	225 (95%)	11 (5%)	23	52
12	L	149/159 (94%)	130 (87%)	19 (13%)	4	16
13	M	108/109 (99%)	103 (95%)	5 (5%)	24	53
14	N	175/176 (99%)	165 (94%)	10 (6%)	18	46
15	O	160/162 (99%)	145 (91%)	15 (9%)	8	29
16	P	145/146 (99%)	133 (92%)	12 (8%)	10	33
17	Q	110/151 (73%)	105 (96%)	5 (4%)	24	53
18	R	129/154 (84%)	117 (91%)	12 (9%)	8	29
19	S	155/156 (99%)	147 (95%)	8 (5%)	21	49
20	T	102/137 (74%)	88 (86%)	14 (14%)	3	14
21	U	93/107 (87%)	92 (99%)	1 (1%)	65	76
22	V	104/105 (99%)	96 (92%)	8 (8%)	12	36
23	W	211/213 (99%)	191 (90%)	20 (10%)	8	28
24	X	117/118 (99%)	105 (90%)	12 (10%)	7	25
25	Y	109/110 (99%)	103 (94%)	6 (6%)	19	47
26	Z	115/116 (99%)	109 (95%)	6 (5%)	21	49
27	a	76/119 (64%)	69 (91%)	7 (9%)	8	29
28	b	568/573 (99%)	506 (89%)	62 (11%)	6	23
29	c	81/88 (92%)	77 (95%)	4 (5%)	22	51
30	d	94/97 (97%)	85 (90%)	9 (10%)	8	28
31	e	109/111 (98%)	105 (96%)	4 (4%)	30	58

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	f	90/91 (99%)	82 (91%)	8 (9%)	9	31
33	g	95/103 (92%)	89 (94%)	6 (6%)	16	43
34	h	104/105 (99%)	94 (90%)	10 (10%)	8	28
35	i	81/82 (99%)	73 (90%)	8 (10%)	7	27
36	j	70/71 (99%)	67 (96%)	3 (4%)	26	55
37	k	68/69 (99%)	67 (98%)	1 (2%)	57	73
38	l	45/46 (98%)	38 (84%)	7 (16%)	2	11
39	m	413/428 (96%)	353 (86%)	60 (14%)	3	13
40	n	334/548 (61%)	312 (93%)	22 (7%)	15	41
41	o	118/199 (59%)	104 (88%)	14 (12%)	5	19
42	p	71/72 (99%)	68 (96%)	3 (4%)	26	55
43	q	171/420 (41%)	160 (94%)	11 (6%)	16	42
44	r	203/229 (89%)	185 (91%)	18 (9%)	9	31
45	s	62/445 (14%)	61 (98%)	1 (2%)	55	72
46	t	256/287 (89%)	238 (93%)	18 (7%)	14	39
47	u	133/180 (74%)	123 (92%)	10 (8%)	12	37
48	v	258/309 (84%)	254 (98%)	4 (2%)	55	72
49	w	161/179 (90%)	154 (96%)	7 (4%)	26	55
50	x	428/451 (95%)	411 (96%)	17 (4%)	28	56
51	y	210/211 (100%)	197 (94%)	13 (6%)	16	43
52	z	48/95 (50%)	44 (92%)	4 (8%)	10	33
56	4	453/520 (87%)	413 (91%)	40 (9%)	9	31
57	5	67/106 (63%)	57 (85%)	10 (15%)	3	12
All	All	9034/10780 (84%)	8290 (92%)	744 (8%)	13	34

5 of 744 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	h	20	GLN
40	n	448	LEU
35	i	57	LEU
33	g	86	LYS
39	m	299	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 162 such sidechains are listed below:

Mol	Chain	Res	Type
43	q	228	ASN
51	y	11	ASN
44	r	49	GLN
49	w	57	ASN
56	4	26	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	1	3048/3396 (89%)	944 (30%)	216 (7%)
54	2	157/158 (99%)	39 (24%)	5 (3%)
55	3	120/121 (99%)	22 (18%)	4 (3%)
58	6	64/232 (27%)	41 (64%)	10 (15%)
All	All	3389/3907 (86%)	1046 (30%)	235 (6%)

5 of 1046 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
53	1	7	C
53	1	11	A
53	1	13	A
53	1	14	U
53	1	16	A

5 of 235 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	1	2411	U
55	3	52	G
53	1	2658	G
54	2	88	A
53	1	3195	U

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
60	GTP	m	501	61	33,34,34	1.15	3 (9%)	50,54,54	1.82	9 (18%)
60	GTP	b	701	61	33,34,34	1.17	3 (9%)	50,54,54	1.73	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
60	GTP	m	501	61	-	1/22/38/38	0/3/3/3
60	GTP	b	701	61	-	2/22/38/38	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	b	701	GTP	C5-C4	3.13	1.47	1.38
60	m	501	GTP	C5-C4	2.96	1.46	1.38
60	m	501	GTP	C6-N1	-2.80	1.33	1.38
60	m	501	GTP	C5-N7	-2.69	1.33	1.39
60	b	701	GTP	C6-N1	-2.31	1.34	1.38

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	m	501	GTP	C5-C4-N3	-6.43	118.16	128.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	b	701	GTP	C5-C4-N3	-5.92	118.96	128.39
60	m	501	GTP	C2-N3-C4	5.13	121.13	112.30
60	b	701	GTP	C2-N3-C4	5.12	121.11	112.30
60	m	501	GTP	N9-C4-N3	4.73	135.41	125.95

There are no chirality outliers.

All (3) torsion outliers are listed below:

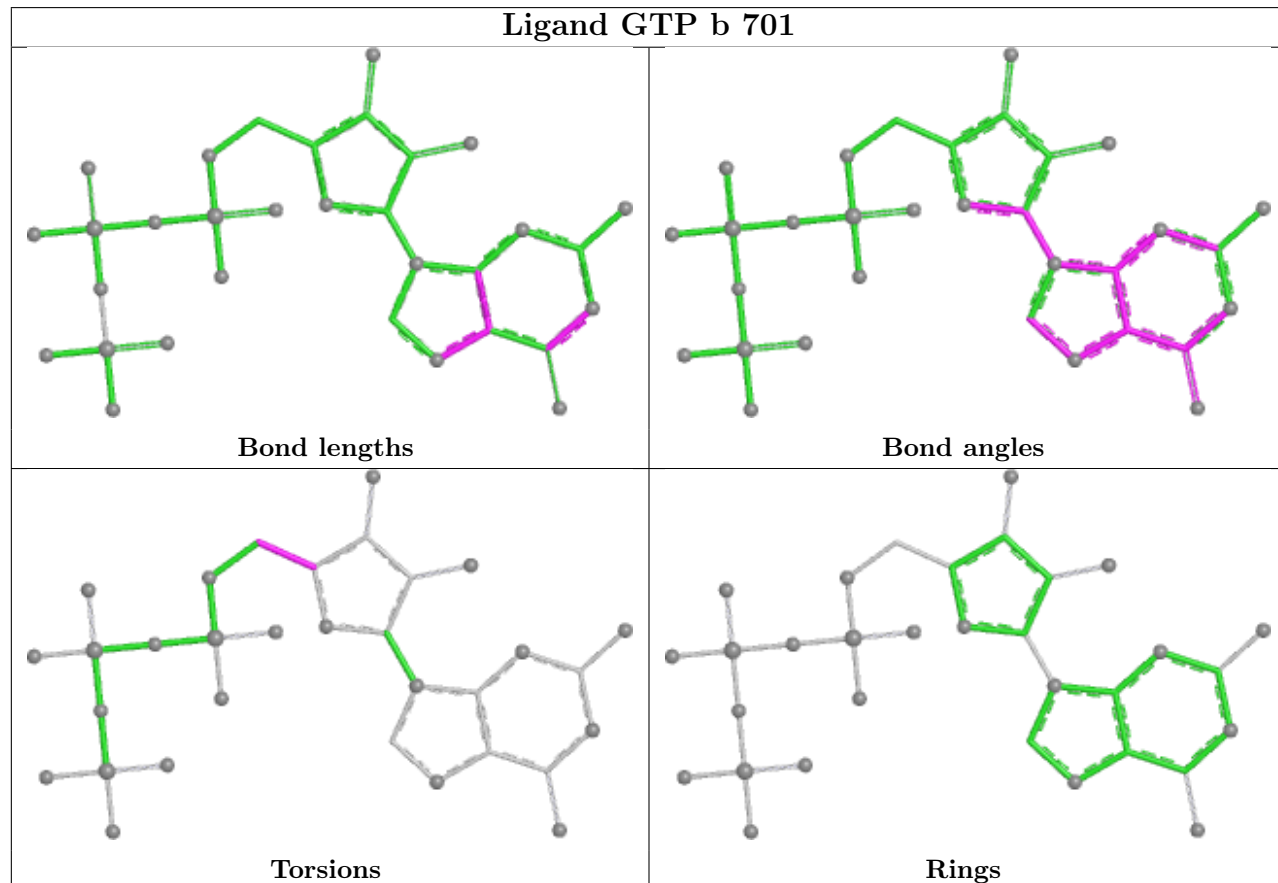
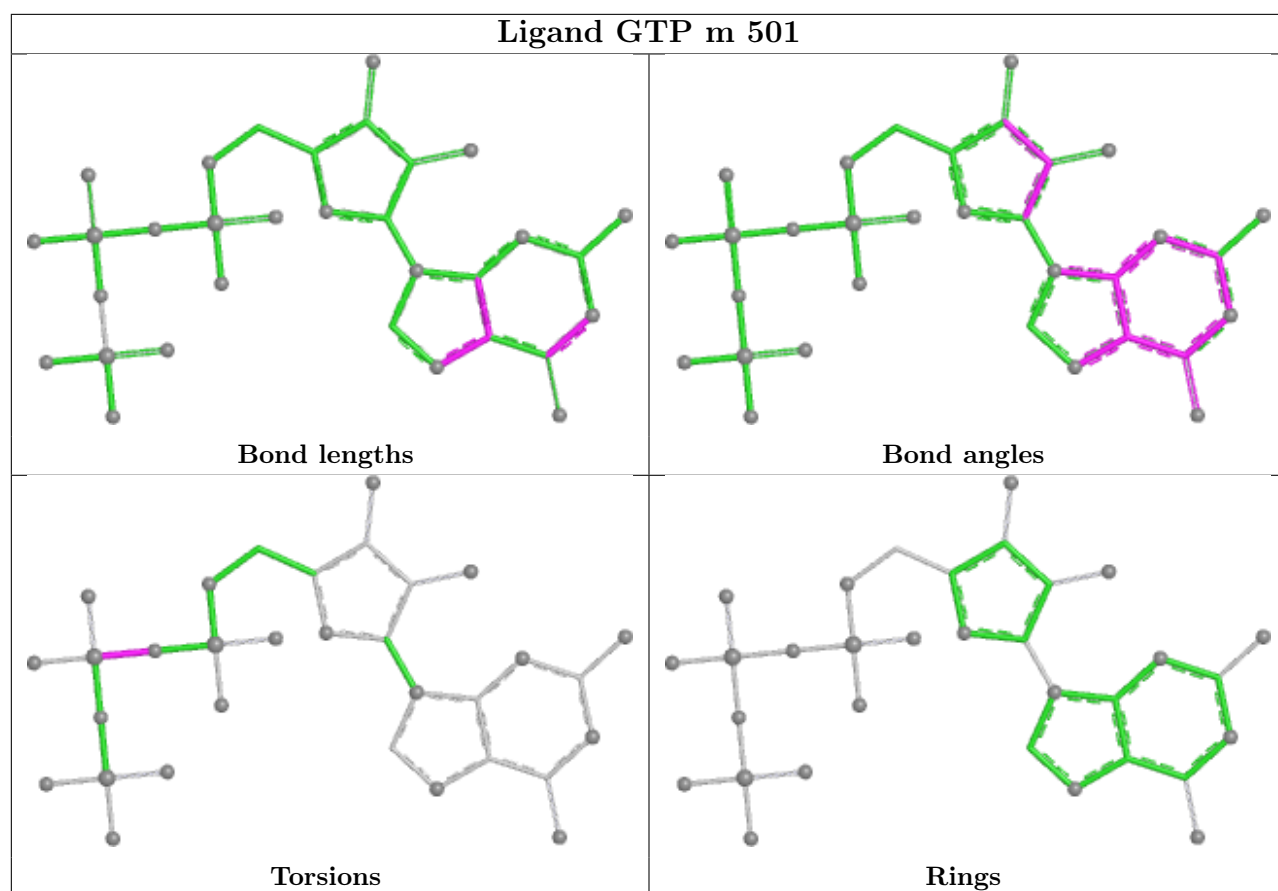
Mol	Chain	Res	Type	Atoms
60	b	701	GTP	C3'-C4'-C5'-O5'
60	b	701	GTP	O4'-C4'-C5'-O5'
60	m	501	GTP	PA-O3A-PB-O2B

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	m	501	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.

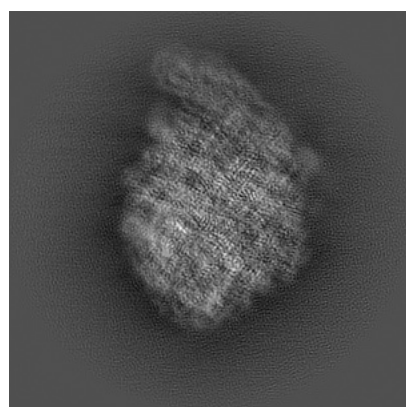
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6615. These allow visual inspection of the internal detail of the map and identification of artifacts.

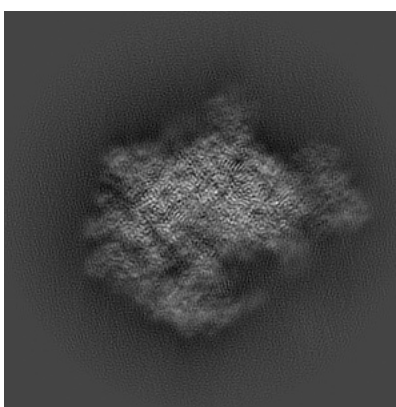
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

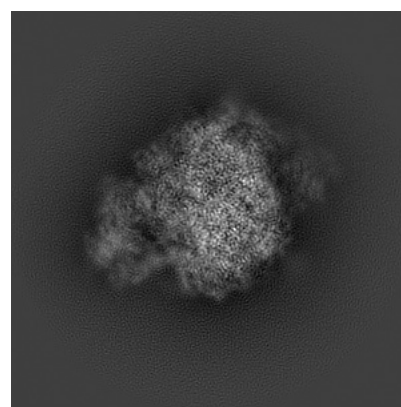
6.1.1 Primary map



X



Y

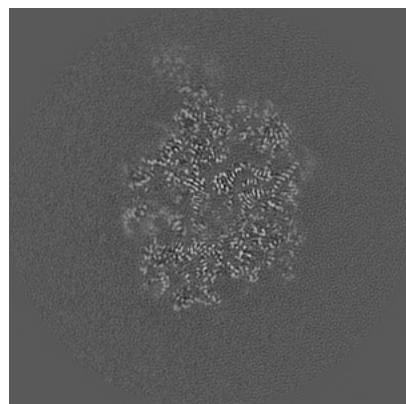


Z

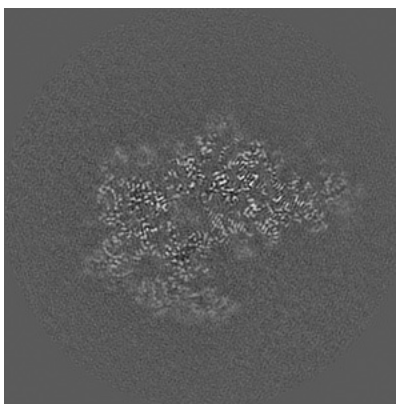
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

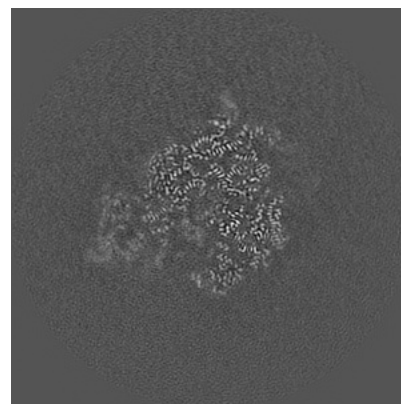
6.2.1 Primary map



X Index: 160



Y Index: 160

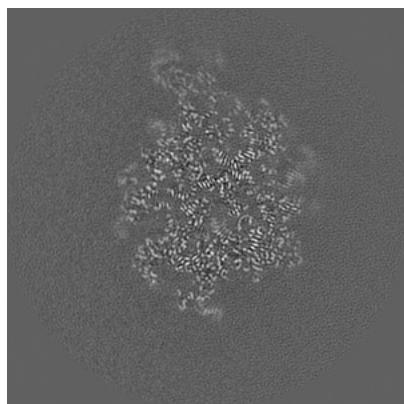


Z Index: 160

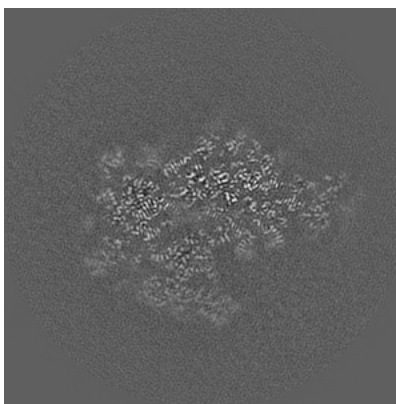
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

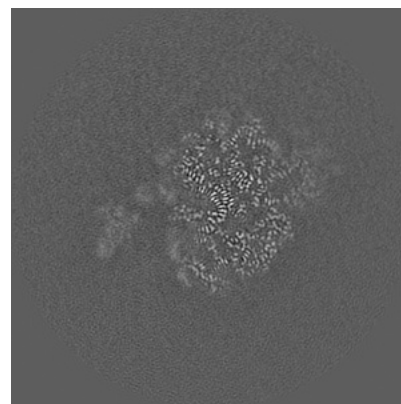
6.3.1 Primary map



X Index: 168



Y Index: 157

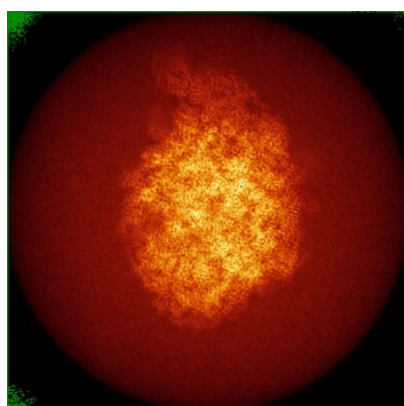


Z Index: 178

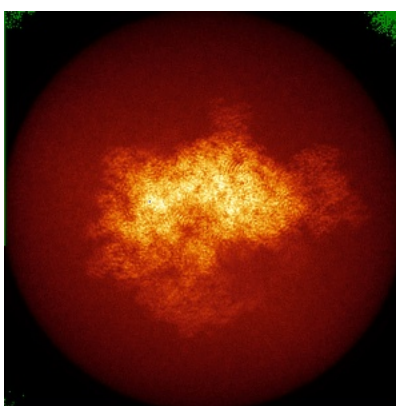
The images above show the largest variance slices of the map in three orthogonal directions.

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

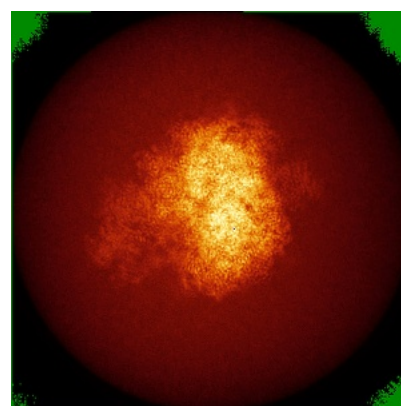
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views

This section was not generated.

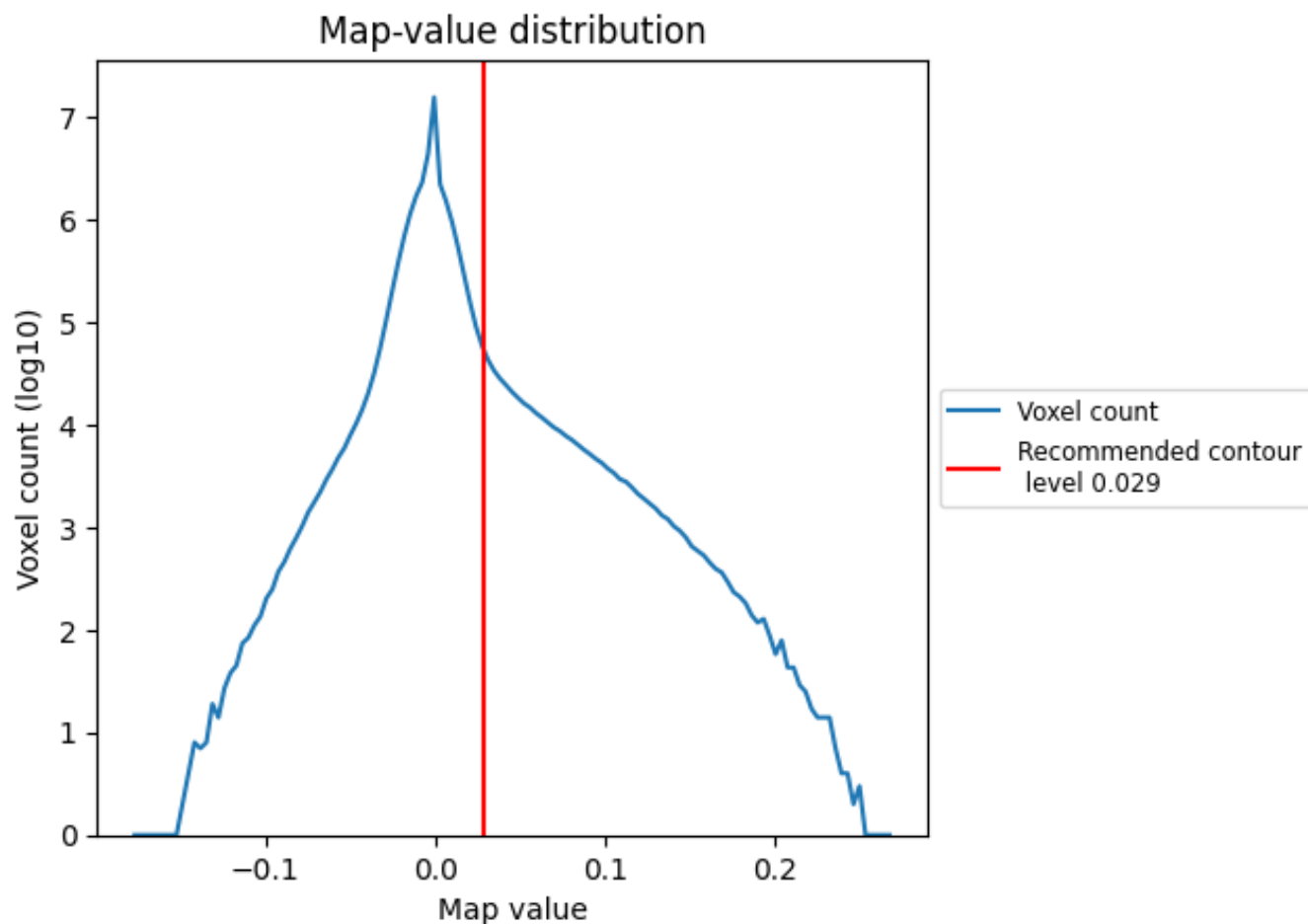
6.6 Mask visualisation

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

7 Map analysis [i](#)

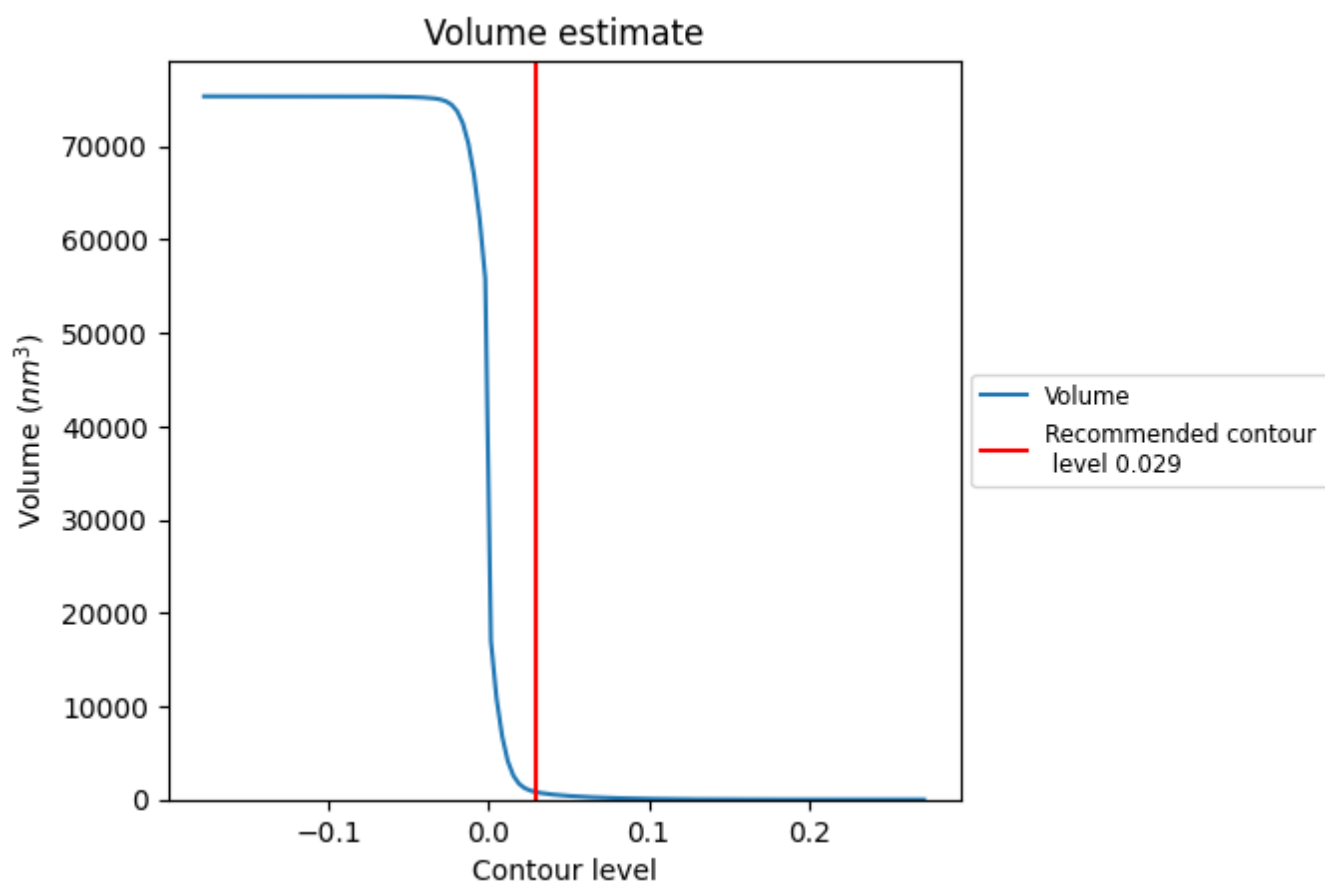
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

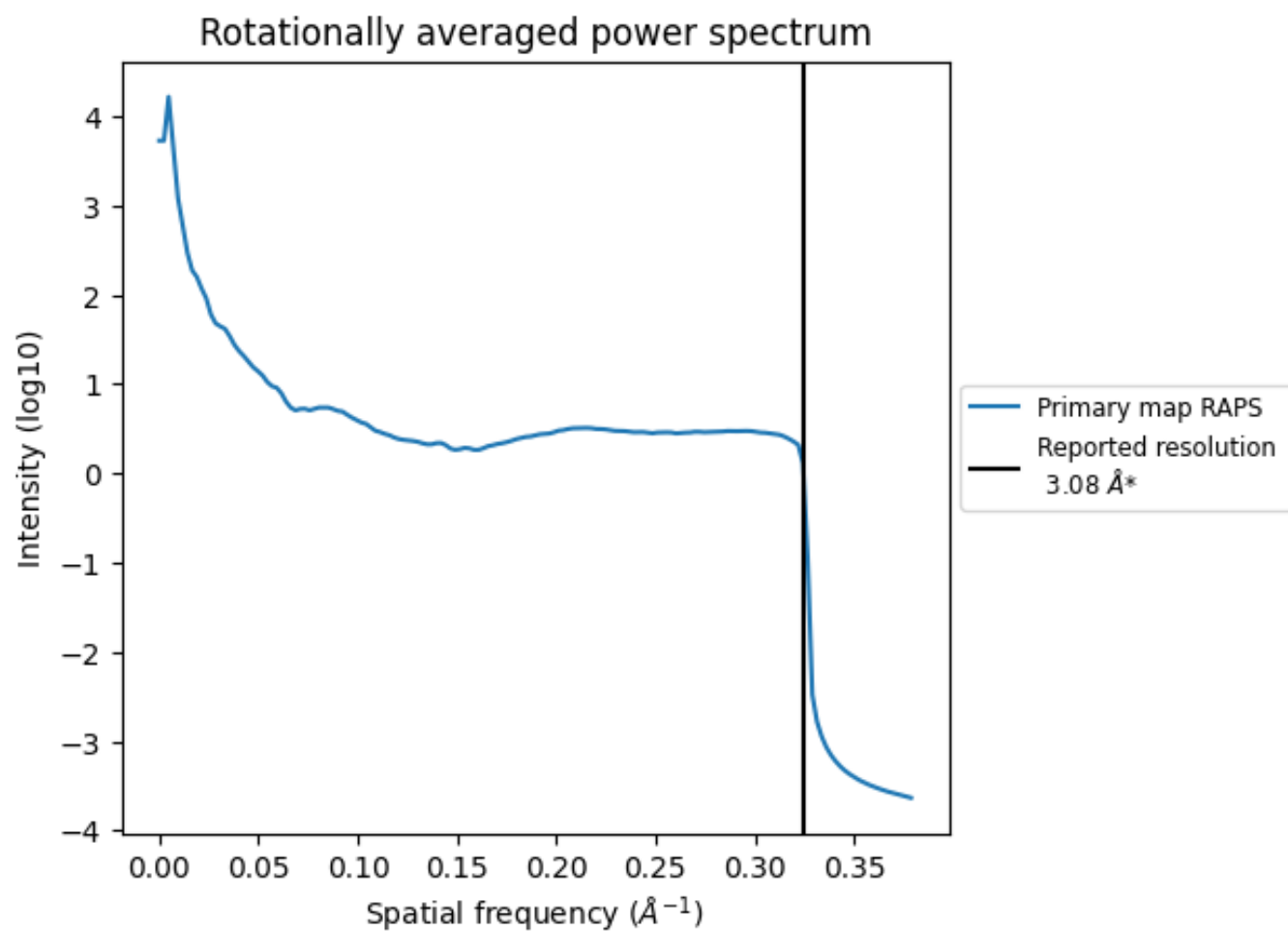
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 835 nm³; this corresponds to an approximate mass of 754 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 ⓘ

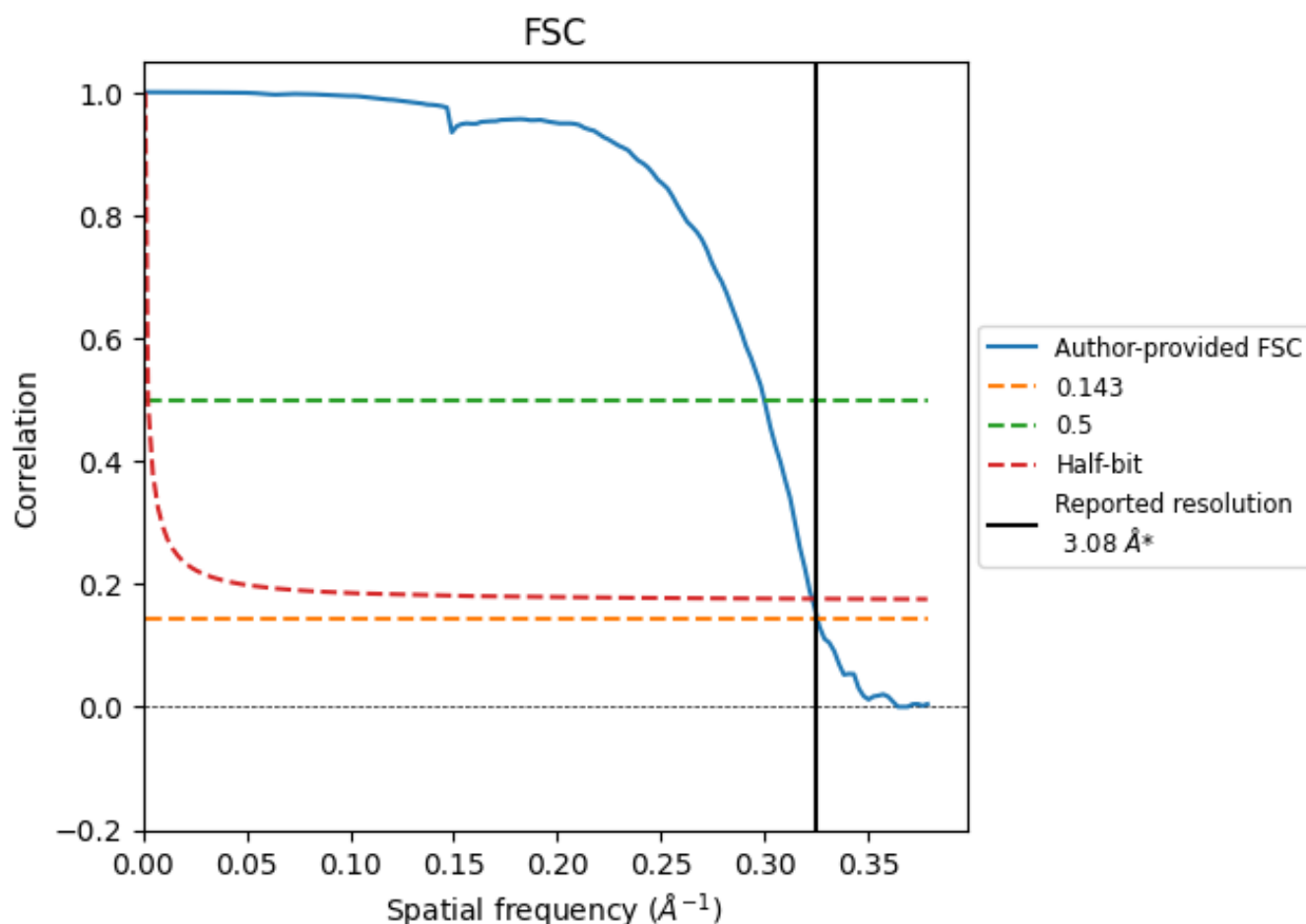


*Reported resolution corresponds to spatial frequency of 0.325 $\text{\AA}^{-1}$

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 0.325 Å⁻¹

8.2 Resolution estimates [i](#)

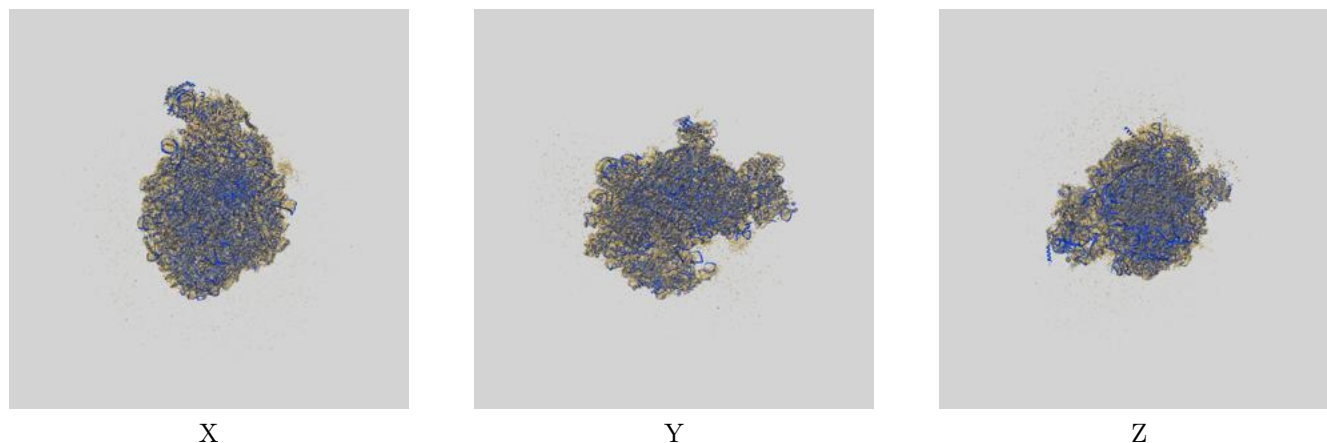
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	-	-
Author-provided FSC curve	3.07	3.33	3.10
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

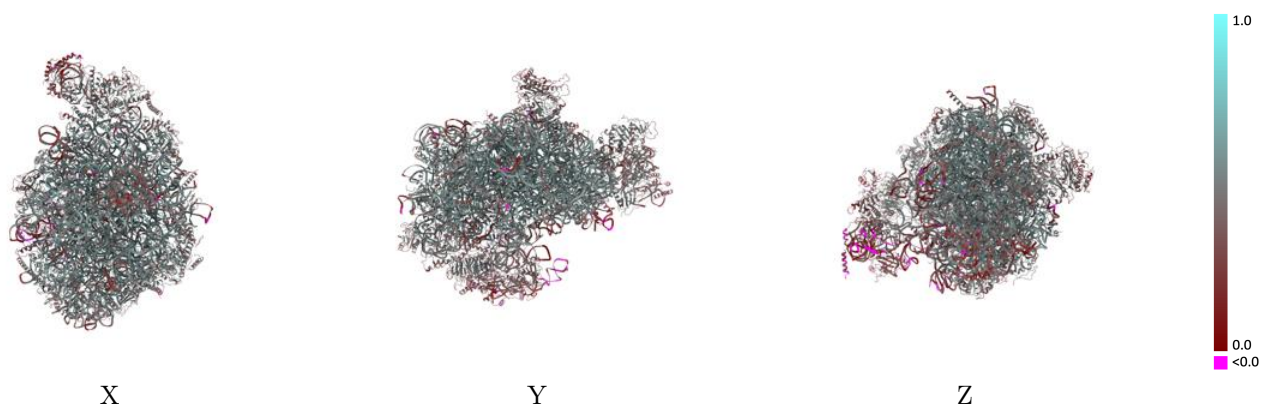
This section contains information regarding the fit between EMDB map EMD-6615 and PDB model 3JCT. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



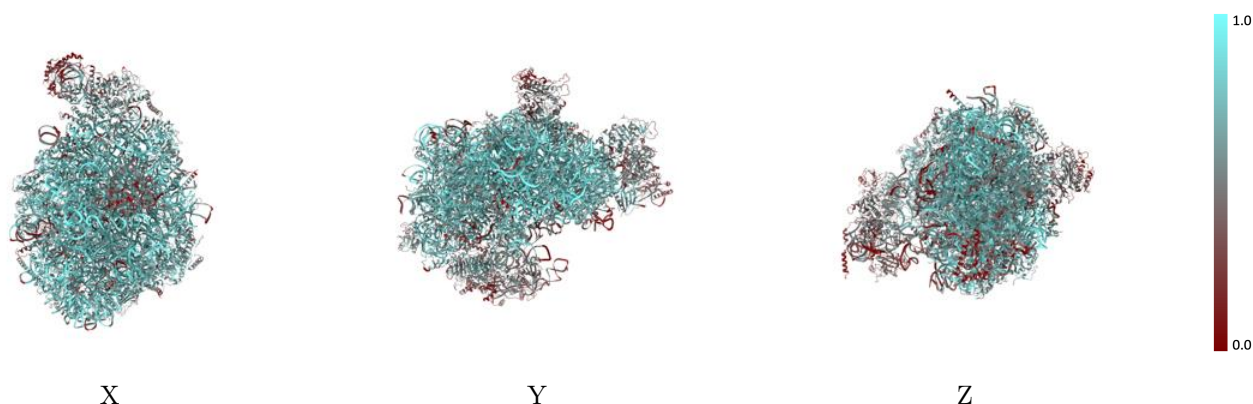
The images above show the 3D surface view of the map at the recommended contour level 0.029 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



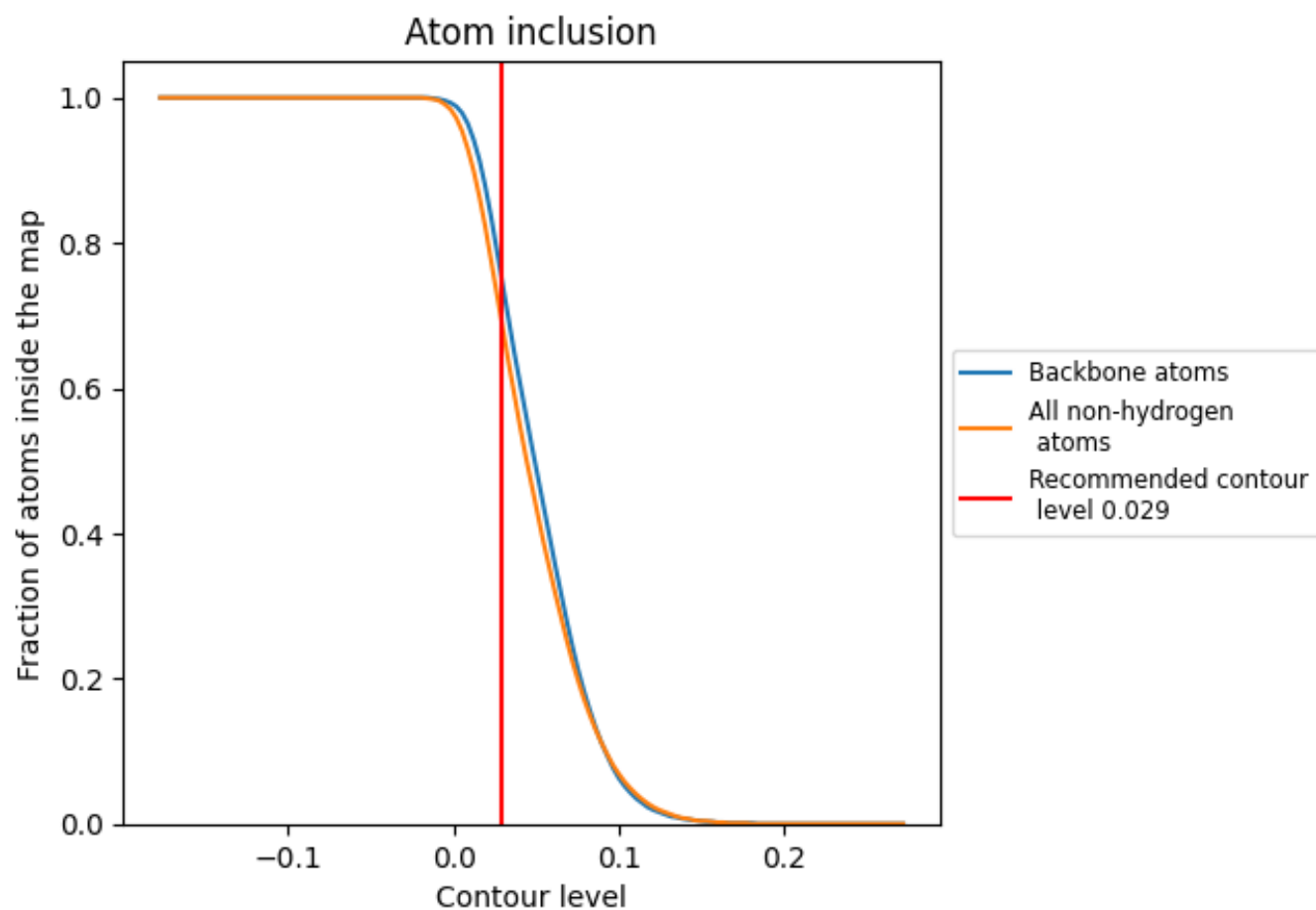
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.029).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 69% 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 (0.029) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6910	 0.4680
1	 0.7970	 0.4940
2	 0.9070	 0.5580
3	 0.4460	 0.2050
4	 0.3710	 0.3860
5	 0.2000	 0.3230
6	 0.5340	 0.3660
A	 0.7480	 0.5390
B	 0.7620	 0.5080
C	 0.7380	 0.5110
D	 0.3330	 0.2520
E	 0.6760	 0.4580
F	 0.7460	 0.4940
G	 0.6600	 0.4580
H	 0.7270	 0.4970
I	 0.5960	 0.4790
J	 0.1700	 0.1600
K	 0.3440	 0.3450
L	 0.6760	 0.4820
M	 0.7120	 0.4920
N	 0.7820	 0.5370
O	 0.7890	 0.5340
P	 0.7060	 0.5020
Q	 0.6640	 0.4850
R	 0.7160	 0.5160
S	 0.6420	 0.4480
T	 0.4860	 0.3930
U	 0.6630	 0.4570
V	 0.7390	 0.5120
W	 0.5170	 0.4090
X	 0.7250	 0.5190
Y	 0.6850	 0.4930
Z	 0.7010	 0.4760
a	 0.6430	 0.4620
b	 0.6370	 0.4710



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
c	 0.6390	 0.4540
d	 0.6920	 0.4910
e	 0.7300	 0.5320
f	 0.7990	 0.5460
g	 0.7310	 0.5180
h	 0.7210	 0.5010
i	 0.6110	 0.4390
j	 0.8280	 0.5620
k	 0.4760	 0.4090
l	 0.7980	 0.5640
m	 0.6660	 0.4900
n	 0.5910	 0.4710
o	 0.4800	 0.3930
p	 0.7400	 0.5070
q	 0.5040	 0.4310
r	 0.7240	 0.5180
s	 0.4840	 0.4200
t	 0.4910	 0.4300
u	 0.7130	 0.4900
v	 0.4350	 0.3600
w	 0.4690	 0.3850
x	 0.4780	 0.3820
y	 0.6860	 0.4930
z	 0.5740	 0.4480