



wwPDB EM Validation Summary Report ⓘ

Oct 6, 2024 – 03:00 AM JST

PDB ID : 7BTB
EMDB ID : EMD-30174
Title : Cryo-EM structure of pre-60S ribosome from *Saccharomyces cerevisiae* rpl4delta63-87 strain at 3.22 Angstroms resolution(state R2)
Authors : Li, Y.; Wilson, D.M.
Deposited on : 2020-04-01
Resolution : 3.22 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

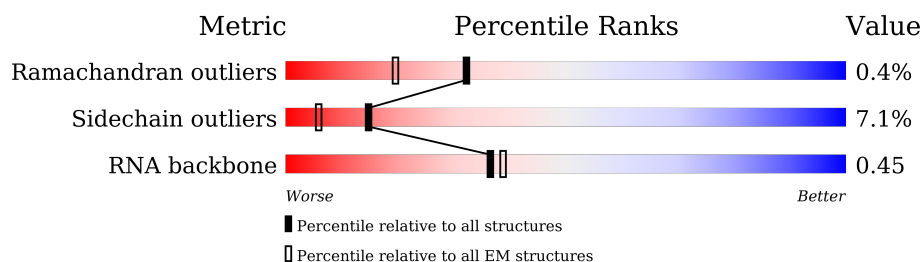
EMDB validation analysis : 0.0.1.dev113
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

1 Overall quality at a glance

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

The reported resolution of this entry is 3.22 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	L	199	
2	a	149	
3	A	254	
4	B	387	
5	C	362	
6	D	297	
7	E	176	
8	F	244	

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Mol	Chain	Length	Quality of chain
9	G	256	
10	H	191	
11	J	174	
12	K	376	
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	b	647	
28	c	105	
29	d	113	
30	e	130	
31	f	107	
32	g	121	
33	h	120	

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Mol	Chain	Length	Quality of chain
34	i	100	
35	j	88	
36	k	78	
37	m	486	
38	n	605	
39	o	220	
40	p	92	
41	q	455	
42	r	261	
43	t	322	
44	u	199	
45	v	344	
46	w	203	
47	x	515	
48	y	245	
49	z	106	
50	1	3396	
51	2	158	
52	3	121	
53	6	232	

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 147931 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 L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	L	185	Total	C	N	O	0	0
			1484	923	305	256		

- Molecule 2 is a protein called 60S ribosomal protein L28.

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

- Molecule 3 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	A	193	Total	C	N	O	0	0
			1492	938	294	260		

- Molecule 4 is a protein called 60S ribosomal protein L3.

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

- Molecule 5 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	336	Total	C	N	O	S	0	0
			2576	1628	483	462	3		

- Molecule 6 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	274	Total	C	N	O	S	0	0
			2197	1388	388	419	2		

- Molecule 7 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 8 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 9 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	227	Total	C	N	O	S	0	0
			1775	1136	318	318	3		

- Molecule 10 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	188	Total	C	N	O	S	0	0
			1493	948	271	270	4		

- Molecule 11 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	167	Total	C	N	O	S	0	0
			1336	838	249	245	4		

- Molecule 12 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	253	Total	C	N	O	S	0	0
			2044	1318	339	384	3		

- 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	104	Total	C	N	O	0	0
			826	534	134	158		

- 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 Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	509	Total	C	N	O	S	0	0
			4137	2624	723	771	19		

- Molecule 28 is a protein called 60S ribosomal protein L30.

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

- Molecule 29 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	105	Total	C	N	O	S	0	0
			856	544	163	148	1		

- Molecule 30 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	125	Total	C	N	O	S	0	0
			1007	638	203	165	1		

- Molecule 31 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 32 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 33 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 34 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 35 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	85	Total	C	N	O	S	0	0
			670	408	146	111	5		

- Molecule 36 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	76	Total	C	N	O	S	0	0
			604	385	114	105			

- Molecule 37 is a protein called Nucleolar GTP-binding protein 2.

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

- Molecule 38 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	n	366	Total	C	N	O	S	0	0
			2988	1936	517	525	10		

- Molecule 39 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	o	129	Total	C	N	O	S	0	0
			1064	685	192	183	4		

- Molecule 40 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 41 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	q	158	Total	C	N	O	S	0	0
			1313	827	235	250	1		

- Molecule 42 is a protein called Ribosome biogenesis protein NSA2.

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

- Molecule 43 is a protein called Ribosome biogenesis protein RLP7.

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

- Molecule 44 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	u	142	Total	C	N	O	S	0	0
			1196	751	239	197	9		

- Molecule 45 is a protein called Ribosome biogenesis protein RPF2.

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

- Molecule 46 is a protein called Regulator of ribosome biosynthesis.

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

- Molecule 47 is a protein called Ribosome assembly protein 4.

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

- Molecule 48 is a protein called Eukaryotic translation initiation factor 6.

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

- Molecule 49 is a protein called UPF0642 protein YBL028C.

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

- Molecule 50 is a RNA chain called RDN25-1 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	1	3058	Total	C	N	O	P	0	0
			65427	29223	11807	21339	3058		

- Molecule 51 is a RNA chain called RDN5.8-1 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	2	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 52 is a RNA chain called RDN5-2 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 53 is a RNA chain called ITS2-1 miscRNA.

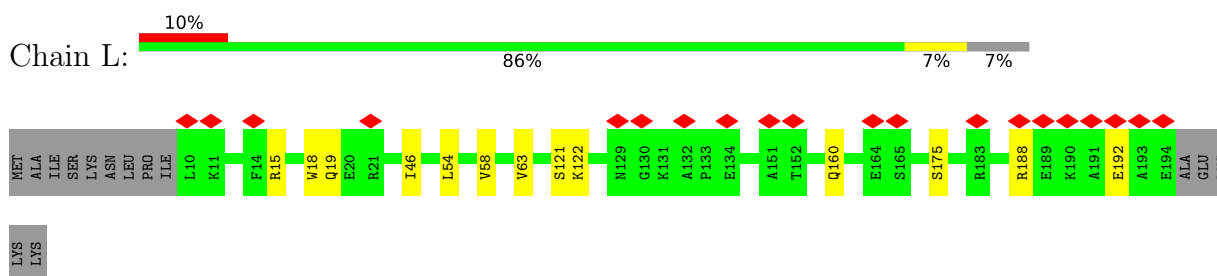
Mol	Chain	Residues	Atoms					AltConf	Trace
53	6	65	Total	C	N	O	P	0	0
			1370	614	228	463	65		

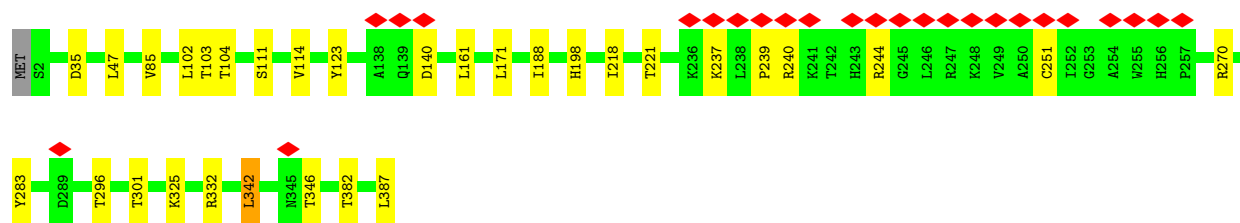
- Molecule 54 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

3 Residue-property plots [i](#)

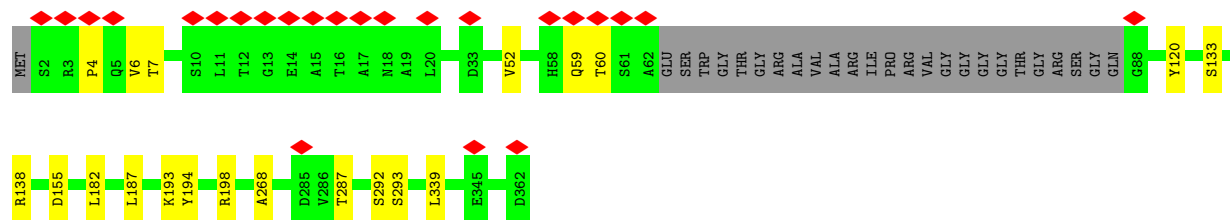
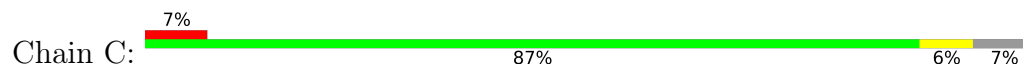
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 L13-A

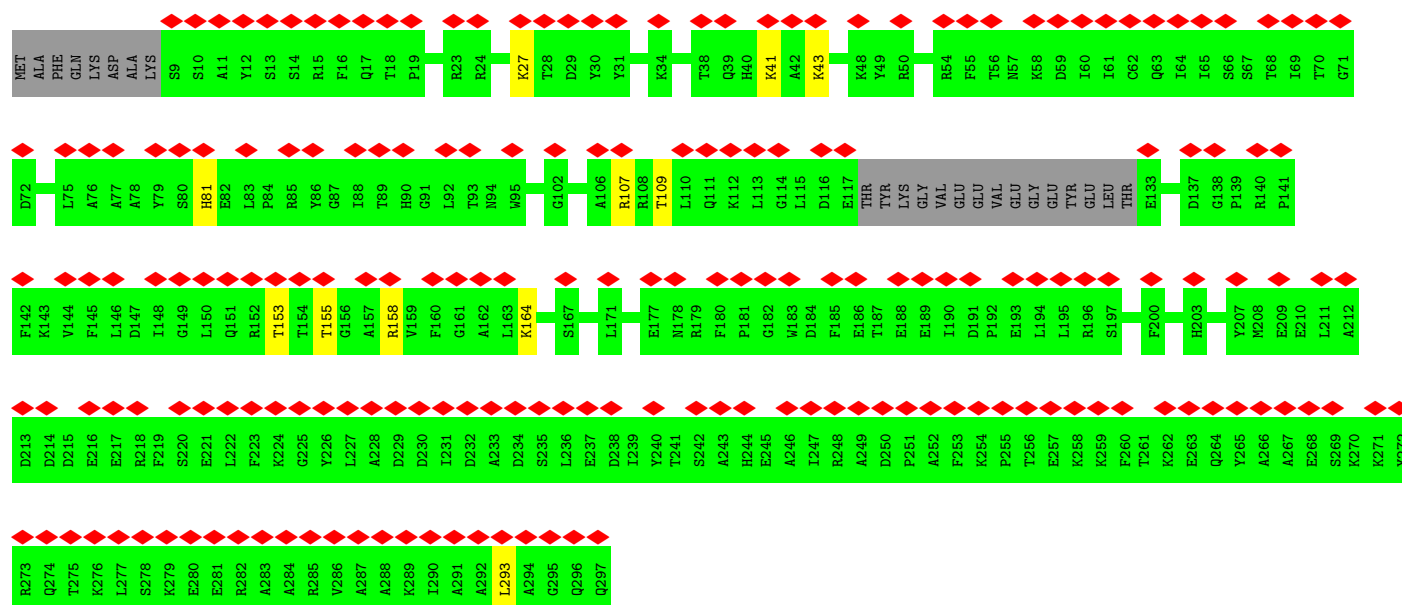
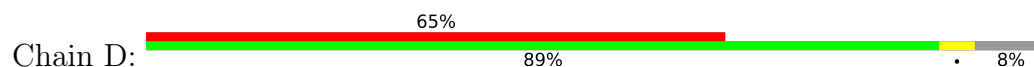




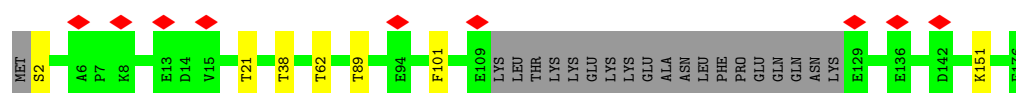
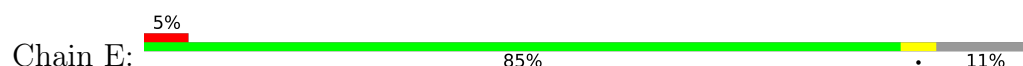
• Molecule 5: 60S ribosomal protein L4-A




• Molecule 6: 60S ribosomal protein L5

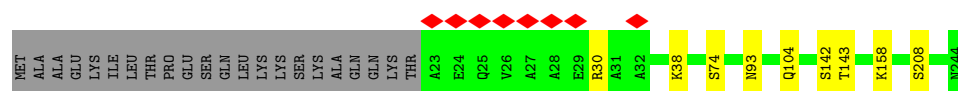


• Molecule 7: 60S ribosomal protein L6-A




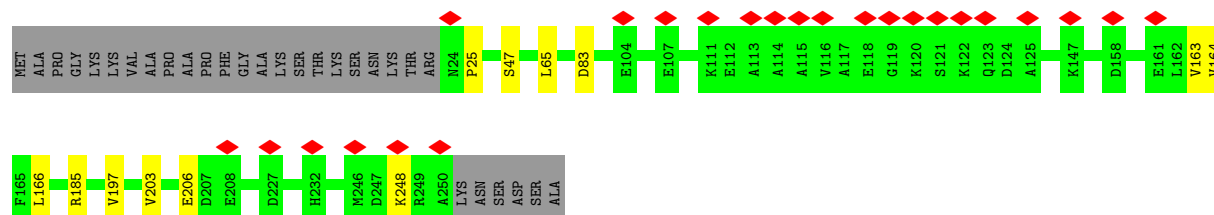
• Molecule 8: 60S ribosomal protein L7-A

Chain F:  87% 9%



• Molecule 9: 60S ribosomal protein L8-A

Chain G:  84% 5% 11%

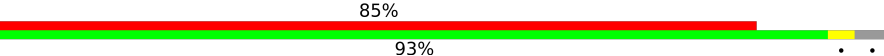


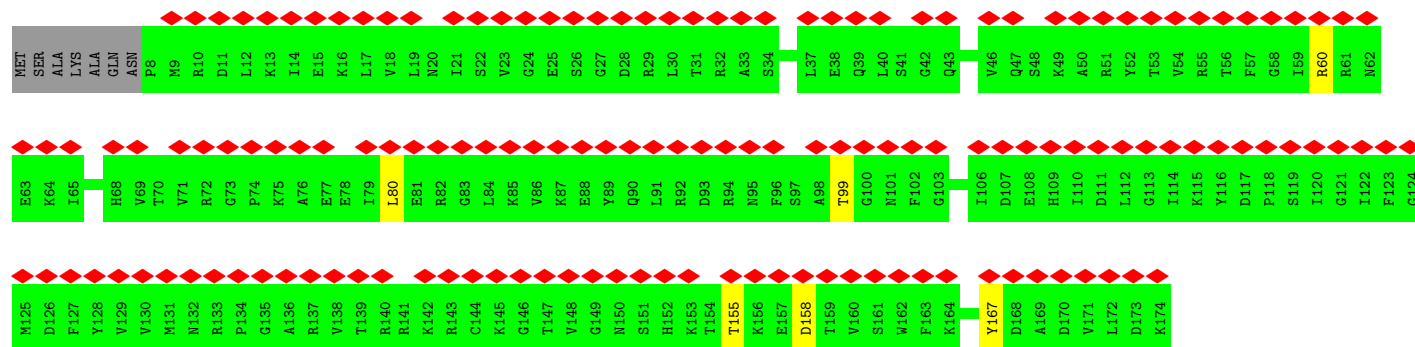
• Molecule 10: 60S ribosomal protein L9-A

Chain H:  93% 5%



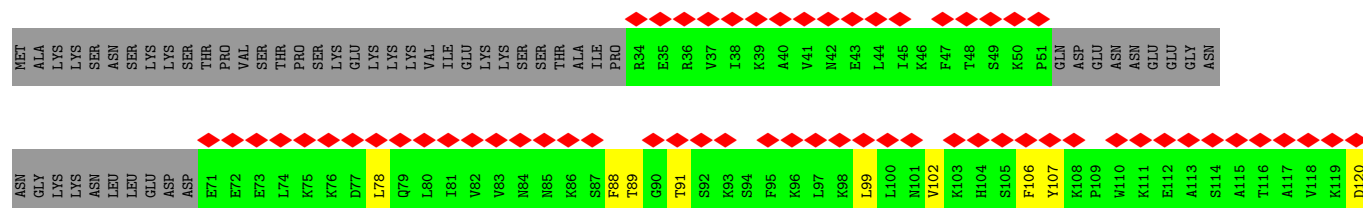
• Molecule 11: 60S ribosomal protein L11-A

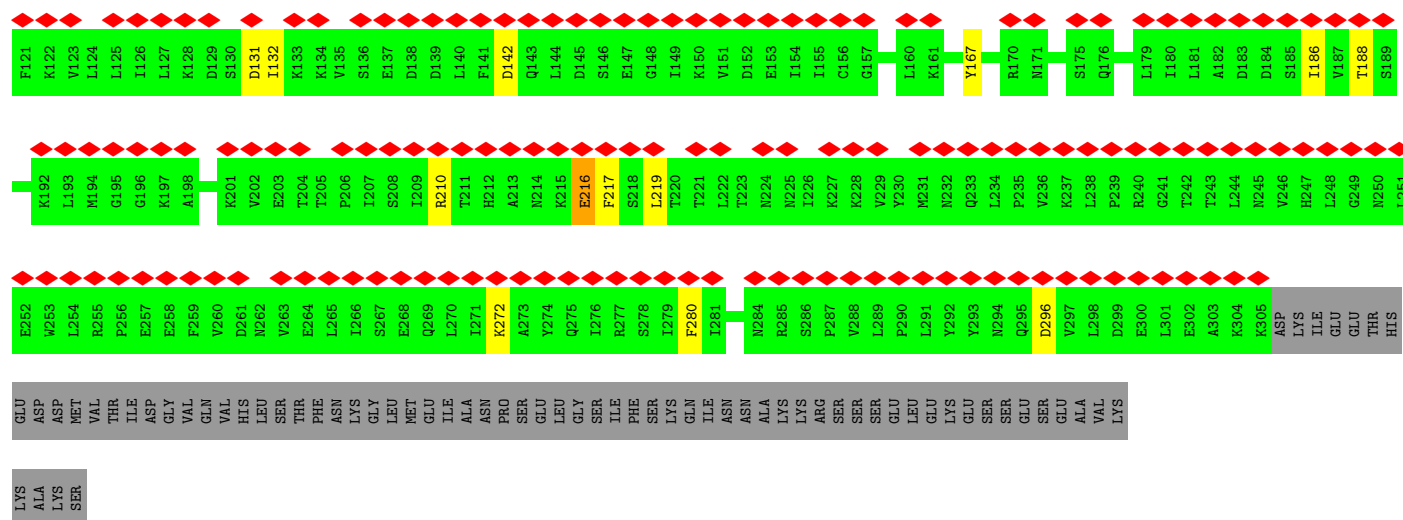
Chain J:  85% 93%



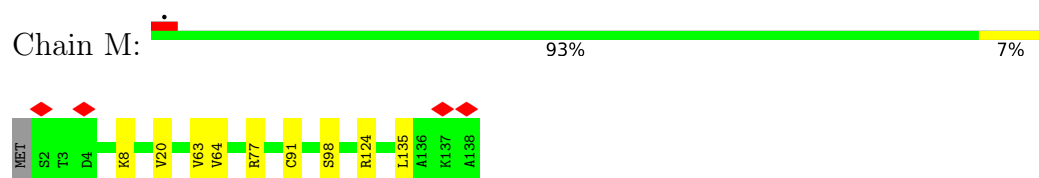
• Molecule 12: Proteasome-interacting protein CIC1

Chain K:  57% 61% 6% 33%

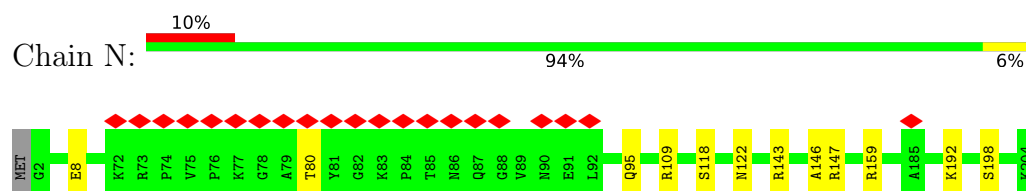




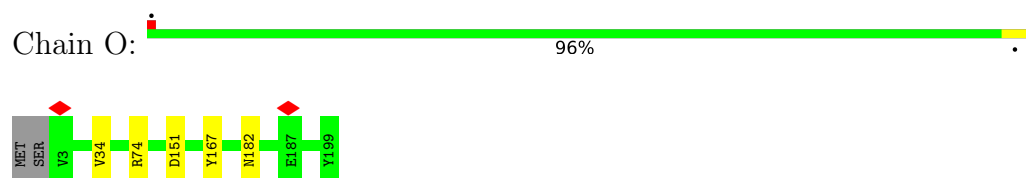
- Molecule 13: 60S ribosomal protein L14-A



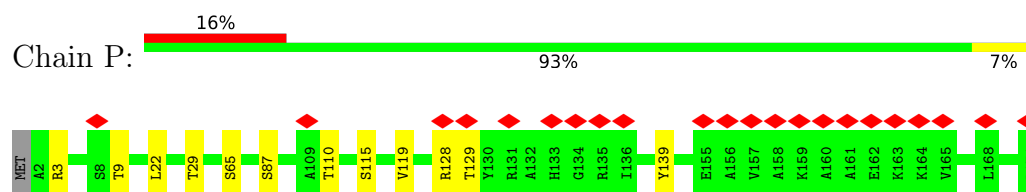
- Molecule 14: 60S ribosomal protein L15-A



- Molecule 15: 60S ribosomal protein L16-A

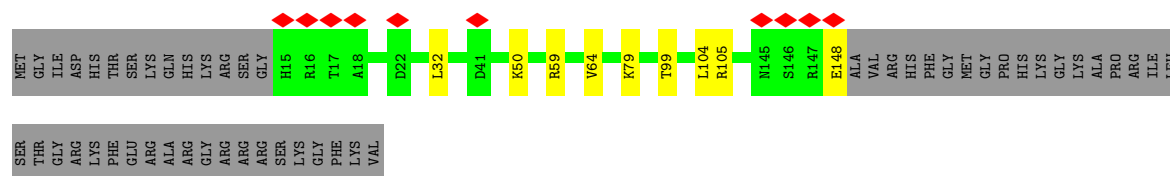


- Molecule 16: 60S ribosomal protein L17-A

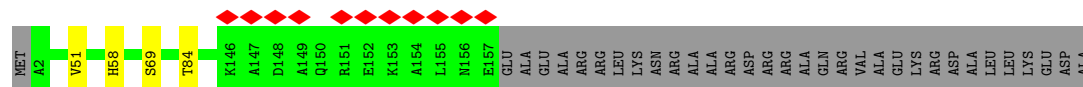
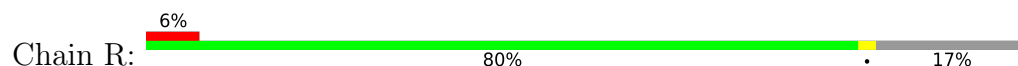


- Molecule 17: 60S ribosomal protein L18-A

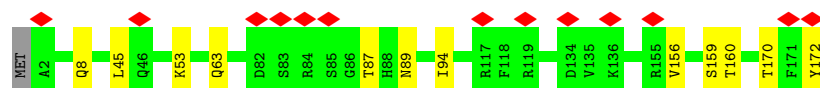




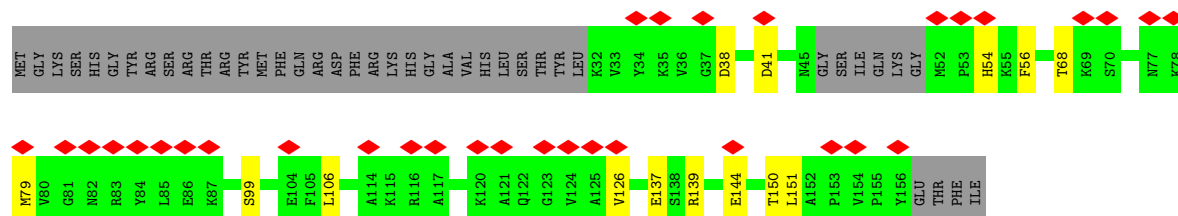
- Molecule 18: 60S ribosomal protein L19-A



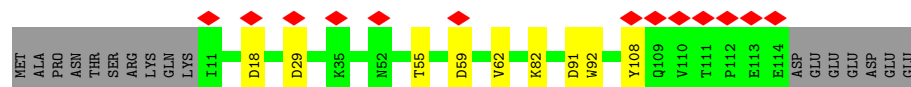
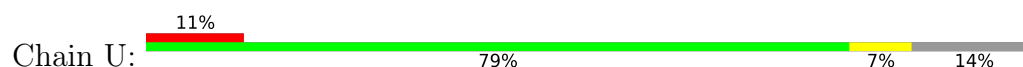
- Molecule 19: 60S ribosomal protein L20-A



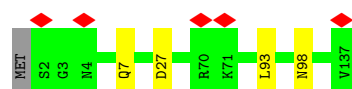
- Molecule 20: 60S ribosomal protein L21-A



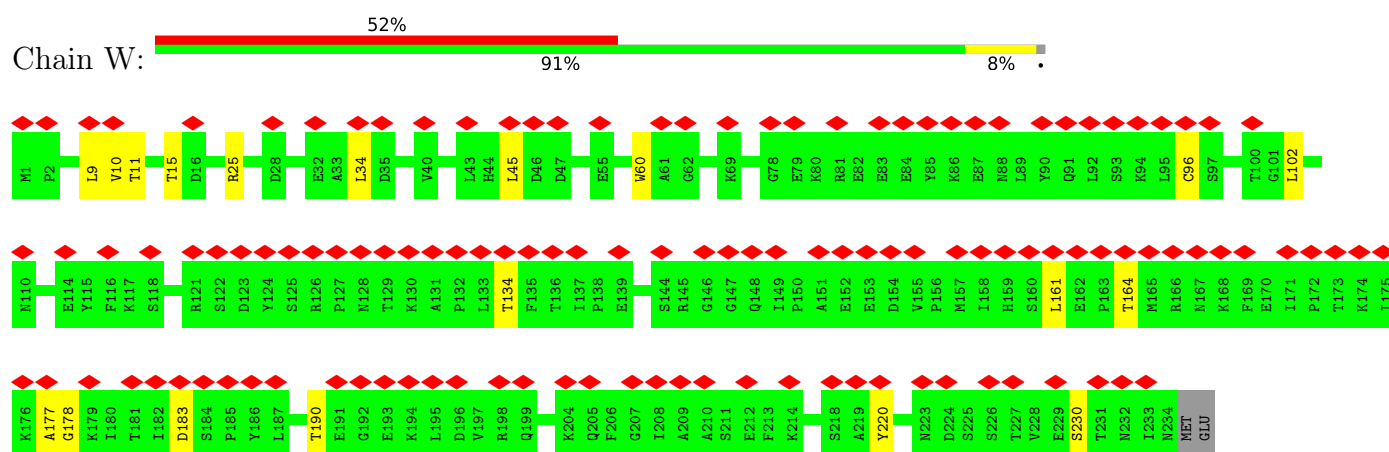
- Molecule 21: 60S ribosomal protein L22-A



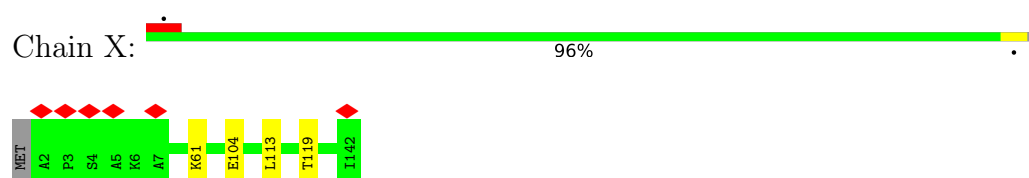
- Molecule 22: 60S ribosomal protein L23-A



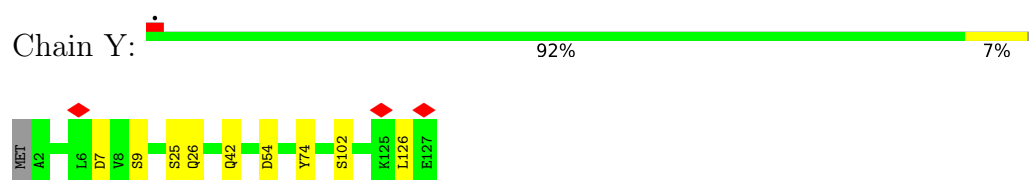
- Molecule 23: Ribosome assembly factor MRT4



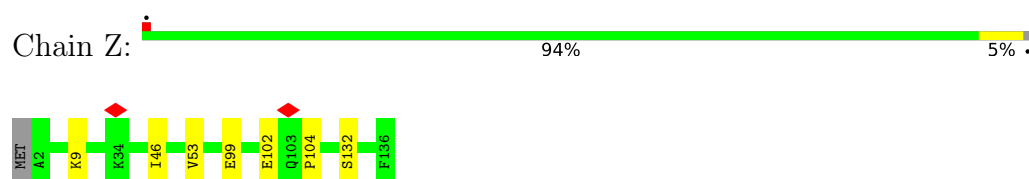
- Molecule 24: 60S ribosomal protein L25



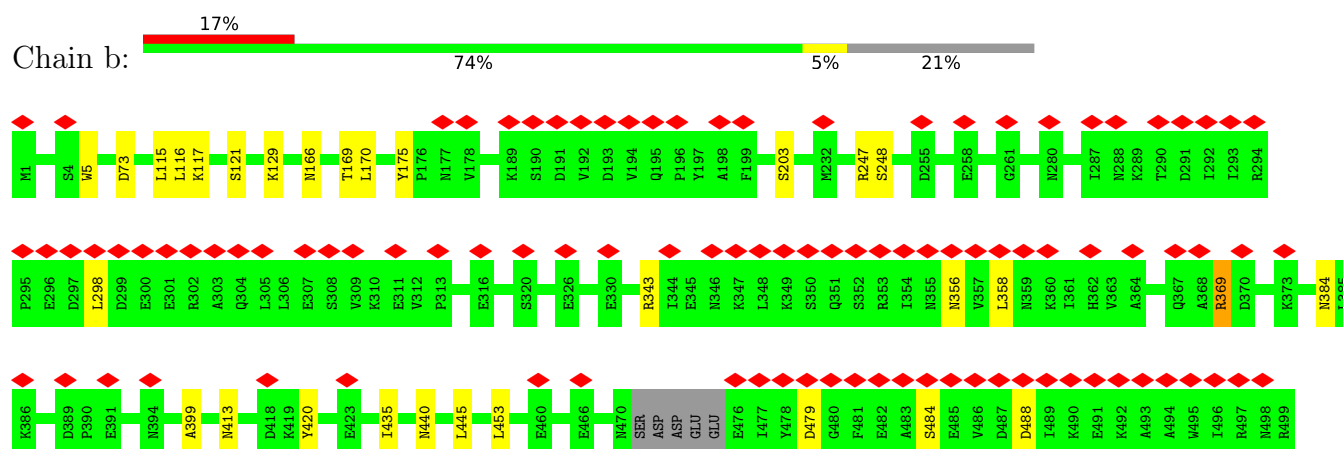
- Molecule 25: 60S ribosomal protein L26-A

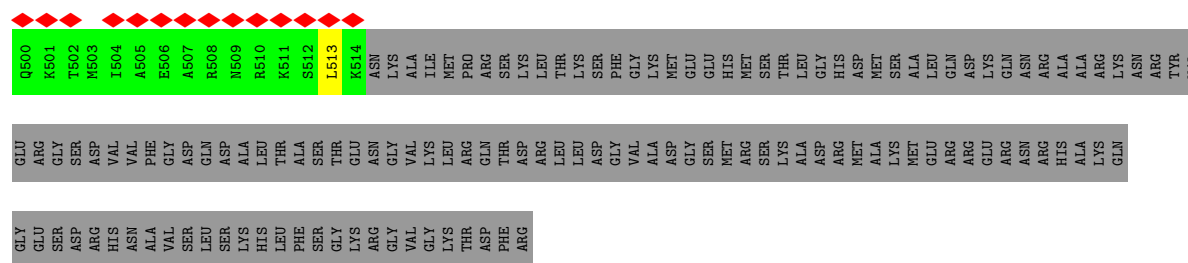


- Molecule 26: 60S ribosomal protein L27-A

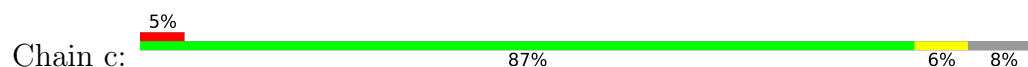


- Molecule 27: Nucleolar GTP-binding protein 1

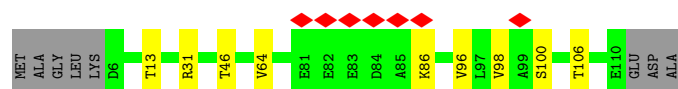
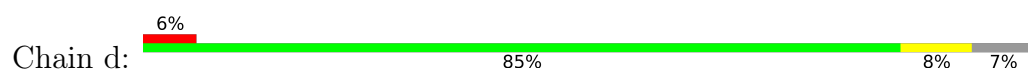




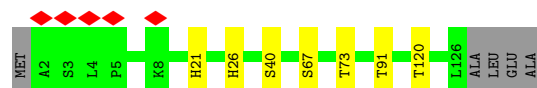
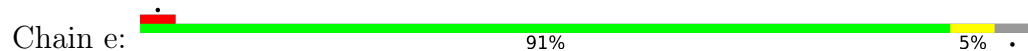
• Molecule 28: 60S ribosomal protein L30



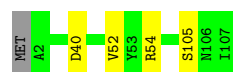
• Molecule 29: 60S ribosomal protein L31-A



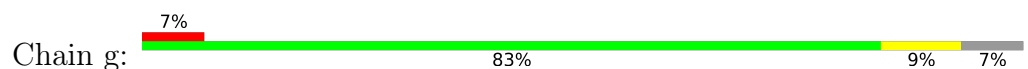
• Molecule 30: 60S ribosomal protein L32



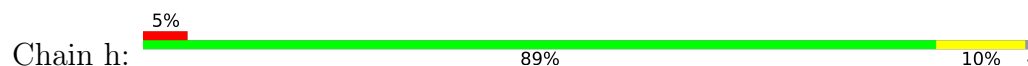
• Molecule 31: 60S ribosomal protein L33-A

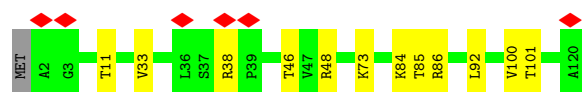


• Molecule 32: 60S ribosomal protein L34-A

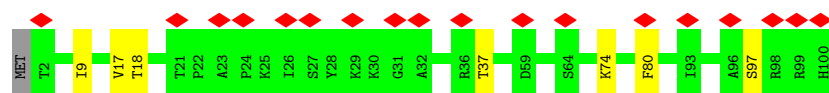
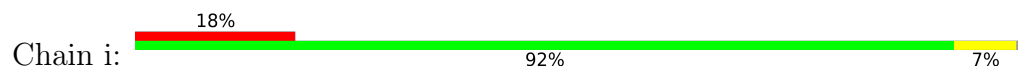


• Molecule 33: 60S ribosomal protein L35-A

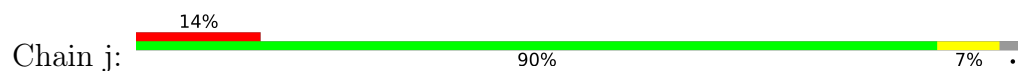




- Molecule 34: 60S ribosomal protein L36-A



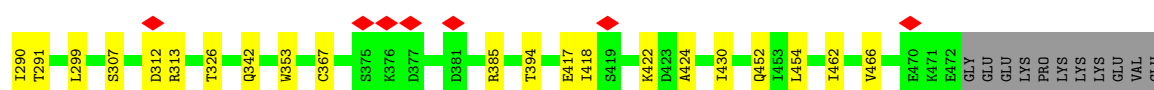
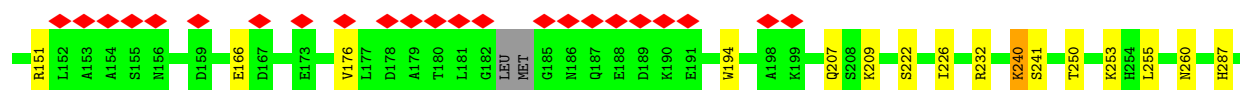
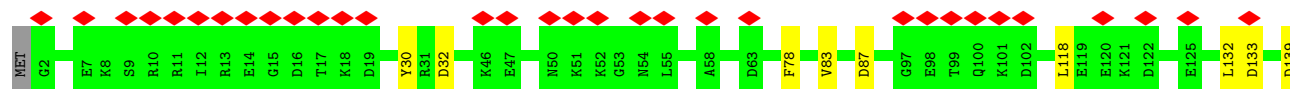
- Molecule 35: 60S ribosomal protein L37-A



- Molecule 36: 60S ribosomal protein L38



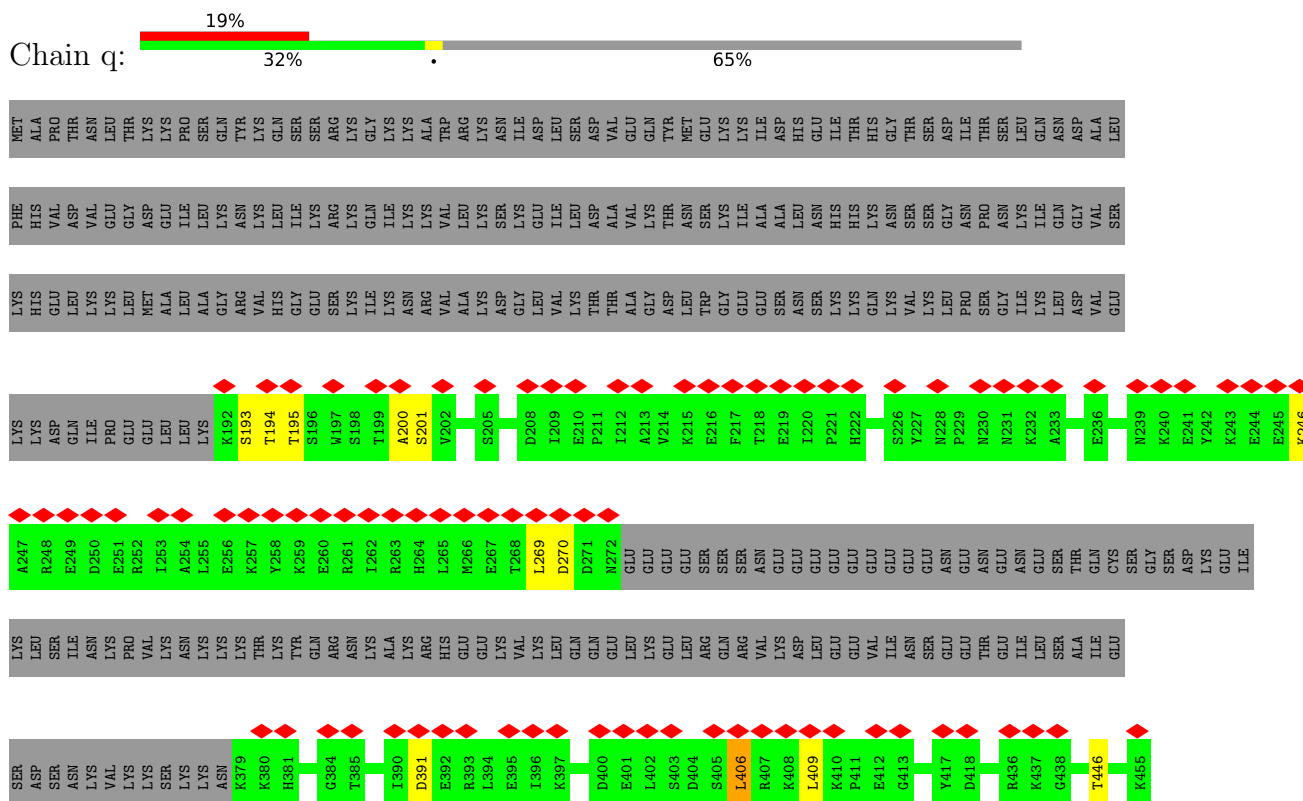
- Molecule 37: Nucleolar GTP-binding protein 2



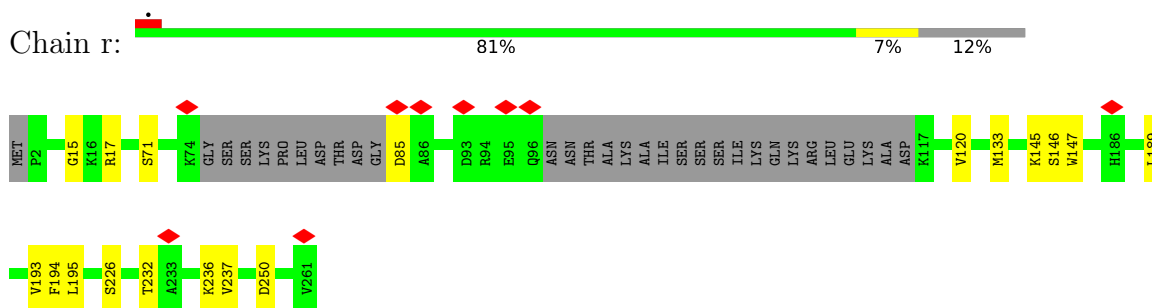
- Molecule 38: Pescadillo homolog



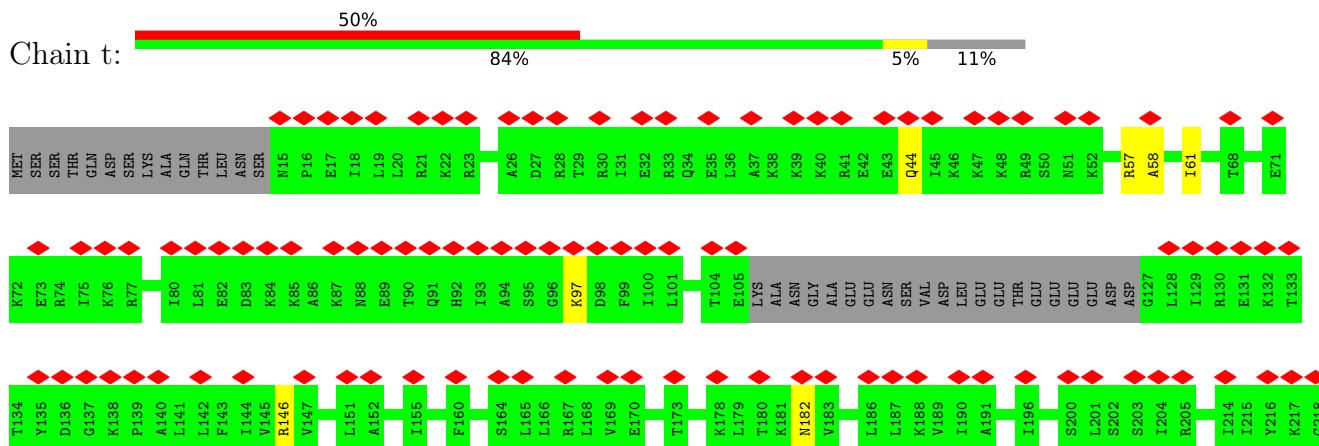
- Molecule 41: Ribosome biogenesis protein NOP53

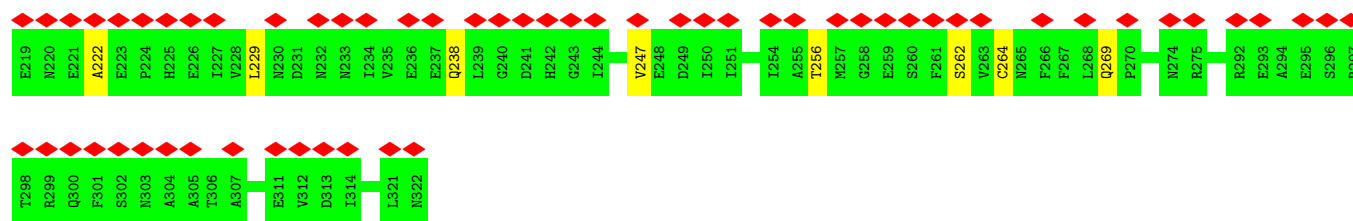


- Molecule 42: Ribosome biogenesis protein NSA2

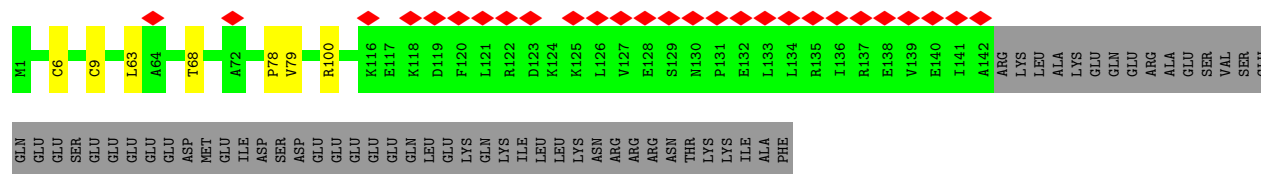


- Molecule 43: Ribosome biogenesis protein RLP7

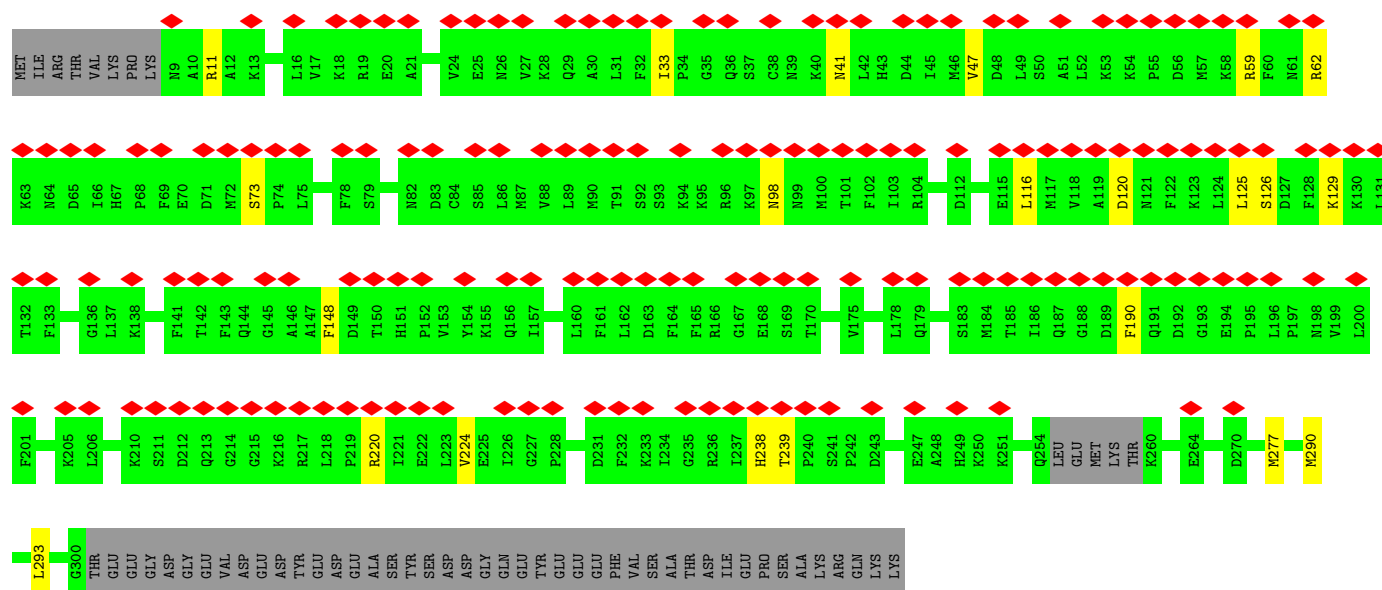
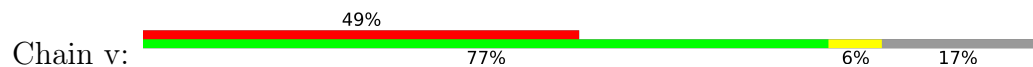




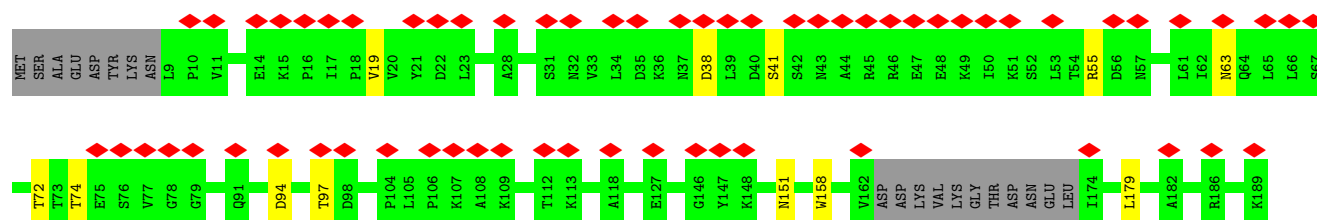
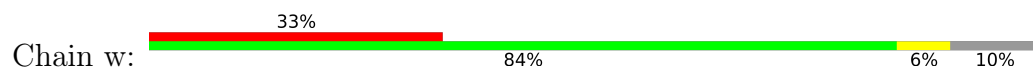
• Molecule 44: Ribosome biogenesis protein RLP24

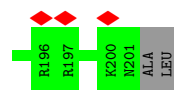


• Molecule 45: Ribosome biogenesis protein RPF2

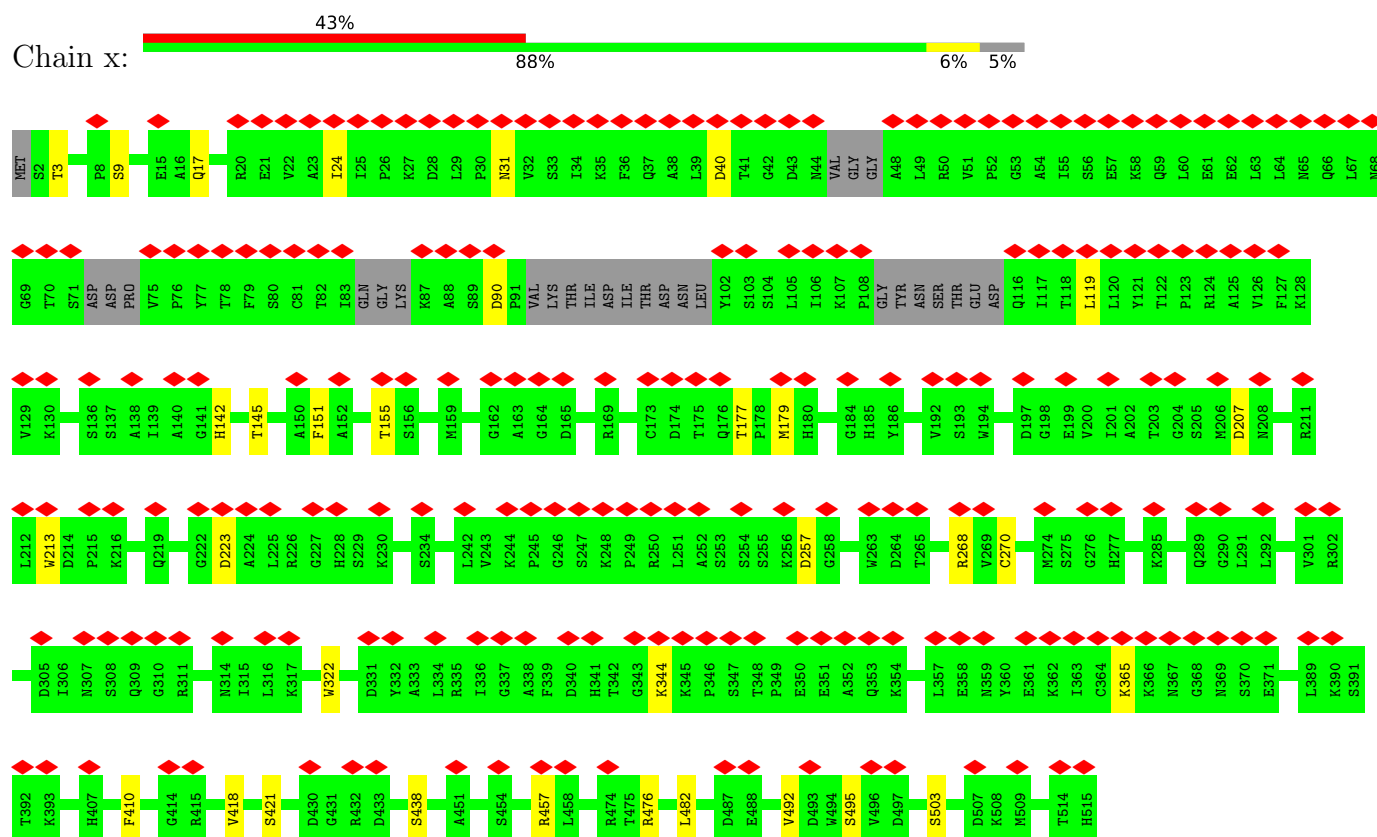


• Molecule 46: Regulator of ribosome biosynthesis

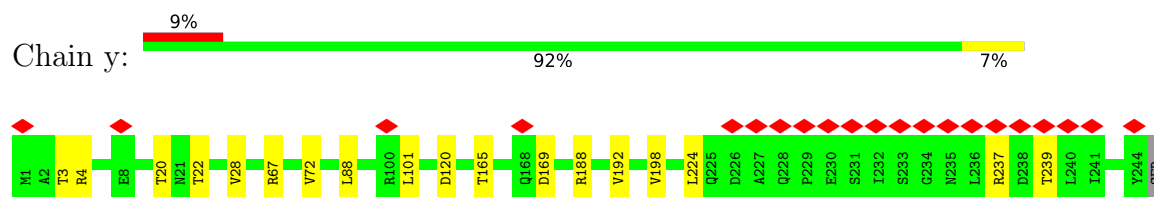




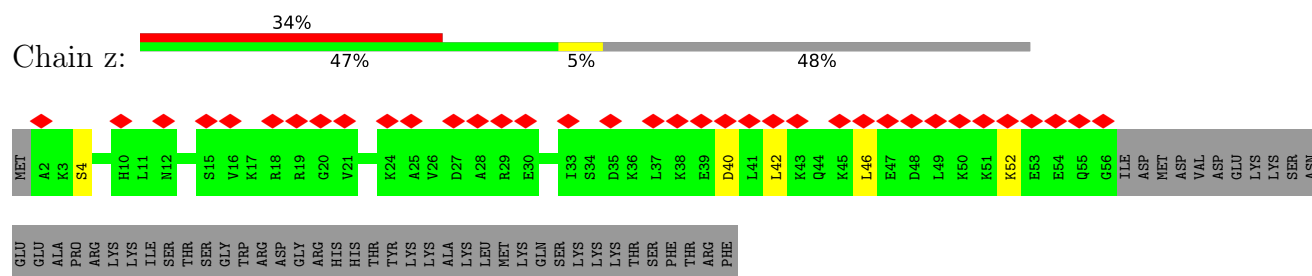
• Molecule 47: Ribosome assembly protein 4



• Molecule 48: Eukaryotic translation initiation factor 6



• Molecule 49: UPF0642 protein YBL028C

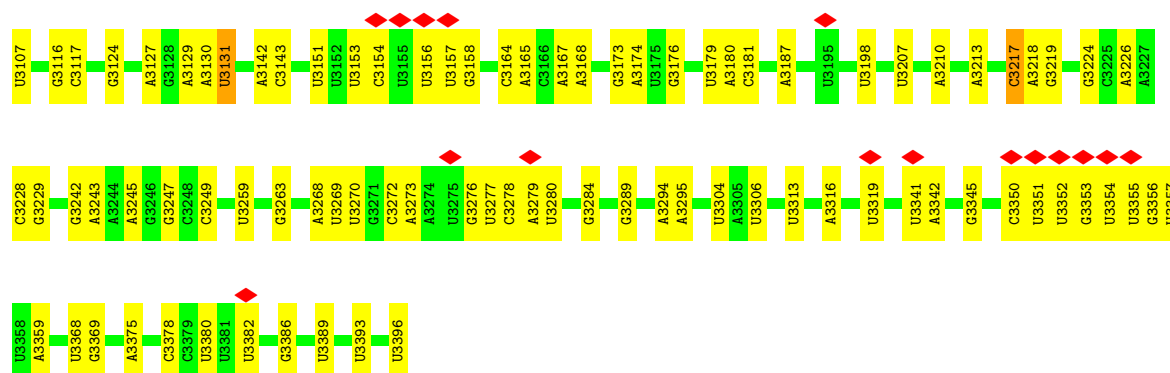


• Molecule 50: RDN25-1 rRNA

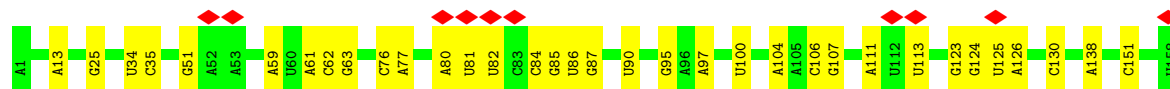
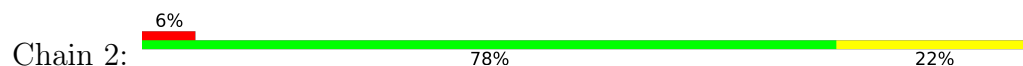




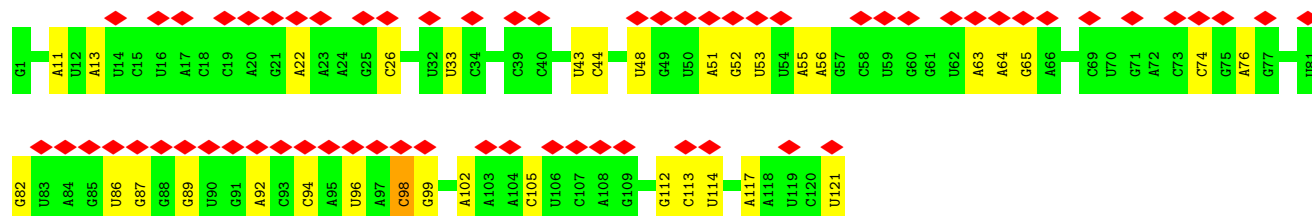




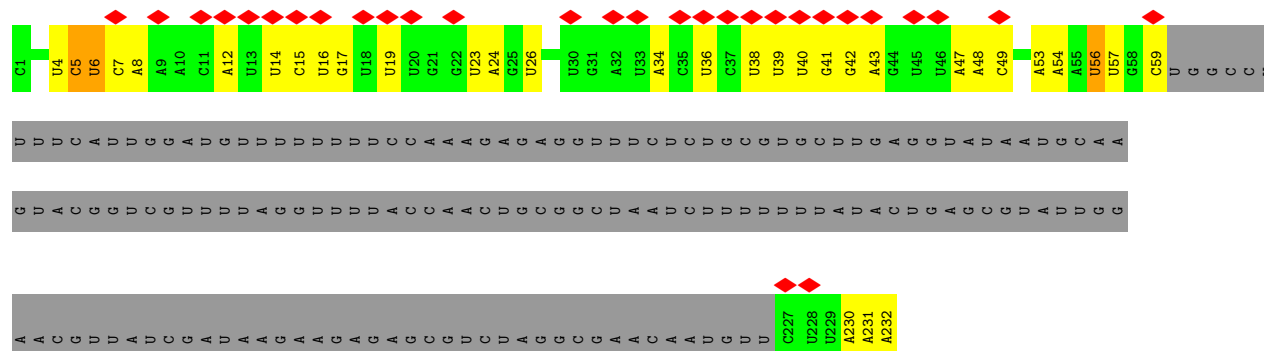
- Molecule 51: RDN5.8-1 rRNA



- Molecule 52: RDN5-2 rRNA



- Molecule 53: ITS2-1 miscRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	47025	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 ($e^-/\text{\AA}^2$)	1.9	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.208	Depositor
Minimum map value	-0.120	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	412.02, 412.02, 412.02	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3734, 1.3734, 1.3734	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	L	0.37	0/1508	0.53	0/2024
2	a	0.36	0/751	0.50	0/1013
3	A	0.41	0/1520	0.51	0/2043
4	B	0.41	0/3152	0.52	0/4239
5	C	0.38	0/2624	0.52	1/3553 (0.0%)
6	D	0.30	0/2243	0.48	0/3025
7	E	0.34	0/1260	0.49	0/1694
8	F	0.40	0/1821	0.50	0/2451
9	G	0.37	0/1807	0.52	0/2439
10	H	0.39	0/1514	0.50	0/2039
11	J	0.25	0/1357	0.51	0/1818
12	K	0.28	0/2077	0.51	0/2800
13	M	0.36	0/1074	0.48	0/1446
14	N	0.41	0/1757	0.51	0/2354
15	O	0.44	0/1585	0.48	0/2128
16	P	0.38	0/1465	0.51	0/1968
17	Q	0.36	0/1050	0.48	0/1419
18	R	0.38	0/1275	0.46	0/1702
19	S	0.39	0/1473	0.49	0/1980
20	T	0.31	0/957	0.51	0/1285
21	U	0.37	0/843	0.51	0/1144
22	V	0.40	0/1018	0.52	0/1369
23	W	0.30	0/1918	0.50	0/2586
24	X	0.40	0/1116	0.50	0/1503
25	Y	0.35	0/1004	0.53	0/1341
26	Z	0.37	0/1118	0.53	0/1497
27	b	0.36	0/4211	0.50	0/5675
28	c	0.37	0/751	0.46	0/1008
29	d	0.42	0/870	0.47	0/1168
30	e	0.39	0/1028	0.47	0/1376
31	f	0.43	0/868	0.50	0/1168
32	g	0.45	0/891	0.53	0/1191

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.39	0/978	0.48	0/1301
34	i	0.31	0/778	0.47	0/1034
35	j	0.42	0/685	0.51	0/908
36	k	0.33	0/610	0.52	0/815
37	m	0.37	0/3848	0.52	0/5181
38	n	0.33	0/3057	0.52	1/4127 (0.0%)
39	o	0.31	0/1083	0.54	0/1440
40	p	0.46	0/701	0.52	0/934
41	q	0.29	0/1336	0.49	0/1788
42	r	0.38	0/1892	0.53	0/2528
43	t	0.29	0/2333	0.47	0/3128
44	u	0.36	0/1218	0.49	0/1621
45	v	0.29	0/2361	0.48	0/3153
46	w	0.30	0/1471	0.50	0/1980
47	x	0.29	0/3897	0.51	1/5282 (0.0%)
48	y	0.36	0/1872	0.54	0/2548
49	z	0.25	0/445	0.40	0/585
50	1	0.67	0/73234	0.92	97/114167 (0.1%)
51	2	0.73	0/3746	0.89	1/5832 (0.0%)
52	3	0.33	0/2883	0.93	1/4491 (0.0%)
53	6	0.37	0/1527	0.98	9/2371 (0.4%)
All	All	0.53	0/157861	0.77	111/229660 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	L	0	1
4	B	0	2
8	F	0	1
11	J	0	1
12	K	0	1
23	W	0	1
29	d	0	1
32	g	0	1
37	m	0	3
38	n	0	3
39	o	0	1
41	q	0	2
42	r	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
44	u	0	2
47	x	0	1
All	All	0	23

There are no bond length outliers.

The worst 5 of 111 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	1	922	U	C2-N1-C1'	9.37	128.95	117.70
50	1	2846	U	C2-N1-C1'	8.03	127.34	117.70
50	1	2788	C	N1-C2-O2	7.99	123.70	118.90
50	1	2788	C	N3-C2-O2	-7.90	116.37	121.90
50	1	3058	U	C2-N1-C1'	7.89	127.17	117.70

There are no chirality outliers.

5 of 23 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	B	221	THR	Peptide
4	B	346	THR	Peptide
8	F	158	LYS	Peptide
11	J	167	TYR	Peptide
1	L	46	ILE	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	L	183/199 (92%)	157 (86%)	25 (14%)	1 (0%)	25	59
2	a	91/149 (61%)	79 (87%)	11 (12%)	1 (1%)	12	43
3	A	191/254 (75%)	172 (90%)	19 (10%)	0	100	100
4	B	384/387 (99%)	330 (86%)	51 (13%)	3 (1%)	16	50
5	C	332/362 (92%)	282 (85%)	47 (14%)	3 (1%)	14	48
6	D	270/297 (91%)	246 (91%)	24 (9%)	0	100	100
7	E	152/176 (86%)	136 (90%)	16 (10%)	0	100	100
8	F	220/244 (90%)	204 (93%)	16 (7%)	0	100	100
9	G	225/256 (88%)	196 (87%)	29 (13%)	0	100	100
10	H	186/191 (97%)	169 (91%)	16 (9%)	1 (0%)	25	59
11	J	165/174 (95%)	136 (82%)	29 (18%)	0	100	100
12	K	249/376 (66%)	217 (87%)	30 (12%)	2 (1%)	16	50
13	M	135/138 (98%)	124 (92%)	11 (8%)	0	100	100
14	N	201/204 (98%)	185 (92%)	14 (7%)	2 (1%)	13	45
15	O	195/199 (98%)	188 (96%)	7 (4%)	0	100	100
16	P	181/184 (98%)	163 (90%)	18 (10%)	0	100	100
17	Q	132/186 (71%)	120 (91%)	12 (9%)	0	100	100
18	R	154/189 (82%)	145 (94%)	9 (6%)	0	100	100
19	S	169/172 (98%)	154 (91%)	15 (9%)	0	100	100
20	T	115/160 (72%)	98 (85%)	17 (15%)	0	100	100
21	U	102/121 (84%)	90 (88%)	12 (12%)	0	100	100
22	V	134/137 (98%)	124 (92%)	10 (8%)	0	100	100
23	W	232/236 (98%)	209 (90%)	22 (10%)	1 (0%)	30	63
24	X	139/142 (98%)	131 (94%)	8 (6%)	0	100	100
25	Y	124/127 (98%)	118 (95%)	6 (5%)	0	100	100
26	Z	133/136 (98%)	113 (85%)	18 (14%)	2 (2%)	8	37
27	b	505/647 (78%)	430 (85%)	72 (14%)	3 (1%)	22	56
28	c	95/105 (90%)	91 (96%)	4 (4%)	0	100	100
29	d	103/113 (91%)	91 (88%)	12 (12%)	0	100	100
30	e	123/130 (95%)	113 (92%)	10 (8%)	0	100	100
31	f	104/107 (97%)	99 (95%)	5 (5%)	0	100	100
32	g	110/121 (91%)	103 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	h	117/120 (98%)	106 (91%)	10 (8%)	1 (1%)	14	48
34	i	97/100 (97%)	86 (89%)	11 (11%)	0	100	100
35	j	83/88 (94%)	75 (90%)	8 (10%)	0	100	100
36	k	74/78 (95%)	67 (90%)	7 (10%)	0	100	100
37	m	465/486 (96%)	389 (84%)	70 (15%)	6 (1%)	10	40
38	n	360/605 (60%)	311 (86%)	46 (13%)	3 (1%)	16	50
39	o	127/220 (58%)	110 (87%)	16 (13%)	1 (1%)	16	50
40	p	89/92 (97%)	80 (90%)	9 (10%)	0	100	100
41	q	154/455 (34%)	128 (83%)	24 (16%)	2 (1%)	10	40
42	r	224/261 (86%)	188 (84%)	33 (15%)	3 (1%)	10	40
43	t	283/322 (88%)	238 (84%)	42 (15%)	3 (1%)	12	43
44	u	140/199 (70%)	126 (90%)	14 (10%)	0	100	100
45	v	283/344 (82%)	265 (94%)	18 (6%)	0	100	100
46	w	178/203 (88%)	158 (89%)	20 (11%)	0	100	100
47	x	476/515 (92%)	422 (89%)	54 (11%)	0	100	100
48	y	242/245 (99%)	213 (88%)	29 (12%)	0	100	100
49	z	53/106 (50%)	51 (96%)	2 (4%)	0	100	100
All	All	9279/11058 (84%)	8226 (89%)	1015 (11%)	38 (0%)	32	63

5 of 38 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	C	339	LEU
12	K	216	GLU
26	Z	102	GLU
37	m	241	SER
1	L	63	VAL

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	L	147/159 (92%)	136 (92%)	11 (8%)	11	38
2	a	76/119 (64%)	70 (92%)	6 (8%)	10	36
3	A	152/196 (78%)	138 (91%)	14 (9%)	7	28
4	B	322/323 (100%)	295 (92%)	27 (8%)	9	33
5	C	273/289 (94%)	257 (94%)	16 (6%)	16	47
6	D	226/245 (92%)	215 (95%)	11 (5%)	21	53
7	E	134/153 (88%)	127 (95%)	7 (5%)	19	50
8	F	186/205 (91%)	178 (96%)	8 (4%)	25	55
9	G	186/208 (89%)	174 (94%)	12 (6%)	14	44
10	H	168/171 (98%)	159 (95%)	9 (5%)	18	50
11	J	145/150 (97%)	140 (97%)	5 (3%)	32	61
12	K	234/346 (68%)	214 (92%)	20 (8%)	8	32
13	M	108/109 (99%)	99 (92%)	9 (8%)	9	34
14	N	175/176 (99%)	165 (94%)	10 (6%)	17	48
15	O	160/162 (99%)	155 (97%)	5 (3%)	35	64
16	P	145/146 (99%)	133 (92%)	12 (8%)	9	34
17	Q	110/151 (73%)	101 (92%)	9 (8%)	9	34
18	R	129/154 (84%)	125 (97%)	4 (3%)	35	64
19	S	155/156 (99%)	143 (92%)	12 (8%)	10	37
20	T	102/137 (74%)	88 (86%)	14 (14%)	3	14
21	U	91/107 (85%)	82 (90%)	9 (10%)	6	26
22	V	104/105 (99%)	100 (96%)	4 (4%)	28	59
23	W	211/213 (99%)	194 (92%)	17 (8%)	9	35
24	X	117/118 (99%)	113 (97%)	4 (3%)	32	61
25	Y	109/110 (99%)	100 (92%)	9 (8%)	9	34
26	Z	115/116 (99%)	110 (96%)	5 (4%)	25	55
27	b	457/573 (80%)	428 (94%)	29 (6%)	15	45
28	c	81/88 (92%)	75 (93%)	6 (7%)	11	39
29	d	92/97 (95%)	84 (91%)	8 (9%)	8	31
30	e	108/111 (97%)	101 (94%)	7 (6%)	14	44
31	f	90/91 (99%)	86 (96%)	4 (4%)	24	55
32	g	95/103 (92%)	85 (90%)	10 (10%)	5	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	h	104/105 (99%)	93 (89%)	11 (11%)	5	23
34	i	81/82 (99%)	74 (91%)	7 (9%)	8	32
35	j	69/71 (97%)	63 (91%)	6 (9%)	8	31
36	k	67/69 (97%)	63 (94%)	4 (6%)	16	46
37	m	413/428 (96%)	375 (91%)	38 (9%)	7	28
38	n	329/548 (60%)	298 (91%)	31 (9%)	7	28
39	o	114/199 (57%)	104 (91%)	10 (9%)	8	31
40	p	71/72 (99%)	67 (94%)	4 (6%)	17	49
41	q	147/420 (35%)	138 (94%)	9 (6%)	15	46
42	r	203/229 (89%)	190 (94%)	13 (6%)	14	44
43	t	256/287 (89%)	244 (95%)	12 (5%)	22	53
44	u	126/180 (70%)	121 (96%)	5 (4%)	27	58
45	v	258/309 (84%)	236 (92%)	22 (8%)	8	32
46	w	161/179 (90%)	149 (92%)	12 (8%)	11	38
47	x	428/451 (95%)	397 (93%)	31 (7%)	12	40
48	y	210/211 (100%)	192 (91%)	18 (9%)	8	32
49	z	48/95 (50%)	43 (90%)	5 (10%)	5	24
All	All	8088/9522 (85%)	7517 (93%)	571 (7%)	15	40

5 of 571 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	r	232	THR
43	t	264	CYS
42	r	226	SER
47	x	24	ILE
18	R	84	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 115 such sidechains are listed below:

Mol	Chain	Res	Type
27	b	333	ASN
47	x	443	HIS
37	m	276	HIS
47	x	402	GLN

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Mol	Chain	Res	Type
45	v	286	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	1	3048/3396 (89%)	815 (26%)	64 (2%)
51	2	157/158 (99%)	32 (20%)	1 (0%)
52	3	120/121 (99%)	33 (27%)	1 (0%)
53	6	63/232 (27%)	33 (52%)	2 (3%)
All	All	3388/3907 (86%)	913 (26%)	68 (2%)

5 of 913 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	1	5	G
50	1	7	C
50	1	14	U
50	1	18	G
50	1	38	U

5 of 68 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	1	2857	C
50	1	2875	U
52	3	52	G
50	1	1307	G
50	1	1302	A

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 7 ligands modelled in this entry, 5 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
54	GTP	m	501	-	26,34,34	1.28	4 (15%)	32,54,54	1.71	7 (21%)
54	GTP	b	701	55	26,34,34	1.14	1 (3%)	32,54,54	1.65	7 (21%)

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
54	GTP	m	501	-	-	7/18/38/38	0/3/3/3
54	GTP	b	701	55	-	3/18/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	m	501	GTP	C5-C6	-4.22	1.38	1.47
54	b	701	GTP	C5-C6	-4.13	1.39	1.47
54	m	501	GTP	C2-N3	2.04	1.38	1.33
54	m	501	GTP	O4'-C4'	-2.03	1.40	1.45
54	m	501	GTP	C5-C4	-2.02	1.37	1.43

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	m	501	GTP	PA-O3A-PB	-4.29	118.09	132.83
54	b	701	GTP	PA-O3A-PB	-4.17	118.50	132.83
54	b	701	GTP	PB-O3B-PG	-3.83	119.67	132.83
54	m	501	GTP	C5-C6-N1	3.52	120.16	113.95
54	m	501	GTP	C8-N7-C5	3.31	109.30	102.99

There are no chirality outliers.

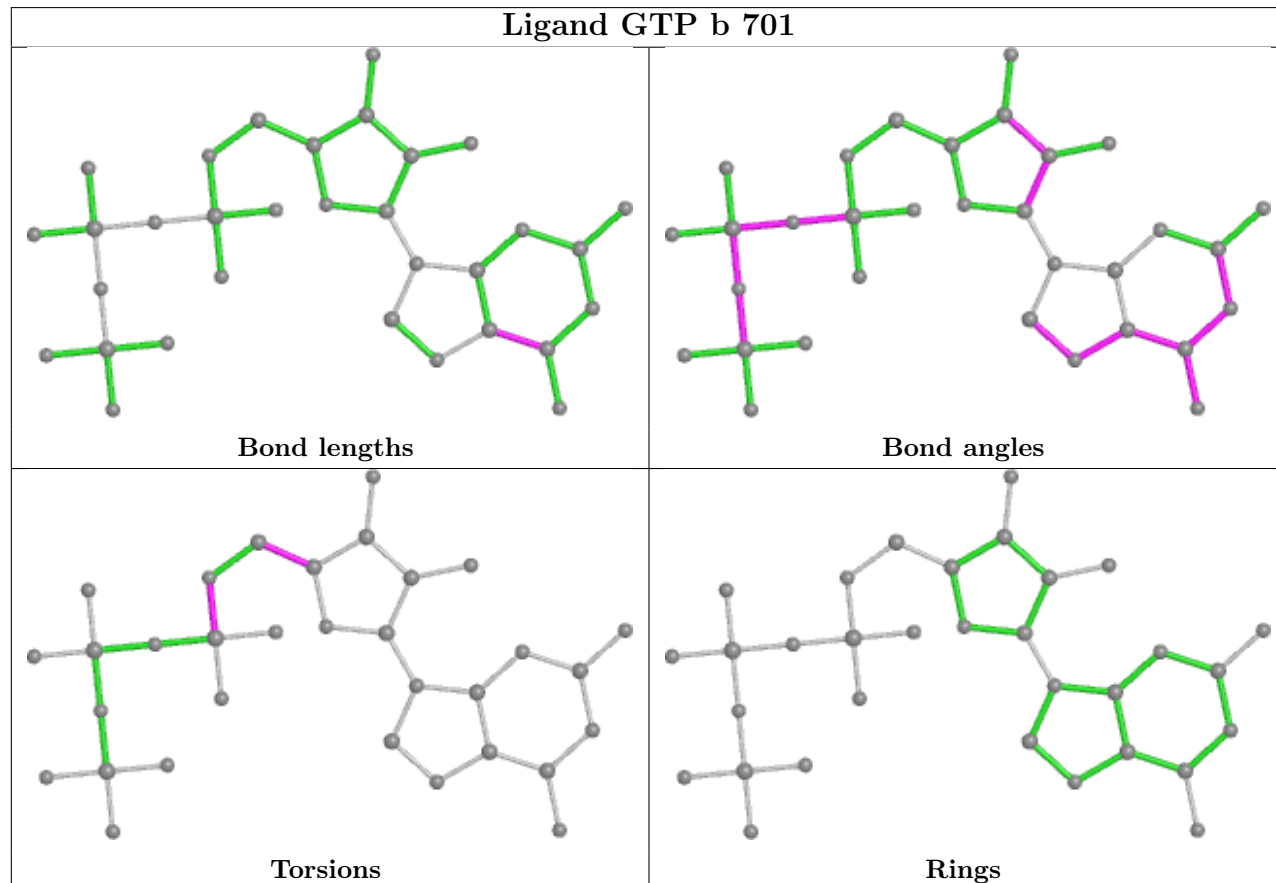
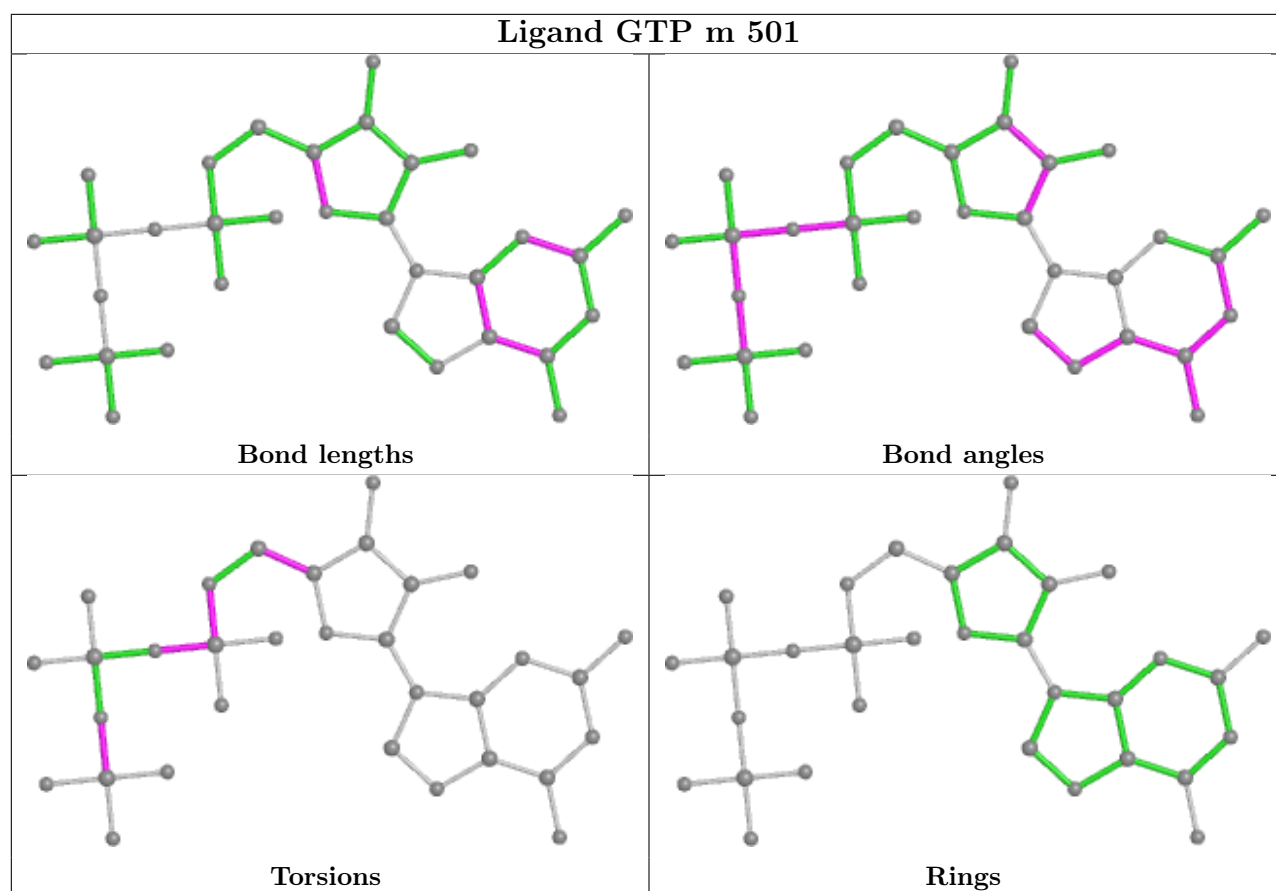
5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
54	m	501	GTP	O4'-C4'-C5'-O5'
54	m	501	GTP	C3'-C4'-C5'-O5'
54	b	701	GTP	C3'-C4'-C5'-O5'
54	m	501	GTP	PB-O3B-PG-O1G
54	b	701	GTP	O4'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

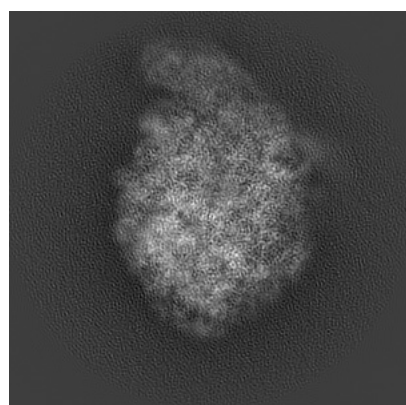
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30174. These allow visual inspection of the internal detail of the map and identification of artifacts.

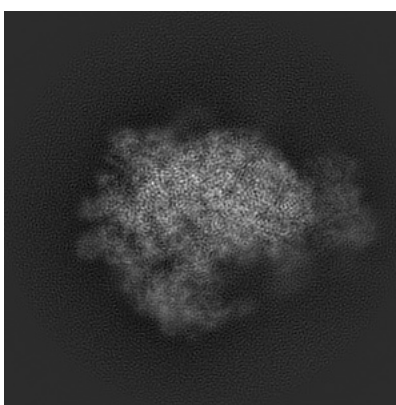
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

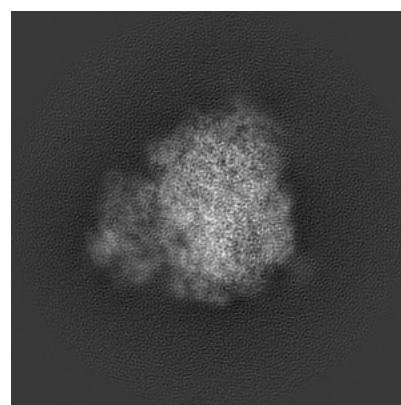
6.1.1 Primary map



X



Y

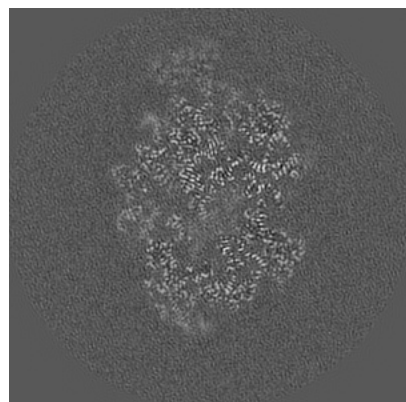


Z

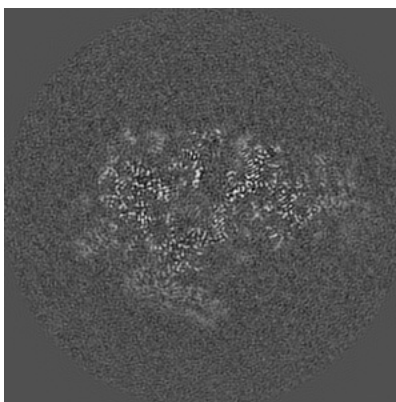
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

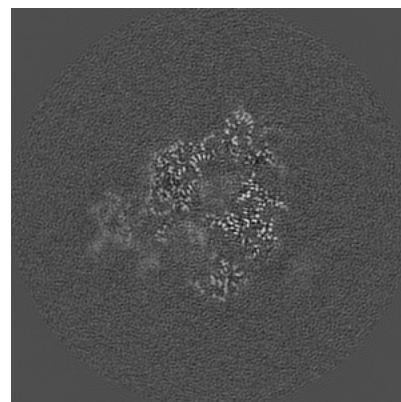
6.2.1 Primary map



X Index: 150



Y Index: 150

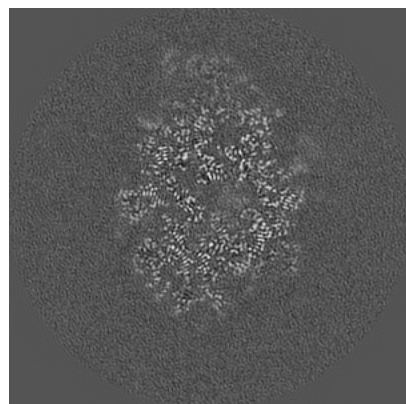


Z Index: 150

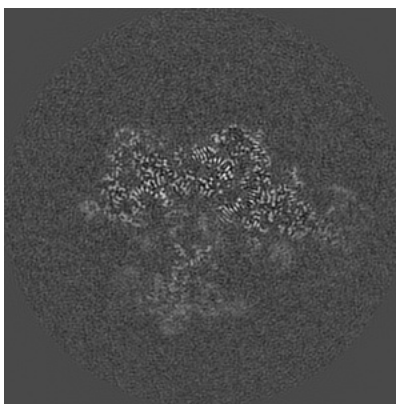
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

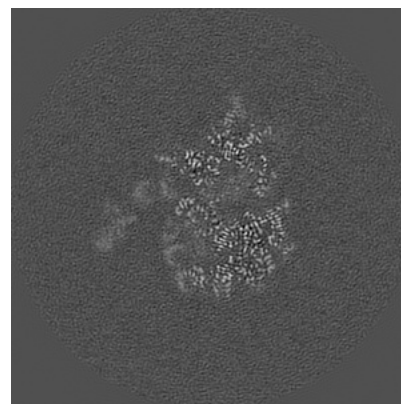
6.3.1 Primary map



X Index: 162



Y Index: 133

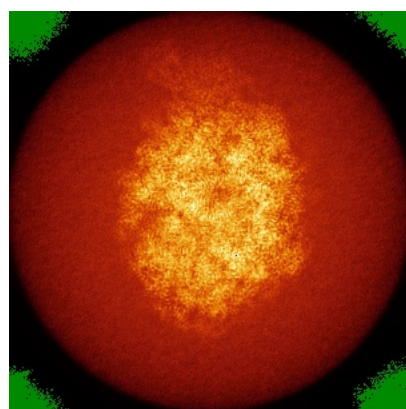


Z Index: 162

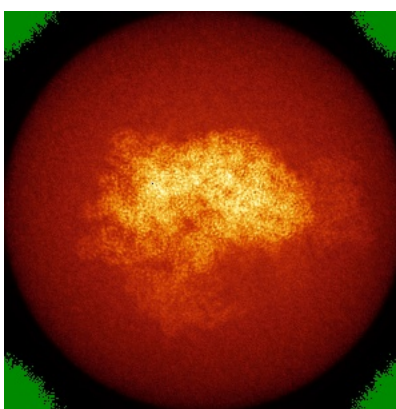
The images above show the largest variance slices of the map in three orthogonal directions.

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

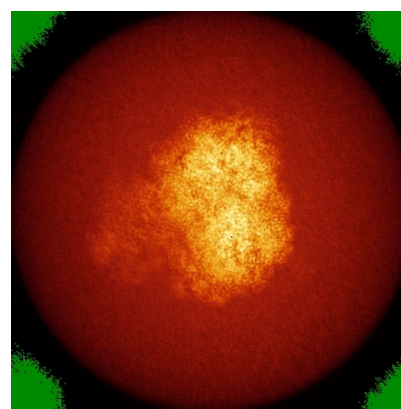
6.4.1 Primary map



X



Y

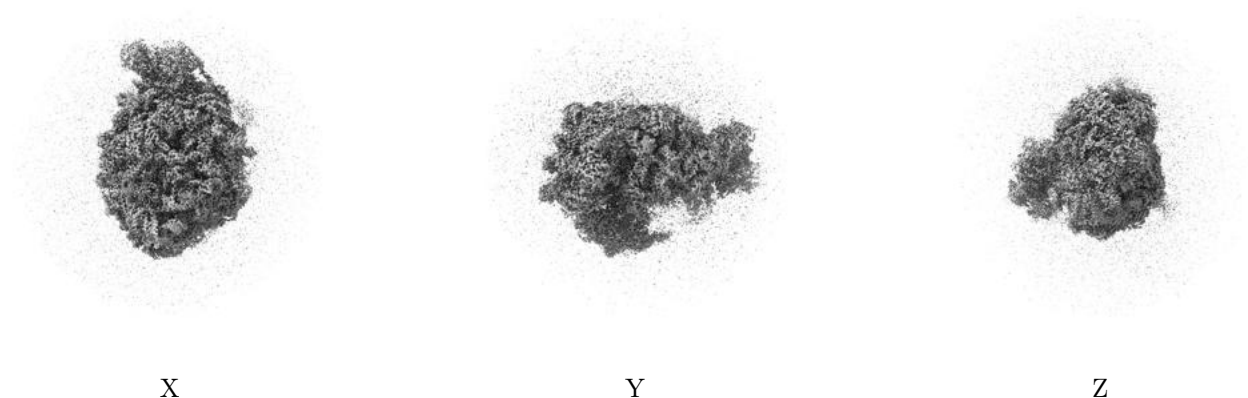


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

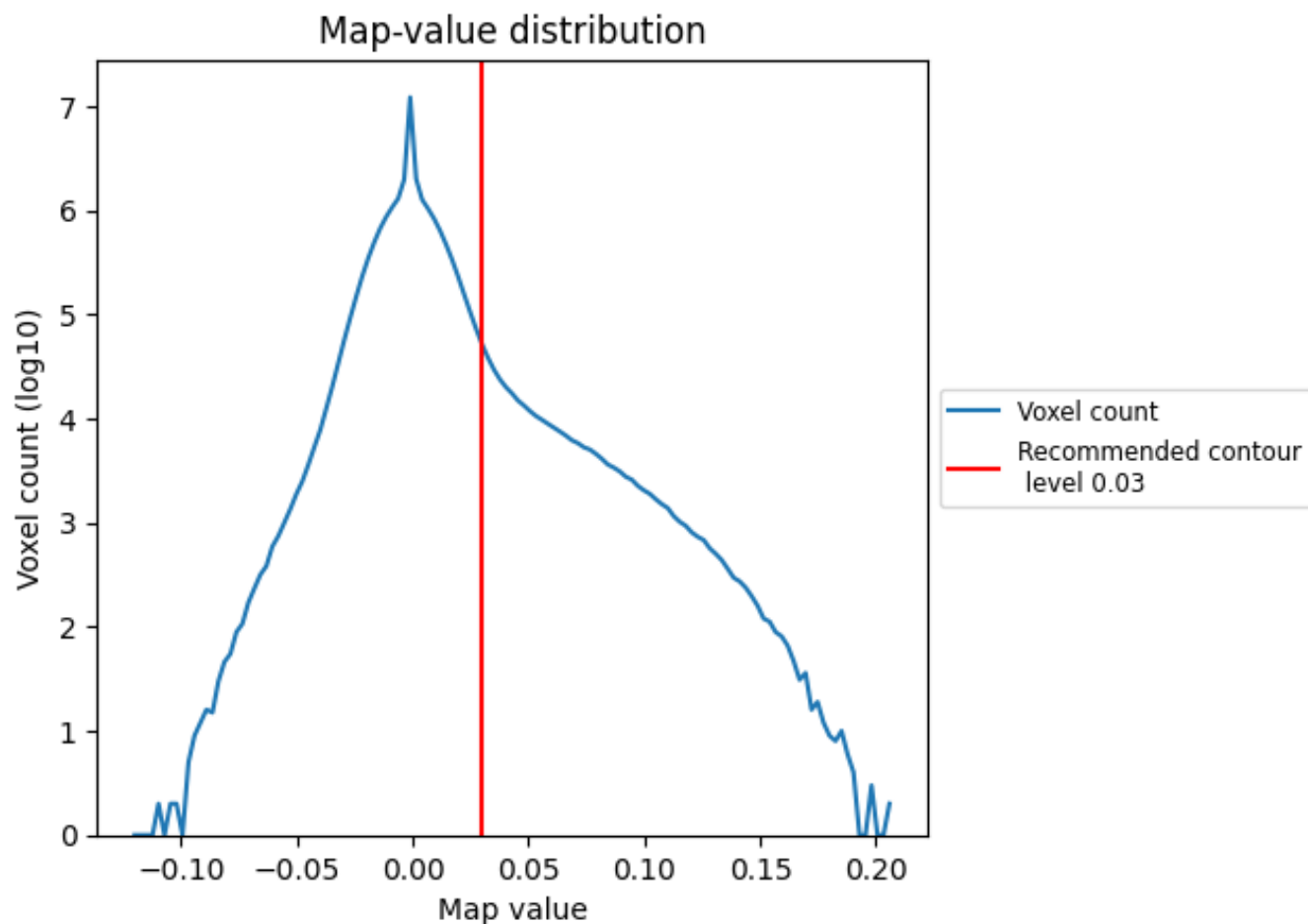
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

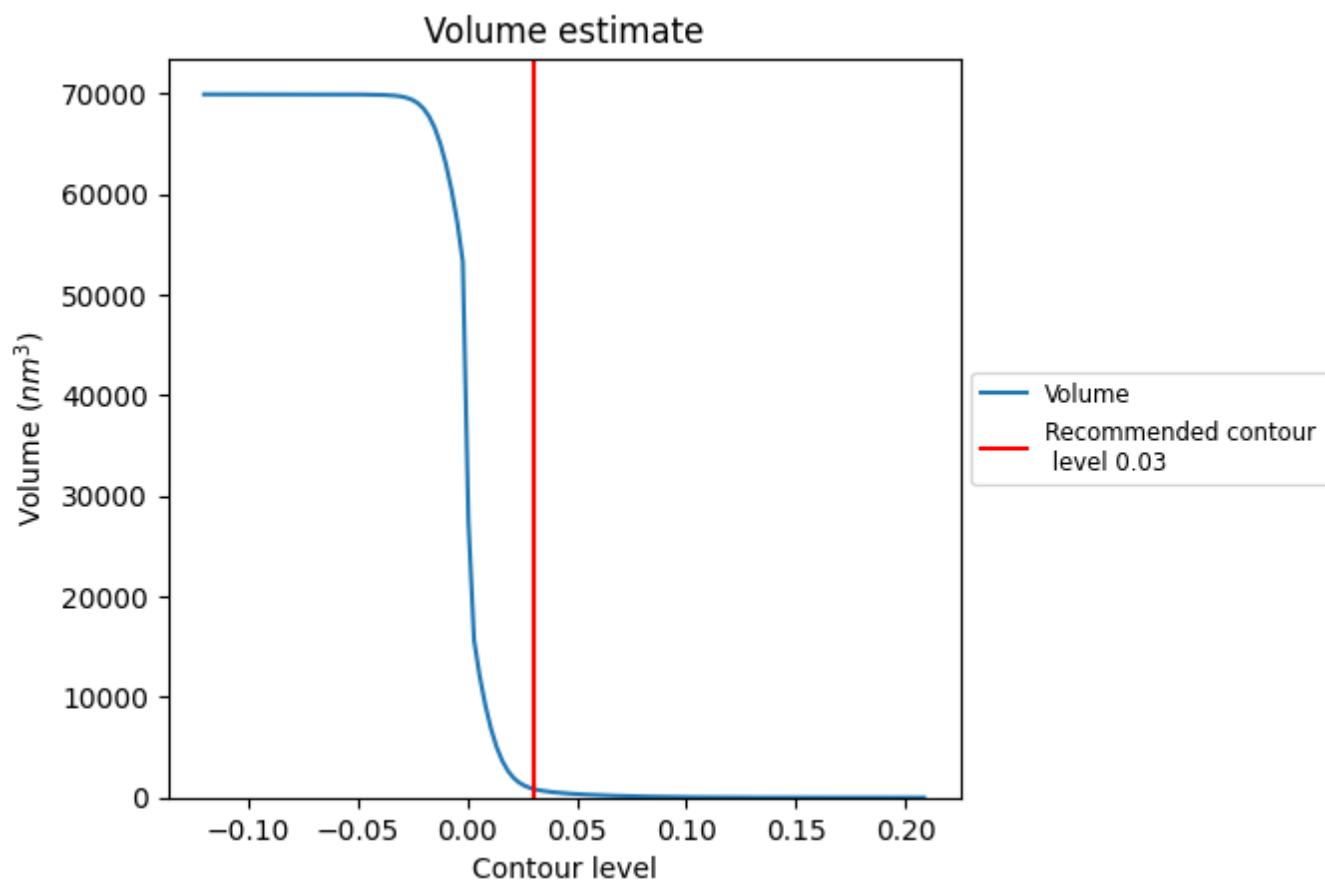
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

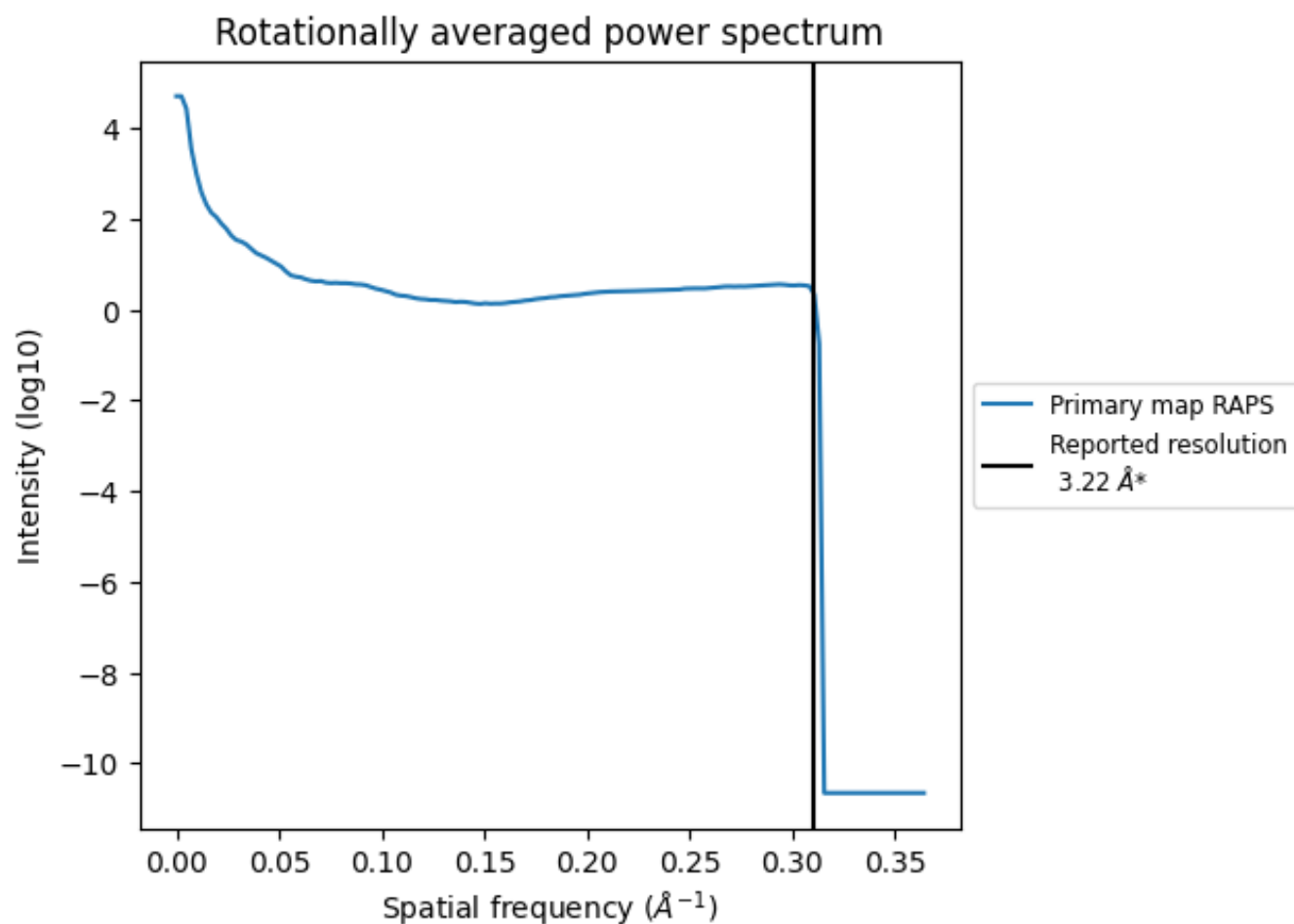
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 879 nm³; this corresponds to an approximate mass of 794 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 0.311 Å⁻¹

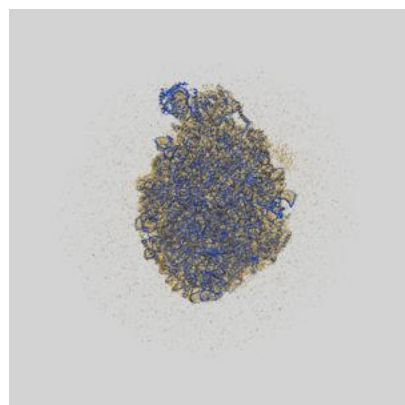
8 Fourier-Shell correlation

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

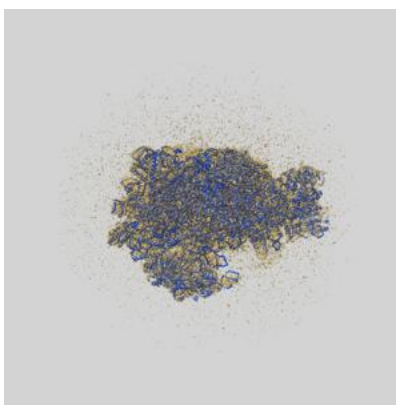
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30174 and PDB model 7BTB. Per-residue inclusion information can be found in section 3 on page 14.

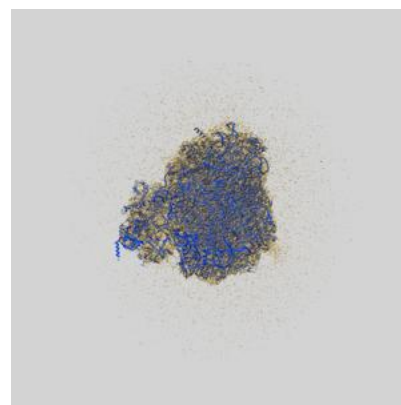
9.1 Map-model overlay [i](#)



X



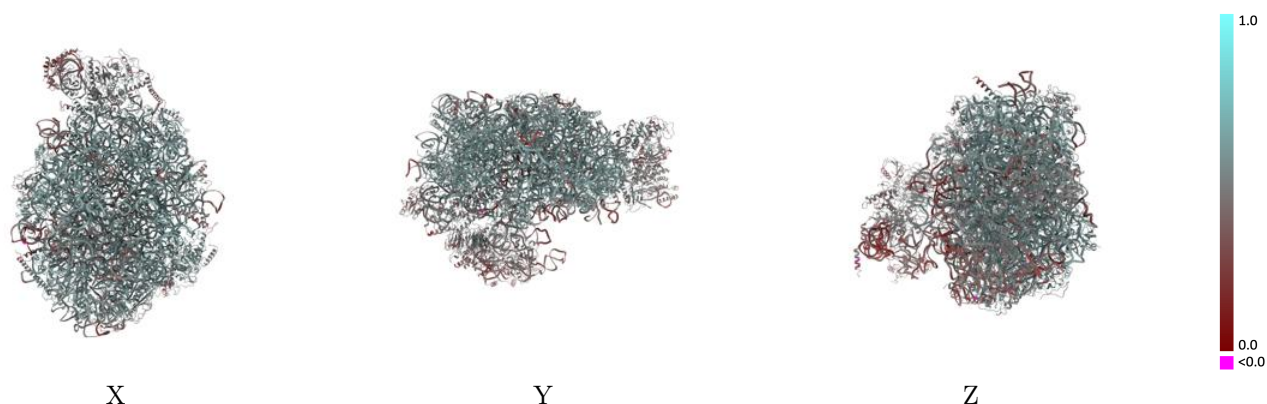
Y



Z

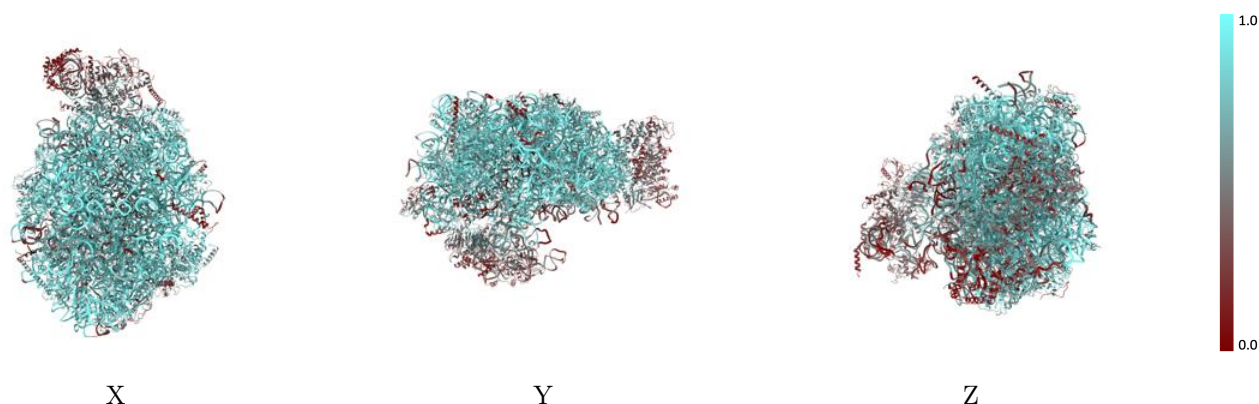
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



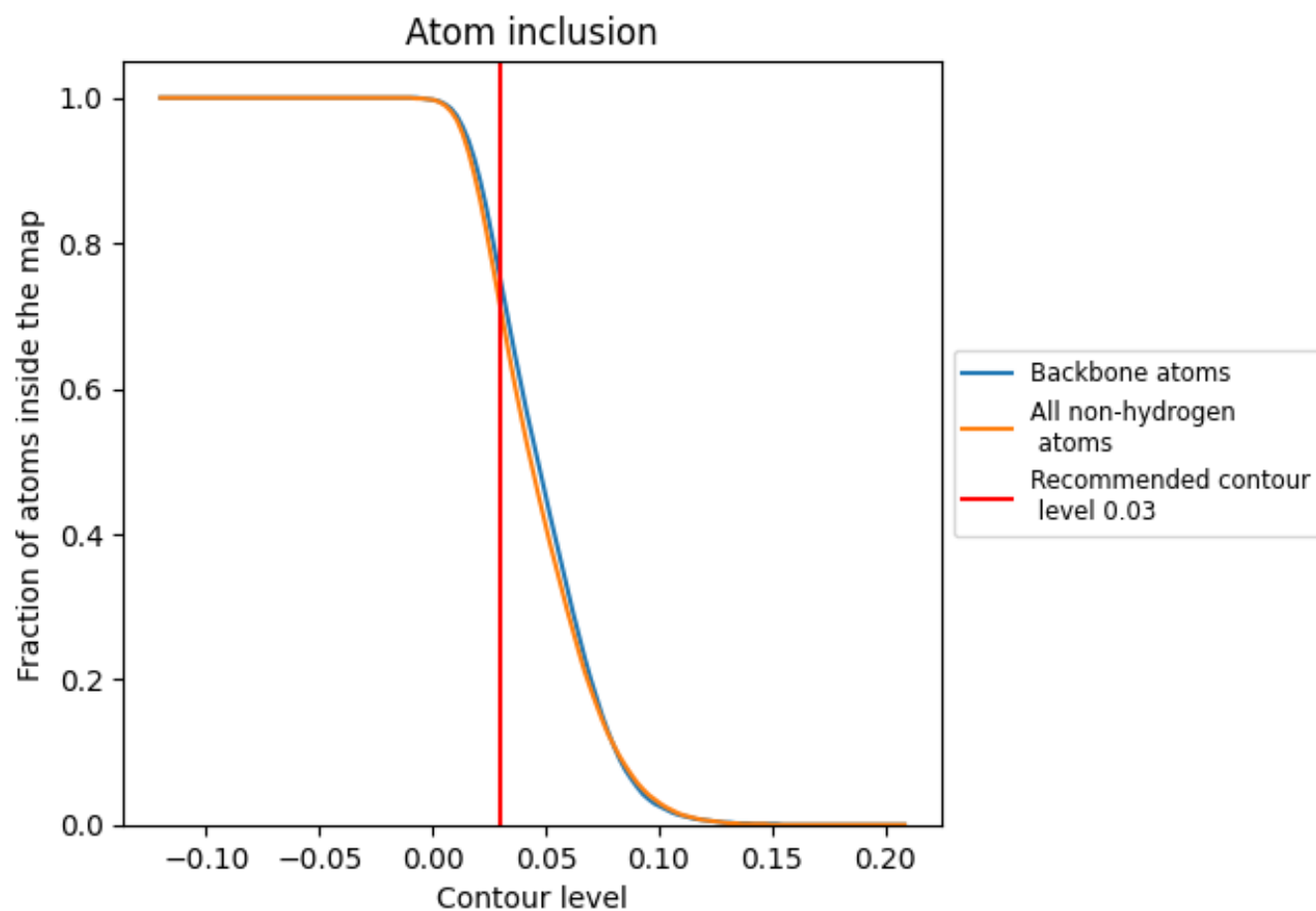
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 71% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7110	 0.5100
1	 0.8040	 0.5140
2	 0.8900	 0.5560
3	 0.3970	 0.2790
6	 0.4140	 0.3910
A	 0.8090	 0.5840
B	 0.8060	 0.5650
C	 0.7910	 0.5630
D	 0.2930	 0.3840
E	 0.7340	 0.5370
F	 0.8030	 0.5620
G	 0.7080	 0.5340
H	 0.8120	 0.5680
J	 0.1700	 0.3260
K	 0.2040	 0.4020
L	 0.7400	 0.5360
M	 0.8010	 0.5580
N	 0.7700	 0.5650
O	 0.8500	 0.5860
P	 0.7340	 0.5480
Q	 0.7600	 0.5520
R	 0.7990	 0.5600
S	 0.7320	 0.5350
T	 0.5200	 0.4760
U	 0.6560	 0.5090
V	 0.8210	 0.5790
W	 0.4070	 0.4260
X	 0.7970	 0.5710
Y	 0.8060	 0.5730
Z	 0.7780	 0.5560
a	 0.7180	 0.5340
b	 0.6150	 0.5010
c	 0.7500	 0.5470
d	 0.7960	 0.5680
e	 0.8180	 0.5740



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Chain	Atom inclusion	Q-score
f	 0.8690	 0.6000
g	 0.8000	 0.5670
h	 0.7890	 0.5530
i	 0.6310	 0.5020
j	 0.7640	 0.5670
k	 0.6750	 0.5310
m	 0.7100	 0.5360
n	 0.5060	 0.4950
o	 0.3810	 0.4530
p	 0.8130	 0.5690
q	 0.4080	 0.4910
r	 0.7590	 0.5550
t	 0.3730	 0.4630
u	 0.7060	 0.5380
v	 0.3920	 0.4360
w	 0.4820	 0.4560
x	 0.4330	 0.4390
y	 0.7380	 0.5430
z	 0.3430	 0.4870