



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:14 AM UTC

PDB ID : 6YLH / pdb_00006ylh
EMDB ID : EMD-10839
Title : Rix1-Rea1 pre-60S particle - full composite structure
Authors : Kater, L.; Beckmann, R.
Deposited on : 2020-04-07
Resolution : 3.10 Å (reported)
Based on initial models : 6QTA, 6OR5, 6N8J, 6HYD, 3JCT, 6HYP

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

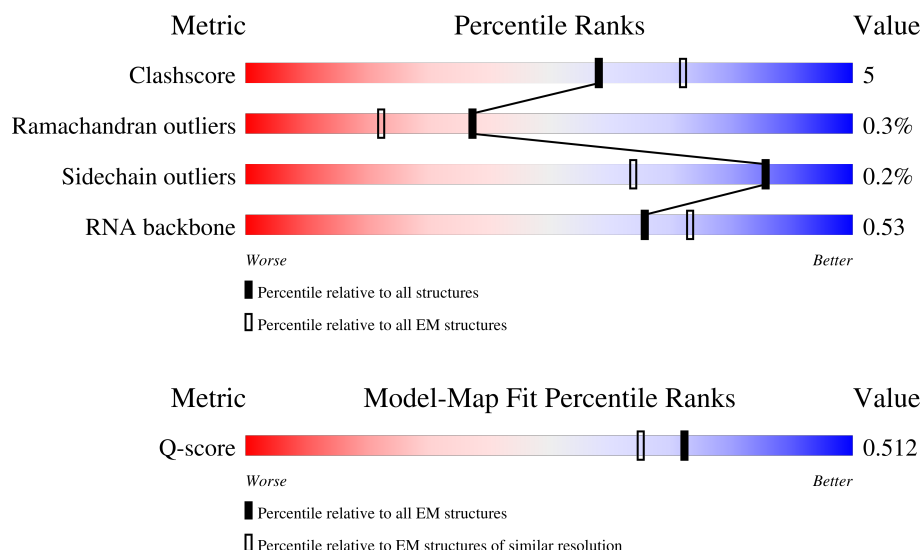
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.10 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	14724 (2.60 - 3.60)

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	1	3396	
2	2	158	
3	3	121	

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Mol	Chain	Length	Quality of chain
4	4	593	
5	5	120	
6	A	254	
7	B	387	
8	C	362	
9	D	297	
10	E	176	
11	F	244	
12	G	256	
13	H	191	
14	I	166	
15	J	174	
16	K	334	
17	L	199	
18	M	138	
19	N	204	
20	O	199	
21	P	184	
22	Q	186	
23	R	189	
24	S	172	
25	T	160	
26	U	121	
27	V	137	
28	W	236	

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Mol	Chain	Length	Quality of chain
29	X	142	
30	Y	127	
31	Z	136	
32	a	149	
33	b	647	
34	c	175	
35	d	113	
36	e	130	
37	f	107	
38	g	121	
39	h	120	
40	i	100	
41	j	88	
42	k	78	
43	l	51	
44	m	486	
45	n	105	
46	o	217	
47	p	92	
48	q	165	
49	r	261	
50	s	520	
51	t	767	
52	u	199	
53	x	515	

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Mol	Chain	Length	Quality of chain
54	y	245	
55	z	106	
56	v	4910	
57	0	555	
57	w	555	
58	6	763	
58	7	763	

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 180897 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	3039	Total	C	N	O	P	0	0
			65028	29041	11740	21208	3039		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	154	Total	C	N	O	P	0	0
			3273	1464	576	1079	154		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	117	Total	C	N	O	P	0	0
			2494	1114	446	817	117		

- Molecule 4 is a protein called Probable metalloprotease ARX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	509	Total	C	N	O	S	0	0
			3945	2503	673	754	15		

- Molecule 5 is a protein called rRNA-processing protein CGR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	78	Total	C	N	O	S	0	0
			681	419	140	119	3		

- Molecule 6 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	245	Total	C	N	O	S	0	0
			1863	1162	376	324	1		

- Molecule 7 is a protein called 60S ribosomal protein L3.

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

- Molecule 8 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 9 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	243	Total	C	N	O	S	0	0
			1969	1250	344	373	2		

- Molecule 10 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 11 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	216	Total	C	N	O	S	0	0
			1744	1127	317	299	1		

- Molecule 12 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	228	Total	C	N	O	S	0	0
			1784	1142	320	319	3		

- Molecule 13 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	187	Total	C	N	O	S	0	0
			1486	944	270	268	4		

- Molecule 14 is a protein called Bud site selection protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	130	Total	C	N	O	S	0	0
			1051	657	194	197	3		

- Molecule 15 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	168	Total	C	N	O	S	0	0
			1344	841	251	248	4		

- Molecule 16 is a protein called Pre-rRNA-processing protein IPI1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	258	Total	C	N	O	S	0	0
			2089	1346	367	368	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	181	Total	C	N	O	S	0	0
			1456	907	301	248			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	134	Total	C	N	O	S	0	0
			1040	666	196	176	2		

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

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

- Molecule 20 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	P	171	Total	C	N	O	0	0
			1360	845	272	243		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
22	Q	144	Total	C	N	O	S	0
			1110	704	213	192	1	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
23	R	151	Total	C	N	O		0
			1219	757	258	204		0

- Molecule 24 is a protein called 60S ribosomal protein L20-A.

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
25	T	124	Total	C	N	O	S	0
			983	619	188	173	3	0

- Molecule 26 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	U	101	Total	C	N	O		0
			800	518	131	151		0

- Molecule 27 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	V	134	Total	C	N	O	S	0
			993	623	187	176	7	0

- Molecule 28 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	W	233	Total	C	N	O	S	0	0
			1877	1189	322	361	5		

- Molecule 29 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	X	140	Total	C	N	O	S	0	0
			1092	699	195	196	2		

- Molecule 30 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y	125	Total	C	N	O		0	0
			984	620	191	173			

- Molecule 31 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 32 is a protein called 60S ribosomal protein L28.

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

- Molecule 33 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	613	Total	C	N	O	S	0	0
			4953	3110	892	926	25		

- Molecule 34 is a protein called Ribosome biogenesis protein ALB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	109	Total	C	N	O		0	0
			872	543	171	158			

- Molecule 35 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 36 is a protein called 60S ribosomal protein L32.

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

- Molecule 37 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 38 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	107	Total	C	N	O	S	0	0
			846	525	173	144	4		

- Molecule 39 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 40 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	i	96	Total	C	N	O	S	0	0
			743	465	148	128	2		

- Molecule 41 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	j	84	Total	C	N	O	S	0	0
			665	405	145	110	5		

- Molecule 42 is a protein called 60S ribosomal protein L38.

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

- Molecule 43 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	l	49	Total	C	N	O	S	0	0
			428	266	96	64	2		

- Molecule 44 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	m	439	Total	C	N	O	S	0	0
			3546	2249	647	641	9		

- Molecule 45 is a protein called 60S ribosomal protein L30.

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

- Molecule 46 is a protein called 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	o	177	Total	C	N	O	0	0
			877	523	177	177		

- Molecule 47 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	p	89	Total	C	N	O	S	0	0
			680	421	136	117	6		

- Molecule 48 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	q	126	Total	C	N	O	S	0	0
			961	606	171	182	2		

- Molecule 49 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	r	225	Total	C	N	O	S	0	0
			1818	1152	345	314	7		

- Molecule 50 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	s	56	Total	C	N	O	S	0	0
			463	291	94	77	1		

- Molecule 51 is a protein called Protein SDA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	t	431	Total	C	N	O	S	0	0
			3395	2156	587	629	23		

- Molecule 52 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	148	Total	C	N	O	S	0	0
			1247	783	250	205	9		

- Molecule 53 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	x	459	Total	C	N	O	S	0	0
			3385	2110	620	635	20		

- Molecule 54 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	y	243	Total	C	N	O	S	0	0
			1841	1141	318	376	6		

- Molecule 55 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	z	77	Total	C	N	O	S	0	0
			643	403	130	109	1		

- Molecule 56 is a protein called Midasin.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	v	3629	Total	C	N	O	0	0
			18010	10752	3629	3629		

- Molecule 57 is a protein called Pre-rRNA-processing protein IPI3.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	w	399	Total	C	N	O	S	0	0
			3139	2004	520	601	14		
57	0	415	Total	C	N	O	S	0	0
			3260	2077	548	621	14		

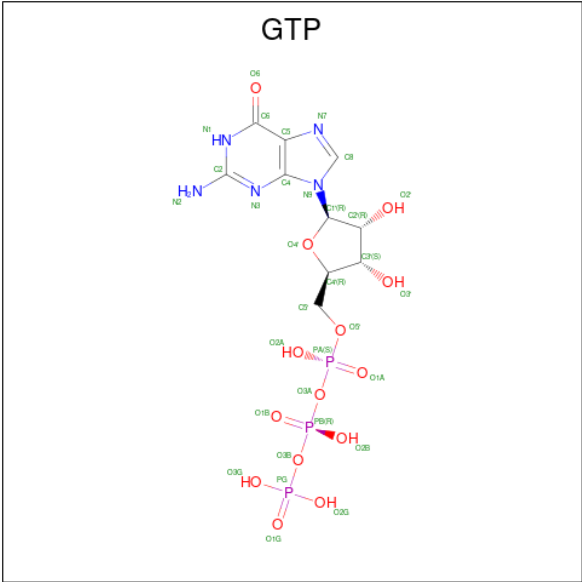
- Molecule 58 is a protein called Pre-rRNA-processing protein RIX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	6	545	Total	C	N	O	S	0	0
			4352	2847	711	777	17		
58	7	547	Total	C	N	O	S	0	0
			4380	2862	720	782	16		

- 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	

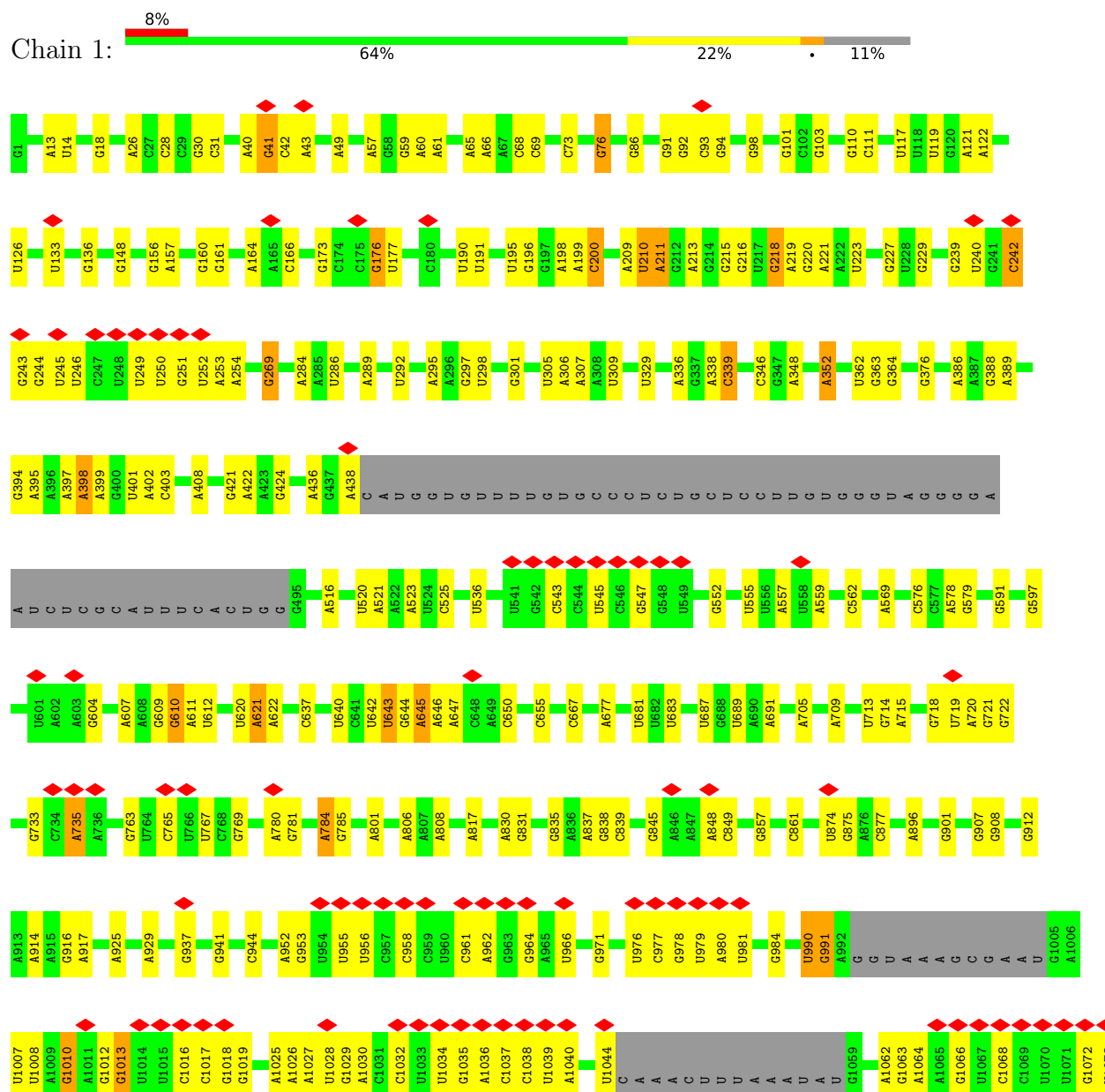
- Molecule 61 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

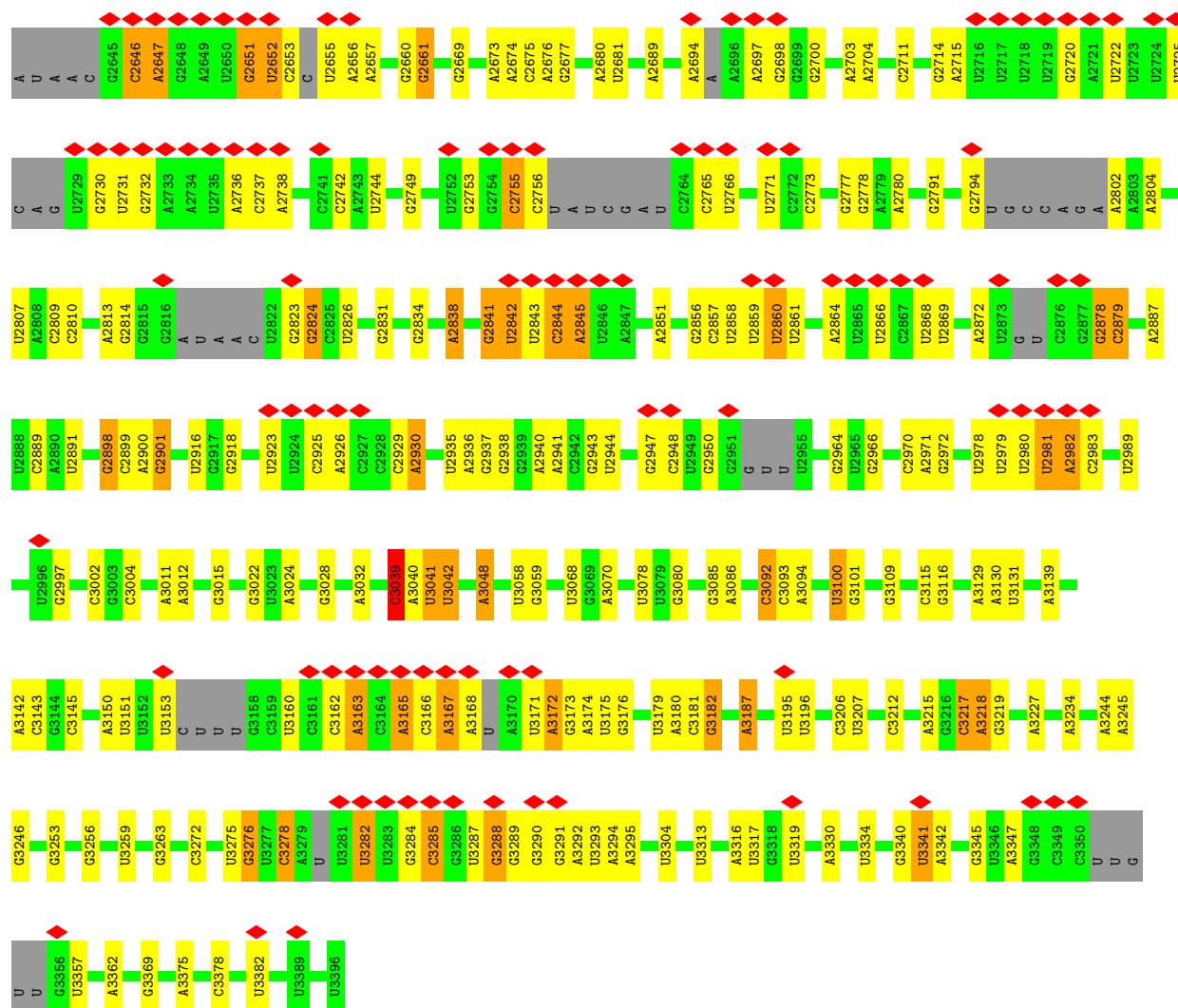
3 Residue-property plots

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.

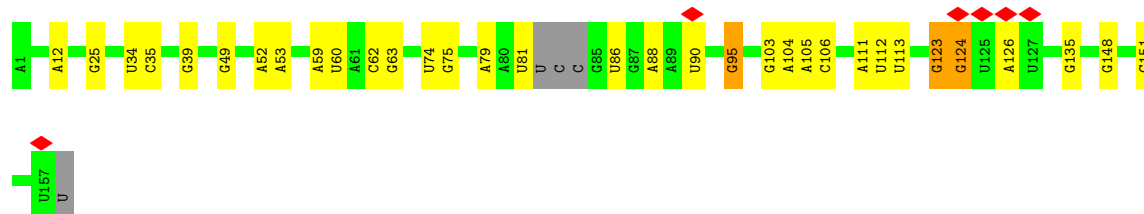
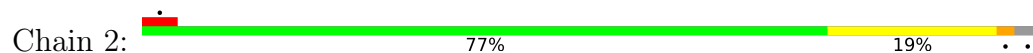
• Molecule 1: 25S rRNA



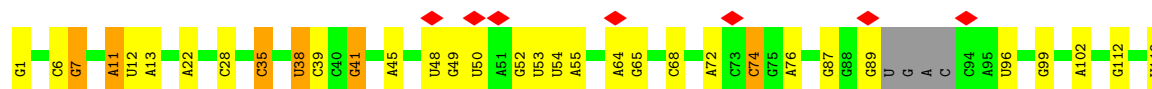




• Molecule 2: 5.8S rRNA

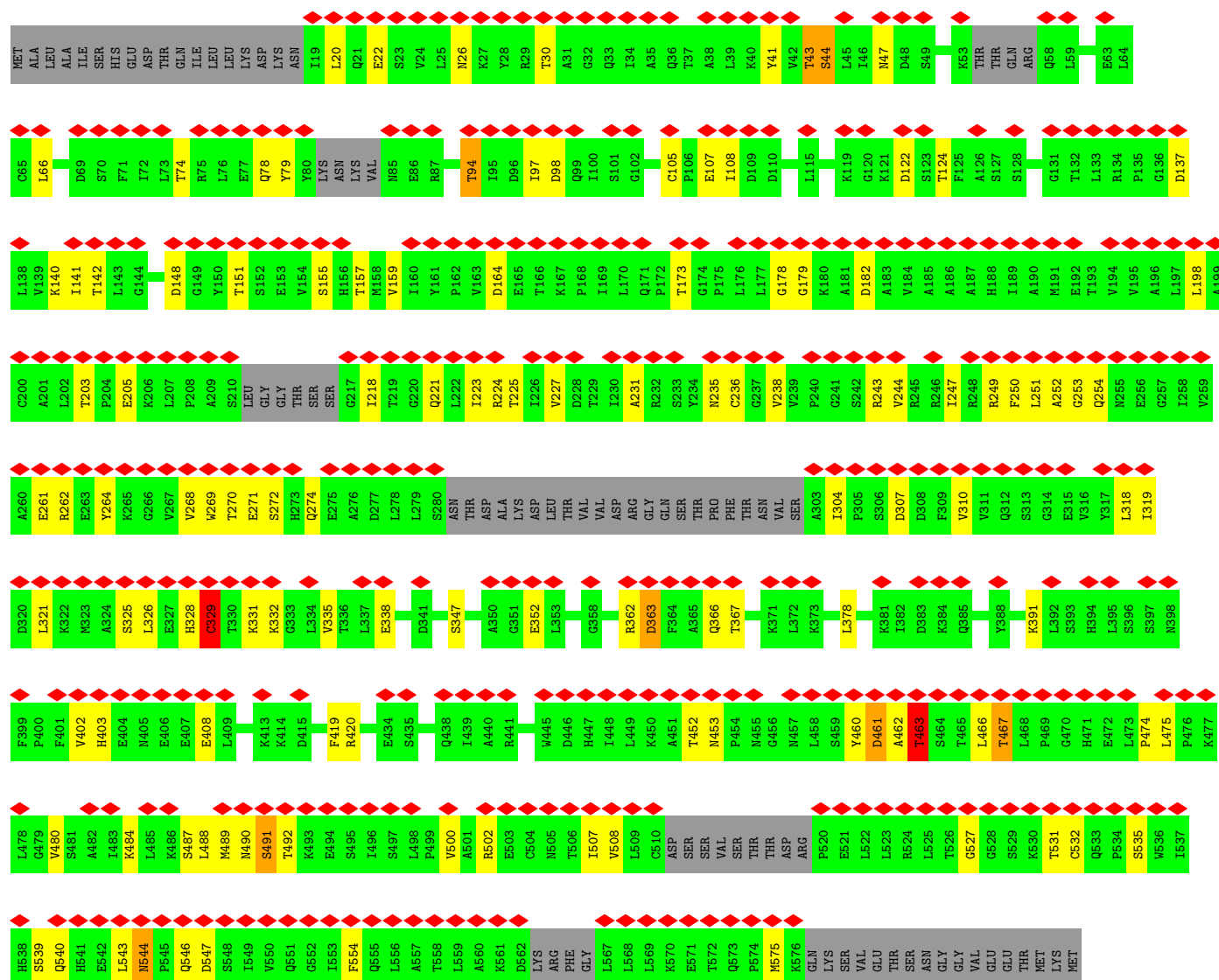


• Molecule 3: 5S rRNA

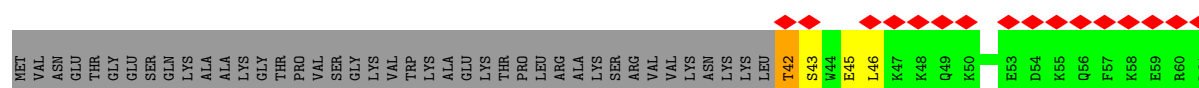


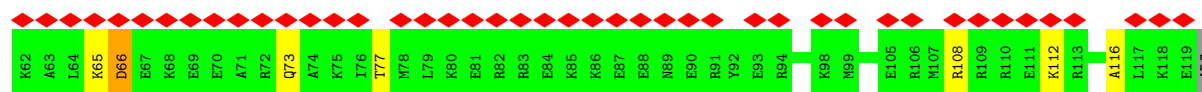


• Molecule 4: Probable metalloprotease ARX1



• Molecule 5: rRNA-processing protein CGR1

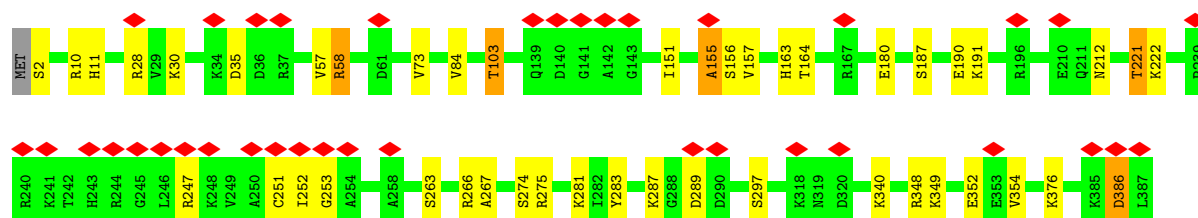




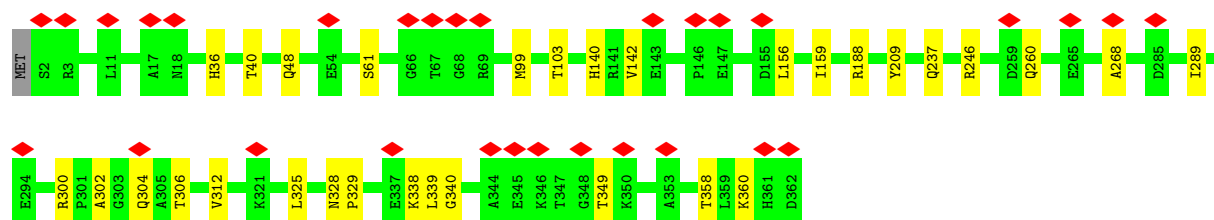
• Molecule 6: 60S ribosomal protein L2-A



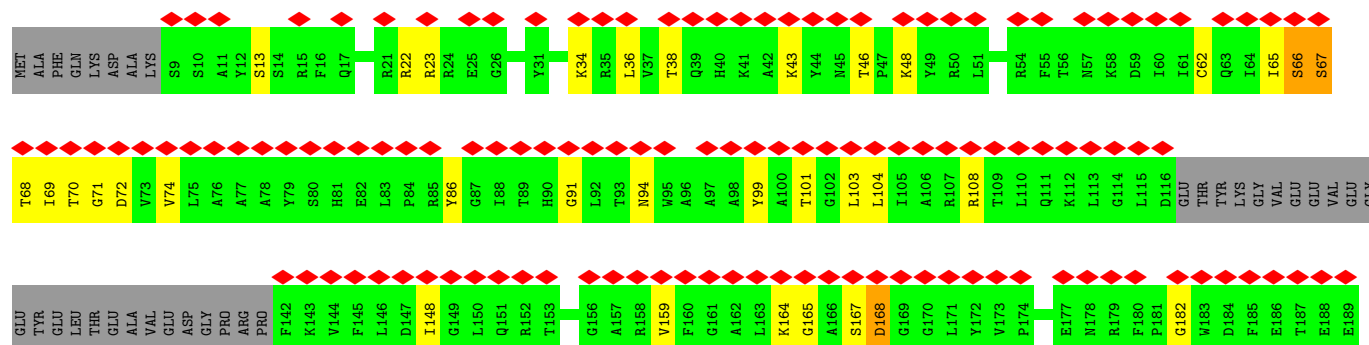
• Molecule 7: 60S ribosomal protein L3

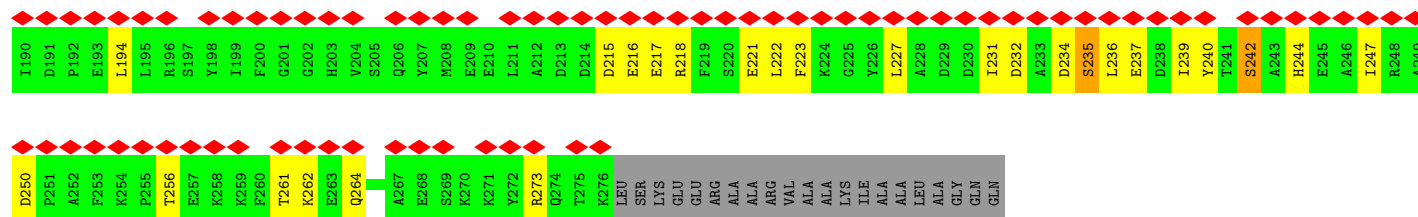


• Molecule 8: 60S ribosomal protein L4-A

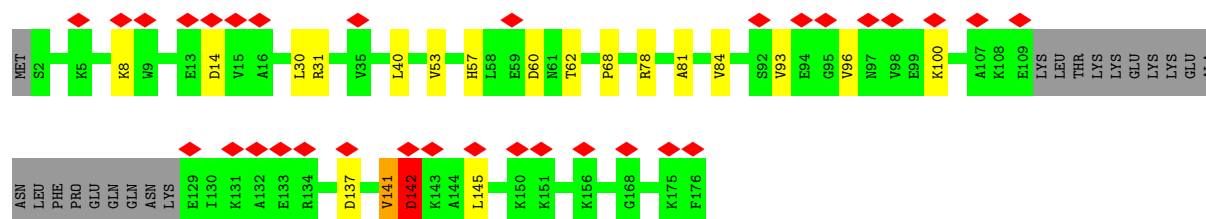
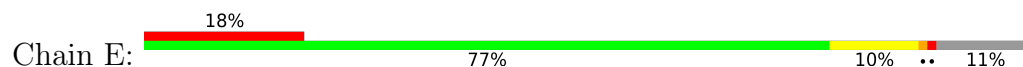


• Molecule 9: 60S ribosomal protein L5

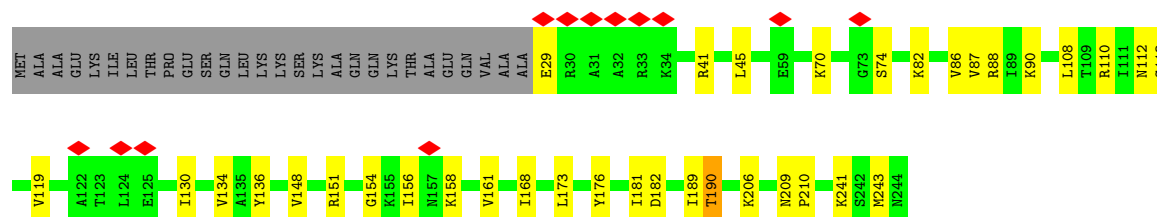
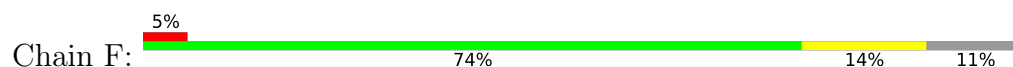




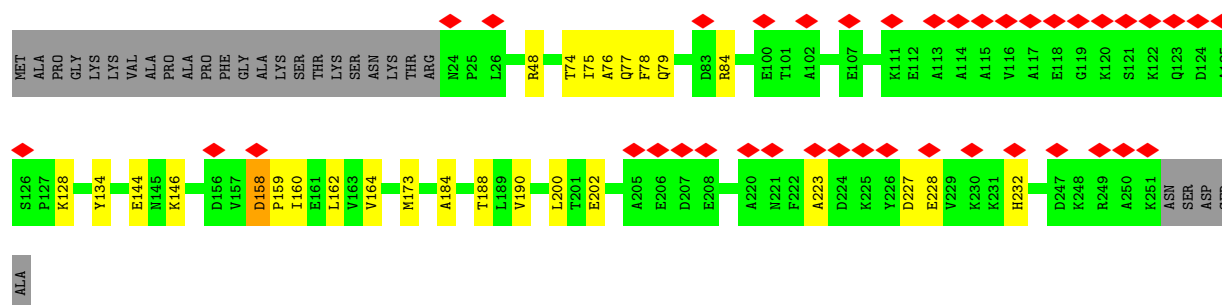
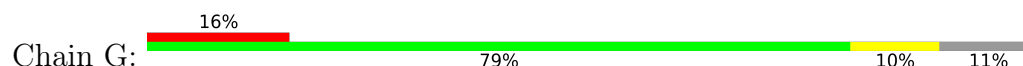
• Molecule 10: 60S ribosomal protein L6-A



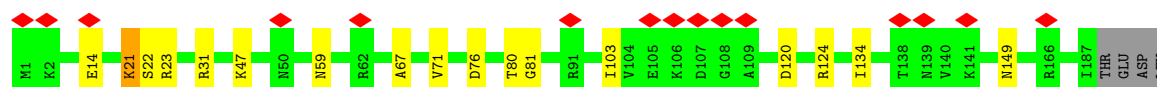
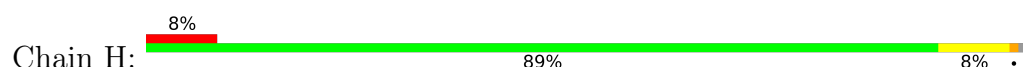
• Molecule 11: 60S ribosomal protein L7-A



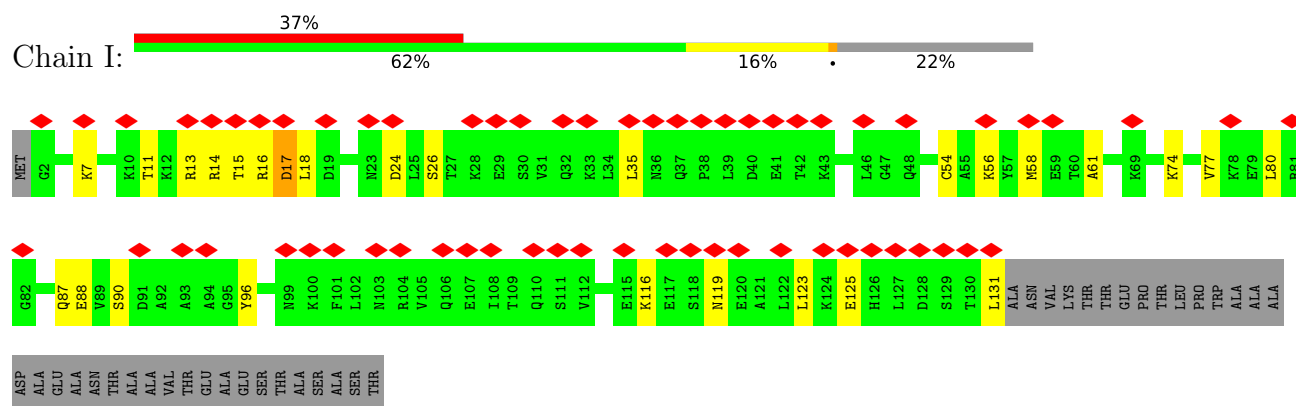
• Molecule 12: 60S ribosomal protein L8-A



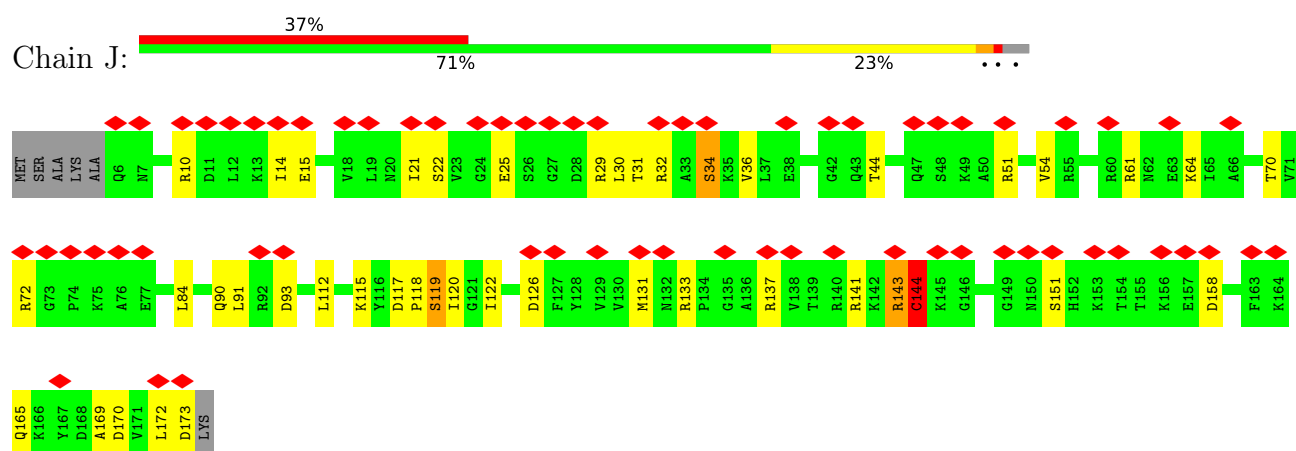
• Molecule 13: 60S ribosomal protein L9-A



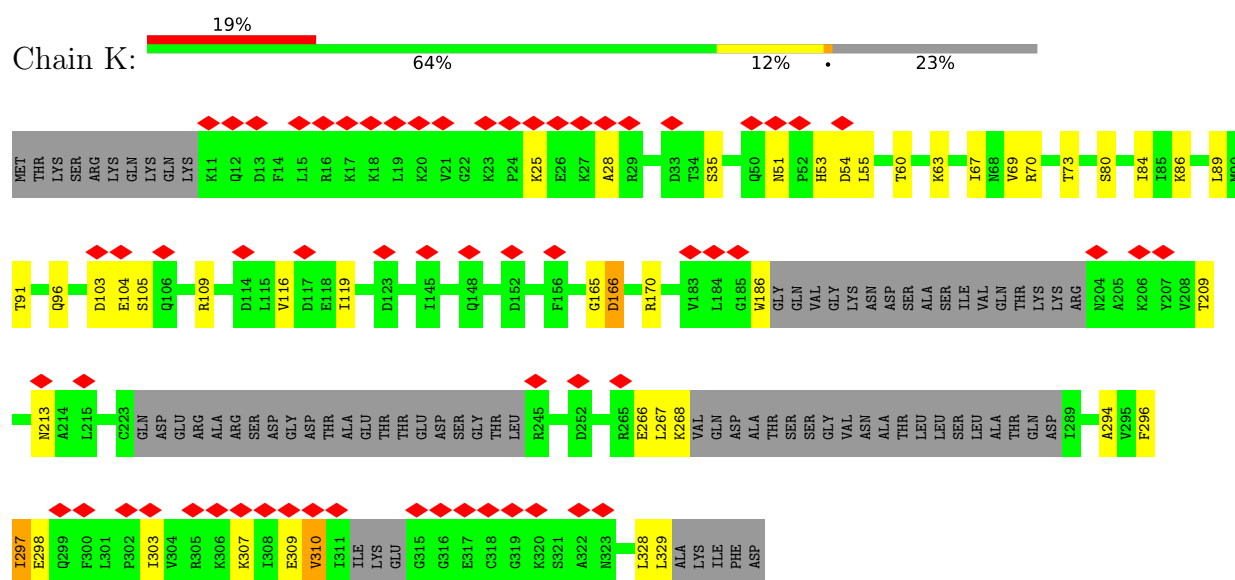
- Molecule 14: Bud site selection protein 20



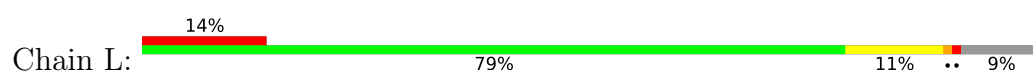
- Molecule 15: 60S ribosomal protein L11-A

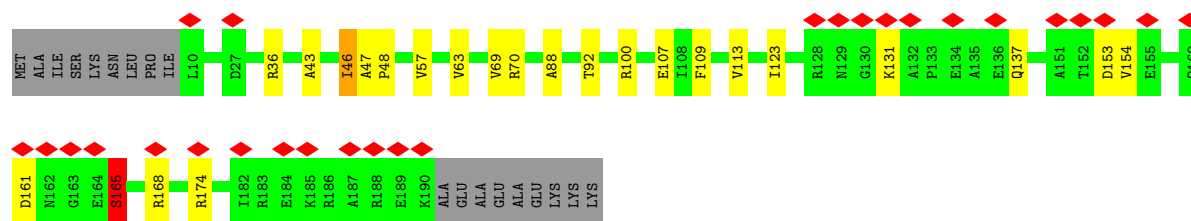


- Molecule 16: Pre-rRNA-processing protein IPI1

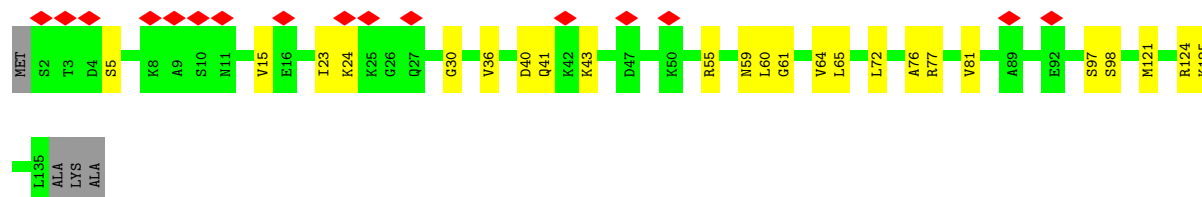
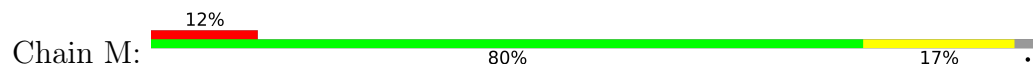


- Molecule 17: 60S ribosomal protein L13-A

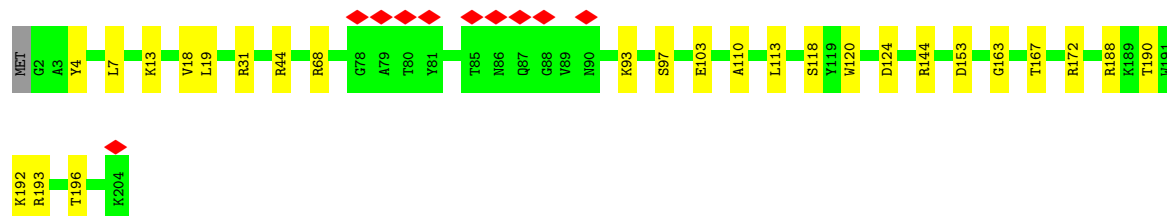
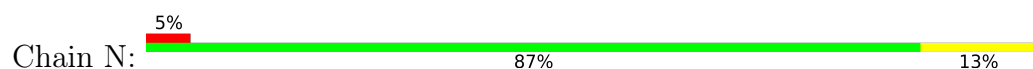




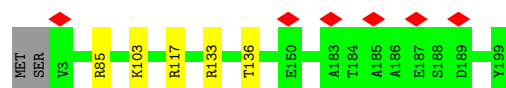
- Molecule 18: 60S ribosomal protein L14-A



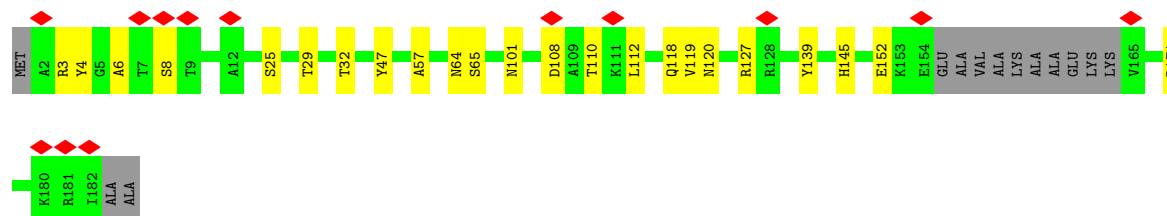
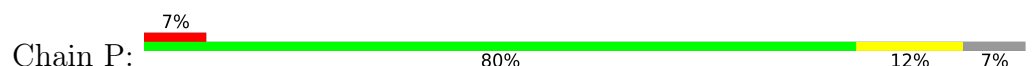
- Molecule 19: 60S ribosomal protein L15-A



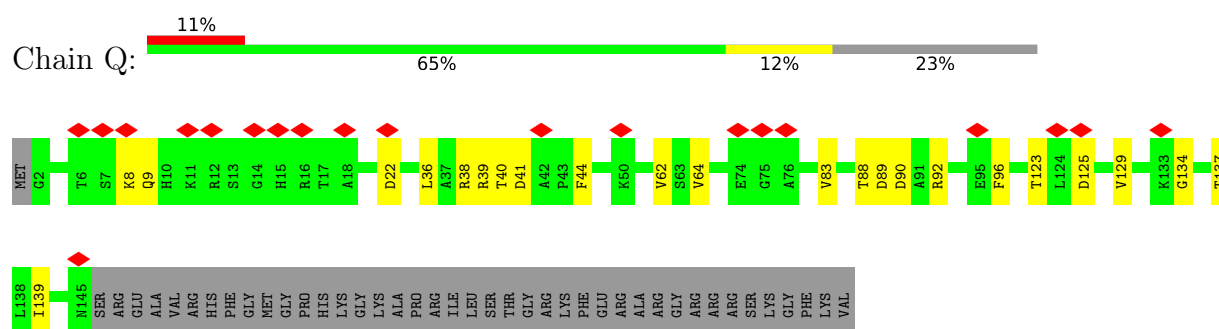
- Molecule 20: 60S ribosomal protein L16-A



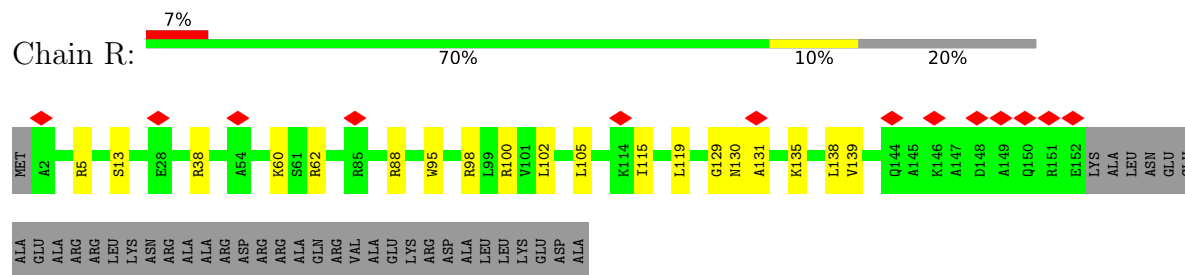
- Molecule 21: 60S ribosomal protein L17-A



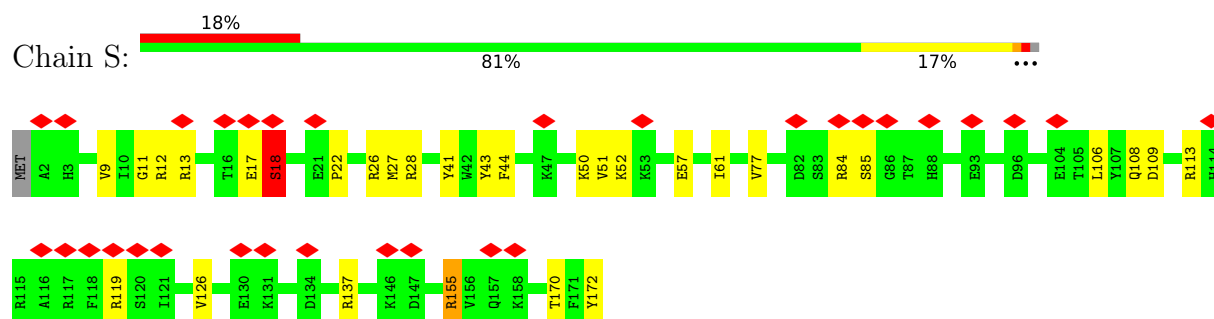
- Molecule 22: 60S ribosomal protein L18-A



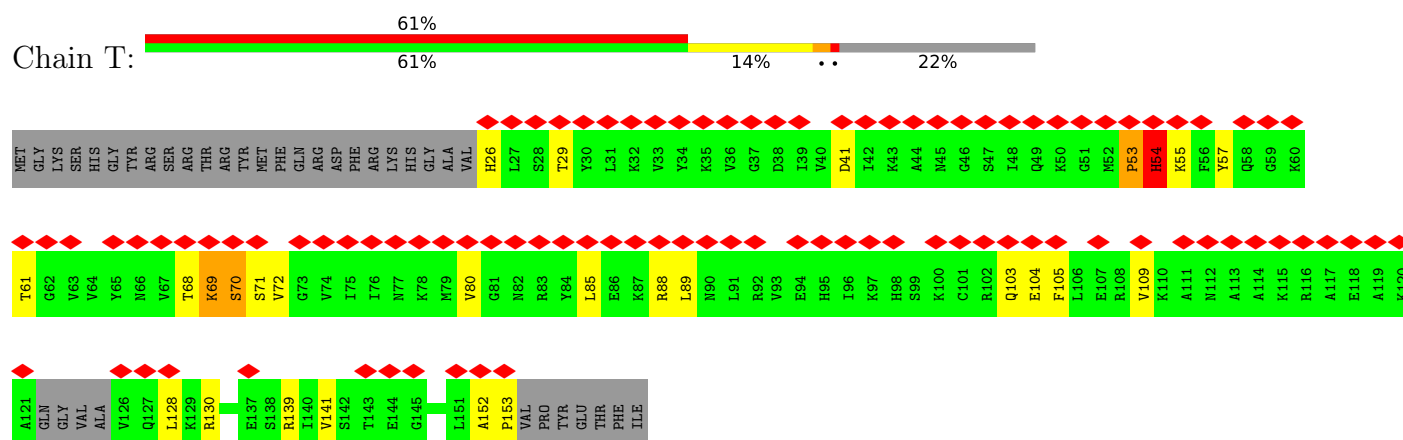
• Molecule 23: 60S ribosomal protein L19-A



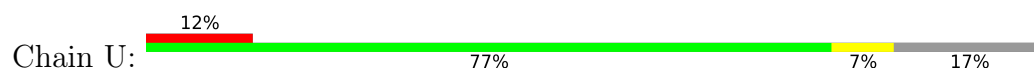
• Molecule 24: 60S ribosomal protein L20-A

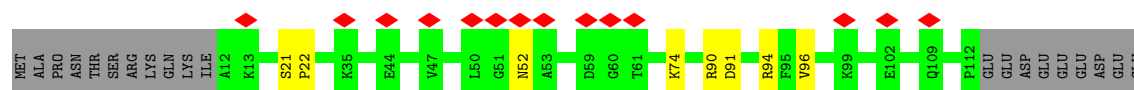


• Molecule 25: 60S ribosomal protein L21-A

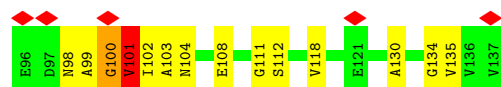
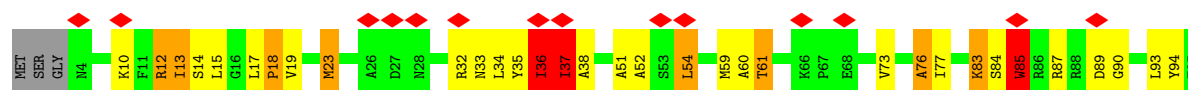


• Molecule 26: 60S ribosomal protein L22-A

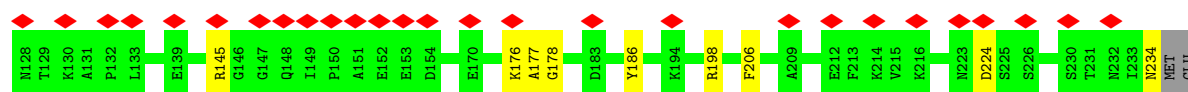
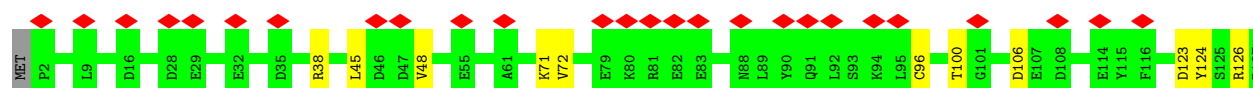




- Molecule 27: 60S ribosomal protein L23-A



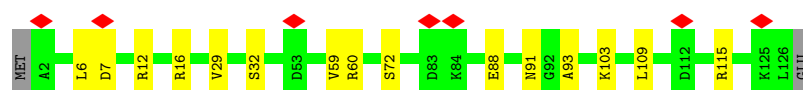
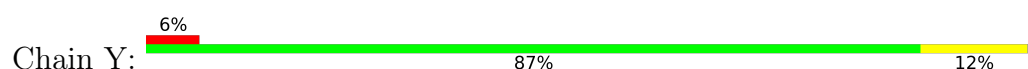
- Molecule 28: Ribosome assembly factor MRT4



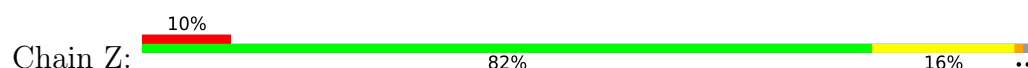
- Molecule 29: 60S ribosomal protein L25



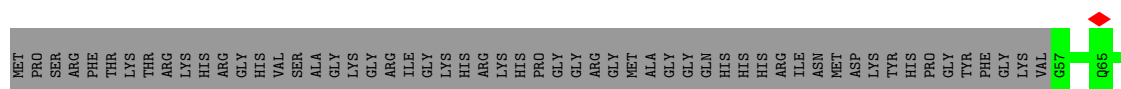
- Molecule 30: 60S ribosomal protein L26-A



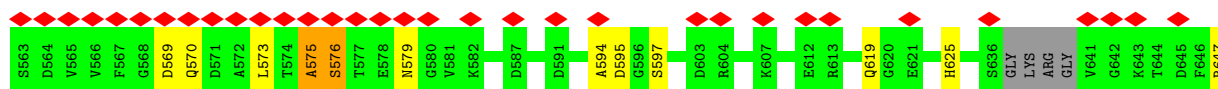
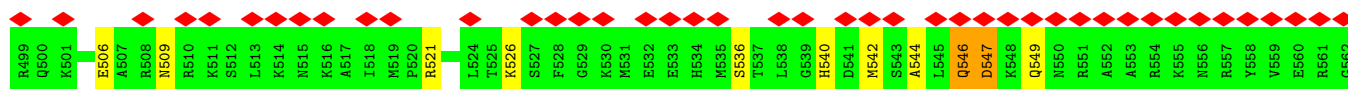
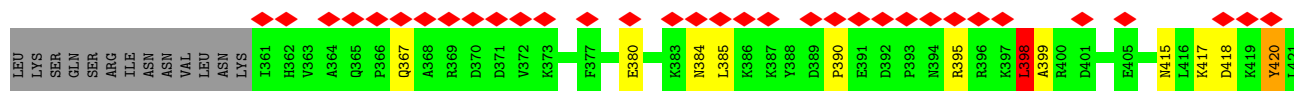
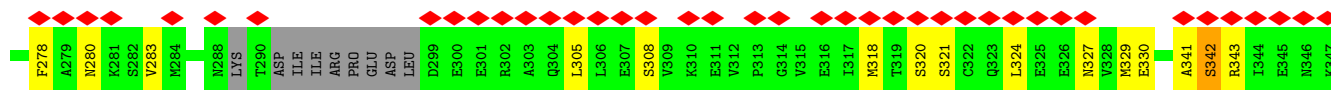
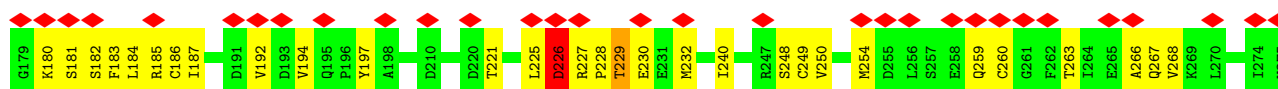
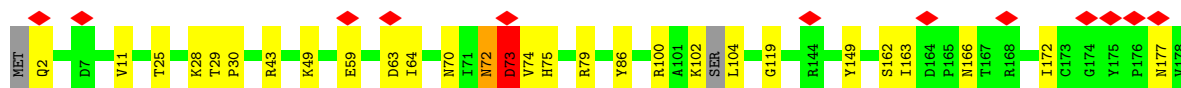
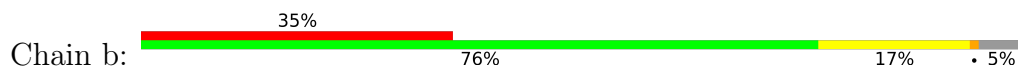
- Molecule 31: 60S ribosomal protein L27-A



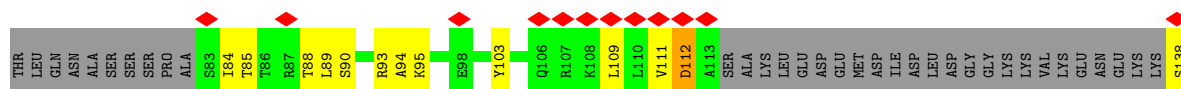
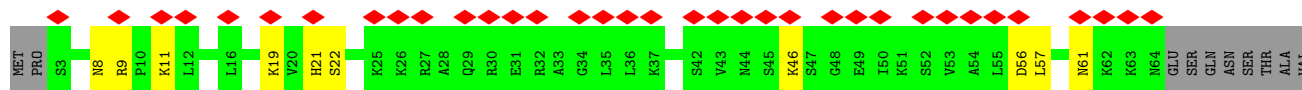
- Molecule 32: 60S ribosomal protein L28

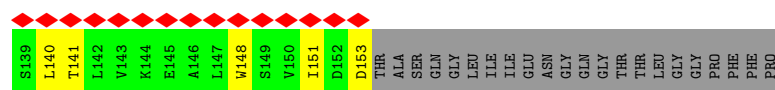


• Molecule 33: Nucleolar GTP-binding protein 1

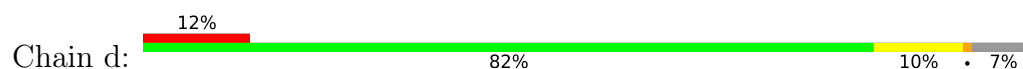


• Molecule 34: Ribosome biogenesis protein ALB1

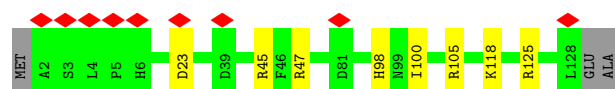




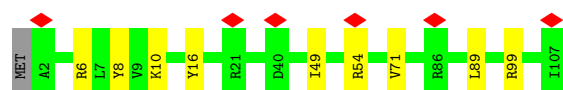
- Molecule 35: 60S ribosomal protein L31-A



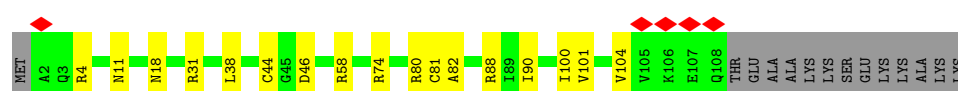
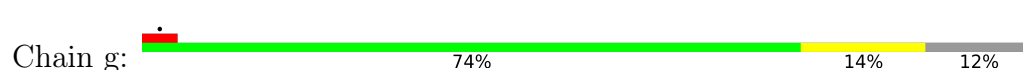
- Molecule 36: 60S ribosomal protein L32



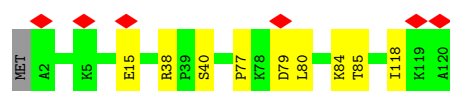
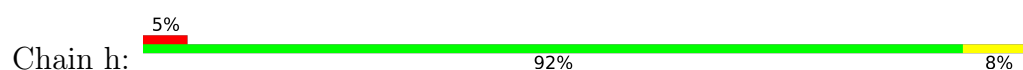
- Molecule 37: 60S ribosomal protein L33-A



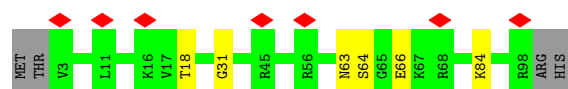
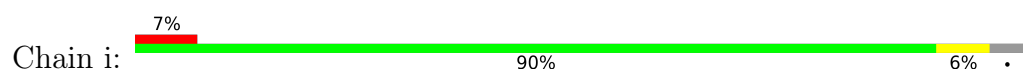
- Molecule 38: 60S ribosomal protein L34-A



- Molecule 39: 60S ribosomal protein L35-A



- Molecule 40: 60S ribosomal protein L36-A



- Molecule 41: 60S ribosomal protein L37-A

Chain j:  89% 7% 5%



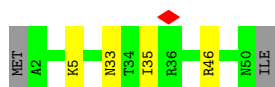
- Molecule 42: 60S ribosomal protein L38

Chain k:  32% 88% 9% ..



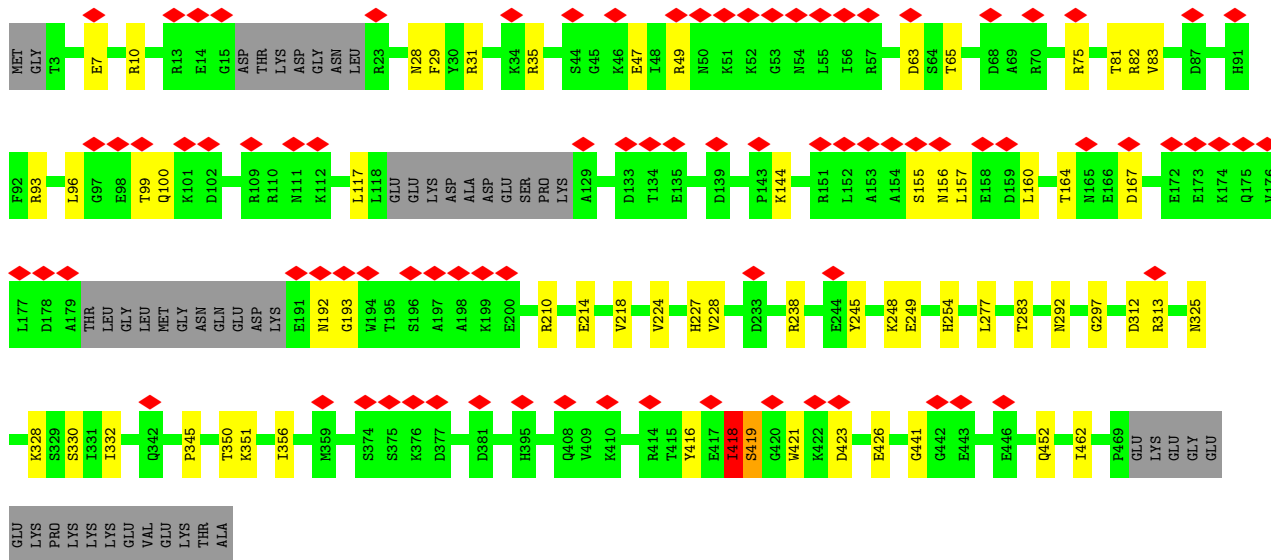
- Molecule 43: 60S ribosomal protein L39

Chain l:  88% 8% .



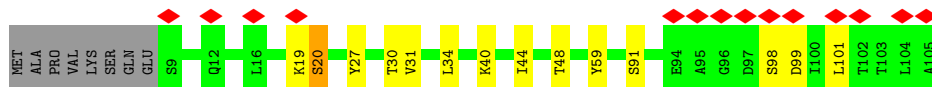
- Molecule 44: Nucleolar GTP-binding protein 2

Chain m:  17% 78% 12% 10%

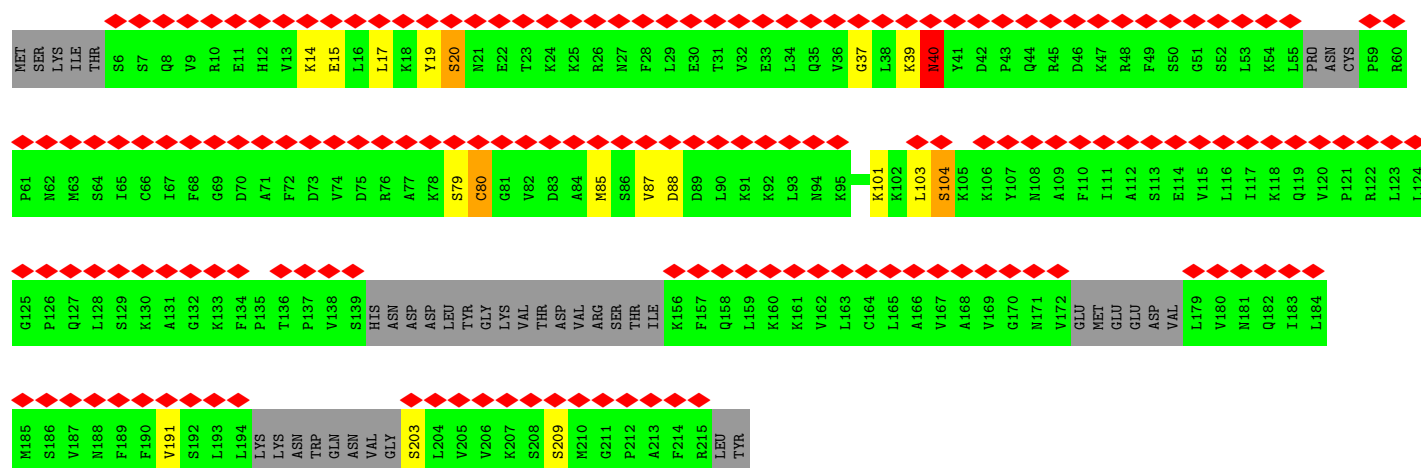
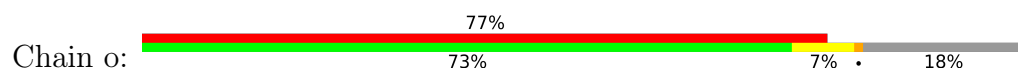


- Molecule 45: 60S ribosomal protein L30

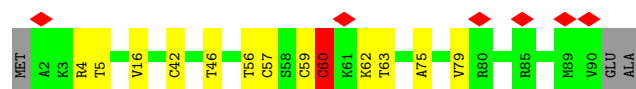
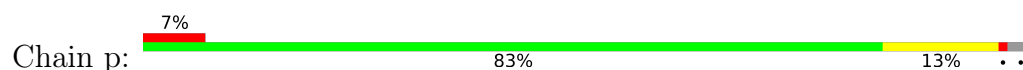
Chain n:  13% 79% 12% 8%



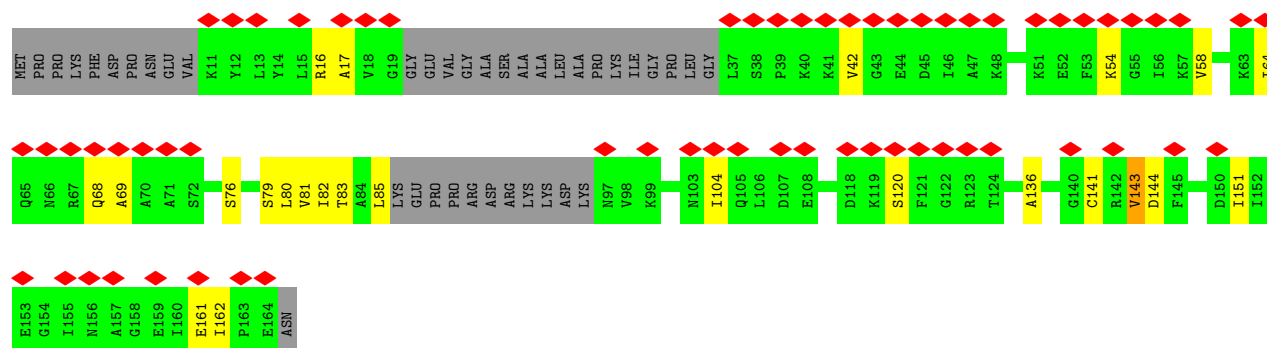
- Molecule 46: 60S ribosomal protein L1-A



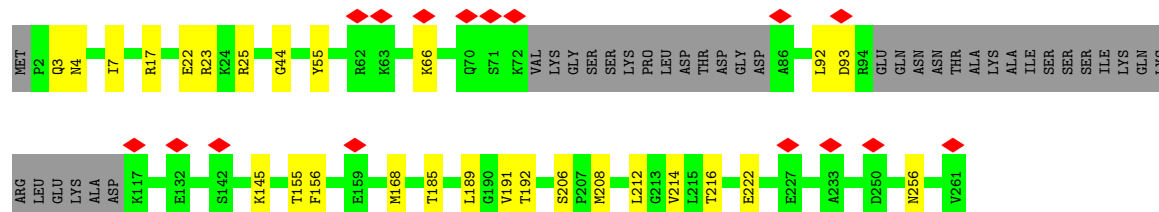
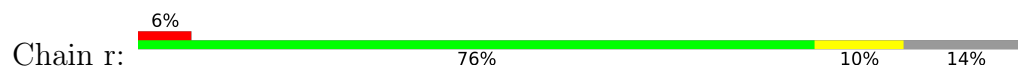
• Molecule 47: 60S ribosomal protein L43-A



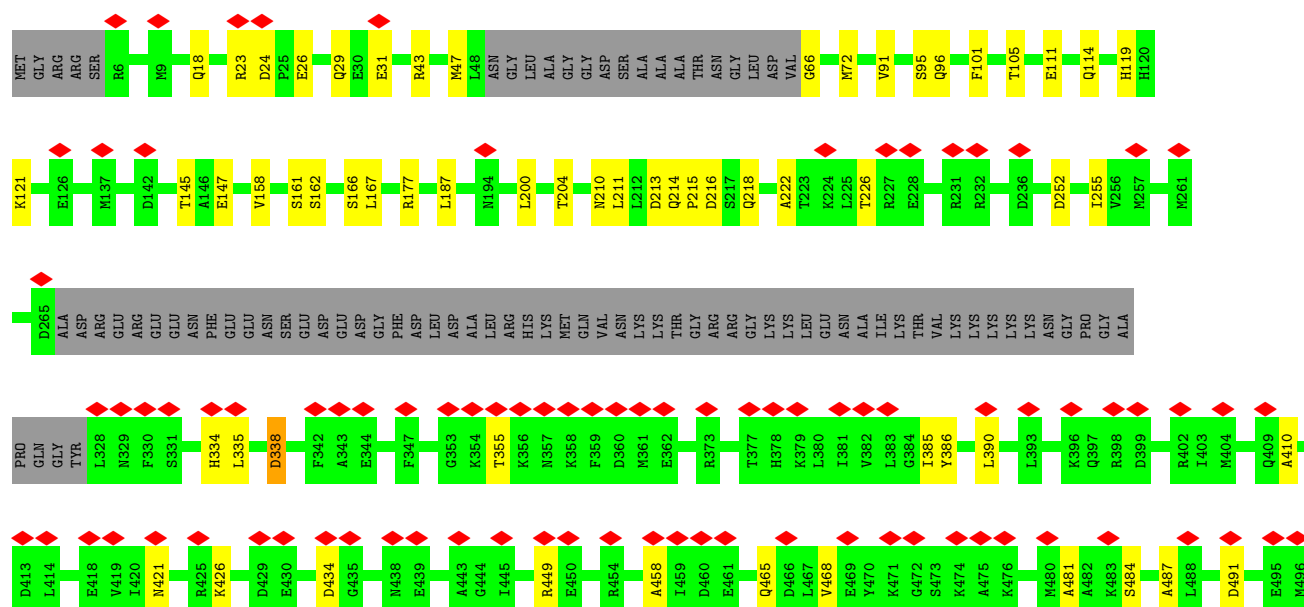
• Molecule 48: 60S ribosomal protein L12-A



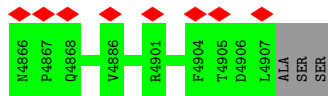
• Molecule 49: Ribosome biogenesis protein NSA2



Chain s: 8% 10% 89%

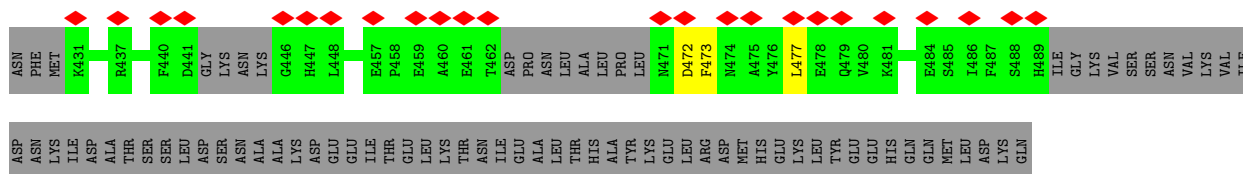




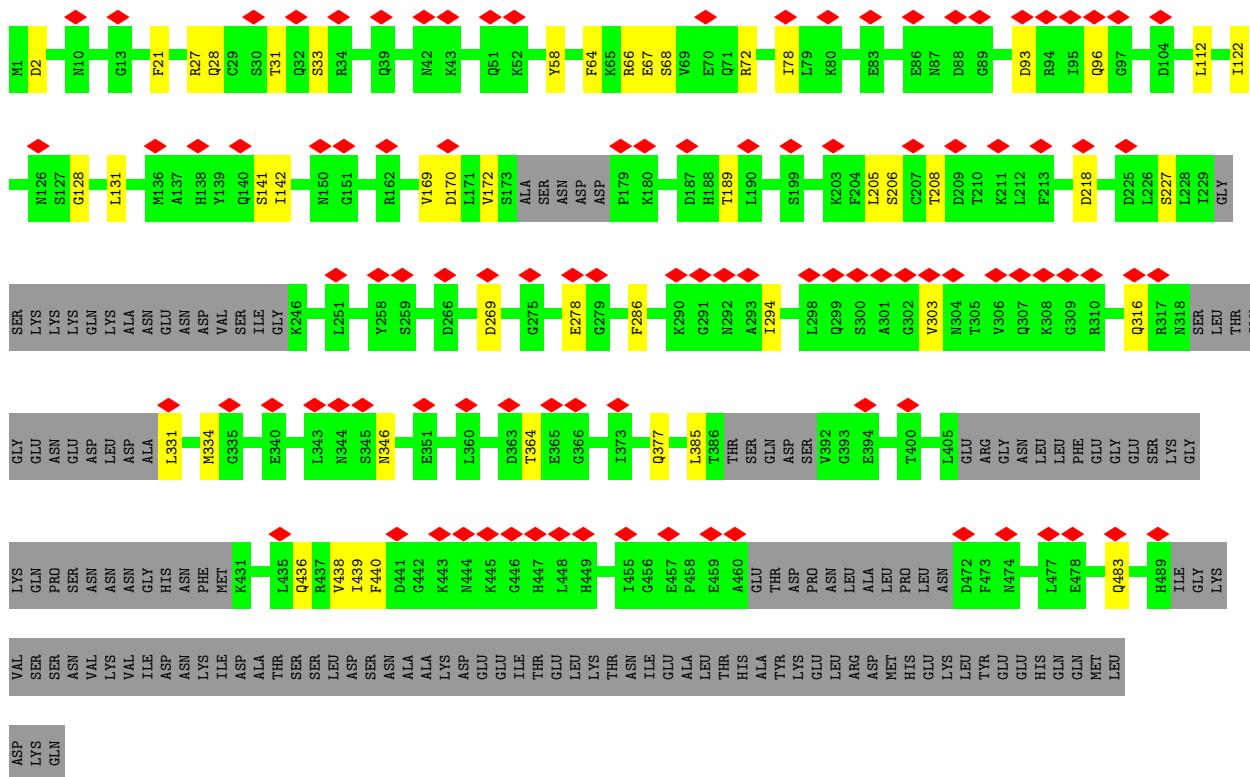


Chain w: 27% 64% 8% 28%





• Molecule 57: Pre-rRNA-processing protein IPI3



LYS	LYS	ALA	VAL	SER	GLN	THR	LYS	GLU	GLU	GLU	LYS	PRO	MET	GLU	ASP	SER	GLU	ASP	GLU	GLU	GLN	GLU	GLU	PHE	GLU	ILE	PRO	ALA	ILE	GLU	LEU	SER	ASP	ASP	GLU	GLU	GLU	GLU	GLU	GLU	GLU
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	114398	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	75	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.138	Depositor
Minimum map value	-0.036	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.025	Depositor
Map size ($\text{\AA}$)	635.4, 635.4, 635.4	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.059, 1.059, 1.059	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	1	0.18	1/72767 (0.0%)	0.36	27/113396 (0.0%)
2	2	0.17	0/3657	0.33	0/5692
3	3	0.13	0/2787	0.29	0/4339
4	4	0.21	0/4015	0.69	13/5447 (0.2%)
5	5	0.24	0/685	0.71	3/895 (0.3%)
6	A	0.26	0/1897	0.57	3/2550 (0.1%)
7	B	0.28	0/3152	0.71	5/4239 (0.1%)
8	C	0.24	0/2801	0.54	0/3792
9	D	0.21	0/2013	0.64	9/2715 (0.3%)
10	E	0.22	0/1260	0.59	5/1694 (0.3%)
11	F	0.23	0/1781	0.55	0/2396
12	G	0.25	0/1816	0.54	1/2450 (0.0%)
13	H	0.22	0/1507	0.53	0/2029
14	I	0.22	0/1067	0.67	2/1433 (0.1%)
15	J	0.23	0/1365	0.75	10/1831 (0.5%)
16	K	0.23	0/2125	0.68	9/2862 (0.3%)
17	L	0.26	0/1480	0.61	1/1986 (0.1%)
18	M	0.22	0/1055	0.53	2/1421 (0.1%)
19	N	0.26	0/1757	0.53	0/2354
20	O	0.24	0/1585	0.53	2/2128 (0.1%)
21	P	0.26	0/1382	0.49	0/1856
22	Q	0.24	0/1127	0.48	0/1521
23	R	0.25	0/1236	0.52	2/1650 (0.1%)
24	S	0.25	0/1473	0.61	2/1980 (0.1%)
25	T	0.23	0/997	0.71	3/1336 (0.2%)
26	U	0.22	0/817	0.54	0/1109
27	V	0.39	0/1008	1.50	25/1356 (1.8%)
28	W	0.21	0/1910	0.53	0/2575
29	X	0.22	0/1108	0.48	0/1492
30	Y	0.23	0/995	0.58	2/1329 (0.2%)
31	Z	0.25	0/1118	0.61	1/1497 (0.1%)
32	a	0.23	0/751	0.57	0/1013

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	b	0.23	0/5032	0.80	30/6756 (0.4%)
34	c	0.20	0/879	0.65	6/1171 (0.5%)
35	d	0.23	0/870	0.61	3/1168 (0.3%)
36	e	0.22	0/1041	0.43	0/1394
37	f	0.25	0/868	0.45	0/1168
38	g	0.25	0/856	0.56	0/1144
39	h	0.23	0/978	0.47	0/1301
40	i	0.23	0/749	0.61	2/995 (0.2%)
41	j	0.25	0/680	0.52	0/901
42	k	0.24	0/618	0.49	0/826
43	l	0.27	0/435	0.49	0/577
44	m	0.24	0/3617	0.67	5/4870 (0.1%)
45	n	0.19	0/751	0.59	3/1008 (0.3%)
46	o	0.20	0/872	0.97	13/1208 (1.1%)
47	p	0.23	0/687	0.51	0/915
48	q	0.23	0/969	0.59	0/1301
49	r	0.26	0/1850	0.60	0/2472
50	s	0.21	0/467	0.65	1/609 (0.2%)
51	t	0.19	0/3447	0.54	6/4643 (0.1%)
52	u	0.24	0/1269	0.83	5/1687 (0.3%)
53	x	0.22	0/3457	0.55	6/4691 (0.1%)
54	y	0.31	0/1864	1.35	41/2538 (1.6%)
55	z	0.19	0/650	0.56	0/854
56	v	0.30	0/17970	0.68	3/25013 (0.0%)
57	0	0.40	0/3312	0.65	1/4487 (0.0%)
57	w	0.36	0/3187	0.60	0/4316
58	6	0.39	0/4443	0.61	1/6029 (0.0%)
58	7	0.37	0/4472	0.58	0/6067
All	All	0.24	1/190784 (0.0%)	0.55	253/274472 (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
4	4	0	4
5	5	0	3
6	A	0	4
7	B	0	3
9	D	0	3
10	E	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
11	F	0	2
12	G	0	2
13	H	0	1
14	I	0	1
15	J	0	3
16	K	0	3
17	L	0	1
18	M	0	1
24	S	0	4
25	T	0	4
27	V	0	7
28	W	0	1
30	Y	0	1
31	Z	0	2
33	b	0	11
34	c	0	1
40	i	0	1
42	k	0	2
44	m	0	1
45	n	0	1
46	o	0	6
47	p	0	1
48	q	0	2
49	r	0	1
52	u	0	1
54	y	0	5
56	v	0	14
57	0	0	1
57	w	0	1
58	6	0	2
All	All	0	102

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2318	U	C1'-N1	6.74	1.57	1.47

The worst 5 of 253 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	b	385	LEU	CA-C-N	16.00	144.75	122.19
33	b	385	LEU	C-N-CA	16.00	144.75	122.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	V	23	MET	CA-C-N	12.56	138.55	120.71
27	V	23	MET	C-N-CA	12.56	138.55	120.71
52	u	23	ARG	CA-C-N	12.38	140.41	120.60

There are no chirality outliers.

5 of 102 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	4	329	CYS	Mainchain
4	4	362	ARG	Peptide
4	4	461	ASP	Mainchain
4	4	463	THR	Peptide
5	5	42	THR	Mainchain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	65028	0	32701	304	0
2	2	3273	0	1654	7	0
3	3	2494	0	1262	19	0
4	4	3945	0	4016	99	0
5	5	681	0	732	11	0
6	A	1863	0	1930	18	0
7	B	3081	0	3165	29	0
8	C	2749	0	2863	24	0
9	D	1969	0	1926	62	0
10	E	1239	0	1326	11	0
11	F	1744	0	1824	25	0
12	G	1784	0	1883	22	0
13	H	1486	0	1559	15	0
14	I	1051	0	1077	14	0
15	J	1344	0	1370	38	0
16	K	2089	0	2192	45	0
17	L	1456	0	1517	23	0
18	M	1040	0	1131	18	0
19	N	1720	0	1779	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	O	1555	0	1659	4	0
21	P	1360	0	1394	27	0
22	Q	1110	0	1190	19	0
23	R	1219	0	1300	22	0
24	S	1437	0	1475	22	0
25	T	983	0	1037	41	0
26	U	800	0	811	5	0
27	V	993	0	1040	54	0
28	W	1877	0	1910	11	0
29	X	1092	0	1176	8	0
30	Y	984	0	1075	9	0
31	Z	1092	0	1155	17	0
32	a	735	0	776	10	0
33	b	4953	0	4993	108	0
34	c	872	0	940	25	0
35	d	856	0	904	7	0
36	e	1020	0	1090	7	0
37	f	850	0	880	7	0
38	g	846	0	910	14	0
39	h	969	0	1078	6	0
40	i	743	0	822	3	0
41	j	665	0	668	5	0
42	k	612	0	682	20	0
43	l	428	0	464	3	0
44	m	3546	0	3627	54	0
45	n	743	0	797	8	0
46	o	877	0	377	6	0
47	p	680	0	724	13	0
48	q	961	0	1010	15	0
49	r	1818	0	1925	18	0
50	s	463	0	522	3	0
51	t	3395	0	3495	69	0
52	u	1247	0	1299	13	0
53	x	3385	0	3125	44	0
54	y	1841	0	1824	57	0
55	z	643	0	693	9	0
56	v	18010	0	7839	53	0
57	0	3260	0	3302	64	0
57	w	3139	0	3169	35	0
58	6	4352	0	4525	37	0
58	7	4380	0	4554	58	0
59	I	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	j	1	0	0	0	0
59	p	1	0	0	0	0
59	u	1	0	0	0	0
60	b	32	0	12	2	0
60	m	32	0	12	3	0
61	b	1	0	0	0	0
61	m	1	0	0	0	0
All	All	180897	0	138167	1483	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 5.

The worst 5 of 1483 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)
56:v:921:LYS:CB	57:0:438:VAL:C	1.80	1.52
51:t:121:LYS:CD	57:0:21:PHE:O	1.66	1.43
16:K:268:LYS:H	51:t:114:GLN:CG	1.14	1.35
1:1:2458:A:N3	58:7:147:LYS:HE3	1.41	1.32
1:1:2458:A:N3	58:7:147:LYS:CE	1.91	1.31

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	
4	4	495/593 (84%)	456 (92%)	34 (7%)	5 (1%)	12	41
5	5	76/120 (63%)	71 (93%)	5 (7%)	0	100	100
6	A	243/254 (96%)	227 (93%)	16 (7%)	0	100	100
7	B	384/387 (99%)	342 (89%)	41 (11%)	1 (0%)	36	67

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	C	359/362 (99%)	336 (94%)	21 (6%)	2 (1%)	21	52
9	D	239/297 (80%)	218 (91%)	21 (9%)	0	100	100
10	E	152/176 (86%)	148 (97%)	4 (3%)	0	100	100
11	F	214/244 (88%)	195 (91%)	19 (9%)	0	100	100
12	G	226/256 (88%)	209 (92%)	17 (8%)	0	100	100
13	H	185/191 (97%)	172 (93%)	13 (7%)	0	100	100
14	I	128/166 (77%)	113 (88%)	13 (10%)	2 (2%)	7	30
15	J	166/174 (95%)	145 (87%)	20 (12%)	1 (1%)	21	52
16	K	248/334 (74%)	231 (93%)	15 (6%)	2 (1%)	16	47
17	L	179/199 (90%)	165 (92%)	12 (7%)	2 (1%)	11	39
18	M	132/138 (96%)	126 (96%)	6 (4%)	0	100	100
19	N	201/204 (98%)	187 (93%)	14 (7%)	0	100	100
20	O	195/199 (98%)	194 (100%)	1 (0%)	0	100	100
21	P	167/184 (91%)	155 (93%)	12 (7%)	0	100	100
22	Q	142/186 (76%)	131 (92%)	11 (8%)	0	100	100
23	R	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
24	S	169/172 (98%)	156 (92%)	10 (6%)	3 (2%)	6	28
25	T	120/160 (75%)	115 (96%)	5 (4%)	0	100	100
26	U	99/121 (82%)	95 (96%)	4 (4%)	0	100	100
27	V	132/137 (96%)	120 (91%)	10 (8%)	2 (2%)	8	32
28	W	231/236 (98%)	225 (97%)	4 (2%)	2 (1%)	14	44
29	X	138/142 (97%)	130 (94%)	8 (6%)	0	100	100
30	Y	123/127 (97%)	119 (97%)	4 (3%)	0	100	100
31	Z	133/136 (98%)	118 (89%)	15 (11%)	0	100	100
32	a	91/149 (61%)	84 (92%)	5 (6%)	2 (2%)	5	24
33	b	600/647 (93%)	538 (90%)	58 (10%)	4 (1%)	18	49
34	c	103/175 (59%)	99 (96%)	4 (4%)	0	100	100
35	d	103/113 (91%)	100 (97%)	3 (3%)	0	100	100
36	e	125/130 (96%)	122 (98%)	3 (2%)	0	100	100
37	f	104/107 (97%)	103 (99%)	1 (1%)	0	100	100
38	g	105/121 (87%)	104 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	h	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
40	i	94/100 (94%)	85 (90%)	8 (8%)	1 (1%)	11	39
41	j	82/88 (93%)	80 (98%)	2 (2%)	0	100	100
42	k	75/78 (96%)	71 (95%)	4 (5%)	0	100	100
43	l	47/51 (92%)	44 (94%)	3 (6%)	0	100	100
44	m	431/486 (89%)	390 (90%)	38 (9%)	3 (1%)	18	49
45	n	95/105 (90%)	92 (97%)	3 (3%)	0	100	100
46	o	167/217 (77%)	145 (87%)	22 (13%)	0	100	100
47	p	87/92 (95%)	84 (97%)	2 (2%)	1 (1%)	11	39
48	q	120/165 (73%)	101 (84%)	16 (13%)	3 (2%)	4	21
49	r	219/261 (84%)	197 (90%)	20 (9%)	2 (1%)	14	44
50	s	52/520 (10%)	47 (90%)	3 (6%)	2 (4%)	2	15
51	t	425/767 (55%)	399 (94%)	26 (6%)	0	100	100
52	u	146/199 (73%)	139 (95%)	7 (5%)	0	100	100
53	x	445/515 (86%)	417 (94%)	28 (6%)	0	100	100
54	y	241/245 (98%)	220 (91%)	20 (8%)	1 (0%)	30	61
55	z	73/106 (69%)	67 (92%)	6 (8%)	0	100	100
56	v	3549/4910 (72%)	3232 (91%)	313 (9%)	4 (0%)	48	78
57	0	401/555 (72%)	393 (98%)	8 (2%)	0	100	100
57	w	379/555 (68%)	375 (99%)	4 (1%)	0	100	100
58	6	535/763 (70%)	527 (98%)	8 (2%)	0	100	100
58	7	541/763 (71%)	533 (98%)	8 (2%)	0	100	100
All	All	14977/19187 (78%)	13942 (93%)	990 (7%)	45 (0%)	37	67

5 of 45 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	C	339	LEU
28	W	177	ALA
33	b	398	LEU
33	b	399	ALA
56	v	241	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	4	445/520 (86%)	445 (100%)	0	100	100
5	5	70/106 (66%)	70 (100%)	0	100	100
6	A	188/196 (96%)	188 (100%)	0	100	100
7	B	322/323 (100%)	321 (100%)	1 (0%)	86	87
8	C	288/289 (100%)	288 (100%)	0	100	100
9	D	205/245 (84%)	205 (100%)	0	100	100
10	E	134/153 (88%)	134 (100%)	0	100	100
11	F	183/205 (89%)	183 (100%)	0	100	100
12	G	187/208 (90%)	187 (100%)	0	100	100
13	H	167/171 (98%)	167 (100%)	0	100	100
14	I	116/141 (82%)	116 (100%)	0	100	100
15	J	146/150 (97%)	146 (100%)	0	100	100
16	K	238/302 (79%)	238 (100%)	0	100	100
17	L	145/159 (91%)	145 (100%)	0	100	100
18	M	107/109 (98%)	106 (99%)	1 (1%)	70	80
19	N	175/176 (99%)	175 (100%)	0	100	100
20	O	160/162 (99%)	160 (100%)	0	100	100
21	P	139/146 (95%)	139 (100%)	0	100	100
22	Q	118/151 (78%)	118 (100%)	0	100	100
23	R	125/154 (81%)	125 (100%)	0	100	100
24	S	155/156 (99%)	155 (100%)	0	100	100
25	T	107/137 (78%)	106 (99%)	1 (1%)	70	80
26	U	88/107 (82%)	87 (99%)	1 (1%)	65	78
27	V	103/105 (98%)	101 (98%)	2 (2%)	50	73
28	W	210/213 (99%)	210 (100%)	0	100	100
29	X	116/118 (98%)	116 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	Y	108/110 (98%)	108 (100%)	0	100	100
31	Z	115/116 (99%)	115 (100%)	0	100	100
32	a	76/119 (64%)	76 (100%)	0	100	100
33	b	541/573 (94%)	539 (100%)	2 (0%)	84	86
34	c	99/153 (65%)	99 (100%)	0	100	100
35	d	92/97 (95%)	92 (100%)	0	100	100
36	e	109/111 (98%)	109 (100%)	0	100	100
37	f	90/91 (99%)	90 (100%)	0	100	100
38	g	92/103 (89%)	92 (100%)	0	100	100
39	h	104/105 (99%)	104 (100%)	0	100	100
40	i	78/82 (95%)	78 (100%)	0	100	100
41	j	69/71 (97%)	69 (100%)	0	100	100
42	k	68/69 (99%)	68 (100%)	0	100	100
43	l	44/46 (96%)	44 (100%)	0	100	100
44	m	388/428 (91%)	385 (99%)	3 (1%)	73	81
45	n	81/88 (92%)	81 (100%)	0	100	100
47	p	70/72 (97%)	70 (100%)	0	100	100
48	q	105/136 (77%)	105 (100%)	0	100	100
49	r	198/229 (86%)	197 (100%)	1 (0%)	81	85
50	s	50/445 (11%)	50 (100%)	0	100	100
51	t	379/665 (57%)	379 (100%)	0	100	100
52	u	131/180 (73%)	130 (99%)	1 (1%)	73	81
53	x	338/451 (75%)	338 (100%)	0	100	100
54	y	209/211 (99%)	209 (100%)	0	100	100
55	z	69/95 (73%)	69 (100%)	0	100	100
57	0	375/497 (76%)	373 (100%)	2 (0%)	81	85
57	w	362/497 (73%)	362 (100%)	0	100	100
58	6	503/707 (71%)	500 (99%)	3 (1%)	78	83
58	7	505/707 (71%)	505 (100%)	0	100	100
All	All	9885/12156 (81%)	9867 (100%)	18 (0%)	85	89

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
57	0	316	GLN
58	6	397	LEU
58	6	269	GLN
44	m	28	ASN
57	0	78	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 80 such sidechains are listed below:

Mol	Chain	Res	Type
51	t	29	GLN
58	6	376	GLN
52	u	24	ASN
57	0	23	GLN
58	7	60	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3013/3396 (88%)	603 (20%)	26 (0%)
2	2	152/158 (96%)	27 (17%)	1 (0%)
3	3	115/121 (95%)	19 (16%)	1 (0%)
All	All	3280/3675 (89%)	649 (19%)	28 (0%)

5 of 649 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	13	A
1	1	14	U
1	1	18	G
1	1	26	A
1	1	30	G

5 of 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2318	U
3	3	52	G
1	1	2444	C
1	1	3042	U
1	1	2339	C

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 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	b	701	61	33,34,34	0.94	1 (3%)	50,54,54	1.65	8 (16%)
60	GTP	m	501	61	33,34,34	0.87	0	50,54,54	1.55	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	b	701	61	-	1/22/38/38	0/3/3/3
60	GTP	m	501	61	-	6/22/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	b	701	GTP	C2-N3	2.27	1.38	1.33

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	b	701	GTP	C5-C4-N3	-5.20	120.12	128.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	m	501	GTP	C5-C4-N3	-4.85	120.67	128.39
60	b	701	GTP	C2-N3-C4	4.61	120.24	112.30
60	m	501	GTP	C2-N3-C4	4.50	120.05	112.30
60	b	701	GTP	N9-C4-N3	3.47	132.89	125.95

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	b	701	GTP	C5'-O5'-PA-O1A
60	m	501	GTP	C5'-O5'-PA-O3A
60	m	501	GTP	C5'-O5'-PA-O2A
60	m	501	GTP	O4'-C4'-C5'-O5'
60	m	501	GTP	C3'-C4'-C5'-O5'

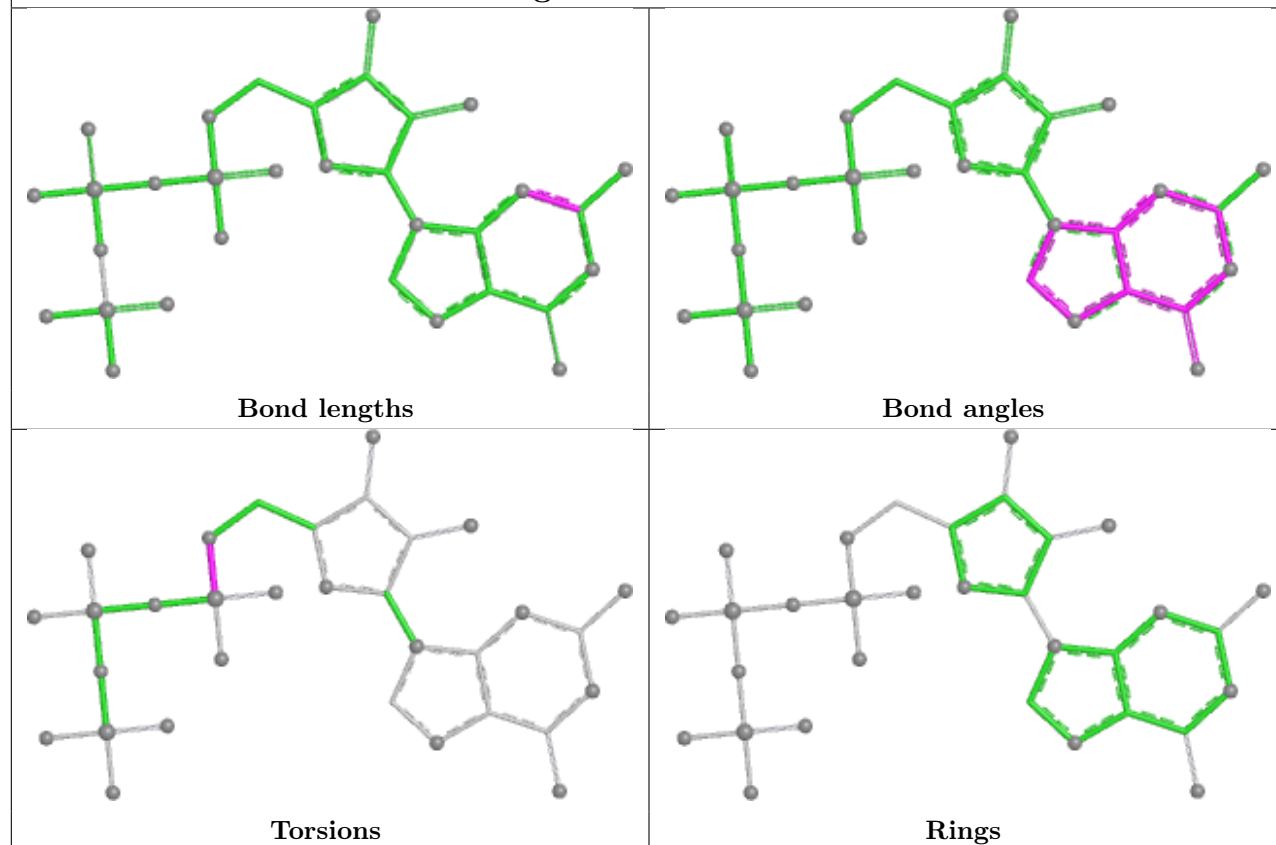
There are no ring outliers.

2 monomers are involved in 5 short contacts:

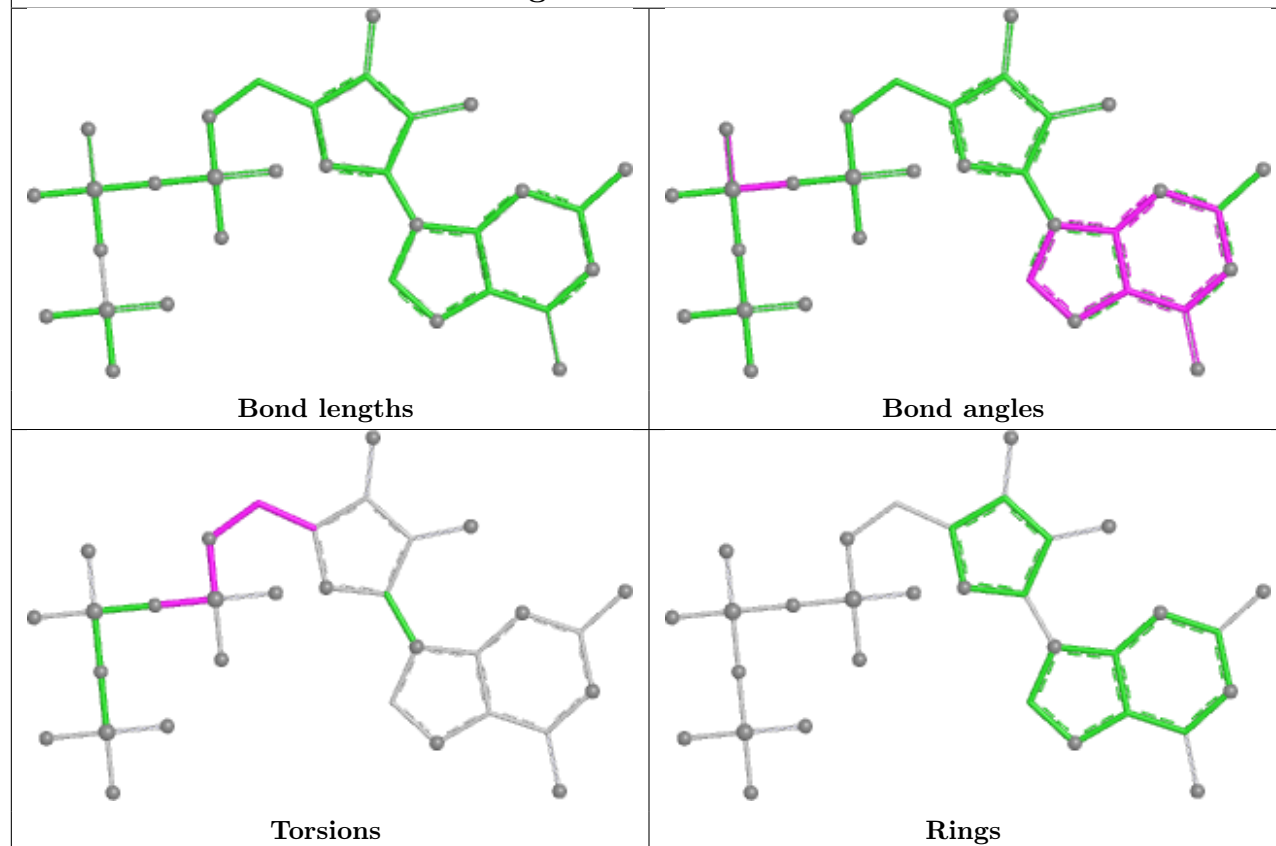
Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	b	701	GTP	2	0
60	m	501	GTP	3	0

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.

Ligand GTP b 701



Ligand GTP m 501



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
56	v	3
1	1	3

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	v	3595:LEU	C	3599:ARG	N	4.97
1	1	3167:A	O3'	3168:A	P	4.92
1	v	3575:LEU	C	3579:VAL	N	3.43
1	v	3587:MET	C	3591:ARG	N	3.23
1	1	1012:G	O3'	1013:G	P	3.13

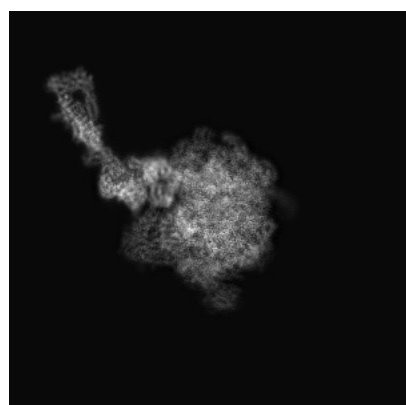
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10839. These allow visual inspection of the internal detail of the map and identification of artifacts.

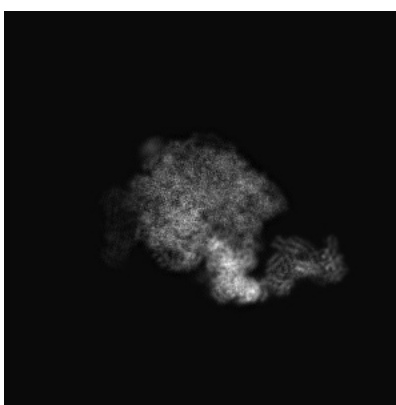
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

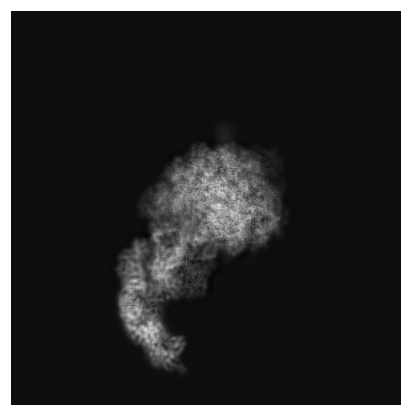
6.1.1 Primary map



X



Y

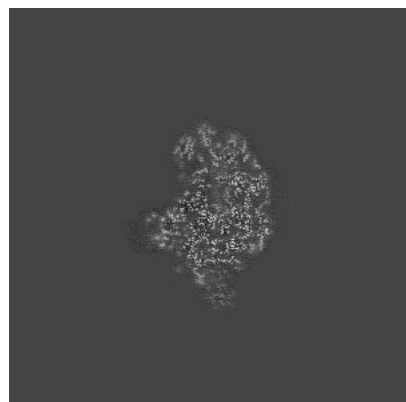


Z

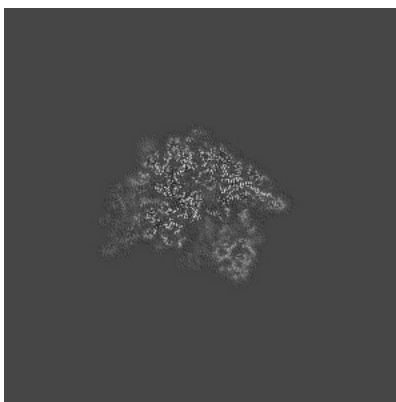
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

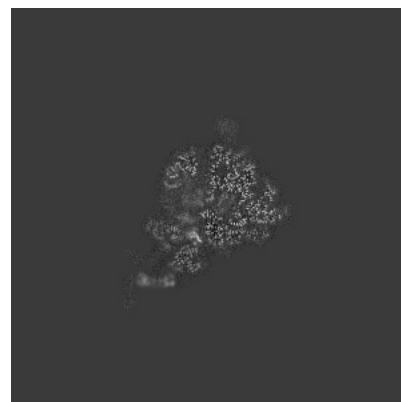
6.2.1 Primary map



X Index: 300



Y Index: 300



Z Index: 300

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

6.3 Largest variance slices [i](#)

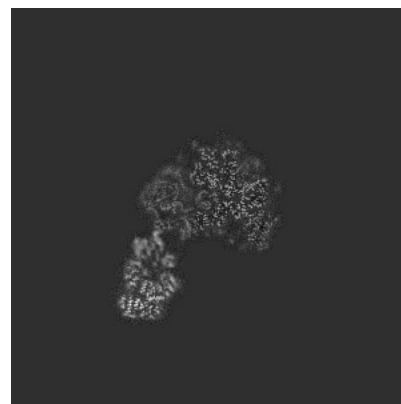
6.3.1 Primary map



X Index: 219



Y Index: 303

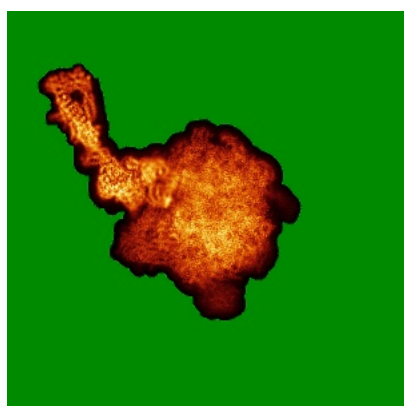


Z Index: 336

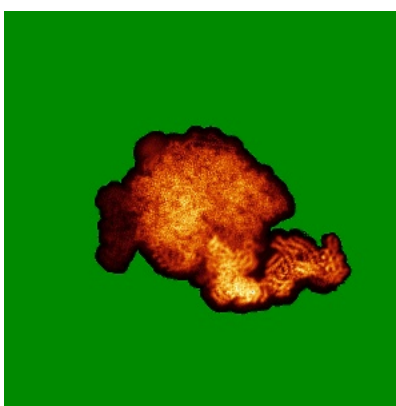
The images above show the largest variance slices of the map in three orthogonal directions.

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

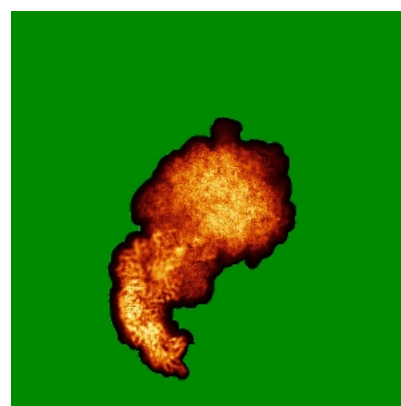
6.4.1 Primary map



X



Y

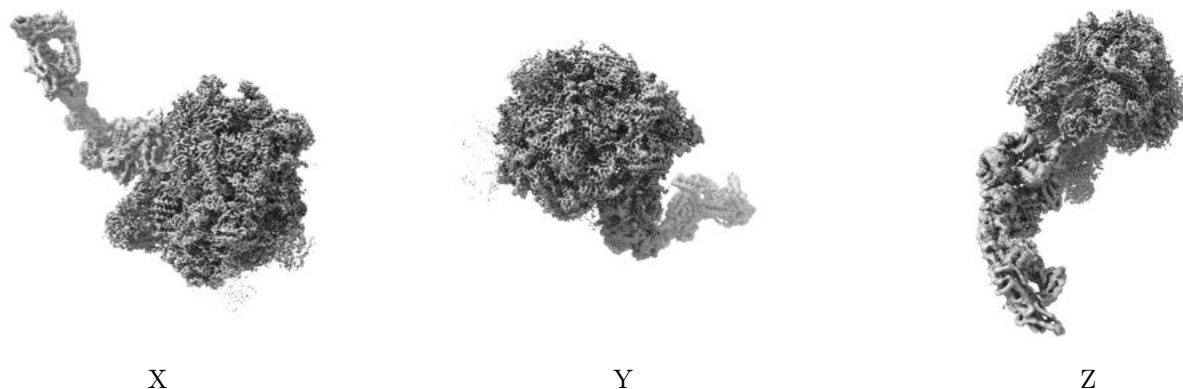


Z

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

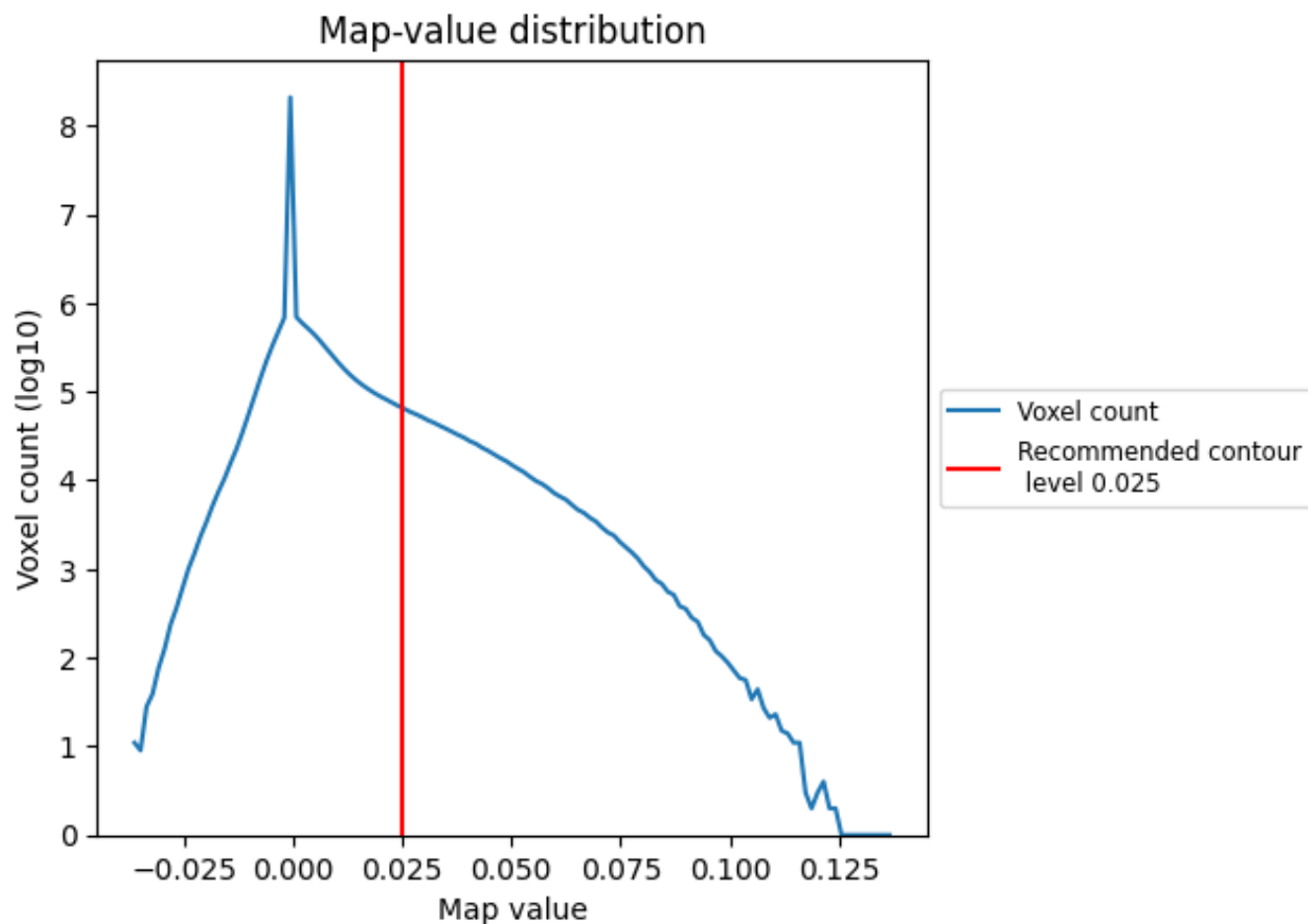
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

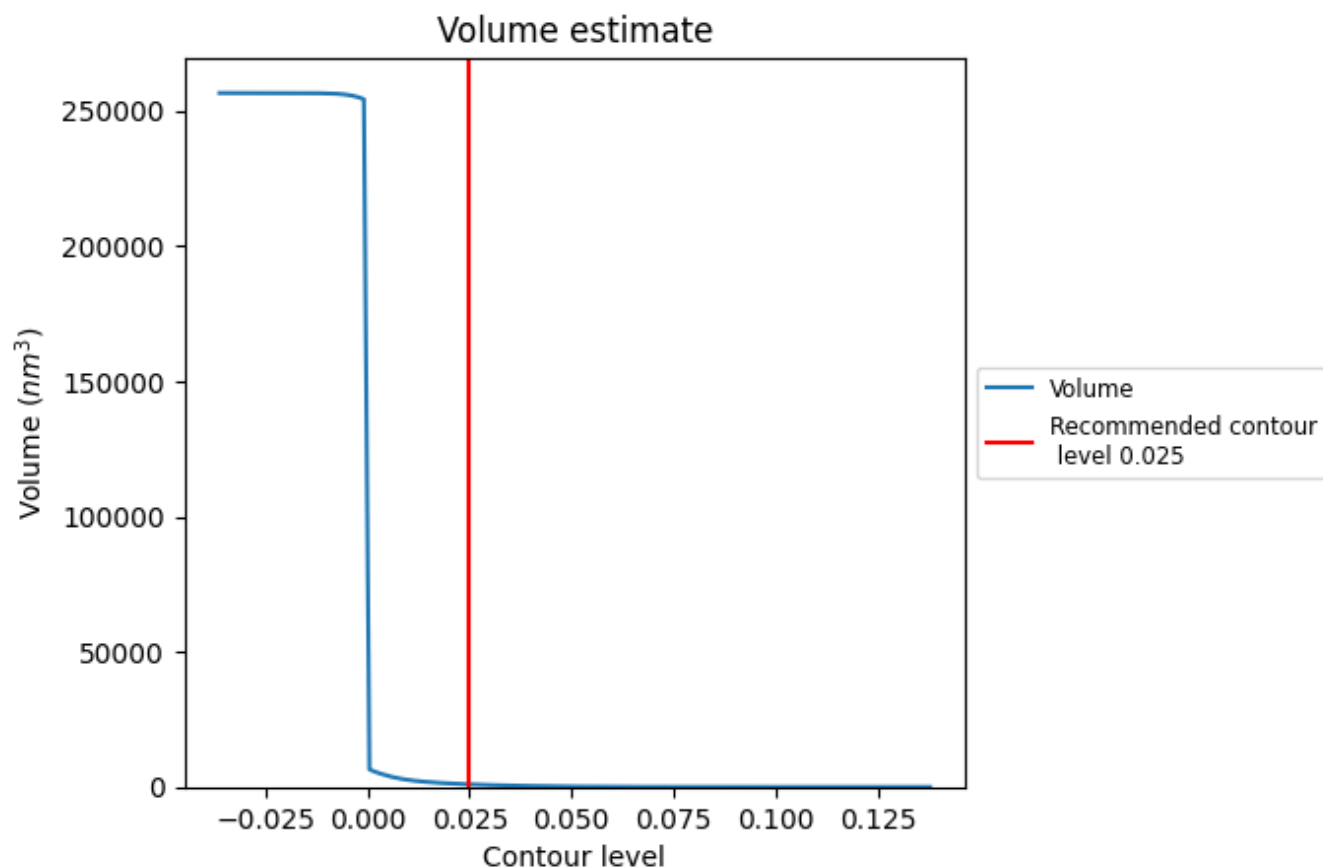
This section contains the results of statistical analysis of the map.

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.

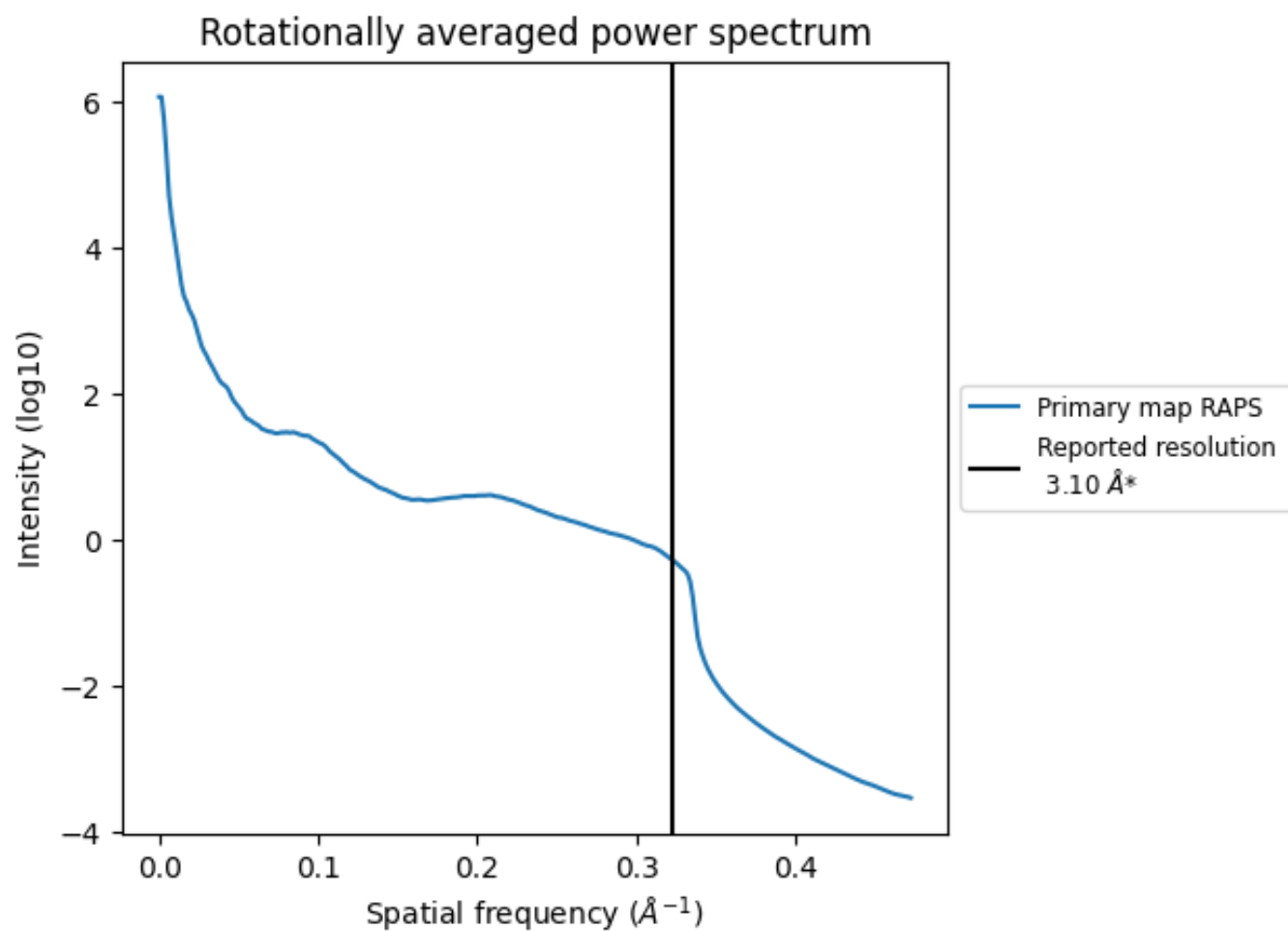
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 970 nm^3 ; this corresponds to an approximate mass of 876 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 0.323 Å⁻¹

8 Fourier-Shell correlation

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

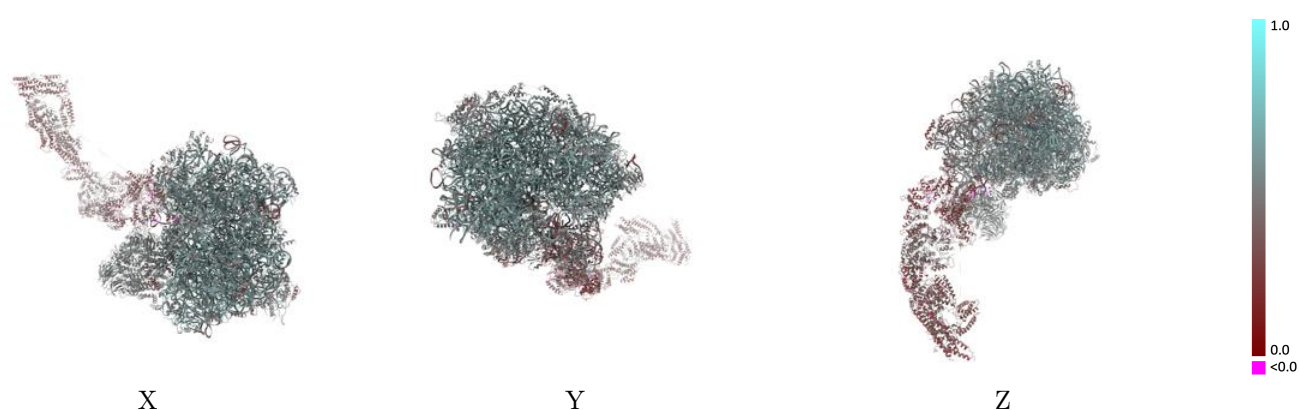
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10839 and PDB model 6YLH. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)

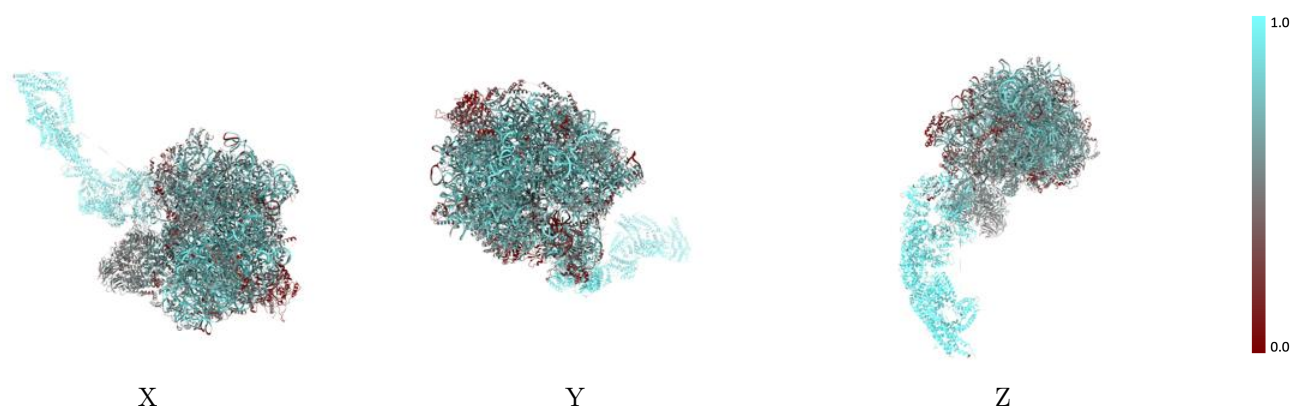
This section was not generated.

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



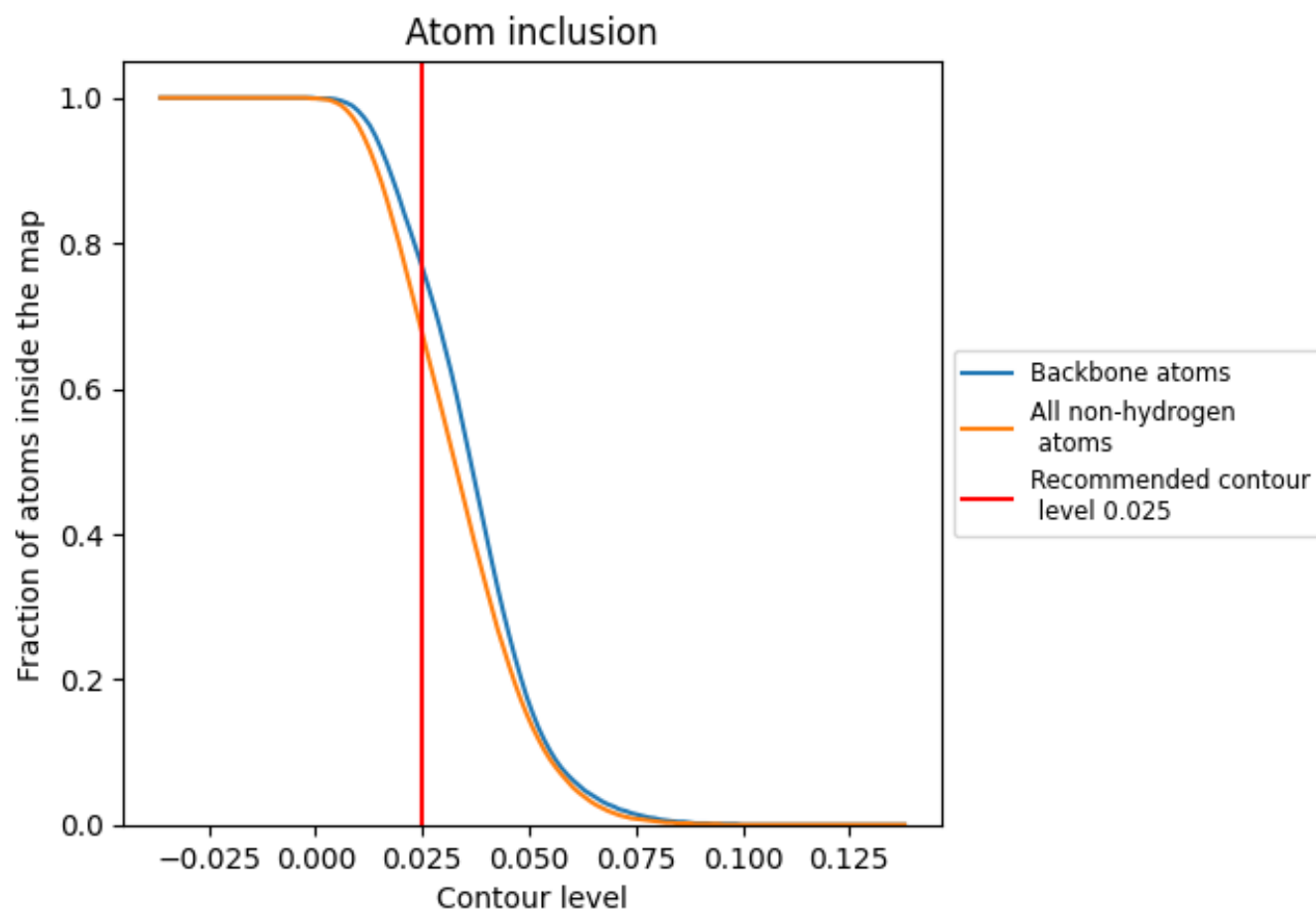
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 68% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6770	 0.5120
0	 0.5160	 0.4940
1	 0.7870	 0.5480
2	 0.8580	 0.5820
3	 0.6800	 0.4900
4	 0.2700	 0.4940
5	 0.3130	 0.4510
6	 0.4990	 0.4750
7	 0.4880	 0.4760
A	 0.7320	 0.5940
B	 0.6650	 0.5690
C	 0.6460	 0.5630
D	 0.2140	 0.4160
E	 0.5640	 0.5370
F	 0.6510	 0.5490
G	 0.5850	 0.5290
H	 0.6260	 0.5570
I	 0.4290	 0.5260
J	 0.4950	 0.4410
K	 0.5600	 0.4690
L	 0.6300	 0.5460
M	 0.6000	 0.5500
N	 0.7280	 0.5850
O	 0.6880	 0.5710
P	 0.6820	 0.5740
Q	 0.6140	 0.5490
R	 0.6600	 0.5570
S	 0.5720	 0.5370
T	 0.2310	 0.4690
U	 0.5570	 0.5320
V	 0.6040	 0.5070
W	 0.5160	 0.5000
X	 0.5850	 0.5660
Y	 0.6450	 0.5640
Z	 0.6320	 0.5360



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Chain	Atom inclusion	Q-score
a	 0.6440	 0.5570
b	 0.4750	 0.5120
c	 0.3450	 0.5350
d	 0.6370	 0.5660
e	 0.6450	 0.5770
f	 0.7080	 0.5950
g	 0.6760	 0.5700
h	 0.6550	 0.5610
i	 0.5980	 0.5390
j	 0.7640	 0.5940
k	 0.5040	 0.5280
l	 0.7220	 0.5970
m	 0.6000	 0.5450
n	 0.5900	 0.5340
o	 0.0800	 0.3960
p	 0.6690	 0.5750
q	 0.3760	 0.4680
r	 0.6470	 0.5650
s	 0.2710	 0.5010
t	 0.5640	 0.4930
u	 0.5940	 0.5420
v	 0.9180	 0.3230
w	 0.4490	 0.4900
x	 0.5710	 0.4990
y	 0.5480	 0.5020
z	 0.4430	 0.5340