



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 10:38 AM UTC

PDB ID : 7NAC / pdb_00007nac
EMDB ID : EMD-24269
Title : State E2 nucleolar 60S ribosomal biogenesis intermediate - Composite model
Authors : Cruz, V.E.; Sekulski, K.; Peddada, N.; Erzberger, J.P.
Deposited on : 2021-06-21
Resolution : 3.04 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

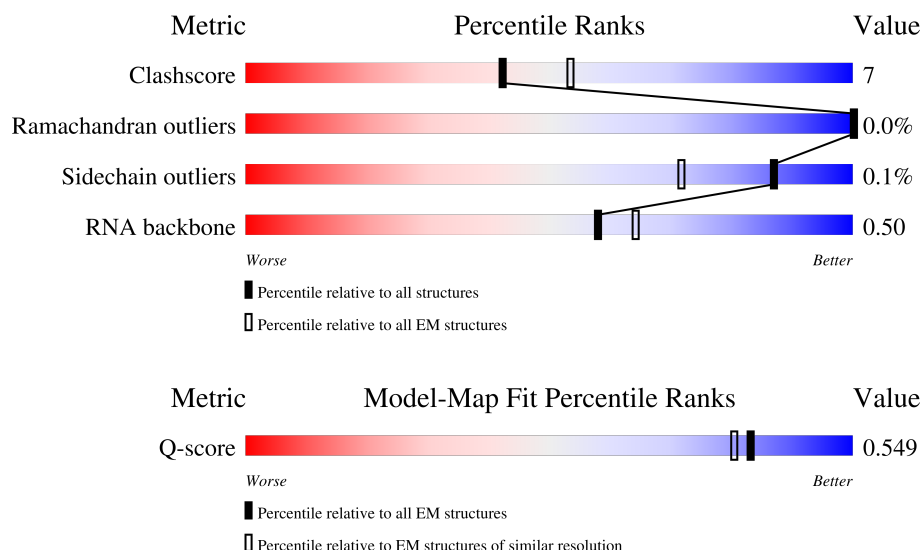
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.04 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	13952 (2.54 - 3.54)

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	7	204	

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Mol	Chain	Length	Quality of chain
4	A	291	
5	B	387	
6	C	362	
7	E	176	
8	F	244	
9	H	191	
10	J	427	
11	L	199	
12	M	138	
13	N	204	
14	O	199	
15	P	184	
16	Q	186	
17	S	172	
18	T	160	
19	W	236	
20	X	142	
21	Y	127	
22	b	647	
23	d	113	
24	e	130	
25	f	107	
26	h	120	
27	i	100	
28	j	88	

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Mol	Chain	Length	Quality of chain
29	l	181	
30	m	807	
31	q	618	
32	r	261	
33	s	520	
34	u	199	
35	v	231	
36	y	245	
37	z	106	
38	8	710	
39	I	663	
40	K	376	
41	V	137	
42	R	189	
43	G	256	
44	Z	136	
45	U	121	
46	c	105	
47	g	121	
48	k	78	
49	n	605	
50	p	460	
51	t	322	
52	6	87	
53	D	505	

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Mol	Chain	Length	Quality of chain
54	o	220	
55	w	841	
56	a	217	
57	5	235	
58	x	606	

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 158246 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	2661	Total	C	N	O	P	0	0
			56944	25427	10267	18590	2660		

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

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

- Molecule 3 is a protein called 60S ribosomal subunit assembly/export protein LOC1.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	7	129	Total	C	N	O	0	0
			1048	650	204	194		

- Molecule 4 is a protein called Ribosome biogenesis protein BRX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	266	Total	C	N	O	S	0	0
			2174	1382	386	400	6		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	335	Total	C	N	O	S	0	0
			2661	1691	492	472	6		

- Molecule 6 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	359	Total	C	N	O	S	0	0
			2731	1720	518	490	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	164	Total	C	N	O	S	0	0
			1309	845	234	229	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 L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	190	Total	C	N	O	S	0	0
			1510	957	273	276	4		

- Molecule 10 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	145	Total	C	N	O	S	0	0
			1215	759	225	228	3		

- Molecule 11 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	121	Total	C	N	O	S	0	0
			991	623	208	160			

- Molecule 12 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 13 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	189	Total	C	N	O	S	0	0
			1621	1015	343	262	1		

- Molecule 14 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 15 is a protein called 60S ribosomal protein L17-A.

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

- Molecule 16 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 17 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	S	170	Total	C	N	O	S	0	0
			1432	922	265	242	3		

- Molecule 18 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	52	Total	C	N	O	S	0	0
			401	244	82	74	1		

- Molecule 19 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	W	232	Total	C	N	O	S	0	0
			1870	1184	321	360	5		

- Molecule 20 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	X	137	Total	C	N	O	S	0	0
			1068	682	192	192	2		

- Molecule 21 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 22 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	b	502	Total	C	N	O	S	0	0
			4066	2581	710	754	21		

- Molecule 23 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 24 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	e	125	Total	C	N	O	S	0	0
			1009	641	203	164	1		

- Molecule 25 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 26 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 27 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	i	79	Total	C	N	O	S	0	0
			628	388	130	108	2		

- Molecule 28 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	j	73	Total	C	N	O	S	0	0
			580	353	126	96	5		

- Molecule 29 is a protein called 60S ribosome subunit biogenesis protein NIP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	l	176	Total	C	N	O	S	0	0
			1394	896	244	247	7		

- Molecule 30 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	m	666	Total	C	N	O	S	0	0
			5377	3421	936	1005	15		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
m	551	ALA	GLU	conflict	UNP Q04660

- Molecule 31 is a protein called 25S rRNA (cytosine(2870)-C(5))-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	q	358	Total	C	N	O	S	0	0
			2799	1779	490	518	12		

- Molecule 32 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	r	176	Total	C	N	O	S	0	0
			1438	906	279	248	5		

- Molecule 33 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	s	36	Total	C	N	O	S	0	0
			301	184	69	46	2		

- Molecule 34 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	u	140	Total	C	N	O	S	0	0
			1183	742	237	195	9		

- Molecule 35 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	v	130	Total	C	N	O	S	0	0
			1087	678	211	195	3		

- Molecule 36 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	y	225	Total	C	N	O	S	0	0
			1701	1056	295	343	7		

- Molecule 37 is a protein called UPF0642 protein YBL028C.

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

- Molecule 38 is a protein called NOC2 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	8	470	Total	C	N	O	S	0	0
			3567	2269	632	655	11		

- Molecule 39 is a protein called Nucleolar complex-associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	I	533	Total	C	N	O	S	0	0
			4247	2693	726	808	20		

- Molecule 40 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	K	284	Total	C	N	O	S	0	0
			2274	1462	375	433	4		

- Molecule 41 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 42 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	R	134	Total	C	N	O		0	0
			1082	679	220	183			

- Molecule 43 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	G	198	Total	C	N	O	S	0	0
			1549	998	271	277	3		

- Molecule 44 is a protein called 60S ribosomal protein L27-A.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	U	102	Total	C	N	O		0	0
			808	524	132	152			

- Molecule 46 is a protein called 60S ribosomal protein L30.

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

- Molecule 47 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 48 is a protein called 60S ribosomal protein L38.

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

- Molecule 49 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	n	425	Total	C	N	O	S	0	0
			3470	2241	600	615	14		

- Molecule 50 is a protein called YTM1 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	p	337	Total	C	N	O	S	0	0
			2628	1633	470	518	7		

- Molecule 51 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	t	285	Total	C	N	O	S	0	0
			2293	1453	425	412	3		

- Molecule 52 is a RNA chain called 5.8S ribosomal RNA gene and internal transcribed spacer 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	6	87	Total	C	N	O	P	0	0
			1838	823	309	619	87		

- Molecule 53 is a protein called ATP-dependent RNA helicase HAS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	D	432	Total	C	N	O	S	0	0
			3451	2227	591	621	12		

- Molecule 54 is a protein called Ribosome biogenesis protein 15.

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

- Molecule 55 is a protein called 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	w	672	Total	C	N	O	S	0	0
			5451	3430	980	1013	28		

- Molecule 56 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	a	214	Total	C	N	O	S	0	0
			1695	1083	295	308	9		

- Molecule 57 is a protein called RRP17 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	5	141	Total	C	N	O	S	0	0
			1208	749	226	232	1		

- Molecule 58 is a protein called ATP-dependent rRNA helicase SPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	x	539	Total	C	N	O	S	0	0
			4340	2781	744	795	20		

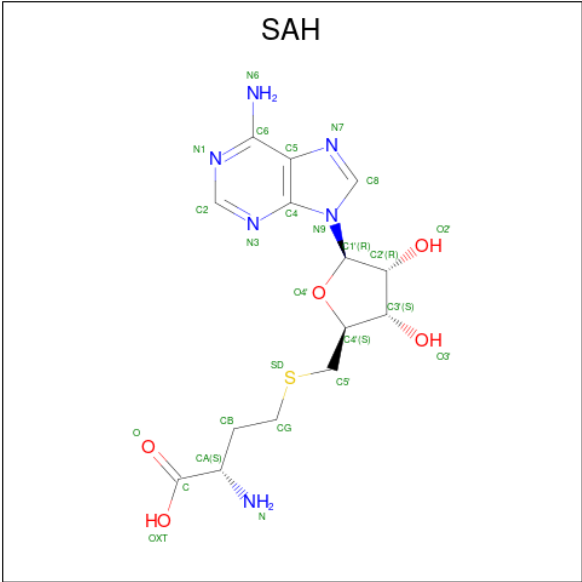
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	405	ALA	THR	conflict	UNP A7A237

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

Mol	Chain	Residues	Atoms		AltConf
59	j	1	Total	Zn	0
			1	1	
59	g	1	Total	Zn	0
			1	1	

- Molecule 60 is S-ADENOSYL-L-HOMOCYSTEINE (CCD ID: SAH) (formula: C₁₄H₂₀N₆O₅S) (labeled as "Ligand of Interest" by depositor).

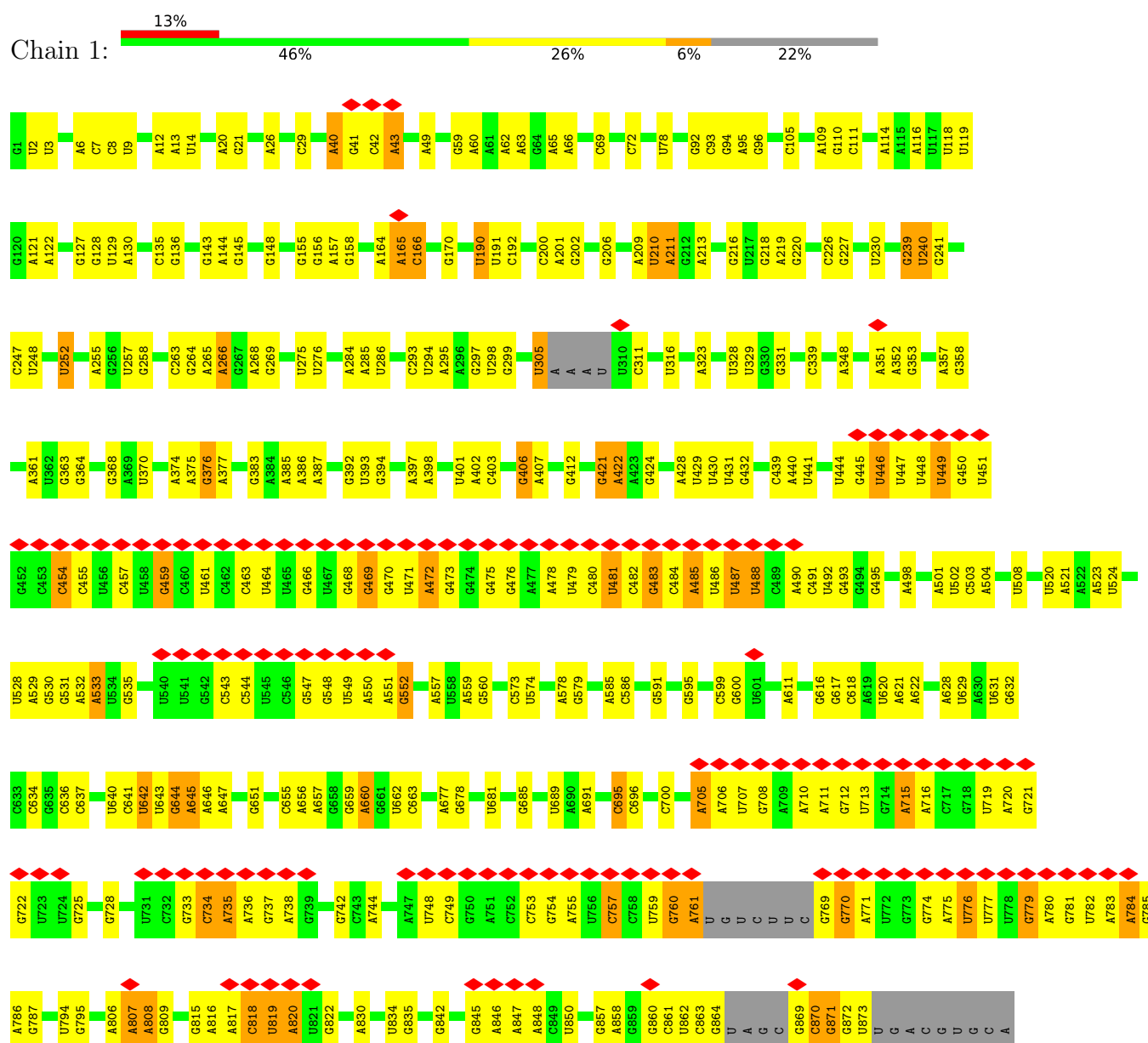


Mol	Chain	Residues	Atoms					AltConf
60	w	1	Total	C	N	O	S	0
			26	14	6	5	1	

3 Residue-property plots

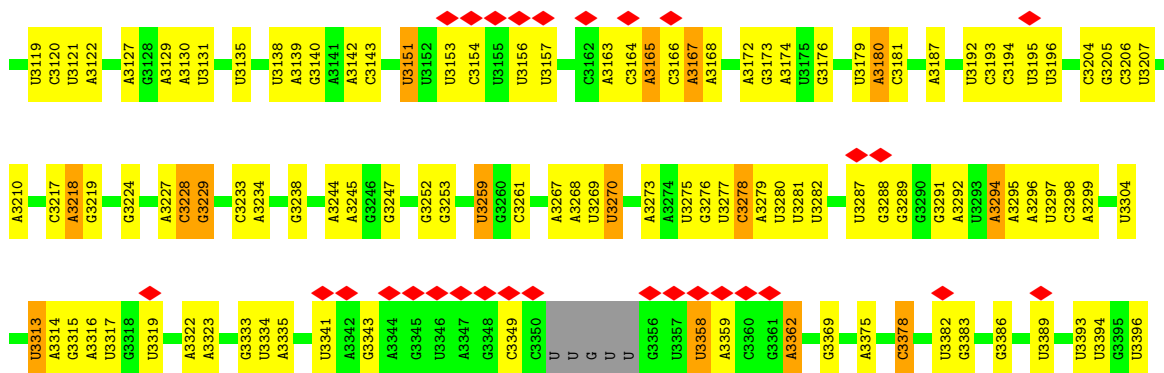
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

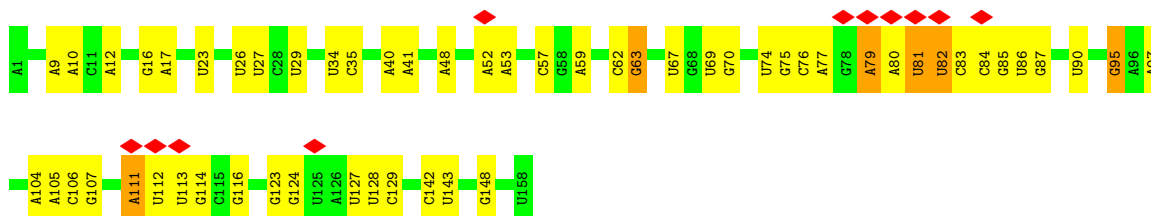




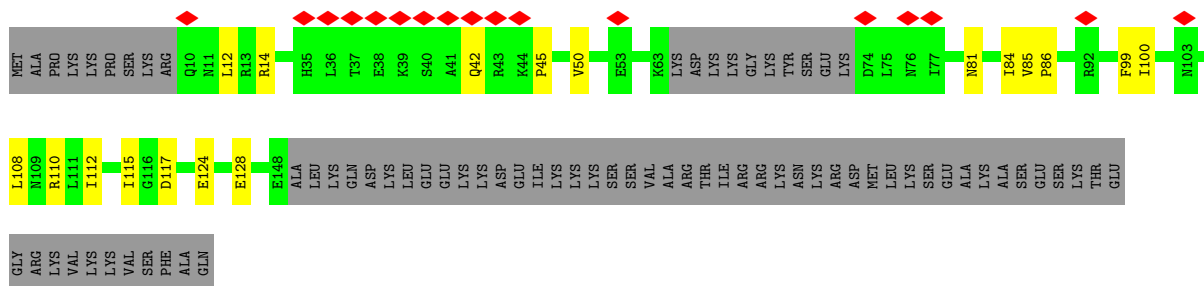




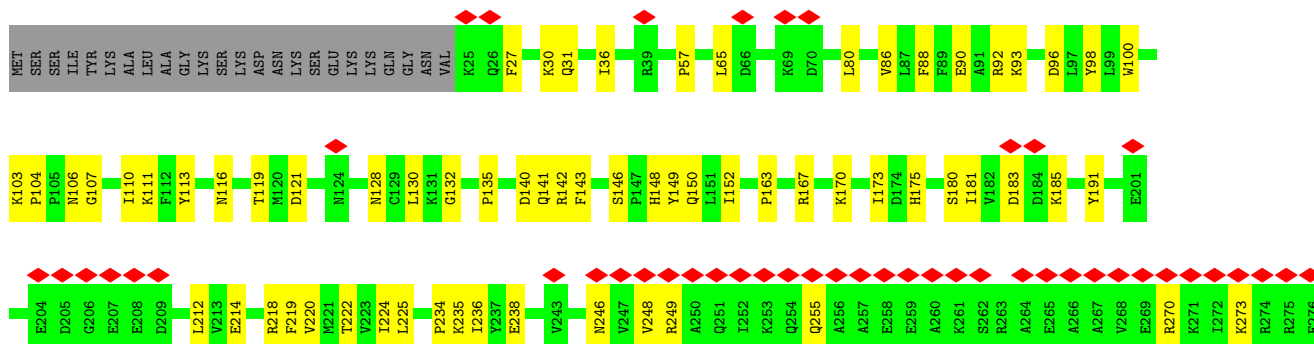
- Molecule 2: 5.8S rRNA

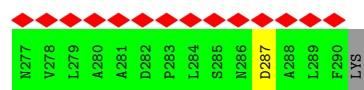


- Molecule 3: 60S ribosomal subunit assembly/export protein LOC1



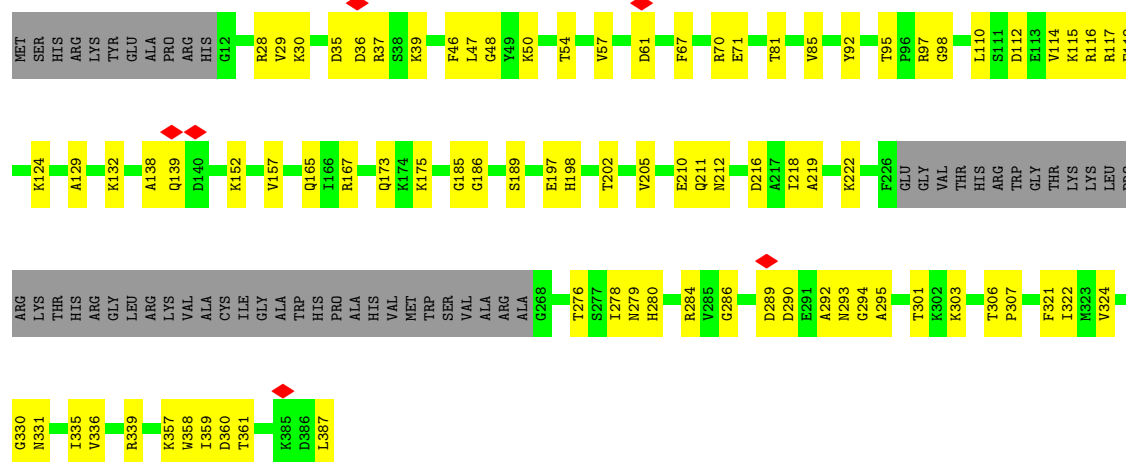
- Molecule 4: Ribosome biogenesis protein BRX1





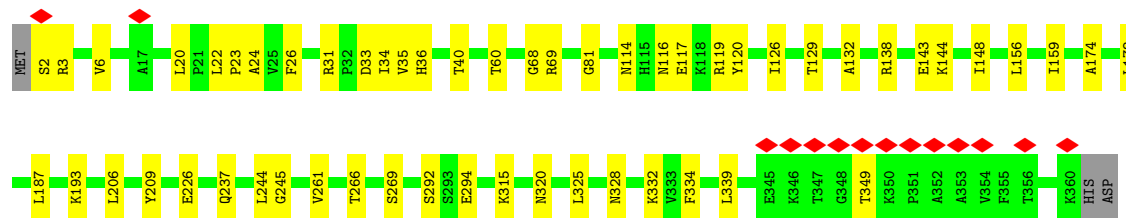
• Molecule 5: 60S ribosomal protein L3

Chain B: 65% 22% 13%



• Molecule 6: 60S ribosomal protein L4-A

Chain C: 84% 15%



• Molecule 7: 60S ribosomal protein L6-A

Chain E: 9% 81% 12% 7%

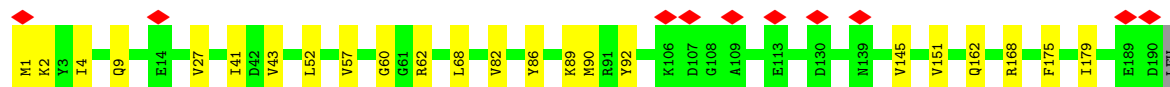
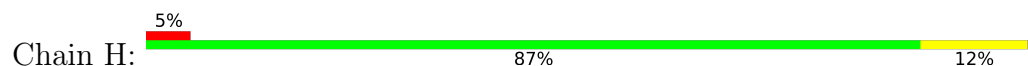


• Molecule 8: 60S ribosomal protein L7-A

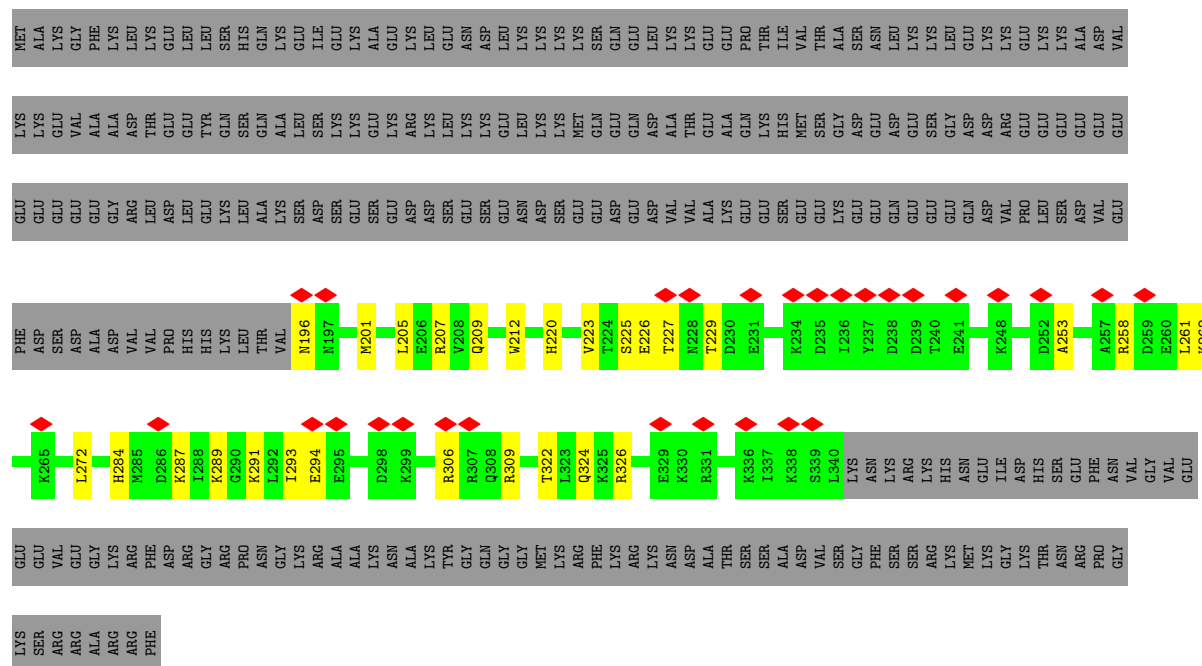
Chain F: 77% 14% 9%



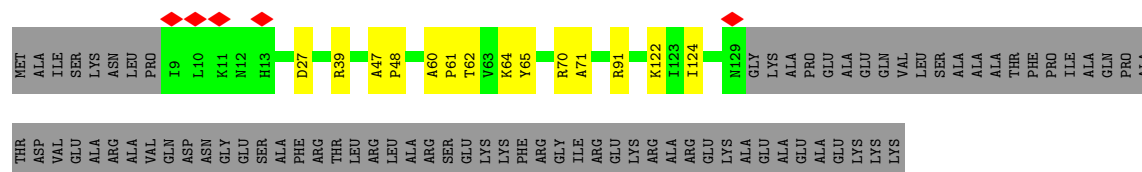
- Molecule 9: 60S ribosomal protein L9-A



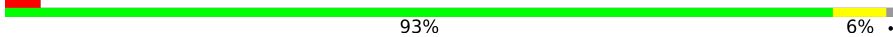
- Molecule 10: rRNA-processing protein EBP2

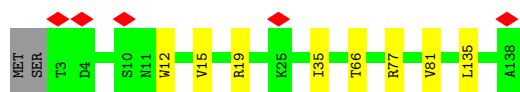


- Molecule 11: 60S ribosomal protein L13-A



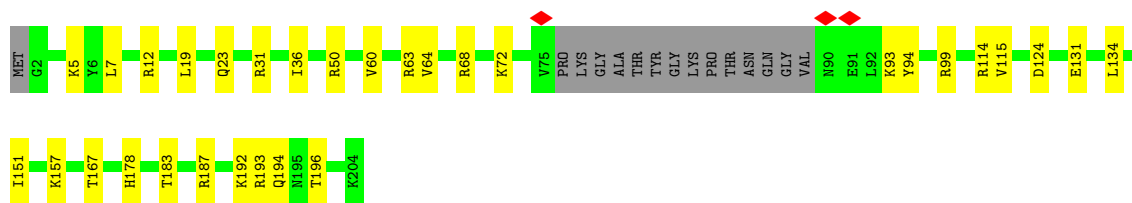
- Molecule 12: 60S ribosomal protein L14-A

Chain M:  93% 6%

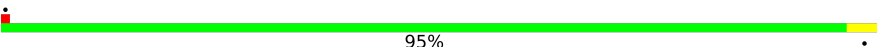


- Molecule 13: 60S ribosomal protein L15-A

Chain N:  77% 15% 7%



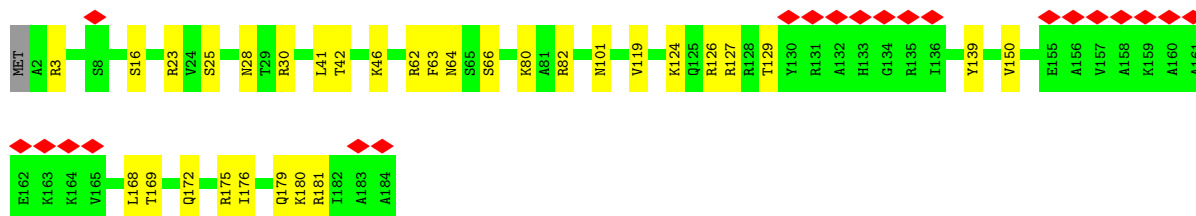
- Molecule 14: 60S ribosomal protein L16-A

Chain O:  95%



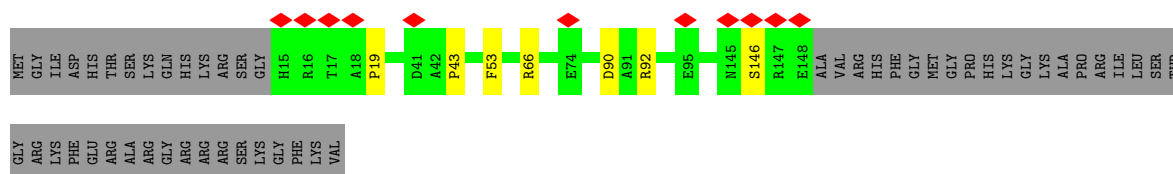
- Molecule 15: 60S ribosomal protein L17-A

Chain P:  11% 83% 17%



- Molecule 16: 60S ribosomal protein L18-A

Chain Q:  6% 68% 28%



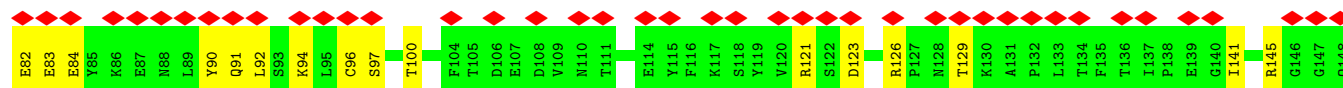
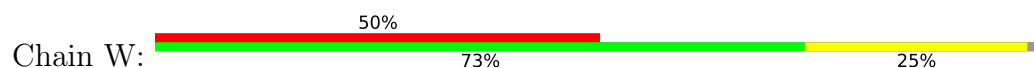
- Molecule 17: 60S ribosomal protein L20-A

Chain S:  12% 84% 15%

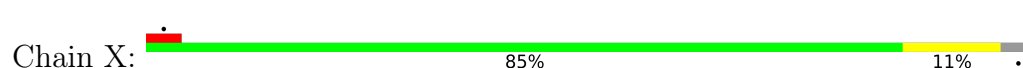
- Molecule 18: 60S ribosomal protein L21-A



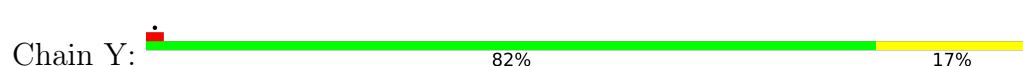
- Molecule 19: Ribosome assembly factor MRT4



- Molecule 20: 60S ribosomal protein L25

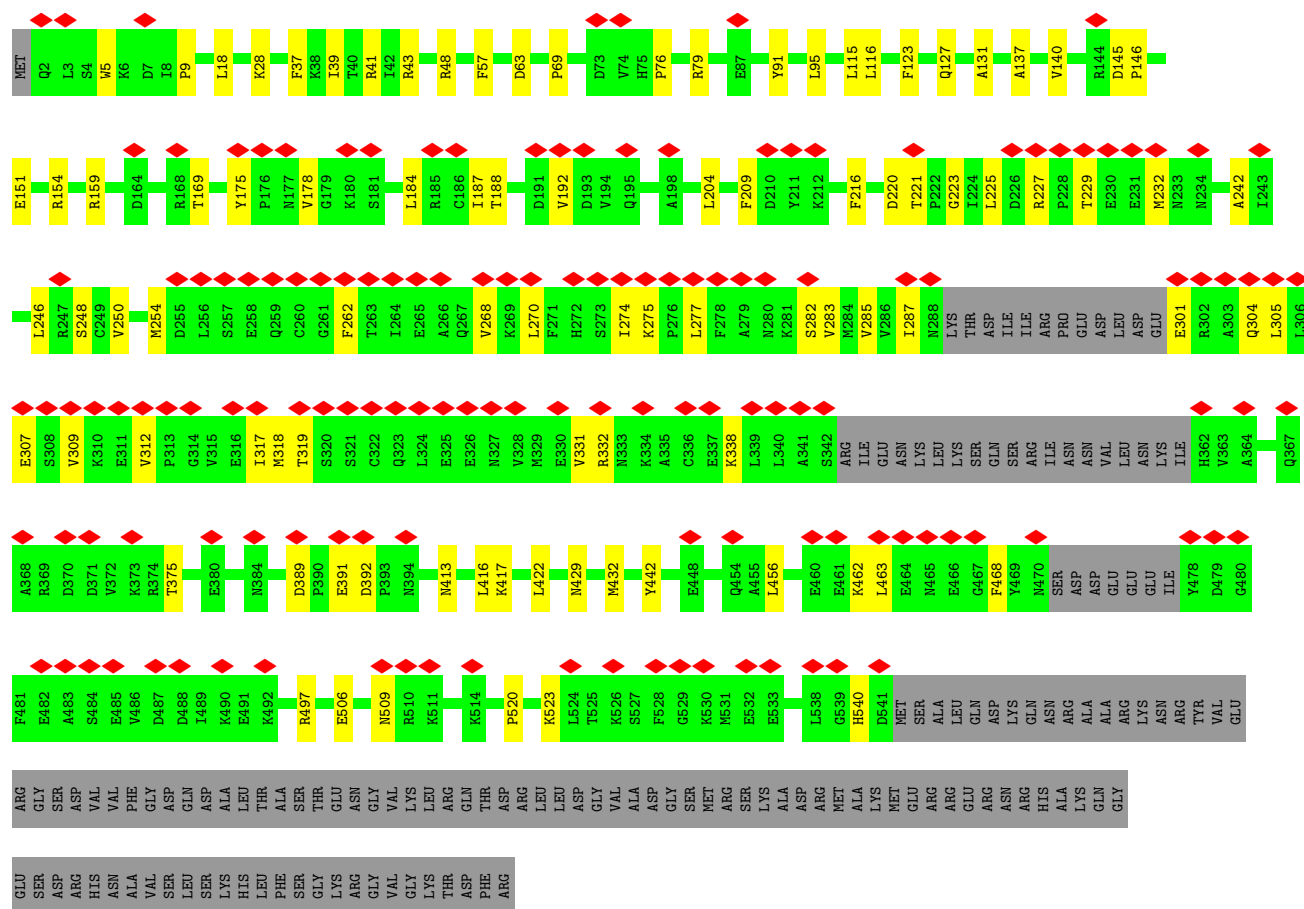


- Molecule 21: 60S ribosomal protein L26-A

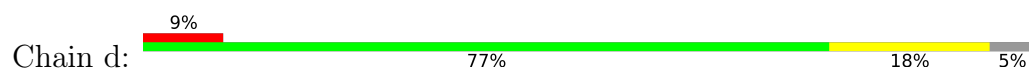




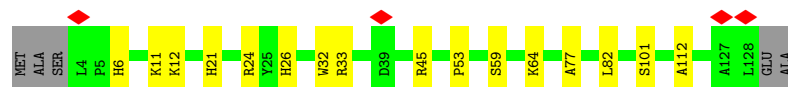
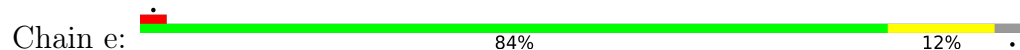
• Molecule 22: Nucleolar GTP-binding protein 1



• Molecule 23: 60S ribosomal protein L31-A



• Molecule 24: 60S ribosomal protein L32

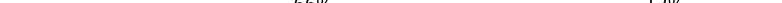


• Molecule 25: 60S ribosomal protein L33-A

MET
A2
Y16
R21
I49
Y53
R54
R65
V66
M67
V71
H75
V80
L89
P90
R99
L102
I107

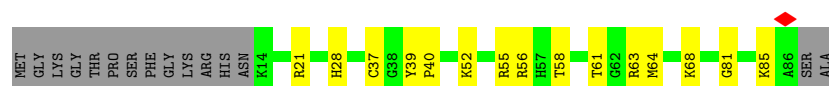
- Chain h: 86% 13%

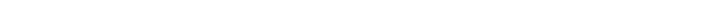


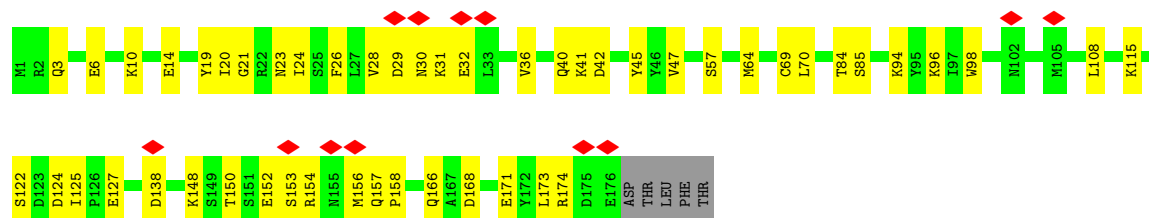
- Chain i: 

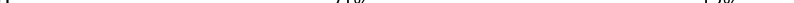


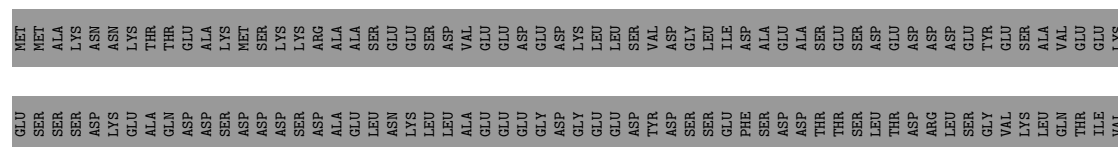
- Chain j:

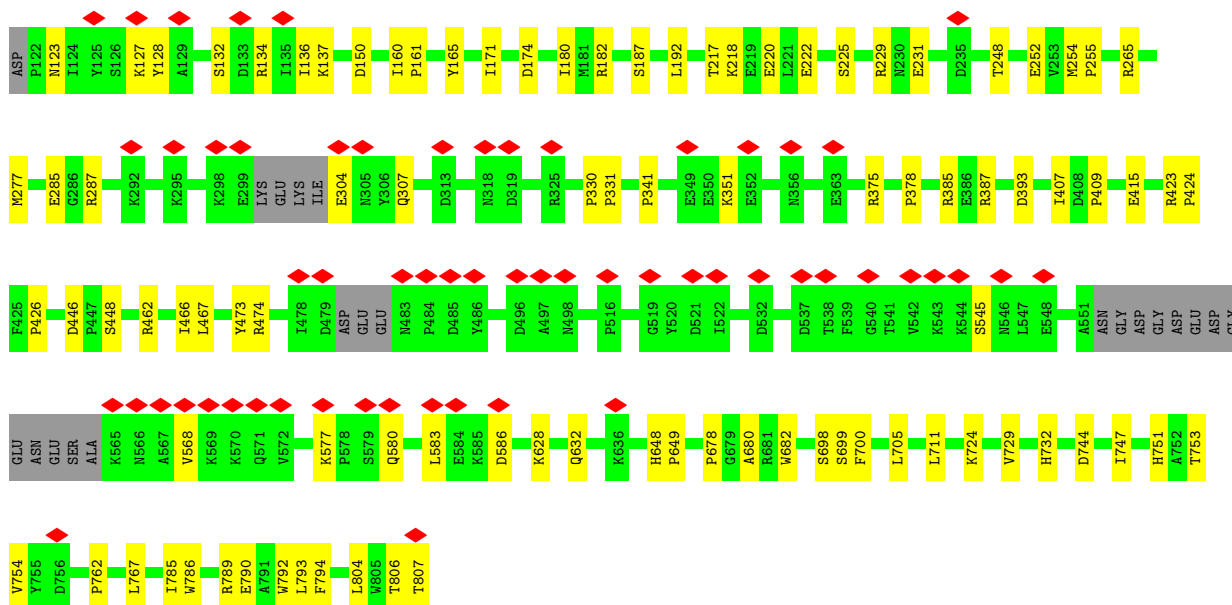


- Chain 1:  7% 70% 28%

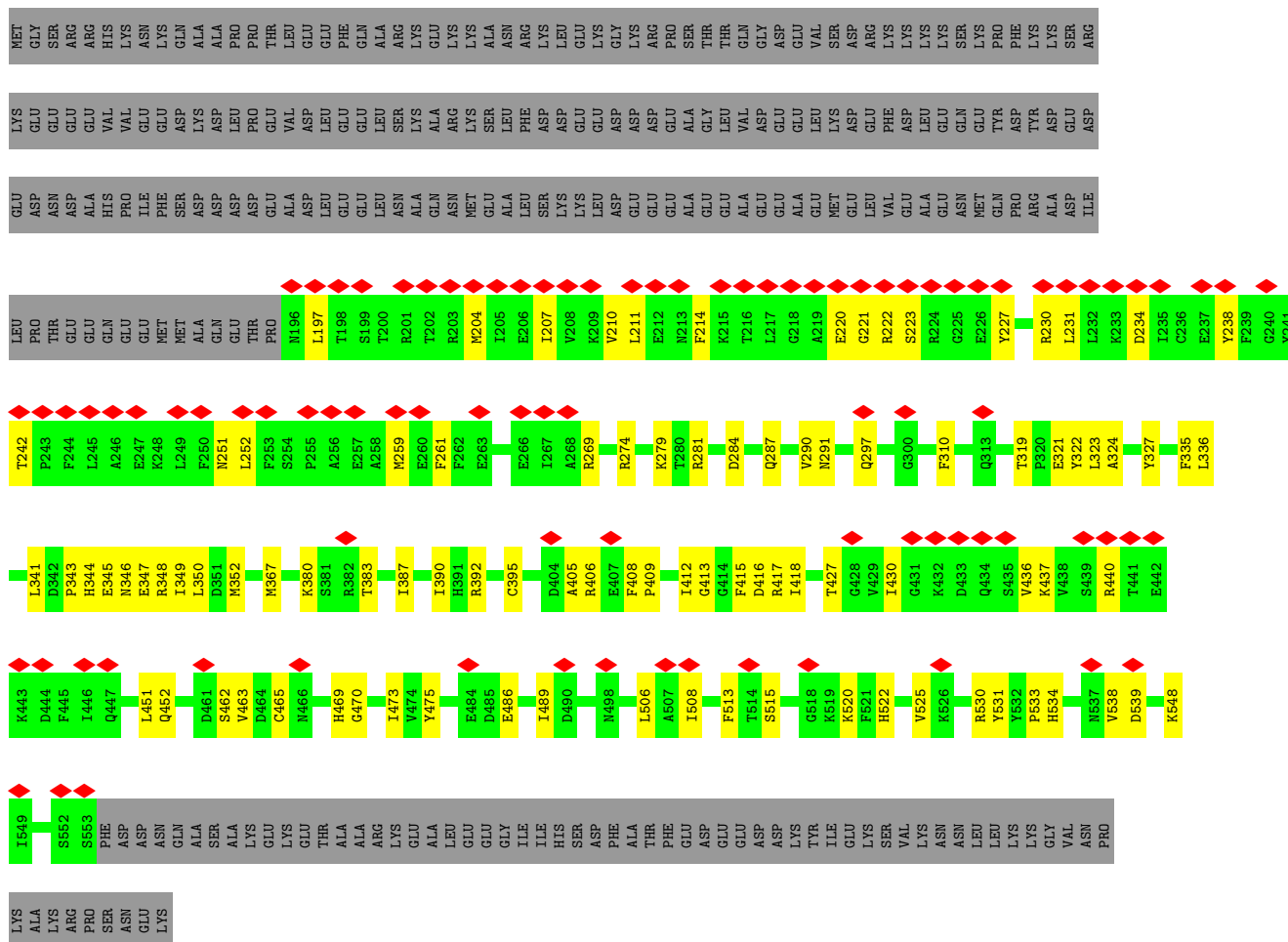


- Chain m: 

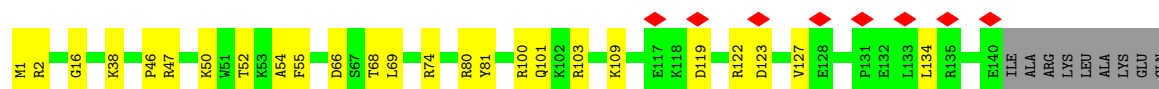




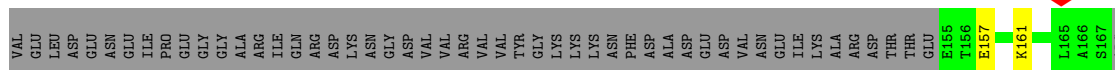
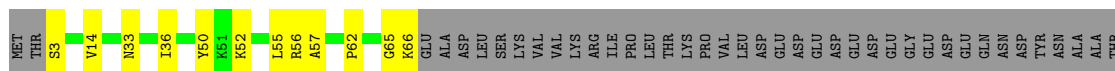
• Molecule 31: 25S rRNA (cytosine(2870)-C(5))-methyltransferase



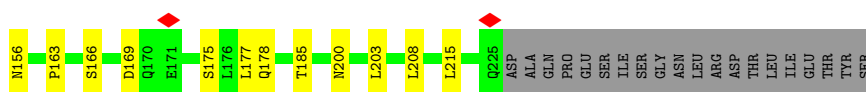
Chain r:



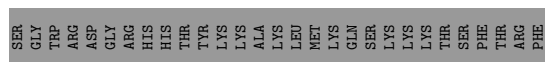
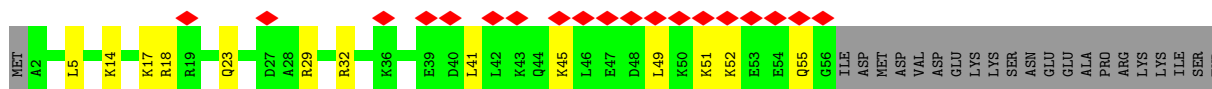
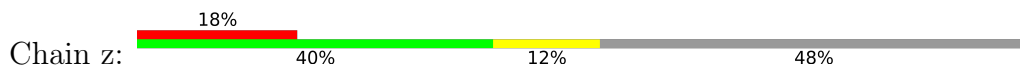
- Molecule 35: Nucleolar protein 16



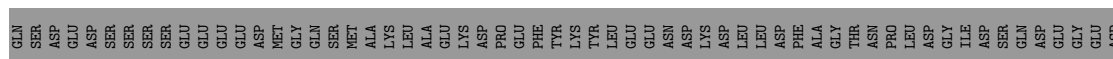
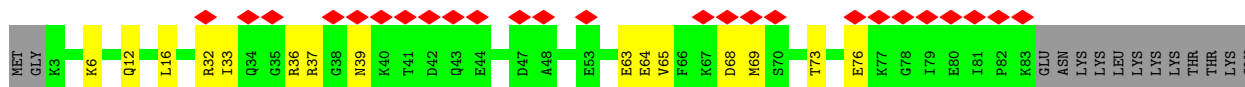
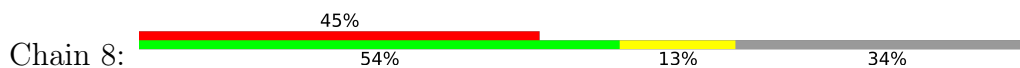
- Molecule 36: Eukaryotic translation initiation factor 6



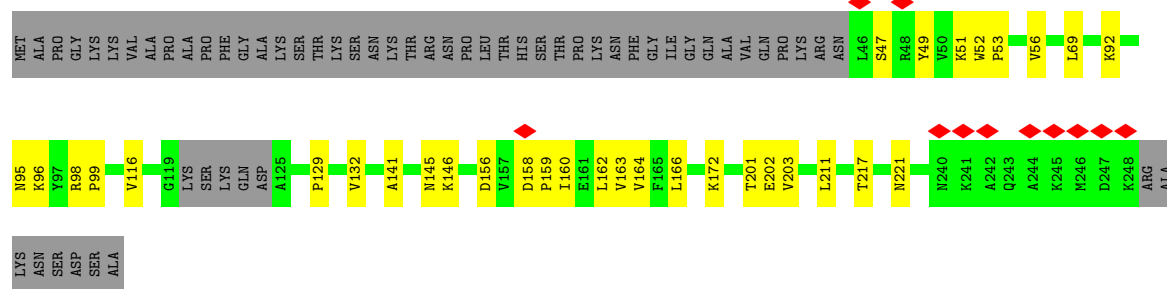
- Molecule 37: UPF0642 protein YBL028C



- Molecule 38: NOC2 isoform 1

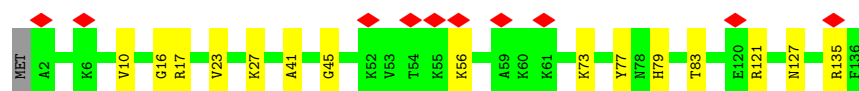


Chain G: 



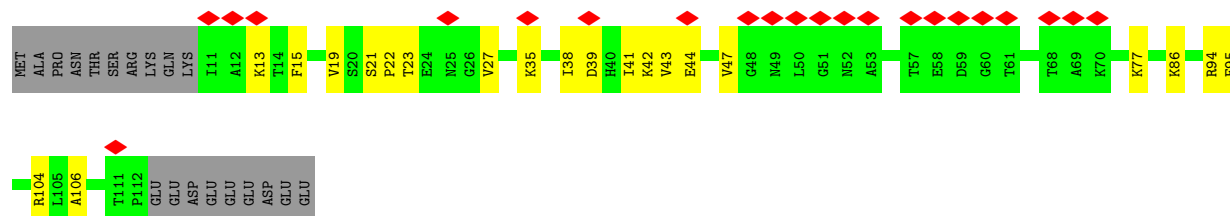
- Molecule 44: 60S ribosomal protein L27-A

Chain Z: 



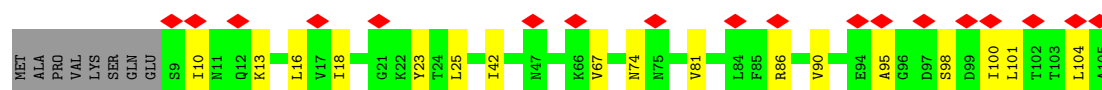
- Molecule 45: 60S ribosomal protein L22-A

Chain U: 



- Molecule 46: 60S ribosomal protein L30

Chain c: 



- Molecule 47: 60S ribosomal protein L34-A

Chain g: 

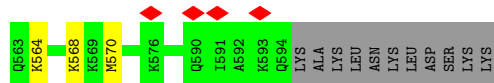
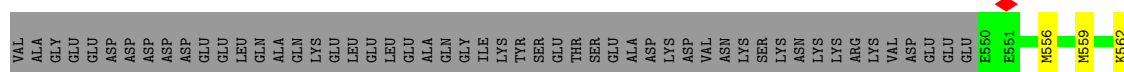
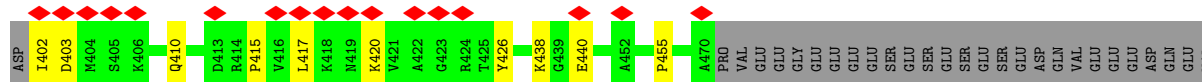
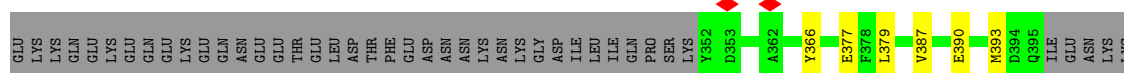
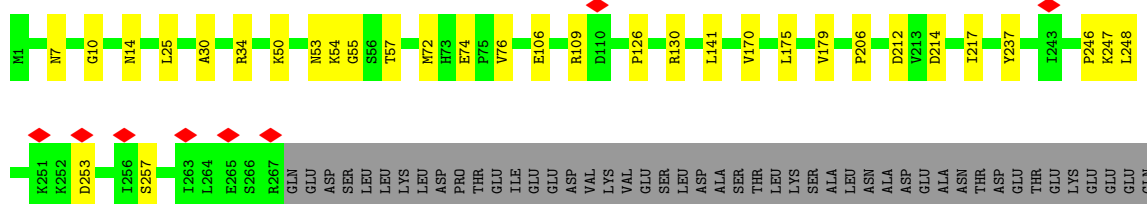


- Molecule 48: 60S ribosomal protein L38

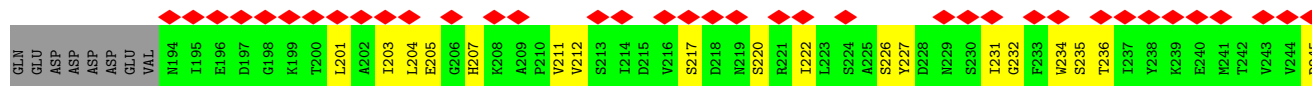
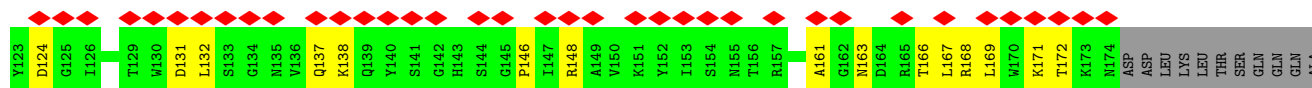
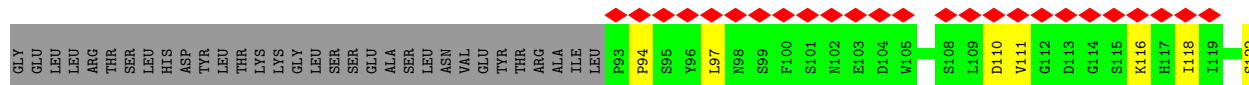
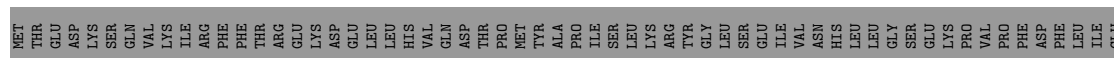
Chain k: 

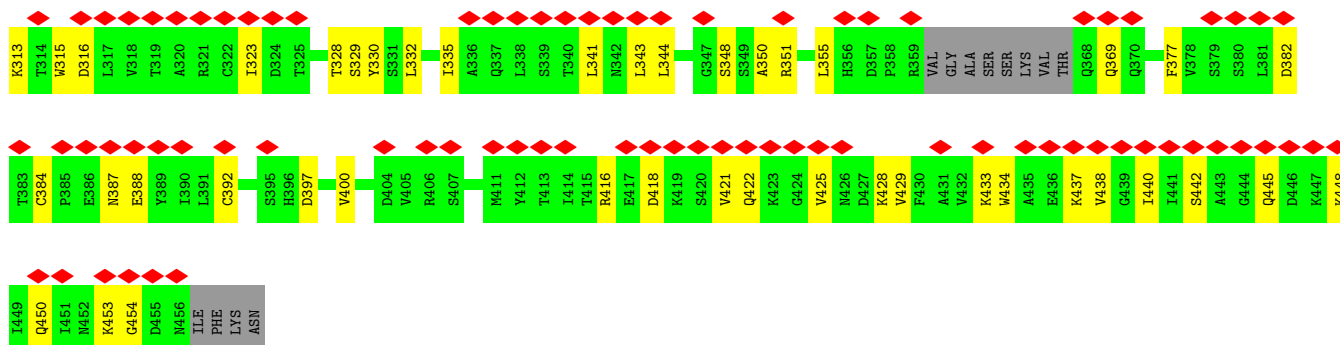


• Molecule 49: Pescadillo homolog

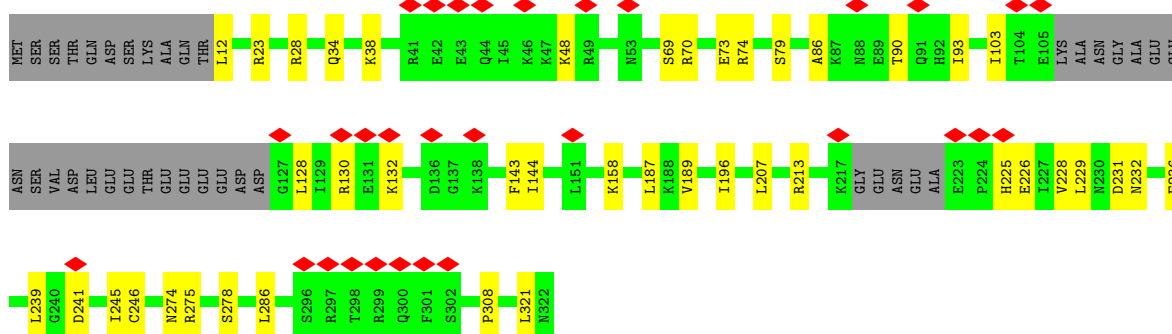
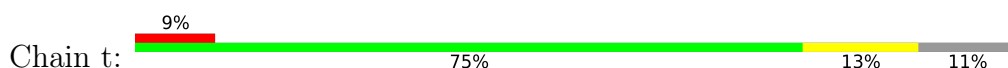


• Molecule 50: YTM1 isoform 1

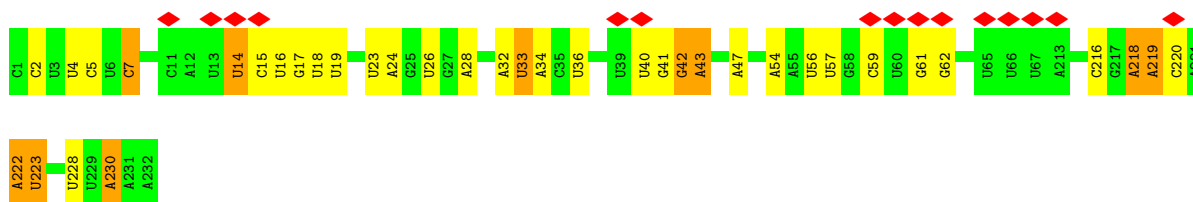




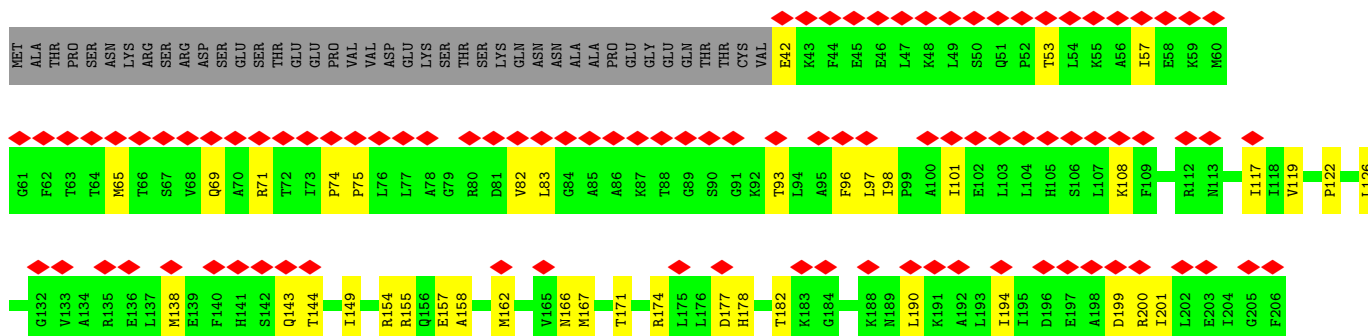
• Molecule 51: Ribosome biogenesis protein RLP7



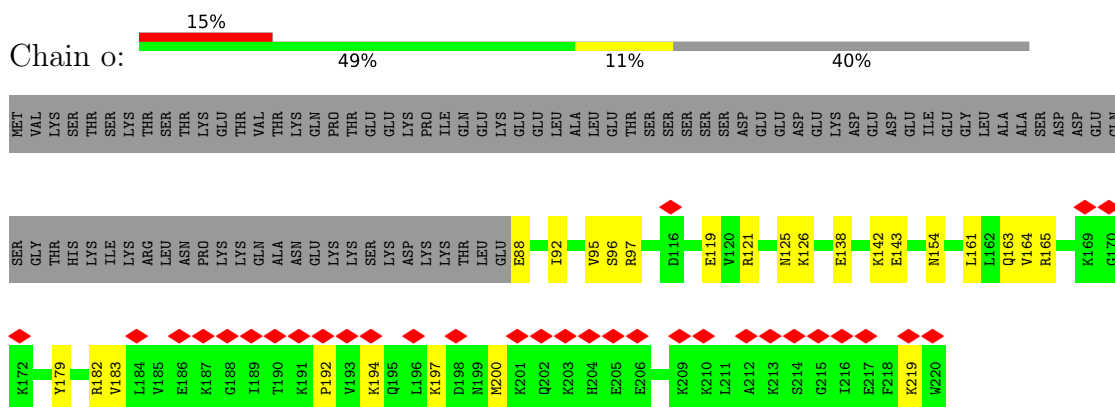
• Molecule 52: 5.8S ribosomal RNA gene and internal transcribed spacer 2



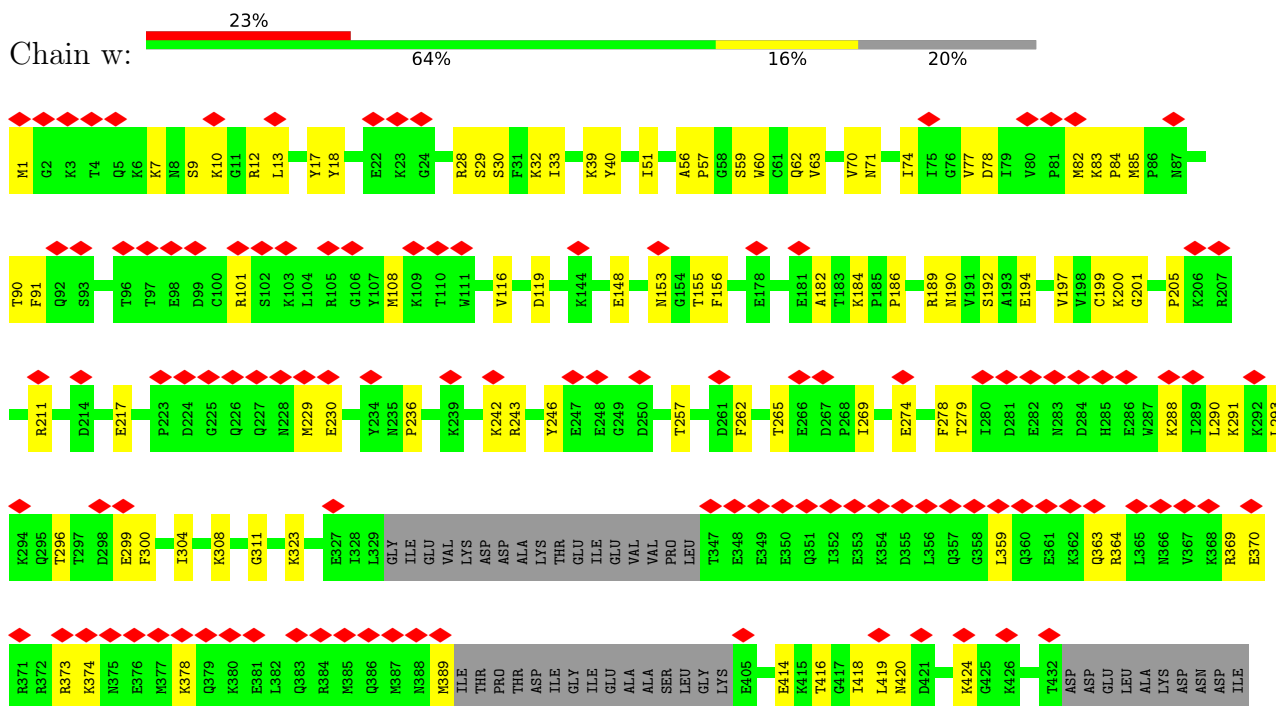
• Molecule 53: ATP-dependent RNA helicase HAS1

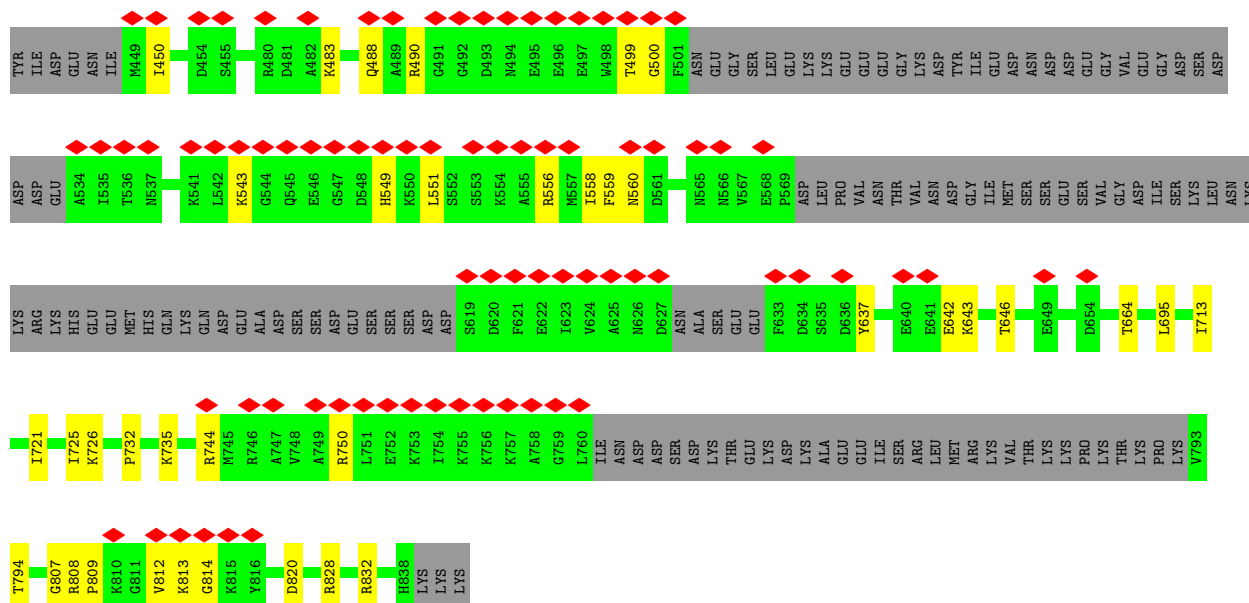


- Molecule 54: Ribosome biogenesis protein 15



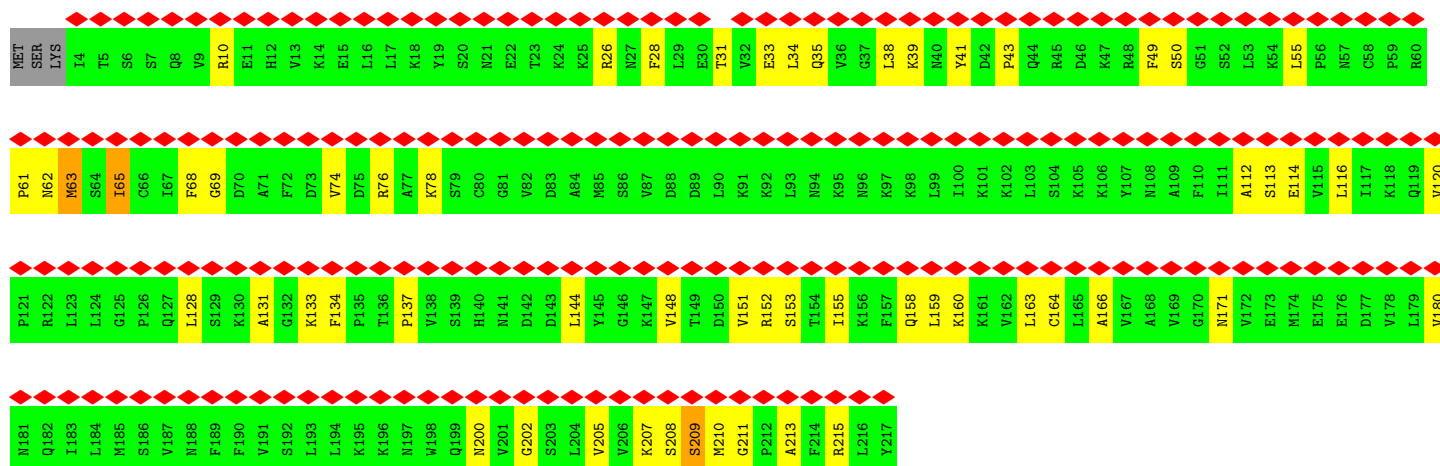
- Molecule 55: 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase





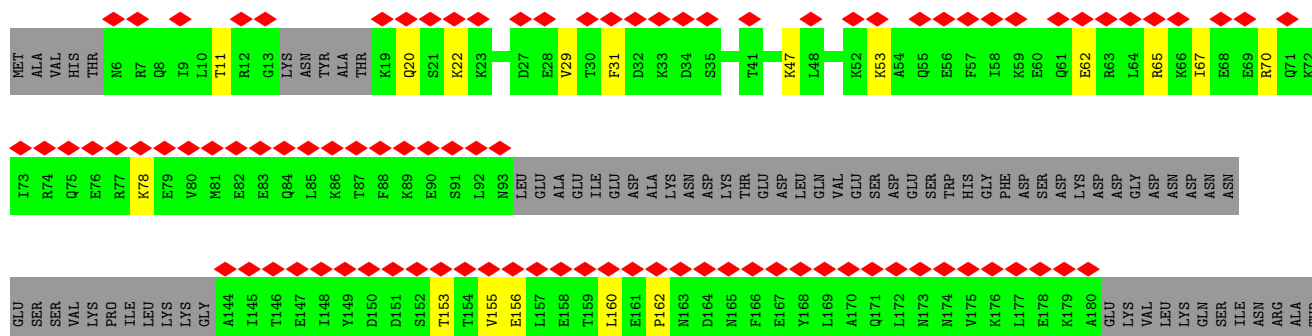
• Molecule 56: Ribosomal protein

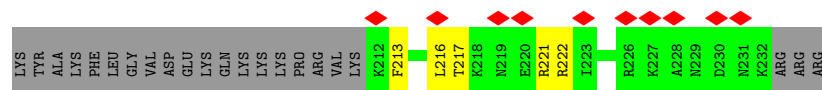
Chain a: 98% 72% 25% ..



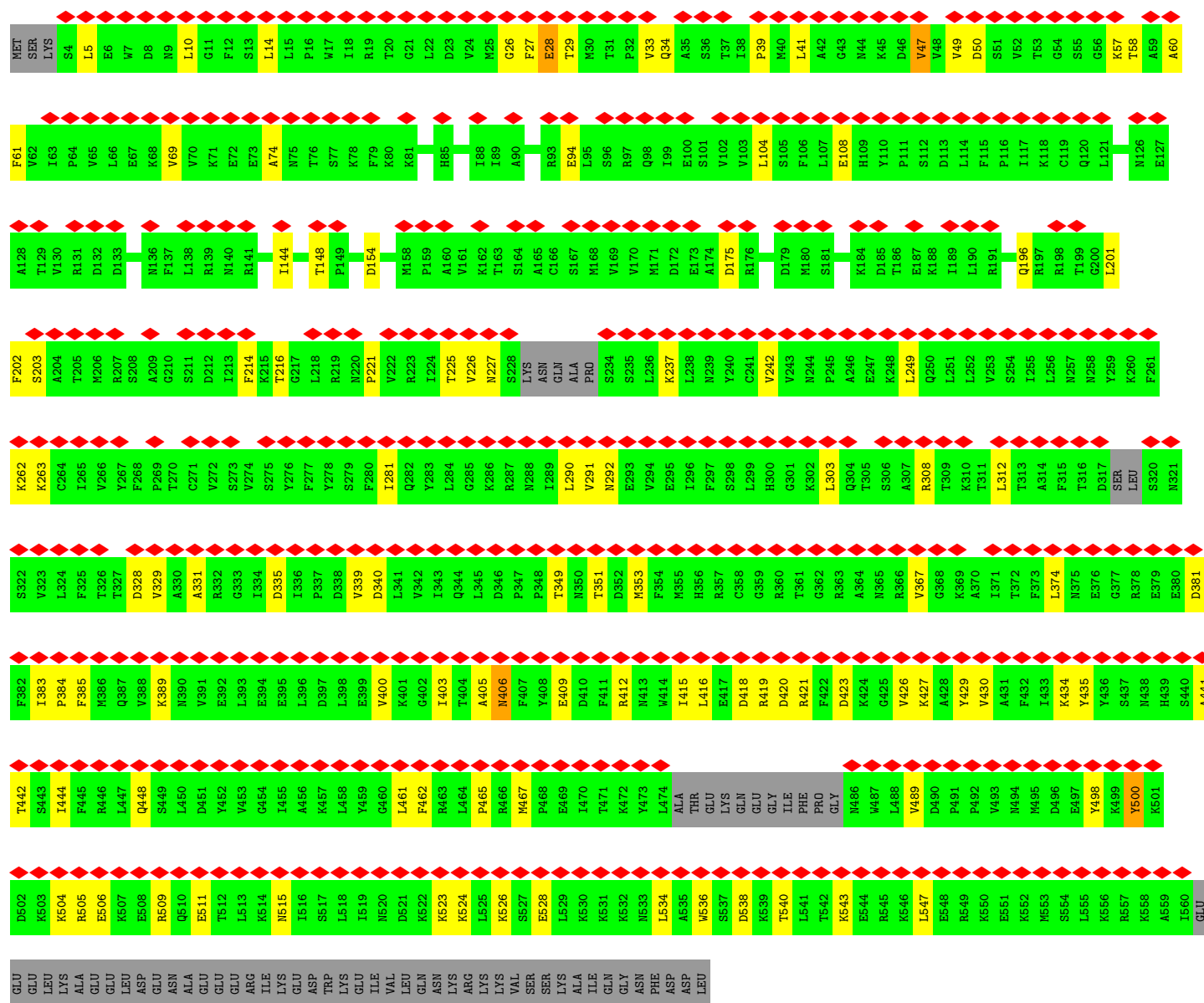
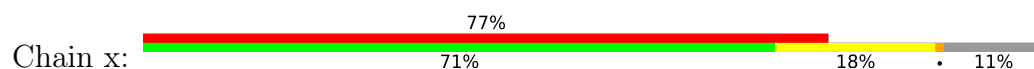
• Molecule 57: RRP17 isoform 1

Chain 5: 44% 51% 9% 40%





• Molecule 58: ATP-dependent rRNA helicase SPB4



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	198000	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 ($e^-/\text{\AA}^2$)	1.2	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.216	Depositor
Minimum map value	-0.125	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0275	Depositor
Map size ($\text{\AA}$)	453.6, 453.6, 453.6	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.08, 1.08, 1.08	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, PSU, OMU, SAH, OMG, A2M

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	0.19	0/63625	0.30	4/99173 (0.0%)
2	2	0.22	0/3746	0.33	0/5832
3	7	0.16	0/1056	0.31	0/1408
4	A	0.16	0/2222	0.32	0/2998
5	B	0.20	0/2715	0.34	0/3647
6	C	0.18	0/2782	0.30	0/3766
7	E	0.16	0/1332	0.29	0/1791
8	F	0.17	0/1821	0.32	0/2451
9	H	0.17	0/1531	0.31	0/2062
10	J	0.13	0/1232	0.27	0/1642
11	L	0.19	0/1009	0.33	0/1355
12	M	0.16	0/1068	0.28	0/1438
13	N	0.20	0/1654	0.28	0/2212
14	O	0.18	0/1585	0.29	0/2128
15	P	0.17	0/1465	0.32	0/1968
16	Q	0.15	0/1050	0.26	0/1419
17	S	0.16	0/1468	0.33	0/1973
18	T	0.12	0/404	0.33	0/542
19	W	0.13	0/1902	0.33	0/2564
20	X	0.17	0/1083	0.30	0/1458
21	Y	0.20	0/1004	0.35	0/1341
22	b	0.14	0/4141	0.30	0/5575
23	d	0.16	0/887	0.32	0/1191
24	e	0.17	0/1030	0.29	0/1379
25	f	0.20	0/868	0.31	0/1168
26	h	0.17	0/978	0.29	0/1301
27	i	0.17	0/633	0.32	0/839
28	j	0.22	0/592	0.40	0/785
29	l	0.15	0/1425	0.32	0/1922
30	m	0.15	0/5511	0.31	0/7471
31	q	0.15	0/2854	0.35	0/3860
32	r	0.15	0/1462	0.30	0/1952

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	s	0.18	0/301	0.26	0/386
34	u	0.14	0/1205	0.26	0/1603
35	v	0.17	0/1100	0.31	0/1456
36	y	0.15	0/1722	0.31	0/2343
37	z	0.13	0/445	0.26	0/585
38	8	0.14	0/3624	0.32	1/4891 (0.0%)
39	I	0.13	0/4310	0.29	0/5807
40	K	0.14	0/2310	0.31	0/3118
41	V	0.16	0/1008	0.34	0/1356
42	R	0.14	0/1095	0.26	0/1465
43	G	0.18	0/1575	0.28	0/2125
44	Z	0.14	0/1118	0.26	0/1497
45	U	0.14	0/825	0.29	0/1120
46	c	0.13	0/751	0.29	0/1008
47	g	0.16	0/891	0.28	0/1191
48	k	0.19	0/618	0.33	0/826
49	n	0.16	0/3544	0.29	0/4766
50	p	0.13	0/2674	0.34	0/3623
51	t	0.14	0/2319	0.27	0/3108
52	6	0.15	0/2050	0.30	0/3186
53	D	0.13	0/3516	0.30	0/4741
54	o	0.14	0/1129	0.30	0/1502
55	w	0.13	0/5531	0.31	0/7389
56	a	0.12	0/1722	0.35	0/2313
57	5	0.10	0/1217	0.28	0/1613
58	x	0.15	0/4419	0.31	0/5958
All	All	0.17	0/167154	0.31	5/239587 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2600	C	C2'-C3'-O3'	7.84	121.25	109.50
1	1	906	A	C2'-C3'-O3'	7.19	124.49	113.70
1	1	906	A	C3'-C2'-O2'	6.67	120.71	110.70
38	8	306	PRO	N-CA-CB	6.55	110.13	103.25
1	1	2600	C	C4'-C3'-O3'	5.29	117.34	109.40

There are no chirality outliers.

There are no planarity outliers.

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	56944	0	28630	609	0
2	2	3353	0	1695	30	0
3	7	1048	0	1117	15	0
4	A	2174	0	2179	48	0
5	B	2661	0	2738	58	0
6	C	2731	0	2852	41	0
7	E	1309	0	1394	17	0
8	F	1784	0	1862	24	0
9	H	1510	0	1576	17	0
10	J	1215	0	1245	22	0
11	L	991	0	1044	13	0
12	M	1053	0	1149	6	0
13	N	1621	0	1678	22	0
14	O	1555	0	1659	8	0
15	P	1442	0	1485	23	0
16	Q	1035	0	1115	6	0
17	S	1432	0	1470	24	0
18	T	401	0	418	16	0
19	W	1870	0	1902	40	0
20	X	1068	0	1153	11	0
21	Y	993	0	1081	17	0
22	b	4066	0	4111	66	0
23	d	873	0	914	14	0
24	e	1009	0	1080	15	0
25	f	850	0	880	9	0
26	h	969	0	1078	15	0
27	i	628	0	675	11	0
28	j	580	0	584	14	0
29	l	1394	0	1426	42	0
30	m	5377	0	5366	65	0
31	q	2799	0	2834	61	0
32	r	1438	0	1515	31	0
33	s	301	0	359	2	0
34	u	1183	0	1227	20	0
35	v	1087	0	1133	16	0
36	y	1701	0	1697	27	0
37	z	444	0	478	12	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	8	3567	0	3408	68	0
39	I	4247	0	4386	67	0
40	K	2274	0	2352	38	0
41	V	993	0	1040	17	0
42	R	1082	0	1160	28	0
43	G	1549	0	1637	23	0
44	Z	1092	0	1155	12	0
45	U	808	0	822	14	0
46	c	743	0	797	12	0
47	g	881	0	945	15	0
48	k	612	0	682	8	0
49	n	3470	0	3586	35	0
50	p	2628	0	2612	68	0
51	t	2293	0	2449	30	0
52	6	1838	0	927	21	0
53	D	3451	0	3578	59	0
54	o	1107	0	1159	19	0
55	w	5451	0	5578	102	0
56	a	1695	0	1781	41	0
57	5	1208	0	1228	31	0
58	x	4340	0	4468	85	0
59	g	1	0	0	0	0
59	j	1	0	0	0	0
60	w	26	0	19	3	0
All	All	158246	0	130568	1904	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 7.

The worst 5 of 1904 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)
57:5:156:GLU:HG3	58:x:225:THR:OG1	1.48	1.10
42:R:105:LEU:HD11	42:R:109:TYR:CZ	1.95	1.02
1:1:909:G:H4'	55:w:750:ARG:HH22	1.28	0.97
1:1:909:G:C5'	55:w:750:ARG:HH22	1.79	0.96
31:q:269:ARG:HH21	31:q:533:PRO:HB2	1.32	0.94

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	7	125/204 (61%)	117 (94%)	8 (6%)	0	100	100
4	A	264/291 (91%)	245 (93%)	19 (7%)	0	100	100
5	B	331/387 (86%)	315 (95%)	16 (5%)	0	100	100
6	C	357/362 (99%)	347 (97%)	10 (3%)	0	100	100
7	E	160/176 (91%)	150 (94%)	10 (6%)	0	100	100
8	F	220/244 (90%)	213 (97%)	7 (3%)	0	100	100
9	H	188/191 (98%)	179 (95%)	9 (5%)	0	100	100
10	J	143/427 (34%)	136 (95%)	7 (5%)	0	100	100
11	L	119/199 (60%)	113 (95%)	6 (5%)	0	100	100
12	M	134/138 (97%)	128 (96%)	6 (4%)	0	100	100
13	N	185/204 (91%)	181 (98%)	4 (2%)	0	100	100
14	O	195/199 (98%)	193 (99%)	2 (1%)	0	100	100
15	P	181/184 (98%)	173 (96%)	8 (4%)	0	100	100
16	Q	132/186 (71%)	130 (98%)	2 (2%)	0	100	100
17	S	168/172 (98%)	162 (96%)	6 (4%)	0	100	100
18	T	50/160 (31%)	45 (90%)	5 (10%)	0	100	100
19	W	230/236 (98%)	217 (94%)	13 (6%)	0	100	100
20	X	135/142 (95%)	127 (94%)	8 (6%)	0	100	100
21	Y	124/127 (98%)	122 (98%)	2 (2%)	0	100	100
22	b	494/647 (76%)	473 (96%)	21 (4%)	0	100	100
23	d	105/113 (93%)	102 (97%)	3 (3%)	0	100	100
24	e	123/130 (95%)	119 (97%)	4 (3%)	0	100	100
25	f	104/107 (97%)	103 (99%)	1 (1%)	0	100	100
26	h	117/120 (98%)	114 (97%)	3 (3%)	0	100	100
27	i	75/100 (75%)	69 (92%)	6 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	j	71/88 (81%)	69 (97%)	2 (3%)	0	100	100
29	l	174/181 (96%)	164 (94%)	9 (5%)	1 (1%)	21	53
30	m	658/807 (82%)	629 (96%)	29 (4%)	0	100	100
31	q	356/618 (58%)	330 (93%)	26 (7%)	0	100	100
32	r	170/261 (65%)	165 (97%)	5 (3%)	0	100	100
33	s	34/520 (6%)	34 (100%)	0	0	100	100
34	u	138/199 (69%)	137 (99%)	1 (1%)	0	100	100
35	v	124/231 (54%)	119 (96%)	5 (4%)	0	100	100
36	y	223/245 (91%)	213 (96%)	10 (4%)	0	100	100
37	z	53/106 (50%)	53 (100%)	0	0	100	100
38	8	456/710 (64%)	435 (95%)	21 (5%)	0	100	100
39	I	531/663 (80%)	511 (96%)	20 (4%)	0	100	100
40	K	278/376 (74%)	267 (96%)	11 (4%)	0	100	100
41	V	132/137 (96%)	128 (97%)	4 (3%)	0	100	100
42	R	130/189 (69%)	128 (98%)	2 (2%)	0	100	100
43	G	194/256 (76%)	190 (98%)	4 (2%)	0	100	100
44	Z	133/136 (98%)	129 (97%)	4 (3%)	0	100	100
45	U	100/121 (83%)	94 (94%)	6 (6%)	0	100	100
46	c	95/105 (90%)	95 (100%)	0	0	100	100
47	g	110/121 (91%)	109 (99%)	1 (1%)	0	100	100
48	k	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
49	n	417/605 (69%)	401 (96%)	16 (4%)	0	100	100
50	p	331/460 (72%)	303 (92%)	28 (8%)	0	100	100
51	t	279/322 (87%)	271 (97%)	8 (3%)	0	100	100
53	D	426/505 (84%)	413 (97%)	13 (3%)	0	100	100
54	o	131/220 (60%)	128 (98%)	3 (2%)	0	100	100
55	w	656/841 (78%)	614 (94%)	42 (6%)	0	100	100
56	a	212/217 (98%)	192 (91%)	17 (8%)	3 (1%)	9	33
57	5	133/235 (57%)	126 (95%)	7 (5%)	0	100	100
58	x	531/606 (88%)	508 (96%)	22 (4%)	1 (0%)	43	73
All	All	11810/15605 (76%)	11302 (96%)	503 (4%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
56	a	63	MET
58	x	406	ASN
56	a	209	SER
56	a	65	ILE
29	l	41	LYS

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	
3	7	114/181 (63%)	114 (100%)	0	100	100
4	A	242/263 (92%)	242 (100%)	0	100	100
5	B	281/323 (87%)	281 (100%)	0	100	100
6	C	286/289 (99%)	286 (100%)	0	100	100
7	E	142/153 (93%)	142 (100%)	0	100	100
8	F	186/205 (91%)	186 (100%)	0	100	100
9	H	170/171 (99%)	170 (100%)	0	100	100
10	J	133/383 (35%)	133 (100%)	0	100	100
11	L	100/159 (63%)	100 (100%)	0	100	100
12	M	107/109 (98%)	107 (100%)	0	100	100
13	N	165/176 (94%)	165 (100%)	0	100	100
14	O	160/162 (99%)	160 (100%)	0	100	100
15	P	145/146 (99%)	145 (100%)	0	100	100
16	Q	110/151 (73%)	110 (100%)	0	100	100
17	S	155/156 (99%)	155 (100%)	0	100	100
18	T	41/137 (30%)	41 (100%)	0	100	100
19	W	209/213 (98%)	209 (100%)	0	100	100
20	X	114/118 (97%)	114 (100%)	0	100	100
21	Y	109/110 (99%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	b	447/573 (78%)	447 (100%)	0	100	100
23	d	94/97 (97%)	94 (100%)	0	100	100
24	e	108/111 (97%)	108 (100%)	0	100	100
25	f	90/91 (99%)	90 (100%)	0	100	100
26	h	104/105 (99%)	104 (100%)	0	100	100
27	i	65/82 (79%)	65 (100%)	0	100	100
28	j	60/71 (84%)	60 (100%)	0	100	100
29	l	151/156 (97%)	151 (100%)	0	100	100
30	m	599/722 (83%)	599 (100%)	0	100	100
31	q	304/535 (57%)	304 (100%)	0	100	100
32	r	156/229 (68%)	156 (100%)	0	100	100
33	s	32/445 (7%)	32 (100%)	0	100	100
34	u	125/180 (69%)	125 (100%)	0	100	100
35	v	116/205 (57%)	116 (100%)	0	100	100
36	y	193/211 (92%)	193 (100%)	0	100	100
37	z	48/95 (50%)	48 (100%)	0	100	100
38	8	351/647 (54%)	350 (100%)	1 (0%)	86	88
39	I	484/602 (80%)	484 (100%)	0	100	100
40	K	261/346 (75%)	261 (100%)	0	100	100
41	V	103/105 (98%)	103 (100%)	0	100	100
42	R	112/154 (73%)	112 (100%)	0	100	100
43	G	161/208 (77%)	161 (100%)	0	100	100
44	Z	115/116 (99%)	115 (100%)	0	100	100
45	U	89/107 (83%)	89 (100%)	0	100	100
46	c	81/88 (92%)	81 (100%)	0	100	100
47	g	95/103 (92%)	95 (100%)	0	100	100
48	k	68/69 (99%)	68 (100%)	0	100	100
49	n	381/548 (70%)	381 (100%)	0	100	100
50	p	300/413 (73%)	299 (100%)	1 (0%)	86	88
51	t	256/287 (89%)	256 (100%)	0	100	100
53	D	378/440 (86%)	378 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	o	118/199 (59%)	118 (100%)	0	100	100
55	w	592/745 (80%)	592 (100%)	0	100	100
56	a	195/198 (98%)	195 (100%)	0	100	100
57	5	133/217 (61%)	133 (100%)	0	100	100
58	x	489/548 (89%)	479 (98%)	10 (2%)	48	73
All	All	10423/13653 (76%)	10411 (100%)	12 (0%)	87	91

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
58	x	400	VAL
58	x	403	ILE
58	x	538	ASP
58	x	435	TYR
58	x	47	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 91 such sidechains are listed below:

Mol	Chain	Res	Type
43	G	61	GLN
51	t	157	ASN
45	U	40	HIS
49	n	590	GLN
53	D	287	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2643/3396 (77%)	555 (20%)	38 (1%)
2	2	157/158 (99%)	24 (15%)	1 (0%)
52	6	85/87 (97%)	24 (28%)	4 (4%)
All	All	2885/3641 (79%)	603 (20%)	43 (1%)

5 of 603 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U
1	1	3	U

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Mol	Chain	Res	Type
1	1	6	A
1	1	7	C
1	1	14	U

5 of 43 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2496	C
1	1	3218	A
1	1	2500	A
1	1	2602	G
1	1	3269	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	PSU	1	2923	1	18,21,22	1.37	2 (11%)	21,30,33	2.02	4 (19%)
1	OMU	1	2921	1	19,22,23	0.73	0	25,31,34	1.00	2 (8%)
1	A2M	1	2946	1	22,25,26	1.45	3 (13%)	30,36,39	1.04	2 (6%)
1	OMG	1	2922	1	23,26,27	1.14	3 (13%)	32,38,41	0.88	1 (3%)

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
1	PSU	1	2923	1	-	1/7/25/26	0/2/2/2
1	OMU	1	2921	1	-	0/9/27/28	0/2/2/2
1	A2M	1	2946	1	-	1/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMG	1	2922	1	-	1/9/27/28	0/3/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2946	A2M	O5'-C5'	-3.43	1.34	1.44
1	1	2923	PSU	C6-C5	3.28	1.38	1.35
1	1	2922	OMG	C6-N1	2.80	1.44	1.38
1	1	2923	PSU	C4-N3	-2.62	1.33	1.38
1	1	2922	OMG	C2-N2	2.62	1.40	1.34

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2923	PSU	N1-C2-N3	6.31	121.83	115.17
1	1	2923	PSU	C4-N3-C2	-4.08	120.75	126.37
1	1	2923	PSU	O2-C2-N1	-3.54	119.14	122.79
1	1	2921	OMU	CM2-O2'-C2'	-2.56	107.89	114.47
1	1	2921	OMU	C4-N3-C2	-2.43	123.60	126.61

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1	2922	OMG	O4'-C4'-C5'-O5'
1	1	2923	PSU	O4'-C1'-C5-C4
1	1	2946	A2M	C4'-C5'-O5'-P

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	2923	PSU	3	0
1	1	2946	A2M	1	0
1	1	2922	OMG	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
60	SAH	w	901	-	27,28,28	1.10	4 (14%)	36,40,40	2.02	9 (25%)

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	SAH	w	901	-	-	6/15/31/31	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	w	901	SAH	C2-N3	2.53	1.38	1.33
60	w	901	SAH	C2-N1	2.51	1.38	1.33
60	w	901	SAH	OXT-C	-2.24	1.23	1.30
60	w	901	SAH	C8-N7	2.09	1.35	1.31

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	w	901	SAH	N3-C2-N1	-5.50	120.26	128.58
60	w	901	SAH	C5-C4-N3	-4.52	120.50	126.72
60	w	901	SAH	C5'-SD-CG	-3.89	90.71	102.26
60	w	901	SAH	N9-C8-N7	-3.81	108.52	113.94
60	w	901	SAH	C2-N3-C4	3.42	120.19	111.83

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

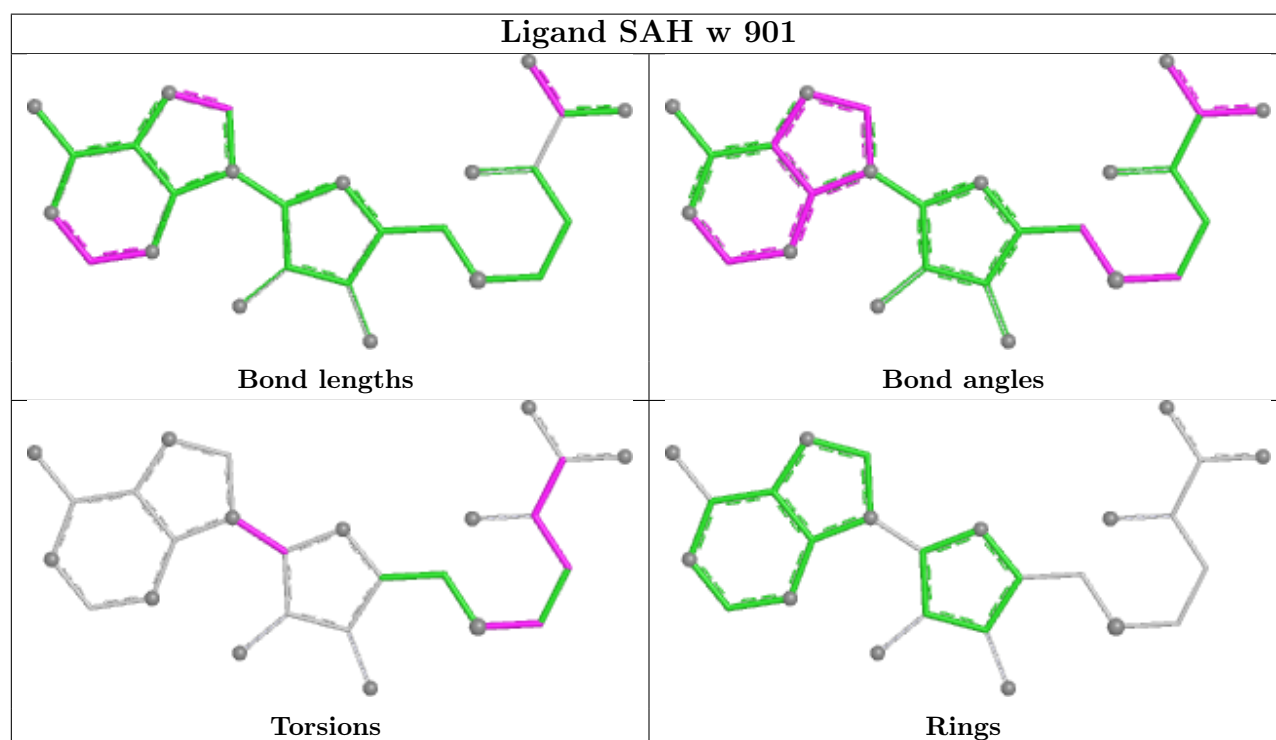
Mol	Chain	Res	Type	Atoms
60	w	901	SAH	C-CA-CB-CG
60	w	901	SAH	N-CA-CB-CG
60	w	901	SAH	OXT-C-CA-N
60	w	901	SAH	CB-CG-SD-C5'
60	w	901	SAH	C2'-C1'-N9-C8

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	w	901	SAH	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.



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
52	6	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	6	67:U	O3'	213:A	P	14.86

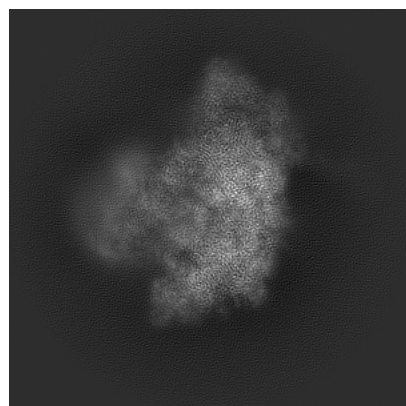
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24269. These allow visual inspection of the internal detail of the map and identification of artifacts.

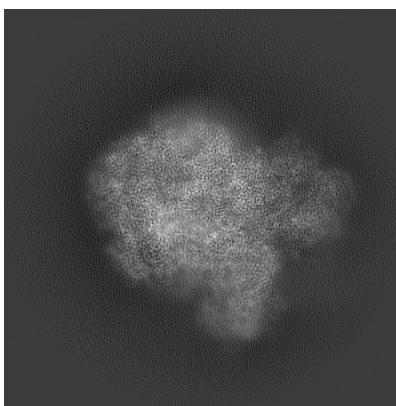
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

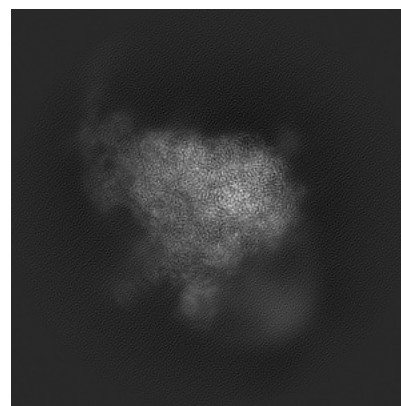
6.1.1 Primary map



X

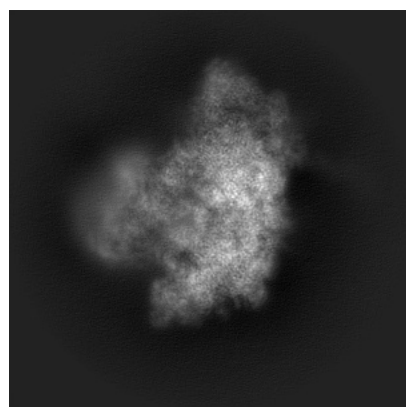


Y

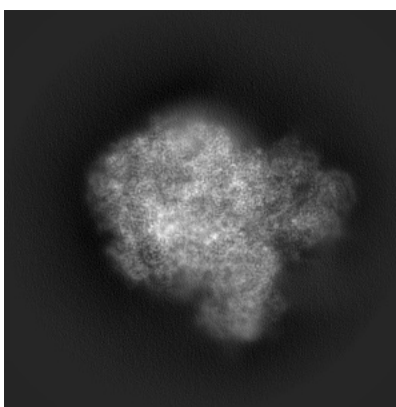


Z

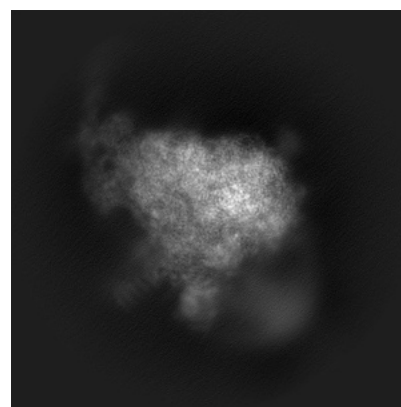
6.1.2 Raw map



X



Y

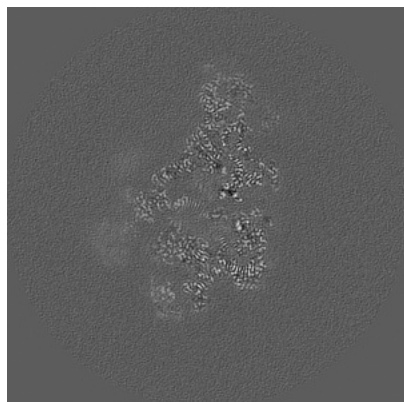


Z

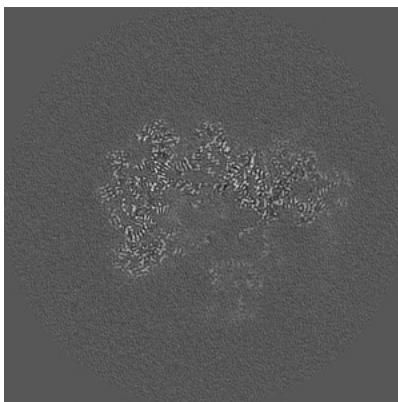
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

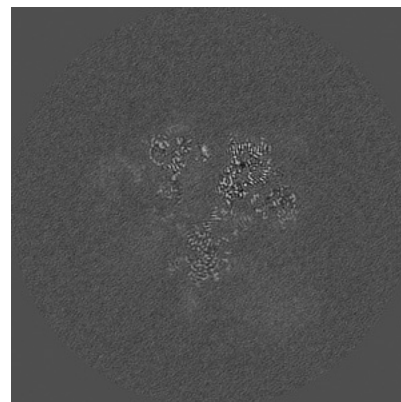
6.2.1 Primary map



X Index: 210

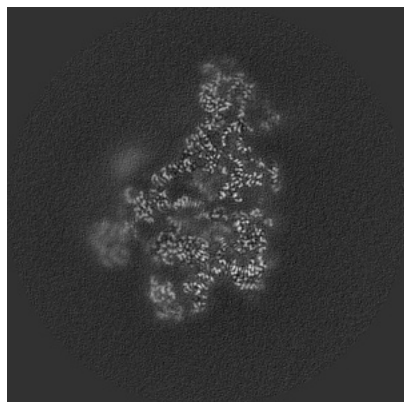


Y Index: 210

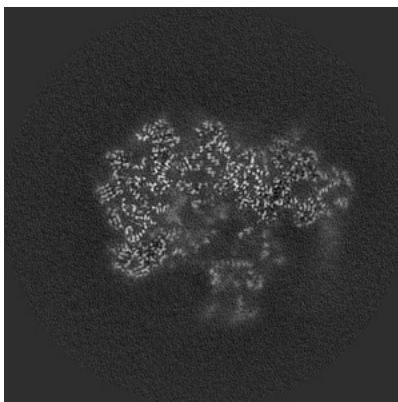


Z Index: 210

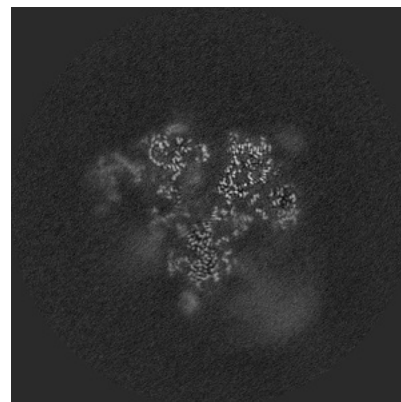
6.2.2 Raw map



X Index: 210



Y Index: 210

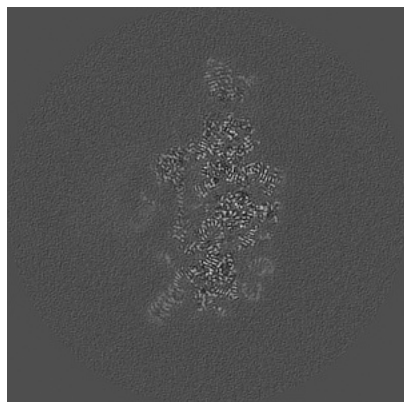


Z Index: 210

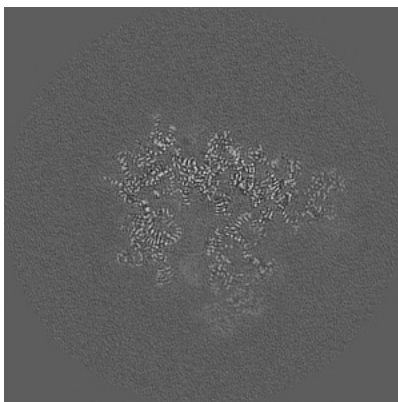
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

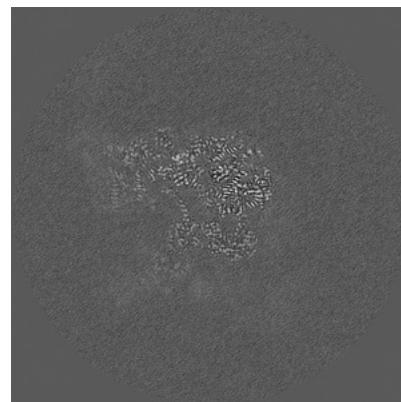
6.3.1 Primary map



X Index: 234

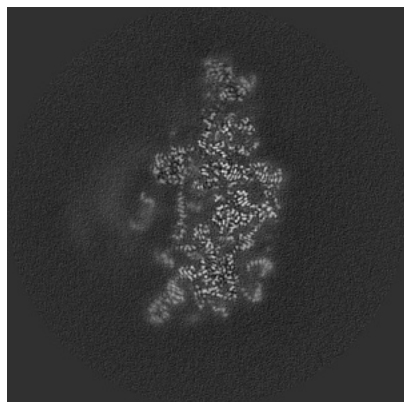


Y Index: 233

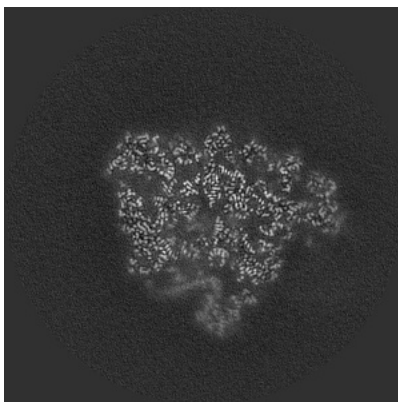


Z Index: 247

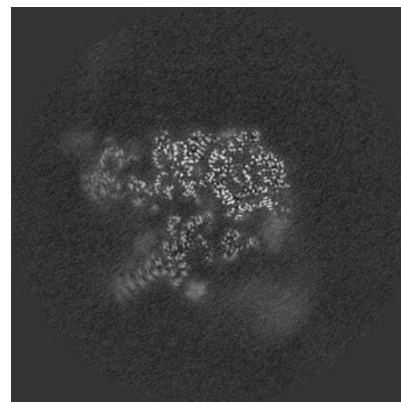
6.3.2 Raw map



X Index: 236



Y Index: 246

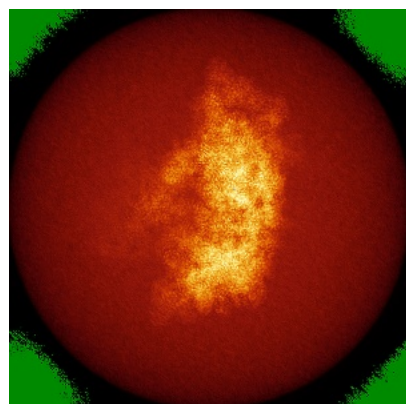


Z Index: 235

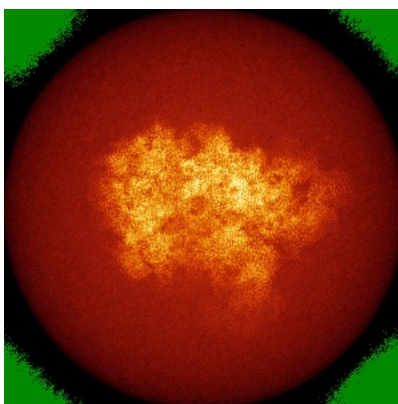
The images above show the largest variance slices of the map in three orthogonal directions.

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

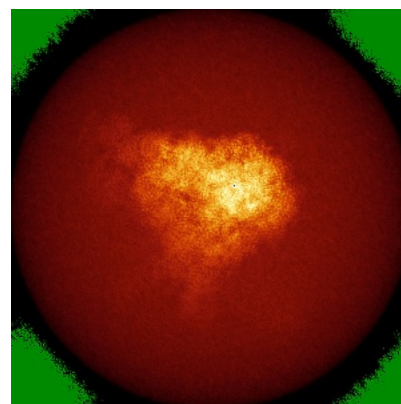
6.4.1 Primary map



X

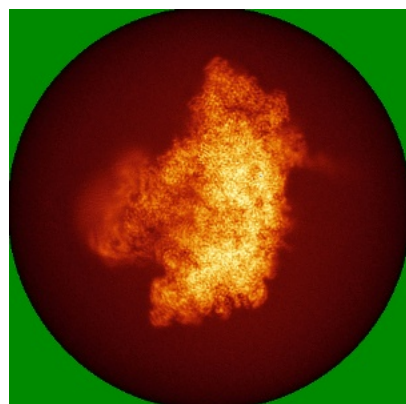


Y

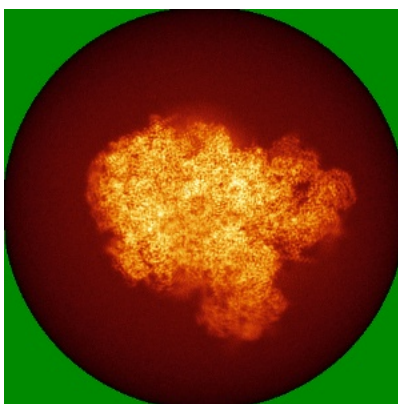


Z

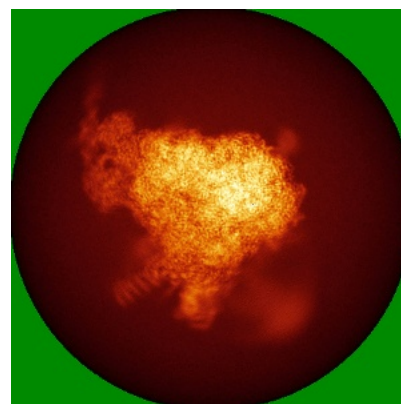
6.4.2 Raw map



X



Y

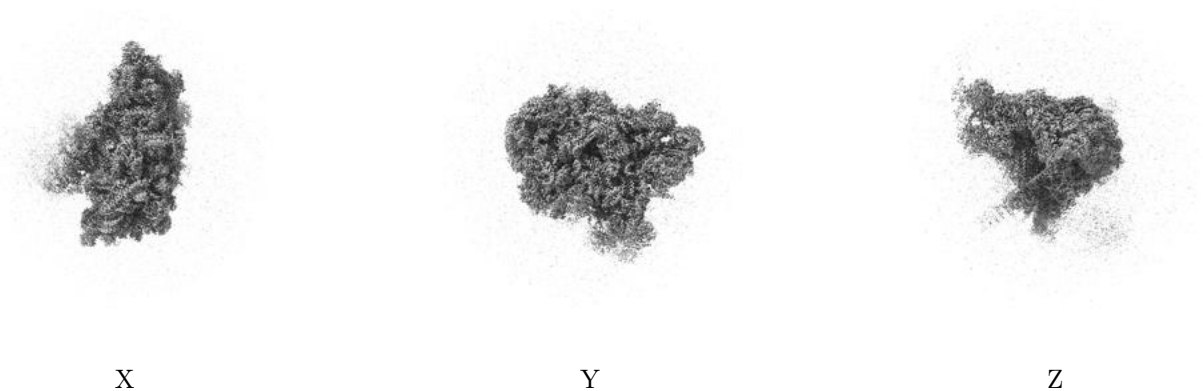


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0275. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

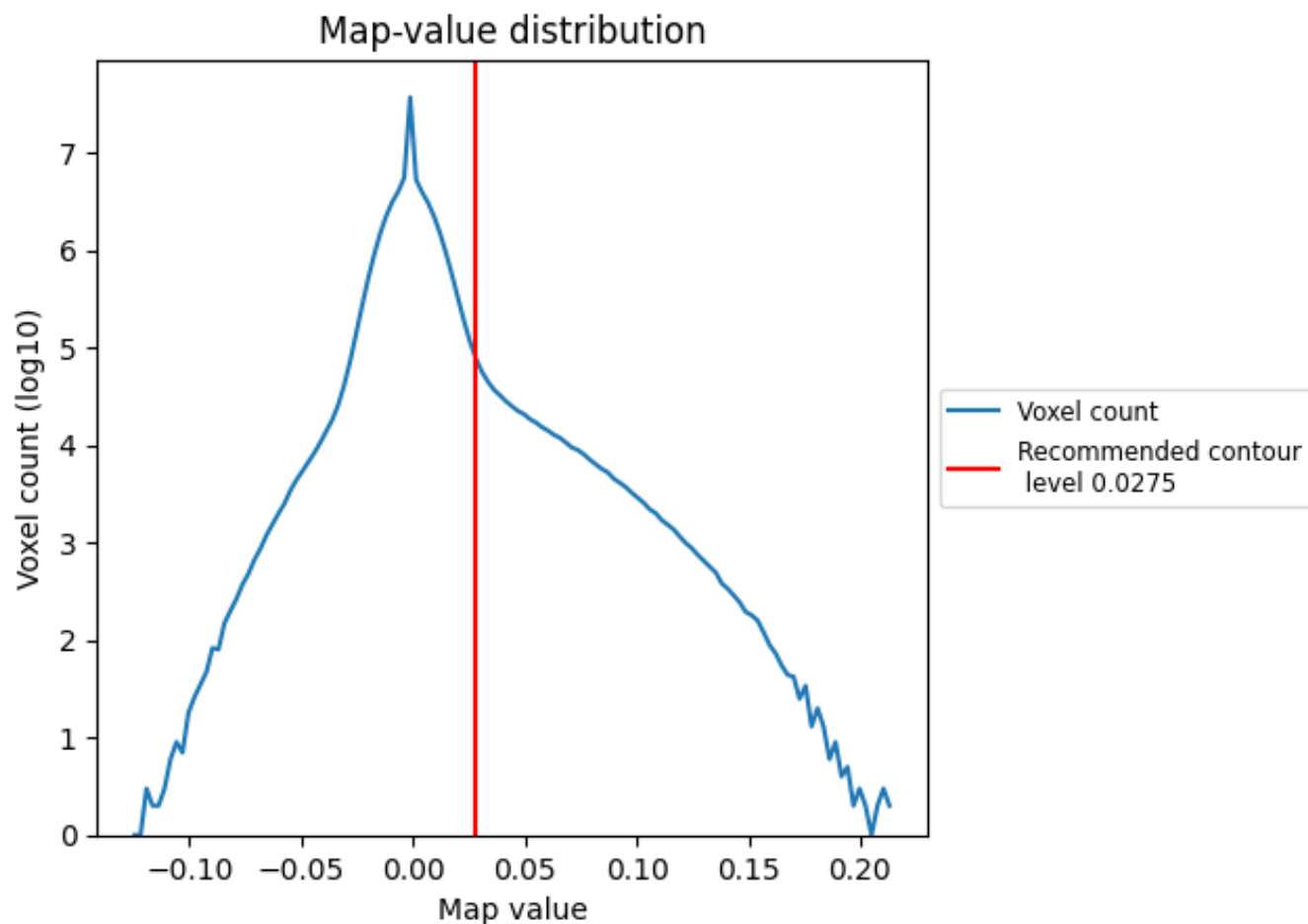
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

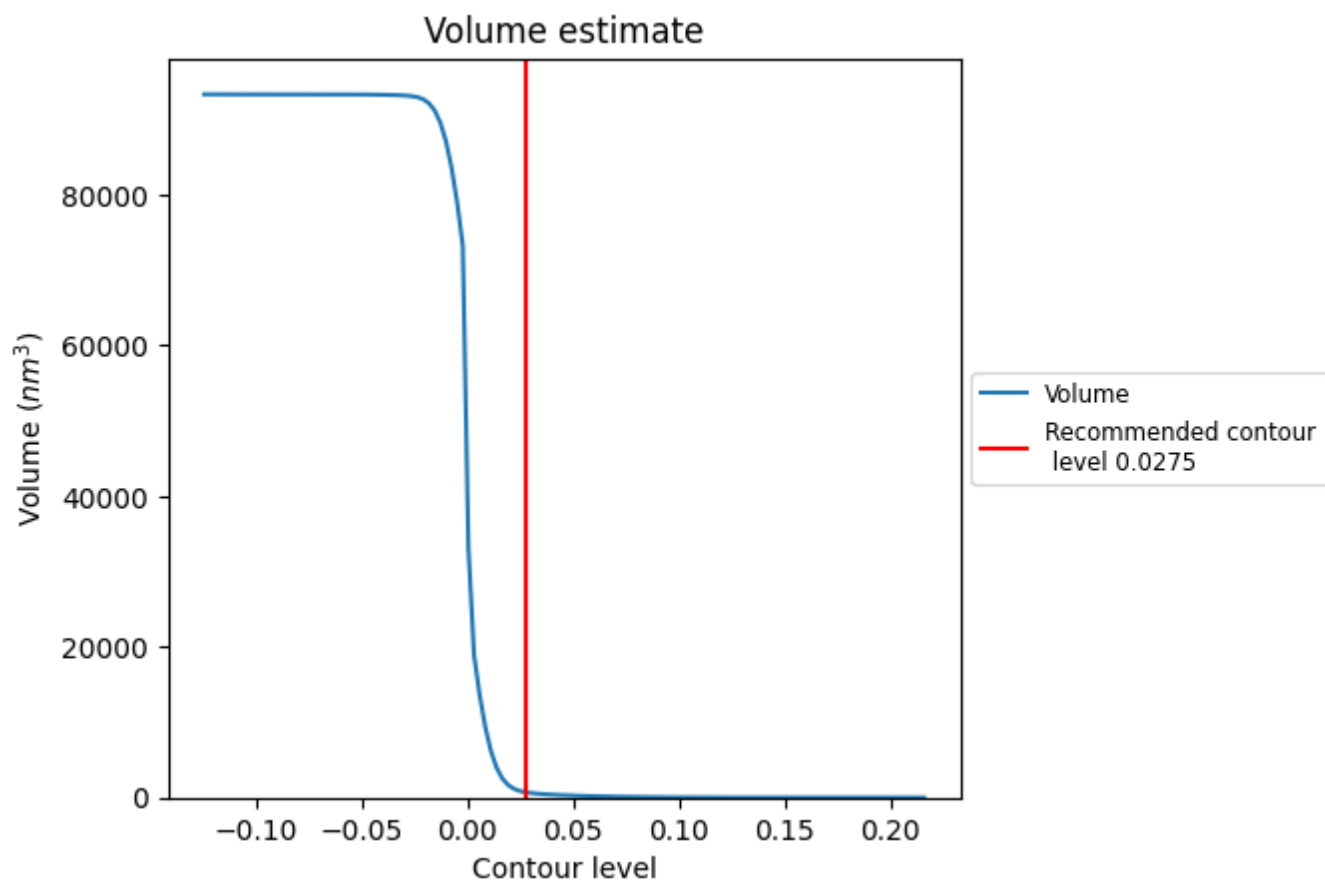
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

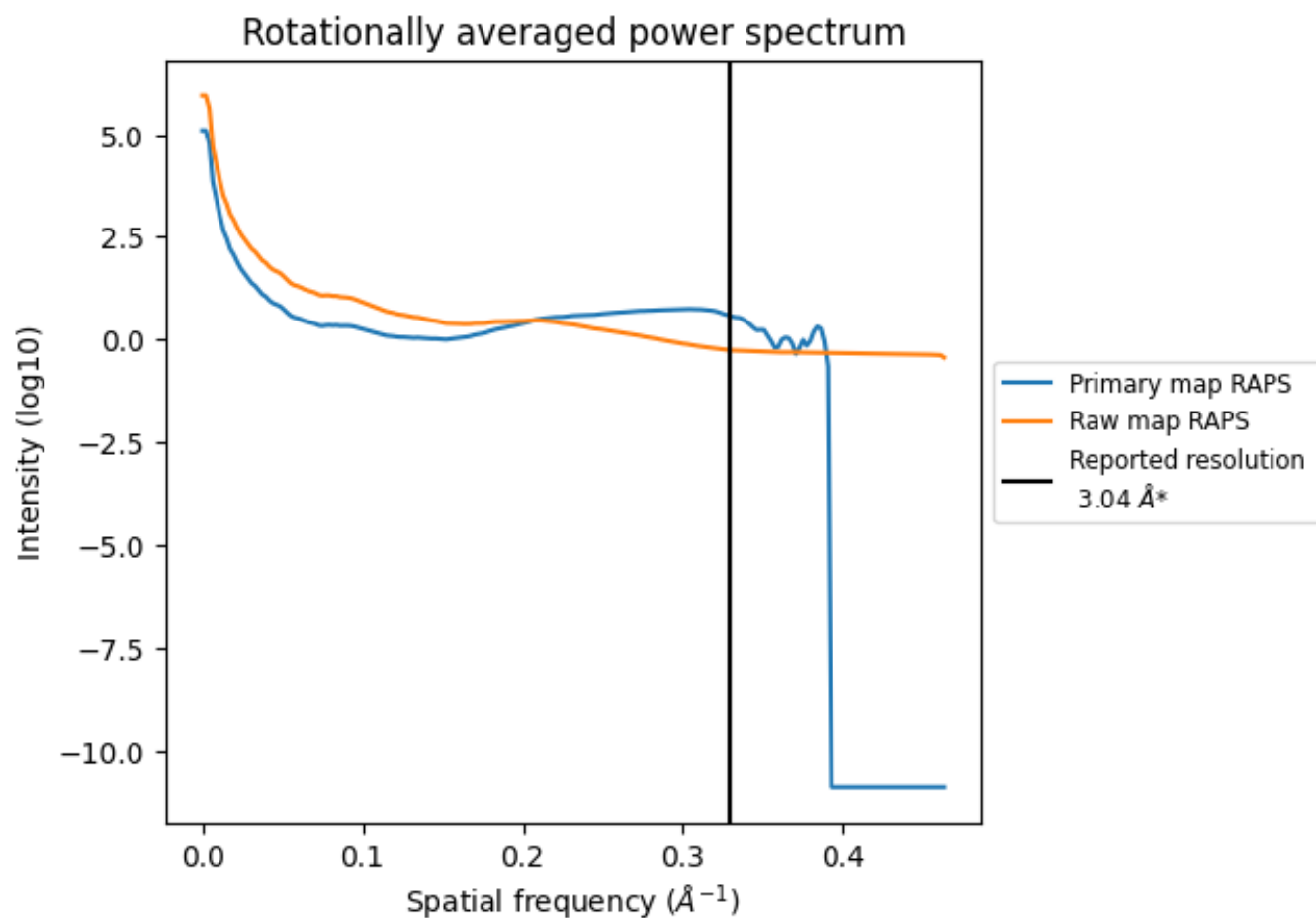
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 704 nm³; this corresponds to an approximate mass of 636 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 ⓘ

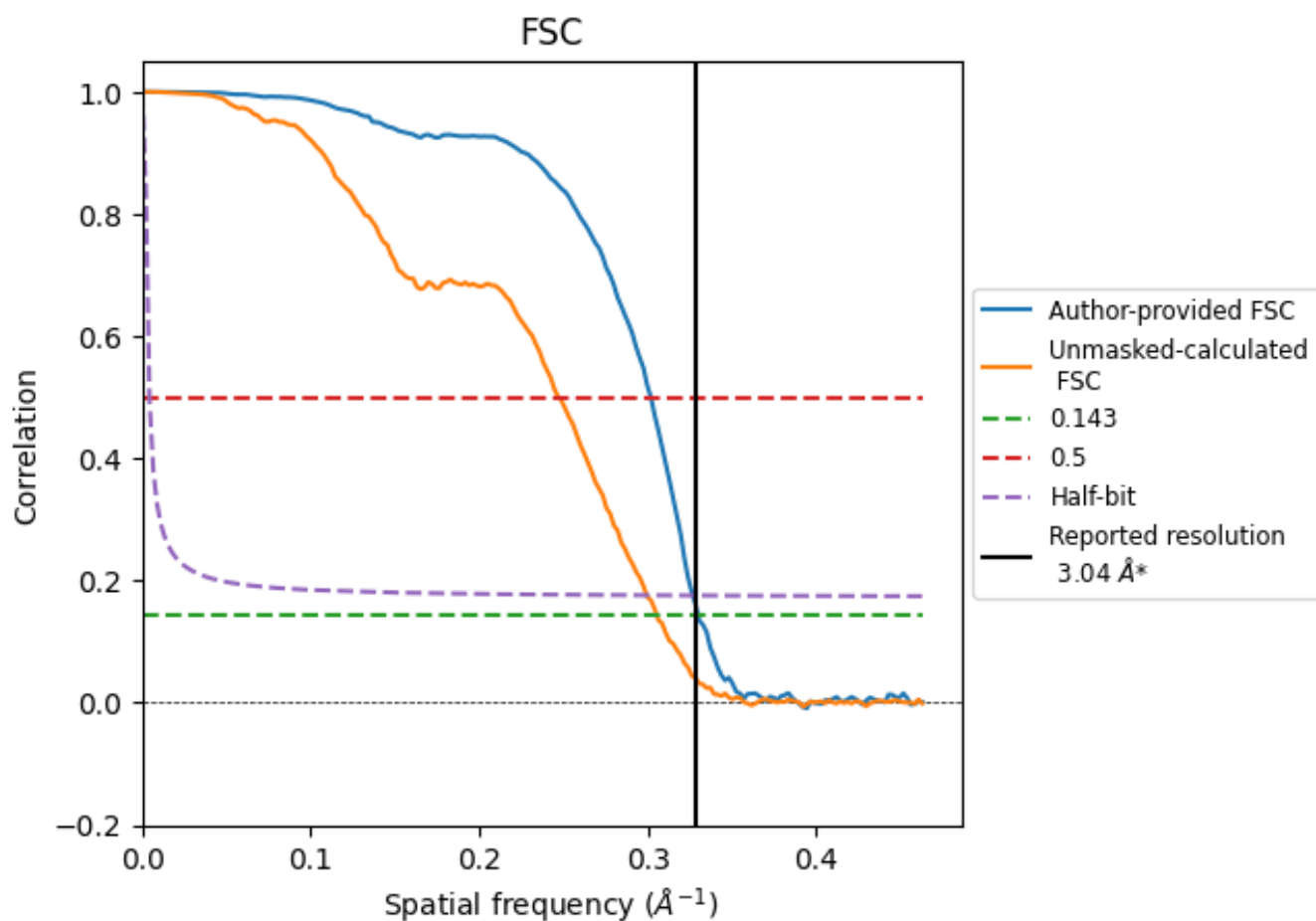


*Reported resolution corresponds to spatial frequency of $0.329 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.329 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

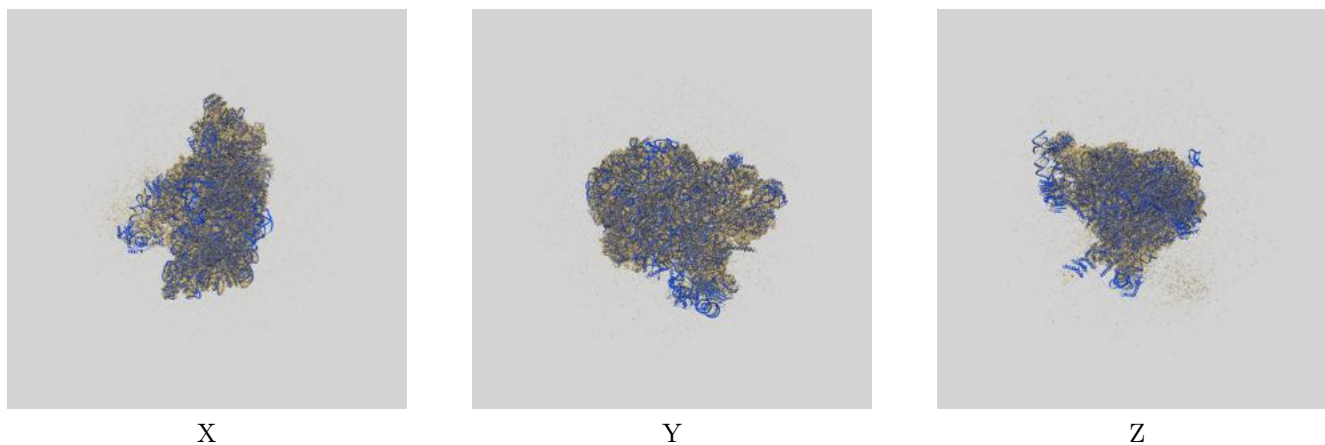
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.04	-	-
Author-provided FSC curve	3.03	3.31	3.06
Unmasked-calculated*	3.27	4.05	3.34

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

9 Map-model fit [i](#)

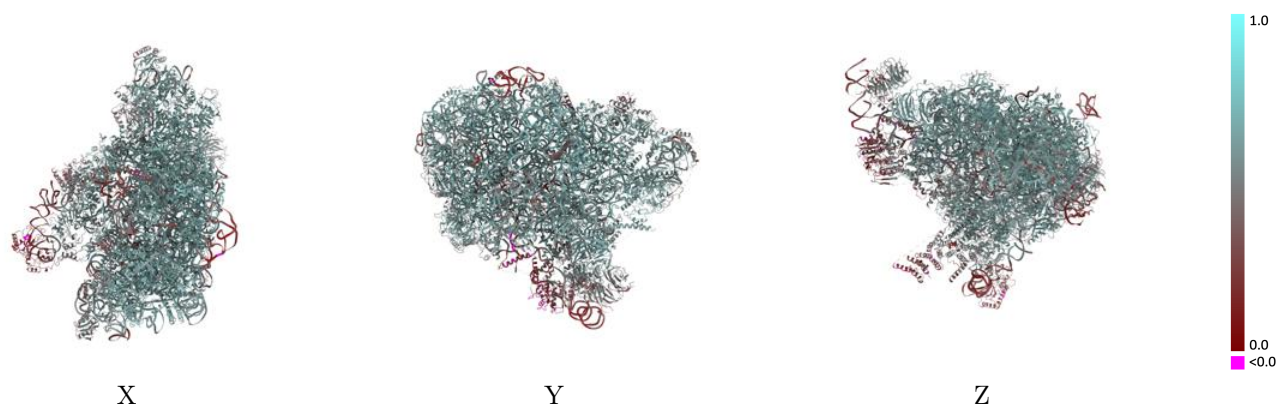
This section contains information regarding the fit between EMDB map EMD-24269 and PDB model 7NAC. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.0275 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](#)

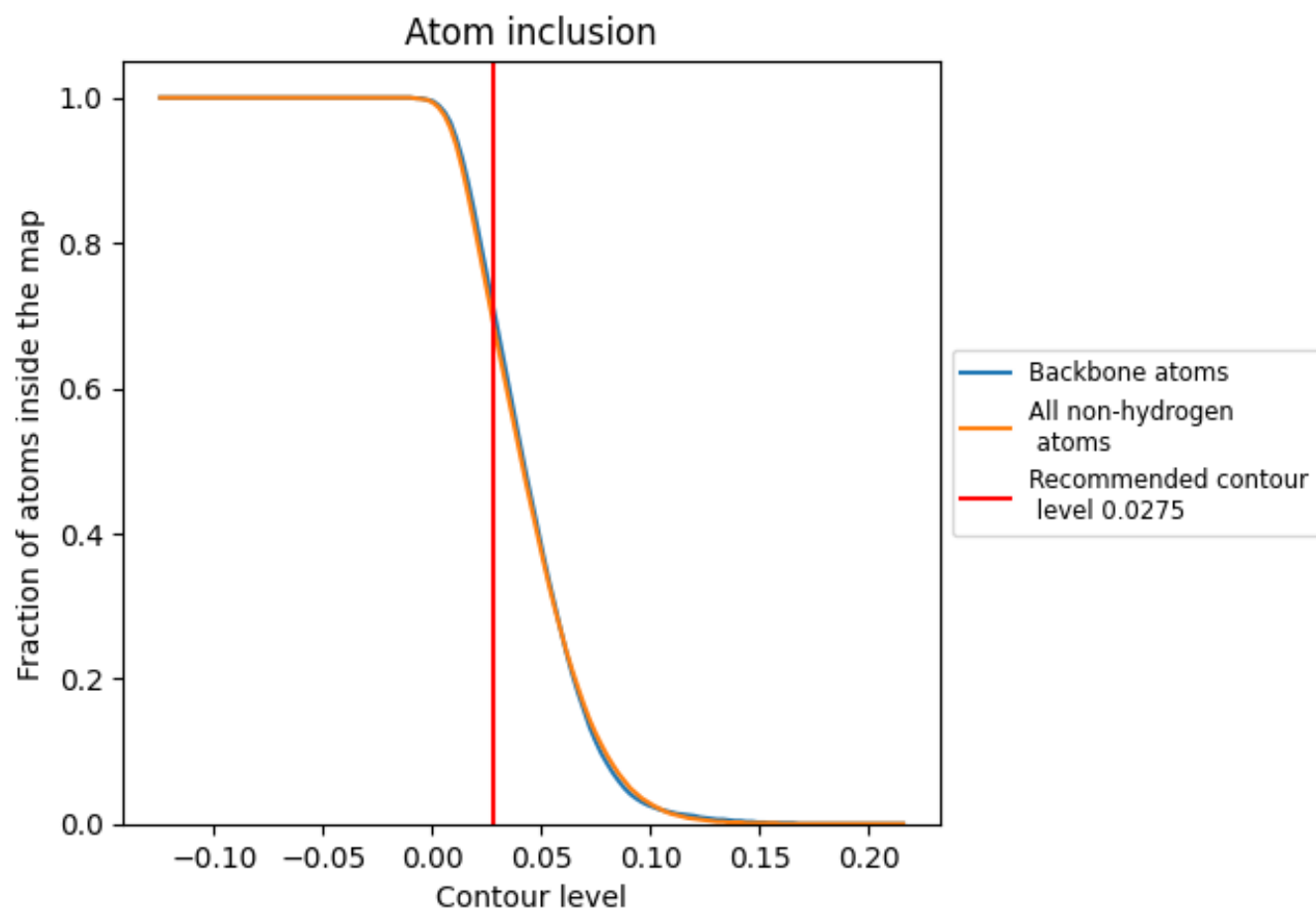


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 70% 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 (0.0275) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6970	 0.5490
1	 0.7670	 0.5470
2	 0.9030	 0.6080
5	 0.2830	 0.4650
6	 0.7140	 0.5480
7	 0.6390	 0.5610
8	 0.3090	 0.4270
A	 0.6680	 0.5390
B	 0.8900	 0.6200
C	 0.8700	 0.6250
D	 0.4970	 0.5230
E	 0.7690	 0.5870
F	 0.8230	 0.6100
G	 0.8380	 0.6120
H	 0.8040	 0.6050
I	 0.6150	 0.5450
J	 0.6210	 0.5550
K	 0.6280	 0.5510
L	 0.8710	 0.6240
M	 0.8310	 0.6110
N	 0.9340	 0.6420
O	 0.9030	 0.6290
P	 0.7790	 0.5880
Q	 0.8090	 0.6090
R	 0.6550	 0.5550
S	 0.7390	 0.5850
T	 0.0330	 0.3610
U	 0.6250	 0.5490
V	 0.8300	 0.6170
W	 0.4160	 0.4790
X	 0.8200	 0.6170
Y	 0.8850	 0.6230
Z	 0.7620	 0.5990
a	 0.0230	 0.2310
b	 0.5820	 0.5370



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Chain	Atom inclusion	Q-score
c	 0.6210	 0.5600
d	 0.7530	 0.5810
e	 0.8820	 0.6320
f	 0.9460	 0.6500
g	 0.8280	 0.6130
h	 0.8660	 0.6260
i	 0.7870	 0.5850
j	 0.9080	 0.6390
k	 0.6930	 0.5830
l	 0.7590	 0.5940
m	 0.7530	 0.5940
n	 0.7830	 0.6010
o	 0.6510	 0.5500
p	 0.3150	 0.4580
q	 0.5830	 0.5280
r	 0.6930	 0.5770
s	 0.7750	 0.6040
t	 0.7190	 0.5860
u	 0.7490	 0.5890
v	 0.8220	 0.6080
w	 0.5630	 0.5320
x	 0.1590	 0.3020
y	 0.8050	 0.5930
z	 0.4950	 0.5320