



wwPDB EM Validation Summary Report ⓘ

Dec 30, 2024 – 01:40 AM EST

PDB ID : 8A3D
EMDB ID : EMD-15113
Title : Human mature large subunit of the ribosome with eIF6 and homoharringtonine bound
Authors : Faille, A.; Warren, A.J.; Dent, K.C.
Deposited on : 2022-06-08
Resolution : 1.67 Å(reported)
Based on initial model : 6EK0

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

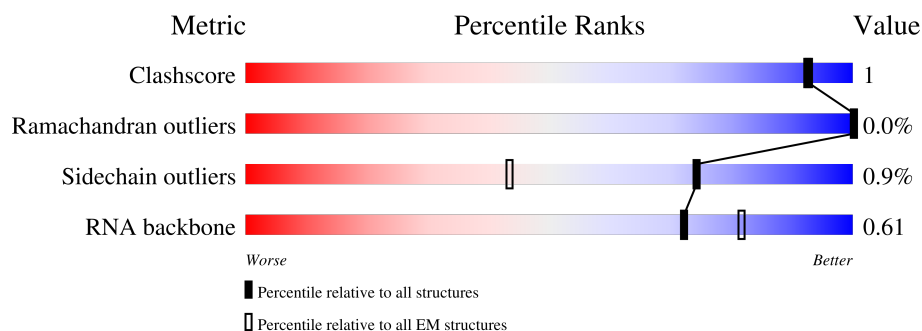
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 1.67 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	A	5069	<div> <div>16%</div> <div>46%</div> <div>16%</div> <div>•</div> <div>35%</div> </div>
2	B	121	<div> <div>11%</div> <div>84%</div> <div>13%</div> <div>••</div> </div>
3	C	157	<div> <div>16%</div> <div>65%</div> <div>22%</div> <div>6%</div> <div>•</div> <div>6%</div> </div>
4	D	257	<div> <div>5%</div> <div>92%</div> <div>•</div> <div>•</div> </div>
5	E	403	<div> <div>20%</div> <div>94%</div> <div>••</div> </div>
6	F	427	<div> <div>10%</div> <div>81%</div> <div>•</div> <div>16%</div> </div>
7	G	297	<div> <div>45%</div> <div>93%</div> <div>••</div> </div>

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Mol	Chain	Length	Quality of chain
8	H	288	
9	m	248	
10	n	266	
11	o	192	
12	p	214	
13	q	178	
14	r	211	
15	s	220	
16	l	204	
17	I	203	
18	J	184	
19	K	188	
20	L	196	
21	M	176	
22	N	160	
23	O	128	
24	P	140	
25	Q	157	
26	R	156	
27	S	145	
28	T	136	
29	U	148	
30	V	159	
31	W	115	
32	X	125	

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Mol	Chain	Length	Quality of chain
33	Y	135	
34	Z	110	
35	a	117	
36	b	196	
37	c	105	
38	d	97	
39	e	70	
40	f	51	
41	g	99	
42	i	106	
43	j	92	
44	k	137	
45	h	245	

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 142233 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 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3303	Total	C	N	O	P	1	0
			70928	31625	12983	23017	3303		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	4910	A	G	conflict	GB 86475748

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	148	Total	C	N	O	P	0	0
			3153	1408	563	1035	147		

- Molecule 4 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	246	Total	C	N	O	S	0	0
			1887	1183	387	311	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	395	Total	C	N	O	S	1	0
			3194	2034	600	545	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	359	Total	C	N	O	S	0	0
			2855	1797	571	474	13		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	285	Total	C	N	O	S	0	0
			2308	1460	419	415	14		

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	219	Total	C	N	O	S	0	0
			1757	1132	333	288	4		

- Molecule 9 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	m	212	Total	C	N	O	S	0	0
			1755	1127	334	285	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	n	223	Total	C	N	O	S	0	0
			1809	1153	349	303	4		

- Molecule 11 is a protein called 60S ribosomal protein L9.

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

- Molecule 12 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	p	204	Total	C	N	O	S	0	0
			1654	1051	318	272	13		

- Molecule 13 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	q	170	Total	C	N	O	S	0	0
			1358	858	253	241	6		

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	r	206	Total	C	N	O	S	0	0
			1664	1041	345	274	4		

- Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	s	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	l	203	Total	C	N	O	S	1	0
			1708	1077	360	267	4		

- Molecule 17 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	199	Total	C	N	O	S	0	0
			1634	1053	319	257	5		

- Molecule 18 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	152	Total	C	N	O	S	0	0
			1233	771	240	213	9		

- Molecule 19 is a protein called 60S ribosomal protein L18.

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

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	157	Total	C	N	O	S	0	0
			1304	813	280	202	9		

- Molecule 21 is a protein called 60S ribosomal protein L18a.

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

- Molecule 22 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 23 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	99	Total	C	N	O	S	0	0
			804	516	140	146	2		

- Molecule 24 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	132	Total	C	N	O	S	0	0
			985	621	185	174	5		

- Molecule 25 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	62	Total	C	N	O	S	0	0
			519	332	101	83	3		

- Molecule 26 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

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

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

- Molecule 28 is a protein called 60S ribosomal protein L27.

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

- Molecule 29 is a protein called 60S ribosomal protein L27a.

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

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	V	94	Total	C	N	O	S	0	0
			773	480	171	119	3		

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	W	100	Total	C	N	O	S	0	0
			772	490	136	139	7		

- Molecule 32 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	X	106	Total	C	N	O	S	0	0
			868	551	170	145	2		

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Y	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 34 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z	109	Total	C	N	O	S	1	0
			879	557	174	144	4		

- Molecule 35 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	a	106	Total	C	N	O	S	0	0
			845	530	174	135	6		

- Molecule 36 is a protein called Ribosomal protein uL29.

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

- Molecule 37 is a protein called 60S ribosomal protein L36.

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

- Molecule 38 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	d	86	Total	C	N	O	S	1	0
			713	442	155	111	5		

- Molecule 39 is a protein called 60S ribosomal protein L38.

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

- Molecule 40 is a protein called 60S ribosomal protein L39.

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

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	g	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 42 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	i	103	Total	C	N	O	S	0	0
			842	528	172	136	6		

- Molecule 43 is a protein called 60S ribosomal protein L37a.

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

- Molecule 44 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	k	124	Total	C	N	O	S	0	0
			992	615	206	167	4		

- Molecule 45 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	h	225	Total	C	N	O	S	0	0
			1712	1065	295	340	12		

- Molecule 46 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
46	A	214	Total	Mg	0
			214	214	
46	B	3	Total	Mg	0
			3	3	
46	C	6	Total	Mg	0
			6	6	
46	J	1	Total	Mg	0
			1	1	
46	L	2	Total	Mg	0
			2	2	
46	P	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
46	U	1	Total 1	Mg 1	0
46	d	1	Total 1	Mg 1	0

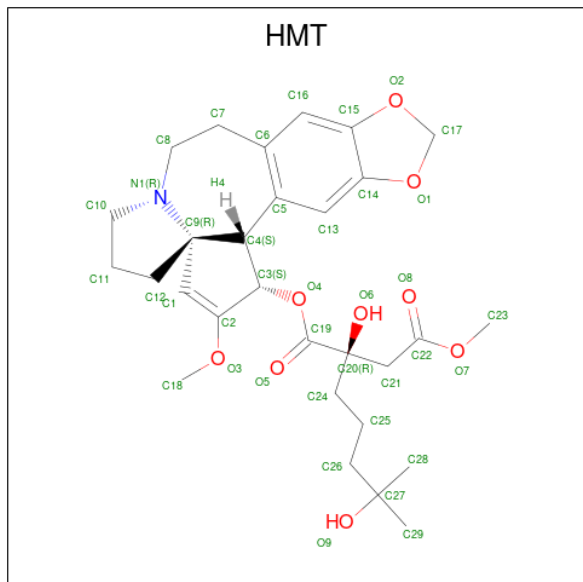
- Molecule 47 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
47	A	139	Total 139	K 139	0
47	B	1	Total 1	K 1	0
47	D	3	Total 3	K 3	0
47	o	1	Total 1	K 1	0
47	p	1	Total 1	K 1	0
47	l	2	Total 2	K 2	0
47	J	1	Total 1	K 1	0
47	N	1	Total 1	K 1	0
47	V	1	Total 1	K 1	0
47	Y	1	Total 1	K 1	0
47	Z	1	Total 1	K 1	0
47	a	1	Total 1	K 1	0
47	f	1	Total 1	K 1	0
47	i	1	Total 1	K 1	0

- Molecule 48 is SODIUM ION (three-letter code: NA) (formula: Na).

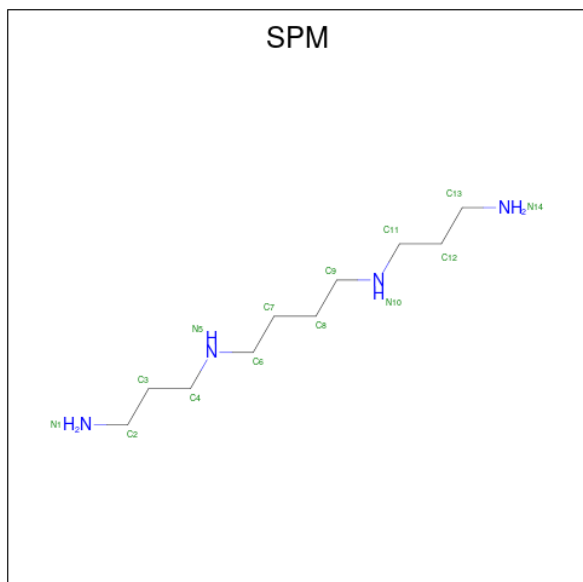
Mol	Chain	Residues	Atoms		AltConf
48	A	2	Total 2	Na 2	0

- Molecule 49 is (3beta)-O 3 -[(2R)-2,6-dihydroxy-2-(2-methoxy-2-oxoethyl)-6-methylheptano yl]cephalotaxine (three-letter code: HMT) (formula: $C_{29}H_{39}NO_9$).



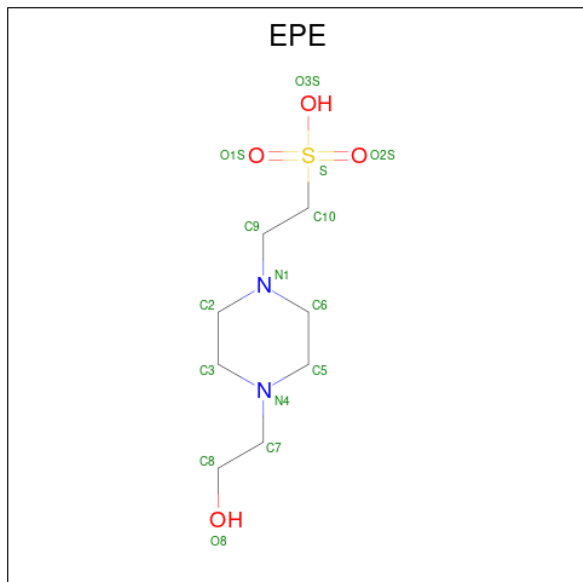
Mol	Chain	Residues	Atoms			AltConf
49	A	1	Total	C	N	O
			39	29	1	9
						0

- Molecule 50 is SPERMINE (three-letter code: SPM) (formula: $C_{10}H_{26}N_4$).



Mol	Chain	Residues	Atoms			AltConf
50	A	1	Total	C	N	
			14	10	4	0

- Molecule 51 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms					AltConf
51	A	1	Total	C	N	O	S	0
			15	8	2	4	1	

- Molecule 52 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
52	a	1	Total	Zn	0
			1	1	
52	d	1	Total	Zn	0
			1	1	
52	g	1	Total	Zn	0
			1	1	
52	i	1	Total	Zn	0
			1	1	
52	j	1	Total	Zn	0
			1	1	

- Molecule 53 is water.

Mol	Chain	Residues	Atoms		AltConf
53	A	8641	Total	O	0
			8641	8641	
53	B	261	Total	O	0
			261	261	

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Mol	Chain	Residues	Atoms		AltConf
53	C	363	Total 363	O 363	0
53	D	131	Total 131	O 131	0
53	E	177	Total 177	O 177	0
53	F	202	Total 202	O 202	0
53	G	67	Total 67	O 67	0
53	H	49	Total 49	O 49	0
53	m	131	Total 131	O 131	0
53	n	46	Total 46	O 46	0
53	o	43	Total 43	O 43	0
53	p	81	Total 81	O 81	0
53	q	13	Total 13	O 13	0
53	r	101	Total 101	O 101	0
53	s	38	Total 38	O 38	0
53	l	155	Total 155	O 155	0
53	I	117	Total 117	O 117	0
53	J	63	Total 63	O 63	0
53	K	139	Total 139	O 139	0
53	L	57	Total 57	O 57	0
53	M	100	Total 100	O 100	0
53	N	87	Total 87	O 87	0
53	O	5	Total 5	O 5	0

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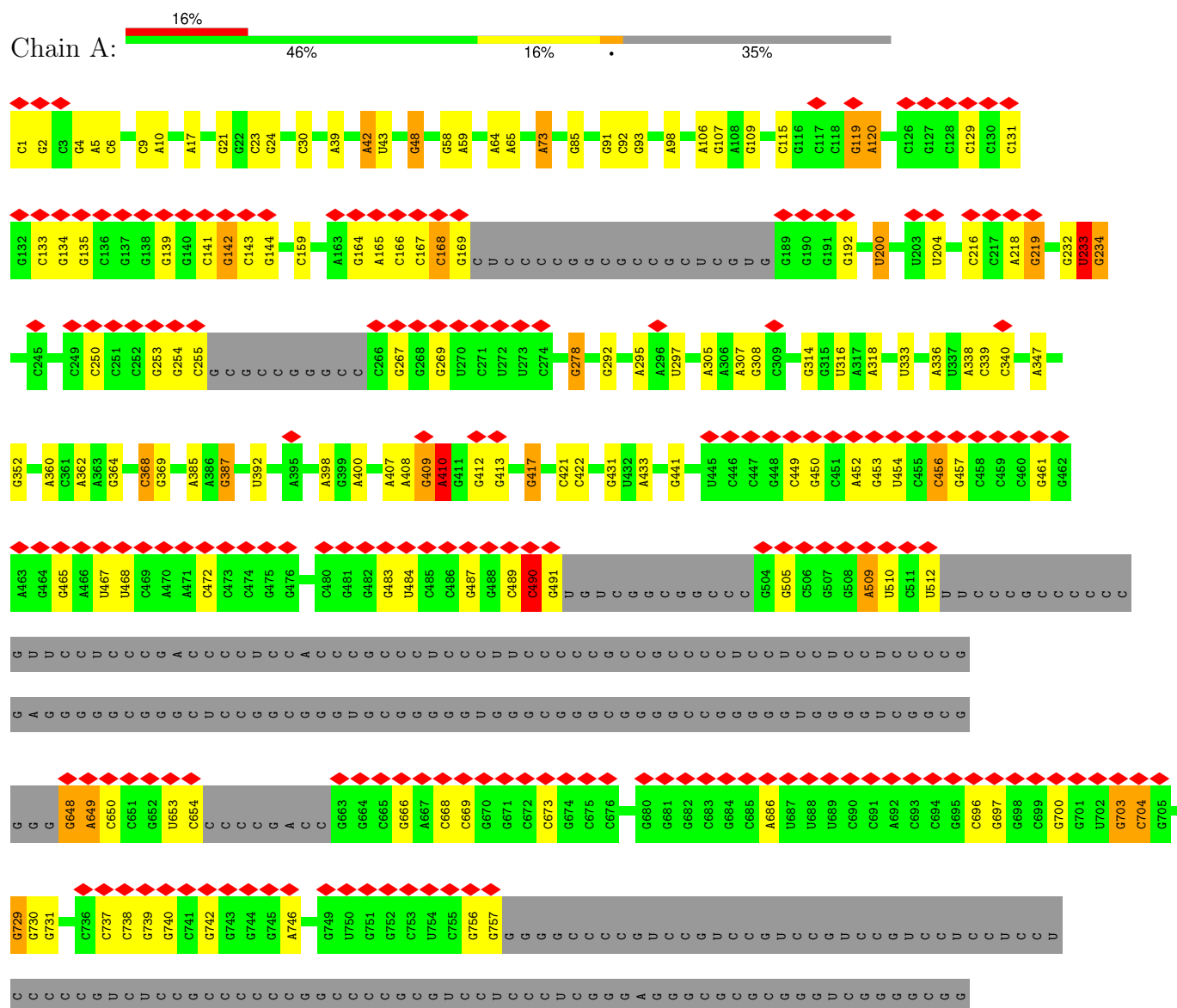
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Mol	Chain	Residues	Atoms		AltConf
53	P	40	Total 40	O 40	0
53	Q	21	Total 21	O 21	0
53	R	35	Total 35	O 35	0
53	S	49	Total 49	O 49	0
53	T	13	Total 13	O 13	0
53	U	92	Total 92	O 92	0
53	V	39	Total 39	O 39	0
53	W	9	Total 9	O 9	0
53	X	37	Total 37	O 37	0
53	Y	112	Total 112	O 112	0
53	Z	72	Total 72	O 72	0
53	a	58	Total 58	O 58	0
53	b	29	Total 29	O 29	0
53	c	32	Total 32	O 32	0
53	d	62	Total 62	O 62	0
53	e	3	Total 3	O 3	0
53	f	19	Total 19	O 19	0
53	g	14	Total 14	O 14	0
53	i	52	Total 52	O 52	0
53	j	40	Total 40	O 40	0
53	k	78	Total 78	O 78	0

3 Residue-property plots [i](#)

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

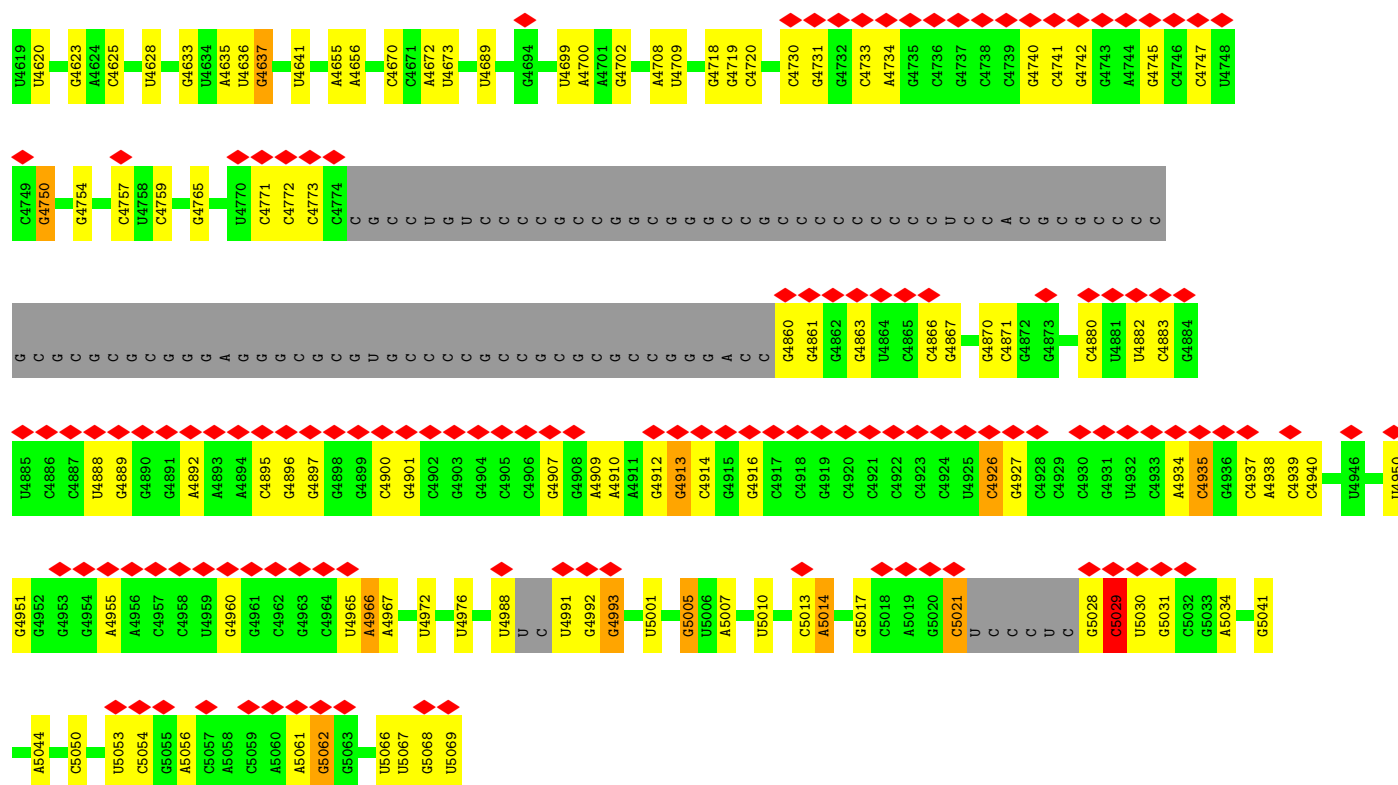
• Molecule 1: 28S ribosomal RNA



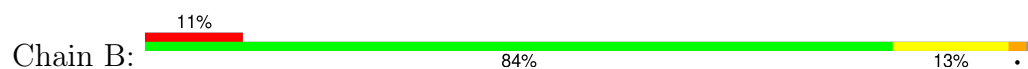




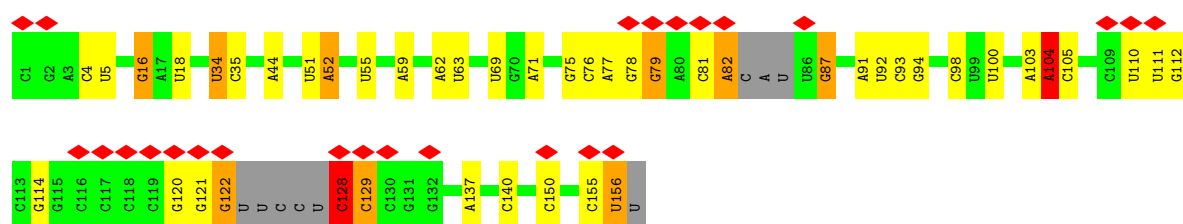




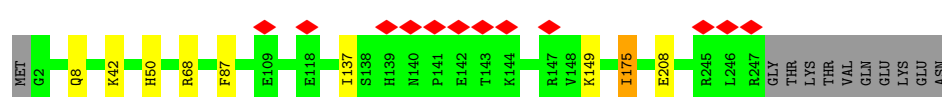
• Molecule 2: 5S ribosomal RNA

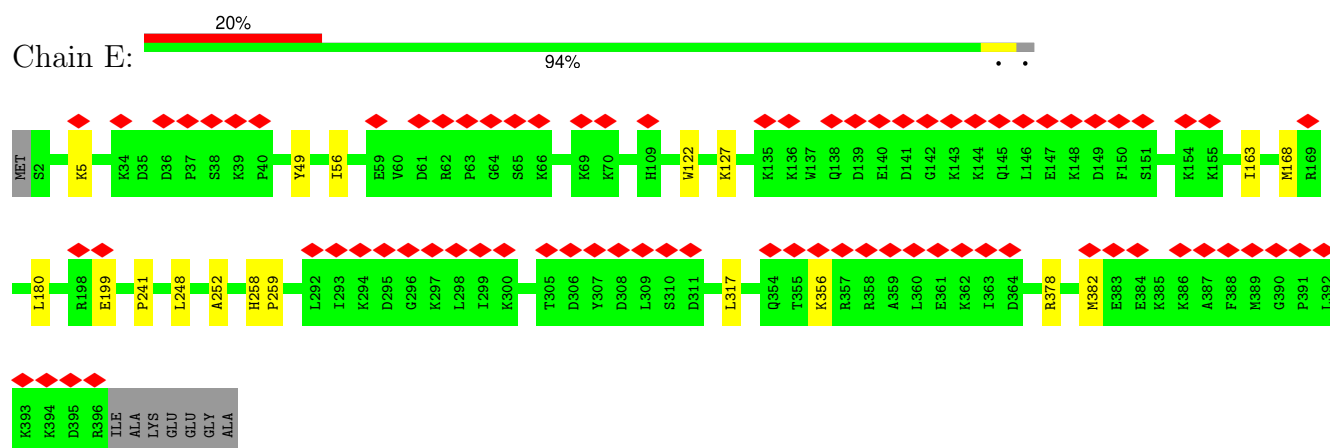


• Molecule 3: 5.8S ribosomal RNA

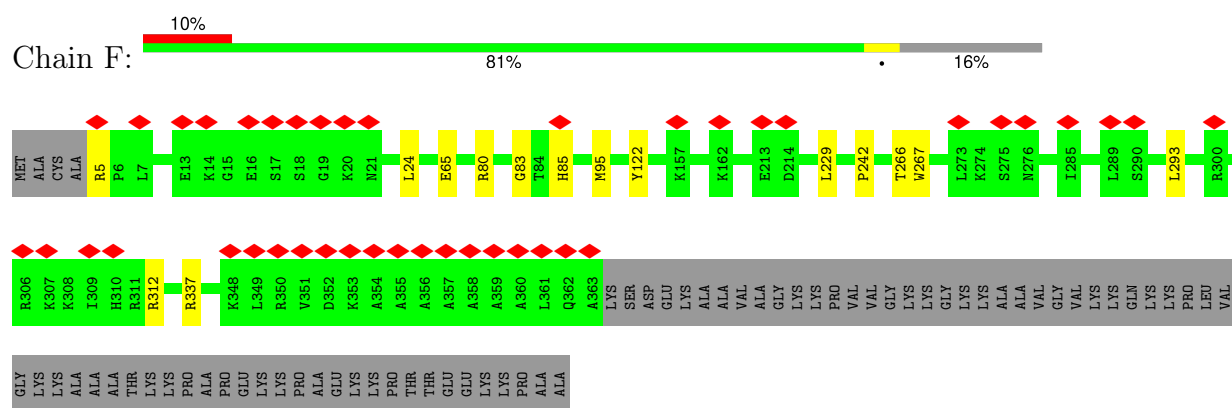


• Molecule 4: 60S ribosomal protein L8

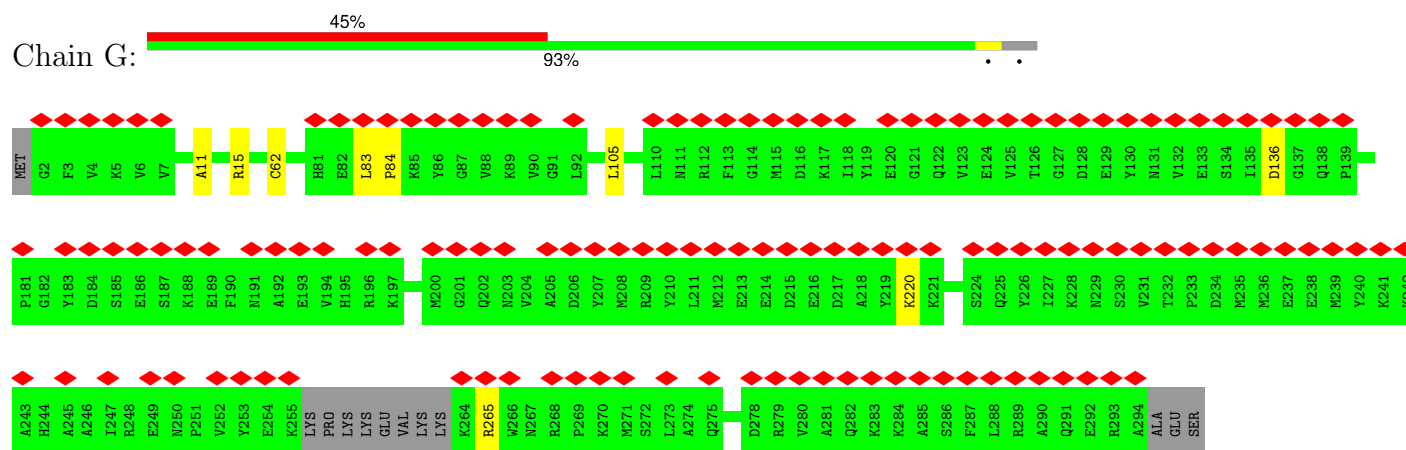




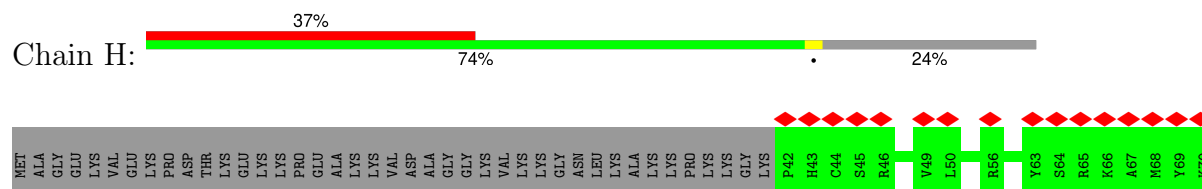
- Molecule 6: 60S ribosomal protein L4

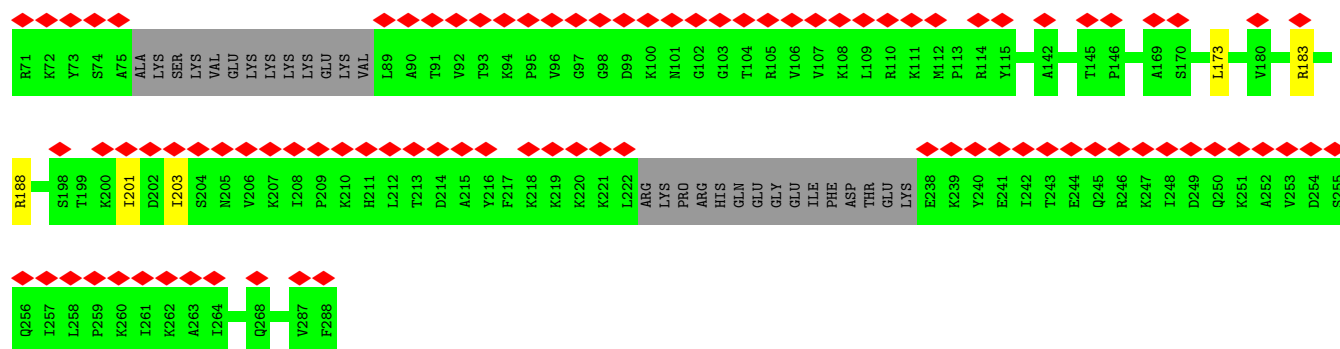


- Molecule 7: 60S ribosomal protein L5

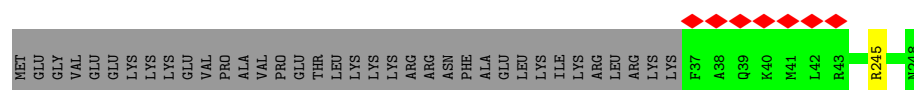
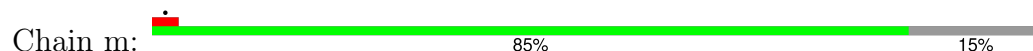


- Molecule 8: 60S ribosomal protein L6

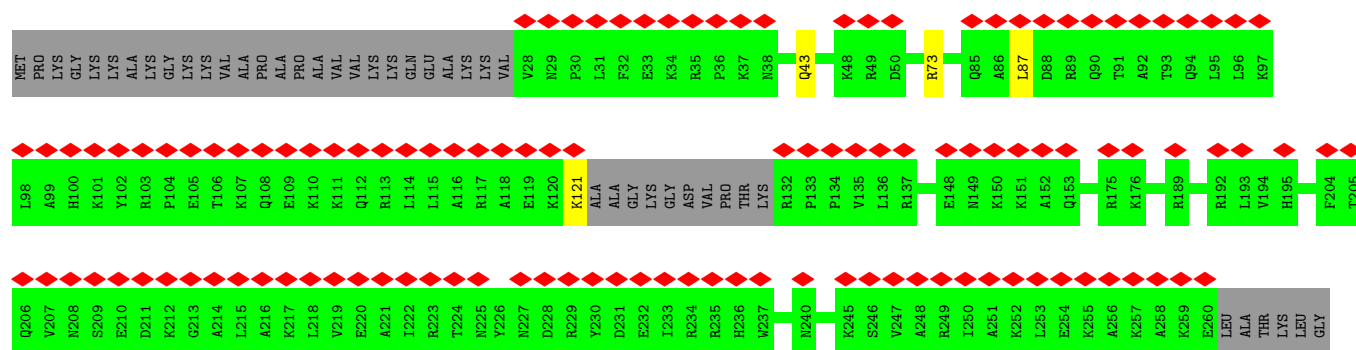
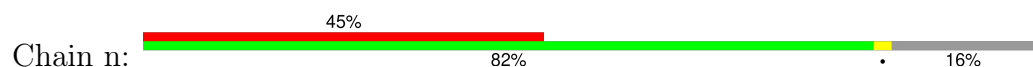




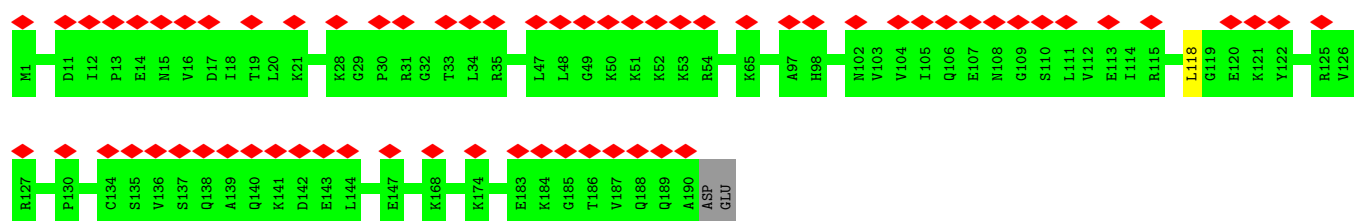
• Molecule 9: 60S ribosomal protein L7



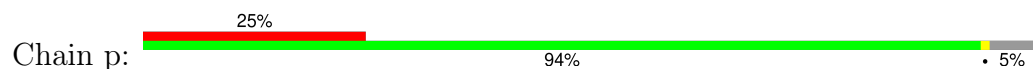
• Molecule 10: 60S ribosomal protein L7a

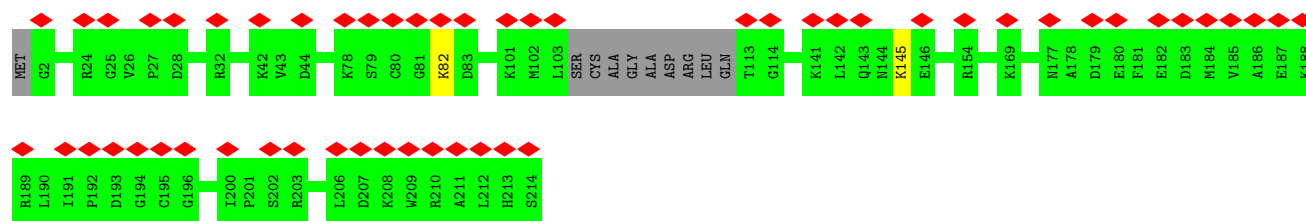


• Molecule 11: 60S ribosomal protein L9



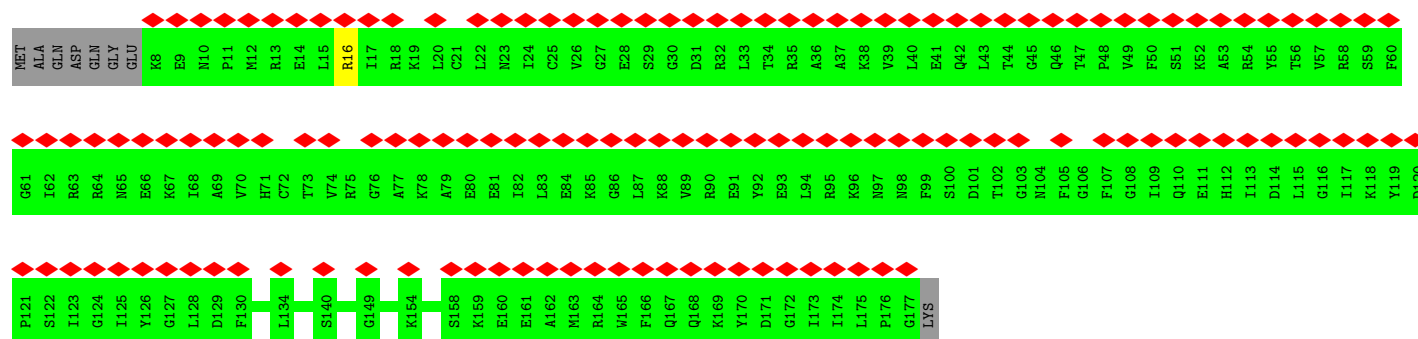
• Molecule 12: 60S ribosomal protein L10





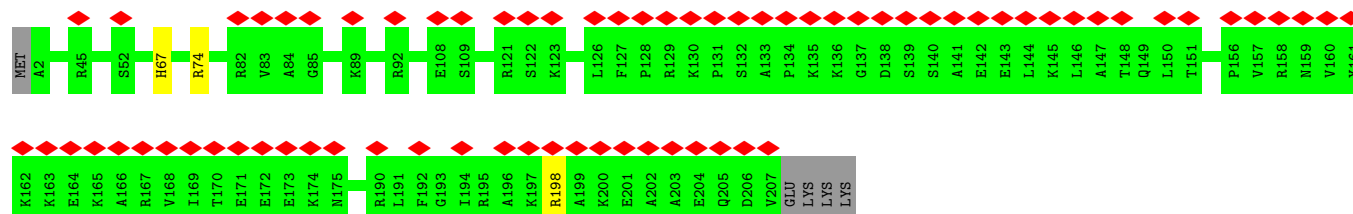
• Molecule 13: 60S ribosomal protein L11

Chain q:



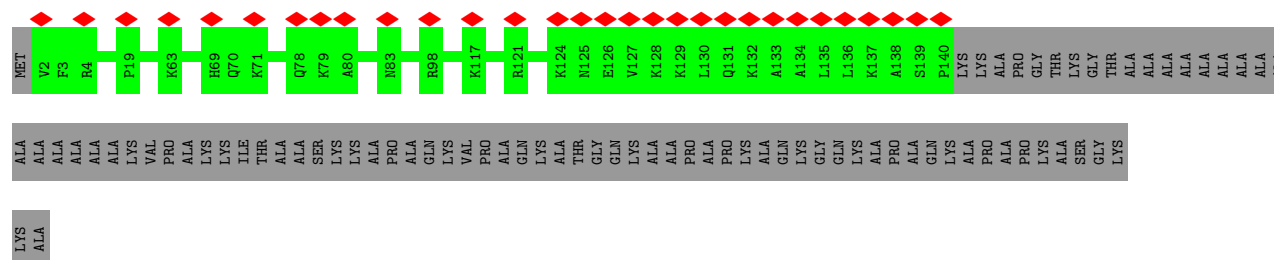
• Molecule 14: 60S ribosomal protein L13

Chain r:



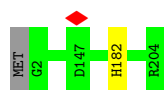
• Molecule 15: 60S ribosomal protein L14

Chain s:



• Molecule 16: 60S ribosomal protein L15

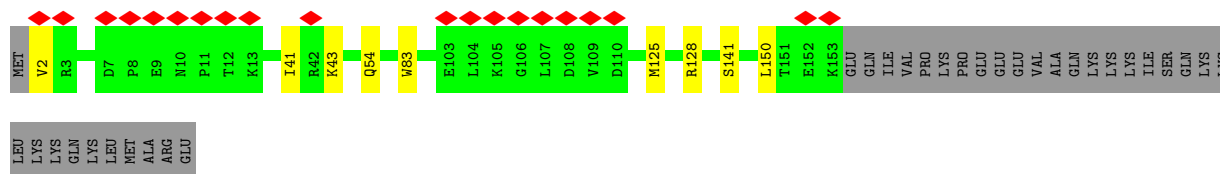
Chain l:



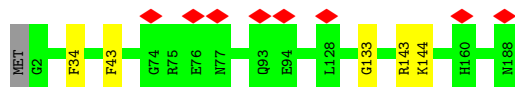
- Molecule 17: 60S ribosomal protein L13a



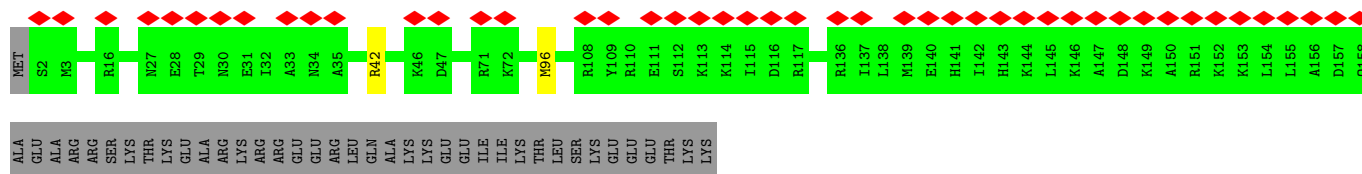
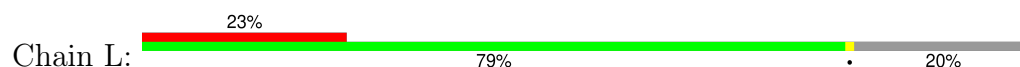
- Molecule 18: 60S ribosomal protein L17



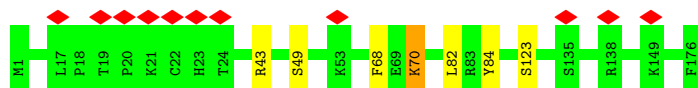
- Molecule 19: 60S ribosomal protein L18



- Molecule 20: 60S ribosomal protein L19

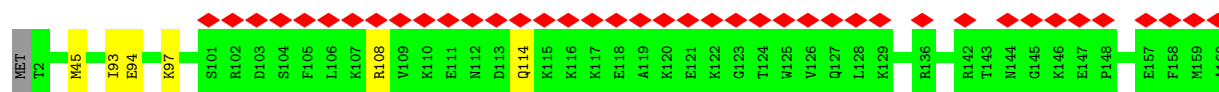


- Molecule 21: 60S ribosomal protein L18a

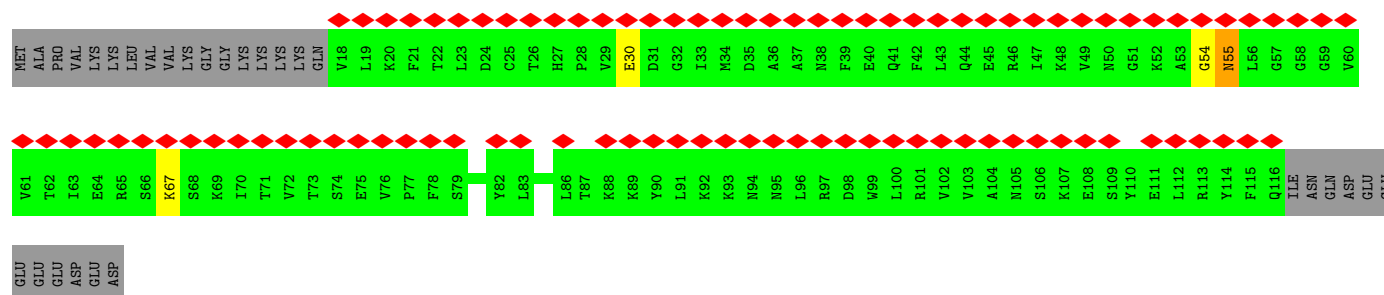
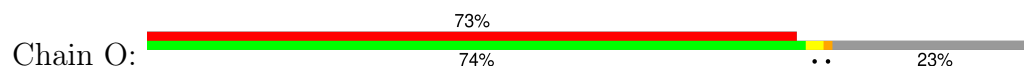


- Molecule 22: 60S ribosomal protein L21

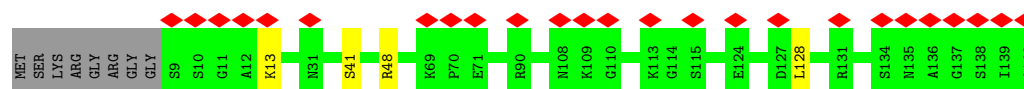




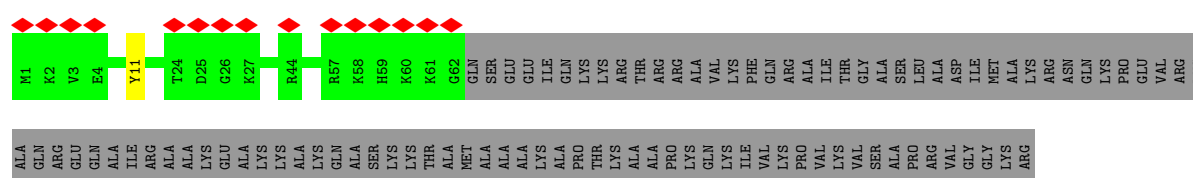
• Molecule 23: 60S ribosomal protein L22



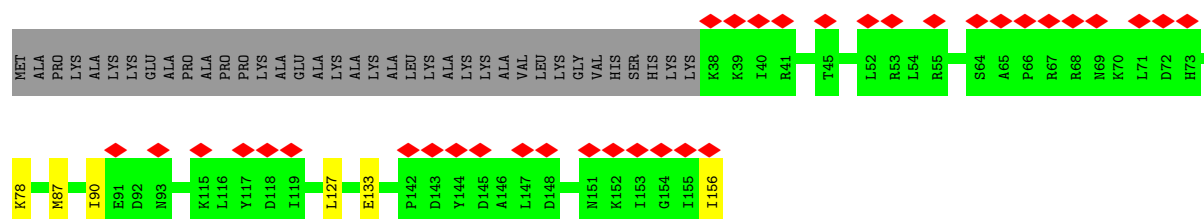
• Molecule 24: 60S ribosomal protein L23



• Molecule 25: 60S ribosomal protein L24

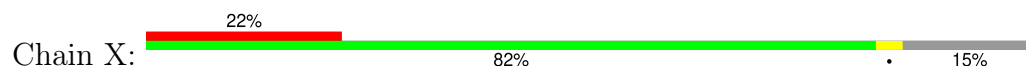


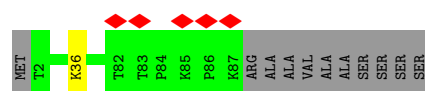
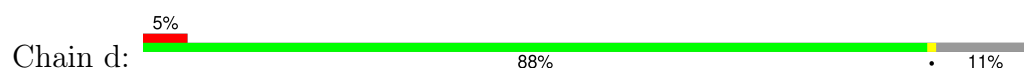
• Molecule 26: 60S ribosomal protein L23a



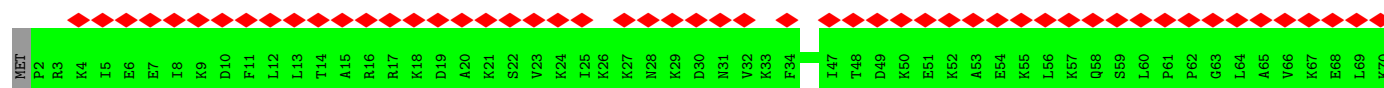
• Molecule 27: 60S ribosomal protein L26



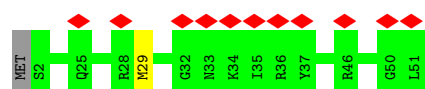




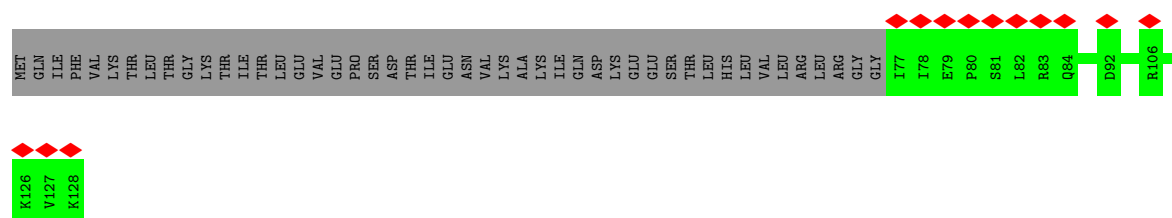
- Molecule 39: 60S ribosomal protein L38



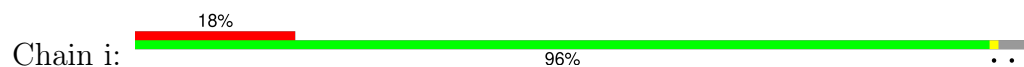
- Molecule 40: 60S ribosomal protein L39



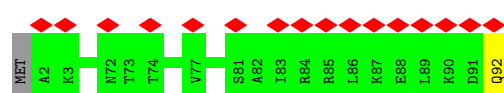
- Molecule 41: Ubiquitin-60S ribosomal protein L40



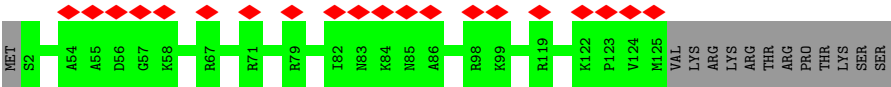
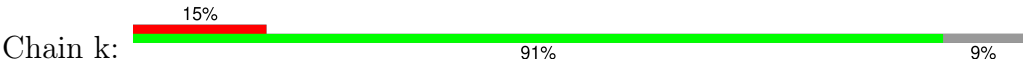
- Molecule 42: 60S ribosomal protein L36a



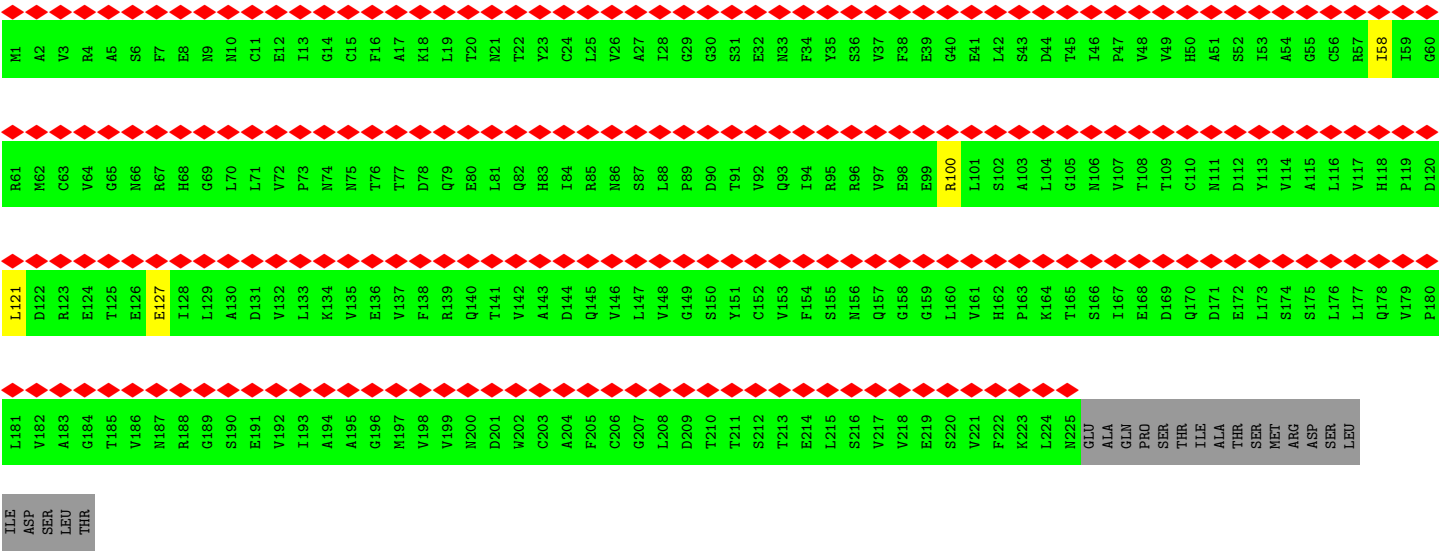
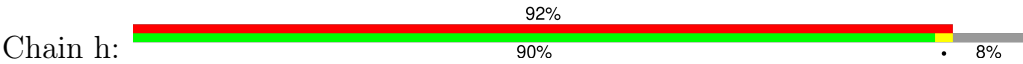
- Molecule 43: 60S ribosomal protein L37a



- Molecule 44: 60S ribosomal protein L28



• Molecule 45: Eukaryotic translation initiation factor 6



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1088709	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	51	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.602	Depositor
Minimum map value	-0.207	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	424.448, 424.448, 424.448	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.829, 0.829, 0.829	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMG, OMU, EPE, NA, 1MA, OMC, ZN, 6MZ, A2M, UR3, MG, HMT, 5MC, PSU, SPM, K

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.81	10/76619 (0.0%)	1.32	313/119498 (0.3%)
2	B	0.75	0/2858	1.27	7/4455 (0.2%)
3	C	0.78	0/3450	1.33	15/5372 (0.3%)
4	D	0.57	0/1925	0.85	0/2581
5	E	0.58	0/3265	0.79	0/4369
6	F	0.58	0/2909	0.82	0/3908
7	G	0.60	0/2352	0.76	0/3152
8	H	0.60	0/1791	0.75	0/2403
9	m	0.56	0/1789	0.80	1/2388 (0.0%)
10	n	0.60	0/1840	0.79	1/2476 (0.0%)
11	o	0.59	0/1537	0.78	0/2066
12	p	0.58	0/1692	0.77	0/2258
13	q	0.62	0/1381	0.78	0/1848
14	r	0.59	0/1695	0.82	1/2270 (0.0%)
15	s	0.57	0/1161	0.76	0/1554
16	l	0.57	0/1753	0.89	0/2348
17	I	0.56	0/1666	0.83	1/2228 (0.0%)
18	J	0.58	0/1259	0.81	0/1689
19	K	0.58	0/1537	0.90	1/2052 (0.0%)
20	L	0.59	0/1320	0.79	1/1749 (0.1%)
21	M	0.55	0/1501	0.80	0/2013
22	N	0.58	0/1326	0.80	0/1770
23	O	0.64	0/818	0.81	0/1098
24	P	0.59	0/999	0.81	0/1340
25	Q	0.58	0/532	0.76	0/708
26	R	0.57	0/993	0.73	0/1334
27	S	0.59	0/1132	0.81	0/1504
28	T	0.60	0/1130	0.80	0/1507
29	U	0.57	0/1191	0.83	0/1591
30	V	0.62	0/786	0.88	2/1038 (0.2%)
31	W	0.62	0/783	0.75	0/1052
32	X	0.57	0/883	0.81	0/1190

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Y	0.59	0/1071	0.86	2/1429 (0.1%)
34	Z	0.55	0/901	0.81	0/1206
35	a	0.61	0/855	0.85	0/1140
36	b	0.59	0/1023	0.80	1/1351 (0.1%)
37	c	0.59	0/843	0.86	0/1115
38	d	0.61	0/732	0.92	0/968
39	e	0.62	0/575	0.79	0/761
40	f	0.58	0/454	0.83	0/599
41	g	0.63	0/435	0.81	0/575
42	i	0.60	0/855	0.86	0/1128
43	j	0.65	0/718	0.80	0/953
44	k	0.58	0/1007	0.82	0/1351
45	h	0.70	0/1736	0.79	0/2362
All	All	0.73	10/137078 (0.0%)	1.17	346/201747 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	16
3	C	0	1
All	All	0	17

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	4291	G	P-O5'	6.95	1.66	1.59
1	A	4633	G	P-O5'	-6.86	1.52	1.59
1	A	2090	U	P-O5'	6.08	1.65	1.59
1	A	1723	A	P-O5'	5.84	1.65	1.59
1	A	347	A	P-O5'	5.45	1.65	1.59

The worst 5 of 346 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	417	G	O4'-C1'-N9	12.12	117.89	108.20
1	A	1925	G	O5'-P-OP2	-11.77	95.11	105.70
1	A	1947	U	P-O3'-C3'	-10.87	106.66	119.70
1	A	73	A	O5'-P-OP1	-10.40	96.34	105.70
1	A	3776	G	O4'-C1'-N9	9.95	116.16	108.20

There are no chirality outliers.

5 of 17 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	292	G	Sidechain
1	A	307	A	Sidechain
1	A	369	G	Sidechain
1	A	417	G	Sidechain
1	A	93	G	Sidechain

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	A	70928	0	35879	138	0
2	B	2558	0	1295	3	0
3	C	3153	0	1603	15	0
4	D	1887	0	1983	6	0
5	E	3194	0	3336	14	0
6	F	2855	0	3021	13	0
7	G	2308	0	2318	3	0
8	H	1757	0	1910	2	0
9	m	1755	0	1859	0	0
10	n	1809	0	1941	0	0
11	o	1518	0	1600	0	0
12	p	1654	0	1705	0	0
13	q	1358	0	1388	0	0
14	r	1664	0	1773	0	0
15	s	1138	0	1204	0	0
16	l	1708	0	1756	0	0
17	I	1634	0	1779	1	0
18	J	1233	0	1263	5	0
19	K	1513	0	1628	3	0
20	L	1304	0	1433	0	0
21	M	1461	0	1502	6	0
22	N	1298	0	1366	4	0
23	O	804	0	825	1	0
24	P	985	0	1044	2	0
25	Q	519	0	533	1	0
26	R	976	0	1053	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	S	1115	0	1205	1	0
28	T	1107	0	1182	1	0
29	U	1162	0	1213	2	0
30	V	773	0	828	2	0
31	W	772	0	808	4	0
32	X	868	0	913	2	0
33	Y	1053	0	1147	5	0
34	Z	879	0	917	3	0
35	a	845	0	933	0	0
36	b	1015	0	1148	0	0
37	c	832	0	917	0	0
38	d	713	0	746	0	0
39	e	569	0	637	0	0
40	f	444	0	482	0	0
41	g	429	0	465	0	0
42	i	842	0	912	0	0
43	j	708	0	756	0	0
44	k	992	0	1052	0	0
45	h	1712	0	1689	0	0
46	A	214	0	0	0	0
46	B	3	0	0	0	0
46	C	6	0	0	0	0
46	J	1	0	0	0	0
46	L	2	0	0	0	0
46	P	1	0	0	0	0
46	U	1	0	0	0	0
46	d	1	0	0	0	0
47	A	139	0	0	0	0
47	B	1	0	0	0	0
47	D	3	0	0	0	0
47	J	1	0	0	0	0
47	N	1	0	0	0	0
47	V	1	0	0	0	0
47	Y	1	0	0	0	0
47	Z	1	0	0	0	0
47	a	1	0	0	0	0
47	f	1	0	0	0	0
47	i	1	0	0	0	0
47	l	2	0	0	0	0
47	o	1	0	0	0	0
47	p	1	0	0	0	0
48	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	A	39	0	39	1	0
50	A	14	0	26	0	0
51	A	15	0	17	0	0
52	a	1	0	0	0	0
52	d	1	0	0	0	0
52	g	1	0	0	0	0
52	i	1	0	0	0	0
52	j	1	0	0	0	0
53	A	8641	0	0	9	0
53	B	261	0	0	0	0
53	C	363	0	0	1	0
53	D	131	0	0	1	0
53	E	177	0	0	0	0
53	F	202	0	0	3	0
53	G	67	0	0	0	0
53	H	49	0	0	0	0
53	I	117	0	0	0	0
53	J	63	0	0	0	0
53	K	139	0	0	0	0
53	L	57	0	0	0	0
53	M	100	0	0	2	0
53	N	87	0	0	1	0
53	O	5	0	0	0	0
53	P	40	0	0	0	0
53	Q	21	0	0	0	0
53	R	35	0	0	0	0
53	S	49	0	0	0	0
53	T	13	0	0	0	0
53	U	92	0	0	0	0
53	V	39	0	0	0	0
53	W	9	0	0	0	0
53	X	37	0	0	0	0
53	Y	112	0	0	0	0
53	Z	72	0	0	2	0
53	a	58	0	0	0	0
53	b	29	0	0	0	0
53	c	32	0	0	0	0
53	d	62	0	0	0	0
53	e	3	0	0	0	0
53	f	19	0	0	0	0
53	g	14	0	0	0	0
53	i	52	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	j	40	0	0	0	0
53	k	78	0	0	0	0
53	l	155	0	0	0	0
53	m	131	0	0	0	0
53	n	46	0	0	0	0
53	o	43	0	0	0	0
53	p	81	0	0	0	0
53	q	13	0	0	0	0
53	r	101	0	0	0	0
53	s	38	0	0	0	0
All	All	142233	0	95029	215	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 1.

The worst 5 of 215 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)
1:A:1721:G:N2	1:A:1841:C:O2	1.87	1.08
34:Z:95:LYS:NZ	53:Z:301:HOH:O	1.81	1.08
1:A:1721:G:N2	1:A:1841:C:C2	2.26	1.03
21:M:70:LYS:NZ	53:M:201:HOH:O	1.94	1.01
1:A:5028:G:O2'	1:A:5029:C:O5'	1.91	0.86

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	D	244/257 (95%)	240 (98%)	4 (2%)	0	100	100
5	E	394/403 (98%)	389 (99%)	5 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	357/427 (84%)	350 (98%)	7 (2%)	0	100	100
7	G	281/297 (95%)	279 (99%)	2 (1%)	0	100	100
8	H	213/288 (74%)	209 (98%)	4 (2%)	0	100	100
9	m	210/248 (85%)	206 (98%)	4 (2%)	0	100	100
10	n	219/266 (82%)	214 (98%)	5 (2%)	0	100	100
11	o	188/192 (98%)	183 (97%)	5 (3%)	0	100	100
12	p	200/214 (94%)	198 (99%)	2 (1%)	0	100	100
13	q	168/178 (94%)	166 (99%)	2 (1%)	0	100	100
14	r	204/211 (97%)	202 (99%)	2 (1%)	0	100	100
15	s	137/220 (62%)	136 (99%)	1 (1%)	0	100	100
16	l	202/204 (99%)	198 (98%)	4 (2%)	0	100	100
17	I	197/203 (97%)	194 (98%)	3 (2%)	0	100	100
18	J	150/184 (82%)	148 (99%)	2 (1%)	0	100	100
19	K	185/188 (98%)	181 (98%)	4 (2%)	0	100	100
20	L	155/196 (79%)	155 (100%)	0	0	100	100
21	M	174/176 (99%)	172 (99%)	2 (1%)	0	100	100
22	N	157/160 (98%)	153 (98%)	4 (2%)	0	100	100
23	O	97/128 (76%)	93 (96%)	3 (3%)	1 (1%)	13	3
24	P	130/140 (93%)	128 (98%)	2 (2%)	0	100	100
25	Q	60/157 (38%)	59 (98%)	1 (2%)	0	100	100
26	R	117/156 (75%)	116 (99%)	1 (1%)	0	100	100
27	S	132/145 (91%)	130 (98%)	2 (2%)	0	100	100
28	T	133/136 (98%)	130 (98%)	3 (2%)	0	100	100
29	U	145/148 (98%)	140 (97%)	4 (3%)	1 (1%)	19	7
30	V	90/159 (57%)	86 (96%)	4 (4%)	0	100	100
31	W	98/115 (85%)	98 (100%)	0	0	100	100
32	X	104/125 (83%)	103 (99%)	1 (1%)	0	100	100
33	Y	126/135 (93%)	125 (99%)	1 (1%)	0	100	100
34	Z	108/110 (98%)	108 (100%)	0	0	100	100
35	a	104/117 (89%)	102 (98%)	2 (2%)	0	100	100
36	b	120/196 (61%)	119 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	c	100/105 (95%)	97 (97%)	3 (3%)	0	100	100
38	d	85/97 (88%)	84 (99%)	1 (1%)	0	100	100
39	e	67/70 (96%)	66 (98%)	1 (2%)	0	100	100
40	f	48/51 (94%)	48 (100%)	0	0	100	100
41	g	50/99 (50%)	50 (100%)	0	0	100	100
42	i	101/106 (95%)	100 (99%)	1 (1%)	0	100	100
43	j	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
44	k	122/137 (89%)	121 (99%)	1 (1%)	0	100	100
45	h	223/245 (91%)	215 (96%)	7 (3%)	1 (0%)	30	16
All	All	6484/7481 (87%)	6375 (98%)	106 (2%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
23	O	67	LYS
29	U	15	VAL
45	h	58	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D	189/199 (95%)	187 (99%)	2 (1%)	70	57
5	E	345/349 (99%)	343 (99%)	2 (1%)	84	77
6	F	297/348 (85%)	295 (99%)	2 (1%)	81	74
7	G	237/250 (95%)	234 (99%)	3 (1%)	65	50
8	H	193/252 (77%)	192 (100%)	1 (0%)	86	81
9	m	182/215 (85%)	182 (100%)	0	100	100
10	n	193/223 (86%)	190 (98%)	3 (2%)	58	41
11	o	169/171 (99%)	168 (99%)	1 (1%)	84	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	p	174/181 (96%)	172 (99%)	2 (1%)	70	57
13	q	142/149 (95%)	141 (99%)	1 (1%)	81	74
14	r	172/177 (97%)	170 (99%)	2 (1%)	67	54
15	s	118/161 (73%)	118 (100%)	0	100	100
16	l	172/172 (100%)	171 (99%)	1 (1%)	84	77
17	I	171/174 (98%)	171 (100%)	0	100	100
18	J	133/163 (82%)	131 (98%)	2 (2%)	60	44
19	K	164/165 (99%)	164 (100%)	0	100	100
20	L	138/175 (79%)	137 (99%)	1 (1%)	81	74
21	M	157/157 (100%)	156 (99%)	1 (1%)	84	77
22	N	139/140 (99%)	137 (99%)	2 (1%)	62	47
23	O	88/115 (76%)	86 (98%)	2 (2%)	45	26
24	P	102/107 (95%)	101 (99%)	1 (1%)	73	62
25	Q	54/126 (43%)	54 (100%)	0	100	100
26	R	107/133 (80%)	106 (99%)	1 (1%)	75	66
27	S	124/135 (92%)	123 (99%)	1 (1%)	79	70
28	T	117/118 (99%)	115 (98%)	2 (2%)	56	39
29	U	120/121 (99%)	120 (100%)	0	100	100
30	V	79/126 (63%)	78 (99%)	1 (1%)	65	50
31	W	84/97 (87%)	84 (100%)	0	100	100
32	X	93/110 (84%)	93 (100%)	0	100	100
33	Y	114/121 (94%)	114 (100%)	0	100	100
34	Z	89/89 (100%)	89 (100%)	0	100	100
35	a	92/100 (92%)	91 (99%)	1 (1%)	70	57
36	b	109/153 (71%)	108 (99%)	1 (1%)	75	66
37	c	86/89 (97%)	81 (94%)	5 (6%)	17	4
38	d	74/80 (92%)	73 (99%)	1 (1%)	62	47
39	e	64/65 (98%)	64 (100%)	0	100	100
40	f	47/48 (98%)	46 (98%)	1 (2%)	48	29
41	g	48/91 (53%)	48 (100%)	0	100	100
42	i	91/94 (97%)	90 (99%)	1 (1%)	70	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	j	74/75 (99%)	73 (99%)	1 (1%)	62	47
44	k	107/121 (88%)	107 (100%)	0	100	100
45	h	195/213 (92%)	192 (98%)	3 (2%)	60	44
All	All	5643/6348 (89%)	5595 (99%)	48 (1%)	74	66

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	P	48	ARG
36	b	113	LEU
26	R	156	ILE
28	T	102	ARG
37	c	18	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
43	j	56	HIS
29	U	60	HIS
19	K	45	GLN
16	l	29	GLN
24	P	135	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3278/5069 (64%)	510 (15%)	71 (2%)
2	B	119/121 (98%)	8 (6%)	0
3	C	146/157 (92%)	20 (13%)	2 (1%)
All	All	3543/5347 (66%)	538 (15%)	73 (2%)

5 of 538 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	G
1	A	39	A
1	A	42	A
1	A	43	U
1	A	48	G

5 of 73 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	4116	C
3	C	51	U
1	A	4266	G
1	A	4870	G
1	A	1501	C

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

117 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	A	4312	1	18,21,22	1.44	2 (11%)	21,30,33	2.34	4 (19%)
1	1MA	A	1322	1,46	17,25,26	1.30	3 (17%)	17,37,40	1.44	3 (17%)
3	OMG	C	75	3	19,26,27	0.96	0	21,38,41	1.28	3 (14%)
1	PSU	A	1683	1,47	18,21,22	1.41	3 (16%)	21,30,33	2.53	6 (28%)
1	PSU	A	4493	1,47	18,21,22	1.32	3 (16%)	21,30,33	2.51	6 (28%)
1	A2M	A	2815	1,47	18,25,26	0.82	0	20,36,39	1.33	1 (5%)
1	OMC	A	1340	1	19,22,23	0.92	1 (5%)	25,31,34	1.08	1 (4%)
1	UR3	A	4530	1	19,22,23	0.92	1 (5%)	26,32,35	1.93	5 (19%)
1	PSU	A	3853	1,46	18,21,22	1.28	3 (16%)	21,30,33	2.50	5 (23%)
1	PSU	A	3637	1,47	18,21,22	1.34	3 (16%)	21,30,33	2.49	4 (19%)
1	OMG	A	1625	1,47	19,26,27	1.20	1 (5%)	21,38,41	1.53	5 (23%)
1	PSU	A	1792	1,47	18,21,22	1.42	2 (11%)	21,30,33	2.45	8 (38%)
1	A2M	A	3867	1	18,25,26	1.07	1 (5%)	20,36,39	1.51	2 (10%)
1	OMG	A	4499	1	19,26,27	1.05	1 (5%)	21,38,41	1.45	3 (14%)
1	OMC	A	3808	1	19,22,23	0.78	1 (5%)	25,31,34	1.00	1 (4%)
1	OMC	A	4456	1	19,22,23	0.84	0	25,31,34	0.89	1 (4%)
1	PSU	A	4423	1	18,21,22	1.31	3 (16%)	21,30,33	2.04	3 (14%)
1	A2M	A	3724	1	18,25,26	0.93	2 (11%)	20,36,39	1.38	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	A	1860	1	18,21,22	1.37	3 (16%)	21,30,33	2.32	6 (28%)
1	PSU	A	3844	1	18,21,22	1.41	3 (16%)	21,30,33	2.50	5 (23%)
1	PSU	A	5001	1,47	18,21,22	1.46	3 (16%)	21,30,33	2.58	5 (23%)
1	OMG	A	4228	1	19,26,27	0.98	1 (5%)	21,38,41	1.54	4 (19%)
1	OMU	A	4227	1	19,22,23	1.25	3 (15%)	25,31,34	1.96	5 (20%)
1	PSU	A	4689	1	18,21,22	1.28	3 (16%)	21,30,33	2.38	4 (19%)
1	PSU	A	4420	1	18,21,22	1.39	2 (11%)	21,30,33	2.13	5 (23%)
1	PSU	A	2632	1	18,21,22	1.49	3 (16%)	21,30,33	2.27	7 (33%)
1	PSU	A	3715	1	18,21,22	1.31	2 (11%)	21,30,33	2.21	4 (19%)
1	PSU	A	1781	1	18,21,22	1.46	2 (11%)	21,30,33	2.28	5 (23%)
1	A2M	A	3830	1	18,25,26	0.96	1 (5%)	20,36,39	1.65	6 (30%)
1	PSU	A	3884	1,47	18,21,22	1.25	3 (16%)	21,30,33	2.22	6 (28%)
1	PSU	A	2508	1	18,21,22	1.32	3 (16%)	21,30,33	2.14	7 (33%)
1	PSU	A	4431	1,47	18,21,22	1.44	3 (16%)	21,30,33	2.59	7 (33%)
1	OMG	A	3627	1	19,26,27	1.04	1 (5%)	21,38,41	1.34	4 (19%)
1	A2M	A	4523	1,46	18,25,26	0.74	0	20,36,39	1.61	3 (15%)
1	PSU	A	1862	1	18,21,22	1.50	3 (16%)	21,30,33	2.72	6 (28%)
1	OMC	A	2351	1,46	19,22,23	0.77	0	25,31,34	1.49	2 (8%)
1	PSU	A	1582	1,47	18,21,22	1.84	5 (27%)	21,30,33	2.29	5 (23%)
1	OMU	A	4306	1	19,22,23	1.29	3 (15%)	25,31,34	1.87	6 (24%)
1	OMC	A	2365	1,46	19,22,23	1.00	2 (10%)	25,31,34	1.10	2 (8%)
1	OMU	A	4620	1	19,22,23	1.15	2 (10%)	25,31,34	2.31	6 (24%)
1	PSU	A	1782	1	18,21,22	1.64	3 (16%)	21,30,33	2.22	5 (23%)
1	PSU	A	4673	1,47	18,21,22	1.16	3 (16%)	21,30,33	1.96	4 (19%)
1	PSU	A	4552	1	18,21,22	1.54	3 (16%)	21,30,33	2.41	7 (33%)
1	PSU	A	4457	1	18,21,22	1.38	3 (16%)	21,30,33	2.48	5 (23%)
1	6MZ	A	4220	1	17,25,26	1.03	0	15,36,39	2.69	5 (33%)
1	PSU	A	4576	1,47	18,21,22	1.35	3 (16%)	21,30,33	2.35	5 (23%)
1	OMC	A	2824	1	19,22,23	0.87	0	25,31,34	0.99	1 (4%)
1	A2M	A	4590	1	18,25,26	0.74	0	20,36,39	1.63	2 (10%)
1	OMC	A	2422	1,46	19,22,23	1.03	2 (10%)	25,31,34	0.83	1 (4%)
1	OMU	A	3925	1	19,22,23	1.17	2 (10%)	25,31,34	2.03	5 (20%)
1	OMG	A	4494	1	19,26,27	1.12	1 (5%)	21,38,41	1.27	2 (9%)
1	OMG	A	4196	1,46	19,26,27	1.07	1 (5%)	21,38,41	1.37	4 (19%)
1	PSU	A	4972	1,47	18,21,22	1.33	2 (11%)	21,30,33	2.60	6 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	A2M	A	3785	1	18,25,26	0.99	1 (5%)	20,36,39	2.68	7 (35%)
1	PSU	A	1744	1,47	18,21,22	1.38	2 (11%)	21,30,33	2.27	4 (19%)
1	OMG	A	3899	1	19,26,27	0.94	0	21,38,41	1.42	3 (14%)
1	5MC	A	3782	1,46	19,22,23	1.11	1 (5%)	26,32,35	1.35	4 (15%)
1	OMG	A	4618	1,47	19,26,27	0.85	0	21,38,41	1.29	4 (19%)
1	PSU	A	1536	1	18,21,22	1.45	2 (11%)	21,30,33	2.51	5 (23%)
1	A2M	A	1524	1	18,25,26	1.00	0	20,36,39	1.59	2 (10%)
1	OMG	A	4623	1	19,26,27	0.96	1 (5%)	21,38,41	1.36	4 (19%)
1	OMU	A	3818	1,47	19,22,23	1.37	3 (15%)	25,31,34	2.11	6 (24%)
1	OMG	A	3744	1	19,26,27	0.83	0	21,38,41	1.12	3 (14%)
1	PSU	A	4296	1	18,21,22	1.42	3 (16%)	21,30,33	2.24	6 (28%)
1	OMU	A	2837	1	19,22,23	1.32	2 (10%)	25,31,34	2.14	7 (28%)
1	A2M	A	3718	1	18,25,26	0.83	0	20,36,39	1.45	3 (15%)
1	A2M	A	1534	1,46	18,25,26	1.08	3 (16%)	20,36,39	1.91	5 (25%)
1	A2M	A	3825	1	18,25,26	0.83	0	20,36,39	1.36	2 (10%)
1	OMG	A	4637	1,47	19,26,27	1.06	1 (5%)	21,38,41	1.24	2 (9%)
1	PSU	A	3639	1	18,21,22	1.41	2 (11%)	21,30,33	2.29	4 (19%)
1	PSU	A	4293	1	18,21,22	1.50	3 (16%)	21,30,33	2.25	6 (28%)
1	PSU	A	4579	1	18,21,22	1.45	3 (16%)	21,30,33	2.26	4 (19%)
1	PSU	A	1677	1,47	18,21,22	1.64	3 (16%)	21,30,33	2.58	6 (28%)
1	PSU	A	4361	1,47	18,21,22	1.81	4 (22%)	21,30,33	2.29	5 (23%)
1	PSU	A	2839	1	18,21,22	1.40	3 (16%)	21,30,33	2.10	7 (33%)
1	OMC	A	3841	1	19,22,23	0.72	0	25,31,34	1.17	2 (8%)
1	PSU	A	3729	1	18,21,22	1.44	3 (16%)	21,30,33	2.11	5 (23%)
1	A2M	A	1871	1,46	18,25,26	0.68	0	20,36,39	1.61	4 (20%)
1	A2M	A	400	1	18,25,26	1.04	1 (5%)	20,36,39	1.50	1 (5%)
1	OMG	A	4392	1	19,26,27	0.98	1 (5%)	21,38,41	1.22	3 (14%)
1	PSU	A	4532	1,47	18,21,22	1.54	3 (16%)	21,30,33	2.49	6 (28%)
1	OMG	A	1316	1,47	19,26,27	0.99	1 (5%)	21,38,41	1.24	3 (14%)
1	OMG	A	3792	1	19,26,27	0.90	0	21,38,41	1.23	2 (9%)
1	A2M	A	2787	1,46	18,25,26	1.00	1 (5%)	20,36,39	2.29	9 (45%)
1	PSU	A	4299	1	18,21,22	1.41	4 (22%)	21,30,33	2.54	5 (23%)
1	A2M	A	398	1	18,25,26	1.13	2 (11%)	20,36,39	1.48	2 (10%)
1	PSU	A	4521	1,46,47	18,21,22	1.48	3 (16%)	21,30,33	2.59	7 (33%)
1	OMG	A	2364	1	19,26,27	1.07	2 (10%)	21,38,41	1.27	2 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	A	4353	1,47	18,21,22	1.55	3 (16%)	21,30,33	2.57	5 (23%)
1	OMU	A	2415	1	19,22,23	1.36	4 (21%)	25,31,34	1.96	8 (32%)
1	PSU	A	4403	1,47	18,21,22	1.69	2 (11%)	21,30,33	2.35	6 (28%)
1	OMC	A	3887	1	19,22,23	0.83	1 (5%)	25,31,34	1.29	2 (8%)
1	PSU	A	4471	1,47	18,21,22	1.55	3 (16%)	21,30,33	2.06	5 (23%)
1	OMU	A	4498	1,47	19,22,23	1.30	3 (15%)	25,31,34	2.43	7 (28%)
1	OMC	A	2861	1	19,22,23	0.91	2 (10%)	25,31,34	0.90	2 (8%)
1	A2M	A	4571	1	18,25,26	0.98	0	20,36,39	1.66	4 (20%)
3	PSU	C	69	3	18,21,22	1.54	3 (16%)	21,30,33	2.37	6 (28%)
3	PSU	C	55	3	18,21,22	1.24	3 (16%)	21,30,33	2.08	5 (23%)
1	A2M	A	2363	1,46	18,25,26	0.73	0	20,36,39	1.86	4 (20%)
1	PSU	A	3695	1,47	18,21,22	1.35	2 (11%)	21,30,33	2.23	6 (28%)
1	5MC	A	4447	1,47	19,22,23	1.07	2 (10%)	26,32,35	1.57	5 (19%)
1	OMC	A	3701	1,47	19,22,23	0.92	0	25,31,34	1.50	4 (16%)
1	PSU	A	3851	1	18,21,22	1.33	3 (16%)	21,30,33	2.52	6 (28%)
1	A2M	A	1326	1	18,25,26	0.95	0	20,36,39	1.65	2 (10%)
1	OMG	A	1522	1	19,26,27	0.97	0	21,38,41	1.43	3 (14%)
1	OMG	A	2876	1	19,26,27	1.05	1 (5%)	21,38,41	1.52	5 (23%)
1	OMG	A	4370	1	19,26,27	0.83	1 (5%)	21,38,41	1.18	3 (14%)
1	PSU	A	4442	1	18,21,22	1.44	2 (11%)	21,30,33	2.35	6 (28%)
1	PSU	A	5010	1	18,21,22	1.30	3 (16%)	21,30,33	2.09	5 (23%)
1	OMG	A	2424	1	19,26,27	1.18	1 (5%)	21,38,41	1.55	5 (23%)
1	PSU	A	4500	1	18,21,22	1.45	4 (22%)	21,30,33	2.40	5 (23%)
1	PSU	A	3920	1,46	18,21,22	1.27	1 (5%)	21,30,33	2.22	5 (23%)
1	PSU	A	4628	1	18,21,22	1.41	4 (22%)	21,30,33	2.54	6 (28%)
1	A2M	A	2401	1,46	18,25,26	0.80	0	20,36,39	1.66	3 (15%)
1	OMC	A	2804	1	19,22,23	0.86	1 (5%)	25,31,34	1.02	1 (4%)
1	OMC	A	4536	1,46	19,22,23	0.84	1 (5%)	25,31,34	0.92	1 (4%)
1	OMC	A	3869	1	19,22,23	0.81	1 (5%)	25,31,34	1.25	4 (16%)

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	A	4312	1	-	0/7/25/26	0/2/2/2
1	1MA	A	1322	1,46	-	0/3/25/26	0/3/3/3
3	OMG	C	75	3	-	0/5/27/28	0/3/3/3
1	PSU	A	1683	1,47	-	0/7/25/26	0/2/2/2
1	PSU	A	4493	1,47	-	0/7/25/26	0/2/2/2
1	A2M	A	2815	1,47	-	0/5/27/28	0/3/3/3
1	OMC	A	1340	1	-	0/9/27/28	0/2/2/2
1	UR3	A	4530	1	-	0/7/25/26	0/2/2/2
1	PSU	A	3853	1,46	-	0/7/25/26	0/2/2/2
1	PSU	A	3637	1,47	-	0/7/25/26	0/2/2/2
1	OMG	A	1625	1,47	-	0/5/27/28	0/3/3/3
1	PSU	A	1792	1,47	-	0/7/25/26	0/2/2/2
1	A2M	A	3867	1	-	0/5/27/28	0/3/3/3
1	OMG	A	4499	1	-	0/5/27/28	0/3/3/3
1	OMC	A	3808	1	-	0/9/27/28	0/2/2/2
1	OMC	A	4456	1	-	0/9/27/28	0/2/2/2
1	PSU	A	4423	1	-	0/7/25/26	0/2/2/2
1	A2M	A	3724	1	-	0/5/27/28	0/3/3/3
1	PSU	A	1860	1	-	0/7/25/26	0/2/2/2
1	PSU	A	3844	1	-	1/7/25/26	0/2/2/2
1	PSU	A	5001	1,47	-	0/7/25/26	0/2/2/2
1	OMG	A	4228	1	-	0/5/27/28	0/3/3/3
1	OMU	A	4227	1	-	0/9/27/28	0/2/2/2
1	PSU	A	4689	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4420	1	-	0/7/25/26	0/2/2/2
1	PSU	A	2632	1	-	0/7/25/26	0/2/2/2
1	PSU	A	3715	1	-	0/7/25/26	0/2/2/2
1	PSU	A	1781	1	-	0/7/25/26	0/2/2/2
1	A2M	A	3830	1	-	0/5/27/28	0/3/3/3
1	PSU	A	3884	1,47	-	0/7/25/26	0/2/2/2
1	PSU	A	2508	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4431	1,47	-	0/7/25/26	0/2/2/2
1	OMG	A	3627	1	-	0/5/27/28	0/3/3/3
1	A2M	A	4523	1,46	-	0/5/27/28	0/3/3/3
1	PSU	A	1862	1	-	0/7/25/26	0/2/2/2
1	OMC	A	2351	1,46	-	0/9/27/28	0/2/2/2
1	PSU	A	1582	1,47	-	0/7/25/26	0/2/2/2
1	OMU	A	4306	1	-	0/9/27/28	0/2/2/2
1	OMC	A	2365	1,46	-	0/9/27/28	0/2/2/2
1	OMU	A	4620	1	-	0/9/27/28	0/2/2/2
1	PSU	A	1782	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4673	1,47	-	0/7/25/26	0/2/2/2
1	PSU	A	4552	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	A	4457	1	-	0/7/25/26	0/2/2/2
1	6MZ	A	4220	1	-	0/5/27/28	0/3/3/3
1	PSU	A	4576	1,47	-	0/7/25/26	0/2/2/2
1	OMC	A	2824	1	-	0/9/27/28	0/2/2/2
1	A2M	A	4590	1	-	1/5/27/28	0/3/3/3
1	OMC	A	2422	1,46	-	2/9/27/28	0/2/2/2
1	OMU	A	3925	1	-	0/9/27/28	0/2/2/2
1	OMG	A	4494	1	-	1/5/27/28	0/3/3/3
1	OMG	A	4196	1,46	-	0/5/27/28	0/3/3/3
1	PSU	A	4972	1,47	-	0/7/25/26	0/2/2/2
1	A2M	A	3785	1	-	2/5/27/28	0/3/3/3
1	PSU	A	1744	1,47	-	0/7/25/26	0/2/2/2
1	OMG	A	3899	1	-	0/5/27/28	0/3/3/3
1	5MC	A	3782	1,46	-	0/7/25/26	0/2/2/2
1	OMG	A	4618	1,47	-	0/5/27/28	0/3/3/3
1	PSU	A	1536	1	-	0/7/25/26	0/2/2/2
1	A2M	A	1524	1	-	0/5/27/28	0/3/3/3
1	OMG	A	4623	1	-	0/5/27/28	0/3/3/3
1	OMU	A	3818	1,47	-	1/9/27/28	0/2/2/2
1	OMG	A	3744	1	-	0/5/27/28	0/3/3/3
1	PSU	A	4296	1	-	0/7/25/26	0/2/2/2
1	OMU	A	2837	1	-	0/9/27/28	0/2/2/2
1	A2M	A	3718	1	-	0/5/27/28	0/3/3/3
1	A2M	A	1534	1,46	-	1/5/27/28	0/3/3/3
1	A2M	A	3825	1	-	0/5/27/28	0/3/3/3
1	OMG	A	4637	1,47	-	0/5/27/28	0/3/3/3
1	PSU	A	3639	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4293	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4579	1	-	0/7/25/26	0/2/2/2
1	PSU	A	1677	1,47	-	1/7/25/26	0/2/2/2
1	PSU	A	4361	1,47	-	0/7/25/26	0/2/2/2
1	PSU	A	2839	1	-	0/7/25/26	0/2/2/2
1	OMC	A	3841	1	-	0/9/27/28	0/2/2/2
1	PSU	A	3729	1	-	0/7/25/26	0/2/2/2
1	A2M	A	1871	1,46	-	0/5/27/28	0/3/3/3
1	A2M	A	400	1	-	0/5/27/28	0/3/3/3
1	OMG	A	4392	1	-	0/5/27/28	0/3/3/3
1	PSU	A	4532	1,47	-	0/7/25/26	0/2/2/2
1	OMG	A	1316	1,47	-	0/5/27/28	0/3/3/3
1	OMG	A	3792	1	-	0/5/27/28	0/3/3/3
1	A2M	A	2787	1,46	-	0/5/27/28	0/3/3/3
1	PSU	A	4299	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	A2M	A	398	1	-	0/5/27/28	0/3/3/3
1	PSU	A	4521	1,46,47	-	0/7/25/26	0/2/2/2
1	OMG	A	2364	1	-	1/5/27/28	0/3/3/3
1	PSU	A	4353	1,47	-	0/7/25/26	0/2/2/2
1	OMU	A	2415	1	-	1/9/27/28	0/2/2/2
1	PSU	A	4403	1,47	-	0/7/25/26	0/2/2/2
1	OMC	A	3887	1	-	0/9/27/28	0/2/2/2
1	PSU	A	4471	1,47	-	0/7/25/26	0/2/2/2
1	OMU	A	4498	1,47	-	0/9/27/28	0/2/2/2
1	OMC	A	2861	1	-	0/9/27/28	0/2/2/2
1	A2M	A	4571	1	-	0/5/27/28	0/3/3/3
3	PSU	C	69	3	-	0/7/25/26	0/2/2/2
3	PSU	C	55	3	-	0/7/25/26	0/2/2/2
1	A2M	A	2363	1,46	-	1/5/27/28	0/3/3/3
1	PSU	A	3695	1,47	-	0/7/25/26	0/2/2/2
1	5MC	A	4447	1,47	-	4/7/25/26	0/2/2/2
1	OMC	A	3701	1,47	-	4/9/27/28	0/2/2/2
1	PSU	A	3851	1	-	0/7/25/26	0/2/2/2
1	A2M	A	1326	1	-	1/5/27/28	0/3/3/3
1	OMG	A	1522	1	-	0/5/27/28	0/3/3/3
1	OMG	A	2876	1	-	0/5/27/28	0/3/3/3
1	OMG	A	4370	1	-	0/5/27/28	0/3/3/3
1	PSU	A	4442	1	-	0/7/25/26	0/2/2/2
1	PSU	A	5010	1	-	0/7/25/26	0/2/2/2
1	OMG	A	2424	1	-	0/5/27/28	0/3/3/3
1	PSU	A	4500	1	-	1/7/25/26	0/2/2/2
1	PSU	A	3920	1,46	-	0/7/25/26	0/2/2/2
1	PSU	A	4628	1	-	0/7/25/26	0/2/2/2
1	A2M	A	2401	1,46	-	1/5/27/28	0/3/3/3
1	OMC	A	2804	1	-	0/9/27/28	0/2/2/2
1	OMC	A	4536	1,46	-	0/9/27/28	0/2/2/2
1	OMC	A	3869	1	-	0/9/27/28	0/2/2/2

The worst 5 of 213 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	4403	PSU	C6-C5	5.15	1.41	1.35
1	A	4361	PSU	C6-C5	4.93	1.40	1.35
1	A	1782	PSU	C6-C5	4.46	1.40	1.35
1	A	4532	PSU	C6-C5	4.43	1.40	1.35
1	A	2632	PSU	C6-C5	4.40	1.40	1.35

The worst 5 of 503 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4353	PSU	N1-C2-N3	8.31	123.94	115.17
1	A	3785	A2M	O4'-C1'-N9	8.10	119.49	108.75
1	A	1862	PSU	N1-C2-N3	7.97	123.57	115.17
1	A	5001	PSU	N1-C2-N3	7.93	123.53	115.17
1	A	4628	PSU	N1-C2-N3	7.67	123.26	115.17

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	2415	OMU	C1'-C2'-O2'-CM2
1	A	3701	OMC	C2'-C1'-N1-C2
1	A	3701	OMC	C2'-C1'-N1-C6
1	A	4590	A2M	C4'-C5'-O5'-P
1	A	2422	OMC	O4'-C4'-C5'-O5'

There are no ring outliers.

15 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1340	OMC	1	0
1	A	3867	A2M	2	0
1	A	4456	OMC	1	0
1	A	2351	OMC	3	0
1	A	4457	PSU	1	0
1	A	4220	6MZ	1	0
1	A	3818	OMU	1	0
1	A	4293	PSU	1	0
1	A	2787	A2M	1	0
1	A	2364	OMG	1	0
1	A	2415	OMU	1	0
1	A	4498	OMU	1	0
1	A	1326	A2M	1	0
1	A	2876	OMG	1	0
1	A	4500	PSU	1	0

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 394 ligands modelled in this entry, 391 are monoatomic - leaving 3 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	$\# Z > 2$
49	HMT	A	5455	-	41,43,43	0.62	0	43,66,66	0.66	0
51	EPE	A	5457	-	15,15,15	0.92	1 (6%)	19,20,20	1.49	2 (10%)
50	SPM	A	5456	-	13,13,13	0.23	0	12,12,12	0.24	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
49	HMT	A	5455	-	-	0/27/74/74	0/5/5/5
51	EPE	A	5457	-	-	1/9/19/19	0/1/1/1
50	SPM	A	5456	-	-	2/11/11/11	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	A	5457	EPE	O2S-S	3.32	1.54	1.45

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	A	5457	EPE	O2S-S-C10	-5.74	98.06	106.73
51	A	5457	EPE	O3S-S-O1S	2.64	118.01	111.40

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
50	A	5456	SPM	C2-C3-C4-N5

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Mol	Chain	Res	Type	Atoms
51	A	5457	EPE	C9-C10-S-O3S
50	A	5456	SPM	C6-C7-C8-C9

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
49	A	5455	HMT	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

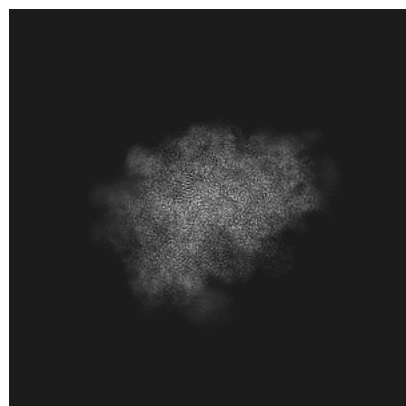
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15113. These allow visual inspection of the internal detail of the map and identification of artifacts.

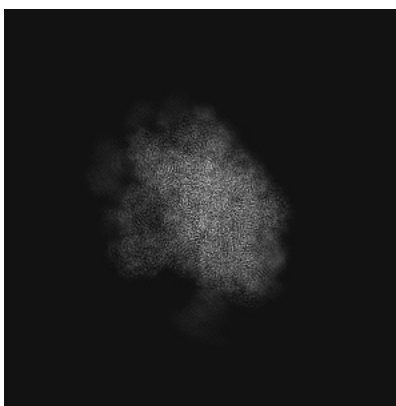
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

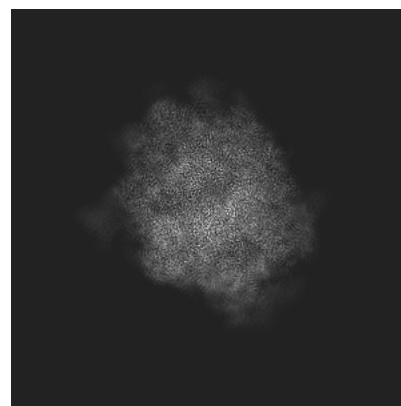
6.1.1 Primary map



X

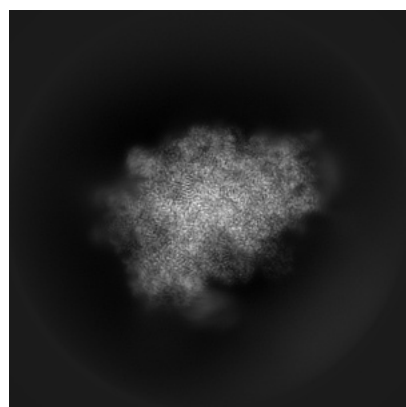


Y

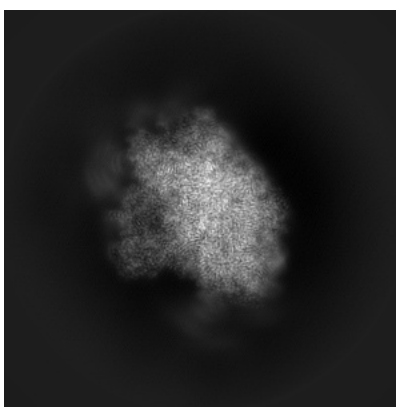


Z

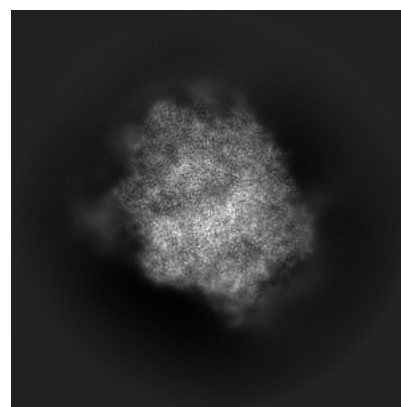
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices [i](#)

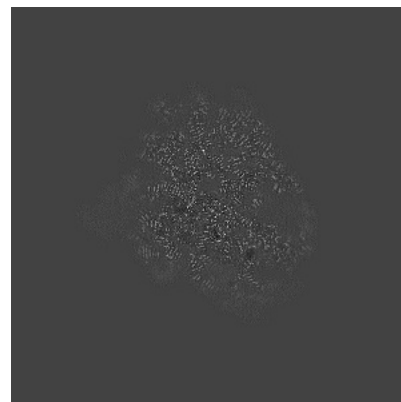
6.2.1 Primary map



X Index: 256

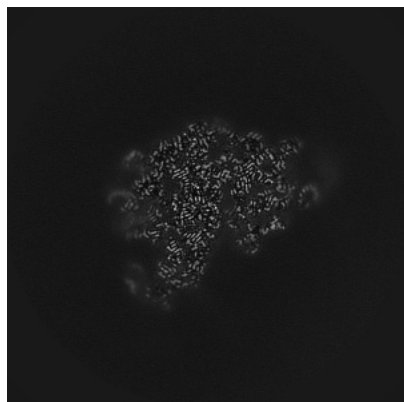


Y Index: 256

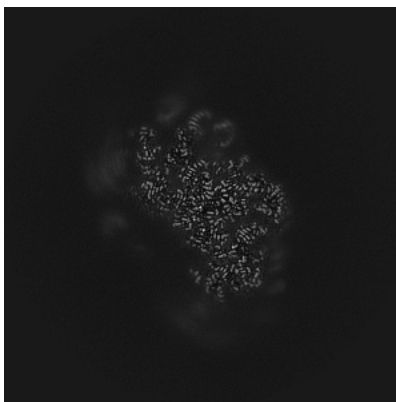


Z Index: 256

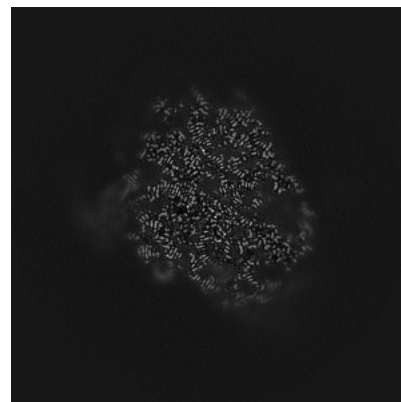
6.2.2 Raw map



X Index: 256



Y Index: 256

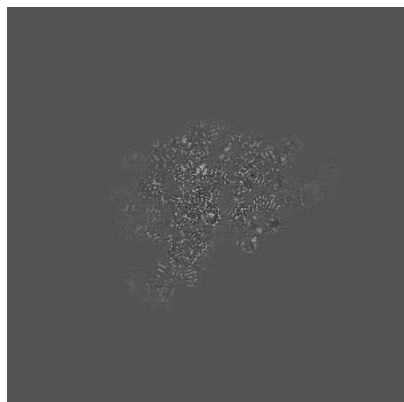


Z Index: 256

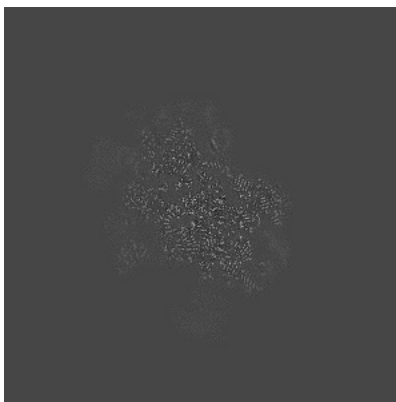
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

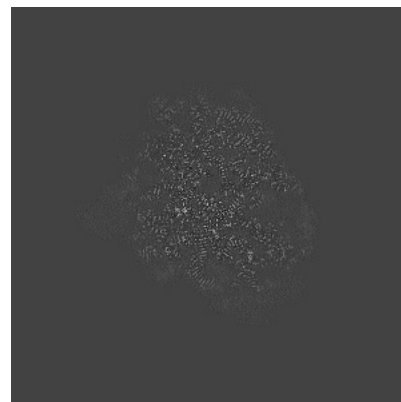
6.3.1 Primary map



X Index: 253

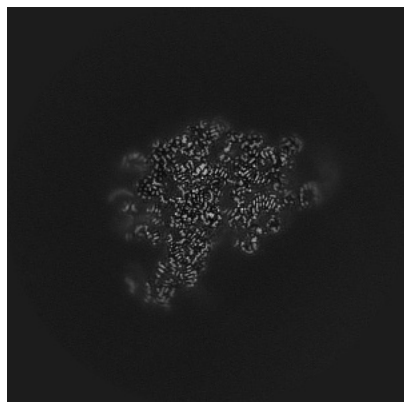


Y Index: 239

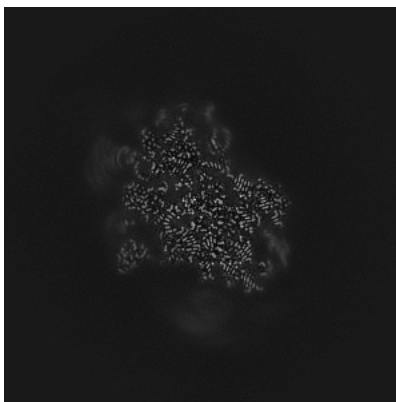


Z Index: 258

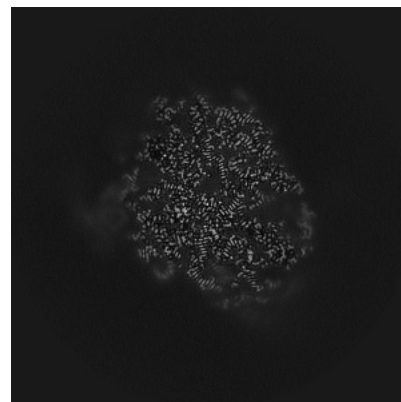
6.3.2 Raw map



X Index: 253



Y Index: 239

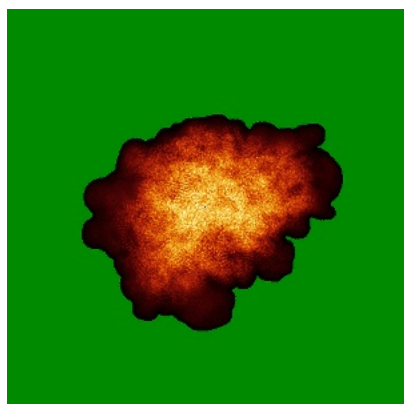


Z Index: 258

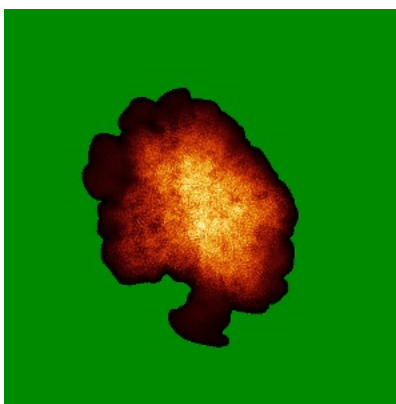
The images above show the largest variance slices of the map in three orthogonal directions.

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

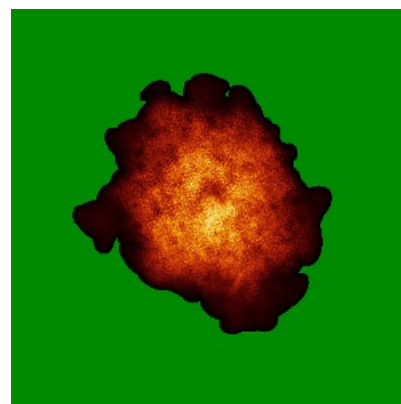
6.4.1 Primary map



X



Y

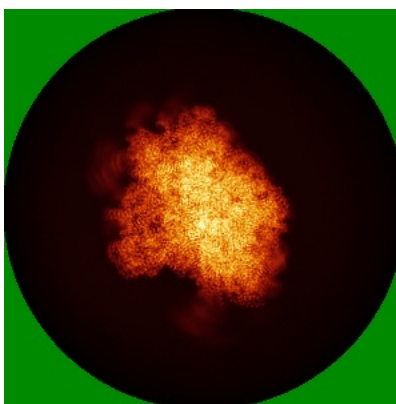


Z

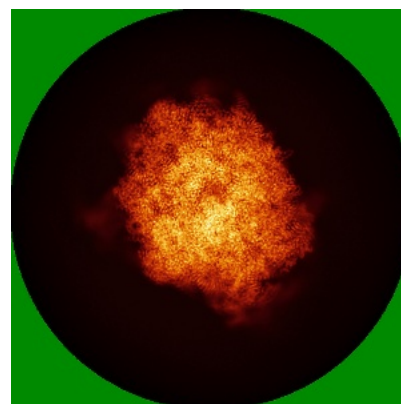
6.4.2 Raw map



X



Y

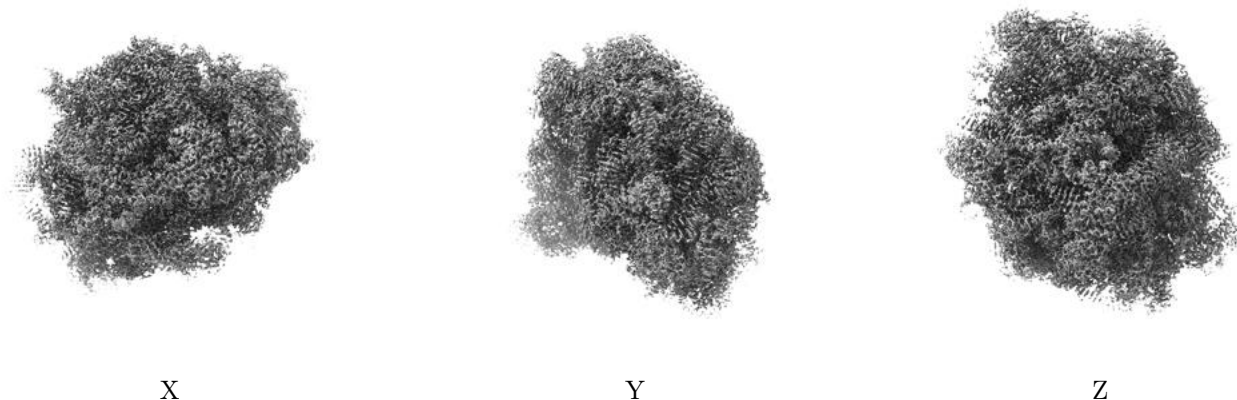


Z

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.

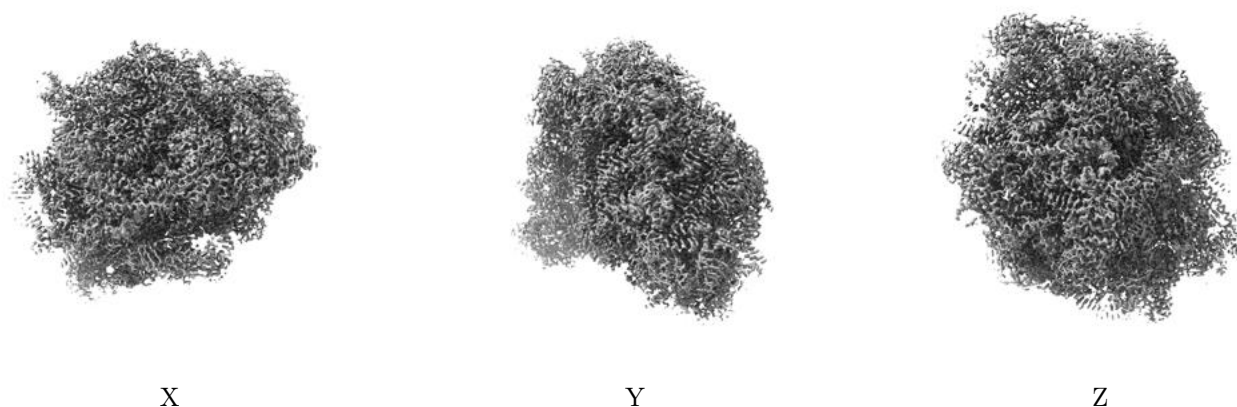
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.07. 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.

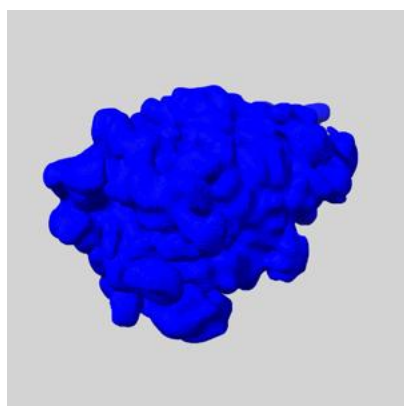
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

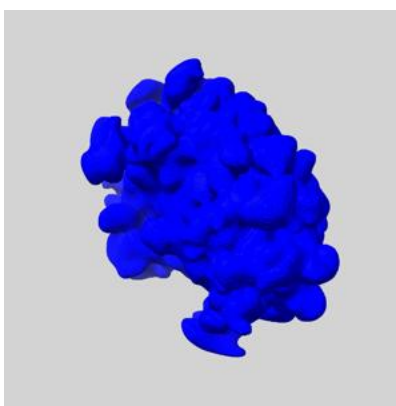
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

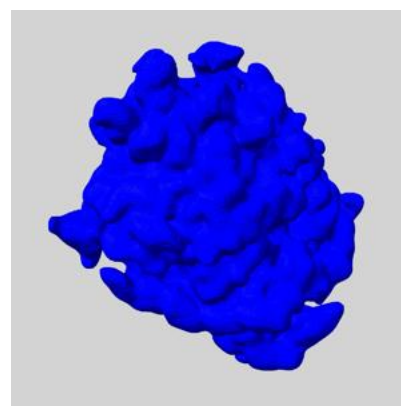
6.6.1 emd_15113_msk_1.map [i](#)



X



Y

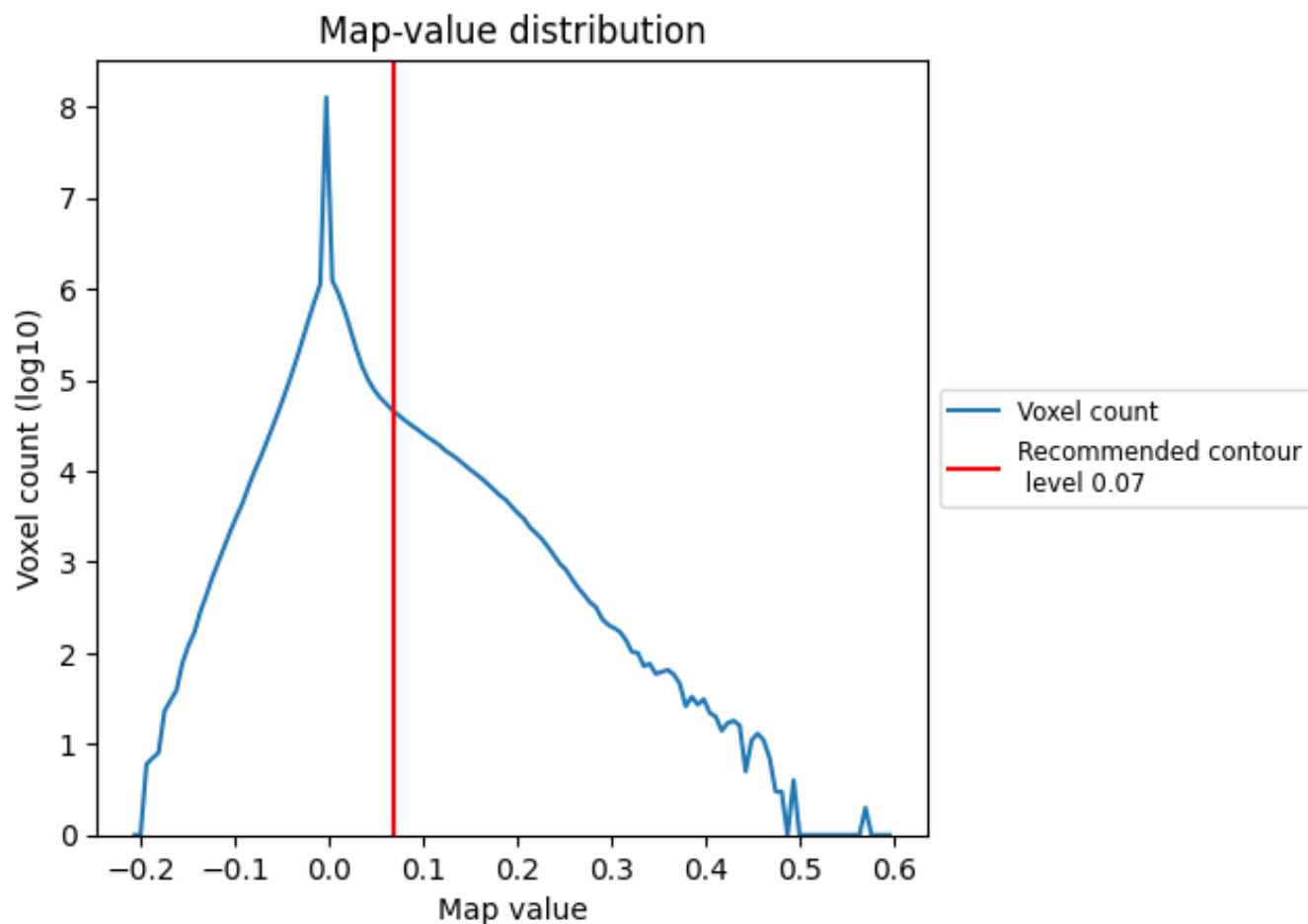


Z

7 Map analysis [i](#)

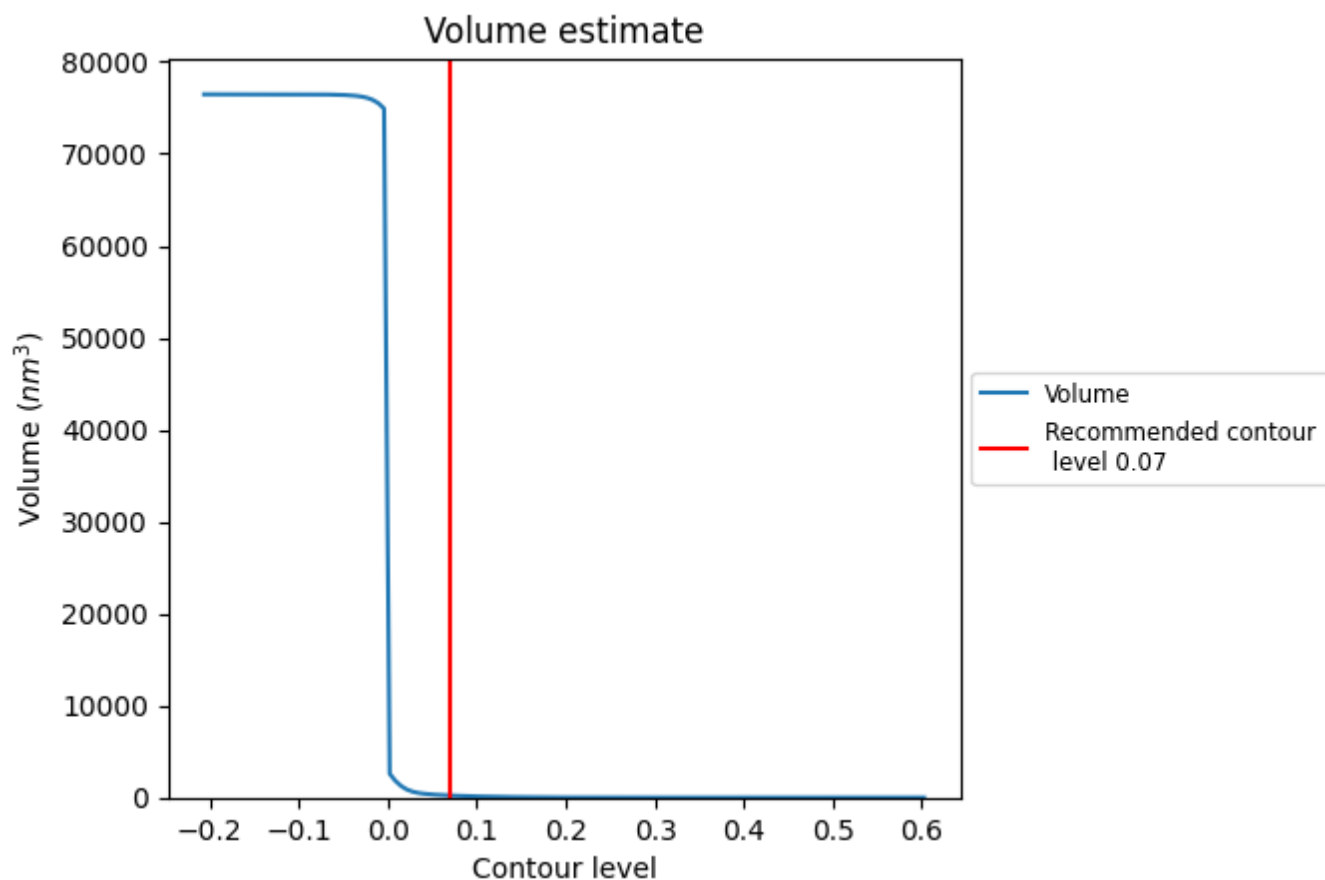
This section contains the results of statistical analysis of the map.

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.

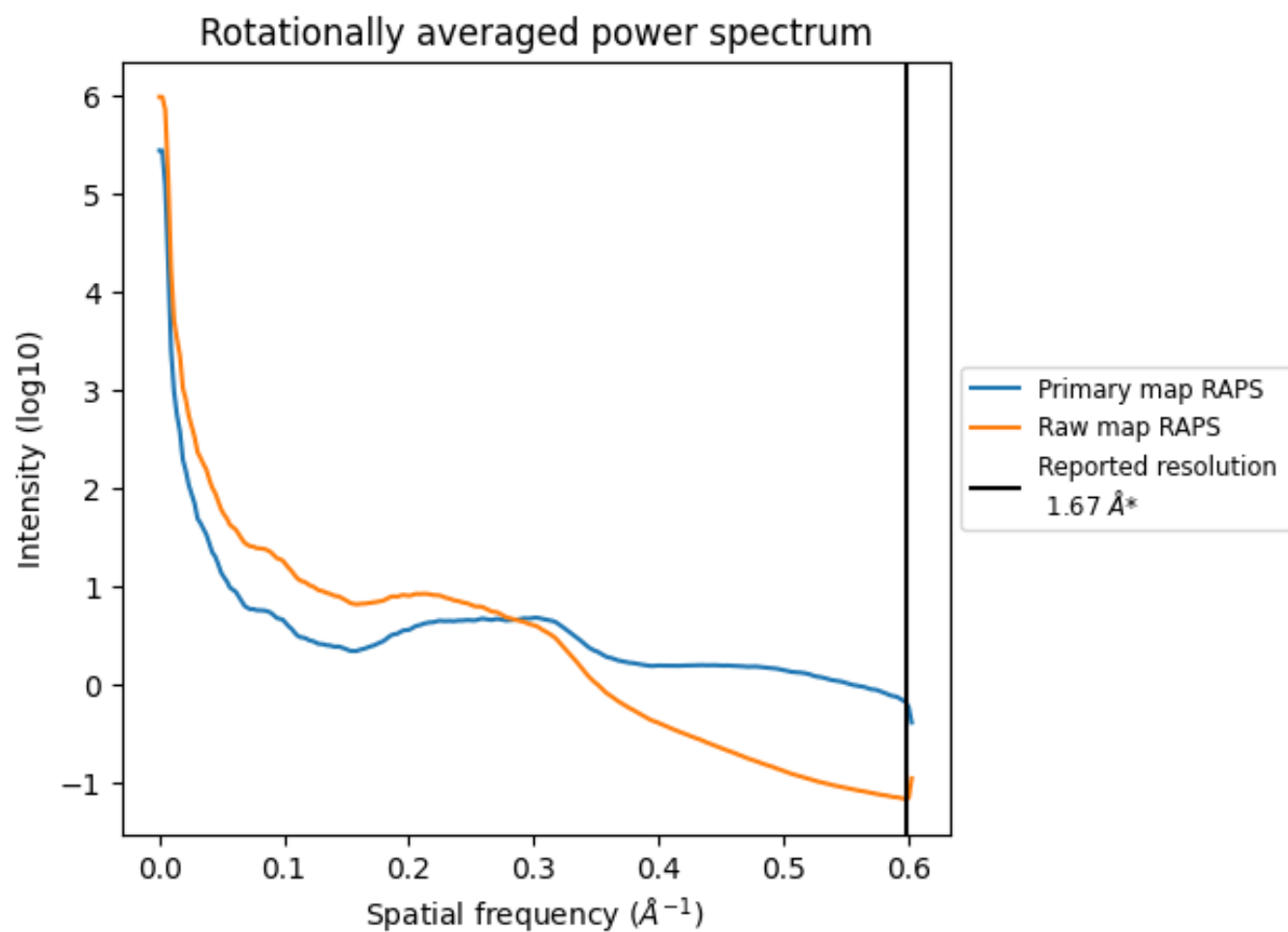
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 222 nm³; this corresponds to an approximate mass of 200 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 ⓘ

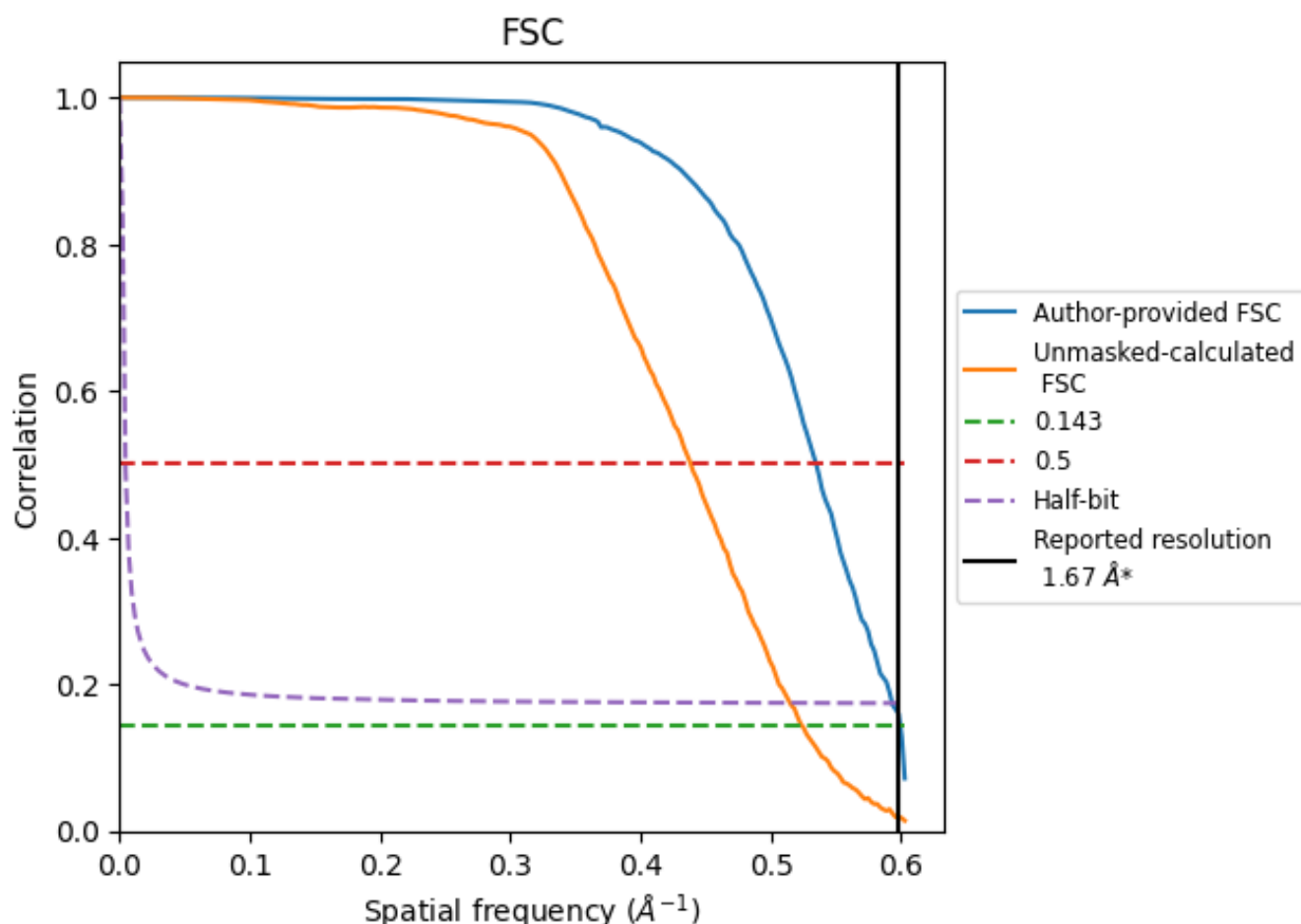


*Reported resolution corresponds to spatial frequency of 0.599 \AA^{-1}

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 0.599 \AA^{-1}

8.2 Resolution estimates [i](#)

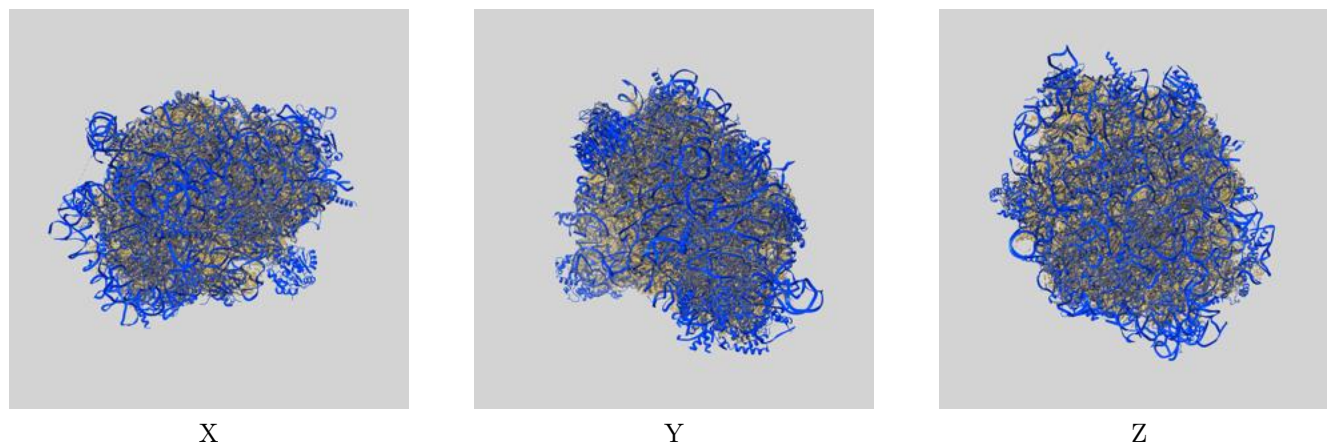
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	1.67	-	-
Author-provided FSC curve	1.67	1.87	1.69
Unmasked-calculated*	1.91	2.28	1.94

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 1.91 differs from the reported value 1.67 by more than 10 %

9 Map-model fit [i](#)

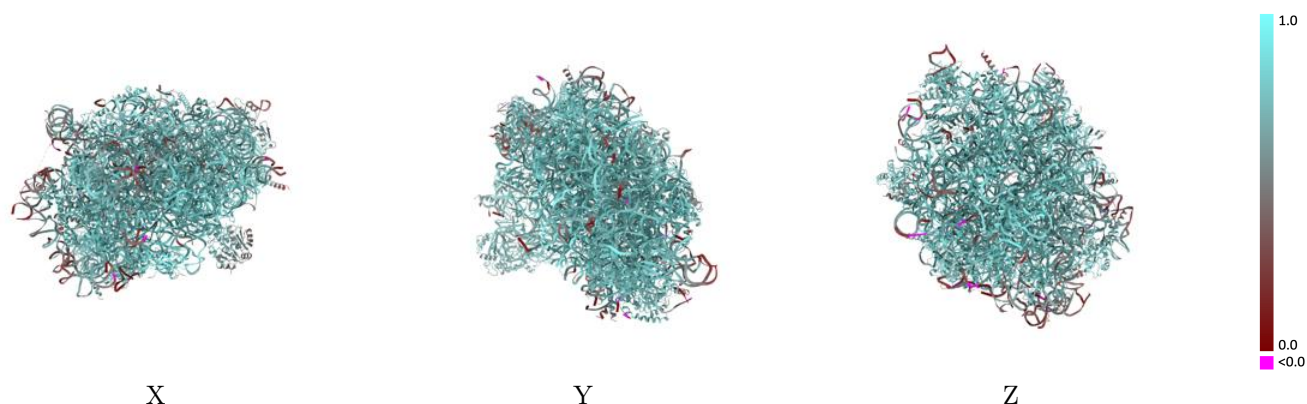
This section contains information regarding the fit between EMDB map EMD-15113 and PDB model 8A3D. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



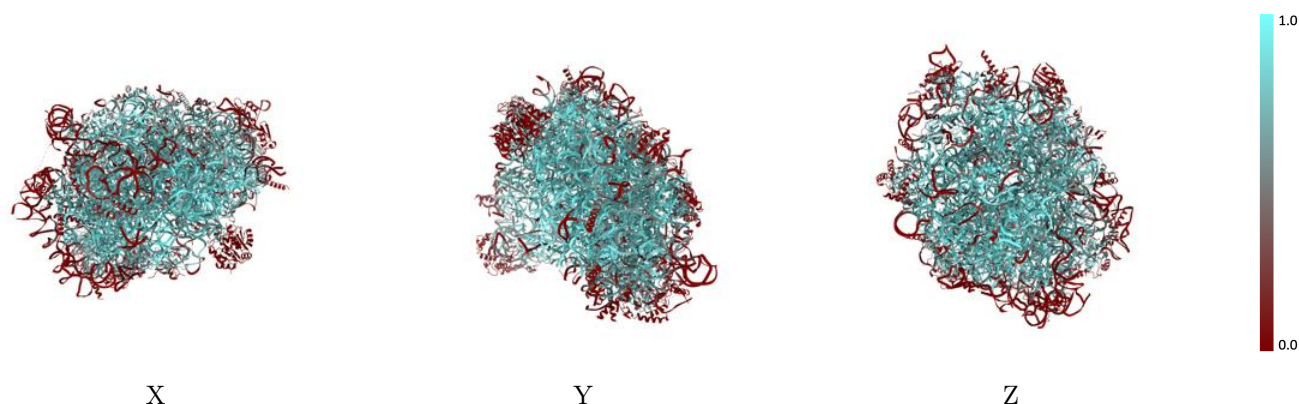
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



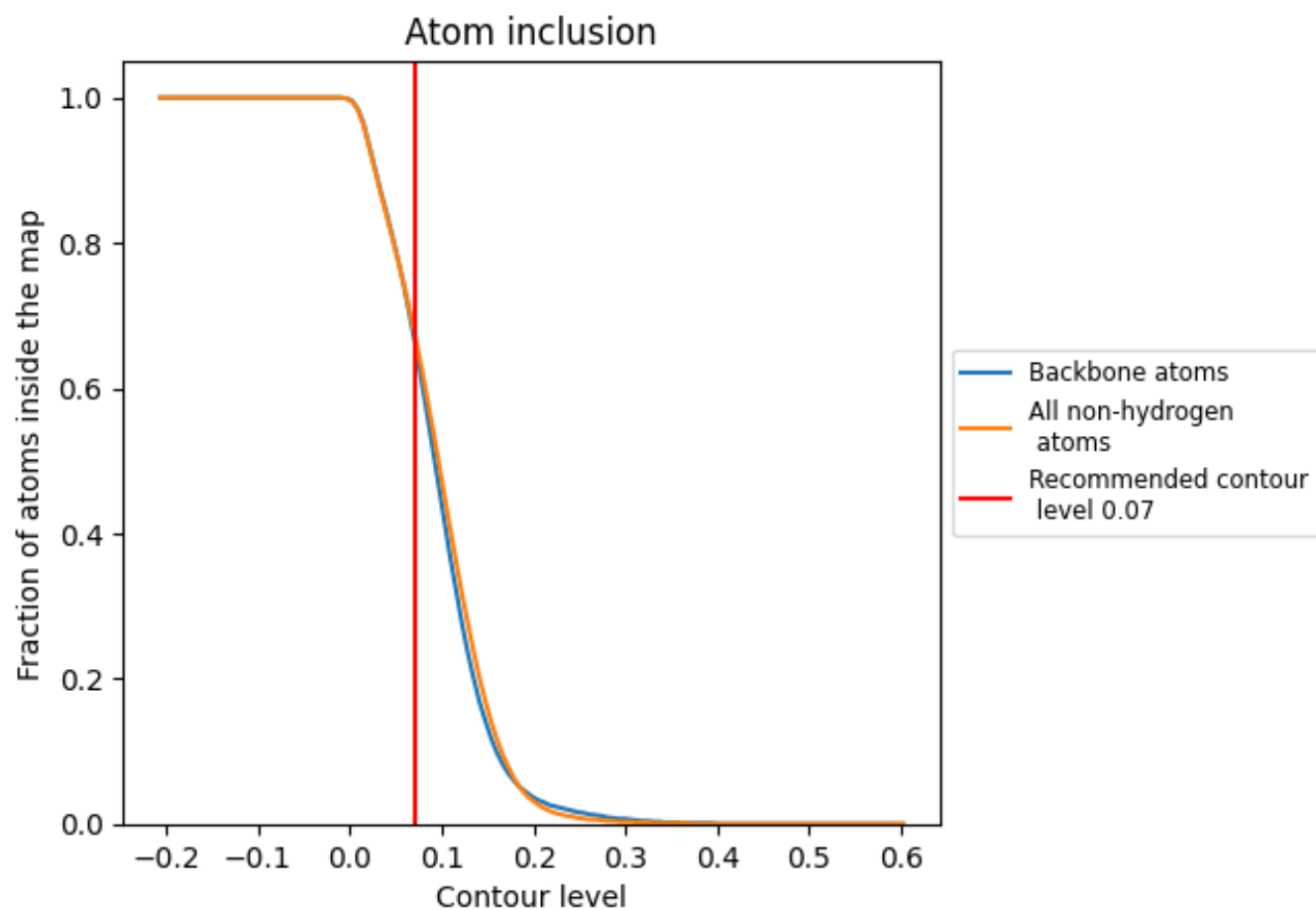
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.07).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 67% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6780	 0.7690
A	 0.7080	 0.7530
B	 0.7760	 0.8070
C	 0.7530	 0.7850
D	 0.8600	 0.8430
E	 0.7290	 0.8170
F	 0.8100	 0.8270
G	 0.4810	 0.7720
H	 0.4480	 0.7450
I	 0.7900	 0.8260
J	 0.7950	 0.8340
K	 0.8480	 0.8450
L	 0.6360	 0.7650
M	 0.8230	 0.8330
N	 0.6770	 0.7700
O	 0.0760	 0.6310
P	 0.7260	 0.8190
Q	 0.6560	 0.8060
R	 0.5980	 0.7930
S	 0.6800	 0.8010
T	 0.3670	 0.7540
U	 0.8020	 0.8270
V	 0.4420	 0.7200
W	 0.3790	 0.7370
X	 0.6270	 0.7870
Y	 0.8380	 0.8400
Z	 0.8640	 0.8480
a	 0.7510	 0.8200
b	 0.5590	 0.7800
c	 0.4710	 0.7460
d	 0.8550	 0.8470
e	 0.2350	 0.6880
f	 0.7030	 0.8080
g	 0.6680	 0.7950
h	 0.0000	 0.5730



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Chain	Atom inclusion	Q-score
i	 0.6770	 0.8140
j	 0.6980	 0.7920
k	 0.7690	 0.8200
l	 0.9170	 0.8500
m	 0.8760	 0.8480
n	 0.4020	 0.7310
o	 0.5350	 0.7840
p	 0.6680	 0.8120
q	 0.1650	 0.6920
r	 0.6020	 0.7690
s	 0.6620	 0.7840