



wwPDB EM Validation Summary Report ⓘ

Jun 19, 2026 – 04:19 am BST

PDB ID : 8AUV / pdb_00008auv
EMDB ID : EMD-15674
Title : Cryo-EM structure of the plant 40S subunit
Authors : Smirnova, J.; Loerke, J.; Kleinau, G.; Schmidt, A.; Buerger, J.; Meyer, E.H.;
Mielke, T.; Scheerer, P.; Bock, R.; Spahn, C.M.T.; Zoschke, R.
Deposited on : 2022-08-25
Resolution : 2.38 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:

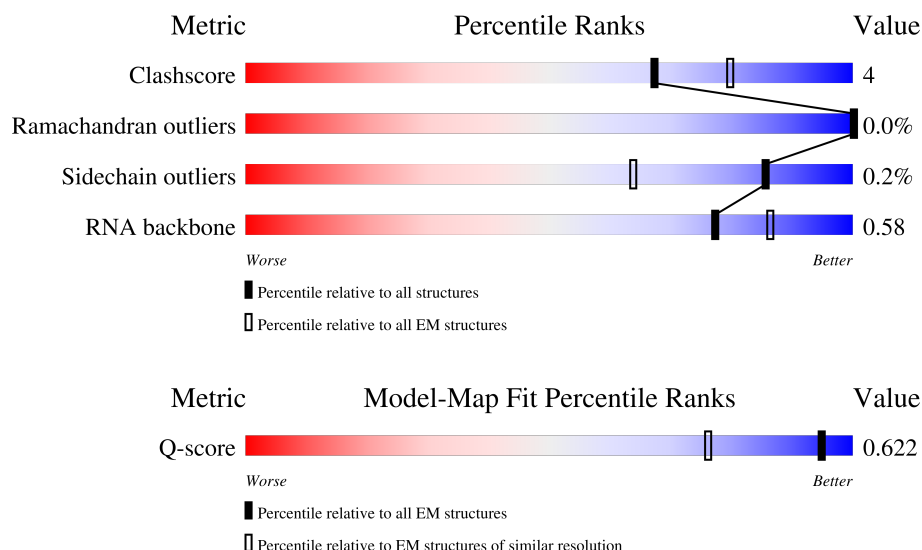
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal 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 2.38 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	4811 (1.88 - 2.88)

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	264	 93% 5% •
2	k	249	 86% 6% 8%
3	h	1808	 61% 25% • 10%

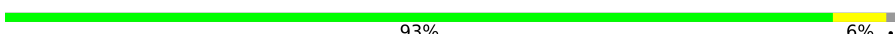
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Mol	Chain	Length	Quality of chain
4	I	208	
5	C	144	
6	D	149	
7	E	143	
8	F	261	
9	G	83	
10	H	133	
11	I	107	
12	J	127	
13	K	86	
14	L	65	
15	M	62	
16	N	156	
17	O	191	
18	P	224	
19	Q	328	
20	R	122	
21	S	150	
22	T	142	
23	U	152	
24	V	56	
25	W	151	
26	X	159	
27	Y	152	
28	Z	336	

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Mol	Chain	Length	Quality of chain
29	a	248	
30	b	197	
31	c	280	
32	d	210	
33	e	130	
34	f	147	
35	B	12	

2 Entry composition

There are 41 unique types of molecules in this entry. The entry contains 132938 atoms, of which 57333 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called eS4 (40S ribosomal protein S4).

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	259	Total	C	H	N	O	S	0	0
			4254	1323	2180	387	357	7		

- Molecule 2 is a protein called eS6 (40S ribosomal protein S6).

Mol	Chain	Residues	Atoms						AltConf	Trace
2	k	230	Total	C	H	N	O	S	0	0
			3816	1156	1965	361	326	8		

- Molecule 3 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	h	1626	Total	C	H	N	O	P	0	0
			52301	15549	17560	6195	11371	1626		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
h	603	UY1	U	modified residue	GB HQ384692
h	1194	B8N	U	modified residue	GB HQ384692
h	1283	4AC	C	modified residue	GB HQ384692

- Molecule 4 is a protein called eS10 (40S ribosomal protein S10).

Mol	Chain	Residues	Atoms						AltConf	Trace
4	l	91	Total	C	H	N	O	S	0	0
			1549	508	776	125	136	4		

- Molecule 5 is a protein called eS12 (40S ribosomal protein S12).

Mol	Chain	Residues	Atoms						AltConf	Trace
5	C	117	Total	C	H	N	O	S	0	0
			1778	553	900	153	165	7		

- Molecule 6 is a protein called eS17 (40S ribosomal protein S17).

Mol	Chain	Residues	Atoms						AltConf	Trace
6	D	119	Total	C	H	N	O	S	0	0
			1989	604	1026	178	177	4		

- Molecule 7 is a protein called eS19 (40S ribosomal protein S19).

Mol	Chain	Residues	Atoms						AltConf	Trace
7	E	136	Total	C	H	N	O	S	0	0
			2172	676	1091	211	190	4		

- Molecule 8 is a protein called eS1 (40S ribosomal protein S3a).

Mol	Chain	Residues	Atoms						AltConf	Trace
8	F	216	Total	C	H	N	O	S	0	0
			3578	1118	1818	314	320	8		

- Molecule 9 is a protein called eS21 (40S ribosomal protein S21).

Mol	Chain	Residues	Atoms						AltConf	Trace
9	G	83	Total	C	H	N	O	S	0	0
			1295	404	643	120	125	3		

- Molecule 10 is a protein called eS24 (40S ribosomal protein S24).

Mol	Chain	Residues	Atoms						AltConf	Trace
10	H	127	Total	C	H	N	O	S	0	0
			2145	657	1111	200	174	3		

- Molecule 11 is a protein called eS25 (40S ribosomal protein S25).

Mol	Chain	Residues	Atoms						AltConf	Trace
11	I	74	Total	C	H	N	O	S	0	0
			1204	365	621	109	106	3		

- Molecule 12 is a protein called eS26 (40S ribosomal protein S26).

Mol	Chain	Residues	Atoms						AltConf	Trace
12	J	98	Total	C	H	N	O	S	0	0
			1610	491	818	161	132	8		

- Molecule 13 is a protein called eS27 (40S ribosomal protein S27).

Mol	Chain	Residues	Atoms						AltConf	Trace
13	K	84	Total	C	H	N	O	S	0	0
			1307	404	656	122	118	7		

- Molecule 14 is a protein called eS28 (40S ribosomal protein S28).

Mol	Chain	Residues	Atoms						AltConf	Trace
14	L	61	Total	C	H	N	O	S	0	0
			1018	303	525	102	86	2		

- Molecule 15 is a protein called eS30 (40S ribosomal protein S30).

Mol	Chain	Residues	Atoms						AltConf	Trace
15	M	52	Total	C	H	N	O	S	0	0
			851	249	442	94	65	1		

- Molecule 16 is a protein called eS31 (ubiquitin-40S ribosomal protein S27a).

Mol	Chain	Residues	Atoms						AltConf	Trace
16	N	69	Total	C	H	N	O	S	0	0
			1143	360	581	103	94	5		

- Molecule 17 is a protein called eS7 (40S ribosomal protein S7).

Mol	Chain	Residues	Atoms						AltConf	Trace
17	O	188	Total	C	H	N	O	S	0	0
			3125	972	1591	281	279	2		

- Molecule 18 is a protein called eS8 (40S ribosomal protein S8).

Mol	Chain	Residues	Atoms						AltConf	Trace
18	P	186	Total	C	H	N	O	S	0	0
			3081	944	1570	300	263	4		

- Molecule 19 is a protein called RACK1 (guanine nucleotide-binding protein subunit beta-like protein).

Mol	Chain	Residues	Atoms						AltConf	Trace
19	Q	309	Total	C	H	N	O	S	0	0
			4756	1512	2362	414	456	12		

- Molecule 20 is a protein called uS10 (40S ribosomal protein S20).

Mol	Chain	Residues	Atoms						AltConf	Trace
20	R	102	Total	C	H	N	O	S	0	0
			1668	505	864	151	145	3		

- Molecule 21 is a protein called uS11 (40S ribosomal protein S14).

Mol	Chain	Residues	Atoms						AltConf	Trace
21	S	132	Total	C	H	N	O	S	0	0
			2026	611	1028	197	185	5		

- Molecule 22 is a protein called uS12 (40S ribosomal protein S23).

Mol	Chain	Residues	Atoms						AltConf	Trace
22	T	141	Total	C	H	N	O	S	0	0
			2264	695	1164	215	187	3		

- Molecule 23 is a protein called uS13 (40S ribosomal protein S18).

Mol	Chain	Residues	Atoms						AltConf	Trace
23	U	142	Total	C	H	N	O	S	0	0
			2337	718	1184	227	202	6		

- Molecule 24 is a protein called uS14 (40S ribosomal protein S29).

Mol	Chain	Residues	Atoms						AltConf	Trace
24	V	55	Total	C	H	N	O	S	0	0
			871	274	430	90	71	6		

- Molecule 25 is a protein called uS15 (40S ribosomal protein S13).

Mol	Chain	Residues	Atoms						AltConf	Trace
25	W	149	Total	C	H	N	O	S	0	0
			2467	762	1278	223	202	2		

- Molecule 26 is a protein called uS17 (40S ribosomal protein S11).

Mol	Chain	Residues	Atoms						AltConf	Trace
26	X	145	Total	C	H	N	O	S	0	0
			2362	734	1207	222	194	5		

- Molecule 27 is a protein called uS19 (40S ribosomal protein S15).

Mol	Chain	Residues	Atoms						AltConf	Trace
27	Y	131	Total	C	H	N	O	S	0	0
			2193	681	1132	199	176	5		

- Molecule 28 is a protein called uS2 (40S ribosomal protein SA).

Mol	Chain	Residues	Atoms						AltConf	Trace
28	Z	202	Total	C	H	N	O	S	0	0
			3233	1023	1623	289	288	10		

- Molecule 29 is a protein called uS3 (40S ribosomal protein S3).

Mol	Chain	Residues	Atoms						AltConf	Trace
29	a	211	Total	C	H	N	O	S	0	0
			3413	1052	1752	306	295	8		

- Molecule 30 is a protein called uS4 (40S ribosomal protein S9).

Mol	Chain	Residues	Atoms						AltConf	Trace
30	b	183	Total	C	H	N	O	S	0	0
			3118	964	1595	301	253	5		

- Molecule 31 is a protein called uS5 (40S ribosomal protein S2).

Mol	Chain	Residues	Atoms						AltConf	Trace
31	c	217	Total	C	H	N	O	S	0	0
			3472	1089	1786	300	289	8		

- Molecule 32 is a protein called uS7 (40S ribosomal protein S5).

Mol	Chain	Residues	Atoms						AltConf	Trace
32	d	194	Total	C	H	N	O	S	0	0
			3103	953	1572	290	280	8		

- Molecule 33 is a protein called uS8 (40S ribosomal protein S15a).

Mol	Chain	Residues	Atoms						AltConf	Trace
33	e	129	Total	C	H	N	O	S	0	0
			2100	659	1068	188	180	5		

- Molecule 34 is a protein called uS9 (40S ribosomal protein S16).

Mol	Chain	Residues	Atoms						AltConf	Trace
34	f	141	Total	C	H	N	O	S	0	0
			2332	722	1197	221	188	4		

- Molecule 35 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	B	12	Total	C	H	N	O	P	0	0
			360	108	120	24	96	12		

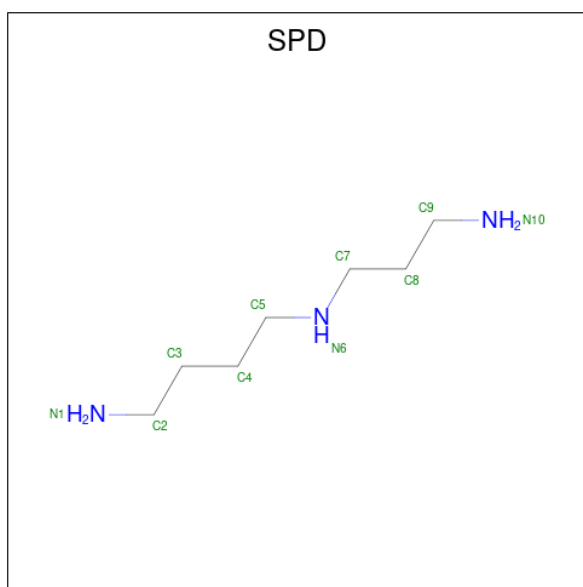
- Molecule 36 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
36	h	73	Total	Mg	0
			73	73	
36	J	1	Total	Mg	0
			1	1	
36	U	1	Total	Mg	0
			1	1	
36	B	1	Total	Mg	0
			1	1	

- Molecule 37 is POTASSIUM ION (CCD ID: K) (formula: K).

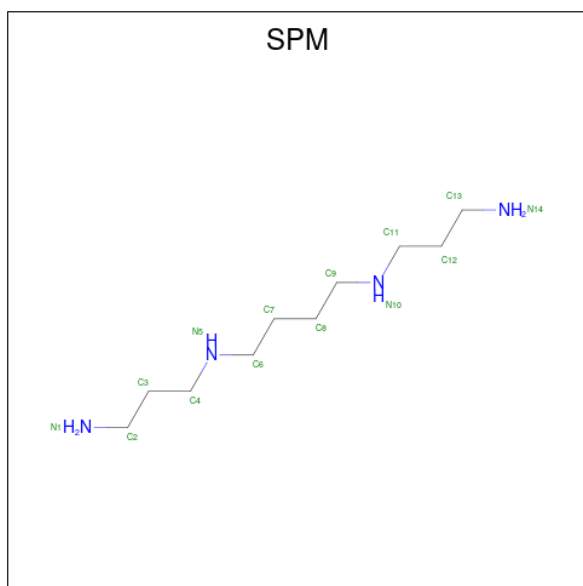
Mol	Chain	Residues	Atoms		AltConf
37	h	41	Total	K	0
			41	41	
37	S	1	Total	K	0
			1	1	
37	T	1	Total	K	0
			1	1	
37	U	1	Total	K	0
			1	1	
37	V	1	Total	K	0
			1	1	
37	W	1	Total	K	0
			1	1	
37	d	1	Total	K	0
			1	1	

- Molecule 38 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).



Mol	Chain	Residues	Atoms				AltConf
38	h	1	Total	C	H	N	0
			29	7	19	3	

- Molecule 39 is SPERMINE (CCD ID: SPM) (formula: $C_{10}H_{26}N_4$).



Mol	Chain	Residues	Atoms				AltConf
39	h	1	Total	C	H	N	0
			40	10	26	4	
39	h	1	Total	C	H	N	0
			40	10	26	4	
39	h	1	Total	C	H	N	0
			40	10	26	4	

- Molecule 40 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
40	J	1	Total 1	Zn 1	0
40	N	1	Total 1	Zn 1	0
40	V	1	Total 1	Zn 1	0

- Molecule 41 is water.

Mol	Chain	Residues	Atoms		AltConf
41	A	10	Total 10	O 10	0
41	k	6	Total 6	O 6	0
41	h	2050	Total 2050	O 2050	0
41	E	10	Total 10	O 10	0
41	F	11	Total 11	O 11	0
41	I	1	Total 1	O 1	0
41	J	29	Total 29	O 29	0
41	K	5	Total 5	O 5	0
41	M	1	Total 1	O 1	0
41	O	1	Total 1	O 1	0
41	P	18	Total 18	O 18	0
41	R	11	Total 11	O 11	0
41	S	26	Total 26	O 26	0
41	T	43	Total 43	O 43	0
41	U	8	Total 8	O 8	0
41	V	5	Total 5	O 5	0

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Mol	Chain	Residues	Atoms		AltConf
41	W	27	Total 27	O 27	0
41	X	22	Total 22	O 22	0
41	Y	6	Total 6	O 6	0
41	Z	1	Total 1	O 1	0
41	a	1	Total 1	O 1	0
41	b	11	Total 11	O 11	0
41	c	11	Total 11	O 11	0
41	d	11	Total 11	O 11	0
41	e	16	Total 16	O 16	0
41	f	15	Total 15	O 15	0
41	B	16	Total 16	O 16	0

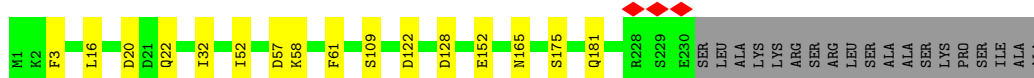
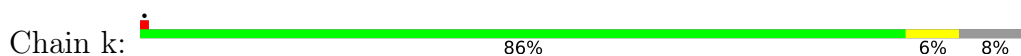
3 Residue-property plots [i](#)

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.

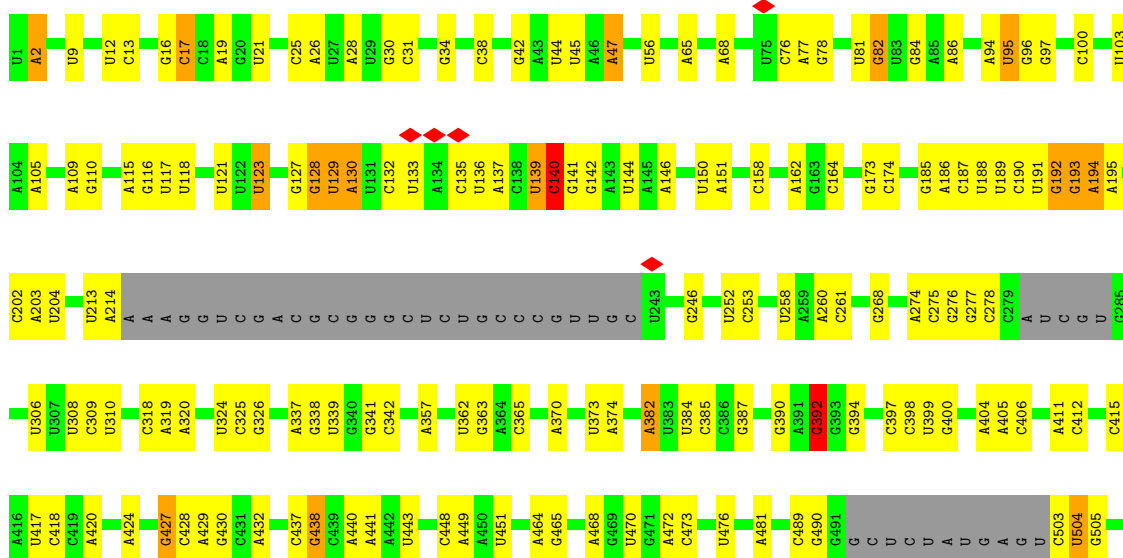
- Molecule 1: eS4 (40S ribosomal protein S4)



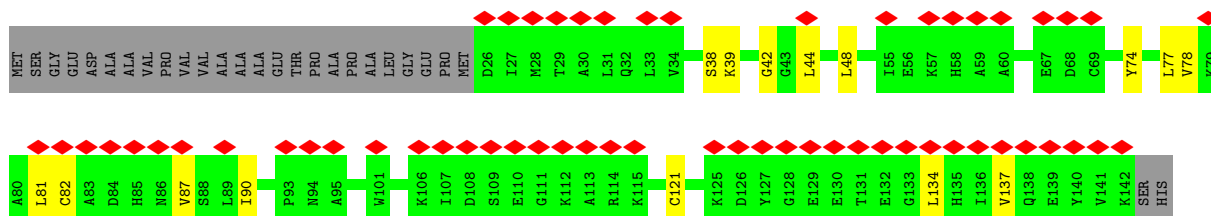
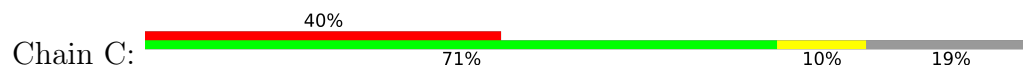
- Molecule 2: eS6 (40S ribosomal protein S6)



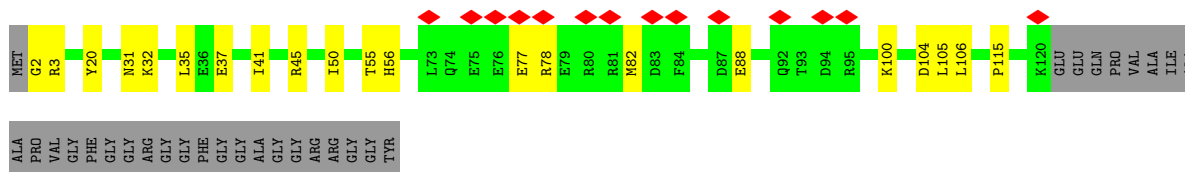
- Molecule 3: 18S rRNA



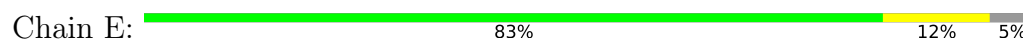
- Molecule 5: eS12 (40S ribosomal protein S12)



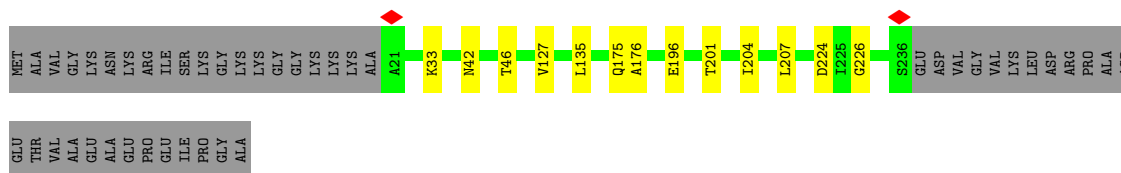
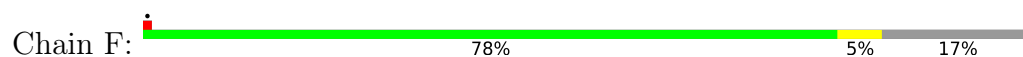
- Molecule 6: eS17 (40S ribosomal protein S17)



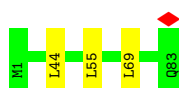
- Molecule 7: eS19 (40S ribosomal protein S19)

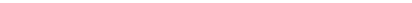


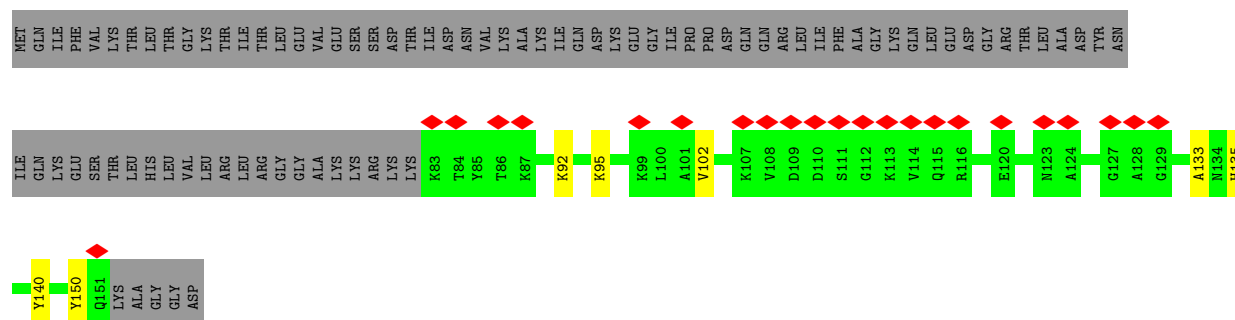
- Molecule 8: eS1 (40S ribosomal protein S3a)



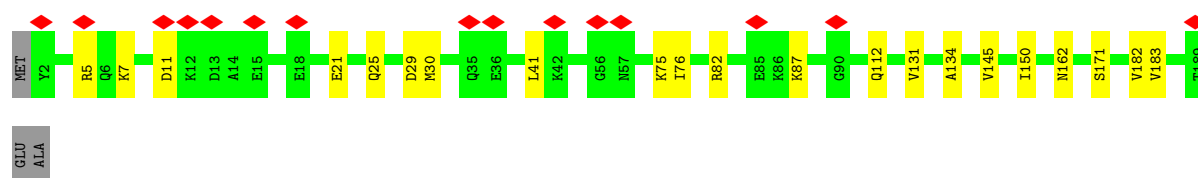
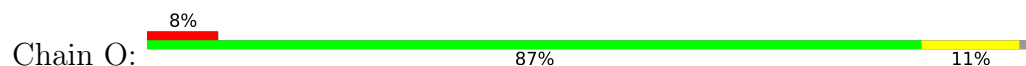
- Molecule 9: eS21 (40S ribosomal protein S21)



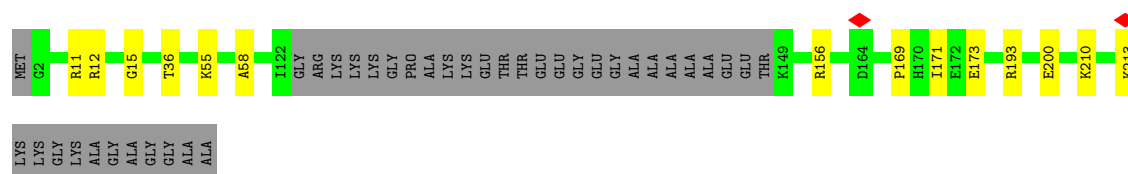
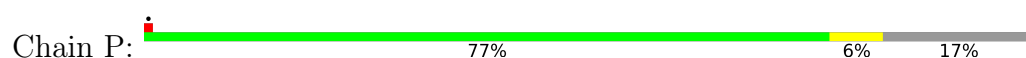
- Chain N:  15% 40% 56%



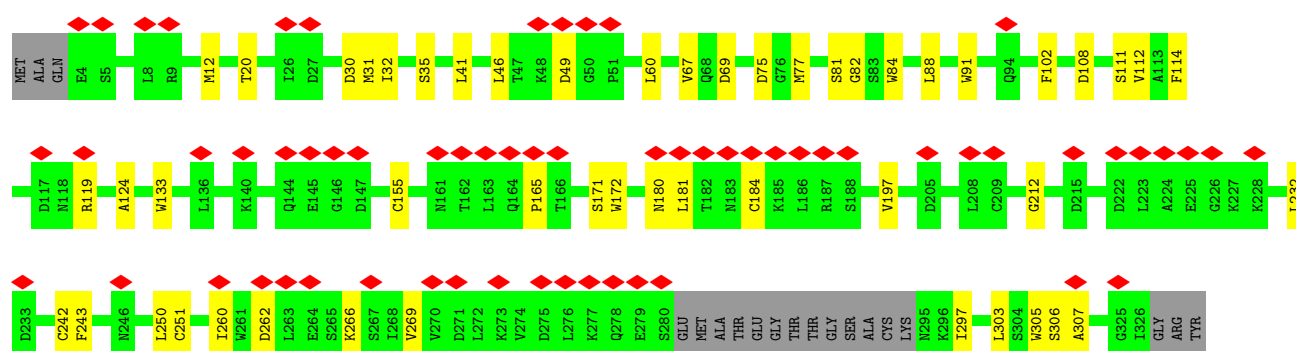
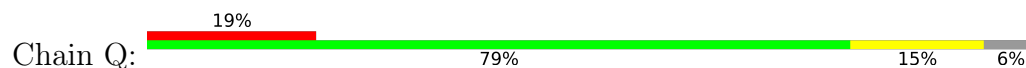
- Molecule 17: eS7 (40S ribosomal protein S7)



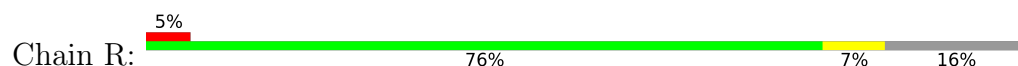
- Molecule 18: eS8 (40S ribosomal protein S8)



- Molecule 19: RACK1 (guanine nucleotide-binding protein subunit beta-like protein)

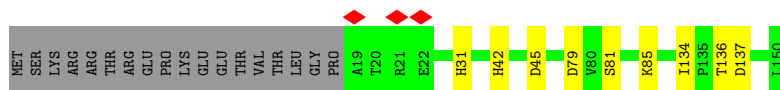
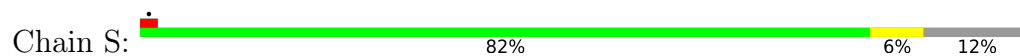


- Molecule 20: uS10 (40S ribosomal protein S20)





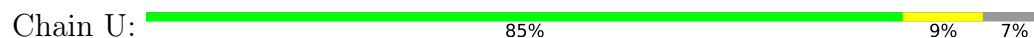
- Molecule 21: uS11 (40S ribosomal protein S14)



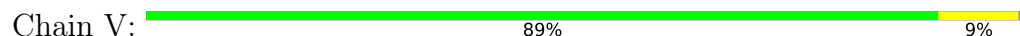
- Molecule 22: uS12 (40S ribosomal protein S23)



- Molecule 23: uS13 (40S ribosomal protein S18)



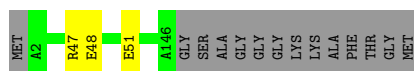
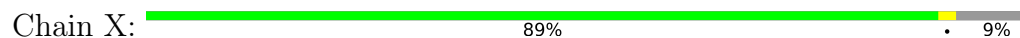
- Molecule 24: uS14 (40S ribosomal protein S29)



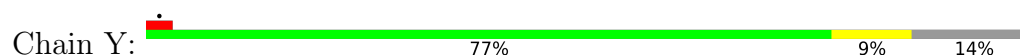
- Molecule 25: uS15 (40S ribosomal protein S13)



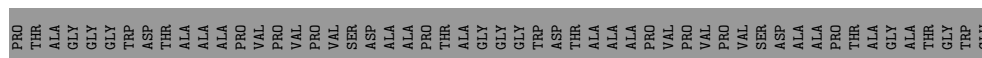
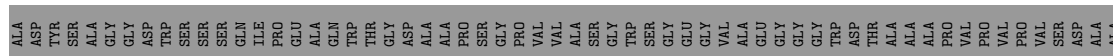
- Molecule 26: uS17 (40S ribosomal protein S11)



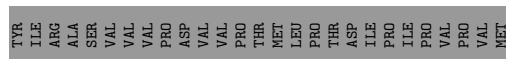
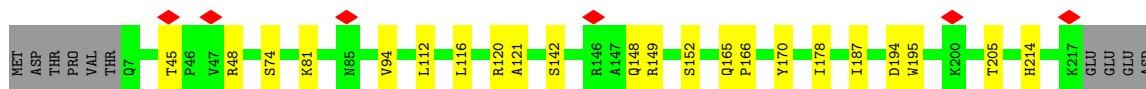
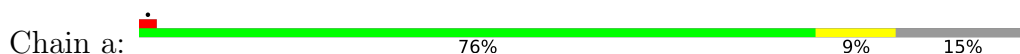
- Molecule 27: uS19 (40S ribosomal protein S15)



- Molecule 28: uS2 (40S ribosomal protein SA)



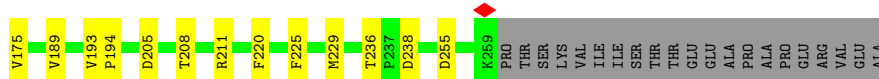
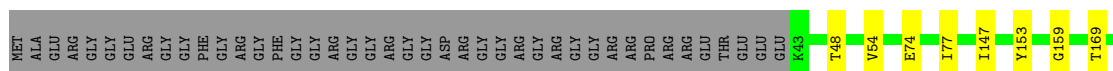
- Molecule 29: uS3 (40S ribosomal protein S3)



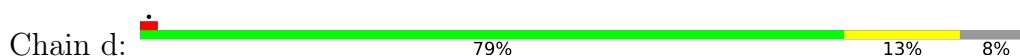
- Molecule 30: uS4 (40S ribosomal protein S9)

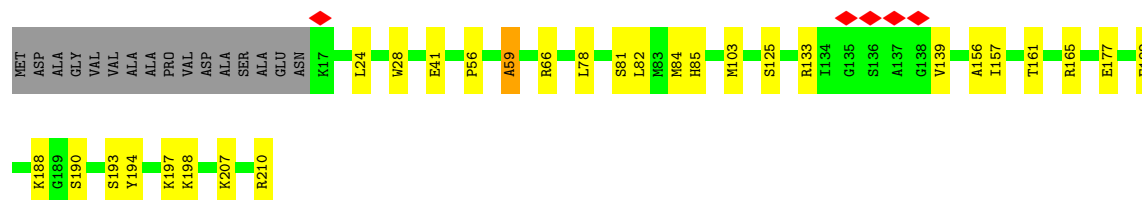


- Molecule 31: uS5 (40S ribosomal protein S2)



- Molecule 32: uS7 (40S ribosomal protein S5)





- Molecule 33: uS8 (40S ribosomal protein S15a)

Chain e: 93% 6% .



- Molecule 34: uS9 (40S ribosomal protein S16)

Chain f: 88% 8% .



- Molecule 35: mRNA

Chain B: 67% 33%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	335672	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 ($e^-/\text{\AA}^2$)	27	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	11.349	Depositor
Minimum map value	-6.212	Depositor
Average map value	0.010	Depositor
Map value standard deviation	0.189	Depositor
Recommended contour level	0.426	Depositor
Map size ($\text{\AA}$)	381.6, 381.6, 381.6	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.848, 0.848, 0.848	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: B8N, 6MZ, MA6, SPM, OMG, K, UY1, OMC, A2M, 4AC, ZN, OMU, MG, PSU, SPD

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	0.13	0/2114	0.26	0/2837
2	k	0.11	0/1875	0.25	0/2494
3	h	0.17	2/36945 (0.0%)	0.26	0/57563
4	l	0.11	0/794	0.23	0/1074
5	C	0.09	0/889	0.21	0/1198
6	D	0.14	0/973	0.29	0/1299
7	E	0.11	0/1103	0.22	0/1480
8	F	0.11	0/1790	0.23	0/2402
9	G	0.10	0/662	0.21	0/891
10	H	0.11	0/1049	0.22	0/1391
11	I	0.14	0/589	0.29	0/789
12	J	0.13	0/805	0.24	0/1076
13	K	0.15	0/662	0.29	0/892
14	L	0.12	0/496	0.22	0/661
15	M	0.16	0/414	0.23	0/544
16	N	0.11	0/574	0.21	0/763
17	O	0.11	0/1560	0.23	0/2097
18	P	0.12	0/1535	0.22	0/2050
19	Q	0.09	0/2446	0.23	0/3324
20	R	0.14	0/813	0.25	0/1095
21	S	0.12	0/1010	0.25	0/1352
22	T	0.13	0/1119	0.25	0/1487
23	U	0.11	0/1170	0.23	0/1562
24	V	0.15	0/453	0.23	0/605
25	W	0.13	0/1214	0.23	0/1632
26	X	0.13	0/1180	0.25	0/1579
27	Y	0.12	0/1084	0.24	0/1450
28	Z	0.12	0/1644	0.24	0/2223
29	a	0.10	0/1684	0.23	0/2257
30	b	0.11	0/1550	0.25	0/2073
31	c	0.12	0/1721	0.25	0/2320
32	d	0.14	0/1553	0.46	2/2095 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.12	0/1050	0.25	0/1405
34	f	0.16	0/1154	0.26	0/1542
35	B	0.11	0/263	0.21	0/404
All	All	0.14	2/75937 (0.0%)	0.25	2/109906 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	h	1272	OMU	O3'-P	5.17	1.61	1.56
3	h	622	A2M	O3'-P	5.01	1.61	1.56

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	d	59	ALA	CA-C-N	10.58	133.97	120.64
32	d	59	ALA	C-N-CA	10.58	133.97	120.64

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	A	2074	2180	2181	10	0
2	k	1851	1965	1969	11	0
3	h	34741	17560	17528	224	0
4	l	773	776	776	4	0
5	C	878	900	905	12	0
6	D	963	1026	1025	22	0
7	E	1081	1091	1091	12	0
8	F	1760	1818	1820	8	0
9	G	652	643	645	1	0
10	H	1034	1111	1110	3	0
11	I	583	621	620	5	0
12	J	792	818	820	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	K	651	656	661	6	0
14	L	493	525	524	6	0
15	M	409	442	440	6	0
16	N	562	581	580	8	0
17	O	1534	1591	1590	14	0
18	P	1511	1570	1570	11	0
19	Q	2394	2362	2368	37	0
20	R	804	864	865	7	0
21	S	998	1028	1028	8	0
22	T	1100	1164	1165	2	0
23	U	1153	1184	1184	8	0
24	V	441	430	430	4	0
25	W	1189	1278	1277	6	0
26	X	1155	1207	1210	2	0
27	Y	1061	1132	1131	9	0
28	Z	1610	1623	1624	16	0
29	a	1661	1752	1754	25	0
30	b	1523	1595	1595	7	0
31	c	1686	1786	1789	15	0
32	d	1531	1572	1573	28	0
33	e	1032	1068	1068	8	0
34	f	1135	1197	1198	8	0
35	B	240	120	121	3	0
36	B	1	0	0	0	0
36	J	1	0	0	0	0
36	U	1	0	0	0	0
36	h	73	0	0	0	0
37	S	1	0	0	0	0
37	T	1	0	0	0	0
37	U	1	0	0	0	0
37	V	1	0	0	0	0
37	W	1	0	0	0	0
37	d	1	0	0	0	0
37	h	41	0	0	0	0
38	h	10	19	19	1	0
39	h	42	78	78	2	0
40	J	1	0	0	0	0
40	N	1	0	0	0	0
40	V	1	0	0	0	0
41	A	10	0	0	0	0
41	B	16	0	0	2	0
41	E	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
41	F	11	0	0	0	0
41	I	1	0	0	0	0
41	J	29	0	0	0	0
41	K	5	0	0	1	0
41	M	1	0	0	0	0
41	O	1	0	0	0	0
41	P	18	0	0	1	0
41	R	11	0	0	1	0
41	S	26	0	0	1	0
41	T	43	0	0	0	0
41	U	8	0	0	0	0
41	V	5	0	0	0	0
41	W	27	0	0	0	0
41	X	22	0	0	0	0
41	Y	6	0	0	0	0
41	Z	1	0	0	0	0
41	a	1	0	0	0	0
41	b	11	0	0	0	0
41	c	11	0	0	0	0
41	d	11	0	0	0	0
41	e	16	0	0	1	0
41	f	15	0	0	0	0
41	h	2050	0	0	49	0
41	k	6	0	0	0	0
All	All	75605	57333	57332	490	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 490 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)
29:a:178:ILE:CD1	29:a:187:ILE:HD12	1.48	1.44
29:a:178:ILE:CD1	29:a:187:ILE:CD1	2.22	1.17
31:c:147:ILE:HD13	31:c:229:MET:HG2	1.28	1.11
19:Q:165:PRO:HB2	19:Q:181:LEU:HD23	1.36	1.06
29:a:178:ILE:HD11	29:a:187:ILE:HD12	1.11	1.04

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	
1	A	257/264 (97%)	253 (98%)	4 (2%)	0	100	100
2	k	228/249 (92%)	228 (100%)	0	0	100	100
4	l	89/208 (43%)	88 (99%)	1 (1%)	0	100	100
5	C	115/144 (80%)	115 (100%)	0	0	100	100
6	D	117/149 (78%)	114 (97%)	3 (3%)	0	100	100
7	E	134/143 (94%)	132 (98%)	2 (2%)	0	100	100
8	F	214/261 (82%)	212 (99%)	2 (1%)	0	100	100
9	G	81/83 (98%)	81 (100%)	0	0	100	100
10	H	125/133 (94%)	122 (98%)	3 (2%)	0	100	100
11	I	72/107 (67%)	72 (100%)	0	0	100	100
12	J	96/127 (76%)	95 (99%)	1 (1%)	0	100	100
13	K	82/86 (95%)	80 (98%)	2 (2%)	0	100	100
14	L	59/65 (91%)	59 (100%)	0	0	100	100
15	M	48/62 (77%)	44 (92%)	4 (8%)	0	100	100
16	N	67/156 (43%)	67 (100%)	0	0	100	100
17	O	186/191 (97%)	182 (98%)	4 (2%)	0	100	100
18	P	182/224 (81%)	180 (99%)	2 (1%)	0	100	100
19	Q	305/328 (93%)	298 (98%)	7 (2%)	0	100	100
20	R	100/122 (82%)	99 (99%)	1 (1%)	0	100	100
21	S	130/150 (87%)	128 (98%)	2 (2%)	0	100	100
22	T	139/142 (98%)	137 (99%)	2 (1%)	0	100	100
23	U	140/152 (92%)	138 (99%)	2 (1%)	0	100	100
24	V	53/56 (95%)	53 (100%)	0	0	100	100
25	W	147/151 (97%)	147 (100%)	0	0	100	100
26	X	143/159 (90%)	140 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	Y	129/152 (85%)	125 (97%)	4 (3%)	0	100	100
28	Z	200/336 (60%)	198 (99%)	2 (1%)	0	100	100
29	a	209/248 (84%)	203 (97%)	6 (3%)	0	100	100
30	b	181/197 (92%)	179 (99%)	2 (1%)	0	100	100
31	c	215/280 (77%)	213 (99%)	2 (1%)	0	100	100
32	d	192/210 (91%)	184 (96%)	7 (4%)	1 (0%)	24	34
33	e	127/130 (98%)	126 (99%)	1 (1%)	0	100	100
34	f	139/147 (95%)	136 (98%)	3 (2%)	0	100	100
All	All	4701/5612 (84%)	4628 (98%)	72 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
32	d	59	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	225/228 (99%)	224 (100%)	1 (0%)	84	91
2	k	199/213 (93%)	199 (100%)	0	100	100
4	l	85/169 (50%)	85 (100%)	0	100	100
5	C	94/112 (84%)	94 (100%)	0	100	100
6	D	109/124 (88%)	109 (100%)	0	100	100
7	E	111/114 (97%)	111 (100%)	0	100	100
8	F	195/228 (86%)	194 (100%)	1 (0%)	81	90
9	G	70/70 (100%)	69 (99%)	1 (1%)	59	77
10	H	108/113 (96%)	108 (100%)	0	100	100
11	I	64/89 (72%)	64 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	J	87/109 (80%)	87 (100%)	0	100	100
13	K	76/78 (97%)	76 (100%)	0	100	100
14	L	54/57 (95%)	54 (100%)	0	100	100
15	M	41/49 (84%)	41 (100%)	0	100	100
16	N	60/134 (45%)	60 (100%)	0	100	100
17	O	169/171 (99%)	169 (100%)	0	100	100
18	P	158/178 (89%)	157 (99%)	1 (1%)	78	88
19	Q	266/279 (95%)	264 (99%)	2 (1%)	73	85
20	R	93/108 (86%)	93 (100%)	0	100	100
21	S	103/120 (86%)	103 (100%)	0	100	100
22	T	113/114 (99%)	113 (100%)	0	100	100
23	U	122/131 (93%)	120 (98%)	2 (2%)	55	74
24	V	46/47 (98%)	46 (100%)	0	100	100
25	W	130/131 (99%)	130 (100%)	0	100	100
26	X	124/131 (95%)	124 (100%)	0	100	100
27	Y	115/130 (88%)	115 (100%)	0	100	100
28	Z	171/256 (67%)	171 (100%)	0	100	100
29	a	179/215 (83%)	179 (100%)	0	100	100
30	b	161/171 (94%)	161 (100%)	0	100	100
31	c	184/226 (81%)	183 (100%)	1 (0%)	81	90
32	d	165/175 (94%)	165 (100%)	0	100	100
33	e	111/112 (99%)	111 (100%)	0	100	100
34	f	116/120 (97%)	116 (100%)	0	100	100
All	All	4104/4702 (87%)	4095 (100%)	9 (0%)	85	94

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	U	59	LEU
31	c	205	ASP
18	P	210	LYS
19	Q	114	PHE
19	Q	133	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
19	Q	149	HIS
33	e	42	GLN
23	U	119	ASN
34	f	65	HIS
31	c	99	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	h	1617/1808 (89%)	225 (13%)	0
35	B	11/12 (91%)	1 (9%)	0
All	All	1628/1820 (89%)	226 (13%)	0

5 of 226 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	h	2	A
3	h	17	C
3	h	25	C
3	h	26	A
3	h	34	G

There are no RNA pucker outliers to report.

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

81 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	$\# Z > 2$
3	PSU	h	1634	3	18,21,22	4.61	8 (44%)	22,30,33	1.80	5 (22%)
3	PSU	h	1535	3	18,21,22	4.64	8 (44%)	22,30,33	1.83	5 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	OMG	h	246	37,3	23,26,27	2.56	8 (34%)	33,38,41	2.24	10 (30%)
3	A2M	h	544	3	22,25,26	3.90	9 (40%)	31,36,39	2.97	14 (45%)
3	PSU	h	607	3	18,21,22	4.60	8 (44%)	22,30,33	1.87	6 (27%)
3	PSU	h	809	3	18,21,22	4.59	8 (44%)	22,30,33	1.83	6 (27%)
3	6MZ	h	1771	37,3,36	22,25,26	2.72	4 (18%)	30,36,39	2.47	11 (36%)
3	PSU	h	95	3	18,21,22	4.62	8 (44%)	22,30,33	1.84	5 (22%)
3	PSU	h	1567	3	18,21,22	4.62	8 (44%)	22,30,33	1.84	5 (22%)
3	PSU	h	753	3	18,21,22	4.62	8 (44%)	22,30,33	1.82	5 (22%)
3	MA6	h	1790	3	23,26,27	1.27	4 (17%)	34,38,41	2.83	15 (44%)
3	PSU	h	1002	3	18,21,22	4.60	8 (44%)	22,30,33	1.76	5 (22%)
3	PSU	h	306	3	18,21,22	4.55	8 (44%)	22,30,33	1.78	5 (22%)
3	A2M	h	977	3	22,25,26	3.91	9 (40%)	31,36,39	2.97	12 (38%)
3	PSU	h	1485	3	18,21,22	4.64	8 (44%)	22,30,33	1.83	5 (22%)
3	OMU	h	886	3	19,22,23	3.21	8 (42%)	26,31,34	1.82	5 (19%)
3	PSU	h	1106	3	18,21,22	4.56	8 (44%)	22,30,33	1.82	5 (22%)
3	PSU	h	470	3	18,21,22	4.61	8 (44%)	22,30,33	1.86	5 (22%)
3	OMC	h	473	3	19,22,23	3.24	8 (42%)	26,31,34	0.69	0
3	B8N	h	1194	3	24,29,30	3.01	7 (29%)	29,42,45	1.72	7 (24%)
3	PSU	h	1304	3	18,21,22	4.59	8 (44%)	22,30,33	1.85	5 (22%)
3	OMG	h	598	3	23,26,27	2.53	8 (34%)	33,38,41	2.22	11 (33%)
3	OMU	h	123	3	19,22,23	3.21	8 (42%)	26,31,34	1.66	4 (15%)
3	OMC	h	418	3	19,22,23	3.27	8 (42%)	26,31,34	0.90	1 (3%)
3	OMG	h	392	3	23,26,27	2.55	9 (39%)	33,38,41	2.19	13 (39%)
3	PSU	h	339	37,3	18,21,22	4.63	8 (44%)	22,30,33	1.86	6 (27%)
3	PSU	h	1178	3	18,21,22	4.57	8 (44%)	22,30,33	1.83	5 (22%)
3	OMU	h	1447	3	19,22,23	3.18	8 (42%)	26,31,34	1.66	4 (15%)
3	OMC	h	1645	3	19,22,23	3.25	8 (42%)	26,31,34	0.75	0
3	PSU	h	1615	3	18,21,22	4.61	8 (44%)	22,30,33	1.80	5 (22%)
3	OMG	h	1274	37,3	23,26,27	2.55	8 (34%)	33,38,41	2.20	11 (33%)
3	PSU	h	362	3	18,21,22	4.58	8 (44%)	22,30,33	1.84	5 (22%)
3	4AC	h	1781	3	21,24,25	3.17	11 (52%)	29,34,37	1.56	4 (13%)
3	OMU	h	1234	3	19,22,23	3.19	8 (42%)	26,31,34	1.66	4 (15%)
3	A2M	h	162	3	22,25,26	3.94	9 (40%)	31,36,39	2.94	12 (38%)
3	A2M	h	28	3,36	22,25,26	3.94	9 (40%)	31,36,39	2.98	12 (38%)
3	A2M	h	440	3	22,25,26	3.92	9 (40%)	31,36,39	3.05	12 (38%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	OMC	h	38	3	19,22,23	3.28	8 (42%)	26,31,34	0.69	0
3	A2M	h	1758	3	22,25,26	3.96	10 (45%)	31,36,39	2.98	13 (41%)
3	UY1	h	603	3	19,22,23	4.13	7 (36%)	22,31,34	1.80	5 (22%)
3	PSU	h	762	3	18,21,22	4.57	8 (44%)	22,30,33	1.76	5 (22%)
3	PSU	h	121	3,36	18,21,22	4.62	8 (44%)	22,30,33	1.79	5 (22%)
3	PSU	h	605	3	18,21,22	4.57	8 (44%)	22,30,33	1.83	5 (22%)
3	PSU	h	417	3	18,21,22	4.57	8 (44%)	22,30,33	1.75	5 (22%)
3	PSU	h	961	37,3	18,21,22	4.61	8 (44%)	22,30,33	1.91	5 (22%)
3	MA6	h	1789	3	23,26,27	1.25	3 (13%)	34,38,41	2.75	14 (41%)
3	OMU	h	581	37,3	19,22,23	3.20	8 (42%)	26,31,34	1.68	4 (15%)
3	PSU	h	1293	3	18,21,22	4.62	8 (44%)	22,30,33	1.82	5 (22%)
3	A2M	h	622	3,36	22,25,26	3.91	10 (45%)	31,36,39	3.15	14 (45%)
3	PSU	h	1524	3	18,21,22	4.68	8 (44%)	22,30,33	1.75	5 (22%)
3	A2M	h	468	3	22,25,26	3.96	9 (40%)	31,36,39	3.02	13 (41%)
3	4AC	h	1283	3	21,24,25	3.14	11 (52%)	29,34,37	1.15	3 (10%)
3	PSU	h	584	3	18,21,22	5.19	10 (55%)	22,30,33	4.36	6 (27%)
3	PSU	h	1217	3	18,21,22	4.62	8 (44%)	22,30,33	1.79	5 (22%)
3	PSU	h	1190	3	18,21,22	4.62	8 (44%)	22,30,33	1.86	5 (22%)
3	OMU	h	373	3	19,22,23	3.19	8 (42%)	26,31,34	1.67	4 (15%)
3	PSU	h	606	3	18,21,22	4.59	8 (44%)	22,30,33	1.76	5 (22%)
3	PSU	h	763	3	18,21,22	4.57	8 (44%)	22,30,33	1.79	5 (22%)
3	PSU	h	950	3	18,21,22	4.59	8 (44%)	22,30,33	1.80	5 (22%)
3	PSU	h	1210	3	18,21,22	4.61	8 (44%)	22,30,33	1.89	5 (22%)
3	PSU	h	1787	3	18,21,22	4.63	8 (44%)	22,30,33	1.91	5 (22%)
3	A2M	h	800	3	22,25,26	3.93	9 (40%)	31,36,39	3.00	12 (38%)
3	PSU	h	1184	3	18,21,22	4.60	8 (44%)	22,30,33	1.90	5 (22%)
3	PSU	h	258	3	18,21,22	4.63	8 (44%)	22,30,33	1.79	5 (22%)
3	PSU	h	1120	3	18,21,22	4.55	8 (44%)	22,30,33	1.85	5 (22%)
3	PSU	h	451	37,3	18,21,22	4.58	8 (44%)	22,30,33	1.83	6 (27%)
3	OMU	h	614	3	19,22,23	3.19	8 (42%)	26,31,34	1.65	4 (15%)
3	OMU	h	1272	3	19,22,23	3.20	8 (42%)	26,31,34	1.67	4 (15%)
3	OMU	h	1383	3,36	19,22,23	3.19	8 (42%)	26,31,34	1.68	4 (15%)
3	PSU	h	103	37,3	18,21,22	4.58	8 (44%)	22,30,33	1.83	5 (22%)
3	OMG	h	1433	3,36	23,26,27	2.54	9 (39%)	33,38,41	2.15	11 (33%)
3	A2M	h	1329	3	22,25,26	3.93	9 (40%)	31,36,39	3.00	13 (41%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PSU	h	1308	3	18,21,22	4.58	8 (44%)	22,30,33	1.83	5 (22%)
3	PSU	h	1027	3	18,21,22	4.62	9 (50%)	22,30,33	1.86	5 (22%)
3	PSU	h	635	3	18,21,22	4.58	8 (44%)	22,30,33	1.82	5 (22%)
3	A2M	h	424	3	22,25,26	3.96	9 (40%)	31,36,39	3.00	13 (41%)
3	OMC	h	1218	3	19,22,23	3.30	8 (42%)	26,31,34	0.79	0
3	OMU	h	1012	3	19,22,23	3.17	8 (42%)	26,31,34	1.69	4 (15%)
3	A2M	h	1579	3	22,25,26	3.95	9 (40%)	31,36,39	3.04	12 (38%)
3	OMC	h	140	3	19,22,23	3.29	8 (42%)	26,31,34	0.73	0
3	PSU	h	310	3	18,21,22	4.61	8 (44%)	22,30,33	1.84	5 (22%)

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
3	PSU	h	1634	3	-	0/7/25/26	0/2/2/2
3	PSU	h	1535	3	-	0/7/25/26	0/2/2/2
3	OMG	h	246	37,3	-	0/9/27/28	0/3/3/3
3	A2M	h	544	3	-	2/9/27/28	0/3/3/3
3	PSU	h	607	3	-	0/7/25/26	0/2/2/2
3	PSU	h	809	3	-	0/7/25/26	0/2/2/2
3	6MZ	h	1771	37,3,36	-	0/9/27/28	0/3/3/3
3	PSU	h	95	3	-	0/7/25/26	0/2/2/2
3	PSU	h	1567	3	-	0/7/25/26	0/2/2/2
3	PSU	h	753	3	-	0/7/25/26	0/2/2/2
3	MA6	h	1790	3	-	3/11/29/30	0/3/3/3
3	PSU	h	1002	3	-	0/7/25/26	0/2/2/2
3	PSU	h	306	3	-	0/7/25/26	0/2/2/2
3	A2M	h	977	3	-	0/9/27/28	0/3/3/3
3	PSU	h	1485	3	-	0/7/25/26	0/2/2/2
3	OMU	h	886	3	-	3/9/27/28	0/2/2/2
3	PSU	h	1106	3	-	0/7/25/26	0/2/2/2
3	PSU	h	470	3	-	0/7/25/26	0/2/2/2
3	OMC	h	473	3	-	0/9/27/28	0/2/2/2
3	B8N	h	1194	3	-	2/16/34/35	0/2/2/2
3	PSU	h	1304	3	-	1/7/25/26	0/2/2/2
3	OMG	h	598	3	-	3/9/27/28	0/3/3/3
3	OMU	h	123	3	-	2/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	OMC	h	418	3	-	2/9/27/28	0/2/2/2
3	OMG	h	392	3	-	2/9/27/28	0/3/3/3
3	PSU	h	339	37,3	-	0/7/25/26	0/2/2/2
3	PSU	h	1178	3	-	0/7/25/26	0/2/2/2
3	OMU	h	1447	3	-	0/9/27/28	0/2/2/2
3	OMC	h	1645	3	-	0/9/27/28	0/2/2/2
3	PSU	h	1615	3	-	0/7/25/26	0/2/2/2
3	OMG	h	1274	37,3	-	2/9/27/28	0/3/3/3
3	PSU	h	362	3	-	0/7/25/26	0/2/2/2
3	4AC	h	1781	3	-	0/11/29/30	0/2/2/2
3	OMU	h	1234	3	-	2/9/27/28	0/2/2/2
3	A2M	h	162	3	-	0/9/27/28	0/3/3/3
3	A2M	h	28	3,36	-	0/9/27/28	0/3/3/3
3	A2M	h	440	3	-	0/9/27/28	0/3/3/3
3	OMC	h	38	3	-	0/9/27/28	0/2/2/2
3	A2M	h	1758	3	-	0/9/27/28	0/3/3/3
3	UY1	h	603	3	-	0/9/27/28	0/2/2/2
3	PSU	h	762	3	-	0/7/25/26	0/2/2/2
3	PSU	h	121	3,36	-	0/7/25/26	0/2/2/2
3	PSU	h	605	3	-	0/7/25/26	0/2/2/2
3	PSU	h	417	3	-	0/7/25/26	0/2/2/2
3	PSU	h	961	37,3	-	2/7/25/26	0/2/2/2
3	MA6	h	1789	3	-	0/11/29/30	0/3/3/3
3	OMU	h	581	37,3	-	2/9/27/28	0/2/2/2
3	PSU	h	1293	3	-	0/7/25/26	0/2/2/2
3	A2M	h	622	3,36	-	5/9/27/28	0/3/3/3
3	PSU	h	1524	3	-	2/7/25/26	0/2/2/2
3	A2M	h	468	3	-	0/9/27/28	0/3/3/3
3	4AC	h	1283	3	-	0/11/29/30	0/2/2/2
3	PSU	h	584	3	-	5/7/25/26	0/2/2/2
3	PSU	h	1217	3	-	0/7/25/26	0/2/2/2
3	PSU	h	1190	3	-	0/7/25/26	0/2/2/2
3	OMU	h	373	3	-	0/9/27/28	0/2/2/2
3	PSU	h	606	3	-	0/7/25/26	0/2/2/2
3	PSU	h	763	3	-	0/7/25/26	0/2/2/2
3	PSU	h	950	3	-	0/7/25/26	0/2/2/2
3	PSU	h	1210	3	-	0/7/25/26	0/2/2/2
3	PSU	h	1787	3	-	2/7/25/26	0/2/2/2
3	A2M	h	800	3	-	0/9/27/28	0/3/3/3
3	PSU	h	1184	3	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PSU	h	258	3	-	2/7/25/26	0/2/2/2
3	PSU	h	1120	3	-	0/7/25/26	0/2/2/2
3	PSU	h	451	37,3	-	0/7/25/26	0/2/2/2
3	OMU	h	614	3	-	1/9/27/28	0/2/2/2
3	OMU	h	1272	3	-	1/9/27/28	0/2/2/2
3	OMU	h	1383	3,36	-	0/9/27/28	0/2/2/2
3	PSU	h	103	37,3	-	0/7/25/26	0/2/2/2
3	OMG	h	1433	3,36	-	1/9/27/28	0/3/3/3
3	A2M	h	1329	3	-	0/9/27/28	0/3/3/3
3	PSU	h	1308	3	-	2/7/25/26	0/2/2/2
3	PSU	h	1027	3	-	0/7/25/26	0/2/2/2
3	PSU	h	635	3	-	0/7/25/26	0/2/2/2
3	A2M	h	424	3	-	0/9/27/28	0/3/3/3
3	OMC	h	1218	3	-	0/9/27/28	0/2/2/2
3	OMU	h	1012	3	-	0/9/27/28	0/2/2/2
3	A2M	h	1579	3	-	2/9/27/28	0/3/3/3
3	OMC	h	140	3	-	2/9/27/28	0/2/2/2
3	PSU	h	310	3	-	0/7/25/26	0/2/2/2

The worst 5 of 658 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	h	1524	PSU	C6-C5	12.31	1.49	1.35
3	h	1485	PSU	C6-C5	12.20	1.49	1.35
3	h	1787	PSU	C6-C5	12.20	1.49	1.35
3	h	1535	PSU	C6-C5	12.19	1.49	1.35
3	h	470	PSU	C6-C5	12.16	1.49	1.35

The worst 5 of 519 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	h	584	PSU	C6-N1-C2	-12.08	110.33	122.68
3	h	584	PSU	C6-C5-C4	-10.84	110.62	118.20
3	h	584	PSU	C5-C6-N1	9.88	136.90	122.11
3	h	1790	MA6	N1-C6-N6	-9.19	107.03	117.08
3	h	1789	MA6	N1-C6-N6	-7.95	108.39	117.08

There are no chirality outliers.

5 of 53 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	h	123	OMU	O4'-C4'-C5'-O5'
3	h	140	OMC	C3'-C4'-C5'-O5'
3	h	140	OMC	O4'-C4'-C5'-O5'
3	h	392	OMG	O4'-C4'-C5'-O5'
3	h	418	OMC	C1'-C2'-O2'-CM2

There are no ring outliers.

15 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	h	95	PSU	1	0
3	h	1790	MA6	3	0
3	h	598	OMG	1	0
3	h	392	OMG	2	0
3	h	1447	OMU	1	0
3	h	1645	OMC	1	0
3	h	1781	4AC	1	0
3	h	1234	OMU	1	0
3	h	603	UY1	1	0
3	h	762	PSU	2	0
3	h	605	PSU	1	0
3	h	1789	MA6	2	0
3	h	763	PSU	1	0
3	h	1383	OMU	1	0
3	h	140	OMC	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 130 ligands modelled in this entry, 126 are monoatomic - leaving 4 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
39	SPM	h	2017	-	13,13,13	0.34	0	12,12,12	0.85	0
39	SPM	h	2016	-	13,13,13	0.34	0	12,12,12	0.78	0
39	SPM	h	2018	-	13,13,13	0.35	0	12,12,12	0.90	0
38	SPD	h	2015	-	9,9,9	0.30	0	8,8,8	0.63	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
39	SPM	h	2017	-	-	4/11/11/11	-
39	SPM	h	2016	-	-	5/11/11/11	-
39	SPM	h	2018	-	-	2/11/11/11	-
38	SPD	h	2015	-	-	3/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
39	h	2016	SPM	C7-C8-C9-N10
38	h	2015	SPD	N6-C7-C8-C9
38	h	2015	SPD	C8-C7-N6-C5
39	h	2016	SPM	C8-C9-N10-C11
39	h	2018	SPM	N5-C6-C7-C8

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
39	h	2016	SPM	1	0
39	h	2018	SPM	1	0
38	h	2015	SPD	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

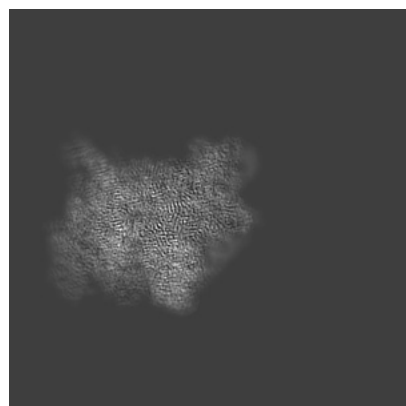
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15674. These allow visual inspection of the internal detail of the map and identification of artifacts.

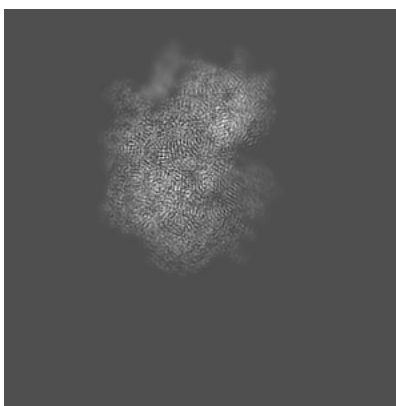
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

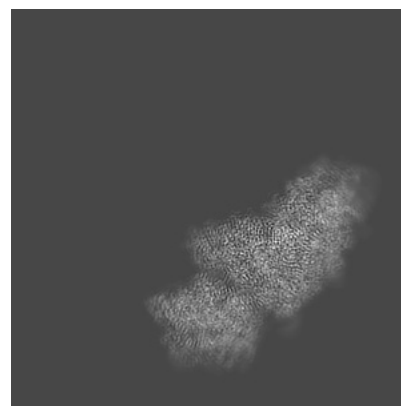
6.1.1 Primary map



X

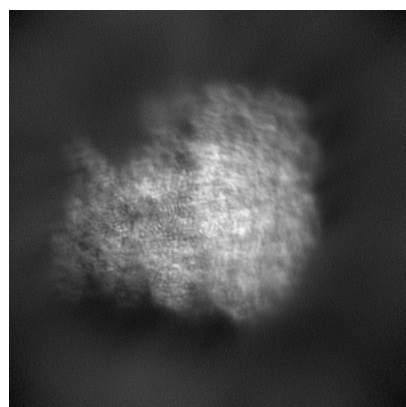


Y

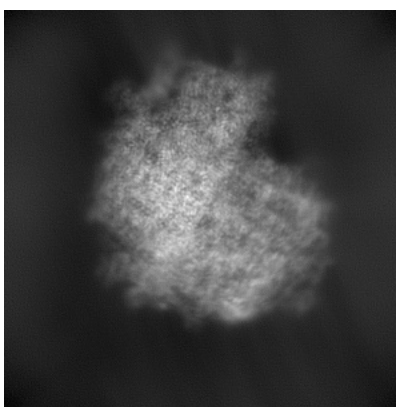


Z

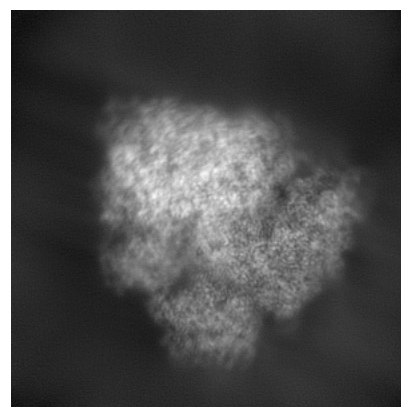
6.1.2 Raw map



X



Y

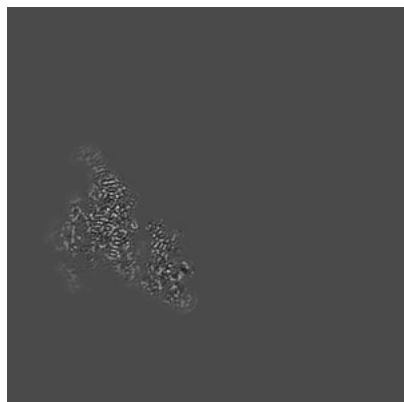


Z

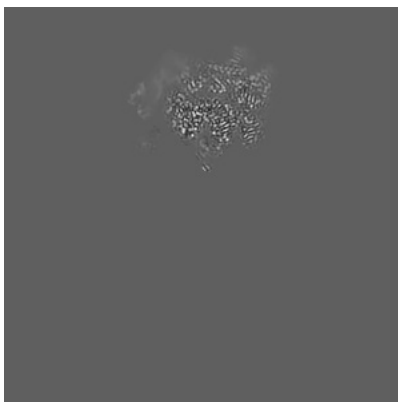
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

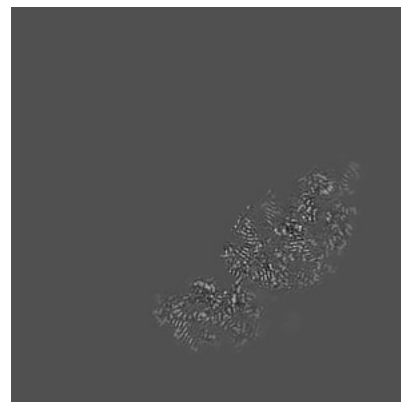
6.2.1 Primary map



X Index: 225

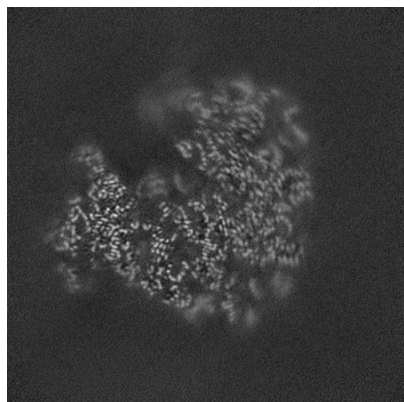


Y Index: 225

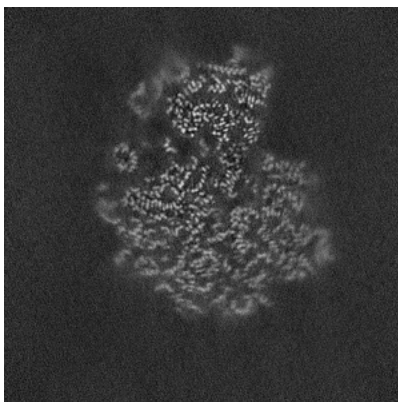


Z Index: 225

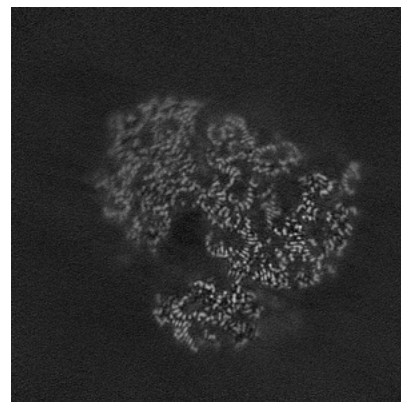
6.2.2 Raw map



X Index: 225



Y Index: 225

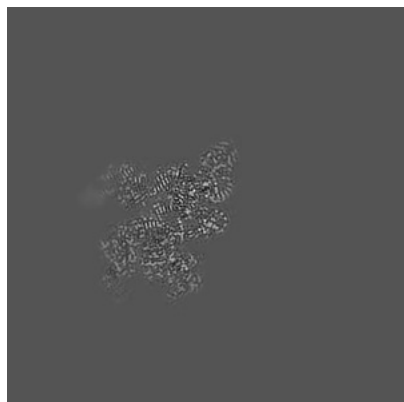


Z Index: 225

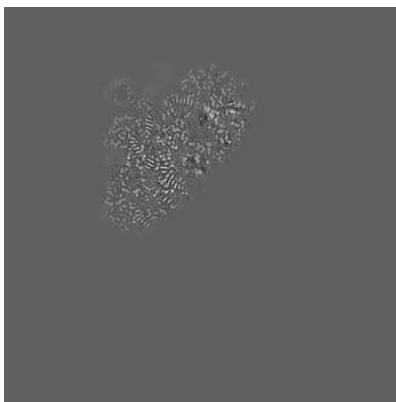
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

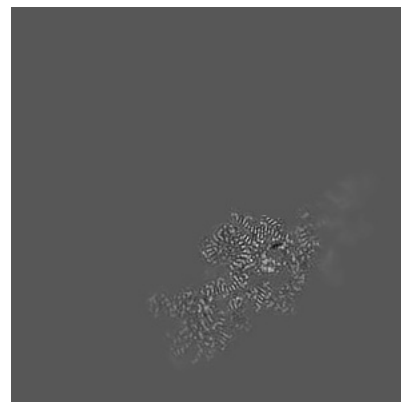
6.3.1 Primary map



X Index: 316

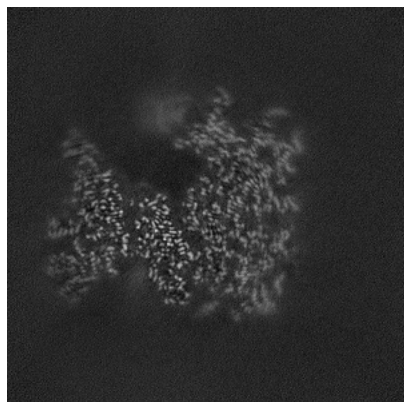


Y Index: 187

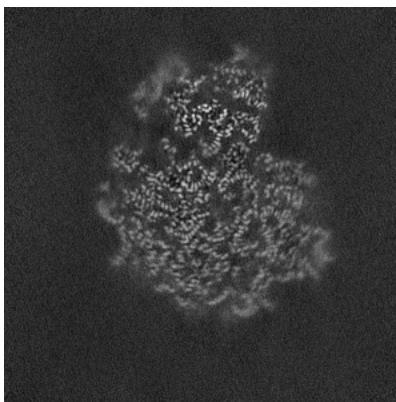


Z Index: 179

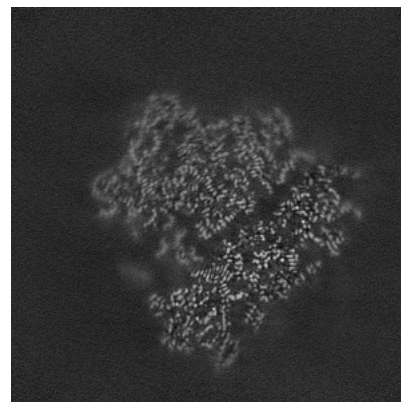
6.3.2 Raw map



X Index: 246



Y Index: 228

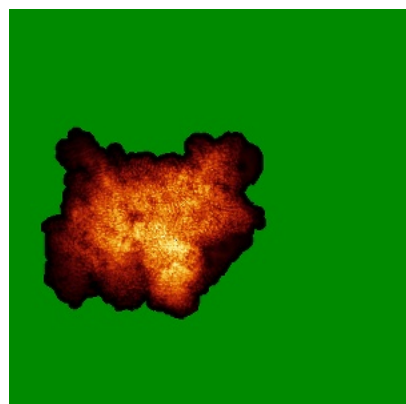


Z Index: 206

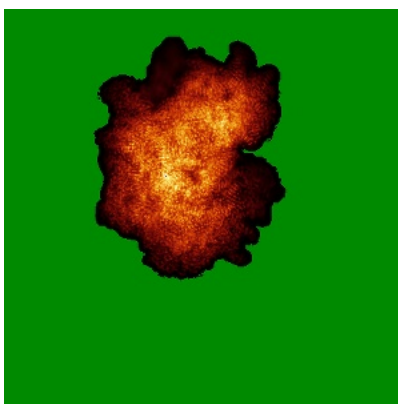
The images above show the largest variance slices of the map in three orthogonal directions.

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

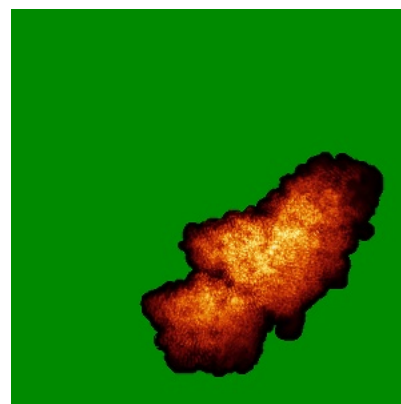
6.4.1 Primary map



X

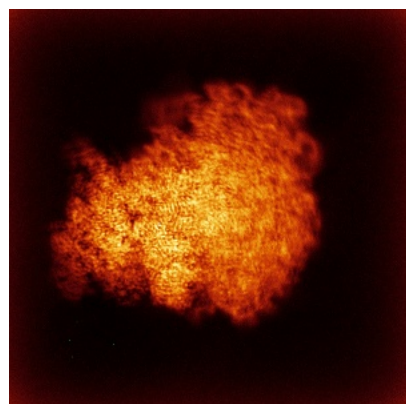


Y

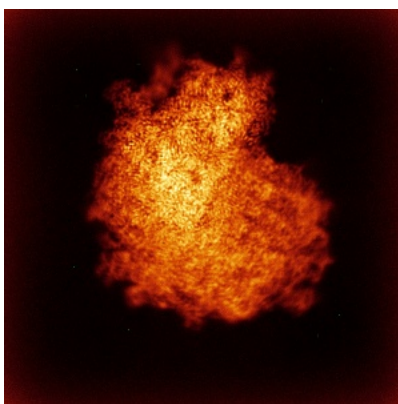


Z

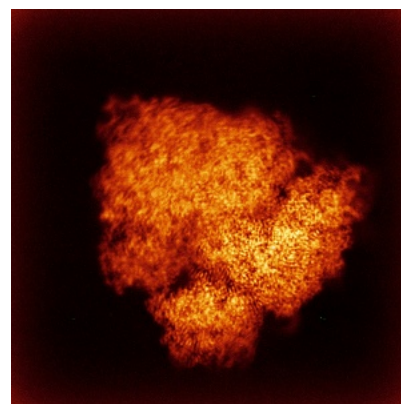
6.4.2 Raw map



X



Y

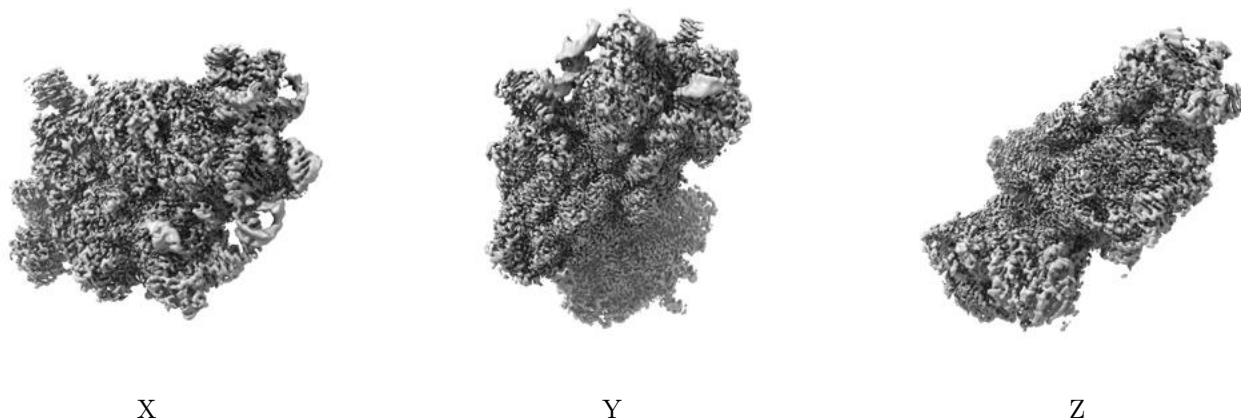


Z

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 0.426. 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.

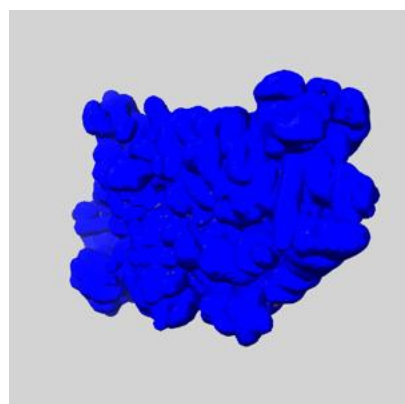
6.6 Mask visualisation [i](#)

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

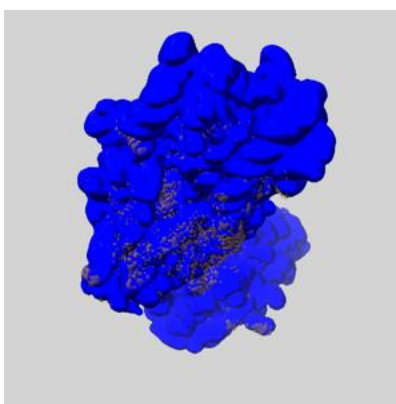
A mask typically either:

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

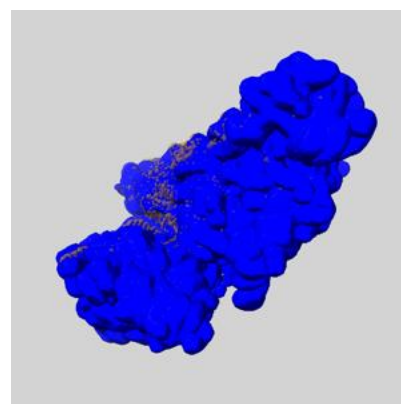
6.6.1 emd_15674_msk_1.map [i](#)



X



Y

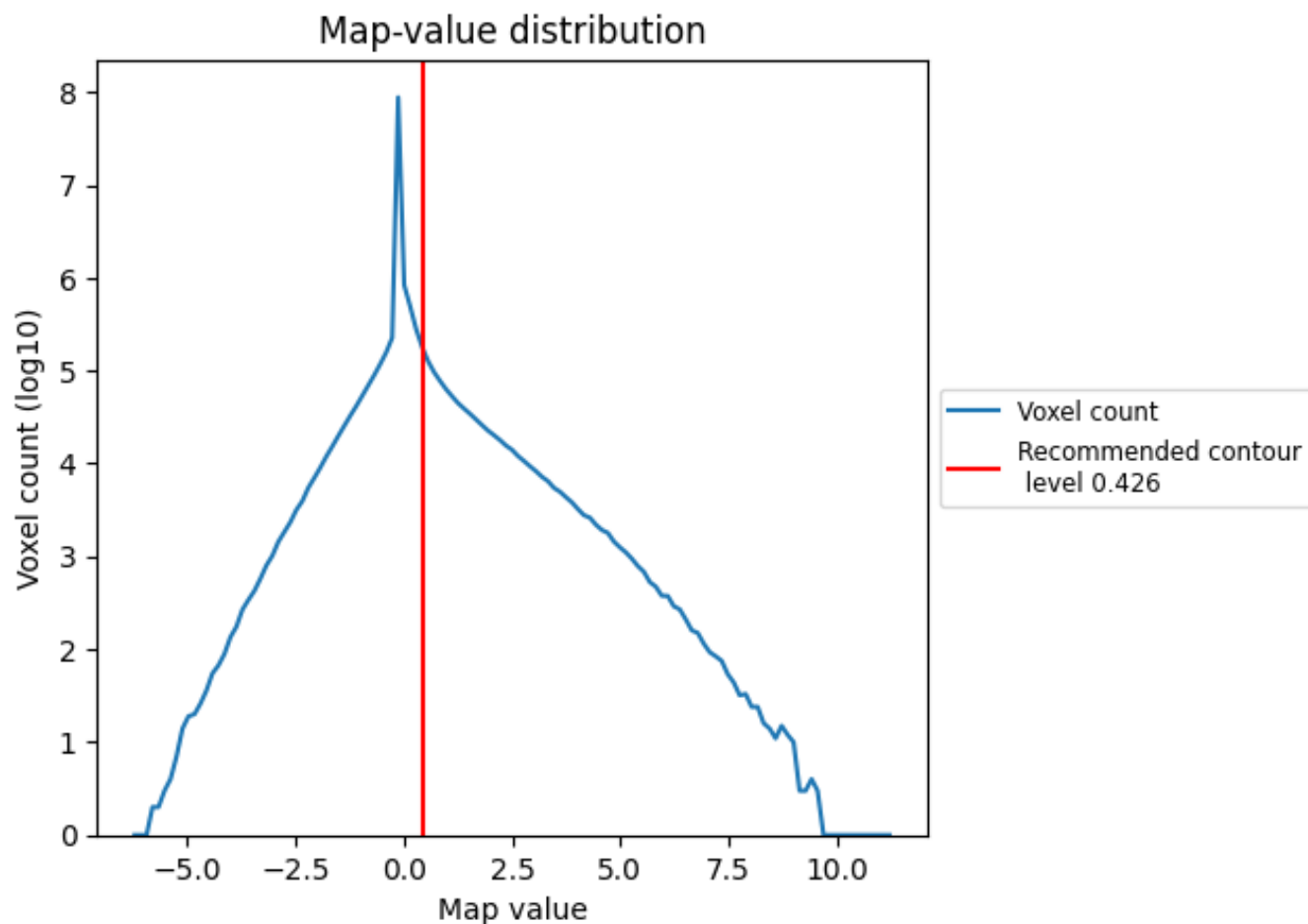


Z

7 Map analysis [i](#)

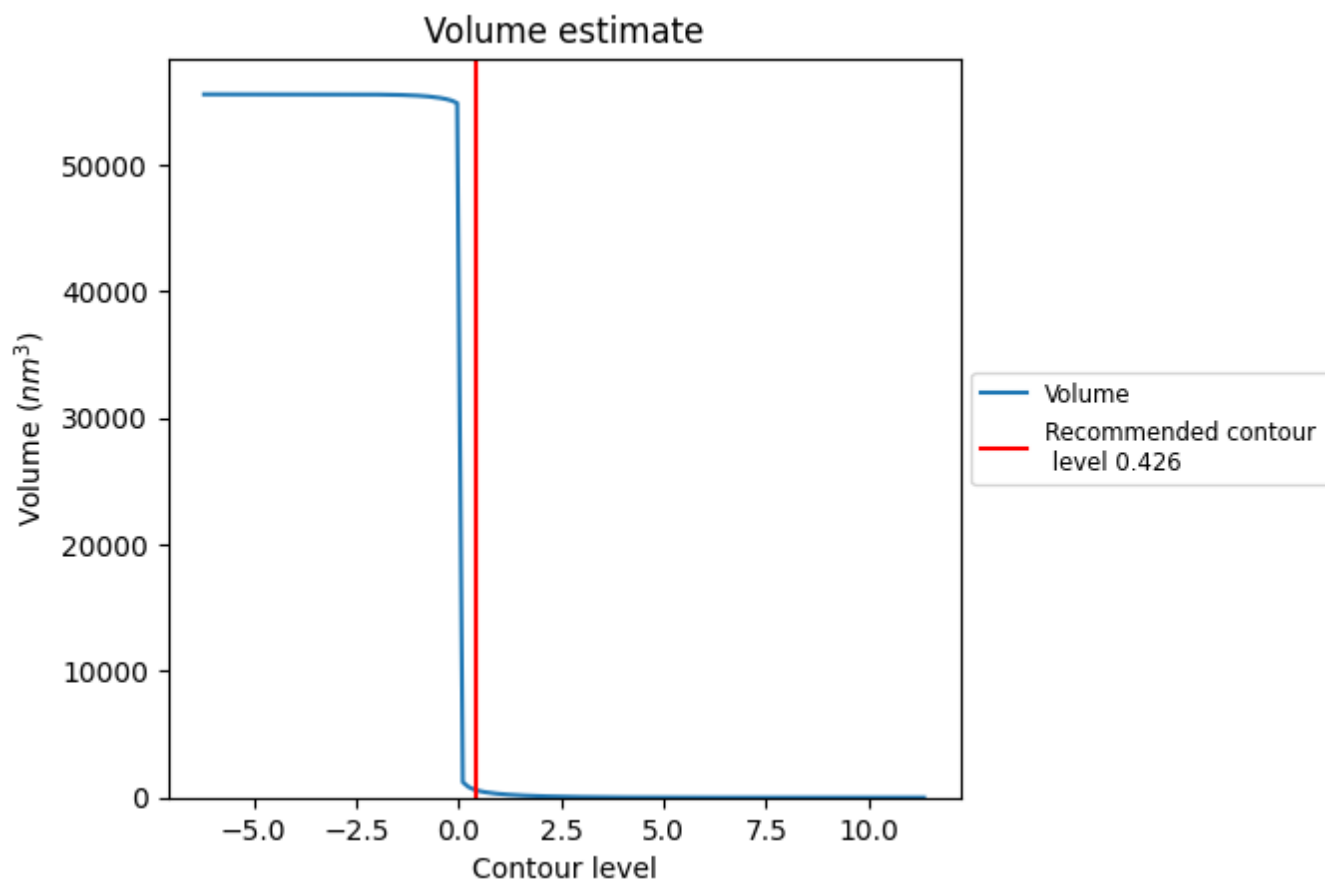
This section contains the results of statistical analysis of the map.

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.

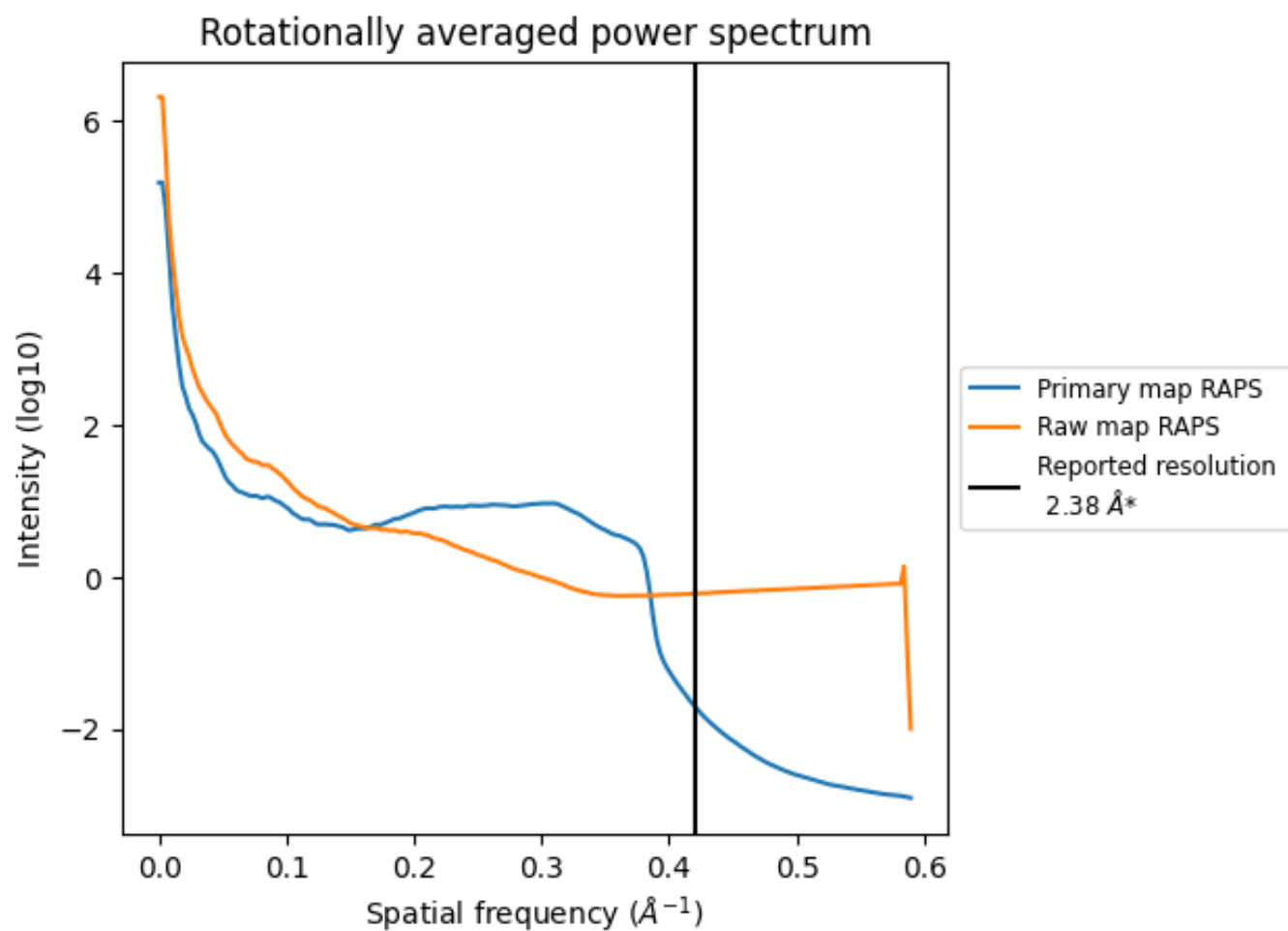
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 588 nm³; this corresponds to an approximate mass of 531 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 ⓘ

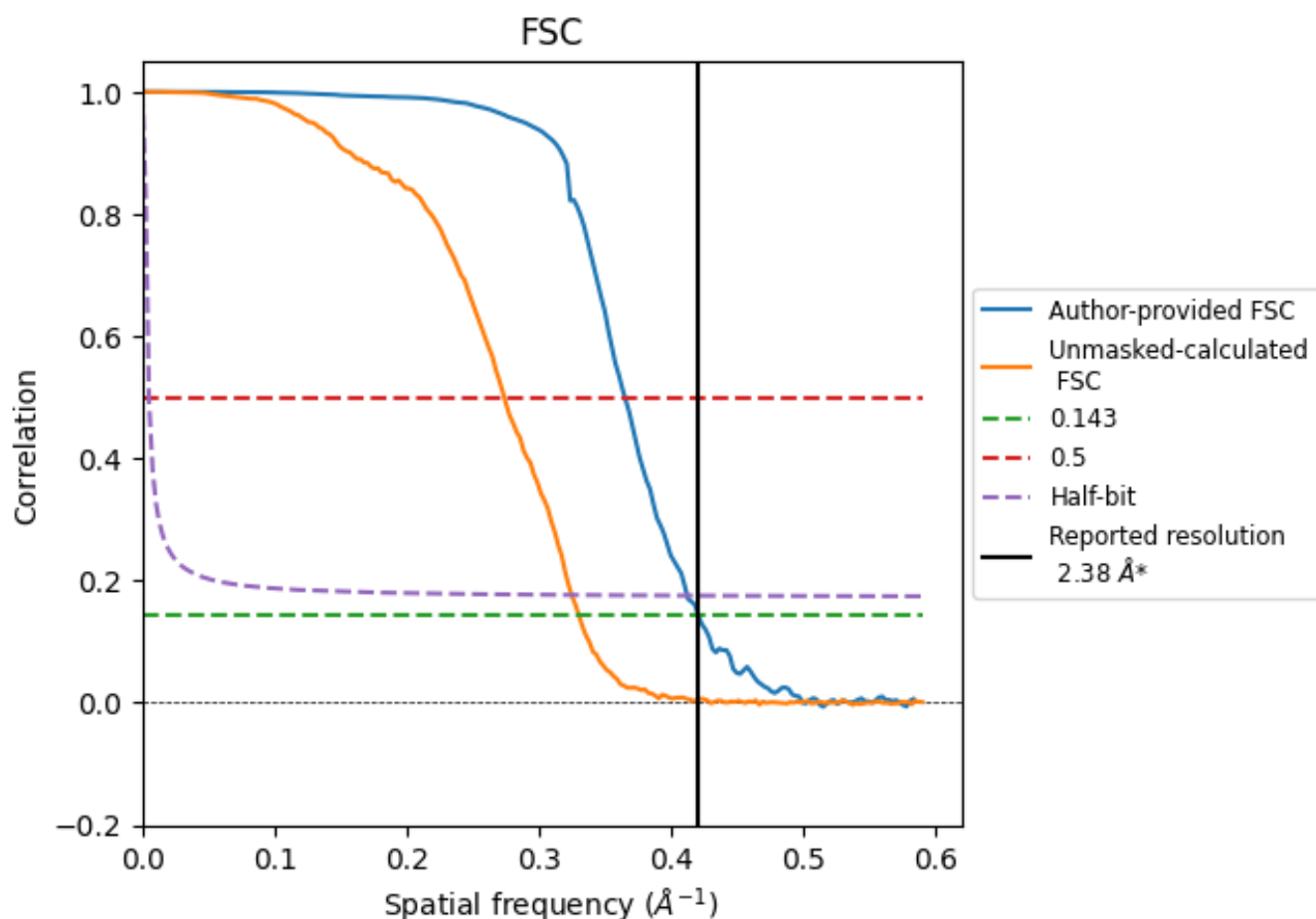


*Reported resolution corresponds to spatial frequency of $0.420 \text{ \AA}^{-1}$

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 0.420 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

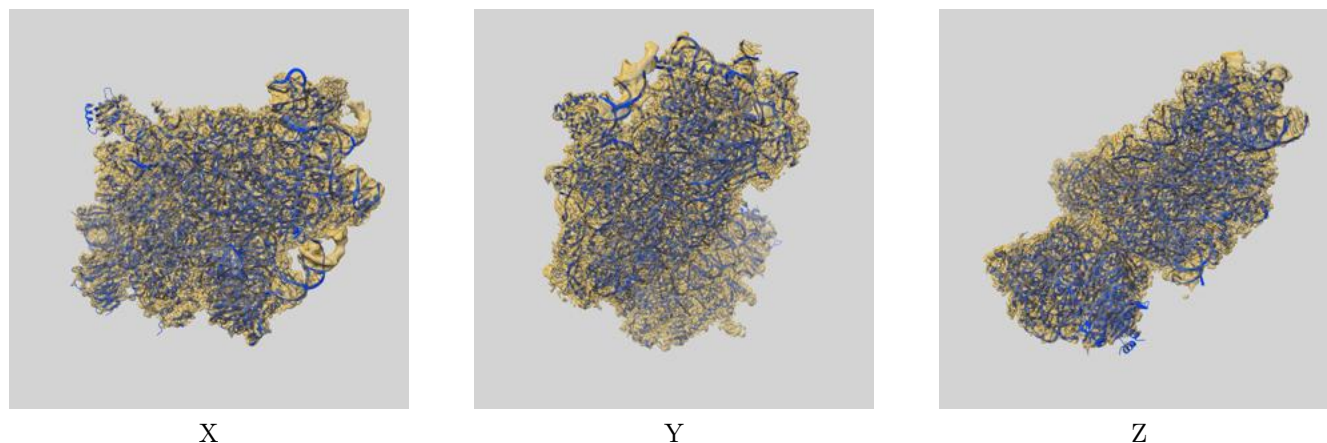
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.38	-	-
Author-provided FSC curve	2.38	2.74	2.43
Unmasked-calculated*	3.03	3.65	3.08

*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 3.03 differs from the reported value 2.38 by more than 10 %

9 Map-model fit [i](#)

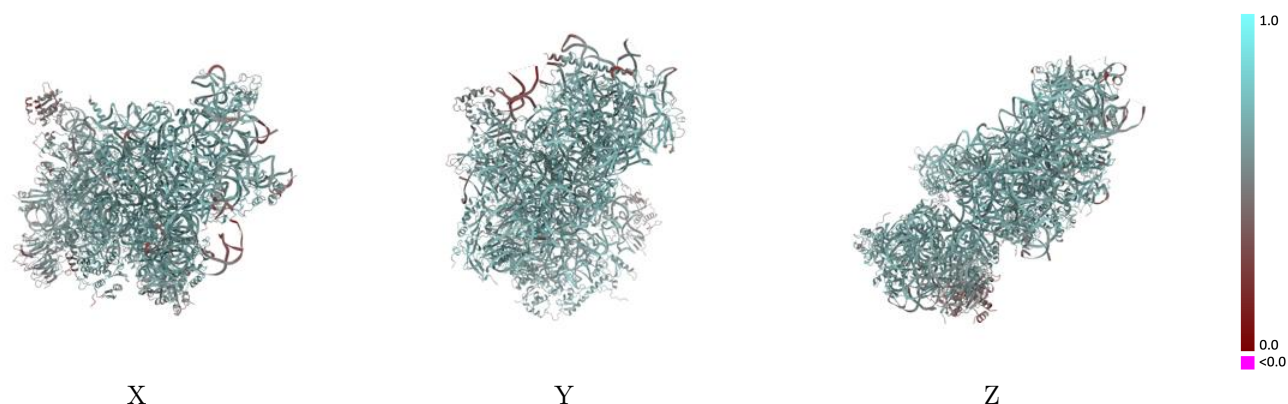
This section contains information regarding the fit between EMDB map EMD-15674 and PDB model 8AUV. Per-residue inclusion information can be found in section [3](#) on page [14](#).

9.1 Map-model overlay [i](#)



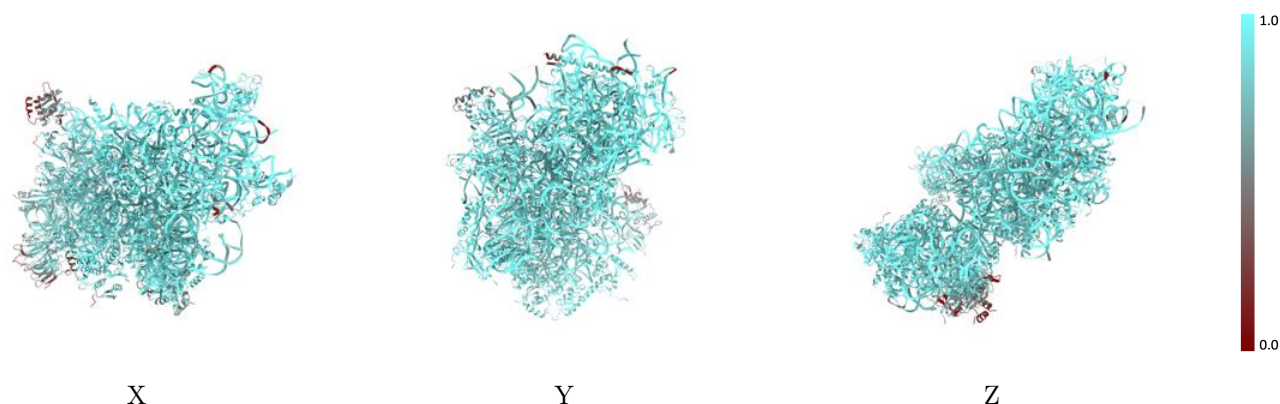
The images above show the 3D surface view of the map at the recommended contour level 0.426 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



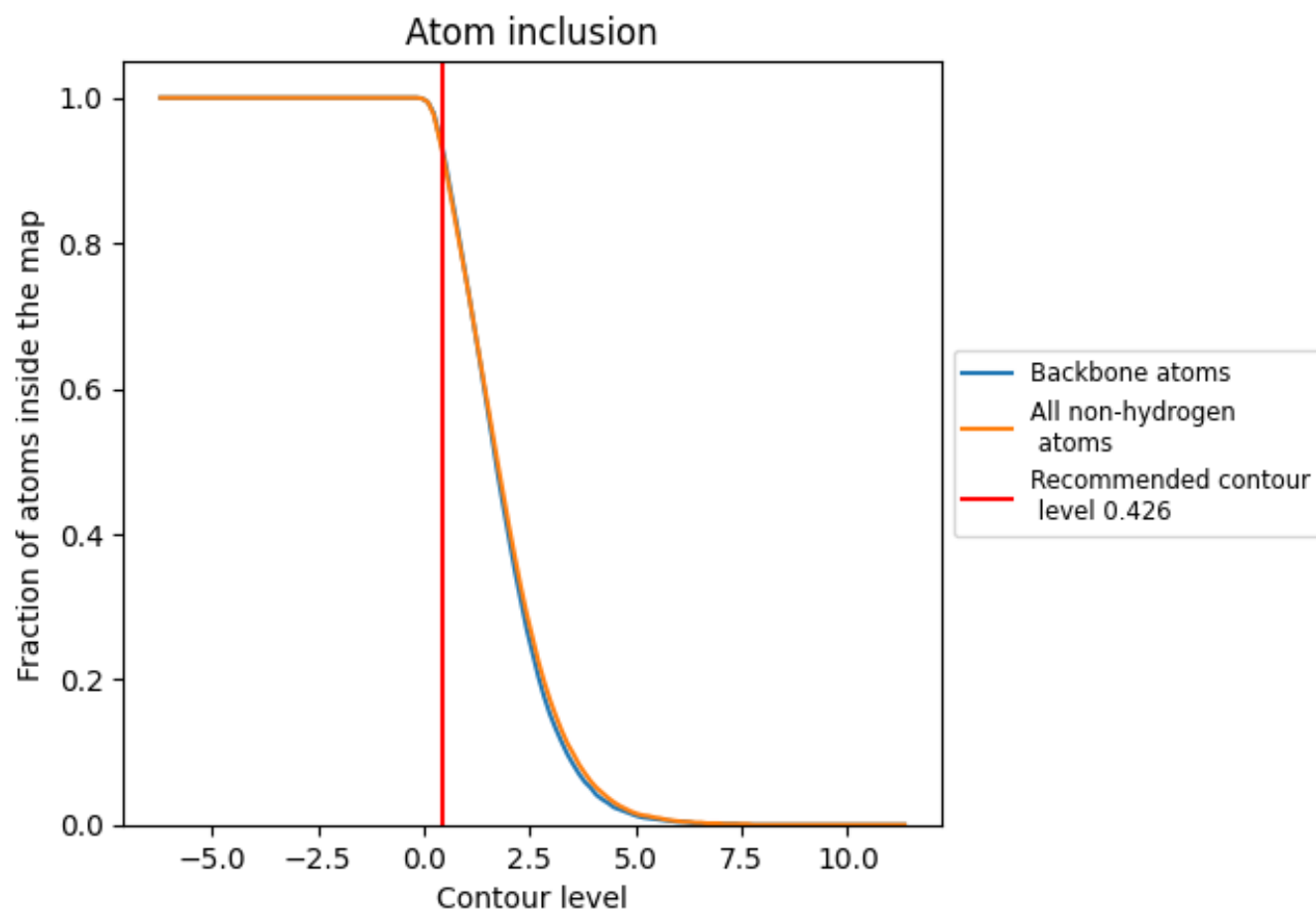
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.426).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 93% 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 (0.426) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9300	 0.6220
A	 0.9670	 0.6530
B	 0.8800	 0.5470
C	 0.3740	 0.3990
D	 0.8060	 0.5530
E	 0.9670	 0.6350
F	 0.9620	 0.6480
G	 0.9250	 0.6170
H	 0.9320	 0.6210
I	 0.8940	 0.5860
J	 0.9630	 0.6630
K	 0.9120	 0.6070
L	 0.8940	 0.5850
M	 0.9290	 0.6230
N	 0.5330	 0.4480
O	 0.8090	 0.5630
P	 0.9480	 0.6440
Q	 0.6600	 0.4980
R	 0.8200	 0.5820
S	 0.9580	 0.6480
T	 0.9800	 0.6820
U	 0.9430	 0.6210
V	 0.9860	 0.6620
W	 0.9660	 0.6520
X	 0.9820	 0.6710
Y	 0.9160	 0.6000
Z	 0.9480	 0.6370
a	 0.8840	 0.5890
b	 0.9520	 0.6360
c	 0.9690	 0.6640
d	 0.9330	 0.6190
e	 0.9890	 0.6840
f	 0.9470	 0.6290
h	 0.9720	 0.6340
k	 0.8970	 0.6000
l	 0.8790	 0.5760

