wwPDB EM Validation Summary Report

Oct 27, 2024 – 07:52 AM EDT

PDB ID	:	7U0G
EMDB ID	:	EMD-26258
Title	:	structure of LIN28b nucleosome bound 3 OCT4
Authors	:	Lian, T.; Guan, R.; Bai, Y.
Deposited on	:	2022-02-18
Resolution	:	2.60 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

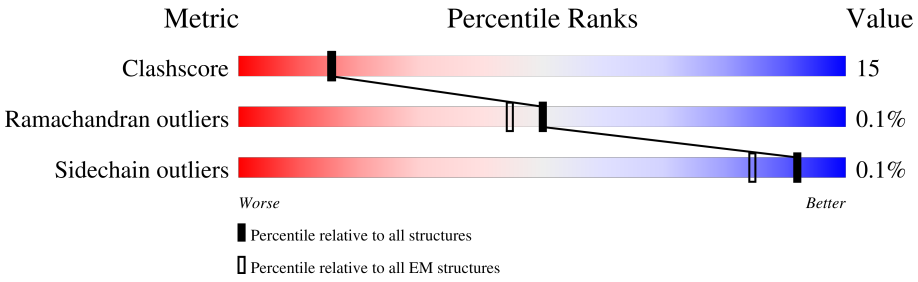
EMDB validation analysis	:	0.0.1.dev113
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	: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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.60 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

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 <=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	136	51% 19% 29%
1	E	136	54% 17% • 29%
2	B	103	65% 17% 18%
2	F	103	• 57% 20% • 20%
3	C	129	64% 19% 17%
3	G	129	65% 19% • 16%
4	D	126	9% 70% 13% 17%
4	H	126	58% 17% 25%

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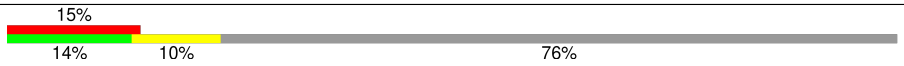
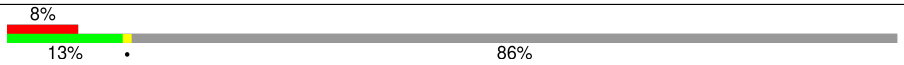
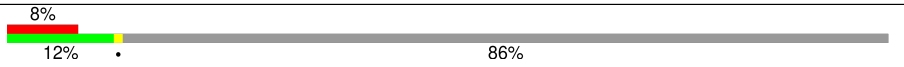
Mol	Chain	Length	Quality of chain
5	I	162	
6	J	162	
7	K	550	
7	L	550	
7	M	550	
8	N	265	
8	O	265	

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 18571 atoms, of which 1244 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 Histone H3.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	96	Total	C	N	O	S	0	0
			790	499	151	136	4		
1	E	97	Total	C	N	O	S	0	0
			801	505	155	137	4		

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	84	Total	C	N	O	S	0	0
			674	425	134	114	1		
2	F	82	Total	C	N	O	S	0	0
			653	412	127	113	1		

- Molecule 3 is a protein called Histone H2A type 2-C.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	107	Total	C	N	O	S	0	0
			816	515	158	142	1		
3	G	109	Total	C	N	O	S	0	0
			840	530	165	144	1		

- Molecule 4 is a protein called Histone H2B type 2-E.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	104	Total	C	N	O	S	0	0
			791	494	143	152	2		
4	H	95	Total	C	N	O	S	0	0
			747	468	136	141	2		

- Molecule 5 is a DNA chain called DNA (162-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	133	Total	C	N	O	P	0	0
			2758	1310	535	780	133		

- Molecule 6 is a DNA chain called DNA (162-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	133	Total	C	N	O	P	0	0
			2695	1295	451	816	133		

- Molecule 7 is a protein called Maltodextrin-binding protein,POU domain, class 5, transcription factor 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	K	134	Total	C	N	O	S		0	0
			1012	643	184	180	5			
7	L	75	Total	C	H	N	O	S	0	0
			1228	392	622	104	107	3		
7	M	75	Total	C	H	N	O	S	0	0
			1228	392	622	104	107	3		

There are 99 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	-251	MET	-	initiating methionine	UNP A0A376KDN7
K	-250	LYS	-	expression tag	UNP A0A376KDN7
K	-249	GLU	-	expression tag	UNP A0A376KDN7
K	1	UNK	THR	conflict	UNP A0A376KDN7
K	114	ALA	LYS	conflict	UNP A0A376KDN7
K	115	ALA	ASP	conflict	UNP A0A376KDN7
K	119	ASN	-	linker	UNP A0A376KDN7
K	120	ALA	-	linker	UNP A0A376KDN7
K	121	GLY	-	linker	UNP A0A376KDN7
K	122	SER	-	linker	UNP A0A376KDN7
K	123	GLU	-	linker	UNP A0A376KDN7
K	124	ASN	-	linker	UNP A0A376KDN7
K	125	LEU	-	linker	UNP A0A376KDN7
K	126	TYR	-	linker	UNP A0A376KDN7
K	127	PHE	-	linker	UNP A0A376KDN7
K	128	GLN	-	linker	UNP A0A376KDN7
K	129	GLY	-	linker	UNP A0A376KDN7
K	130	SER	-	linker	UNP A0A376KDN7
K	131	VAL	-	linker	UNP A0A376KDN7
K	132	ASP	-	linker	UNP A0A376KDN7

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Chain	Residue	Modelled	Actual	Comment	Reference
K	133	SER	-	linker	UNP A0A376KDN7
K	134	ALA	-	linker	UNP A0A376KDN7
K	135	ALA	-	linker	UNP A0A376KDN7
K	136	ALA	-	linker	UNP A0A376KDN7
K	137	SER	-	linker	UNP A0A376KDN7
K	291	GLU	-	expression tag	UNP Q01860
K	292	PHE	-	expression tag	UNP Q01860
K	293	HIS	-	expression tag	UNP Q01860
K	294	HIS	-	expression tag	UNP Q01860
K	295	HIS	-	expression tag	UNP Q01860
K	296	HIS	-	expression tag	UNP Q01860
K	297	HIS	-	expression tag	UNP Q01860
K	298	HIS	-	expression tag	UNP Q01860
L	-251	MET	-	initiating methionine	UNP A0A376KDN7
L	-250	LYS	-	expression tag	UNP A0A376KDN7
L	-249	GLU	-	expression tag	UNP A0A376KDN7
L	1	UNK	THR	conflict	UNP A0A376KDN7
L	114	ALA	LYS	conflict	UNP A0A376KDN7
L	115	ALA	ASP	conflict	UNP A0A376KDN7
L	119	ASN	-	linker	UNP A0A376KDN7
L	120	ALA	-	linker	UNP A0A376KDN7
L	121	GLY	-	linker	UNP A0A376KDN7
L	122	SER	-	linker	UNP A0A376KDN7
L	123	GLU	-	linker	UNP A0A376KDN7
L	124	ASN	-	linker	UNP A0A376KDN7
L	125	LEU	-	linker	UNP A0A376KDN7
L	126	TYR	-	linker	UNP A0A376KDN7
L	127	PHE	-	linker	UNP A0A376KDN7
L	128	GLN	-	linker	UNP A0A376KDN7
L	129	GLY	-	linker	UNP A0A376KDN7
L	130	SER	-	linker	UNP A0A376KDN7
L	131	VAL	-	linker	UNP A0A376KDN7
L	132	ASP	-	linker	UNP A0A376KDN7
L	133	SER	-	linker	UNP A0A376KDN7
L	134	ALA	-	linker	UNP A0A376KDN7
L	135	ALA	-	linker	UNP A0A376KDN7
L	136	ALA	-	linker	UNP A0A376KDN7
L	137	SER	-	linker	UNP A0A376KDN7
L	291	GLU	-	expression tag	UNP Q01860
L	292	PHE	-	expression tag	UNP Q01860
L	293	HIS	-	expression tag	UNP Q01860
L	294	HIS	-	expression tag	UNP Q01860

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Chain	Residue	Modelled	Actual	Comment	Reference
L	295	HIS	-	expression tag	UNP Q01860
L	296	HIS	-	expression tag	UNP Q01860
L	297	HIS	-	expression tag	UNP Q01860
L	298	HIS	-	expression tag	UNP Q01860
M	-251	MET	-	initiating methionine	UNP A0A376KDN7
M	-250	LYS	-	expression tag	UNP A0A376KDN7
M	-249	GLU	-	expression tag	UNP A0A376KDN7
M	1	UNK	THR	conflict	UNP A0A376KDN7
M	114	ALA	LYS	conflict	UNP A0A376KDN7
M	115	ALA	ASP	conflict	UNP A0A376KDN7
M	119	ASN	-	linker	UNP A0A376KDN7
M	120	ALA	-	linker	UNP A0A376KDN7
M	121	GLY	-	linker	UNP A0A376KDN7
M	122	SER	-	linker	UNP A0A376KDN7
M	123	GLU	-	linker	UNP A0A376KDN7
M	124	ASN	-	linker	UNP A0A376KDN7
M	125	LEU	-	linker	UNP A0A376KDN7
M	126	TYR	-	linker	UNP A0A376KDN7
M	127	PHE	-	linker	UNP A0A376KDN7
M	128	GLN	-	linker	UNP A0A376KDN7
M	129	GLY	-	linker	UNP A0A376KDN7
M	130	SER	-	linker	UNP A0A376KDN7
M	131	VAL	-	linker	UNP A0A376KDN7
M	132	ASP	-	linker	UNP A0A376KDN7
M	133	SER	-	linker	UNP A0A376KDN7
M	134	ALA	-	linker	UNP A0A376KDN7
M	135	ALA	-	linker	UNP A0A376KDN7
M	136	ALA	-	linker	UNP A0A376KDN7
M	137	SER	-	linker	UNP A0A376KDN7
M	291	GLU	-	expression tag	UNP Q01860
M	292	PHE	-	expression tag	UNP Q01860
M	293	HIS	-	expression tag	UNP Q01860
M	294	HIS	-	expression tag	UNP Q01860
M	295	HIS	-	expression tag	UNP Q01860
M	296	HIS	-	expression tag	UNP Q01860
M	297	HIS	-	expression tag	UNP Q01860
M	298	HIS	-	expression tag	UNP Q01860

- Molecule 8 is a protein called Single-chain variable fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	226	Total	C	N	O	S	0	0
			1769	1115	289	357	8		

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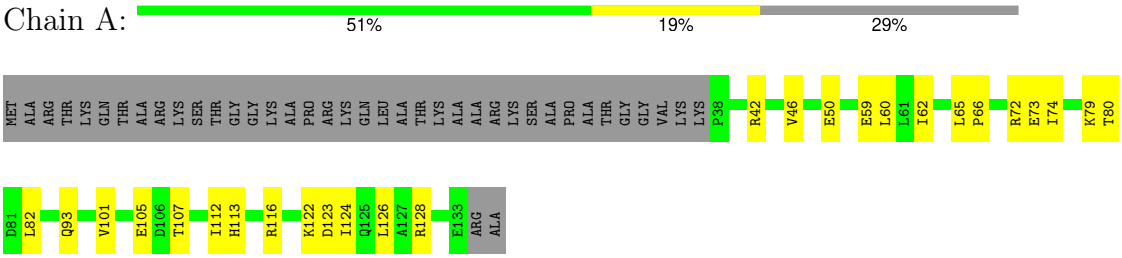
Mol	Chain	Residues	Atoms					AltConf	Trace
8	O	226	Total	C	N	O	S	0	0
			1769	1115	289	357	8		

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.

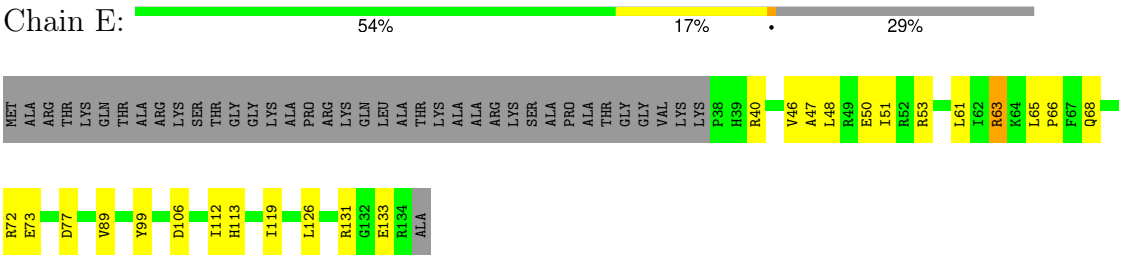
• Molecule 1: Histone H3.1

Chain A:



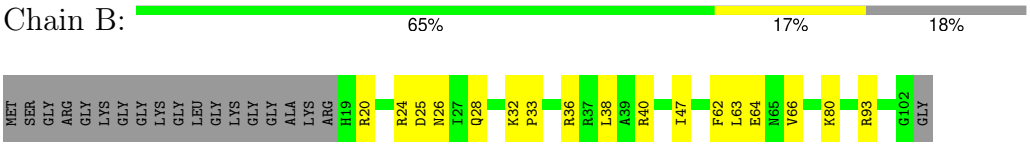
• Molecule 1: Histone H3.1

Chain E:



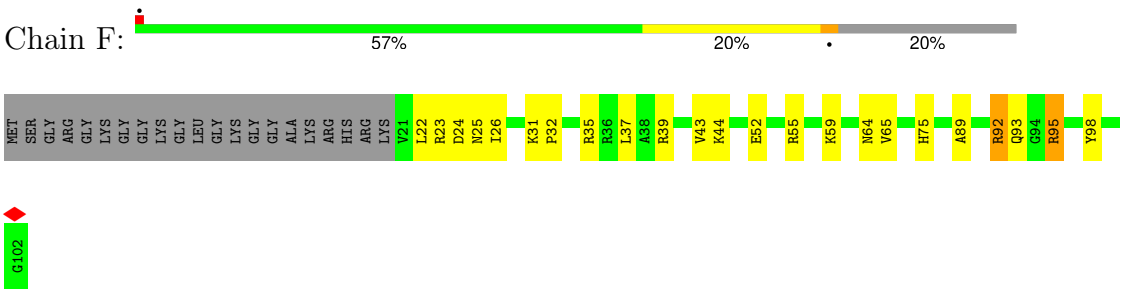
• Molecule 2: Histone H4

Chain B:



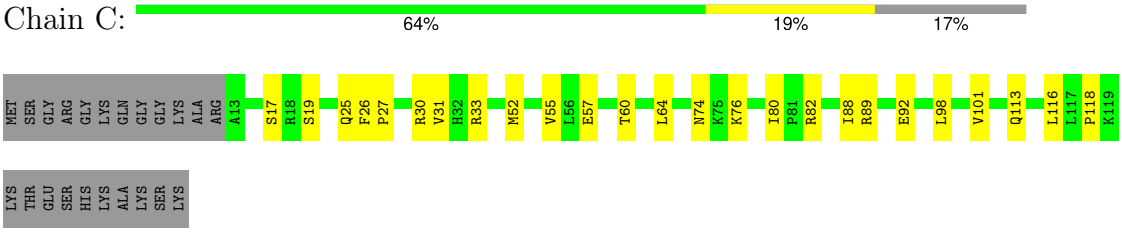
• Molecule 2: Histone H4

Chain F:



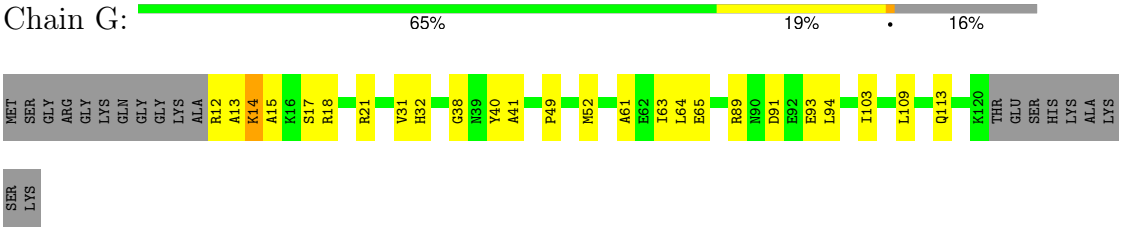
• Molecule 3: Histone H2A type 2-C

Chain C:



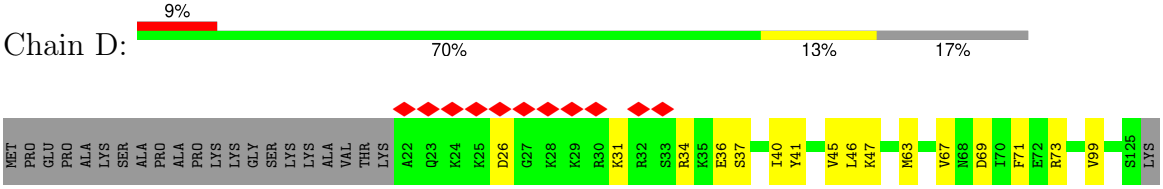
• Molecule 3: Histone H2A type 2-C

Chain G:



• Molecule 4: Histone H2B type 2-E

Chain D:

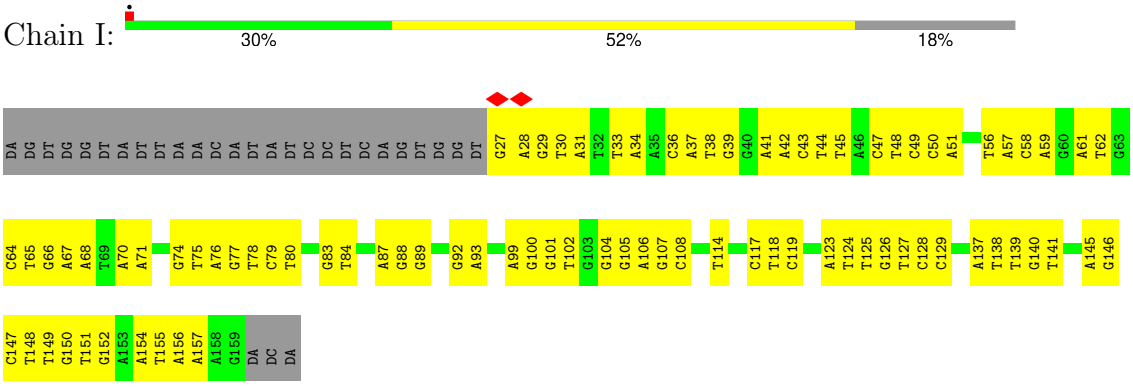


• Molecule 4: Histone H2B type 2-E

Chain H:

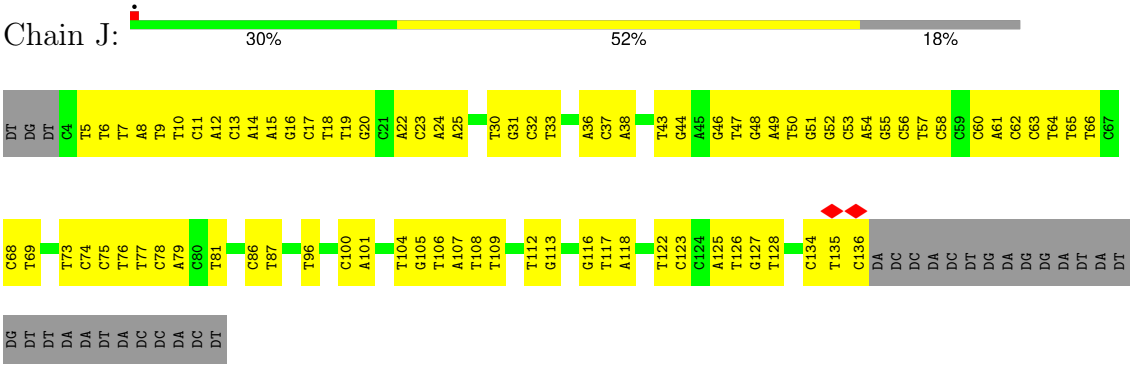
• Molecule 5: DNA (162-MER)

Chain I:



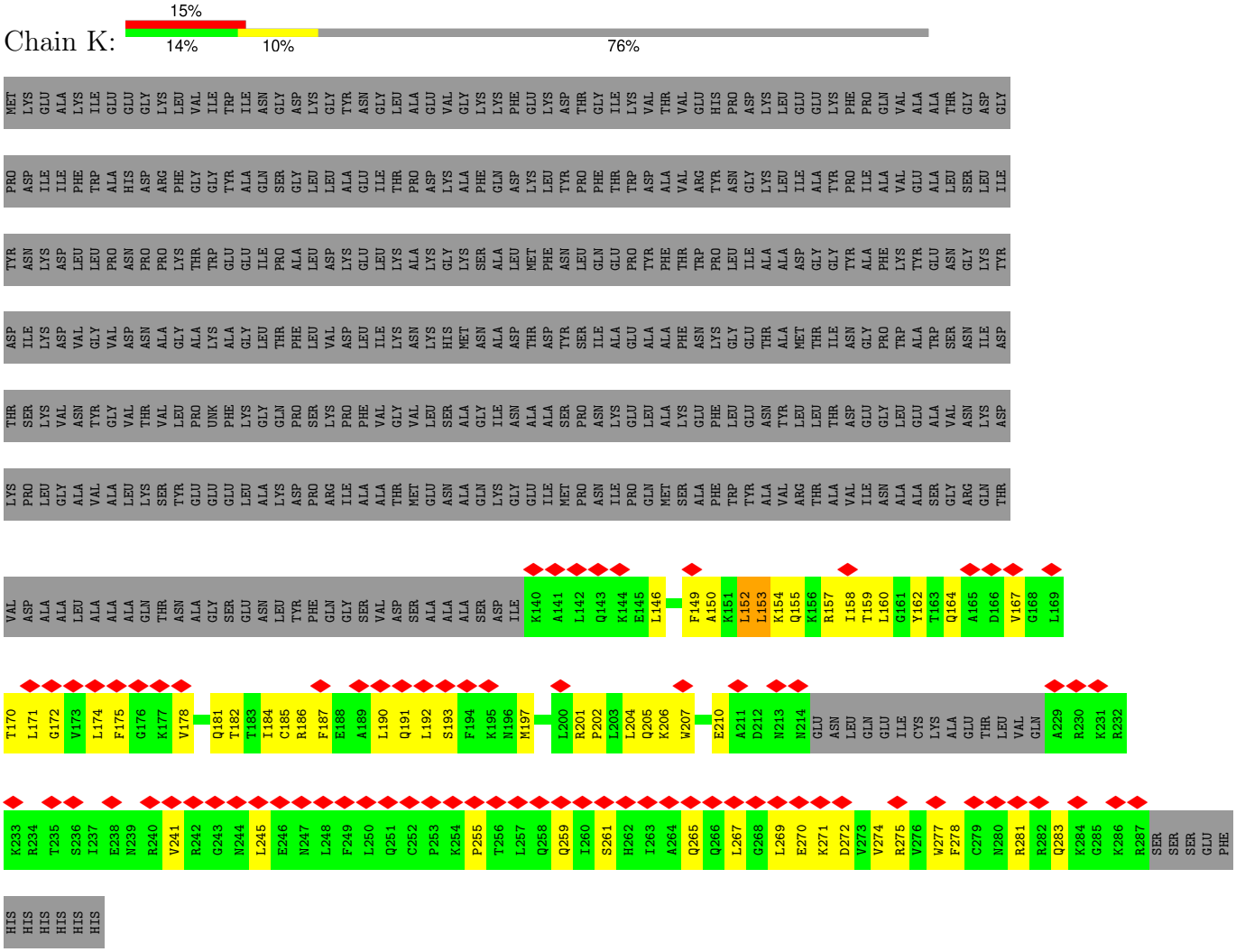
• Molecule 6: DNA (162-MER)

Chain J:



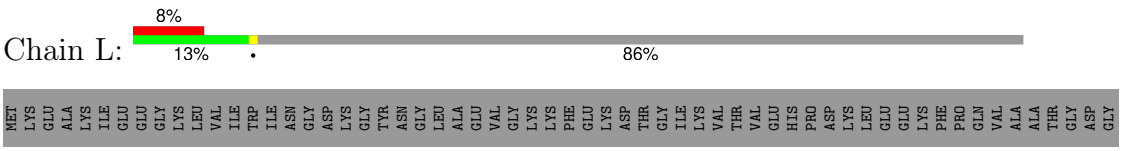
• Molecule 7: Maltodextrin-binding protein,POU domain, class 5, transcription factor 1

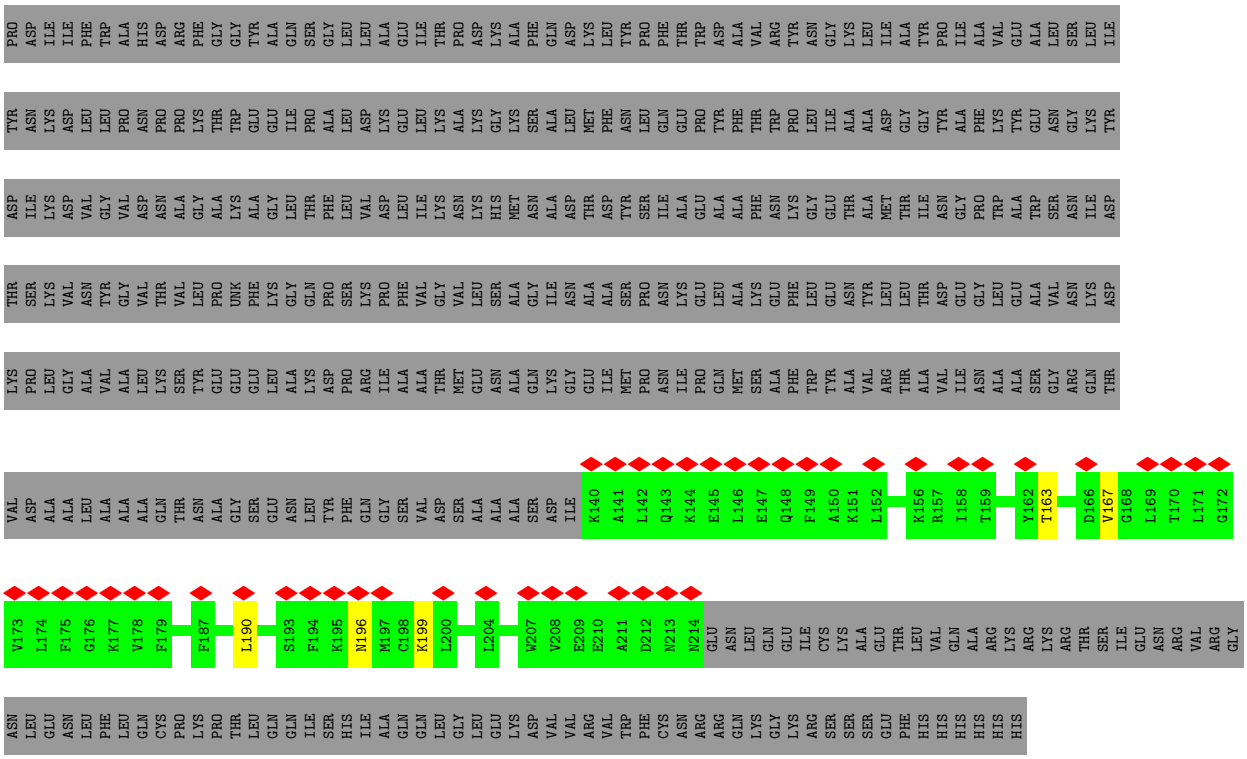
Chain K:



• Molecule 7: Maltodextrin-binding protein,POU domain, class 5, transcription factor 1

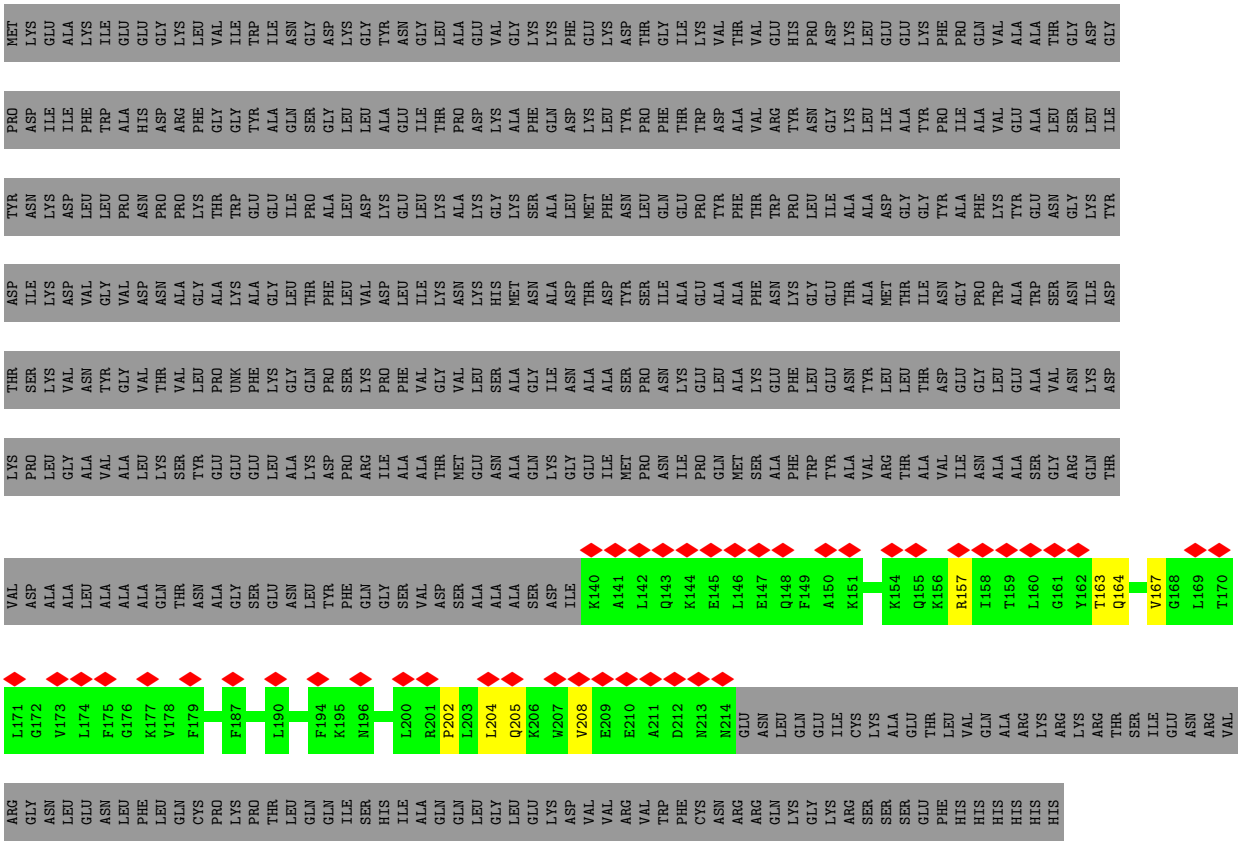
Chain L:





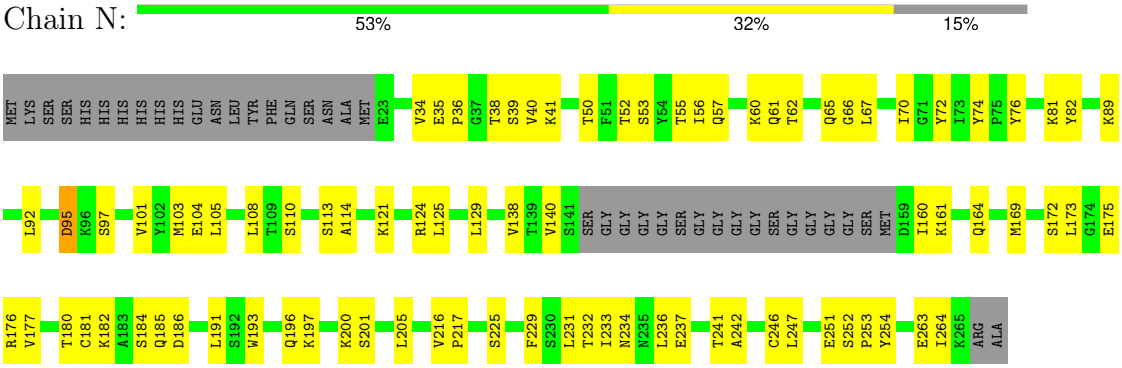
• Molecule 7: Maltodextrin-binding protein,POU domain, class 5, transcription factor 1

Chain M:



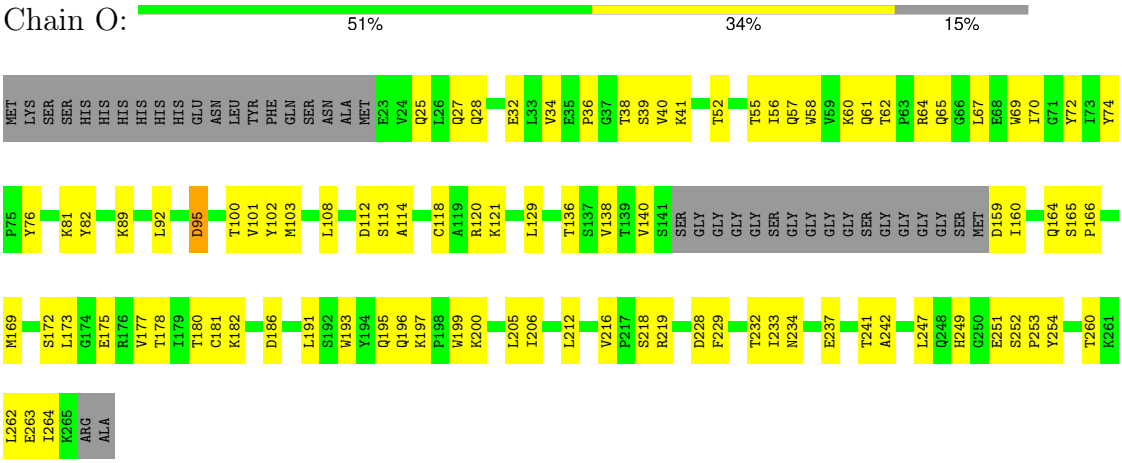
• Molecule 8: Single-chain variable fragment

Chain N:



• Molecule 8: Single-chain variable fragment

Chain O:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	112532	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 ($e^-/Å^2$)	53.8	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.478	Depositor
Minimum map value	-0.934	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.067	Depositor
Recommended contour level	0.17	Depositor
Map size (Å)	253.44, 253.44, 253.44	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.056, 1.056, 1.056	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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	0.32	0/802	0.53	0/1076
1	E	0.50	1/813 (0.1%)	0.54	0/1090
2	B	0.44	1/682 (0.1%)	0.58	0/914
2	F	0.44	0/660	0.67	2/883 (0.2%)
3	C	0.42	1/826 (0.1%)	0.63	2/1114 (0.2%)
3	G	0.44	2/850 (0.2%)	0.62	2/1143 (0.2%)
4	D	0.36	0/802	0.53	1/1079 (0.1%)
4	H	0.40	0/758	0.49	0/1016
5	I	0.54	0/3106	0.94	0/4797
6	J	0.52	0/3010	0.98	0/4638
7	K	0.26	0/1025	0.64	3/1385 (0.2%)
7	L	0.34	0/614	0.75	2/822 (0.2%)
7	M	0.35	0/614	0.67	0/822
8	N	0.33	0/1811	0.63	3/2454 (0.1%)
8	O	0.33	0/1811	0.63	2/2454 (0.1%)
All	All	0.43	5/18184 (0.0%)	0.76	17/25687 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	52	MET	C-O	-5.58	1.12	1.23
1	E	63	ARG	C-O	-5.50	1.12	1.23
3	G	52	MET	C-O	-5.07	1.13	1.23
2	B	93	ARG	C-O	-5.03	1.13	1.23
3	G	52	MET	CG-SD	-5.01	1.68	1.81

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	N	186	ASP	CB-CG-OD1	9.98	127.29	118.30
7	K	153	LEU	CA-CB-CG	9.76	137.75	115.30
8	O	186	ASP	CB-CG-OD1	9.69	127.02	118.30
2	F	24	ASP	CB-CG-OD1	7.87	125.38	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	N	95	ASP	CB-CG-OD1	7.85	125.37	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	790	0	826	19	0
1	E	801	0	839	28	0
2	B	674	0	715	16	0
2	F	653	0	696	16	0
3	C	816	0	869	21	0
3	G	840	0	906	30	0
4	D	791	0	790	14	0
4	H	747	0	771	18	0
5	I	2758	0	1494	83	0
6	J	2695	0	1512	90	0
7	K	1012	0	974	51	0
7	L	606	622	640	2	0
7	M	606	622	640	5	0
8	N	1769	0	1708	66	0
8	O	1769	0	1708	88	0
All	All	17327	1244	15088	473	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 15.

The worst 5 of 473 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:E:63:ARG:NH2	6:J:65:DT:H5”	1.49	1.27
3:G:89:ARG:HB3	3:G:109:LEU:HD11	1.29	1.12
1:E:63:ARG:HH22	6:J:65:DT:C5’	1.71	1.02
1:E:63:ARG:NH2	6:J:65:DT:C5’	2.23	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:63:ARG:HH22	6:J:65:DT:H5"	0.79	0.94

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	
1	A	94/136 (69%)	94 (100%)	0	0	100	100
1	E	95/136 (70%)	95 (100%)	0	0	100	100
2	B	82/103 (80%)	77 (94%)	5 (6%)	0	100	100
2	F	80/103 (78%)	77 (96%)	3 (4%)	0	100	100
3	C	105/129 (81%)	97 (92%)	8 (8%)	0	100	100
3	G	107/129 (83%)	105 (98%)	1 (1%)	1 (1%)	14	31
4	D	102/126 (81%)	95 (93%)	7 (7%)	0	100	100
4	H	93/126 (74%)	89 (96%)	4 (4%)	0	100	100
7	K	130/550 (24%)	127 (98%)	3 (2%)	0	100	100
7	L	73/550 (13%)	73 (100%)	0	0	100	100
7	M	73/550 (13%)	73 (100%)	0	0	100	100
8	N	222/265 (84%)	209 (94%)	13 (6%)	0	100	100
8	O	222/265 (84%)	210 (95%)	12 (5%)	0	100	100
All	All	1478/3168 (47%)	1421 (96%)	56 (4%)	1 (0%)	50	71

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	G	14	LYS

5.3.2 Protein sidechains (i)

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	84/111 (76%)	84 (100%)	0	100 100
1	E	85/111 (77%)	85 (100%)	0	100 100
2	B	69/79 (87%)	69 (100%)	0	100 100
2	F	67/79 (85%)	66 (98%)	1 (2%)	60 81
3	C	82/99 (83%)	82 (100%)	0	100 100
3	G	85/99 (86%)	85 (100%)	0	100 100
4	D	83/106 (78%)	83 (100%)	0	100 100
4	H	82/106 (77%)	82 (100%)	0	100 100
7	K	97/451 (22%)	97 (100%)	0	100 100
7	L	66/451 (15%)	66 (100%)	0	100 100
7	M	66/451 (15%)	66 (100%)	0	100 100
8	N	199/224 (89%)	199 (100%)	0	100 100
8	O	199/224 (89%)	199 (100%)	0	100 100
All	All	1264/2591 (49%)	1263 (100%)	1 (0%)	92 98

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	92	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
3	G	32	HIS
7	K	164	GLN
7	K	283	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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.

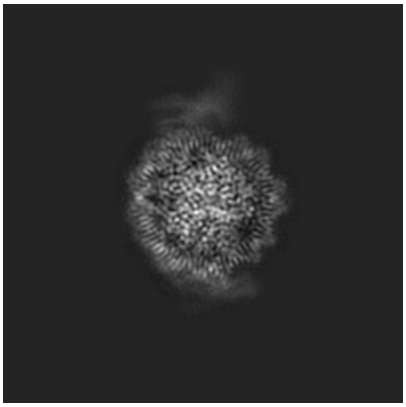
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-26258. These allow visual inspection of the internal detail of the map and identification of artifacts.

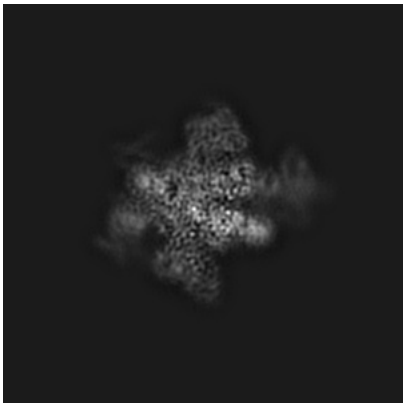
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

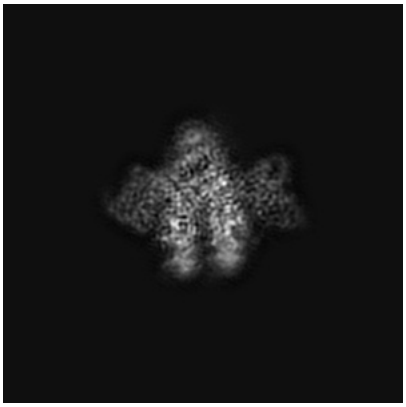
6.1.1 Primary map



X



Y

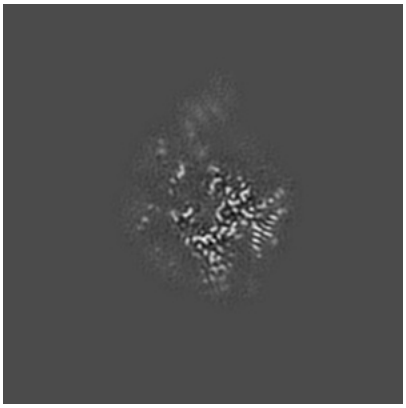


Z

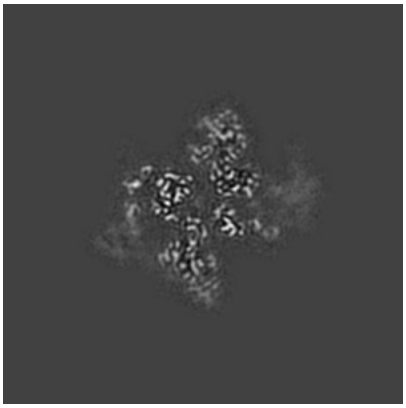
The images above show the map projected in three orthogonal directions.

6.2 Central slices

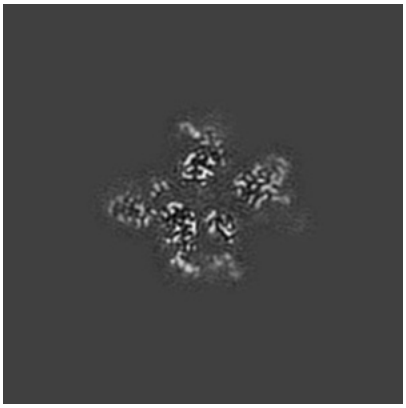
6.2.1 Primary map



X Index: 120



Y Index: 120

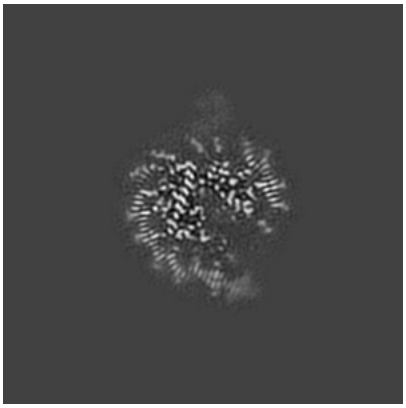


Z Index: 120

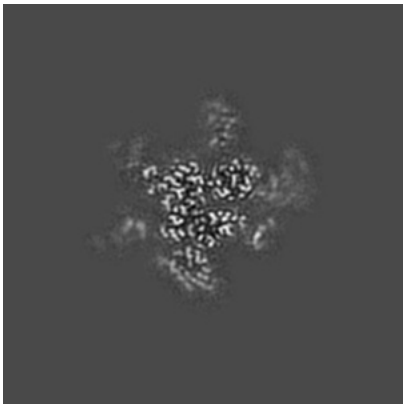
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

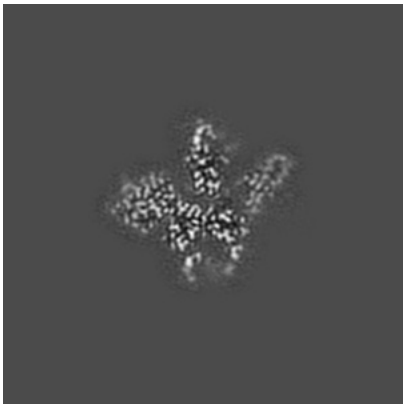
6.3.1 Primary map



X Index: 111



Y Index: 110

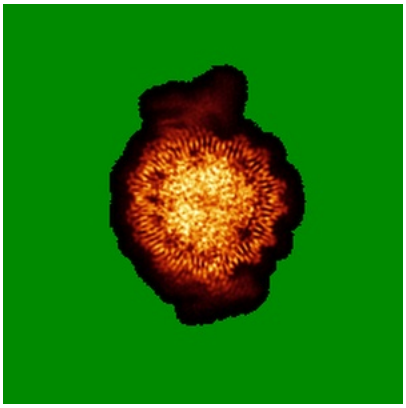


Z Index: 114

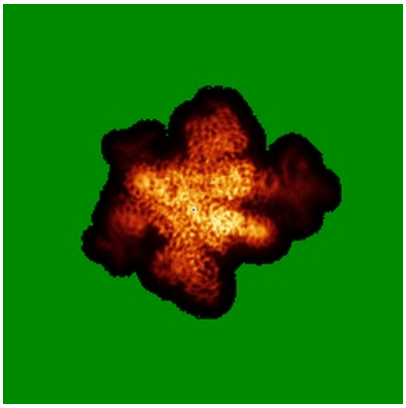
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

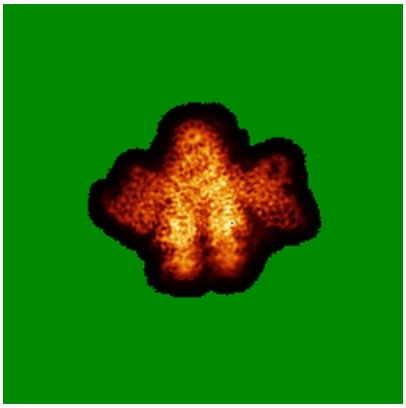
6.4.1 Primary map



X



Y

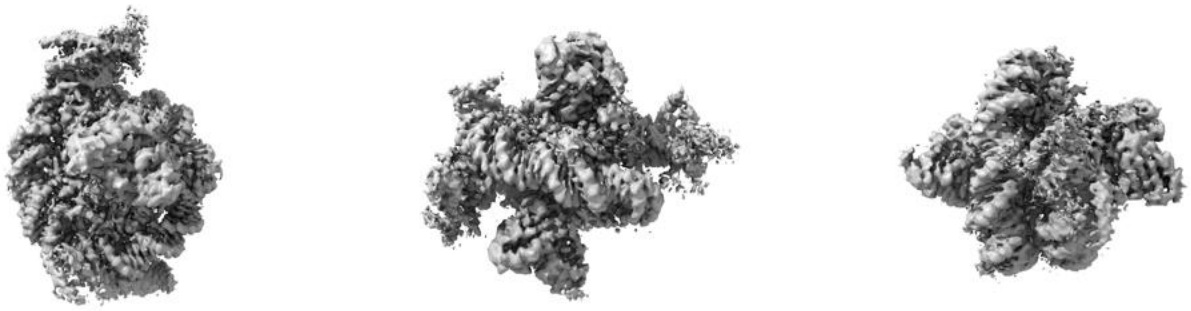


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.17. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

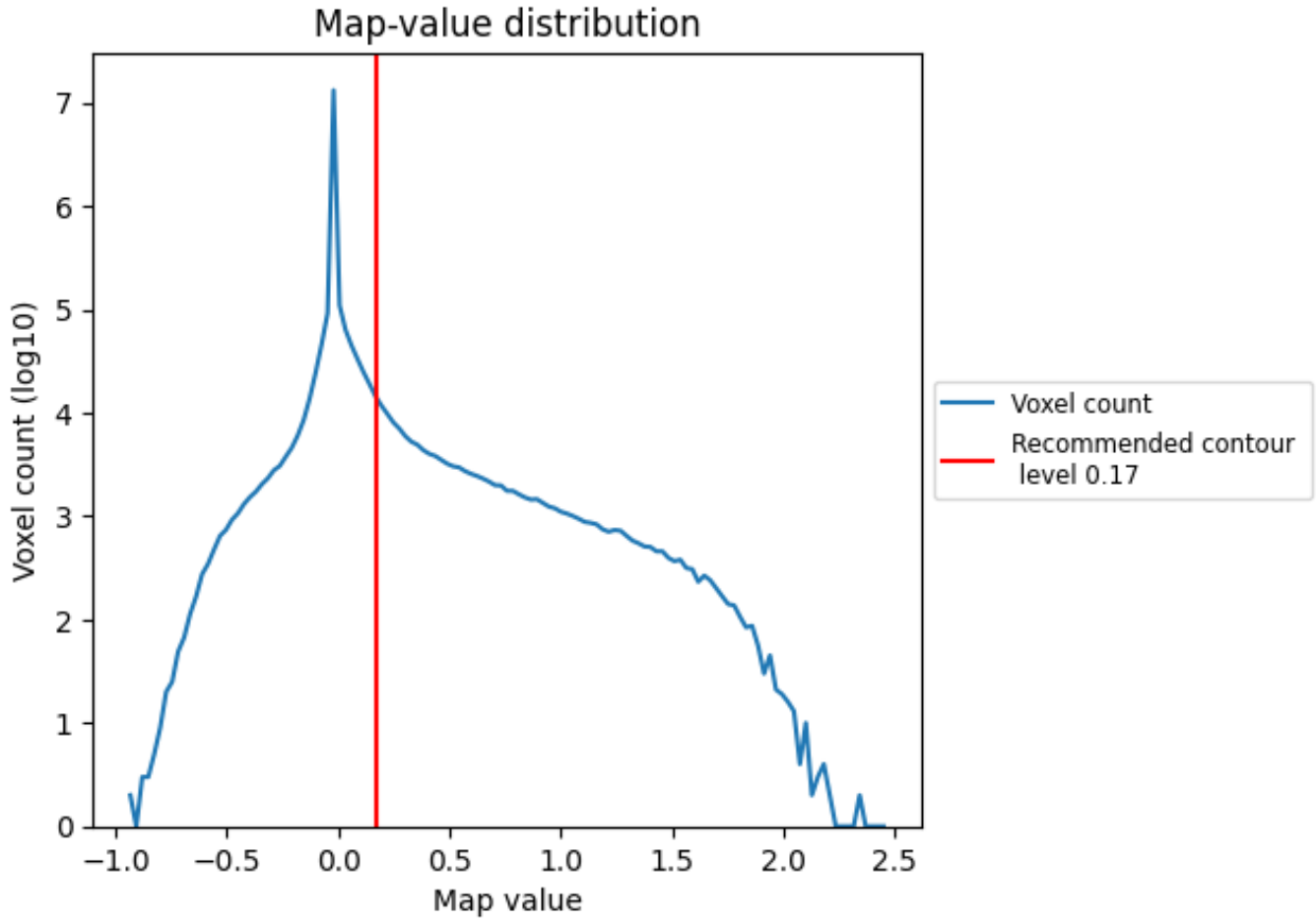
6.6 Mask visualisation (i)

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

7 Map analysis

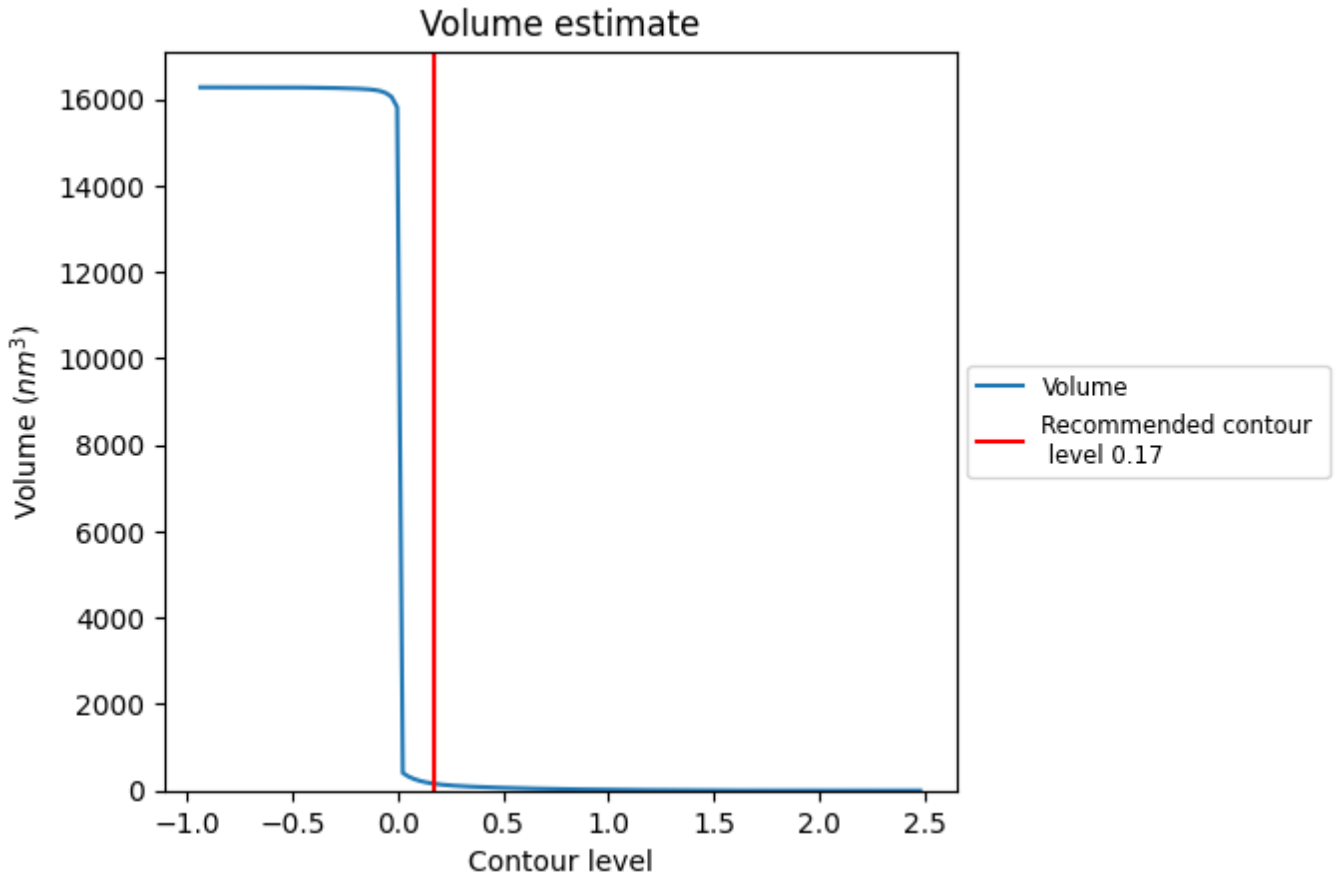
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

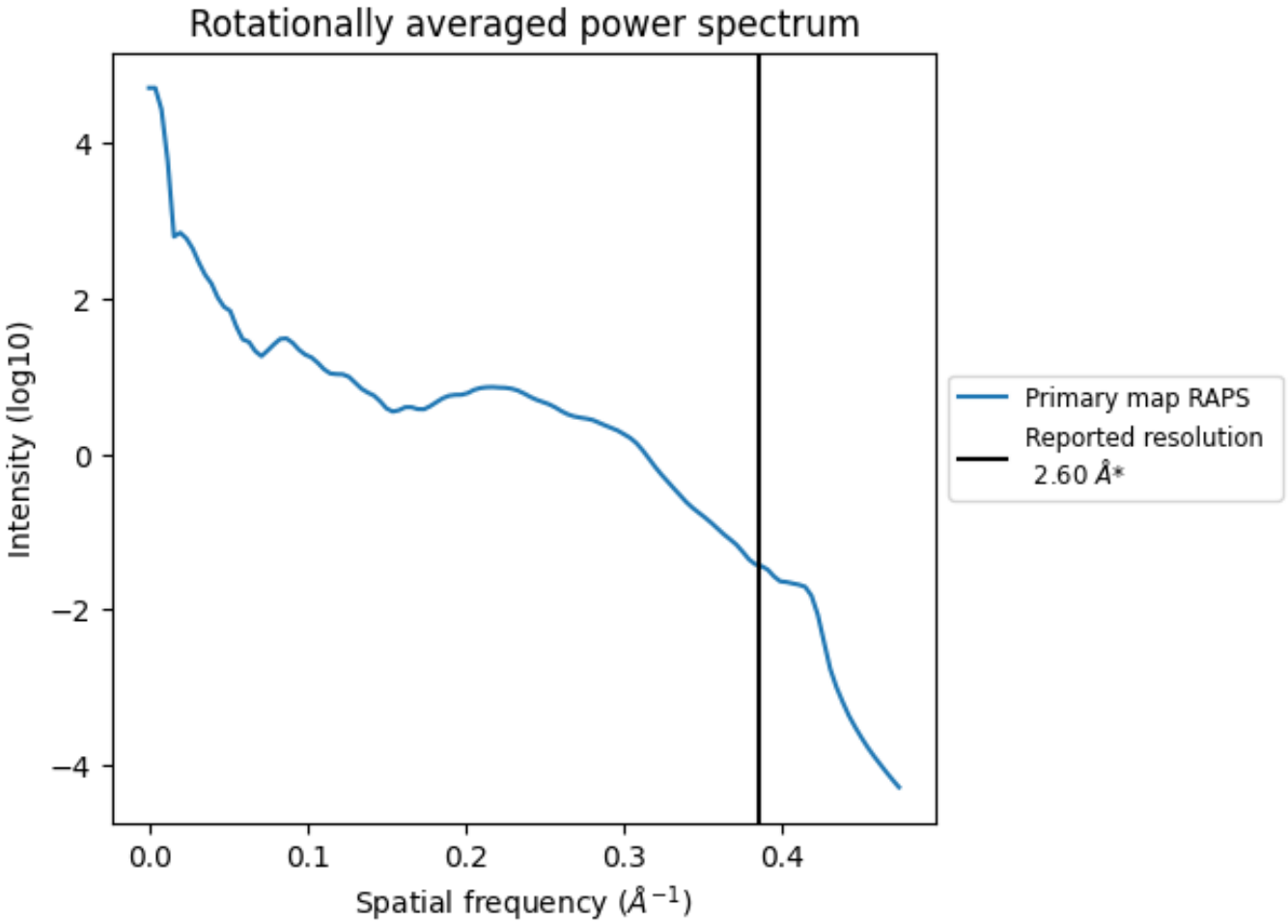
7.2 Volume estimate (i)



The volume at the recommended contour level is 162 nm^3; this corresponds to an approximate mass of 146 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 (i)



*Reported resolution corresponds to spatial frequency of 0.385 $Å^{-1}$

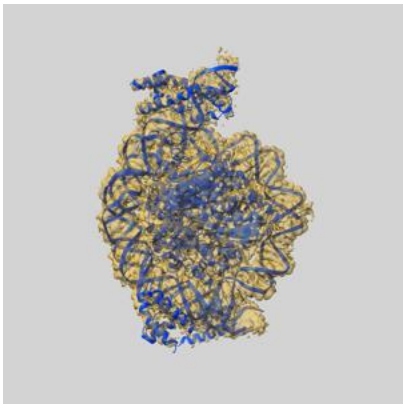
8 Fourier-Shell correlation

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

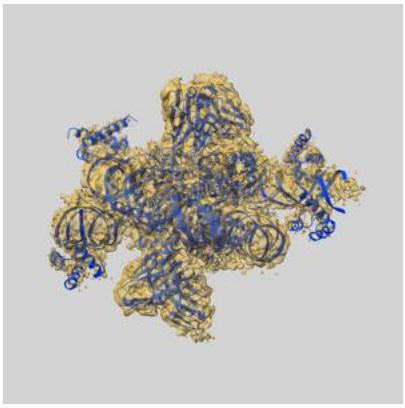
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-26258 and PDB model 7U0G. Per-residue inclusion information can be found in section 3 on page 9.

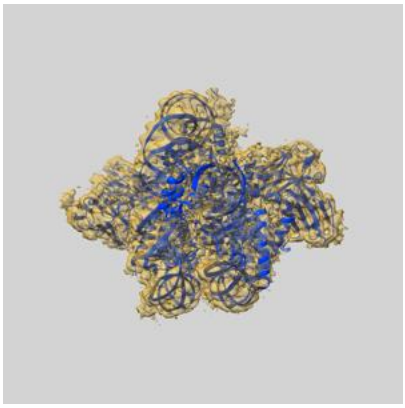
9.1 Map-model overlay



X



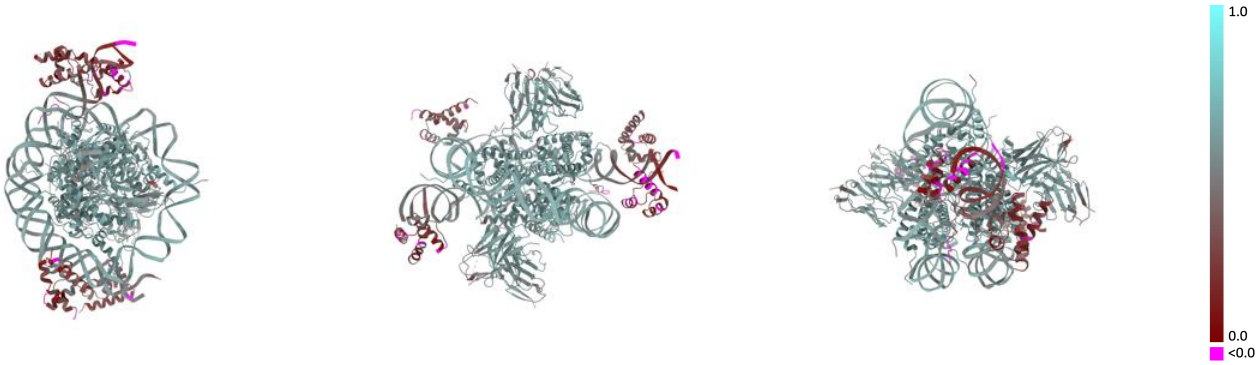
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.17 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.

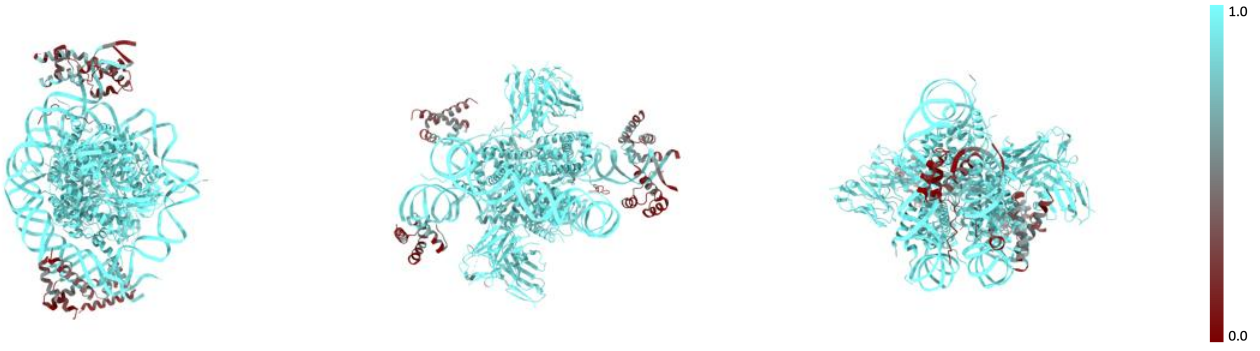
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

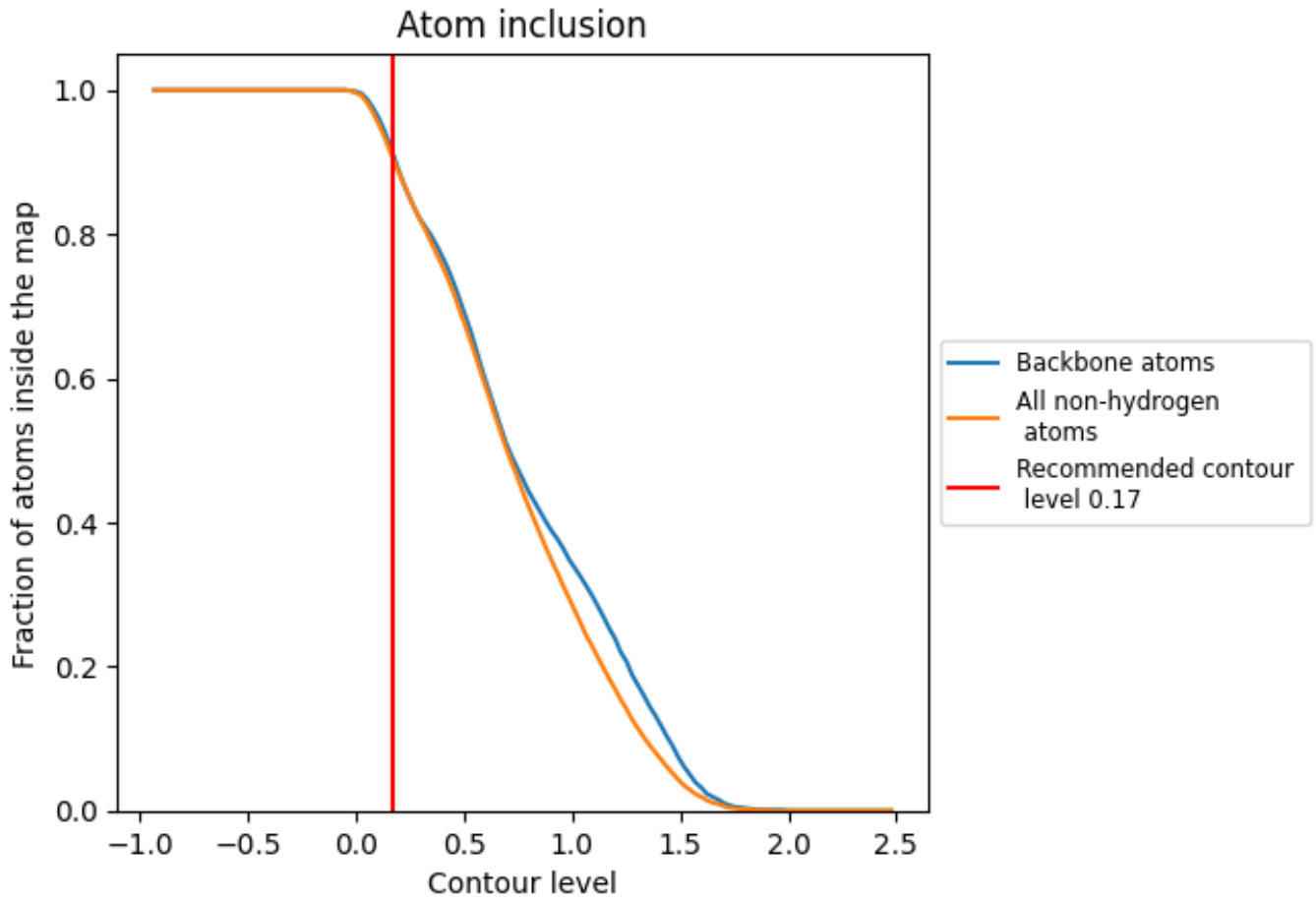
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.17).

9.4 Atom inclusion (i)



At the recommended contour level, 91% of all backbone atoms, 91% 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 (0.17) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9060	0.5310
A	0.9870	0.6250
B	0.9800	0.6240
C	0.9750	0.6150
D	0.8980	0.5700
E	0.9860	0.6200
F	0.9760	0.6270
G	0.9770	0.6120
H	0.9710	0.6140
I	0.9670	0.5500
J	0.9660	0.5380
K	0.3510	0.1920
L	0.3710	0.2800
M	0.3590	0.2310
N	0.9690	0.5630
O	0.9710	0.5620