



wwPDB EM Validation Summary Report ⓘ

Jul 15, 2024 – 07:32 pm BST

PDB ID : 8CLJ
EMDB ID : EMD-16714
Title : TFIIC TauB-DNA dimer
Authors : Seifert-Davila, W.; Girbig, M.; Hauptmann, L.; Hoffmann, T.; Eustermann, S.; Mueller, C.W.
Deposited on : 2023-02-16
Resolution : 3.20 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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

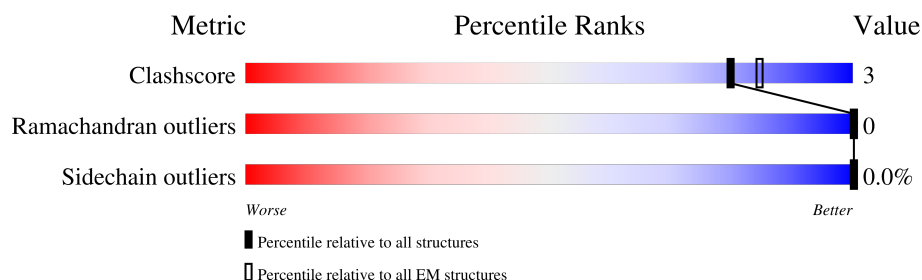
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	2158	24% 75%
1	F	2158	24% 75%
2	B	822	76% 8% 16%
2	G	822	77% 6% 16%
3	C	925	58% 37%
3	H	925	59% 37%
4	D	35	54% 43%
4	I	35	60% 40%

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Mol	Chain	Length	Quality of chain
5	E	35	 69%31%
5	J	35	 63%37%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 31910 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 protein called General transcription factor 3C polypeptide 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	542	Total	C	N	O	S	0	0
			4421	2789	803	802	27		
1	F	542	Total	C	N	O	S	0	0
			4421	2789	803	802	27		

There are 98 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2110	GLY	-	expression tag	UNP Q12789
A	2111	GLY	-	expression tag	UNP Q12789
A	2112	GLY	-	expression tag	UNP Q12789
A	2113	SER	-	expression tag	UNP Q12789
A	2114	GLY	-	expression tag	UNP Q12789
A	2115	GLY	-	expression tag	UNP Q12789
A	2116	GLY	-	expression tag	UNP Q12789
A	2117	SER	-	expression tag	UNP Q12789
A	2118	GLY	-	expression tag	UNP Q12789
A	2119	GLY	-	expression tag	UNP Q12789
A	2120	SER	-	expression tag	UNP Q12789
A	2121	LEU	-	expression tag	UNP Q12789
A	2122	GLU	-	expression tag	UNP Q12789
A	2123	VAL	-	expression tag	UNP Q12789
A	2124	LEU	-	expression tag	UNP Q12789
A	2125	PHE	-	expression tag	UNP Q12789
A	2126	GLN	-	expression tag	UNP Q12789
A	2127	GLY	-	expression tag	UNP Q12789
A	2128	PRO	-	expression tag	UNP Q12789
A	2129	GLY	-	expression tag	UNP Q12789
A	2130	SER	-	expression tag	UNP Q12789
A	2131	GLY	-	expression tag	UNP Q12789
A	2132	SER	-	expression tag	UNP Q12789
A	2133	ASP	-	expression tag	UNP Q12789
A	2134	TYR	-	expression tag	UNP Q12789
A	2135	LYS	-	expression tag	UNP Q12789

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Chain	Residue	Modelled	Actual	Comment	Reference
A	2136	ASP	-	expression tag	UNP Q12789
A	2137	ASP	-	expression tag	UNP Q12789
A	2138	ASP	-	expression tag	UNP Q12789
A	2139	ASP	-	expression tag	UNP Q12789
A	2140	LYS	-	expression tag	UNP Q12789
A	2141	GLY	-	expression tag	UNP Q12789
A	2142	ASP	-	expression tag	UNP Q12789
A	2143	TYR	-	expression tag	UNP Q12789
A	2144	LYS	-	expression tag	UNP Q12789
A	2145	ASP	-	expression tag	UNP Q12789
A	2146	ASP	-	expression tag	UNP Q12789
A	2147	ASP	-	expression tag	UNP Q12789
A	2148	ASP	-	expression tag	UNP Q12789
A	2149	LYS	-	expression tag	UNP Q12789
A	2150	GLY	-	expression tag	UNP Q12789
A	2151	ASP	-	expression tag	UNP Q12789
A	2152	TYR	-	expression tag	UNP Q12789
A	2153	LYS	-	expression tag	UNP Q12789
A	2154	ASP	-	expression tag	UNP Q12789
A	2155	ASP	-	expression tag	UNP Q12789
A	2156	ASP	-	expression tag	UNP Q12789
A	2157	ASP	-	expression tag	UNP Q12789
A	2158	LYS	-	expression tag	UNP Q12789
F	2110	GLY	-	expression tag	UNP Q12789
F	2111	GLY	-	expression tag	UNP Q12789
F	2112	GLY	-	expression tag	UNP Q12789
F	2113	SER	-	expression tag	UNP Q12789
F	2114	GLY	-	expression tag	UNP Q12789
F	2115	GLY	-	expression tag	UNP Q12789
F	2116	GLY	-	expression tag	UNP Q12789
F	2117	SER	-	expression tag	UNP Q12789
F	2118	GLY	-	expression tag	UNP Q12789
F	2119	GLY	-	expression tag	UNP Q12789
F	2120	SER	-	expression tag	UNP Q12789
F	2121	LEU	-	expression tag	UNP Q12789
F	2122	GLU	-	expression tag	UNP Q12789
F	2123	VAL	-	expression tag	UNP Q12789
F	2124	LEU	-	expression tag	UNP Q12789
F	2125	PHE	-	expression tag	UNP Q12789
F	2126	GLN	-	expression tag	UNP Q12789
F	2127	GLY	-	expression tag	UNP Q12789
F	2128	PRO	-	expression tag	UNP Q12789

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Chain	Residue	Modelled	Actual	Comment	Reference
F	2129	GLY	-	expression tag	UNP Q12789
F	2130	SER	-	expression tag	UNP Q12789
F	2131	GLY	-	expression tag	UNP Q12789
F	2132	SER	-	expression tag	UNP Q12789
F	2133	ASP	-	expression tag	UNP Q12789
F	2134	TYR	-	expression tag	UNP Q12789
F	2135	LYS	-	expression tag	UNP Q12789
F	2136	ASP	-	expression tag	UNP Q12789
F	2137	ASP	-	expression tag	UNP Q12789
F	2138	ASP	-	expression tag	UNP Q12789
F	2139	ASP	-	expression tag	UNP Q12789
F	2140	LYS	-	expression tag	UNP Q12789
F	2141	GLY	-	expression tag	UNP Q12789
F	2142	ASP	-	expression tag	UNP Q12789
F	2143	TYR	-	expression tag	UNP Q12789
F	2144	LYS	-	expression tag	UNP Q12789
F	2145	ASP	-	expression tag	UNP Q12789
F	2146	ASP	-	expression tag	UNP Q12789
F	2147	ASP	-	expression tag	UNP Q12789
F	2148	ASP	-	expression tag	UNP Q12789
F	2149	LYS	-	expression tag	UNP Q12789
F	2150	GLY	-	expression tag	UNP Q12789
F	2151	ASP	-	expression tag	UNP Q12789
F	2152	TYR	-	expression tag	UNP Q12789
F	2153	LYS	-	expression tag	UNP Q12789
F	2154	ASP	-	expression tag	UNP Q12789
F	2155	ASP	-	expression tag	UNP Q12789
F	2156	ASP	-	expression tag	UNP Q12789
F	2157	ASP	-	expression tag	UNP Q12789
F	2158	LYS	-	expression tag	UNP Q12789

- Molecule 2 is a protein called General transcription factor 3C polypeptide 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	689	Total	C	N	O	S	0	0
			5496	3519	947	991	39		
2	G	689	Total	C	N	O	S	0	0
			5496	3519	947	991	39		

- Molecule 3 is a protein called General transcription factor 3C polypeptide 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	579	Total	C	N	O	S	0	0
			4601	2964	802	808	27		
3	H	579	Total	C	N	O	S	0	0
			4601	2964	802	808	27		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-13	MET	-	initiating methionine	UNP Q8WUA4
C	-12	HIS	-	expression tag	UNP Q8WUA4
C	-11	HIS	-	expression tag	UNP Q8WUA4
C	-10	HIS	-	expression tag	UNP Q8WUA4
C	-9	HIS	-	expression tag	UNP Q8WUA4
C	-8	HIS	-	expression tag	UNP Q8WUA4
C	-7	HIS	-	expression tag	UNP Q8WUA4
C	-6	GLU	-	expression tag	UNP Q8WUA4
C	-5	ASN	-	expression tag	UNP Q8WUA4
C	-4	LEU	-	expression tag	UNP Q8WUA4
C	-3	TYR	-	expression tag	UNP Q8WUA4
C	-2	PHE	-	expression tag	UNP Q8WUA4
C	-1	GLN	-	expression tag	UNP Q8WUA4
C	0	GLY	-	expression tag	UNP Q8WUA4
H	-13	MET	-	initiating methionine	UNP Q8WUA4
H	-12	HIS	-	expression tag	UNP Q8WUA4
H	-11	HIS	-	expression tag	UNP Q8WUA4
H	-10	HIS	-	expression tag	UNP Q8WUA4
H	-9	HIS	-	expression tag	UNP Q8WUA4
H	-8	HIS	-	expression tag	UNP Q8WUA4
H	-7	HIS	-	expression tag	UNP Q8WUA4
H	-6	GLU	-	expression tag	UNP Q8WUA4
H	-5	ASN	-	expression tag	UNP Q8WUA4
H	-4	LEU	-	expression tag	UNP Q8WUA4
H	-3	TYR	-	expression tag	UNP Q8WUA4
H	-2	PHE	-	expression tag	UNP Q8WUA4
H	-1	GLN	-	expression tag	UNP Q8WUA4
H	0	GLY	-	expression tag	UNP Q8WUA4

- Molecule 4 is a DNA chain called tDNA (35-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	35	Total	C	N	O	P	0	0
			721	342	132	212	35		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	I	35	Total	C	N	O	P	0	0
			721	342	132	212	35		

- Molecule 5 is a DNA chain called tDNA (35-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	35	Total	C	N	O	P	0	0
			714	339	132	208	35		
5	J	35	Total	C	N	O	P	0	0
			714	339	132	208	35		

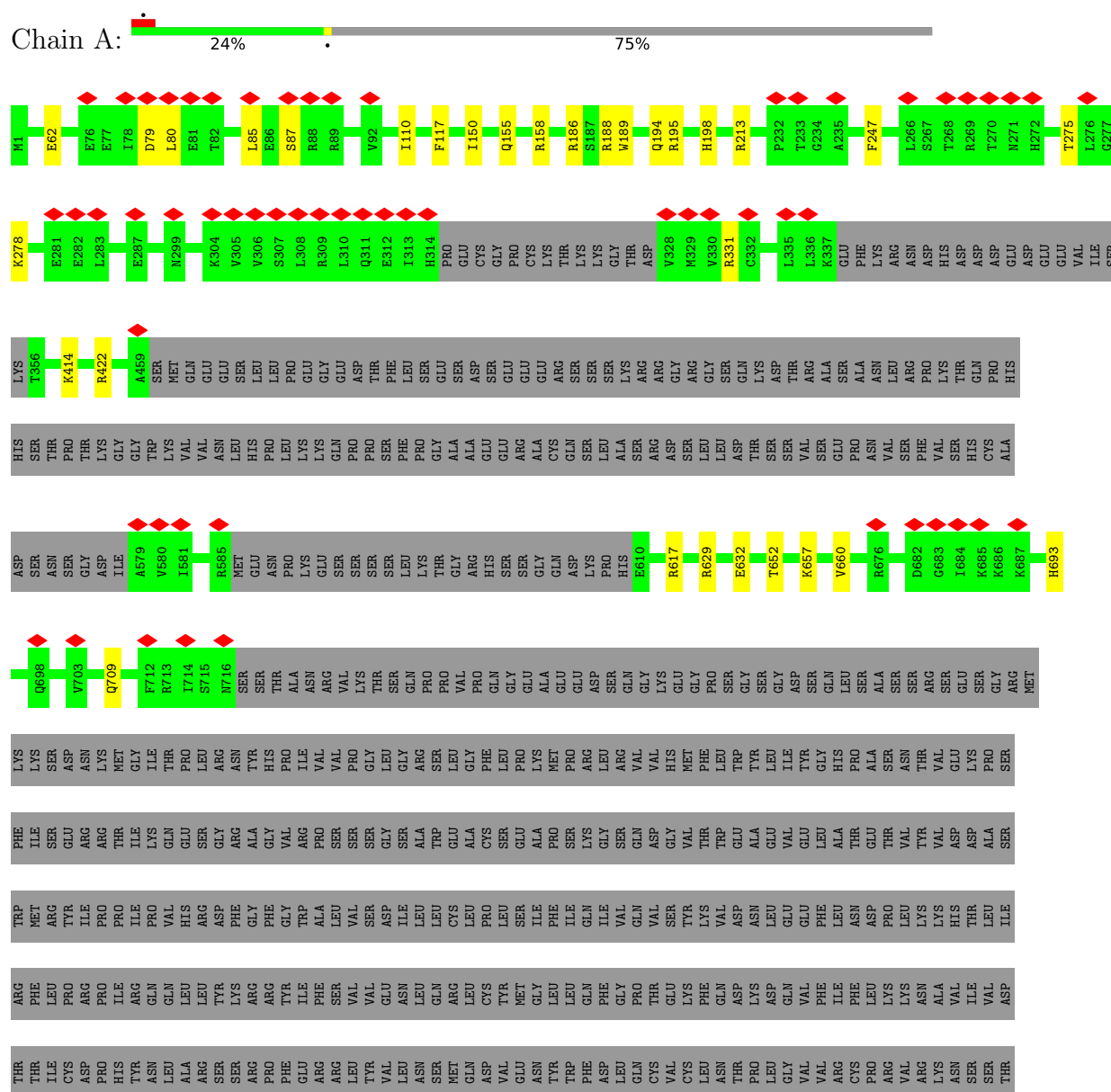
- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
6	B	2	Total	Zn	0
			2	2	
6	G	2	Total	Zn	0
			2	2	

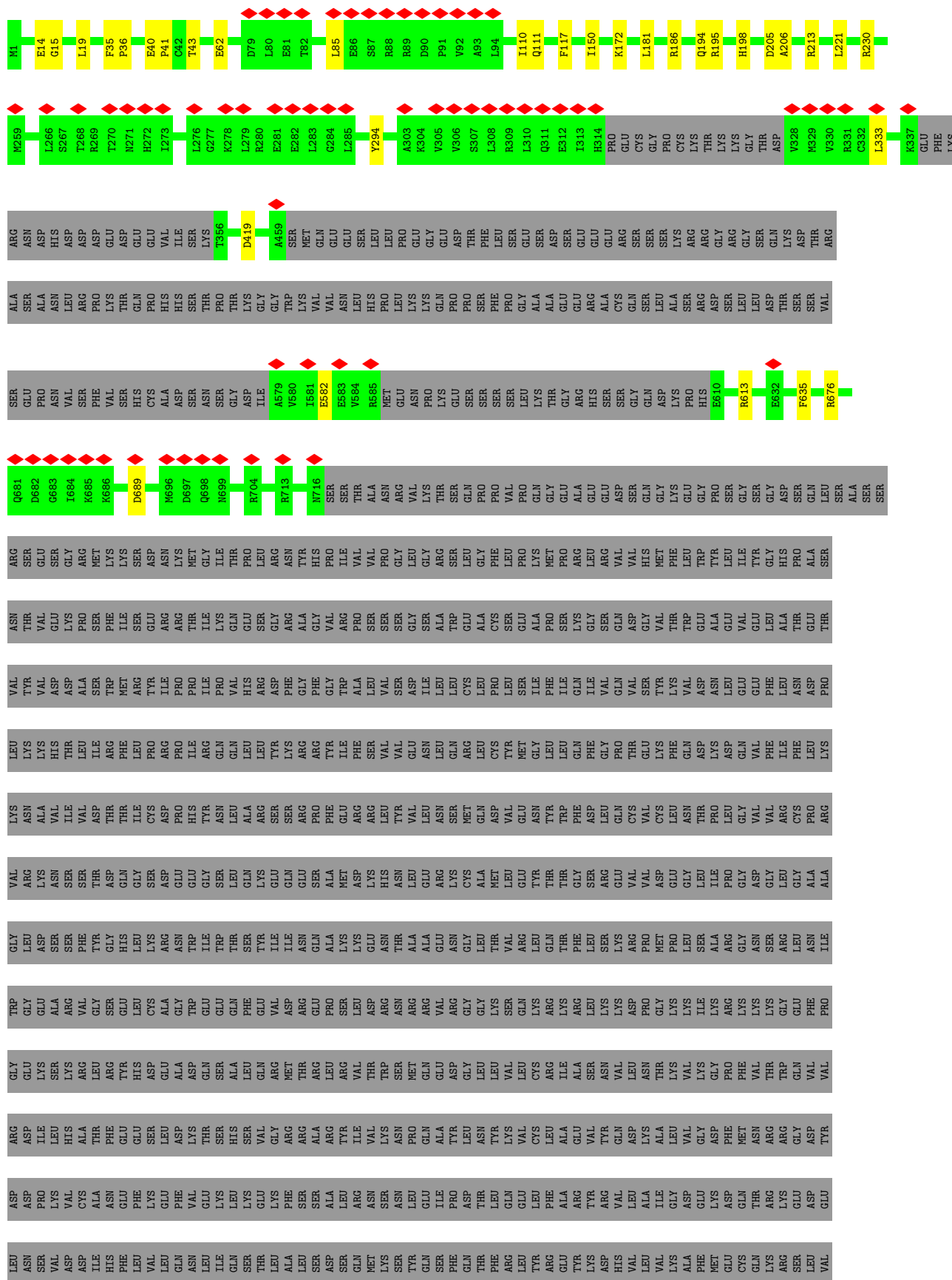
3 Residue-property plots

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

- Molecule 1: General transcription factor 3C polypeptide 1



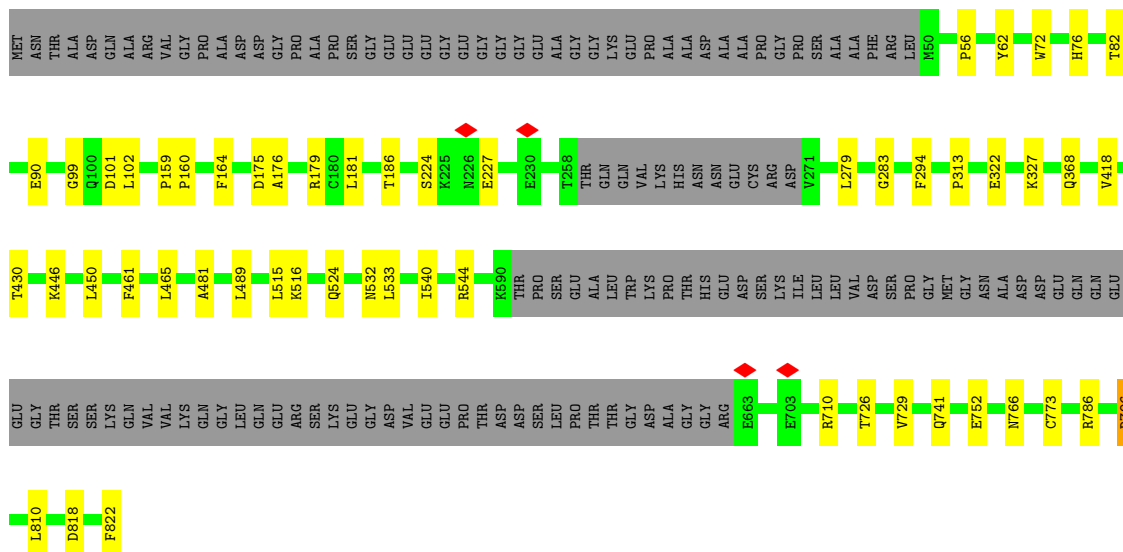






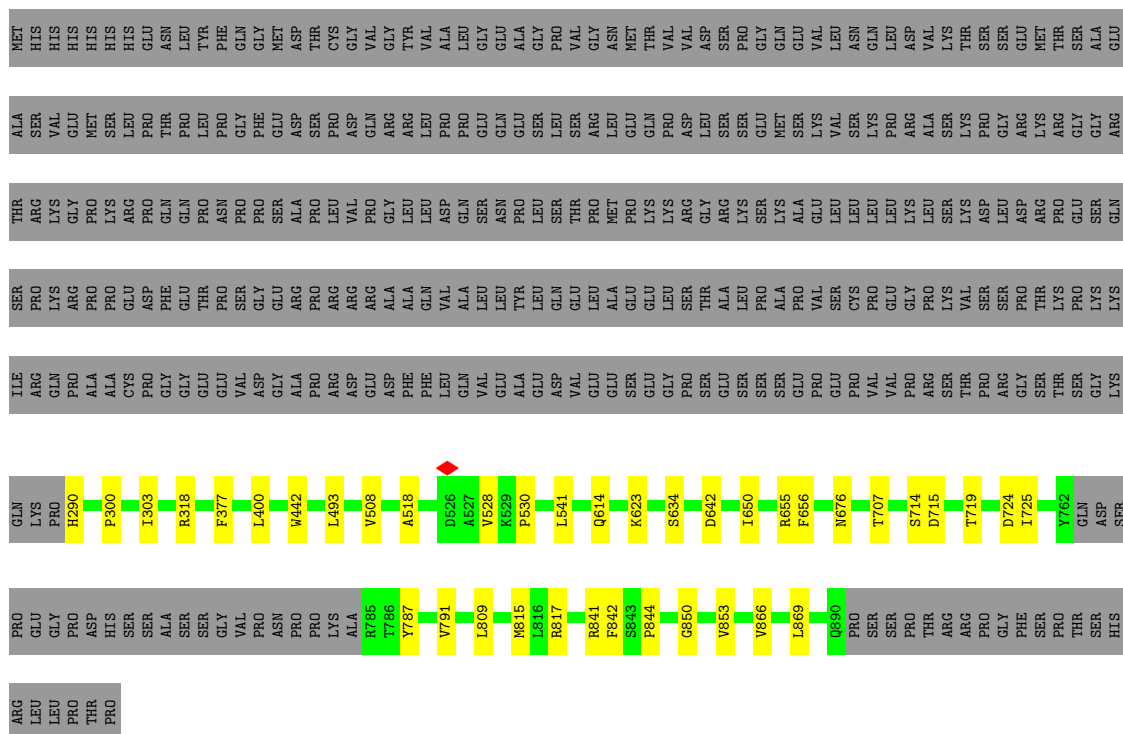
- Molecule 2: General transcription factor 3C polypeptide 4

Chain G:



- Molecule 3: General transcription factor 3C polypeptide 2

Chain C:



- Molecule 3: General transcription factor 3C polypeptide 2

Chain H:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35379	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 ($e^-/\text{\AA}^2$)	42.8	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	5.808	Depositor
Minimum map value	-3.396	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.115	Depositor
Recommended contour level	0.6	Depositor
Map size (Å)	394.56, 394.56, 394.56	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82199997, 0.82199997, 0.82199997	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.25	0/4484	0.54	0/6029
1	F	0.25	0/4484	0.54	0/6029
2	B	0.28	0/5626	0.51	0/7626
2	G	0.30	0/5626	0.52	0/7626
3	C	0.30	0/4750	0.54	0/6472
3	H	0.29	0/4750	0.54	0/6472
4	D	0.71	0/808	1.13	2/1246 (0.2%)
4	I	0.70	0/808	1.15	2/1246 (0.2%)
5	E	0.65	0/800	1.03	0/1231
5	J	0.64	0/800	1.03	0/1231
All	All	0.34	0/32936	0.62	4/45208 (0.0%)

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	2
2	B	0	1
2	G	0	1
3	C	0	1
3	H	0	1
All	All	0	6

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	3	DA	O4'-C1'-N9	6.44	112.51	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	3	DA	O4'-C1'-N9	5.87	112.11	108.00
4	I	2	DA	O4'-C1'-N9	5.55	111.89	108.00
4	D	5	DG	P-O3'-C3'	5.05	125.76	119.70

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	186	ARG	Sidechain
1	A	617	ARG	Sidechain
2	B	796	ARG	Sidechain
3	C	841	ARG	Sidechain
2	G	796	ARG	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	4421	0	4580	17	0
1	F	4421	0	4580	18	0
2	B	5496	0	5532	34	0
2	G	5496	0	5532	30	0
3	C	4601	0	4494	20	0
3	H	4601	0	4494	19	0
4	D	721	0	395	12	0
4	I	721	0	395	10	0
5	E	714	0	393	10	0
5	J	714	0	393	8	0
6	B	2	0	0	0	0
6	G	2	0	0	0	0
All	All	31910	0	30788	171	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 3.

The worst 5 of 171 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)
3:C:676:ASN:H	3:C:707:THR:HG22	1.51	0.74
5:E:15:DG:C8	5:E:15:DG:H5'	2.27	0.69
5:J:15:DG:C8	5:J:15:DG:H5'	2.27	0.68
1:F:194:GLN:OE1	1:F:213:ARG:NH1	2.25	0.67
3:H:350:PRO:O	3:H:376:ARG:NH1	2.26	0.66

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	532/2158 (25%)	523 (98%)	9 (2%)	0	100	100
1	F	532/2158 (25%)	523 (98%)	9 (2%)	0	100	100
2	B	683/822 (83%)	663 (97%)	20 (3%)	0	100	100
2	G	683/822 (83%)	657 (96%)	26 (4%)	0	100	100
3	C	575/925 (62%)	568 (99%)	7 (1%)	0	100	100
3	H	575/925 (62%)	566 (98%)	9 (2%)	0	100	100
All	All	3580/7810 (46%)	3500 (98%)	80 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	493/1898 (26%)	493 (100%)	0	100	100
1	F	493/1898 (26%)	493 (100%)	0	100	100
2	B	617/718 (86%)	616 (100%)	1 (0%)	93	98
2	G	617/718 (86%)	617 (100%)	0	100	100
3	C	489/791 (62%)	489 (100%)	0	100	100
3	H	489/791 (62%)	489 (100%)	0	100	100
All	All	3198/6814 (47%)	3197 (100%)	1 (0%)	100	100

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

Mol	Chain	Res	Type
2	B	251	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
3	H	570	HIS
3	H	857	GLN
1	F	111	GLN
1	F	272	HIS
1	F	627	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

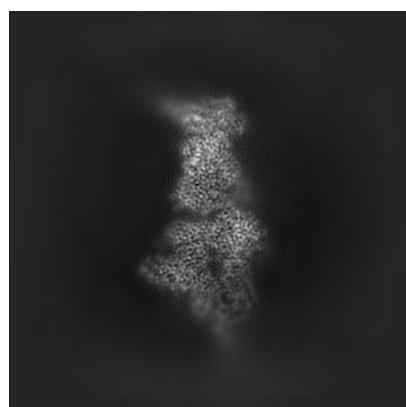
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16714. These allow visual inspection of the internal detail of the map and identification of artifacts.

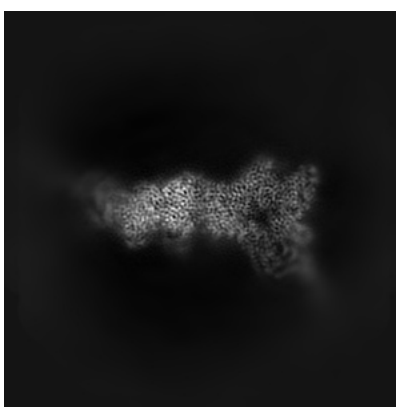
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

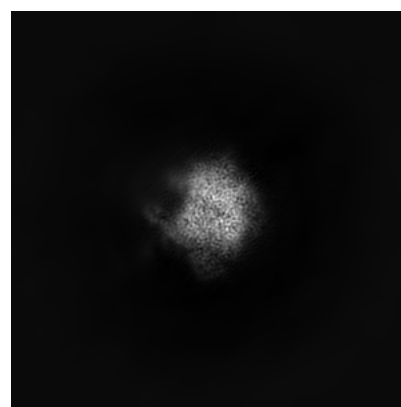
6.1.1 Primary map



X



Y

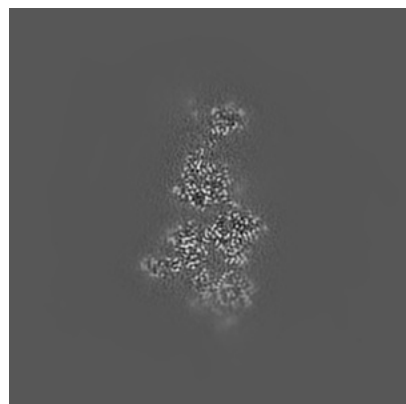


Z

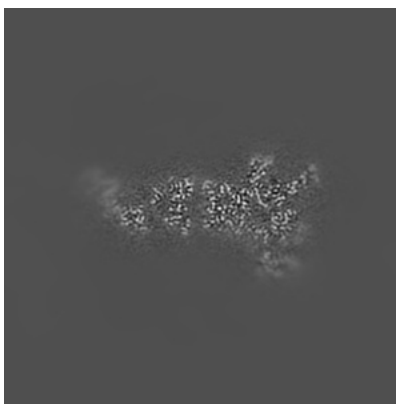
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

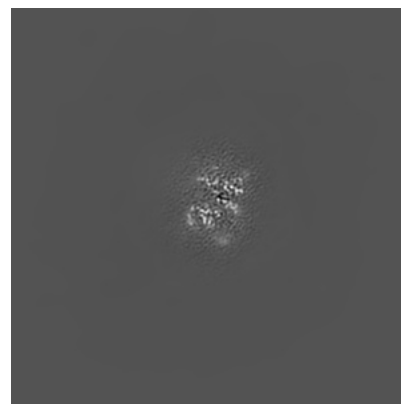
6.2.1 Primary map



X Index: 240



Y Index: 240

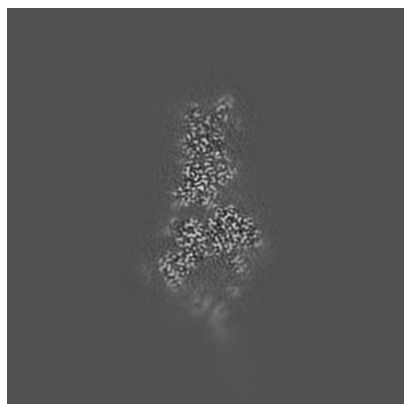


Z Index: 240

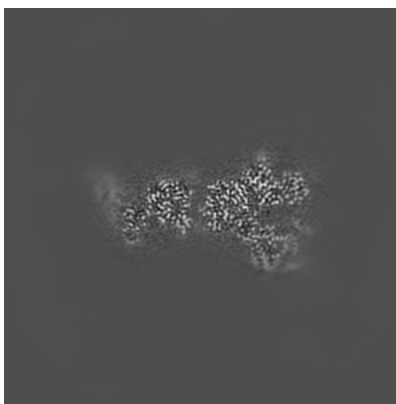
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

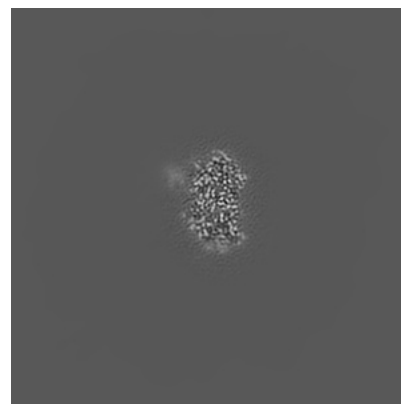
6.3.1 Primary map



X Index: 258



Y Index: 227

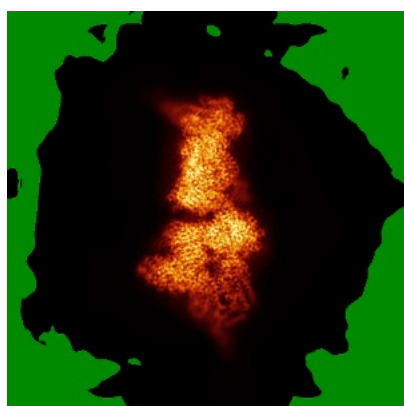


Z Index: 211

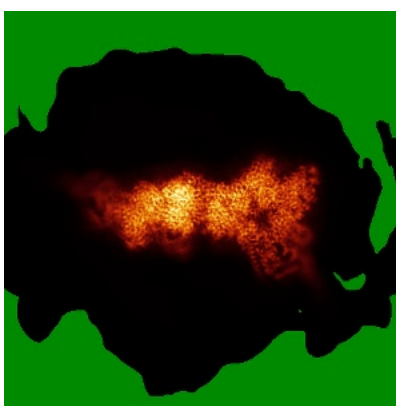
The images above show the largest variance slices of the map in three orthogonal directions.

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

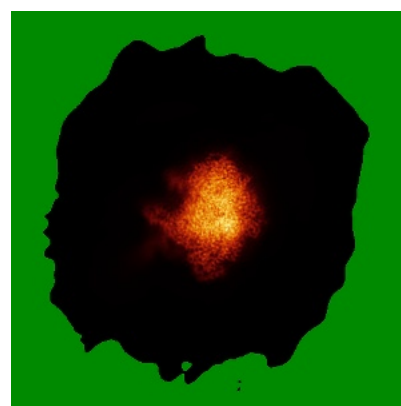
6.4.1 Primary map



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](#)

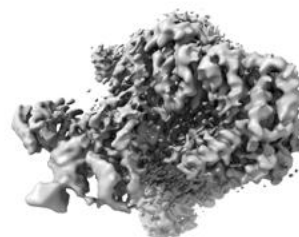
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.6. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

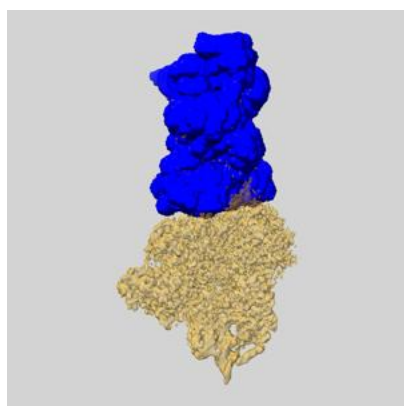
6.6 Mask visualisation [i](#)

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

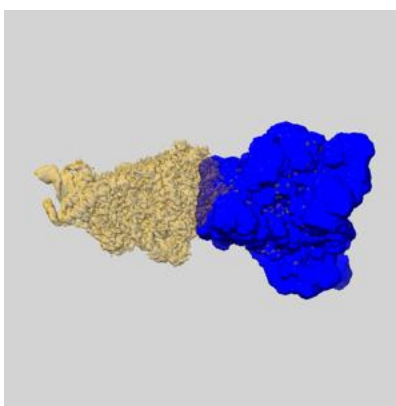
A mask typically either:

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

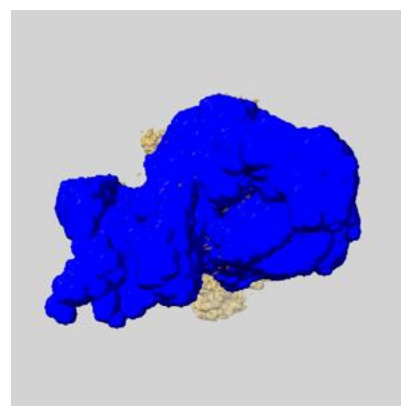
6.6.1 emd_16714_msk_1.map [i](#)



X

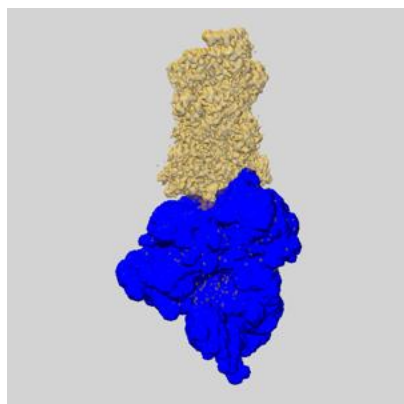


Y

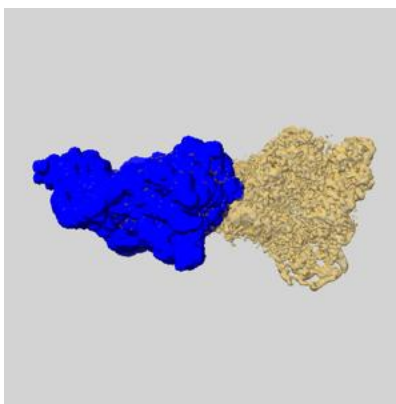


Z

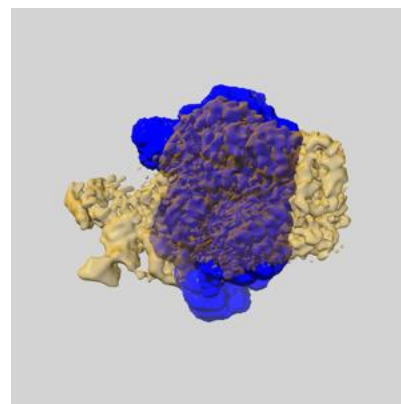
6.6.2 emd_16714_msk_2.map [i](#)



X



Y

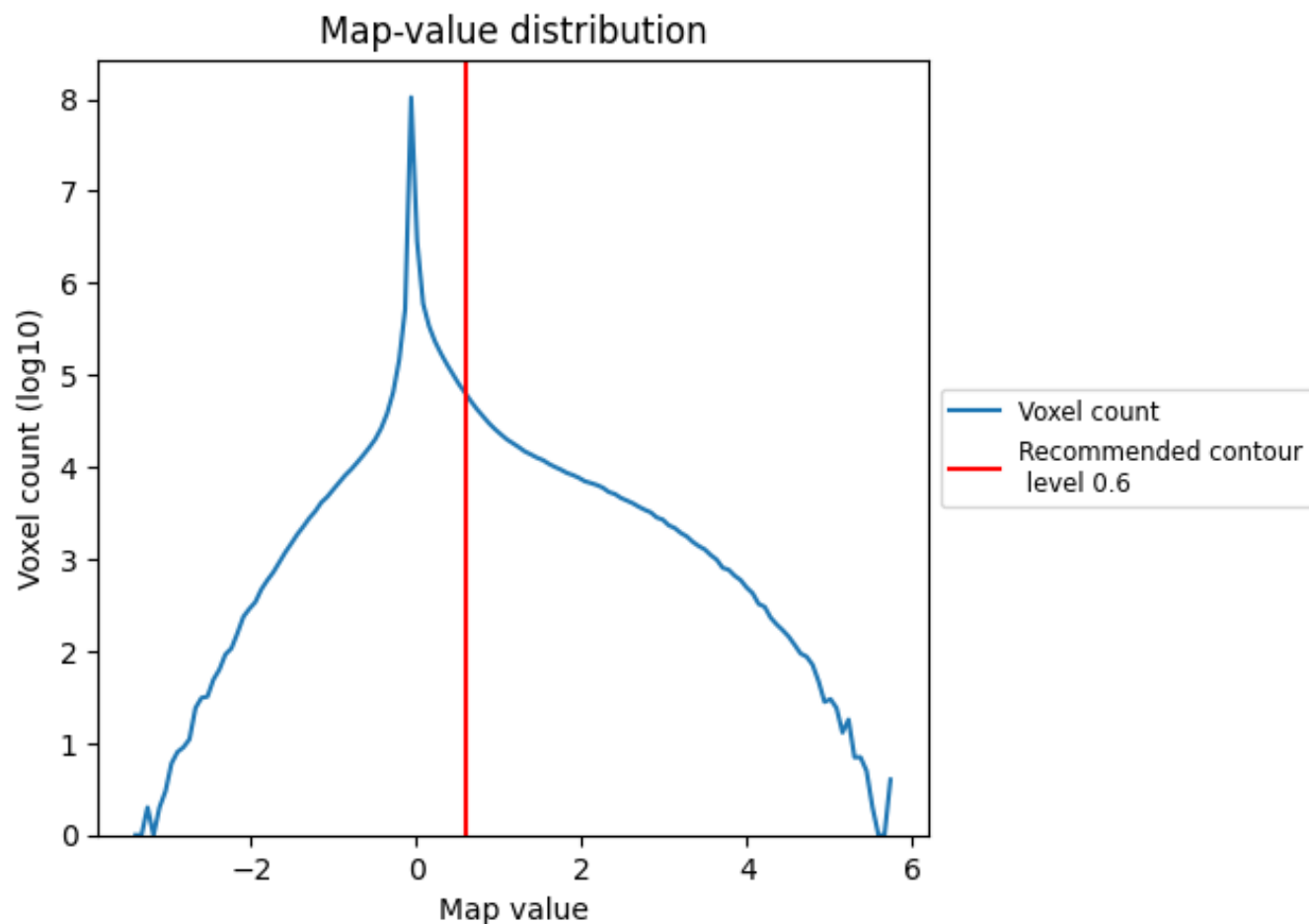


Z

7 Map analysis [i](#)

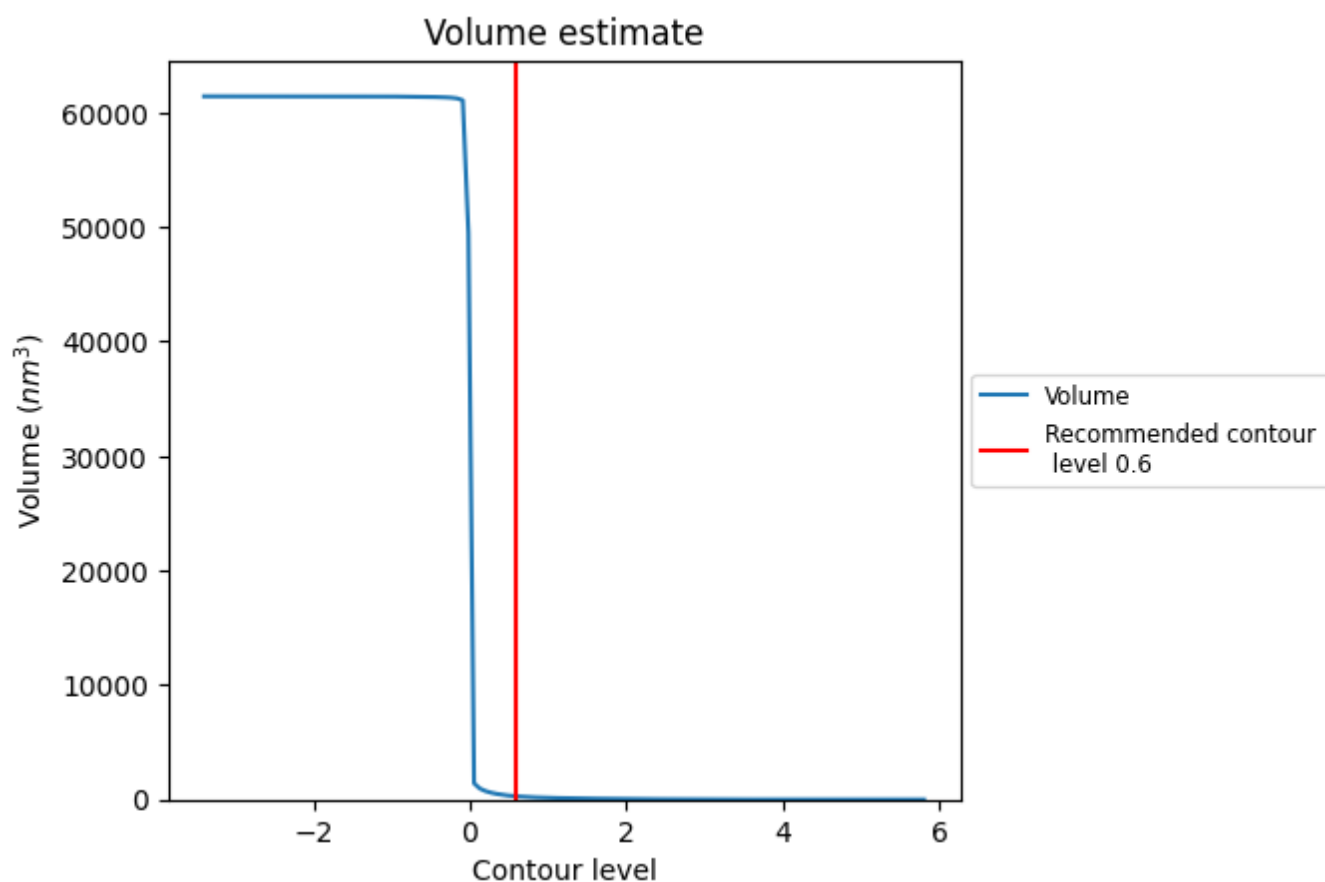
This section contains the results of statistical analysis of the map.

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.

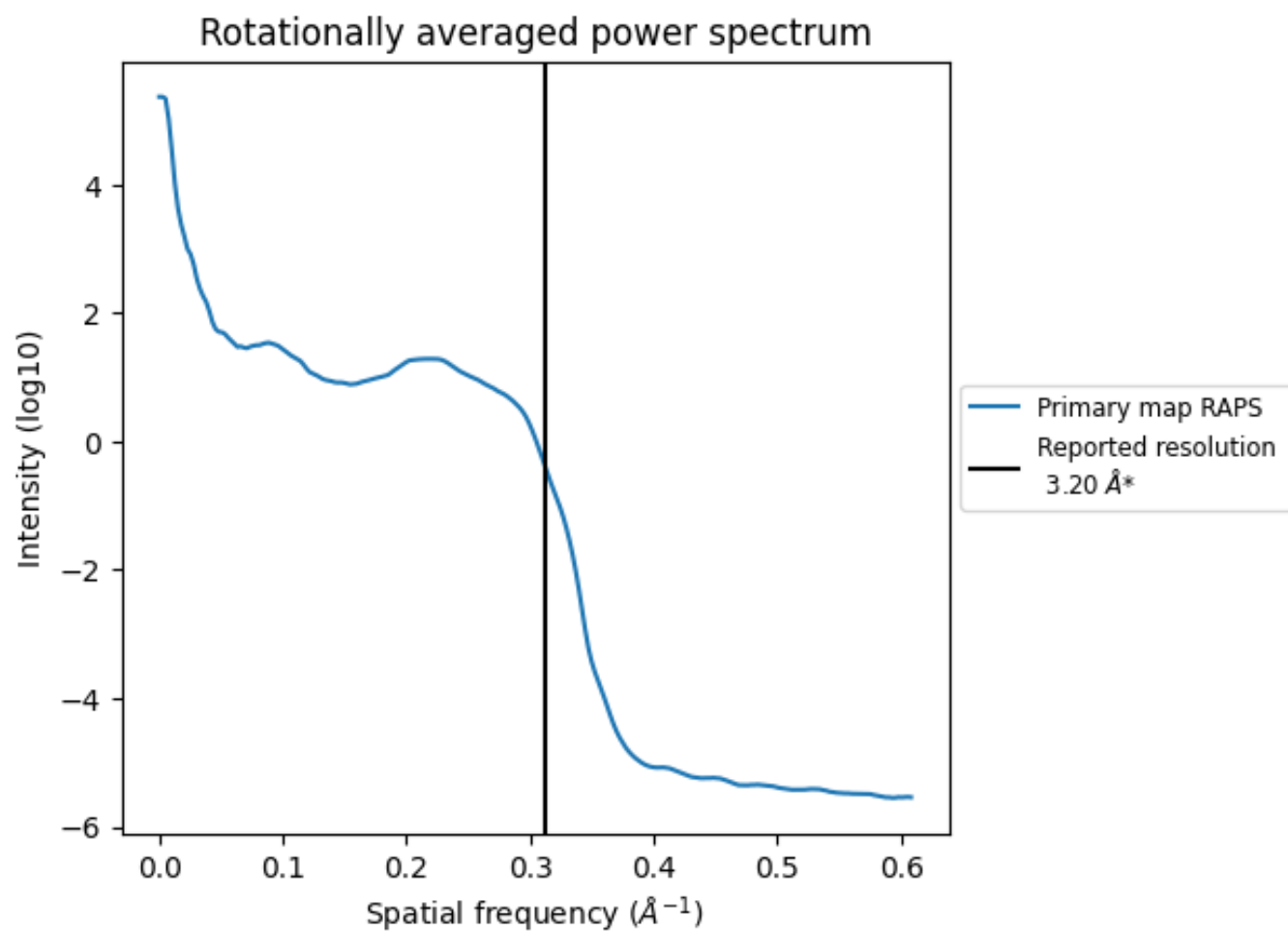
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 284 nm³; this corresponds to an approximate mass of 257 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 0.312 Å⁻¹

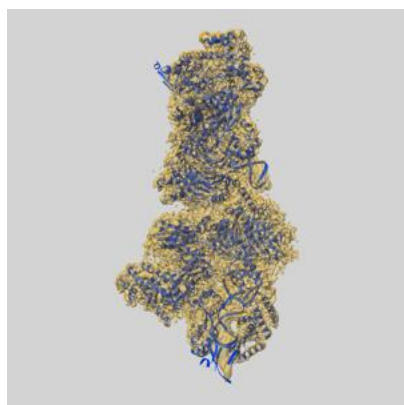
8 Fourier-Shell correlation

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

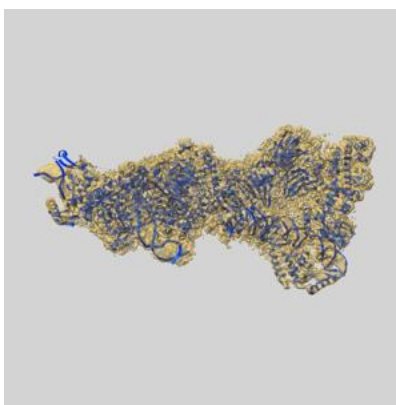
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-16714 and PDB model 8CLJ. Per-residue inclusion information can be found in section [3](#) on page [9](#).

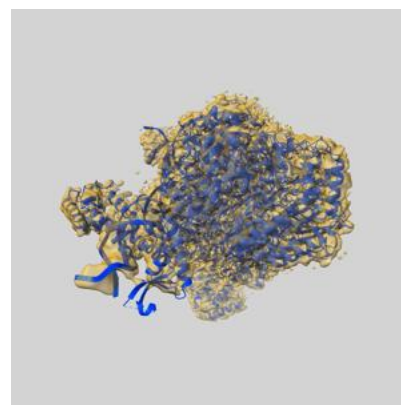
9.1 Map-model overlay [i](#)



X



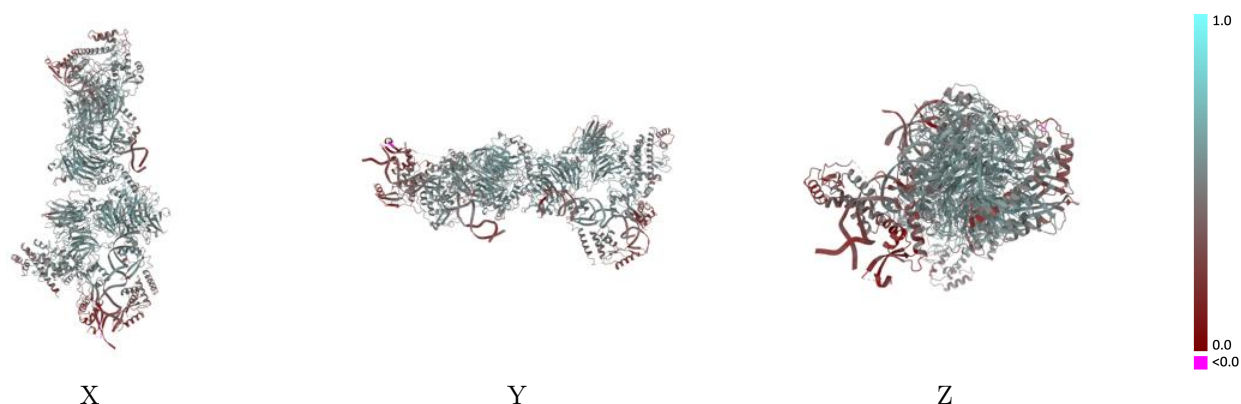
Y



Z

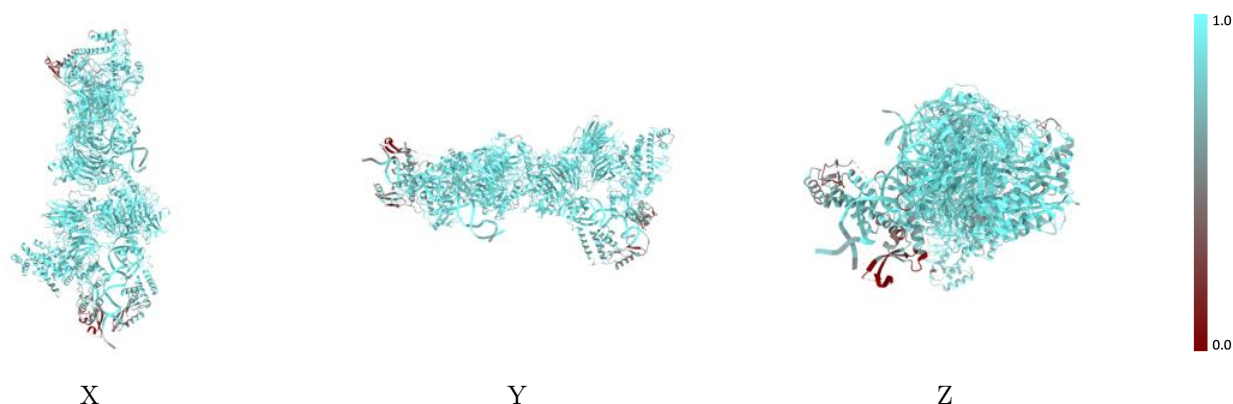
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



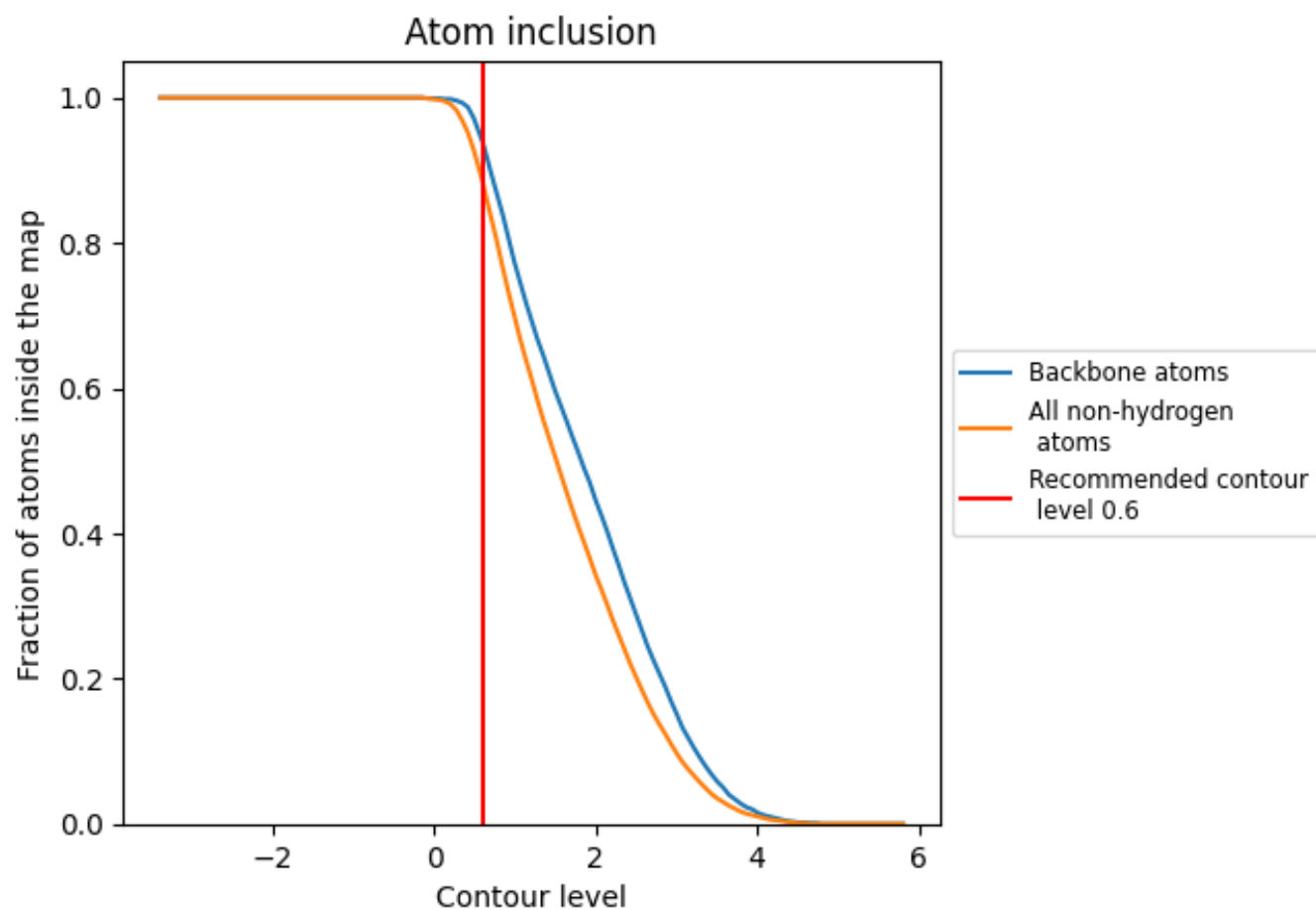
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.6).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 88% 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 (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8830	<div></div> 0.4900
A	<div></div> 0.7680	<div></div> 0.4310
B	<div></div> 0.9120	<div></div> 0.5120
C	<div></div> 0.9630	<div></div> 0.5590
D	<div></div> 0.8920	<div></div> 0.4070
E	<div></div> 0.8800	<div></div> 0.3980
F	<div></div> 0.7670	<div></div> 0.4200
G	<div></div> 0.9120	<div></div> 0.5090
H	<div></div> 0.9520	<div></div> 0.5540
I	<div></div> 0.8970	<div></div> 0.3970
J	<div></div> 0.8810	<div></div> 0.3970

1.0

0.0

<0.0