



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 03:02 PM UTC

PDB ID : 9OT1 / pdb_00009ot1
EMDB ID : EMD-70818
Title : Helical assembly of the IL-17RA/RB/ACT1 complex
Authors : Zhang, H.; Bai, X.; Zhang, X.
Deposited on : 2025-05-26
Resolution : 3.00 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:

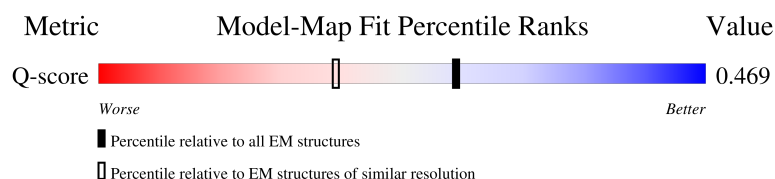
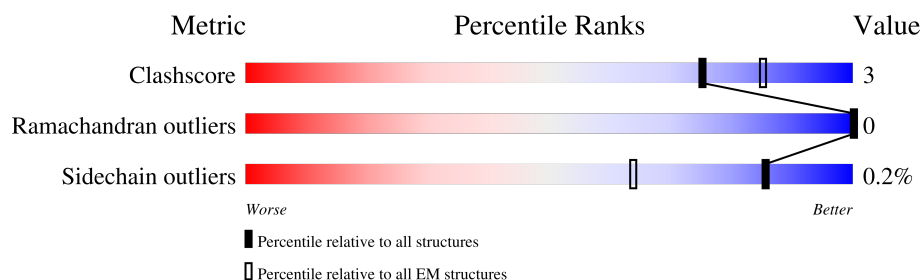
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.00 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	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	683	
1	B	683	
1	C	683	
1	D	683	

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Mol	Chain	Length	Quality of chain
2	E	207	
2	F	207	
2	G	207	
2	H	207	
2	I	207	
2	J	207	
2	K	207	
2	L	207	
2	M	207	
2	N	207	
2	O	207	
2	P	207	
2	Q	207	
2	R	207	
2	S	207	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 57949 atoms, of which 29239 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 Interleukin-17 receptor B, Interleukin-17 receptor A.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	B	142	Total	C	H	N	O	S	0	0
			2296	748	1143	189	206	10		
1	A	140	Total	C	H	N	O	S	0	0
			2271	741	1132	186	202	10		
1	C	320	Total	C	H	N	O	S	0	0
			4902	1563	2449	431	442	17		
1	D	309	Total	C	H	N	O	S	0	0
			4784	1526	2395	420	427	16		

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	324	GLY	-	expression tag	UNP Q9NRM6
B	325	PRO	-	expression tag	UNP Q9NRM6
B	326	LEU	-	expression tag	UNP Q9NRM6
B	327	GLU	-	expression tag	UNP Q9NRM6
B	484	GLN	-	linker	UNP Q9NRM6
B	485	GLY	-	linker	UNP Q9NRM6
B	486	GLY	-	linker	UNP Q9NRM6
B	487	GLY	-	linker	UNP Q9NRM6
B	488	SER	-	linker	UNP Q9NRM6
B	489	GLY	-	linker	UNP Q9NRM6
B	490	GLY	-	linker	UNP Q9NRM6
B	491	GLY	-	linker	UNP Q9NRM6
B	492	SER	-	linker	UNP Q9NRM6
B	493	GLY	-	linker	UNP Q9NRM6
B	494	GLY	-	linker	UNP Q9NRM6
B	495	GLY	-	linker	UNP Q9NRM6
B	496	SER	-	linker	UNP Q9NRM6
B	497	GLY	-	linker	UNP Q9NRM6
B	498	GLY	-	linker	UNP Q9NRM6
B	499	GLY	-	linker	UNP Q9NRM6
B	500	SER	-	linker	UNP Q9NRM6
A	324	GLY	-	expression tag	UNP Q9NRM6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	325	PRO	-	expression tag	UNP Q9NRM6
A	326	LEU	-	expression tag	UNP Q9NRM6
A	327	GLU	-	expression tag	UNP Q9NRM6
A	484	GLN	-	linker	UNP Q9NRM6
A	485	GLY	-	linker	UNP Q9NRM6
A	486	GLY	-	linker	UNP Q9NRM6
A	487	GLY	-	linker	UNP Q9NRM6
A	488	SER	-	linker	UNP Q9NRM6
A	489	GLY	-	linker	UNP Q9NRM6
A	490	GLY	-	linker	UNP Q9NRM6
A	491	GLY	-	linker	UNP Q9NRM6
A	492	SER	-	linker	UNP Q9NRM6
A	493	GLY	-	linker	UNP Q9NRM6
A	494	GLY	-	linker	UNP Q9NRM6
A	495	GLY	-	linker	UNP Q9NRM6
A	496	SER	-	linker	UNP Q9NRM6
A	497	GLY	-	linker	UNP Q9NRM6
A	498	GLY	-	linker	UNP Q9NRM6
A	499	GLY	-	linker	UNP Q9NRM6
A	500	SER	-	linker	UNP Q9NRM6
C	184	GLY	-	expression tag	UNP Q9NRM6
C	185	PRO	-	expression tag	UNP Q9NRM6
C	186	LEU	-	expression tag	UNP Q9NRM6
C	187	GLU	-	expression tag	UNP Q9NRM6
C	344	GLN	-	linker	UNP Q9NRM6
C	345	GLY	-	linker	UNP Q9NRM6
C	346	GLY	-	linker	UNP Q9NRM6
C	347	GLY	-	linker	UNP Q9NRM6
C	348	SER	-	linker	UNP Q9NRM6
C	349	GLY	-	linker	UNP Q9NRM6
C	350	GLY	-	linker	UNP Q9NRM6
C	351	GLY	-	linker	UNP Q9NRM6
C	352	SER	-	linker	UNP Q9NRM6
C	353	GLY	-	linker	UNP Q9NRM6
C	354	GLY	-	linker	UNP Q9NRM6
C	355	GLY	-	linker	UNP Q9NRM6
C	356	SER	-	linker	UNP Q9NRM6
C	357	GLY	-	linker	UNP Q9NRM6
C	358	GLY	-	linker	UNP Q9NRM6
C	359	GLY	-	linker	UNP Q9NRM6
C	360	SER	-	linker	UNP Q9NRM6
D	184	GLY	-	expression tag	UNP Q9NRM6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	185	PRO	-	expression tag	UNP Q9NRM6
D	186	LEU	-	expression tag	UNP Q9NRM6
D	187	GLU	-	expression tag	UNP Q9NRM6
D	344	GLN	-	linker	UNP Q9NRM6
D	345	GLY	-	linker	UNP Q9NRM6
D	346	GLY	-	linker	UNP Q9NRM6
D	347	GLY	-	linker	UNP Q9NRM6
D	348	SER	-	linker	UNP Q9NRM6
D	349	GLY	-	linker	UNP Q9NRM6
D	350	GLY	-	linker	UNP Q9NRM6
D	351	GLY	-	linker	UNP Q9NRM6
D	352	SER	-	linker	UNP Q9NRM6
D	353	GLY	-	linker	UNP Q9NRM6
D	354	GLY	-	linker	UNP Q9NRM6
D	355	GLY	-	linker	UNP Q9NRM6
D	356	SER	-	linker	UNP Q9NRM6
D	357	GLY	-	linker	UNP Q9NRM6
D	358	GLY	-	linker	UNP Q9NRM6
D	359	GLY	-	linker	UNP Q9NRM6
D	360	SER	-	linker	UNP Q9NRM6

- Molecule 2 is a protein called E3 ubiquitin ligase TRAF3IP2.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	E	177	Total	C	H	N	O	S	0	0
			2969	953	1502	249	258	7		
2	F	177	Total	C	H	N	O	S	0	0
			2969	953	1502	249	258	7		
2	G	177	Total	C	H	N	O	S	0	0
			2970	953	1503	249	258	7		
2	H	177	Total	C	H	N	O	S	0	0
			2970	953	1503	249	258	7		
2	I	177	Total	C	H	N	O	S	0	0
			2970	953	1503	249	258	7		
2	J	177	Total	C	H	N	O	S	0	0
			2970	953	1503	249	258	7		
2	K	177	Total	C	H	N	O	S	0	0
			2969	953	1502	249	258	7		
2	L	177	Total	C	H	N	O	S	0	0
			2970	953	1503	249	258	7		
2	M	177	Total	C	H	N	O	S	0	0
			2970	953	1503	249	258	7		

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Mol	Chain	Residues	Atoms						AltConf	Trace
2	N	177	Total	C	H	N	O	S	0	0
			2970	953	1503	249	258	7		
2	O	177	Total	C	H	N	O	S	0	0
			2970	953	1503	249	258	7		
2	P	177	Total	C	H	N	O	S	0	0
			2970	953	1503	249	258	7		
2	Q	171	Total	C	H	N	O	S	0	0
			2883	928	1457	242	249	7		
2	R	161	Total	C	H	N	O	S	0	0
			2737	882	1388	230	230	7		
2	S	143	Total	C	H	N	O	S	0	0
			2437	787	1242	205	196	7		

There are 75 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	368	GLY	-	expression tag	UNP O43734
E	369	PRO	-	expression tag	UNP O43734
E	370	LEU	-	expression tag	UNP O43734
E	371	GLU	-	expression tag	UNP O43734
E	558	PHE	TYR	conflict	UNP O43734
F	368	GLY	-	expression tag	UNP O43734
F	369	PRO	-	expression tag	UNP O43734
F	370	LEU	-	expression tag	UNP O43734
F	371	GLU	-	expression tag	UNP O43734
F	558	PHE	TYR	conflict	UNP O43734
G	368	GLY	-	expression tag	UNP O43734
G	369	PRO	-	expression tag	UNP O43734
G	370	LEU	-	expression tag	UNP O43734
G	371	GLU	-	expression tag	UNP O43734
G	558	PHE	TYR	conflict	UNP O43734
H	368	GLY	-	expression tag	UNP O43734
H	369	PRO	-	expression tag	UNP O43734
H	370	LEU	-	expression tag	UNP O43734
H	371	GLU	-	expression tag	UNP O43734
H	558	PHE	TYR	conflict	UNP O43734
I	368	GLY	-	expression tag	UNP O43734
I	369	PRO	-	expression tag	UNP O43734
I	370	LEU	-	expression tag	UNP O43734
I	371	GLU	-	expression tag	UNP O43734
I	558	PHE	TYR	conflict	UNP O43734
J	368	GLY	-	expression tag	UNP O43734
J	369	PRO	-	expression tag	UNP O43734

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Chain	Residue	Modelled	Actual	Comment	Reference
J	370	LEU	-	expression tag	UNP O43734
J	371	GLU	-	expression tag	UNP O43734
J	558	PHE	TYR	conflict	UNP O43734
K	368	GLY	-	expression tag	UNP O43734
K	369	PRO	-	expression tag	UNP O43734
K	370	LEU	-	expression tag	UNP O43734
K	371	GLU	-	expression tag	UNP O43734
K	558	PHE	TYR	conflict	UNP O43734
L	368	GLY	-	expression tag	UNP O43734
L	369	PRO	-	expression tag	UNP O43734
L	370	LEU	-	expression tag	UNP O43734
L	371	GLU	-	expression tag	UNP O43734
L	558	PHE	TYR	conflict	UNP O43734
M	368	GLY	-	expression tag	UNP O43734
M	369	PRO	-	expression tag	UNP O43734
M	370	LEU	-	expression tag	UNP O43734
M	371	GLU	-	expression tag	UNP O43734
M	558	PHE	TYR	conflict	UNP O43734
N	368	GLY	-	expression tag	UNP O43734
N	369	PRO	-	expression tag	UNP O43734
N	370	LEU	-	expression tag	UNP O43734
N	371	GLU	-	expression tag	UNP O43734
N	558	PHE	TYR	conflict	UNP O43734
O	368	GLY	-	expression tag	UNP O43734
O	369	PRO	-	expression tag	UNP O43734
O	370	LEU	-	expression tag	UNP O43734
O	371	GLU	-	expression tag	UNP O43734
O	558	PHE	TYR	conflict	UNP O43734
P	368	GLY	-	expression tag	UNP O43734
P	369	PRO	-	expression tag	UNP O43734
P	370	LEU	-	expression tag	UNP O43734
P	371	GLU	-	expression tag	UNP O43734
P	558	PHE	TYR	conflict	UNP O43734
Q	368	GLY	-	expression tag	UNP O43734
Q	369	PRO	-	expression tag	UNP O43734
Q	370	LEU	-	expression tag	UNP O43734
Q	371	GLU	-	expression tag	UNP O43734
Q	558	PHE	TYR	conflict	UNP O43734
R	368	GLY	-	expression tag	UNP O43734
R	369	PRO	-	expression tag	UNP O43734
R	370	LEU	-	expression tag	UNP O43734
R	371	GLU	-	expression tag	UNP O43734

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Chain	Residue	Modelled	Actual	Comment	Reference
R	558	PHE	TYR	conflict	UNP O43734
S	368	GLY	-	expression tag	UNP O43734
S	369	PRO	-	expression tag	UNP O43734
S	370	LEU	-	expression tag	UNP O43734
S	371	GLU	-	expression tag	UNP O43734
S	558	PHE	TYR	conflict	UNP O43734

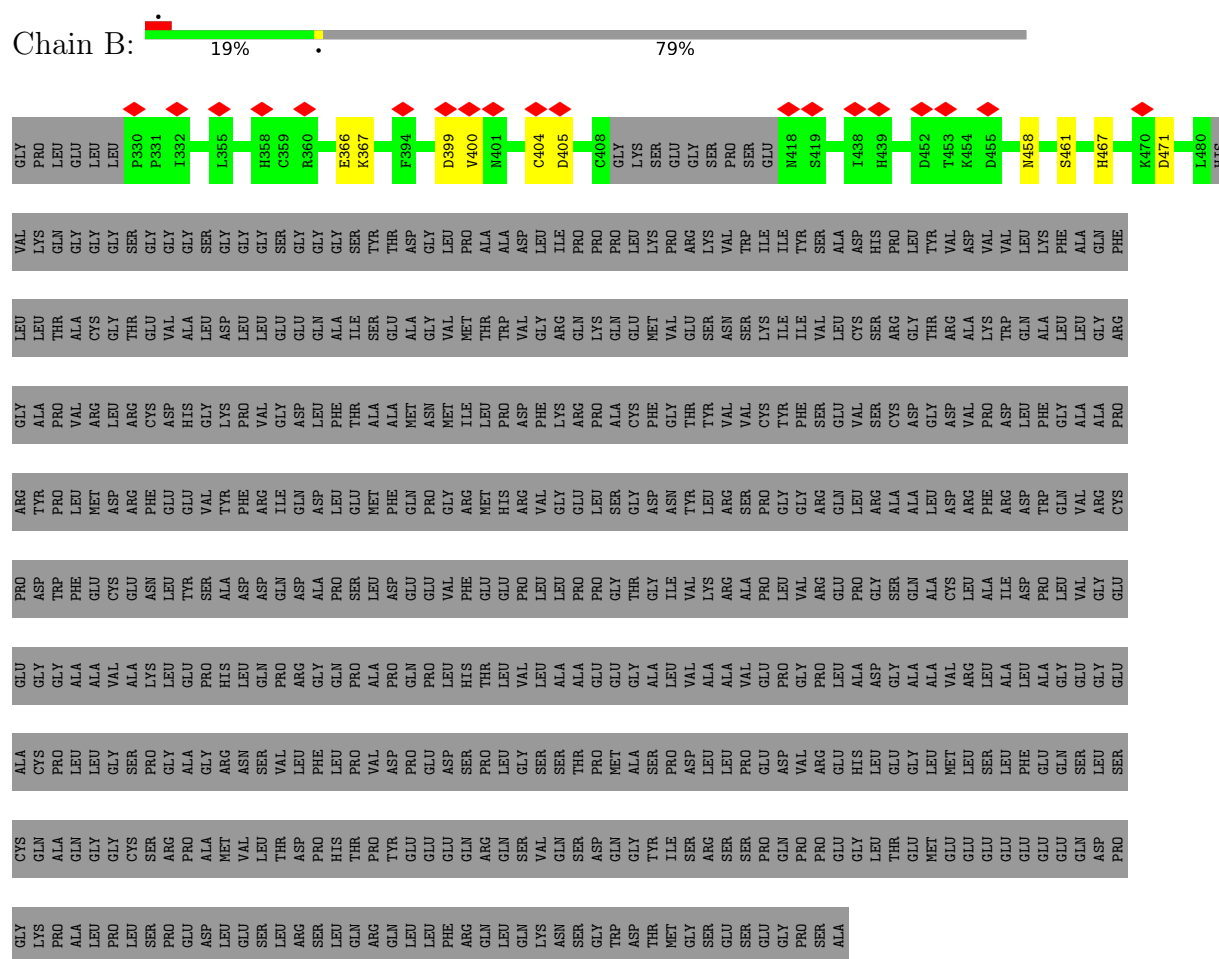
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
3	B	1	Total Zn 1 1	0
3	A	1	Total Zn 1 1	0

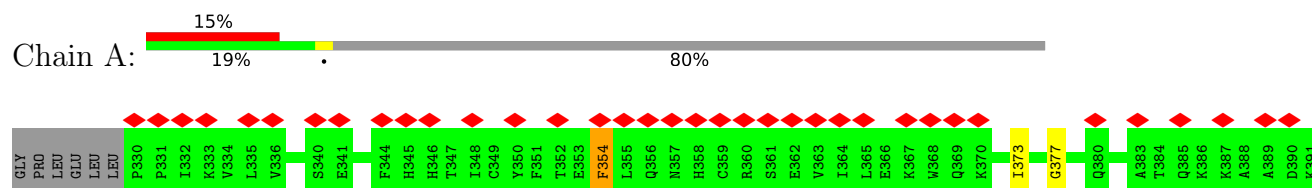
3 Residue-property plots

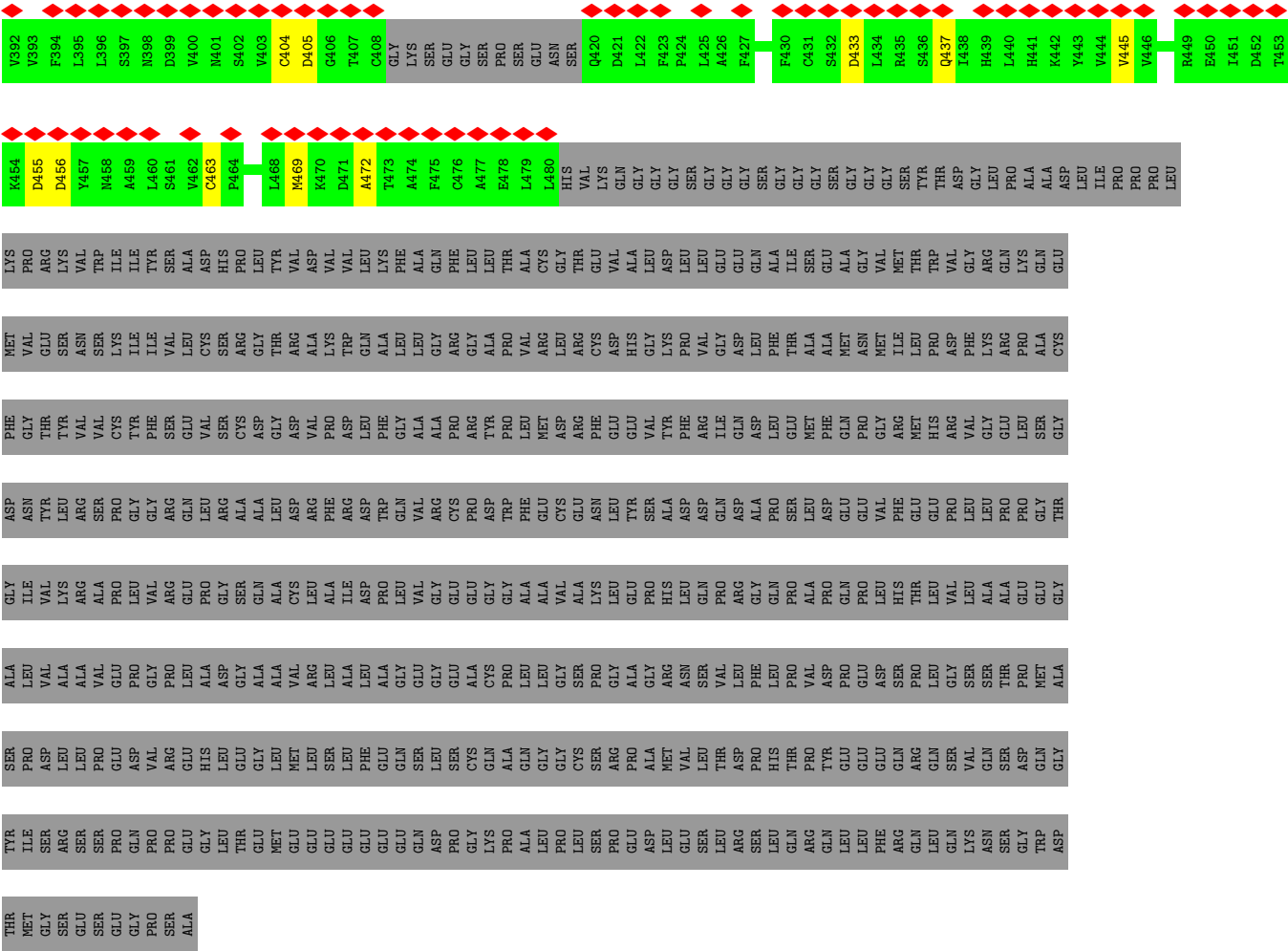
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Interleukin-17 receptor B, Interleukin-17 receptor A

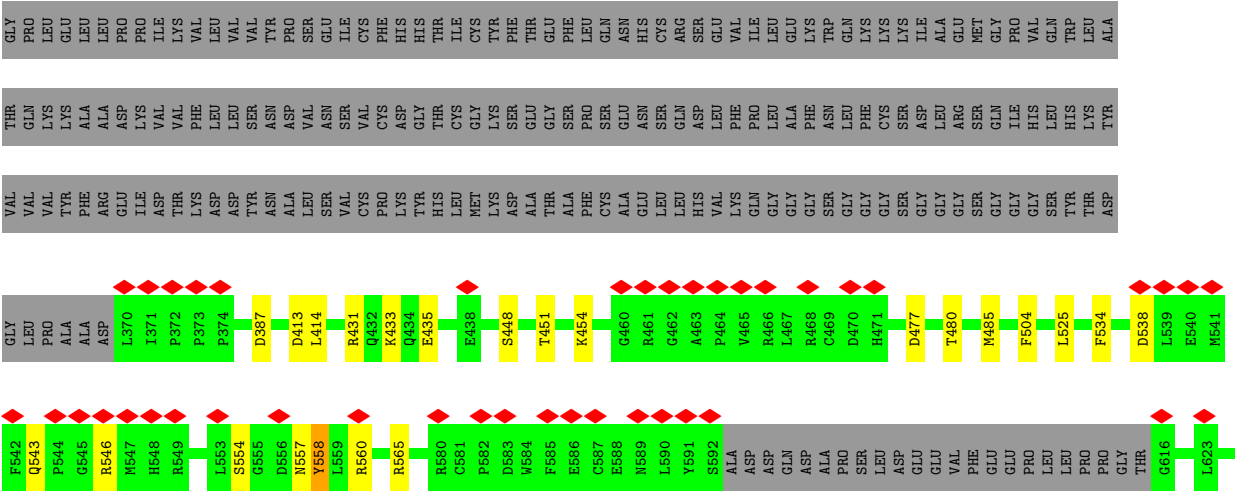


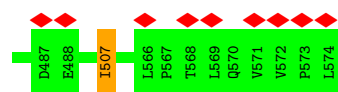
- Molecule 1: Interleukin-17 receptor B, Interleukin-17 receptor A



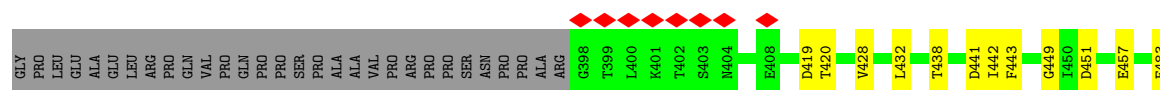
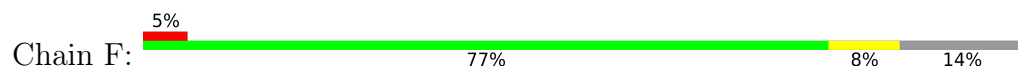


● Molecule 1: Interleukin-17 receptor B,Interleukin-17 receptor A

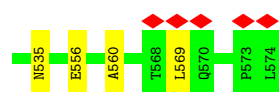
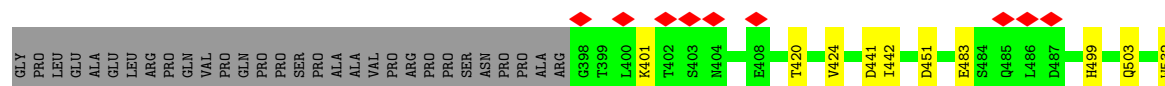
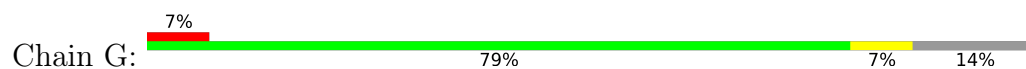




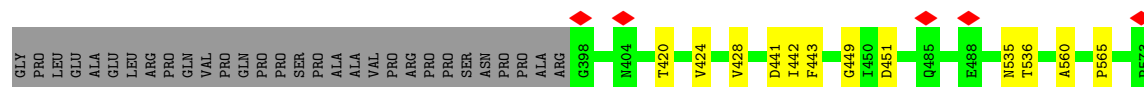
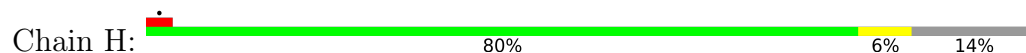
- Molecule 2: E3 ubiquitin ligase TRAF3IP2



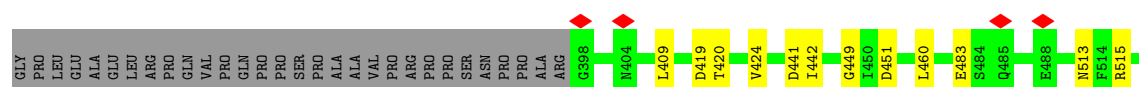
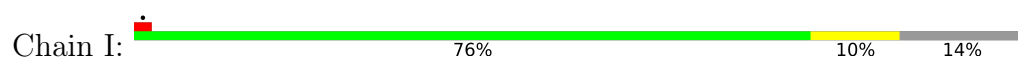
- Molecule 2: E3 ubiquitin ligase TRAF3IP2



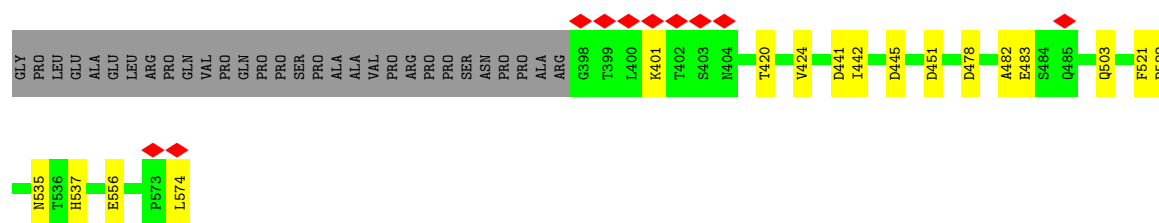
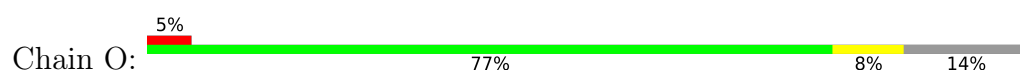
- Molecule 2: E3 ubiquitin ligase TRAF3IP2



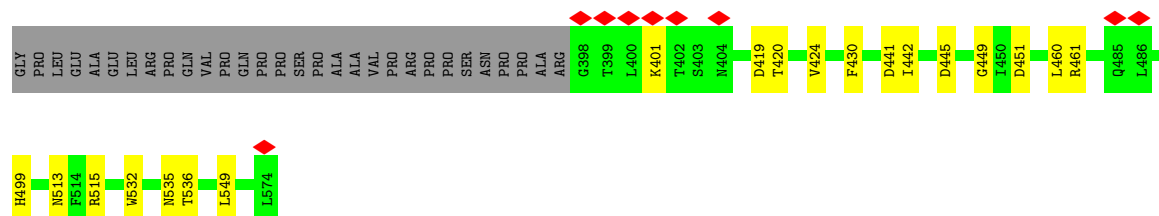
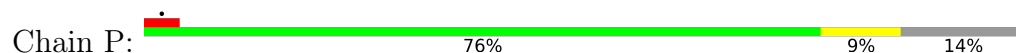
- Molecule 2: E3 ubiquitin ligase TRAF3IP2



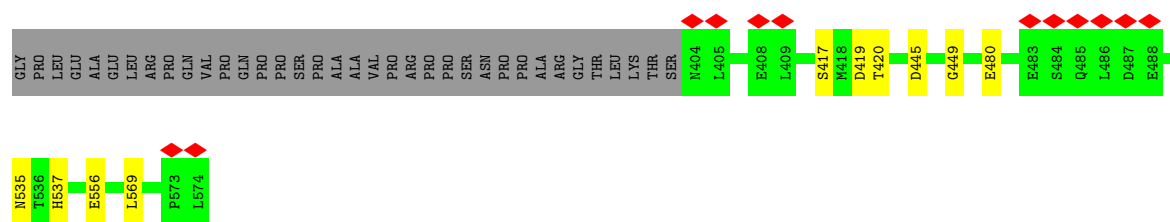
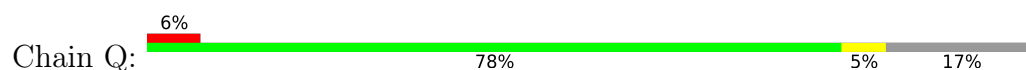
- Molecule 2: E3 ubiquitin ligase TRAF3IP2



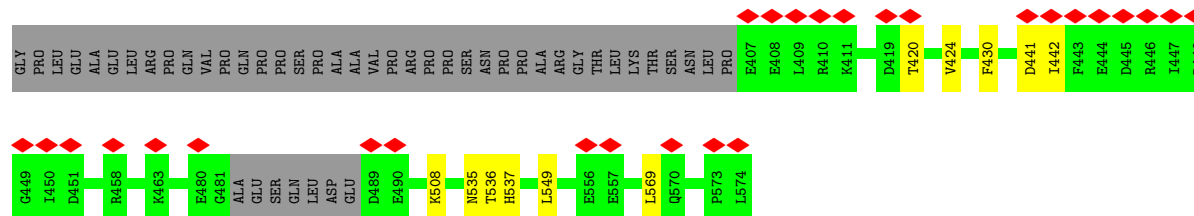
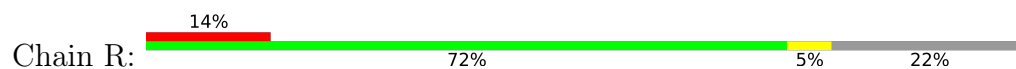
- Molecule 2: E3 ubiquitin ligase TRAF3IP2



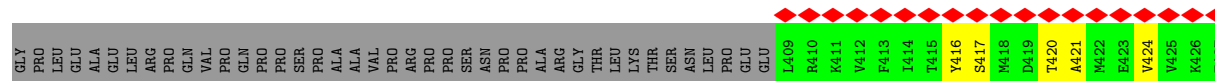
- Molecule 2: E3 ubiquitin ligase TRAF3IP2

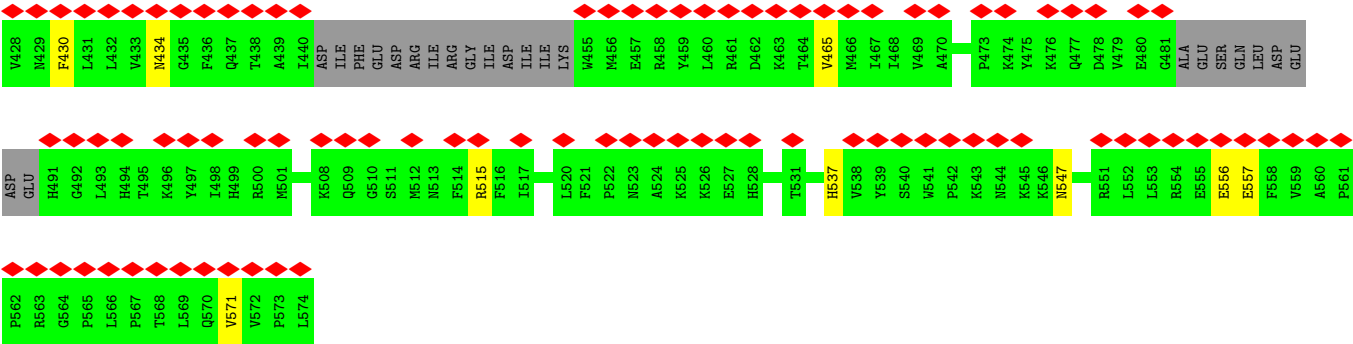


- Molecule 2: E3 ubiquitin ligase TRAF3IP2



- Molecule 2: E3 ubiquitin ligase TRAF3IP2





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	157029	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	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	33.333	Depositor
Minimum map value	-12.773	Depositor
Average map value	0.036	Depositor
Map value standard deviation	0.582	Depositor
Recommended contour level	5	Depositor
Map size (Å)	428.00003, 428.00003, 428.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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	0.10	0/1168	0.28	0/1582
1	B	0.11	0/1182	0.30	0/1601
1	C	0.14	0/2513	0.32	0/3415
1	D	0.15	0/2449	0.32	0/3331
2	E	0.18	0/1503	0.31	0/2032
2	F	0.22	0/1503	0.32	0/2032
2	G	0.22	0/1503	0.33	0/2032
2	H	0.24	0/1503	0.34	0/2032
2	I	0.22	0/1503	0.33	0/2032
2	J	0.21	0/1503	0.32	0/2032
2	K	0.21	0/1503	0.33	0/2032
2	L	0.23	0/1503	0.34	0/2032
2	M	0.22	0/1503	0.34	0/2032
2	N	0.22	0/1503	0.33	0/2032
2	O	0.21	0/1503	0.32	0/2032
2	P	0.19	0/1503	0.32	0/2032
2	Q	0.15	0/1462	0.31	0/1977
2	R	0.13	0/1383	0.29	0/1867
2	S	0.10	0/1227	0.27	0/1657
All	All	0.19	0/29420	0.32	0/39814

There are no bond length outliers.

There are no bond angle outliers.

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	1139	1132	1131	7	0
1	B	1153	1143	1142	5	0
1	C	2453	2449	2447	24	0
1	D	2389	2395	2393	27	0
2	E	1467	1502	1500	12	0
2	F	1467	1502	1500	13	0
2	G	1467	1503	1500	11	0
2	H	1467	1503	1500	11	0
2	I	1467	1503	1500	15	0
2	J	1467	1503	1500	10	0
2	K	1467	1502	1500	18	0
2	L	1467	1503	1500	14	0
2	M	1467	1503	1500	10	0
2	N	1467	1503	1500	10	0
2	O	1467	1503	1500	13	0
2	P	1467	1503	1500	13	0
2	Q	1426	1457	1454	9	0
2	R	1349	1388	1384	8	0
2	S	1195	1242	1237	9	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
All	All	28710	29239	29188	181	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 181 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)
2:F:451:ASP:OD1	2:H:535:ASN:ND2	2.06	0.88
2:H:451:ASP:OD1	2:J:535:ASN:ND2	2.07	0.87
2:L:451:ASP:OD1	2:N:535:ASN:ND2	2.07	0.85
2:Q:556:GLU:N	2:Q:556:GLU:OE1	2.17	0.78
2:S:417:SER:O	2:S:421:ALA:N	2.16	0.78

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	136/683 (20%)	134 (98%)	2 (2%)	0	100	100
1	B	138/683 (20%)	134 (97%)	4 (3%)	0	100	100
1	C	316/683 (46%)	304 (96%)	12 (4%)	0	100	100
1	D	305/683 (45%)	290 (95%)	15 (5%)	0	100	100
2	E	175/207 (84%)	173 (99%)	2 (1%)	0	100	100
2	F	175/207 (84%)	171 (98%)	4 (2%)	0	100	100
2	G	175/207 (84%)	172 (98%)	3 (2%)	0	100	100
2	H	175/207 (84%)	173 (99%)	2 (1%)	0	100	100
2	I	175/207 (84%)	170 (97%)	5 (3%)	0	100	100
2	J	175/207 (84%)	172 (98%)	3 (2%)	0	100	100
2	K	175/207 (84%)	171 (98%)	4 (2%)	0	100	100
2	L	175/207 (84%)	171 (98%)	4 (2%)	0	100	100
2	M	175/207 (84%)	167 (95%)	8 (5%)	0	100	100
2	N	175/207 (84%)	171 (98%)	4 (2%)	0	100	100
2	O	175/207 (84%)	168 (96%)	7 (4%)	0	100	100
2	P	175/207 (84%)	172 (98%)	3 (2%)	0	100	100
2	Q	169/207 (82%)	168 (99%)	1 (1%)	0	100	100
2	R	157/207 (76%)	154 (98%)	3 (2%)	0	100	100
2	S	137/207 (66%)	136 (99%)	1 (1%)	0	100	100
All	All	3458/5837 (59%)	3371 (98%)	87 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	129/571 (23%)	128 (99%)	1 (1%)	73	86
1	B	131/571 (23%)	131 (100%)	0	100	100
1	C	255/571 (45%)	254 (100%)	1 (0%)	84	90
1	D	251/571 (44%)	250 (100%)	1 (0%)	84	90
2	E	164/189 (87%)	163 (99%)	1 (1%)	78	88
2	F	164/189 (87%)	164 (100%)	0	100	100
2	G	164/189 (87%)	164 (100%)	0	100	100
2	H	164/189 (87%)	164 (100%)	0	100	100
2	I	164/189 (87%)	164 (100%)	0	100	100
2	J	164/189 (87%)	164 (100%)	0	100	100
2	K	164/189 (87%)	163 (99%)	1 (1%)	78	88
2	L	164/189 (87%)	164 (100%)	0	100	100
2	M	164/189 (87%)	164 (100%)	0	100	100
2	N	164/189 (87%)	164 (100%)	0	100	100
2	O	164/189 (87%)	164 (100%)	0	100	100
2	P	164/189 (87%)	164 (100%)	0	100	100
2	Q	159/189 (84%)	159 (100%)	0	100	100
2	R	150/189 (79%)	149 (99%)	1 (1%)	76	86
2	S	133/189 (70%)	133 (100%)	0	100	100
All	All	3176/5119 (62%)	3170 (100%)	6 (0%)	85	92

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	507	ILE
2	K	444	GLU
2	R	508	LYS
1	C	558	TYR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	354	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	547	ASN
2	S	509	GLN
2	K	494	HIS
2	R	499	HIS
2	I	491	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 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.

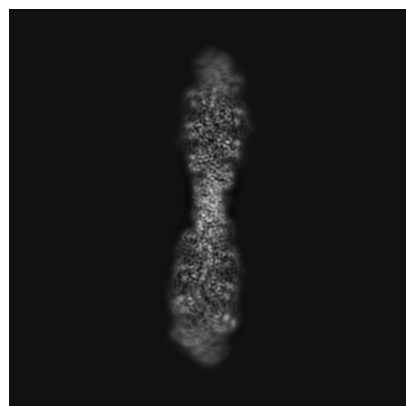
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-70818. These allow visual inspection of the internal detail of the map and identification of artifacts.

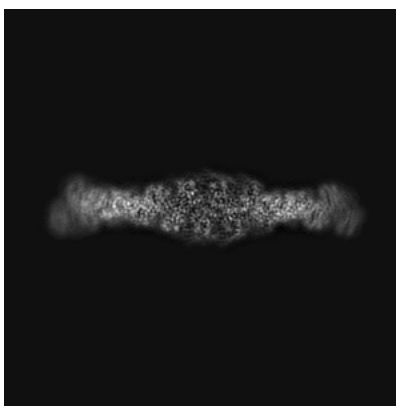
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

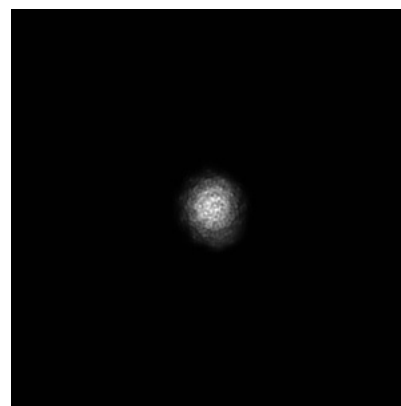
6.1.1 Primary map



X

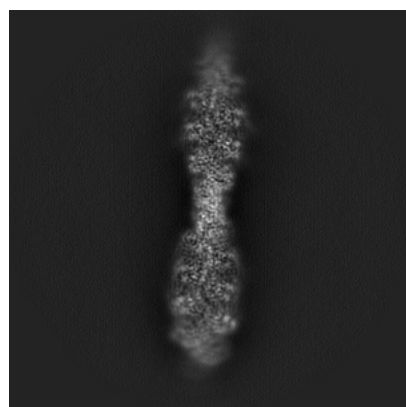


Y

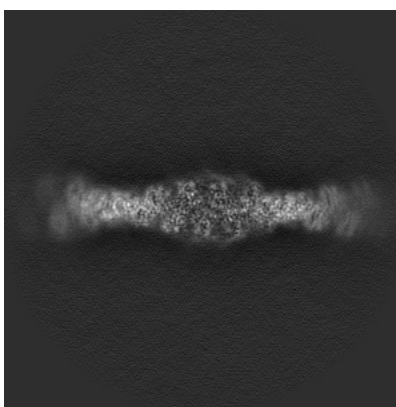


Z

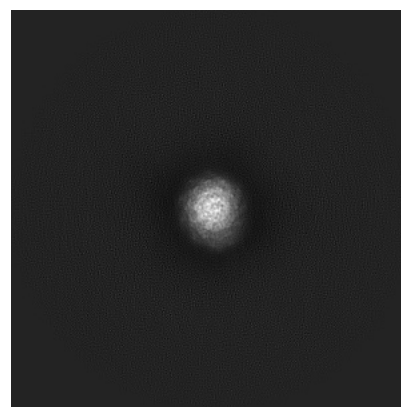
6.1.2 Raw map



X



Y

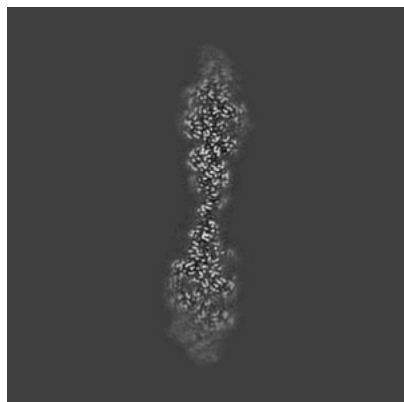


Z

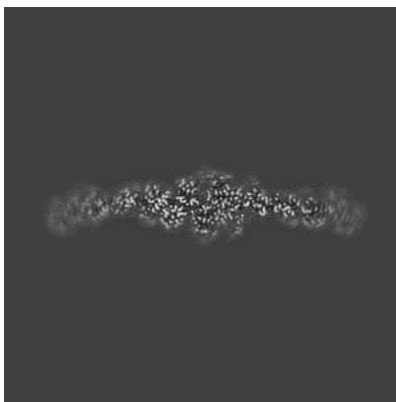
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

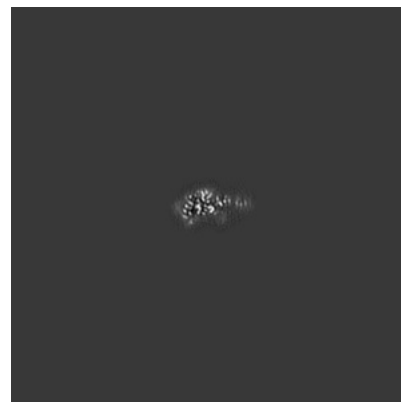
6.2.1 Primary map



X Index: 200

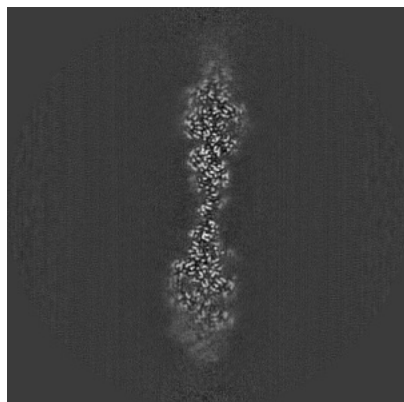


Y Index: 200

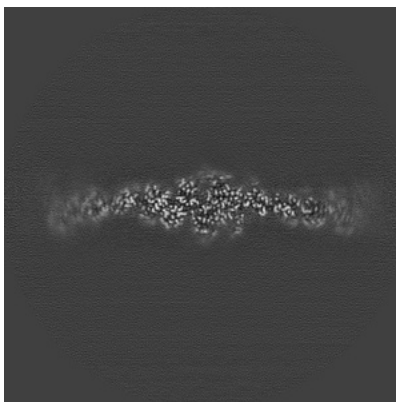


Z Index: 200

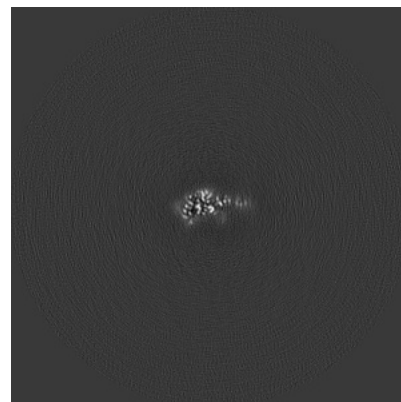
6.2.2 Raw map



X Index: 200



Y Index: 200

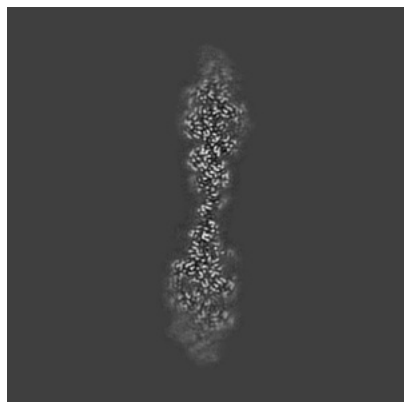


Z Index: 200

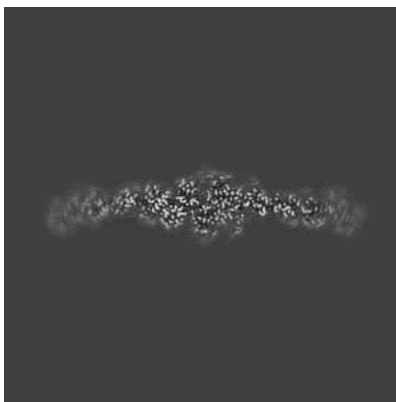
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

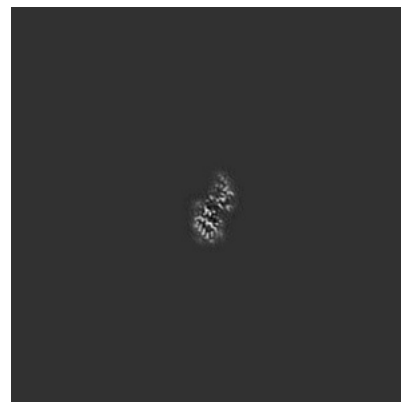
6.3.1 Primary map



X Index: 200

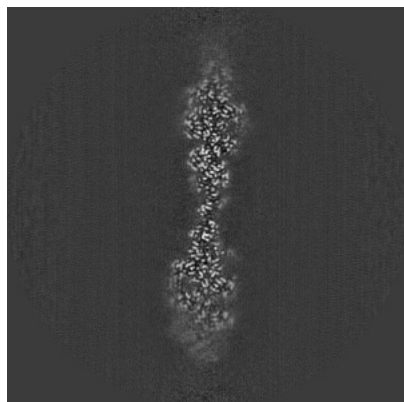


Y Index: 200

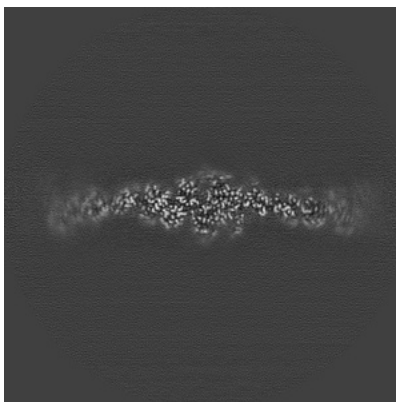


Z Index: 142

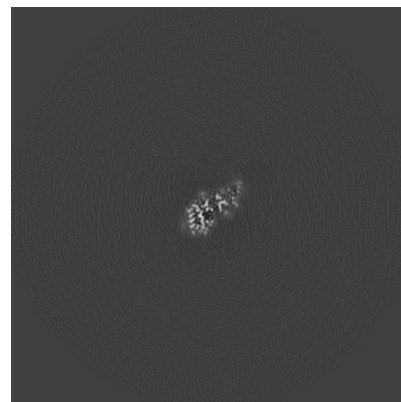
6.3.2 Raw map



X Index: 200



Y Index: 200

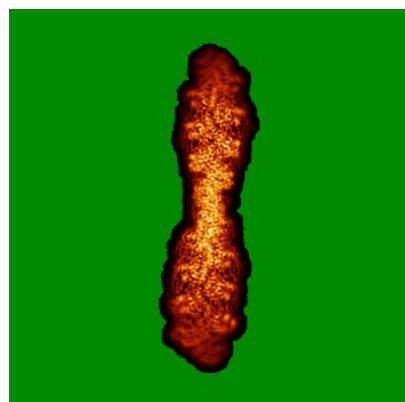


Z Index: 173

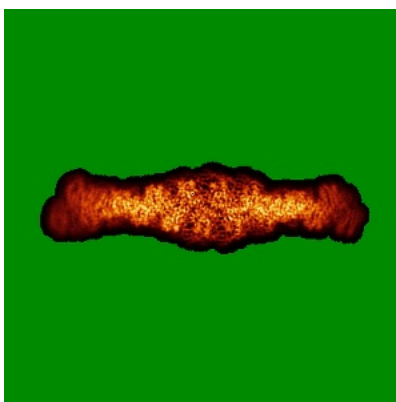
The images above show the largest variance slices of the map in three orthogonal directions.

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

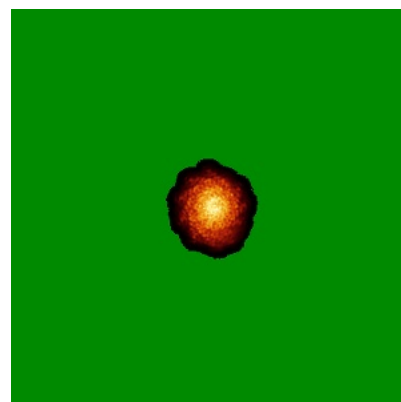
6.4.1 Primary map



X

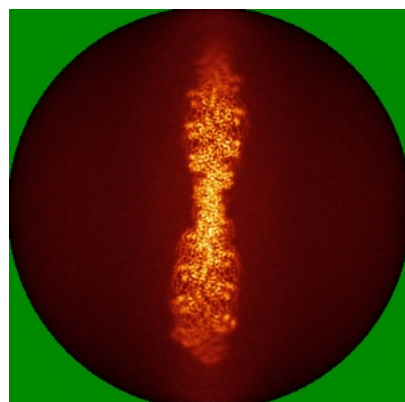


Y

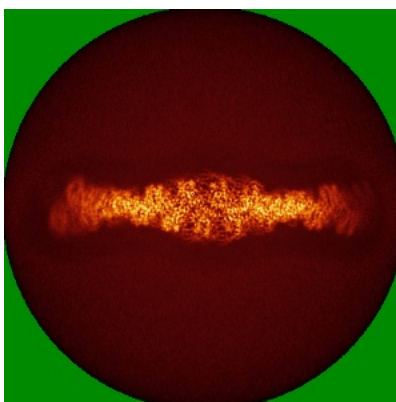


Z

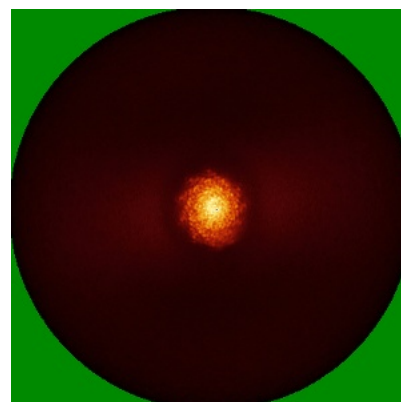
6.4.2 Raw map



X



Y

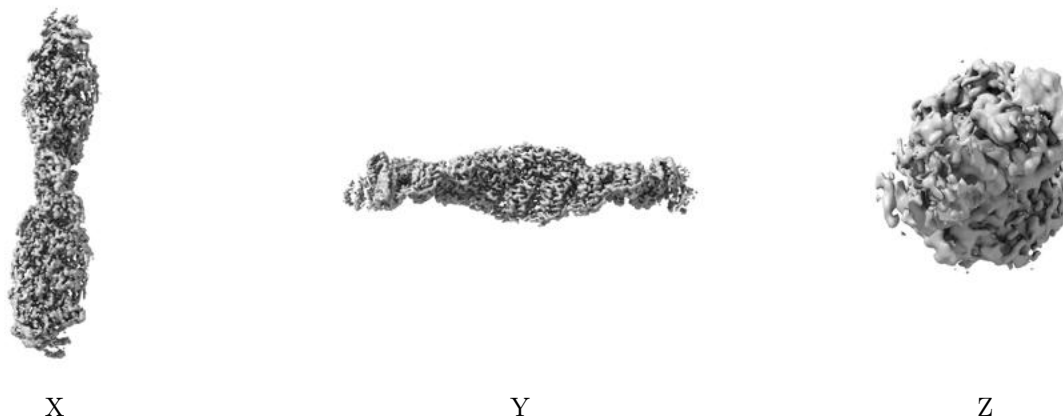


Z

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.

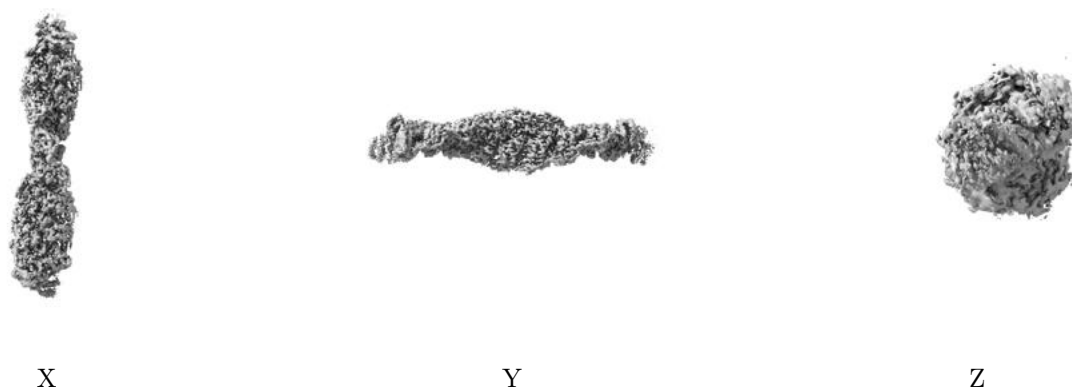
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 5.0. 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.

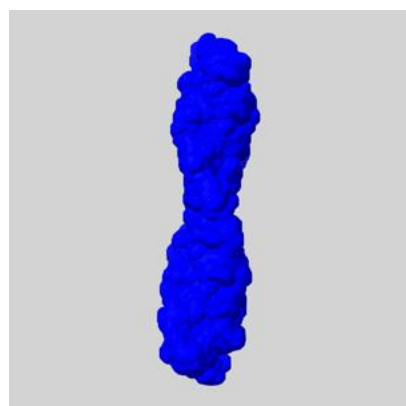
6.6 Mask visualisation [i](#)

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

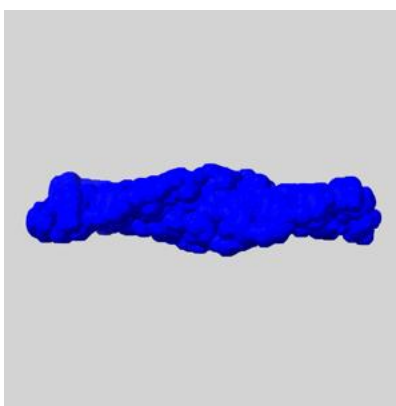
A mask typically either:

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

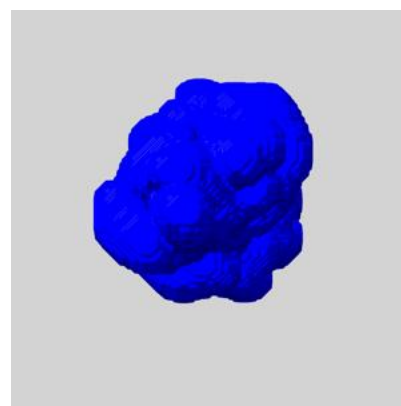
6.6.1 emd_70818_msk_1.map [i](#)



X



Y

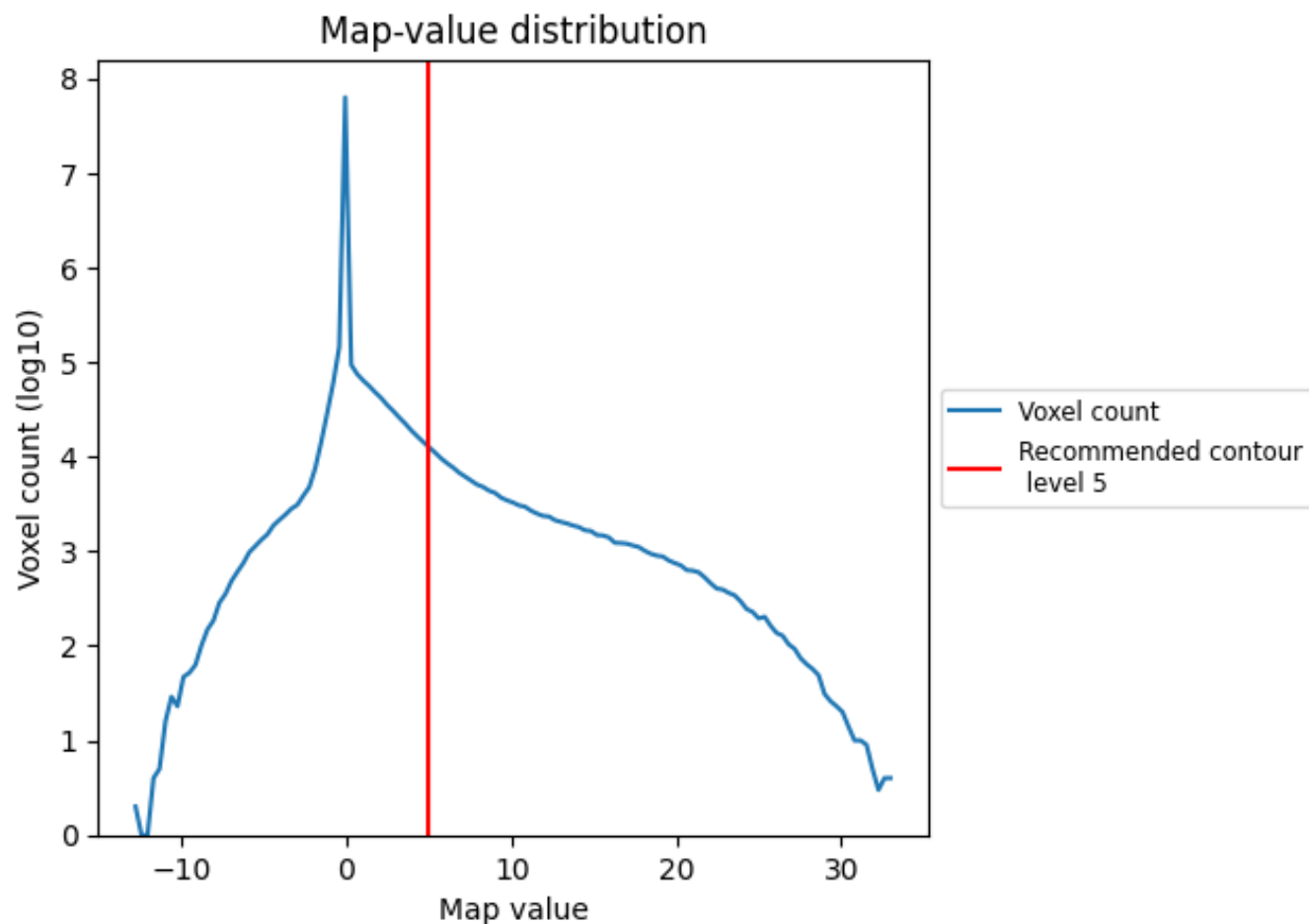


Z

7 Map analysis [i](#)

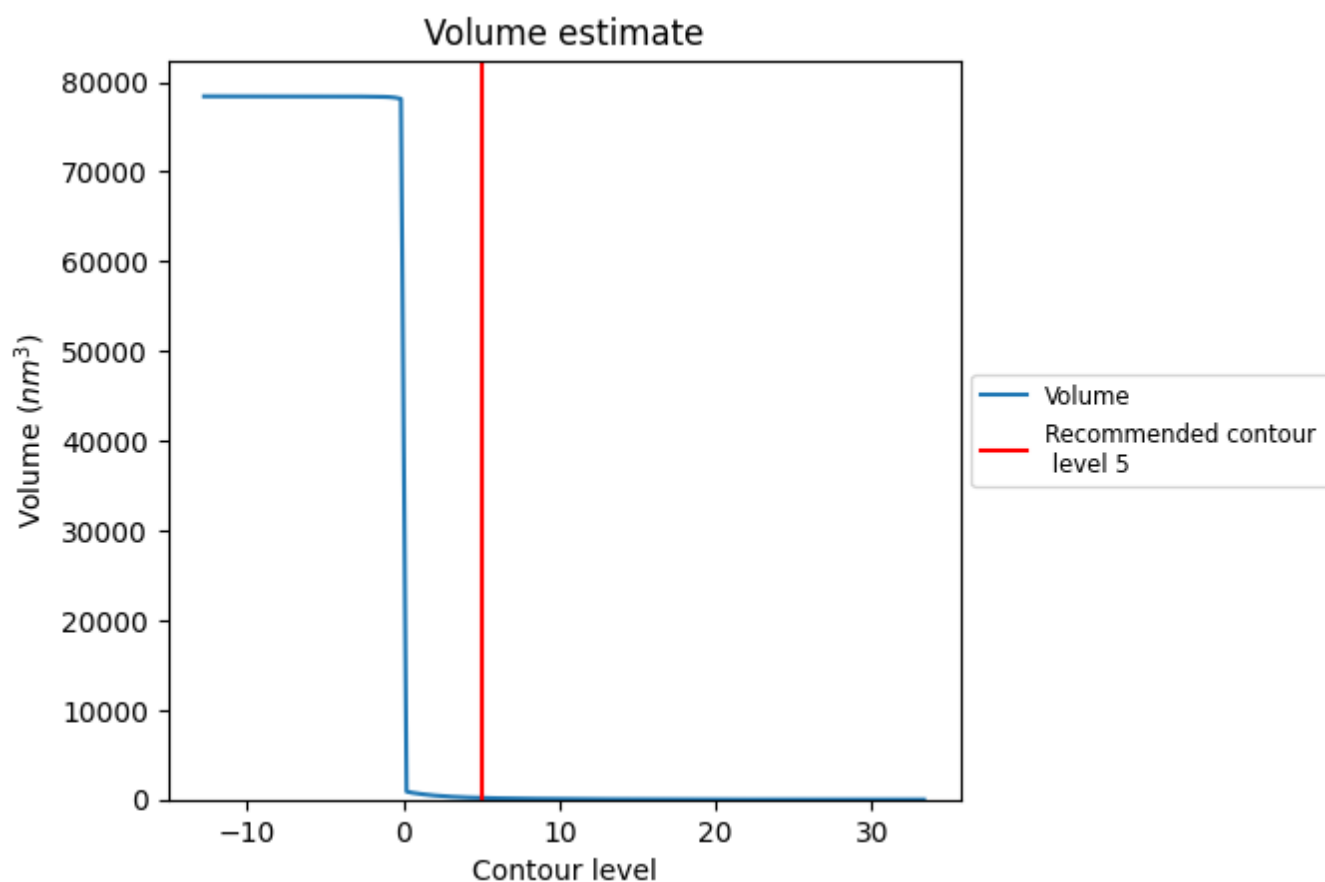
This section contains the results of statistical analysis of the map.

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.

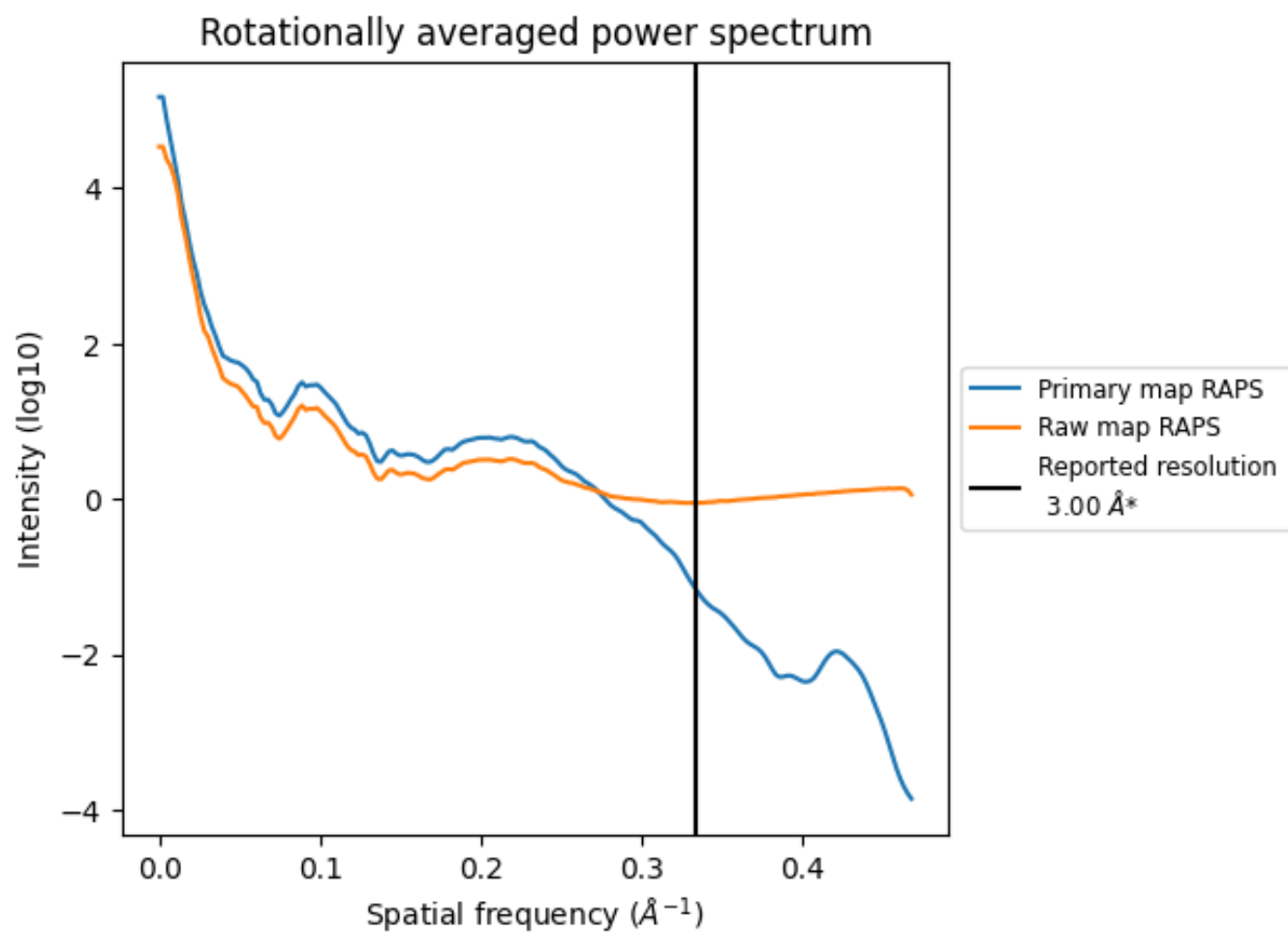
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 183 nm^3 ; this corresponds to an approximate mass of 165 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 ⓘ

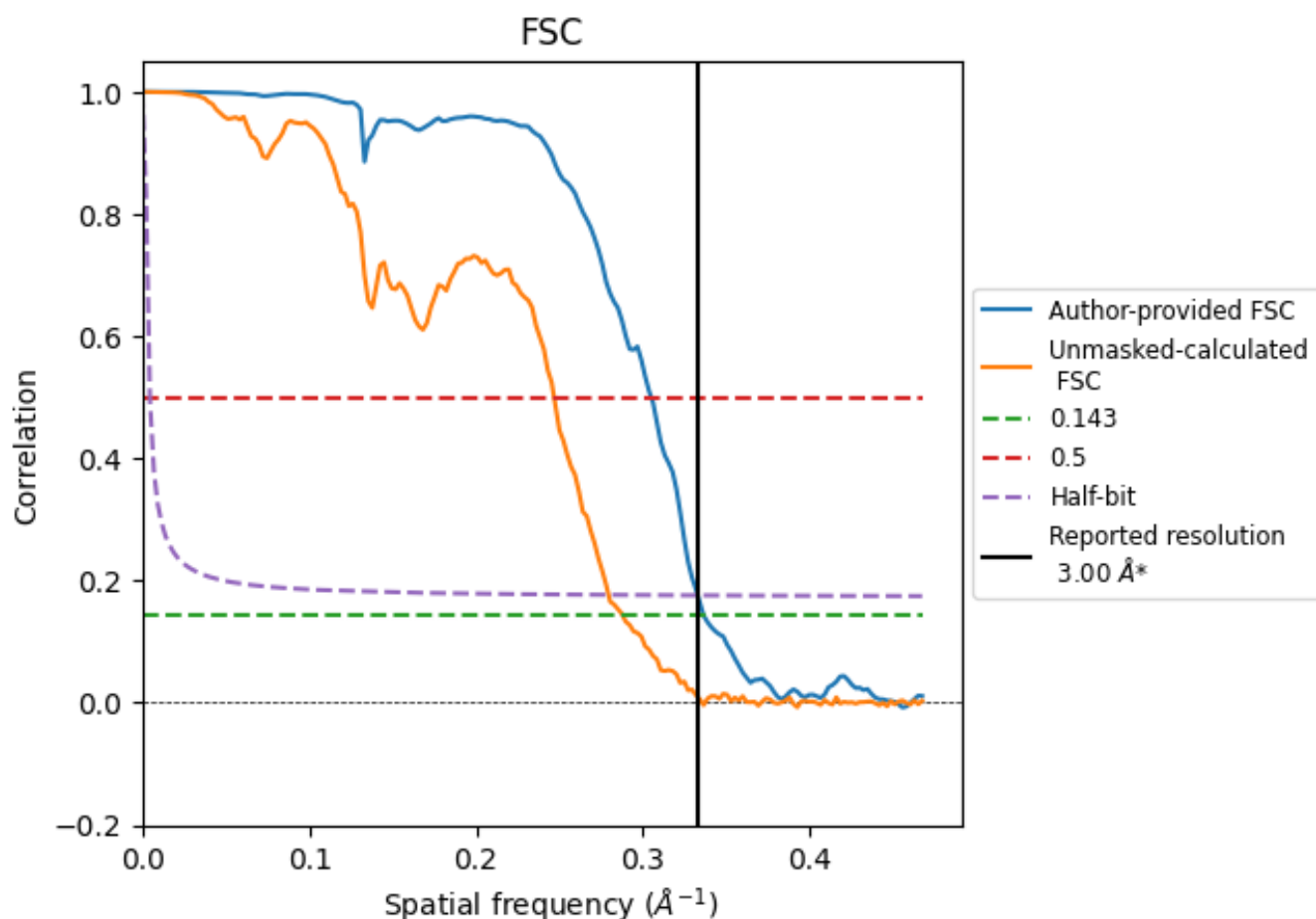


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

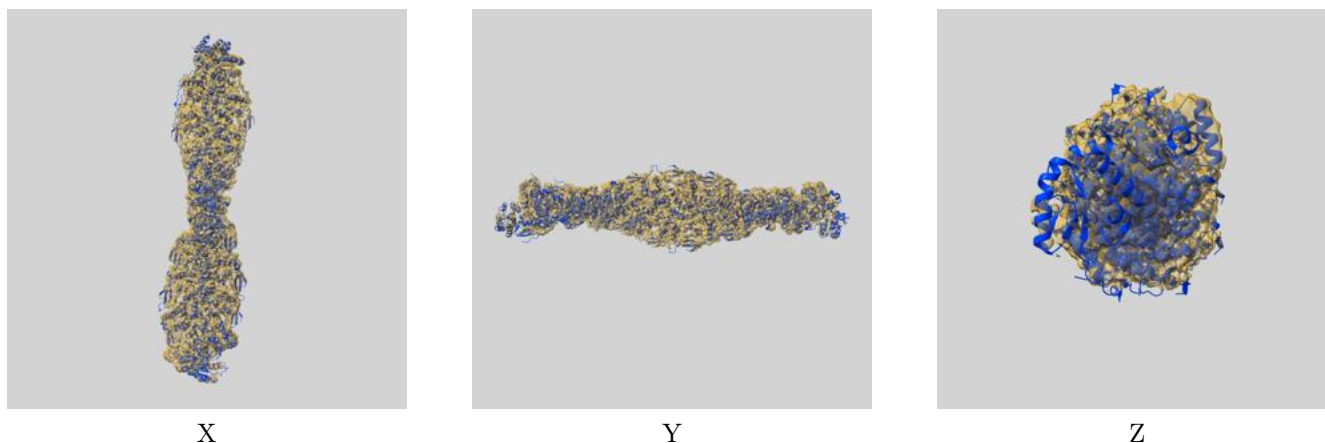
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	2.97	3.28	3.00
Unmasked-calculated*	3.47	4.05	3.58

*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 3.47 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

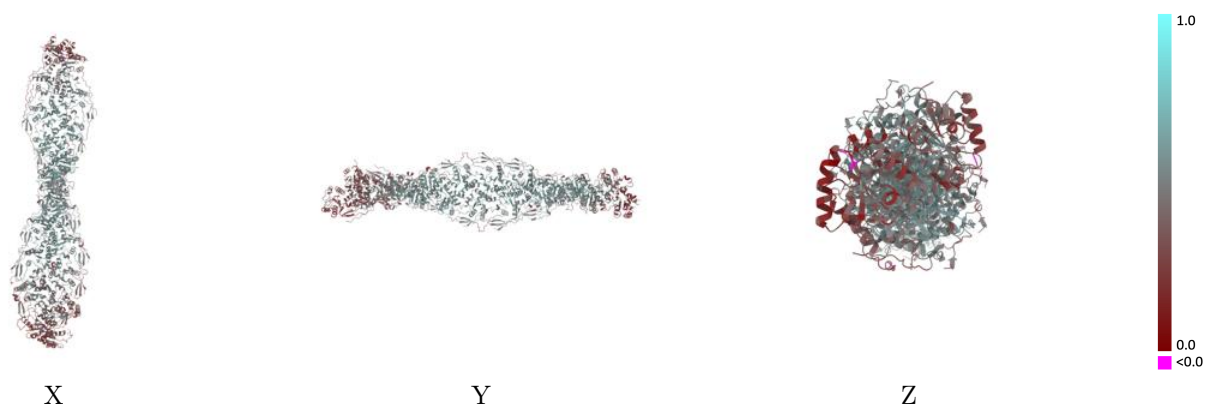
This section contains information regarding the fit between EMDB map EMD-70818 and PDB model 9OT1. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

9.1 Map-model overlay [i](#)



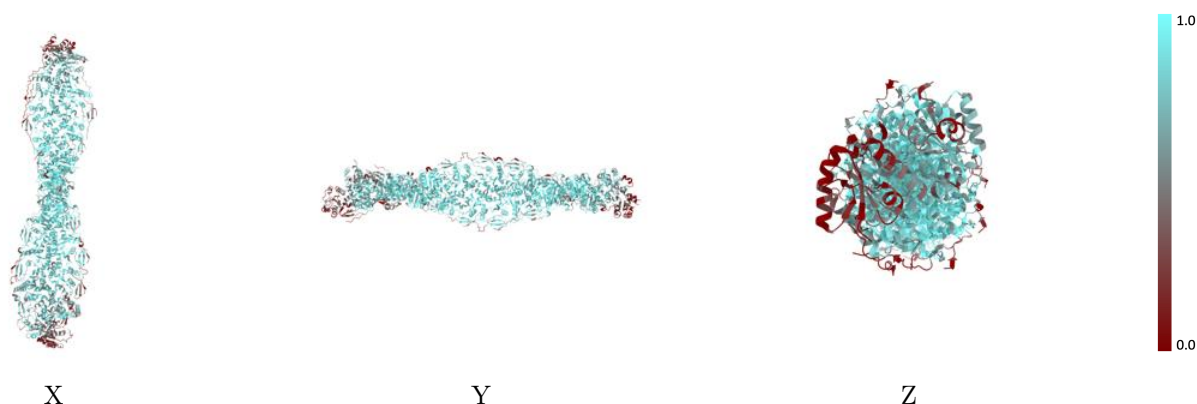
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



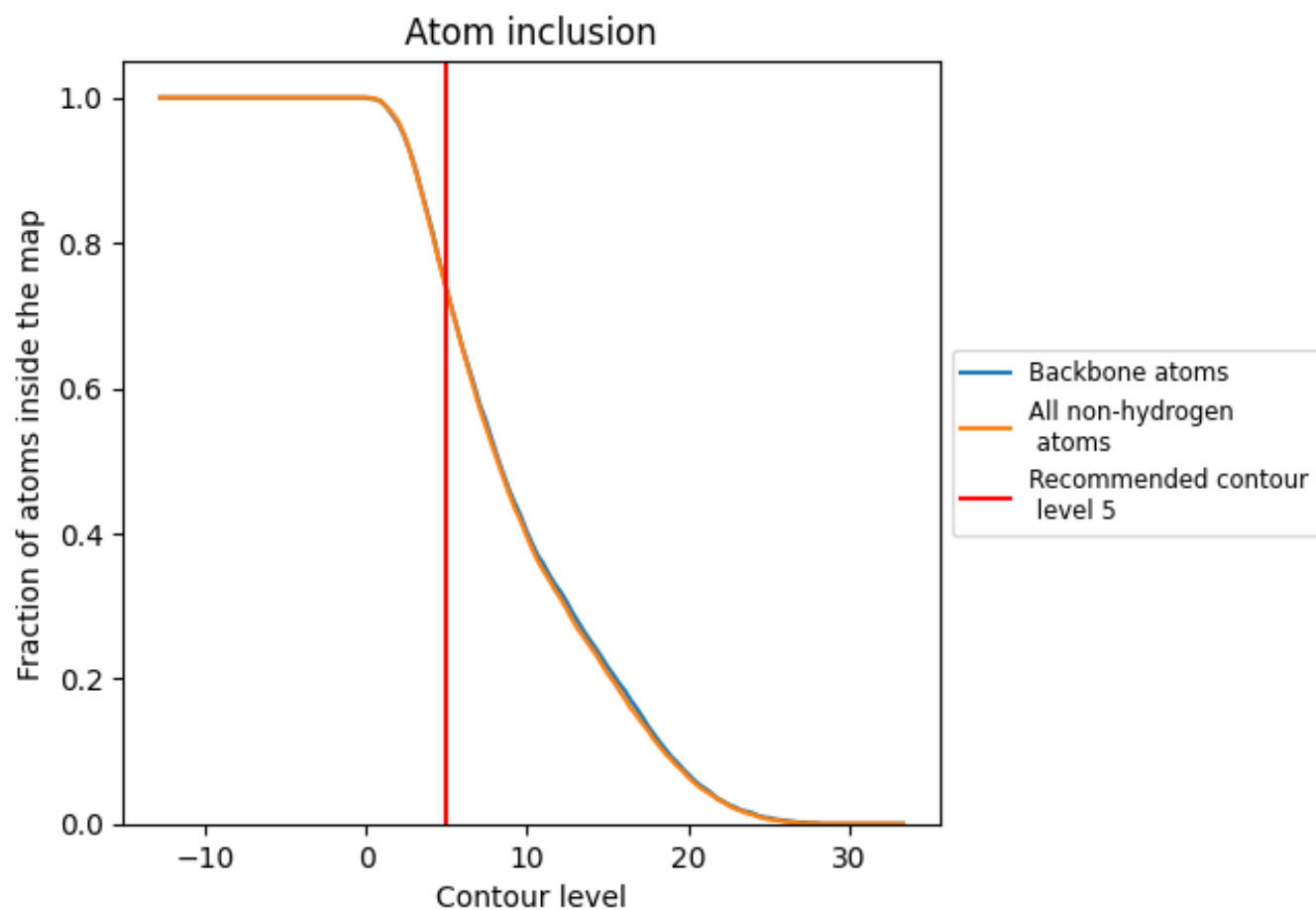
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 74% 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 (5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7350	 0.4690
A	 0.2610	 0.2700
B	 0.6210	 0.3080
C	 0.5900	 0.3710
D	 0.6830	 0.4290
E	 0.7800	 0.4750
F	 0.8460	 0.5280
G	 0.8420	 0.5330
H	 0.8880	 0.5460
I	 0.8660	 0.5460
J	 0.8740	 0.5410
K	 0.8520	 0.5380
L	 0.8760	 0.5430
M	 0.8620	 0.5440
N	 0.8740	 0.5410
O	 0.8590	 0.5380
P	 0.8290	 0.5210
Q	 0.7560	 0.4590
R	 0.6280	 0.3790
S	 0.2250	 0.2660

