wwPDB EM Validation Summary Report (i)

Sep 21, 2026 – 06:50 PM JST

PDB ID	:	8ZJX / pdb_00008zjx
EMDB ID	:	EMD-60159
Title	:	Cryo-EM structure of the full length pAg-bound BTN2A1-BTN3A1-BTN3A2 in complex with Vgamma9-Vdelta2 TCR (MOP genotype)
Authors	:	Xin, W.; Huang, B.; Su, Q.; Zhou, Q.
Deposited on	:	2024-05-15
Resolution	:	3.35 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 (i) 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 (i)) were used in the production of this report:

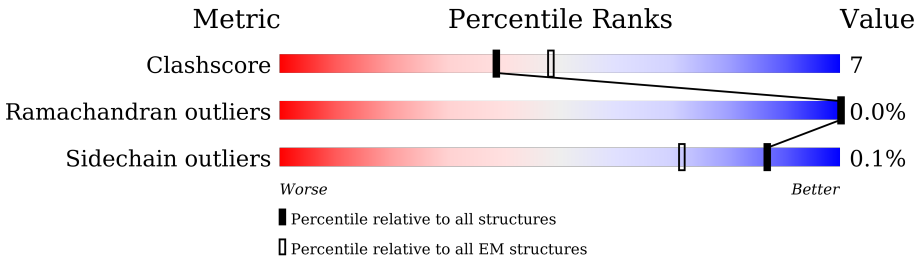
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using 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)	:	2.50

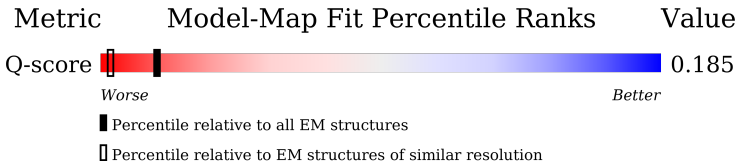
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.35 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	14390 (2.85 - 3.85)

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	534	27% 72% 20% 8%
1	B	534	16% 80% 12% 8%
2	D	332	. 51% 11% 38%
3	E	340	14% 75% 11% 14%

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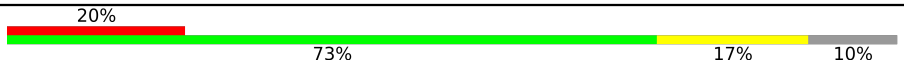
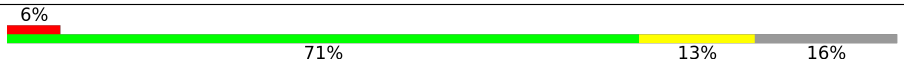
Mol	Chain	Length	Quality of chain
4	F	539	
5	G	267	

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 17386 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 Butyrophilin subfamily 2 member A1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	493	Total	C	N	O	S	0	0
			3946	2503	692	728	23		
1	B	493	Total	C	N	O	S	0	0
			3946	2503	692	728	23		

There are 70 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	MET	-	initiating methionine	UNP Q7KYR7
A	8	ASP	-	expression tag	UNP Q7KYR7
A	9	MET	-	expression tag	UNP Q7KYR7
A	10	ARG	-	expression tag	UNP Q7KYR7
A	11	VAL	-	expression tag	UNP Q7KYR7
A	12	PRO	-	expression tag	UNP Q7KYR7
A	13	ALA	-	expression tag	UNP Q7KYR7
A	14	GLN	-	expression tag	UNP Q7KYR7
A	15	LEU	-	expression tag	UNP Q7KYR7
A	16	LEU	-	expression tag	UNP Q7KYR7
A	17	GLY	-	expression tag	UNP Q7KYR7
A	18	LEU	-	expression tag	UNP Q7KYR7
A	19	LEU	-	expression tag	UNP Q7KYR7
A	20	LEU	-	expression tag	UNP Q7KYR7
A	21	LEU	-	expression tag	UNP Q7KYR7
A	22	TRP	-	expression tag	UNP Q7KYR7
A	23	LEU	-	expression tag	UNP Q7KYR7
A	24	SER	-	expression tag	UNP Q7KYR7
A	25	GLY	-	expression tag	UNP Q7KYR7
A	26	ALA	-	expression tag	UNP Q7KYR7
A	27	ARG	-	expression tag	UNP Q7KYR7
A	28	CYS	-	expression tag	UNP Q7KYR7
A	528	GLY	-	expression tag	UNP Q7KYR7
A	529	SER	-	expression tag	UNP Q7KYR7
A	530	SER	-	expression tag	UNP Q7KYR7
A	531	GLY	-	expression tag	UNP Q7KYR7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	532	MET	-	expression tag	UNP Q7KYR7
A	533	ASP	-	expression tag	UNP Q7KYR7
A	534	TYR	-	expression tag	UNP Q7KYR7
A	535	LYS	-	expression tag	UNP Q7KYR7
A	536	ASP	-	expression tag	UNP Q7KYR7
A	537	ASP	-	expression tag	UNP Q7KYR7
A	538	ASP	-	expression tag	UNP Q7KYR7
A	539	ASP	-	expression tag	UNP Q7KYR7
A	540	LYS	-	expression tag	UNP Q7KYR7
B	7	MET	-	initiating methionine	UNP Q7KYR7
B	8	ASP	-	expression tag	UNP Q7KYR7
B	9	MET	-	expression tag	UNP Q7KYR7
B	10	ARG	-	expression tag	UNP Q7KYR7
B	11	VAL	-	expression tag	UNP Q7KYR7
B	12	PRO	-	expression tag	UNP Q7KYR7
B	13	ALA	-	expression tag	UNP Q7KYR7
B	14	GLN	-	expression tag	UNP Q7KYR7
B	15	LEU	-	expression tag	UNP Q7KYR7
B	16	LEU	-	expression tag	UNP Q7KYR7
B	17	GLY	-	expression tag	UNP Q7KYR7
B	18	LEU	-	expression tag	UNP Q7KYR7
B	19	LEU	-	expression tag	UNP Q7KYR7
B	20	LEU	-	expression tag	UNP Q7KYR7
B	21	LEU	-	expression tag	UNP Q7KYR7
B	22	TRP	-	expression tag	UNP Q7KYR7
B	23	LEU	-	expression tag	UNP Q7KYR7
B	24	SER	-	expression tag	UNP Q7KYR7
B	25	GLY	-	expression tag	UNP Q7KYR7
B	26	ALA	-	expression tag	UNP Q7KYR7
B	27	ARG	-	expression tag	UNP Q7KYR7
B	28	CYS	-	expression tag	UNP Q7KYR7
B	528	GLY	-	expression tag	UNP Q7KYR7
B	529	SER	-	expression tag	UNP Q7KYR7
B	530	SER	-	expression tag	UNP Q7KYR7
B	531	GLY	-	expression tag	UNP Q7KYR7
B	532	MET	-	expression tag	UNP Q7KYR7
B	533	ASP	-	expression tag	UNP Q7KYR7
B	534	TYR	-	expression tag	UNP Q7KYR7
B	535	LYS	-	expression tag	UNP Q7KYR7
B	536	ASP	-	expression tag	UNP Q7KYR7
B	537	ASP	-	expression tag	UNP Q7KYR7
B	538	ASP	-	expression tag	UNP Q7KYR7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	539	ASP	-	expression tag	UNP Q7KYR7
B	540	LYS	-	expression tag	UNP Q7KYR7

- Molecule 2 is a protein called T cell receptor delta variable 2,T cell receptor delta constant 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	205	Total	C	N	O	S	0	0
			1605	1021	269	307	8		

- Molecule 3 is a protein called Butyrophilin subfamily 3 member A2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	293	Total	C	N	O	S	0	0
			2256	1428	384	434	10		

There are 35 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	8	MET	-	initiating methionine	UNP P78410
E	9	ASP	-	expression tag	UNP P78410
E	10	MET	-	expression tag	UNP P78410
E	11	ARG	-	expression tag	UNP P78410
E	12	VAL	-	expression tag	UNP P78410
E	13	PRO	-	expression tag	UNP P78410
E	14	ALA	-	expression tag	UNP P78410
E	15	GLN	-	expression tag	UNP P78410
E	16	LEU	-	expression tag	UNP P78410
E	17	LEU	-	expression tag	UNP P78410
E	18	GLY	-	expression tag	UNP P78410
E	19	LEU	-	expression tag	UNP P78410
E	20	LEU	-	expression tag	UNP P78410
E	21	LEU	-	expression tag	UNP P78410
E	22	LEU	-	expression tag	UNP P78410
E	23	TRP	-	expression tag	UNP P78410
E	24	LEU	-	expression tag	UNP P78410
E	25	SER	-	expression tag	UNP P78410
E	26	GLY	-	expression tag	UNP P78410
E	27	ALA	-	expression tag	UNP P78410
E	28	ARG	-	expression tag	UNP P78410
E	29	CYS	-	expression tag	UNP P78410
E	335	GLY	-	expression tag	UNP P78410

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Chain	Residue	Modelled	Actual	Comment	Reference
E	336	SER	-	expression tag	UNP P78410
E	337	SER	-	expression tag	UNP P78410
E	338	GLY	-	expression tag	UNP P78410
E	339	MET	-	expression tag	UNP P78410
E	340	ASP	-	expression tag	UNP P78410
E	341	TYR	-	expression tag	UNP P78410
E	342	LYS	-	expression tag	UNP P78410
E	343	ASP	-	expression tag	UNP P78410
E	344	ASP	-	expression tag	UNP P78410
E	345	ASP	-	expression tag	UNP P78410
E	346	ASP	-	expression tag	UNP P78410
E	347	LYS	-	expression tag	UNP P78410

- Molecule 4 is a protein called Butyrophilin subfamily 3 member A1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	484	Total	C	N	O	S	0	0
			3832	2438	666	712	16		

There are 55 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	8	MET	-	initiating methionine	UNP O00481
F	9	ASP	-	expression tag	UNP O00481
F	10	MET	-	expression tag	UNP O00481
F	11	ARG	-	expression tag	UNP O00481
F	12	VAL	-	expression tag	UNP O00481
F	13	PRO	-	expression tag	UNP O00481
F	14	ALA	-	expression tag	UNP O00481
F	15	GLN	-	expression tag	UNP O00481
F	16	LEU	-	expression tag	UNP O00481
F	17	LEU	-	expression tag	UNP O00481
F	18	GLY	-	expression tag	UNP O00481
F	19	LEU	-	expression tag	UNP O00481
F	20	LEU	-	expression tag	UNP O00481
F	21	LEU	-	expression tag	UNP O00481
F	22	LEU	-	expression tag	UNP O00481
F	23	TRP	-	expression tag	UNP O00481
F	24	LEU	-	expression tag	UNP O00481
F	25	SER	-	expression tag	UNP O00481
F	26	GLY	-	expression tag	UNP O00481
F	27	ALA	-	expression tag	UNP O00481

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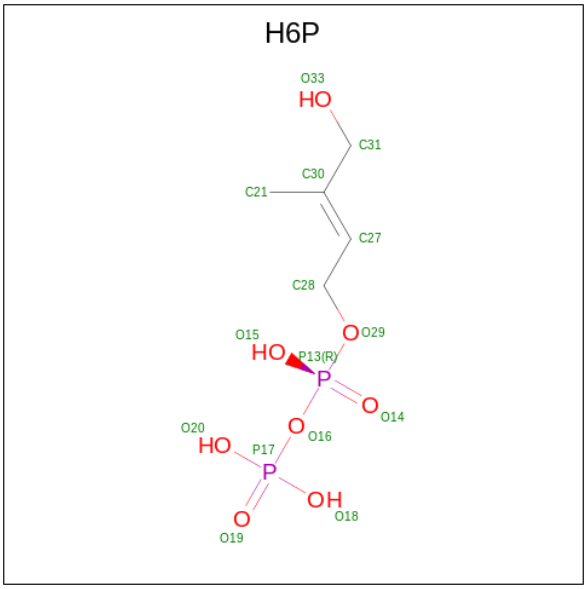
Chain	Residue	Modelled	Actual	Comment	Reference
F	28	ARG	-	expression tag	UNP O00481
F	29	CYS	-	expression tag	UNP O00481
F	514	GLY	-	expression tag	UNP O00481
F	515	SER	-	expression tag	UNP O00481
F	516	SER	-	expression tag	UNP O00481
F	517	GLY	-	expression tag	UNP O00481
F	518	ALA	-	expression tag	UNP O00481
F	519	TRP	-	expression tag	UNP O00481
F	520	SER	-	expression tag	UNP O00481
F	521	HIS	-	expression tag	UNP O00481
F	522	PRO	-	expression tag	UNP O00481
F	523	GLN	-	expression tag	UNP O00481
F	524	PHE	-	expression tag	UNP O00481
F	525	GLU	-	expression tag	UNP O00481
F	526	LYS	-	expression tag	UNP O00481
F	527	GLY	-	expression tag	UNP O00481
F	528	GLY	-	expression tag	UNP O00481
F	529	GLY	-	expression tag	UNP O00481
F	530	SER	-	expression tag	UNP O00481
F	531	GLY	-	expression tag	UNP O00481
F	532	GLY	-	expression tag	UNP O00481
F	533	GLY	-	expression tag	UNP O00481
F	534	SER	-	expression tag	UNP O00481
F	535	GLY	-	expression tag	UNP O00481
F	536	GLY	-	expression tag	UNP O00481
F	537	SER	-	expression tag	UNP O00481
F	538	ALA	-	expression tag	UNP O00481
F	539	TRP	-	expression tag	UNP O00481
F	540	SER	-	expression tag	UNP O00481
F	541	HIS	-	expression tag	UNP O00481
F	542	PRO	-	expression tag	UNP O00481
F	543	GLN	-	expression tag	UNP O00481
F	544	PHE	-	expression tag	UNP O00481
F	545	GLU	-	expression tag	UNP O00481
F	546	LYS	-	expression tag	UNP O00481

- Molecule 5 is a protein called T cell receptor gamma variable 9,T cell receptor gamma constant 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	225	Total	C	N	O	S	0	0
			1786	1141	298	341	6		

- Molecule 6 is (2E)-4-hydroxy-3-methylbut-2-en-1-yl trihydrogen diphosphate (CCD ID: H6P) (formula: $C_5H_{12}O_8P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
6	F	1	15	5	8	2	0

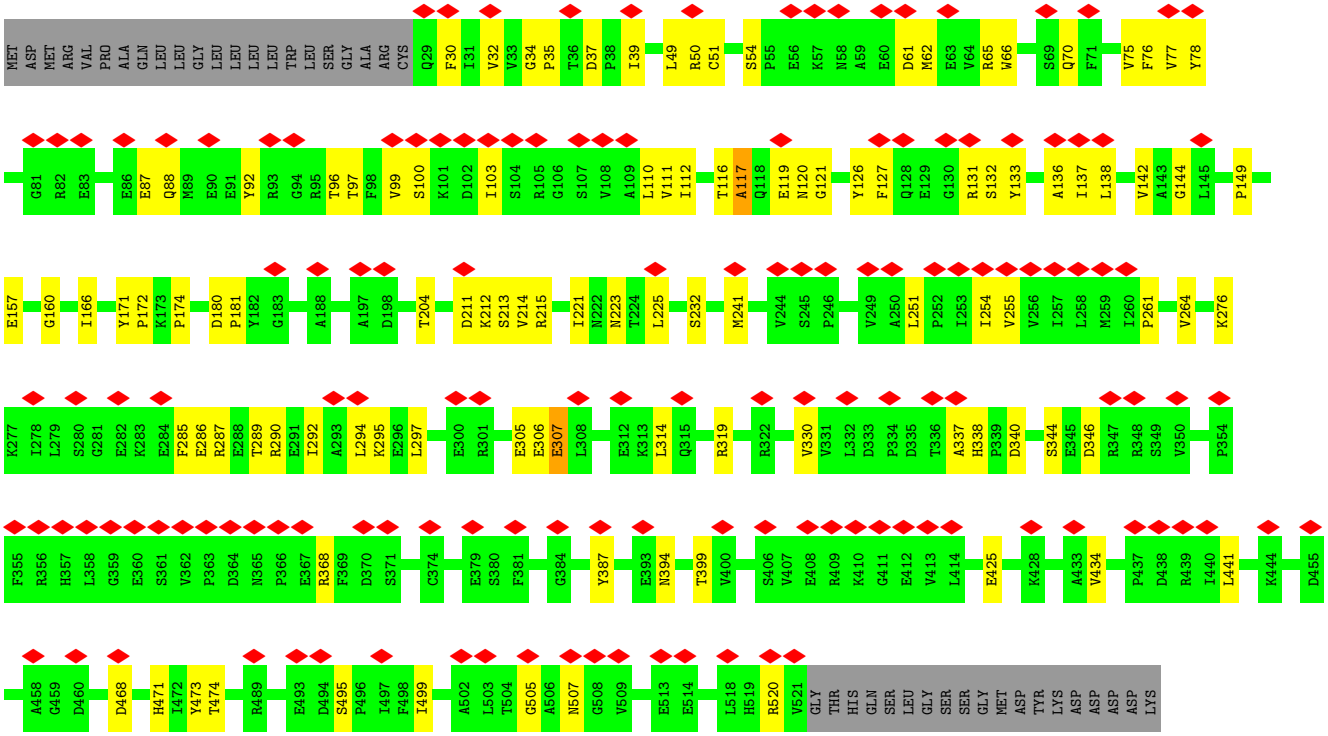
3 Residue-property plots (i)

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

• Molecule 1: Butyrophilin subfamily 2 member A1

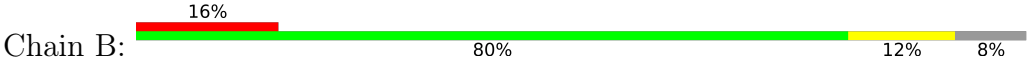
Chain A:

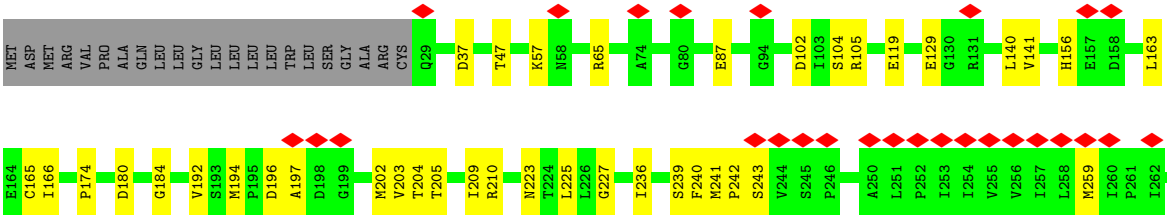


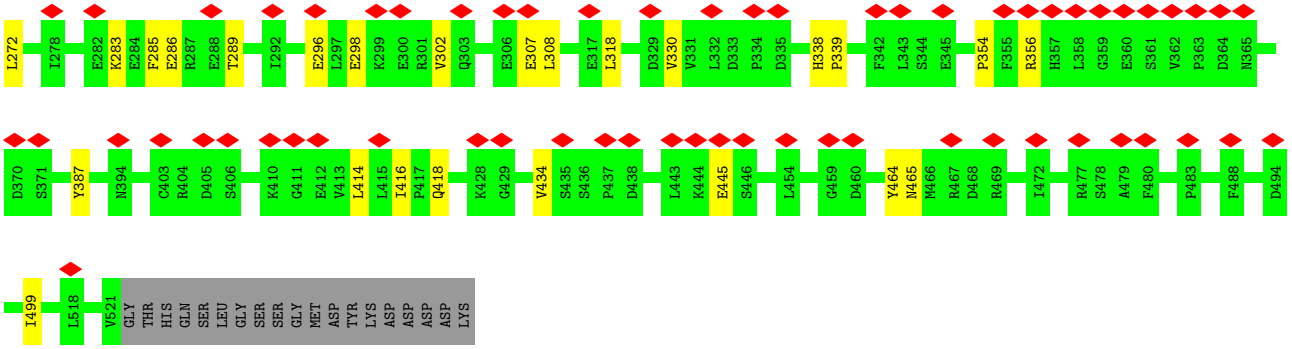


• Molecule 1: Butyrophilin subfamily 2 member A1

Chain B:



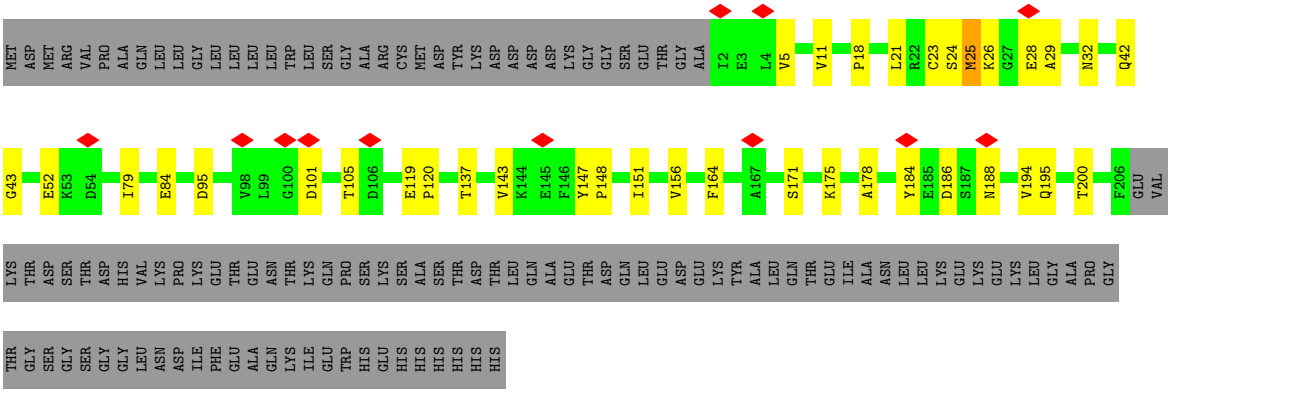




• Molecule 2: T cell receptor delta variable 2,T cell receptor delta constant 1

Chain D:

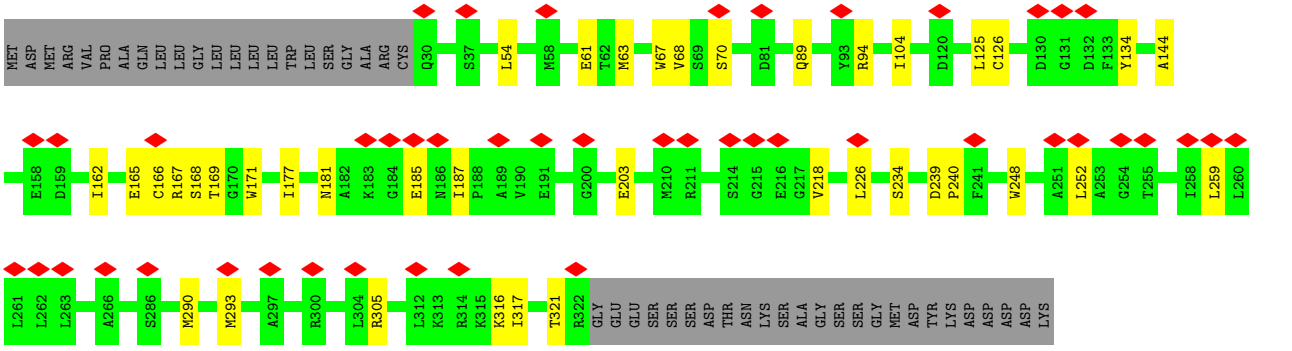




• Molecule 3: Butyrophilin subfamily 3 member A2

Chain E:

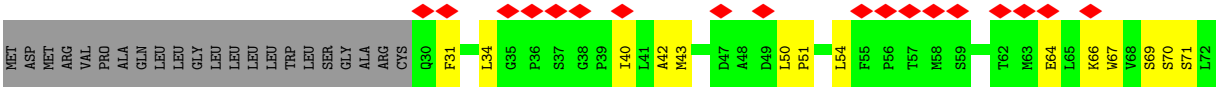


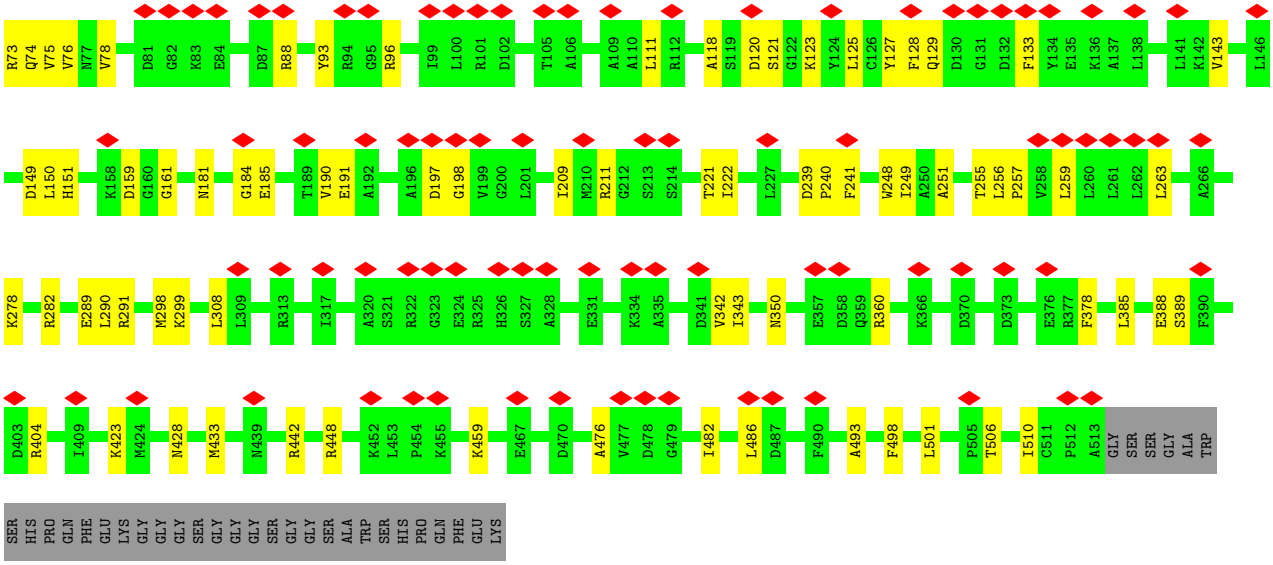


• Molecule 4: Butyrophilin subfamily 3 member A1

Chain F:



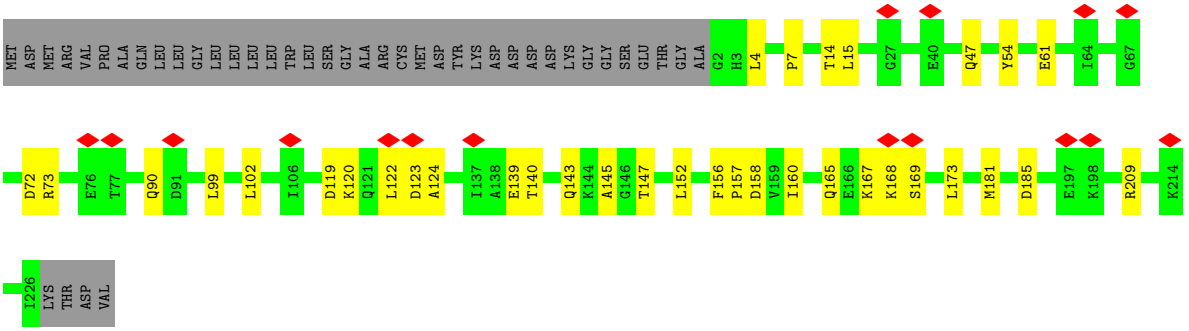




• Molecule 5: T cell receptor gamma variable 9,T cell receptor gamma constant 1

Chain G:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	572509	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 ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.057	Depositor
Minimum map value	-0.010	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0132	Depositor
Map size (Å)	430.91998, 430.91998, 430.91998	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0773, 1.0773, 1.0773	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: H6P

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	0.14	0/4037	0.33	0/5468
1	B	0.14	0/4037	0.29	0/5468
2	D	0.19	0/1641	0.47	4/2225 (0.2%)
3	E	0.15	0/2299	0.30	0/3112
4	F	0.14	0/3926	0.31	0/5322
5	G	0.18	0/1823	0.38	2/2467 (0.1%)
All	All	0.15	0/17763	0.33	6/24062 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	25	MET	CA-C-N	6.26	132.97	121.70
2	D	25	MET	C-N-CA	6.26	132.97	121.70
2	D	43	GLY	CA-C-N	5.79	132.13	121.70
2	D	43	GLY	C-N-CA	5.79	132.13	121.70
5	G	167	LYS	CA-C-N	5.09	130.87	121.70

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	3946	0	3924	81	0
1	B	3946	0	3924	52	0
2	D	1605	0	1594	24	0
3	E	2256	0	2247	26	0
4	F	3832	0	3792	69	0
5	G	1786	0	1818	24	0
6	F	15	0	9	3	0
All	All	17386	0	17308	254	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 7.

The worst 5 of 254 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:B:156:HIS:NE2	1:B:240:PHE:O	2.06	0.88
1:A:212:LYS:NZ	1:A:241:MET:O	2.14	0.80
1:B:47:THR:HG21	1:B:140:LEU:HD11	1.65	0.78
3:E:317:ILE:O	3:E:321:THR:HG23	1.85	0.77
4:F:96:ARG:NH2	4:F:120:ASP:OD2	2.19	0.76

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	491/534 (92%)	462 (94%)	28 (6%)	1 (0%)	43	70
1	B	491/534 (92%)	469 (96%)	22 (4%)	0	100	100
2	D	203/332 (61%)	189 (93%)	14 (7%)	0	100	100
3	E	291/340 (86%)	277 (95%)	14 (5%)	0	100	100
4	F	482/539 (89%)	461 (96%)	21 (4%)	0	100	100

Continued on next page...

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	G	223/267 (84%)	210 (94%)	13 (6%)	0	100	100
All	All	2181/2546 (86%)	2068 (95%)	112 (5%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	117	ALA

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	438/472 (93%)	437 (100%)	1 (0%)	87	85
1	B	438/472 (93%)	438 (100%)	0	100	100
2	D	181/288 (63%)	181 (100%)	0	100	100
3	E	239/278 (86%)	239 (100%)	0	100	100
4	F	412/451 (91%)	412 (100%)	0	100	100
5	G	205/239 (86%)	205 (100%)	0	100	100
All	All	1913/2200 (87%)	1912 (100%)	1 (0%)	87	88

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

Mol	Chain	Res	Type
1	A	307	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	36	ASN
4	F	77	ASN
5	G	212	ASN
5	G	6	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	G	143	GLN

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)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
6	H6P	F	601	-	11,14,14	1.07	1 (9%)	13,20,20	1.35	2 (15%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	H6P	F	601	-	-	7/15/15/15	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	F	601	H6P	O29-C28	-2.31	1.40	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	F	601	H6P	C28-C27-C30	-2.76	121.27	126.04
6	F	601	H6P	P13-O16-P17	-2.40	124.58	132.83

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	F	601	H6P	P13-O16-P17-O20
6	F	601	H6P	C21-C30-C31-O33
6	F	601	H6P	C27-C30-C31-O33
6	F	601	H6P	P13-O16-P17-O18
6	F	601	H6P	P17-O16-P13-O15

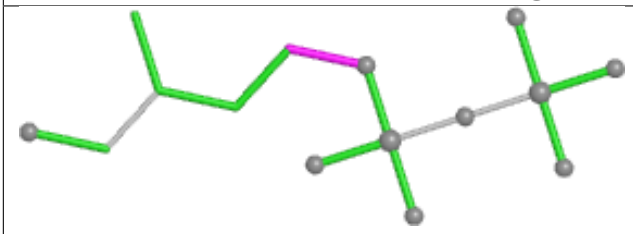
There are no ring outliers.

1 monomer is involved in 3 short contacts:

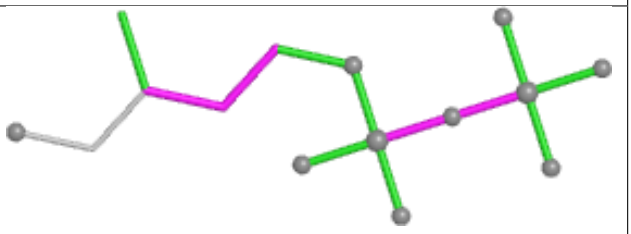
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	F	601	H6P	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

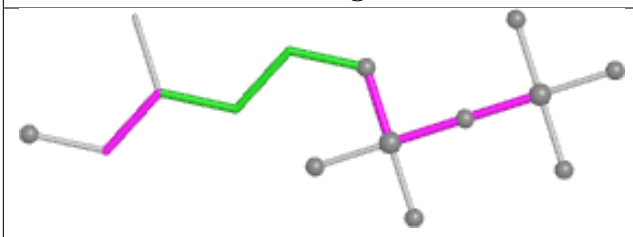
Ligand H6P F 601



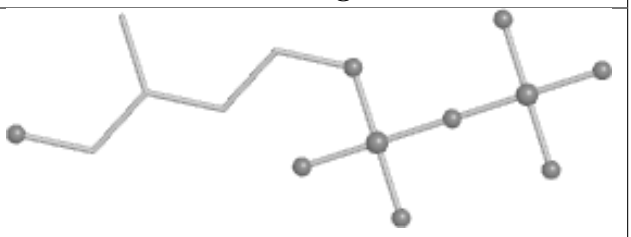
Bond lengths



Bond angles



Torsions



Rings

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.

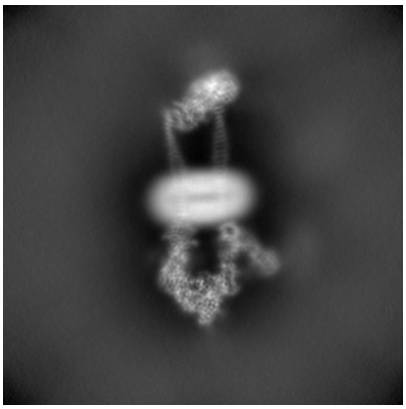
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-60159. These allow visual inspection of the internal detail of the map and identification of artifacts.

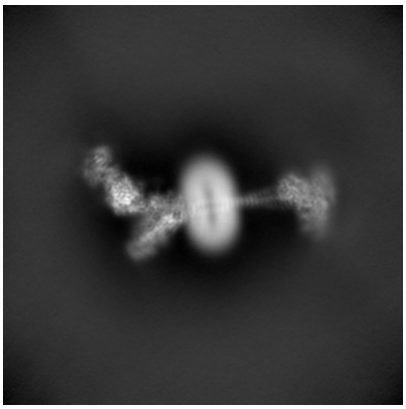
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

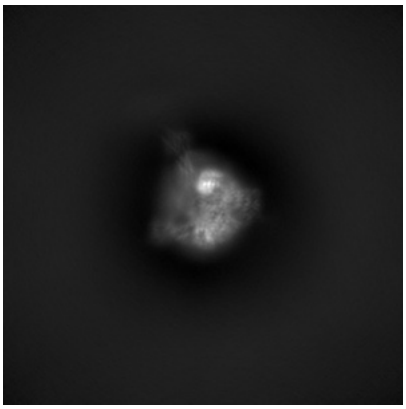
6.1.1 Primary map



X

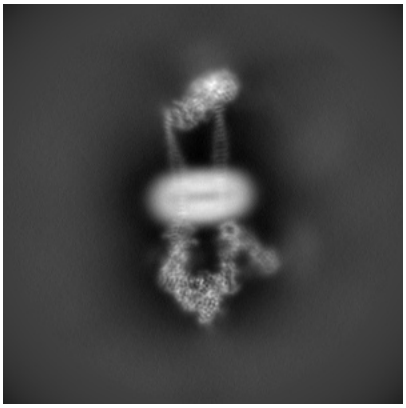


Y

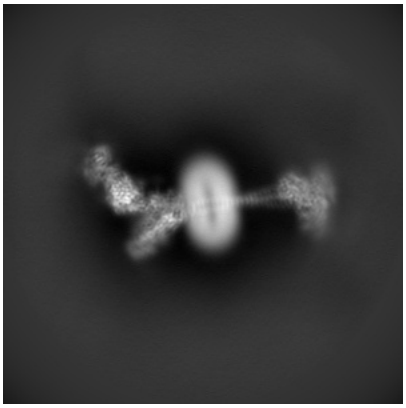


Z

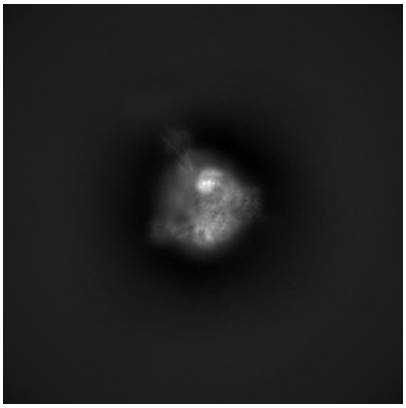
6.1.2 Raw map



X



Y

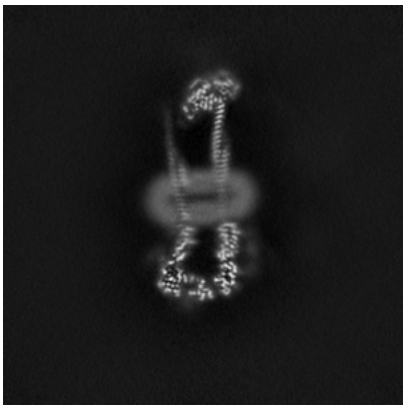


Z

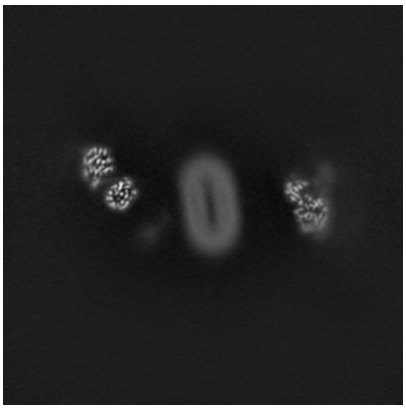
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

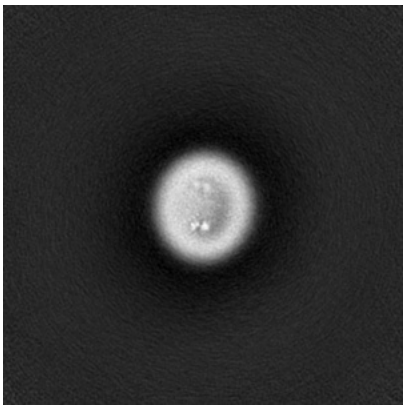
6.2.1 Primary map



X Index: 200

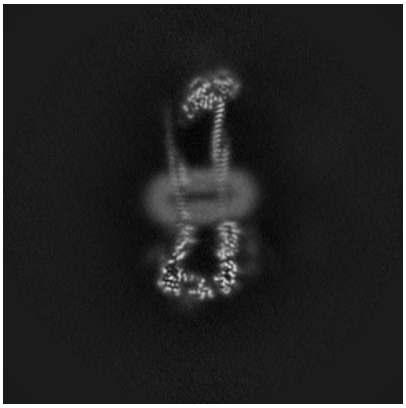


Y Index: 200

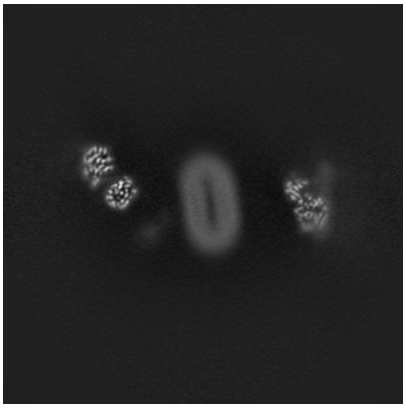


Z Index: 200

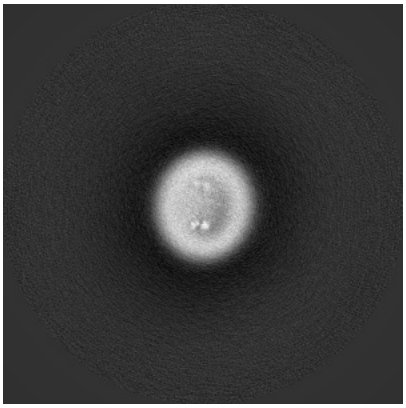
6.2.2 Raw map



X Index: 200



Y Index: 200

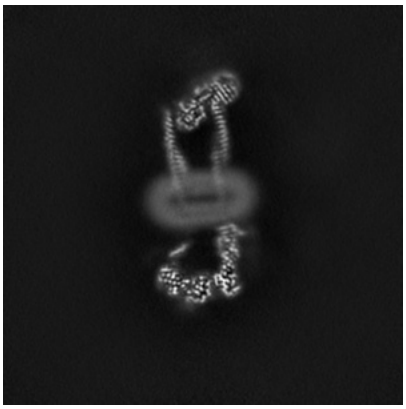


Z Index: 200

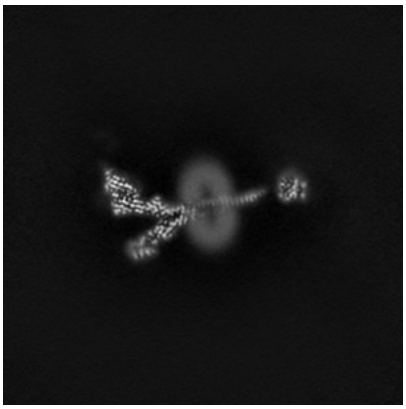
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

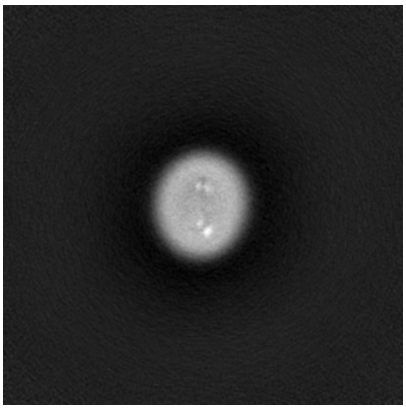
6.3.1 Primary map



X Index: 206

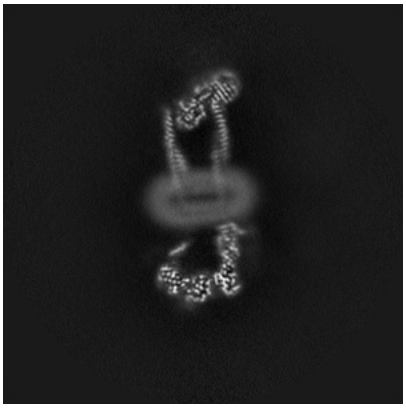


Y Index: 175

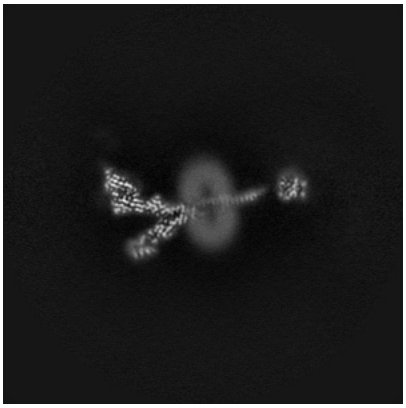


Z Index: 218

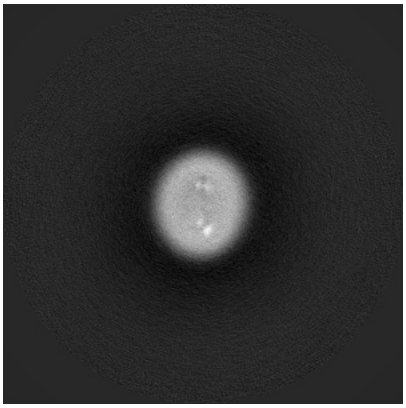
6.3.2 Raw map



X Index: 206



Y Index: 175

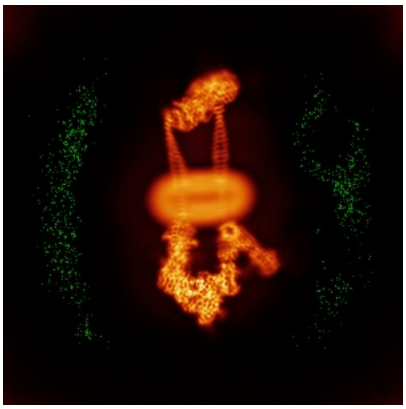


Z Index: 218

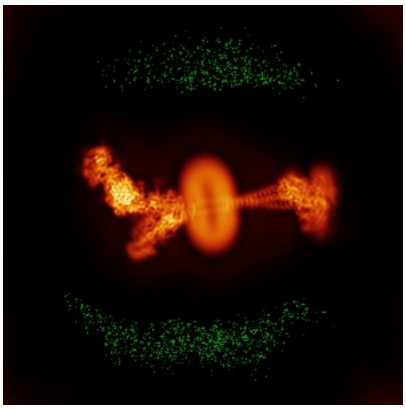
The images above show the largest variance slices of the map in three orthogonal directions.

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

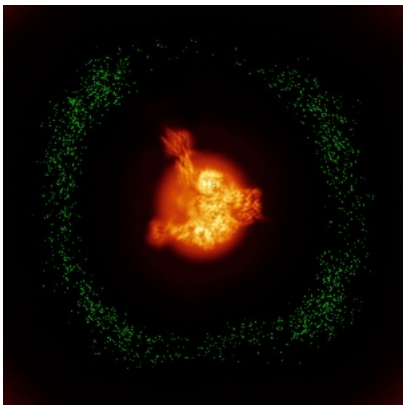
6.4.1 Primary map



X



Y

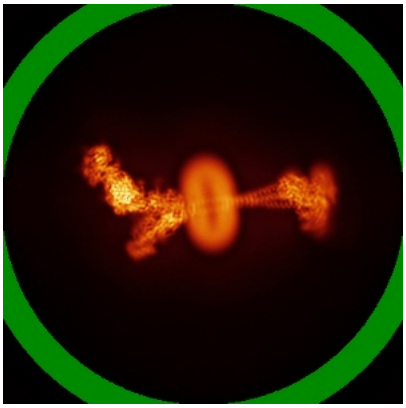


Z

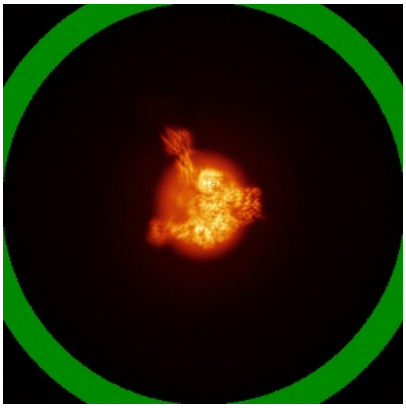
6.4.2 Raw map



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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0132. 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



X Y Z

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.

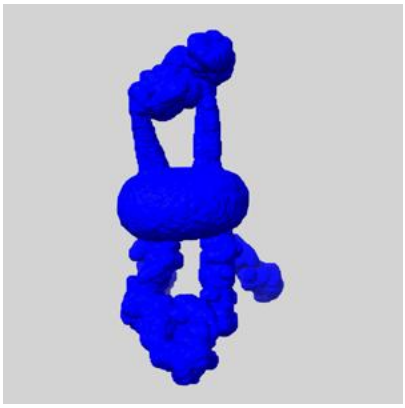
6.6 Mask visualisation (i)

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

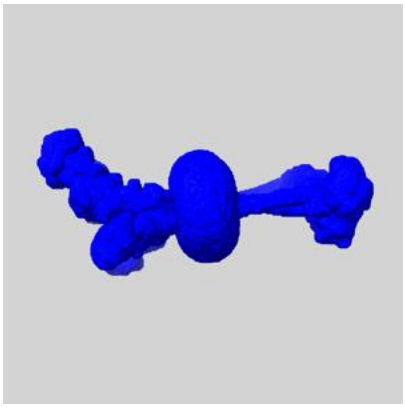
A mask typically either:

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

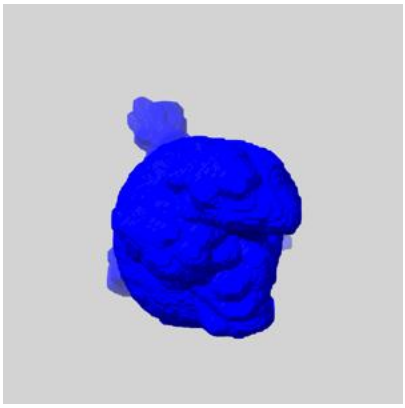
6.6.1 emd_60159_msk_1.map (i)



X



Y

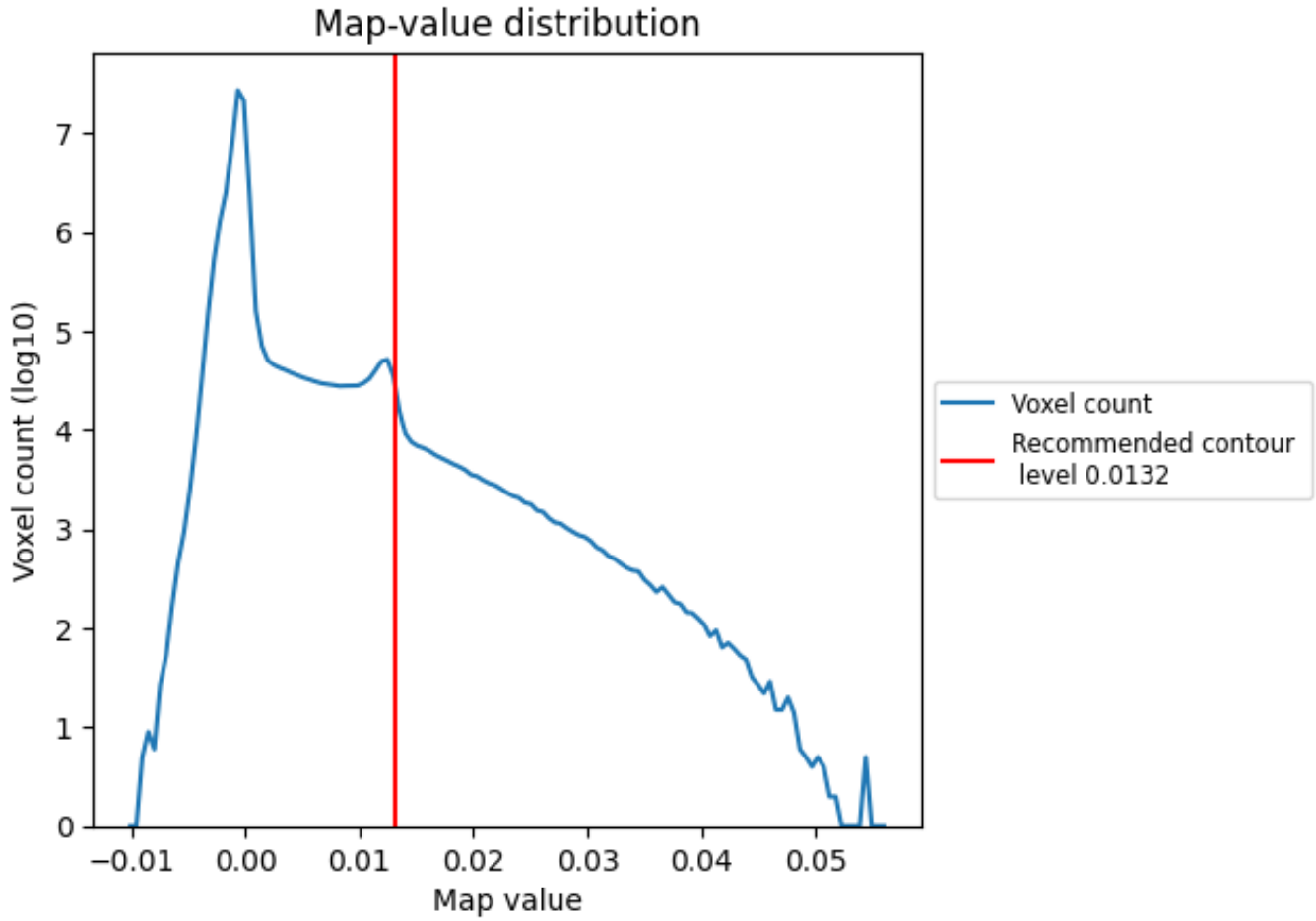


Z

7 Map analysis

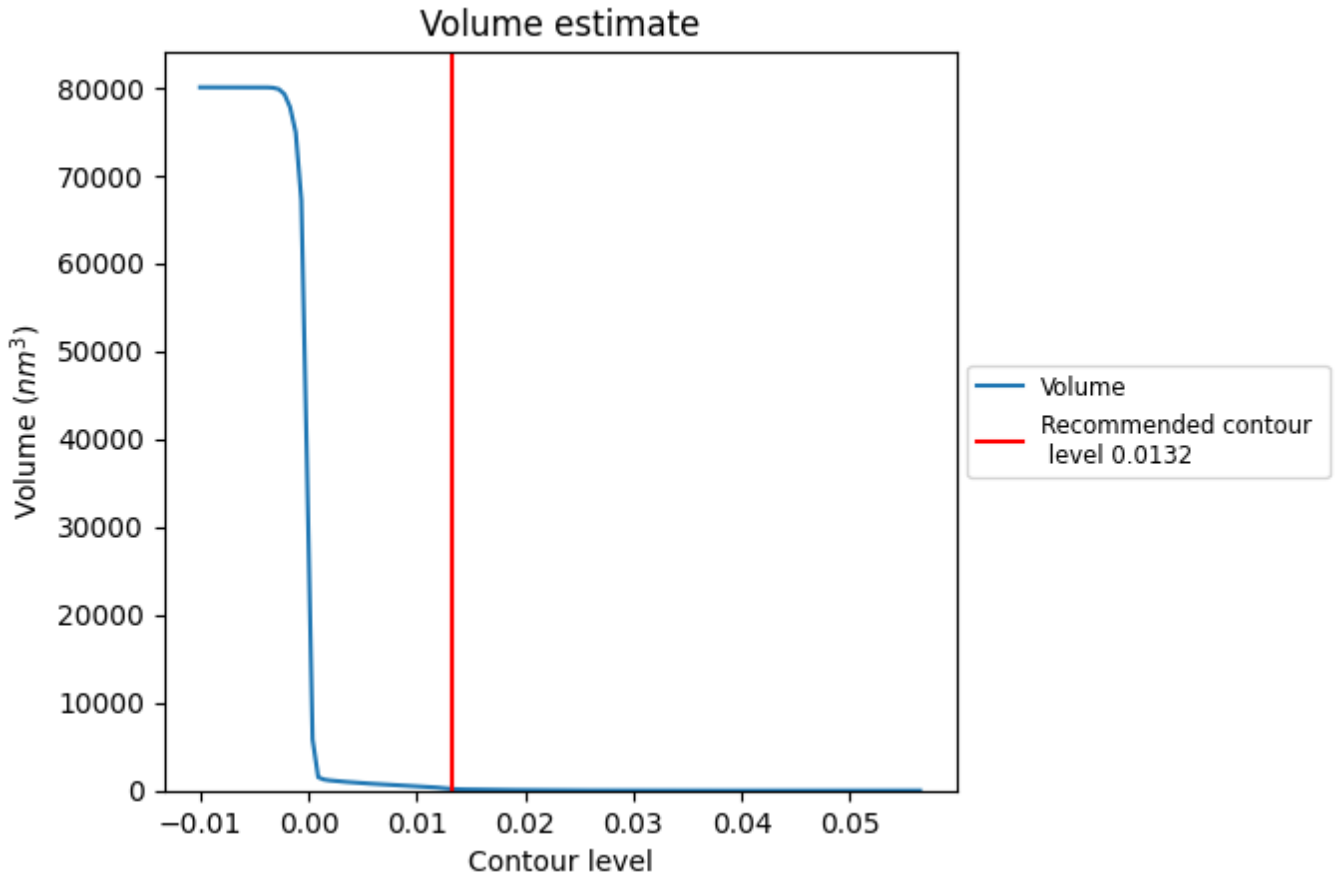
This section contains the results of statistical analysis of the map.

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.

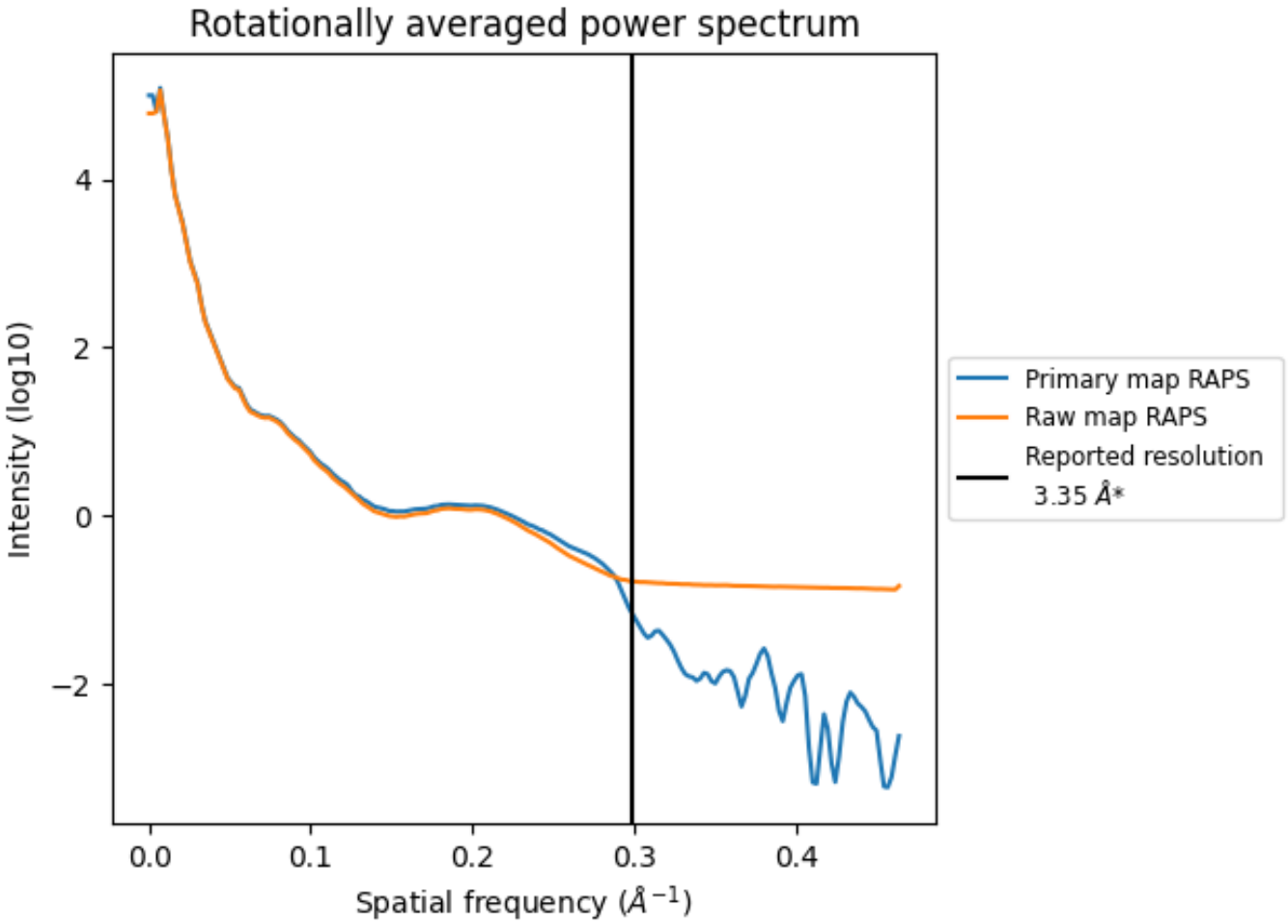
7.2 Volume estimate (i)



The volume at the recommended contour level is 186 nm^3; this corresponds to an approximate mass of 168 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)

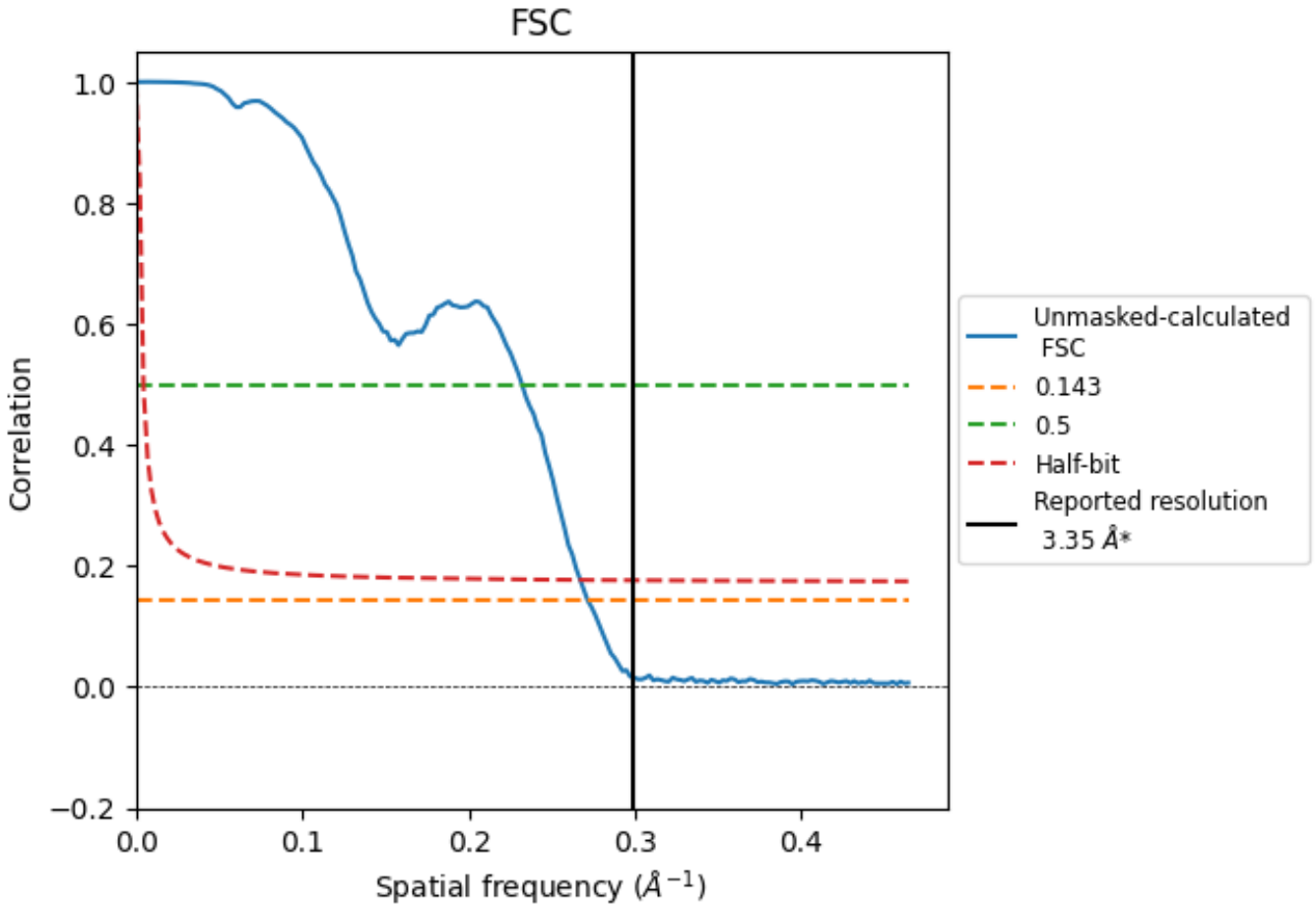


*Reported resolution corresponds to spatial frequency of 0.299 $Å^{-1}$

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.299 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.35	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.68	4.31	3.75

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

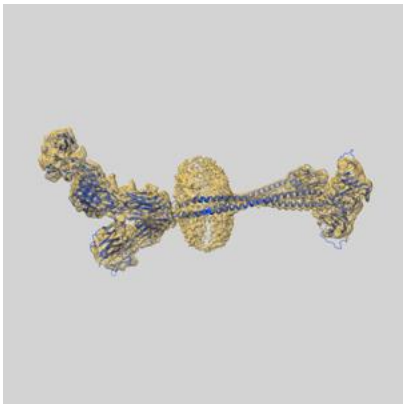
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-60159 and PDB model 8ZJX. Per-residue inclusion information can be found in section 3 on page 10.

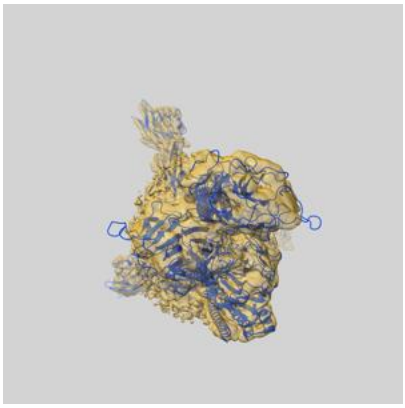
9.1 Map-model overlay



X



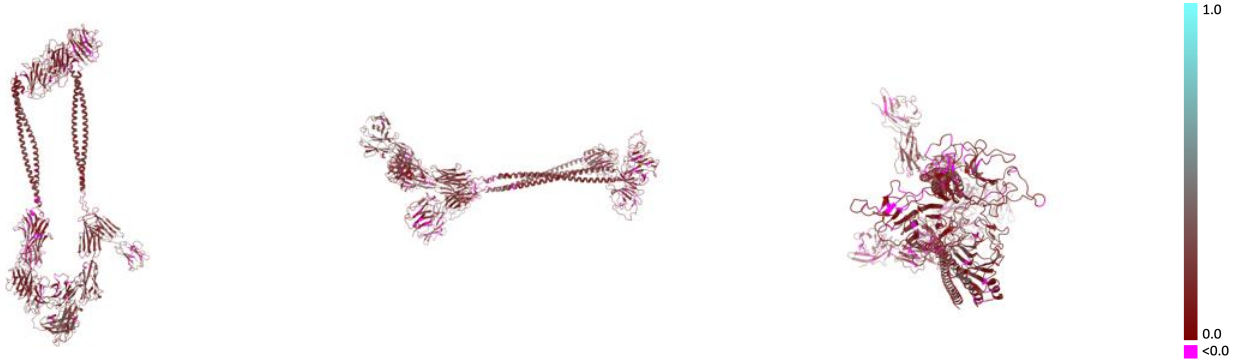
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0132 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.

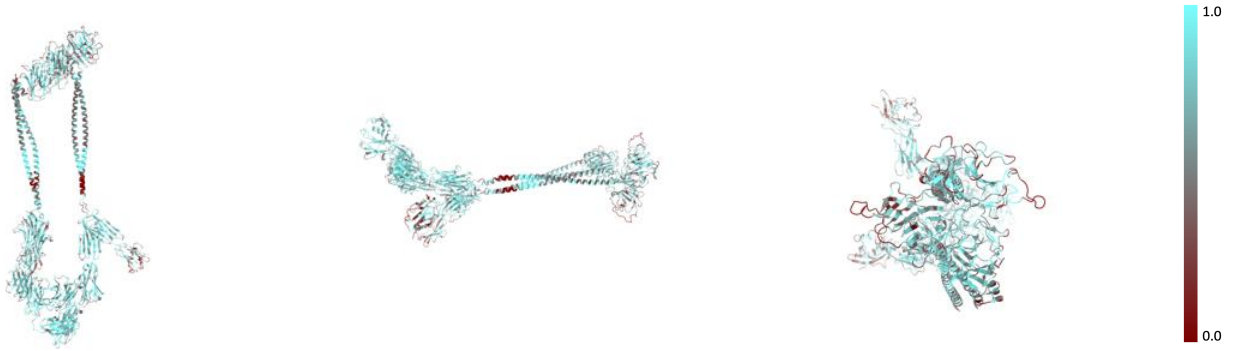
9.2 Q-score mapped to coordinate model (i)



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.

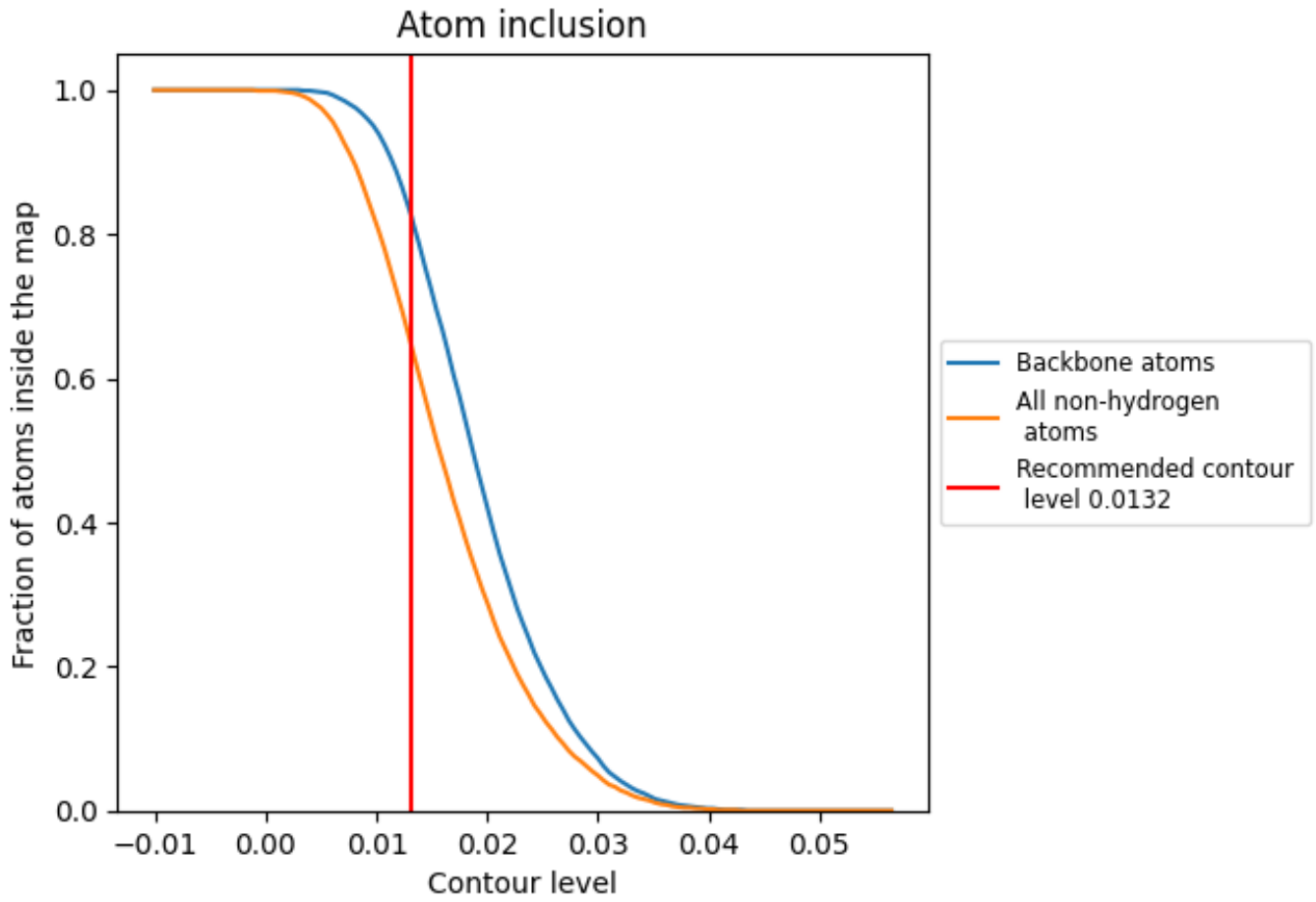
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.0132).

9.4 Atom inclusion (i)



At the recommended contour level, 82% of all backbone atoms, 64% 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 (0.0132) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6430	0.1850
A	0.5560	0.1640
B	0.6500	0.1840
D	0.7440	0.2420
E	0.6760	0.1750
F	0.6220	0.1720
G	0.7360	0.2240

