



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 08:36 PM UTC

PDB ID : 7STJ / pdb_00007stj
EMDB ID : EMD-25430
Title : Full-length insulin receptor bound with unsaturated insulin WT (2 insulins bound) asymmetric conformation (Conformation 1)
Authors : Bai, X.C.; Choi, E.
Deposited on : 2021-11-14
Resolution : 4.40 Å(reported)

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

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A user guide is available at

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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

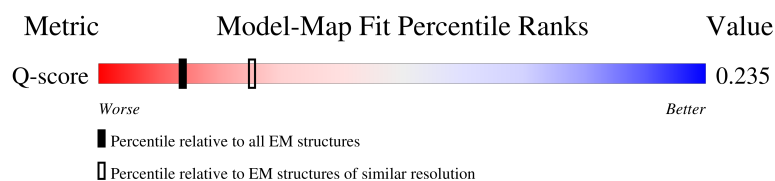
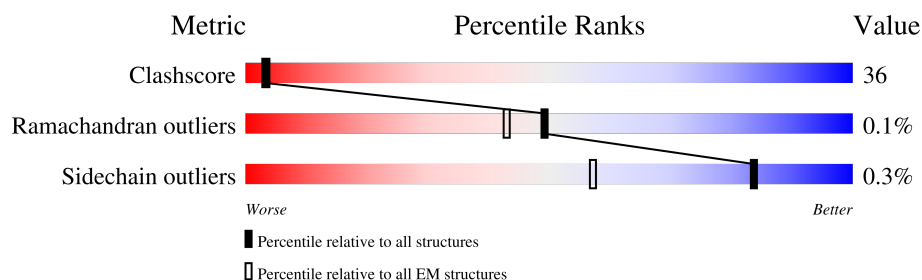
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.40 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	3132 (3.91 - 4.90)

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	1372	
1	B	1372	
2	C	110	
2	D	110	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13515 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 Insulin receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	786	Total	C	N	O	S	0	0
			6378	4061	1099	1171	47		
1	B	797	Total	C	N	O	S	0	0
			6441	4095	1110	1187	49		

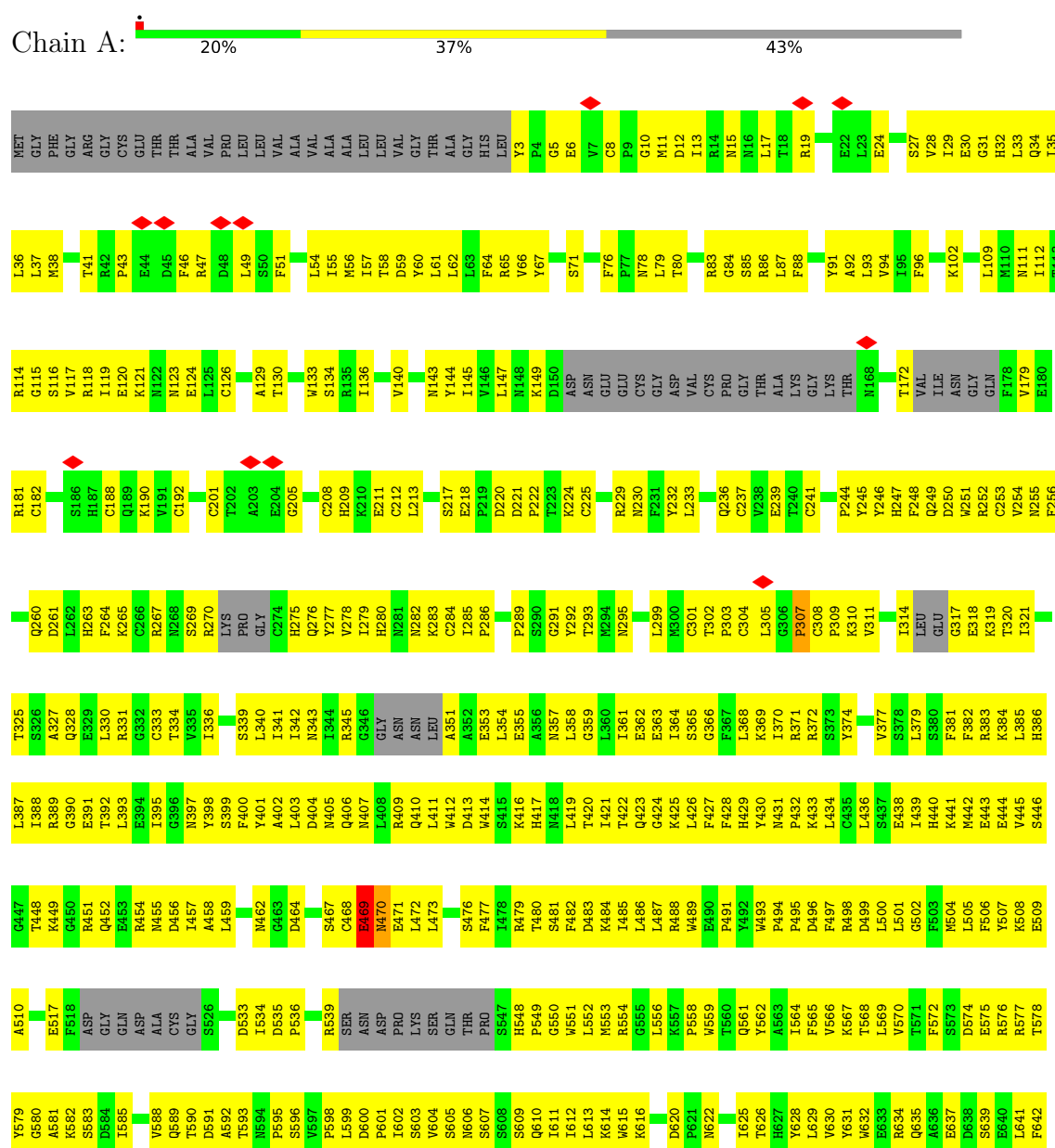
- Molecule 2 is a protein called Insulin.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	48	Total	C	N	O	S	0	0
			376	238	61	71	6		
2	D	41	Total	C	N	O	S	0	0
			320	203	50	61	6		

3 Residue-property plots

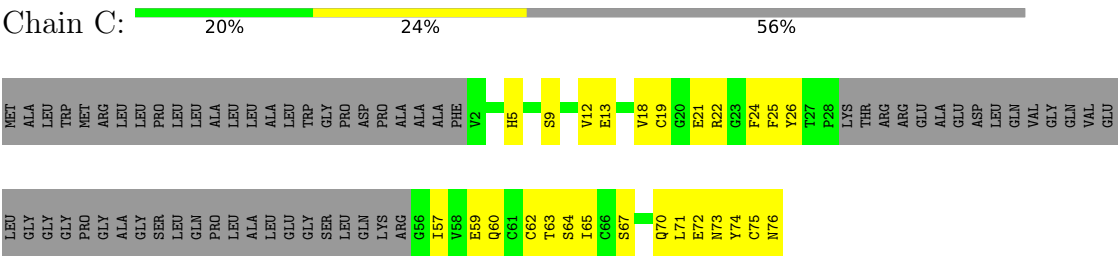
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

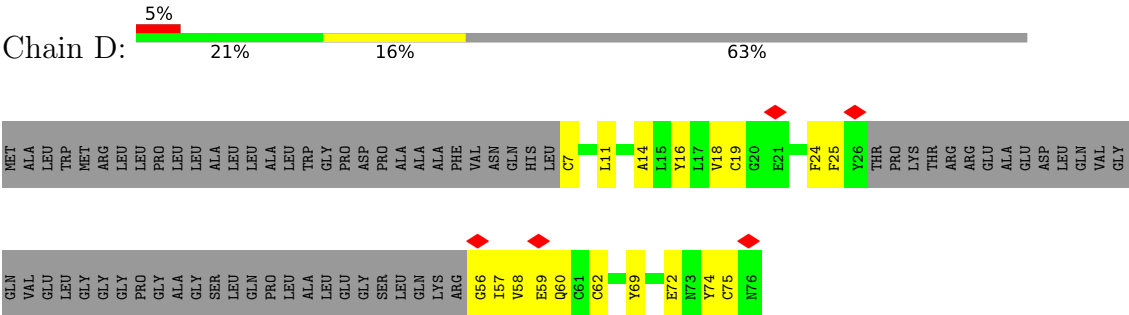


HIS	PHE	GLN	PHE	LEU	THR	GLU	P900	N825	GLU	GLN	H624	T560	P494	G424	G338	H263
ILE	PRO	GLY	GLY	ARG	VAL	TYR	PRO	N826	H756	ILE	I625	Q561	P494	G424	S339	F264
THR	GLU	SER	TYR	PRO	ASN	LEU	TYR	V827	R757	LEU	I626	Y562	F497	F428	S339	K265
THR	VAL	SER	TYR	GLU	GLY	SER	GLY	V828	R757	LEU	H627	A563	F498	H429	I341	C266
HIS	PHE	ASN	GLY	ALA	SER	ALA	ASN	H829	V762	LEU	I629	I564	F498	Y430	R267	
MET	PHE	ASN	GLY	ASN	SER	SER	ASN	M831	K765	LEU	L629	F565	L501	M431	I344	
ASN	TYR	ASN	ILE	VAL	ASP	VAL	THR	H832	E766	GLU	L630	V566	G502	P432	R345	R270
GLY	THR	VAL	THR	PHE	THR	VAL	THR	H833	E767	GLU	L631	K567	F503	K433	LYS	
GLY	THR	VAL	THR	PHE	THR	VAL	THR	H834	E768	SER	Y632	T568	M504	L434	PRO	
LYS	GLY	PHE	GLY	ARG	ARG	GLY	TYR	E834	L768	SER	E633	L569	L505	C435	GLY	
ASN	VAL	VAL	ASP	VAL	ASP	VAL	ASP	P835	V769	PHE	R634	D574	F506	L436	C274	
GLY	ALA	ASP	VAL	VAL	VAL	VAL	VAL	P838	I770	ARG	Q635	E575	Y507	S437	H275	
ASN	THR	THR	PRO	PRO	THR	THR	PRO	N839	L773	LYS	A636	R576	G509	I439	Q276	
GLY	ARG	GLY	ASN	THR	PHE	THR	ASN	G840	R774	THR	L641	R577	A510	H440	Y277	
VAL	GLY	GLY	PRO	GLU	ASN	VAL	ASN	L841	H775	THR	F642	R578	P511	M442	I279	
THR	GLY	THR	ILE	GLU	GLY	GLU	ILE	I842	T776	ARG	L641	Y579	P512	E362	GLY	
LEU	GLY	GLY	ALA	GLU	ALA	GLU	ALA	V843	T777	ARG	Y646	G580	Q513	M442	I364	
LEU	GLY	GLY	ALA	GLU	ALA	GLU	ALA	L844	G778	THR	C647	A581	Q513	E443	S365	
PRO	GLY	GLY	ILE	GLU	VAL	GLU	ILE	Y845	T779	THR		K582	N514			N282
GLN	PRO	PRO	ILE	VAL	VAL	VAL	ILE	E846	R780	THR	L651	S583	F518	S446	K369	K283
ASN	THR	THR	ILE	VAL	VAL	VAL	ILE		I781	PRO	L652	I586	ASP	T448	P286	C284
ASN	VAL	VAL	ILE	VAL	VAL	VAL	ILE	Y849	E782	PRO	A652	Y587	GLY	T448	I370	
GLY	THR	THR	GLY	THR	GLY	THR	GLY	R850	L783	SER	L653	V588	GLN	R451	R371	P289
THR	PHE	PHE	PHE	ALA	THR	THR	THR	R851	L784	ARG	P654	Q588	ASP	Q452	R372	S290
GLY	THR	THR	THR	THR	THR	THR	THR	Y852	A785	ARG	S655	T590	ALA	Q452	S373	G291
ASP	THR	THR	THR	THR	THR	THR	THR	G853	C786	LYS	S656	D591	CYS	E453	L376	Y292
THR	THR	THR	THR	THR	THR	THR	THR	E854	Q788	ARG	S656	T592	GLY	E453		M294
LEU	THR	THR	THR	THR	THR	THR	THR	E855	Q789	SER	S656	D593	ASN	E458	R382	
LEU	THR	THR	THR	THR	THR	THR	THR		S790	SER	S656	D594	ASN	E458	R383	
LEU	THR	THR	THR	THR	THR	THR	THR	L859	T791	LEU	S656	D595	ASP	E458	K384	C301
ASP	THR	THR	THR	THR	THR	THR	THR	C860	D792	GLU	S656	S596	ASP	E458	L385	C304
GLY	THR	THR	THR	THR	THR	THR	THR	V861	E793	GLU	S656	S597	GLY	E458	H386	L305
VAL	THR	THR	THR	THR	THR	THR	THR	R862	R794	VAL	S656	P598	ASP	E458	L387	G306
VAL	THR	THR	THR	THR	THR	THR	THR	R863	C795	GLY	S656	L599	ASP	E458	I388	P307
LEU	THR	THR	THR	THR	THR	THR	THR		S796	ASN	S656	D600	ASP	E458	R389	
LEU	THR	THR	THR	THR	THR	THR	THR	R873	V797	VAL	S656	D601	ASP	E458	E384	C368
LEU	THR	THR	THR	THR	THR	THR	THR	L874	A798	THR	S656	P601	ASP	E458	P309	P309
LEU	THR	THR	THR	THR	THR	THR	THR	R875	E799	ALA	S656	I602	ASP	E458	K310	V311
LEU	THR	THR	THR	THR	THR	THR	THR	G876	Y800	THR	S656	S603	ASP	E458	V311	C312
LEU	THR	THR	THR	THR	THR	THR	THR	L877		THR	S656	V604	ASP	E458	Q313	Q313
LEU	THR	THR	THR	THR	THR	THR	THR	R878		THR	S656	S605	ASP	E458	I314	I314
LEU	THR	THR	THR	THR	THR	THR	THR	S879		THR	S656	S606	ASP	E458	Y401	
LEU	THR	THR	THR	THR	THR	THR	THR	G880		THR	S656	S607	ASP	E458	Y401	
LEU	THR	THR	THR	THR	THR	THR	THR	N881		THR	S656	S608	ASP	E458	N405	G317
LEU	THR	THR	THR	THR	THR	THR	THR	Y882		THR	S656	S609	ASP	E458	E318	E318
LEU	THR	THR	THR	THR	THR	THR	THR	S883		THR	S656	S610	ASP	E458	K319	K319
LEU	THR	THR	THR	THR	THR	THR	THR	V884		THR	S656	S611	ASP	E458	T320	T320
LEU	THR	THR	THR	THR	THR	THR	THR	R885		THR	S656	S612	ASP	E458	I321	I321
LEU	THR	THR	THR	THR	THR	THR	THR	V886		THR	S656	S613	ASP	E458	D322	D322
LEU	THR	THR	THR	THR	THR	THR	THR	R887		THR	S656	S614	ASP	E458	S323	S323
LEU	THR	THR	THR	THR	THR	THR	THR	A888		THR	S656	S615	ASP	E458	W412	W412
LEU	THR	THR	THR	THR	THR	THR	THR	T889		THR	S656	S616	ASP	E458	D413	D413
LEU	THR	THR	THR	THR	THR	THR	THR	V889		THR	S656	S617	ASP	E458	W414	W414
LEU	THR	THR	THR	THR	THR	THR	THR	S890		THR	S656	S618	ASP	E458	S415	S415
LEU	THR	THR	THR	THR	THR	THR	THR	L891		THR	S656	S619	ASP	E458	L486	L486
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S620	ASP	E458	K416	K416
LEU	THR	THR	THR	THR	THR	THR	THR	N894		THR	S656	S621	ASP	E458	T420	T420
LEU	THR	THR	THR	THR	THR	THR	THR	G895		THR	S656	S622	ASP	E458	I421	I421
LEU	THR	THR	THR	THR	THR	THR	THR	S896		THR	S656	S623	ASP	E458	T422	T422
LEU	THR	THR	THR	THR	THR	THR	THR	W897		THR	S656	S624	ASP	E458	Q423	Q423
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S625	ASP	E458		
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S626	ASP	E458		
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S627	ASP	E458		
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S628	ASP	E458		
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S629	ASP	E458		
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S630	ASP	E458		
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S631	ASP	E458		
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S632	ASP	E458		
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S633	ASP	E458		
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S634	ASP	E458		
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S635	ASP	E458		
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S636	ASP	E458		
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S637	ASP	E458		
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S638	ASP	E458		
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LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S640	ASP	E458		
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S641	ASP	E458		
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S642	ASP	E458		
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S643	ASP	E458		
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S644	ASP	E458		
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S645	ASP	E458		
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LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S660	ASP	E458		
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LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S663	ASP	E458		
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S664	ASP	E458		
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LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S669	ASP	E458		
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LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S671	ASP	E458		
LEU	THR	THR	THR	THR	THR	THR	THR			THR	S656	S672	ASP	E458		
LEU	THR	THR	THR													

● Molecule 2: Insulin



● Molecule 2: Insulin



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	12430	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.098	Depositor
Minimum map value	-0.037	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	324.0, 324.0, 324.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.23	0/6534	0.40	1/8849 (0.0%)
1	B	0.28	0/6602	0.41	0/8952
2	C	0.29	0/383	0.43	0/518
2	D	0.13	0/325	0.39	0/437
All	All	0.25	0/13844	0.41	1/18756 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	469	GLU	N-CA-C	-9.36	101.76	113.55

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6378	0	6210	514	0
1	B	6441	0	6257	438	0
2	C	376	0	346	21	0
2	D	320	0	291	16	0
All	All	13515	0	13104	970	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 36.

The worst 5 of 970 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:476:SER:H	1:B:489:TRP:HA	1.23	1.04
1:A:387:LEU:HB3	1:A:389:ARG:HH12	1.30	0.96
1:B:454:ARG:HE	1:B:455:ASN:H	1.14	0.95
1:A:469:GLU:HG3	1:A:580:GLY:H	1.36	0.90
1:B:552:LEU:O	1:B:554:ARG:NH1	2.05	0.89

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	766/1372 (56%)	691 (90%)	74 (10%)	1 (0%)	48	83
1	B	783/1372 (57%)	699 (89%)	83 (11%)	1 (0%)	48	83
2	C	44/110 (40%)	41 (93%)	3 (7%)	0	100	100
2	D	37/110 (34%)	34 (92%)	3 (8%)	0	100	100
All	All	1630/2964 (55%)	1465 (90%)	163 (10%)	2 (0%)	49	83

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	470	ASN
1	A	307	PRO

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	718/1228 (58%)	713 (99%)	5 (1%)	76	79
1	B	725/1228 (59%)	725 (100%)	0	100	100
2	C	43/88 (49%)	43 (100%)	0	100	100
2	D	36/88 (41%)	36 (100%)	0	100	100
All	All	1522/2632 (58%)	1517 (100%)	5 (0%)	84	84

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	305	LEU
1	A	310	LYS
1	A	311	VAL
1	A	469	GLU
1	A	470	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	431	ASN
2	D	76	ASN
2	C	60	GLN
1	A	470	ASN
1	B	418	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

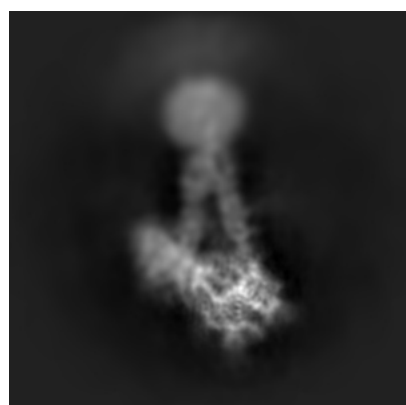
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25430. These allow visual inspection of the internal detail of the map and identification of artifacts.

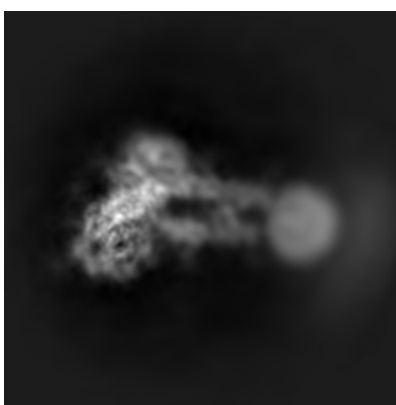
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

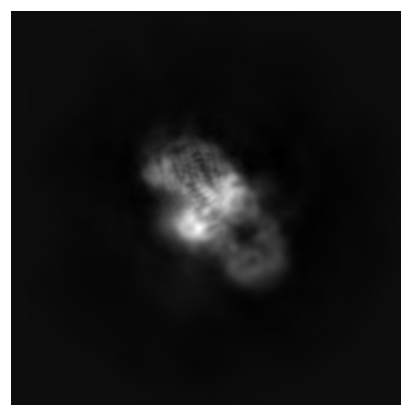
6.1.1 Primary map



X



Y

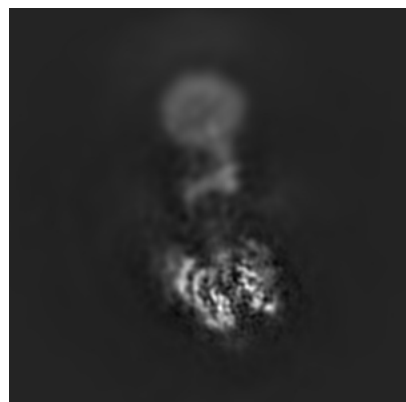


Z

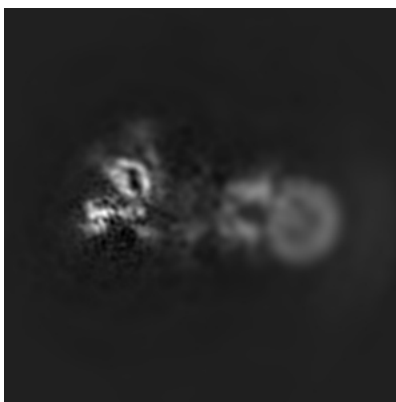
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

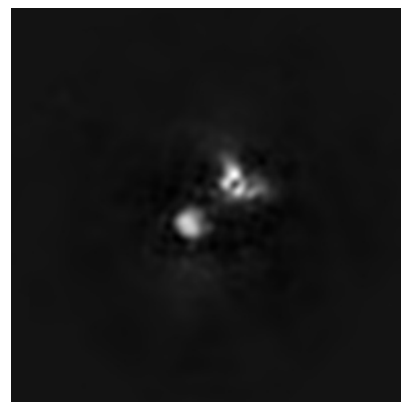
6.2.1 Primary map



X Index: 150



Y Index: 150

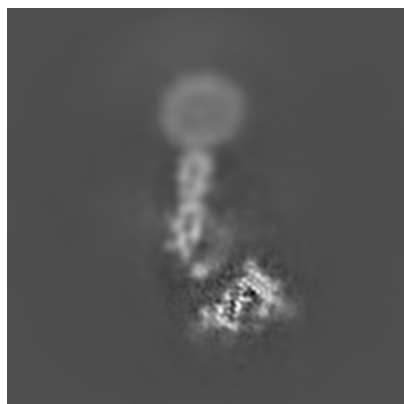


Z Index: 150

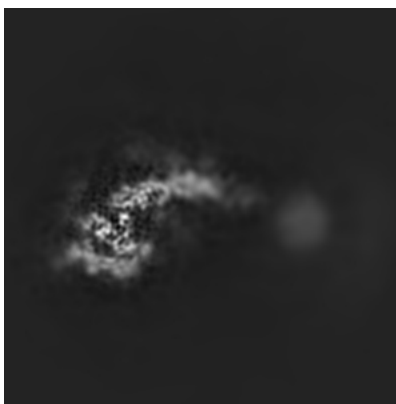
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

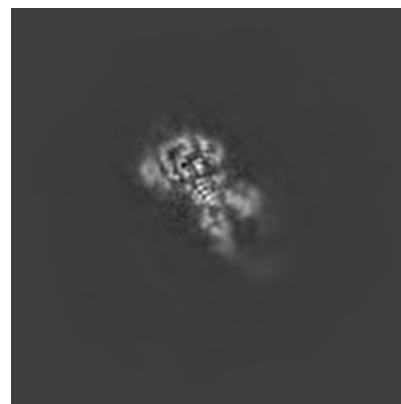
6.3.1 Primary map



X Index: 133



Y Index: 173



Z Index: 83

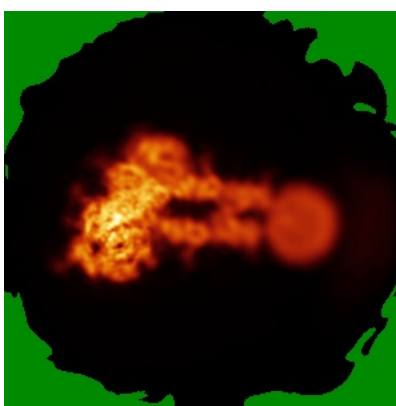
The images above show the largest variance slices of the map in three orthogonal directions.

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

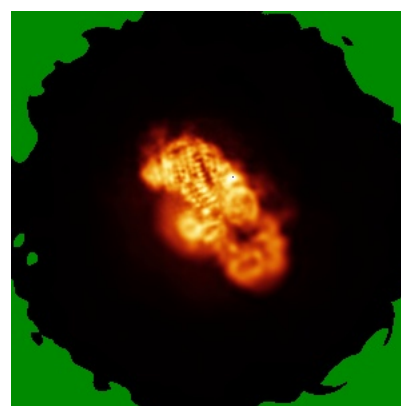
6.4.1 Primary map



X



Y



Z

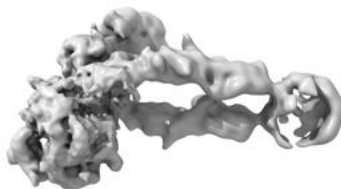
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

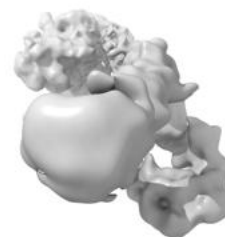
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

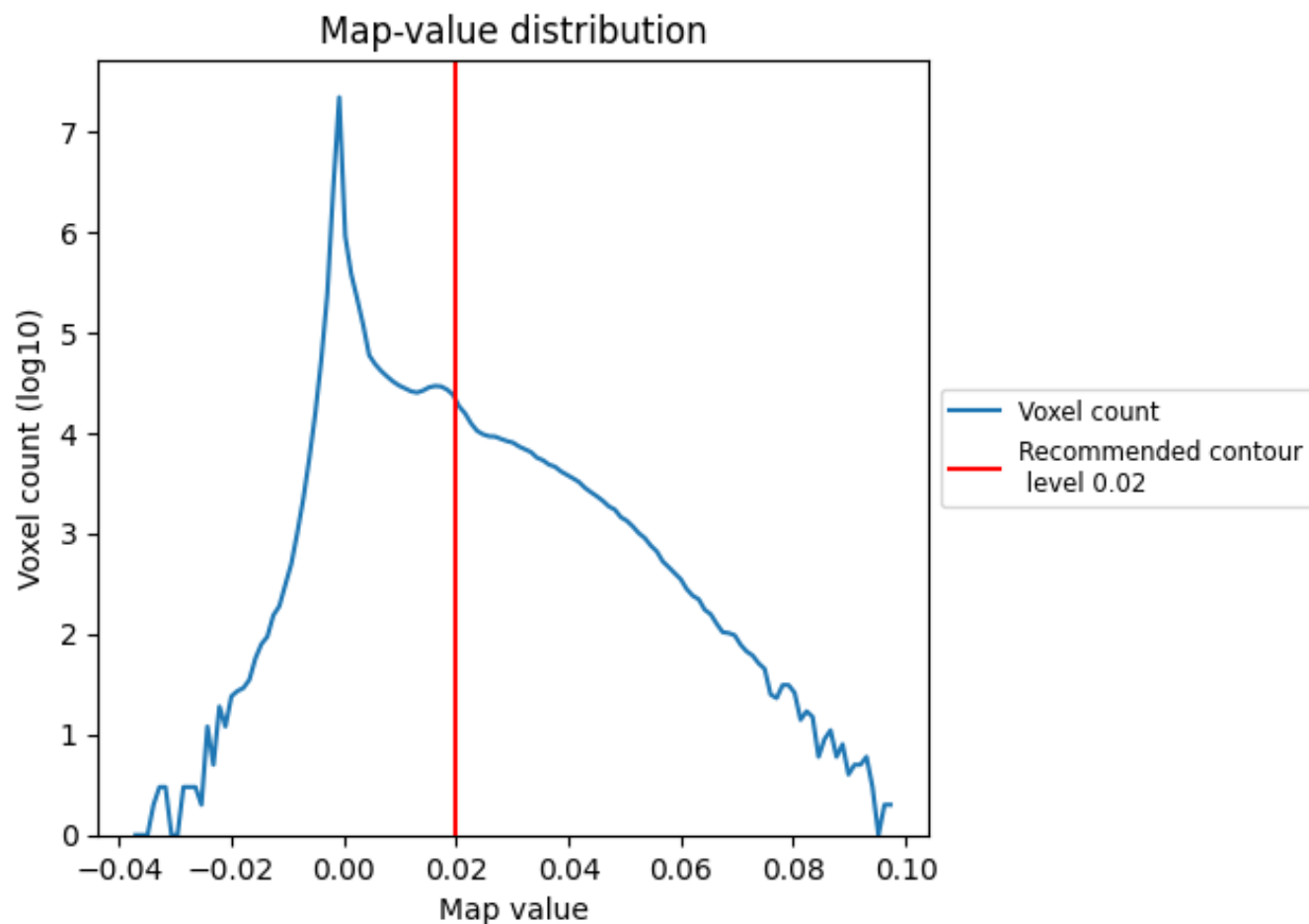
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

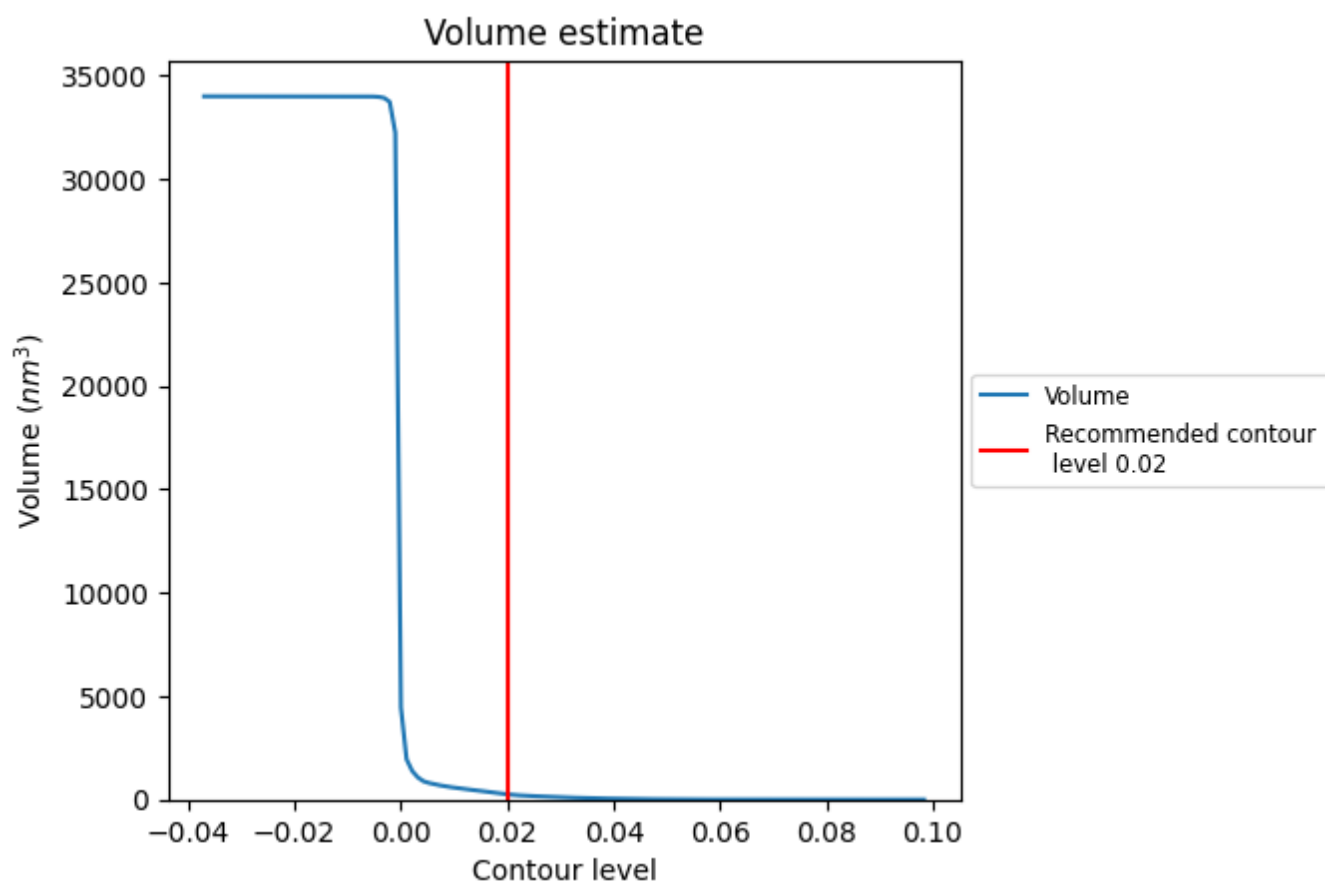
This section contains the results of statistical analysis of the map.

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.

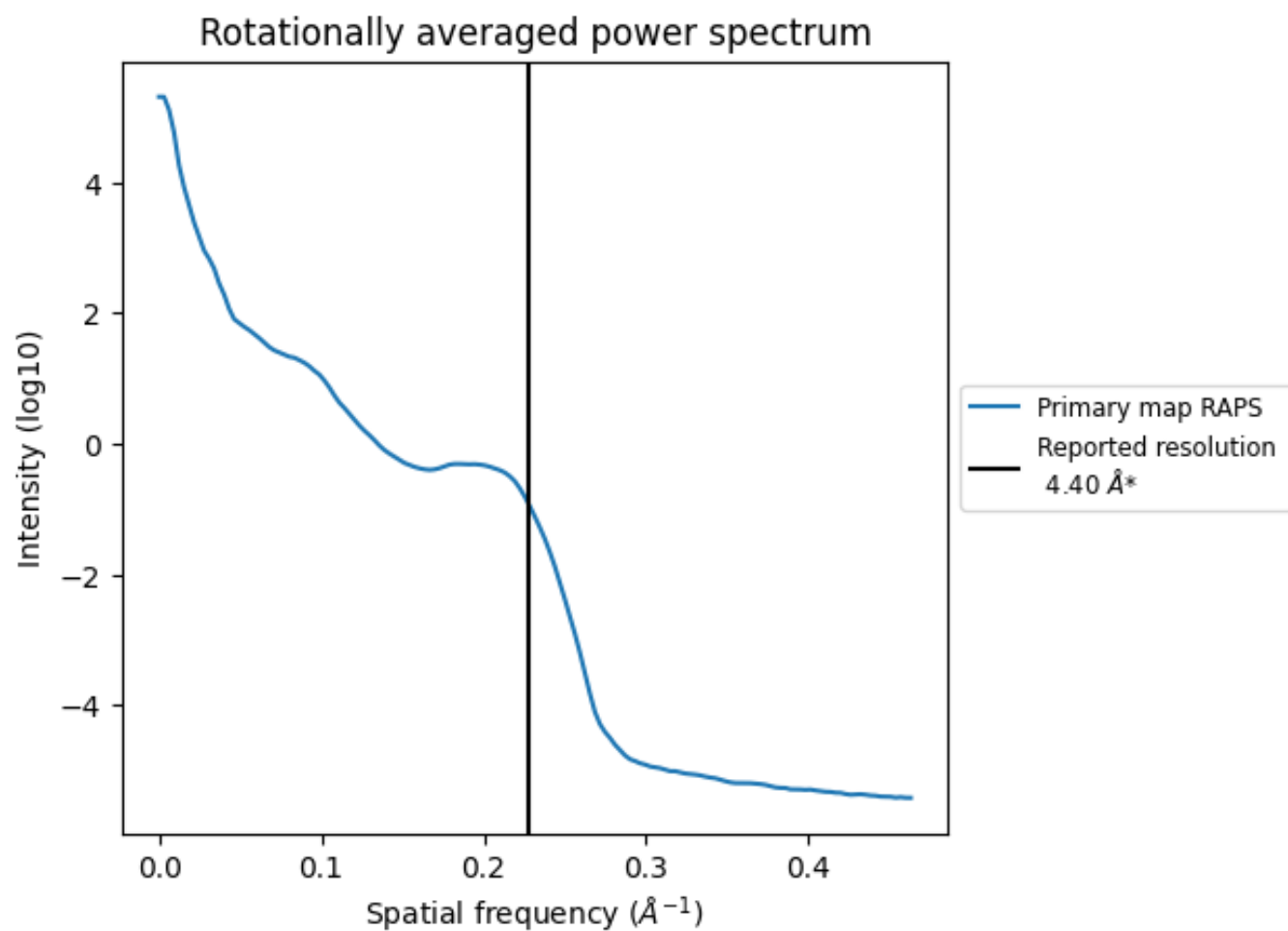
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 255 nm³; this corresponds to an approximate mass of 230 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 0.227 Å⁻¹

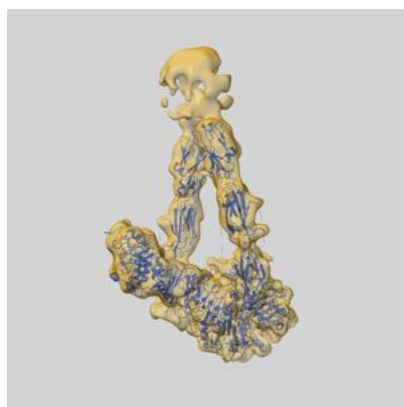
8 Fourier-Shell correlation

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

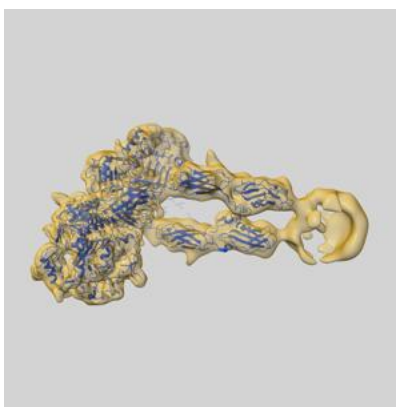
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25430 and PDB model 7STJ. Per-residue inclusion information can be found in section [3](#) on page [4](#).

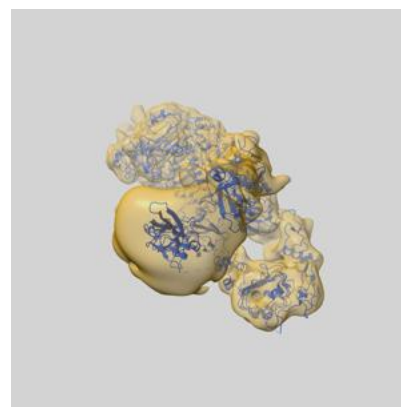
9.1 Map-model overlay [i](#)



X



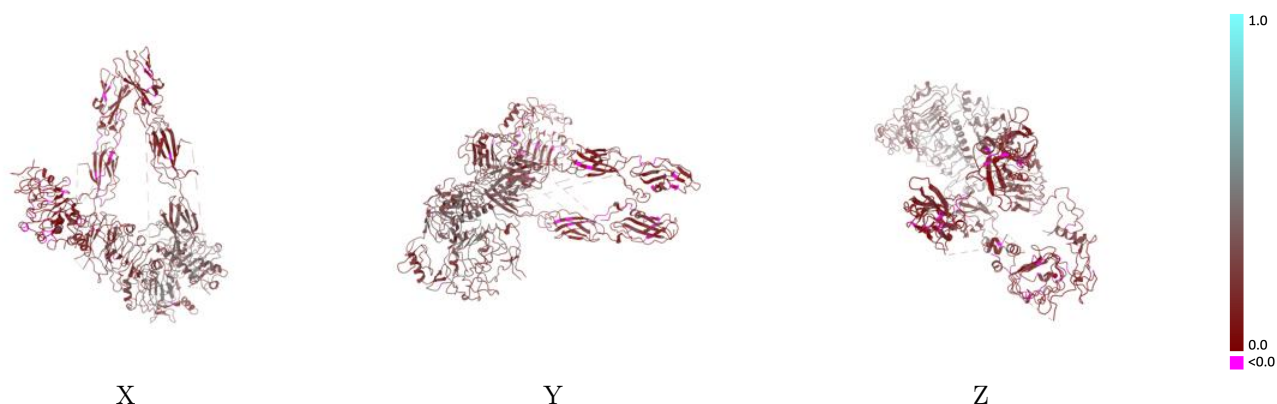
Y



Z

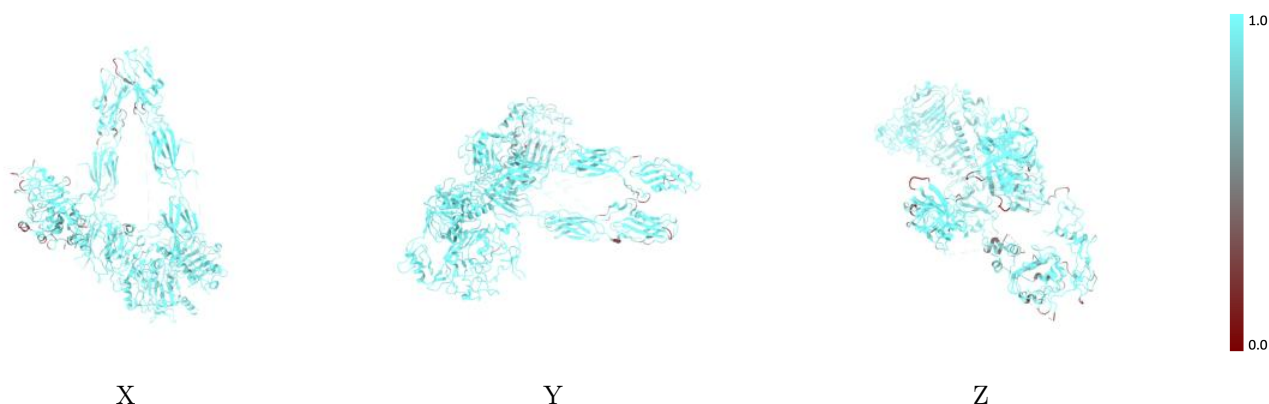
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



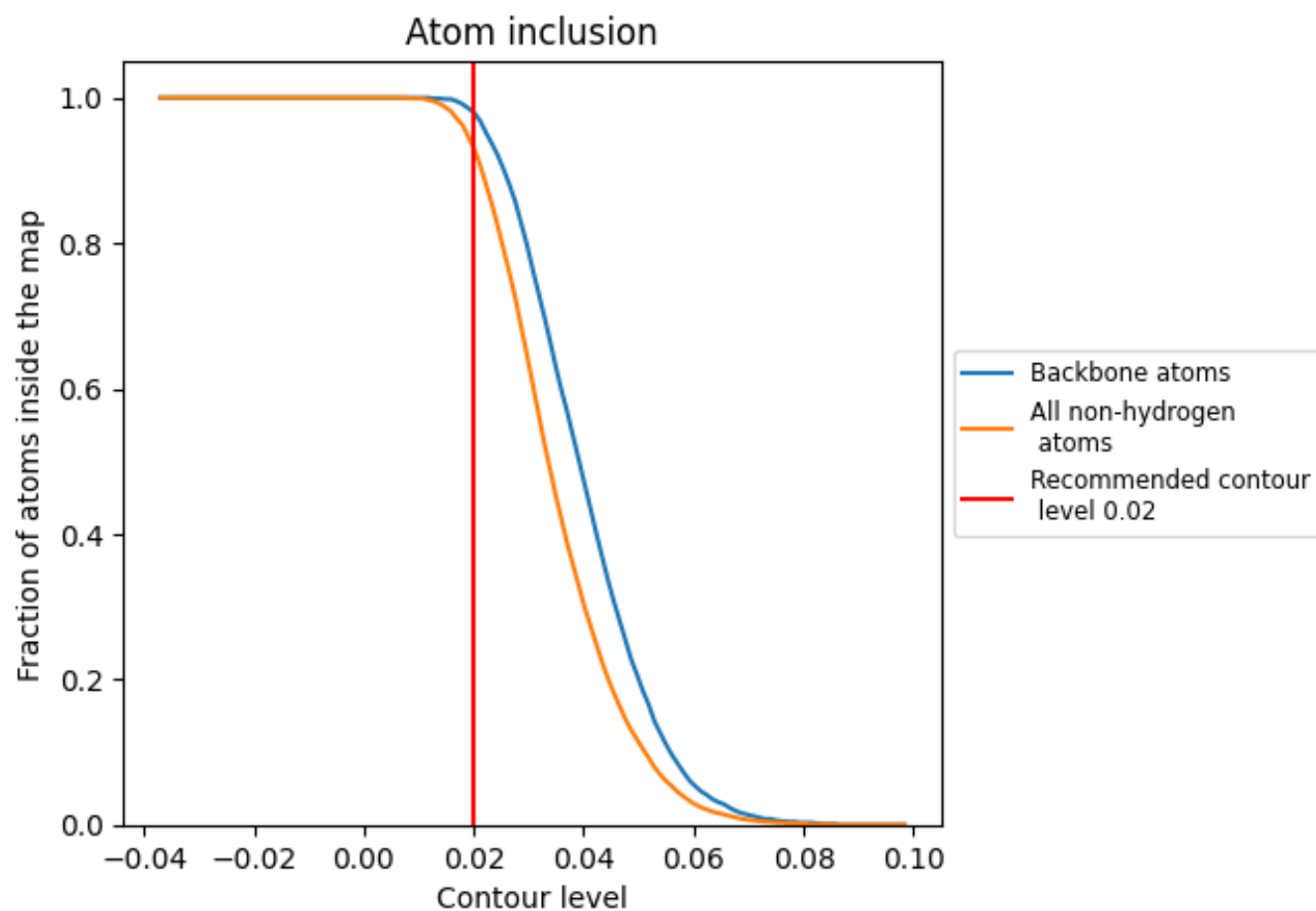
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9300	0.2350
A	0.9200	0.2020
B	0.9450	0.2670
C	0.9700	0.3120
D	0.7740	0.1470

