Full wwPDB EM Validation Report ⓘ

Oct 12, 2024 – 03:32 PM EDT

PDB ID	:	6PXV
EMDB ID	:	EMD-20522
Title	:	Cryo-EM structure of full-length insulin receptor bound to 4 insulin. 3D refinement was focused on the extracellular region.
Authors	:	Uchikawa, E.; Choi, E.; Shang, G.J.; Yu, H.T.; Bai, X.C.
Deposited on	:	2019-07-27
Resolution	:	3.20 Å(reported)

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

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

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

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

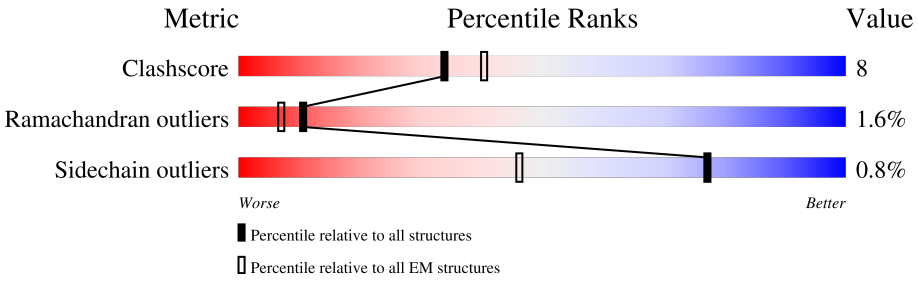
EMDB validation analysis	:	0.0.1.dev113
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	: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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1354	12% 50% 11% 39%
1	C	1354	12% 50% 11% 39%
2	D	74	55% 9% 35%
2	E	74	57% 8% 35%
2	F	74	14% 45% 15% 41%
2	G	74	14% 46% 14% 41%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 14774 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	823	Total	C	N	O	S	0	0
			6664	4231	1149	1236	48		
1	C	823	Total	C	N	O	S	0	0
			6664	4231	1149	1236	48		

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	960	PHE	TYR	conflict	UNP P06213
A	962	THR	SER	conflict	UNP P06213
A	1120	ASN	ASP	conflict	UNP P06213
A	1333	ALA	ARG	conflict	UNP P06213
A	1334	ALA	ILE	conflict	UNP P06213
A	1335	ALA	LEU	conflict	UNP P06213
A	1337	ALA	LEU	conflict	UNP P06213
A	1344	LEU	-	expression tag	UNP P06213
A	1345	GLU	-	expression tag	UNP P06213
A	1346	SER	-	expression tag	UNP P06213
A	1347	SER	-	expression tag	UNP P06213
A	1348	GLY	-	expression tag	UNP P06213
A	1349	LEU	-	expression tag	UNP P06213
A	1350	GLU	-	expression tag	UNP P06213
A	1351	VAL	-	expression tag	UNP P06213
A	1352	LEU	-	expression tag	UNP P06213
A	1353	PHE	-	expression tag	UNP P06213
A	1354	GLN	-	expression tag	UNP P06213
C	960	PHE	TYR	conflict	UNP P06213
C	962	THR	SER	conflict	UNP P06213
C	1120	ASN	ASP	conflict	UNP P06213
C	1333	ALA	ARG	conflict	UNP P06213
C	1334	ALA	ILE	conflict	UNP P06213
C	1335	ALA	LEU	conflict	UNP P06213
C	1337	ALA	LEU	conflict	UNP P06213
C	1344	LEU	-	expression tag	UNP P06213

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1345	GLU	-	expression tag	UNP P06213
C	1346	SER	-	expression tag	UNP P06213
C	1347	SER	-	expression tag	UNP P06213
C	1348	GLY	-	expression tag	UNP P06213
C	1349	LEU	-	expression tag	UNP P06213
C	1350	GLU	-	expression tag	UNP P06213
C	1351	VAL	-	expression tag	UNP P06213
C	1352	LEU	-	expression tag	UNP P06213
C	1353	PHE	-	expression tag	UNP P06213
C	1354	GLN	-	expression tag	UNP P06213

- Molecule 2 is a protein called Insulin.

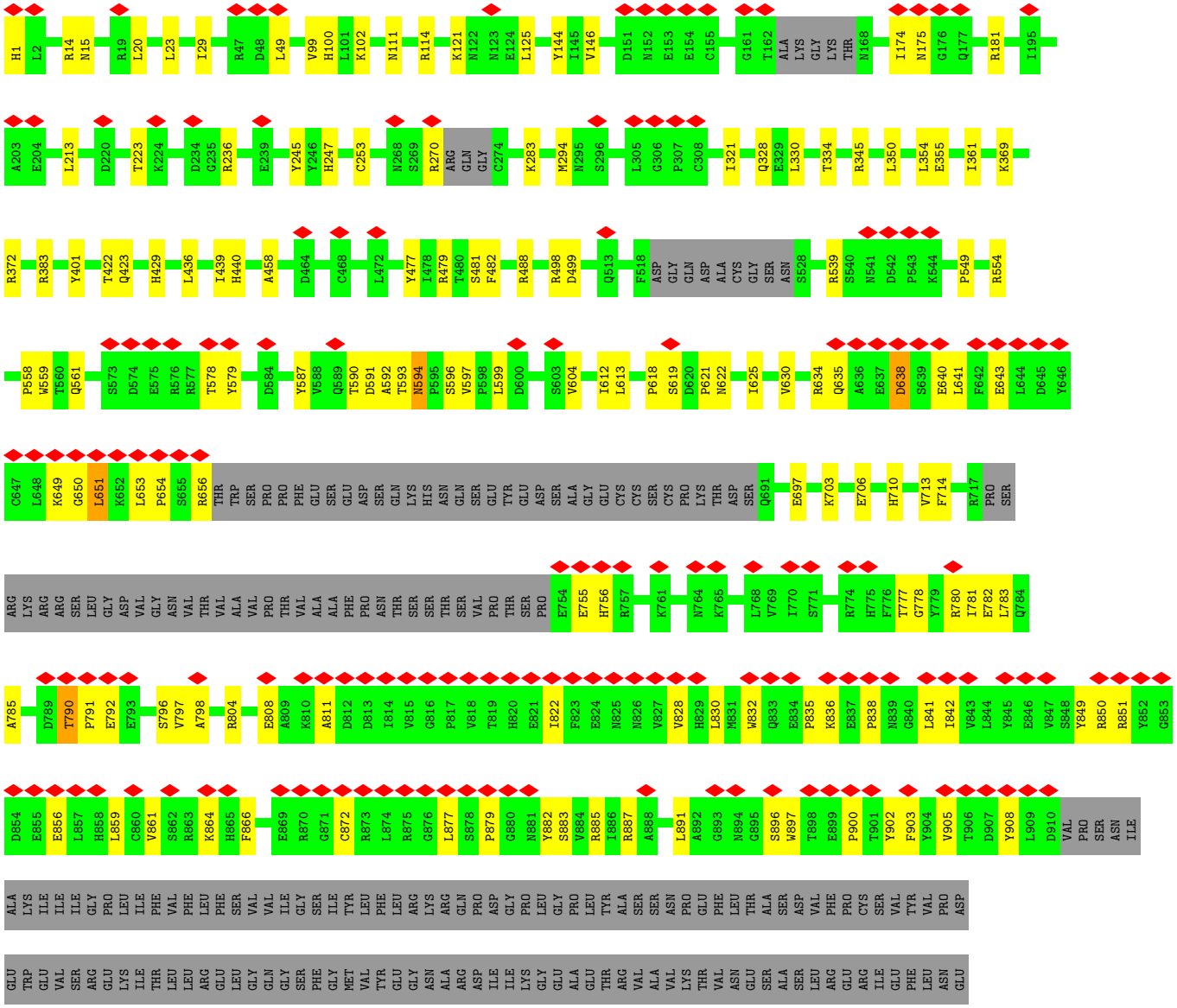
Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	48	Total	C	N	O	S	0	0
			376	238	61	71	6		
2	E	48	Total	C	N	O	S	0	0
			376	238	61	71	6		
2	F	44	Total	C	N	O	S	0	0
			347	220	56	65	6		
2	G	44	Total	C	N	O	S	0	0
			347	220	56	65	6		

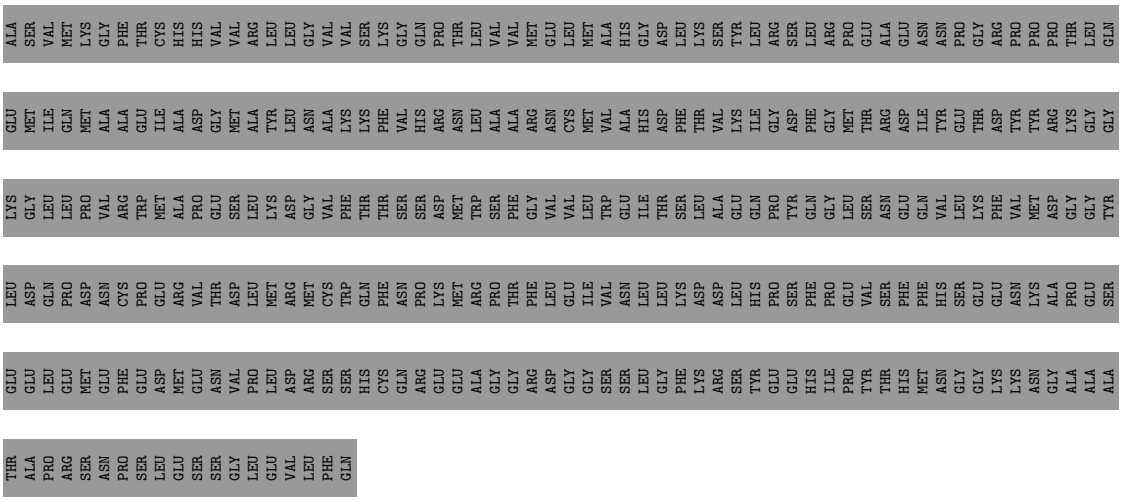
3 Residue-property plots (i)

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: Insulin receptor

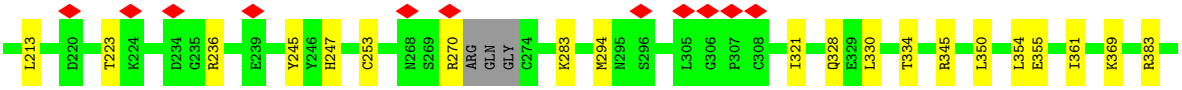
Chain A:

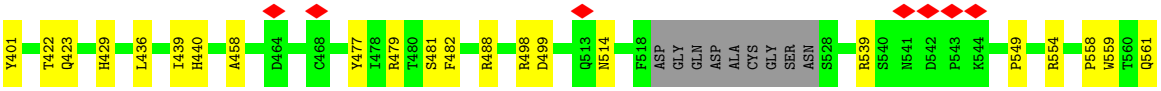


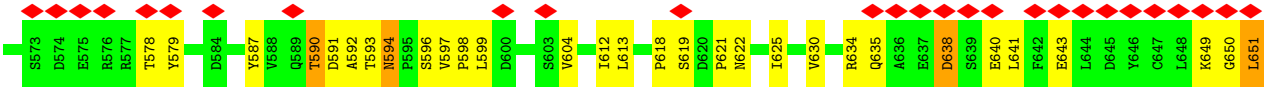


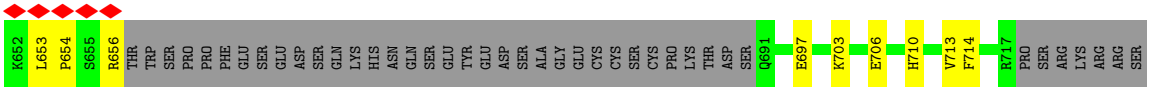
• Molecule 1: Insulin receptor

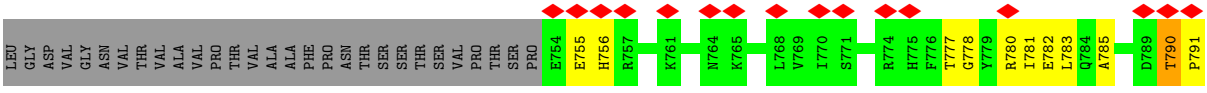
Chain C:

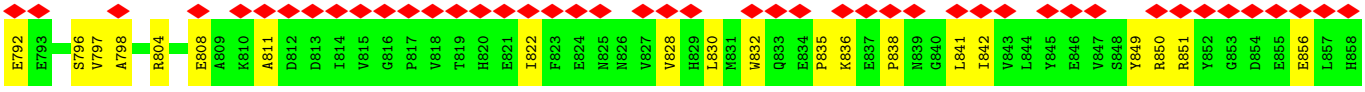


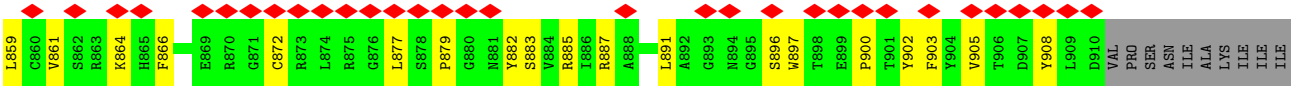


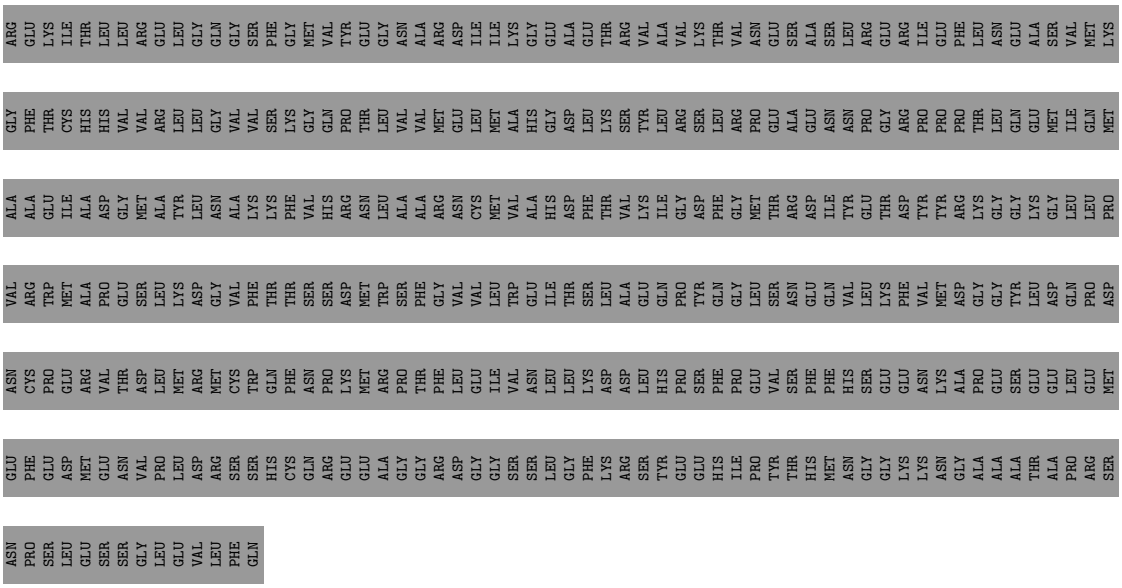






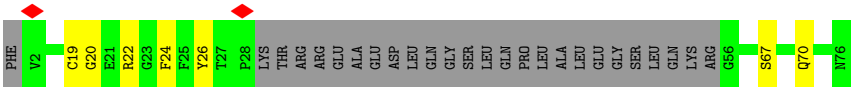






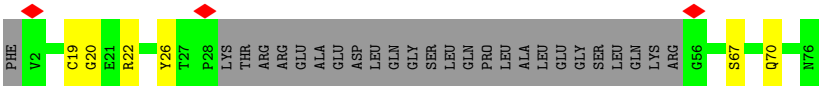
• Molecule 2: Insulin

Chain D:



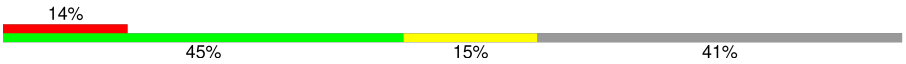
• Molecule 2: Insulin

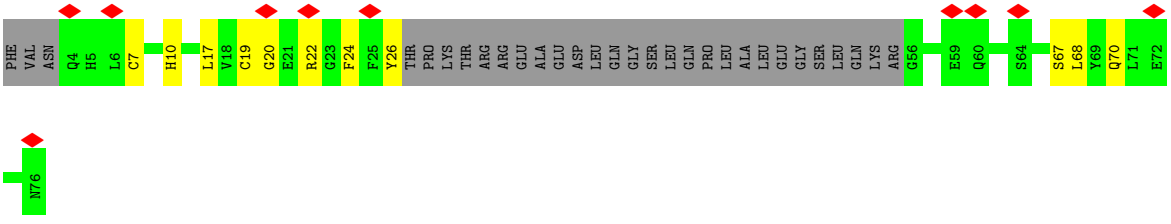
Chain E:



• Molecule 2: Insulin

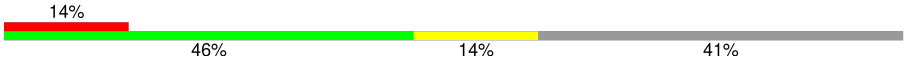
Chain F:

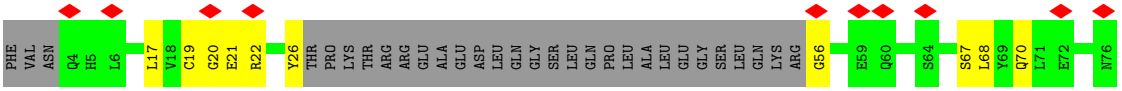




• Molecule 2: Insulin

Chain G:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	235707	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)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 IS (4k x 4k)	Depositor
Maximum map value	0.121	Depositor
Minimum map value	-0.054	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.036	Depositor
Map size (Å)	321.00003, 321.00003, 321.00003	wwPDB
Map dimensions	300, 300, 300	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

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	0.46	0/6828	0.69	0/9258
1	C	0.46	0/6828	0.70	0/9258
2	D	0.35	0/383	0.51	0/518
2	E	0.35	0/383	0.51	0/518
2	F	0.37	0/353	0.54	0/475
2	G	0.37	0/353	0.54	0/475
All	All	0.45	0/15128	0.68	0/20502

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	578	THR	Peptide
1	C	578	THR	Peptide

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	6664	0	6478	108	0
1	C	6664	0	6478	114	0
2	D	376	0	346	5	0
2	E	376	0	346	4	0
2	F	347	0	317	8	0
2	G	347	0	317	9	0
All	All	14774	0	14282	232	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 8.

All (232) 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:C:482:PHE:CZ	1:C:593:THR:HG21	1.45	1.50
1:A:482:PHE:CZ	1:A:593:THR:HG21	1.58	1.36
1:A:482:PHE:CE1	1:A:593:THR:HB	1.60	1.33
1:C:482:PHE:CZ	1:C:593:THR:CG2	2.13	1.30
1:C:482:PHE:CE1	1:C:593:THR:CG2	2.14	1.30
1:A:482:PHE:HE1	1:A:593:THR:CB	1.45	1.28
1:C:482:PHE:CE1	1:C:593:THR:HB	1.74	1.23
1:C:482:PHE:HE1	1:C:593:THR:CB	1.52	1.21
1:A:559:TRP:HB2	1:A:592:ALA:HB2	1.25	1.14
1:C:482:PHE:CE1	1:C:593:THR:CB	2.29	1.12
1:A:482:PHE:CZ	1:A:593:THR:CG2	2.34	1.10
1:C:559:TRP:HB2	1:C:592:ALA:HB2	1.17	1.10
1:A:482:PHE:CE1	1:A:593:THR:CB	2.26	1.09
1:A:482:PHE:CE1	1:A:593:THR:CG2	2.35	1.08
1:A:559:TRP:HB2	1:A:592:ALA:CB	1.88	1.03
1:A:482:PHE:HZ	1:A:593:THR:HG21	0.91	1.02
1:C:482:PHE:HE1	1:C:593:THR:HB	1.06	0.97
1:A:482:PHE:HE1	1:A:593:THR:HB	0.80	0.94
1:C:482:PHE:CE1	1:C:593:THR:HG22	2.02	0.93
1:A:559:TRP:CB	1:A:592:ALA:HB2	2.04	0.88
1:C:482:PHE:HZ	1:C:593:THR:CG2	1.66	0.86
1:A:790:THR:HB	1:A:791:PRO:HD3	1.57	0.86
1:C:790:THR:HB	1:C:791:PRO:HD3	1.57	0.85
1:C:482:PHE:HE1	1:C:593:THR:CG2	1.69	0.85
1:C:482:PHE:HZ	1:C:593:THR:HG21	0.88	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:559:TRP:HB2	1:C:592:ALA:CB	2.07	0.78
1:A:755:GLU:HG2	1:A:756:HIS:N	1.99	0.76
1:A:755:GLU:HG2	1:A:756:HIS:H	1.51	0.75
1:C:755:GLU:HG2	1:C:756:HIS:N	1.99	0.75
1:C:350:LEU:O	1:C:354:LEU:HB2	1.88	0.74
1:A:350:LEU:O	1:A:354:LEU:HB2	1.88	0.72
1:C:755:GLU:HG2	1:C:756:HIS:H	1.51	0.72
1:C:599:LEU:HD11	1:C:619:SER:HB3	1.72	0.72
1:A:599:LEU:HD11	1:A:619:SER:HB3	1.72	0.72
1:A:885:ARG:HE	1:A:897:TRP:HB3	1.56	0.70
1:C:885:ARG:HE	1:C:897:TRP:HB3	1.56	0.69
1:A:590:THR:OG1	1:A:591:ASP:N	2.27	0.68
1:C:482:PHE:CZ	1:C:593:THR:HG22	2.14	0.67
1:C:590:THR:OG1	1:C:591:ASP:N	2.27	0.67
1:C:785:ALA:H	1:C:796:SER:HB3	1.60	0.66
1:A:651:LEU:HD23	1:A:651:LEU:H	1.62	0.64
1:A:785:ALA:H	1:A:796:SER:HB3	1.60	0.64
1:A:597:VAL:HG22	1:A:797:VAL:CG2	2.28	0.64
1:C:651:LEU:H	1:C:651:LEU:HD23	1.62	0.63
1:A:808:GLU:HB2	1:A:811:ALA:HB2	1.80	0.63
1:C:808:GLU:HB2	1:C:811:ALA:HB2	1.81	0.63
1:C:597:VAL:HG22	1:C:797:VAL:CG2	2.28	0.62
1:C:559:TRP:CB	1:C:592:ALA:HB2	2.10	0.62
1:C:879:PRO:HA	1:C:905:VAL:HG23	1.82	0.61
1:A:879:PRO:HA	1:A:905:VAL:HG23	1.82	0.61
1:C:223:THR:HG22	1:C:236:ARG:HG2	1.82	0.61
1:A:643:GLU:HA	1:A:864:LYS:HE3	1.82	0.60
1:A:223:THR:HG22	1:A:236:ARG:HG2	1.82	0.60
1:C:643:GLU:HA	1:C:864:LYS:HE3	1.82	0.60
1:C:593:THR:O	1:C:594:ASN:O	2.20	0.59
1:A:558:PRO:HB3	1:A:592:ALA:HA	1.84	0.59
1:C:422:THR:HG22	1:C:423:GLN:HG3	1.86	0.57
1:C:822:ILE:HG12	1:C:828:VAL:HG22	1.86	0.57
1:C:482:PHE:HA	1:C:591:ASP:OD1	2.05	0.57
1:A:634:ARG:HD2	1:A:777:THR:HG21	1.87	0.56
1:A:422:THR:HG22	1:A:423:GLN:HG3	1.86	0.56
1:A:593:THR:O	1:A:622:ASN:HB2	2.05	0.56
1:A:822:ILE:HG12	1:A:828:VAL:HG22	1.86	0.56
1:C:634:ARG:HD2	1:C:777:THR:HG21	1.87	0.56
1:C:885:ARG:NH1	1:C:900:PRO:HD3	2.21	0.56
1:A:604:VAL:HB	1:A:612:ILE:HG13	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:835:PRO:HD2	1:A:842:ILE:HD12	1.88	0.56
1:C:835:PRO:HD2	1:C:842:ILE:HD12	1.88	0.55
1:A:885:ARG:NH1	1:A:900:PRO:HD3	2.21	0.55
1:C:558:PRO:HB3	1:C:592:ALA:HA	1.88	0.55
1:C:499:ASP:OD1	1:C:703:LYS:NZ	2.37	0.55
1:C:604:VAL:HB	1:C:612:ILE:HG13	1.88	0.55
1:C:436:LEU:O	1:C:440:HIS:ND1	2.34	0.53
1:A:482:PHE:HA	1:A:591:ASP:OD1	2.08	0.53
1:A:593:THR:O	1:A:594:ASN:O	2.25	0.53
1:C:613:LEU:HD22	1:C:781:ILE:HG21	1.91	0.53
1:C:479:ARG:NH2	2:F:17:LEU:O	2.41	0.53
1:A:477:TYR:HB3	1:A:488:ARG:HB2	1.92	0.52
1:C:355:GLU:OE2	1:C:383:ARG:NH2	2.33	0.52
1:C:477:TYR:HB3	1:C:488:ARG:HB2	1.92	0.52
1:A:479:ARG:NH2	2:G:17:LEU:O	2.42	0.52
1:A:436:LEU:O	1:A:440:HIS:ND1	2.34	0.52
1:A:613:LEU:HD22	1:A:781:ILE:HG21	1.91	0.52
1:C:593:THR:O	1:C:622:ASN:HB2	2.10	0.52
2:F:67:SER:OG	2:F:70:GLN:NE2	2.43	0.52
1:A:654:PRO:HG2	1:A:656:ARG:HH21	1.73	0.52
1:A:499:ASP:OD1	1:A:703:LYS:NZ	2.36	0.52
1:C:654:PRO:HG2	1:C:656:ARG:HH21	1.73	0.52
1:A:355:GLU:OE2	1:A:383:ARG:NH2	2.33	0.51
2:D:67:SER:OG	2:D:70:GLN:NE2	2.43	0.51
2:G:67:SER:OG	2:G:70:GLN:NE2	2.43	0.51
1:A:482:PHE:CE1	1:A:593:THR:HG22	2.41	0.51
1:A:597:VAL:HG22	1:A:797:VAL:HG23	1.92	0.51
1:C:154:GLU:OE2	2:G:56:GLY:N	2.44	0.51
1:C:597:VAL:HG22	1:C:797:VAL:HG23	1.92	0.51
1:A:23:LEU:HD11	1:A:29:ILE:HD11	1.93	0.51
1:A:247:HIS:HB2	1:A:283:LYS:HG2	1.93	0.50
1:A:635:GLN:HE21	1:A:780:ARG:HB2	1.76	0.50
2:E:67:SER:OG	2:E:70:GLN:NE2	2.43	0.50
1:A:597:VAL:HG22	1:A:797:VAL:HG22	1.93	0.50
1:A:144:TYR:CE2	1:A:146:VAL:HG12	2.46	0.50
1:C:597:VAL:HG22	1:C:797:VAL:HG22	1.93	0.50
1:A:488:ARG:HE	2:G:68:LEU:HD21	1.77	0.50
1:A:630:VAL:HG22	1:A:783:LEU:HD13	1.94	0.50
1:C:482:PHE:CE1	1:C:593:THR:HG21	1.97	0.50
1:A:144:TYR:CE2	1:A:146:VAL:CG1	2.95	0.49
1:C:247:HIS:HB2	1:C:283:LYS:HG2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:635:GLN:HE21	1:C:780:ARG:HB2	1.76	0.49
1:C:23:LEU:HD11	1:C:29:ILE:HD11	1.93	0.49
1:C:111:ASN:HD22	1:C:213:LEU:HD11	1.76	0.49
1:C:630:VAL:HG22	1:C:783:LEU:HD13	1.94	0.49
1:A:436:LEU:HD23	1:A:439:ILE:HD12	1.95	0.48
1:A:111:ASN:HD22	1:A:213:LEU:HD11	1.76	0.48
1:A:114:ARG:HH22	1:A:328:GLN:HE21	1.60	0.48
1:A:1:HIS:N	1:A:223:THR:O	2.37	0.48
1:A:481:SER:HB2	2:G:17:LEU:HD21	1.96	0.48
1:A:877:LEU:HD12	1:A:877:LEU:N	2.29	0.48
1:C:114:ARG:HH22	1:C:328:GLN:HE21	1.60	0.48
1:C:436:LEU:HD23	1:C:439:ILE:HD12	1.95	0.48
1:C:481:SER:HB2	2:F:17:LEU:HD21	1.96	0.48
1:A:593:THR:O	1:A:594:ASN:C	2.51	0.48
1:C:782:GLU:HG3	1:C:798:ALA:HB1	1.96	0.47
1:A:830:LEU:HB2	1:A:872:CYS:HB3	1.96	0.47
1:C:1:HIS:N	1:C:223:THR:O	2.37	0.47
1:C:144:TYR:CE2	1:C:146:VAL:HG12	2.49	0.47
2:E:67:SER:H	2:E:70:GLN:HE21	1.61	0.47
1:C:851:ARG:HB2	1:C:882:TYR:CE2	2.49	0.47
1:A:14:ARG:NH2	1:C:713:VAL:O	2.35	0.47
2:F:67:SER:H	2:F:70:GLN:HE21	1.61	0.47
1:A:559:TRP:HB2	1:A:592:ALA:HB3	1.88	0.47
1:A:481:SER:O	1:A:591:ASP:OD1	2.33	0.47
1:A:782:GLU:HG3	1:A:798:ALA:HB1	1.97	0.47
1:A:851:ARG:HB2	1:A:882:TYR:CE2	2.49	0.47
1:A:345:ARG:NH1	1:C:697:GLU:OE1	2.46	0.47
1:C:877:LEU:HD12	1:C:877:LEU:N	2.29	0.47
2:G:67:SER:H	2:G:70:GLN:HE21	1.61	0.47
2:D:67:SER:H	2:D:70:GLN:HE21	1.61	0.47
1:C:859:LEU:HD23	1:C:872:CYS:SG	2.55	0.47
2:E:19:CYS:SG	2:E:22:ARG:NH2	2.88	0.46
2:G:19:CYS:SG	2:G:22:ARG:NH2	2.88	0.46
1:A:706:GLU:O	1:A:710:HIS:ND1	2.45	0.46
2:D:19:CYS:SG	2:D:22:ARG:NH2	2.88	0.46
1:C:830:LEU:HB2	1:C:872:CYS:HB3	1.96	0.46
2:F:19:CYS:SG	2:F:22:ARG:NH2	2.88	0.46
1:C:334:THR:HA	1:C:361:ILE:HA	1.97	0.46
1:A:621:PRO:HB3	1:A:625:ILE:HD11	1.98	0.46
1:C:144:TYR:CE2	1:C:146:VAL:CG1	2.98	0.46
1:A:697:GLU:OE1	1:C:345:ARG:NH1	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:477:TYR:OH	2:G:21:GLU:OE2	2.34	0.46
1:C:481:SER:O	1:C:591:ASP:OD1	2.34	0.46
1:C:593:THR:O	1:C:594:ASN:C	2.54	0.46
1:C:885:ARG:HH12	1:C:900:PRO:HD3	1.81	0.46
1:C:498:ARG:NH1	1:C:706:GLU:OE1	2.48	0.45
1:A:334:THR:HA	1:A:361:ILE:HA	1.97	0.45
1:A:859:LEU:HD23	1:A:872:CYS:SG	2.55	0.45
1:C:706:GLU:O	1:C:710:HIS:ND1	2.45	0.45
2:F:24:PHE:CD2	2:F:26:TYR:HB2	2.51	0.45
2:G:26:TYR:CD1	2:G:26:TYR:C	2.90	0.45
1:A:885:ARG:HH12	1:A:900:PRO:HD3	1.81	0.45
1:C:621:PRO:HB3	1:C:625:ILE:HD11	1.98	0.45
1:C:828:VAL:HG21	1:C:903:PHE:CE1	2.51	0.45
1:A:713:VAL:O	1:C:14:ARG:NH2	2.35	0.45
1:A:861:VAL:HG12	1:A:866:PHE:HB2	1.99	0.45
1:A:828:VAL:HG21	1:A:903:PHE:CE1	2.52	0.44
1:C:369:LYS:HG3	1:C:401:TYR:HB3	1.99	0.44
1:A:498:ARG:NH1	1:A:706:GLU:OE1	2.48	0.44
1:A:369:LYS:HG3	1:A:401:TYR:HB3	1.99	0.44
1:C:832:TRP:HH2	1:C:872:CYS:HB2	1.82	0.44
1:A:832:TRP:HH2	1:A:872:CYS:HB2	1.82	0.44
1:A:849:TYR:HA	1:A:883:SER:O	2.17	0.44
1:C:755:GLU:CG	1:C:756:HIS:H	2.27	0.44
1:A:640:GLU:CD	1:A:640:GLU:H	2.21	0.44
1:A:641:LEU:HB3	1:A:841:LEU:HD21	1.99	0.44
2:F:7:CYS:O	2:F:10:HIS:HB2	2.18	0.44
1:C:641:LEU:HB3	1:C:841:LEU:HD21	1.99	0.44
1:C:850:ARG:NH2	1:C:856:GLU:HB2	2.33	0.43
1:C:849:TYR:HA	1:C:883:SER:O	2.17	0.43
1:C:861:VAL:HG12	1:C:866:PHE:HB2	1.99	0.43
1:C:102:LYS:HA	1:C:125:LEU:HA	2.00	0.43
1:A:651:LEU:H	1:A:651:LEU:CD2	2.30	0.43
1:A:710:HIS:HD2	1:A:714:PHE:HE2	1.66	0.43
1:A:144:TYR:HE2	1:A:146:VAL:HG12	1.83	0.43
1:C:429:HIS:CE1	1:C:458:ALA:HB2	2.54	0.43
1:A:832:TRP:CH2	1:A:872:CYS:HB2	2.54	0.43
1:A:850:ARG:NH2	1:A:856:GLU:HB2	2.33	0.43
1:C:640:GLU:CD	1:C:640:GLU:H	2.21	0.43
1:A:596:SER:HB3	1:A:618:PRO:HB2	2.01	0.43
1:C:778:GLY:HA2	1:C:804:ARG:HA	2.01	0.43
1:C:832:TRP:CH2	1:C:872:CYS:HB2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:ILE:HB	1:A:181:ARG:HH22	1.84	0.43
1:C:596:SER:HB3	1:C:618:PRO:HB2	2.01	0.42
1:C:710:HIS:HD2	1:C:714:PHE:HE2	1.66	0.42
1:C:790:THR:HB	1:C:791:PRO:CD	2.40	0.42
1:A:654:PRO:HB2	1:A:656:ARG:HE	1.84	0.42
1:C:593:THR:O	1:C:622:ASN:CB	2.67	0.42
1:A:429:HIS:CE1	1:A:458:ALA:HB2	2.54	0.42
1:C:14:ARG:CZ	2:E:26:TYR:HB2	2.49	0.42
1:A:245:TYR:HB3	1:A:253:CYS:HB3	2.01	0.42
1:C:653:LEU:HD21	1:C:891:LEU:HD23	2.01	0.42
1:A:102:LYS:HA	1:A:125:LEU:HA	2.01	0.42
1:C:654:PRO:HB2	1:C:656:ARG:HE	1.84	0.42
1:A:561:GLN:HE21	1:A:587:TYR:HB3	1.85	0.42
1:A:778:GLY:HA2	1:A:804:ARG:HA	2.01	0.42
1:C:321:ILE:HD11	1:C:330:LEU:HD12	2.01	0.42
1:A:593:THR:O	1:A:622:ASN:CB	2.67	0.41
1:A:653:LEU:HD21	1:A:891:LEU:HD23	2.01	0.41
1:C:147:LEU:HD23	1:C:147:LEU:HA	1.93	0.41
1:C:558:PRO:CB	1:C:592:ALA:HA	2.50	0.41
1:C:514:ASN:OD1	1:C:514:ASN:N	2.51	0.41
1:C:174:ILE:HB	1:C:181:ARG:HH22	1.84	0.41
1:C:245:TYR:HB3	1:C:253:CYS:HB3	2.01	0.41
1:C:488:ARG:HE	2:F:68:LEU:HD21	1.84	0.41
1:A:15:ASN:HD21	2:D:24:PHE:H	1.68	0.41
1:C:887:ARG:HB2	1:C:897:TRP:CD2	2.56	0.41
1:A:321:ILE:HD11	1:A:330:LEU:HD12	2.01	0.41
1:A:14:ARG:CZ	2:D:26:TYR:HB2	2.51	0.41
1:C:561:GLN:HE21	1:C:587:TYR:HB3	1.85	0.41
1:C:598:PRO:HG2	1:C:783:LEU:HG	2.03	0.41
1:A:121:LYS:NZ	1:C:706:GLU:OE2	2.44	0.41
1:A:885:ARG:HE	1:A:897:TRP:CB	2.29	0.41
1:A:887:ARG:HB2	1:A:897:TRP:CD2	2.56	0.41
1:C:350:LEU:O	1:C:354:LEU:CB	2.65	0.41
1:A:345:ARG:HH21	1:A:372:ARG:HD2	1.86	0.41
1:C:99:VAL:HG12	1:C:100:HIS:CD2	2.56	0.41
1:C:597:VAL:HA	1:C:796:SER:HG	1.86	0.41
1:A:882:TYR:O	1:A:902:TYR:HA	2.21	0.40
1:A:20:LEU:HD23	1:A:49:LEU:HD21	2.03	0.40
1:C:755:GLU:CG	1:C:756:HIS:N	2.77	0.40
1:A:99:VAL:HG12	1:A:100:HIS:CD2	2.56	0.40
1:C:882:TYR:O	1:C:902:TYR:HA	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:TYR:HE2	1:A:146:VAL:CG1	2.33	0.40
1:C:20:LEU:HD23	1:C:49:LEU:HD21	2.03	0.40

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	811/1354 (60%)	719 (89%)	80 (10%)	12 (2%)	8	38
1	C	811/1354 (60%)	719 (89%)	79 (10%)	13 (2%)	8	37
2	D	44/74 (60%)	41 (93%)	2 (4%)	1 (2%)	5	29
2	E	44/74 (60%)	41 (93%)	2 (4%)	1 (2%)	5	29
2	F	40/74 (54%)	37 (92%)	2 (5%)	1 (2%)	4	28
2	G	40/74 (54%)	37 (92%)	2 (5%)	1 (2%)	4	28
All	All	1790/3004 (60%)	1594 (89%)	167 (9%)	29 (2%)	10	37

All (29) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	649	LYS
1	A	790	THR
1	A	896	SER
1	C	649	LYS
1	C	790	THR
1	C	896	SER
1	A	579	TYR
1	A	638	ASP
1	C	579	TYR
1	C	594	ASN

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Mol	Chain	Res	Type
1	C	638	ASP
1	A	650	GLY
1	C	650	GLY
1	A	594	ASN
1	A	792	GLU
1	C	792	GLU
1	A	836	LYS
1	A	908	TYR
1	C	590	THR
1	C	836	LYS
1	C	908	TYR
1	A	838	PRO
1	C	838	PRO
1	A	549	PRO
2	D	20	GLY
2	E	20	GLY
2	F	20	GLY
2	G	20	GLY
1	C	549	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	751/1209 (62%)	744 (99%)	7 (1%)	75 89
1	C	751/1209 (62%)	744 (99%)	7 (1%)	75 89
2	D	43/65 (66%)	43 (100%)	0	100 100
2	E	43/65 (66%)	43 (100%)	0	100 100
2	F	39/65 (60%)	39 (100%)	0	100 100
2	G	39/65 (60%)	39 (100%)	0	100 100
All	All	1666/2678 (62%)	1652 (99%)	14 (1%)	77 90

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	175	ASN
1	A	270	ARG
1	A	294	MET
1	A	539	ARG
1	A	554	ARG
1	A	638	ASP
1	A	651	LEU
1	C	175	ASN
1	C	270	ARG
1	C	294	MET
1	C	539	ARG
1	C	554	ARG
1	C	638	ASP
1	C	651	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	ASN
1	A	32	HIS
1	A	34	GLN
1	A	100	HIS
1	A	175	ASN
1	A	209	HIS
1	A	546	GLN
1	A	561	GLN
1	A	610	GLN
1	A	635	GLN
1	C	15	ASN
1	C	32	HIS
1	C	34	GLN
1	C	100	HIS
1	C	175	ASN
1	C	209	HIS
1	C	546	GLN
1	C	561	GLN
1	C	610	GLN
1	C	635	GLN
2	D	3	ASN
2	D	70	GLN
2	E	3	ASN
2	E	10	HIS
2	E	70	GLN

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Mol	Chain	Res	Type
2	F	70	GLN
2	G	70	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)

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.

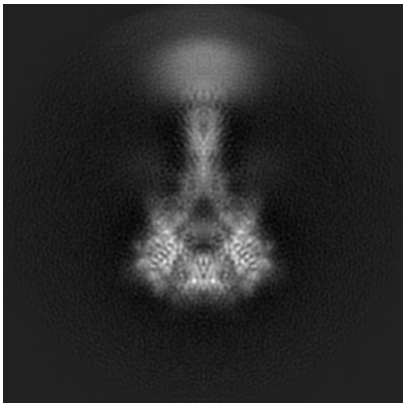
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-20522. These allow visual inspection of the internal detail of the map and identification of artifacts.

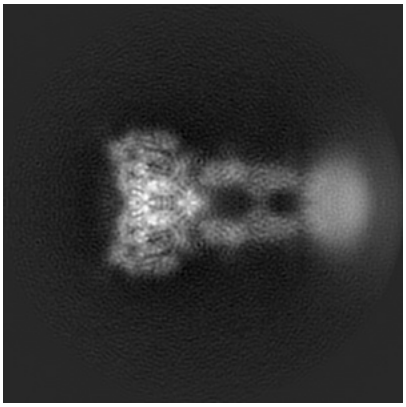
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

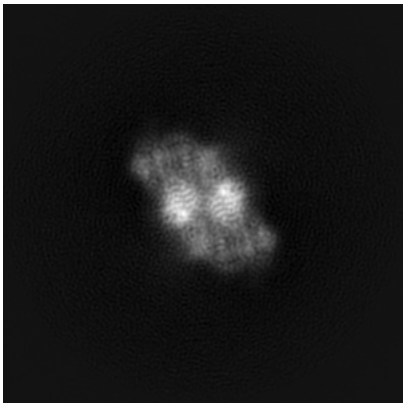
6.1.1 Primary map



X



Y

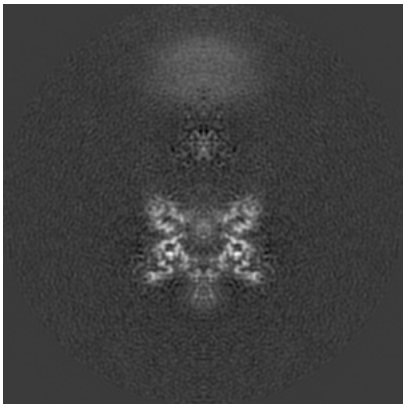


Z

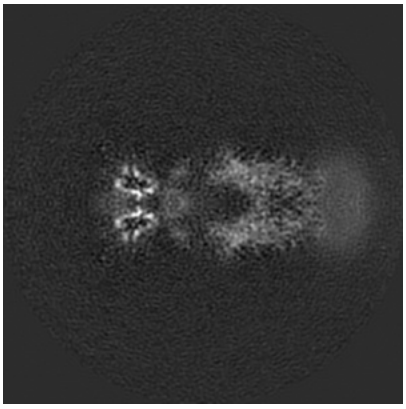
The images above show the map projected in three orthogonal directions.

6.2 Central slices

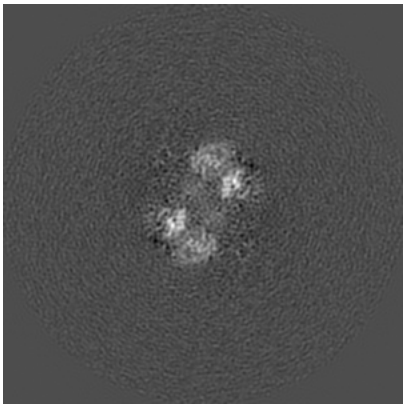
6.2.1 Primary map



X Index: 150



Y Index: 150

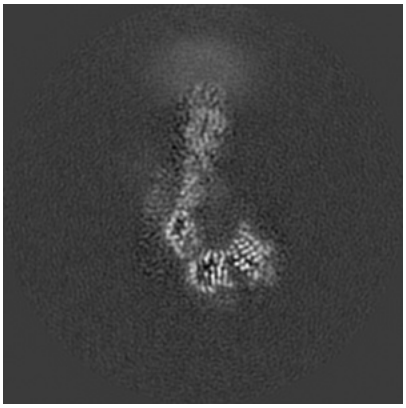


Z Index: 150

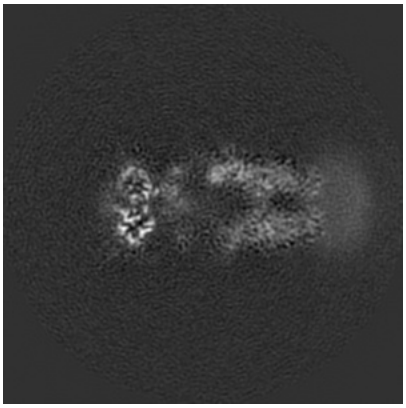
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

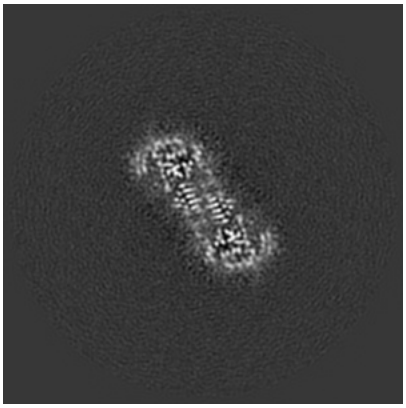
6.3.1 Primary map



X Index: 135



Y Index: 153

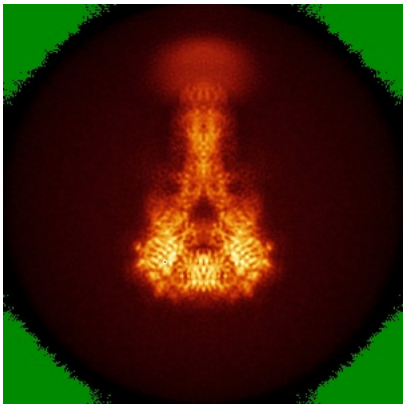


Z Index: 107

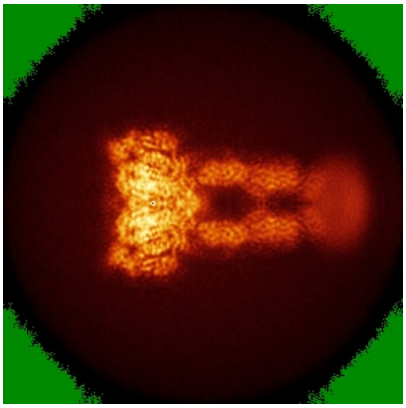
The images above show the largest variance slices of the map in three orthogonal directions.

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

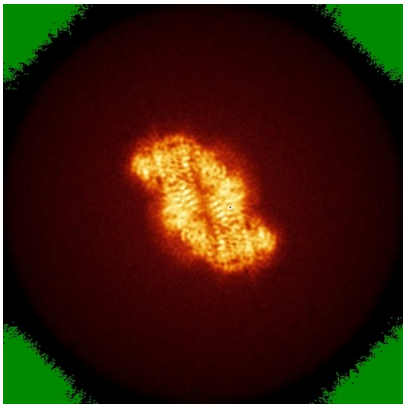
6.4.1 Primary map



X



Y

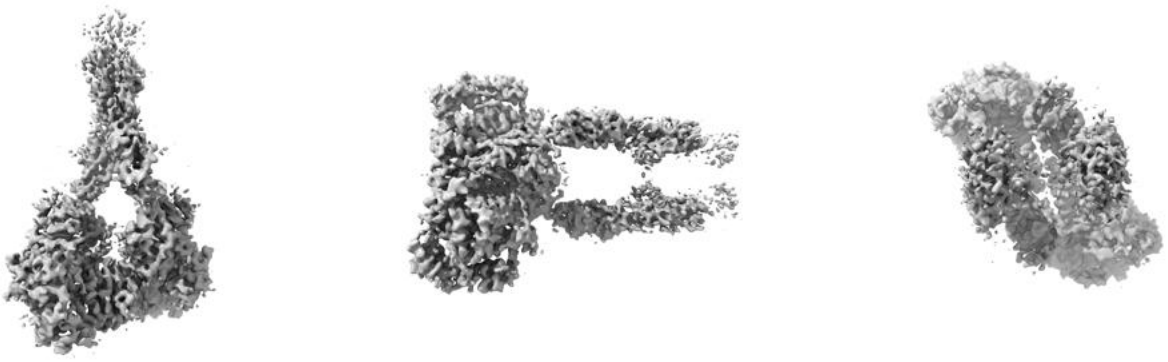


Z

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 0.036. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

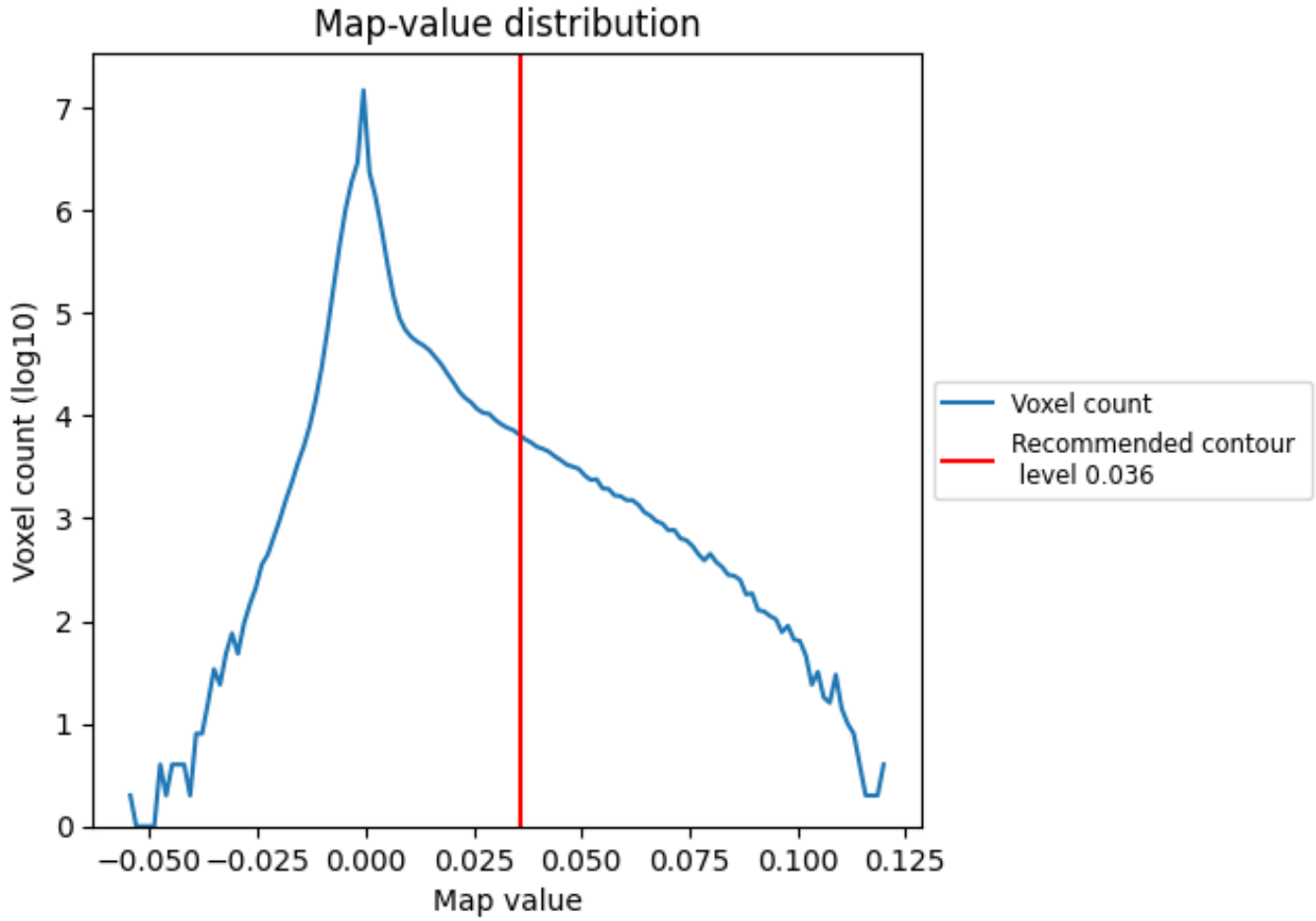
6.6 Mask visualisation (i)

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

7 Map analysis

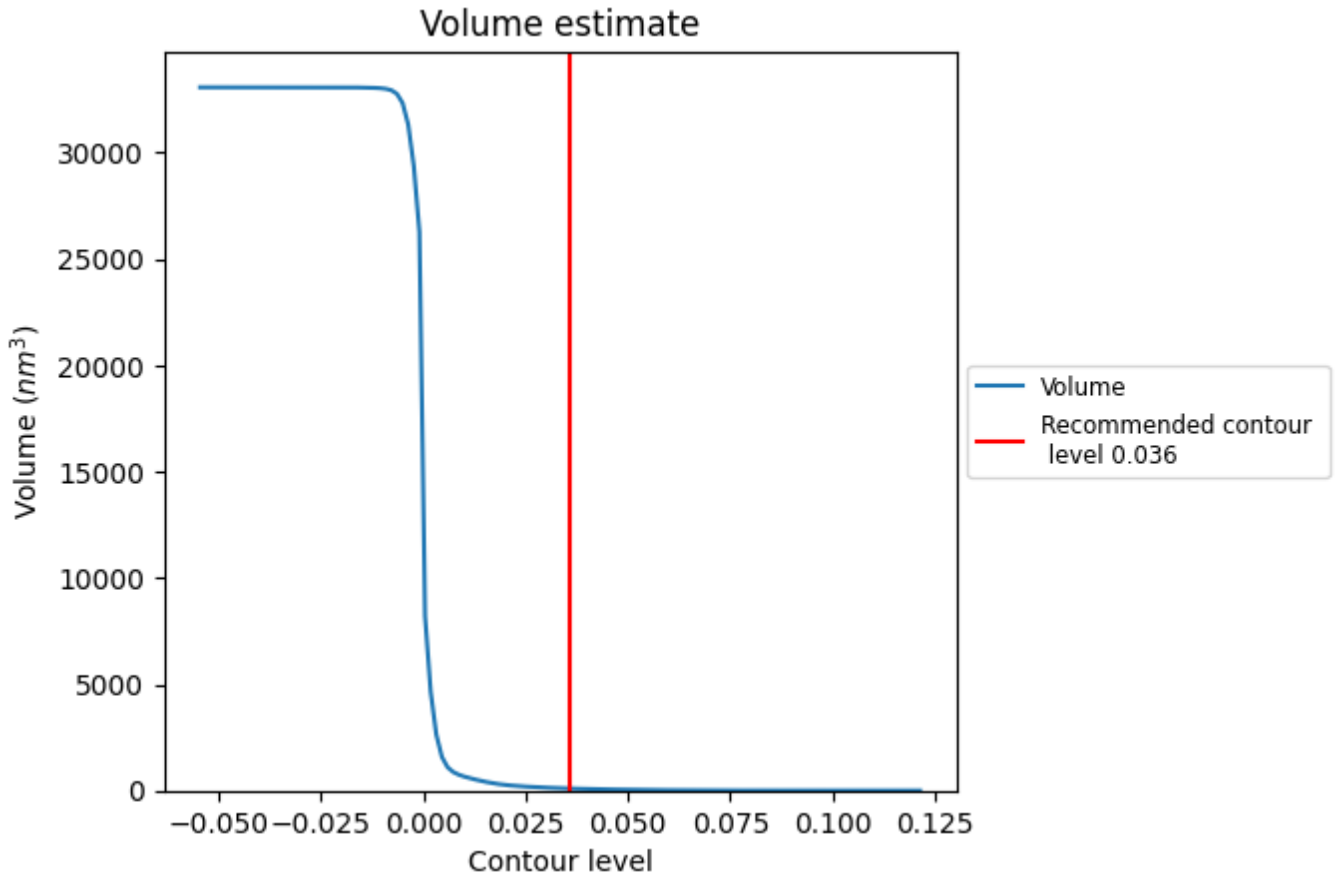
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

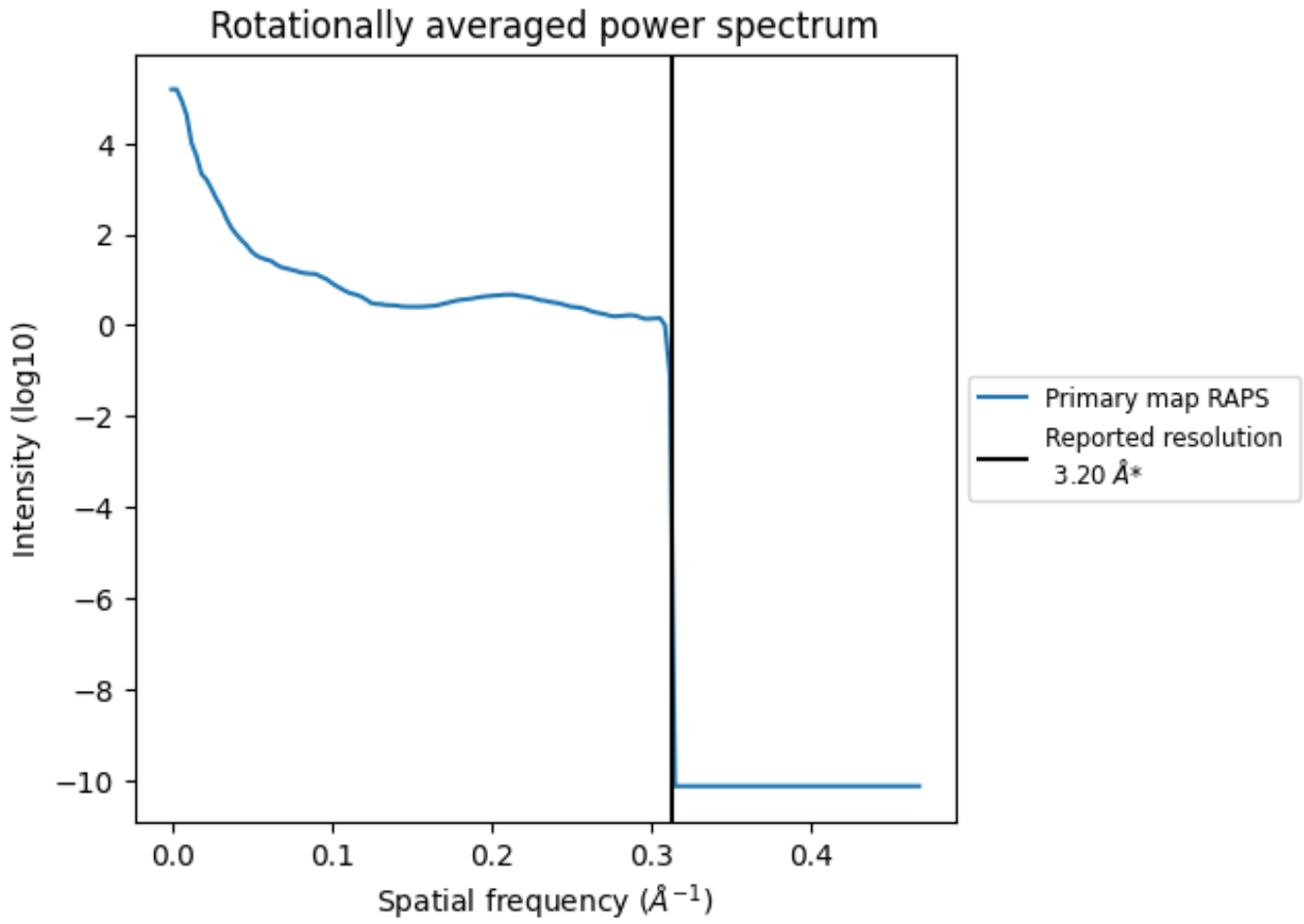
7.2 Volume estimate



The volume at the recommended contour level is 95 nm^3; this corresponds to an approximate mass of 86 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 0.312 Å^{-1}

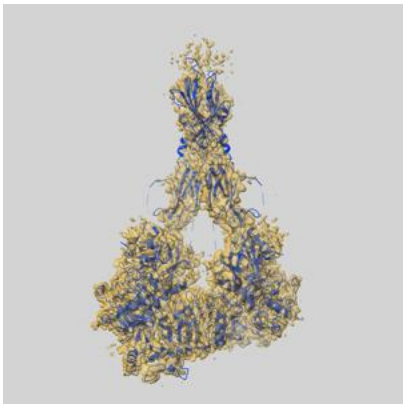
8 Fourier-Shell correlation

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

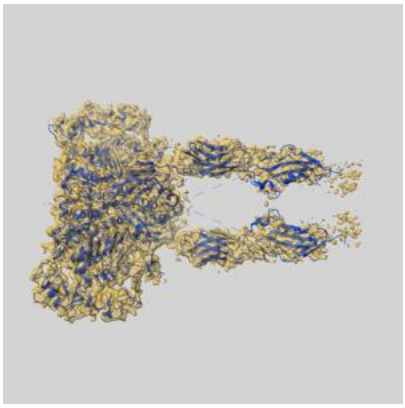
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-20522 and PDB model 6PXV. Per-residue inclusion information can be found in section 3 on page 5.

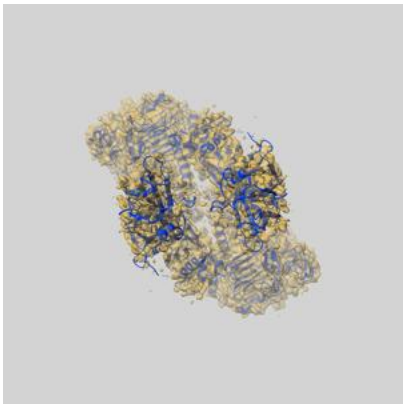
9.1 Map-model overlay



X



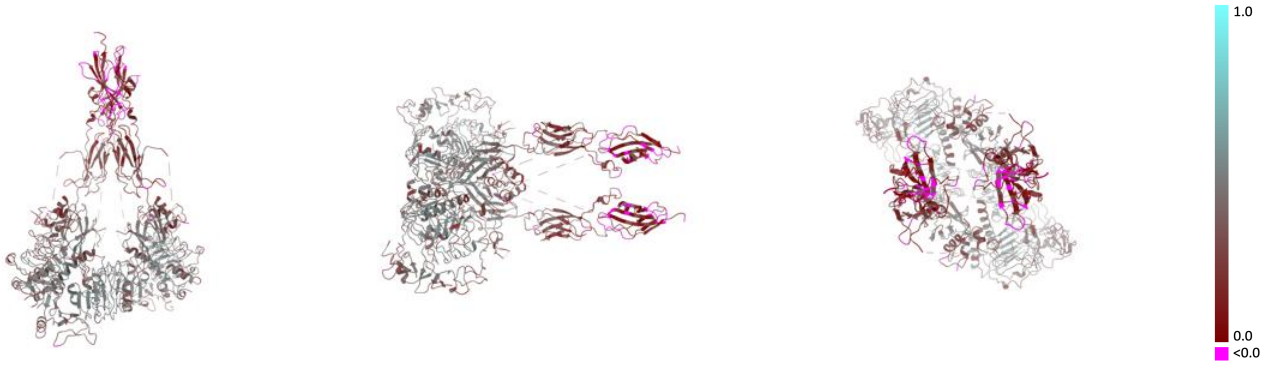
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.036 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.

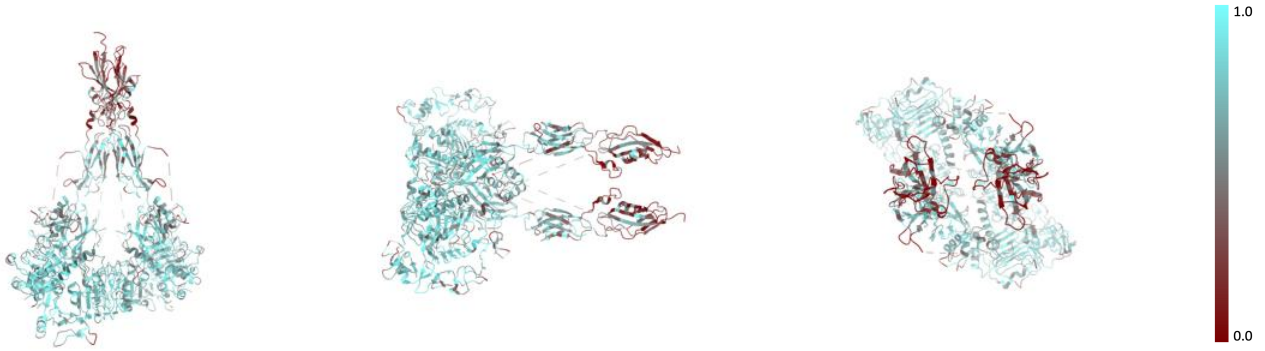
9.2 Q-score mapped to coordinate model (i)



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.

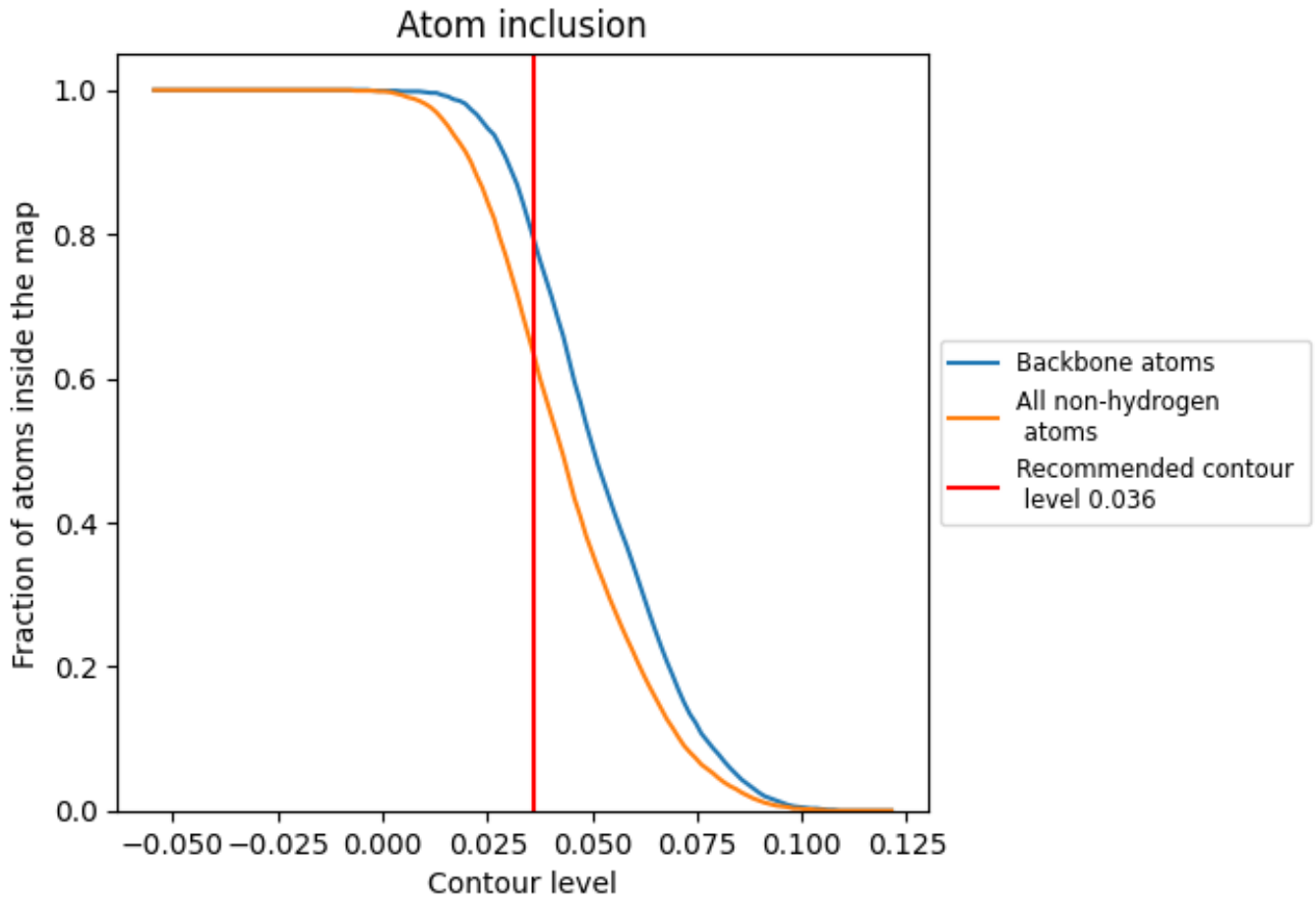
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.036).

9.4 Atom inclusion (i)



At the recommended contour level, 79% of all backbone atoms, 63% 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 (0.036) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6340	0.3520
A	0.6320	0.3540
C	0.6340	0.3530
D	0.7080	0.3970
E	0.6970	0.3940
F	0.5780	0.2860
G	0.5780	0.2840