



Full wwPDB EM Validation Report ⓘ

Nov 15, 2022 – 12:36 AM EST

PDB ID : 6W4O
EMDB ID : EMD-21535
Title : CaMKII alpha-30 Cryo-EM reconstruction
Authors : Chao, L.H.; Stratton, M.M.
Deposited on : 2020-03-11
Resolution : 4.80 Å(reported)
Based on initial models : 5IG3, 3SOA

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:

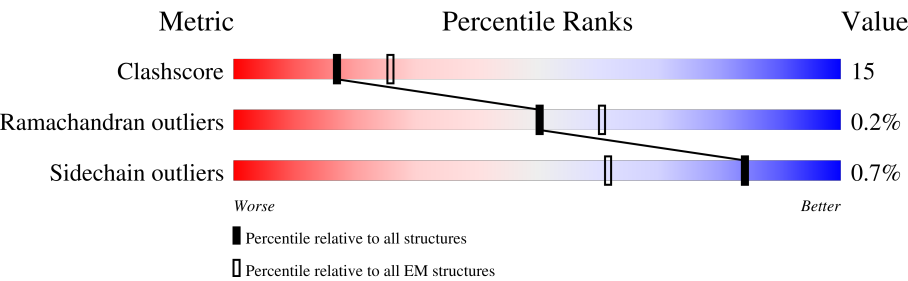
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 4.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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

Mol	Chain	Length	Quality of chain
1	A	473	<div><div>25%</div><div>73%</div></div>
1	B	473	<div><div>23%</div><div>73%</div></div>
1	C	473	<div><div>22%</div><div>73%</div></div>
1	D	473	<div><div>22%</div><div>74%</div></div>
1	E	473	<div><div>21%</div><div>5%</div><div>74%</div></div>
1	F	473	<div><div>22%</div><div>74%</div></div>
1	G	473	<div><div>25%</div><div>73%</div></div>
1	I	473	<div><div>23%</div><div>73%</div></div>

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Mol	Chain	Length	Quality of chain
1	J	473	<div><div></div><div>21%5%73%</div></div>
1	K	473	<div><div></div><div>22%.74%</div></div>
1	L	473	<div><div></div><div>22%.74%</div></div>
1	M	473	<div><div></div><div>22%.74%</div></div>
2	O	473	<div><div></div><div>26%34%.38%</div></div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 14475 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 Calcium/calmodulin-dependent protein kinase type II subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	128	Total	C	N	O	S	0	0
			1040	658	186	191	5		
1	B	126	Total	C	N	O	S	0	0
			1023	650	181	187	5		
1	C	126	Total	C	N	O	S	0	0
			1022	648	181	188	5		
1	D	123	Total	C	N	O	S	0	0
			994	630	176	183	5		
1	E	123	Total	C	N	O	S	0	0
			994	630	176	183	5		
1	F	122	Total	C	N	O	S	0	0
			988	625	176	182	5		
1	G	128	Total	C	N	O	S	0	0
			1041	658	187	191	5		
1	I	126	Total	C	N	O	S	0	0
			1023	650	181	187	5		
1	J	126	Total	C	N	O	S	0	0
			1022	648	181	188	5		
1	K	123	Total	C	N	O	S	0	0
			994	630	176	183	5		
1	L	123	Total	C	N	O	S	0	0
			994	630	176	183	5		
1	M	122	Total	C	N	O	S	0	0
			988	625	176	182	5		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-322	SER	-	expression tag	UNP Q9UQM7
B	-337	SER	-	expression tag	UNP Q9UQM7
C	-332	SER	-	expression tag	UNP Q9UQM7
D	-334	SER	-	expression tag	UNP Q9UQM7
E	-336	SER	-	expression tag	UNP Q9UQM7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-337	SER	-	expression tag	UNP Q9UQM7
G	-322	SER	-	expression tag	UNP Q9UQM7
I	-337	SER	-	expression tag	UNP Q9UQM7
J	-332	SER	-	expression tag	UNP Q9UQM7
K	-334	SER	-	expression tag	UNP Q9UQM7
L	-336	SER	-	expression tag	UNP Q9UQM7
M	-337	SER	-	expression tag	UNP Q9UQM7

- Molecule 2 is a protein called Calcium/calmodulin-dependent protein kinase type II subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	O	293	Total	C	N	O	S	0	0
			2352	1503	415	423	11		

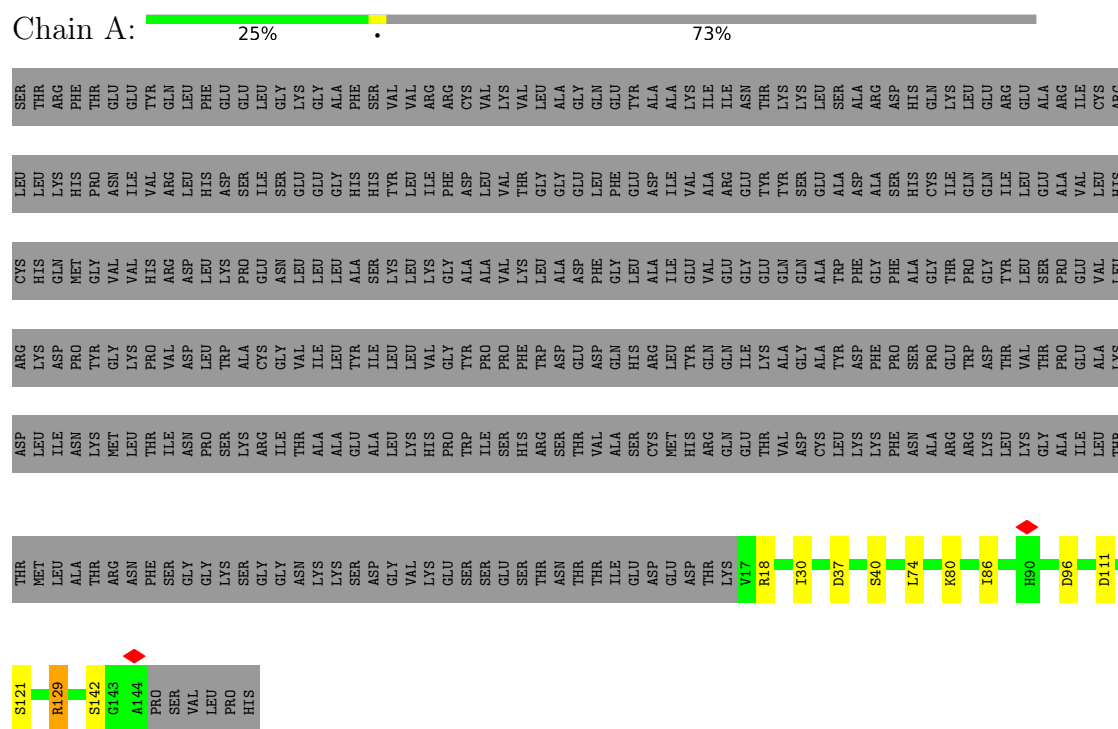
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	0	SER	-	expression tag	UNP Q9UQM7
O	34	MET	LYS	engineered mutation	UNP Q9UQM7
O	127	ASN	ASP	conflict	UNP Q9UQM7

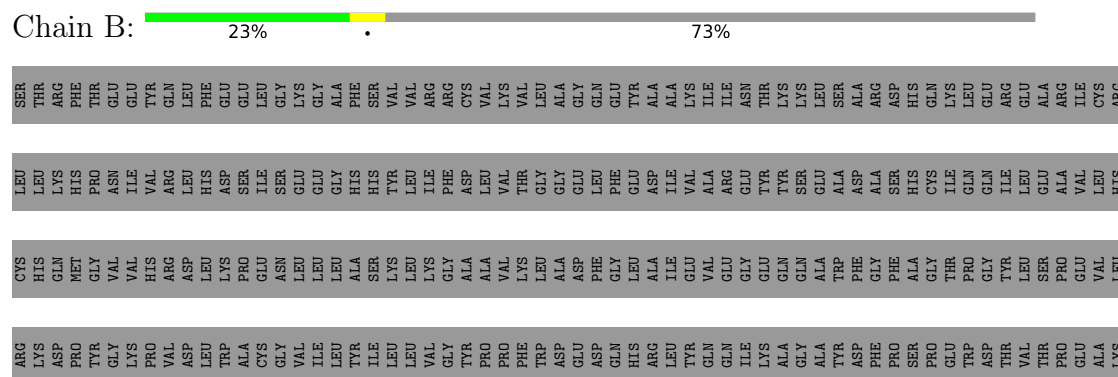
3 Residue-property plots

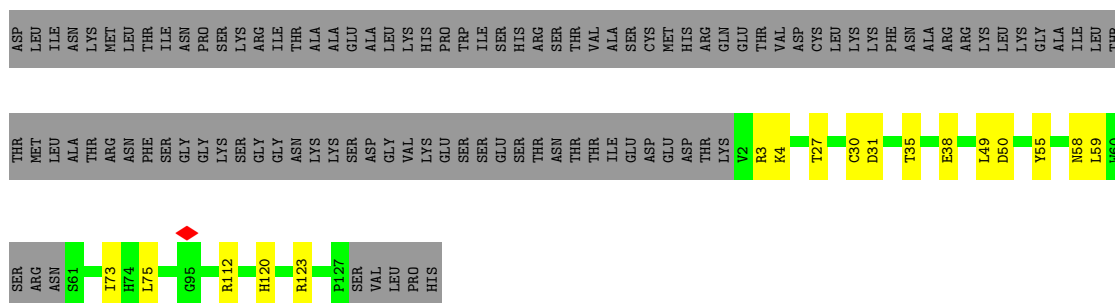
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Calcium/calmodulin-dependent protein kinase type II subunit alpha



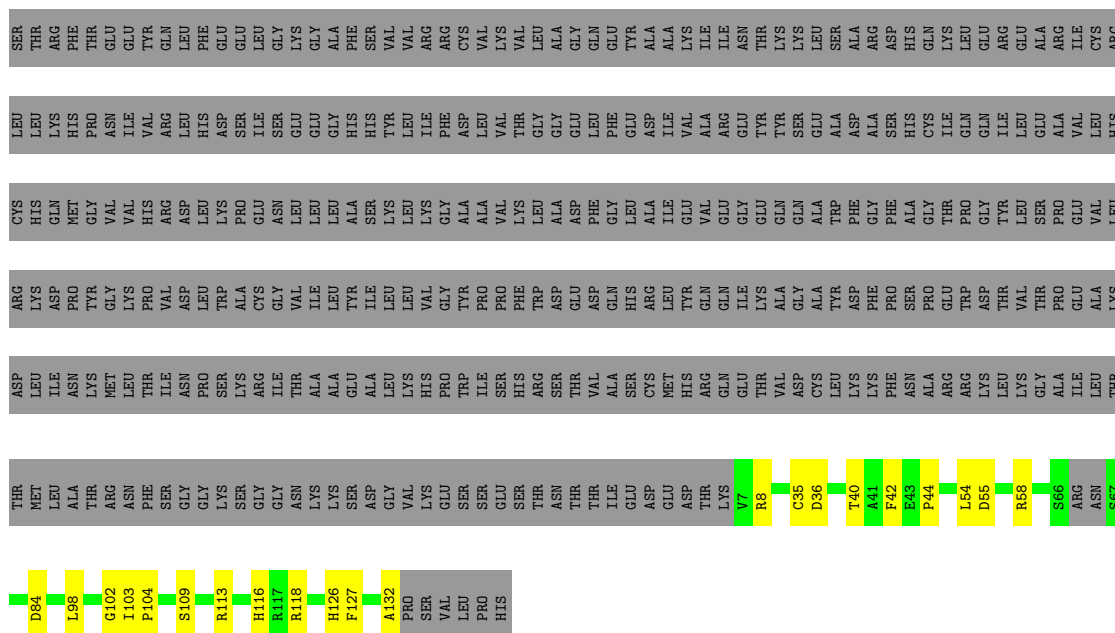
- Molecule 1: Calcium/calmodulin-dependent protein kinase type II subunit alpha





- Molecule 1: Calcium/calmodulin-dependent protein kinase type II subunit alpha

Chain C:  22%  73%



- Molecule 1: Calcium/calmodulin-dependent protein kinase type II subunit alpha

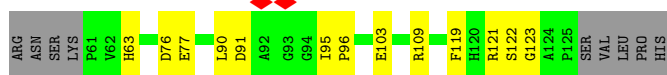
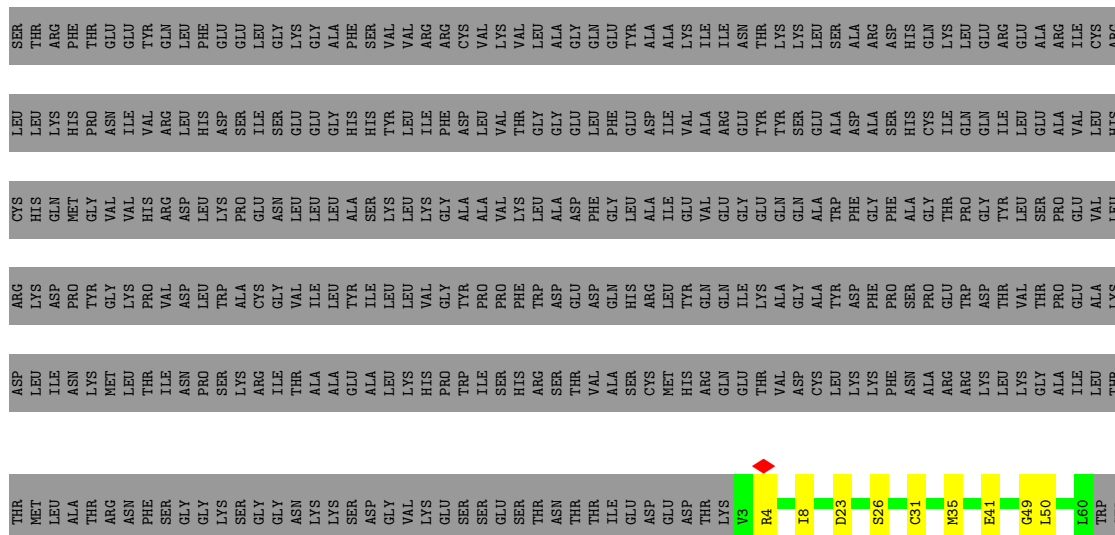
Chain D:  22%  74%





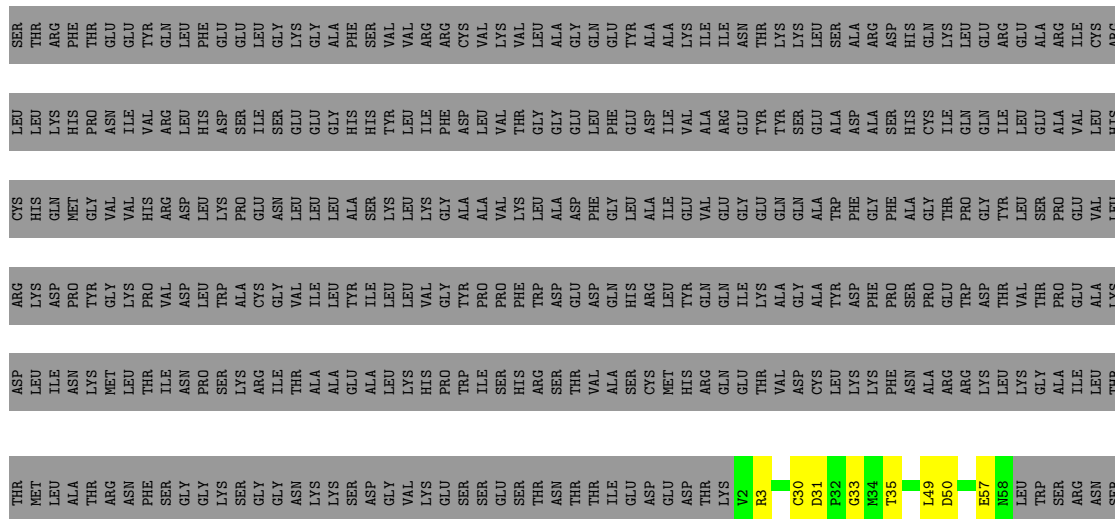
- Molecule 1: Calcium/calmodulin-dependent protein kinase type II subunit alpha

Chain E: 21% 5% 74%



- Molecule 1: Calcium/calmodulin-dependent protein kinase type II subunit alpha

Chain F: 22% 1% 74%



R212	R213	I217	K218	D223	F224	P225	S226	P227	E228	W229	D230	T231	V232	T233	P234	E235	A236	L239	I240	L244	I252	T253	A254	A255	L258	K259	H260	P261	W262	I263	S264	H265	R266	S267	T268	V269	A270	S271	C272	M273	H274	R275	T278	V279	L282	W286	R289	K290	L291										
K292	C293	ALA	ILE	LEU	THR	THR	MET	LEU	ALA	THR	THR	ARG	ASN	PHE	SER	GLY	GLY	LYS	SER	GLY	ASN	LYS	LYS	SER	ASP	GLY	VAL	LYS	GLU	SER	THR	ASN	THR	THR	ILE	GLU	ASP	GLU	ASP	THR	LYS	VAL	ARG	LYS	GLN	GLU	ILE	ILE	LYS	THR	VAL	THR	ILE	GLN	ASN	PRO	HIS	ILE	GLU
ALA	ILE	SER	ASN	GLY	ASP	PHE	GLU	SER	TYR	ALA	THR	LYS	MET	CYS	ASP	GLY	PRO	GLY	MET	THR	ALA	PHE	GLU	PRO	GLU	ALA	LEU	GLY	ASN	PHE	HIS	ARG	THR	ASP	TYR	PHE	GLU	ASN	LYS	PRO	VAL	SER	GLY	ALA	THR	THR	ILE	LEU	ASN	PRO	HIS	ILE							
HIS	LEU	MET	GLY	ASP	GLU	SER	ALA	CYS	ILE	ILE	ALA	TYR	ILE	ARG	ILE	THR	GLN	TYR	LEU	ASP	ALA	ALA	GLY	ILE	PRO	ARG	THR	ALA	GLN	SER	GLU	GLY	TRP	GLN	ILE	VAL	HIS	PHE	HIS	ARG	SER	GLY	ALA	PRO	SER	VAL	LEU	PRO	HIS										

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	160211	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	52	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.026	Depositor
Minimum map value	-0.011	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0072	Depositor
Map size (Å)	364.0, 364.0, 364.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.91, 0.91, 0.91	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	0.25	0/1067	0.42	0/1443
1	B	0.26	0/1050	0.42	0/1421
1	C	0.25	0/1048	0.42	0/1417
1	D	0.25	0/1019	0.41	0/1378
1	E	0.26	0/1019	0.42	0/1378
1	F	0.25	0/1012	0.41	0/1367
1	G	0.25	0/1068	0.42	0/1445
1	I	0.26	0/1050	0.41	0/1421
1	J	0.25	0/1048	0.42	0/1417
1	K	0.25	0/1019	0.42	0/1378
1	L	0.26	0/1019	0.42	0/1378
1	M	0.25	0/1012	0.41	0/1367
2	O	0.37	0/2407	0.65	2/3254 (0.1%)
All	All	0.28	0/14838	0.46	2/20064 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	O	0	3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	O	269	VAL	N-CA-C	5.71	126.42	111.00
2	O	151	LEU	N-CA-C	-5.12	97.17	111.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	O	149	PHE	Peptide
2	O	150	GLY	Peptide
2	O	40	LYS	Peptide

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	1040	0	1002	9	0
1	B	1023	0	985	12	0
1	C	1022	0	983	12	0
1	D	994	0	958	10	0
1	E	994	0	958	16	0
1	F	988	0	952	11	0
1	G	1041	0	1003	7	0
1	I	1023	0	985	13	0
1	J	1022	0	982	77	0
1	K	994	0	957	51	0
1	L	994	0	958	16	0
1	M	988	0	952	11	0
2	O	2352	0	2355	319	0
All	All	14475	0	14030	440	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 15.

All (440) 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:J:14:LYS:HD3	2:O:291:LEU:CB	1.31	1.57
1:J:14:LYS:HB2	2:O:291:LEU:CG	1.29	1.53
1:K:27:GLU:CG	2:O:164:GLY:HA2	1.17	1.50
1:J:14:LYS:CB	2:O:291:LEU:CD1	1.95	1.42
1:K:27:GLU:HG2	2:O:162:TRP:NE1	1.35	1.42
1:J:14:LYS:HD3	2:O:291:LEU:CG	1.52	1.38
1:J:14:LYS:CB	2:O:291:LEU:HG	1.57	1.34
1:J:14:LYS:CB	2:O:291:LEU:CG	2.05	1.33

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:14:LYS:HB2	2:O:291:LEU:CD1	1.54	1.30
1:K:27:GLU:HG3	2:O:164:GLY:CA	1.02	1.29
1:K:27:GLU:CG	2:O:164:GLY:CA	1.74	1.27
1:J:14:LYS:HD3	2:O:291:LEU:CA	1.66	1.25
1:J:14:LYS:CD	2:O:291:LEU:HG	1.66	1.24
1:J:14:LYS:CB	2:O:291:LEU:HD11	1.62	1.22
1:J:25:ASN:HB3	2:O:15:LYS:NZ	1.55	1.21
1:J:14:LYS:CG	2:O:291:LEU:CD1	2.20	1.20
1:J:14:LYS:CD	2:O:291:LEU:CG	2.19	1.19
1:J:14:LYS:CG	2:O:291:LEU:HD12	1.71	1.19
1:J:14:LYS:CD	2:O:291:LEU:CB	2.22	1.18
1:K:60:GLU:HA	2:O:44:ARG:HG3	1.26	1.13
1:J:14:LYS:CD	2:O:291:LEU:HA	1.78	1.12
1:J:14:LYS:HB3	2:O:291:LEU:HD11	1.33	1.11
2:O:99:TYR:OH	2:O:198:LEU:O	1.69	1.09
1:K:30:THR:O	2:O:179:LYS:NZ	1.86	1.08
1:J:14:LYS:CG	2:O:291:LEU:HG	1.83	1.08
2:O:266:ARG:HB3	2:O:270:ALA:HB2	1.30	1.08
1:J:25:ASN:HB3	2:O:15:LYS:HZ1	0.97	1.08
1:J:69:PRO:HB3	2:O:41:LEU:HD23	1.37	1.06
1:K:27:GLU:HG3	2:O:164:GLY:HA3	1.35	1.05
1:C:36:ASP:OD2	1:C:118:ARG:NH1	1.90	1.05
1:J:14:LYS:CG	2:O:291:LEU:CG	2.32	1.05
1:J:36:ASP:OD2	1:J:118:ARG:NH1	1.90	1.04
1:J:14:LYS:HG2	2:O:291:LEU:HD12	1.06	1.04
1:J:14:LYS:HZ2	2:O:291:LEU:HA	1.22	1.02
1:I:31:ASP:OD1	1:I:112:ARG:NH1	1.93	1.02
1:K:27:GLU:CG	2:O:164:GLY:HA3	1.83	1.02
1:J:14:LYS:NZ	2:O:291:LEU:HA	1.74	1.01
1:B:31:ASP:OD1	1:B:112:ARG:NH1	1.93	1.01
2:O:261:PRO:HB2	2:O:265:HIS:H	1.26	1.00
1:J:14:LYS:HB2	2:O:291:LEU:CD2	1.92	1.00
1:K:31:LYS:HA	2:O:179:LYS:HZ2	1.27	0.97
1:K:27:GLU:HG2	2:O:162:TRP:HE1	1.15	0.96
1:J:25:ASN:CB	2:O:15:LYS:NZ	2.29	0.95
1:K:31:LYS:HA	2:O:179:LYS:NZ	1.80	0.95
2:O:266:ARG:HB3	2:O:270:ALA:CB	1.97	0.95
1:J:14:LYS:CD	2:O:291:LEU:CA	2.35	0.94
2:O:100:SER:HB2	2:O:272:CYS:HA	1.47	0.94
2:O:42:SER:O	2:O:46:HIS:ND1	1.99	0.94
1:K:27:GLU:CG	2:O:162:TRP:NE1	2.30	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:67:LEU:HA	2:O:81:PHE:HA	1.49	0.93
1:J:14:LYS:HG2	2:O:291:LEU:CD1	1.89	0.93
2:O:65:VAL:HG13	2:O:82:ASP:HB3	1.50	0.93
2:O:265:HIS:O	2:O:269:VAL:N	2.03	0.92
2:O:233:THR:HG23	2:O:236:ALA:H	1.35	0.91
1:K:30:THR:C	2:O:179:LYS:HZ3	1.72	0.91
2:O:125:HIS:CE1	2:O:127:ASN:O	2.24	0.90
1:K:30:THR:HG21	2:O:165:PHE:CD2	2.06	0.90
1:J:25:ASN:CG	2:O:15:LYS:HE2	1.91	0.89
2:O:152:ALA:O	2:O:153:ILE:HG13	1.73	0.89
2:O:2:ARG:HH22	2:O:71:ILE:HG12	1.38	0.89
2:O:40:LYS:HE3	2:O:45:ASP:OD2	1.73	0.87
1:J:14:LYS:NZ	2:O:291:LEU:CA	2.37	0.87
1:K:31:LYS:HA	2:O:179:LYS:CD	2.04	0.86
2:O:90:PHE:HB3	2:O:286:ASN:HD21	1.39	0.85
1:J:14:LYS:HD3	2:O:291:LEU:HB2	1.56	0.85
2:O:34:MET:HB3	2:O:36:ILE:HD11	1.60	0.84
2:O:3:PHE:HB2	2:O:71:ILE:HD12	1.57	0.84
1:J:14:LYS:CE	2:O:291:LEU:HA	2.07	0.84
1:K:27:GLU:HG2	2:O:162:TRP:CD1	2.13	0.83
1:J:14:LYS:HB2	2:O:291:LEU:HG	1.17	0.83
1:J:14:LYS:NZ	2:O:290:LYS:C	2.33	0.82
1:K:27:GLU:HG2	2:O:164:GLY:HA2	1.57	0.82
1:K:31:LYS:HA	2:O:179:LYS:HD2	1.61	0.81
2:O:262:TRP:O	2:O:266:ARG:HB2	1.80	0.81
1:K:30:THR:HG21	2:O:165:PHE:CG	2.16	0.80
1:J:25:ASN:CB	2:O:15:LYS:HZ1	1.87	0.80
2:O:86:GLY:HA3	2:O:135:LEU:O	1.82	0.79
1:J:69:PRO:CB	2:O:41:LEU:HD23	2.11	0.79
2:O:261:PRO:HB3	2:O:264:SER:HB2	1.64	0.79
2:O:232:VAL:CG2	2:O:275:ARG:HH22	1.95	0.78
1:J:14:LYS:HZ3	2:O:291:LEU:N	1.81	0.78
2:O:2:ARG:NH2	2:O:71:ILE:HG12	1.98	0.78
2:O:105:SER:HB3	2:O:263:ILE:HA	1.66	0.76
1:J:14:LYS:HZ2	2:O:291:LEU:CA	1.95	0.76
2:O:235:GLU:HG3	2:O:266:ARG:NH2	2.02	0.75
2:O:41:LEU:O	2:O:42:SER:C	2.25	0.75
2:O:261:PRO:HG2	2:O:265:HIS:ND1	2.02	0.75
1:I:50:ASP:OD2	1:L:63:HIS:NE2	2.20	0.74
1:B:50:ASP:OD2	1:E:63:HIS:NE2	2.20	0.74
1:J:14:LYS:NZ	2:O:291:LEU:N	2.35	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:2:ARG:HH21	2:O:71:ILE:HG23	1.49	0.74
1:K:27:GLU:OE2	2:O:163:PHE:N	2.07	0.74
2:O:263:ILE:HG13	2:O:264:SER:N	2.02	0.74
2:O:263:ILE:HG13	2:O:264:SER:H	1.52	0.74
1:J:14:LYS:HZ3	2:O:290:LYS:C	1.90	0.73
2:O:259:LYS:O	2:O:261:PRO:HD3	1.90	0.72
1:K:31:LYS:CA	2:O:179:LYS:HZ2	2.02	0.72
2:O:147:ALA:HB1	2:O:149:PHE:CE2	2.25	0.72
2:O:63:ASN:O	2:O:145:LYS:HA	1.90	0.71
1:K:31:LYS:CA	2:O:179:LYS:HD2	2.17	0.71
2:O:232:VAL:HG22	2:O:275:ARG:HH22	1.55	0.71
2:O:188:LEU:HD13	2:O:252:ILE:O	1.90	0.71
1:M:31:ASP:OD2	1:M:33:GLY:N	2.23	0.70
2:O:98:TYR:HA	2:O:274:HIS:ND1	2.06	0.70
2:O:147:ALA:HB1	2:O:149:PHE:CZ	2.25	0.70
1:C:8:ARG:NH1	1:C:84:ASP:O	2.24	0.70
1:J:25:ASN:HB3	2:O:15:LYS:CE	2.21	0.70
1:J:8:ARG:NH1	1:J:84:ASP:O	2.24	0.70
2:O:223:ASP:O	2:O:225:PRO:HD3	1.92	0.69
2:O:153:ILE:CD1	2:O:163:PHE:HB3	2.22	0.69
2:O:34:MET:HB3	2:O:36:ILE:CD1	2.22	0.69
1:G:18:ARG:NH1	1:G:96:ASP:O	2.25	0.69
2:O:151:LEU:HG	2:O:166:ALA:HB1	1.72	0.69
1:A:18:ARG:NH1	1:A:96:ASP:O	2.25	0.69
1:K:27:GLU:HG2	2:O:162:TRP:CE2	2.26	0.68
1:J:14:LYS:CD	2:O:291:LEU:HB2	2.18	0.68
2:O:261:PRO:HG2	2:O:265:HIS:CG	2.29	0.68
2:O:253:THR:HG22	2:O:254:ALA:N	2.08	0.68
2:O:235:GLU:HG3	2:O:266:ARG:HH21	1.57	0.68
2:O:41:LEU:H	2:O:45:ASP:HB2	1.58	0.68
2:O:94:VAL:CG1	2:O:282:LEU:HD22	2.25	0.67
1:J:25:ASN:ND2	2:O:15:LYS:HE2	2.10	0.66
2:O:125:HIS:O	2:O:151:LEU:O	2.13	0.66
2:O:227:PRO:HA	2:O:230:ASP:OD2	1.95	0.66
1:F:31:ASP:OD2	1:F:33:GLY:N	2.23	0.66
1:K:27:GLU:OE2	2:O:162:TRP:C	2.34	0.66
2:O:61:HIS:CD2	2:O:62:PRO:HD2	2.29	0.66
1:J:14:LYS:NZ	2:O:290:LYS:O	2.28	0.66
2:O:266:ARG:CB	2:O:270:ALA:HB2	2.18	0.65
1:K:31:LYS:CA	2:O:179:LYS:NZ	2.56	0.65
2:O:161:ALA:HB3	2:O:163:PHE:CE1	2.32	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:269:VAL:HG12	2:O:269:VAL:O	1.96	0.65
2:O:70:SER:HG	2:O:77:HIS:HE2	1.45	0.64
2:O:23:VAL:HG22	2:O:30:GLU:HG2	1.78	0.64
1:K:31:LYS:NZ	2:O:176:VAL:O	2.30	0.64
1:B:35:THR:O	1:B:120:HIS:HA	1.98	0.63
1:F:90:ASP:O	1:F:92:GLY:N	2.31	0.63
1:K:60:GLU:CA	2:O:44:ARG:HG3	2.18	0.63
1:J:14:LYS:HB2	2:O:291:LEU:HD21	1.78	0.63
2:O:2:ARG:HH22	2:O:71:ILE:CG1	2.11	0.63
1:M:90:ASP:O	1:M:92:GLY:N	2.31	0.63
2:O:73:GLU:HG2	2:O:74:GLU:H	1.63	0.63
2:O:275:ARG:CD	2:O:278:THR:HB	2.28	0.63
2:O:235:GLU:HG3	2:O:266:ARG:NE	2.14	0.63
2:O:61:HIS:CE1	2:O:63:ASN:HB2	2.34	0.63
1:I:35:THR:O	1:I:120:HIS:HA	1.98	0.62
2:O:235:GLU:HG3	2:O:266:ARG:CZ	2.28	0.62
2:O:41:LEU:HD12	2:O:45:ASP:OD1	1.99	0.62
2:O:148:ASP:O	2:O:149:PHE:CD1	2.51	0.62
2:O:275:ARG:HD2	2:O:278:THR:HB	1.82	0.61
1:A:80:LYS:NZ	1:A:111:ASP:O	2.33	0.61
1:J:14:LYS:HD2	2:O:291:LEU:HA	1.80	0.61
1:M:3:ARG:NH2	1:M:75:ASP:OD1	2.34	0.61
1:F:35:THR:O	1:F:117:HIS:HA	2.00	0.61
1:I:59:LEU:HD22	1:L:96:PRO:HG3	1.82	0.61
2:O:261:PRO:HB2	2:O:265:HIS:N	2.08	0.61
2:O:55:ILE:HG22	2:O:148:ASP:OD2	1.99	0.61
1:G:80:LYS:NZ	1:G:111:ASP:O	2.33	0.61
1:K:31:LYS:HD2	2:O:179:LYS:HA	1.82	0.60
1:M:35:THR:O	1:M:117:HIS:HA	2.00	0.60
1:F:3:ARG:NH2	1:F:75:ASP:OD1	2.34	0.60
1:J:14:LYS:HB2	2:O:291:LEU:HD11	1.37	0.60
2:O:61:HIS:ND1	2:O:63:ASN:HB2	2.17	0.60
2:O:153:ILE:HD13	2:O:163:PHE:HB3	1.84	0.60
2:O:94:VAL:HG12	2:O:282:LEU:HD22	1.83	0.59
1:B:59:LEU:HD22	1:E:96:PRO:HG3	1.82	0.59
2:O:40:LYS:HB3	2:O:45:ASP:OD2	2.02	0.59
2:O:105:SER:HB3	2:O:263:ILE:CA	2.33	0.59
2:O:65:VAL:HG11	2:O:81:PHE:CD1	2.38	0.59
1:C:8:ARG:NH1	1:C:84:ASP:HA	2.18	0.59
2:O:2:ARG:HH21	2:O:71:ILE:CG2	2.16	0.59
2:O:3:PHE:CD1	2:O:80:ILE:HD11	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:61:HIS:CG	2:O:62:PRO:HD2	2.37	0.59
2:O:235:GLU:CG	2:O:266:ARG:HH21	2.16	0.58
2:O:125:HIS:HE1	2:O:127:ASN:O	1.80	0.58
2:O:67:LEU:HD12	2:O:80:ILE:O	2.02	0.58
1:J:14:LYS:CE	2:O:291:LEU:CA	2.74	0.58
2:O:3:PHE:CE1	2:O:80:ILE:HD11	2.38	0.58
1:J:25:ASN:CB	2:O:15:LYS:HZ3	2.15	0.58
2:O:108:ILE:CG2	2:O:263:ILE:HG21	2.33	0.58
1:K:31:LYS:HA	2:O:179:LYS:CE	2.33	0.58
2:O:278:THR:CG2	2:O:279:VAL:N	2.67	0.58
1:J:8:ARG:NH1	1:J:84:ASP:HA	2.18	0.58
2:O:51:ARG:HA	2:O:54:ARG:NH2	2.17	0.58
2:O:172:LEU:O	2:O:217:ILE:HG21	2.03	0.58
2:O:175:GLU:HA	2:O:178:ARG:NH1	2.19	0.57
2:O:261:PRO:C	2:O:263:ILE:H	2.08	0.57
1:J:14:LYS:HD3	2:O:291:LEU:HG	1.32	0.57
2:O:275:ARG:O	2:O:278:THR:HG22	2.04	0.57
2:O:60:LYS:HA	2:O:66:ARG:HG2	1.87	0.57
2:O:3:PHE:HB2	2:O:71:ILE:CD1	2.31	0.57
2:O:278:THR:HG23	2:O:279:VAL:N	2.19	0.57
2:O:261:PRO:C	2:O:263:ILE:N	2.56	0.56
1:K:65:HIS:NE2	1:M:50:ASP:OD2	2.37	0.56
2:O:116:LEU:O	2:O:120:GLN:HG3	2.04	0.56
2:O:253:THR:HG22	2:O:254:ALA:H	1.70	0.56
1:E:41:GLU:OE1	1:E:121:ARG:NH2	2.38	0.56
1:J:14:LYS:CA	2:O:291:LEU:HG	2.33	0.56
1:L:41:GLU:OE1	1:L:121:ARG:NH2	2.39	0.56
2:O:168:THR:O	2:O:172:LEU:HG	2.06	0.56
2:O:104:ALA:HB1	2:O:198:LEU:HG	1.88	0.56
2:O:106:HIS:O	2:O:109:GLN:HG2	2.05	0.56
1:B:30:CYS:HB2	1:B:49:LEU:HD21	1.88	0.56
2:O:178:ARG:NH1	2:O:180:ASP:OD2	2.36	0.56
2:O:205:PHE:O	2:O:206:TRP:HB2	2.06	0.56
1:B:58:ASN:HB3	1:E:90:LEU:HD11	1.88	0.55
1:I:30:CYS:HB2	1:I:49:LEU:HD21	1.88	0.55
1:B:3:ARG:HD2	1:B:75:LEU:HD13	1.89	0.55
2:O:232:VAL:HG23	2:O:275:ARG:HH22	1.71	0.55
1:I:58:ASN:HB3	1:L:90:LEU:HD11	1.89	0.55
2:O:235:GLU:HG3	2:O:266:ARG:HE	1.71	0.55
2:O:109:GLN:O	2:O:113:GLU:HG2	2.07	0.55
2:O:265:HIS:O	2:O:268:THR:HB	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:55:ASP:OD1	1:C:58:ARG:NH1	2.41	0.54
1:I:3:ARG:HD2	1:I:75:LEU:HD13	1.89	0.54
1:L:35:MET:O	1:L:49:GLY:N	2.33	0.54
1:E:23:ASP:OD2	1:E:26:SER:OG	2.15	0.54
2:O:31:TYR:C	2:O:83:LEU:HB2	2.28	0.54
1:E:35:MET:O	1:E:49:GLY:N	2.33	0.54
1:G:18:ARG:NH1	1:G:96:ASP:HA	2.22	0.54
1:K:60:GLU:HA	2:O:44:ARG:CG	2.18	0.54
2:O:24:LYS:O	2:O:28:GLY:HA2	2.07	0.54
2:O:105:SER:CB	2:O:263:ILE:HA	2.38	0.54
2:O:60:LYS:HB3	2:O:66:ARG:CD	2.38	0.54
2:O:90:PHE:HB3	2:O:286:ASN:ND2	2.18	0.54
1:K:30:THR:HG21	2:O:165:PHE:CB	2.38	0.54
1:J:40:THR:O	1:J:126:HIS:HA	2.08	0.53
2:O:153:ILE:CG2	2:O:154:GLU:N	2.71	0.53
1:J:55:ASP:OD1	1:J:58:ARG:NH1	2.41	0.53
2:O:108:ILE:HG22	2:O:263:ILE:HG21	1.90	0.53
1:A:18:ARG:NH1	1:A:96:ASP:HA	2.23	0.53
1:J:25:ASN:CG	2:O:15:LYS:CE	2.72	0.53
2:O:152:ALA:O	2:O:153:ILE:CG1	2.53	0.53
1:C:102:GLY:HA2	1:C:103:ILE:HB	1.91	0.53
2:O:200:VAL:HG11	2:O:229:TRP:CE2	2.43	0.53
2:O:259:LYS:O	2:O:261:PRO:CD	2.57	0.53
1:J:44:PRO:HG2	1:J:132:ALA:H	1.74	0.53
2:O:38:THR:HG23	2:O:75:GLY:C	2.29	0.53
1:C:40:THR:O	1:C:126:HIS:HA	2.08	0.52
2:O:200:VAL:HG11	2:O:229:TRP:NE1	2.24	0.52
2:O:91:GLU:O	2:O:94:VAL:HG22	2.09	0.52
1:K:31:LYS:CG	2:O:162:TRP:CE2	2.86	0.52
2:O:153:ILE:HD13	2:O:163:PHE:CD2	2.45	0.52
2:O:147:ALA:CB	2:O:149:PHE:CE2	2.93	0.52
1:K:33:CYS:HB2	1:K:52:LEU:HD21	1.92	0.52
2:O:64:ILE:HD11	2:O:114:ALA:HB1	1.92	0.52
2:O:40:LYS:HB3	2:O:45:ASP:CB	2.39	0.51
1:A:74:LEU:HD22	1:F:95:PRO:HG3	1.92	0.51
2:O:116:LEU:HD22	2:O:258:LEU:HD12	1.93	0.51
1:J:102:GLY:HA2	1:J:103:ILE:HB	1.91	0.51
2:O:42:SER:O	2:O:46:HIS:CE1	2.62	0.51
2:O:153:ILE:HD13	2:O:163:PHE:CG	2.45	0.51
2:O:239:LEU:HD22	2:O:262:TRP:HD1	1.75	0.51
1:F:57:GLU:N	1:F:57:GLU:OE1	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:14:LYS:CE	2:O:291:LEU:HB2	2.40	0.51
1:D:33:CYS:HB2	1:D:52:LEU:HD21	1.92	0.51
1:J:25:ASN:CB	2:O:15:LYS:CE	2.83	0.51
2:O:40:LYS:HB3	2:O:45:ASP:HB3	1.92	0.51
2:O:48:LYS:HG2	2:O:51:ARG:HH22	1.76	0.51
2:O:70:SER:OG	2:O:77:HIS:NE2	2.34	0.51
1:M:57:GLU:N	1:M:57:GLU:OE1	2.44	0.51
1:A:121:SER:HA	1:A:142:SER:O	2.11	0.51
1:D:65:HIS:NE2	1:F:50:ASP:OD2	2.37	0.51
1:K:27:GLU:CG	2:O:162:TRP:CD1	2.89	0.51
2:O:153:ILE:HD11	2:O:163:PHE:HB3	1.92	0.51
1:K:31:LYS:HA	2:O:179:LYS:CG	2.40	0.50
2:O:183:GLY:C	2:O:185:PRO:HD2	2.32	0.50
1:C:44:PRO:HG2	1:C:132:ALA:H	1.74	0.50
1:G:74:LEU:HD22	1:M:95:PRO:HG3	1.93	0.50
2:O:97:GLU:O	2:O:274:HIS:CE1	2.64	0.50
1:G:18:ARG:NH2	1:G:129:ARG:HH22	2.09	0.50
1:K:30:THR:C	2:O:179:LYS:NZ	2.45	0.50
2:O:192:GLY:C	2:O:244:LEU:HD21	2.31	0.50
2:O:260:HIS:C	2:O:260:HIS:ND1	2.63	0.50
1:A:18:ARG:NH2	1:A:129:ARG:HH22	2.09	0.50
1:K:30:THR:CG2	2:O:165:PHE:CG	2.92	0.50
2:O:65:VAL:HG12	2:O:81:PHE:HB2	1.92	0.50
1:G:121:SER:HA	1:G:142:SER:O	2.12	0.50
2:O:225:PRO:HD2	2:O:229:TRP:CD1	2.47	0.50
2:O:253:THR:CG2	2:O:254:ALA:N	2.73	0.50
1:J:14:LYS:NZ	2:O:290:LYS:HG2	2.26	0.50
2:O:48:LYS:HG2	2:O:51:ARG:NH2	2.27	0.50
1:K:27:GLU:CB	2:O:164:GLY:HA3	2.40	0.49
2:O:91:GLU:HA	2:O:91:GLU:OE1	2.12	0.49
2:O:182:TYR:CD2	2:O:186:VAL:HG11	2.47	0.49
1:K:7:LYS:HB3	1:K:73:ILE:HD12	1.95	0.49
2:O:40:LYS:HB3	2:O:45:ASP:CG	2.33	0.49
2:O:60:LYS:HB3	2:O:66:ARG:HD3	1.94	0.49
2:O:65:VAL:HG13	2:O:82:ASP:CB	2.32	0.49
2:O:173:SER:HB2	2:O:175:GLU:OE2	2.12	0.49
1:K:21:ILE:HA	1:K:59:PHE:HE1	1.78	0.49
1:L:23:ASP:OD2	1:L:26:SER:OG	2.15	0.49
2:O:67:LEU:HD12	2:O:80:ILE:C	2.33	0.49
2:O:153:ILE:HD13	2:O:163:PHE:CB	2.43	0.49
2:O:282:LEU:C	2:O:282:LEU:HD23	2.32	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:10:GLN:HE21	2:O:291:LEU:HD23	1.78	0.49
1:J:14:LYS:CE	2:O:291:LEU:CB	2.88	0.49
1:D:7:LYS:HB3	1:D:73:ILE:HD12	1.95	0.49
2:O:264:SER:O	2:O:267:SER:HB2	2.13	0.49
1:D:21:ILE:HA	1:D:59:PHE:HE1	1.78	0.48
1:F:74:GLY:HA3	1:L:77:GLU:OE2	2.13	0.48
1:J:25:ASN:CB	2:O:15:LYS:HE2	2.44	0.48
1:L:4:ARG:HE	1:L:109:ARG:HH22	1.62	0.48
1:E:4:ARG:HE	1:E:109:ARG:HH22	1.62	0.48
1:J:10:GLN:O	2:O:291:LEU:HD21	2.12	0.48
1:J:25:ASN:ND2	2:O:15:LYS:CE	2.76	0.48
2:O:2:ARG:NH2	2:O:71:ILE:CG1	2.70	0.48
2:O:262:TRP:CD1	2:O:263:ILE:HG23	2.49	0.48
2:O:136:ALA:HB2	2:O:145:LYS:HE2	1.95	0.48
1:B:4:LYS:HB3	1:B:73:ILE:HD12	1.95	0.48
1:K:31:LYS:HA	2:O:179:LYS:HG3	1.96	0.48
2:O:39:LYS:O	2:O:39:LYS:HG3	2.14	0.48
2:O:176:VAL:HG22	2:O:182:TYR:CD1	2.49	0.48
1:L:31:CYS:HB2	1:L:50:LEU:HD21	1.95	0.47
2:O:65:VAL:HG11	2:O:81:PHE:HD1	1.79	0.47
2:O:153:ILE:HG22	2:O:154:GLU:N	2.29	0.47
2:O:209:ASP:HB3	2:O:212:ARG:HD2	1.97	0.47
1:E:31:CYS:HB2	1:E:50:LEU:HD21	1.95	0.47
1:I:4:LYS:HB3	1:I:73:ILE:HD12	1.95	0.47
1:E:91:ASP:OD2	1:E:95:ILE:N	2.41	0.47
1:M:30:CYS:HB2	1:M:49:LEU:HD21	1.96	0.47
2:O:6:GLU:HB2	2:O:7:TYR:CD1	2.50	0.47
2:O:213:LEU:O	2:O:217:ILE:HG13	2.15	0.47
2:O:286:ASN:O	2:O:289:ARG:HG2	2.15	0.47
1:L:122:SER:HA	1:L:123:GLY:HA2	1.66	0.47
1:D:39:ALA:HB3	1:D:49:VAL:HG23	1.97	0.47
1:E:103:GLU:HG2	1:E:121:ARG:HG3	1.97	0.47
1:K:39:ALA:HB3	1:K:49:VAL:HG23	1.97	0.47
2:O:262:TRP:O	2:O:262:TRP:CD2	2.68	0.47
1:C:35:CYS:HB2	1:C:54:LEU:HD21	1.97	0.46
2:O:209:ASP:OD1	2:O:211:HIS:HB3	2.15	0.46
2:O:253:THR:CG2	2:O:254:ALA:H	2.28	0.46
2:O:189:TRP:CD1	2:O:189:TRP:C	2.89	0.46
2:O:195:LEU:HD12	2:O:198:LEU:HD23	1.97	0.46
1:J:10:GLN:HE21	2:O:291:LEU:CD2	2.28	0.46
2:O:118:CYS:O	2:O:121:MET:N	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:137:SER:H	2:O:142:ALA:HB1	1.80	0.46
2:O:253:THR:HG22	2:O:255:ALA:H	1.81	0.46
1:L:103:GLU:HG2	1:L:121:ARG:HG3	1.97	0.46
1:J:35:CYS:HB2	1:J:54:LEU:HD21	1.97	0.46
2:O:34:MET:HG2	2:O:81:PHE:HE2	1.81	0.46
1:B:27:THR:HG22	1:B:49:LEU:HD22	1.98	0.46
2:O:125:HIS:ND1	2:O:127:ASN:O	2.46	0.46
1:J:14:LYS:HZ1	2:O:290:LYS:HG2	1.81	0.45
1:K:30:THR:CG2	2:O:165:PHE:CD2	2.91	0.45
1:F:30:CYS:HB2	1:F:49:LEU:HD21	1.97	0.45
2:O:184:LYS:N	2:O:185:PRO:HD2	2.32	0.45
2:O:165:PHE:CD1	2:O:179:LYS:HE2	2.52	0.45
1:J:69:PRO:HG3	2:O:41:LEU:HA	1.99	0.45
2:O:41:LEU:N	2:O:45:ASP:HB2	2.30	0.45
1:J:10:GLN:HG3	2:O:291:LEU:HD22	1.97	0.45
1:K:38:THR:O	1:K:120:HIS:HA	2.16	0.45
2:O:2:ARG:NH2	2:O:2:ARG:HB2	2.32	0.45
2:O:286:ASN:HA	2:O:289:ARG:HE	1.82	0.45
1:I:27:THR:HG22	1:I:49:LEU:HD22	1.98	0.45
2:O:108:ILE:HG12	2:O:195:LEU:HD13	1.99	0.45
1:C:98:LEU:HD23	1:C:104:PRO:HA	1.99	0.45
2:O:193:VAL:HG13	2:O:204:PRO:CG	2.47	0.44
2:O:279:VAL:O	2:O:282:LEU:HB3	2.17	0.44
1:D:37:MET:HA	1:D:119:VAL:O	2.17	0.44
1:F:90:ASP:O	1:F:93:GLY:N	2.39	0.44
1:J:98:LEU:HD23	1:J:104:PRO:HA	1.99	0.44
1:K:30:THR:HG21	2:O:165:PHE:HB3	1.99	0.44
1:D:38:THR:O	1:D:120:HIS:HA	2.16	0.44
1:L:4:ARG:O	1:L:8:ILE:HG12	2.18	0.44
2:O:30:GLU:HB3	2:O:83:LEU:CD2	2.47	0.44
2:O:60:LYS:HA	2:O:66:ARG:CG	2.46	0.44
2:O:168:THR:HG23	2:O:169:PRO:HD2	2.00	0.44
2:O:184:LYS:N	2:O:185:PRO:CD	2.80	0.44
1:A:37:ASP:OD2	1:A:40:SER:OG	2.23	0.44
2:O:94:VAL:HA	2:O:279:VAL:HG13	1.99	0.44
2:O:1:THR:H1	2:O:73:GLU:HA	1.83	0.44
2:O:32:ALA:HB2	2:O:83:LEU:CD1	2.48	0.44
2:O:129:LYS:HB2	2:O:130:PRO:HD2	2.00	0.44
1:C:116:HIS:CD2	1:C:118:ARG:HE	2.36	0.44
1:K:37:MET:HA	1:K:119:VAL:O	2.17	0.44
2:O:112:LEU:HB2	2:O:258:LEU:HD21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:126:ARG:HD3	2:O:153:ILE:HD12	1.99	0.44
1:E:4:ARG:O	1:E:8:ILE:HG12	2.18	0.43
2:O:11:GLU:O	2:O:11:GLU:HG2	2.17	0.43
2:O:36:ILE:HD12	2:O:36:ILE:N	2.33	0.43
2:O:101:GLU:HB2	2:O:271:SER:O	2.18	0.43
2:O:36:ILE:HG23	2:O:40:LYS:HD3	2.00	0.43
2:O:88:GLU:HG2	2:O:89:LEU:N	2.32	0.43
2:O:118:CYS:SG	2:O:119:HIS:N	2.90	0.43
2:O:119:HIS:O	2:O:184:LYS:NZ	2.38	0.43
2:O:174:PRO:HB3	2:O:218:LYS:HA	2.00	0.43
1:E:77:GLU:OE2	1:M:74:GLY:HA3	2.17	0.43
1:L:119:PHE:CZ	1:L:121:ARG:HB2	2.54	0.43
2:O:240:ILE:O	2:O:244:LEU:HG	2.18	0.43
2:O:137:SER:OG	2:O:139:LEU:HB2	2.18	0.43
2:O:152:ALA:C	2:O:153:ILE:HG13	2.38	0.43
2:O:193:VAL:O	2:O:197:ILE:HG13	2.19	0.43
1:B:38:GLU:OE2	1:B:123:ARG:NH2	2.52	0.43
1:I:50:ASP:OD2	1:L:63:HIS:CE1	2.71	0.43
1:E:119:PHE:CZ	1:E:121:ARG:HB2	2.54	0.43
1:J:116:HIS:CD2	1:J:118:ARG:HE	2.36	0.43
2:O:88:GLU:OE2	2:O:289:ARG:NH2	2.51	0.43
1:D:69:LEU:HB2	1:D:86:ILE:HB	2.01	0.42
2:O:130:PRO:HD3	2:O:171:TYR:CZ	2.54	0.42
1:M:90:ASP:O	1:M:93:GLY:N	2.39	0.42
2:O:110:GLN:O	2:O:113:GLU:HB2	2.18	0.42
1:G:18:ARG:HH12	1:G:96:ASP:HA	1.83	0.42
1:K:31:LYS:HG3	2:O:162:TRP:CE2	2.53	0.42
1:I:38:GLU:OE2	1:I:123:ARG:NH2	2.52	0.42
2:O:41:LEU:H	2:O:45:ASP:CB	2.26	0.42
2:O:266:ARG:HD2	2:O:270:ALA:HB2	2.02	0.42
1:K:69:LEU:HB2	1:K:86:ILE:HB	2.02	0.42
2:O:41:LEU:O	2:O:42:SER:O	2.37	0.42
2:O:73:GLU:HG2	2:O:74:GLU:N	2.31	0.42
1:D:121:PHE:CE2	1:D:123:ARG:NH1	2.88	0.42
2:O:182:TYR:HB2	2:O:186:VAL:CG1	2.50	0.41
2:O:60:LYS:HB3	2:O:66:ARG:HD2	2.02	0.41
2:O:73:GLU:CG	2:O:74:GLU:H	2.32	0.41
2:O:89:LEU:HD13	2:O:135:LEU:HD21	2.03	0.41
1:C:113:ARG:HD3	1:C:127:PHE:HB2	2.02	0.41
1:K:121:PHE:CE2	1:K:123:ARG:NH1	2.88	0.41
1:B:50:ASP:OD2	1:E:63:HIS:CE1	2.72	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:176:VAL:HG22	2:O:182:TYR:CE1	2.55	0.41
1:F:65:ILE:HG22	1:F:68:PRO:HG3	2.02	0.41
2:O:34:MET:HB2	2:O:79:LEU:HB2	2.03	0.41
2:O:263:ILE:CG1	2:O:264:SER:N	2.78	0.41
1:A:30:ILE:HD12	1:A:86:ILE:HD11	2.03	0.41
2:O:32:ALA:HB2	2:O:83:LEU:HD12	2.03	0.41
1:B:55:TYR:HE1	1:E:96:PRO:HB2	1.86	0.41
1:C:109:SER:HB3	1:C:132:ALA:HB2	2.02	0.41
1:E:122:SER:HA	1:E:123:GLY:HA2	1.66	0.41
1:J:109:SER:HB3	1:J:132:ALA:HB2	2.02	0.41
1:J:113:ARG:HD3	1:J:127:PHE:HB2	2.02	0.41
2:O:168:THR:O	2:O:171:TYR:N	2.54	0.41
1:A:18:ARG:HH12	1:A:96:ASP:HA	1.84	0.41
1:M:65:ILE:HG22	1:M:68:PRO:HG3	2.03	0.40
1:I:40:GLU:O	1:L:98:THR:HG21	2.21	0.40
1:K:31:LYS:N	2:O:179:LYS:HZ3	2.15	0.40
2:O:135:LEU:O	2:O:136:ALA:C	2.60	0.40
2:O:197:ILE:HG12	2:O:203:PRO:HA	2.03	0.40
1:I:55:TYR:HE1	1:L:96:PRO:HB2	1.86	0.40
1:J:10:GLN:HG3	2:O:291:LEU:CD2	2.50	0.40
1:D:126:ALA:HA	1:D:127:PRO:HD3	1.96	0.40
2:O:101:GLU:HB3	2:O:262:TRP:CZ3	2.56	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	126/473 (27%)	123 (98%)	3 (2%)	0	100	100
1	B	122/473 (26%)	119 (98%)	3 (2%)	0	100	100
1	C	122/473 (26%)	116 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	119/473 (25%)	116 (98%)	3 (2%)	0	100	100
1	E	119/473 (25%)	116 (98%)	3 (2%)	0	100	100
1	F	118/473 (25%)	117 (99%)	0	1 (1%)	19	59
1	G	126/473 (27%)	123 (98%)	3 (2%)	0	100	100
1	I	122/473 (26%)	119 (98%)	3 (2%)	0	100	100
1	J	122/473 (26%)	116 (95%)	6 (5%)	0	100	100
1	K	119/473 (25%)	116 (98%)	3 (2%)	0	100	100
1	L	119/473 (25%)	116 (98%)	3 (2%)	0	100	100
1	M	118/473 (25%)	117 (99%)	0	1 (1%)	19	59
2	O	289/473 (61%)	270 (93%)	17 (6%)	2 (1%)	22	62
All	All	1741/6149 (28%)	1684 (97%)	53 (3%)	4 (0%)	50	81

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	91	ALA
1	M	91	ALA
2	O	42	SER
2	O	261	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	110/405 (27%)	109 (99%)	1 (1%)	78	87
1	B	109/405 (27%)	109 (100%)	0	100	100
1	C	109/405 (27%)	108 (99%)	1 (1%)	78	87
1	D	106/405 (26%)	105 (99%)	1 (1%)	78	87
1	E	106/405 (26%)	105 (99%)	1 (1%)	78	87
1	F	105/405 (26%)	105 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	111/405 (27%)	110 (99%)	1 (1%)	78	87
1	I	109/405 (27%)	109 (100%)	0	100	100
1	J	109/405 (27%)	108 (99%)	1 (1%)	78	87
1	K	106/405 (26%)	105 (99%)	1 (1%)	78	87
1	L	106/405 (26%)	105 (99%)	1 (1%)	78	87
1	M	105/405 (26%)	105 (100%)	0	100	100
2	O	250/405 (62%)	247 (99%)	3 (1%)	71	84
All	All	1541/5265 (29%)	1530 (99%)	11 (1%)	84	90

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	129	ARG
1	C	42	PHE
1	D	121	PHE
1	E	76	ASP
1	G	129	ARG
1	J	42	PHE
1	K	121	PHE
1	L	76	ASP
2	O	1	THR
2	O	45	ASP
2	O	260	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	140	HIS
1	D	122	HIS
1	E	120	HIS
1	G	73	ASN
1	G	140	HIS
1	I	72	HIS
1	J	10	GLN
1	L	120	HIS
2	O	286	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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.

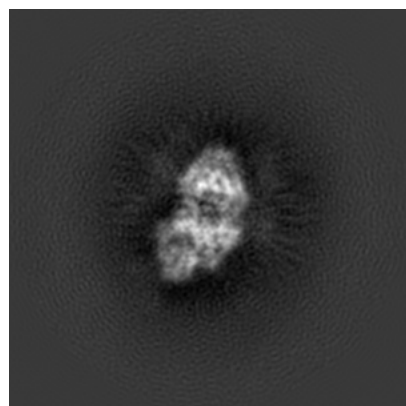
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21535. These allow visual inspection of the internal detail of the map and identification of artifacts.

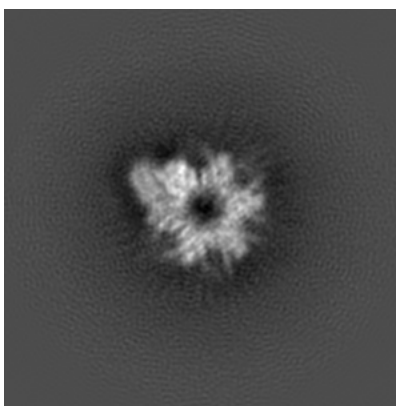
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

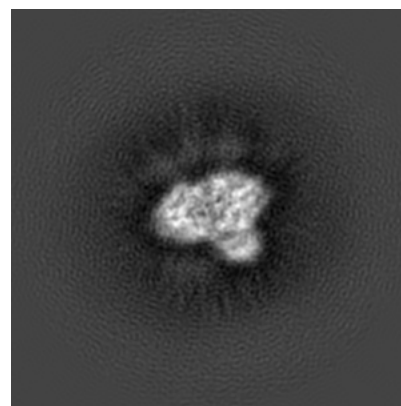
6.1.1 Primary map



X

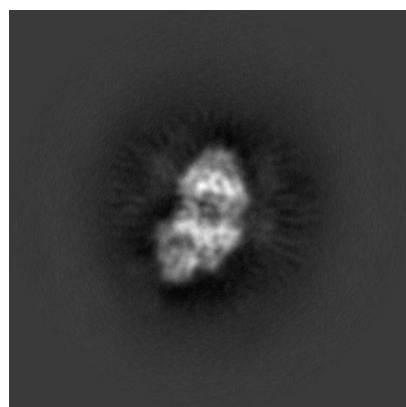


Y

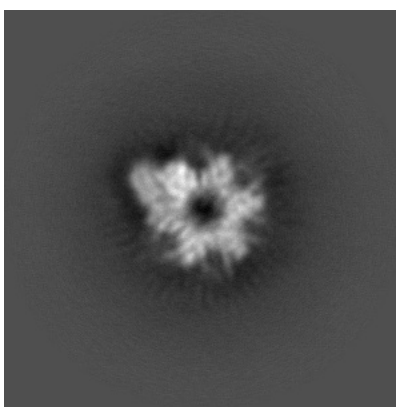


Z

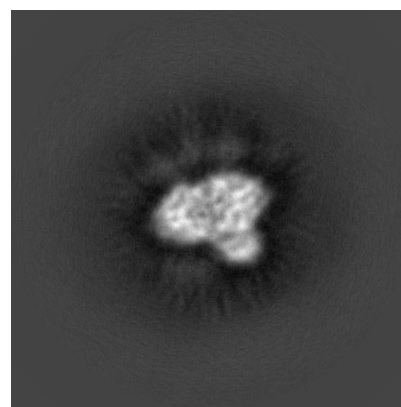
6.1.2 Raw map



X



Y

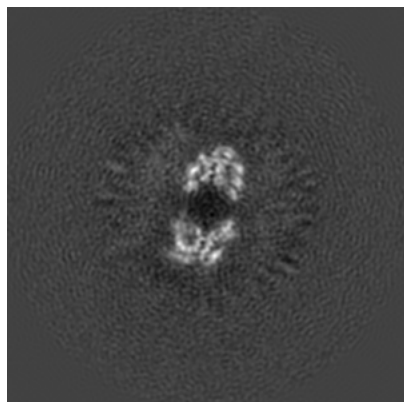


Z

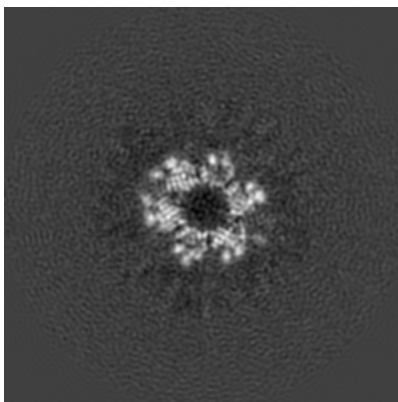
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

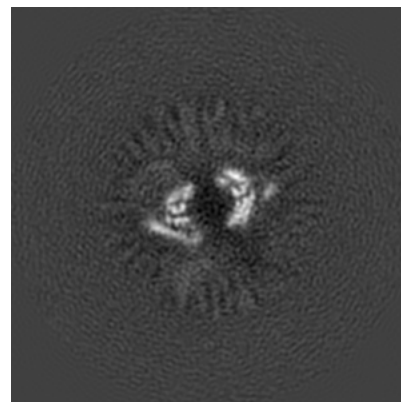
6.2.1 Primary map



X Index: 200

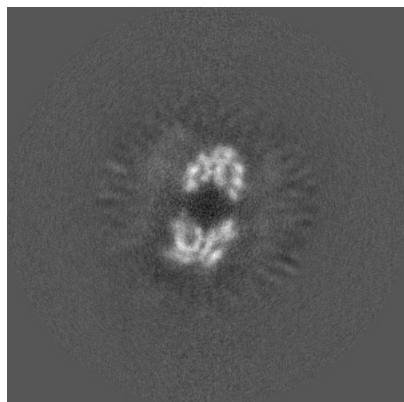


Y Index: 200

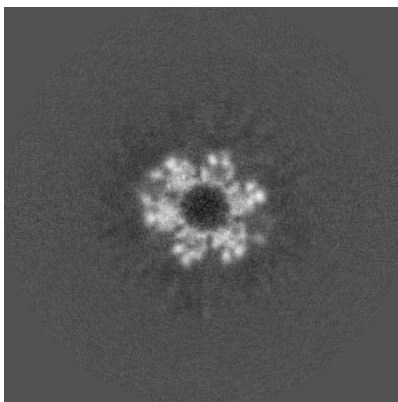


Z Index: 200

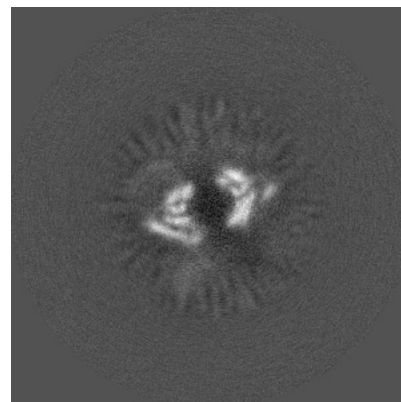
6.2.2 Raw map



X Index: 200



Y Index: 200

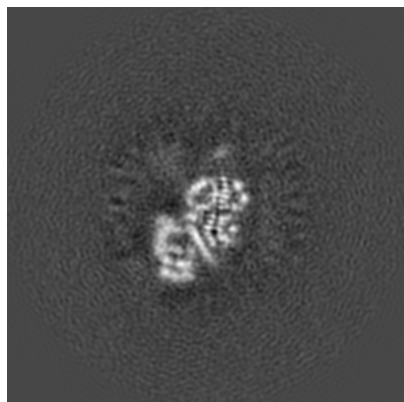


Z Index: 200

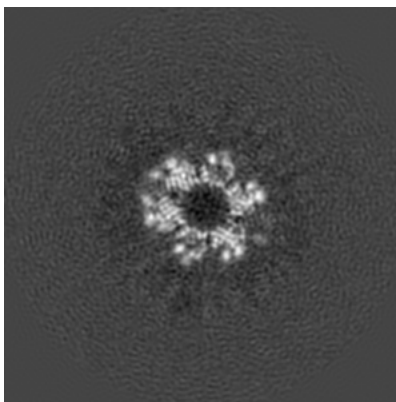
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

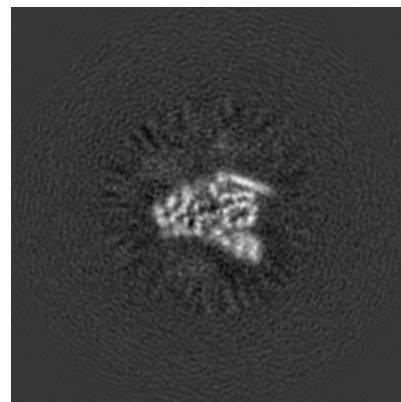
6.3.1 Primary map



X Index: 230

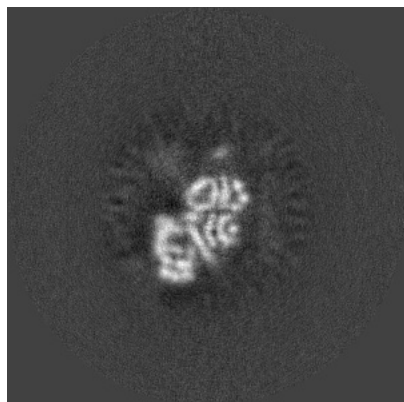


Y Index: 201

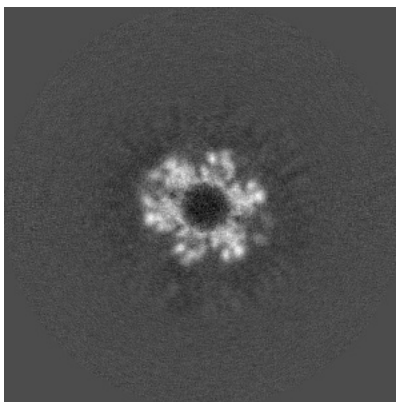


Z Index: 178

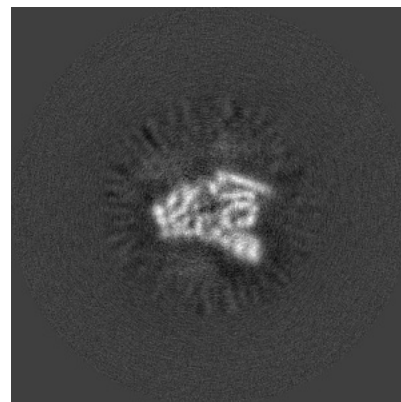
6.3.2 Raw map



X Index: 230



Y Index: 202

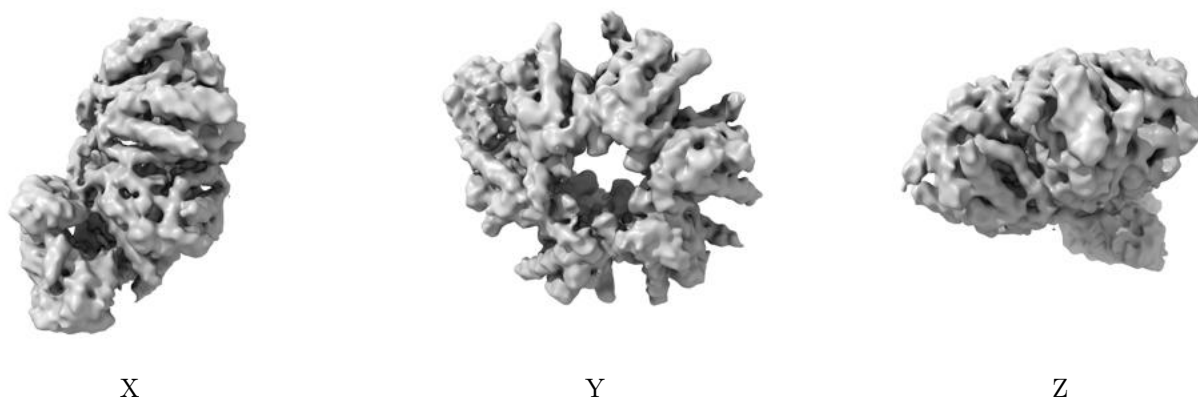


Z Index: 179

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

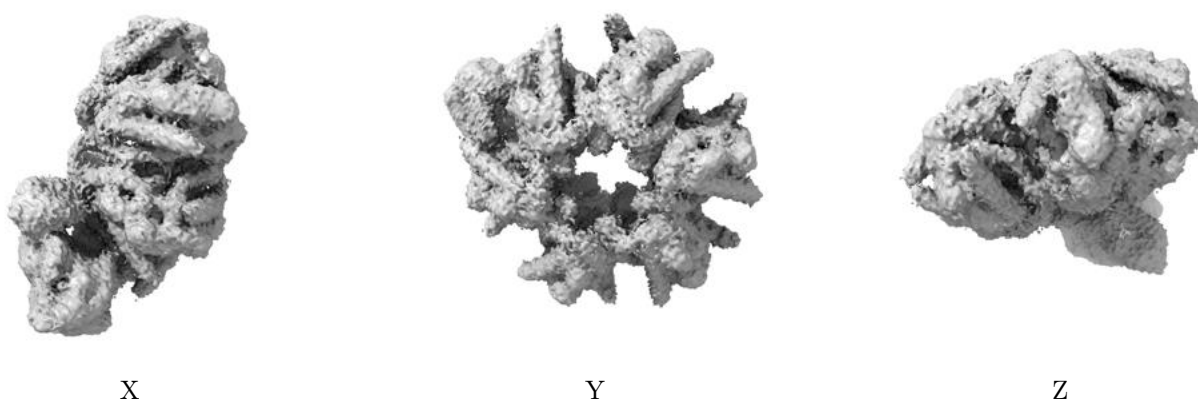
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0072. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

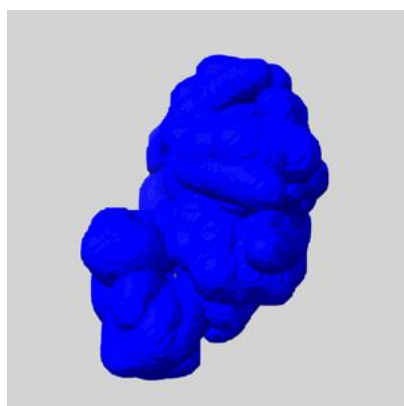
6.5 Mask visualisation [i](#)

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

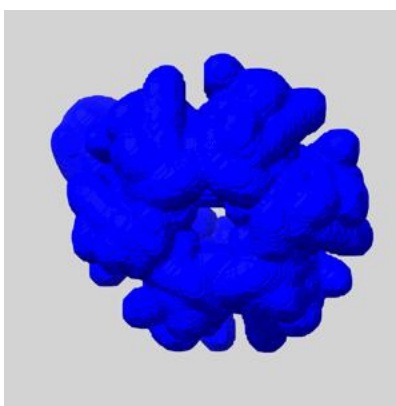
A mask typically either:

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

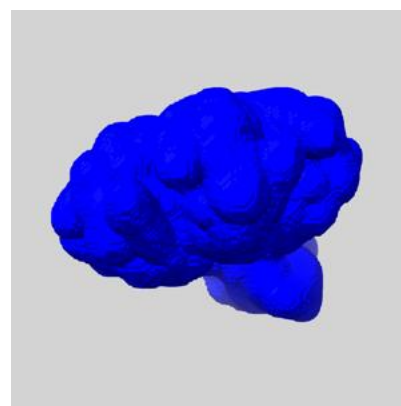
6.5.1 emd_21535_msk_1.map [i](#)



X



Y

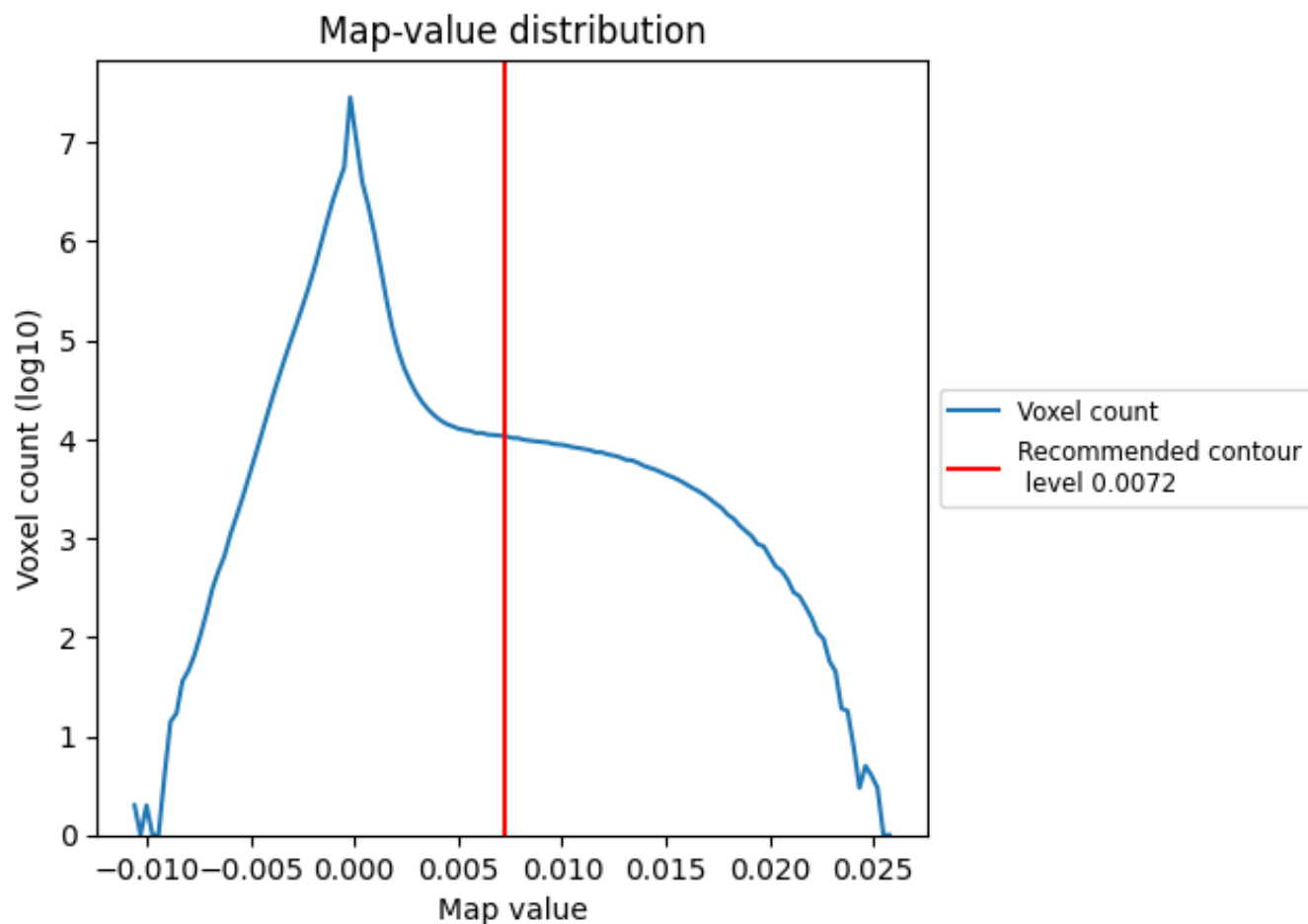


Z

7 Map analysis [i](#)

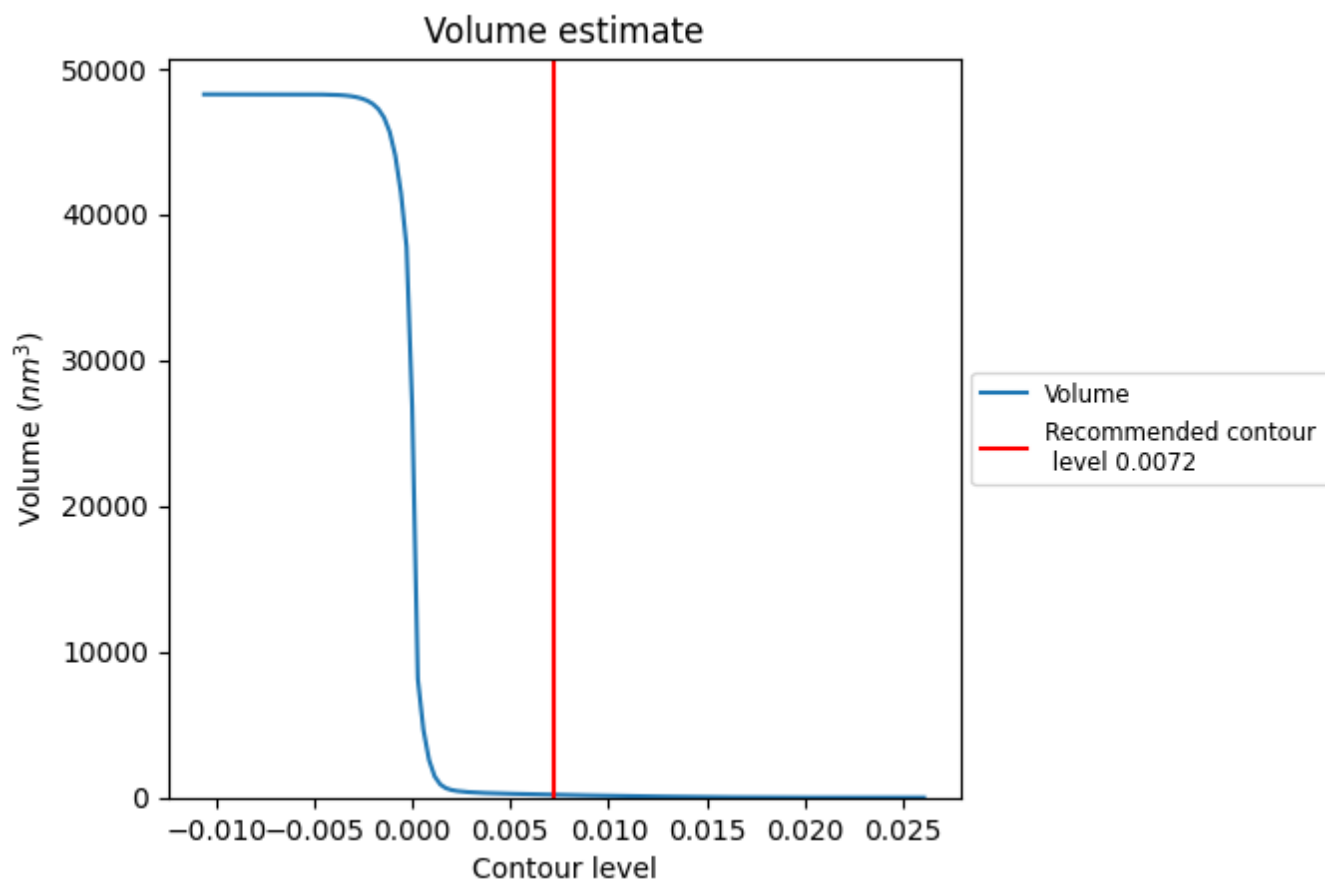
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

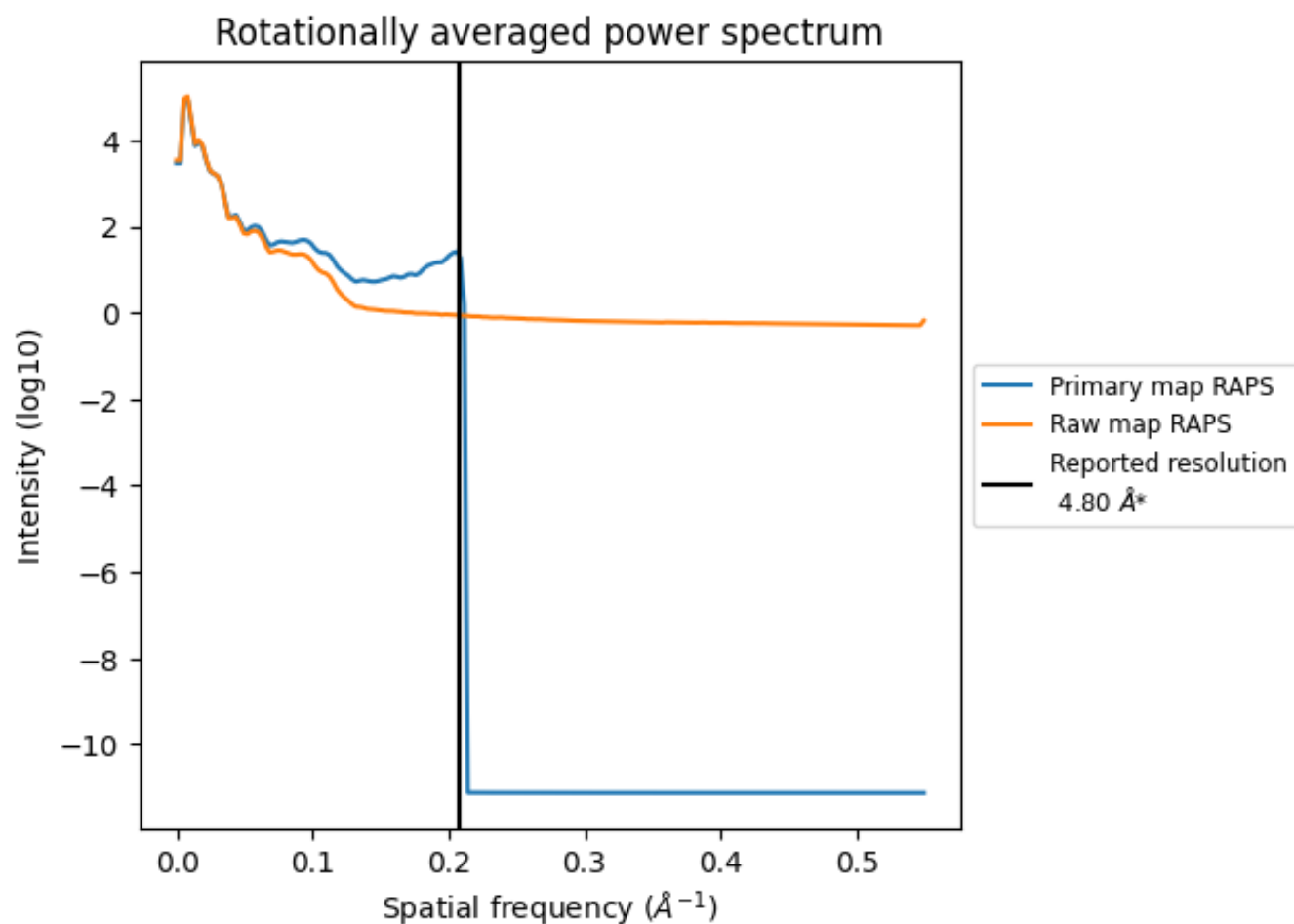
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 194 nm³; this corresponds to an approximate mass of 176 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 ⓘ

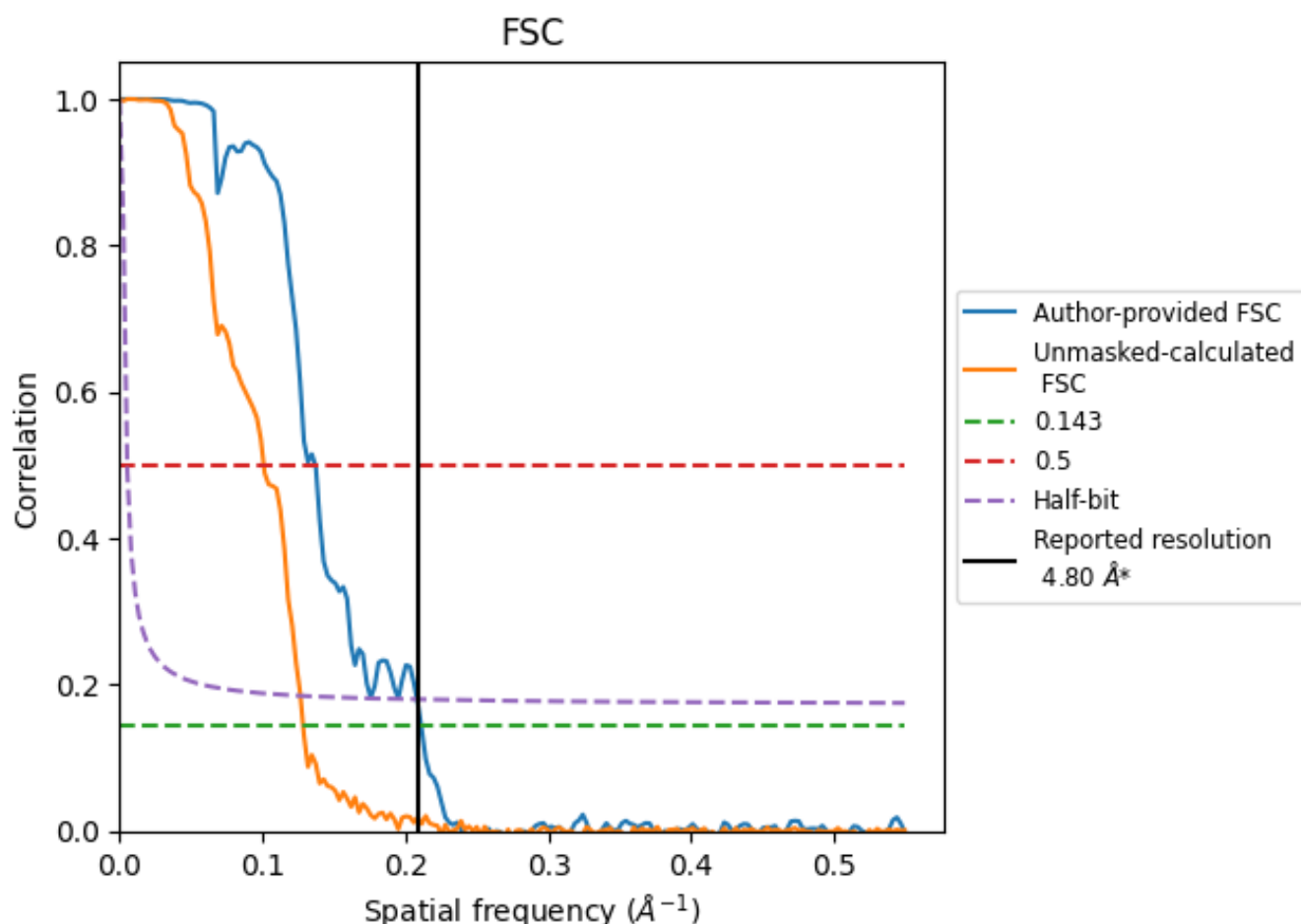


*Reported resolution corresponds to spatial frequency of 0.208 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.208 Å⁻¹

8.2 Resolution estimates [i](#)

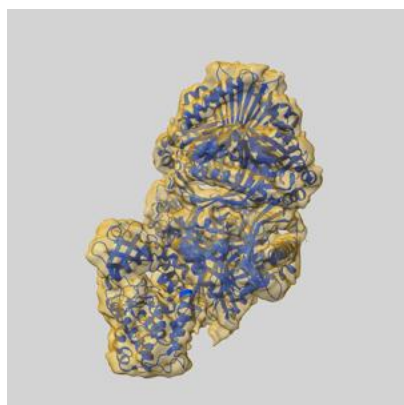
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.80	-	-
Author-provided FSC curve	4.73	7.30	4.80
Unmasked-calculated*	7.78	9.90	7.90

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.78 differs from the reported value 4.8 by more than 10 %

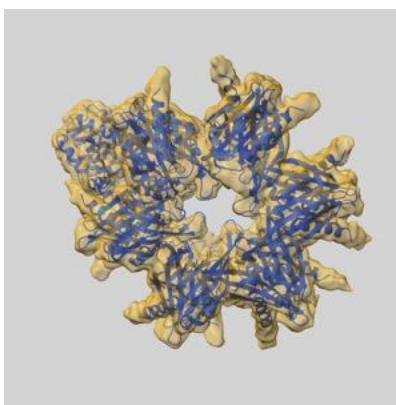
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21535 and PDB model 6W4O. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

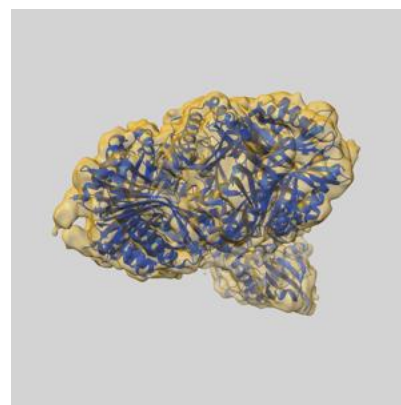
9.1 Map-model overlay [i](#)



X



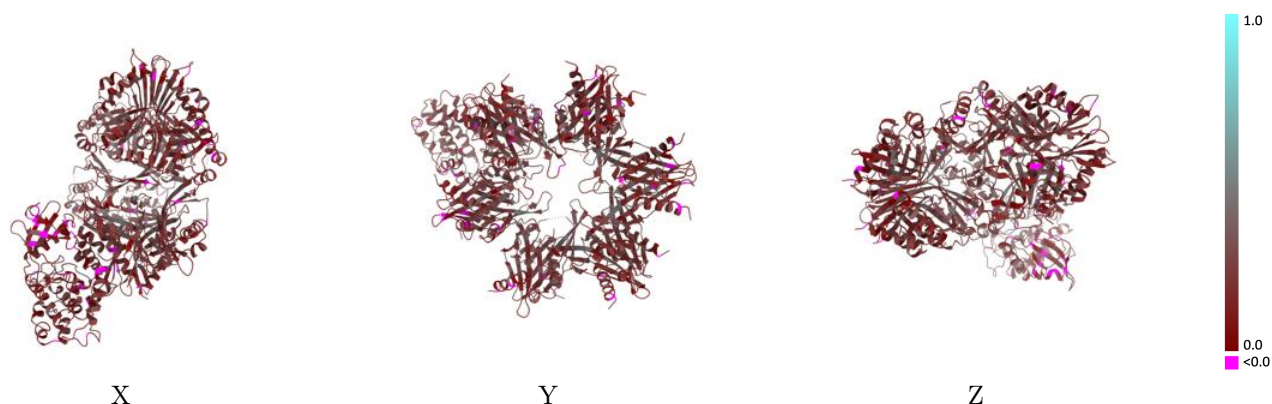
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0072 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



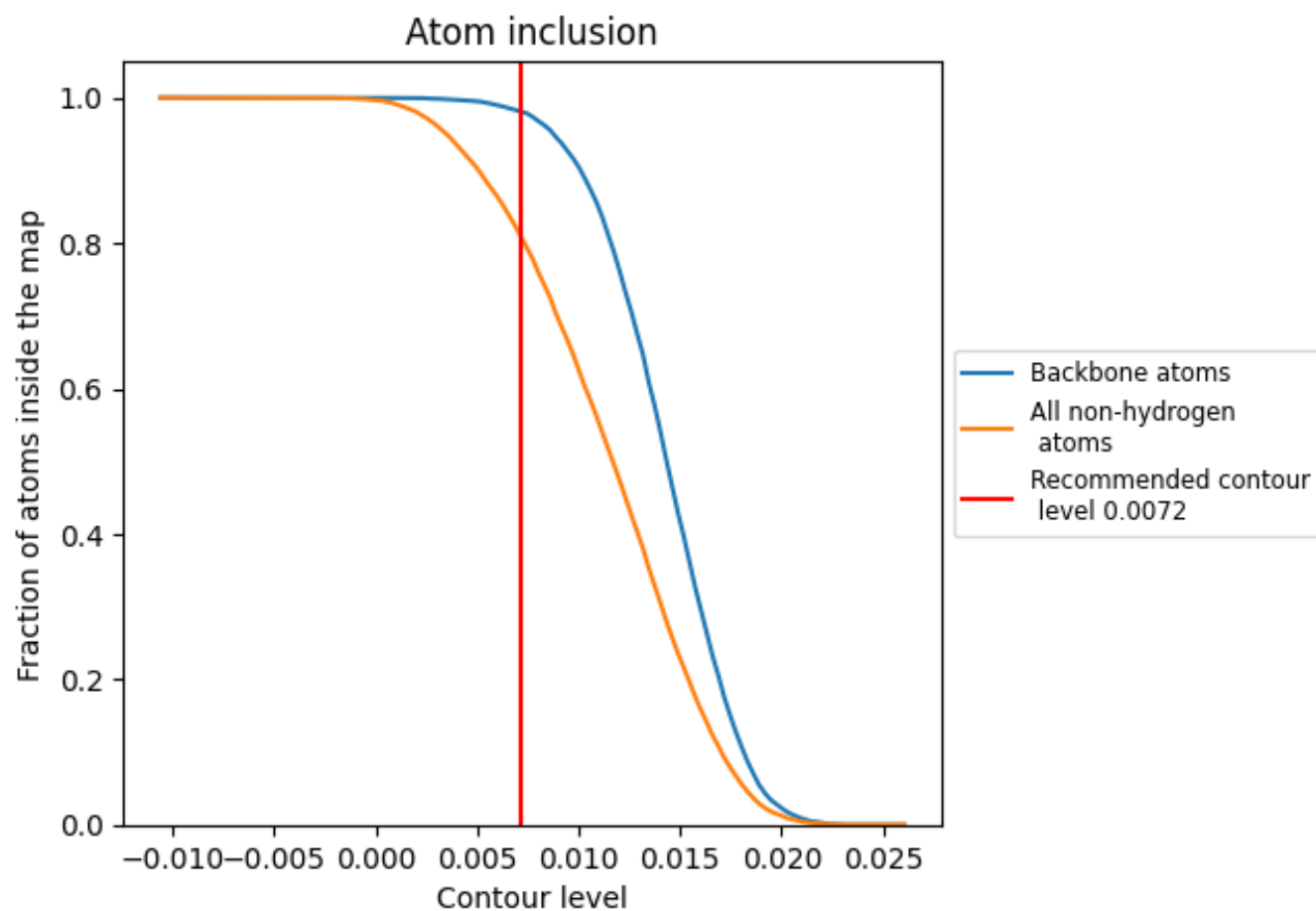
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0072).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 81% 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 (0.0072) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8068</div>	<div><div></div>0.2130</div>
A	<div><div></div>0.7941</div>	<div><div></div>0.2140</div>
B	<div><div></div>0.7890</div>	<div><div></div>0.2160</div>
C	<div><div></div>0.7998</div>	<div><div></div>0.2260</div>
D	<div><div></div>0.8117</div>	<div><div></div>0.2150</div>
E	<div><div></div>0.7912</div>	<div><div></div>0.2130</div>
F	<div><div></div>0.8126</div>	<div><div></div>0.2290</div>
G	<div><div></div>0.7894</div>	<div><div></div>0.2170</div>
I	<div><div></div>0.7880</div>	<div><div></div>0.2110</div>
J	<div><div></div>0.7838</div>	<div><div></div>0.2360</div>
K	<div><div></div>0.7963</div>	<div><div></div>0.2270</div>
L	<div><div></div>0.8056</div>	<div><div></div>0.2180</div>
M	<div><div></div>0.7909</div>	<div><div></div>0.2270</div>
O	<div><div></div>0.8627</div>	<div><div></div>0.1750</div>

1.0

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