



## Full wwPDB EM Validation Report ⓘ

May 18, 2024 – 05:04 PM EDT

PDB ID : 7L7S  
EMDB ID : EMD-23217  
Title : Human mitochondrial chaperonin mHsp60  
Authors : Chen, L.; Wang, J.C.Y.  
Deposited on : 2020-12-30  
Resolution : 3.50 Å (reported)  
Based on initial model : 1PCQ

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev92  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

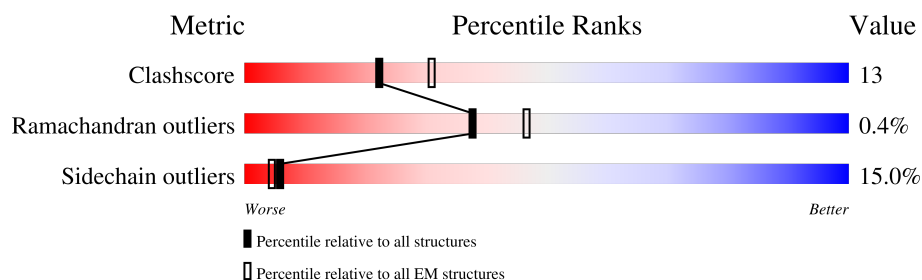
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.50 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  $\geq 3$ , 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	H	524	
1	I	524	
1	J	524	
1	K	524	
1	L	524	
1	M	524	
1	N	524	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 27363 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.

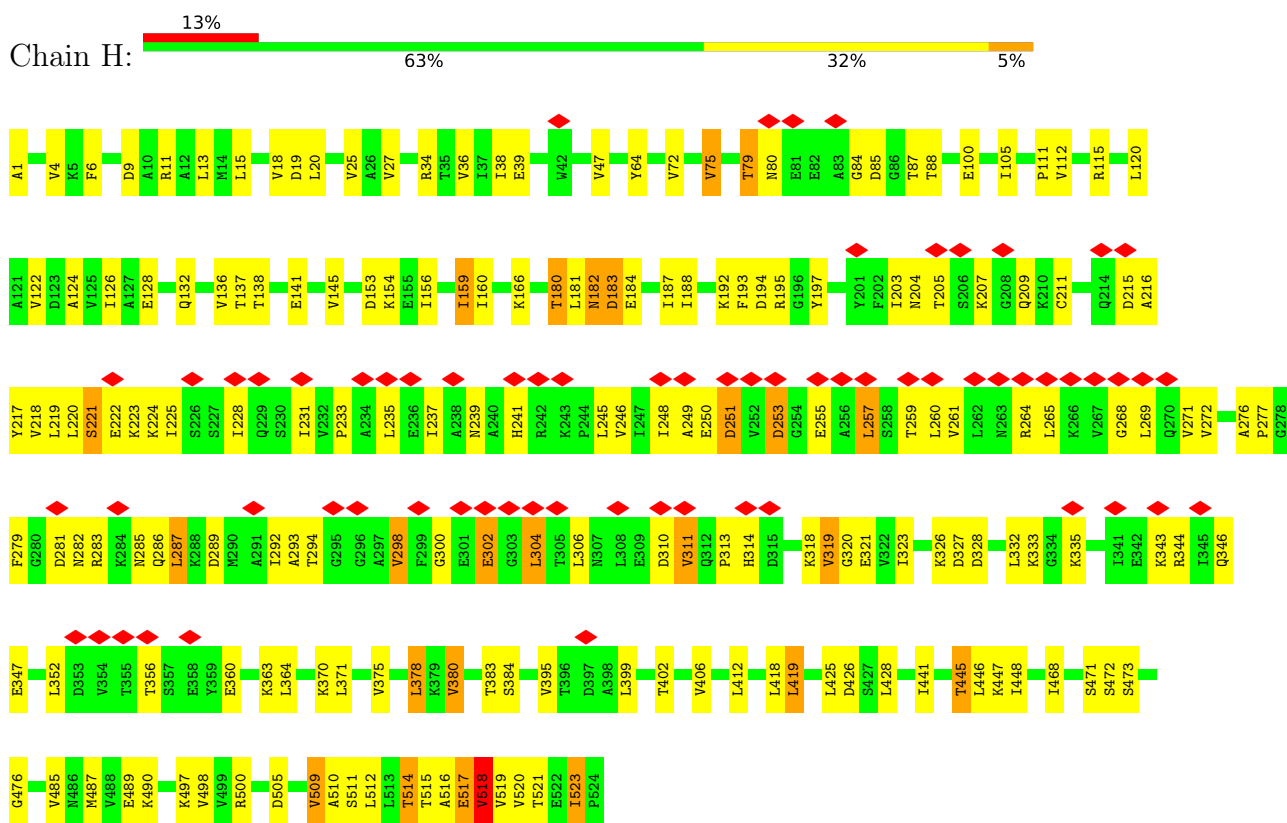
- Molecule 1 is a protein called 60 kDa heat shock protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	H	524	Total	C	N	O	S	0	0
			3909	2451	667	777	14		
1	I	524	Total	C	N	O	S	0	0
			3909	2451	667	777	14		
1	J	524	Total	C	N	O	S	0	0
			3909	2451	667	777	14		
1	K	524	Total	C	N	O	S	0	0
			3909	2451	667	777	14		
1	L	524	Total	C	N	O	S	0	0
			3909	2451	667	777	14		
1	M	524	Total	C	N	O	S	0	0
			3909	2451	667	777	14		
1	N	524	Total	C	N	O	S	0	0
			3909	2451	667	777	14		

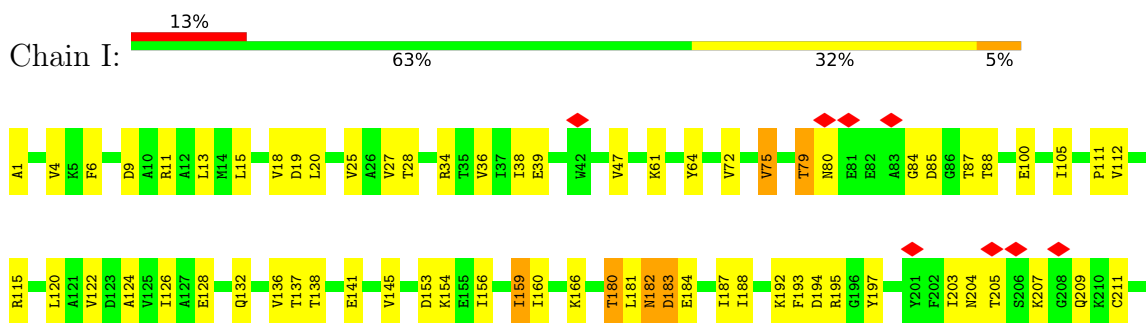
### 3 Residue-property plots

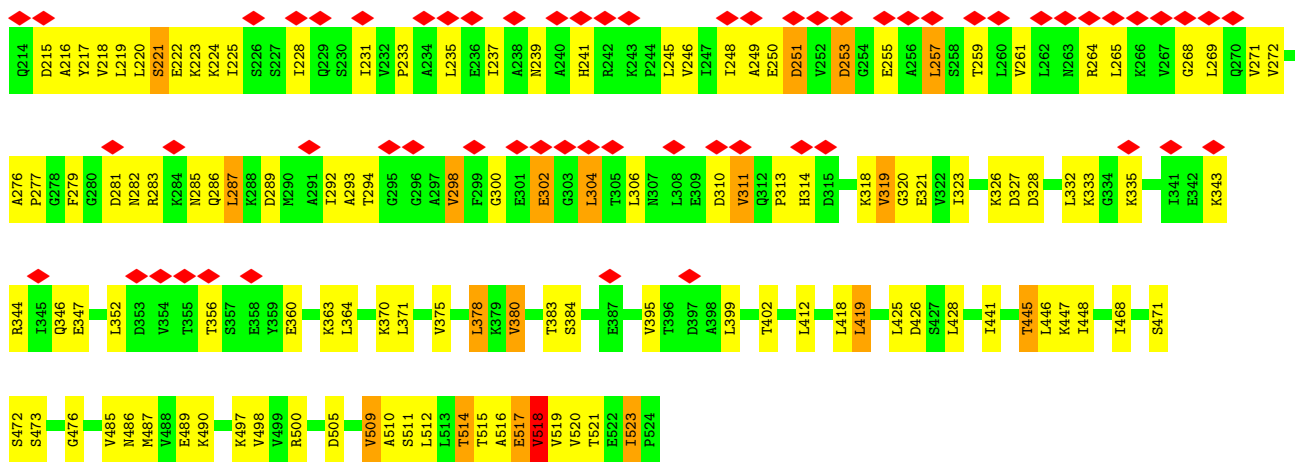
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 60 kDa heat shock protein, mitochondrial

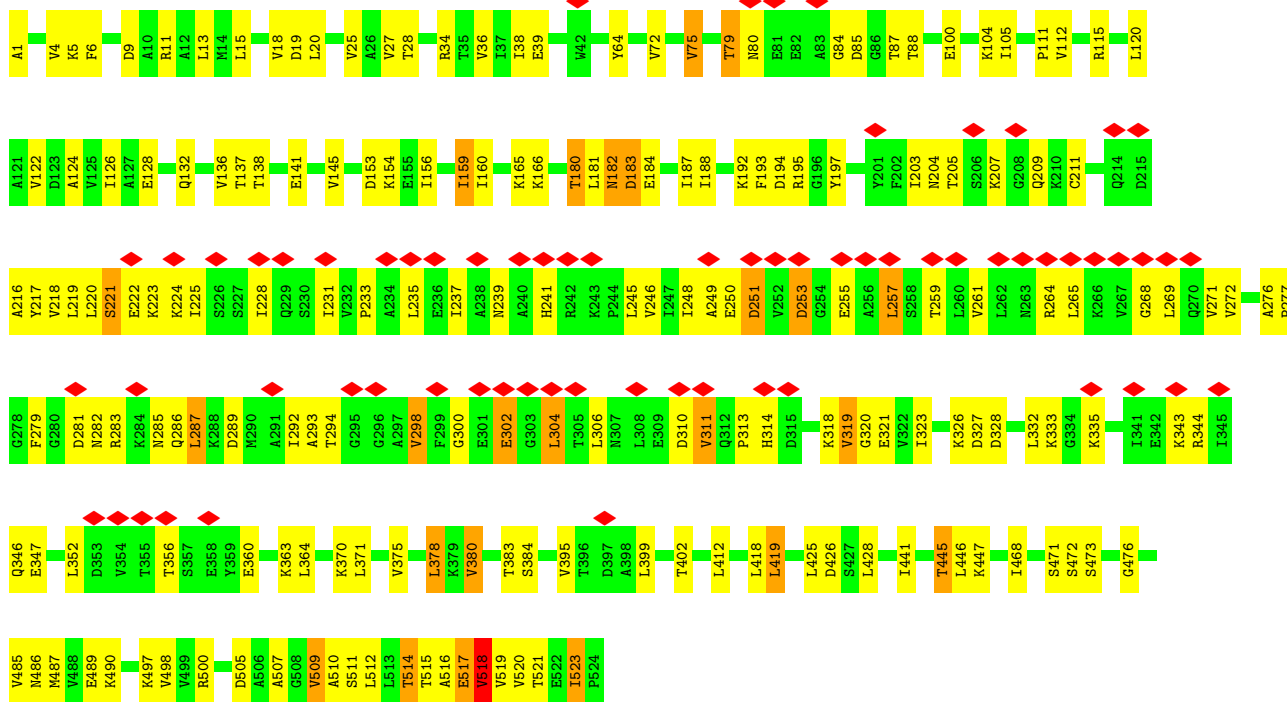


- Molecule 1: 60 kDa heat shock protein, mitochondrial

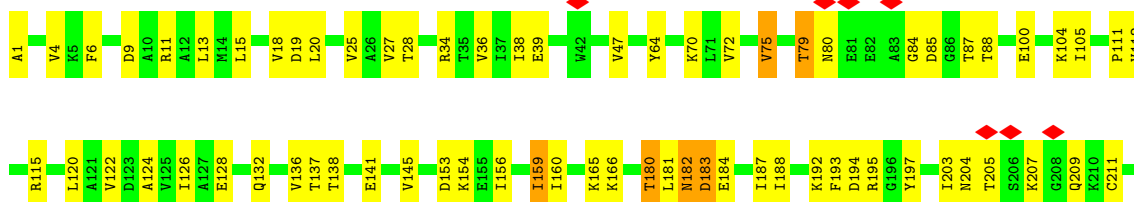


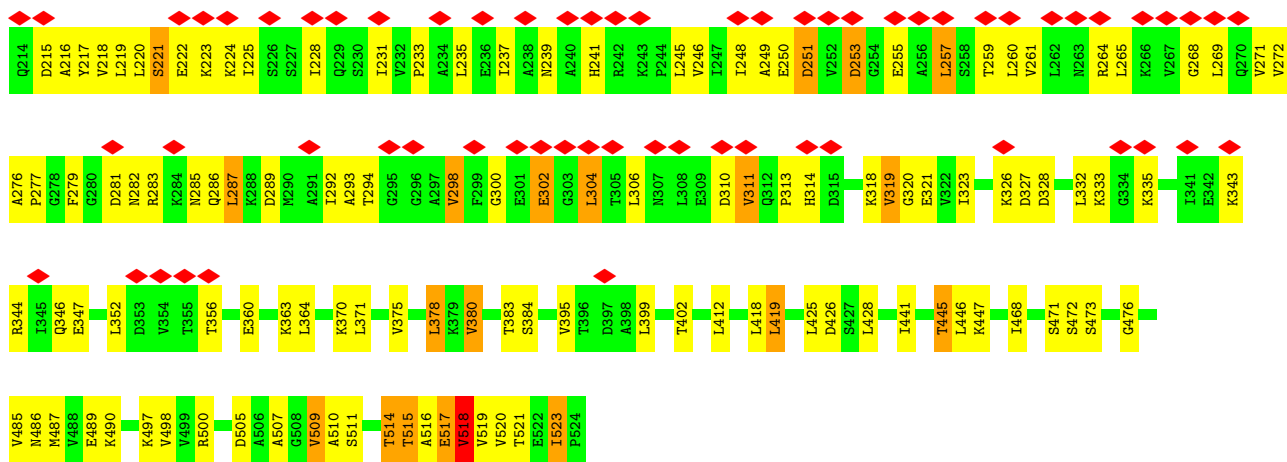


- Molecule 1: 60 kDa heat shock protein, mitochondrial

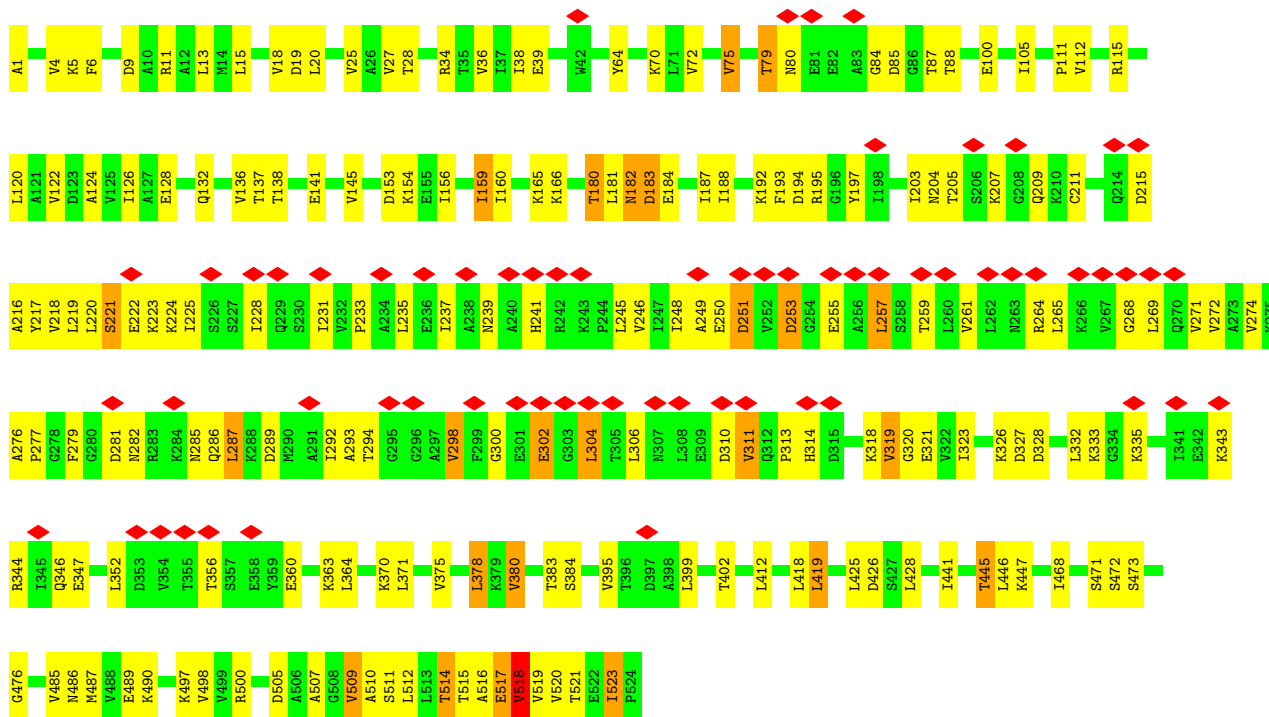


- Molecule 1: 60 kDa heat shock protein, mitochondrial

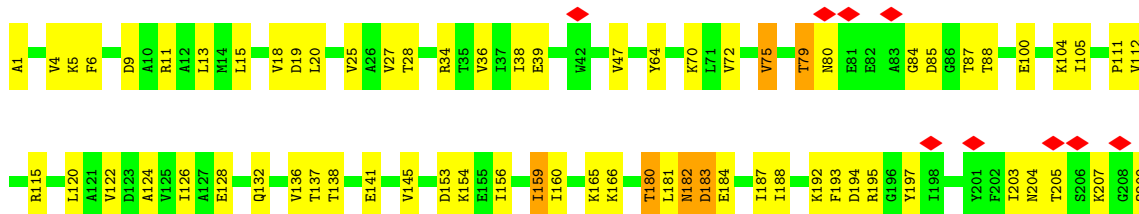


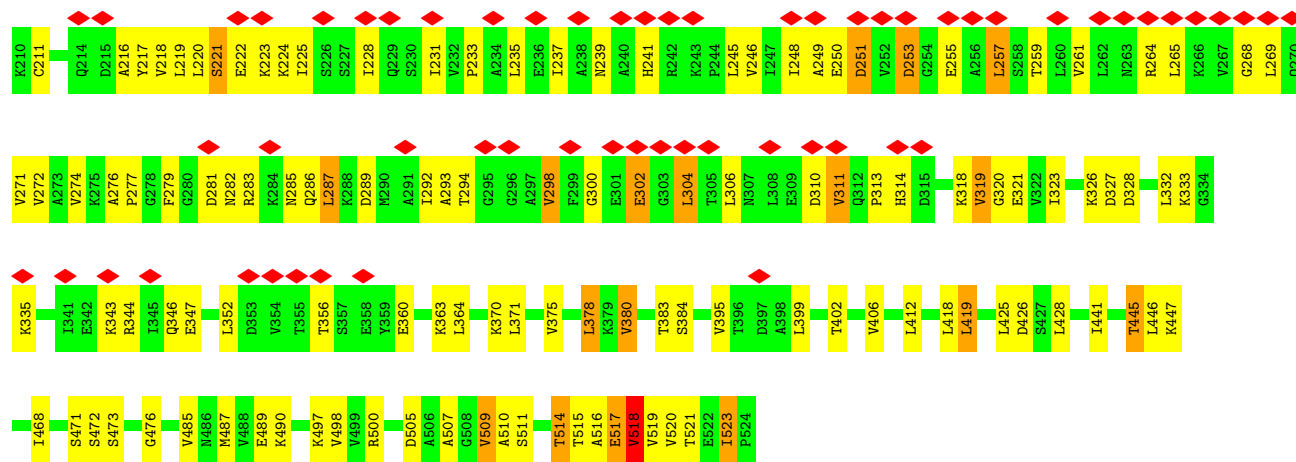


- Molecule 1: 60 kDa heat shock protein, mitochondrial

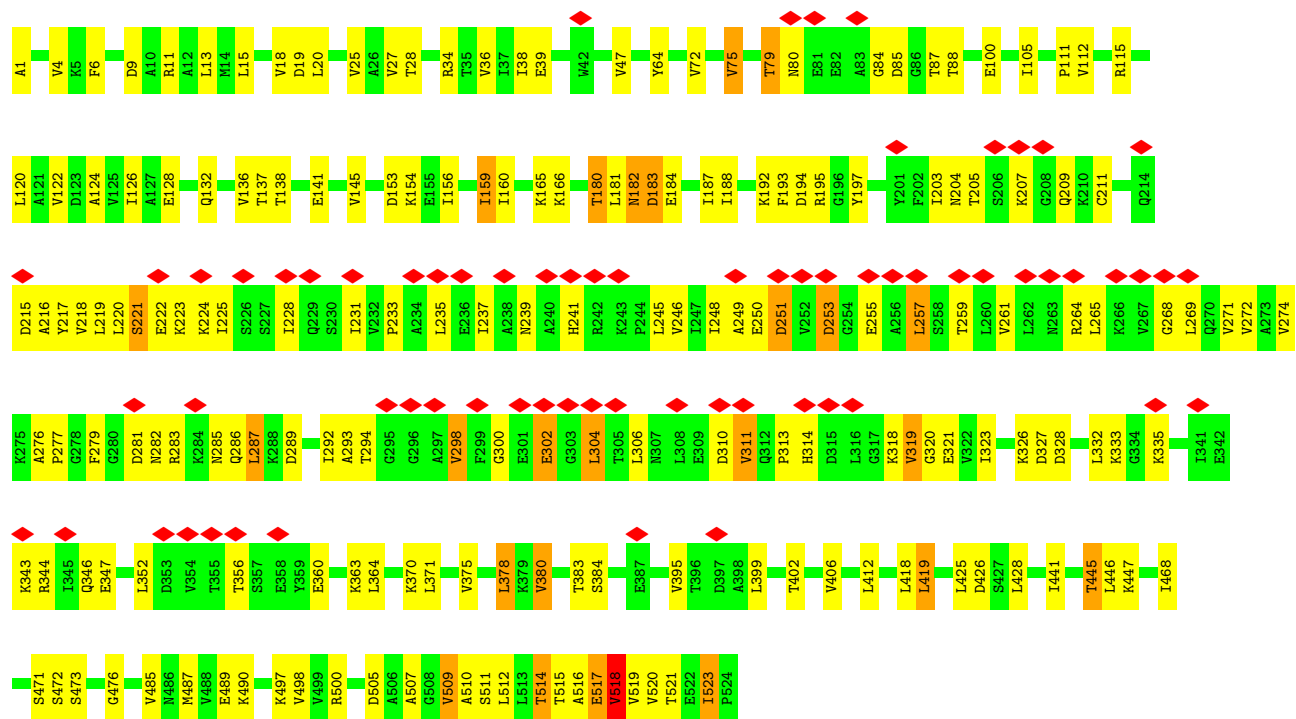


- Molecule 1: 60 kDa heat shock protein, mitochondrial





- Molecule 1: 60 kDa heat shock protein, mitochondrial



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, POINT	Depositor
Number of particles used	196060, 182600	Depositor
Resolution determination method	FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION, PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	44, 53	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k), GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.254	Depositor
Minimum map value	-0.173	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.019	Depositor
Map size (Å)	268.8, 268.8, 268.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.84, 0.84, 0.84	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	H	0.37	0/3940	0.49	0/5313
1	I	0.37	0/3940	0.49	0/5313
1	J	0.37	0/3940	0.49	0/5313
1	K	0.37	0/3940	0.49	0/5313
1	L	0.37	0/3940	0.49	0/5313
1	M	0.37	0/3940	0.49	0/5313
1	N	0.37	0/3940	0.49	0/5313
All	All	0.37	0/27580	0.49	0/37191

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	H	0	1
1	I	0	1
1	J	0	1
1	K	0	1
1	L	0	1
1	M	0	1
1	N	0	1
All	All	0	7

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	517	GLU	Peptide

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Mol	Chain	Res	Type	Group
1	I	517	GLU	Peptide
1	J	517	GLU	Peptide
1	K	517	GLU	Peptide
1	L	517	GLU	Peptide
1	M	517	GLU	Peptide
1	N	517	GLU	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	H	3909	0	4087	100	0
1	I	3909	0	4087	101	0
1	J	3909	0	4087	105	0
1	K	3909	0	4087	108	0
1	L	3909	0	4087	104	0
1	M	3909	0	4087	104	0
1	N	3909	0	4087	102	0
All	All	27363	0	28609	711	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 13.

All (711) 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:H:277:PRO:O	1:H:286:GLN:NE2	2.16	0.79
1:I:277:PRO:O	1:I:286:GLN:NE2	2.16	0.79
1:J:277:PRO:O	1:J:286:GLN:NE2	2.16	0.79
1:L:277:PRO:O	1:L:286:GLN:NE2	2.16	0.79
1:K:277:PRO:O	1:K:286:GLN:NE2	2.16	0.79
1:N:277:PRO:O	1:N:286:GLN:NE2	2.16	0.79
1:M:277:PRO:O	1:M:286:GLN:NE2	2.16	0.78
1:N:383:THR:O	1:N:384:SER:N	2.18	0.76
1:H:383:THR:O	1:H:384:SER:N	2.18	0.76
1:L:383:THR:O	1:L:384:SER:N	2.18	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:383:THR:O	1:I:384:SER:N	2.18	0.75
1:K:383:THR:O	1:K:384:SER:N	2.18	0.75
1:J:383:THR:O	1:J:384:SER:N	2.18	0.75
1:M:383:THR:O	1:M:384:SER:N	2.18	0.75
1:I:251:ASP:OD1	1:I:251:ASP:N	2.19	0.75
1:J:251:ASP:OD1	1:J:251:ASP:N	2.19	0.75
1:L:38:ILE:HG22	1:M:520:VAL:HB	1.69	0.74
1:H:251:ASP:N	1:H:251:ASP:OD1	2.19	0.74
1:N:281:ASP:O	1:N:285:ASN:ND2	2.21	0.74
1:K:281:ASP:O	1:K:285:ASN:ND2	2.21	0.74
1:H:281:ASP:O	1:H:285:ASN:ND2	2.21	0.73
1:L:251:ASP:OD1	1:L:251:ASP:N	2.19	0.73
1:L:281:ASP:O	1:L:285:ASN:ND2	2.21	0.73
1:I:281:ASP:O	1:I:285:ASN:ND2	2.21	0.73
1:J:281:ASP:O	1:J:285:ASN:ND2	2.21	0.73
1:M:237:ILE:HG21	1:M:313:PRO:HB3	1.71	0.73
1:M:281:ASP:O	1:M:285:ASN:ND2	2.21	0.73
1:L:237:ILE:HG21	1:L:313:PRO:HB3	1.71	0.73
1:N:237:ILE:HG21	1:N:313:PRO:HB3	1.71	0.72
1:L:217:TYR:HB2	1:L:245:LEU:HD22	1.71	0.72
1:I:237:ILE:HG21	1:I:313:PRO:HB3	1.71	0.72
1:H:237:ILE:HG21	1:H:313:PRO:HB3	1.71	0.72
1:K:237:ILE:HG21	1:K:313:PRO:HB3	1.71	0.72
1:K:217:TYR:HB2	1:K:245:LEU:HD22	1.72	0.71
1:J:237:ILE:HG21	1:J:313:PRO:HB3	1.71	0.71
1:H:217:TYR:HB2	1:H:245:LEU:HD22	1.72	0.71
1:H:126:ILE:HD12	1:H:500:ARG:HG3	1.73	0.71
1:I:217:TYR:HB2	1:I:245:LEU:HD22	1.71	0.71
1:I:126:ILE:HD12	1:I:500:ARG:HG3	1.73	0.71
1:K:251:ASP:OD1	1:K:251:ASP:N	2.19	0.71
1:M:126:ILE:HD12	1:M:500:ARG:HG3	1.73	0.71
1:M:217:TYR:HB2	1:M:245:LEU:HD22	1.72	0.71
1:N:221:SER:HB3	1:N:249:ALA:HB1	1.73	0.71
1:L:126:ILE:HD12	1:L:500:ARG:HG3	1.73	0.70
1:J:126:ILE:HD12	1:J:500:ARG:HG3	1.73	0.70
1:M:221:SER:HB3	1:M:249:ALA:HB1	1.73	0.70
1:N:217:TYR:HB2	1:N:245:LEU:HD22	1.71	0.70
1:J:217:TYR:HB2	1:J:245:LEU:HD22	1.71	0.70
1:J:221:SER:HB3	1:J:249:ALA:HB1	1.73	0.70
1:L:221:SER:HB3	1:L:249:ALA:HB1	1.73	0.70
1:H:221:SER:HB3	1:H:249:ALA:HB1	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:126:ILE:HD12	1:K:500:ARG:HG3	1.73	0.69
1:N:279:PHE:O	1:N:282:ASN:ND2	2.26	0.69
1:J:510:ALA:O	1:J:514:THR:OG1	2.10	0.69
1:K:221:SER:HB3	1:K:249:ALA:HB1	1.74	0.69
1:N:126:ILE:HD12	1:N:500:ARG:HG3	1.73	0.69
1:N:251:ASP:OD1	1:N:251:ASP:N	2.19	0.69
1:N:510:ALA:O	1:N:514:THR:OG1	2.10	0.69
1:K:510:ALA:O	1:K:514:THR:OG1	2.10	0.68
1:L:510:ALA:O	1:L:514:THR:OG1	2.10	0.68
1:M:279:PHE:O	1:M:282:ASN:ND2	2.26	0.68
1:H:279:PHE:O	1:H:282:ASN:ND2	2.26	0.68
1:I:221:SER:HB3	1:I:249:ALA:HB1	1.73	0.68
1:K:38:ILE:HG22	1:L:520:VAL:HB	1.75	0.68
1:I:510:ALA:O	1:I:514:THR:OG1	2.10	0.68
1:K:279:PHE:O	1:K:282:ASN:ND2	2.26	0.68
1:H:510:ALA:O	1:H:514:THR:OG1	2.10	0.68
1:M:510:ALA:O	1:M:514:THR:OG1	2.10	0.68
1:J:279:PHE:O	1:J:282:ASN:ND2	2.26	0.68
1:L:279:PHE:O	1:L:282:ASN:ND2	2.26	0.68
1:I:279:PHE:O	1:I:282:ASN:ND2	2.26	0.67
1:M:251:ASP:N	1:M:251:ASP:OD1	2.19	0.66
1:K:194:ASP:O	1:K:195:ARG:NH1	2.28	0.66
1:I:228:ILE:HD11	1:I:255:GLU:HB2	1.78	0.66
1:M:38:ILE:HG22	1:N:520:VAL:HB	1.78	0.66
1:H:228:ILE:HD11	1:H:255:GLU:HB2	1.78	0.66
1:H:520:VAL:HB	1:N:38:ILE:HG22	1.76	0.66
1:J:228:ILE:HD11	1:J:255:GLU:HB2	1.78	0.65
1:L:194:ASP:O	1:L:195:ARG:NH1	2.28	0.65
1:M:194:ASP:O	1:M:195:ARG:NH1	2.28	0.65
1:K:166:LYS:HB3	1:K:187:ILE:HD11	1.79	0.65
1:M:228:ILE:HD11	1:M:255:GLU:HB2	1.78	0.64
1:I:166:LYS:HB3	1:I:187:ILE:HD11	1.79	0.64
1:L:166:LYS:HB3	1:L:187:ILE:HD11	1.79	0.64
1:H:38:ILE:HG22	1:I:520:VAL:HB	1.78	0.64
1:J:166:LYS:HB3	1:J:187:ILE:HD11	1.79	0.64
1:L:4:VAL:HG22	1:L:520:VAL:HG22	1.79	0.64
1:L:228:ILE:HD11	1:L:255:GLU:HB2	1.78	0.64
1:M:166:LYS:HB3	1:M:187:ILE:HD11	1.79	0.64
1:N:228:ILE:HD11	1:N:255:GLU:HB2	1.78	0.64
1:K:4:VAL:HG22	1:K:520:VAL:HG22	1.80	0.64
1:H:166:LYS:HB3	1:H:187:ILE:HD11	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:261:VAL:O	1:M:265:LEU:HB3	1.98	0.64
1:N:166:LYS:HB3	1:N:187:ILE:HD11	1.79	0.64
1:N:261:VAL:O	1:N:265:LEU:HB3	1.98	0.64
1:I:261:VAL:O	1:I:265:LEU:HB3	1.98	0.64
1:N:222:GLU:HG2	1:N:300:GLY:HA3	1.80	0.63
1:I:222:GLU:HG2	1:I:300:GLY:HA3	1.81	0.63
1:J:4:VAL:HG22	1:J:520:VAL:HG22	1.80	0.63
1:H:222:GLU:HG2	1:H:300:GLY:HA3	1.80	0.63
1:H:261:VAL:O	1:H:265:LEU:HB3	1.98	0.63
1:J:222:GLU:HG2	1:J:300:GLY:HA3	1.80	0.63
1:K:228:ILE:HD11	1:K:255:GLU:HB2	1.78	0.63
1:M:4:VAL:HG22	1:M:520:VAL:HG22	1.80	0.63
1:M:222:GLU:HG2	1:M:300:GLY:HA3	1.80	0.63
1:N:194:ASP:O	1:N:195:ARG:NH1	2.28	0.63
1:J:38:ILE:HG22	1:K:520:VAL:HB	1.80	0.63
1:L:261:VAL:O	1:L:265:LEU:HB3	1.98	0.63
1:H:194:ASP:O	1:H:195:ARG:NH1	2.28	0.63
1:L:222:GLU:HG2	1:L:300:GLY:HA3	1.80	0.63
1:K:222:GLU:HG2	1:K:300:GLY:HA3	1.81	0.62
1:I:4:VAL:HG22	1:I:520:VAL:HG22	1.80	0.62
1:J:261:VAL:O	1:J:265:LEU:HB3	1.98	0.62
1:K:261:VAL:O	1:K:265:LEU:HB3	1.98	0.62
1:N:4:VAL:HG22	1:N:520:VAL:HG22	1.80	0.62
1:K:128:GLU:OE2	1:K:132:GLN:NE2	2.30	0.62
1:L:128:GLU:OE2	1:L:132:GLN:NE2	2.30	0.62
1:H:4:VAL:HG22	1:H:520:VAL:HG22	1.80	0.61
1:H:183:ASP:HB3	1:H:380:VAL:HA	1.82	0.61
1:I:128:GLU:OE2	1:I:132:GLN:NE2	2.30	0.61
1:I:194:ASP:O	1:I:195:ARG:NH1	2.28	0.61
1:I:183:ASP:HB3	1:I:380:VAL:HA	1.82	0.61
1:H:332:LEU:HD11	1:H:375:VAL:HG21	1.83	0.61
1:J:194:ASP:O	1:J:195:ARG:NH1	2.28	0.61
1:N:332:LEU:HD11	1:N:375:VAL:HG21	1.83	0.61
1:J:128:GLU:OE2	1:J:132:GLN:NE2	2.30	0.61
1:N:183:ASP:HB3	1:N:380:VAL:HA	1.82	0.61
1:H:471:SER:OG	1:H:472:SER:N	2.34	0.61
1:I:471:SER:OG	1:I:472:SER:N	2.35	0.60
1:J:471:SER:OG	1:J:472:SER:N	2.34	0.60
1:M:332:LEU:HD11	1:M:375:VAL:HG21	1.83	0.60
1:I:332:LEU:HD11	1:I:375:VAL:HG21	1.83	0.60
1:K:471:SER:OG	1:K:472:SER:N	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:183:ASP:HB3	1:M:380:VAL:HA	1.82	0.60
1:I:38:ILE:HG22	1:J:520:VAL:HB	1.84	0.60
1:M:128:GLU:OE2	1:M:132:GLN:NE2	2.30	0.60
1:N:471:SER:OG	1:N:472:SER:N	2.34	0.60
1:K:180:THR:OG1	1:K:181:LEU:N	2.35	0.60
1:K:183:ASP:HB3	1:K:380:VAL:HA	1.82	0.60
1:N:180:THR:OG1	1:N:181:LEU:N	2.35	0.60
1:L:180:THR:OG1	1:L:181:LEU:N	2.35	0.60
1:J:183:ASP:HB3	1:J:380:VAL:HA	1.82	0.60
1:M:180:THR:OG1	1:M:181:LEU:N	2.35	0.60
1:N:115:ARG:HG3	1:N:511:SER:HB2	1.84	0.60
1:K:332:LEU:HD11	1:K:375:VAL:HG21	1.83	0.60
1:L:183:ASP:HB3	1:L:380:VAL:HA	1.82	0.60
1:L:115:ARG:HG3	1:L:511:SER:HB2	1.84	0.60
1:M:115:ARG:HG3	1:M:511:SER:HB2	1.84	0.60
1:K:115:ARG:HG3	1:K:511:SER:HB2	1.84	0.59
1:H:192:LYS:O	1:H:370:LYS:NZ	2.35	0.59
1:J:6:PHE:HA	1:J:518:VAL:HG13	1.84	0.59
1:K:6:PHE:HA	1:K:518:VAL:HG13	1.84	0.59
1:L:332:LEU:HD11	1:L:375:VAL:HG21	1.83	0.59
1:H:180:THR:OG1	1:H:181:LEU:N	2.35	0.59
1:J:332:LEU:HD11	1:J:375:VAL:HG21	1.83	0.59
1:K:192:LYS:O	1:K:370:LYS:NZ	2.35	0.59
1:I:192:LYS:O	1:I:370:LYS:NZ	2.36	0.59
1:M:192:LYS:O	1:M:370:LYS:NZ	2.35	0.59
1:N:192:LYS:O	1:N:370:LYS:NZ	2.36	0.59
1:L:192:LYS:O	1:L:370:LYS:NZ	2.35	0.59
1:H:115:ARG:HG3	1:H:511:SER:HB2	1.84	0.59
1:I:6:PHE:HA	1:I:518:VAL:HG13	1.84	0.59
1:J:115:ARG:HG3	1:J:511:SER:HB2	1.84	0.59
1:J:180:THR:OG1	1:J:181:LEU:N	2.35	0.59
1:L:6:PHE:HA	1:L:518:VAL:HG13	1.84	0.59
1:L:471:SER:OG	1:L:472:SER:N	2.34	0.59
1:I:180:THR:OG1	1:I:181:LEU:N	2.35	0.58
1:N:6:PHE:HA	1:N:518:VAL:HG13	1.84	0.58
1:H:6:PHE:HA	1:H:518:VAL:HG13	1.84	0.58
1:J:192:LYS:O	1:J:370:LYS:NZ	2.35	0.58
1:K:228:ILE:HG21	1:K:259:THR:HG21	1.86	0.58
1:L:228:ILE:HG21	1:L:259:THR:HG21	1.86	0.58
1:M:471:SER:OG	1:M:472:SER:N	2.35	0.58
1:N:128:GLU:OE2	1:N:132:GLN:NE2	2.30	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:441:ILE:O	1:I:445:THR:HG23	2.04	0.58
1:J:441:ILE:O	1:J:445:THR:HG23	2.04	0.58
1:H:228:ILE:HG21	1:H:259:THR:HG21	1.86	0.58
1:H:441:ILE:O	1:H:445:THR:HG23	2.04	0.57
1:J:228:ILE:HG21	1:J:259:THR:HG21	1.86	0.57
1:M:6:PHE:HA	1:M:518:VAL:HG13	1.84	0.57
1:I:228:ILE:HG21	1:I:259:THR:HG21	1.86	0.57
1:I:115:ARG:HG3	1:I:511:SER:HB2	1.84	0.57
1:N:441:ILE:O	1:N:445:THR:HG23	2.04	0.57
1:I:136:VAL:HG11	1:I:145:VAL:HG21	1.87	0.57
1:K:441:ILE:O	1:K:445:THR:HG23	2.04	0.57
1:K:304:LEU:HD12	1:K:306:LEU:HD23	1.86	0.57
1:L:441:ILE:O	1:L:445:THR:HG23	2.04	0.57
1:N:304:LEU:HD12	1:N:306:LEU:HD23	1.86	0.57
1:H:136:VAL:HG11	1:H:145:VAL:HG21	1.87	0.57
1:N:228:ILE:HG21	1:N:259:THR:HG21	1.86	0.57
1:H:304:LEU:HD12	1:H:306:LEU:HD23	1.86	0.57
1:I:160:ILE:HG21	1:I:402:THR:HG21	1.86	0.57
1:J:136:VAL:HG11	1:J:145:VAL:HG21	1.87	0.57
1:J:160:ILE:HG21	1:J:402:THR:HG21	1.86	0.57
1:L:304:LEU:HD12	1:L:306:LEU:HD23	1.86	0.57
1:M:441:ILE:O	1:M:445:THR:HG23	2.04	0.57
1:J:304:LEU:HD12	1:J:306:LEU:HD23	1.86	0.56
1:K:136:VAL:HG11	1:K:145:VAL:HG21	1.87	0.56
1:N:136:VAL:HG11	1:N:145:VAL:HG21	1.87	0.56
1:N:485:VAL:HG11	1:N:490:LYS:HD3	1.87	0.56
1:H:485:VAL:HG11	1:H:490:LYS:HD3	1.88	0.56
1:I:485:VAL:HG11	1:I:490:LYS:HD3	1.88	0.56
1:M:160:ILE:HG21	1:M:402:THR:HG21	1.86	0.56
1:M:228:ILE:HG21	1:M:259:THR:HG21	1.86	0.56
1:N:160:ILE:HG21	1:N:402:THR:HG21	1.86	0.56
1:J:485:VAL:HG11	1:J:490:LYS:HD3	1.88	0.56
1:L:136:VAL:HG11	1:L:145:VAL:HG21	1.87	0.56
1:M:136:VAL:HG11	1:M:145:VAL:HG21	1.87	0.56
1:J:188:ILE:HD11	1:J:332:LEU:HG	1.88	0.56
1:K:188:ILE:HD11	1:K:332:LEU:HG	1.88	0.56
1:K:485:VAL:HG11	1:K:490:LYS:HD3	1.87	0.56
1:L:160:ILE:HG21	1:L:402:THR:HG21	1.86	0.56
1:M:304:LEU:HD12	1:M:306:LEU:HD23	1.86	0.56
1:M:485:VAL:HG11	1:M:490:LYS:HD3	1.88	0.56
1:H:160:ILE:HG21	1:H:402:THR:HG21	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:156:ILE:HG23	1:N:395:VAL:HG23	1.88	0.56
1:L:360:GLU:OE1	1:L:360:GLU:N	2.37	0.56
1:H:156:ILE:HG23	1:H:395:VAL:HG23	1.88	0.55
1:K:160:ILE:HG21	1:K:402:THR:HG21	1.86	0.55
1:I:304:LEU:HD12	1:I:306:LEU:HD23	1.86	0.55
1:L:188:ILE:HD11	1:L:332:LEU:HG	1.88	0.55
1:I:188:ILE:HD11	1:I:332:LEU:HG	1.88	0.55
1:M:156:ILE:HG23	1:M:395:VAL:HG23	1.88	0.55
1:M:320:GLY:N	1:M:332:LEU:O	2.36	0.55
1:K:153:ASP:OD1	1:K:154:LYS:N	2.40	0.55
1:H:128:GLU:OE2	1:H:132:GLN:NE2	2.30	0.55
1:L:485:VAL:HG11	1:L:490:LYS:HD3	1.88	0.55
1:I:360:GLU:OE1	1:I:360:GLU:N	2.37	0.55
1:L:153:ASP:OD1	1:L:154:LYS:N	2.40	0.55
1:M:153:ASP:OD1	1:M:154:LYS:N	2.40	0.55
1:M:188:ILE:HD11	1:M:332:LEU:HG	1.88	0.55
1:N:188:ILE:HD11	1:N:332:LEU:HG	1.88	0.55
1:N:153:ASP:OD1	1:N:154:LYS:N	2.40	0.55
1:I:153:ASP:OD1	1:I:154:LYS:N	2.40	0.54
1:J:153:ASP:OD1	1:J:154:LYS:N	2.40	0.54
1:M:360:GLU:OE1	1:M:360:GLU:N	2.37	0.54
1:J:138:THR:N	1:J:141:GLU:OE2	2.37	0.54
1:H:188:ILE:HD11	1:H:332:LEU:HG	1.88	0.54
1:I:156:ILE:HG23	1:I:395:VAL:HG23	1.88	0.54
1:J:360:GLU:OE1	1:J:360:GLU:N	2.37	0.54
1:H:153:ASP:OD1	1:H:154:LYS:N	2.40	0.54
1:L:156:ILE:HG23	1:L:395:VAL:HG23	1.88	0.54
1:M:18:VAL:HG23	1:M:72:VAL:HG21	1.90	0.54
1:H:224:LYS:HA	1:H:250:GLU:HB3	1.90	0.54
1:H:360:GLU:OE1	1:H:360:GLU:N	2.37	0.54
1:N:224:LYS:HA	1:N:250:GLU:HB3	1.90	0.54
1:H:320:GLY:N	1:H:332:LEU:O	2.36	0.53
1:N:18:VAL:HG23	1:N:72:VAL:HG21	1.90	0.53
1:L:138:THR:N	1:L:141:GLU:OE2	2.37	0.53
1:N:360:GLU:OE1	1:N:360:GLU:N	2.37	0.53
1:J:156:ILE:HG23	1:J:395:VAL:HG23	1.88	0.53
1:I:18:VAL:HG23	1:I:72:VAL:HG21	1.90	0.53
1:L:18:VAL:HG23	1:L:72:VAL:HG21	1.90	0.53
1:M:224:LYS:HA	1:M:250:GLU:HB3	1.90	0.53
1:I:224:LYS:HA	1:I:250:GLU:HB3	1.90	0.53
1:K:156:ILE:HG23	1:K:395:VAL:HG23	1.88	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:18:VAL:HG23	1:J:72:VAL:HG21	1.90	0.53
1:K:18:VAL:HG23	1:K:72:VAL:HG21	1.90	0.53
1:H:18:VAL:HG23	1:H:72:VAL:HG21	1.90	0.52
1:L:224:LYS:HA	1:L:250:GLU:HB3	1.90	0.52
1:K:224:LYS:HA	1:K:250:GLU:HB3	1.90	0.52
1:K:360:GLU:OE1	1:K:360:GLU:N	2.37	0.52
1:L:320:GLY:N	1:L:332:LEU:O	2.36	0.52
1:K:138:THR:N	1:K:141:GLU:OE2	2.37	0.52
1:J:224:LYS:HA	1:J:250:GLU:HB3	1.90	0.52
1:M:138:THR:N	1:M:141:GLU:OE2	2.37	0.52
1:K:318:LYS:HD2	1:K:335:LYS:HB2	1.92	0.51
1:I:138:THR:N	1:I:141:GLU:OE2	2.37	0.51
1:L:289:ASP:HA	1:L:292:ILE:HG22	1.92	0.51
1:N:318:LYS:HD2	1:N:335:LYS:HB2	1.92	0.51
1:H:182:ASN:OD1	1:H:182:ASN:N	2.44	0.51
1:H:472:SER:OG	1:H:473:SER:N	2.44	0.51
1:L:318:LYS:HD2	1:L:335:LYS:HB2	1.92	0.51
1:M:472:SER:OG	1:M:473:SER:N	2.44	0.51
1:N:472:SER:OG	1:N:473:SER:N	2.44	0.51
1:N:289:ASP:HA	1:N:292:ILE:HG22	1.92	0.51
1:M:289:ASP:HA	1:M:292:ILE:HG22	1.93	0.51
1:H:221:SER:HA	1:H:298:VAL:HG23	1.93	0.51
1:J:318:LYS:HD2	1:J:335:LYS:HB2	1.92	0.51
1:L:472:SER:OG	1:L:473:SER:N	2.44	0.51
1:I:472:SER:OG	1:I:473:SER:N	2.44	0.51
1:N:221:SER:HA	1:N:298:VAL:HG23	1.93	0.51
1:I:221:SER:HA	1:I:298:VAL:HG23	1.93	0.51
1:M:318:LYS:HD2	1:M:335:LYS:HB2	1.92	0.51
1:N:182:ASN:OD1	1:N:182:ASN:N	2.44	0.51
1:L:352:LEU:HD23	1:L:364:LEU:HD11	1.93	0.51
1:I:318:LYS:HD2	1:I:335:LYS:HB2	1.92	0.50
1:K:320:GLY:N	1:K:332:LEU:O	2.36	0.50
1:L:105:ILE:HD13	1:L:111:PRO:HB3	1.94	0.50
1:M:72:VAL:HG12	1:M:509:VAL:HG11	1.93	0.50
1:M:105:ILE:HD13	1:M:111:PRO:HB3	1.93	0.50
1:I:80:ASN:HB2	1:I:87:THR:OG1	2.12	0.50
1:J:352:LEU:HD23	1:J:364:LEU:HD11	1.93	0.50
1:K:352:LEU:HD23	1:K:364:LEU:HD11	1.93	0.50
1:H:289:ASP:HA	1:H:292:ILE:HG22	1.93	0.50
1:J:289:ASP:HA	1:J:292:ILE:HG22	1.92	0.50
1:K:289:ASP:HA	1:K:292:ILE:HG22	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:105:ILE:HD13	1:N:111:PRO:HB3	1.93	0.50
1:H:318:LYS:HD2	1:H:335:LYS:HB2	1.92	0.50
1:I:418:LEU:HB3	1:I:446:LEU:HG	1.93	0.50
1:J:418:LEU:HB3	1:J:446:LEU:HG	1.93	0.50
1:K:105:ILE:HD13	1:K:111:PRO:HB3	1.93	0.50
1:L:72:VAL:HG12	1:L:509:VAL:HG11	1.93	0.50
1:N:72:VAL:HG12	1:N:509:VAL:HG11	1.93	0.50
1:I:289:ASP:HA	1:I:292:ILE:HG22	1.93	0.50
1:M:264:ARG:O	1:M:268:GLY:N	2.41	0.50
1:M:352:LEU:HD23	1:M:364:LEU:HD11	1.93	0.50
1:H:105:ILE:HD13	1:H:111:PRO:HB3	1.93	0.50
1:K:80:ASN:HB2	1:K:87:THR:OG1	2.12	0.50
1:K:418:LEU:HB3	1:K:446:LEU:HG	1.93	0.50
1:L:80:ASN:HB2	1:L:87:THR:OG1	2.12	0.50
1:J:221:SER:HA	1:J:298:VAL:HG23	1.93	0.50
1:J:472:SER:OG	1:J:473:SER:N	2.44	0.50
1:K:72:VAL:HG12	1:K:509:VAL:HG11	1.93	0.50
1:H:72:VAL:HG12	1:H:509:VAL:HG11	1.93	0.50
1:H:80:ASN:HB2	1:H:87:THR:OG1	2.12	0.50
1:I:352:LEU:HD23	1:I:364:LEU:HD11	1.93	0.49
1:J:105:ILE:HD13	1:J:111:PRO:HB3	1.94	0.49
1:K:472:SER:OG	1:K:473:SER:N	2.44	0.49
1:M:221:SER:HA	1:M:298:VAL:HG23	1.93	0.49
1:N:138:THR:N	1:N:141:GLU:OE2	2.37	0.49
1:N:352:LEU:HD23	1:N:364:LEU:HD11	1.93	0.49
1:H:352:LEU:HD23	1:H:364:LEU:HD11	1.93	0.49
1:I:105:ILE:HD13	1:I:111:PRO:HB3	1.94	0.49
1:K:182:ASN:OD1	1:K:182:ASN:N	2.44	0.49
1:N:264:ARG:O	1:N:268:GLY:N	2.41	0.49
1:H:418:LEU:HB3	1:H:446:LEU:HG	1.93	0.49
1:J:72:VAL:HG12	1:J:509:VAL:HG11	1.93	0.49
1:N:80:ASN:HB2	1:N:87:THR:OG1	2.12	0.49
1:H:138:THR:N	1:H:141:GLU:OE2	2.37	0.49
1:I:72:VAL:HG12	1:I:509:VAL:HG11	1.93	0.49
1:I:182:ASN:OD1	1:I:182:ASN:N	2.44	0.49
1:K:246:VAL:HG13	1:K:272:VAL:HG21	1.95	0.49
1:L:221:SER:HA	1:L:298:VAL:HG23	1.93	0.49
1:H:197:TYR:CD2	1:H:326:LYS:HA	2.48	0.49
1:L:246:VAL:HG13	1:L:272:VAL:HG21	1.95	0.49
1:L:418:LEU:HB3	1:L:446:LEU:HG	1.93	0.49
1:M:80:ASN:HB2	1:M:87:THR:OG1	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:246:VAL:HG13	1:M:272:VAL:HG21	1.95	0.49
1:N:197:TYR:CD2	1:N:326:LYS:HA	2.48	0.49
1:J:182:ASN:OD1	1:J:182:ASN:N	2.44	0.49
1:K:197:TYR:CD2	1:K:326:LYS:HA	2.48	0.49
1:K:221:SER:HA	1:K:298:VAL:HG23	1.93	0.49
1:L:182:ASN:OD1	1:L:182:ASN:N	2.44	0.49
1:L:264:ARG:O	1:L:268:GLY:N	2.41	0.49
1:M:182:ASN:OD1	1:M:182:ASN:N	2.44	0.49
1:J:80:ASN:HB2	1:J:87:THR:OG1	2.12	0.49
1:I:320:GLY:N	1:I:332:LEU:O	2.36	0.48
1:J:246:VAL:HG13	1:J:272:VAL:HG21	1.95	0.48
1:K:203:ILE:HA	1:K:211:CYS:HB2	1.95	0.48
1:M:418:LEU:HB3	1:M:446:LEU:HG	1.93	0.48
1:I:197:TYR:CD2	1:I:326:LYS:HA	2.48	0.48
1:N:418:LEU:HB3	1:N:446:LEU:HG	1.93	0.48
1:J:159:ILE:HD12	1:J:378:LEU:HD21	1.96	0.48
1:N:246:VAL:HG13	1:N:272:VAL:HG21	1.95	0.48
1:H:203:ILE:HA	1:H:211:CYS:HB2	1.95	0.48
1:J:197:TYR:CD2	1:J:326:LYS:HA	2.48	0.48
1:K:159:ILE:HD12	1:K:378:LEU:HD21	1.96	0.48
1:M:159:ILE:HD12	1:M:378:LEU:HD21	1.96	0.48
1:J:203:ILE:HA	1:J:211:CYS:HB2	1.95	0.48
1:L:203:ILE:HA	1:L:211:CYS:HB2	1.95	0.48
1:N:159:ILE:HD12	1:N:378:LEU:HD21	1.96	0.48
1:L:197:TYR:CD2	1:L:326:LYS:HA	2.48	0.48
1:I:203:ILE:HA	1:I:211:CYS:HB2	1.95	0.48
1:I:246:VAL:HG13	1:I:272:VAL:HG21	1.95	0.48
1:L:159:ILE:HD12	1:L:378:LEU:HD21	1.96	0.48
1:M:203:ILE:HA	1:M:211:CYS:HB2	1.95	0.48
1:I:419:LEU:HD13	1:I:447:LYS:HB3	1.96	0.48
1:N:203:ILE:HA	1:N:211:CYS:HB2	1.95	0.48
1:N:419:LEU:HD13	1:N:447:LYS:HB3	1.96	0.48
1:H:419:LEU:HD13	1:H:447:LYS:HB3	1.96	0.48
1:I:159:ILE:HD12	1:I:378:LEU:HD21	1.96	0.48
1:J:11:ARG:HD2	1:J:516:ALA:H	1.79	0.48
1:J:419:LEU:HD13	1:J:447:LYS:HB3	1.96	0.48
1:M:11:ARG:HD2	1:M:516:ALA:H	1.79	0.48
1:M:419:LEU:HD13	1:M:447:LYS:HB3	1.96	0.48
1:N:11:ARG:HD2	1:N:516:ALA:H	1.79	0.48
1:H:159:ILE:HD12	1:H:378:LEU:HD21	1.96	0.48
1:M:197:TYR:CD2	1:M:326:LYS:HA	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:419:LEU:HD13	1:L:447:LYS:HB3	1.96	0.47
1:I:138:THR:O	1:I:141:GLU:HG2	2.14	0.47
1:K:419:LEU:HD13	1:K:447:LYS:HB3	1.96	0.47
1:N:343:LYS:O	1:N:347:GLU:HG3	2.14	0.47
1:H:246:VAL:HG13	1:H:272:VAL:HG21	1.95	0.47
1:J:28:THR:O	1:J:28:THR:OG1	2.30	0.47
1:L:138:THR:O	1:L:141:GLU:HG2	2.14	0.47
1:L:343:LYS:O	1:L:347:GLU:HG3	2.14	0.47
1:M:28:THR:O	1:M:28:THR:OG1	2.30	0.47
1:M:343:LYS:O	1:M:347:GLU:HG3	2.14	0.47
1:N:302:GLU:HG3	1:N:304:LEU:HG	1.96	0.47
1:J:138:THR:O	1:J:141:GLU:HG2	2.14	0.47
1:L:11:ARG:HD2	1:L:516:ALA:H	1.79	0.47
1:M:302:GLU:HG3	1:M:304:LEU:HG	1.96	0.47
1:H:11:ARG:HD2	1:H:516:ALA:H	1.79	0.47
1:H:343:LYS:O	1:H:347:GLU:HG3	2.14	0.47
1:I:11:ARG:HD2	1:I:516:ALA:H	1.79	0.47
1:I:302:GLU:HG3	1:I:304:LEU:HG	1.96	0.47
1:J:302:GLU:HG3	1:J:304:LEU:HG	1.96	0.47
1:K:1:ALA:O	1:K:523:ILE:HB	2.15	0.47
1:H:138:THR:O	1:H:141:GLU:HG2	2.14	0.47
1:H:302:GLU:HG3	1:H:304:LEU:HG	1.96	0.47
1:I:28:THR:O	1:I:28:THR:OG1	2.30	0.47
1:M:138:THR:O	1:M:141:GLU:HG2	2.14	0.47
1:N:138:THR:O	1:N:141:GLU:HG2	2.14	0.47
1:J:1:ALA:O	1:J:523:ILE:HB	2.15	0.47
1:J:13:LEU:HD23	1:J:64:TYR:HB2	1.97	0.47
1:L:122:VAL:O	1:L:126:ILE:HG12	2.15	0.47
1:H:264:ARG:O	1:H:268:GLY:N	2.41	0.47
1:K:28:THR:O	1:K:28:THR:OG1	2.30	0.47
1:H:13:LEU:HD23	1:H:64:TYR:HB2	1.97	0.46
1:K:11:ARG:HD2	1:K:516:ALA:H	1.79	0.46
1:L:302:GLU:HG3	1:L:304:LEU:HG	1.96	0.46
1:H:1:ALA:O	1:H:523:ILE:HB	2.15	0.46
1:J:104:LYS:HD3	1:J:104:LYS:HA	1.68	0.46
1:M:122:VAL:O	1:M:126:ILE:HG12	2.15	0.46
1:N:320:GLY:N	1:N:332:LEU:O	2.36	0.46
1:I:1:ALA:O	1:I:523:ILE:HB	2.15	0.46
1:I:122:VAL:O	1:I:126:ILE:HG12	2.15	0.46
1:J:343:LYS:O	1:J:347:GLU:HG3	2.14	0.46
1:K:138:THR:O	1:K:141:GLU:HG2	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:195:ARG:NE	1:J:276:ALA:O	2.48	0.46
1:J:320:GLY:N	1:J:332:LEU:O	2.36	0.46
1:K:264:ARG:O	1:K:268:GLY:N	2.41	0.46
1:K:343:LYS:O	1:K:347:GLU:HG3	2.14	0.46
1:M:195:ARG:NE	1:M:276:ALA:O	2.48	0.46
1:N:13:LEU:HD23	1:N:64:TYR:HB2	1.97	0.46
1:N:122:VAL:O	1:N:126:ILE:HG12	2.15	0.46
1:H:122:VAL:O	1:H:126:ILE:HG12	2.15	0.46
1:J:197:TYR:CZ	1:J:203:ILE:HG22	2.51	0.46
1:M:197:TYR:CZ	1:M:203:ILE:HG22	2.51	0.46
1:N:195:ARG:NE	1:N:276:ALA:O	2.48	0.46
1:I:197:TYR:CZ	1:I:203:ILE:HG22	2.51	0.46
1:I:343:LYS:O	1:I:347:GLU:HG3	2.14	0.46
1:J:122:VAL:O	1:J:126:ILE:HG12	2.15	0.46
1:K:320:GLY:HA3	1:K:333:LYS:HB3	1.97	0.46
1:L:1:ALA:O	1:L:523:ILE:HB	2.15	0.46
1:L:197:TYR:CZ	1:L:203:ILE:HG22	2.51	0.46
1:L:320:GLY:HA3	1:L:333:LYS:HB3	1.98	0.46
1:H:320:GLY:HA3	1:H:333:LYS:HB3	1.97	0.46
1:K:197:TYR:CZ	1:K:203:ILE:HG22	2.51	0.46
1:N:28:THR:O	1:N:28:THR:OG1	2.30	0.46
1:N:197:TYR:CZ	1:N:203:ILE:HG22	2.51	0.46
1:I:13:LEU:HD23	1:I:64:TYR:HB2	1.97	0.46
1:I:195:ARG:NE	1:I:276:ALA:O	2.48	0.46
1:K:302:GLU:HG3	1:K:304:LEU:HG	1.96	0.46
1:N:1:ALA:O	1:N:523:ILE:HB	2.15	0.46
1:K:122:VAL:O	1:K:126:ILE:HG12	2.15	0.46
1:K:195:ARG:NE	1:K:276:ALA:O	2.48	0.46
1:M:1:ALA:O	1:M:523:ILE:HB	2.15	0.45
1:H:195:ARG:NE	1:H:276:ALA:O	2.48	0.45
1:I:320:GLY:HA3	1:I:333:LYS:HB3	1.97	0.45
1:K:184:GLU:N	1:K:184:GLU:OE1	2.50	0.45
1:L:195:ARG:NE	1:L:276:ALA:O	2.48	0.45
1:N:233:PRO:HB2	1:N:311:VAL:HG13	1.98	0.45
1:N:320:GLY:HA3	1:N:333:LYS:HB3	1.98	0.45
1:H:184:GLU:N	1:H:184:GLU:OE1	2.50	0.45
1:I:253:ASP:O	1:I:255:GLU:N	2.46	0.45
1:J:233:PRO:HB2	1:J:311:VAL:HG13	1.98	0.45
1:K:13:LEU:HD23	1:K:64:TYR:HB2	1.97	0.45
1:K:124:ALA:HB1	1:K:425:LEU:HD13	1.99	0.45
1:M:233:PRO:HB2	1:M:311:VAL:HG13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:320:GLY:HA3	1:M:333:LYS:HB3	1.97	0.45
1:J:124:ALA:HB1	1:J:425:LEU:HD13	1.99	0.45
1:L:184:GLU:OE1	1:L:184:GLU:N	2.50	0.45
1:M:221:SER:H	1:M:249:ALA:HA	1.82	0.45
1:H:197:TYR:CZ	1:H:203:ILE:HG22	2.51	0.45
1:L:25:VAL:HG12	1:L:88:THR:HG23	1.99	0.45
1:N:264:ARG:HE	1:N:264:ARG:HB2	1.58	0.45
1:I:75:VAL:O	1:I:79:THR:HG23	2.17	0.45
1:I:264:ARG:O	1:I:268:GLY:N	2.41	0.45
1:K:253:ASP:O	1:K:255:GLU:N	2.46	0.45
1:L:221:SER:H	1:L:249:ALA:HA	1.82	0.45
1:M:13:LEU:HD23	1:M:64:TYR:HB2	1.97	0.45
1:I:221:SER:H	1:I:249:ALA:HA	1.82	0.45
1:I:293:ALA:HB2	1:I:371:LEU:HD11	1.99	0.45
1:J:75:VAL:O	1:J:79:THR:HG23	2.17	0.45
1:J:320:GLY:HA3	1:J:333:LYS:HB3	1.98	0.45
1:H:75:VAL:O	1:H:79:THR:HG23	2.17	0.45
1:H:264:ARG:HA	1:H:269:LEU:H	1.82	0.45
1:I:124:ALA:HB1	1:I:425:LEU:HD13	1.99	0.45
1:J:184:GLU:OE1	1:J:184:GLU:N	2.50	0.45
1:K:25:VAL:HG12	1:K:88:THR:HG23	1.99	0.45
1:L:28:THR:O	1:L:28:THR:OG1	2.30	0.45
1:H:124:ALA:HB1	1:H:425:LEU:HD13	1.99	0.45
1:H:233:PRO:HB2	1:H:311:VAL:HG13	1.98	0.45
1:H:293:ALA:HB2	1:H:371:LEU:HD11	1.99	0.45
1:I:233:PRO:HB2	1:I:311:VAL:HG13	1.98	0.45
1:J:25:VAL:HG12	1:J:88:THR:HG23	1.99	0.45
1:K:287:LEU:HD13	1:K:287:LEU:HA	1.81	0.45
1:L:75:VAL:O	1:L:79:THR:HG23	2.17	0.45
1:N:75:VAL:O	1:N:79:THR:HG23	2.17	0.45
1:N:221:SER:H	1:N:249:ALA:HA	1.82	0.45
1:N:264:ARG:HA	1:N:269:LEU:H	1.82	0.45
1:K:75:VAL:O	1:K:79:THR:HG23	2.17	0.45
1:M:75:VAL:O	1:M:79:THR:HG23	2.17	0.45
1:M:104:LYS:HA	1:M:104:LYS:HD3	1.68	0.45
1:J:264:ARG:HA	1:J:269:LEU:H	1.82	0.44
1:L:233:PRO:HB2	1:L:311:VAL:HG13	1.98	0.44
1:M:264:ARG:HA	1:M:269:LEU:H	1.82	0.44
1:N:184:GLU:N	1:N:184:GLU:OE1	2.50	0.44
1:N:287:LEU:HD13	1:N:287:LEU:HA	1.81	0.44
1:I:264:ARG:HA	1:I:269:LEU:H	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:221:SER:H	1:J:249:ALA:HA	1.82	0.44
1:K:221:SER:H	1:K:249:ALA:HA	1.82	0.44
1:M:25:VAL:HG12	1:M:88:THR:HG23	1.99	0.44
1:H:512:LEU:HD11	1:N:47:VAL:HG11	1.99	0.44
1:J:264:ARG:HE	1:J:264:ARG:HB2	1.58	0.44
1:L:216:ALA:O	1:L:319:VAL:HG12	2.18	0.44
1:N:293:ALA:HB2	1:N:371:LEU:HD11	1.99	0.44
1:H:253:ASP:O	1:H:255:GLU:N	2.46	0.44
1:I:160:ILE:HD12	1:I:399:LEU:HD13	2.00	0.44
1:I:264:ARG:HE	1:I:264:ARG:HB2	1.58	0.44
1:J:264:ARG:O	1:J:268:GLY:N	2.40	0.44
1:J:293:ALA:HB2	1:J:371:LEU:HD11	1.99	0.44
1:K:233:PRO:HB2	1:K:311:VAL:HG13	1.98	0.44
1:L:13:LEU:HD23	1:L:64:TYR:HB2	1.98	0.44
1:L:124:ALA:HB1	1:L:425:LEU:HD13	1.99	0.44
1:H:160:ILE:HD12	1:H:399:LEU:HD13	2.00	0.44
1:I:184:GLU:N	1:I:184:GLU:OE1	2.50	0.44
1:I:216:ALA:O	1:I:319:VAL:HG12	2.18	0.44
1:K:160:ILE:HD12	1:K:399:LEU:HD13	2.00	0.44
1:M:184:GLU:N	1:M:184:GLU:OE1	2.50	0.44
1:I:25:VAL:HG12	1:I:88:THR:HG23	1.99	0.44
1:N:124:ALA:HB1	1:N:425:LEU:HD13	1.99	0.44
1:N:216:ALA:O	1:N:319:VAL:HG12	2.18	0.44
1:H:216:ALA:O	1:H:319:VAL:HG12	2.18	0.44
1:H:425:LEU:HD23	1:H:425:LEU:HA	1.81	0.44
1:J:160:ILE:HD12	1:J:399:LEU:HD13	2.00	0.44
1:K:216:ALA:O	1:K:319:VAL:HG12	2.18	0.44
1:L:160:ILE:HD12	1:L:399:LEU:HD13	2.00	0.44
1:L:225:ILE:HG21	1:L:231:ILE:HD11	2.00	0.44
1:L:264:ARG:HA	1:L:269:LEU:H	1.82	0.44
1:H:287:LEU:HD13	1:H:287:LEU:HA	1.81	0.44
1:J:269:LEU:HD23	1:J:269:LEU:HA	1.80	0.44
1:K:264:ARG:HA	1:K:269:LEU:H	1.82	0.44
1:M:85:ASP:HB3	1:M:498:VAL:HG11	2.00	0.44
1:M:225:ILE:HG21	1:M:231:ILE:HD11	2.00	0.44
1:H:25:VAL:HG12	1:H:88:THR:HG23	1.99	0.44
1:H:47:VAL:HG11	1:I:512:LEU:HD11	1.99	0.44
1:K:193:PHE:HZ	1:K:248:ILE:HD13	1.83	0.44
1:K:225:ILE:HG21	1:K:231:ILE:HD11	2.00	0.44
1:N:160:ILE:HD12	1:N:399:LEU:HD13	2.00	0.44
1:N:225:ILE:HG21	1:N:231:ILE:HD11	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:47:VAL:HG11	1:L:512:LEU:HD11	2.00	0.43
1:L:85:ASP:HB3	1:L:498:VAL:HG11	2.00	0.43
1:L:293:ALA:HB2	1:L:371:LEU:HD11	1.99	0.43
1:M:124:ALA:HB1	1:M:425:LEU:HD13	1.99	0.43
1:M:216:ALA:O	1:M:319:VAL:HG12	2.18	0.43
1:M:293:ALA:HB2	1:M:371:LEU:HD11	1.99	0.43
1:H:193:PHE:HZ	1:H:248:ILE:HD13	1.83	0.43
1:H:221:SER:H	1:H:249:ALA:HA	1.82	0.43
1:K:85:ASP:HB3	1:K:498:VAL:HG11	2.00	0.43
1:M:160:ILE:HD12	1:M:399:LEU:HD13	2.00	0.43
1:N:193:PHE:HZ	1:N:248:ILE:HD13	1.83	0.43
1:J:468:ILE:HD12	1:J:476:GLY:HA2	2.00	0.43
1:K:293:ALA:HB2	1:K:371:LEU:HD11	1.99	0.43
1:K:468:ILE:HD12	1:K:476:GLY:HA2	2.00	0.43
1:M:193:PHE:HZ	1:M:248:ILE:HD13	1.83	0.43
1:M:287:LEU:HD13	1:M:287:LEU:HA	1.81	0.43
1:N:25:VAL:HG12	1:N:88:THR:HG23	1.99	0.43
1:N:85:ASP:HB3	1:N:498:VAL:HG11	2.00	0.43
1:J:193:PHE:HZ	1:J:248:ILE:HD13	1.83	0.43
1:L:425:LEU:HA	1:L:425:LEU:HD23	1.81	0.43
1:M:412:LEU:HG	1:M:487:MET:HB2	2.01	0.43
1:N:257:LEU:O	1:N:261:VAL:HG23	2.19	0.43
1:H:412:LEU:HG	1:H:487:MET:HB2	2.01	0.43
1:I:193:PHE:HZ	1:I:248:ILE:HD13	1.83	0.43
1:J:216:ALA:O	1:J:319:VAL:HG12	2.18	0.43
1:I:468:ILE:HD12	1:I:476:GLY:HA2	2.00	0.43
1:J:225:ILE:HG21	1:J:231:ILE:HD11	2.00	0.43
1:J:253:ASP:O	1:J:255:GLU:N	2.46	0.43
1:K:425:LEU:HD23	1:K:425:LEU:HA	1.81	0.43
1:H:468:ILE:HD12	1:H:476:GLY:HA2	2.00	0.43
1:K:257:LEU:O	1:K:261:VAL:HG23	2.19	0.43
1:L:412:LEU:HG	1:L:487:MET:HB2	2.01	0.43
1:N:412:LEU:HG	1:N:487:MET:HB2	2.01	0.43
1:H:225:ILE:HG21	1:H:231:ILE:HD11	2.00	0.43
1:H:304:LEU:HD23	1:H:304:LEU:H	1.84	0.43
1:I:47:VAL:HG11	1:J:512:LEU:HD11	2.00	0.43
1:I:85:ASP:HB3	1:I:498:VAL:HG11	2.00	0.43
1:I:412:LEU:HG	1:I:487:MET:HB2	2.01	0.43
1:J:85:ASP:HB3	1:J:498:VAL:HG11	2.00	0.43
1:L:165:LYS:HB2	1:L:165:LYS:HE3	1.83	0.43
1:M:257:LEU:O	1:M:261:VAL:HG23	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:253:ASP:O	1:N:255:GLU:N	2.46	0.43
1:K:264:ARG:HE	1:K:264:ARG:HB2	1.58	0.43
1:L:304:LEU:H	1:L:304:LEU:HD23	1.84	0.43
1:H:85:ASP:HB3	1:H:498:VAL:HG11	2.00	0.42
1:H:257:LEU:O	1:H:261:VAL:HG23	2.19	0.42
1:H:446:LEU:HD12	1:H:446:LEU:HA	1.81	0.42
1:I:225:ILE:HG21	1:I:231:ILE:HD11	2.00	0.42
1:K:446:LEU:HD12	1:K:446:LEU:HA	1.81	0.42
1:L:468:ILE:HD12	1:L:476:GLY:HA2	2.00	0.42
1:I:269:LEU:HD23	1:I:269:LEU:HA	1.80	0.42
1:J:257:LEU:O	1:J:261:VAL:HG23	2.19	0.42
1:J:412:LEU:HG	1:J:487:MET:HB2	2.01	0.42
1:L:84:GLY:O	1:L:85:ASP:HB2	2.20	0.42
1:I:61:LYS:HB2	1:J:1:ALA:HB1	2.00	0.42
1:K:412:LEU:HG	1:K:487:MET:HB2	2.01	0.42
1:L:193:PHE:HZ	1:L:248:ILE:HD13	1.83	0.42
1:M:468:ILE:HD12	1:M:476:GLY:HA2	2.00	0.42
1:N:304:LEU:H	1:N:304:LEU:HD23	1.84	0.42
1:J:165:LYS:HB2	1:J:165:LYS:HE3	1.83	0.42
1:J:304:LEU:HD23	1:J:304:LEU:H	1.84	0.42
1:N:446:LEU:HD12	1:N:446:LEU:HA	1.81	0.42
1:I:287:LEU:HD13	1:I:287:LEU:HA	1.81	0.42
1:J:84:GLY:O	1:J:85:ASP:HB2	2.20	0.42
1:K:269:LEU:HD23	1:K:269:LEU:HA	1.80	0.42
1:L:205:THR:HG22	1:L:207:LYS:H	1.85	0.42
1:N:205:THR:HG22	1:N:207:LYS:H	1.85	0.42
1:N:468:ILE:HD12	1:N:476:GLY:HA2	2.00	0.42
1:H:205:THR:HG22	1:H:207:LYS:H	1.85	0.42
1:I:257:LEU:O	1:I:261:VAL:HG23	2.19	0.42
1:K:205:THR:HG22	1:K:207:LYS:H	1.85	0.42
1:L:257:LEU:O	1:L:261:VAL:HG23	2.19	0.42
1:M:165:LYS:HB2	1:M:165:LYS:HE3	1.83	0.42
1:K:165:LYS:HB2	1:K:165:LYS:HE3	1.83	0.42
1:I:425:LEU:HD23	1:I:425:LEU:HA	1.81	0.42
1:K:304:LEU:HD23	1:K:304:LEU:H	1.84	0.42
1:J:425:LEU:HD23	1:J:425:LEU:HA	1.81	0.42
1:M:304:LEU:HD23	1:M:304:LEU:H	1.84	0.42
1:K:515:THR:O	1:K:515:THR:OG1	2.38	0.41
1:L:224:LYS:HE3	1:L:224:LYS:HB2	1.87	0.41
1:M:15:LEU:HA	1:M:18:VAL:HG12	2.02	0.41
1:N:15:LEU:HA	1:N:18:VAL:HG12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:15:LEU:HA	1:H:18:VAL:HG12	2.02	0.41
1:I:448:ILE:HD13	1:I:448:ILE:HA	1.93	0.41
1:K:160:ILE:HD13	1:K:160:ILE:HA	1.94	0.41
1:K:224:LYS:HE3	1:K:224:LYS:HB2	1.87	0.41
1:L:15:LEU:HA	1:L:18:VAL:HG12	2.02	0.41
1:M:224:LYS:HE3	1:M:224:LYS:HB2	1.87	0.41
1:M:75:VAL:HG13	1:M:505:ASP:HB3	2.02	0.41
1:I:84:GLY:O	1:I:85:ASP:HB2	2.20	0.41
1:J:205:THR:HG22	1:J:207:LYS:H	1.85	0.41
1:L:160:ILE:HD13	1:L:160:ILE:HA	1.94	0.41
1:N:193:PHE:CE2	1:N:195:ARG:HB2	2.56	0.41
1:K:84:GLY:O	1:K:85:ASP:HB2	2.20	0.41
1:L:287:LEU:HD13	1:L:287:LEU:HA	1.81	0.41
1:M:193:PHE:CE2	1:M:195:ARG:HB2	2.56	0.41
1:N:75:VAL:HG13	1:N:505:ASP:HB3	2.03	0.41
1:I:75:VAL:HG13	1:I:505:ASP:HB3	2.02	0.41
1:J:253:ASP:O	1:J:255:GLU:HG2	2.21	0.41
1:L:75:VAL:HG13	1:L:505:ASP:HB3	2.02	0.41
1:H:75:VAL:HG13	1:H:505:ASP:HB3	2.02	0.41
1:I:215:ASP:HA	1:I:320:GLY:O	2.21	0.41
1:I:304:LEU:HD23	1:I:304:LEU:H	1.84	0.41
1:L:122:VAL:HG21	1:L:507:ALA:HB2	2.03	0.41
1:L:446:LEU:HD12	1:L:446:LEU:HA	1.81	0.41
1:M:205:THR:HG22	1:M:207:LYS:H	1.85	0.41
1:N:215:ASP:HA	1:N:320:GLY:O	2.21	0.41
1:N:253:ASP:O	1:N:255:GLU:HG2	2.21	0.41
1:H:84:GLY:O	1:H:85:ASP:HB2	2.19	0.41
1:J:75:VAL:HG13	1:J:505:ASP:HB3	2.02	0.41
1:J:446:LEU:HD12	1:J:446:LEU:HA	1.81	0.41
1:K:70:LYS:HA	1:K:70:LYS:HD2	1.82	0.41
1:K:104:LYS:HD3	1:K:104:LYS:HA	1.68	0.41
1:K:122:VAL:HG21	1:K:507:ALA:HB2	2.03	0.41
1:M:84:GLY:O	1:M:85:ASP:HB2	2.19	0.41
1:N:84:GLY:O	1:N:85:ASP:HB2	2.20	0.41
1:N:136:VAL:HG23	1:N:406:VAL:HA	2.03	0.41
1:I:15:LEU:HA	1:I:18:VAL:HG12	2.02	0.41
1:I:193:PHE:CE2	1:I:195:ARG:HB2	2.55	0.41
1:J:287:LEU:HA	1:J:287:LEU:HD13	1.81	0.41
1:K:15:LEU:HA	1:K:18:VAL:HG12	2.02	0.41
1:K:419:LEU:HD12	1:K:419:LEU:HA	1.87	0.41
1:L:70:LYS:HD2	1:L:70:LYS:HA	1.81	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:122:VAL:HG21	1:M:507:ALA:HB2	2.03	0.41
1:M:248:ILE:HG23	1:M:274:VAL:HB	2.03	0.41
1:M:425:LEU:HD23	1:M:425:LEU:HA	1.81	0.41
1:M:446:LEU:HD12	1:M:446:LEU:HA	1.81	0.41
1:N:248:ILE:HG23	1:N:274:VAL:HB	2.03	0.41
1:H:193:PHE:CE2	1:H:195:ARG:HB2	2.56	0.41
1:H:260:LEU:HD13	1:H:260:LEU:HA	1.89	0.41
1:K:75:VAL:HG13	1:K:505:ASP:HB3	2.03	0.41
1:K:215:ASP:HA	1:K:320:GLY:O	2.21	0.41
1:K:260:LEU:HD13	1:K:260:LEU:HA	1.89	0.41
1:N:279:PHE:N	1:N:283:ARG:HB2	2.36	0.41
1:H:279:PHE:N	1:H:283:ARG:HB2	2.37	0.40
1:I:205:THR:HG22	1:I:207:LYS:H	1.85	0.40
1:I:279:PHE:N	1:I:283:ARG:HB2	2.37	0.40
1:J:15:LEU:HA	1:J:18:VAL:HG12	2.02	0.40
1:J:279:PHE:N	1:J:283:ARG:HB2	2.36	0.40
1:K:193:PHE:CE2	1:K:195:ARG:HB2	2.56	0.40
1:L:264:ARG:HE	1:L:264:ARG:HB2	1.58	0.40
1:M:253:ASP:O	1:M:255:GLU:N	2.46	0.40
1:N:165:LYS:HE3	1:N:165:LYS:HB2	1.83	0.40
1:H:136:VAL:HG23	1:H:406:VAL:HA	2.03	0.40
1:H:215:ASP:HA	1:H:320:GLY:O	2.21	0.40
1:I:253:ASP:O	1:I:255:GLU:HG2	2.21	0.40
1:J:5:LYS:HG3	1:J:64:TYR:CZ	2.57	0.40
1:J:122:VAL:HG21	1:J:507:ALA:HB2	2.03	0.40
1:L:215:ASP:HA	1:L:320:GLY:O	2.21	0.40
1:L:248:ILE:HG23	1:L:274:VAL:HB	2.04	0.40
1:L:253:ASP:O	1:L:255:GLU:HG2	2.21	0.40
1:H:253:ASP:O	1:H:255:GLU:HG2	2.21	0.40
1:H:448:ILE:HD13	1:H:448:ILE:HA	1.93	0.40
1:J:193:PHE:CE2	1:J:195:ARG:HB2	2.56	0.40
1:K:253:ASP:O	1:K:255:GLU:HG2	2.21	0.40
1:L:193:PHE:CE2	1:L:195:ARG:HB2	2.56	0.40
1:L:253:ASP:O	1:L:255:GLU:N	2.47	0.40
1:M:5:LYS:HG3	1:M:64:TYR:CZ	2.56	0.40
1:M:70:LYS:HD2	1:M:70:LYS:HA	1.82	0.40
1:M:136:VAL:HG23	1:M:406:VAL:HA	2.03	0.40
1:M:253:ASP:O	1:M:255:GLU:HG2	2.21	0.40
1:M:279:PHE:N	1:M:283:ARG:HB2	2.37	0.40
1:J:160:ILE:HD13	1:J:160:ILE:HA	1.94	0.40
1:M:47:VAL:HG11	1:N:512:LEU:HD11	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:122:VAL:HG21	1:N:507:ALA:HB2	2.03	0.40
1:J:419:LEU:HD12	1:J:419:LEU:HA	1.87	0.40
1:K:279:PHE:N	1:K:283:ARG:HB2	2.37	0.40
1:L:5:LYS:HG3	1:L:64:TYR:CZ	2.57	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	H	520/524 (99%)	462 (89%)	56 (11%)	2 (0%)	34	72
1	I	520/524 (99%)	462 (89%)	56 (11%)	2 (0%)	34	72
1	J	520/524 (99%)	462 (89%)	56 (11%)	2 (0%)	34	72
1	K	520/524 (99%)	462 (89%)	56 (11%)	2 (0%)	34	72
1	L	520/524 (99%)	462 (89%)	56 (11%)	2 (0%)	34	72
1	M	520/524 (99%)	462 (89%)	56 (11%)	2 (0%)	34	72
1	N	520/524 (99%)	462 (89%)	56 (11%)	2 (0%)	34	72
All	All	3640/3668 (99%)	3234 (89%)	392 (11%)	14 (0%)	38	72

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	518	VAL
1	I	518	VAL
1	J	518	VAL
1	K	518	VAL
1	L	518	VAL
1	M	518	VAL
1	N	518	VAL

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Mol	Chain	Res	Type
1	H	517	GLU
1	I	517	GLU
1	J	517	GLU
1	K	517	GLU
1	L	517	GLU
1	M	517	GLU
1	N	517	GLU

### 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	H	424/424 (100%)	361 (85%)	63 (15%)	3	17
1	I	424/424 (100%)	360 (85%)	64 (15%)	3	17
1	J	424/424 (100%)	360 (85%)	64 (15%)	3	17
1	K	424/424 (100%)	360 (85%)	64 (15%)	3	17
1	L	424/424 (100%)	360 (85%)	64 (15%)	3	17
1	M	424/424 (100%)	361 (85%)	63 (15%)	3	17
1	N	424/424 (100%)	361 (85%)	63 (15%)	3	17
All	All	2968/2968 (100%)	2523 (85%)	445 (15%)	6	17

All (445) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	9	ASP
1	H	19	ASP
1	H	20	LEU
1	H	27	VAL
1	H	34	ARG
1	H	36	VAL
1	H	39	GLU
1	H	75	VAL
1	H	79	THR
1	H	100	GLU

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Mol	Chain	Res	Type
1	H	112	VAL
1	H	120	LEU
1	H	137	THR
1	H	159	ILE
1	H	180	THR
1	H	182	ASN
1	H	183	ASP
1	H	204	ASN
1	H	209	GLN
1	H	218	VAL
1	H	219	LEU
1	H	220	LEU
1	H	221	SER
1	H	223	LYS
1	H	235	LEU
1	H	239	ASN
1	H	241	HIS
1	H	251	ASP
1	H	253	ASP
1	H	257	LEU
1	H	271	VAL
1	H	287	LEU
1	H	294	THR
1	H	298	VAL
1	H	302	GLU
1	H	304	LEU
1	H	310	ASP
1	H	311	VAL
1	H	314	HIS
1	H	319	VAL
1	H	321	GLU
1	H	323	ILE
1	H	327	ASP
1	H	328	ASP
1	H	344	ARG
1	H	346	GLN
1	H	356	THR
1	H	363	LYS
1	H	378	LEU
1	H	380	VAL
1	H	419	LEU
1	H	426	ASP

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Mol	Chain	Res	Type
1	H	428	LEU
1	H	445	THR
1	H	489	GLU
1	H	497	LYS
1	H	509	VAL
1	H	514	THR
1	H	515	THR
1	H	518	VAL
1	H	519	VAL
1	H	521	THR
1	H	523	ILE
1	I	9	ASP
1	I	19	ASP
1	I	20	LEU
1	I	27	VAL
1	I	34	ARG
1	I	36	VAL
1	I	39	GLU
1	I	75	VAL
1	I	79	THR
1	I	100	GLU
1	I	112	VAL
1	I	120	LEU
1	I	137	THR
1	I	159	ILE
1	I	180	THR
1	I	182	ASN
1	I	183	ASP
1	I	204	ASN
1	I	209	GLN
1	I	218	VAL
1	I	219	LEU
1	I	220	LEU
1	I	221	SER
1	I	223	LYS
1	I	235	LEU
1	I	239	ASN
1	I	241	HIS
1	I	251	ASP
1	I	253	ASP
1	I	257	LEU
1	I	271	VAL

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Mol	Chain	Res	Type
1	I	287	LEU
1	I	294	THR
1	I	298	VAL
1	I	302	GLU
1	I	304	LEU
1	I	310	ASP
1	I	311	VAL
1	I	314	HIS
1	I	319	VAL
1	I	321	GLU
1	I	323	ILE
1	I	327	ASP
1	I	328	ASP
1	I	344	ARG
1	I	346	GLN
1	I	356	THR
1	I	363	LYS
1	I	378	LEU
1	I	380	VAL
1	I	419	LEU
1	I	426	ASP
1	I	428	LEU
1	I	445	THR
1	I	486	ASN
1	I	489	GLU
1	I	497	LYS
1	I	509	VAL
1	I	514	THR
1	I	515	THR
1	I	518	VAL
1	I	519	VAL
1	I	521	THR
1	I	523	ILE
1	J	9	ASP
1	J	19	ASP
1	J	20	LEU
1	J	27	VAL
1	J	34	ARG
1	J	36	VAL
1	J	39	GLU
1	J	75	VAL
1	J	79	THR

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Mol	Chain	Res	Type
1	J	100	GLU
1	J	112	VAL
1	J	120	LEU
1	J	137	THR
1	J	159	ILE
1	J	180	THR
1	J	182	ASN
1	J	183	ASP
1	J	204	ASN
1	J	209	GLN
1	J	218	VAL
1	J	219	LEU
1	J	220	LEU
1	J	221	SER
1	J	223	LYS
1	J	235	LEU
1	J	239	ASN
1	J	241	HIS
1	J	251	ASP
1	J	253	ASP
1	J	257	LEU
1	J	271	VAL
1	J	287	LEU
1	J	294	THR
1	J	298	VAL
1	J	302	GLU
1	J	304	LEU
1	J	310	ASP
1	J	311	VAL
1	J	314	HIS
1	J	319	VAL
1	J	321	GLU
1	J	323	ILE
1	J	327	ASP
1	J	328	ASP
1	J	344	ARG
1	J	346	GLN
1	J	356	THR
1	J	363	LYS
1	J	378	LEU
1	J	380	VAL
1	J	419	LEU

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Mol	Chain	Res	Type
1	J	426	ASP
1	J	428	LEU
1	J	445	THR
1	J	486	ASN
1	J	489	GLU
1	J	497	LYS
1	J	509	VAL
1	J	514	THR
1	J	515	THR
1	J	518	VAL
1	J	519	VAL
1	J	521	THR
1	J	523	ILE
1	K	9	ASP
1	K	19	ASP
1	K	20	LEU
1	K	27	VAL
1	K	34	ARG
1	K	36	VAL
1	K	39	GLU
1	K	75	VAL
1	K	79	THR
1	K	100	GLU
1	K	112	VAL
1	K	120	LEU
1	K	137	THR
1	K	159	ILE
1	K	180	THR
1	K	182	ASN
1	K	183	ASP
1	K	204	ASN
1	K	209	GLN
1	K	218	VAL
1	K	219	LEU
1	K	220	LEU
1	K	221	SER
1	K	223	LYS
1	K	235	LEU
1	K	239	ASN
1	K	241	HIS
1	K	251	ASP
1	K	253	ASP

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Mol	Chain	Res	Type
1	K	257	LEU
1	K	271	VAL
1	K	287	LEU
1	K	294	THR
1	K	298	VAL
1	K	302	GLU
1	K	304	LEU
1	K	310	ASP
1	K	311	VAL
1	K	314	HIS
1	K	319	VAL
1	K	321	GLU
1	K	323	ILE
1	K	327	ASP
1	K	328	ASP
1	K	344	ARG
1	K	346	GLN
1	K	356	THR
1	K	363	LYS
1	K	378	LEU
1	K	380	VAL
1	K	419	LEU
1	K	426	ASP
1	K	428	LEU
1	K	445	THR
1	K	486	ASN
1	K	489	GLU
1	K	497	LYS
1	K	509	VAL
1	K	514	THR
1	K	515	THR
1	K	518	VAL
1	K	519	VAL
1	K	521	THR
1	K	523	ILE
1	L	9	ASP
1	L	19	ASP
1	L	20	LEU
1	L	27	VAL
1	L	34	ARG
1	L	36	VAL
1	L	39	GLU

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Mol	Chain	Res	Type
1	L	75	VAL
1	L	79	THR
1	L	100	GLU
1	L	112	VAL
1	L	120	LEU
1	L	137	THR
1	L	159	ILE
1	L	180	THR
1	L	182	ASN
1	L	183	ASP
1	L	204	ASN
1	L	209	GLN
1	L	218	VAL
1	L	219	LEU
1	L	220	LEU
1	L	221	SER
1	L	223	LYS
1	L	235	LEU
1	L	239	ASN
1	L	241	HIS
1	L	251	ASP
1	L	253	ASP
1	L	257	LEU
1	L	271	VAL
1	L	287	LEU
1	L	294	THR
1	L	298	VAL
1	L	302	GLU
1	L	304	LEU
1	L	310	ASP
1	L	311	VAL
1	L	314	HIS
1	L	319	VAL
1	L	321	GLU
1	L	323	ILE
1	L	327	ASP
1	L	328	ASP
1	L	344	ARG
1	L	346	GLN
1	L	356	THR
1	L	363	LYS
1	L	378	LEU

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Mol	Chain	Res	Type
1	L	380	VAL
1	L	419	LEU
1	L	426	ASP
1	L	428	LEU
1	L	445	THR
1	L	486	ASN
1	L	489	GLU
1	L	497	LYS
1	L	509	VAL
1	L	514	THR
1	L	515	THR
1	L	518	VAL
1	L	519	VAL
1	L	521	THR
1	L	523	ILE
1	M	9	ASP
1	M	19	ASP
1	M	20	LEU
1	M	27	VAL
1	M	34	ARG
1	M	36	VAL
1	M	39	GLU
1	M	75	VAL
1	M	79	THR
1	M	100	GLU
1	M	112	VAL
1	M	120	LEU
1	M	137	THR
1	M	159	ILE
1	M	180	THR
1	M	182	ASN
1	M	183	ASP
1	M	204	ASN
1	M	209	GLN
1	M	218	VAL
1	M	219	LEU
1	M	220	LEU
1	M	221	SER
1	M	223	LYS
1	M	235	LEU
1	M	239	ASN
1	M	241	HIS

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Mol	Chain	Res	Type
1	M	251	ASP
1	M	253	ASP
1	M	257	LEU
1	M	271	VAL
1	M	287	LEU
1	M	294	THR
1	M	298	VAL
1	M	302	GLU
1	M	304	LEU
1	M	310	ASP
1	M	311	VAL
1	M	314	HIS
1	M	319	VAL
1	M	321	GLU
1	M	323	ILE
1	M	327	ASP
1	M	328	ASP
1	M	344	ARG
1	M	346	GLN
1	M	356	THR
1	M	363	LYS
1	M	378	LEU
1	M	380	VAL
1	M	419	LEU
1	M	426	ASP
1	M	428	LEU
1	M	445	THR
1	M	489	GLU
1	M	497	LYS
1	M	509	VAL
1	M	514	THR
1	M	515	THR
1	M	518	VAL
1	M	519	VAL
1	M	521	THR
1	M	523	ILE
1	N	9	ASP
1	N	19	ASP
1	N	20	LEU
1	N	27	VAL
1	N	34	ARG
1	N	36	VAL

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Mol	Chain	Res	Type
1	N	39	GLU
1	N	75	VAL
1	N	79	THR
1	N	100	GLU
1	N	112	VAL
1	N	120	LEU
1	N	137	THR
1	N	159	ILE
1	N	180	THR
1	N	182	ASN
1	N	183	ASP
1	N	204	ASN
1	N	209	GLN
1	N	218	VAL
1	N	219	LEU
1	N	220	LEU
1	N	221	SER
1	N	223	LYS
1	N	235	LEU
1	N	239	ASN
1	N	241	HIS
1	N	251	ASP
1	N	253	ASP
1	N	257	LEU
1	N	271	VAL
1	N	287	LEU
1	N	294	THR
1	N	298	VAL
1	N	302	GLU
1	N	304	LEU
1	N	310	ASP
1	N	311	VAL
1	N	314	HIS
1	N	319	VAL
1	N	321	GLU
1	N	323	ILE
1	N	327	ASP
1	N	328	ASP
1	N	344	ARG
1	N	346	GLN
1	N	356	THR
1	N	363	LYS

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Mol	Chain	Res	Type
1	N	378	LEU
1	N	380	VAL
1	N	419	LEU
1	N	426	ASP
1	N	428	LEU
1	N	445	THR
1	N	489	GLU
1	N	497	LYS
1	N	509	VAL
1	N	514	THR
1	N	515	THR
1	N	518	VAL
1	N	519	VAL
1	N	521	THR
1	N	523	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	282	ASN
1	H	285	ASN
1	H	286	GLN
1	I	282	ASN
1	I	285	ASN
1	I	286	GLN
1	J	282	ASN
1	J	285	ASN
1	J	286	GLN
1	K	282	ASN
1	K	285	ASN
1	K	286	GLN
1	L	282	ASN
1	L	285	ASN
1	L	286	GLN
1	M	282	ASN
1	M	285	ASN
1	M	286	GLN
1	N	282	ASN
1	N	285	ASN
1	N	286	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 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	H	1
1	I	1
1	J	1
1	K	1
1	L	1
1	M	1
1	N	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	H	383:THR	C	384:SER	N	3.19
1	I	383:THR	C	384:SER	N	3.19
1	J	383:THR	C	384:SER	N	3.19
1	K	383:THR	C	384:SER	N	3.19
1	L	383:THR	C	384:SER	N	3.19

*Continued on next page...*

*Continued from previous page...*

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	M	383:THR	C	384:SER	N	3.19
1	N	383:THR	C	384:SER	N	3.19

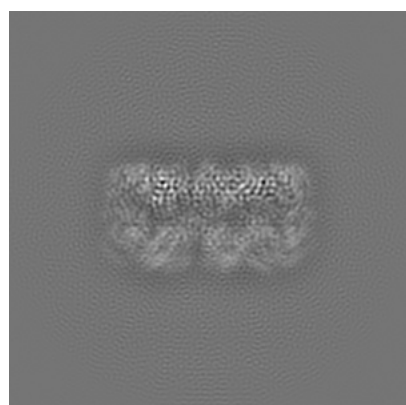
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23217. These allow visual inspection of the internal detail of the map and identification of artifacts.

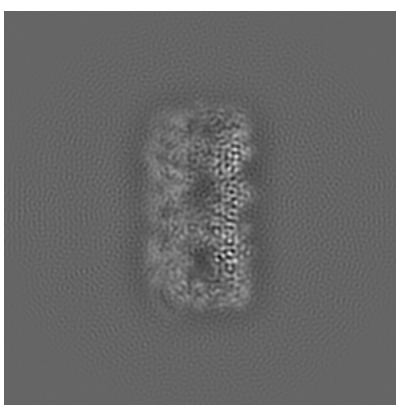
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

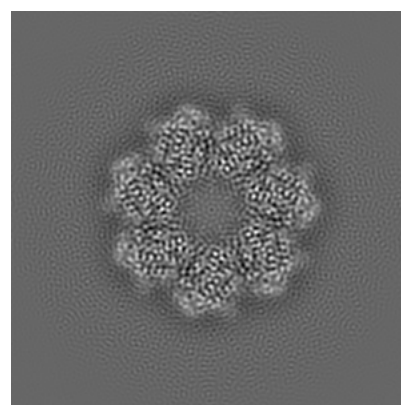
#### 6.1.1 Primary map



X



Y

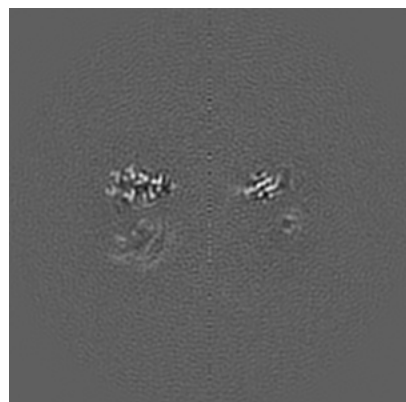


Z

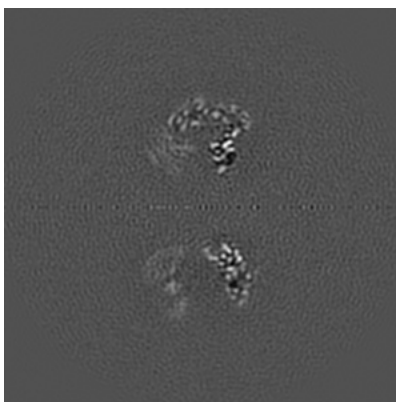
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

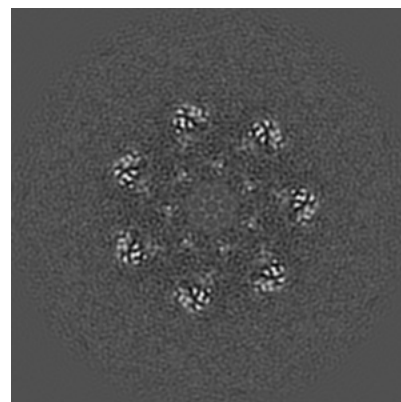
#### 6.2.1 Primary map



X Index: 160



Y Index: 160

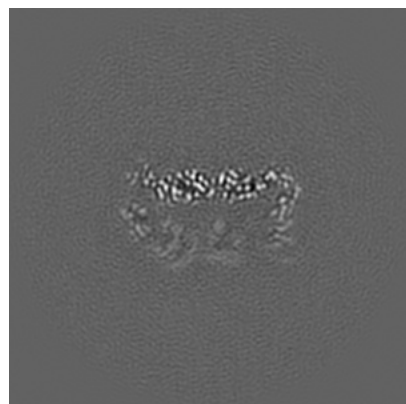


Z Index: 160

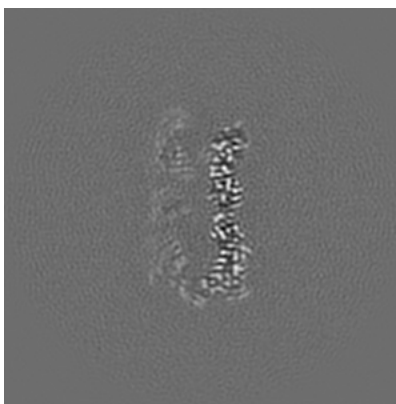
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

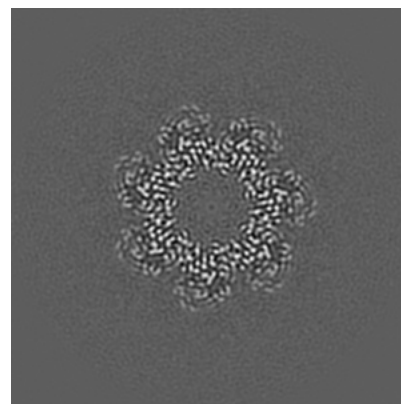
### 6.3.1 Primary map



X Index: 198



Y Index: 122

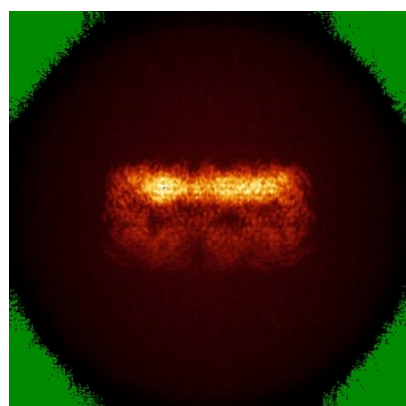


Z Index: 180

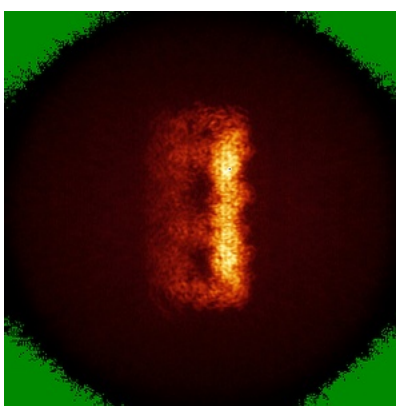
The images above show the largest variance slices of the map in three orthogonal directions.

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

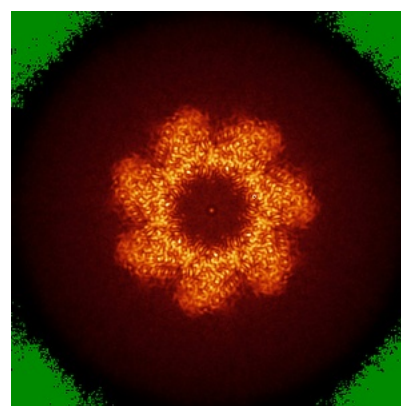
### 6.4.1 Primary map



X



Y

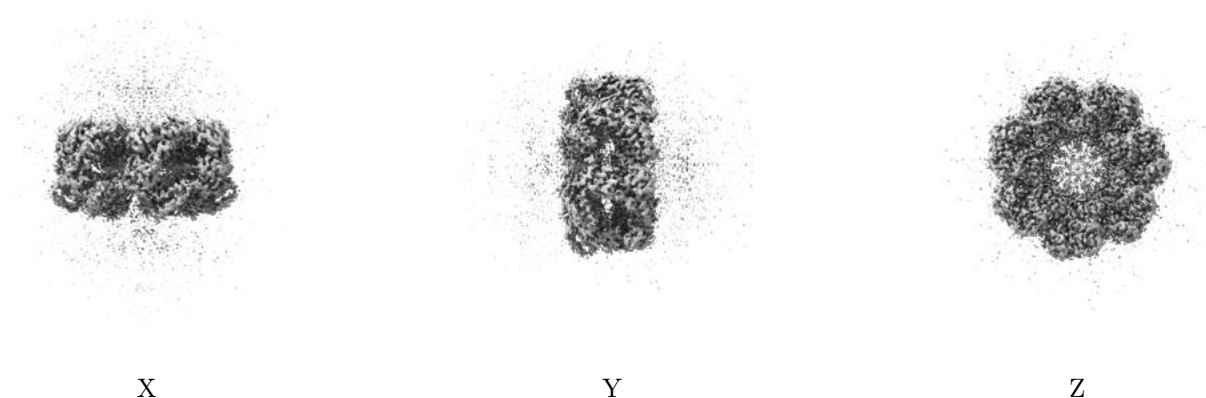


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.019. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

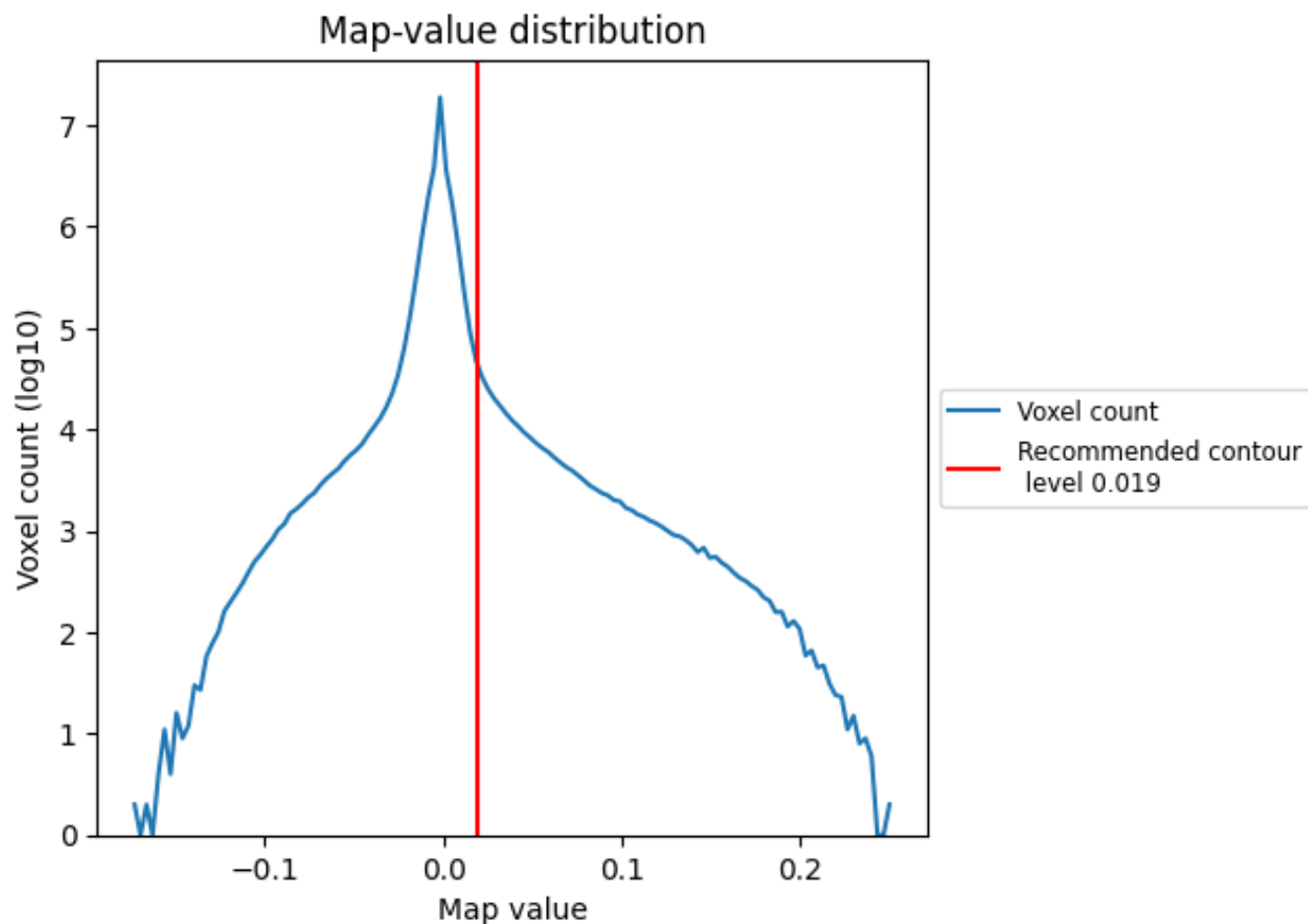
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

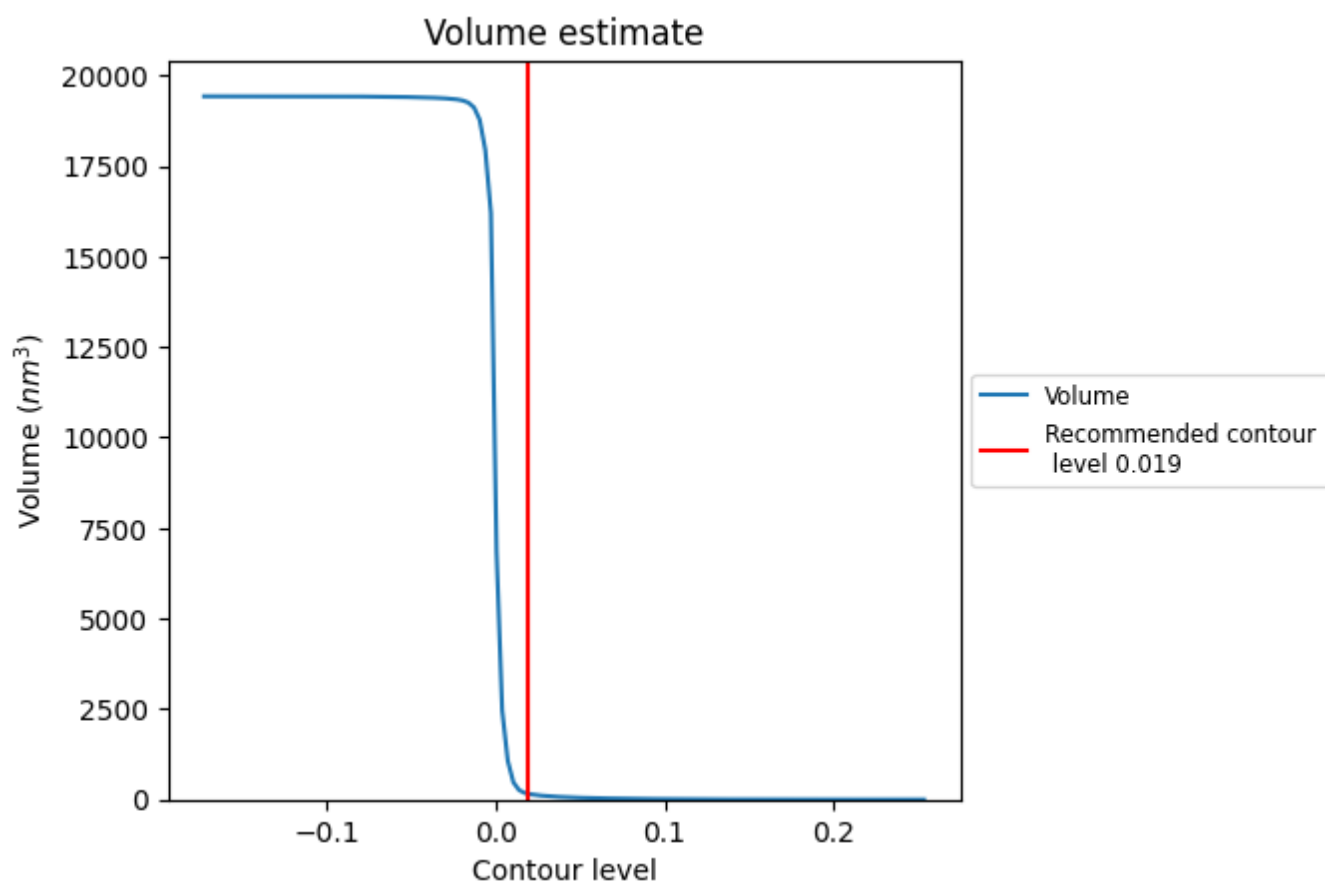
This section contains the results of statistical analysis of the map.

### 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.

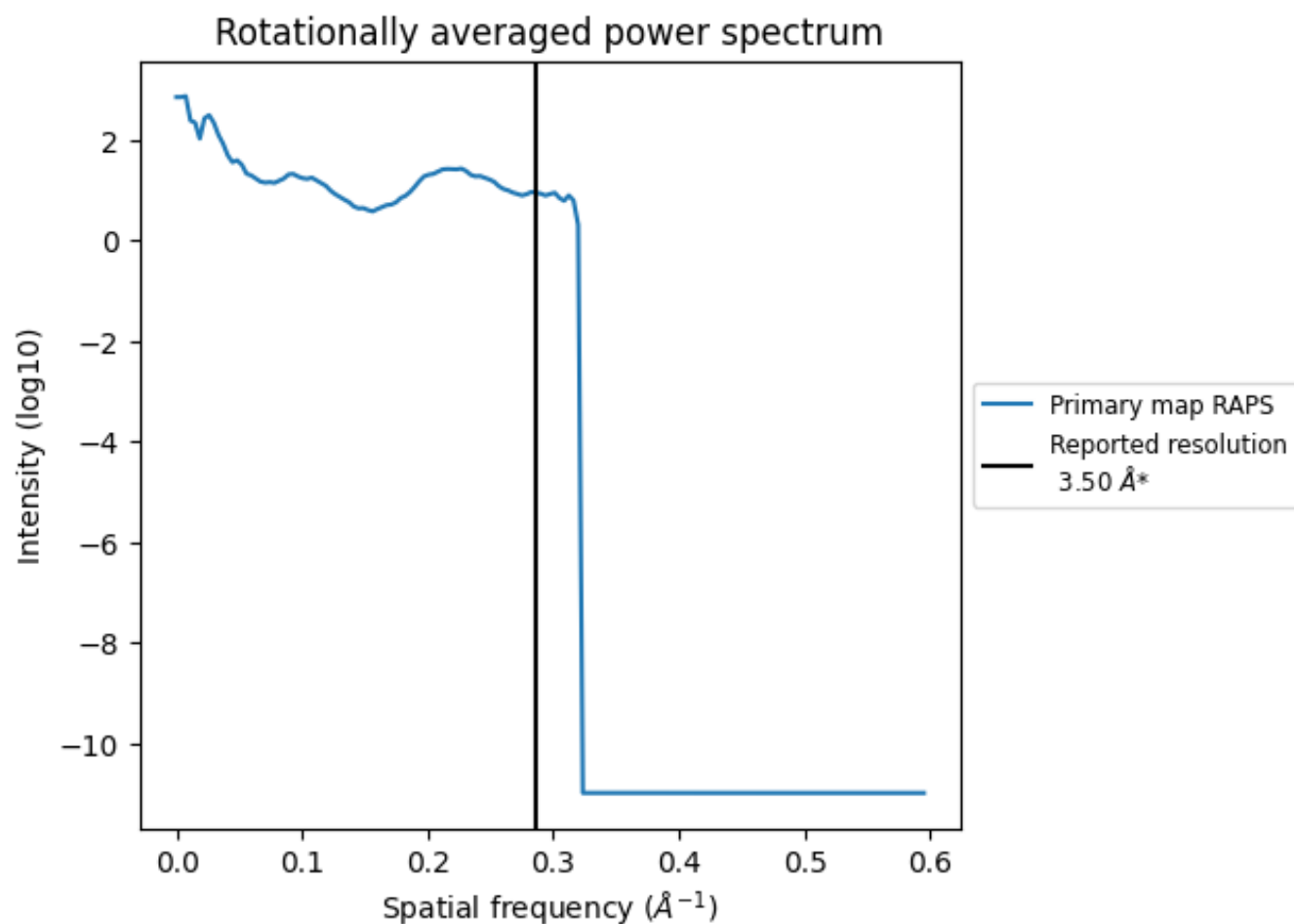
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 162 nm<sup>3</sup>; this corresponds to an approximate mass of 146 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 ⓘ



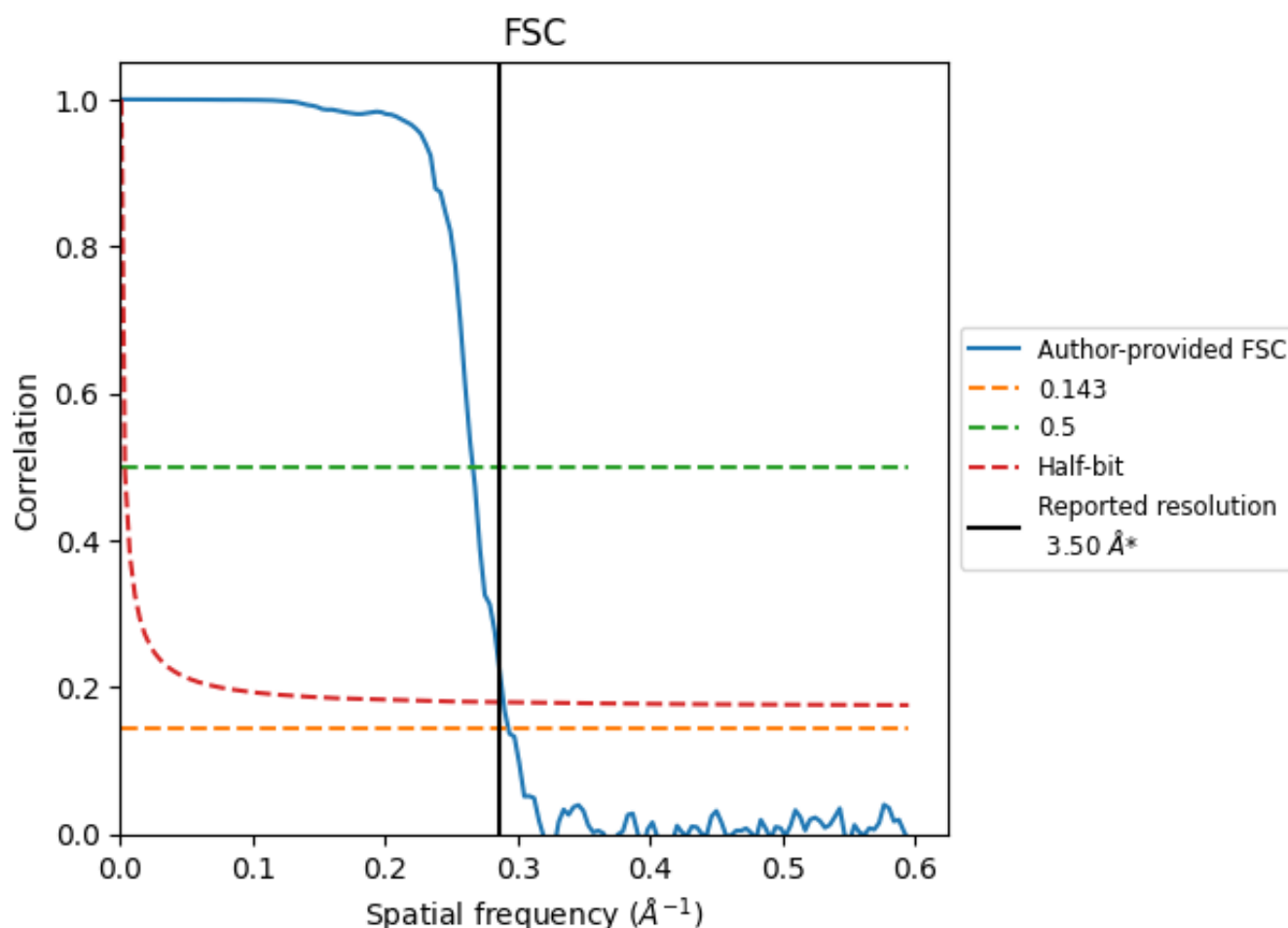
\*Reported resolution corresponds to spatial frequency of 0.286 Å<sup>-1</sup>



## 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 0.286  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

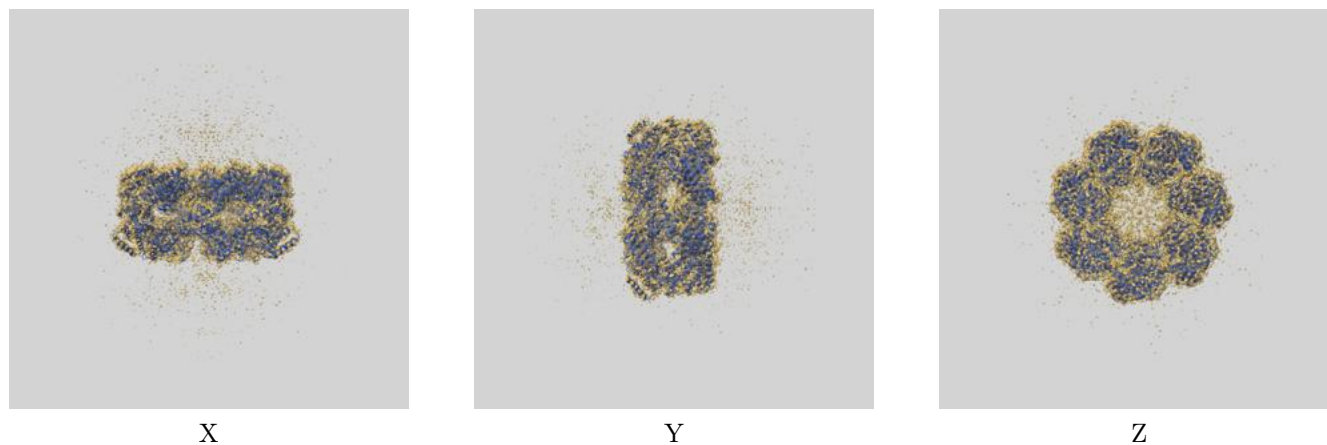
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	-	-
Author-provided FSC curve	3.41	3.76	3.46
Unmasked-calculated*	-	-	-

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

## 9 Map-model fit [i](#)

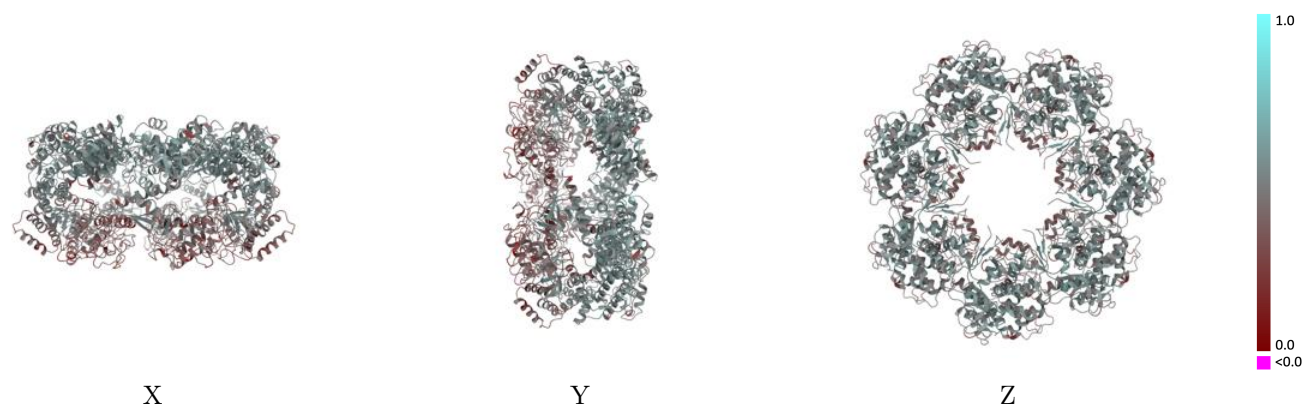
This section contains information regarding the fit between EMDB map EMD-23217 and PDB model 7L7S. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

### 9.1 Map-model overlay [i](#)



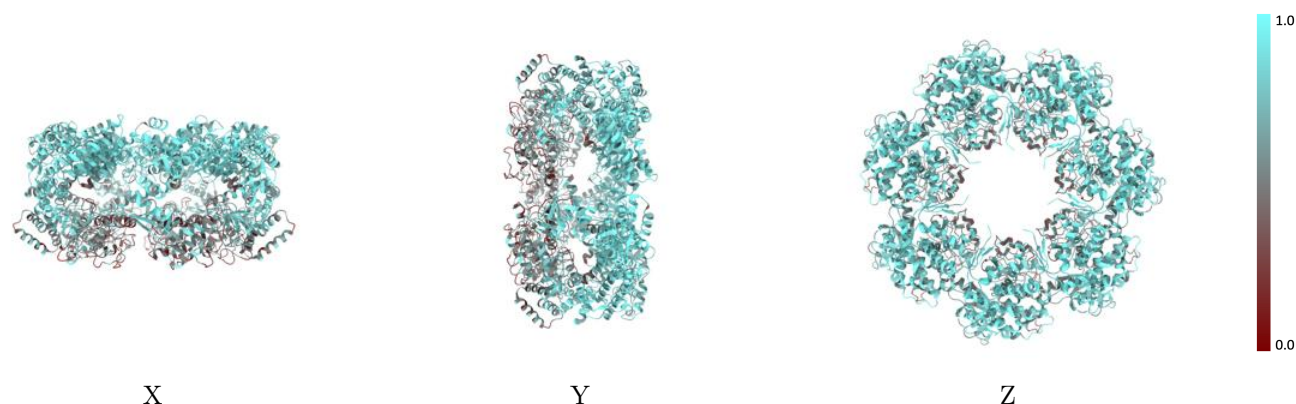
The images above show the 3D surface view of the map at the recommended contour level 0.019 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



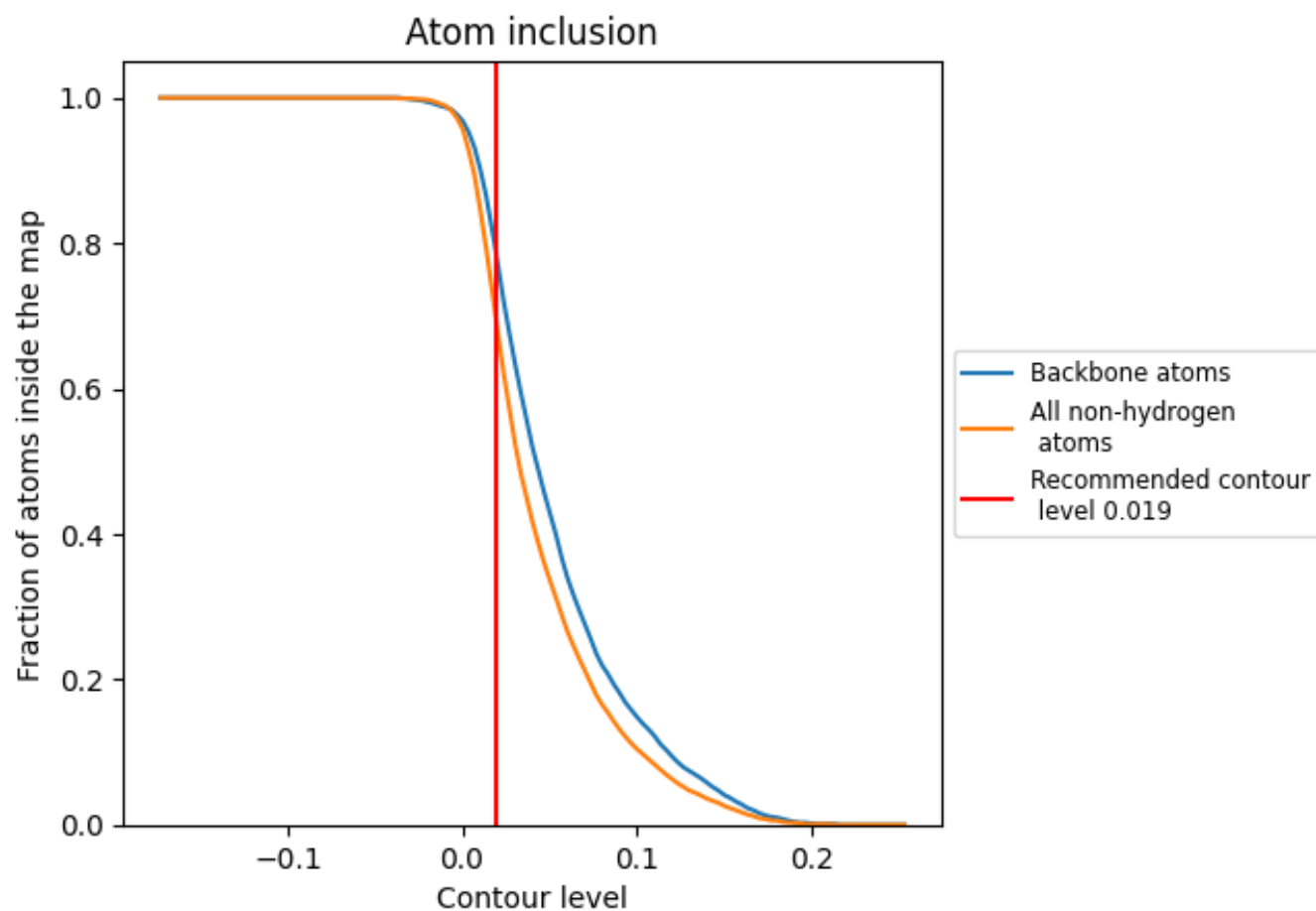
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.019).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 70% 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 (0.019) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.7030	<div><div></div></div> 0.4550
H	<div><div></div></div> 0.7030	<div><div></div></div> 0.4560
I	<div><div></div></div> 0.7020	<div><div></div></div> 0.4550
J	<div><div></div></div> 0.7020	<div><div></div></div> 0.4570
K	<div><div></div></div> 0.7020	<div><div></div></div> 0.4530
L	<div><div></div></div> 0.7050	<div><div></div></div> 0.4540
M	<div><div></div></div> 0.7040	<div><div></div></div> 0.4550
N	<div><div></div></div> 0.7050	<div><div></div></div> 0.4550

1.0

0.0

<0.0