



Full wwPDB EM Validation Report ⓘ

Nov 8, 2022 – 10:21 AM JST

PDB ID : 5ZQZ
EMDB ID : EMD-6940
Title : Structure of human mitochondrial trifunctional protein, tetramer
Authors : Liang, K.; Li, N.; Dai, J.; Wang, X.; Liu, P.; Chen, X.; Wang, C.; Gao, N.;
Xiao, J.
Deposited on : 2018-04-20
Resolution : 4.20 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.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

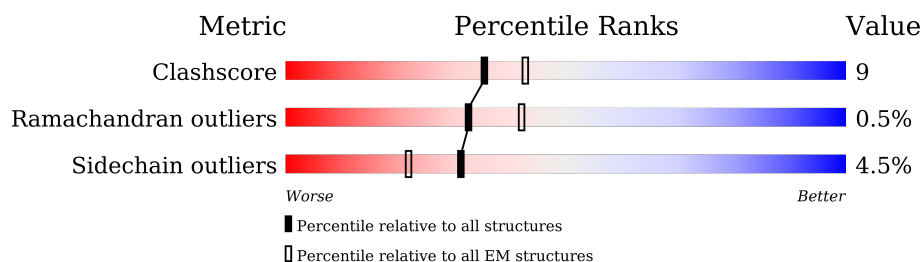
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	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	763	<p>20% 72% 20% • 7%</p>
1	C	763	<p>20% 71% 21% • 7%</p>
2	B	474	<p>6% 66% 20% •• 11%</p>
2	D	474	<p>5% 67% 19% •• 11%</p>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 17174 atoms, of which 0 are hydrogens and 0 are deuteriums.

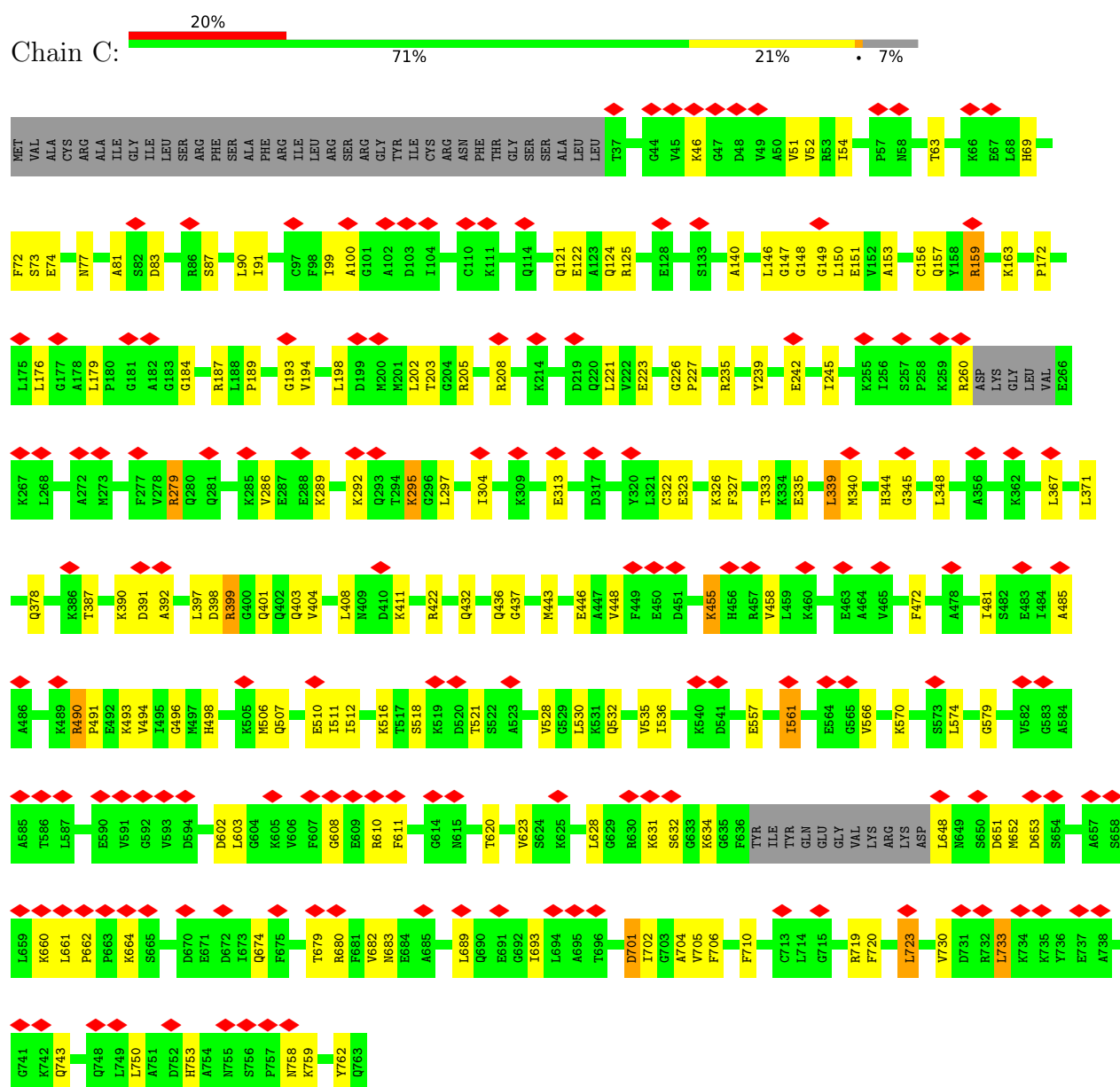
In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Trifunctional enzyme subunit alpha, mitochondrial.

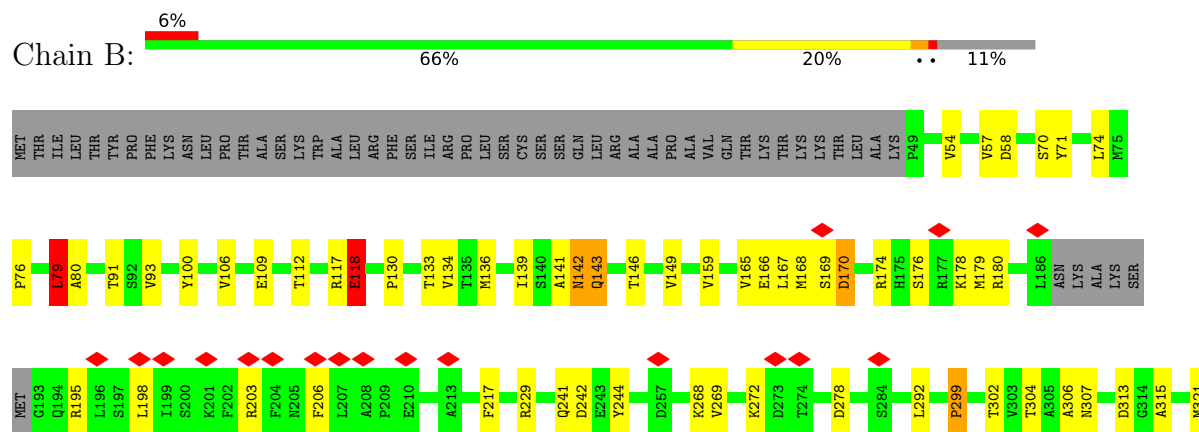
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	711	Total	C	N	O	S	0	0
			5410	3443	923	1015	29		
1	C	711	Total	C	N	O	S	0	0
			5410	3443	923	1015	29		

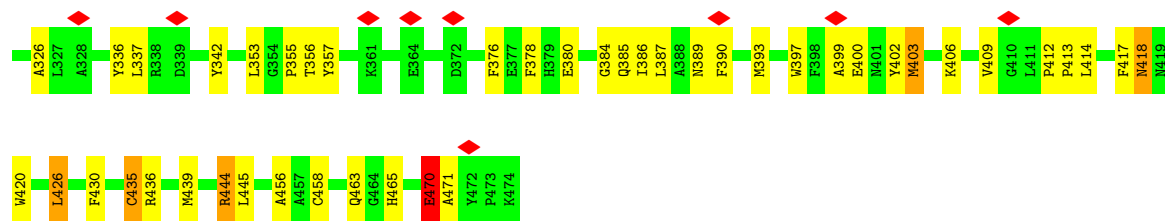
- Molecule 2 is a protein called Trifunctional enzyme subunit beta, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	420	Total	C	N	O	S	0	0
			3177	2015	549	592	21		
2	D	420	Total	C	N	O	S	0	0
			3177	2015	549	592	21		

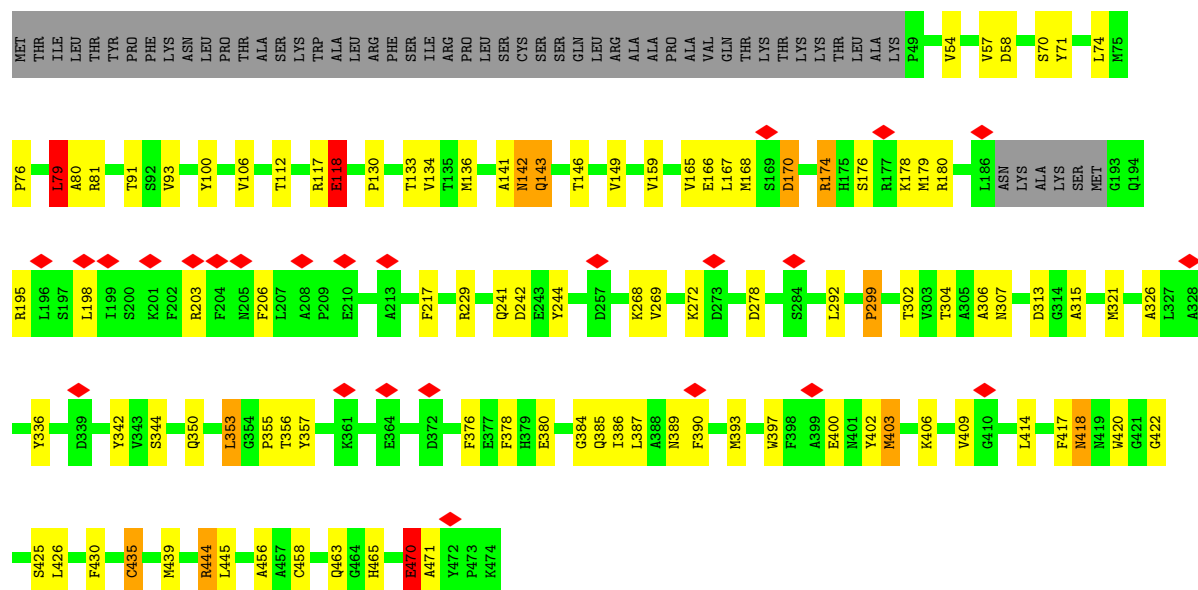


- Molecule 2: Trifunctional enzyme subunit beta, mitochondrial





- Molecule 2: Trifunctional enzyme subunit beta, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	426969	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	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	0.340	Depositor
Minimum map value	-0.173	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	237.6, 237.6, 237.6	wwPDB
Map dimensions	180, 180, 180	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.32, 1.32, 1.32	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.40	0/5494	0.71	5/7400 (0.1%)
1	C	0.40	0/5494	0.71	5/7400 (0.1%)
2	B	0.51	0/3239	0.79	5/4376 (0.1%)
2	D	0.51	0/3239	0.79	5/4376 (0.1%)
All	All	0.45	0/17466	0.74	20/23552 (0.1%)

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	B	0	5
2	D	0	5
All	All	0	10

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	118	GLU	CA-CB-CG	8.89	132.97	113.40
2	D	118	GLU	CA-CB-CG	8.88	132.94	113.40
1	A	723	LEU	CA-CB-CG	8.12	133.99	115.30
1	C	723	LEU	CA-CB-CG	8.12	133.97	115.30
1	A	159	ARG	CA-CB-CG	7.07	128.96	113.40
1	C	159	ARG	CA-CB-CG	7.07	128.95	113.40
1	A	51	VAL	CG1-CB-CG2	-6.77	100.07	110.90
1	C	51	VAL	CG1-CB-CG2	-6.76	100.08	110.90
2	B	470	GLU	CA-CB-CG	6.62	127.96	113.40
2	D	470	GLU	CA-CB-CG	6.61	127.94	113.40
1	C	661	LEU	CA-CB-CG	6.50	130.25	115.30
1	A	661	LEU	CA-CB-CG	6.50	130.25	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	159	ARG	CB-CG-CD	6.44	128.34	111.60
1	A	159	ARG	CB-CG-CD	6.42	128.30	111.60
2	D	414	LEU	CA-CB-CG	6.06	129.23	115.30
2	B	414	LEU	CA-CB-CG	6.05	129.22	115.30
2	D	198	LEU	CA-CB-CG	5.25	127.38	115.30
2	B	79	LEU	CB-CG-CD2	-5.24	102.09	111.00
2	D	79	LEU	CB-CG-CD2	-5.24	102.09	111.00
2	B	198	LEU	CA-CB-CG	5.24	127.34	115.30

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	142	ASN	Peptide
2	B	174	ARG	Peptide
2	B	272	LYS	Peptide
2	B	376	PHE	Peptide
2	B	435	CYS	Peptide
2	D	142	ASN	Peptide
2	D	174	ARG	Peptide
2	D	272	LYS	Peptide
2	D	376	PHE	Peptide
2	D	435	CYS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5410	0	5613	97	0
1	C	5410	0	5613	89	0
2	B	3177	0	3210	61	0
2	D	3177	0	3210	61	0
All	All	17174	0	17646	301	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 9.

All (301) 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:A:194:VAL:O	1:A:198:LEU:HB2	1.73	0.89
1:C:194:VAL:O	1:C:198:LEU:HB2	1.73	0.88
1:A:257:SER:HB2	1:A:259:LYS:HD3	1.60	0.84
1:A:148:GLY:O	1:A:151:GLU:HB2	1.86	0.76
1:A:257:SER:CB	1:A:259:LYS:HD3	2.16	0.75
1:C:148:GLY:O	1:C:151:GLU:HB2	1.86	0.75
1:A:260:ARG:HD3	1:A:260:ARG:C	2.09	0.71
2:D:393:MET:SD	2:D:393:MET:N	2.65	0.70
1:A:628:LEU:HB3	1:A:632:SER:HB3	1.75	0.69
2:B:393:MET:SD	2:B:393:MET:N	2.65	0.67
1:C:628:LEU:HB3	1:C:632:SER:HB3	1.75	0.67
1:A:397:LEU:HB3	1:A:401:GLN:HE22	1.60	0.66
1:A:257:SER:HB2	1:A:259:LYS:CD	2.26	0.66
1:A:701:ASP:N	1:A:701:ASP:OD1	2.27	0.66
2:B:292:LEU:HD22	2:B:306:ALA:HB2	1.78	0.65
1:C:701:ASP:OD1	1:C:701:ASP:N	2.27	0.65
1:C:397:LEU:HB3	1:C:401:GLN:HE22	1.60	0.65
1:C:223:GLU:HG3	2:D:229:ARG:HE	1.62	0.65
2:D:292:LEU:HD22	2:D:306:ALA:HB2	1.78	0.65
1:A:344:HIS:O	1:A:348:LEU:HB2	1.96	0.65
1:C:344:HIS:O	1:C:348:LEU:HB2	1.96	0.65
2:B:170:ASP:N	2:B:170:ASP:OD1	2.30	0.64
1:C:472:PHE:HB3	1:C:494:VAL:HG22	1.80	0.64
1:C:408:LEU:O	1:C:411:LYS:HB3	1.98	0.63
2:D:170:ASP:N	2:D:170:ASP:OD1	2.30	0.63
1:A:472:PHE:HB3	1:A:494:VAL:HG22	1.80	0.63
1:A:408:LEU:O	1:A:411:LYS:HB3	1.98	0.62
2:B:439:MET:N	2:B:439:MET:SD	2.73	0.62
1:A:156:CYS:SG	1:A:157:GLN:N	2.72	0.62
2:D:439:MET:SD	2:D:439:MET:N	2.73	0.62
1:C:156:CYS:SG	1:C:157:GLN:N	2.72	0.61
1:C:557:GLU:OE2	1:C:680:ARG:NH2	2.34	0.61
2:D:176:SER:O	2:D:180:ARG:NE	2.33	0.61
1:A:557:GLU:OE2	1:A:680:ARG:NH2	2.34	0.61
2:B:242:ASP:OD1	2:B:307:ASN:ND2	2.33	0.60
2:B:79:LEU:HD21	2:B:167:LEU:HD11	1.84	0.60
1:A:223:GLU:HG3	2:B:229:ARG:HE	1.67	0.59
2:D:242:ASP:OD1	2:D:307:ASN:ND2	2.33	0.59
2:B:176:SER:O	2:B:180:ARG:NE	2.33	0.59
2:D:79:LEU:HD21	2:D:167:LEU:HD11	1.84	0.59
1:A:399:ARG:HH12	1:A:403:GLN:HE21	1.52	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:470:GLU:OE1	2:B:471:ALA:N	2.37	0.58
1:C:399:ARG:HH12	1:C:403:GLN:HE21	1.52	0.57
2:D:470:GLU:OE1	2:D:471:ALA:N	2.37	0.57
1:A:378:GLN:HA	1:A:404:VAL:HG23	1.86	0.57
1:C:378:GLN:HA	1:C:404:VAL:HG23	1.86	0.57
2:B:54:VAL:HG21	2:B:149:VAL:HG23	1.88	0.56
2:D:378:PHE:HD2	2:D:417:PHE:HE1	1.54	0.56
1:A:333:THR:HG23	1:A:335:GLU:H	1.71	0.56
2:B:378:PHE:HD2	2:B:417:PHE:HE1	1.54	0.56
1:C:333:THR:HG23	1:C:335:GLU:H	1.71	0.56
1:C:52:VAL:O	1:C:90:LEU:HA	2.06	0.56
2:D:91:THR:HG23	2:D:93:VAL:H	1.70	0.56
1:A:52:VAL:O	1:A:90:LEU:HA	2.06	0.56
2:D:385:GLN:NE2	2:D:458:CYS:SG	2.77	0.56
2:D:244:TYR:OH	2:D:380:GLU:OE2	2.23	0.55
2:B:91:THR:HG23	2:B:93:VAL:H	1.70	0.55
2:B:385:GLN:NE2	2:B:458:CYS:SG	2.77	0.55
1:A:257:SER:OG	1:A:259:LYS:HD3	2.07	0.55
2:D:54:VAL:HG21	2:D:149:VAL:HG23	1.88	0.55
2:D:134:VAL:HG11	2:D:143:GLN:HE21	1.72	0.55
2:B:134:VAL:HG11	2:B:143:GLN:HE21	1.72	0.55
2:B:244:TYR:OH	2:B:380:GLU:OE2	2.23	0.54
2:B:406:LYS:HD3	2:B:409:VAL:HG11	1.90	0.54
2:D:106:VAL:HG11	2:D:430:PHE:HD2	1.72	0.54
2:B:106:VAL:HG11	2:B:430:PHE:HD2	1.72	0.54
2:D:406:LYS:HD3	2:D:409:VAL:HG11	1.90	0.54
1:C:448:VAL:HB	1:C:455:LYS:HD2	1.90	0.54
1:C:566:VAL:O	1:C:570:LYS:NZ	2.41	0.53
1:A:566:VAL:O	1:A:570:LYS:NZ	2.41	0.53
1:C:498:HIS:HB3	1:C:510:GLU:HG3	1.90	0.53
1:A:91:ILE:HD13	1:A:140:ALA:HB3	1.91	0.53
2:D:159:VAL:HG12	2:D:321:MET:HA	1.91	0.53
1:C:719:ARG:NH2	1:C:762:TYR:OH	2.42	0.53
1:A:448:VAL:HB	1:A:455:LYS:HD2	1.90	0.53
1:C:91:ILE:HD13	1:C:140:ALA:HB3	1.91	0.53
1:A:719:ARG:NH2	1:A:762:TYR:OH	2.42	0.52
1:A:680:ARG:NH2	1:A:743:GLN:OE1	2.42	0.52
1:A:432:GLN:NE2	1:A:436:GLN:O	2.43	0.52
1:A:498:HIS:HB3	1:A:510:GLU:HG3	1.90	0.52
2:D:278:ASP:N	2:D:278:ASP:OD1	2.43	0.52
1:A:69:HIS:HA	1:A:72:PHE:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:432:GLN:NE2	1:C:436:GLN:O	2.43	0.52
2:D:355:PRO:HD3	2:D:458:CYS:HB3	1.92	0.52
1:A:574:LEU:O	1:A:674:GLN:NE2	2.40	0.52
2:B:159:VAL:HG12	2:B:321:MET:HA	1.91	0.52
1:C:680:ARG:NH2	1:C:743:GLN:OE1	2.42	0.52
2:B:355:PRO:HD3	2:B:458:CYS:HB3	1.92	0.51
2:B:168:MET:N	2:B:313:ASP:OD1	2.41	0.51
2:B:176:SER:HG	2:B:179:MET:H	1.57	0.51
1:C:73:SER:OG	1:C:74:GLU:OE1	2.29	0.51
1:C:574:LEU:O	1:C:674:GLN:NE2	2.40	0.51
2:D:176:SER:HG	2:D:179:MET:H	1.58	0.51
1:A:259:LYS:N	1:A:259:LYS:HD2	2.25	0.51
1:A:258:PRO:HD2	1:A:259:LYS:HZ2	1.75	0.51
2:D:397:TRP:N	2:D:400:GLU:OE1	2.43	0.51
1:C:69:HIS:HA	1:C:72:PHE:HB3	1.92	0.51
2:B:397:TRP:N	2:B:400:GLU:OE1	2.43	0.50
2:B:336:TYR:HB2	2:B:470:GLU:HG3	1.93	0.50
2:D:100:TYR:HD1	2:D:130:PRO:HG2	1.77	0.50
2:D:168:MET:N	2:D:313:ASP:OD1	2.41	0.50
1:A:279:ARG:NH1	1:A:313:GLU:OE2	2.44	0.50
2:D:336:TYR:HB2	2:D:470:GLU:HG3	1.93	0.50
1:C:367:LEU:HB3	1:C:446:GLU:HA	1.94	0.50
1:A:73:SER:OG	1:A:74:GLU:OE1	2.29	0.50
1:A:122:GLU:OE2	1:A:125:ARG:NH2	2.36	0.49
1:C:367:LEU:HA	1:C:390:LYS:HB3	1.94	0.49
2:B:463:GLN:NE2	2:D:117:ARG:HD2	2.26	0.49
1:C:279:ARG:NH1	1:C:313:GLU:OE2	2.44	0.49
2:B:278:ASP:OD1	2:B:278:ASP:N	2.43	0.49
2:B:100:TYR:HD1	2:B:130:PRO:HG2	1.77	0.49
1:A:496:GLY:HA3	1:A:512:ILE:HB	1.95	0.49
2:B:136:MET:SD	2:B:342:TYR:OH	2.71	0.49
1:A:367:LEU:HA	1:A:390:LYS:HB3	1.94	0.48
1:A:367:LEU:HB3	1:A:446:GLU:HA	1.94	0.48
1:C:398:ASP:N	1:C:398:ASP:OD1	2.44	0.48
1:A:653:ASP:N	1:A:653:ASP:OD1	2.47	0.48
2:D:136:MET:SD	2:D:342:TYR:OH	2.71	0.48
1:A:367:LEU:HD12	1:A:390:LYS:HG2	1.95	0.48
1:C:367:LEU:HD12	1:C:390:LYS:HG2	1.95	0.48
1:C:496:GLY:HA3	1:C:512:ILE:HB	1.95	0.48
1:A:295:LYS:HE3	1:A:579:GLY:HA2	1.95	0.48
2:B:71:TYR:HA	2:B:74:LEU:HD23	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:112:THR:HG21	2:B:118:GLU:HG3	1.96	0.48
1:C:176:LEU:HA	1:C:339:LEU:HD12	1.95	0.48
1:C:295:LYS:HE3	1:C:579:GLY:HA2	1.95	0.48
1:A:705:VAL:HA	1:A:710:PHE:HB3	1.96	0.47
2:B:117:ARG:HD2	2:D:463:GLN:NE2	2.29	0.47
2:D:79:LEU:HD12	2:D:315:ALA:HB2	1.96	0.47
2:B:142:ASN:OD1	2:B:465:HIS:NE2	2.47	0.47
1:C:750:LEU:HA	1:C:753:HIS:CE1	2.50	0.47
1:A:398:ASP:N	1:A:398:ASP:OD1	2.44	0.47
1:C:653:ASP:N	1:C:653:ASP:OD1	2.47	0.47
1:C:121:GLN:HA	1:C:124:GLN:HE22	1.79	0.47
2:D:456:ALA:HA	2:D:465:HIS:O	2.15	0.47
1:A:750:LEU:HA	1:A:753:HIS:CE1	2.50	0.47
1:A:753:HIS:HB2	1:A:759:LYS:HB2	1.97	0.47
2:B:79:LEU:HD12	2:B:315:ALA:HB2	1.96	0.47
1:C:753:HIS:HB2	1:C:759:LYS:HB2	1.97	0.47
1:A:121:GLN:HA	1:A:124:GLN:HE22	1.79	0.47
2:B:70:SER:HB2	2:B:269:VAL:HG11	1.96	0.47
2:B:456:ALA:HA	2:B:465:HIS:O	2.15	0.47
2:D:70:SER:HB2	2:D:269:VAL:HG11	1.96	0.47
2:D:112:THR:HG21	2:D:118:GLU:HG3	1.96	0.47
1:A:176:LEU:HA	1:A:339:LEU:HD12	1.95	0.47
1:C:455:LYS:HA	1:C:458:VAL:HB	1.97	0.47
2:D:142:ASN:OD1	2:D:465:HIS:NE2	2.47	0.47
1:A:664:LYS:H	1:A:664:LYS:HG3	1.40	0.47
1:C:491:PRO:HB2	1:C:516:LYS:HD3	1.97	0.47
2:B:80:ALA:HB2	2:B:165:VAL:HG11	1.97	0.47
1:A:455:LYS:HA	1:A:458:VAL:HB	1.97	0.46
1:A:679:THR:HA	1:A:682:VAL:HG22	1.96	0.46
1:C:203:THR:HG23	1:C:205:ARG:H	1.79	0.46
1:A:258:PRO:HD2	1:A:259:LYS:NZ	2.30	0.46
1:C:679:THR:HA	1:C:682:VAL:HG22	1.96	0.46
1:C:705:VAL:HA	1:C:710:PHE:HB3	1.96	0.46
1:A:189:PRO:HA	1:A:193:GLY:H	1.81	0.46
2:D:71:TYR:HA	2:D:74:LEU:HD23	1.96	0.46
1:A:203:THR:HG23	1:A:205:ARG:H	1.79	0.46
1:C:146:LEU:HD12	1:C:172:PRO:HG3	1.98	0.46
1:C:163:LYS:HB2	1:C:221:LEU:HD23	1.98	0.46
1:C:235:ARG:O	1:C:239:TYR:N	2.49	0.45
1:A:491:PRO:HB2	1:A:516:LYS:HD3	1.97	0.45
1:A:235:ARG:O	1:A:239:TYR:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:146:THR:HA	2:D:149:VAL:HG12	1.98	0.45
1:C:147:GLY:H	1:C:172:PRO:HD2	1.82	0.45
2:D:80:ALA:HB2	2:D:165:VAL:HG11	1.97	0.45
1:A:391:ASP:OD1	1:A:392:ALA:N	2.49	0.45
1:C:189:PRO:HA	1:C:193:GLY:H	1.81	0.45
2:D:241:GLN:HA	2:D:387:LEU:HD21	1.98	0.45
2:D:420:TRP:CD1	2:D:444:ARG:HG3	2.52	0.45
1:C:227:PRO:HG2	2:D:350:GLN:HG3	1.97	0.45
1:A:710:PHE:HZ	1:A:720:PHE:HE2	1.65	0.45
1:C:122:GLU:OE2	1:C:125:ARG:NH2	2.36	0.45
1:A:83:ASP:OD1	1:A:83:ASP:N	2.50	0.45
1:A:163:LYS:HB2	1:A:221:LEU:HD23	1.98	0.45
1:A:179:LEU:HG	1:A:327:PHE:HD1	1.82	0.45
1:A:651:ASP:N	1:A:651:ASP:OD1	2.50	0.45
2:B:241:GLN:HA	2:B:387:LEU:HD21	1.98	0.45
1:C:150:LEU:HA	1:C:153:ALA:HB3	1.99	0.45
1:C:179:LEU:HG	1:C:327:PHE:HD1	1.82	0.45
2:D:81:ARG:HE	2:D:81:ARG:HB2	1.58	0.45
1:A:147:GLY:H	1:A:172:PRO:HD2	1.82	0.45
1:A:150:LEU:HA	1:A:153:ALA:HB3	1.99	0.45
2:B:146:THR:HA	2:B:149:VAL:HG12	1.98	0.45
1:C:710:PHE:HZ	1:C:720:PHE:HE2	1.65	0.45
1:A:77:ASN:O	1:A:81:ALA:N	2.50	0.45
1:C:701:ASP:HA	1:C:704:ALA:H	1.83	0.45
1:C:602:ASP:OD1	1:C:602:ASP:N	2.48	0.44
1:C:286:VAL:HA	1:C:289:LYS:HB3	1.99	0.44
1:A:286:VAL:HA	1:A:289:LYS:HB3	1.99	0.44
1:C:83:ASP:OD1	1:C:83:ASP:N	2.50	0.44
1:C:77:ASN:O	1:C:81:ALA:N	2.50	0.44
1:A:528:VAL:O	1:A:532:GLN:HB2	2.17	0.44
2:B:356:THR:OG1	2:B:389:ASN:ND2	2.50	0.44
2:B:420:TRP:CD1	2:B:444:ARG:HG3	2.52	0.44
1:A:507:GLN:HB3	1:A:706:PHE:HE2	1.82	0.44
1:A:610:ARG:HG3	1:A:611:PHE:HD1	1.82	0.44
1:C:202:LEU:HD22	1:C:304:ILE:HD11	1.98	0.44
1:C:603:LEU:O	1:C:608:GLY:N	2.47	0.44
1:A:226:GLY:HA3	1:A:227:PRO:HD3	1.83	0.44
1:A:518:SER:HB3	1:A:521:THR:HG23	1.99	0.44
1:A:634:LYS:HZ1	1:A:648:LEU:N	2.16	0.44
1:C:610:ARG:HG3	1:C:611:PHE:HD1	1.82	0.44
2:D:384:GLY:HA2	2:D:387:LEU:HG	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:146:LEU:HD12	1:A:172:PRO:HG3	1.98	0.43
1:A:561:ILE:H	1:A:561:ILE:HG13	1.56	0.43
1:A:602:ASP:OD1	1:A:602:ASP:N	2.48	0.43
2:B:384:GLY:HA2	2:B:387:LEU:HG	2.00	0.43
1:C:528:VAL:O	1:C:532:GLN:HB2	2.17	0.43
1:A:620:THR:HA	1:A:623:VAL:HG22	2.01	0.43
1:C:507:GLN:HB3	1:C:706:PHE:HE2	1.82	0.43
1:A:701:ASP:HA	1:A:704:ALA:H	1.83	0.43
2:B:166:GLU:OE2	2:B:430:PHE:N	2.52	0.43
2:D:356:THR:OG1	2:D:389:ASN:ND2	2.51	0.43
1:A:202:LEU:HD22	1:A:304:ILE:HD11	1.99	0.43
1:C:651:ASP:N	1:C:651:ASP:OD1	2.50	0.43
1:C:518:SER:HB3	1:C:521:THR:HG23	1.99	0.43
1:A:151:GLU:OE2	1:A:184:GLY:N	2.50	0.43
2:B:389:ASN:HA	2:B:393:MET:HE1	2.01	0.43
2:D:76:PRO:HA	2:D:167:LEU:HD13	2.01	0.43
1:A:371:LEU:HD13	1:A:399:ARG:HH22	1.84	0.43
2:B:169:SER:OG	2:B:170:ASP:OD1	2.31	0.43
2:D:386:ILE:HD12	2:D:386:ILE:HA	1.82	0.42
2:B:337:LEU:HD12	2:B:337:LEU:HA	1.89	0.42
1:C:371:LEU:HD13	1:C:399:ARG:HH22	1.84	0.42
2:D:166:GLU:OE2	2:D:430:PHE:N	2.52	0.42
1:A:242:GLU:HA	1:A:245:ILE:HG22	2.00	0.42
1:A:279:ARG:H	1:A:279:ARG:HG3	1.27	0.42
2:D:387:LEU:HA	2:D:390:PHE:CD2	2.54	0.42
2:B:386:ILE:HD12	2:B:386:ILE:HA	1.81	0.42
1:C:54:ILE:N	1:C:91:ILE:O	2.53	0.42
1:C:345:GLY:HA3	1:C:702:ILE:HG12	2.01	0.42
1:C:561:ILE:H	1:C:561:ILE:HG13	1.56	0.42
1:A:323:GLU:HA	1:A:326:LYS:HB2	2.02	0.42
1:A:566:VAL:HB	1:A:570:LYS:HZ1	1.85	0.42
1:C:151:GLU:OE2	1:C:184:GLY:N	2.50	0.42
2:B:178:LYS:HE3	2:B:206:PHE:HB2	2.00	0.42
1:C:634:LYS:HZ1	1:C:648:LEU:N	2.16	0.42
2:D:178:LYS:HE3	2:D:206:PHE:HB2	2.01	0.42
2:B:76:PRO:HA	2:B:167:LEU:HD13	2.01	0.42
2:D:380:GLU:OE2	2:D:418:ASN:ND2	2.53	0.42
1:A:660:LYS:HA	1:A:660:LYS:HD2	1.43	0.42
1:C:323:GLU:HA	1:C:326:LYS:HB2	2.01	0.42
1:C:689:LEU:HA	1:C:693:ILE:H	1.85	0.42
2:D:422:GLY:O	2:D:425:SER:OG	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:380:GLU:OE2	2:B:418:ASN:ND2	2.53	0.42
1:C:99:ILE:HD11	1:C:149:GLY:HA2	2.02	0.42
1:C:620:THR:HA	1:C:623:VAL:HG22	2.01	0.42
2:D:353:LEU:HD22	2:D:353:LEU:HA	1.87	0.42
1:A:401:GLN:HA	1:A:404:VAL:HG12	2.02	0.41
1:A:503:VAL:H	1:A:503:VAL:HG22	1.62	0.41
1:A:511:ILE:HD11	1:A:536:ILE:HD11	2.02	0.41
1:A:689:LEU:HA	1:A:693:ILE:H	1.85	0.41
2:B:357:TYR:OH	2:B:402:TYR:O	2.20	0.41
2:B:387:LEU:HA	2:B:390:PHE:CD2	2.55	0.41
2:D:100:TYR:CD1	2:D:130:PRO:HG2	2.55	0.41
1:C:511:ILE:HD11	1:C:536:ILE:HD11	2.02	0.41
2:D:321:MET:HG2	2:D:326:ALA:HB2	2.01	0.41
1:A:289:LYS:HA	1:A:292:LYS:HG2	2.02	0.41
1:A:345:GLY:HA3	1:A:702:ILE:HG12	2.01	0.41
1:A:481:ILE:O	1:A:485:ALA:N	2.54	0.41
1:A:490:ARG:HG3	1:A:493:LYS:HB2	2.02	0.41
2:B:412:PRO:HA	2:B:413:PRO:HD3	1.82	0.41
1:C:242:GLU:HA	1:C:245:ILE:HG22	2.01	0.41
1:A:506:MET:HE2	1:A:506:MET:HB2	1.98	0.41
2:B:139:ILE:H	2:B:139:ILE:HG13	1.74	0.41
1:A:257:SER:HB2	1:A:259:LYS:CE	2.50	0.41
2:B:241:GLN:OE1	2:B:302:THR:OG1	2.35	0.41
1:C:401:GLN:HA	1:C:404:VAL:HG12	2.02	0.41
1:C:481:ILE:O	1:C:485:ALA:N	2.54	0.41
2:D:403:MET:HE1	2:D:406:LYS:HB2	2.01	0.41
1:A:423:ASP:OD2	2:D:81:ARG:NH1	2.53	0.41
2:B:57:VAL:HG12	2:B:58:ASP:H	1.85	0.41
1:C:226:GLY:HA3	1:C:227:PRO:HD3	1.83	0.41
1:C:432:GLN:HE22	1:C:437:GLY:HA3	1.86	0.41
2:D:141:ALA:HB1	2:D:435:CYS:SG	2.61	0.41
1:A:322:CYS:SG	1:A:323:GLU:N	2.94	0.41
2:B:100:TYR:CD1	2:B:130:PRO:HG2	2.55	0.41
2:D:357:TYR:OH	2:D:402:TYR:O	2.20	0.41
1:C:63:THR:HA	1:C:100:ALA:HB3	2.03	0.41
2:D:344:SER:HA	2:D:463:GLN:HA	2.03	0.41
2:B:141:ALA:HB1	2:B:435:CYS:SG	2.61	0.41
1:C:54:ILE:HD11	1:C:90:LEU:HD12	2.03	0.41
1:C:289:LYS:HA	1:C:292:LYS:HG2	2.02	0.41
1:C:490:ARG:HG3	1:C:493:LYS:HB2	2.02	0.41
2:D:304:THR:HG23	2:D:306:ALA:H	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:411:LYS:HE3	1:A:411:LYS:HB2	1.90	0.41
2:B:399:ALA:HB1	2:B:403:MET:HE2	2.03	0.41
1:C:322:CYS:SG	1:C:323:GLU:N	2.94	0.41
2:D:241:GLN:OE1	2:D:302:THR:OG1	2.35	0.41
2:B:304:THR:HG23	2:B:306:ALA:H	1.86	0.40
2:B:109:GLU:CD	2:D:174:ARG:HH12	2.25	0.40
2:B:426:LEU:HD11	2:B:436:ARG:NH1	2.36	0.40
1:C:295:LYS:HE2	1:C:297:LEU:HB2	2.03	0.40
2:D:57:VAL:HG12	2:D:58:ASP:H	1.85	0.40
2:B:321:MET:HG2	2:B:326:ALA:HB2	2.01	0.40
1:C:391:ASP:OD1	1:C:392:ALA:N	2.49	0.40
1:C:631:LYS:HE2	1:C:631:LYS:HB2	1.92	0.40
1:A:63:THR:HA	1:A:100:ALA:HB3	2.03	0.40
1:C:730:VAL:HA	1:C:733:LEU:HD23	2.04	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	705/763 (92%)	626 (89%)	76 (11%)	3 (0%)	34	72
1	C	705/763 (92%)	626 (89%)	77 (11%)	2 (0%)	41	76
2	B	416/474 (88%)	353 (85%)	60 (14%)	3 (1%)	22	62
2	D	416/474 (88%)	352 (85%)	61 (15%)	3 (1%)	22	62
All	All	2242/2474 (91%)	1957 (87%)	274 (12%)	11 (0%)	32	68

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	758	ASN

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Mol	Chain	Res	Type
1	C	758	ASN
1	A	259	LYS
1	A	662	PRO
2	B	217	PHE
2	B	299	PRO
2	B	418	ASN
1	C	662	PRO
2	D	217	PHE
2	D	299	PRO
2	D	418	ASN

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	589/632 (93%)	562 (95%)	27 (5%)	27	54
1	C	589/632 (93%)	562 (95%)	27 (5%)	27	54
2	B	335/382 (88%)	320 (96%)	15 (4%)	27	54
2	D	335/382 (88%)	320 (96%)	15 (4%)	27	54
All	All	1848/2028 (91%)	1764 (96%)	84 (4%)	31	54

All (84) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	LYS
1	A	87	SER
1	A	159	ARG
1	A	187	ARG
1	A	208	ARG
1	A	260	ARG
1	A	279	ARG
1	A	295	LYS
1	A	339	LEU
1	A	340	MET
1	A	387	THR

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Mol	Chain	Res	Type
1	A	399	ARG
1	A	422	ARG
1	A	443	MET
1	A	455	LYS
1	A	490	ARG
1	A	506	MET
1	A	530	LEU
1	A	535	VAL
1	A	561	ILE
1	A	652	MET
1	A	660	LYS
1	A	664	LYS
1	A	683	ASN
1	A	701	ASP
1	A	723	LEU
1	A	733	LEU
2	B	79	LEU
2	B	118	GLU
2	B	133	THR
2	B	143	GLN
2	B	170	ASP
2	B	195	ARG
2	B	203	ARG
2	B	268	LYS
2	B	299	PRO
2	B	353	LEU
2	B	403	MET
2	B	426	LEU
2	B	444	ARG
2	B	445	LEU
2	B	470	GLU
1	C	46	LYS
1	C	87	SER
1	C	159	ARG
1	C	187	ARG
1	C	208	ARG
1	C	260	ARG
1	C	279	ARG
1	C	295	LYS
1	C	339	LEU
1	C	340	MET
1	C	387	THR

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Mol	Chain	Res	Type
1	C	399	ARG
1	C	422	ARG
1	C	443	MET
1	C	455	LYS
1	C	490	ARG
1	C	506	MET
1	C	530	LEU
1	C	535	VAL
1	C	561	ILE
1	C	652	MET
1	C	660	LYS
1	C	664	LYS
1	C	683	ASN
1	C	701	ASP
1	C	723	LEU
1	C	733	LEU
2	D	79	LEU
2	D	118	GLU
2	D	133	THR
2	D	143	GLN
2	D	170	ASP
2	D	195	ARG
2	D	203	ARG
2	D	268	LYS
2	D	299	PRO
2	D	353	LEU
2	D	403	MET
2	D	426	LEU
2	D	444	ARG
2	D	445	LEU
2	D	470	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	401	GLN
1	A	403	GLN
1	A	432	GLN
1	A	683	ASN
2	B	132	HIS
2	B	143	GLN
2	B	385	GLN

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Mol	Chain	Res	Type
2	B	389	ASN
1	C	401	GLN
1	C	403	GLN
1	C	432	GLN
1	C	683	ASN
2	D	132	HIS
2	D	143	GLN
2	D	385	GLN
2	D	389	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.

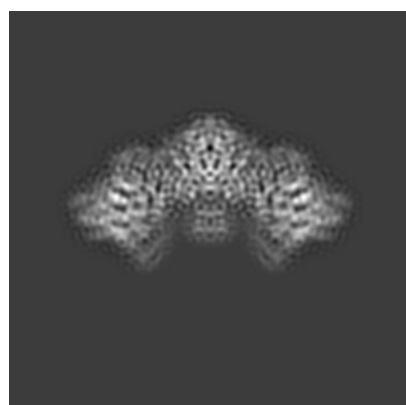
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6940. These allow visual inspection of the internal detail of the map and identification of artifacts.

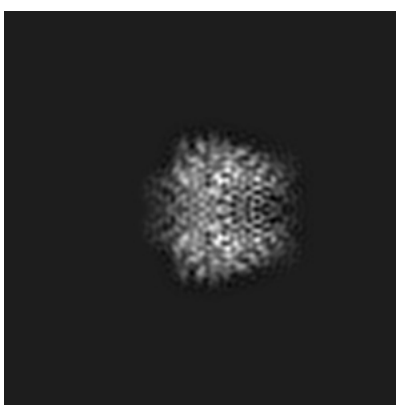
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

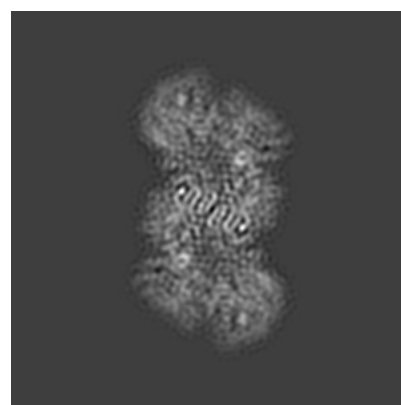
6.1.1 Primary map



X



Y

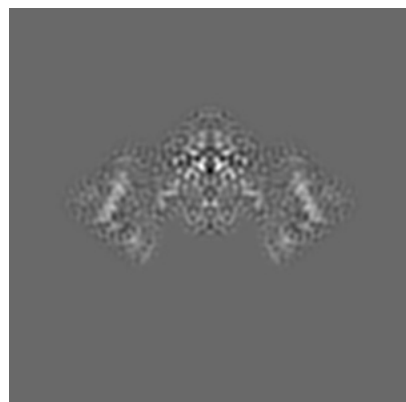


Z

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

6.2 Central slices [i](#)

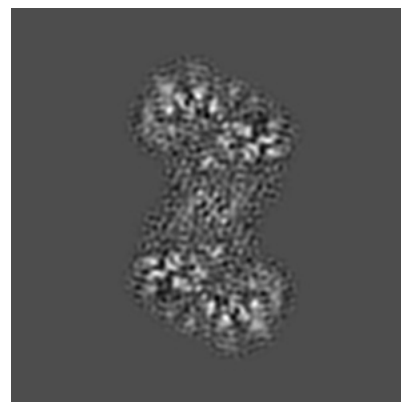
6.2.1 Primary map



X Index: 90



Y Index: 90

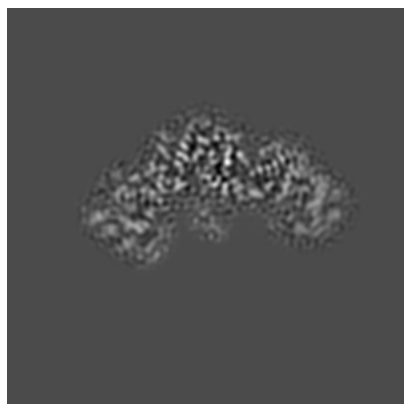


Z Index: 90

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

6.3 Largest variance slices [i](#)

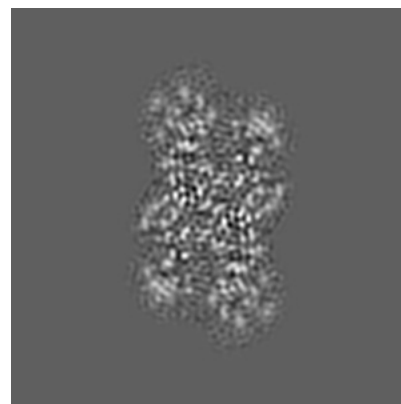
6.3.1 Primary map



X Index: 77



Y Index: 86

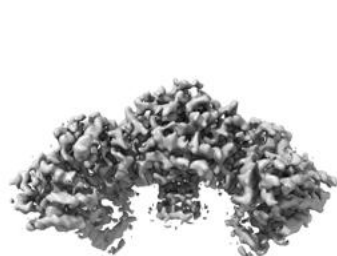


Z Index: 100

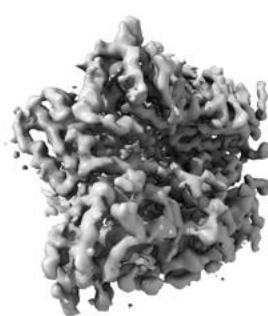
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

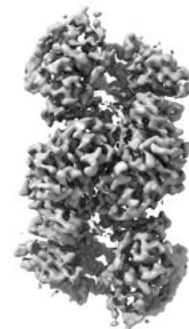
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

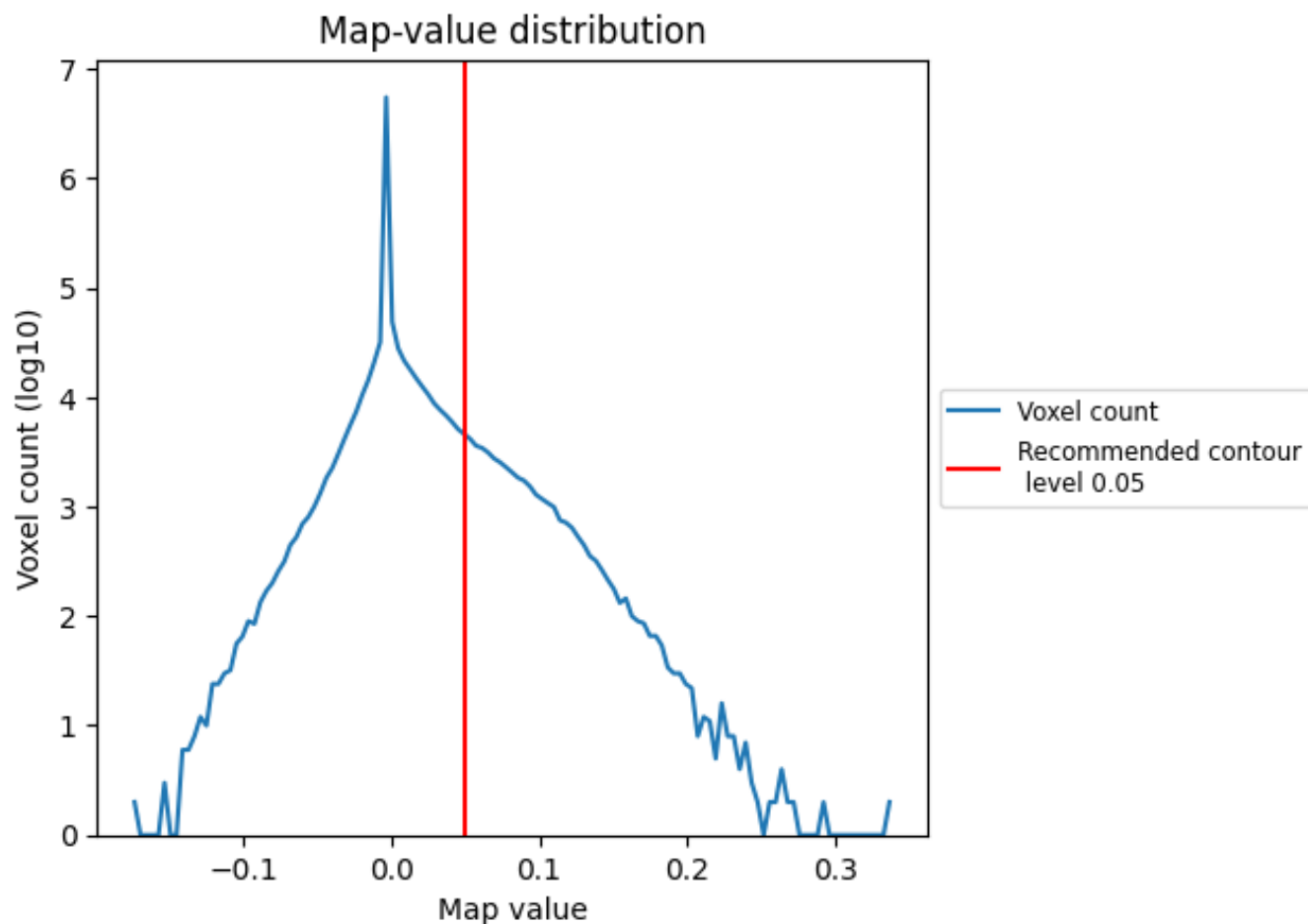
6.5 Mask visualisation

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

7 Map analysis [i](#)

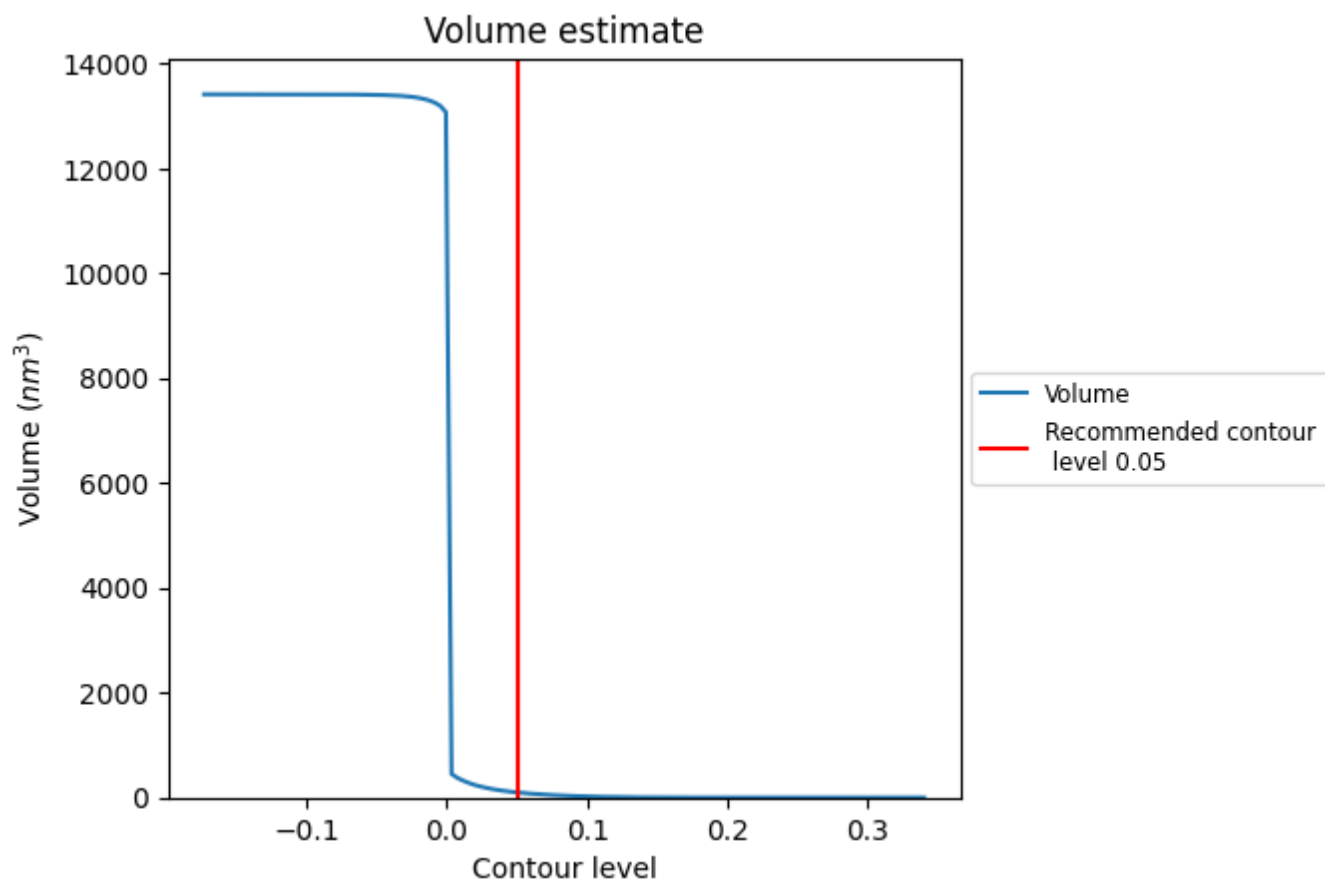
This section contains the results of statistical analysis of the map.

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.

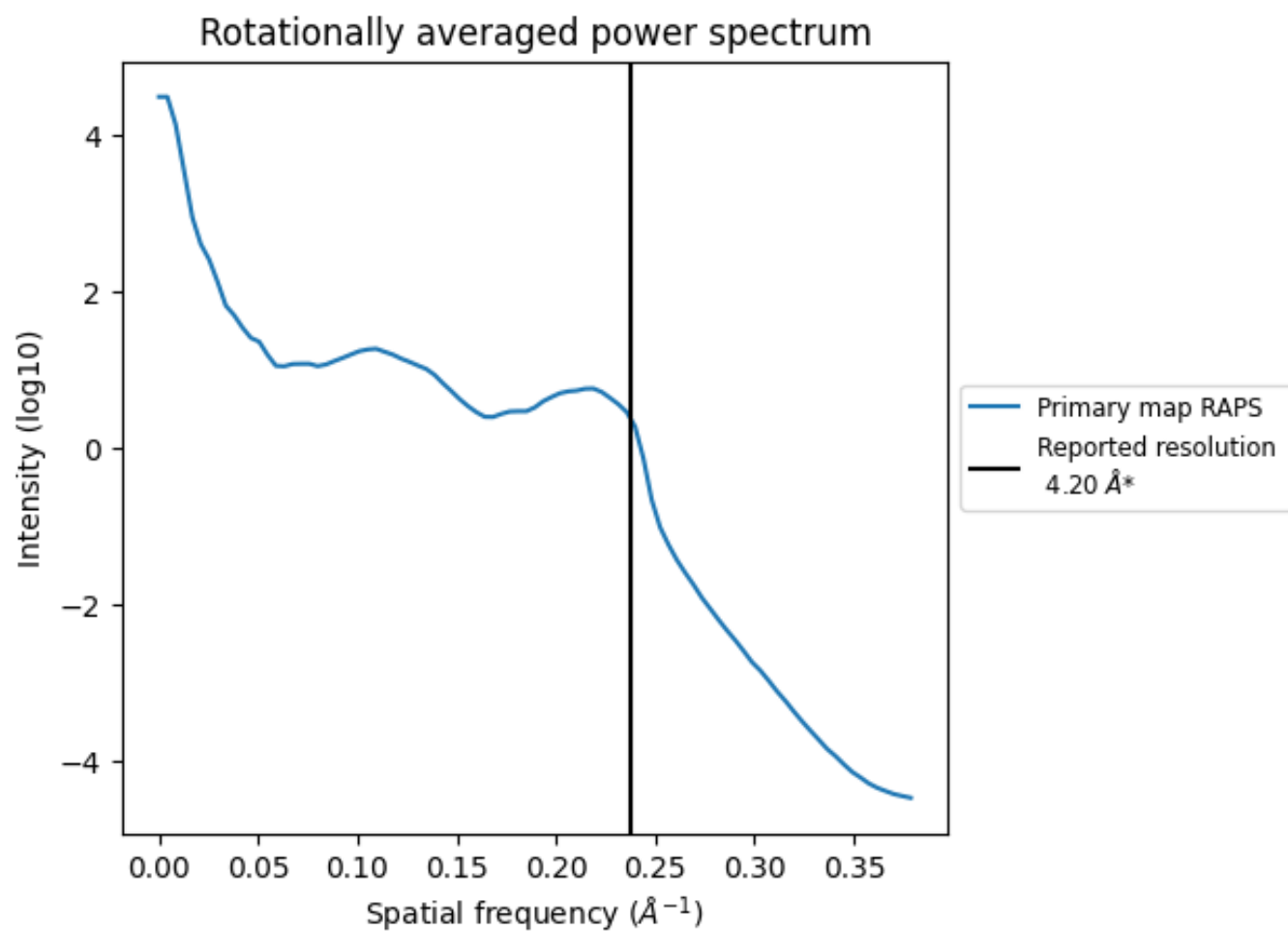
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 98 nm³; this corresponds to an approximate mass of 89 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 0.238 \AA^{-1}

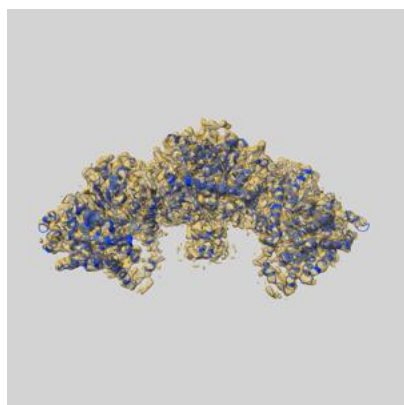
8 Fourier-Shell correlation ⓘ

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

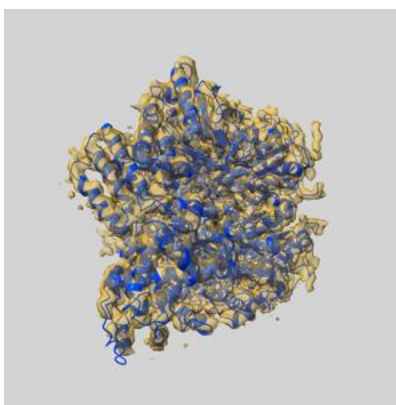
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6940 and PDB model 5ZQZ. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

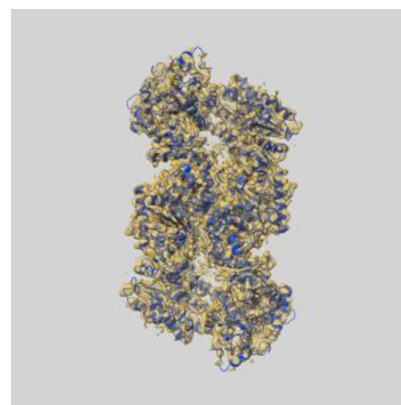
9.1 Map-model overlay [i](#)



X



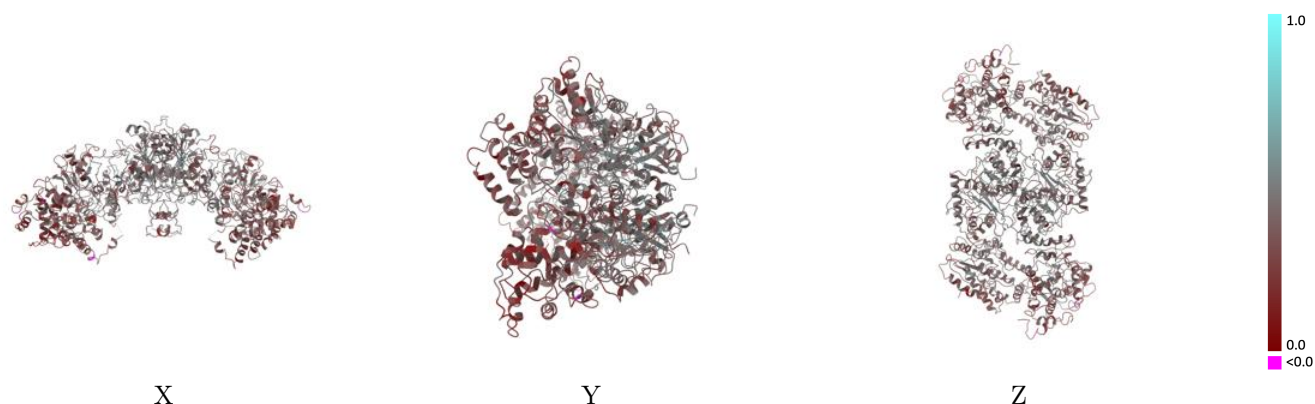
Y



Z

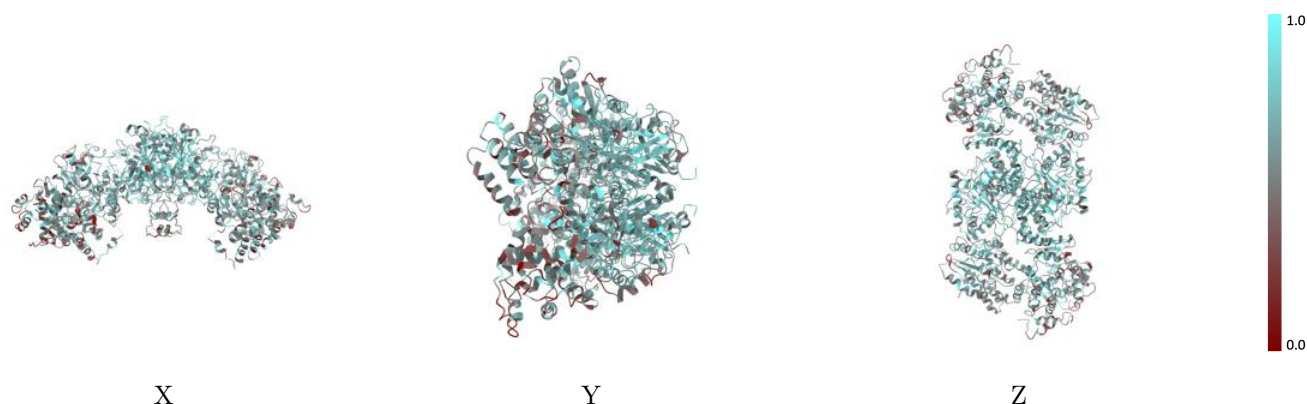
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



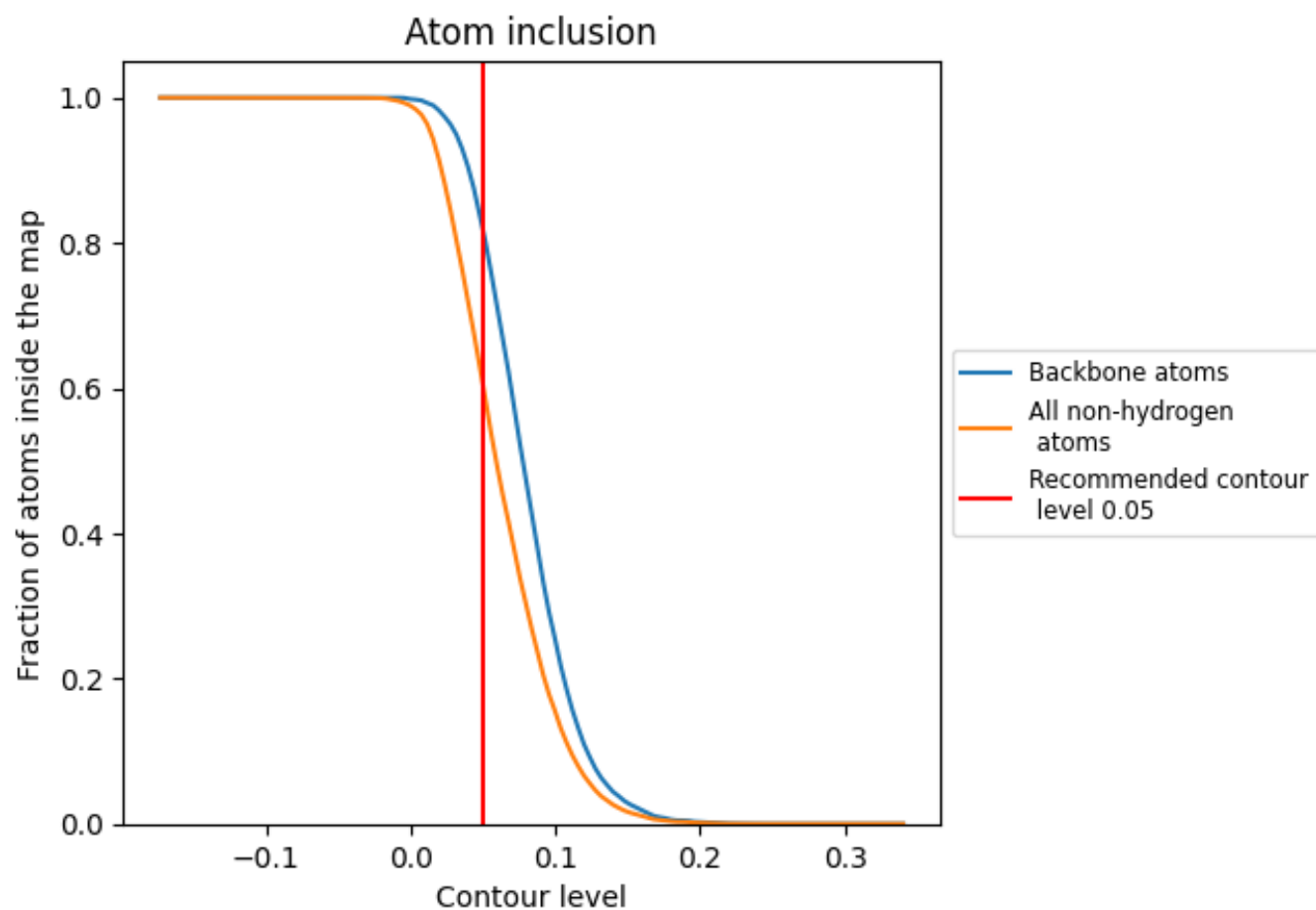
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 60% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6023	<div></div> 0.3770
A	<div></div> 0.5586	<div></div> 0.3500
B	<div></div> 0.6747	<div></div> 0.4230
C	<div></div> 0.5601	<div></div> 0.3500
D	<div></div> 0.6769	<div></div> 0.4230

