



Full wwPDB EM Validation Report ⓘ

Jun 5, 2024 – 02:24 PM EDT

PDB ID : 8U72
EMDB ID : EMD-41966
Title : Cryo-EM structure of the SPARTA oligomer with guide RNA and target DNA
Authors : Malik, R.; Kottur, J.; Aggarwal, A.K.
Deposited on : 2023-09-14
Resolution : 3.15 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.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

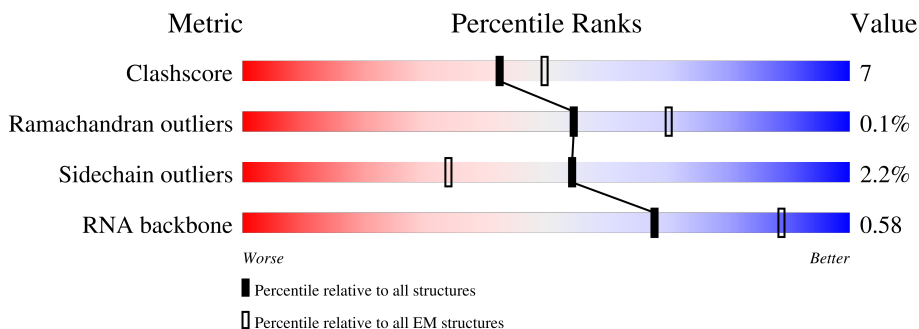
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.15 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
RNA backbone	4643	859

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	M	21	48% (green), 43% (yellow), 10% (grey)
1	S	21	57% (green), 33% (yellow), 10% (grey)
1	U	21	52% (green), 38% (yellow), 10% (grey)
1	X	21	33% (green), 52% (yellow), 5% (orange), 10% (grey)
2	N	45	22% (green), 18% (yellow), 60% (grey)
2	T	45	31% (green), 9% (yellow), 60% (grey)
2	V	45	22% (green), 16% (yellow), 1% (orange), 60% (grey)

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Mol	Chain	Length	Quality of chain
2	Y	45	 20% 20% 60%
3	B	450	 75% 17% 7%
3	D	450	 71% 19% 9%
3	F	450	 74% 18% 8%
3	H	450	 77% 16% 7%
4	C	507	 75% 14% 11%
4	E	507	 78% 11% 11%
4	G	507	 77% 12% 11%
4	I	507	 74% 15% 10%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 29712 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 RNA chain called RNA (5'-R(P*UP*GP*AP*GP*GP*UP*AP*GP*UP*AP*GP*GP*UP*UP*GP*UP*AP*UP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	U	19	411	183	74	135	19	0	0
1	M	19	411	183	74	135	19	0	0
1	S	19	411	183	74	135	19	0	0
1	X	19	411	183	74	135	19	0	0

- Molecule 2 is a DNA chain called DNA (5'-D(P*TP*AP*TP*AP*CP*AP*AP*CP*CP*TP*AP*CP*TP*AP*CP*CP*TP*C)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	V	18	359	173	61	107	18	0	0
2	N	18	359	173	61	107	18	0	0
2	T	18	359	173	61	107	18	0	0
2	Y	18	359	173	61	107	18	0	0

- Molecule 3 is a protein called TIR domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	H	417	3143	2068	545	523	7	0	0
3	D	411	3142	2066	539	529	8	0	0
3	B	417	3166	2093	538	527	8	0	0
3	F	416	3170	2091	543	529	7	0	0

- Molecule 4 is a protein called Piwi domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	I	454	Total 3533	C 2312	N 591	O 619	S 11	1	0
4	E	452	Total 3452	C 2268	N 577	O 596	S 11	0	0
4	C	452	Total 3489	C 2282	N 580	O 616	S 11	0	0
4	G	450	Total 3476	C 2273	N 583	O 609	S 11	1	0

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
5	I	1	Total 1	Mg 1	0
5	E	1	Total 1	Mg 1	0
5	C	1	Total 1	Mg 1	0
5	G	1	Total 1	Mg 1	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		AltConf
			Total	O	
6	U	1	Total 1	O 1	0
6	H	8	Total 8	O 8	0
6	I	2	Total 2	O 2	0
6	E	1	Total 1	O 1	0
6	M	1	Total 1	O 1	0
6	N	1	Total 1	O 1	0
6	D	7	Total 7	O 7	0
6	B	17	Total 17	O 17	0

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Mol	Chain	Residues	Atoms		AltConf
6	C	4	Total 4	O 4	0
6	F	12	Total 12	O 12	0
6	G	3	Total 3	O 3	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

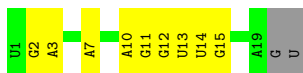
- Molecule 1: RNA (5'-R(P*UP*GP*AP*GP*GP*UP*AP*GP*UP*AP*GP*GP*UP*UP*GP*UP*AP*UP*A)-3')

Chain U: 



- Molecule 1: RNA (5'-R(P*UP*GP*AP*GP*GP*UP*AP*GP*UP*AP*GP*GP*UP*UP*GP*UP*AP*UP*A)-3')

Chain M: 



- Molecule 1: RNA (5'-R(P*UP*GP*AP*GP*GP*UP*AP*GP*UP*AP*GP*GP*UP*UP*GP*UP*AP*UP*A)-3')

Chain S: 



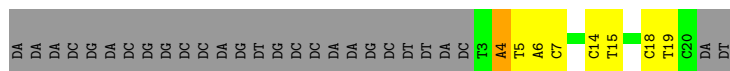
- Molecule 1: RNA (5'-R(P*UP*GP*AP*GP*GP*UP*AP*GP*UP*AP*GP*GP*UP*UP*GP*UP*AP*UP*A)-3')

Chain X: 

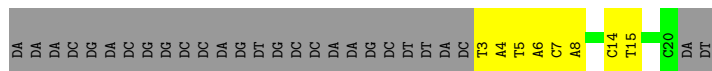


- Molecule 2: DNA (5'-D(P*TP*AP*TP*AP*CP*AP*AP*CP*CP*TP*AP*CP*TP*AP*CP*C P*TP*C)-3')

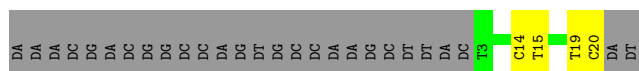
Chain V: 



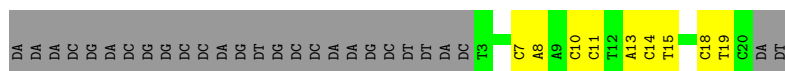
• Molecule 2: DNA (5'-D(P*TP*AP*TP*AP*CP*AP*AP*CP*CP*TP*AP*CP*TP*AP*CP*C P*TP*C)-3')



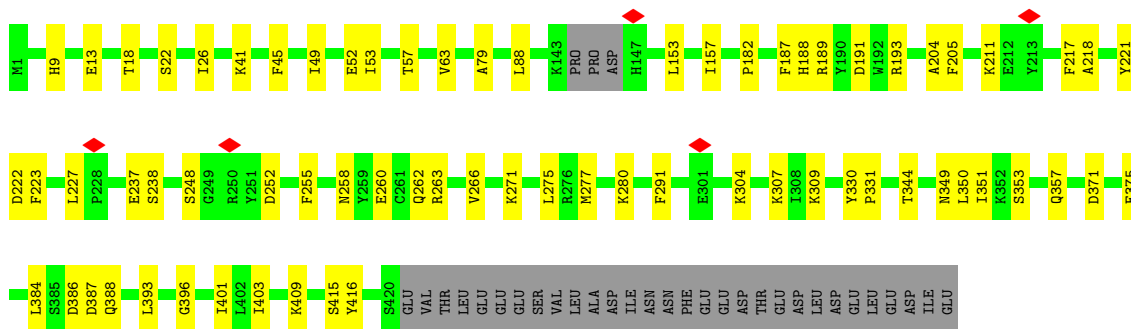
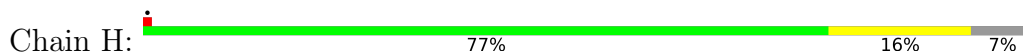
• Molecule 2: DNA (5'-D(P*TP*AP*TP*AP*CP*AP*AP*CP*CP*TP*AP*CP*TP*AP*CP*C P*TP*C)-3')



• Molecule 2: DNA (5'-D(P*TP*AP*TP*AP*CP*AP*AP*CP*CP*TP*AP*CP*TP*AP*CP*C P*TP*C)-3')

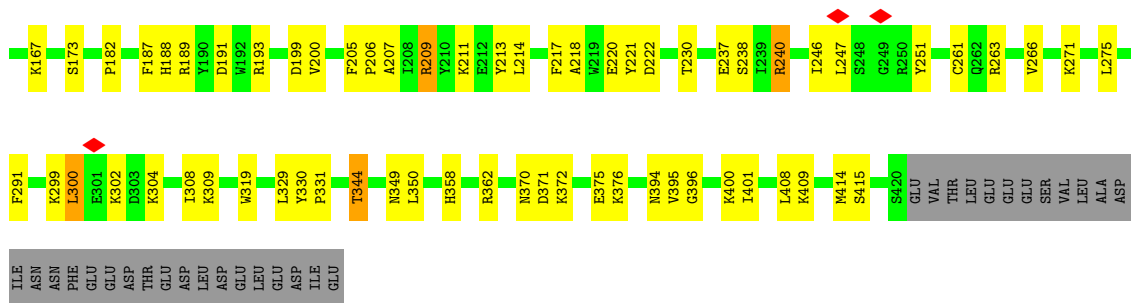


• Molecule 3: TIR domain-containing protein



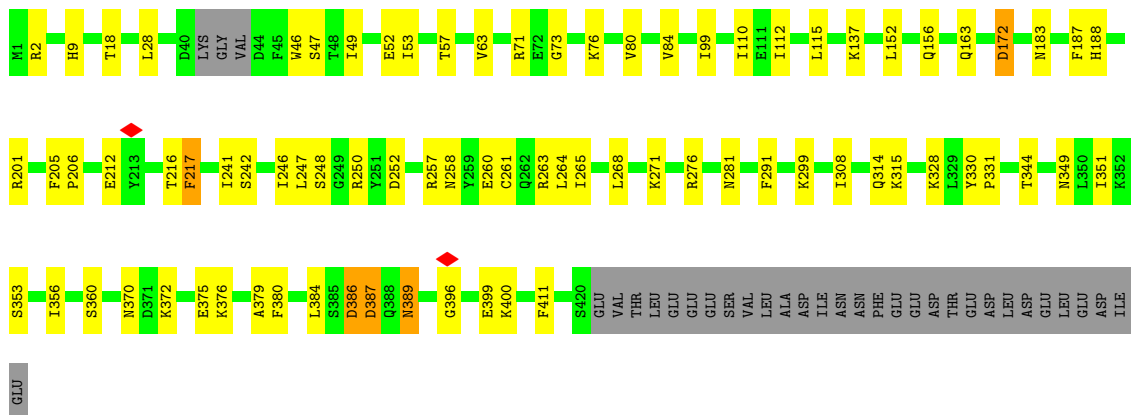
• Molecule 3: TIR domain-containing protein





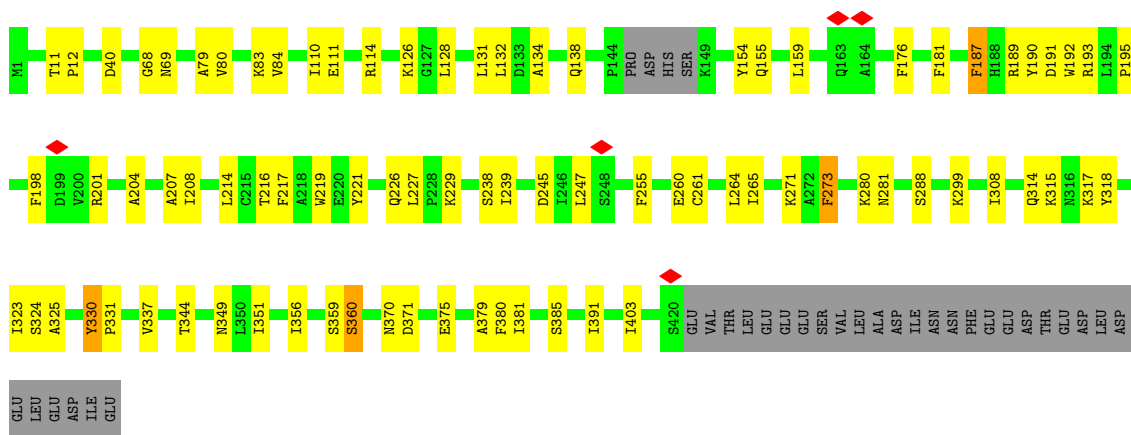
- Molecule 3: TIR domain-containing protein

Chain B: 75% 17% 7%



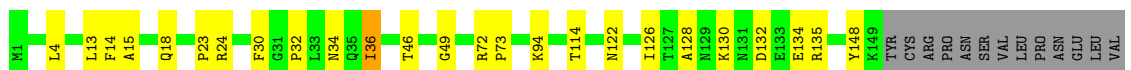
- Molecule 3: TIR domain-containing protein

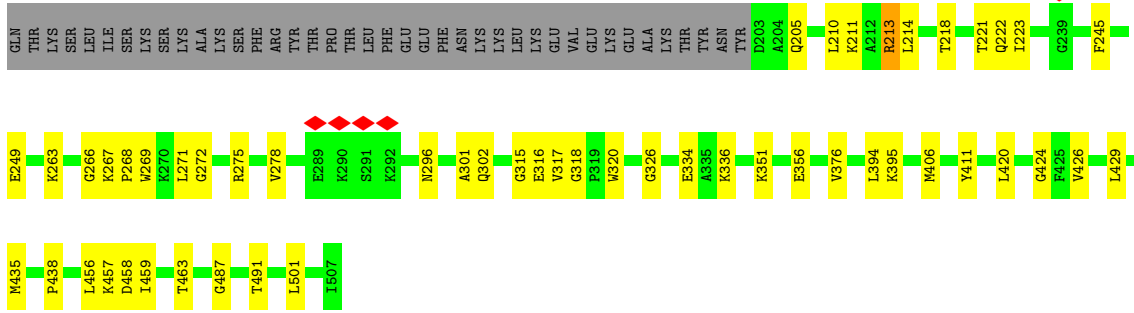
Chain F: 74% 18% 8%



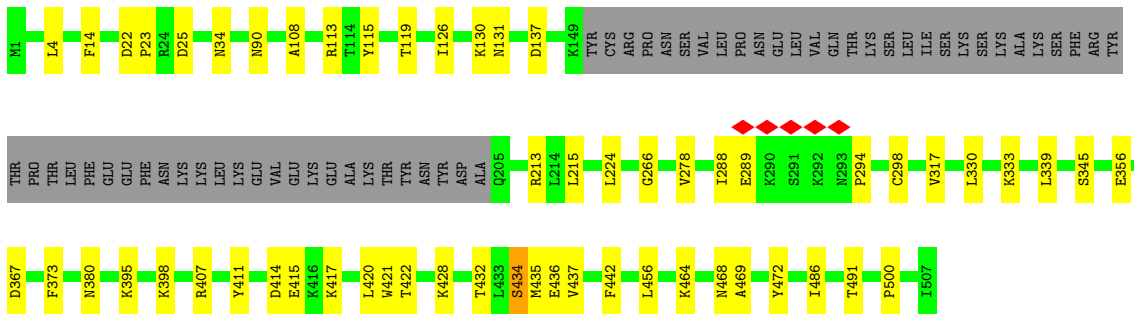
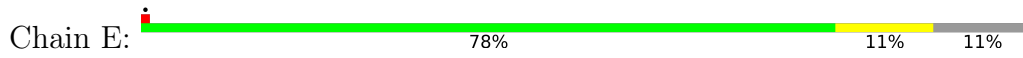
- Molecule 4: Piwi domain-containing protein

Chain I: 74% 15% 10%

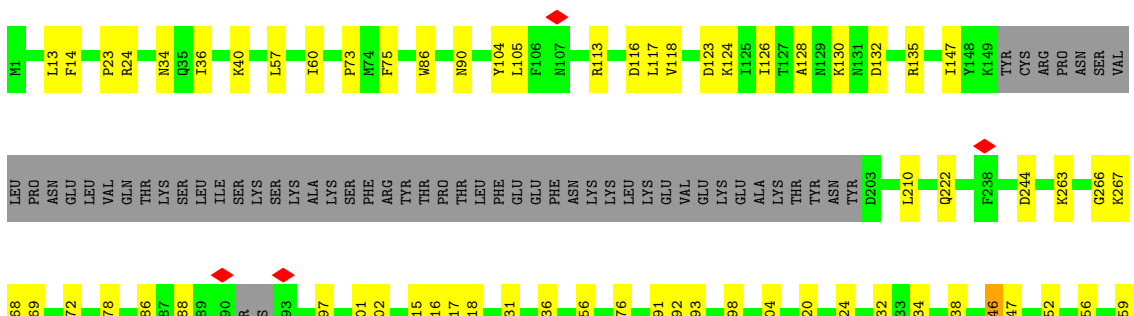
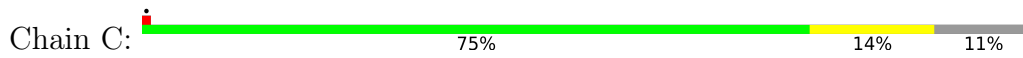




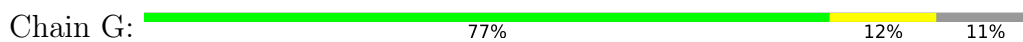
• Molecule 4: Piwi domain-containing protein

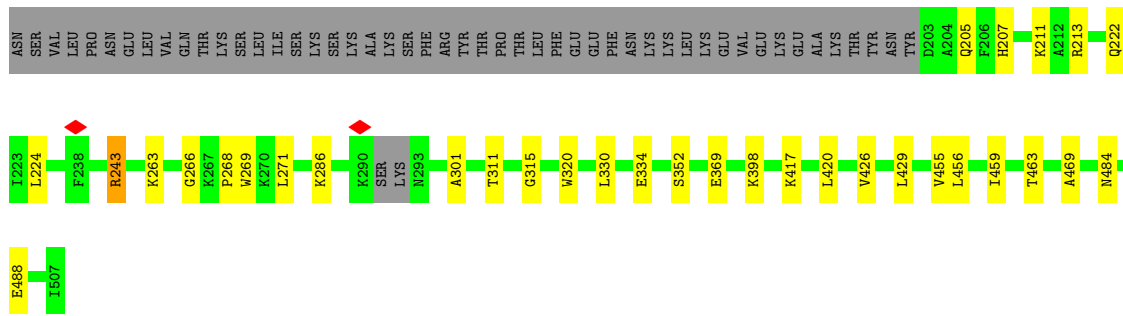


• Molecule 4: Piwi domain-containing protein



• Molecule 4: Piwi domain-containing protein





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	238432	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 ($e^-/\text{\AA}^2$)	51.11	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	4.539	Depositor
Minimum map value	-0.412	Depositor
Average map value	0.025	Depositor
Map value standard deviation	0.065	Depositor
Recommended contour level	0.564	Depositor
Map size (\AA)	519.83997, 519.83997, 519.83997	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.083, 1.083, 1.083	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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	M	0.29	0/460	0.79	0/716
1	S	0.34	0/460	0.79	0/716
1	U	0.29	0/460	0.80	0/716
1	X	0.32	0/460	0.87	0/716
2	N	0.63	0/400	0.93	0/612
2	T	0.64	0/400	0.95	0/612
2	V	0.64	0/400	1.03	1/612 (0.2%)
2	Y	0.65	0/400	0.94	0/612
3	B	0.27	0/3247	0.51	0/4412
3	D	0.27	0/3221	0.50	0/4378
3	F	0.29	0/3249	0.53	0/4410
3	H	0.27	0/3220	0.51	0/4377
4	C	0.27	0/3578	0.46	0/4865
4	E	0.28	0/3541	0.48	0/4816
4	G	0.27	0/3566	0.47	0/4846
4	I	0.27	0/3630	0.48	1/4932 (0.0%)
All	All	0.31	0/30692	0.56	2/42348 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	H	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	V	4	DA	O3'-P-O5'	8.39	119.95	104.00
4	I	36	ILE	N-CA-C	-5.44	96.32	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	H	189	ARG	Sidechain

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	M	411	0	203	8	0
1	S	411	0	203	8	0
1	U	411	0	203	7	0
1	X	411	0	203	9	0
2	N	359	0	204	6	0
2	T	359	0	204	2	0
2	V	359	0	204	6	0
2	Y	359	0	204	6	0
3	B	3166	0	2963	52	0
3	D	3142	0	2944	67	0
3	F	3170	0	2981	53	0
3	H	3143	0	2936	51	0
4	C	3489	0	3363	44	0
4	E	3452	0	3304	35	0
4	G	3476	0	3357	39	0
4	I	3533	0	3440	42	0
5	C	1	0	0	0	0
5	E	1	0	0	0	0
5	G	1	0	0	0	0
5	I	1	0	0	0	0
6	B	17	0	0	1	0
6	C	4	0	0	0	0
6	D	7	0	0	0	0
6	E	1	0	0	0	0
6	F	12	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	G	3	0	0	0	0
6	H	8	0	0	0	0
6	I	2	0	0	1	0
6	M	1	0	0	0	0
6	N	1	0	0	0	0
6	U	1	0	0	0	0
All	All	29712	0	26916	406	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 7.

All (406) 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)
3:D:344:THR:HG22	3:D:349:ASN:O	1.42	1.14
4:E:414:ASP:OD2	4:E:415:GLU:N	2.15	0.80
3:D:344:THR:HG23	3:D:350:LEU:HA	1.64	0.79
3:H:263:ARG:NH2	1:S:15:G:N2	2.33	0.77
3:D:189:ARG:HD2	3:D:214:LEU:HG	1.68	0.75
3:D:189:ARG:CD	3:D:214:LEU:HG	2.18	0.74
3:F:370:ASN:HD21	4:G:398:LYS:H	1.34	0.74
3:F:204:ALA:H	3:F:226:GLN:HE22	1.36	0.73
3:H:263:ARG:NH2	1:S:15:G:H21	1.87	0.73
3:H:9:HIS:HD2	3:H:18:THR:HG21	1.55	0.71
3:D:344:THR:HG22	3:D:349:ASN:C	2.11	0.71
3:H:13:GLU:N	3:H:13:GLU:OE2	2.24	0.70
3:D:344:THR:CG2	3:D:350:LEU:HA	2.22	0.69
4:G:420:LEU:HD12	4:G:456:LEU:HD22	1.74	0.69
3:D:188:HIS:HA	3:D:237:GLU:HG3	1.75	0.69
3:D:52:GLU:OE1	3:D:56:ASN:ND2	2.27	0.68
3:H:260:GLU:OE1	3:H:263:ARG:NH2	2.25	0.68
2:V:7:DC:O2	3:B:263:ARG:NH1	2.27	0.67
3:D:344:THR:CG2	3:D:349:ASN:O	2.34	0.67
4:I:278:VAL:HG12	4:I:356:GLU:HB3	1.77	0.67
4:C:135:ARG:NH1	4:G:137:ASP:OD2	2.28	0.67
4:C:278:VAL:HG12	4:C:356:GLU:HB3	1.76	0.67
3:H:188:HIS:HA	3:H:237:GLU:HG3	1.76	0.67
4:E:464:LYS:NZ	4:E:472:TYR:O	2.28	0.66
3:H:211:LYS:NZ	3:H:255:PHE:O	2.30	0.65
4:E:317:VAL:HG11	4:E:486:ILE:HG21	1.79	0.65
4:C:34:ASN:HD21	4:C:266:GLY:HA2	1.60	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:211:LYS:HG2	3:H:217:PHE:HZ	1.63	0.64
4:I:501:LEU:HB2	4:E:131:ASN:HB3	1.78	0.64
4:G:14:PHE:HZ	4:G:23:PRO:HA	1.62	0.64
4:E:119:THR:HG22	4:E:213:ARG:HH22	1.62	0.64
3:F:126:LYS:HE3	3:F:126:LYS:HA	1.79	0.64
3:F:195:PRO:HG2	3:F:198:PHE:HB2	1.79	0.64
3:B:276:ARG:NH2	3:B:386:ASP:OD1	2.31	0.64
1:U:14:U:H2'	1:U:15:G:H8	1.63	0.63
3:F:68:GLY:O	3:F:69:ASN:ND2	2.32	0.63
3:B:152:LEU:O	3:B:156:GLN:NE2	2.30	0.63
3:D:211:LYS:HG2	3:D:217:PHE:HZ	1.63	0.63
4:G:205:GLN:N	4:G:205:GLN:OE1	2.29	0.62
3:B:63:VAL:HG13	3:B:99:ILE:HD12	1.81	0.62
3:F:308:ILE:HD13	3:F:375:GLU:HB3	1.80	0.62
3:F:245:ASP:O	3:F:247:LEU:N	2.32	0.62
3:F:308:ILE:HD12	3:F:379:ALA:HB2	1.82	0.61
4:I:420:LEU:HD12	4:I:456:LEU:HD22	1.82	0.61
4:C:222:GLN:OE1	4:C:263:LYS:NZ	2.32	0.61
3:F:314:GLN:NE2	3:F:360:SER:OG	2.34	0.61
4:I:301:ALA:HA	4:I:315:GLY:HA2	1.82	0.61
4:G:100:GLU:O	4:G:104:TYR:HB2	2.01	0.61
3:B:308:ILE:HD13	3:B:375:GLU:HB3	1.81	0.60
2:N:3:DT:H2'	2:N:4:DA:H8	1.66	0.60
3:B:370:ASN:HD22	4:C:404:PRO:HA	1.65	0.60
3:H:371:ASP:O	3:H:375:GLU:HG2	2.01	0.60
4:G:330:LEU:N	4:G:369:GLU:OE2	2.27	0.60
4:E:108:ALA:HB3	4:E:113:ARG:HG3	1.83	0.60
3:B:370:ASN:HD21	4:C:398:LYS:H	1.50	0.60
3:H:263:ARG:CZ	1:S:15:G:N2	2.64	0.59
3:D:49:ILE:O	3:D:53:ILE:HG13	2.02	0.59
4:I:426:VAL:HG11	4:I:429:LEU:HD12	1.83	0.59
3:B:71:ARG:O	3:B:73:GLY:N	2.35	0.59
1:U:14:U:H2'	1:U:15:G:C8	2.38	0.59
3:H:304:LYS:HE3	3:H:307:LYS:HA	1.85	0.58
2:V:5:DT:H2''	2:V:6:DA:OP2	2.03	0.58
3:B:188:HIS:HB2	3:B:216:THR:HB	1.84	0.58
3:F:391:ILE:HB	3:F:403:ILE:HB	1.85	0.58
4:I:424:GLY:HA2	4:I:438:PRO:HG3	1.86	0.58
3:B:281:ASN:HB3	3:B:299:LYS:HE2	1.86	0.58
3:B:330:TYR:HB3	3:B:331:PRO:HD3	1.86	0.58
4:G:54:LYS:HG2	4:G:88:SER:HB2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:61:GLN:NE2	4:G:86:TRP:O	2.37	0.58
3:H:344:THR:OG1	3:H:349:ASN:O	2.20	0.57
3:H:415:SER:OG	3:H:416:TYR:N	2.38	0.57
3:F:344:THR:OG1	3:F:349:ASN:O	2.22	0.57
3:H:271:LYS:O	3:H:275:LEU:HD12	2.04	0.57
4:I:46:THR:HG23	4:I:49:GLY:H	1.69	0.57
3:B:187:PHE:HE1	3:B:217:PHE:CE1	2.23	0.57
3:B:344:THR:OG1	3:B:349:ASN:O	2.23	0.57
3:D:187:PHE:HB2	3:D:238:SER:HB3	1.86	0.57
4:C:446:ASN:ND2	4:C:446:ASN:O	2.38	0.57
4:E:34:ASN:HD21	4:E:266:GLY:HA2	1.70	0.57
3:B:308:ILE:HD12	3:B:379:ALA:HB2	1.85	0.57
4:I:114:THR:HG21	4:I:205:GLN:HB3	1.87	0.57
3:B:261:CYS:HA	3:B:264:LEU:HD12	1.86	0.57
4:C:288:ILE:HD11	4:C:297:ALA:HB2	1.87	0.57
3:D:167:LYS:HB3	3:D:415:SER:HB2	1.87	0.56
4:C:117:LEU:HD13	4:C:147:ILE:HG23	1.86	0.56
3:B:399:GLU:O	3:B:400:LYS:NZ	2.31	0.56
3:F:281:ASN:O	3:F:299:LYS:NZ	2.35	0.56
2:N:8:DA:H1'	3:D:263:ARG:HD3	1.87	0.56
4:E:398:LYS:H	3:D:370:ASN:HD21	1.51	0.56
4:E:435:MET:HG2	4:E:436:GLU:HG3	1.87	0.56
2:Y:18:DC:H2'	2:Y:19:DT:C6	2.41	0.56
4:G:271:LEU:H	4:G:311:THR:HG21	1.69	0.56
3:H:280:LYS:NZ	3:H:384:LEU:O	2.34	0.56
3:D:218:ALA:HB1	3:D:220:GLU:O	2.06	0.56
3:H:280:LYS:NZ	3:H:386:ASP:OD1	2.37	0.56
4:I:222:GLN:OE1	4:I:263:LYS:NZ	2.38	0.56
3:H:211:LYS:HA	1:S:17:A:H4'	1.87	0.56
1:X:14:U:H2'	1:X:15:G:H8	1.70	0.55
4:C:301:ALA:HA	4:C:315:GLY:HA2	1.88	0.55
3:F:273:PHE:CE1	3:F:325:ALA:HB3	2.42	0.55
3:D:371:ASP:O	3:D:375:GLU:HG2	2.07	0.55
3:F:187:PHE:HA	3:F:216:THR:O	2.06	0.55
3:B:396:GLY:O	3:B:400:LYS:NZ	2.39	0.55
1:U:17:A:H4'	3:B:212:GLU:H	1.71	0.55
3:F:191:ASP:C	3:F:193:ARG:H	2.11	0.54
4:G:301:ALA:HA	4:G:315:GLY:HA2	1.89	0.54
3:D:207:ALA:HA	3:D:217:PHE:O	2.07	0.54
3:D:237:GLU:N	3:D:237:GLU:OE1	2.40	0.54
4:I:214:LEU:O	4:I:218:THR:N	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:104:TYR:CE1	4:G:116:ASP:HB3	2.43	0.54
3:H:182:PRO:HD3	3:H:401:ILE:HG12	1.89	0.54
4:I:135:ARG:NH1	4:E:137:ASP:OD2	2.40	0.54
4:I:459:ILE:O	4:I:463:THR:HG23	2.07	0.54
4:C:36:ILE:HG13	4:C:36:ILE:O	2.07	0.54
3:D:182:PRO:HD3	3:D:401:ILE:HG12	1.90	0.54
3:F:330:TYR:HB3	3:F:331:PRO:HD3	1.91	0.54
4:E:417:LYS:HD3	4:E:442:PHE:HZ	1.72	0.53
4:E:22:ASP:HB2	4:E:428:LYS:HE2	1.89	0.53
1:X:14:U:H2'	1:X:15:G:C8	2.43	0.53
3:D:319:TRP:HH2	3:D:376:LYS:HZ1	1.54	0.53
4:G:320:TRP:HB3	4:G:334:GLU:HB3	1.90	0.53
1:S:13:U:H2'	1:S:14:U:C6	2.43	0.53
2:N:7:DC:H2'	2:N:8:DA:C8	2.43	0.53
3:F:371:ASP:OD1	3:F:371:ASP:N	2.42	0.53
3:B:246:ILE:HG22	3:B:247:LEU:H	1.73	0.53
3:H:205:PHE:CD2	3:H:396:GLY:HA2	2.45	0.52
3:D:200:VAL:HG21	3:D:209:ARG:HG3	1.92	0.52
3:B:206:PRO:HB3	3:B:271:LYS:HG2	1.91	0.52
3:D:309:LYS:O	3:D:376:LYS:NZ	2.41	0.52
4:G:455:VAL:O	4:G:459:ILE:HG12	2.10	0.52
1:S:14:U:H2'	1:S:15:G:H8	1.74	0.52
1:X:2:G:H5'	4:G:224:LEU:HD23	1.92	0.52
2:Y:14:DC:H2'	2:Y:15:DT:C6	2.44	0.52
3:B:9:HIS:CD2	3:B:18:THR:HG21	2.45	0.52
3:H:237:GLU:N	3:H:237:GLU:OE1	2.43	0.52
3:D:15:ASP:O	3:D:18:THR:OG1	2.23	0.52
4:E:278:VAL:HG12	4:E:356:GLU:HB3	1.92	0.51
4:E:432:THR:HG22	4:E:434:SER:H	1.75	0.51
4:G:89:GLN:OE1	4:G:89:GLN:N	2.42	0.51
1:U:13:U:H2'	1:U:14:U:H6	1.74	0.51
3:D:266:VAL:HG12	3:D:329:LEU:HD13	1.92	0.51
4:G:426:VAL:HG13	4:G:429:LEU:HB2	1.91	0.51
1:M:13:U:H2'	1:M:14:U:C6	2.46	0.51
3:D:9:HIS:CG	3:D:18:THR:HG21	2.45	0.51
3:D:187:PHE:HE2	3:D:217:PHE:CZ	2.29	0.51
3:D:344:THR:CG2	3:D:349:ASN:C	2.78	0.51
3:F:201:ARG:HG3	3:F:271:LYS:HZ1	1.76	0.51
4:I:320:TRP:HB3	4:I:334:GLU:HB3	1.91	0.51
3:D:372:LYS:O	3:D:376:LYS:HG3	2.11	0.51
4:C:420:LEU:HD13	4:C:456:LEU:HD22	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:13:U:H2'	1:S:14:U:H6	1.74	0.50
3:D:344:THR:HG23	3:D:350:LEU:HD23	1.92	0.50
3:B:217:PHE:CZ	3:B:264:LEU:HD13	2.46	0.50
3:B:183:ASN:OD1	3:B:183:ASN:N	2.44	0.50
4:C:105:LEU:HD12	4:C:113:ARG:HD3	1.93	0.50
4:C:302:GLN:HB2	4:C:316:GLU:HG2	1.93	0.50
4:G:484:ASN:O	4:G:488:GLU:HG3	2.11	0.50
3:F:155:GLN:HG2	3:F:159:LEU:HD23	1.93	0.50
3:D:240:ARG:NH1	3:D:251:TYR:O	2.45	0.50
4:C:123:ASP:OD1	4:C:124:LYS:N	2.45	0.50
3:F:134:ALA:O	3:F:138:GLN:HG3	2.11	0.50
3:H:271:LYS:HG3	3:H:275:LEU:HD11	1.94	0.50
3:B:257:ARG:NE	6:B:503:HOH:O	2.44	0.50
3:H:187:PHE:HE1	3:H:217:PHE:CE2	2.30	0.50
1:X:13:U:H2'	1:X:14:U:H6	1.77	0.50
2:N:3:DT:H2'	2:N:4:DA:C8	2.45	0.50
1:U:12:G:H2'	1:U:13:U:C6	2.47	0.49
3:D:71:ARG:HB3	3:D:74:VAL:HG12	1.93	0.49
3:D:308:ILE:HG12	3:D:375:GLU:HB3	1.93	0.49
4:C:268:PRO:HB2	4:C:269:TRP:CE3	2.47	0.49
4:C:446:ASN:HD22	4:C:446:ASN:C	2.14	0.49
4:E:395:LYS:HE3	4:E:437:VAL:HB	1.93	0.49
1:M:14:U:H2'	1:M:15:G:H8	1.77	0.49
4:C:446:ASN:O	4:C:447:LYS:HG2	2.12	0.49
4:E:398:LYS:N	3:D:370:ASN:HD21	2.10	0.49
4:G:123:ASP:OD1	4:G:124:LYS:N	2.45	0.49
3:H:218:ALA:HB3	3:H:223:PHE:HZ	1.77	0.49
3:F:80:VAL:O	3:F:84:VAL:HG23	2.12	0.49
3:B:380:PHE:HE1	3:B:384:LEU:HD11	1.78	0.49
4:C:432:THR:OG1	4:C:434:SER:O	2.25	0.49
1:M:14:U:H2'	1:M:15:G:C8	2.47	0.49
4:C:459:ILE:O	4:C:463:THR:HG23	2.13	0.49
3:H:351:ILE:HB	3:H:357:GLN:HE21	1.77	0.49
1:M:13:U:H2'	1:M:14:U:H6	1.78	0.48
3:B:46:TRP:O	3:B:47:SER:OG	2.29	0.48
3:F:208:ILE:HD11	3:F:264:LEU:HG	1.95	0.48
3:H:153:LEU:O	3:H:157:ILE:HG13	2.12	0.48
4:E:126:ILE:O	4:E:130:LYS:HG2	2.13	0.48
3:D:330:TYR:HB3	3:D:331:PRO:HD3	1.95	0.48
3:F:187:PHE:CD1	3:F:238:SER:HB2	2.48	0.48
2:V:6:DA:O3'	3:B:201:ARG:NH1	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:112:ILE:HA	3:D:115:LEU:HD12	1.95	0.48
3:B:387:ASP:OD1	3:B:389:ASN:N	2.44	0.48
4:G:50:LEU:HD11	4:G:91:ILE:HG21	1.96	0.48
3:D:149:LYS:O	3:D:153:LEU:HG	2.14	0.48
3:D:221:TYR:CG	3:D:222:ASP:N	2.82	0.48
4:C:494:THR:OG1	4:C:495:GLU:N	2.47	0.48
3:F:201:ARG:HG3	3:F:271:LYS:NZ	2.29	0.48
4:I:72:ARG:NH1	6:I:701:HOH:O	2.46	0.48
3:B:351:ILE:HG21	3:B:356:ILE:HD11	1.95	0.48
4:E:420:LEU:HD22	4:E:456:LEU:HD22	1.96	0.48
4:I:24:ARG:HD2	4:I:73:PRO:HD2	1.95	0.48
2:N:5:DT:H2'	2:N:6:DA:H8	1.77	0.48
3:F:330:TYR:HE2	4:G:417:LYS:HD2	1.78	0.48
1:U:13:U:H2'	1:U:14:U:C6	2.49	0.48
3:H:221:TYR:CG	3:H:222:ASP:N	2.82	0.48
1:S:14:U:H2'	1:S:15:G:C8	2.49	0.47
3:D:395:VAL:HG22	3:D:400:LYS:HA	1.96	0.47
4:C:391:SER:O	4:C:391:SER:OG	2.28	0.47
3:H:409:LYS:HB3	3:H:409:LYS:HE3	1.61	0.47
3:H:227:LEU:HD12	3:H:227:LEU:O	2.14	0.47
3:F:11:THR:O	3:F:12:PRO:C	2.53	0.47
2:V:4:DA:H2''	2:V:5:DT:OP1	2.14	0.47
4:E:14:PHE:HZ	4:E:23:PRO:HA	1.80	0.47
3:H:41:LYS:HD2	3:D:118:ILE:HG12	1.95	0.47
2:V:18:DC:H2'	2:V:19:DT:C6	2.50	0.47
3:H:205:PHE:HB2	3:H:223:PHE:HE1	1.79	0.47
2:T:14:DC:H2'	2:T:15:DT:C6	2.50	0.47
3:D:189:ARG:HD2	3:D:214:LEU:CG	2.42	0.47
3:B:380:PHE:CE1	3:B:384:LEU:HD11	2.50	0.47
3:B:389:ASN:O	3:B:389:ASN:ND2	2.46	0.47
4:C:118:VAL:HG13	4:C:210:LEU:HD13	1.96	0.47
3:H:387:ASP:OD1	3:H:388:GLN:N	2.45	0.47
4:G:117:LEU:HD13	4:G:147:ILE:HG23	1.96	0.47
3:D:16:ASP:HA	3:D:19:ARG:HG3	1.97	0.47
4:I:296:ASN:ND2	4:I:326:GLY:O	2.48	0.47
3:F:260:GLU:HG3	3:F:264:LEU:HD13	1.97	0.47
4:I:336:LYS:HA	4:I:376:VAL:HG21	1.97	0.46
1:X:13:U:H2'	1:X:14:U:C6	2.50	0.46
3:D:191:ASP:O	3:D:193:ARG:HG3	2.16	0.46
4:C:104:TYR:CD2	4:C:116:ASP:HB3	2.49	0.46
4:C:126:ILE:O	4:C:130:LYS:HG2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:80:VAL:O	3:D:84:VAL:HG23	2.15	0.46
4:E:25:ASP:OD2	3:D:154:TYR:OH	2.34	0.46
2:N:14:DC:H2'	2:N:15:DT:C6	2.51	0.46
3:H:262:GLN:O	3:H:266:VAL:HG23	2.15	0.46
4:I:210:LEU:HD22	4:I:223:ILE:HD11	1.97	0.46
2:T:19:DT:H4'	2:T:20:DC:C2	2.51	0.46
1:X:12:G:H2'	1:X:13:U:C6	2.51	0.46
4:G:56:TYR:O	4:G:60:ILE:HG23	2.16	0.46
2:V:14:DC:H2'	2:V:15:DT:C6	2.50	0.46
3:F:191:ASP:O	3:F:193:ARG:N	2.49	0.46
3:F:239:ILE:H	3:F:239:ILE:HG13	1.54	0.46
3:D:18:THR:O	3:D:22:SER:OG	2.25	0.46
3:F:273:PHE:HE1	3:F:325:ALA:HB3	1.80	0.46
4:G:268:PRO:HB2	4:G:269:TRP:CE3	2.51	0.46
4:I:128:ALA:O	4:I:132:ASP:HB2	2.16	0.46
4:I:268:PRO:HB2	4:I:269:TRP:CE3	2.51	0.46
3:B:261:CYS:O	3:B:265:ILE:HG13	2.15	0.46
4:E:215:LEU:HD21	4:E:500:PRO:HD2	1.98	0.45
4:E:469:ALA:HB2	1:M:3:A:H4'	1.98	0.45
3:F:351:ILE:HG21	3:F:356:ILE:HD11	1.98	0.45
4:G:105:LEU:HD13	4:G:117:LEU:HD11	1.97	0.45
1:U:12:G:H2'	1:U:13:U:H6	1.81	0.45
3:B:112:ILE:HA	3:B:115:LEU:HD12	1.99	0.45
3:F:187:PHE:CE1	3:F:238:SER:HB2	2.52	0.45
3:F:128:LEU:O	3:F:132:LEU:HD23	2.16	0.45
3:D:358:HIS:O	3:D:362:ARG:HG2	2.16	0.45
4:C:244:ASP:OD1	4:C:244:ASP:N	2.48	0.45
4:G:14:PHE:CZ	4:G:23:PRO:HA	2.49	0.45
4:I:14:PHE:HZ	4:I:23:PRO:HA	1.81	0.45
4:E:224:LEU:HD23	1:M:2:G:H5'	1.99	0.45
3:D:33:TRP:NE1	3:D:52:GLU:OE2	2.49	0.45
3:D:199:ASP:OD1	3:D:199:ASP:N	2.49	0.45
3:H:9:HIS:HA	3:H:63:VAL:HG22	1.98	0.45
4:I:394:LEU:HD12	4:I:395:LYS:H	1.82	0.45
3:B:49:ILE:O	3:B:53:ILE:HG13	2.17	0.45
3:B:52:GLU:O	3:B:57:THR:HG23	2.16	0.45
3:F:79:ALA:O	3:F:83:LYS:HG2	2.17	0.45
4:G:57:LEU:O	4:G:61:GLN:HG2	2.17	0.45
4:G:286:LYS:HB3	4:G:286:LYS:HE3	1.65	0.45
4:I:126:ILE:O	4:I:130:LYS:HG2	2.17	0.44
4:I:275:ARG:NH2	4:I:458:ASP:OD2	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:501:LEU:HB2	4:E:131:ASN:CB	2.45	0.44
4:I:211:LYS:HE2	4:I:221:THR:HG23	1.99	0.44
4:I:487:GLY:O	4:I:491:THR:HG23	2.16	0.44
3:H:353:SER:O	3:H:357:GLN:HG3	2.18	0.44
4:E:4:LEU:HD22	4:E:411:TYR:HB2	1.99	0.44
3:B:28:LEU:HD12	3:B:28:LEU:HA	1.75	0.44
3:F:385:SER:HA	3:F:391:ILE:HD13	1.99	0.44
3:F:110:ILE:O	3:F:111:GLU:HG2	2.18	0.44
4:E:288:ILE:HD13	4:E:491:THR:HG23	2.00	0.44
4:I:94:LYS:HE2	4:I:128:ALA:HB2	1.99	0.44
4:I:302:GLN:HB2	4:I:316:GLU:HG2	2.00	0.44
4:E:289:GLU:HA	4:E:294:PRO:HA	1.99	0.43
4:E:339:LEU:HD22	4:E:373:PHE:CD1	2.53	0.43
3:F:227:LEU:O	3:F:229:LYS:N	2.51	0.43
4:I:15:ALA:HB2	4:I:32:PRO:O	2.18	0.43
4:G:34:ASN:HD21	4:G:266:GLY:HA2	1.82	0.43
3:H:52:GLU:O	3:H:57:THR:HG23	2.17	0.43
1:M:12:G:H2'	1:M:13:U:C6	2.53	0.43
3:B:137:LYS:HE2	3:F:40:ASP:OD1	2.17	0.43
3:F:318:TYR:HB2	3:F:344:THR:HG22	2.00	0.43
3:D:187:PHE:N	3:D:238:SER:O	2.46	0.43
3:H:191:ASP:C	3:H:193:ARG:H	2.22	0.43
3:D:246:ILE:HG22	3:D:247:LEU:H	1.83	0.43
3:B:372:LYS:O	3:B:376:LYS:HG3	2.18	0.43
4:G:222:GLN:OE1	4:G:263:LYS:NZ	2.45	0.43
4:C:13:LEU:HD13	4:C:272:GLY:HA3	2.01	0.43
4:C:424:GLY:HA2	4:C:438:PRO:HG3	1.99	0.43
3:H:252:ASP:HB3	3:H:258:ASN:HB2	1.99	0.43
3:H:304:LYS:HG2	3:H:309:LYS:HG3	2.00	0.43
3:D:173:SER:OG	3:D:408:LEU:O	2.28	0.43
3:B:260:GLU:HG3	3:B:264:LEU:HD11	2.01	0.43
3:H:211:LYS:HG2	3:H:217:PHE:CZ	2.47	0.43
3:B:328:LYS:NZ	3:B:331:PRO:HD2	2.34	0.43
4:C:267:LYS:H	4:C:267:LYS:HG3	1.68	0.43
4:I:351:LYS:HA	4:I:351:LYS:HD3	1.87	0.43
3:B:80:VAL:O	3:B:84:VAL:HG23	2.18	0.43
4:C:452:ILE:HD12	4:C:452:ILE:HA	1.91	0.43
3:F:176:PHE:CE2	3:F:381:ILE:HG12	2.54	0.43
4:C:331:LYS:HA	4:C:331:LYS:HD3	1.85	0.43
4:G:57:LEU:HD23	4:G:57:LEU:HA	1.85	0.43
4:G:207:HIS:CE1	4:G:211:LYS:HG3	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:457:LYS:HB3	4:I:457:LYS:HE2	1.91	0.42
4:C:24:ARG:HD2	4:C:73:PRO:HD2	2.00	0.42
4:I:122:ASN:ND2	4:I:213:ARG:HB2	2.34	0.42
3:D:189:ARG:HD3	3:D:214:LEU:CD2	2.49	0.42
4:C:57:LEU:HA	4:C:57:LEU:HD12	1.79	0.42
3:D:206:PRO:HG3	3:D:275:LEU:HD21	2.01	0.42
3:B:217:PHE:HD2	3:B:268:LEU:HD11	1.84	0.42
3:B:328:LYS:HZ3	3:B:331:PRO:HD2	1.84	0.42
4:C:14:PHE:HZ	4:C:23:PRO:HA	1.84	0.42
4:C:57:LEU:HD11	4:C:86:TRP:CE2	2.54	0.42
2:Y:7:DC:H2'	2:Y:8:DA:C8	2.54	0.42
3:D:263:ARG:HD2	3:D:263:ARG:O	2.19	0.42
4:I:315:GLY:O	4:I:501:LEU:HG	2.19	0.42
4:C:392:LYS:HA	4:C:393:PRO:HD3	1.86	0.42
3:H:277:MET:SD	3:H:384:LEU:HD13	2.60	0.42
1:X:5:G:H2'	1:X:6:U:C6	2.54	0.42
3:F:280:LYS:HD2	3:F:280:LYS:HA	1.92	0.42
4:I:13:LEU:HD13	4:I:272:GLY:HA3	2.02	0.42
3:B:201:ARG:HE	3:B:201:ARG:HB2	1.67	0.42
3:F:132:LEU:HD12	3:F:154:TYR:HE1	1.85	0.42
3:H:49:ILE:O	3:H:53:ILE:HG13	2.19	0.41
3:B:183:ASN:O	3:B:241:ILE:HA	2.20	0.41
3:F:131:LEU:HD23	3:F:131:LEU:HA	1.82	0.41
3:H:9:HIS:CD2	3:H:18:THR:HG21	2.45	0.41
3:H:350:LEU:HD23	3:H:350:LEU:HA	1.89	0.41
1:X:9:U:OP2	3:F:288:SER:OG	2.34	0.41
3:F:261:CYS:O	3:F:265:ILE:HG13	2.20	0.41
4:G:119:THR:OG1	4:G:213:ARG:NH2	2.54	0.41
4:I:317:VAL:HG22	4:I:318:GLY:H	1.85	0.41
3:D:22:SER:O	3:D:26:ILE:HG13	2.21	0.41
3:F:187:PHE:HD2	3:F:217:PHE:CE1	2.39	0.41
3:F:330:TYR:CD1	3:F:330:TYR:C	2.93	0.41
4:G:15:ALA:HB2	4:G:32:PRO:O	2.20	0.41
4:G:243[A]:ARG:HA	4:G:243[A]:ARG:HD2	1.80	0.41
4:I:18:GLN:HG3	4:I:30:PHE:CE1	2.55	0.41
4:I:245:PHE:O	4:I:249:GLU:HG3	2.20	0.41
4:I:271:LEU:HD23	4:I:271:LEU:HA	1.91	0.41
2:Y:13:DA:H2''	2:Y:14:DC:H6	1.84	0.41
3:D:302:LYS:O	3:D:304:LYS:HG3	2.20	0.41
3:B:314:GLN:CG	3:B:315:LYS:H	2.33	0.41
3:F:207:ALA:HA	3:F:217:PHE:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:214:LEU:HD13	3:F:255:PHE:CE1	2.56	0.41
4:E:22:ASP:HB3	4:E:25:ASP:HB2	2.02	0.41
3:D:271:LYS:O	3:D:275:LEU:HG	2.20	0.41
3:F:325:ALA:HB2	3:F:337:VAL:HA	2.02	0.41
3:H:205:PHE:CD1	3:H:205:PHE:N	2.87	0.41
1:X:3:A:H4'	4:G:469:ALA:HB2	2.02	0.41
3:D:110:ILE:HG22	3:D:111:GLU:H	1.85	0.41
3:D:299:LYS:O	3:D:300:LEU:HB2	2.21	0.41
3:B:205:PHE:HE2	3:B:396:GLY:C	2.24	0.41
4:C:420:LEU:HD21	4:C:460:LEU:HD13	2.02	0.41
4:I:4:LEU:HD22	4:I:411:TYR:HB2	2.02	0.41
4:E:14:PHE:CZ	4:E:23:PRO:HA	2.55	0.41
4:E:468:ASN:ND2	1:M:3:A:H5'	2.36	0.41
3:D:409:LYS:HE3	3:D:409:LYS:HB3	1.65	0.41
4:C:128:ALA:O	4:C:132:ASP:HB2	2.21	0.41
4:C:317:VAL:HG22	4:C:318:GLY:H	1.85	0.41
3:F:315:LYS:O	3:F:317:LYS:HG3	2.21	0.41
4:G:459:ILE:O	4:G:463:THR:HG23	2.21	0.41
3:H:79:ALA:HB2	3:F:114:ARG:NH1	2.36	0.41
3:H:204:ALA:C	3:H:205:PHE:HD1	2.24	0.41
3:H:330:TYR:HB3	3:H:331:PRO:HD3	2.01	0.41
3:B:248:SER:O	3:B:250:ARG:N	2.47	0.41
4:C:40:LYS:HE3	4:C:40:LYS:HB3	1.85	0.41
4:C:301:ALA:HB3	4:C:479:THR:HG23	2.03	0.41
4:G:113:ARG:O	4:G:117:LEU:HG	2.21	0.41
3:H:187:PHE:HB2	3:H:238:SER:HB3	2.03	0.40
3:H:393:LEU:HD11	3:H:403:ILE:HD11	2.04	0.40
4:E:330:LEU:HD12	4:E:330:LEU:HA	1.94	0.40
3:D:152:LEU:O	3:D:156:GLN:HG3	2.21	0.40
3:B:2:ARG:HA	3:B:2:ARG:NE	2.36	0.40
3:F:323:ILE:HG12	3:F:380:PHE:CE1	2.56	0.40
4:I:134:GLU:H	4:I:134:GLU:HG3	1.68	0.40
4:I:34:ASN:HD21	4:I:266:GLY:HA2	1.85	0.40
4:E:115:TYR:O	4:E:119:THR:HG23	2.22	0.40
4:E:407:ARG:NH1	4:E:422:THR:O	2.48	0.40
2:Y:10:DC:H2'	2:Y:11:DC:H6	1.86	0.40
3:D:191:ASP:C	3:D:193:ARG:H	2.24	0.40
3:D:205:PHE:CE2	3:D:396:GLY:HA2	2.56	0.40
3:D:213:TYR:O	3:D:214:LEU:C	2.58	0.40
4:C:336:LYS:HG2	4:C:376:VAL:HG23	2.03	0.40
4:G:128:ALA:O	4:G:132:ASP:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Y:10:DC:H2'	2:Y:11:DC:C6	2.57	0.40
3:B:76:LYS:O	3:B:80:VAL:HG23	2.20	0.40
3:B:172:ASP:N	3:B:172:ASP:OD1	2.54	0.40
4:C:286:LYS:HE3	4:C:286:LYS:HB3	1.77	0.40
3:H:22:SER:O	3:H:26:ILE:HG13	2.21	0.40
3:H:88:LEU:HD12	3:H:88:LEU:HA	1.93	0.40
4:E:333:LYS:HB3	4:E:333:LYS:HE2	1.92	0.40
3:D:46:TRP:HE1	3:B:110:ILE:HB	1.86	0.40
3:D:152:LEU:HD12	3:D:152:LEU:HA	1.90	0.40
4:C:60:ILE:HG23	4:C:75:PHE:HE2	1.86	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	
3	B	413/450 (92%)	353 (86%)	60 (14%)	0	100	100
3	D	407/450 (90%)	368 (90%)	38 (9%)	1 (0%)	47	78
3	F	412/450 (92%)	354 (86%)	56 (14%)	2 (0%)	29	65
3	H	413/450 (92%)	370 (90%)	42 (10%)	1 (0%)	47	78
4	C	446/507 (88%)	416 (93%)	30 (7%)	0	100	100
4	E	448/507 (88%)	419 (94%)	29 (6%)	0	100	100
4	G	443/507 (87%)	417 (94%)	26 (6%)	0	100	100
4	I	451/507 (89%)	427 (95%)	24 (5%)	0	100	100
All	All	3433/3828 (90%)	3124 (91%)	305 (9%)	4 (0%)	54	83

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	H	248	SER
3	F	192	TRP
3	D	300	LEU
3	F	189	ARG

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	
3	B	279/415 (67%)	266 (95%)	13 (5%)	26	60
3	D	284/415 (68%)	273 (96%)	11 (4%)	32	64
3	F	284/415 (68%)	274 (96%)	10 (4%)	36	67
3	H	279/415 (67%)	277 (99%)	2 (1%)	84	93
4	C	335/446 (75%)	333 (99%)	2 (1%)	86	94
4	E	319/446 (72%)	312 (98%)	7 (2%)	52	77
4	G	333/446 (75%)	329 (99%)	4 (1%)	71	87
4	I	344/446 (77%)	337 (98%)	7 (2%)	55	79
All	All	2457/3444 (71%)	2401 (98%)	56 (2%)	54	76

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	H	45	PHE
3	H	291	PHE
4	I	36	ILE
4	I	148	TYR
4	I	213	ARG
4	I	267[A]	LYS
4	I	267[B]	LYS
4	I	406	MET
4	I	435	MET
4	E	90	ASN
4	E	298	CYS
4	E	345	SER

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Mol	Chain	Res	Type
4	E	367	ASP
4	E	380	ASN
4	E	421	TRP
4	E	434	SER
3	D	71	ARG
3	D	87	HIS
3	D	111	GLU
3	D	209	ARG
3	D	230	THR
3	D	240	ARG
3	D	261	CYS
3	D	291	PHE
3	D	344	THR
3	D	394	ASN
3	D	414	MET
3	B	163	GLN
3	B	172	ASP
3	B	217	PHE
3	B	242	SER
3	B	252	ASP
3	B	258	ASN
3	B	291	PHE
3	B	353	SER
3	B	360	SER
3	B	386	ASP
3	B	387	ASP
3	B	389	ASN
3	B	411	PHE
4	C	90	ASN
4	C	446	ASN
3	F	181	PHE
3	F	187	PHE
3	F	190	TYR
3	F	219	TRP
3	F	221	TYR
3	F	273	PHE
3	F	324	SER
3	F	330	TYR
3	F	359	SER
3	F	360	SER
4	G	104	TYR
4	G	243[A]	ARG

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Mol	Chain	Res	Type
4	G	243[B]	ARG
4	G	352	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
3	D	320	HIS
3	D	370	ASN
3	B	370	ASN
3	F	314	GLN
3	F	370	ASN
4	G	61	GLN
4	G	207	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	M	18/21 (85%)	3 (16%)	0
1	S	18/21 (85%)	3 (16%)	0
1	U	18/21 (85%)	3 (16%)	0
1	X	18/21 (85%)	4 (22%)	0
All	All	72/84 (85%)	13 (18%)	0

All (13) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	U	2	G
1	U	7	A
1	U	10	A
1	M	7	A
1	M	10	A
1	M	11	G
1	S	2	G
1	S	7	A
1	S	11	G
1	X	2	G
1	X	7	A
1	X	10	A
1	X	11	G

There are no RNA pucker outliers to report.

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](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

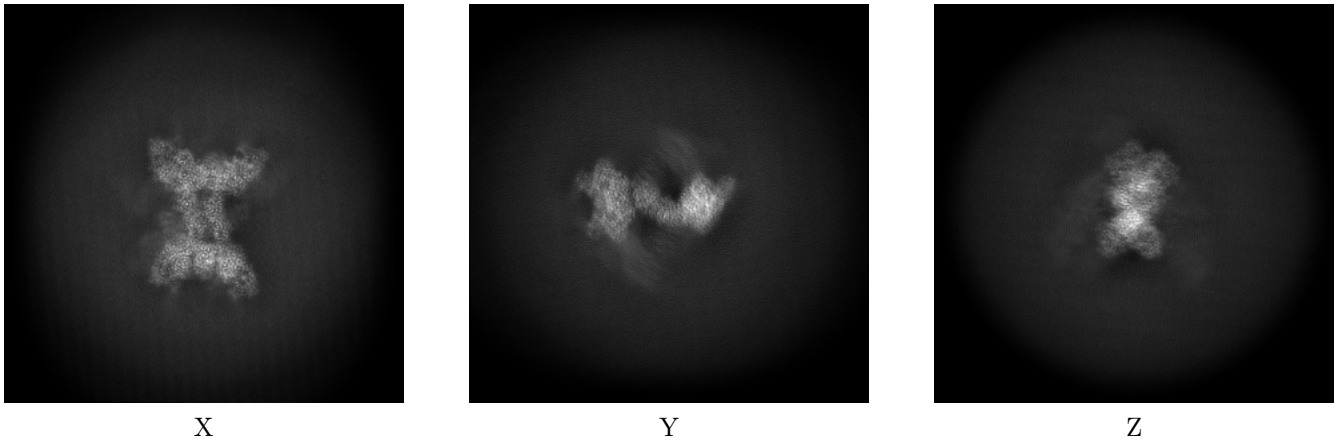
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41966. 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](#)

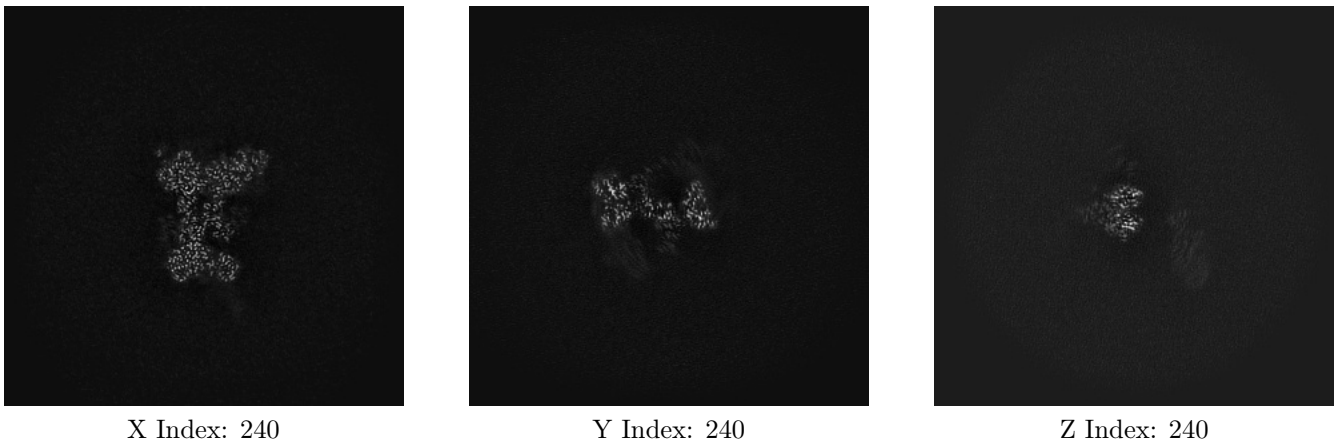
6.1.1 Primary map



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

6.2 Central slices [i](#)

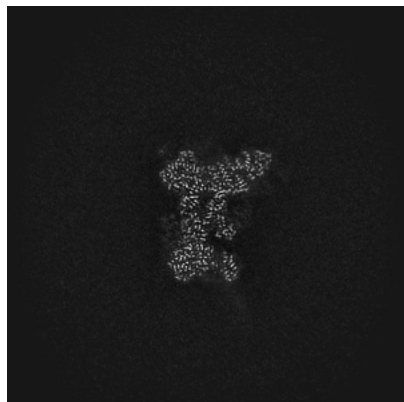
6.2.1 Primary map



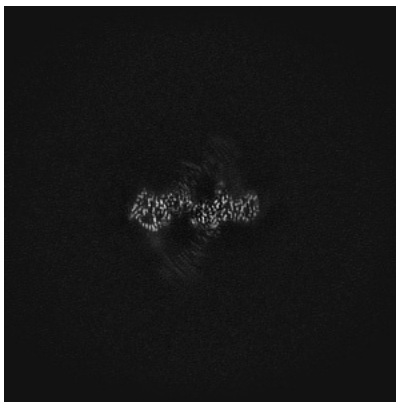
The images above show central slices of the map in three orthogonal directions.

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

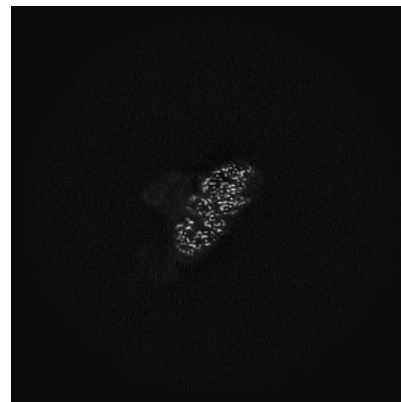
6.3.1 Primary map



X Index: 238



Y Index: 220



Z Index: 171

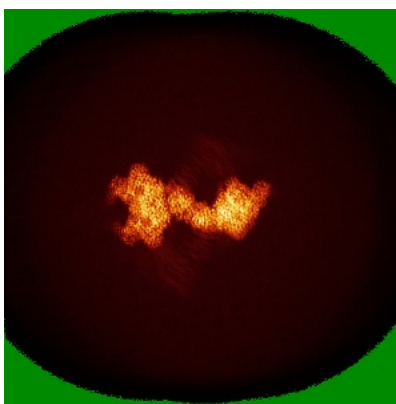
The images above show the largest variance slices of the map in three orthogonal directions.

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

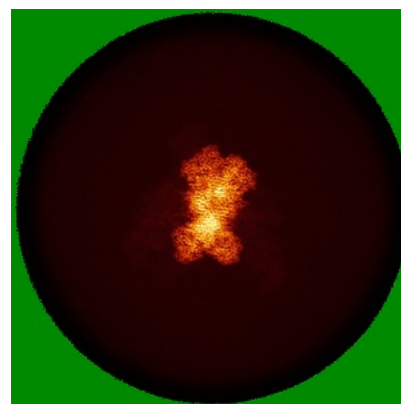
6.4.1 Primary map



X



Y

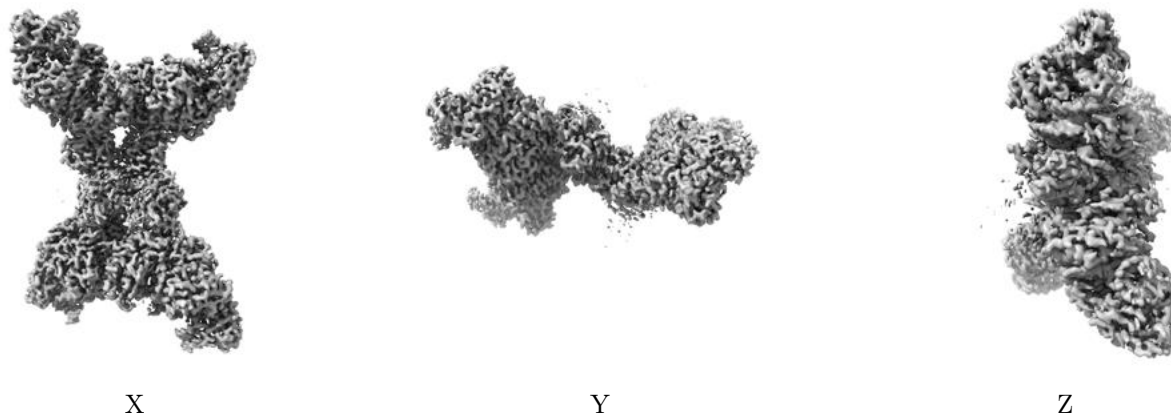


Z

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

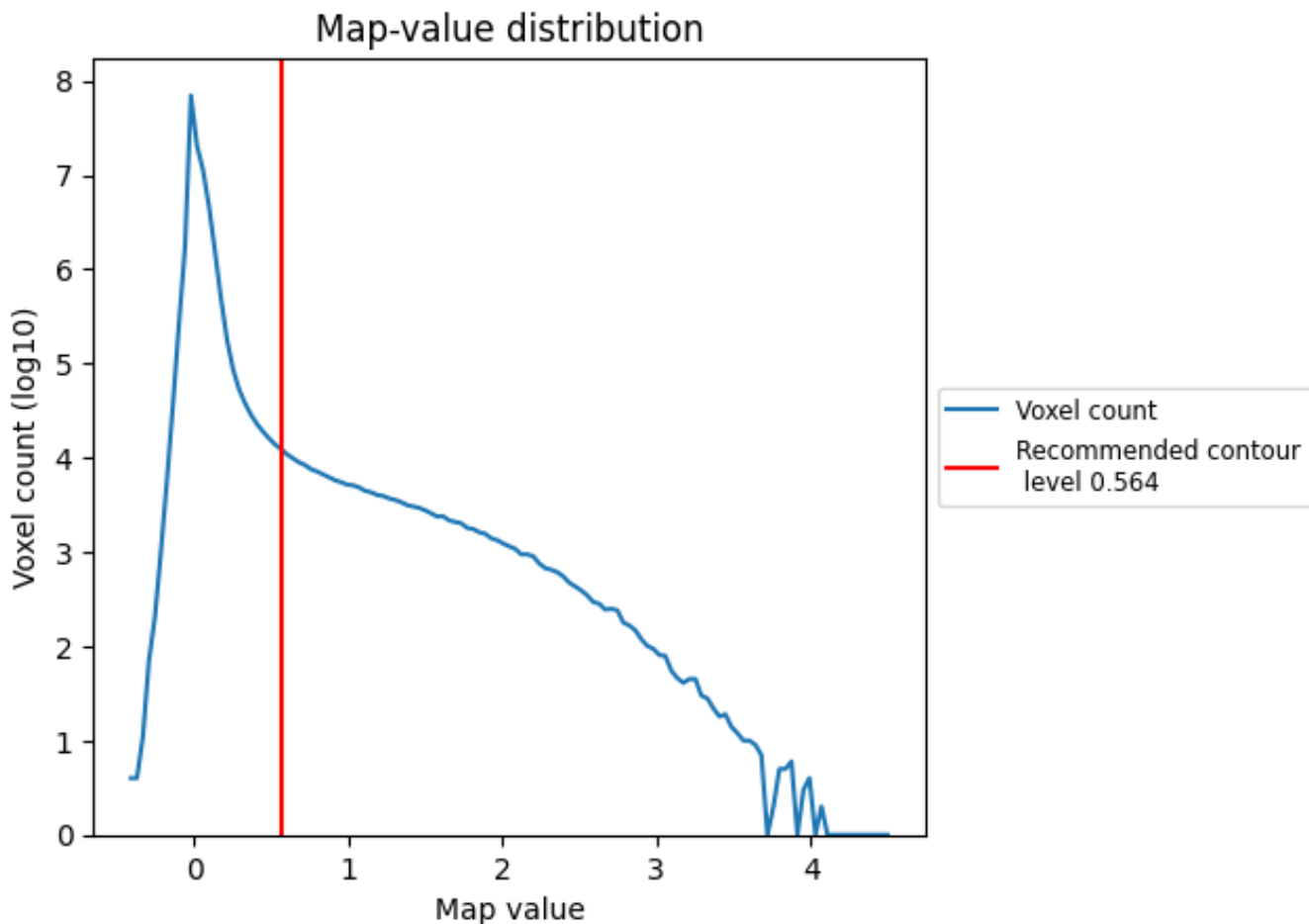
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

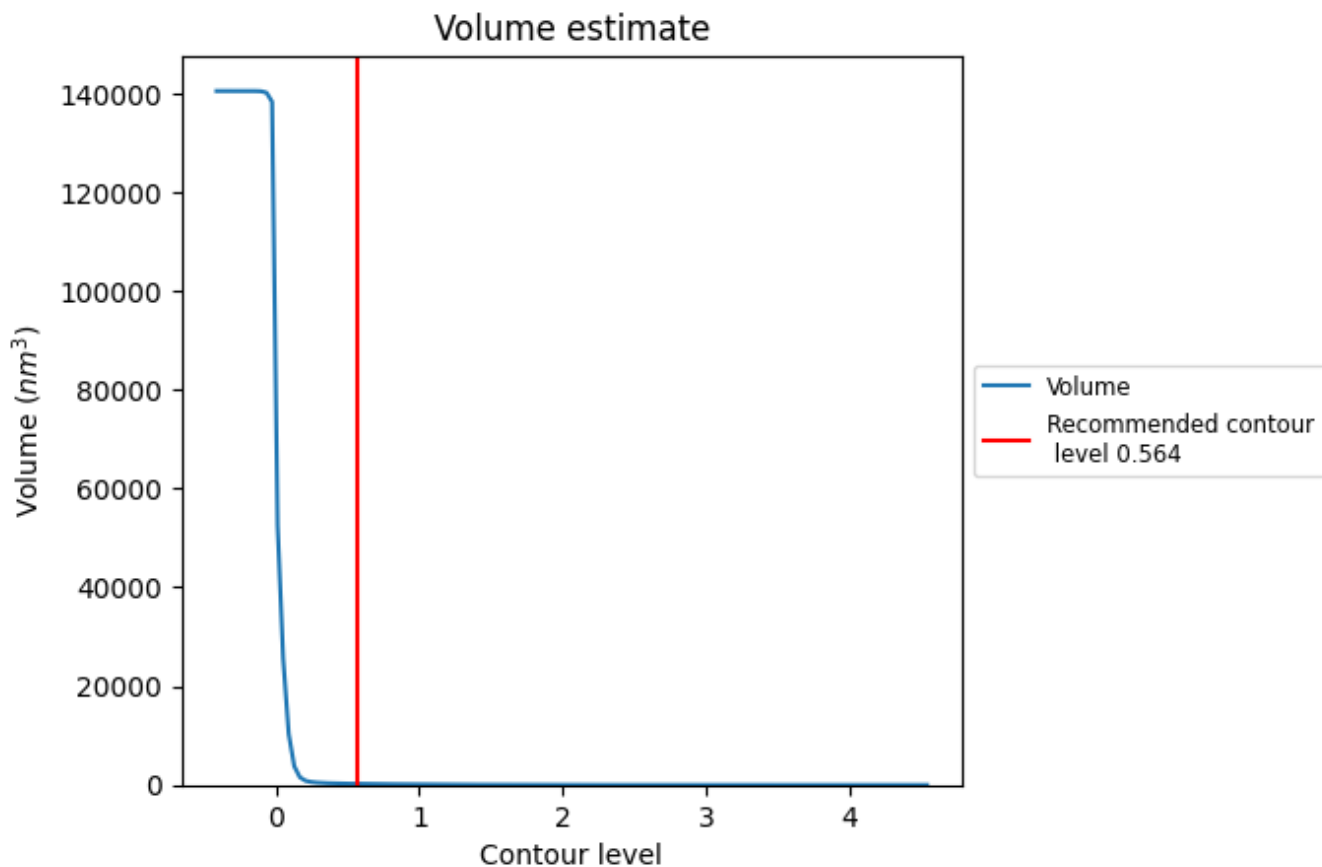
This section contains the results of statistical analysis of the map.

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.

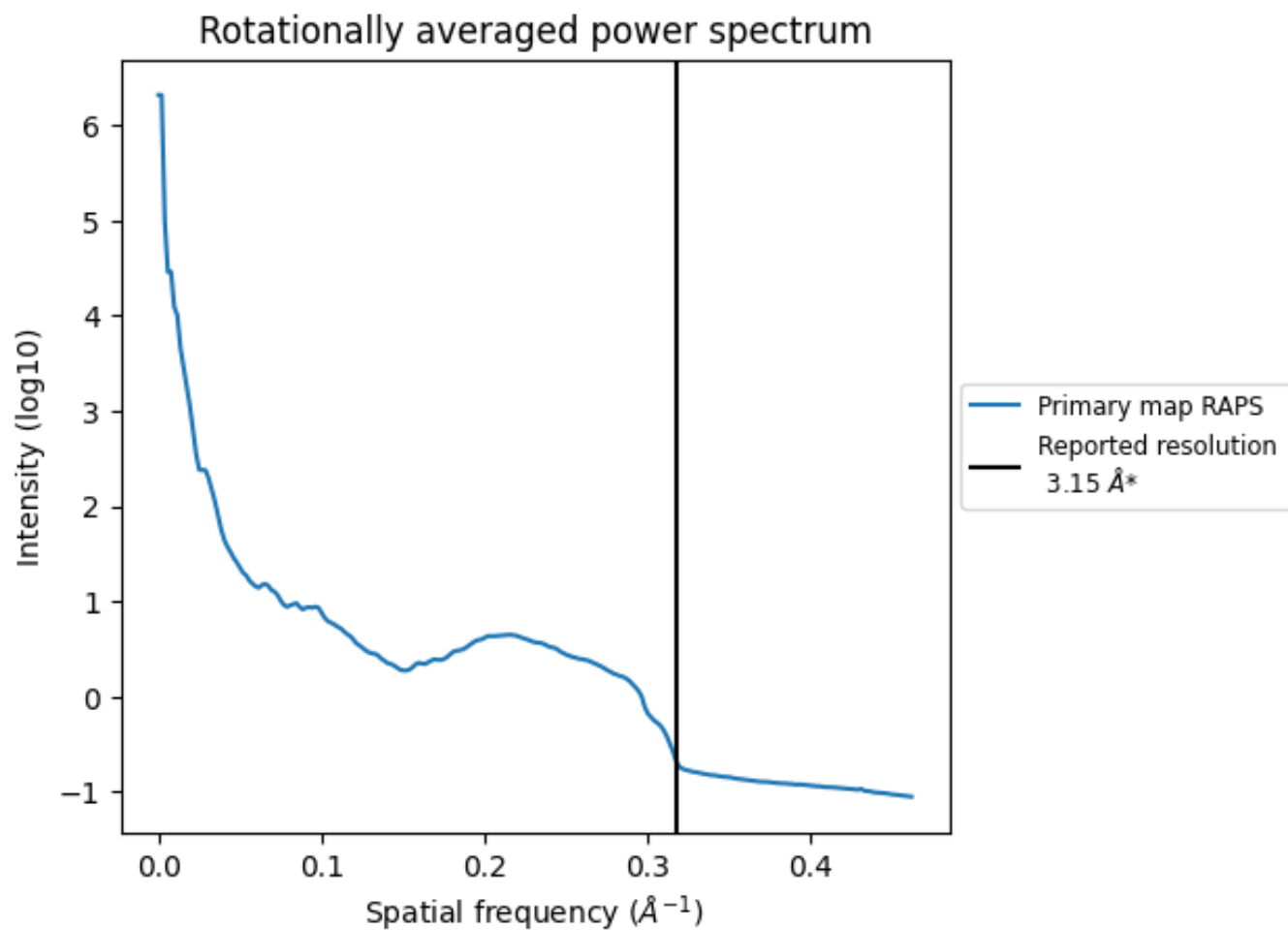
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 229 nm³; this corresponds to an approximate mass of 207 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.317 Å⁻¹

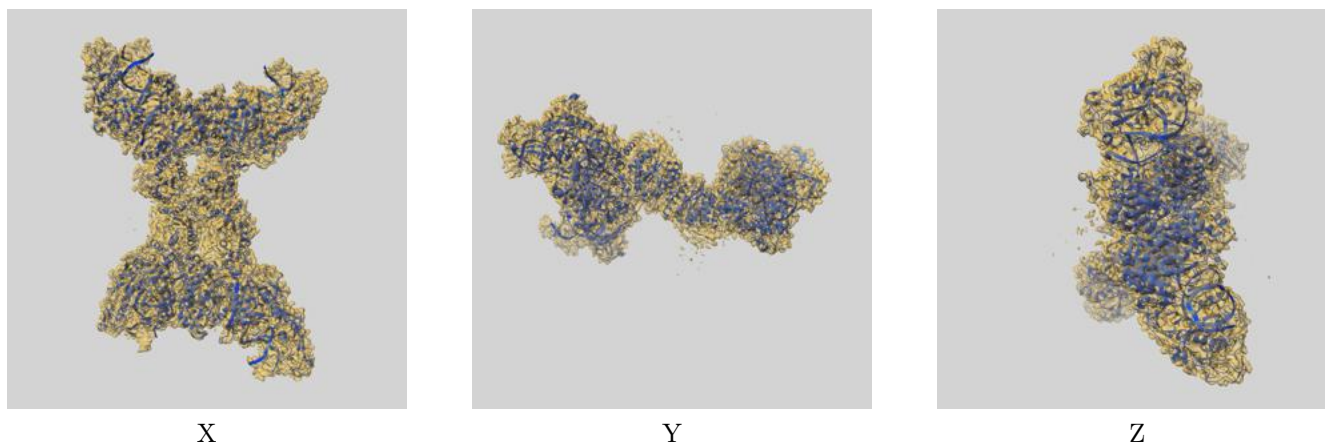
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

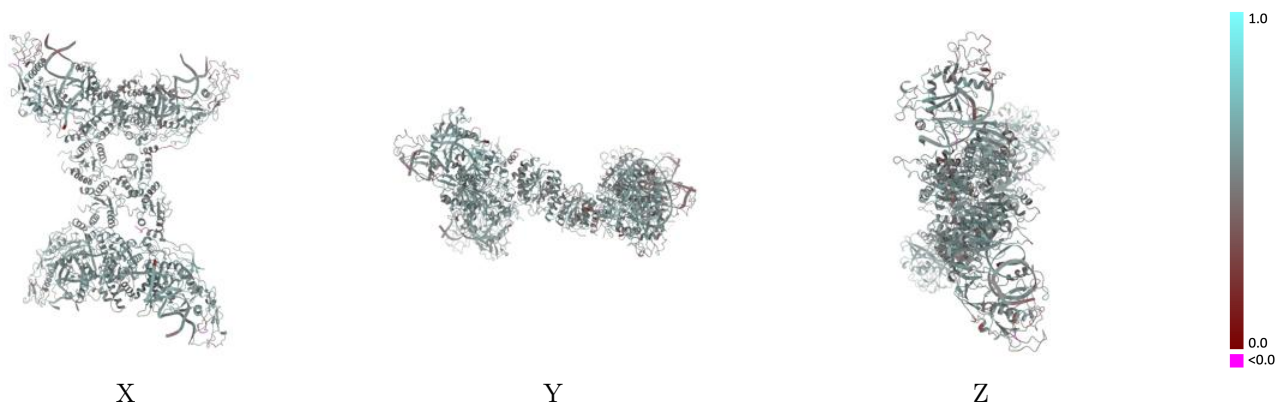
This section contains information regarding the fit between EMDB map EMD-41966 and PDB model 8U72. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



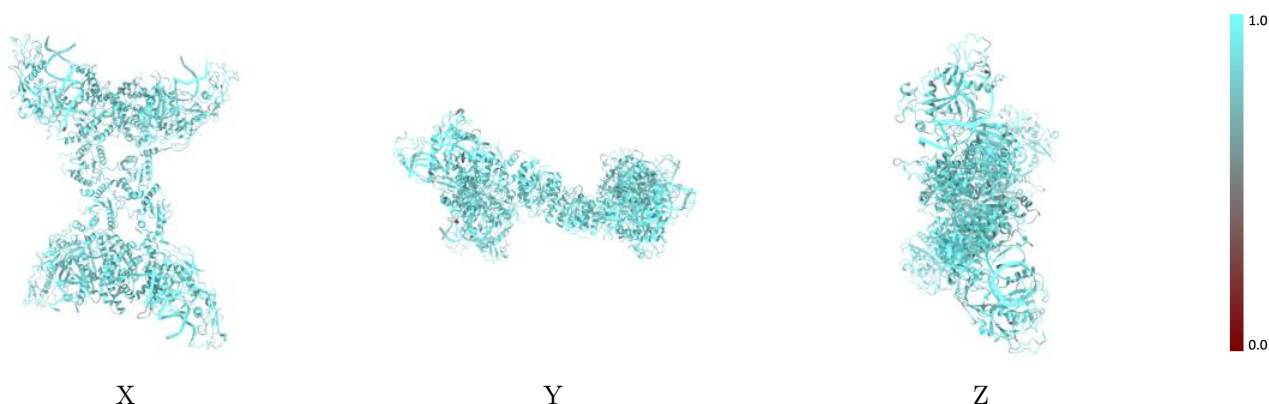
The images above show the 3D surface view of the map at the recommended contour level 0.564 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



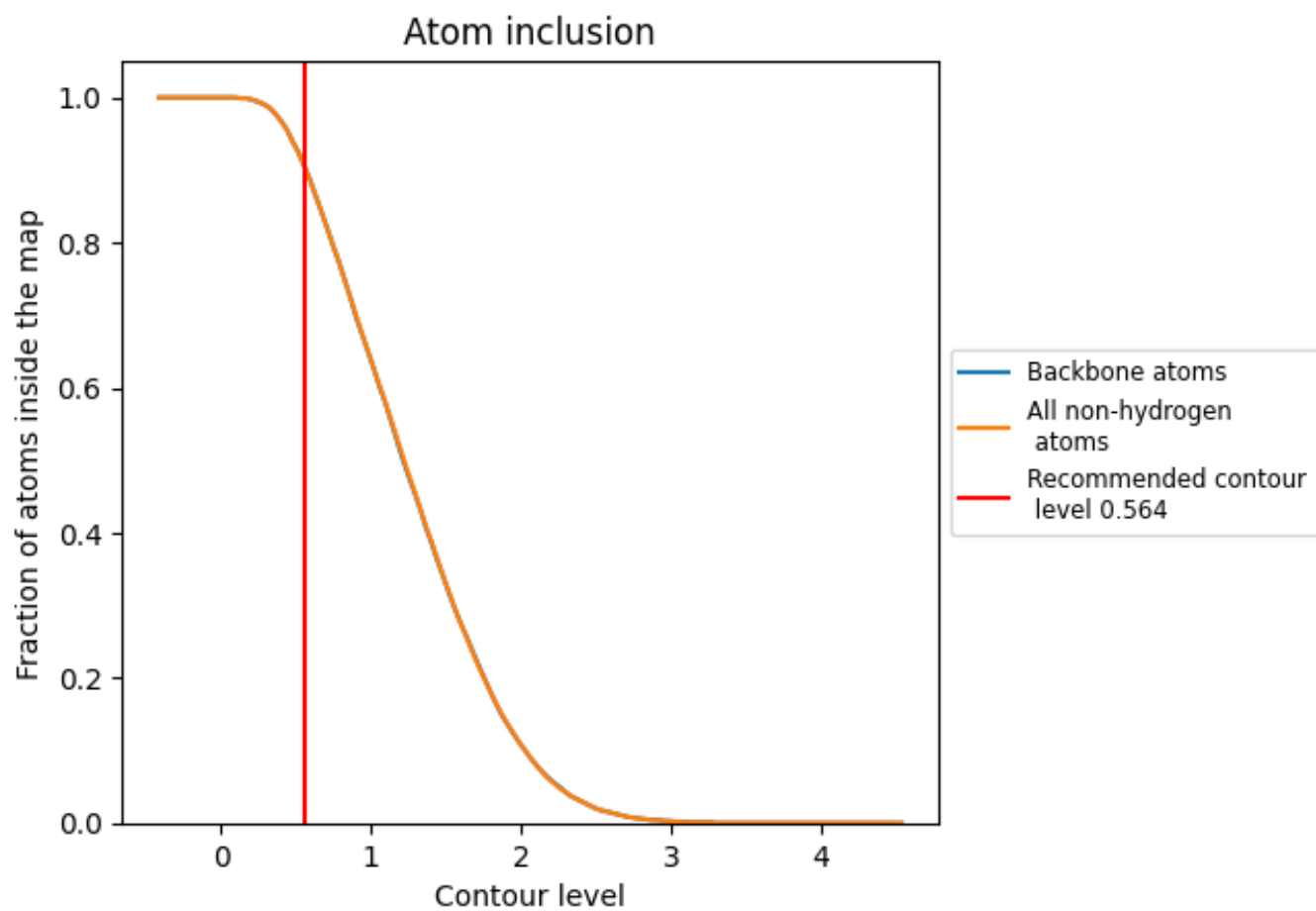
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.564).



































9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 90% 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 (0.564) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9020	 0.5330
B	 0.8820	 0.5110
C	 0.8950	 0.5410
D	 0.9040	 0.5310
E	 0.9240	 0.5580
F	 0.8820	 0.5090
G	 0.9020	 0.5370
H	 0.9070	 0.5270
I	 0.9030	 0.5520
M	 0.9710	 0.5540
N	 0.9390	 0.5310
S	 0.9680	 0.5540
T	 0.9330	 0.5250
U	 0.9470	 0.5280
V	 0.8910	 0.5110
X	 0.9660	 0.5350
Y	 0.8660	 0.4750

