Full wwPDB EM Validation Report ⓘ

Nov 22, 2022 – 04:03 AM EST

PDB ID	:	7SVW
EMDB ID	:	EMD-25455
Title	:	Strand-transfer complex of TnsB from ShCAST
Authors	:	Park, J.; Tsai, A.W.T.; Kellogg, E.H.
Deposited on	:	2021-11-19
Resolution	:	3.69 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:

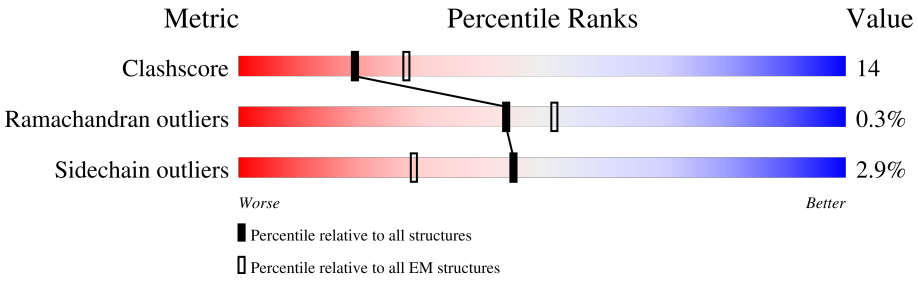
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

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 3.69 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 <=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	1	70	37% 34% 29%
1	4	70	37% 34% 29%
2	2	45	33% 33% 33%
2	5	45	29% 36% 33%
3	3	20	15% 35% 40% 25%
3	6	20	15% 35% 40% 25%
4	A	584	43% 6% 49%
4	B	584	64% 11% 24%

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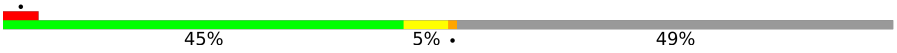
Mol	Chain	Length	Quality of chain
4	C	584	
4	D	584	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 15830 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 DNA chain called STC_LE_For.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	50	Total	C	N	O	P	0	0
			1021	487	188	297	49		
1	4	50	Total	C	N	O	P	0	0
			1021	487	188	297	49		

- Molecule 2 is a DNA chain called STC_LE_Rev1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	30	Total	C	N	O	P	0	0
			615	295	110	181	29		
2	5	30	Total	C	N	O	P	0	0
			615	295	110	181	29		

- Molecule 3 is a DNA chain called STC_LE_Rev2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	15	Total	C	N	O	P	0	0
			301	145	56	86	14		
3	6	15	Total	C	N	O	P	0	0
			301	145	56	86	14		

- Molecule 4 is a protein called TnsB.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	296	Total	C	N	O	S	0	0
			2382	1494	433	445	10		
4	B	446	Total	C	N	O	S	0	0
			3595	2254	659	670	12		
4	C	296	Total	C	N	O	S	0	0
			2382	1494	433	445	10		
4	D	446	Total	C	N	O	S	0	0
			3595	2254	659	670	12		

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

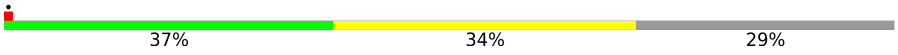
Mol	Chain	Residues	Atoms	AltConf
5	B	1	Total Mg 1 1	0
5	D	1	Total Mg 1 1	0

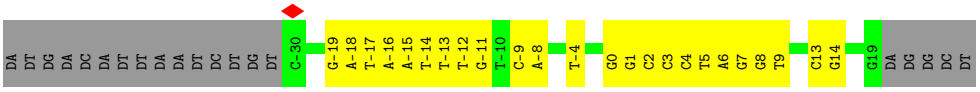
3 Residue-property plots (i)

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: STC_LE_For

Chain 1:



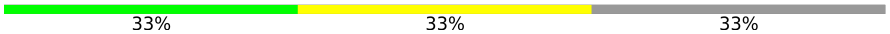


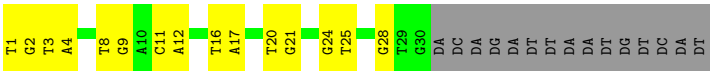
• Molecule 1: STC_LE_For

Chain 4:

• Molecule 2: STC_LE_Rev1

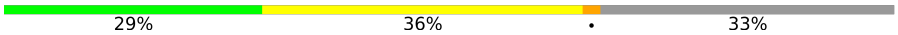
Chain 2:





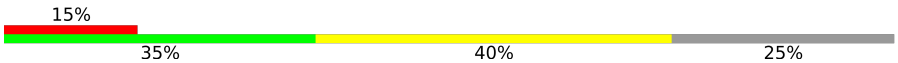
• Molecule 2: STC_LE_Rev1

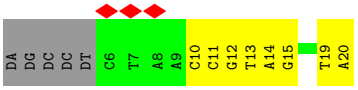
Chain 5:



• Molecule 3: STC_LE_Rev2

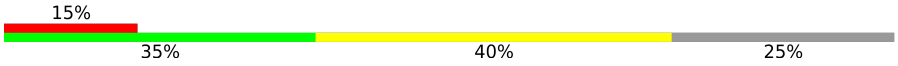
Chain 3:

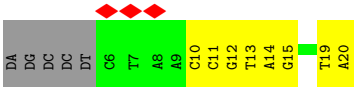




• Molecule 3: STC_LE_Rev2

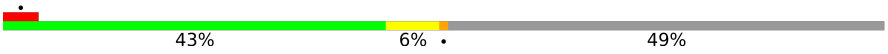
Chain 6:

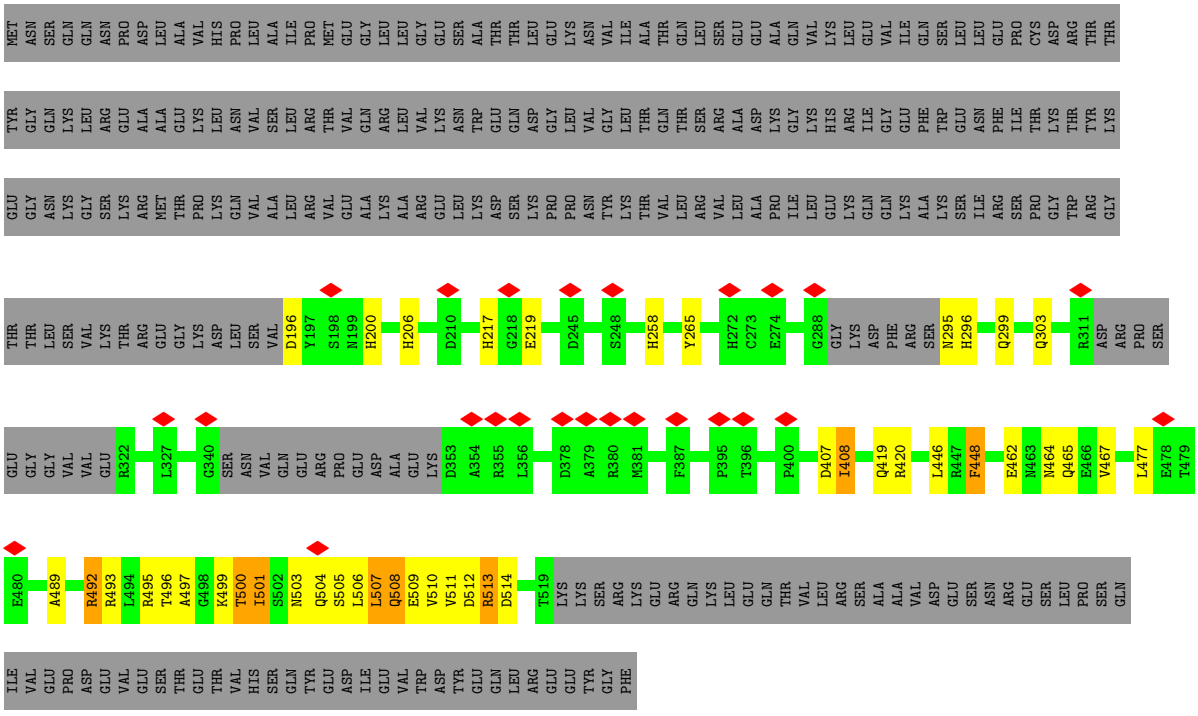




• Molecule 4: TnsB

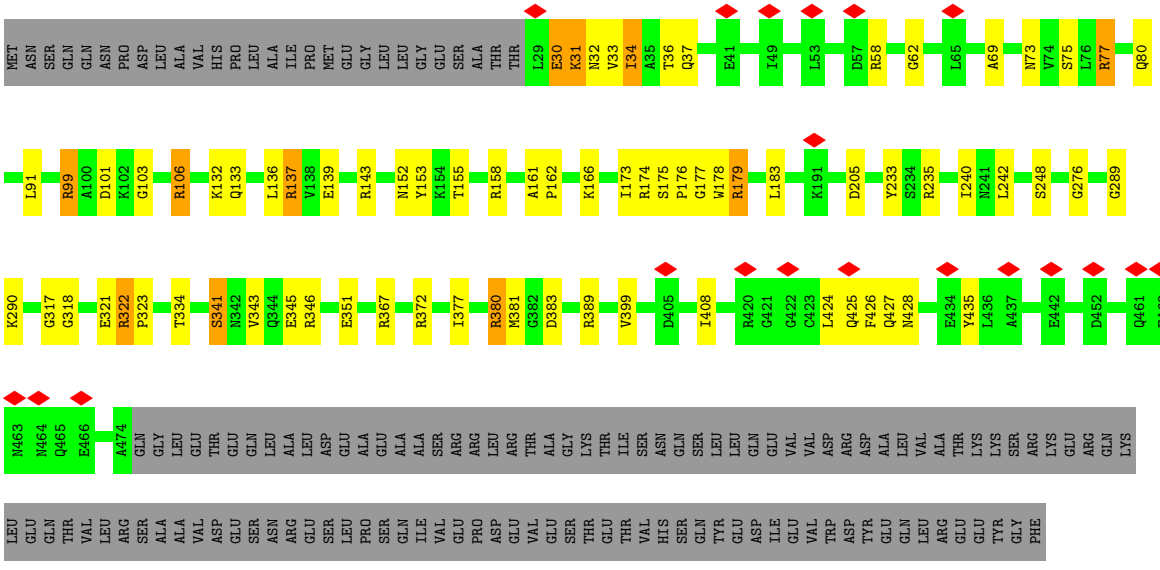
Chain A:





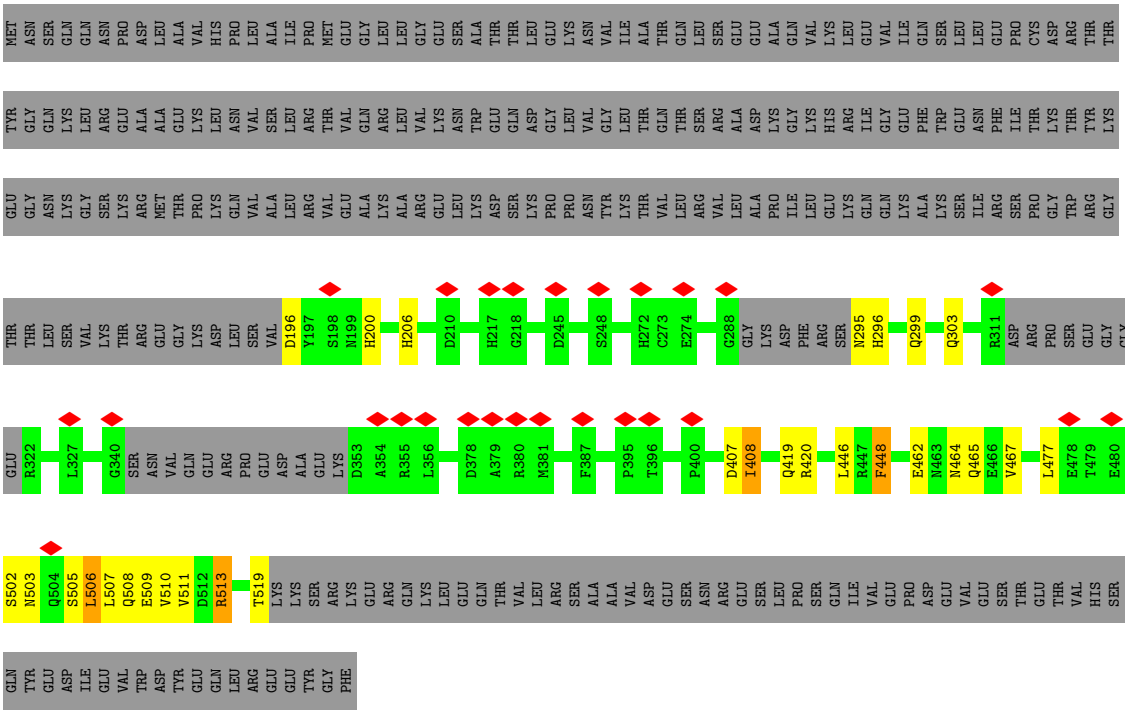
• Molecule 4: TnsB

Chain B:



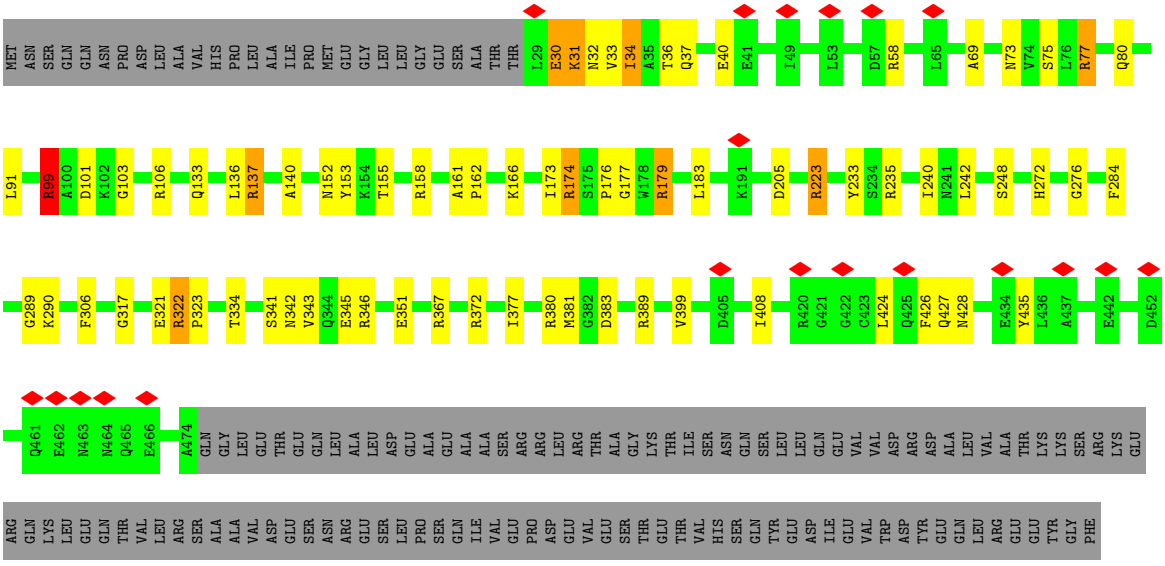
• Molecule 4: TnsB

Chain C:



• Molecule 4: TnsB

Chain D:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	46568	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	49	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.107	Depositor
Minimum map value	-0.063	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.017	Depositor
Map size (Å)	399.0, 399.0, 399.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.33, 1.33, 1.33	Depositor

5 Model quality

5.1 Standard geometry

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	1	0.49	0/1145	0.88	0/1765
1	4	0.48	0/1145	0.88	0/1765
2	2	0.52	0/689	0.92	0/1063
2	5	0.58	1/689 (0.1%)	0.90	0/1063
3	3	0.47	0/337	0.84	0/517
3	6	0.47	0/337	0.83	0/517
4	A	0.73	0/2428	0.79	0/3289
4	B	0.81	0/3665	0.73	2/4952 (0.0%)
4	C	0.74	0/2428	0.79	0/3289
4	D	0.80	0/3665	0.72	2/4952 (0.0%)
All	All	0.72	1/16528 (0.0%)	0.79	4/23172 (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
4	A	0	2
4	B	0	3
4	C	0	2
4	D	0	4
All	All	0	11

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	5	3	DT	O3'-P	-5.32	1.54	1.61

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	317	GLY	N-CA-C	-5.79	98.62	113.10
4	D	317	GLY	N-CA-C	-5.79	98.63	113.10
4	B	276	GLY	N-CA-C	5.18	126.05	113.10
4	D	276	GLY	N-CA-C	5.18	126.04	113.10

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	A	206	HIS	Mainchain
4	A	448	PHE	Mainchain
4	B	166	LYS	Mainchain
4	B	380	ARG	Sidechain
4	B	389	ARG	Mainchain
4	C	206	HIS	Mainchain
4	C	448	PHE	Mainchain
4	D	106	ARG	Sidechain
4	D	166	LYS	Mainchain
4	D	389	ARG	Mainchain
4	D	99	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	1	1021	0	564	35	0
1	4	1021	0	564	34	0
2	2	615	0	342	40	0
2	5	615	0	342	40	0
3	3	301	0	169	13	0
3	6	301	0	169	12	0
4	A	2382	0	2337	80	0
4	B	3595	0	3601	182	0
4	C	2382	0	2337	79	0
4	D	3595	0	3603	141	0
5	B	1	0	0	0	0
5	D	1	0	0	0	0
All	All	15830	0	14028	425	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 14.

All (425) 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)
4:A:420:ARG:CG	4:B:173:ILE:HG21	1.13	1.61
4:C:420:ARG:CG	4:D:173:ILE:HG21	1.14	1.57
4:A:420:ARG:HG3	4:B:173:ILE:CG2	1.10	1.56
4:C:420:ARG:HG3	4:D:173:ILE:CG2	1.11	1.54
4:A:501:ILE:CD1	4:B:377:ILE:HD11	1.38	1.49
4:C:509:GLU:OE1	4:D:272:HIS:NE2	1.59	1.34
4:A:501:ILE:HD11	4:B:377:ILE:CD1	1.61	1.28
4:C:501:ILE:HD11	4:D:383:ASP:OD1	1.32	1.24
4:C:507:LEU:CD1	4:D:372:ARG:HD2	1.67	1.23
2:5:6:DA:C2'	4:B:132:LYS:HD2	1.78	1.12
2:5:6:DA:H3'	4:B:132:LYS:HD3	1.12	1.11
4:C:510:VAL:HA	4:D:367:ARG:HH12	0.96	1.11
4:A:299:GLN:NE2	4:B:37:GLN:OE1	1.84	1.11
2:5:6:DA:C3'	4:B:132:LYS:HD3	1.82	1.09
2:5:6:DA:H2'	4:B:132:LYS:HD2	1.30	1.09
4:A:420:ARG:HG2	4:B:173:ILE:HG21	1.14	1.09
4:C:299:GLN:NE2	4:D:37:GLN:OE1	1.85	1.09
4:B:205:ASP:OD2	4:B:321:GLU:OE2	1.70	1.09
4:A:501:ILE:CD1	4:B:377:ILE:CD1	2.25	1.08
4:B:143:ARG:NE	4:C:508:GLN:OE1	1.86	1.08
4:C:420:ARG:HG3	4:D:173:ILE:HG22	1.17	1.08
4:C:420:ARG:CG	4:D:173:ILE:CG2	1.91	1.08
4:C:420:ARG:HG2	4:D:173:ILE:HG21	1.16	1.07
4:D:205:ASP:OD2	4:D:321:GLU:OE2	1.70	1.07
4:A:510:VAL:HA	4:B:367:ARG:HH12	0.93	1.07
4:A:420:ARG:HG3	4:B:173:ILE:HG22	1.15	1.06
2:2:1:DT:H2'	4:B:177:GLY:O	1.53	1.06
4:B:77:ARG:HH11	4:B:77:ARG:HB2	1.17	1.05
4:A:510:VAL:HA	4:B:367:ARG:NH1	1.72	1.04
2:2:1:DT:C6	4:B:178:TRP:HA	1.93	1.04
4:C:510:VAL:HA	4:D:367:ARG:NH1	1.73	1.03
4:A:504:GLN:HG3	4:A:505:SER:H	1.19	1.03
2:5:6:DA:H3'	4:B:132:LYS:CD	1.88	1.03
1:4:-23:DG:O6	4:B:77:ARG:NH2	1.90	1.02
4:A:420:ARG:CG	4:B:173:ILE:CG2	1.90	1.02
4:A:501:ILE:HD12	4:B:377:ILE:HD11	1.38	1.02
4:C:507:LEU:O	4:C:510:VAL:HG12	1.59	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:16:DT:O2	4:D:99:ARG:NH1	1.92	1.01
3:3:13:DT:P	4:D:428:ASN:HD21	1.83	1.00
4:C:507:LEU:CD1	4:D:372:ARG:CD	2.38	1.00
2:5:6:DA:H2'	4:B:132:LYS:CD	1.93	0.99
2:2:28:DG:H21	4:D:58:ARG:NH1	1.62	0.97
2:5:6:DA:O5'	4:B:132:LYS:NZ	1.98	0.97
4:C:501:ILE:CD1	4:D:383:ASP:OD1	2.11	0.97
1:4:7:DG:H21	4:B:290:LYS:HG3	1.27	0.96
4:C:507:LEU:HD11	4:D:372:ARG:HD2	1.48	0.95
2:5:6:DA:C2'	4:B:132:LYS:CD	2.44	0.95
2:2:1:DT:C2'	4:B:177:GLY:O	2.15	0.95
4:A:492:ARG:HH11	4:A:492:ARG:HG3	1.34	0.93
1:4:7:DG:N2	4:B:290:LYS:HG3	1.84	0.93
2:5:6:DA:OP2	4:B:132:LYS:NZ	2.01	0.92
4:B:77:ARG:O	4:B:80:GLN:OE1	1.88	0.92
2:5:1:DT:H2"	4:D:177:GLY:O	1.70	0.91
4:A:501:ILE:HD11	4:B:377:ILE:HD11	0.92	0.91
4:A:511:VAL:HG21	4:D:136:LEU:CD2	2.02	0.90
2:2:21:DG:P	4:D:75:SER:HG	1.94	0.89
2:5:6:DA:P	4:B:132:LYS:NZ	2.46	0.89
4:A:467:VAL:HG22	4:B:33:VAL:HG13	1.55	0.88
4:C:467:VAL:HG22	4:D:33:VAL:HG13	1.54	0.88
4:B:136:LEU:CD2	4:C:511:VAL:HG21	2.04	0.87
4:C:507:LEU:HD11	4:D:372:ARG:CD	2.01	0.87
4:C:507:LEU:HD12	4:D:372:ARG:HD2	1.54	0.87
4:D:77:ARG:HG3	4:D:77:ARG:HH11	1.37	0.86
4:B:99:ARG:HG3	4:B:99:ARG:HH11	1.39	0.86
2:5:6:DA:C3'	4:B:132:LYS:CD	2.48	0.86
2:2:3:DT:P	4:B:380:ARG:HH22	2.00	0.85
4:A:504:GLN:HG3	4:A:505:SER:N	1.91	0.85
4:B:132:LYS:HG2	4:B:153:TYR:CZ	2.12	0.84
4:A:420:ARG:HD2	4:B:173:ILE:HB	1.59	0.84
1:4:-15:DA:N3	4:B:99:ARG:NH1	2.25	0.83
4:B:77:ARG:HH11	4:B:77:ARG:CB	1.90	0.83
4:C:507:LEU:HD13	4:D:372:ARG:HG3	1.60	0.83
2:5:7:DG:OP2	4:B:132:LYS:HG3	1.79	0.83
1:1:7:DG:H21	4:D:290:LYS:HG3	1.44	0.83
2:2:2:DG:OP1	4:B:175:SER:OG	1.97	0.82
4:C:420:ARG:HD2	4:D:173:ILE:HB	1.60	0.82
2:5:23:DC:H42	4:B:77:ARG:HH22	1.29	0.80
4:A:497:ALA:O	4:A:500:THR:HG23	1.80	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:503:ASN:OD1	4:A:503:ASN:O	1.99	0.80
4:C:509:GLU:CD	4:D:272:HIS:NE2	2.35	0.80
2:2:17:DA:O4'	4:D:99:ARG:NH2	2.16	0.79
4:A:511:VAL:HG21	4:D:136:LEU:HD22	1.65	0.79
3:3:13:DT:OP1	4:D:428:ASN:ND2	2.16	0.79
2:2:28:DG:H21	4:D:58:ARG:HH12	1.26	0.78
1:1:3:DC:H5	4:B:351:GLU:OE2	1.66	0.78
1:1:-12:DT:H73	4:D:158:ARG:NH1	1.99	0.78
4:B:322:ARG:HD2	4:B:322:ARG:O	1.84	0.78
2:2:28:DG:N2	4:D:58:ARG:HH12	1.82	0.77
4:A:303:GLN:HB2	4:B:91:LEU:CD1	2.14	0.77
4:B:136:LEU:HD21	4:C:511:VAL:HG21	1.66	0.77
1:4:-12:DT:H73	4:B:158:ARG:NH1	1.99	0.77
2:5:28:DG:H21	4:B:58:ARG:NH1	1.82	0.77
4:C:303:GLN:HB2	4:D:91:LEU:CD1	2.15	0.77
4:A:462:GLU:HB2	4:A:465:GLN:HG3	1.65	0.77
4:A:477:LEU:H	4:A:477:LEU:HD23	1.49	0.77
4:C:462:GLU:HB2	4:C:465:GLN:HG3	1.65	0.76
4:A:511:VAL:HG21	4:D:136:LEU:HD21	1.67	0.76
1:4:3:DC:H5	4:D:351:GLU:OE2	1.69	0.76
4:A:464:ASN:C	4:B:36:THR:OG1	2.24	0.76
4:C:501:ILE:HD11	4:D:383:ASP:CG	2.07	0.76
1:4:7:DG:H21	4:B:290:LYS:CG	1.98	0.75
4:C:464:ASN:C	4:D:36:THR:OG1	2.25	0.75
2:5:1:DT:HO5'	2:5:1:DT:H6	1.33	0.75
4:A:219:GLU:OE1	4:A:492:ARG:NH2	2.18	0.75
4:B:77:ARG:HB2	4:B:77:ARG:NH1	2.00	0.75
4:D:322:ARG:HD2	4:D:322:ARG:O	1.86	0.75
4:A:492:ARG:HG3	4:A:492:ARG:NH1	2.00	0.75
4:C:477:LEU:H	4:C:477:LEU:HD23	1.49	0.75
4:C:507:LEU:HD11	4:D:372:ARG:NE	2.02	0.75
2:2:21:DG:P	4:D:75:SER:OG	2.44	0.74
2:5:21:DG:P	4:B:75:SER:OG	2.46	0.74
3:6:20:DA:H5'	4:B:289:GLY:CA	2.17	0.74
2:2:28:DG:N2	4:D:58:ARG:NH1	2.36	0.74
4:B:143:ARG:HE	4:C:508:GLN:CD	1.92	0.73
1:1:7:DG:N2	4:D:290:LYS:HG3	2.03	0.73
4:A:217:HIS:CE1	4:A:493:ARG:HE	2.06	0.73
4:D:80:GLN:N	4:D:80:GLN:OE1	2.21	0.73
4:B:99:ARG:HG3	4:B:99:ARG:NH1	1.99	0.73
1:1:-14:DT:H5'	4:D:99:ARG:HB2	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:1:DT:C2'	4:D:177:GLY:O	2.37	0.73
4:B:136:LEU:HD22	4:C:511:VAL:HG21	1.70	0.73
1:1:3:DC:C5	4:B:351:GLU:OE2	2.42	0.72
1:4:3:DC:C5	4:D:351:GLU:OE2	2.41	0.72
2:2:21:DG:OP2	4:D:75:SER:OG	2.08	0.72
4:C:510:VAL:CA	4:D:367:ARG:HH12	1.88	0.72
4:B:322:ARG:HD2	4:B:322:ARG:C	2.09	0.72
4:C:407:ASP:O	4:D:34:ILE:HD12	1.90	0.72
4:B:80:GLN:OE1	4:B:80:GLN:N	2.21	0.72
4:C:303:GLN:OE1	4:D:91:LEU:HD12	1.90	0.71
4:A:496:THR:O	4:A:500:THR:HG22	1.90	0.71
4:A:407:ASP:O	4:B:34:ILE:HD12	1.90	0.71
4:A:497:ALA:O	4:B:383:ASP:OD1	2.07	0.71
4:A:510:VAL:CA	4:B:367:ARG:HH12	1.87	0.70
2:2:4:DA:OP2	4:B:380:ARG:NH1	2.23	0.70
4:A:303:GLN:OE1	4:B:91:LEU:HD12	1.90	0.70
4:C:420:ARG:CD	4:D:173:ILE:CG2	2.70	0.69
2:5:21:DG:OP2	4:B:75:SER:OG	2.10	0.69
2:5:23:DC:N4	4:B:77:ARG:HH22	1.91	0.69
4:A:420:ARG:CD	4:B:173:ILE:CG2	2.69	0.69
4:C:510:VAL:HG13	4:C:511:VAL:N	2.08	0.68
3:6:12:DG:O3'	4:B:428:ASN:OD1	2.10	0.68
4:C:507:LEU:O	4:C:510:VAL:CG1	2.40	0.68
4:C:507:LEU:HD13	4:D:372:ARG:CG	2.23	0.68
4:A:489:ALA:HA	4:A:492:ARG:HD3	1.76	0.68
2:2:1:DT:H72	4:B:178:TRP:HB3	1.73	0.68
3:3:20:DA:H5'	4:D:289:GLY:CA	2.24	0.68
4:A:507:LEU:CD1	4:B:372:ARG:HD2	2.24	0.68
4:A:408:ILE:HD13	4:A:408:ILE:H	1.60	0.67
4:A:303:GLN:OE1	4:A:408:ILE:HG21	1.96	0.66
4:C:408:ILE:HD13	4:C:408:ILE:H	1.60	0.66
4:D:152:ASN:OD1	4:D:153:TYR:N	2.28	0.66
4:A:501:ILE:HD11	4:B:377:ILE:HD12	1.74	0.66
4:C:303:GLN:OE1	4:C:408:ILE:HG21	1.96	0.66
2:5:6:DA:P	4:B:132:LYS:HZ3	2.12	0.66
2:2:1:DT:H6	4:B:178:TRP:HA	1.57	0.65
4:B:143:ARG:CD	4:C:508:GLN:OE1	2.44	0.65
4:B:152:ASN:OD1	4:B:153:TYR:N	2.28	0.65
4:D:322:ARG:HD2	4:D:322:ARG:C	2.11	0.65
1:1:2:DC:C4	4:B:343:VAL:CG2	2.80	0.64
4:B:30:GLU:HG2	4:B:31:LYS:HG2	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:34:ILE:HG12	4:B:34:ILE:O	1.97	0.64
1:1:2:DC:N3	4:B:343:VAL:HG21	2.12	0.64
2:5:1:DT:H1'	4:D:177:GLY:O	1.98	0.64
4:D:77:ARG:HG3	4:D:77:ARG:NH1	2.10	0.64
2:2:3:DT:OP1	4:B:380:ARG:NH2	2.31	0.63
2:5:1:DT:H6	2:5:1:DT:O5'	1.81	0.63
1:1:2:DC:C4	4:B:343:VAL:HG21	2.34	0.63
1:4:2:DC:H3'	4:D:346:ARG:HH12	1.63	0.63
4:D:30:GLU:HG2	4:D:31:LYS:HG2	1.80	0.63
2:5:6:DA:P	4:B:132:LYS:HZ1	2.12	0.62
3:6:12:DG:C3'	4:B:428:ASN:OD1	2.48	0.62
4:D:34:ILE:HG12	4:D:34:ILE:O	1.97	0.62
1:4:-15:DA:C2	4:B:99:ARG:NH2	2.67	0.62
4:B:341:SER:OG	4:B:345:GLU:OE2	2.16	0.62
1:4:-12:DT:C7	4:B:158:ARG:NH1	2.63	0.62
2:2:1:DT:C5	4:B:178:TRP:HA	2.19	0.61
4:D:322:ARG:HB3	4:D:323:PRO:HD3	1.81	0.61
4:C:509:GLU:HG2	4:D:367:ARG:HH22	1.65	0.61
1:1:-14:DT:H5'	4:D:99:ARG:CB	2.31	0.61
4:A:501:ILE:HD12	4:B:377:ILE:CD1	2.13	0.60
1:1:-12:DT:C7	4:D:158:ARG:NH1	2.65	0.60
4:A:511:VAL:HG13	4:D:137:ARG:NH2	2.16	0.60
4:C:507:LEU:HD13	4:D:372:ARG:CD	2.30	0.60
4:A:510:VAL:HG22	4:B:367:ARG:NH1	2.17	0.59
2:5:17:DA:H5'	4:B:101:ASP:OD2	2.02	0.59
4:A:508:GLN:HG3	4:D:140:ALA:HA	1.84	0.59
4:B:334:THR:CG2	4:D:133:GLN:HE22	2.15	0.59
3:3:12:DG:OP1	4:D:426:PHE:O	2.21	0.59
2:5:1:DT:C1'	4:D:177:GLY:O	2.50	0.59
4:B:132:LYS:CG	4:B:153:TYR:OH	2.50	0.59
4:A:303:GLN:HB2	4:B:91:LEU:HD11	1.83	0.59
4:B:36:THR:HG22	4:B:37:GLN:N	2.18	0.59
4:B:334:THR:CG2	4:D:133:GLN:NE2	2.66	0.59
1:4:2:DC:H3'	4:D:346:ARG:NH1	2.18	0.59
4:C:303:GLN:HB2	4:D:91:LEU:HD11	1.84	0.59
1:1:2:DC:H3'	4:B:346:ARG:HH12	1.67	0.58
1:4:-17:DT:H2"	1:4:-16:DA:C8	2.38	0.58
4:B:179:ARG:HA	4:B:179:ARG:NE	2.17	0.58
4:B:106:ARG:HH11	4:B:106:ARG:CG	2.16	0.58
4:D:399:VAL:HG13	4:D:399:VAL:O	2.03	0.58
4:D:174:ARG:O	4:D:174:ARG:HG2	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:179:ARG:HA	4:D:179:ARG:NE	2.17	0.57
1:1:-17:DT:H2”	1:1:-16:DA:C8	2.38	0.57
2:2:2:DG:H5”	4:B:178:TRP:HE1	1.68	0.57
4:B:399:VAL:O	4:B:399:VAL:HG13	2.03	0.57
4:D:36:THR:HG22	4:D:37:GLN:N	2.18	0.57
1:1:13:DC:H2”	1:1:14:DG:N7	2.19	0.57
4:A:507:LEU:HD11	4:B:372:ARG:CD	2.35	0.57
1:4:13:DC:H2”	1:4:14:DG:N7	2.20	0.56
4:A:477:LEU:H	4:A:477:LEU:CD2	2.18	0.56
4:A:446:LEU:HD12	4:A:446:LEU:O	2.05	0.56
4:C:446:LEU:HD12	4:C:446:LEU:O	2.05	0.56
2:2:17:DA:H5’	4:D:101:ASP:OD2	2.06	0.56
4:B:133:GLN:HE22	4:D:334:THR:CG2	2.18	0.56
4:C:519:THR:O	4:C:519:THR:HG22	2.03	0.56
1:1:7:DG:H2’	1:1:8:DG:C8	2.41	0.56
4:A:507:LEU:HD13	4:B:372:ARG:HD2	1.87	0.56
2:2:3:DT:H3’	4:B:380:ARG:HH12	1.71	0.56
1:4:5:DT:H2”	1:4:6:DA:C8	2.42	0.56
3:3:13:DT:P	4:D:428:ASN:ND2	2.66	0.55
1:1:7:DG:H21	4:D:290:LYS:CG	2.16	0.55
4:B:343:VAL:HG22	4:B:343:VAL:O	2.06	0.55
4:B:133:GLN:NE2	4:D:334:THR:CG2	2.70	0.55
4:C:477:LEU:H	4:C:477:LEU:CD2	2.18	0.55
1:4:7:DG:H2’	1:4:8:DG:C8	2.42	0.55
2:5:6:DA:O5’	4:B:132:LYS:CE	2.54	0.55
2:2:1:DT:C5’	2:2:1:DT:O2	2.55	0.55
4:B:77:ARG:HH11	4:B:77:ARG:CG	2.18	0.55
1:4:-11:DG:OP2	4:B:155:THR:OG1	2.22	0.55
4:A:497:ALA:O	4:A:500:THR:CG2	2.54	0.54
1:1:5:DT:H2”	1:1:6:DA:C8	2.43	0.54
4:A:508:GLN:HG3	4:D:140:ALA:CB	2.37	0.54
3:6:12:DG:OP1	4:B:425:GLN:HB3	2.08	0.54
1:4:-13:DT:OP1	4:B:103:GLY:N	2.23	0.53
1:4:-15:DA:N3	4:B:99:ARG:CZ	2.71	0.53
4:A:462:GLU:HB2	4:A:465:GLN:CG	2.37	0.53
4:C:510:VAL:CG1	4:C:511:VAL:N	2.72	0.53
2:2:1:DT:H72	4:B:178:TRP:CB	2.29	0.53
2:2:17:DA:C1’	4:D:99:ARG:HH22	2.21	0.53
4:A:420:ARG:CG	4:B:173:ILE:CB	2.81	0.53
1:1:2:DC:H3’	4:B:346:ARG:NH1	2.25	0.52
2:2:1:DT:C4	4:B:178:TRP:CE3	2.98	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:4:-9:DC:H2"	1:4:-8:DA:C8	2.44	0.52
4:A:303:GLN:CD	4:A:408:ILE:HG21	2.30	0.52
3:3:12:DG:O3'	4:D:428:ASN:OD1	2.28	0.52
4:C:303:GLN:CD	4:C:408:ILE:HG21	2.30	0.52
1:1:-9:DC:H2"	1:1:-8:DA:C8	2.44	0.51
4:B:106:ARG:CG	4:B:106:ARG:NH1	2.73	0.51
4:B:132:LYS:CG	4:B:153:TYR:CZ	2.89	0.51
4:A:407:ASP:OD2	4:B:32:ASN:ND2	2.43	0.51
4:A:509:GLU:HA	4:A:509:GLU:OE1	2.09	0.51
4:B:132:LYS:HG3	4:B:153:TYR:HH	1.75	0.51
4:C:506:LEU:N	4:C:506:LEU:CD1	2.73	0.51
2:5:6:DA:H8	4:B:132:LYS:NZ	2.08	0.51
1:4:8:DG:H2'	1:4:9:DT:C6	2.46	0.51
4:B:99:ARG:HH11	4:B:99:ARG:CG	2.13	0.51
4:C:501:ILE:HD12	4:C:501:ILE:H	1.75	0.51
3:3:19:DT:H2"	3:3:20:DA:C8	2.46	0.51
4:A:508:GLN:HG3	4:D:140:ALA:CA	2.41	0.51
1:1:8:DG:H2'	1:1:9:DT:C6	2.46	0.50
3:3:12:DG:C3'	4:D:428:ASN:OD1	2.60	0.50
4:C:407:ASP:OD2	4:D:32:ASN:ND2	2.42	0.50
4:C:507:LEU:HD11	4:D:372:ARG:CZ	2.41	0.50
4:A:503:ASN:ND2	4:A:507:LEU:HB2	2.26	0.50
4:C:462:GLU:HB2	4:C:465:GLN:CG	2.37	0.50
2:2:1:DT:O2	2:2:1:DT:O4'	2.30	0.50
1:4:7:DG:H4'	4:B:248:SER:OG	2.11	0.50
2:5:6:DA:H2'	4:B:132:LYS:NZ	2.26	0.50
4:B:322:ARG:HB3	4:B:323:PRO:HD3	1.92	0.50
4:C:420:ARG:HD2	4:D:173:ILE:CB	2.36	0.50
4:C:420:ARG:CG	4:D:173:ILE:CB	2.83	0.50
4:A:508:GLN:CG	4:D:140:ALA:HA	2.42	0.50
4:C:419:GLN:OE1	4:D:176:PRO:HB3	2.11	0.49
4:C:196:ASP:N	4:C:200:HIS:HD1	2.10	0.49
3:6:19:DT:H2"	3:6:20:DA:C8	2.48	0.49
4:A:419:GLN:OE1	4:B:176:PRO:HB3	2.12	0.49
4:A:508:GLN:HG3	4:D:140:ALA:HB2	1.94	0.49
4:B:77:ARG:NH1	4:B:77:ARG:CG	2.74	0.49
1:1:0:DG:H2'	1:1:1:DG:C8	2.47	0.49
4:A:508:GLN:N	4:A:508:GLN:OE1	2.46	0.49
4:B:137:ARG:CZ	4:C:511:VAL:CG1	2.90	0.49
4:C:446:LEU:HD12	4:C:446:LEU:C	2.33	0.49
4:D:408:ILE:C	4:D:408:ILE:HD12	2.33	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:6:20:DA:H5'	4:B:289:GLY:HA3	1.94	0.49
4:A:446:LEU:HD12	4:A:446:LEU:C	2.33	0.49
4:B:318:GLY:O	4:B:322:ARG:HB2	2.12	0.49
3:3:12:DG:H4'	4:D:428:ASN:OD1	2.12	0.49
4:A:420:ARG:HD2	4:B:173:ILE:CB	2.35	0.49
4:B:143:ARG:HD2	4:C:508:GLN:OE1	2.13	0.49
1:4:0:DG:H2'	1:4:1:DG:C8	2.47	0.48
1:1:2:DC:C4	4:B:343:VAL:HG23	2.48	0.48
4:B:132:LYS:HG3	4:B:153:TYR:OH	2.13	0.48
4:A:196:ASP:N	4:A:200:HIS:HD1	2.10	0.48
4:B:408:ILE:C	4:B:408:ILE:HD12	2.33	0.48
4:C:501:ILE:HG12	4:D:377:ILE:HD11	1.94	0.48
2:2:3:DT:OP2	4:B:178:TRP:HD1	1.95	0.48
3:3:11:DC:H2"	3:3:12:DG:C8	2.49	0.48
4:A:513:ARG:HD2	4:A:513:ARG:HA	1.48	0.48
4:B:161:ALA:N	4:B:162:PRO:HD2	2.29	0.48
2:2:16:DT:H2"	2:2:17:DA:N7	2.29	0.47
3:6:11:DC:H2"	3:6:12:DG:C8	2.49	0.47
1:4:-12:DT:C5	4:B:158:ARG:NH1	2.82	0.47
3:6:13:DT:P	4:B:428:ASN:HD21	2.37	0.47
4:D:161:ALA:N	4:D:162:PRO:HD2	2.29	0.47
3:3:14:DA:H2"	3:3:15:DG:H8	1.79	0.47
3:6:13:DT:P	4:B:428:ASN:OD1	2.73	0.47
4:B:183:LEU:HD23	4:B:183:LEU:N	2.30	0.47
4:B:242:LEU:HD23	4:B:242:LEU:H	1.80	0.47
2:5:16:DT:H2"	2:5:17:DA:N7	2.29	0.47
4:B:139:GLU:HG2	4:C:508:GLN:HE21	1.80	0.47
4:C:507:LEU:CD1	4:D:372:ARG:CG	2.85	0.47
4:D:342:ASN:HB3	4:D:343:VAL:H	1.57	0.47
1:4:7:DG:H4'	4:B:248:SER:HG	1.79	0.47
1:1:-17:DT:H2"	1:1:-16:DA:N7	2.30	0.47
1:4:-17:DT:H2"	1:4:-16:DA:N7	2.30	0.47
4:D:77:ARG:NH1	4:D:77:ARG:CG	2.73	0.47
4:D:183:LEU:N	4:D:183:LEU:HD23	2.30	0.47
1:1:-14:DT:C5'	4:D:99:ARG:HB2	2.41	0.46
3:6:12:DG:OP1	4:B:426:PHE:O	2.32	0.46
3:6:14:DA:H2"	3:6:15:DG:H8	1.80	0.46
4:D:242:LEU:HD23	4:D:242:LEU:H	1.80	0.46
4:A:420:ARG:CG	4:B:173:ILE:HG22	2.04	0.46
4:B:137:ARG:NH1	4:C:511:VAL:HG13	2.31	0.46
4:B:426:PHE:CG	4:B:427:GLN:N	2.84	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:6:DA:H8	4:B:132:LYS:HZ2	1.63	0.46
4:C:501:ILE:HD12	4:C:501:ILE:N	2.30	0.46
2:2:2:DG:H5"	4:B:178:TRP:NE1	2.31	0.46
4:A:503:ASN:OD1	4:A:503:ASN:C	2.53	0.46
1:1:4:DC:H2'	1:1:5:DT:H71	1.98	0.46
4:A:504:GLN:CG	4:A:505:SER:N	2.63	0.46
4:A:501:ILE:H	4:A:501:ILE:HG12	1.64	0.45
4:B:137:ARG:CZ	4:C:511:VAL:HG13	2.46	0.45
1:1:-14:DT:H5'	4:D:99:ARG:HD3	1.98	0.45
1:4:3:DC:OP2	4:D:223:ARG:NH1	2.49	0.45
1:4:4:DC:H2'	1:4:5:DT:H71	1.97	0.45
4:B:106:ARG:NH1	4:B:106:ARG:HG3	2.31	0.45
2:2:28:DG:H21	4:D:58:ARG:HH11	1.55	0.45
4:A:303:GLN:HB2	4:B:91:LEU:HD12	1.97	0.45
2:5:28:DG:H21	4:B:58:ARG:HH12	1.60	0.45
1:1:7:DG:H4'	4:D:248:SER:OG	2.17	0.45
4:D:343:VAL:HG22	4:D:343:VAL:O	2.17	0.45
2:5:24:DG:H2'	2:5:25:DT:H71	1.99	0.45
4:B:161:ALA:HB3	4:B:162:PRO:CD	2.47	0.45
4:D:99:ARG:NH2	4:D:99:ARG:HG2	2.32	0.45
4:D:136:LEU:C	4:D:136:LEU:HD23	2.38	0.44
4:D:426:PHE:CG	4:D:427:GLN:N	2.84	0.44
2:2:3:DT:H2"	2:2:4:DA:C8	2.52	0.44
2:2:20:DT:H2"	2:2:21:DG:H5"	1.99	0.44
4:D:161:ALA:HB3	4:D:162:PRO:CD	2.47	0.44
1:4:-26:DG:OP1	4:B:62:GLY:CA	2.65	0.44
4:C:509:GLU:OE1	4:D:272:HIS:CD2	2.56	0.44
4:C:509:GLU:OE1	4:D:272:HIS:CE1	2.56	0.44
3:6:10:DC:H2"	3:6:11:DC:C5	2.52	0.44
4:B:242:LEU:HD23	4:B:242:LEU:N	2.32	0.44
3:3:10:DC:H2"	3:3:11:DC:C5	2.53	0.44
1:4:-16:DA:H2"	1:4:-15:DA:C8	2.53	0.44
4:D:240:ILE:C	4:D:240:ILE:HD12	2.38	0.44
4:D:322:ARG:C	4:D:322:ARG:CD	2.86	0.44
4:B:132:LYS:HG2	4:B:153:TYR:CE1	2.52	0.43
1:1:-4:DT:O4	4:B:174:ARG:HG3	2.18	0.43
4:B:424:LEU:HD12	4:B:424:LEU:C	2.38	0.43
4:D:242:LEU:HD23	4:D:242:LEU:N	2.32	0.43
4:B:136:LEU:C	4:B:136:LEU:HD23	2.38	0.43
4:D:322:ARG:HD2	4:D:322:ARG:HA	1.70	0.43
1:4:-19:DG:H2"	1:4:-18:DA:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:69:ALA:O	4:D:73:ASN:N	2.51	0.43
1:1:-16:DA:H2"	1:1:-15:DA:C8	2.53	0.43
2:2:24:DG:H2'	2:2:25:DT:H71	1.99	0.43
4:B:69:ALA:O	4:B:73:ASN:N	2.51	0.43
4:D:399:VAL:O	4:D:399:VAL:CG1	2.67	0.43
2:5:20:DT:H2"	2:5:21:DG:H5"	1.99	0.43
4:A:465:GLN:N	4:B:36:THR:OG1	2.52	0.43
1:1:-19:DG:H2"	1:1:-18:DA:C8	2.54	0.43
4:D:36:THR:CG2	4:D:37:GLN:N	2.82	0.43
4:A:295:ASN:OD1	4:A:296:HIS:N	2.52	0.43
4:B:240:ILE:C	4:B:240:ILE:HD12	2.38	0.43
1:1:-15:DA:H1'	4:D:99:ARG:HD2	2.01	0.42
1:1:-15:DA:N3	4:D:99:ARG:HD2	2.34	0.42
4:D:424:LEU:HD12	4:D:424:LEU:O	2.19	0.42
4:D:424:LEU:HD12	4:D:424:LEU:C	2.38	0.42
2:5:3:DT:H2"	2:5:4:DA:C8	2.54	0.42
4:B:424:LEU:HD12	4:B:424:LEU:O	2.19	0.42
4:C:507:LEU:HD12	4:C:510:VAL:HG11	2.01	0.42
3:3:20:DA:H5'	4:D:289:GLY:HA3	1.98	0.42
4:C:501:ILE:CG1	4:D:377:ILE:HD11	2.50	0.42
2:2:1:DT:C6	4:B:177:GLY:O	2.73	0.42
2:5:28:DG:N2	4:B:58:ARG:NH1	2.60	0.42
2:2:1:DT:H71	4:B:179:ARG:HB2	1.78	0.42
4:B:36:THR:CG2	4:B:37:GLN:N	2.82	0.42
4:C:465:GLN:N	4:D:36:THR:OG1	2.53	0.42
1:1:-11:DG:OP2	4:D:155:THR:OG1	2.30	0.42
4:C:506:LEU:HD13	4:C:506:LEU:H	1.85	0.42
2:5:8:DT:H2"	2:5:9:DG:C8	2.55	0.41
2:5:11:DC:H2"	2:5:12:DA:C8	2.55	0.41
2:5:6:DA:H2'	4:B:132:LYS:CE	2.48	0.41
4:B:322:ARG:HH11	4:B:322:ARG:CG	2.33	0.41
4:D:380:ARG:HB3	4:D:381:MET:CE	2.49	0.41
4:C:513:ARG:HA	4:C:513:ARG:HD2	1.41	0.41
4:C:503:ASN:HB2	4:C:507:LEU:H	1.86	0.41
1:4:-12:DT:C6	4:B:158:ARG:NH1	2.89	0.41
4:A:477:LEU:HD23	4:A:477:LEU:N	2.24	0.41
4:A:504:GLN:CG	4:A:505:SER:H	2.01	0.41
4:B:380:ARG:HB3	4:B:381:MET:CE	2.50	0.41
4:C:448:PHE:CD2	4:C:448:PHE:C	2.93	0.41
1:4:-15:DA:C2	4:B:99:ARG:CZ	3.03	0.41
4:C:303:GLN:HB2	4:D:91:LEU:HD12	1.98	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:-9:DC:OP2	4:A:499:LYS:NZ	2.50	0.41
2:2:1:DT:H6	4:B:177:GLY:O	2.04	0.41
2:2:11:DC:H2"	2:2:12:DA:C8	2.55	0.41
4:C:295:ASN:OD1	4:C:296:HIS:N	2.52	0.41
4:A:217:HIS:CE1	4:A:493:ARG:NE	2.82	0.41
4:A:448:PHE:CD2	4:A:448:PHE:C	2.93	0.41
4:B:334:THR:HG21	4:D:133:GLN:NE2	2.35	0.41
4:D:341:SER:N	4:D:345:GLU:OE2	2.54	0.41
1:1:-13:DT:OP1	4:D:103:GLY:N	2.28	0.41
4:B:233:TYR:O	4:B:235:ARG:NH1	2.54	0.41
1:4:-15:DA:C4	4:B:99:ARG:NH1	2.88	0.40
4:B:399:VAL:O	4:B:399:VAL:CG1	2.67	0.40
4:D:40:GLU:H	4:D:40:GLU:CD	2.24	0.40
2:5:3:DT:H6	2:5:3:DT:H2'	1.73	0.40
4:D:306:PHE:CD1	4:D:306:PHE:C	2.95	0.40
2:2:1:DT:O2	2:2:1:DT:H5"	2.21	0.40
2:2:8:DT:H2"	2:2:9:DG:C8	2.56	0.40
4:A:258:HIS:CE1	4:A:265:TYR:HH	2.39	0.40
4:D:233:TYR:O	4:D:235:ARG:NH1	2.54	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	
4	A	288/584 (49%)	276 (96%)	11 (4%)	1 (0%)	41	74
4	B	444/584 (76%)	426 (96%)	17 (4%)	1 (0%)	47	78
4	C	288/584 (49%)	275 (96%)	12 (4%)	1 (0%)	41	74
4	D	444/584 (76%)	425 (96%)	18 (4%)	1 (0%)	47	78
All	All	1464/2336 (63%)	1402 (96%)	58 (4%)	4 (0%)	44	74

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	506	LEU
4	B	435	TYR
4	D	435	TYR
4	C	499	LYS

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	
4	A	256/512 (50%)	246 (96%)	10 (4%)	32	60
4	B	391/512 (76%)	381 (97%)	10 (3%)	46	69
4	C	256/512 (50%)	250 (98%)	6 (2%)	50	71
4	D	391/512 (76%)	380 (97%)	11 (3%)	43	67
All	All	1294/2048 (63%)	1257 (97%)	37 (3%)	45	66

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	408	ILE
4	A	492	ARG
4	A	495	ARG
4	A	500	THR
4	A	501	ILE
4	A	507	LEU
4	A	508	GLN
4	A	512	ASP
4	A	513	ARG
4	A	514	ASP
4	B	30	GLU
4	B	31	LYS
4	B	34	ILE
4	B	77	ARG
4	B	99	ARG
4	B	106	ARG

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Mol	Chain	Res	Type
4	B	137	ARG
4	B	179	ARG
4	B	322	ARG
4	B	341	SER
4	C	408	ILE
4	C	500	THR
4	C	502	SER
4	C	505	SER
4	C	506	LEU
4	C	513	ARG
4	D	30	GLU
4	D	31	LYS
4	D	34	ILE
4	D	77	ARG
4	D	99	ARG
4	D	137	ARG
4	D	174	ARG
4	D	179	ARG
4	D	223	ARG
4	D	284	PHE
4	D	322	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
4	D	342	ASN
4	D	428	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

Of 2 ligands modelled in this entry, 2 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

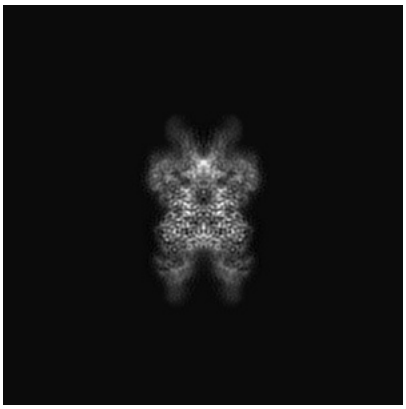
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-25455. These allow visual inspection of the internal detail of the map and identification of artifacts.

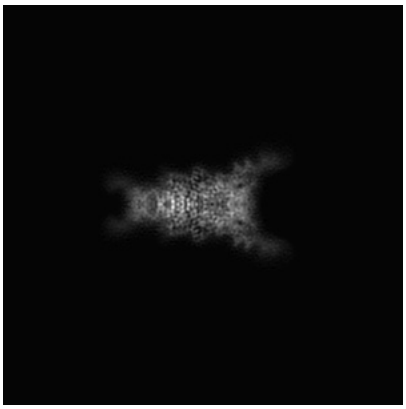
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

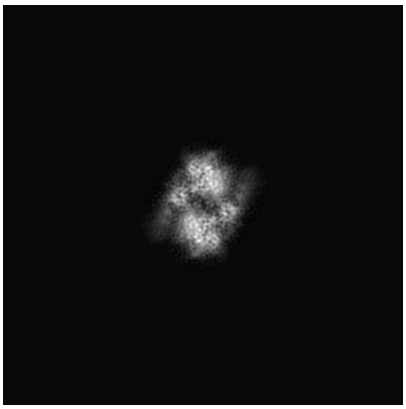
6.1.1 Primary map



X

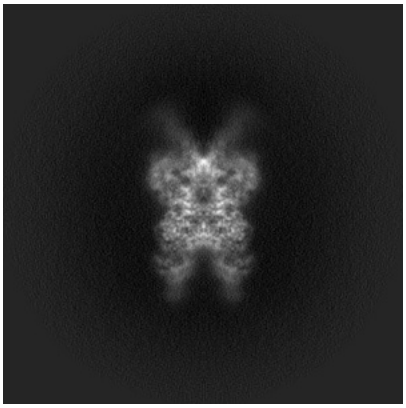


Y

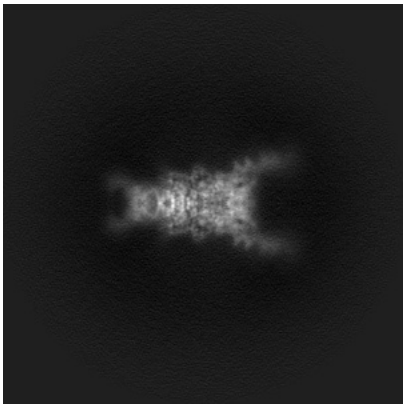


Z

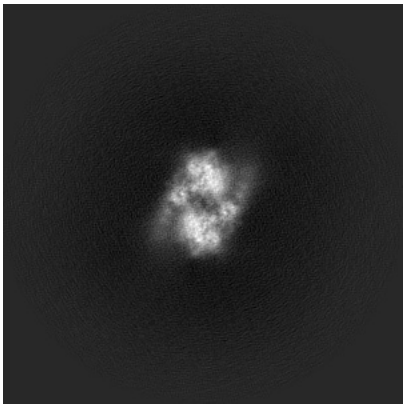
6.1.2 Raw map



X



Y

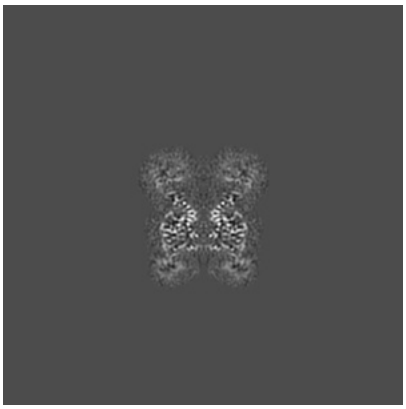


Z

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

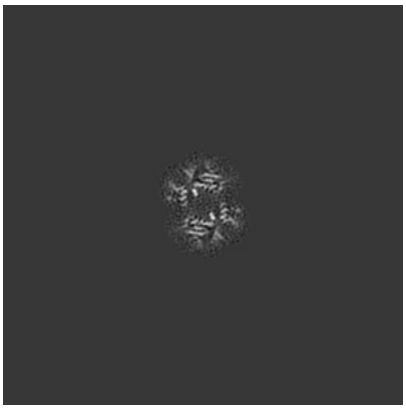
6.2 Central slices (i)

6.2.1 Primary map



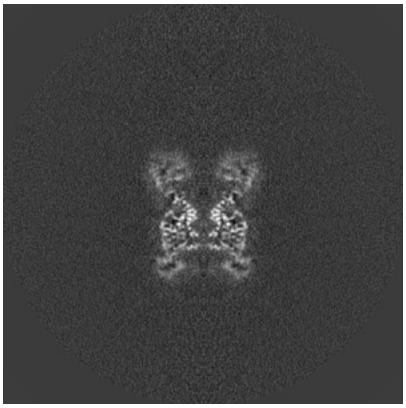
X Index: 150

Y Index: 150

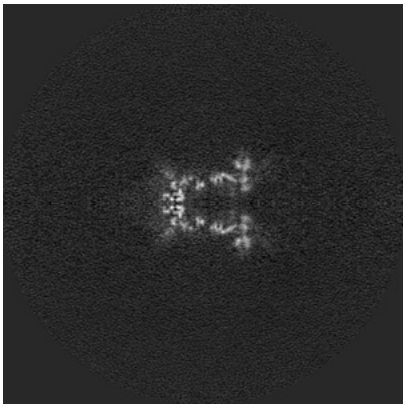


Z Index: 150

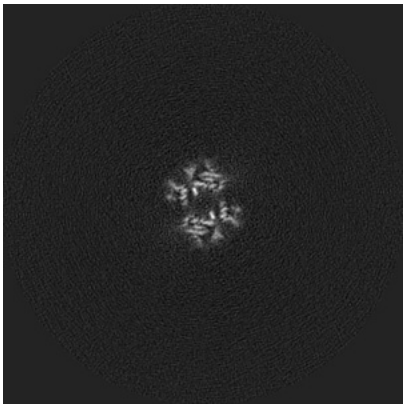
6.2.2 Raw map



X Index: 150



Y Index: 150

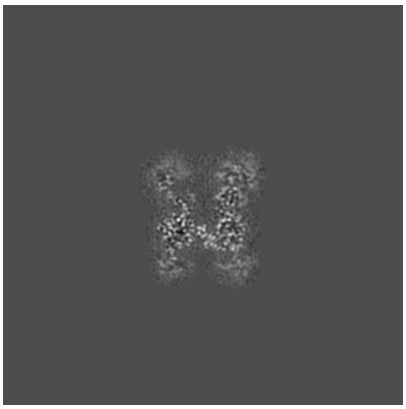


Z Index: 150

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

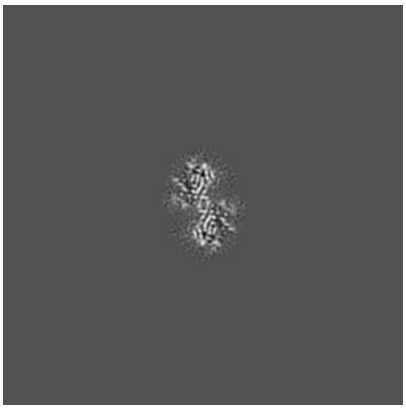
6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 153

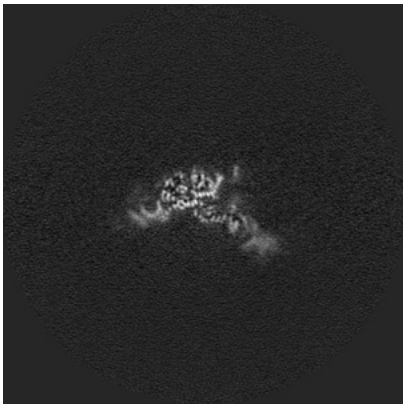
Y Index: 139



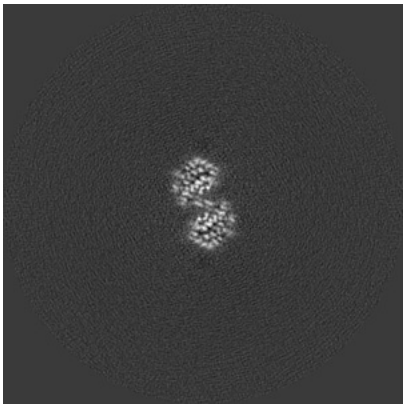
Z Index: 127

6.3.2 Raw map

X Index: 154



Y Index: 139



Z Index: 134

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

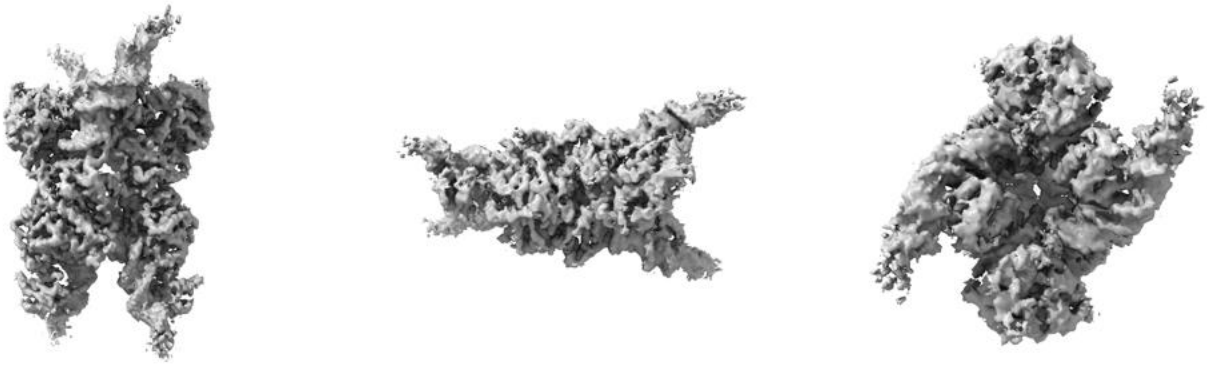
6.4 Orthogonal surface views (i)

6.4.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.017. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



X Y Z

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

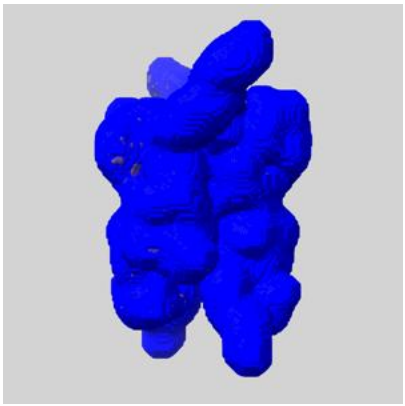
6.5 Mask visualisation (i)

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

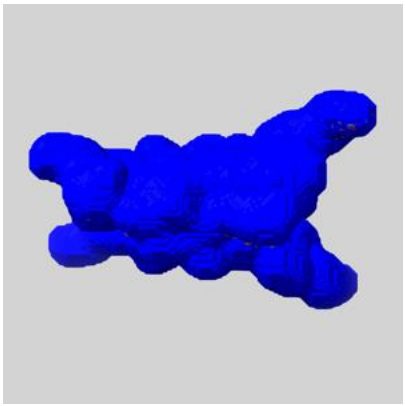
A mask typically either:

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

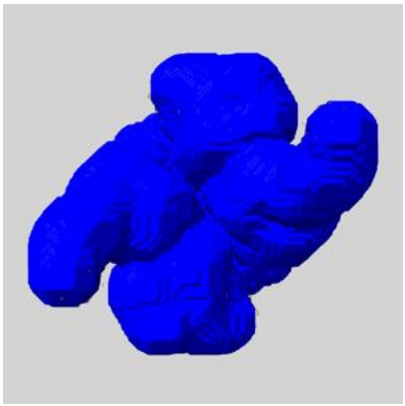
6.5.1 emd_25455_msk_1.map (i)



X



Y

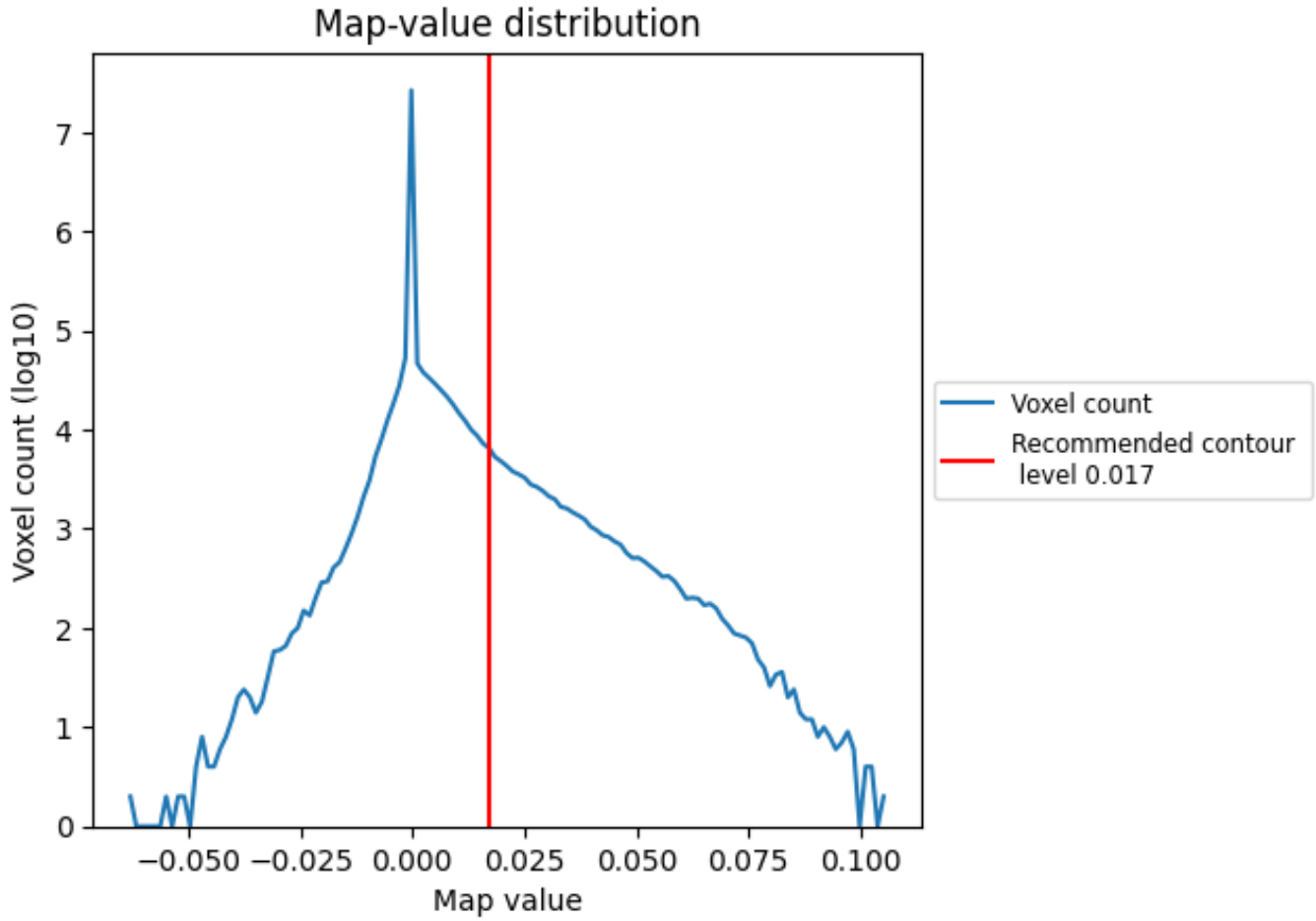


Z

7 Map analysis

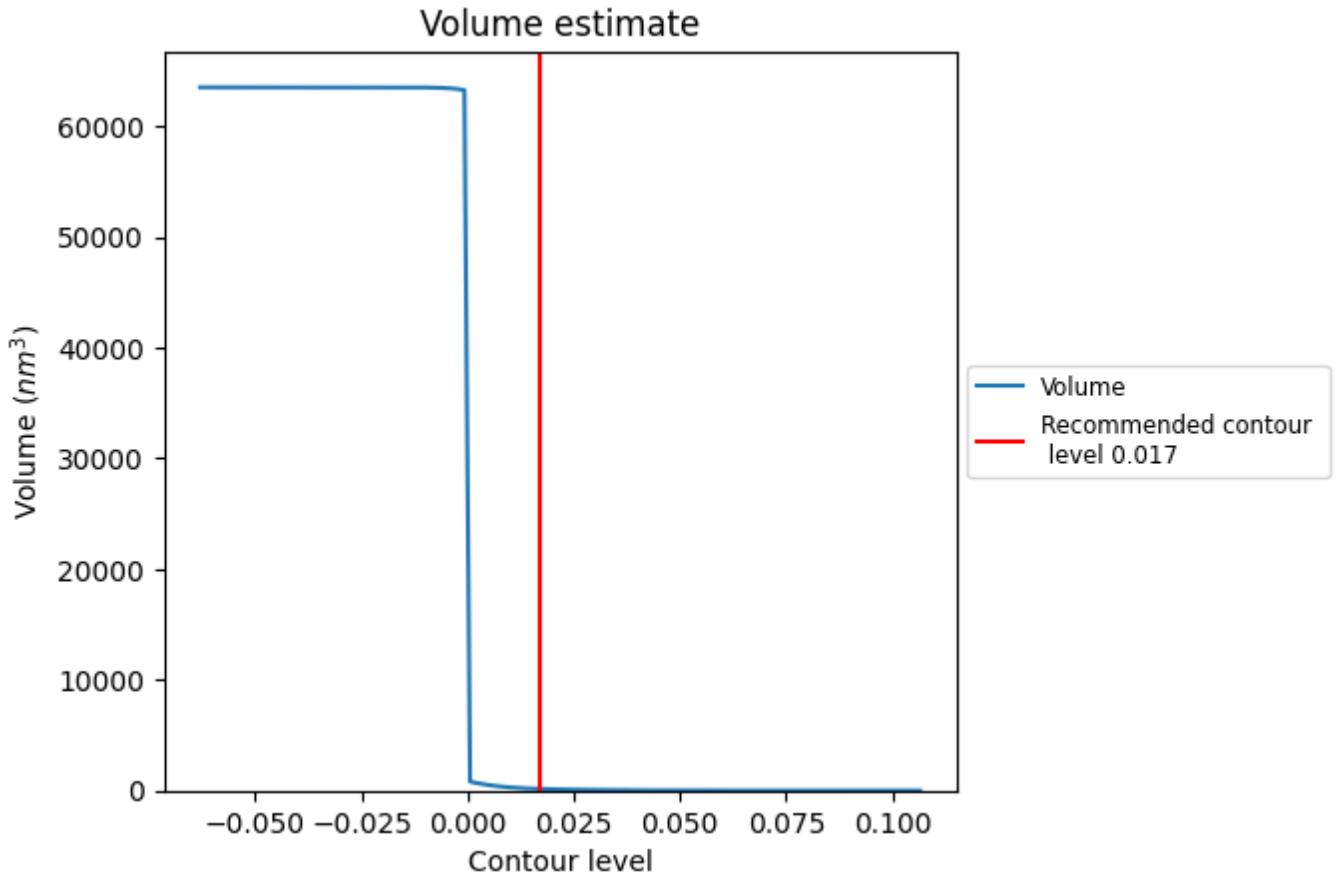
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

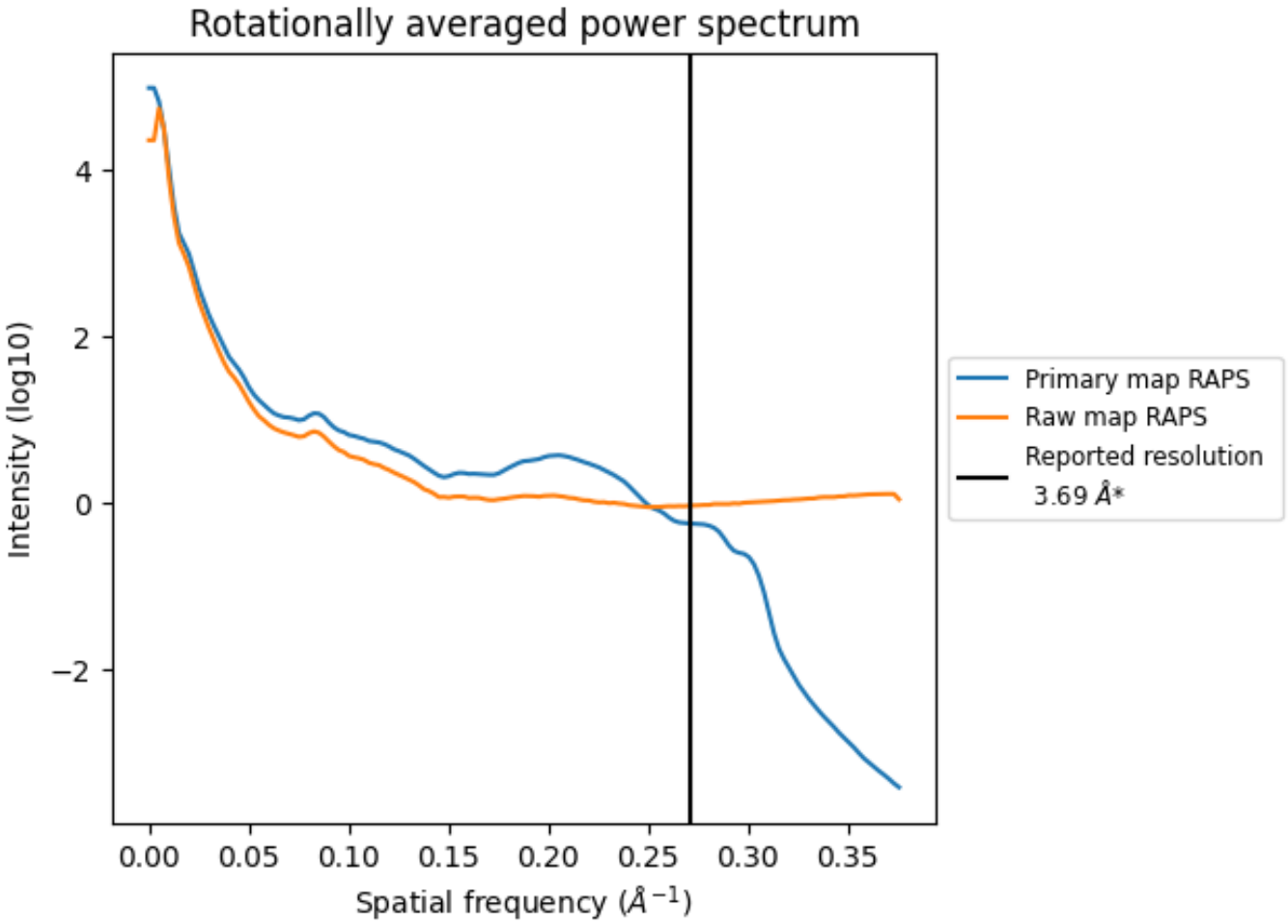
7.2 Volume estimate (i)



The volume at the recommended contour level is 147 nm^3; this corresponds to an approximate mass of 133 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)

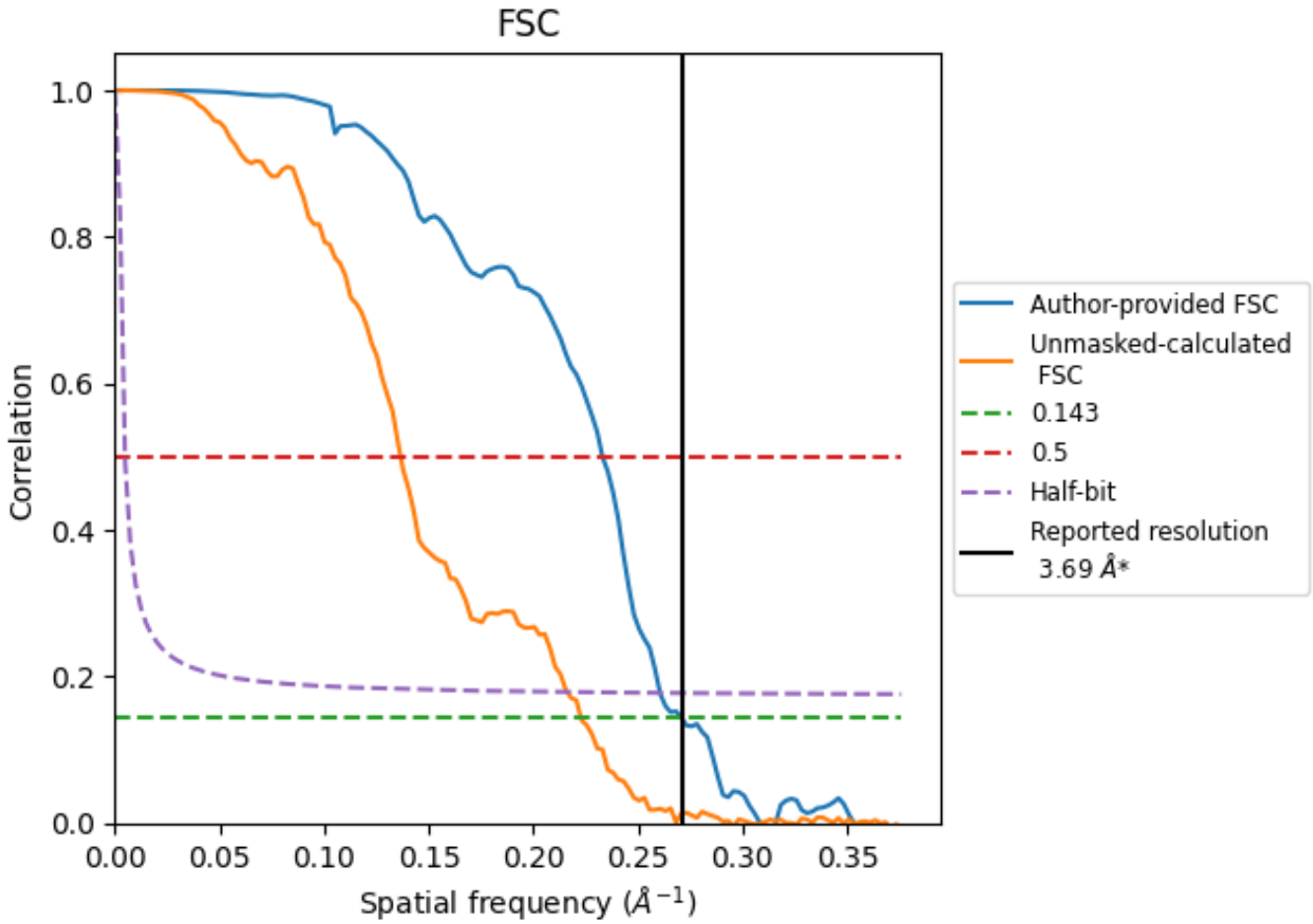


*Reported resolution corresponds to spatial frequency of 0.271 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.271 Å^{-1}

8.2 Resolution estimates (i)

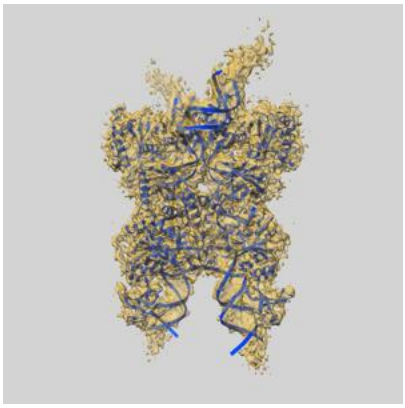
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.69	-	-
Author-provided FSC curve	3.69	4.29	3.84
Unmasked-calculated*	4.49	7.32	4.62

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.49 differs from the reported value 3.69 by more than 10 %

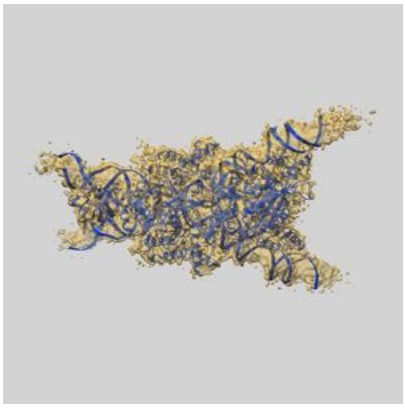
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-25455 and PDB model 7SVW. Per-residue inclusion information can be found in section 3 on page 6.

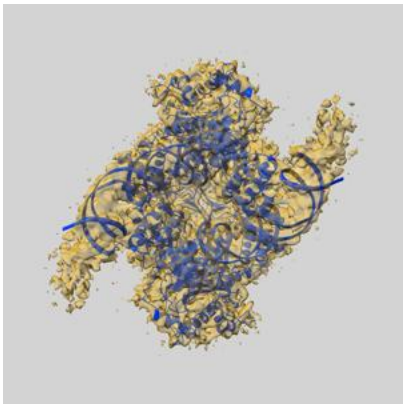
9.1 Map-model overlay



X



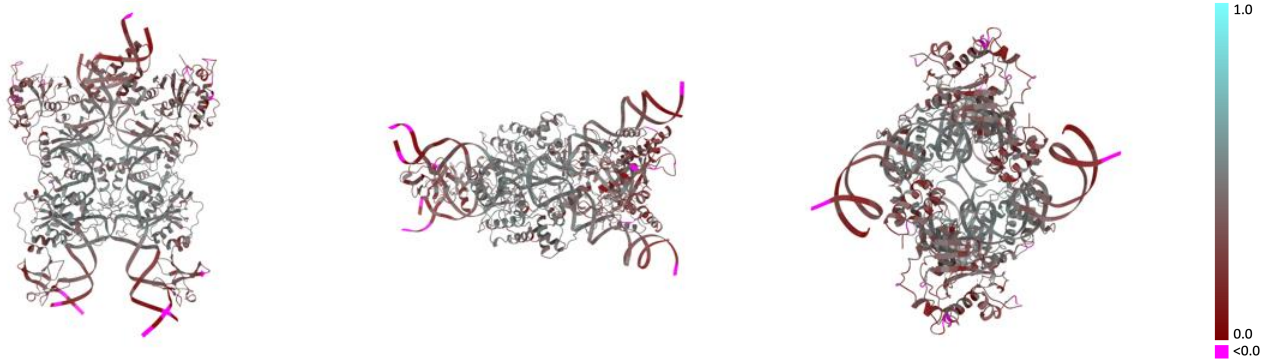
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.017 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

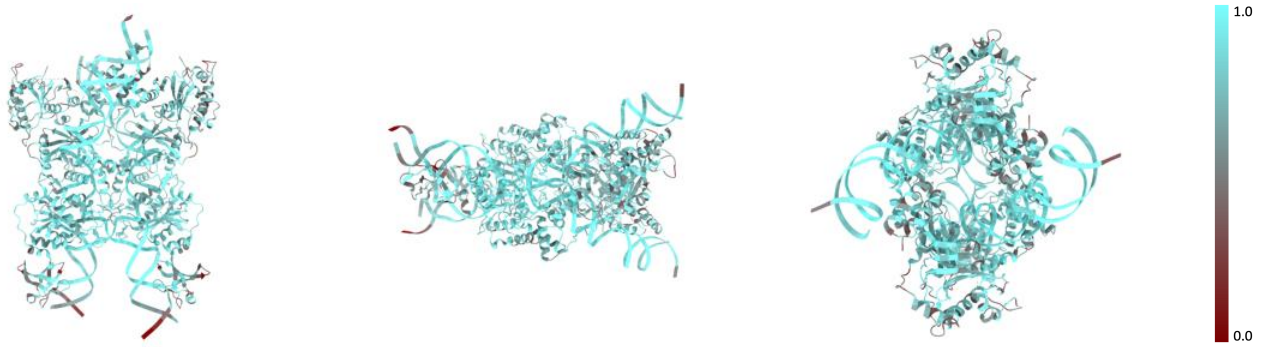
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

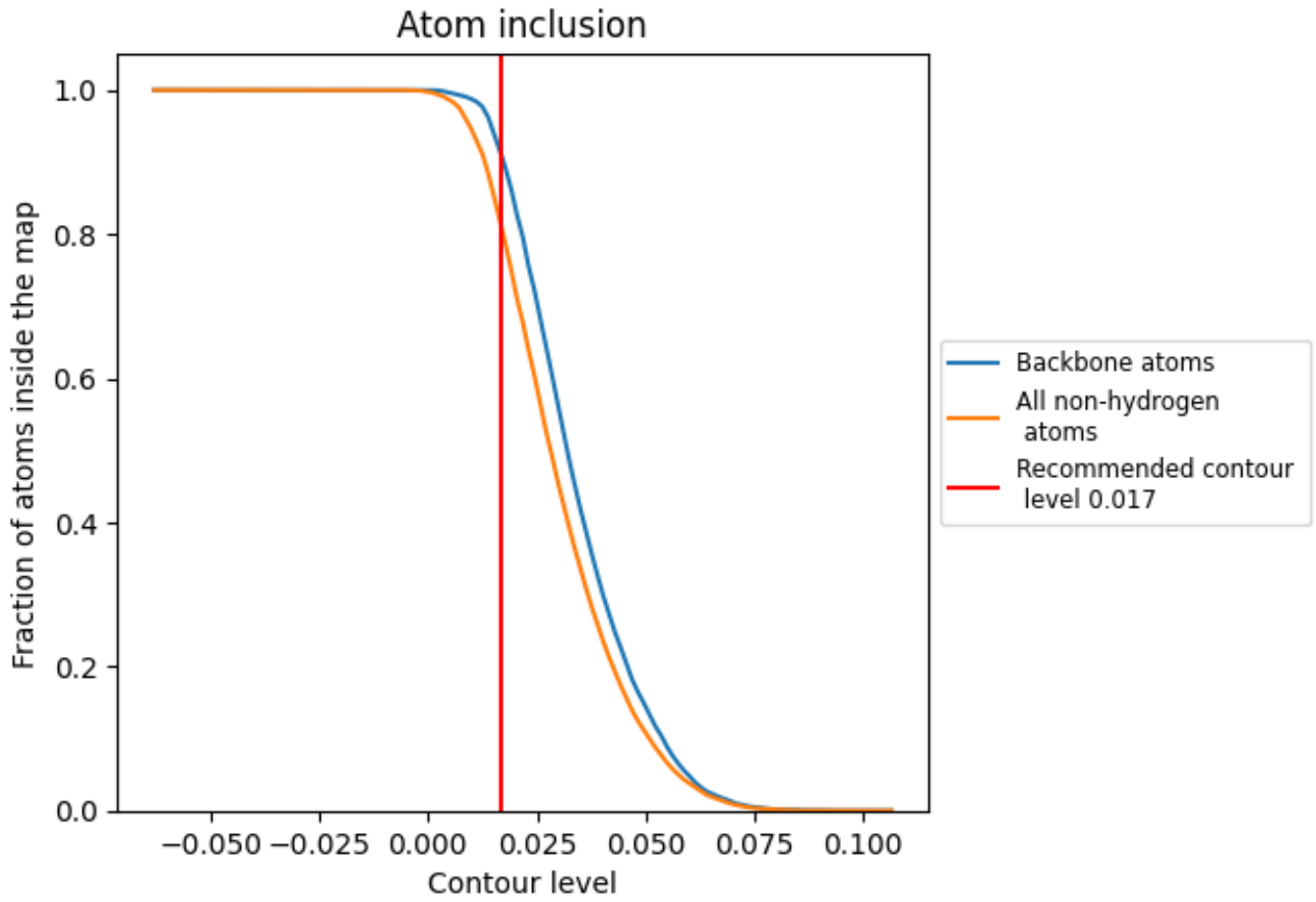
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.017).

9.4 Atom inclusion (i)



At the recommended contour level, 91% of all backbone atoms, 81% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.017) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8070	0.3850
1	0.8981	0.3570
2	0.9220	0.3840
3	0.7641	0.2710
4	0.8952	0.3610
5	0.9268	0.3860
6	0.7674	0.2670
A	0.7451	0.3550
B	0.8074	0.4230
C	0.7369	0.3520
D	0.8072	0.4230