



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 04:21 AM UTC

PDB ID : 6YUF / pdb_00006yuf
EMDB ID : EMD-10930
Title : Cohesin complex with loader gripping DNA
Authors : Higashi, T.L.; Eickhoff, P.; Sousa, J.S.; Costa, A.; Uhlmann, F.
Deposited on : 2020-04-27
Resolution : 3.94 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:

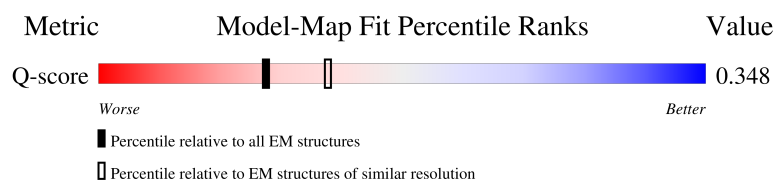
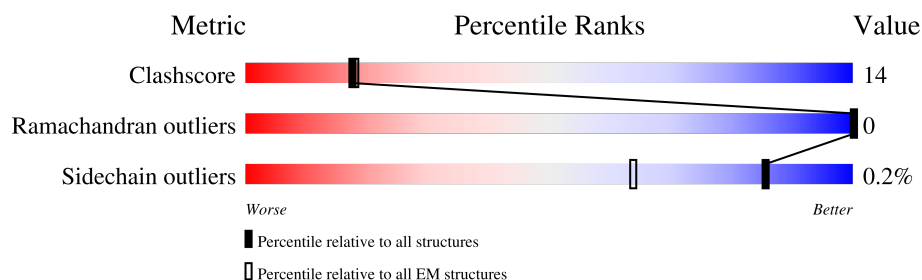
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMD archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.94 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	7757 (3.44 - 4.43)

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	B	628	 17% 7% 76%
2	D	1587	 7% 54% 25% 14%
3	A	1228	 23% 8% 69%
4	C	1194	 27% 10% 63%

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Mol	Chain	Length	Quality of chain
5	X	32	 72% 28%
6	Y	32	 84% 16%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 19528 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 Cohesin subunit rad21.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	152	Total	C	N	O	S	0	0
			1195	758	206	225	6		

- Molecule 2 is a protein called Sister chromatid cohesion protein mis4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	1272	Total	C	N	O	S	0	0
			10247	6604	1687	1910	46		

- Molecule 3 is a protein called Structural maintenance of chromosomes protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	384	Total	C	N	O	S	0	0
			3047	1932	521	587	7		

- Molecule 4 is a protein called Structural maintenance of chromosomes protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	456	Total	C	N	O	S	0	0
			3665	2294	644	714	13		

- Molecule 5 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	X	32	Total	C	N	O	P	0	0
			658	312	129	185	32		

- Molecule 6 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Y	32	Total	C	N	O	P	0	0
			654	313	110	199	32		

-
- BEF
- F3
- F
- BE Be⁻ — F F1
- F
- F2

Mol	Chain	Residues	Atoms			AltConf
7	A	1	Total 4	Be 1	F 3	0
7	C	1	Total 4	Be 1	F 3	0

- # ADP

Mol	Chain	Residues	Atoms					AltConf
8	A	1	Total 27	C 10	N 5	O 10	P 2	0

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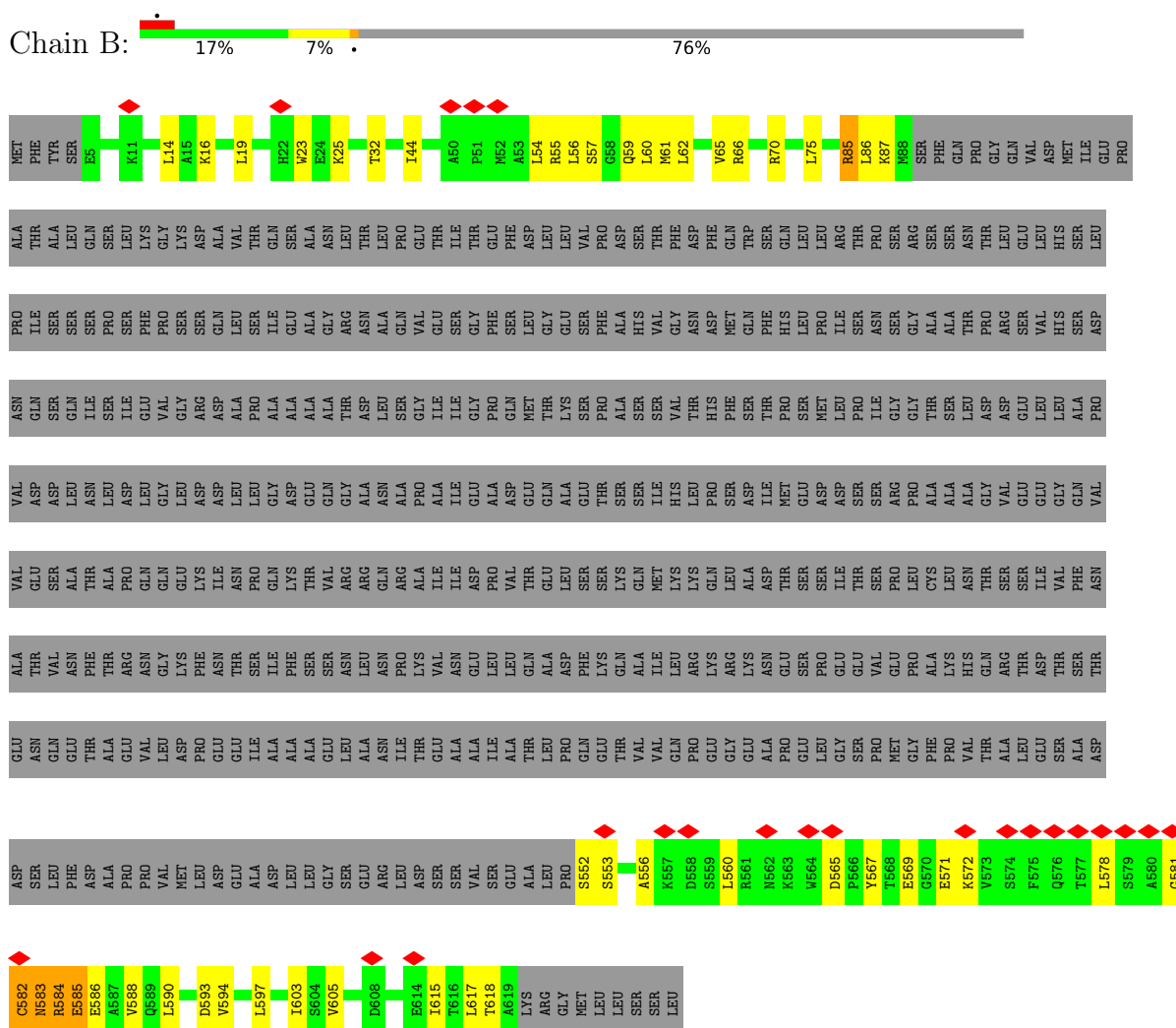
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Mol	Chain	Residues	Atoms					AltConf
8	C	1	Total	C	N	O	P	0
			27	10	5	10	2	

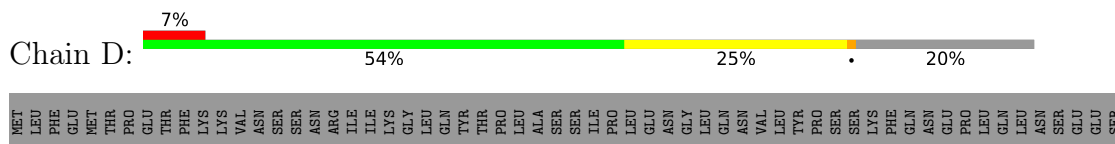
3 Residue-property plots

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

• Molecule 1: Cohesin subunit rad21



• Molecule 2: Sister chromatid cohesion protein mis4









4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	255148	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 ($e^-/\text{\AA}^2$)	33.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	4.069	Depositor
Minimum map value	-1.652	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.065	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	392.40002, 392.40002, 392.40002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	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: BEF, ADP

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	B	0.73	1/1211 (0.1%)	1.16	7/1634 (0.4%)
2	D	0.66	18/10425 (0.2%)	0.88	22/14086 (0.2%)
3	A	0.70	4/3100 (0.1%)	0.85	10/4170 (0.2%)
4	C	0.94	16/3717 (0.4%)	1.10	35/4996 (0.7%)
5	X	0.37	0/740	0.48	0/1139
6	Y	0.40	0/730	0.57	0/1125
All	All	0.71	39/19923 (0.2%)	0.92	74/27150 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
2	D	0	3
4	C	0	2
All	All	0	6

All (39) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	9	GLN	CD-NE2	-25.17	0.80	1.33
4	C	9	GLN	CB-CG	-14.25	1.09	1.52
2	D	1520	ILE	CG1-CD1	-13.20	1.00	1.51
3	A	152	THR	CB-CG2	-11.36	1.15	1.52
4	C	9	GLN	CG-CD	-10.97	1.24	1.52
4	C	220	ARG	CD-NE	-10.30	1.31	1.46
2	D	860	ILE	CG1-CD1	-9.86	1.13	1.51
2	D	325	PHE	CD2-CE2	-9.09	1.11	1.38
4	C	17	TYR	CB-CG	9.00	1.71	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	17	TYR	CG-CD1	8.25	1.56	1.39
2	D	332	LEU	CG-CD2	-7.89	1.26	1.52
4	C	17	TYR	CE1-CZ	-7.67	1.19	1.38
2	D	1107	VAL	C-O	-7.20	1.15	1.24
3	A	160	GLU	CD-OE2	-7.14	1.11	1.25
2	D	1050	LEU	CG-CD1	-7.06	1.29	1.52
2	D	1029	VAL	CB-CG1	-7.02	1.29	1.52
4	C	220	ARG	CG-CD	7.02	1.73	1.52
2	D	992	ILE	CG1-CD1	-6.93	1.24	1.51
2	D	969	LEU	CG-CD2	-6.81	1.30	1.52
2	D	325	PHE	CB-CG	-6.70	1.35	1.50
2	D	1503	LYS	CG-CD	-6.60	1.32	1.52
2	D	1211	MET	CB-CG	-6.39	1.33	1.52
4	C	964	LEU	CG-CD1	6.38	1.73	1.52
2	D	1107	VAL	CA-C	6.21	1.57	1.52
3	A	160	GLU	CB-CG	-6.15	1.34	1.52
2	D	852	THR	CB-CG2	-6.11	1.32	1.52
2	D	1107	VAL	CA-CB	6.11	1.58	1.53
1	B	597	LEU	CG-CD1	-6.02	1.32	1.52
4	C	221	ARG	N-CA	-5.87	1.39	1.46
3	A	182	LYS	CE-NZ	-5.77	1.32	1.49
4	C	9	GLN	CD-OE1	-5.72	1.12	1.23
4	C	1152	PHE	CB-CG	-5.63	1.37	1.50
2	D	332	LEU	CG-CD1	-5.59	1.34	1.52
2	D	1167	ASN	CG-ND2	-5.47	1.21	1.33
4	C	217	ASP	CA-CB	5.43	1.62	1.53
2	D	638	LEU	CG-CD2	-5.27	1.35	1.52
4	C	217	ASP	CB-CG	5.21	1.65	1.52
4	C	1152	PHE	CE1-CZ	-5.14	1.23	1.38
4	C	1152	PHE	CG-CD2	-5.04	1.28	1.38

All (74) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	220	ARG	NE-CZ-NH2	16.52	134.07	119.20
4	C	220	ARG	NE-CZ-NH1	-15.65	105.84	121.50
4	C	9	GLN	CG-CD-NE2	-14.96	93.95	116.40
2	D	1211	MET	CG-SD-CE	-14.57	68.85	100.90
4	C	9	GLN	CG-CD-OE1	10.97	142.74	120.80
2	D	1516	LEU	CD1-CG-CD2	-10.68	87.31	110.80
3	A	1120	MET	CG-SD-CE	-10.42	77.98	100.90
4	C	1156	THR	CB-CA-C	-9.74	93.56	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	617	LEU	CA-CB-CG	9.72	150.31	116.30
4	C	17	TYR	N-CA-CB	9.70	126.39	110.39
2	D	1503	LYS	CD-CE-NZ	-9.63	81.09	111.90
2	D	332	LEU	CB-CG-CD1	-9.35	82.64	110.70
4	C	1161	MET	N-CA-C	-8.90	101.23	112.90
2	D	1227	MET	CG-SD-CE	-8.90	81.33	100.90
3	A	149	ASP	OD1-CG-OD2	-8.65	102.13	122.90
2	D	999	LEU	CB-CA-C	-8.05	96.99	110.68
2	D	1189	LEU	CB-CG-CD2	7.95	134.54	110.70
3	A	1205	VAL	CG1-CB-CG2	-7.60	94.08	110.80
2	D	731	LYS	CG-CD-CE	7.55	128.66	111.30
4	C	17	TYR	CD1-CE1-CZ	-7.41	106.26	119.60
4	C	964	LEU	CB-CG-CD1	7.25	132.44	110.70
4	C	1142	MET	CG-SD-CE	-7.08	85.33	100.90
2	D	1107	VAL	O-C-N	7.05	125.08	120.07
4	C	957	LEU	CB-CG-CD2	-6.86	90.13	110.70
4	C	957	LEU	CB-CG-CD1	-6.83	90.21	110.70
4	C	217	ASP	N-CA-C	-6.80	104.95	113.18
1	B	85	ARG	NE-CZ-NH2	6.75	125.27	119.20
4	C	17	TYR	CE1-CZ-OH	-6.71	99.77	119.90
4	C	963	ALA	CA-C-N	-6.59	108.73	121.58
4	C	963	ALA	C-N-CA	-6.59	108.73	121.58
4	C	1154	CYS	CA-CB-SG	-6.58	99.28	114.40
4	C	220	ARG	N-CA-CB	6.41	120.17	110.30
4	C	1161	MET	CB-CG-SD	6.39	131.87	112.70
4	C	17	TYR	CG-CD1-CE1	6.39	130.78	121.20
2	D	1024	MET	CG-SD-CE	-6.32	87.00	100.90
2	D	1107	VAL	CA-C-N	-6.25	113.18	120.12
2	D	1107	VAL	C-N-CA	-6.25	113.18	120.12
3	A	156	GLN	CB-CA-C	6.25	123.33	110.40
4	C	17	TYR	CB-CG-CD1	6.13	130.00	120.80
4	C	17	TYR	CD1-CG-CD2	-6.08	108.97	118.10
1	B	85	ARG	NH1-CZ-NH2	-6.04	111.45	119.30
4	C	217	ASP	CA-CB-CG	6.03	118.63	112.60
4	C	964	LEU	CB-CG-CD2	-6.03	92.60	110.70
2	D	1047	LYS	CB-CG-CD	5.92	124.93	111.30
3	A	149	ASP	CB-CG-OD2	5.88	131.92	118.40
3	A	1139	MET	CG-SD-CE	-5.88	87.97	100.90
4	C	972	LYS	CA-C-N	5.85	133.63	121.94
4	C	972	LYS	C-N-CA	5.85	133.63	121.94
1	B	571	GLU	N-CA-C	5.79	117.67	111.36
4	C	217	ASP	OD1-CG-OD2	-5.76	109.08	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	188	LYS	CD-CE-NZ	-5.75	93.49	111.90
3	A	39	SER	CB-CA-C	-5.73	100.16	110.35
2	D	1303	LEU	CA-CB-CG	-5.66	96.50	116.30
4	C	964	LEU	CD1-CG-CD2	5.62	123.16	110.80
4	C	219	GLU	CB-CA-C	5.55	120.90	110.63
2	D	1104	MET	CG-SD-CE	-5.54	88.72	100.90
4	C	961	ASN	N-CA-CB	-5.51	102.00	110.20
2	D	744	SER	CA-CB-OG	-5.45	100.19	111.10
4	C	17	TYR	CE1-CZ-CE2	5.41	131.11	120.30
2	D	355	LEU	CD1-CG-CD2	-5.39	98.93	110.80
2	D	1050	LEU	CD1-CG-CD2	-5.38	98.96	110.80
3	A	1058	ARG	CG-CD-NE	5.35	123.78	112.00
4	C	1156	THR	N-CA-CB	5.31	119.15	110.55
4	C	9	GLN	CB-CA-C	-5.30	99.18	109.68
2	D	1520	ILE	CG1-CB-CG2	-5.29	94.82	110.70
4	C	973	LYS	CB-CG-CD	5.26	123.40	111.30
1	B	85	ARG	CD-NE-CZ	5.19	131.67	124.40
2	D	954	ILE	CB-CA-C	-5.12	105.27	111.87
3	A	1149	HIS	CA-CB-CG	-5.12	108.68	113.80
2	D	1147	MET	CG-SD-CE	-5.08	89.71	100.90
2	D	999	LEU	CB-CG-CD2	5.08	125.93	110.70
1	B	581	GLY	CA-C-N	-5.05	115.75	122.72
1	B	581	GLY	C-N-CA	-5.05	115.75	122.72
3	A	156	GLN	N-CA-CB	-5.01	103.28	110.44

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	85	ARG	Sidechain
4	C	220	ARG	Sidechain
4	C	235	ILE	Peptide
2	D	1178	SER	Peptide
2	D	722	LYS	Peptide
2	D	744	SER	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	B	1195	0	1238	52	0
2	D	10247	0	10549	319	0
3	A	3047	0	3045	70	0
4	C	3665	0	3668	93	0
5	X	658	0	358	8	0
6	Y	654	0	365	4	0
7	A	4	0	0	0	0
7	C	4	0	0	1	0
8	A	27	0	11	4	0
8	C	27	0	11	1	0
All	All	19528	0	19245	525	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 (525) 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)
2:D:290:ILE:HD11	2:D:346:LEU:CD1	1.66	1.25
2:D:268:TYR:HB2	2:D:332:LEU:CD2	1.73	1.18
2:D:290:ILE:CD1	2:D:346:LEU:HD12	1.73	1.16
2:D:290:ILE:HD11	2:D:346:LEU:HD12	1.01	1.00
2:D:268:TYR:HB2	2:D:332:LEU:HD21	0.99	0.96
2:D:268:TYR:CB	2:D:332:LEU:HD21	1.94	0.96
2:D:286:GLU:HG3	2:D:346:LEU:HD21	1.50	0.92
1:B:556:ALA:HB3	1:B:593:ASP:OD1	1.69	0.91
4:C:220:ARG:O	4:C:224:GLU:HB2	1.73	0.88
1:B:572:LYS:NZ	1:B:594:VAL:CG1	2.38	0.87
2:D:264:ILE:HG23	2:D:332:LEU:CD1	2.05	0.86
1:B:565:ASP:OD1	1:B:618:THR:HG22	1.76	0.85
2:D:280:CYS:HB2	2:D:340:VAL:HA	1.59	0.84
1:B:556:ALA:CB	1:B:593:ASP:OD1	2.26	0.83
1:B:572:LYS:HZ3	1:B:594:VAL:CG1	1.90	0.83
1:B:572:LYS:HZ3	1:B:594:VAL:HG13	1.44	0.81
2:D:280:CYS:SG	2:D:341:PRO:CD	2.69	0.81
2:D:296:LEU:HD13	2:D:333:VAL:HG11	1.62	0.81
2:D:1222:PHE:HA	2:D:1227:MET:HE1	1.63	0.81
2:D:1223:ILE:HG22	2:D:1303:LEU:HD11	1.63	0.79
2:D:280:CYS:SG	2:D:341:PRO:HD2	2.22	0.79
2:D:1024:MET:HG3	2:D:1027:LEU:HD12	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1195:ASN:O	3:A:1199:SER:HB3	1.82	0.78
1:B:553:SER:HA	1:B:593:ASP:OD2	1.84	0.77
2:D:285:GLU:HG2	2:D:346:LEU:HG	1.65	0.77
2:D:801:ARG:NH1	2:D:804:ASN:OD1	2.18	0.77
2:D:477:LEU:O	2:D:480:PHE:HB3	1.85	0.76
1:B:585:GLU:CD	1:B:585:GLU:H	1.95	0.75
2:D:272:THR:HG22	2:D:276:ARG:HH22	1.52	0.75
2:D:264:ILE:HG23	2:D:332:LEU:HD12	1.69	0.75
3:A:37:GLY:HA3	3:A:1207:ILE:HG21	1.69	0.74
2:D:1044:HIS:HA	2:D:1047:LYS:HE2	1.70	0.73
2:D:1143:ASN:HB3	2:D:1146:LYS:HB2	1.71	0.73
4:C:27:HIS:NE2	4:C:1154:CYS:SG	2.61	0.73
1:B:553:SER:HA	1:B:593:ASP:CG	2.14	0.73
2:D:280:CYS:SG	2:D:341:PRO:HD3	2.29	0.73
2:D:1103:LEU:HG	2:D:1149:ARG:HH22	1.53	0.72
2:D:659:LYS:HB3	2:D:663:PRO:HB3	1.71	0.71
2:D:264:ILE:HG23	2:D:332:LEU:HD11	1.73	0.71
2:D:1298:GLY:HA3	3:A:1123:MET:HE1	1.73	0.70
2:D:1151:ILE:O	2:D:1210:ASN:ND2	2.24	0.70
2:D:264:ILE:CG2	2:D:332:LEU:HD11	2.22	0.69
4:C:56:LEU:HD13	4:C:61:ARG:HB2	1.72	0.69
2:D:290:ILE:HD11	2:D:346:LEU:HD11	1.71	0.69
2:D:251:ARG:NH1	2:D:257:LYS:O	2.25	0.69
4:C:143:ARG:O	4:C:146:SER:OG	2.11	0.69
2:D:1196:LEU:HB3	2:D:1204:ARG:HH21	1.58	0.69
2:D:987:THR:O	2:D:991:GLN:NE2	2.25	0.69
4:C:213:TYR:O	4:C:217:ASP:N	2.24	0.69
4:C:1114:GLN:OE1	4:C:1122:ASN:ND2	2.27	0.68
2:D:1134:LEU:HD22	2:D:1154:ILE:HG13	1.76	0.68
4:C:30:ILE:HB	4:C:1155:THR:HG22	1.75	0.68
2:D:811:SER:HA	2:D:814:ARG:HD3	1.76	0.68
2:D:541:LEU:HG	2:D:544:HIS:H	1.58	0.68
4:C:213:TYR:HE1	4:C:964:LEU:HD13	1.59	0.68
1:B:87:LYS:HA	4:C:199:ARG:HH22	1.59	0.67
3:A:42:MET:HG3	3:A:1158:VAL:HG11	1.77	0.67
4:C:219:GLU:HG3	4:C:220:ARG:HH12	1.60	0.67
1:B:556:ALA:HB3	1:B:593:ASP:CG	2.21	0.66
4:C:141:GLN:OE1	7:C:1201:BEF:F3	2.03	0.66
4:C:213:TYR:HA	4:C:216:LYS:HB3	1.77	0.66
2:D:1152:ASP:HA	2:D:1210:ASN:HD22	1.61	0.66
3:A:2:GLY:N	3:A:93:TYR:HH	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:1148:VAL:HA	2:D:1151:ILE:HG22	1.76	0.66
2:D:347:GLN:NE2	2:D:351:SER:OG	2.29	0.66
2:D:728:GLU:HA	2:D:731:LYS:HD2	1.79	0.65
2:D:790:SER:O	2:D:796:ARG:NH2	2.29	0.65
2:D:296:LEU:O	2:D:300:LEU:HG	1.96	0.65
2:D:286:GLU:CG	2:D:346:LEU:HD21	2.26	0.65
2:D:1095:LEU:HD21	2:D:1106:ILE:HG21	1.78	0.65
2:D:279:ALA:HA	2:D:282:LYS:HD3	1.78	0.65
2:D:466:PRO:HA	2:D:469:ARG:HB2	1.77	0.65
2:D:525:ILE:HG12	2:D:544:HIS:HB3	1.80	0.64
2:D:1501:ARG:HA	2:D:1504:ILE:HG12	1.79	0.64
2:D:296:LEU:CD1	2:D:333:VAL:HG11	2.28	0.64
2:D:502:GLN:O	2:D:505:SER:OG	2.16	0.64
2:D:1469:ILE:HD11	2:D:1526:ILE:HG21	1.80	0.64
1:B:585:GLU:CD	1:B:585:GLU:N	2.56	0.63
3:A:16:ARG:HD3	3:A:1213:GLU:HB3	1.79	0.63
4:C:29:VAL:HG12	4:C:1161:MET:HE3	1.80	0.63
4:C:62:GLN:NE2	4:C:67:GLU:OE2	2.30	0.63
3:A:199:LYS:HB2	3:A:1045:PHE:HE2	1.64	0.63
4:C:172:ARG:O	4:C:176:ASN:ND2	2.29	0.63
2:D:1167:ASN:ND2	2:D:1182:ASP:OD1	2.32	0.62
2:D:261:SER:HA	2:D:264:ILE:HD12	1.80	0.62
3:A:16:ARG:O	3:A:19:GLN:NE2	2.31	0.62
2:D:1130:CYS:HA	2:D:1133:SER:HB2	1.81	0.62
2:D:324:ASP:O	2:D:328:LYS:NZ	2.33	0.62
2:D:213:GLN:HE21	2:D:214:ARG:HH22	1.48	0.62
2:D:272:THR:O	2:D:275:SER:OG	2.16	0.62
4:C:223:LEU:HD12	4:C:957:LEU:HD22	1.82	0.62
2:D:263:ALA:HA	2:D:266:LYS:HE2	1.82	0.61
2:D:1121:GLU:HA	2:D:1124:LYS:HE3	1.82	0.61
2:D:292:VAL:O	2:D:296:LEU:HG	2.00	0.61
2:D:902:ARG:NH2	2:D:905:ASP:OD2	2.33	0.61
2:D:1305:GLN:HG2	2:D:1339:VAL:HG22	1.82	0.61
2:D:226:THR:HG22	2:D:270:ALA:HB1	1.82	0.61
2:D:285:GLU:N	2:D:285:GLU:OE1	2.32	0.61
3:A:157:SER:N	3:A:160:GLU:OE2	2.34	0.61
2:D:264:ILE:CG2	2:D:332:LEU:CD1	2.77	0.61
2:D:864:ILE:O	2:D:902:ARG:NH1	2.34	0.61
1:B:578:LEU:HB2	1:B:586:GLU:HB3	1.82	0.61
2:D:398:ALA:O	2:D:402:ASN:ND2	2.34	0.61
2:D:1268:LEU:HA	2:D:1271:LYS:HB2	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:1516:LEU:O	2:D:1519:TYR:N	2.34	0.60
2:D:1101:ALA:HA	2:D:1104:MET:HE1	1.82	0.60
4:C:1128:ASP:OD1	4:C:1128:ASP:N	2.29	0.60
2:D:1164:ASN:O	2:D:1165:ARG:NH2	2.30	0.60
2:D:1073:LEU:HD13	2:D:1113:LEU:HD21	1.82	0.60
3:A:206:LEU:HD13	3:A:1034:VAL:HG21	1.83	0.60
1:B:584:ARG:HH21	1:B:584:ARG:HG3	1.67	0.60
1:B:62:LEU:HD21	1:B:66:ARG:HH21	1.67	0.60
2:D:249:ILE:O	2:D:257:LYS:HA	2.01	0.60
1:B:16:LYS:NZ	1:B:32:THR:OG1	2.33	0.59
2:D:1295:TRP:HE1	3:A:1095:PRO:HD2	1.66	0.59
3:A:43:ASP:OD2	3:A:57:ARG:NH2	2.35	0.59
4:C:993:GLU:OE1	4:C:996:ARG:NH1	2.35	0.59
3:A:1157:PHE:HE2	3:A:1159:LEU:HD21	1.67	0.59
3:A:1201:SER:OG	3:A:1202:GLU:N	2.34	0.59
2:D:1047:LYS:HA	2:D:1050:LEU:HD13	1.85	0.59
3:A:2:GLY:N	3:A:94:GLU:O	2.35	0.59
2:D:1342:ARG:HH22	3:A:1116:LYS:HD2	1.67	0.58
2:D:603:LEU:HB3	2:D:605:GLU:OE1	2.03	0.58
1:B:25:LYS:O	1:B:70:ARG:NH2	2.37	0.58
2:D:492:THR:HG22	2:D:493:TYR:H	1.69	0.58
3:A:49:LEU:HD11	3:A:1156:PHE:HZ	1.68	0.58
2:D:1114:PHE:O	2:D:1118:ASN:N	2.37	0.58
2:D:524:GLU:HG3	2:D:525:ILE:HG13	1.86	0.58
3:A:4:LEU:HD12	3:A:91:LEU:HD11	1.86	0.58
4:C:13:SER:O	4:C:1178:SER:OG	2.21	0.58
2:D:300:LEU:CD2	2:D:326:ILE:HD11	2.33	0.58
2:D:529:GLU:OE2	2:D:742:GLN:N	2.37	0.58
2:D:681:LEU:HA	2:D:684:LEU:HD12	1.85	0.57
2:D:300:LEU:HD23	2:D:326:ILE:HD11	1.85	0.57
2:D:218:VAL:O	2:D:222:GLN:HG2	2.05	0.57
2:D:634:LYS:HD2	2:D:795:LEU:HD21	1.86	0.57
2:D:397:VAL:HA	2:D:400:VAL:HG22	1.86	0.57
2:D:225:ASP:O	2:D:229:LEU:HG	2.05	0.57
2:D:471:PHE:O	2:D:474:GLU:HB3	2.05	0.57
2:D:836:ASP:HB2	2:D:874:ARG:HD2	1.87	0.56
4:C:1036:VAL:HG12	4:C:1038:ALA:H	1.70	0.56
2:D:290:ILE:HA	2:D:293:LYS:HE2	1.86	0.56
2:D:897:SER:OG	2:D:965:ARG:NH1	2.38	0.56
2:D:942:LEU:HB2	2:D:946:LYS:HE3	1.86	0.56
2:D:1016:THR:HG23	2:D:1019:ILE:HD13	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:139:ARG:NH1	5:X:6:DC:OP1	2.37	0.56
1:B:603:ILE:HG23	1:B:618:THR:H	1.70	0.56
2:D:274:LEU:HD13	2:D:277:LEU:HD11	1.88	0.56
3:A:52:LYS:HE2	5:X:6:DC:H5"	1.86	0.56
4:C:1159:PRO:HB3	4:C:1192:VAL:HG11	1.87	0.56
1:B:86:LEU:O	4:C:199:ARG:NH1	2.38	0.56
3:A:28:THR:HG22	3:A:1203:ALA:HB3	1.88	0.56
2:D:635:ASN:HD22	2:D:798:LYS:HG3	1.71	0.56
3:A:1158:VAL:HG13	3:A:1189:VAL:HG23	1.88	0.56
4:C:112:ASP:OD1	4:C:113:LYS:NZ	2.38	0.56
2:D:846:ILE:HD11	2:D:856:ILE:HG21	1.87	0.56
2:D:867:PRO:O	2:D:872:ARG:NH2	2.39	0.56
2:D:1500:GLU:HG2	2:D:1503:LYS:HE3	1.88	0.56
1:B:572:LYS:NZ	1:B:594:VAL:HG12	2.21	0.55
2:D:544:HIS:O	2:D:547:THR:OG1	2.23	0.55
2:D:1246:LEU:O	2:D:1249:SER:OG	2.20	0.55
4:C:28:ASN:ND2	4:C:1167:ASN:OD1	2.39	0.55
2:D:1193:GLN:NE2	2:D:1226:LEU:O	2.39	0.55
2:D:224:GLN:N	2:D:227:ARG:HH11	2.04	0.55
2:D:286:GLU:HG3	2:D:346:LEU:HD11	1.88	0.55
1:B:553:SER:HA	1:B:593:ASP:OD1	2.07	0.55
2:D:264:ILE:O	2:D:332:LEU:HD11	2.06	0.55
2:D:284:LEU:HD12	2:D:286:GLU:OE1	2.07	0.55
3:A:8:GLU:OE1	3:A:18:HIS:NE2	2.40	0.55
4:C:1136:ARG:NH1	4:C:1160:GLU:OE2	2.40	0.55
2:D:264:ILE:HD11	2:D:325:PHE:CZ	2.41	0.55
4:C:163:ALA:HB2	4:C:1020:THR:HG21	1.87	0.55
2:D:285:GLU:CG	2:D:346:LEU:HG	2.36	0.55
2:D:675:ILE:HD13	2:D:678:ILE:HD13	1.86	0.55
4:C:1040:ARG:NH1	4:C:1086:SER:OG	2.40	0.55
2:D:366:THR:O	2:D:369:GLU:HG3	2.07	0.55
3:A:8:GLU:HB2	3:A:18:HIS:HE2	1.72	0.55
2:D:324:ASP:HA	2:D:327:LEU:HD12	1.89	0.55
2:D:601:LEU:HA	2:D:609:THR:HG21	1.89	0.55
2:D:1167:ASN:O	2:D:1171:LYS:N	2.31	0.55
2:D:351:SER:O	2:D:355:LEU:HD12	2.07	0.54
2:D:1034:PHE:HZ	2:D:1037:LEU:HD22	1.72	0.54
2:D:1143:ASN:O	2:D:1147:MET:N	2.30	0.54
4:C:9:GLN:NE2	4:C:17:TYR:HA	2.22	0.54
1:B:582:CYS:O	1:B:586:GLU:HG2	2.05	0.54
2:D:979:SER:OG	2:D:984:ASN:OD1	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:1159:ARG:HD2	2:D:1213:ARG:HB3	1.89	0.54
4:C:9:GLN:HE21	4:C:17:TYR:HA	1.73	0.54
2:D:297:GLU:O	2:D:301:LYS:HG3	2.08	0.54
3:A:39:SER:OG	8:A:1302:ADP:O1B	2.25	0.54
4:C:133:SER:OG	4:C:134:ASN:N	2.39	0.54
2:D:1490:ILE:HA	2:D:1493:TRP:CD2	2.43	0.54
1:B:65:VAL:HB	4:C:179:MET:HE3	1.90	0.54
1:B:582:CYS:C	1:B:584:ARG:H	2.16	0.53
4:C:229:SER:O	4:C:233:ASP:HB2	2.08	0.53
3:A:1128:ASP:OD1	3:A:1128:ASP:N	2.41	0.53
3:A:6:ARG:NH1	3:A:100:GLN:OE1	2.42	0.53
2:D:850:ARG:NH1	2:D:851:GLU:OE2	2.41	0.53
2:D:874:ARG:NH2	5:X:25:DA:OP1	2.42	0.53
3:A:63:GLU:N	3:A:63:GLU:OE1	2.42	0.53
3:A:1086:LYS:NZ	3:A:1098:GLY:O	2.34	0.53
1:B:578:LEU:CB	1:B:586:GLU:HB3	2.38	0.53
2:D:813:LEU:HD22	2:D:820:LEU:HB2	1.91	0.53
2:D:360:HIS:CG	2:D:420:ARG:HH22	2.27	0.53
2:D:483:LEU:HB2	2:D:589:LEU:HD13	1.91	0.52
3:A:12:PHE:HE2	3:A:40:ASN:HB3	1.74	0.52
3:A:182:LYS:HE3	3:A:182:LYS:HA	1.91	0.52
4:C:210:LEU:HA	4:C:213:TYR:HB3	1.90	0.52
2:D:235:GLU:O	2:D:239:SER:OG	2.21	0.52
2:D:950:GLN:HE22	2:D:995:LEU:HB2	1.73	0.52
2:D:251:ARG:HH11	2:D:257:LYS:H	1.55	0.52
2:D:1034:PHE:HE1	2:D:1037:LEU:HD13	1.75	0.52
4:C:57:SER:H	4:C:60:GLU:HB2	1.74	0.52
2:D:470:ASP:OD1	2:D:470:ASP:N	2.42	0.52
2:D:630:ALA:O	2:D:634:LYS:NZ	2.43	0.52
1:B:585:GLU:HA	1:B:588:VAL:HG12	1.91	0.52
2:D:347:GLN:HE22	2:D:351:SER:HG	1.54	0.52
2:D:250:LYS:HD2	2:D:254:ASP:HB3	1.92	0.52
2:D:873:LYS:O	2:D:877:LYS:NZ	2.41	0.52
4:C:214:HIS:O	4:C:221:ARG:NH1	2.43	0.52
2:D:534:GLU:OE1	2:D:735:ASN:ND2	2.42	0.51
4:C:197:GLU:OE1	4:C:201:ARG:NH2	2.37	0.51
2:D:524:GLU:OE1	2:D:547:THR:OG1	2.29	0.51
3:A:27:PHE:HA	3:A:1188:PHE:O	2.10	0.51
3:A:1149:HIS:CE1	3:A:1157:PHE:HE1	2.28	0.51
2:D:271:LEU:HD13	2:D:335:PHE:HB3	1.91	0.51
2:D:868:SER:O	2:D:872:ARG:NE	2.39	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:918:LEU:O	2:D:922:TRP:HD1	1.93	0.51
1:B:565:ASP:OD1	1:B:618:THR:CG2	2.55	0.51
2:D:582:SER:HA	2:D:586:PHE:HB3	1.91	0.51
4:C:213:TYR:CE1	4:C:964:LEU:HD13	2.42	0.51
4:C:957:LEU:O	4:C:961:ASN:HB2	2.11	0.51
2:D:296:LEU:HA	2:D:299:GLU:OE1	2.11	0.51
2:D:1027:LEU:O	2:D:1031:SER:OG	2.22	0.51
4:C:29:VAL:CG1	4:C:1161:MET:HE3	2.40	0.51
2:D:792:GLN:O	2:D:796:ARG:NH1	2.43	0.50
1:B:19:LEU:HG	1:B:23:TRP:CD1	2.45	0.50
4:C:230:ARG:NH2	4:C:950:SER:OG	2.44	0.50
1:B:572:LYS:HZ2	1:B:594:VAL:CG1	2.24	0.50
2:D:943:GLU:HA	2:D:947:LEU:HD21	1.93	0.50
2:D:1162:ASP:OD2	2:D:1165:ARG:NH2	2.45	0.50
1:B:556:ALA:HB2	1:B:593:ASP:OD1	2.07	0.50
2:D:1168:ASP:O	2:D:1172:HIS:N	2.45	0.50
2:D:733:ILE:HD12	2:D:736:CYS:HB2	1.92	0.50
2:D:1295:TRP:NE1	3:A:1095:PRO:HD2	2.27	0.50
2:D:518:GLN:HE21	2:D:520:LEU:H	1.58	0.50
2:D:1077:LYS:HG2	2:D:1079:ILE:H	1.76	0.50
2:D:836:ASP:OD1	2:D:837:THR:N	2.45	0.50
1:B:75:LEU:HD13	4:C:991:ARG:HD2	1.92	0.50
4:C:1035:LEU:HD13	4:C:1104:LEU:HD11	1.94	0.50
2:D:371:ILE:O	2:D:375:VAL:HG22	2.12	0.49
2:D:605:GLU:OE1	2:D:605:GLU:N	2.44	0.49
3:A:5:LEU:HD11	3:A:94:GLU:HB2	1.94	0.49
1:B:44:ILE:HD13	1:B:60:LEU:HD12	1.94	0.49
2:D:459:GLN:HE21	2:D:514:SER:HB3	1.77	0.49
1:B:583:ASN:HB3	3:A:1226:TYR:HB3	1.95	0.49
2:D:268:TYR:O	2:D:271:LEU:HG	2.12	0.49
2:D:634:LYS:O	2:D:638:LEU:HD23	2.12	0.49
4:C:27:HIS:HB3	4:C:1165:ALA:HA	1.93	0.49
2:D:679:THR:OG1	2:D:736:CYS:SG	2.67	0.49
2:D:726:ASP:HB3	2:D:729:ALA:HB3	1.94	0.49
4:C:957:LEU:C	4:C:957:LEU:HD23	2.38	0.49
2:D:596:ASP:O	2:D:600:MET:HG2	2.11	0.49
4:C:1124:LEU:O	4:C:1154:CYS:HA	2.13	0.49
2:D:1421:SER:O	2:D:1425:ARG:NE	2.46	0.49
3:A:16:ARG:HG2	3:A:1215:SER:HB3	1.93	0.49
3:A:1124:LYS:HE3	3:A:1127:ARG:HE	1.77	0.49
3:A:1222:ASN:OD1	3:A:1223:LEU:N	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:651:LEU:HD23	2:D:774:PHE:HZ	1.76	0.49
3:A:90:LYS:HE2	3:A:104:LYS:HB2	1.93	0.49
3:A:1033:THR:HB	3:A:1037:ARG:HH21	1.76	0.49
2:D:675:ILE:HB	2:D:678:ILE:HB	1.94	0.49
4:C:1095:ASN:OD1	4:C:1102:LYS:NZ	2.28	0.49
2:D:235:GLU:HA	2:D:238:ASN:HD22	1.78	0.48
2:D:513:GLN:NE2	2:D:704:ASN:HB2	2.28	0.48
2:D:513:GLN:HE22	2:D:704:ASN:HB2	1.77	0.48
6:Y:10:DT:H2''	6:Y:11:DC:H5''	1.95	0.48
2:D:1468:SER:OG	2:D:1469:ILE:N	2.44	0.48
3:A:195:SER:HB2	3:A:1045:PHE:CE1	2.49	0.48
1:B:61:MET:HE2	4:C:1005:LEU:HG	1.94	0.48
2:D:268:TYR:CB	2:D:332:LEU:CD2	2.67	0.48
2:D:271:LEU:CD1	2:D:335:PHE:HB3	2.42	0.48
2:D:633:SER:OG	2:D:634:LYS:N	2.46	0.48
2:D:760:ASP:HA	2:D:763:ILE:HD13	1.96	0.48
4:C:100:ARG:NH1	4:C:109:TYR:OH	2.46	0.48
1:B:14:LEU:HD11	1:B:60:LEU:HD13	1.96	0.48
2:D:374:ILE:HG22	2:D:386:GLU:HB3	1.95	0.48
2:D:634:LYS:HE2	2:D:795:LEU:HD11	1.95	0.48
2:D:1138:ARG:HH22	2:D:1194:LYS:HZ3	1.59	0.48
2:D:1311:ILE:O	2:D:1314:SER:OG	2.31	0.48
2:D:1427:LYS:HD2	2:D:1431:GLN:HE22	1.79	0.48
2:D:1112:SER:O	2:D:1116:ARG:NH1	2.47	0.48
2:D:1079:ILE:HG23	2:D:1083:PHE:HD2	1.77	0.48
4:C:1048:ARG:HH11	4:C:1078:ILE:HG21	1.79	0.48
2:D:1034:PHE:CE1	2:D:1037:LEU:HD13	2.49	0.47
2:D:1529:SER:O	2:D:1529:SER:OG	2.32	0.47
4:C:993:GLU:HG3	4:C:997:ARG:HH21	1.78	0.47
2:D:330:THR:O	2:D:334:LEU:HD23	2.15	0.47
2:D:251:ARG:NH1	2:D:257:LYS:H	2.13	0.47
2:D:301:LYS:HB2	2:D:302:GLU:OE2	2.14	0.47
2:D:1501:ARG:HB3	2:D:1505:LEU:HD23	1.95	0.47
3:A:1124:LYS:CE	3:A:1127:ARG:HE	2.27	0.47
2:D:394:LEU:HA	2:D:397:VAL:HG22	1.96	0.47
3:A:31:ILE:O	3:A:1206:GLY:HA2	2.15	0.47
1:B:560:LEU:HD22	1:B:567:TYR:CE2	2.50	0.47
2:D:264:ILE:CD1	2:D:325:PHE:CZ	2.97	0.47
2:D:1159:ARG:NH1	2:D:1252:GLU:OE2	2.47	0.47
2:D:844:THR:HA	2:D:847:MET:HE2	1.97	0.47
2:D:1475:ILE:O	2:D:1478:THR:OG1	2.31	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:1476:ILE:HA	2:D:1479:VAL:HG22	1.97	0.47
2:D:294:GLN:HA	2:D:297:GLU:OE1	2.14	0.47
2:D:386:GLU:OE2	2:D:389:HIS:ND1	2.35	0.47
2:D:1464:ILE:HD12	2:D:1465:PRO:HD2	1.97	0.47
3:A:1106:ASP:OD1	3:A:1109:GLU:N	2.40	0.47
4:C:217:ASP:O	4:C:220:ARG:N	2.45	0.47
2:D:1268:LEU:HD12	2:D:1271:LYS:HB2	1.96	0.47
2:D:1410:GLN:HA	2:D:1464:ILE:HD13	1.97	0.47
1:B:54:LEU:O	1:B:57:SER:OG	2.26	0.47
1:B:590:LEU:HA	1:B:590:LEU:HD23	1.77	0.47
2:D:268:TYR:HE2	2:D:335:PHE:CE1	2.32	0.47
2:D:1435:PRO:HG3	2:D:1453:PHE:HE2	1.80	0.47
1:B:585:GLU:N	1:B:585:GLU:OE2	2.48	0.47
2:D:476:SER:O	2:D:504:TYR:OH	2.33	0.47
2:D:211:LYS:HB2	2:D:214:ARG:O	2.15	0.46
2:D:790:SER:OG	2:D:792:GLN:O	2.30	0.46
2:D:1143:ASN:O	2:D:1146:LYS:N	2.44	0.46
4:C:220:ARG:O	4:C:224:GLU:CB	2.54	0.46
2:D:869:THR:HG23	2:D:910:ILE:HD11	1.97	0.46
3:A:1166:LEU:HD22	3:A:1170:ASN:HD21	1.80	0.46
8:A:1302:ADP:H5'1	4:C:1097:LEU:O	2.14	0.46
2:D:374:ILE:HG13	2:D:375:VAL:HG13	1.97	0.46
2:D:626:ASN:HD21	2:D:629:GLN:HE22	1.64	0.46
1:B:19:LEU:HG	1:B:23:TRP:HD1	1.81	0.46
2:D:285:GLU:HA	2:D:288:SER:HB3	1.97	0.46
2:D:1104:MET:SD	2:D:1104:MET:N	2.88	0.46
1:B:572:LYS:NZ	1:B:594:VAL:HG13	2.14	0.46
2:D:1020:LEU:HB2	2:D:1024:MET:HE1	1.98	0.46
4:C:220:ARG:NH1	4:C:957:LEU:HD21	2.30	0.46
3:A:49:LEU:HD11	3:A:1156:PHE:CZ	2.49	0.46
4:C:212:VAL:O	4:C:216:LYS:N	2.49	0.46
2:D:607:CYS:HB2	2:D:708:TYR:HD2	1.81	0.46
2:D:951:TYR:HD1	2:D:995:LEU:HD11	1.81	0.46
2:D:1039:ASP:OD1	2:D:1041:SER:N	2.44	0.46
1:B:55:ARG:HG3	1:B:56:LEU:HD12	1.97	0.45
2:D:216:GLN:O	2:D:220:LEU:HG	2.16	0.45
2:D:270:ALA:O	2:D:274:LEU:HD23	2.15	0.45
2:D:509:VAL:O	2:D:513:GLN:N	2.48	0.45
2:D:1182:ASP:O	2:D:1184:ALA:N	2.49	0.45
2:D:1267:LYS:HG3	2:D:1271:LYS:HG3	1.98	0.45
4:C:978:PHE:O	4:C:982:THR:OG1	2.21	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:280:CYS:SG	2:D:281:ASP:N	2.89	0.45
2:D:518:GLN:NE2	2:D:520:LEU:HB3	2.31	0.45
1:B:75:LEU:HD23	4:C:189:ILE:HD13	1.98	0.45
1:B:552:SER:O	1:B:593:ASP:OD1	2.35	0.45
2:D:679:THR:HG1	2:D:736:CYS:HG	1.64	0.45
2:D:259:ILE:HG22	2:D:260:SER:O	2.17	0.45
4:C:42:PHE:CD1	4:C:1123:ILE:HD11	2.52	0.45
2:D:446:SER:HA	2:D:449:PHE:CD2	2.51	0.45
2:D:1169:ASP:OD1	2:D:1169:ASP:N	2.47	0.45
2:D:905:ASP:OD1	2:D:906:GLU:N	2.48	0.45
2:D:1193:GLN:NE2	2:D:1230:THR:OG1	2.50	0.45
2:D:856:ILE:HD13	2:D:856:ILE:HA	1.86	0.45
4:C:181:GLU:O	4:C:184:GLN:HG3	2.16	0.45
1:B:560:LEU:HD11	1:B:572:LYS:NZ	2.32	0.45
2:D:487:ARG:HB2	6:Y:10:DT:H3'	1.99	0.45
2:D:1086:SER:O	2:D:1089:SER:OG	2.26	0.45
2:D:1144:PHE:HA	2:D:1147:MET:HG3	1.99	0.45
2:D:291:LEU:HD12	2:D:292:VAL:N	2.33	0.44
4:C:89:PHE:HE1	4:C:124:LEU:HA	1.82	0.44
2:D:794:SER:O	2:D:797:THR:OG1	2.26	0.44
2:D:1411:SER:O	2:D:1415:ILE:HG12	2.18	0.44
2:D:1488:PRO:HB2	3:A:1049:ARG:HH12	1.81	0.44
2:D:1518:ARG:HD3	2:D:1521:LYS:HD2	1.98	0.44
4:C:9:GLN:OE1	4:C:77:TYR:CE1	2.71	0.44
4:C:1187:GLU:OE2	4:C:1187:GLU:N	2.48	0.44
2:D:1478:THR:O	2:D:1481:SER:OG	2.21	0.44
3:A:186:ASP:HA	3:A:189:VAL:HG12	1.98	0.44
4:C:1124:LEU:HB3	4:C:1127:CYS:SG	2.58	0.44
6:Y:13:DC:H2''	6:Y:14:DA:H8	1.83	0.44
2:D:969:LEU:O	2:D:972:SER:OG	2.23	0.44
2:D:988:LEU:O	2:D:992:ILE:HG12	2.17	0.44
8:A:1302:ADP:O2B	4:C:1098:SER:HB2	2.17	0.44
4:C:110:SER:OG	4:C:111:LEU:N	2.50	0.44
4:C:165:THR:O	4:C:165:THR:OG1	2.33	0.44
2:D:423:TYR:OH	4:C:973:LYS:HG2	2.17	0.44
2:D:1334:ILE:HD11	2:D:1344:CYS:SG	2.57	0.44
3:A:114:GLU:HB3	3:A:121:ILE:HD11	1.99	0.44
4:C:110:SER:OG	4:C:111:LEU:O	2.33	0.44
2:D:601:LEU:HD12	2:D:613:ILE:HD12	1.99	0.44
2:D:958:CYS:O	2:D:1025:SER:OG	2.35	0.44
2:D:1046:LEU:HD13	2:D:1050:LEU:HD11	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:217:ASP:OD1	4:C:220:ARG:HB2	2.17	0.44
2:D:1239:ASN:OD1	2:D:1242:GLU:N	2.48	0.44
2:D:280:CYS:HB2	2:D:340:VAL:CA	2.39	0.44
2:D:285:GLU:HA	2:D:289:ILE:HG13	2.00	0.44
2:D:1251:LEU:HD21	2:D:1328:GLU:HG2	1.99	0.44
4:C:1107:LEU:HD12	4:C:1111:PHE:CZ	2.53	0.44
2:D:511:LEU:O	2:D:514:SER:OG	2.30	0.43
2:D:652:PHE:CZ	2:D:656:LEU:HB3	2.53	0.43
3:A:13:LYS:HB2	8:A:1302:ADP:C5	2.53	0.43
3:A:86:THR:HG21	3:A:109:PRO:HD3	1.99	0.43
4:C:1146:MET:HA	4:C:1149:THR:HG22	2.00	0.43
2:D:735:ASN:HA	2:D:738:ASP:HB3	2.00	0.43
3:A:60:ASN:HD22	3:A:63:GLU:CD	2.26	0.43
3:A:191:LEU:O	3:A:195:SER:HB3	2.18	0.43
4:C:134:ASN:HA	4:C:135:PRO:HD3	1.87	0.43
4:C:1045:MET:HA	4:C:1078:ILE:HG12	2.00	0.43
1:B:583:ASN:N	1:B:583:ASN:HD22	2.16	0.43
2:D:293:LYS:HA	2:D:296:LEU:HD12	1.98	0.43
2:D:1104:MET:HE2	2:D:1104:MET:HB2	1.71	0.43
3:A:172:LEU:HD23	3:A:172:LEU:HA	1.90	0.43
2:D:213:GLN:HE21	2:D:214:ARG:NH2	2.14	0.43
2:D:1209:ASP:OD1	2:D:1209:ASP:N	2.49	0.43
4:C:1013:LYS:O	4:C:1017:ILE:HG12	2.18	0.43
4:C:1094:ILE:HD12	4:C:1097:LEU:HD12	2.00	0.43
2:D:332:LEU:HA	2:D:332:LEU:HD23	1.64	0.43
2:D:470:ASP:HA	2:D:473:ILE:HD12	2.00	0.43
2:D:604:PRO:HB2	2:D:692:PHE:HZ	1.83	0.43
2:D:1077:LYS:HZ1	2:D:1084:LEU:HD13	1.84	0.43
3:A:1159:LEU:HD23	3:A:1159:LEU:HA	1.73	0.43
2:D:234:ILE:O	2:D:238:ASN:ND2	2.52	0.43
2:D:568:ALA:O	2:D:572:SER:HB3	2.19	0.43
2:D:670:ASP:OD1	2:D:778:LYS:NZ	2.48	0.43
3:A:117:ILE:HD11	3:A:127:TYR:HA	2.01	0.43
3:A:1119:ALA:H	3:A:1129:MET:HE3	1.84	0.43
4:C:59:GLU:HG2	4:C:60:GLU:OE2	2.19	0.43
1:B:569:GLU:HB2	1:B:615:ILE:HD11	2.01	0.43
2:D:549:GLU:HA	2:D:552:LEU:HD12	2.01	0.43
2:D:280:CYS:CB	2:D:340:VAL:HA	2.41	0.43
2:D:282:LYS:HD2	2:D:282:LYS:N	2.34	0.43
2:D:779:PHE:O	2:D:782:SER:OG	2.34	0.43
3:A:30:ILE:HA	3:A:1205:VAL:HG23	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:165:THR:OG1	4:C:1013:LYS:HE3	2.19	0.43
4:C:185:LYS:HA	4:C:188:LYS:HE2	2.01	0.43
6:Y:36:DG:H8	6:Y:36:DG:OP2	2.02	0.43
2:D:987:THR:HG23	2:D:988:LEU:HD22	2.01	0.42
1:B:556:ALA:CB	1:B:593:ASP:CG	2.84	0.42
2:D:517:ILE:HG12	2:D:708:TYR:HD1	1.84	0.42
2:D:543:GLU:HA	2:D:546:LYS:HB2	2.01	0.42
2:D:1227:MET:HB3	2:D:1227:MET:HE2	1.36	0.42
2:D:1472:PRO:HA	2:D:1475:ILE:HG12	2.01	0.42
4:C:84:ASN:HD22	4:C:88:ARG:HB3	1.84	0.42
2:D:541:LEU:HD23	2:D:544:HIS:CD2	2.54	0.42
2:D:886:THR:O	2:D:892:ARG:NH2	2.53	0.42
4:C:1171:VAL:HG12	4:C:1180:VAL:HG12	1.99	0.42
1:B:59:GLN:HE22	4:C:171:ARG:NH1	2.18	0.42
2:D:370:ALA:HB1	2:D:390:LEU:HD11	2.01	0.42
3:A:1133:SER:HB3	8:C:1202:ADP:H5'1	2.02	0.42
1:B:605:VAL:HG21	3:A:1219:LEU:HD11	2.02	0.42
2:D:418:VAL:HA	2:D:421:ILE:HG12	2.02	0.42
2:D:1438:LEU:HD12	2:D:1438:LEU:HA	1.83	0.42
3:A:42:MET:HG3	3:A:1158:VAL:CG1	2.48	0.42
1:B:584:ARG:HH21	1:B:584:ARG:CG	2.30	0.42
2:D:229:LEU:HA	2:D:232:GLN:OE1	2.20	0.42
2:D:1143:ASN:O	2:D:1147:MET:HG3	2.19	0.42
4:C:29:VAL:HG13	4:C:1165:ALA:HB2	2.01	0.42
5:X:30:DC:H2'	5:X:31:DA:C8	2.55	0.42
2:D:1356:ILE:HG13	2:D:1358:GLU:H	1.83	0.42
2:D:518:GLN:HE21	2:D:520:LEU:HB3	1.83	0.42
4:C:1156:THR:HB	4:C:1157:PHE:H	1.34	0.42
2:D:426:PRO:HB3	2:D:479:ASN:HD21	1.85	0.42
2:D:1208:ILE:HD12	2:D:1208:ILE:HA	1.90	0.42
3:A:1206:GLY:O	3:A:1218:THR:OG1	2.24	0.42
4:C:6:ILE:HG23	4:C:80:VAL:HG12	2.02	0.42
4:C:155:ARG:CD	4:C:1080:ILE:HD11	2.50	0.42
1:B:582:CYS:C	1:B:584:ARG:N	2.77	0.41
2:D:272:THR:C	2:D:275:SER:HG	2.26	0.41
2:D:1004:ILE:HD13	2:D:1004:ILE:HG21	1.87	0.41
2:D:1221:LEU:O	2:D:1224:SER:N	2.43	0.41
4:C:1135:TYR:O	4:C:1139:ILE:HG12	2.20	0.41
2:D:281:ASP:OD1	2:D:342:SER:OG	2.37	0.41
2:D:803:ILE:HG23	2:D:806:MET:HE3	2.02	0.41
2:D:1458:CYS:HB3	2:D:1516:LEU:HD12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X:10:DG:H5'	5:X:10:DG:C8	2.55	0.41
2:D:265:GLU:OE2	2:D:268:TYR:HD1	2.03	0.41
4:C:184:GLN:C	4:C:188:LYS:HZ3	2.28	0.41
4:C:217:ASP:C	4:C:220:ARG:H	2.27	0.41
2:D:1420:LYS:HZ2	5:X:15:DA:H3'	1.85	0.41
2:D:240:GLU:OE2	2:D:257:LYS:HD2	2.21	0.41
3:A:1127:ARG:HB3	3:A:1131:GLN:HE21	1.86	0.41
4:C:134:ASN:N	4:C:134:ASN:OD1	2.52	0.41
2:D:264:ILE:HA	2:D:267:LEU:HD12	2.03	0.41
2:D:803:ILE:HA	2:D:806:MET:HB3	2.01	0.41
2:D:225:ASP:O	2:D:228:LEU:HB3	2.21	0.41
2:D:227:ARG:O	2:D:230:ILE:HB	2.21	0.41
2:D:740:ASN:C	2:D:740:ASN:HD22	2.29	0.41
2:D:948:ARG:HD3	2:D:948:ARG:HA	1.84	0.41
2:D:1221:LEU:O	2:D:1223:ILE:N	2.54	0.41
3:A:1090:LYS:C	3:A:1173:LYS:HZ1	2.28	0.41
3:A:1139:MET:HE3	3:A:1170:ASN:HB2	2.02	0.41
4:C:958:HIS:O	4:C:961:ASN:HB3	2.20	0.41
5:X:2:DA:H2''	5:X:3:DG:C8	2.56	0.41
2:D:209:PRO:C	2:D:218:VAL:HG22	2.45	0.41
2:D:223:LEU:HG	2:D:227:ARG:CZ	2.51	0.41
2:D:405:SER:HA	2:D:457:THR:HG22	2.03	0.41
2:D:570:LEU:O	2:D:574:SER:OG	2.24	0.41
4:C:1004:GLU:O	4:C:1007:THR:OG1	2.34	0.41
2:D:297:GLU:HA	2:D:300:LEU:HD12	2.03	0.41
2:D:451:LYS:HE3	2:D:451:LYS:HB2	1.80	0.41
2:D:494:ARG:HH22	5:X:32:DC:H4'	1.85	0.41
2:D:499:LYS:HA	2:D:499:LYS:HD3	1.89	0.41
2:D:575:LEU:HD21	2:D:637:ALA:HB2	2.02	0.41
2:D:588:ILE:O	2:D:591:LYS:HG2	2.20	0.41
4:C:956:LYS:O	4:C:960:ILE:HG12	2.19	0.41
2:D:1165:ARG:HD3	2:D:1165:ARG:HA	1.82	0.41
3:A:195:SER:OG	3:A:196:PHE:N	2.53	0.41
4:C:995:LEU:O	4:C:998:SER:OG	2.31	0.41
2:D:266:LYS:HA	2:D:269:MET:HE3	2.03	0.40
2:D:286:GLU:HG3	2:D:346:LEU:CD2	2.35	0.40
2:D:645:VAL:HA	2:D:648:VAL:HG12	2.01	0.40
2:D:705:ILE:HD12	2:D:705:ILE:HA	1.89	0.40
2:D:800:LEU:HD23	2:D:800:LEU:HA	1.83	0.40
2:D:941:PHE:O	2:D:945:GLN:HB2	2.21	0.40
2:D:298:LYS:HA	2:D:301:LYS:HE3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:920:LYS:HD3	2:D:920:LYS:HA	1.94	0.40
2:D:1416:VAL:HG21	2:D:1428:LEU:HD21	2.03	0.40
3:A:200:ARG:O	3:A:204:ALA:HB2	2.21	0.40
2:D:286:GLU:OE1	2:D:286:GLU:N	2.41	0.40
2:D:402:ASN:O	2:D:405:SER:OG	2.28	0.40
2:D:739:LYS:HD3	2:D:739:LYS:HA	1.89	0.40
2:D:993:ARG:HD3	2:D:1037:LEU:HD23	2.04	0.40
2:D:1189:LEU:HB3	2:D:1211:MET:HE1	2.04	0.40
2:D:1400:THR:O	2:D:1402:LYS:N	2.52	0.40
3:A:31:ILE:HD12	3:A:31:ILE:HA	1.86	0.40
3:A:1171:VAL:HA	3:A:1174:ILE:HG22	2.03	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	B	148/628 (24%)	137 (93%)	11 (7%)	0	100	100
2	D	1262/1587 (80%)	1148 (91%)	114 (9%)	0	100	100
3	A	378/1228 (31%)	351 (93%)	27 (7%)	0	100	100
4	C	450/1194 (38%)	402 (89%)	48 (11%)	0	100	100
All	All	2238/4637 (48%)	2038 (91%)	200 (9%)	0	100	100

There are no Ramachandran outliers to report.

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	B	132/539 (24%)	128 (97%)	4 (3%)	36	57
2	D	1186/1480 (80%)	1185 (100%)	1 (0%)	88	90
3	A	330/1102 (30%)	330 (100%)	0	100	100
4	C	407/1082 (38%)	407 (100%)	0	100	100
All	All	2055/4203 (49%)	2050 (100%)	5 (0%)	85	88

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	582	CYS
1	B	583	ASN
1	B	584	ARG
1	B	585	GLU
2	D	299	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	583	ASN
2	D	238	ASN
2	D	258	HIS
2	D	459	GLN
2	D	513	GLN
2	D	518	GLN
2	D	557	HIS
2	D	626	ASN
2	D	682	ASN
2	D	725	ASN
2	D	740	ASN
2	D	822	GLN
2	D	938	GLN
2	D	1143	ASN
2	D	1193	GLN
2	D	1238	ASN
2	D	1336	GLN
3	A	60	ASN
3	A	194	HIS
4	C	28	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	C	34	ASN
4	C	84	ASN
4	C	951	ASN
4	C	979	ASN
4	C	1114	GLN
4	C	1122	ASN
4	C	1167	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
7	BEF	C	1201	8	0,3,3	-	-	-		
7	BEF	A	1301	8	0,3,3	-	-	-		
8	ADP	A	1302	7	28,29,29	2.00	4 (14%)	43,45,45	1.62	8 (18%)
8	ADP	C	1202	7	28,29,29	2.01	4 (14%)	43,45,45	1.76	8 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	ADP	A	1302	7	-	8/16/32/32	0/3/3/3
8	ADP	C	1202	7	-	8/16/32/32	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	C	1202	ADP	PA-O5'	7.80	1.89	1.59
8	A	1302	ADP	PA-O5'	7.78	1.89	1.59
8	A	1302	ADP	PA-O3A	-3.43	1.55	1.59
8	C	1202	ADP	PA-O3A	-3.36	1.55	1.59
8	A	1302	ADP	O2'-C2'	-3.25	1.34	1.43
8	C	1202	ADP	O2'-C2'	-3.24	1.34	1.43
8	C	1202	ADP	O5'-C5'	-2.36	1.35	1.44
8	A	1302	ADP	O5'-C5'	-2.33	1.35	1.44

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	C	1202	ADP	O2A-PA-O3A	7.33	127.09	107.27
8	A	1302	ADP	O3A-PA-O1A	5.44	127.06	110.70
8	C	1202	ADP	O5'-PA-O1A	-4.02	93.02	108.94
8	A	1302	ADP	O2A-PA-O5'	-3.20	93.06	107.57
8	A	1302	ADP	O5'-PA-O1A	-2.82	97.77	108.94
8	C	1202	ADP	O3B-PB-O3A	-2.76	95.38	104.64
8	A	1302	ADP	O3B-PB-O3A	-2.75	95.40	104.64
8	C	1202	ADP	C2-N1-C6	-2.36	114.85	118.73
8	A	1302	ADP	O2B-PB-O1B	2.35	119.97	110.83
8	A	1302	ADP	C2-N1-C6	-2.34	114.88	118.73
8	C	1202	ADP	O2B-PB-O1B	2.34	119.97	110.83
8	C	1202	ADP	N3-C4-N9	2.17	130.85	127.17
8	C	1202	ADP	O2A-PA-O5'	-2.15	97.80	107.57
8	A	1302	ADP	N3-C4-N9	2.11	130.75	127.17
8	C	1202	ADP	C3'-C2'-C1'	-2.09	97.52	101.46
8	A	1302	ADP	C3'-C2'-C1'	-2.05	97.58	101.46

There are no chirality outliers.

All (16) torsion outliers are listed below:

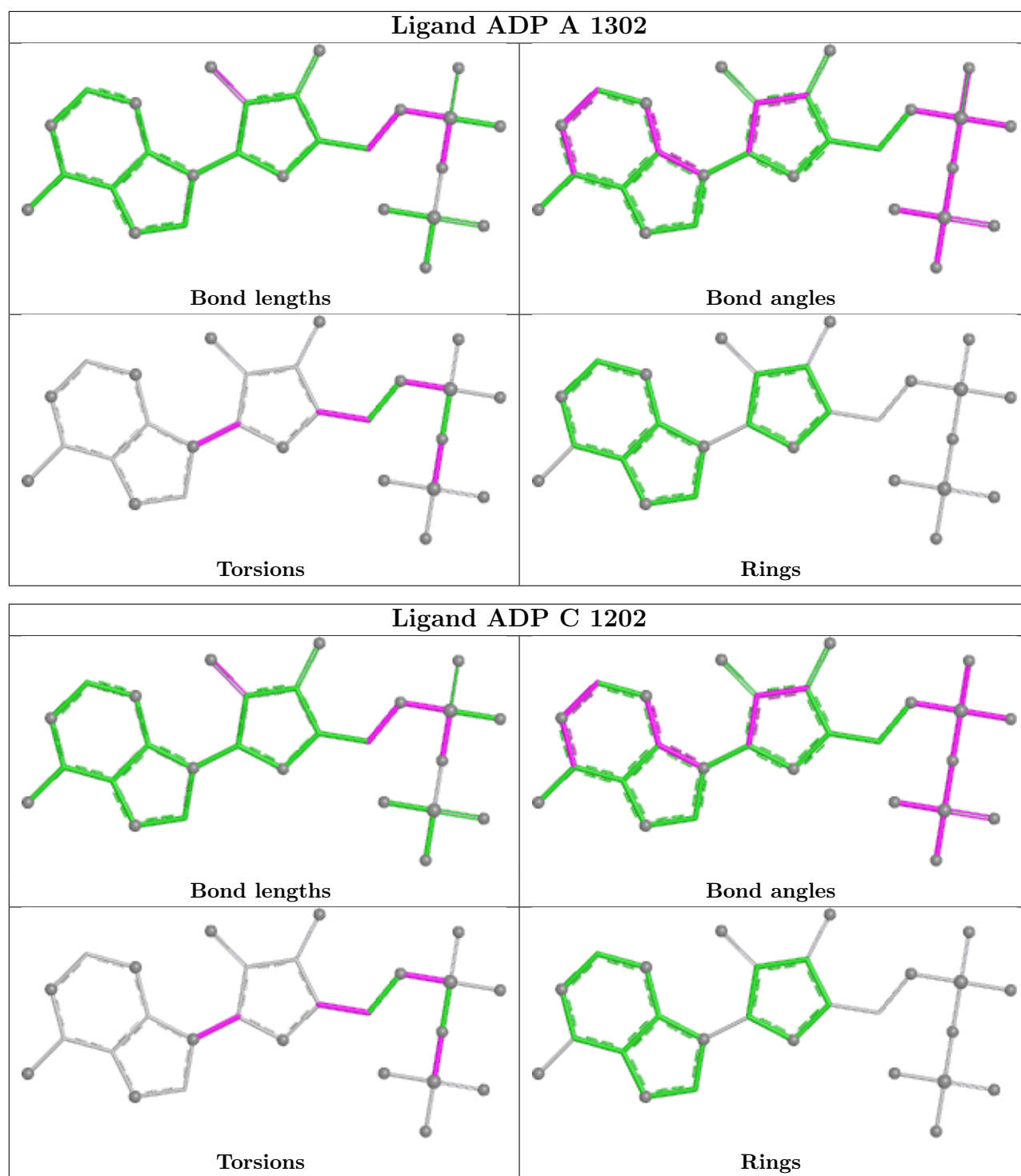
Mol	Chain	Res	Type	Atoms
8	A	1302	ADP	PA-O3A-PB-O2B
8	A	1302	ADP	C5'-O5'-PA-O1A
8	A	1302	ADP	C5'-O5'-PA-O2A
8	A	1302	ADP	C3'-C4'-C5'-O5'
8	C	1202	ADP	PA-O3A-PB-O2B
8	C	1202	ADP	C5'-O5'-PA-O1A
8	C	1202	ADP	C3'-C4'-C5'-O5'
8	A	1302	ADP	O4'-C4'-C5'-O5'
8	C	1202	ADP	O4'-C4'-C5'-O5'
8	A	1302	ADP	PA-O3A-PB-O1B
8	A	1302	ADP	C5'-O5'-PA-O3A
8	C	1202	ADP	C5'-O5'-PA-O2A
8	C	1202	ADP	C5'-O5'-PA-O3A
8	A	1302	ADP	C2'-C1'-N9-C8
8	C	1202	ADP	C2'-C1'-N9-C8
8	C	1202	ADP	PA-O3A-PB-O1B

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	1201	BEF	1	0
8	A	1302	ADP	4	0
8	C	1202	ADP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	D	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	602:SER	C	603:LEU	N	1.20

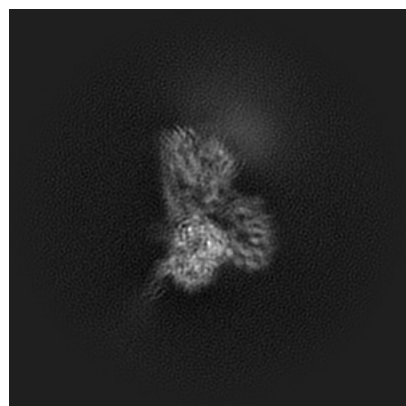
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10930. These allow visual inspection of the internal detail of the map and identification of artifacts.

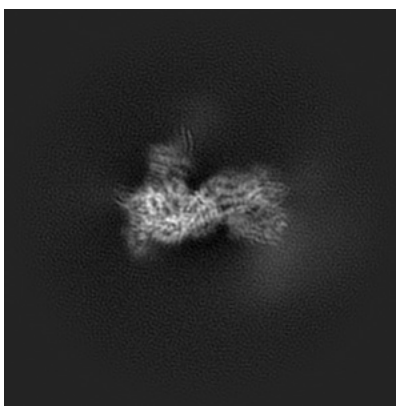
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

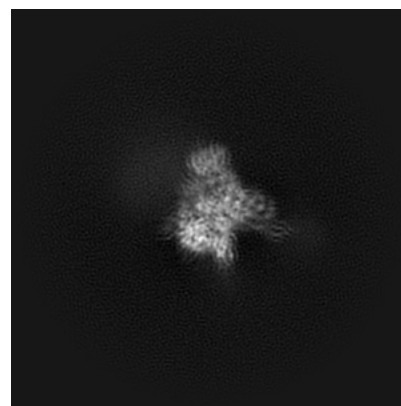
6.1.1 Primary map



X

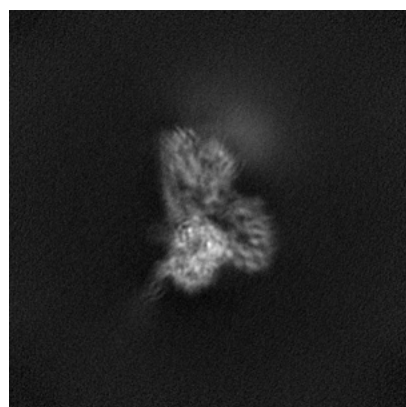


Y

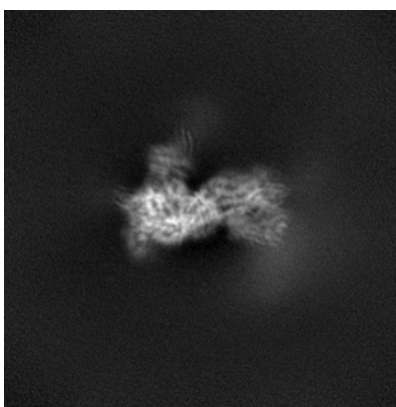


Z

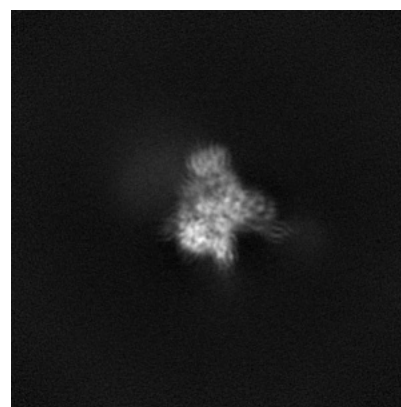
6.1.2 Raw map



X



Y

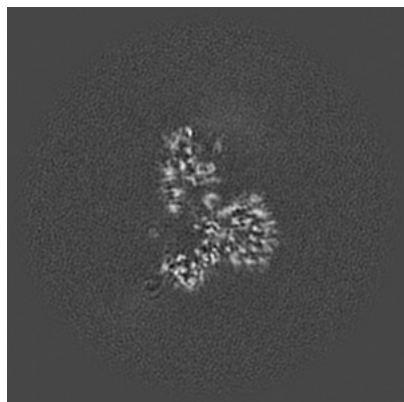


Z

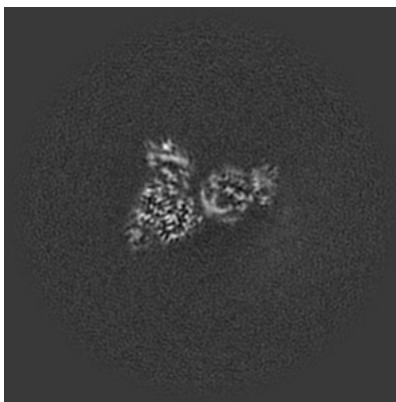
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

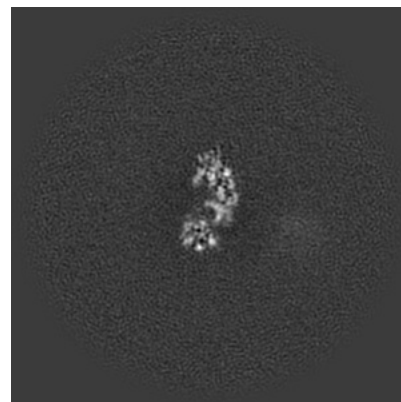
6.2.1 Primary map



X Index: 180

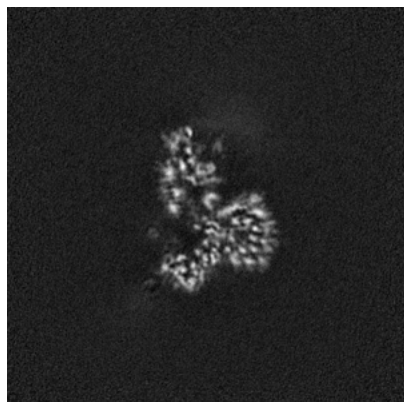


Y Index: 180

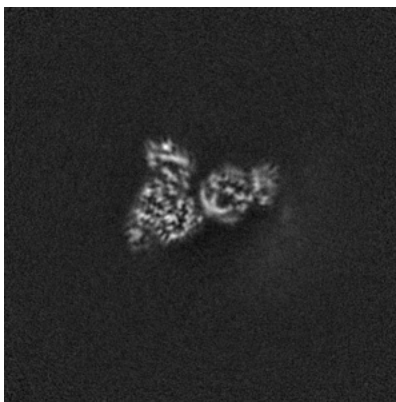


Z Index: 180

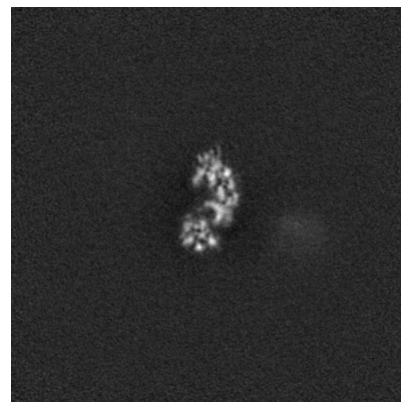
6.2.2 Raw map



X Index: 180



Y Index: 180

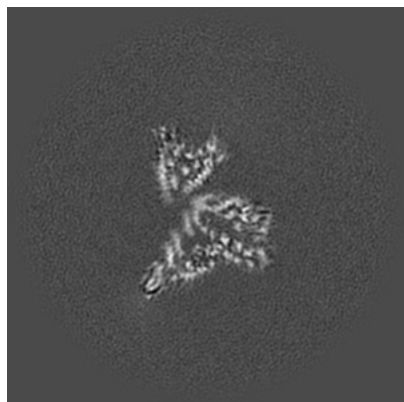


Z Index: 180

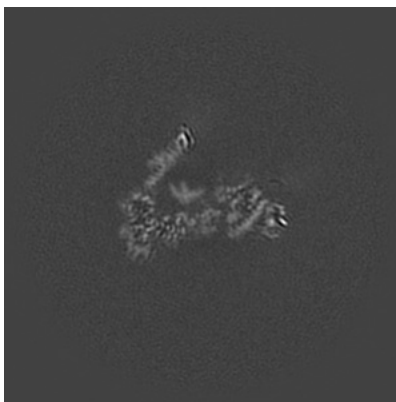
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

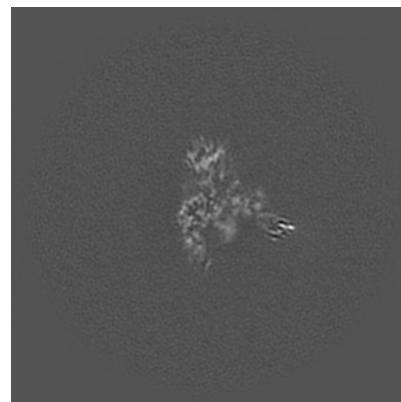
6.3.1 Primary map



X Index: 188

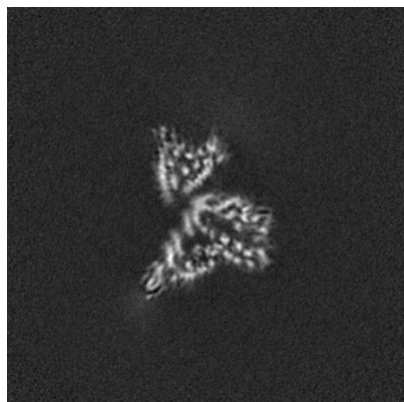


Y Index: 163

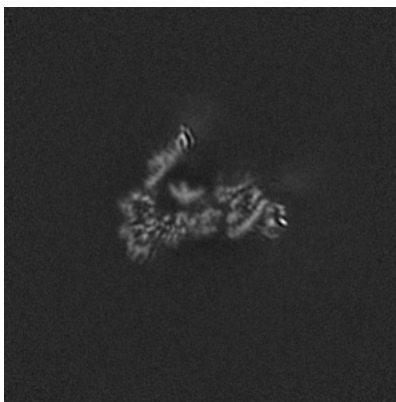


Z Index: 160

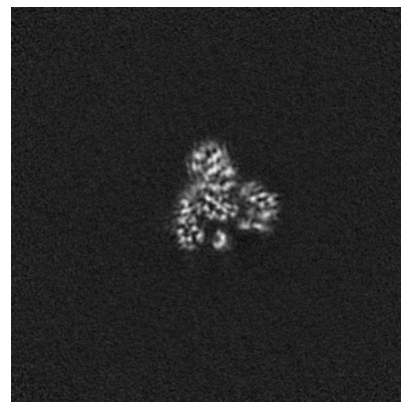
6.3.2 Raw map



X Index: 188



Y Index: 163

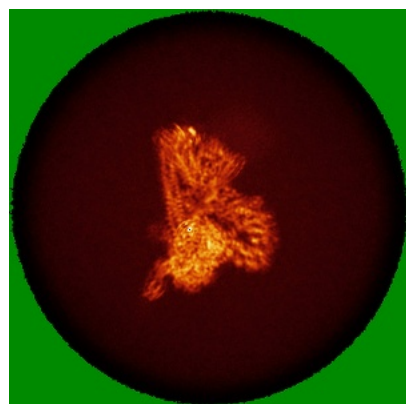


Z Index: 140

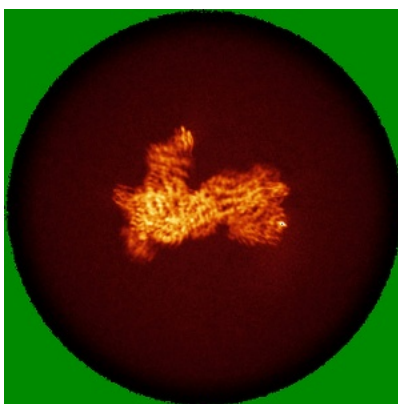
The images above show the largest variance slices of the map in three orthogonal directions.

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

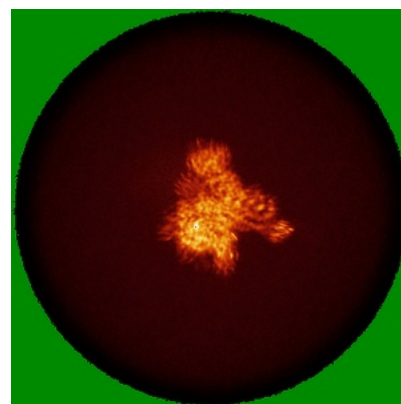
6.4.1 Primary map



X

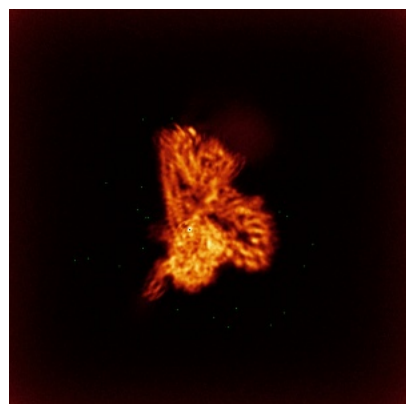


Y

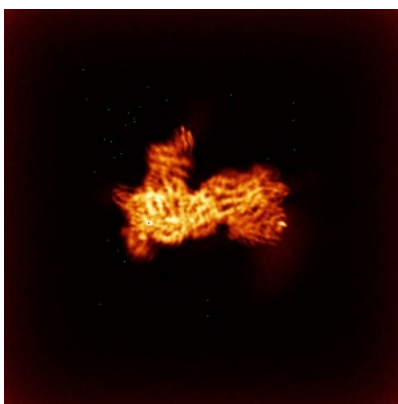


Z

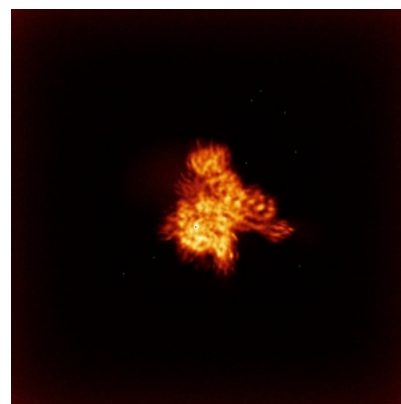
6.4.2 Raw map



X



Y

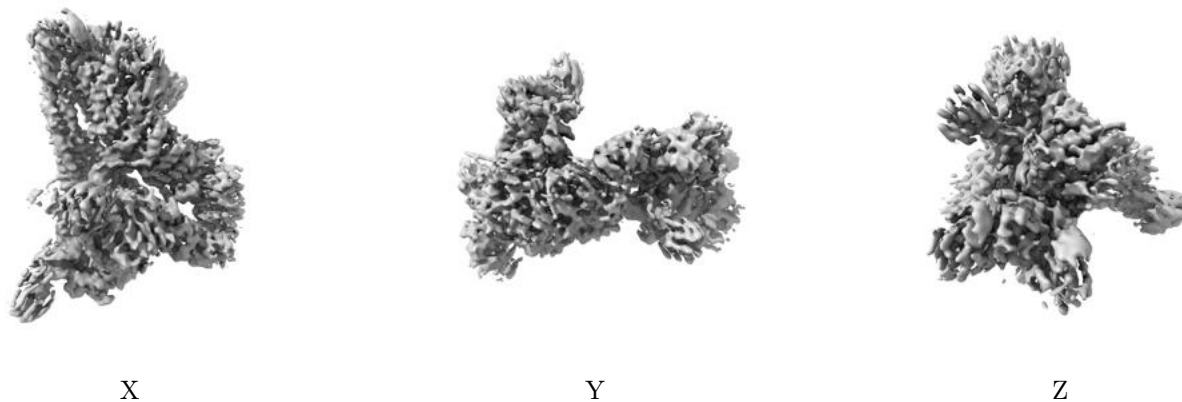


Z

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.

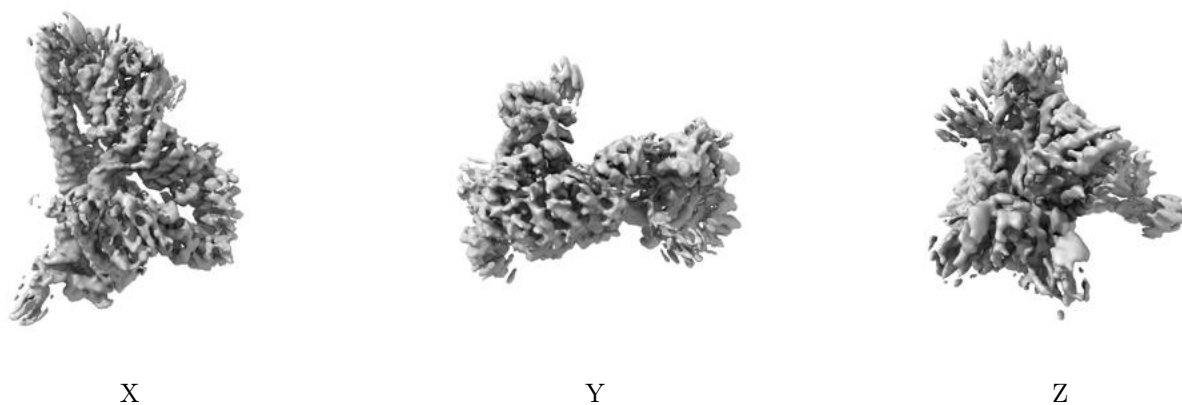
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

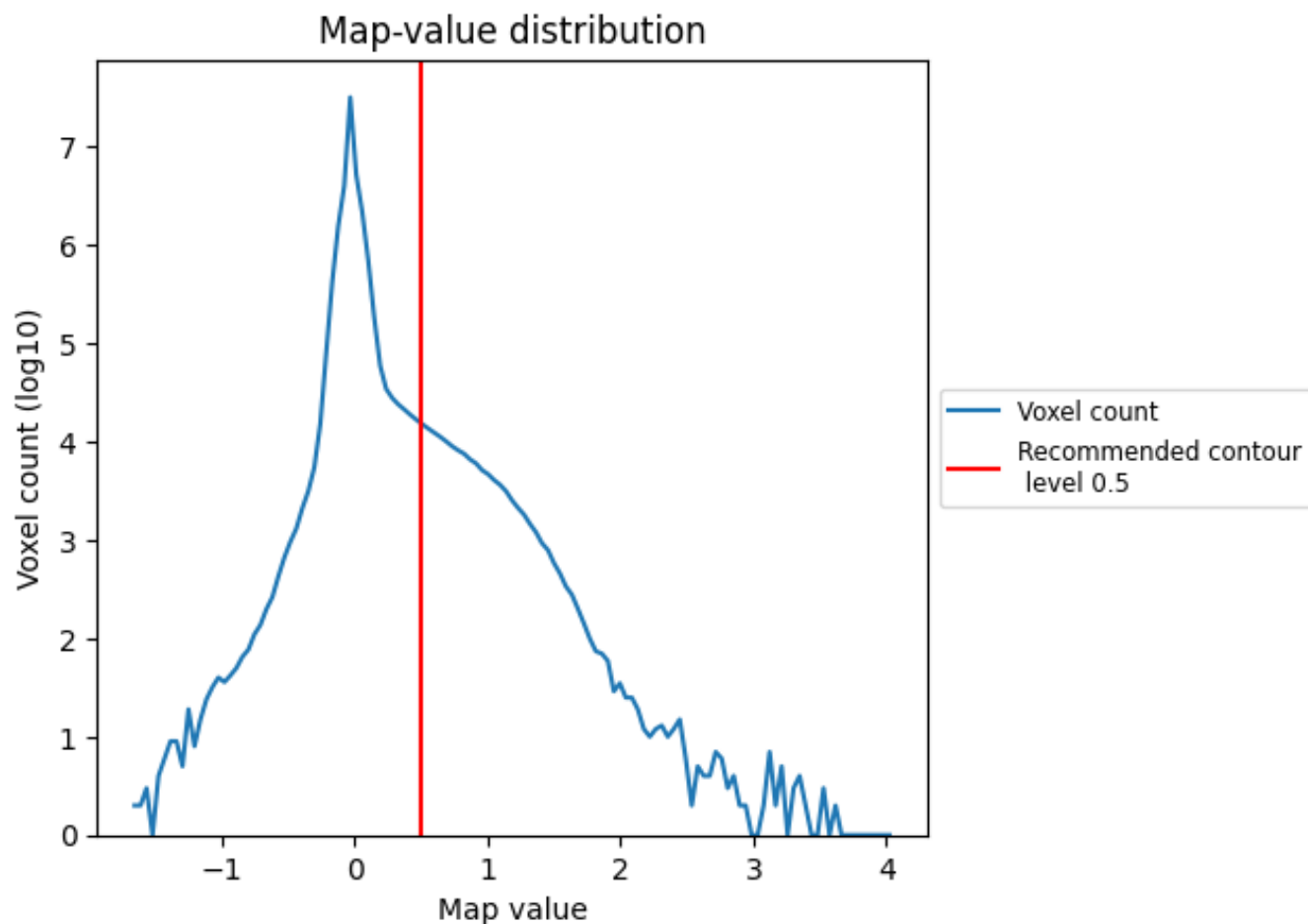
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

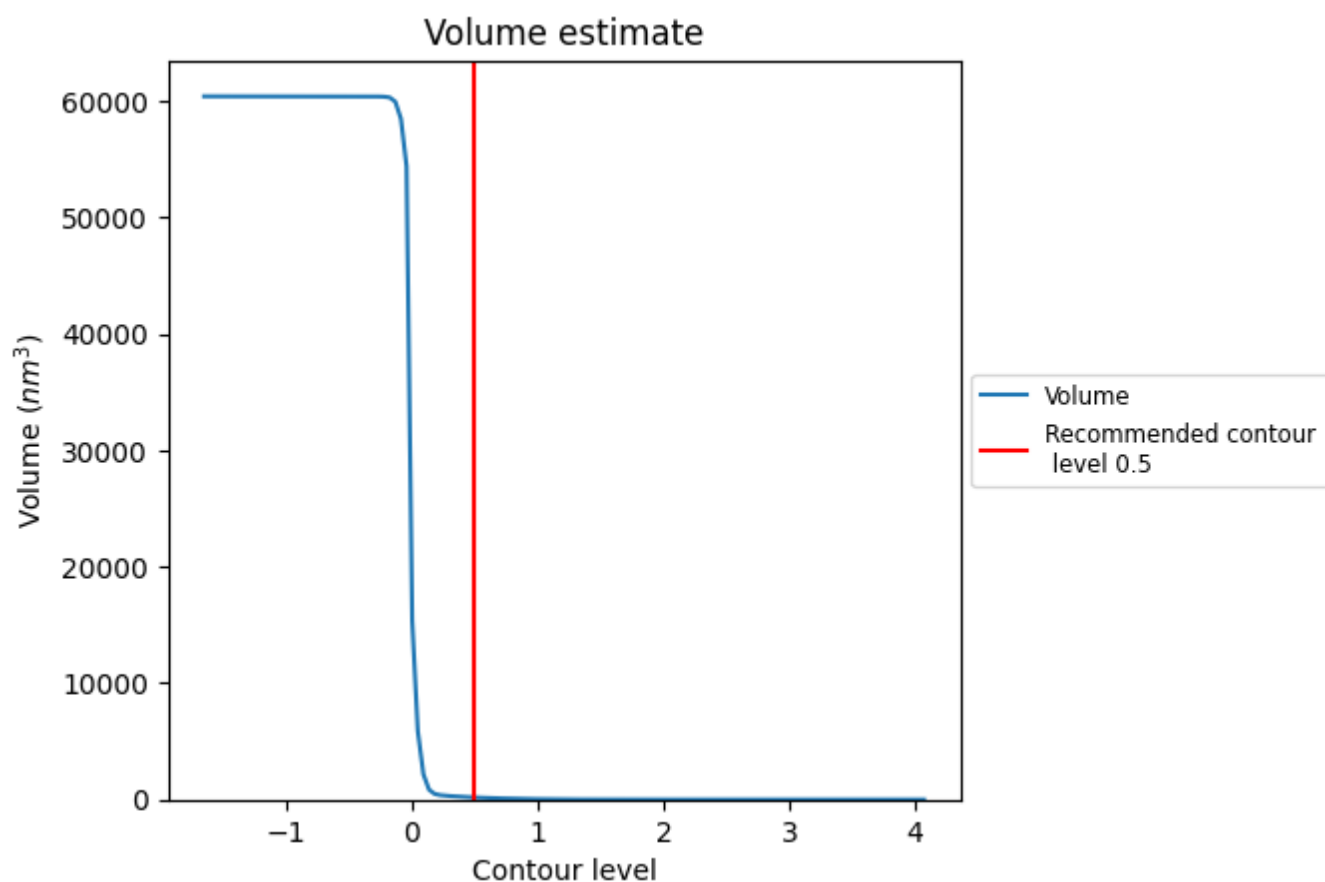
This section contains the results of statistical analysis of the map.

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.

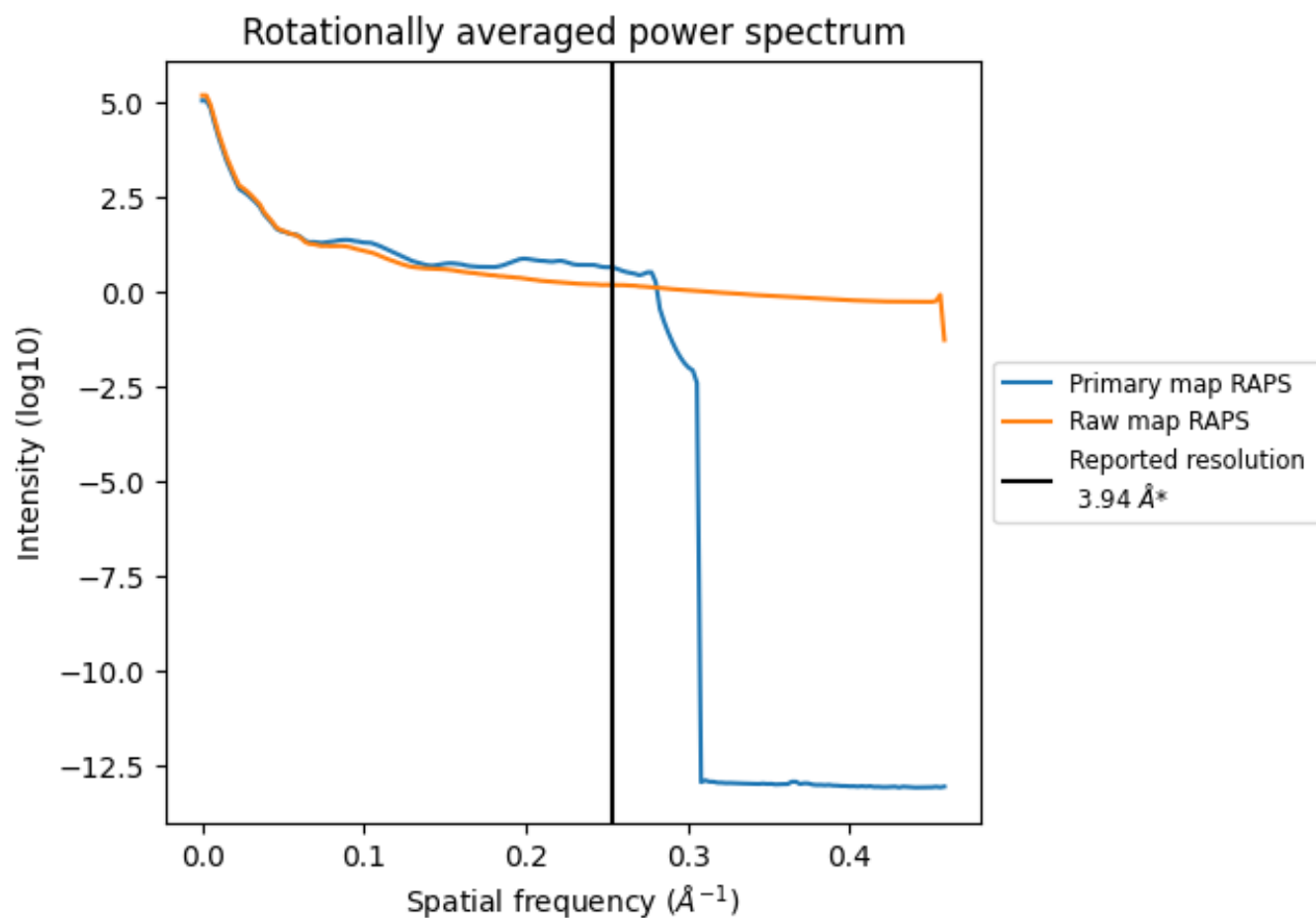
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 179 nm³; this corresponds to an approximate mass of 161 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 ⓘ

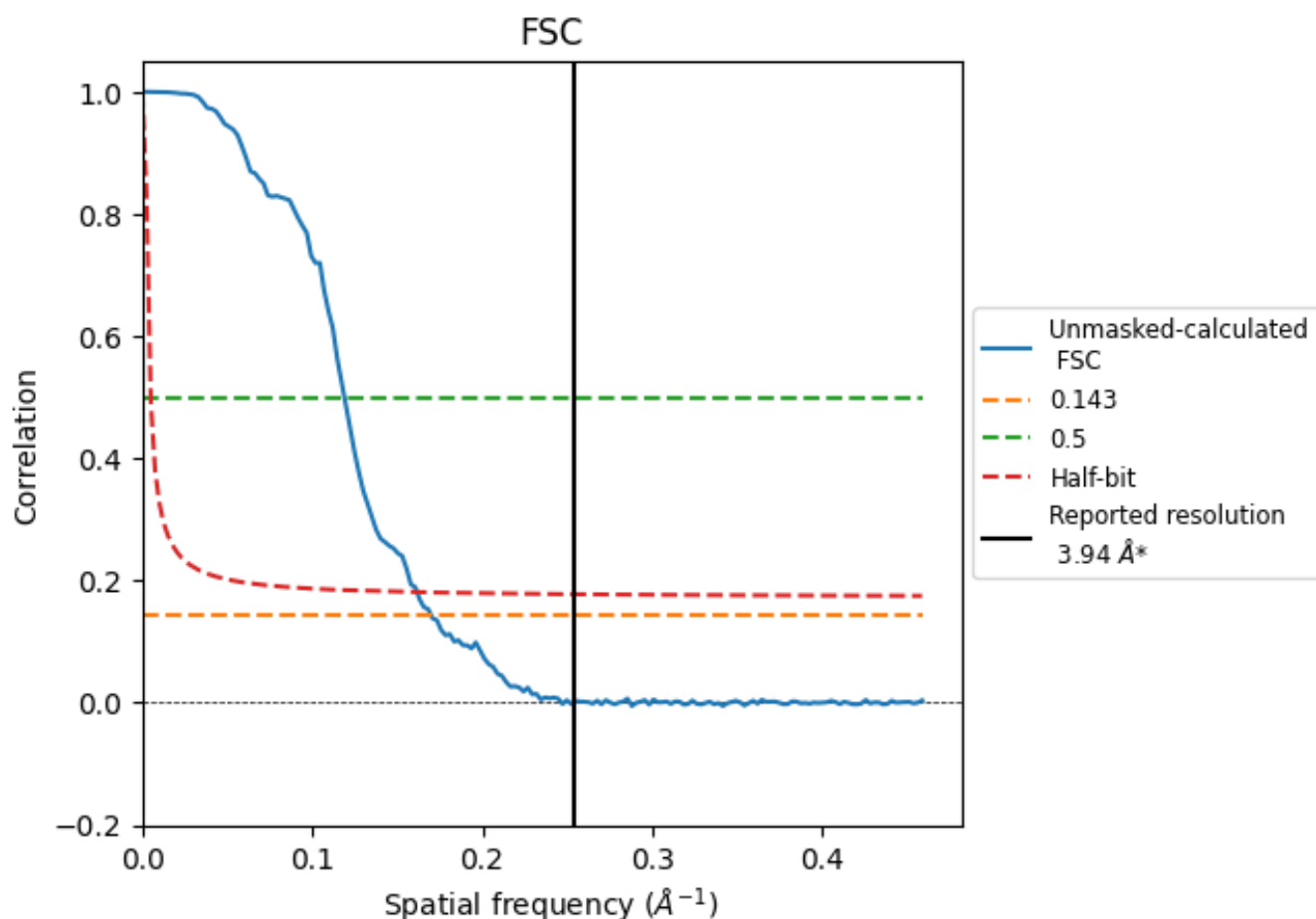


*Reported resolution corresponds to spatial frequency of 0.254 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.254 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

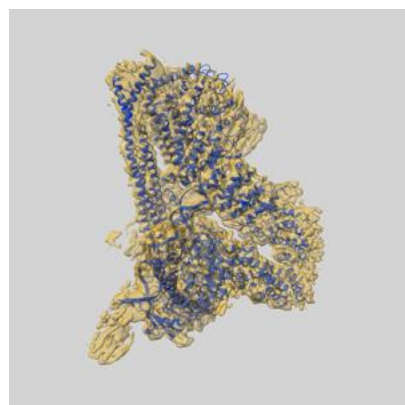
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.94	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.89	8.41	6.19

*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 5.89 differs from the reported value 3.94 by more than 10 %

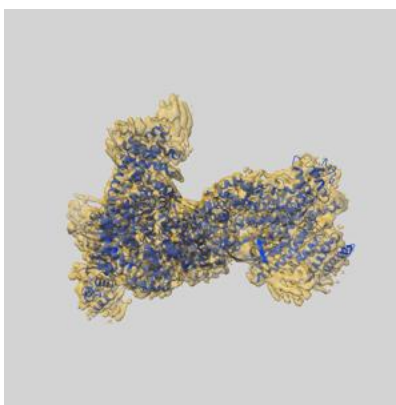
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10930 and PDB model 6YUF. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

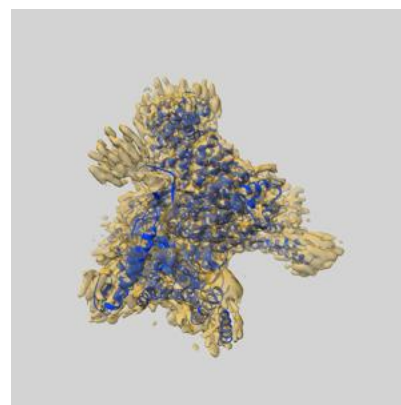
9.1 Map-model overlay [i](#)



X



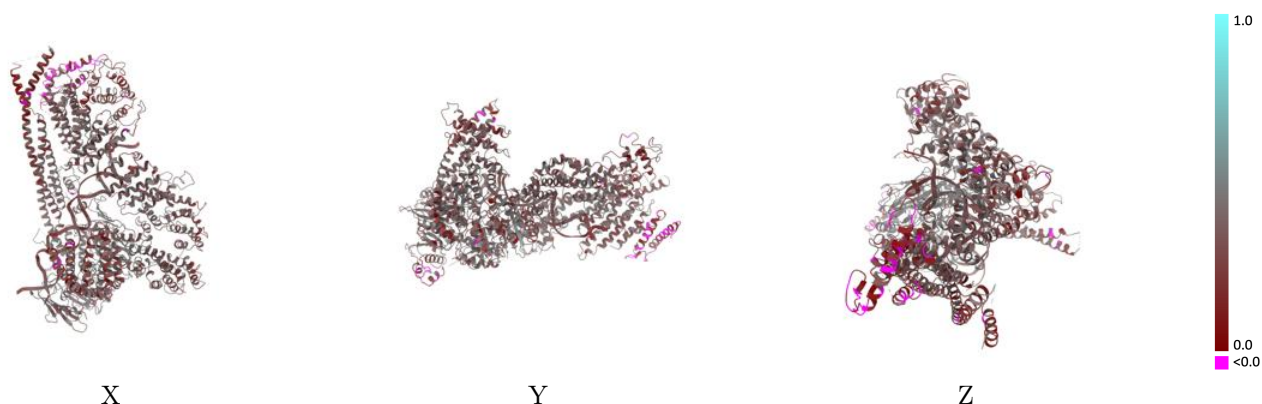
Y



Z

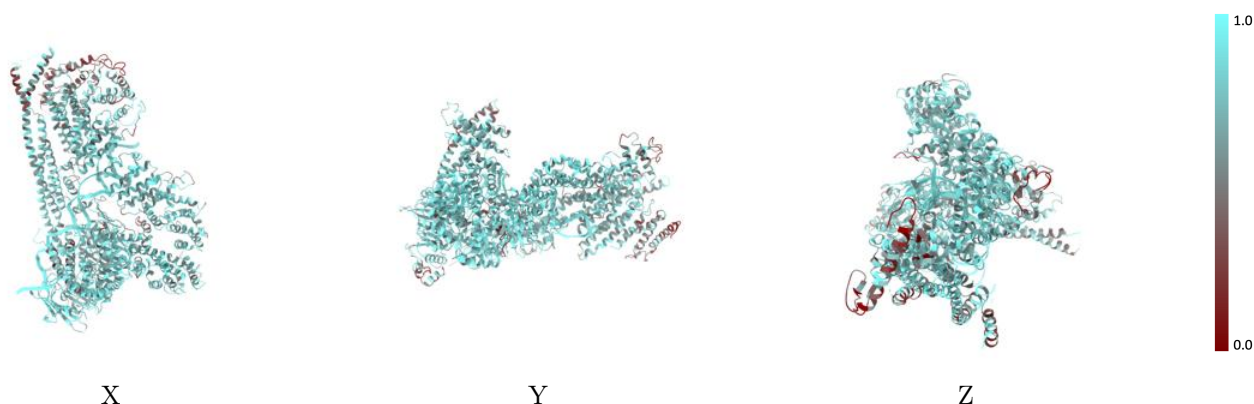
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



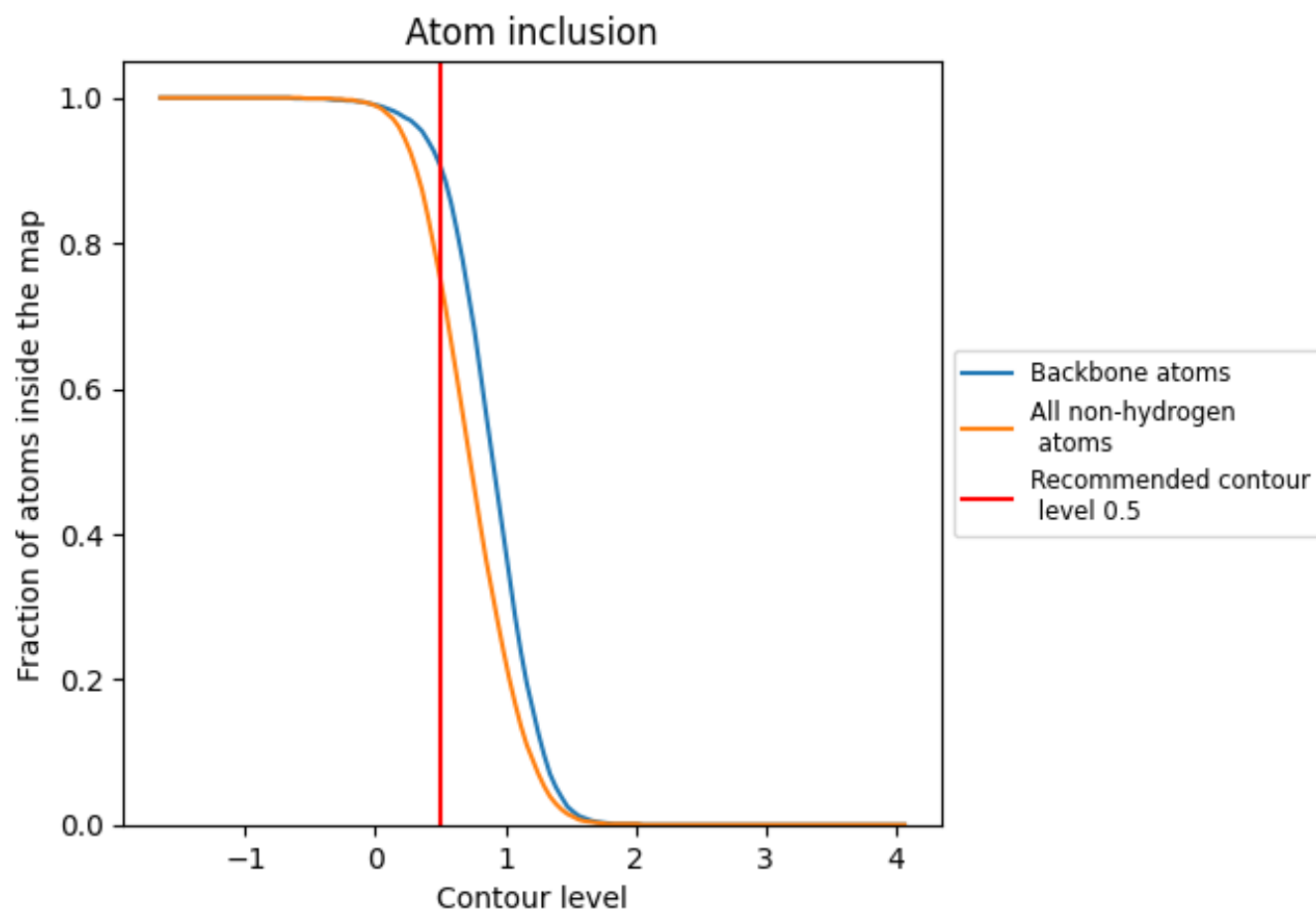
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).

9.4 Atom inclusion ⓘ



At the recommended contour level, 91% of all backbone atoms, 75% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7500	0.3480
A	0.8000	0.3990
B	0.6830	0.3130
C	0.7820	0.3820
D	0.7100	0.3290
X	0.9090	0.3100
Y	0.9220	0.3230

1.0

0.0

<0.0