



## Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 04:30 PM UTC

PDB ID : 7E2C / pdb\_00007e2c  
EMDB ID : EMD-30954  
Title : Monomer of TRAPP11 (open)  
Authors : Sui, S.F.; Sun, S.; Mi, C.C.  
Deposited on : 2021-02-05  
Resolution : 4.18 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

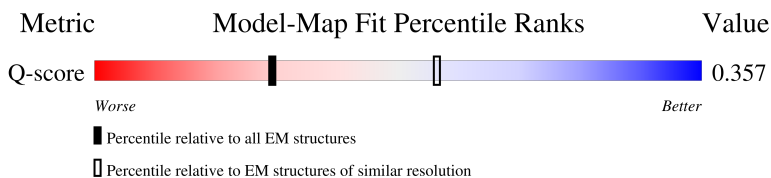
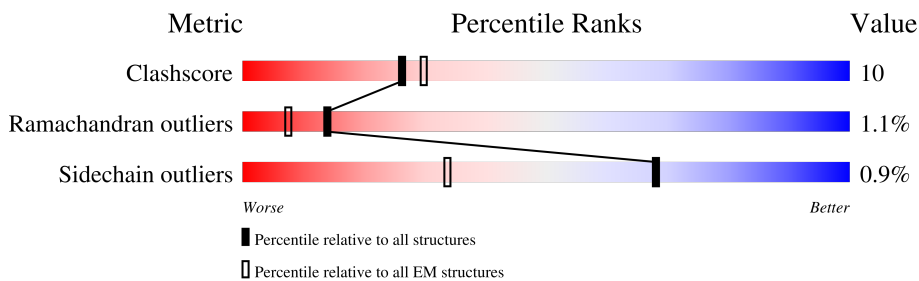
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins)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

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 4.18 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	5389 ( 3.68 - 4.68 )

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	152	
2	B	268	
3	C	193	
3	F	193	

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Mol	Chain	Length	Quality of chain
4	D	159	 <p>75% 19% 5%</p>
5	E	219	 <p>58% 15% 26%</p>
6	G	283	 <p>59% 13% 28%</p>
7	H	175	 <p>62% 18% 17%</p>
8	I	1102	 <p>66% 6% 27%</p>
9	J	1289	 <p>56% 11% 32%</p>
10	K	559	 <p>39% 6% 55%</p>

## 2 Entry composition i

There are 10 unique types of molecules in this entry. The entry contains 23020 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 TRAPP-associated protein TCA17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	150	1206	781	188	233	4	0	0

- Molecule 2 is a protein called Trafficking protein particle complex subunit 33.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	195	1458	939	247	264	8	0	0

- Molecule 3 is a protein called Trafficking protein particle complex subunit BET3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	184	1482	947	244	280	11	0	0
3	F	182	1470	939	242	278	11	0	0

- Molecule 4 is a protein called Trafficking protein particle complex subunit BET5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	151	1234	792	209	227	6	0	0

- Molecule 5 is a protein called Trafficking protein particle complex subunit 23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	161	1295	838	206	242	9	0	0

- Molecule 6 is a protein called Trafficking protein particle complex subunit 31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	G	203	1612	1029	282	292	9	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	41	TYR	ILE	conflict	UNP Q03337
G	42	ILE	PRO	conflict	UNP Q03337

- Molecule 7 is a protein called Trafficking protein particle complex subunit 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	H	146	1172	758	194	215	5	0	0

- Molecule 8 is a protein called Trafficking protein particle complex II-specific subunit 130.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	I	799	4258	2590	822	844	2	0	0


- Molecule 9 is a protein called Trafficking protein particle complex II-specific subunit 120.

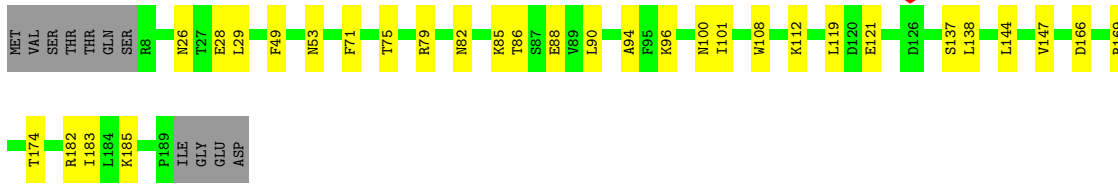
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	J	873	6265	3988	1085	1173	19	0	0

- Molecule 10 is a protein called Trafficking protein particle complex II-specific subunit 65.


Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	K	251	1568	988	278	300	2	0	0

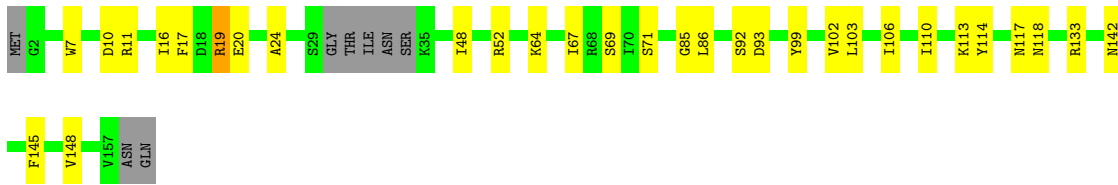


Chain F:  78% 16% 6%



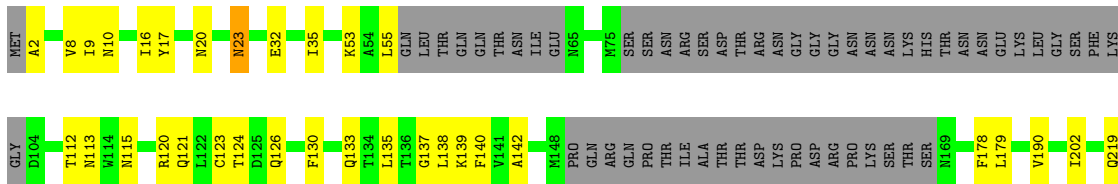
- Molecule 4: Trafficking protein particle complex subunit BET5

Chain D:  75% 19% 5%



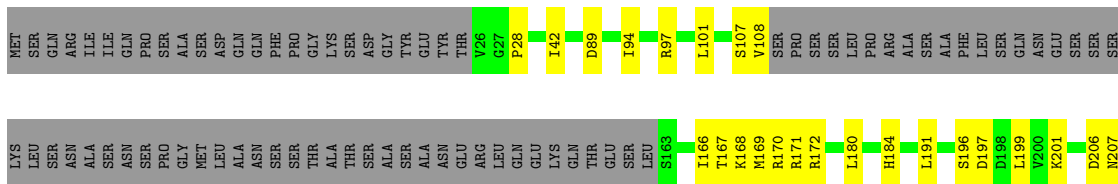
- Molecule 5: Trafficking protein particle complex subunit 23

Chain E:  58% 15% 26%



- Molecule 6: Trafficking protein particle complex subunit 31

Chain G:  59% 13% 28%

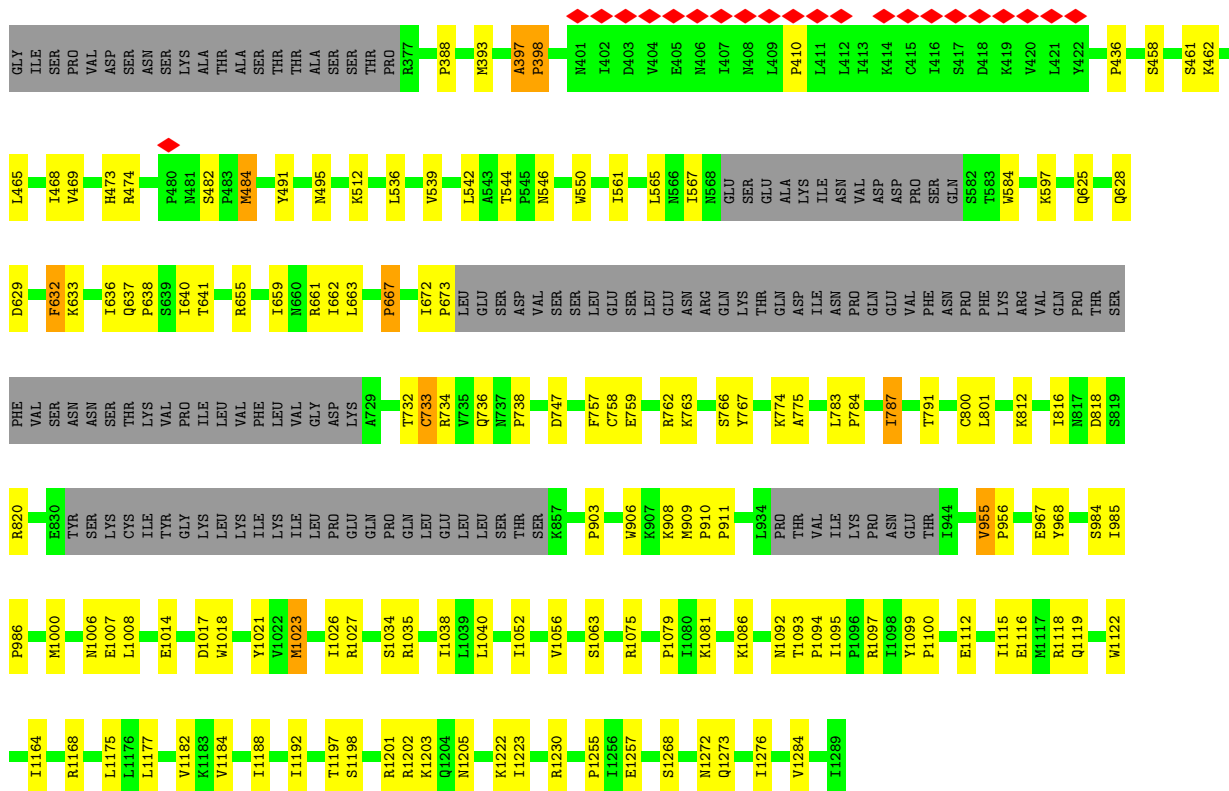


- Molecule 7: Trafficking protein particle complex subunit 20

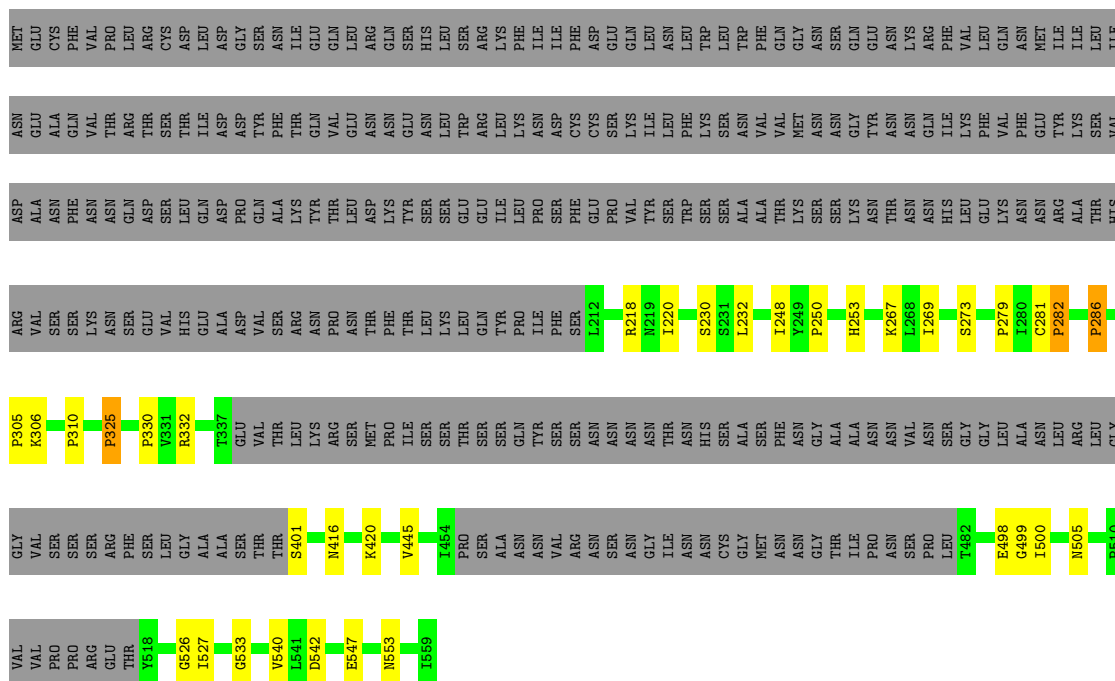
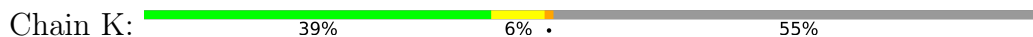
Chain H:  62% 18% 17%







• Molecule 10: Trafficking protein particle complex II-specific subunit 65



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	91346	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.068	Depositor
Minimum map value	-0.037	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	523.68, 523.68, 523.68	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.091, 1.091, 1.091	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.39	0/1226	0.92	4/1655 (0.2%)
2	B	0.42	0/1480	0.87	0/1998
3	C	0.36	0/1509	0.81	2/2040 (0.1%)
3	F	0.40	0/1497	0.85	1/2024 (0.0%)
4	D	0.42	0/1262	0.87	1/1702 (0.1%)
5	E	0.42	0/1319	0.77	2/1779 (0.1%)
6	G	0.43	0/1645	0.84	3/2217 (0.1%)
7	H	0.48	0/1202	0.92	3/1629 (0.2%)
8	I	0.40	0/4279	0.88	15/5936 (0.3%)
9	J	0.43	0/6368	0.96	24/8672 (0.3%)
10	K	0.46	0/1582	1.02	10/2169 (0.5%)
All	All	0.42	0/23369	0.90	65/31821 (0.2%)

There are no bond length outliers.

All (65) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	I	346	PRO	N-CA-CB	10.53	110.18	102.28
8	I	976	PRO	N-CA-CB	9.09	112.80	103.25
8	I	1076	PRO	N-CA-CB	8.38	112.05	103.25
7	H	26	PRO	N-CA-CB	8.24	111.90	103.25
10	K	325	PRO	N-CA-CB	8.14	111.80	103.25
8	I	704	PRO	N-CA-CB	7.87	111.52	103.25
9	J	673	PRO	N-CA-CB	7.80	111.58	103.00
8	I	970	PRO	N-CA-CB	7.78	110.56	103.33
9	J	667	PRO	N-CA-CB	7.72	111.35	103.25
8	I	649	PRO	N-CA-CB	7.71	110.50	103.33
8	I	252	PRO	N-CA-CB	7.57	111.20	103.25
8	I	721	PRO	N-CA-CB	7.57	110.04	103.31
10	K	330	PRO	N-CA-CB	7.55	111.18	103.25
10	K	282	PRO	N-CA-CB	7.35	110.97	103.25
8	I	483	PRO	N-CA-CB	7.30	110.92	103.25
9	J	1255	PRO	N-CA-CB	7.25	110.18	103.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	K	310	PRO	N-CA-CB	7.17	110.95	102.85
8	I	1067	PRO	N-CA-CB	7.01	110.61	103.25
6	G	42	ILE	CG1-CB-CG2	-6.96	89.83	110.70
9	J	1100	PRO	N-CA-CB	6.85	109.71	103.20
10	K	305	PRO	N-CA-CB	6.78	110.50	103.38
10	K	279	PRO	N-CA-CB	6.78	110.36	103.25
7	H	25	ASN	CA-C-N	6.75	128.28	119.84
7	H	25	ASN	C-N-CA	6.75	128.28	119.84
9	J	956	PRO	N-CA-CB	6.70	109.89	103.52
9	J	783	LEU	CA-CB-CG	6.55	139.22	116.30
8	I	980	PRO	N-CA-CB	6.52	110.10	103.25
4	D	16	ILE	CG1-CB-CG2	-6.45	91.35	110.70
9	J	632	PHE	CA-C-N	6.45	133.85	121.54
9	J	632	PHE	C-N-CA	6.45	133.85	121.54
9	J	398	PRO	N-CA-CB	6.40	109.97	103.25
3	F	185	LYS	CA-CB-CG	6.40	126.90	114.10
8	I	646	ILE	CA-C-N	6.39	133.48	121.97
8	I	646	ILE	C-N-CA	6.39	133.48	121.97
8	I	639	PRO	N-CA-CB	6.39	109.96	103.25
8	I	572	PRO	N-CA-CB	6.38	109.94	103.25
9	J	410	PRO	N-CA-CB	6.25	110.14	103.52
9	J	388	PRO	N-CA-CB	6.21	110.10	103.52
9	J	733	CYS	CA-C-N	6.21	131.93	122.93
9	J	733	CYS	C-N-CA	6.21	131.93	122.93
9	J	986	PRO	N-CA-CB	6.19	109.75	103.25
6	G	28	PRO	N-CA-CB	6.17	110.35	103.44
10	K	250	PRO	N-CA-CB	6.12	110.06	103.33
10	K	533	GLY	CA-C-N	6.04	133.08	121.54
10	K	533	GLY	C-N-CA	6.04	133.08	121.54
9	J	436	PRO	N-CA-CB	5.95	110.11	103.44
10	K	286	PRO	N-CA-CB	5.95	109.50	103.25
9	J	787	ILE	CG1-CB-CG2	-5.67	93.68	110.70
9	J	908	LYS	CA-C-N	5.62	135.51	121.80
9	J	908	LYS	C-N-CA	5.62	135.51	121.80
9	J	763	LYS	CA-CB-CG	5.50	125.10	114.10
9	J	550	TRP	CA-C-N	5.43	140.83	121.59
9	J	550	TRP	C-N-CA	5.43	140.83	121.59
1	A	131	LYS	CA-C-N	5.38	131.82	121.54
1	A	131	LYS	C-N-CA	5.38	131.82	121.54
3	C	187	GLU	CA-C-N	5.27	131.88	122.13
3	C	187	GLU	C-N-CA	5.27	131.88	122.13
1	A	30	MET	CA-C-N	5.24	131.54	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	30	MET	C-N-CA	5.24	131.54	121.54
5	E	23	ASN	CA-C-N	5.18	131.44	121.54
5	E	23	ASN	C-N-CA	5.18	131.44	121.54
9	J	909	MET	N-CA-C	-5.17	98.39	109.81
6	G	101	LEU	CA-CB-CG	5.14	134.27	116.30
9	J	1023	MET	CB-CG-SD	5.13	128.10	112.70
9	J	1052	ILE	CG1-CB-CG2	-5.01	95.66	110.70

There are no chirality outliers.

There are no planarity outliers.

## 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	A	1206	0	1228	86	0
2	B	1458	0	1380	60	0
3	C	1482	0	1490	28	0
3	F	1470	0	1476	22	0
4	D	1234	0	1201	24	0
5	E	1295	0	1293	23	0
6	G	1612	0	1554	38	0
7	H	1172	0	1121	53	0
8	I	4258	0	2190	39	0
9	J	6265	0	5496	80	0
10	K	1568	0	1147	13	0
All	All	23020	0	19576	426	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 10.

All (426) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:LYS:HE2	8:I:377:ASP:CB	1.15	1.60
1:A:35:LYS:CE	8:I:377:ASP:CB	1.83	1.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:ILE:CG2	1:A:81:GLN:OE1	1.67	1.39
1:A:63:LEU:HD12	1:A:77:MET:CE	1.58	1.33
1:A:35:LYS:NZ	8:I:377:ASP:HA	1.45	1.30
7:H:37:ASN:HB3	7:H:38:PRO:CD	1.73	1.19
6:G:108:VAL:HG21	6:G:169:MET:HG3	1.20	1.18
2:B:177:LYS:CB	2:B:185:TYR:HE1	1.60	1.15
7:H:32:ASP:OD1	7:H:36:LEU:HD23	1.46	1.15
6:G:108:VAL:CG2	6:G:169:MET:HG3	1.77	1.13
2:B:177:LYS:HB2	2:B:185:TYR:HE1	0.96	1.10
1:A:63:LEU:HD12	1:A:77:MET:HE1	1.19	1.10
2:B:177:LYS:HB2	2:B:185:TYR:CE1	1.85	1.09
1:A:63:LEU:HA	1:A:77:MET:CE	1.84	1.08
7:H:37:ASN:CB	7:H:38:PRO:HD2	1.83	1.07
1:A:63:LEU:HA	1:A:77:MET:HE1	1.07	1.06
1:A:79:ILE:HG23	1:A:81:GLN:CD	1.79	1.05
7:H:37:ASN:CB	7:H:38:PRO:CD	2.35	1.05
1:A:35:LYS:NZ	8:I:377:ASP:CA	2.21	1.02
1:A:61:PRO:HB2	1:A:79:ILE:HD13	1.41	1.02
1:A:79:ILE:HG23	1:A:81:GLN:OE1	0.86	1.01
1:A:63:LEU:CD1	1:A:77:MET:HE1	1.89	1.01
1:A:79:ILE:HG22	1:A:81:GLN:H	1.22	0.99
1:A:63:LEU:CA	1:A:77:MET:HE1	1.91	0.99
1:A:63:LEU:CD1	1:A:77:MET:CE	2.39	0.99
1:A:35:LYS:HE3	8:I:377:ASP:CB	1.94	0.98
6:G:108:VAL:HG22	6:G:169:MET:HA	1.44	0.96
7:H:37:ASN:HB3	7:H:38:PRO:HD2	0.96	0.96
7:H:37:ASN:O	7:H:41:LEU:HG	1.66	0.95
1:A:35:LYS:CE	8:I:377:ASP:CA	2.47	0.93
1:A:35:LYS:HZ1	8:I:377:ASP:HA	1.03	0.91
1:A:54:TRP:NE1	1:A:78:LEU:HD12	1.86	0.90
2:B:176:LEU:HB2	2:B:186:LEU:CD1	2.01	0.89
2:B:174:ASP:O	2:B:187:LEU:HD23	1.73	0.89
7:H:37:ASN:CG	7:H:38:PRO:HD3	1.98	0.88
1:A:62:LEU:O	1:A:77:MET:SD	2.31	0.87
2:B:177:LYS:CB	2:B:185:TYR:CE1	2.49	0.87
1:A:61:PRO:HG2	1:A:79:ILE:HA	1.55	0.86
2:B:187:LEU:HD23	2:B:187:LEU:O	1.77	0.84
1:A:35:LYS:HE2	8:I:377:ASP:CA	2.06	0.84
1:A:61:PRO:HG2	1:A:79:ILE:HD12	1.60	0.83
2:B:176:LEU:HB2	2:B:186:LEU:HD11	1.59	0.82
1:A:79:ILE:CG2	1:A:81:GLN:HB2	2.10	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:61:PRO:CG	1:A:79:ILE:HD12	2.11	0.81
6:G:108:VAL:HG12	6:G:108:VAL:O	1.79	0.81
2:B:181:ARG:HA	2:B:184:PHE:CE1	2.16	0.81
7:H:32:ASP:O	7:H:36:LEU:HG	1.83	0.79
7:H:38:PRO:HB3	9:J:584:TRP:CZ2	2.18	0.79
1:A:61:PRO:HD2	1:A:79:ILE:HD12	1.64	0.78
7:H:38:PRO:O	7:H:42:HIS:N	2.16	0.78
1:A:35:LYS:HZ3	8:I:377:ASP:HA	1.48	0.78
2:B:174:ASP:O	2:B:187:LEU:CD2	2.32	0.78
7:H:37:ASN:CG	7:H:38:PRO:CD	2.57	0.77
2:B:177:LYS:O	2:B:185:TYR:CE1	2.37	0.77
8:I:379:ASN:O	8:I:380:TYR:O	2.02	0.76
1:A:61:PRO:CD	1:A:79:ILE:HD12	2.15	0.76
1:A:61:PRO:CB	1:A:79:ILE:HD13	2.16	0.76
1:A:54:TRP:CE2	1:A:78:LEU:HD12	2.19	0.75
6:G:108:VAL:HG22	6:G:169:MET:HG3	1.71	0.72
9:J:491:TYR:O	9:J:495:ASN:HB2	1.88	0.72
1:A:61:PRO:HG2	1:A:79:ILE:CD1	2.19	0.72
1:A:61:PRO:CG	1:A:79:ILE:CD1	2.67	0.72
1:A:93:LYS:HE3	1:A:93:LYS:C	2.16	0.71
2:B:176:LEU:HD13	2:B:186:LEU:HD13	1.73	0.70
1:A:61:PRO:CG	1:A:79:ILE:HA	2.21	0.70
1:A:54:TRP:HE1	1:A:78:LEU:HD12	1.58	0.69
7:H:38:PRO:O	7:H:42:HIS:HB2	1.94	0.69
1:A:77:MET:HB3	1:A:109:PHE:CE1	2.28	0.68
1:A:63:LEU:HD12	1:A:77:MET:HE2	1.67	0.68
7:H:36:LEU:HD12	7:H:36:LEU:C	2.19	0.67
9:J:662:ILE:O	9:J:736:GLN:CD	2.37	0.67
1:A:79:ILE:HG21	1:A:81:GLN:HB2	1.76	0.66
7:H:2:PRO:HB2	7:H:29:PHE:CE1	2.31	0.66
1:A:54:TRP:CZ2	1:A:78:LEU:CD1	2.80	0.65
1:A:61:PRO:HD2	1:A:79:ILE:CD1	2.25	0.65
1:A:79:ILE:HG22	1:A:81:GLN:N	2.03	0.65
7:H:52:GLN:HG3	7:H:104:ILE:HG21	1.78	0.65
2:B:47:MET:HB2	3:C:63:ILE:HD11	1.78	0.64
1:A:61:PRO:HG2	1:A:79:ILE:CA	2.27	0.64
4:D:20:GLU:HB2	4:D:24:ALA:CB	2.28	0.64
9:J:628:GLN:O	9:J:632:PHE:HB2	1.98	0.64
6:G:108:VAL:CG1	6:G:166:ILE:HD12	2.29	0.63
2:B:183:THR:C	2:B:184:PHE:HD1	2.06	0.63
3:C:49:PHE:HB3	3:C:138:LEU:HB2	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:177:LYS:O	2:B:185:TYR:CD1	2.52	0.62
6:G:108:VAL:HG13	6:G:168:LYS:O	2.00	0.62
5:E:140:PHE:HB3	5:E:179:LEU:HD12	1.81	0.62
7:H:36:LEU:HA	7:H:40:ILE:HG21	1.80	0.62
9:J:393:MET:O	9:J:397:ALA:HB3	2.00	0.62
9:J:1182:VAL:HG11	9:J:1188:ILE:HD11	1.82	0.62
3:C:187:GLU:H	4:D:133:ARG:HH11	1.48	0.61
1:A:93:LYS:HE3	1:A:93:LYS:O	2.00	0.61
7:H:35:GLU:O	7:H:40:ILE:CG2	2.49	0.61
10:K:445:VAL:HG12	10:K:540:VAL:HG12	1.83	0.60
1:A:54:TRP:CE2	1:A:78:LEU:CD1	2.85	0.60
7:H:87:CYS:SG	7:H:88:TYR:N	2.74	0.60
7:H:4:TYR:HB3	7:H:114:ILE:HB	1.84	0.59
2:B:181:ARG:C	2:B:184:PHE:HE1	2.11	0.59
9:J:1075:ARG:HD2	10:K:505:ASN:HB2	1.83	0.58
9:J:1175:LEU:HG	9:J:1192:ILE:HG22	1.85	0.58
9:J:1112:GLU:O	9:J:1116:GLU:HB2	2.02	0.58
3:F:108:TRP:HB3	3:F:112:LYS:HA	1.85	0.58
1:A:105:ILE:HA	1:A:108:ILE:HG12	1.85	0.58
3:F:101:ILE:HD11	3:F:121:GLU:HG3	1.85	0.58
3:C:68:ILE:HD13	3:C:151:SER:HB2	1.84	0.58
3:C:92:LYS:O	3:C:96:LYS:HB2	2.04	0.58
7:H:47:ILE:O	7:H:51:LEU:HB2	2.04	0.58
2:B:181:ARG:HA	2:B:184:PHE:HE1	1.67	0.58
1:A:35:LYS:HZ3	8:I:377:ASP:CA	2.09	0.57
1:A:61:PRO:CB	1:A:79:ILE:HA	2.34	0.57
8:I:1003:THR:O	9:J:1230:ARG:NH2	2.37	0.57
9:J:659:ILE:HG23	9:J:738:PRO:HB3	1.86	0.57
9:J:661:ARG:NH2	9:J:733:CYS:HA	2.20	0.57
8:I:379:ASN:C	8:I:380:TYR:O	2.47	0.57
1:A:61:PRO:HB2	1:A:79:ILE:CD1	2.28	0.57
4:D:19:ARG:HH22	4:D:20:GLU:HG2	1.69	0.57
1:A:62:LEU:C	1:A:77:MET:SD	2.88	0.57
4:D:20:GLU:HB2	4:D:24:ALA:HB1	1.86	0.57
9:J:800:CYS:SG	9:J:801:LEU:N	2.67	0.57
2:B:157:MET:HA	2:B:160:ILE:HG22	1.87	0.56
2:B:238:CYS:SG	2:B:239:LEU:N	2.78	0.56
6:G:107:SER:HB2	6:G:170:ARG:HB2	1.86	0.56
7:H:29:PHE:N	7:H:29:PHE:CD1	2.73	0.56
2:B:42:GLN:H	3:C:23:GLU:HB3	1.69	0.56
3:F:29:LEU:HD12	6:G:191:LEU:HD22	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:ILE:HG21	1:A:81:GLN:OE1	1.90	0.56
9:J:458:SER:O	9:J:462:LYS:NZ	2.39	0.56
5:E:10:ASN:HA	5:E:138:LEU:HD23	1.88	0.56
7:H:88:TYR:OH	7:H:130:MET:SD	2.62	0.55
2:B:187:LEU:HD23	2:B:187:LEU:C	2.31	0.55
1:A:63:LEU:CB	1:A:77:MET:HE1	2.37	0.55
6:G:250:VAL:HG13	6:G:268:ILE:HG22	1.89	0.55
6:G:277:ARG:HH11	7:H:53:TRP:HB3	1.71	0.55
9:J:1017:ASP:N	9:J:1017:ASP:OD1	2.40	0.55
1:A:63:LEU:CD1	1:A:77:MET:HE3	2.32	0.55
9:J:1115:ILE:HD11	9:J:1201:ARG:HH21	1.72	0.55
10:K:416:ASN:O	10:K:420:LYS:NZ	2.37	0.55
2:B:184:PHE:HD1	2:B:184:PHE:N	2.05	0.54
7:H:32:ASP:HA	7:H:35:GLU:CD	2.33	0.54
9:J:1008:LEU:O	9:J:1023:MET:SD	2.65	0.54
1:A:80:LYS:O	1:A:80:LYS:HG2	2.08	0.54
3:F:26:ASN:ND2	3:F:28:GLU:OE2	2.41	0.54
8:I:599:PHE:HA	8:I:636:LYS:HA	1.88	0.54
4:D:103:LEU:HD23	4:D:106:ILE:HD11	1.90	0.54
9:J:638:PRO:HA	9:J:641:THR:HG22	1.90	0.53
2:B:41:SER:HG	2:B:43:SER:HG	1.56	0.53
3:F:71:PHE:O	3:F:75:THR:OG1	2.25	0.53
9:J:542:LEU:HD11	9:J:597:LYS:HB3	1.89	0.53
4:D:92:SER:OG	4:D:93:ASP:N	2.40	0.53
4:D:114:TYR:O	4:D:118:ASN:ND2	2.41	0.53
1:A:61:PRO:CB	1:A:79:ILE:CD1	2.86	0.53
2:B:177:LYS:C	2:B:185:TYR:CE1	2.86	0.53
2:B:187:LEU:CD2	2:B:187:LEU:H	2.22	0.53
3:C:48:ASP:OD1	3:C:48:ASP:N	2.38	0.53
5:E:190:VAL:HG21	5:E:202:ILE:HG23	1.90	0.53
6:G:94:ILE:HA	6:G:97:ARG:HD3	1.90	0.53
2:B:184:PHE:N	2:B:184:PHE:CD1	2.76	0.53
3:C:8:ARG:HE	3:C:10:LEU:H	1.57	0.53
3:C:186:ASP:OD1	4:D:133:ARG:NH1	2.42	0.53
3:F:49:PHE:O	3:F:53:ASN:ND2	2.42	0.53
6:G:89:ASP:N	6:G:89:ASP:OD1	2.42	0.53
3:C:161:VAL:HG12	3:C:178:VAL:HG13	1.91	0.53
5:E:20:ASN:HB2	5:E:23:ASN:HD21	1.74	0.52
9:J:1203:LYS:HG2	9:J:1205:ASN:H	1.73	0.52
5:E:113:ASN:ND2	5:E:115:ASN:OD1	2.43	0.52
7:H:31:GLN:NE2	7:H:31:GLN:CA	2.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:LEU:HA	1:A:86:ILE:HG22	1.92	0.52
1:A:54:TRP:CZ2	1:A:78:LEU:HD12	2.43	0.52
7:H:37:ASN:OD1	7:H:38:PRO:HD3	2.08	0.52
9:J:1006:ASN:ND2	10:K:498:GLU:OE2	2.43	0.52
7:H:37:ASN:O	7:H:41:LEU:CG	2.49	0.52
2:B:139:ILE:HG22	2:B:147:LYS:HB2	1.92	0.52
3:F:49:PHE:HB3	3:F:138:LEU:HB2	1.92	0.52
7:H:2:PRO:CB	7:H:29:PHE:CE1	2.92	0.51
1:A:61:PRO:CD	1:A:79:ILE:CD1	2.85	0.51
3:C:147:VAL:O	3:C:151:SER:HB3	2.10	0.51
4:D:69:SER:OG	5:E:123:CYS:SG	2.66	0.51
3:C:132:MET:HA	3:C:135:MET:HB2	1.92	0.51
1:A:42:ILE:O	1:A:46:TYR:CB	2.59	0.51
2:B:187:LEU:CD2	2:B:187:LEU:N	2.73	0.51
6:G:167:THR:O	7:H:131:ARG:NH2	2.42	0.51
9:J:474:ARG:HH12	9:J:491:TYR:HA	1.75	0.51
9:J:633:LYS:HA	9:J:636:ILE:HG12	1.93	0.51
3:C:86:THR:HA	3:C:89:VAL:HG12	1.92	0.51
5:E:115:ASN:HA	5:E:133:GLN:HE21	1.75	0.51
6:G:108:VAL:HG22	6:G:169:MET:CA	2.28	0.51
3:F:82:ASN:OD1	3:F:85:LYS:N	2.41	0.51
6:G:108:VAL:CG2	6:G:169:MET:CG	2.70	0.51
9:J:1000:MET:HE1	9:J:1040:LEU:HD12	1.92	0.51
2:B:186:LEU:O	2:B:260:PHE:HB2	2.11	0.51
6:G:108:VAL:HG21	6:G:169:MET:CG	2.14	0.51
8:I:994:GLU:CB	8:I:1030:ASP:HA	2.41	0.51
10:K:401:SER:O	10:K:553:ASN:ND2	2.44	0.51
1:A:100:ASP:O	1:A:104:ALA:HB2	2.11	0.50
9:J:1034:SER:OG	9:J:1035:ARG:N	2.44	0.50
3:C:53:ASN:ND2	3:C:139:TRP:O	2.42	0.50
2:B:55:LEU:HD11	3:C:41:LEU:HD21	1.94	0.50
2:B:137:LEU:HD13	2:B:140:PHE:HD2	1.76	0.50
3:C:138:LEU:O	3:C:169:ARG:NH1	2.40	0.50
4:D:71:SER:HB2	5:E:121:GLN:HG2	1.93	0.50
2:B:177:LYS:HB3	2:B:185:TYR:CE1	2.43	0.50
3:F:53:ASN:HD21	3:F:138:LEU:HA	1.76	0.50
9:J:1272:ASN:ND2	9:J:1273:GLN:O	2.44	0.50
2:B:135:SER:HB2	2:B:149:LYS:HE2	1.92	0.50
2:B:181:ARG:CA	2:B:184:PHE:HE1	2.23	0.50
4:D:11:ARG:HG2	4:D:85:GLY:HA3	1.93	0.50
9:J:1268:SER:HA	9:J:1276:ILE:HA	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:185:TYR:HB3	2:B:261:HIS:HA	1.92	0.50
4:D:113:LYS:HA	4:D:117:ASN:HD22	1.77	0.50
5:E:137:GLY:O	5:E:139:LYS:NZ	2.44	0.50
2:B:124:ARG:NH1	2:B:216:GLU:OE2	2.45	0.50
2:B:184:PHE:O	2:B:262:VAL:HG12	2.11	0.49
5:E:8:VAL:HG23	5:E:16:ILE:HB	1.94	0.49
9:J:1014:GLU:OE2	9:J:1027:ARG:NH1	2.45	0.49
2:B:154:LEU:O	2:B:184:PHE:CE2	2.65	0.49
3:C:17:ILE:HA	3:C:20:ASN:HB2	1.95	0.49
5:E:2:ALA:N	5:E:219:GLN:OE1	2.45	0.49
6:G:97:ARG:NH2	7:H:145:LEU:O	2.45	0.49
7:H:2:PRO:CB	7:H:29:PHE:HE1	2.26	0.49
9:J:818:ASP:HB3	9:J:820:ARG:HG3	1.94	0.49
1:A:37:ASN:O	1:A:41:ASN:ND2	2.45	0.49
3:F:144:LEU:HA	3:F:147:VAL:HG12	1.95	0.49
2:B:178:THR:OG1	2:B:184:PHE:CD1	2.52	0.49
2:B:144:PRO:HD2	2:B:147:LYS:HB3	1.93	0.49
6:G:201:LYS:NZ	6:G:206:ASP:OD1	2.46	0.49
9:J:565:LEU:HB2	9:J:567:ILE:HG12	1.94	0.49
8:I:363:TRP:O	8:I:367:VAL:CB	2.61	0.49
4:D:99:TYR:HB3	4:D:102:VAL:HB	1.95	0.48
6:G:108:VAL:O	6:G:108:VAL:CG1	2.52	0.48
9:J:967:GLU:N	9:J:985:ILE:O	2.45	0.48
7:H:31:GLN:NE2	7:H:31:GLN:N	2.61	0.48
9:J:968:TYR:HA	9:J:984:SER:HA	1.95	0.48
7:H:36:LEU:C	7:H:36:LEU:CD1	2.86	0.48
6:G:172:ARG:NH2	7:H:86:ASN:O	2.46	0.48
6:G:168:LYS:HD3	7:H:131:ARG:NH2	2.28	0.48
9:J:1094:PRO:HD3	9:J:1122:TRP:HE1	1.78	0.48
6:G:261:SER:HG	6:G:262:GLN:HE21	1.59	0.48
9:J:762:ARG:HE	9:J:791:THR:HG21	1.79	0.48
10:K:500:ILE:HG22	10:K:526:GLY:HA2	1.96	0.48
2:B:181:ARG:CA	2:B:184:PHE:CE1	2.92	0.47
7:H:157:ARG:NH1	7:H:162:ASP:OD2	2.46	0.47
9:J:1056:VAL:O	9:J:1063:SER:OG	2.32	0.47
4:D:17:PHE:CZ	4:D:20:GLU:HA	2.49	0.47
3:F:182:ARG:NH1	3:F:183:ILE:O	2.47	0.47
10:K:542:ASP:HB3	10:K:547:GLU:HB3	1.96	0.47
3:F:96:LYS:HG2	3:F:100:ASN:HD22	1.78	0.47
6:G:275:LEU:O	6:G:279:GLY:N	2.46	0.47
8:I:379:ASN:O	8:I:380:TYR:C	2.57	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:53:ASN:ND2	3:F:137:SER:O	2.47	0.47
2:B:223:ARG:HE	2:B:235:GLU:HB3	1.79	0.47
2:B:226:LEU:O	2:B:230:GLY:N	2.48	0.47
3:F:82:ASN:O	3:F:86:THR:OG1	2.33	0.47
8:I:940:LEU:O	8:I:944:LEU:N	2.47	0.47
9:J:393:MET:O	9:J:397:ALA:CB	2.62	0.47
6:G:108:VAL:HG12	6:G:166:ILE:HD12	1.96	0.47
7:H:32:ASP:OD1	7:H:36:LEU:CD2	2.39	0.47
2:B:110:LYS:O	2:B:209:LYS:NZ	2.44	0.47
8:I:989:GLN:N	8:I:1082:ASN:O	2.47	0.47
9:J:1021:TYR:HD2	9:J:1079:PRO:HG2	1.79	0.47
10:K:218:ARG:HA	10:K:232:LEU:HA	1.97	0.47
1:A:63:LEU:HA	1:A:77:MET:SD	2.53	0.47
2:B:127:GLY:HA2	2:B:130:ILE:HD12	1.96	0.47
9:J:662:ILE:O	9:J:736:GLN:NE2	2.49	0.47
1:A:35:LYS:HZ1	8:I:377:ASP:CA	1.94	0.46
1:A:79:ILE:CG2	1:A:81:GLN:CB	2.88	0.46
4:D:20:GLU:HB2	4:D:24:ALA:HB3	1.97	0.46
7:H:32:ASP:HA	7:H:35:GLU:OE2	2.15	0.46
9:J:628:GLN:O	9:J:632:PHE:CB	2.63	0.46
4:D:67:ILE:HA	5:E:124:THR:HG22	1.96	0.46
3:F:90:LEU:O	3:F:94:ALA:CB	2.64	0.46
6:G:171:ARG:HD3	7:H:86:ASN:HB2	1.96	0.46
9:J:1092:ASN:O	9:J:1122:TRP:NE1	2.49	0.46
2:B:60:GLU:OE1	2:B:61:ARG:NH2	2.48	0.46
6:G:180:LEU:HD12	6:G:199:LEU:HD12	1.98	0.46
9:J:1197:THR:OG1	9:J:1198:SER:N	2.49	0.46
1:A:61:PRO:CG	1:A:79:ILE:HD13	2.42	0.46
9:J:1119:GLN:OE1	9:J:1168:ARG:NH1	2.49	0.46
2:B:185:TYR:HB2	2:B:260:PHE:O	2.16	0.46
5:E:32:GLU:HA	5:E:35:ILE:HD12	1.98	0.45
6:G:184:HIS:NE2	6:G:196:SER:O	2.50	0.45
8:I:860:ASN:ND2	8:I:966:ARG:O	2.49	0.45
9:J:757:PHE:HA	9:J:766:SER:HB3	1.98	0.45
9:J:1115:ILE:HA	9:J:1118:ARG:HB3	1.98	0.45
6:G:172:ARG:HH12	7:H:104:ILE:HG22	1.81	0.45
7:H:38:PRO:HB3	9:J:584:TRP:CE2	2.49	0.45
3:C:144:LEU:HA	3:C:147:VAL:HG22	1.99	0.45
1:A:24:ASN:ND2	1:A:28:ASN:OD1	2.50	0.45
3:F:85:LYS:HA	3:F:88:GLU:HG2	1.98	0.45
9:J:536:LEU:HA	9:J:539:VAL:HG12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:J:910:PRO:HA	9:J:911:PRO:HD3	1.79	0.45
2:B:174:ASP:O	2:B:187:LEU:O	2.34	0.45
7:H:29:PHE:CD2	7:H:36:LEU:CD2	3.00	0.45
8:I:598:ASP:HA	8:I:603:LYS:HA	1.97	0.45
9:J:903:PRO:HA	9:J:906:TRP:HB3	1.98	0.45
3:C:8:ARG:HG3	3:C:11:LYS:H	1.81	0.45
7:H:165:VAL:O	7:H:169:ALA:N	2.48	0.45
8:I:676:LEU:HA	8:I:689:VAL:HA	1.97	0.45
8:I:793:ARG:NH2	8:I:831:GLY:O	2.49	0.45
5:E:53:LYS:HG2	5:E:55:LEU:HB3	1.99	0.45
1:A:30:MET:SD	1:A:30:MET:N	2.85	0.45
4:D:7:TRP:HA	4:D:17:PHE:HB2	1.99	0.45
4:D:64:LYS:O	5:E:126:GLN:NE2	2.50	0.45
5:E:8:VAL:HG22	5:E:17:TYR:HB3	1.99	0.45
7:H:31:GLN:N	7:H:31:GLN:HE21	2.14	0.45
1:A:79:ILE:HG22	1:A:81:GLN:HB2	1.97	0.44
5:E:112:THR:OG1	5:E:113:ASN:N	2.51	0.44
9:J:663:LEU:HA	9:J:734:ARG:HH21	1.82	0.44
1:A:129:ASP:OD1	1:A:129:ASP:N	2.50	0.44
7:H:31:GLN:NE2	7:H:31:GLN:HA	2.29	0.44
7:H:38:PRO:HB3	9:J:584:TRP:CH2	2.49	0.44
9:J:758:CYS:HA	9:J:801:LEU:HB2	1.99	0.44
1:A:67:PHE:HD2	1:A:74:VAL:HG23	1.82	0.44
5:E:130:PHE:N	5:E:142:ALA:O	2.50	0.44
3:F:119:LEU:O	3:F:174:THR:OG1	2.35	0.44
6:G:167:THR:OG1	6:G:168:LYS:N	2.50	0.44
8:I:399:GLU:O	8:I:403:GLN:N	2.51	0.44
8:I:590:ASP:H	8:I:613:ARG:HA	1.81	0.44
3:F:166:ASP:OD1	3:F:169:ARG:N	2.45	0.44
6:G:197:ASP:OD2	6:G:214:ASN:ND2	2.49	0.44
9:J:774:LYS:HD3	9:J:775:ALA:H	1.81	0.44
1:A:61:PRO:HG2	1:A:79:ILE:O	2.18	0.44
2:B:186:LEU:HD12	2:B:186:LEU:HA	1.78	0.44
4:D:110:ILE:HD11	4:D:148:VAL:HG13	2.00	0.44
6:G:254:ARG:HD3	6:G:262:GLN:HA	2.00	0.44
7:H:171:LYS:HE3	7:H:171:LYS:HB3	1.90	0.44
9:J:662:ILE:O	9:J:736:GLN:OE1	2.36	0.44
1:A:42:ILE:O	1:A:46:TYR:HB3	2.17	0.44
7:H:5:PHE:HB3	7:H:18:ILE:HG22	1.99	0.44
9:J:561:ILE:HD13	9:J:561:ILE:HA	1.88	0.44
3:F:28:GLU:H	3:F:28:GLU:HG2	1.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:PRO:HB3	1:A:20:ILE:HD11	2.00	0.43
9:J:1177:LEU:HD13	9:J:1284:VAL:HG11	2.00	0.43
8:I:803:GLU:O	8:I:856:LYS:N	2.52	0.43
2:B:128:PHE:O	2:B:132:LEU:N	2.47	0.43
4:D:142:ASN:HB2	4:D:145:PHE:HB3	1.99	0.43
6:G:246:PHE:HA	6:G:274:VAL:HG11	2.00	0.43
10:K:267:LYS:H	10:K:273:SER:HA	1.83	0.43
10:K:499:GLY:O	10:K:527:ILE:N	2.51	0.43
1:A:93:LYS:HD2	1:A:93:LYS:HA	1.71	0.43
8:I:583:SER:HA	8:I:617:TYR:HA	2.01	0.43
9:J:738:PRO:HG2	9:J:784:PRO:HG2	1.99	0.43
7:H:93:ASP:HB2	7:H:100:ILE:HD11	2.00	0.43
9:J:1093:THR:OG1	9:J:1118:ARG:NH2	2.47	0.43
9:J:1184:VAL:HG13	9:J:1257:GLU:H	1.84	0.43
9:J:1202:ARG:H	9:J:1202:ARG:HG2	1.58	0.43
4:D:17:PHE:CE2	4:D:20:GLU:HA	2.54	0.43
8:I:853:PHE:O	8:I:974:THR:N	2.51	0.43
3:C:11:LYS:HD2	3:C:92:LYS:HE3	2.00	0.43
6:G:171:ARG:NH2	7:H:84:THR:O	2.46	0.43
9:J:1081:LYS:HB3	9:J:1081:LYS:HE2	1.87	0.43
2:B:178:THR:OG1	2:B:184:PHE:CE1	2.66	0.43
2:B:191:TYR:HD2	2:B:194:ILE:HG12	1.83	0.43
4:D:10:ASP:HA	4:D:86:LEU:HD13	2.01	0.43
9:J:758:CYS:SG	9:J:759:GLU:N	2.91	0.43
2:B:143:ASN:HA	2:B:147:LYS:HD3	2.00	0.43
5:E:115:ASN:HB2	5:E:120:ARG:CZ	2.48	0.43
9:J:484:MET:HE3	9:J:484:MET:HB3	1.87	0.43
9:J:1222:LYS:NZ	9:J:1223:ILE:O	2.42	0.43
1:A:42:ILE:O	1:A:46:TYR:HB2	2.19	0.42
1:A:43:SER:HA	1:A:46:TYR:HB3	2.01	0.42
2:B:187:LEU:H	2:B:187:LEU:HD22	1.84	0.42
3:C:177:LYS:HB3	3:C:177:LYS:HE2	1.89	0.42
3:C:188:ILE:HG23	4:D:133:ARG:HG2	2.01	0.42
3:F:90:LEU:O	3:F:94:ALA:HB2	2.19	0.42
10:K:306:LYS:HA	10:K:332:ARG:HA	2.01	0.42
3:F:26:ASN:OD1	3:F:26:ASN:N	2.50	0.42
9:J:1018:TRP:HB2	9:J:1079:PRO:HG3	2.01	0.42
8:I:675:GLU:O	8:I:690:GLU:N	2.52	0.42
9:J:625:GLN:NE2	9:J:747:ASP:O	2.48	0.42
1:A:79:ILE:CG2	1:A:81:GLN:CD	2.62	0.42
9:J:465:LEU:HA	9:J:468:ILE:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:J:767:TYR:HB2	9:J:787:ILE:HD11	2.02	0.42
7:H:157:ARG:HD2	7:H:157:ARG:HA	1.74	0.42
9:J:544:THR:HG22	9:J:546:ASN:H	1.83	0.42
9:J:629:ASP:HA	9:J:632:PHE:HB3	2.01	0.42
9:J:637:GLN:HA	9:J:640:ILE:HG12	2.01	0.42
9:J:800:CYS:HB3	9:J:812:LYS:HB3	2.02	0.42
6:G:207:ASN:OD1	6:G:207:ASN:N	2.52	0.42
8:I:770:SER:N	8:I:789:ASN:O	2.52	0.42
3:C:141:SER:HB3	3:C:144:LEU:HG	2.02	0.42
9:J:458:SER:O	9:J:461:SER:OG	2.35	0.42
3:C:34:TYR:OH	3:C:140:TYR:O	2.34	0.42
5:E:178:PHE:HD2	5:E:179:LEU:HD22	1.85	0.42
6:G:108:VAL:HG22	6:G:169:MET:CG	2.46	0.42
9:J:1026:ILE:HD12	9:J:1026:ILE:HA	1.94	0.42
1:A:10:LEU:HB2	1:A:18:ILE:HB	2.02	0.41
1:A:117:ILE:HD12	1:A:117:ILE:HA	1.94	0.41
2:B:137:LEU:HD12	3:C:28:GLU:HG3	2.02	0.41
5:E:9:ILE:HB	5:E:139:LYS:HB2	2.01	0.41
9:J:655:ARG:HH11	9:J:816:ILE:HG21	1.84	0.41
9:J:1038:ILE:HD11	9:J:1164:ILE:HD12	2.02	0.41
10:K:220:ILE:HA	10:K:230:SER:HA	2.02	0.41
1:A:17:PRO:HD2	8:I:464:TRP:HB2	2.01	0.41
4:D:48:ILE:O	4:D:52:ARG:N	2.53	0.41
8:I:979:LEU:O	8:I:1075:PHE:N	2.52	0.41
1:A:41:ASN:HA	1:A:44:LEU:HB2	2.01	0.41
1:A:142:ASP:OD1	1:A:142:ASP:N	2.53	0.41
8:I:802:SER:O	8:I:839:TYR:OH	2.38	0.41
1:A:97:GLY:N	1:A:101:GLU:OE1	2.53	0.41
2:B:49:LEU:HD23	2:B:52:MET:HE1	2.02	0.41
3:C:63:ILE:HD12	3:C:63:ILE:HA	1.94	0.41
9:J:1095:ILE:O	9:J:1097:ARG:NH1	2.45	0.41
6:G:172:ARG:HH22	7:H:104:ILE:HB	1.85	0.41
8:I:998:ASP:O	8:I:999:ALA:HB3	2.21	0.41
9:J:1086:LYS:HA	9:J:1086:LYS:HD3	1.74	0.41
2:B:203:ALA:HB3	2:B:206:GLU:HG2	2.02	0.41
3:C:152:LEU:HD22	3:C:157:LEU:HD11	2.03	0.41
6:G:225:GLU:HA	6:G:254:ARG:HH22	1.86	0.41
9:J:512:LYS:HA	9:J:512:LYS:HD2	1.82	0.41
2:B:125:ASN:O	2:B:129:GLN:NE2	2.54	0.41
2:B:160:ILE:HD12	2:B:160:ILE:HA	1.99	0.41
8:I:989:GLN:HA	8:I:1034:TYR:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:LEU:HD23	1:A:4:ARG:HH12	1.86	0.40
7:H:108:GLY:O	7:H:110:LYS:NZ	2.55	0.40
8:I:582:LEU:O	8:I:618:GLY:N	2.54	0.40
9:J:662:ILE:CB	9:J:736:GLN:OE1	2.69	0.40
10:K:248:ILE:O	10:K:253:HIS:N	2.53	0.40
3:C:90:LEU:HD21	3:C:148:LEU:HD22	2.04	0.40
8:I:320:SER:HA	8:I:324:LEU:H	1.86	0.40
1:A:48:GLU:HB2	1:A:54:TRP:HZ3	1.86	0.40
2:B:176:LEU:CB	2:B:186:LEU:CD1	2.87	0.40
1:A:28:ASN:HB3	1:A:29:GLU:H	1.79	0.40
5:E:23:ASN:OD1	5:E:23:ASN:N	2.54	0.40
5:E:135:LEU:HD11	3:F:79:ARG:HE	1.86	0.40
8:I:790:SER:O	8:I:793:ARG:NH1	2.45	0.40
9:J:469:VAL:O	9:J:473:HIS:ND1	2.52	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	148/152 (97%)	128 (86%)	20 (14%)	0	100	100
2	B	189/268 (70%)	165 (87%)	23 (12%)	1 (0%)	24	62
3	C	182/193 (94%)	169 (93%)	13 (7%)	0	100	100
3	F	180/193 (93%)	164 (91%)	16 (9%)	0	100	100
4	D	147/159 (92%)	125 (85%)	22 (15%)	0	100	100
5	E	153/219 (70%)	139 (91%)	14 (9%)	0	100	100
6	G	199/283 (70%)	176 (88%)	23 (12%)	0	100	100
7	H	142/175 (81%)	124 (87%)	16 (11%)	2 (1%)	9	39
8	I	791/1102 (72%)	641 (81%)	129 (16%)	21 (3%)	4	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	J	861/1289 (67%)	691 (80%)	164 (19%)	6 (1%)	18	55
10	K	243/559 (44%)	183 (75%)	55 (23%)	5 (2%)	5	30
All	All	3235/4592 (70%)	2705 (84%)	495 (15%)	35 (1%)	14	45

All (35) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	H	26	PRO
7	H	37	ASN
8	I	252	PRO
8	I	380	TYR
8	I	381	PRO
8	I	638	PHE
8	I	647	VAL
8	I	976	PRO
8	I	980	PRO
8	I	1067	PRO
8	I	1076	PRO
9	J	667	PRO
9	J	1099	TYR
10	K	325	PRO
8	I	639	PRO
8	I	704	PRO
8	I	1054	ILE
10	K	269	ILE
8	I	371	SER
8	I	571	PHE
9	J	398	PRO
9	J	672	ILE
10	K	282	PRO
10	K	286	PRO
8	I	377	ASP
8	I	1004	ILE
9	J	397	ALA
8	I	375	LEU
2	B	99	ILE
8	I	367	VAL
9	J	955	VAL
10	K	281	CYS
8	I	1029	ILE
8	I	345	ASN

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Mol	Chain	Res	Type
8	I	483	PRO

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	140/142 (99%)	135 (96%)	5 (4%)	31	53
2	B	142/248 (57%)	139 (98%)	3 (2%)	47	65
3	C	169/178 (95%)	169 (100%)	0	100	100
3	F	168/178 (94%)	168 (100%)	0	100	100
4	D	135/145 (93%)	134 (99%)	1 (1%)	76	78
5	E	144/199 (72%)	144 (100%)	0	100	100
6	G	169/249 (68%)	169 (100%)	0	100	100
7	H	126/152 (83%)	122 (97%)	4 (3%)	34	56
8	I	78/1023 (8%)	78 (100%)	0	100	100
9	J	551/1213 (45%)	546 (99%)	5 (1%)	70	75
10	K	93/517 (18%)	93 (100%)	0	100	100
All	All	1915/4244 (45%)	1897 (99%)	18 (1%)	68	75

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	LEU
1	A	79	ILE
1	A	80	LYS
1	A	93	LYS
1	A	94	SER
2	B	184	PHE
2	B	186	LEU
2	B	187	LEU
4	D	19	ARG
7	H	29	PHE

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Mol	Chain	Res	Type
7	H	31	GLN
7	H	32	ASP
7	H	40	ILE
9	J	482	SER
9	J	484	MET
9	J	732	THR
9	J	955	VAL
9	J	1007	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	167	GLN
2	B	179	ASN
2	B	261	HIS
2	B	263	GLN
3	C	20	ASN
3	C	104	ASN
3	C	107	ASN
3	C	110	HIS
4	D	14	ASN
4	D	36	GLN
4	D	97	GLN
4	D	117	ASN
5	E	29	ASN
3	F	181	ASN
6	G	72	GLN
6	G	257	GLN
7	H	31	GLN
9	J	471	ASN
9	J	566	ASN
9	J	593	GLN
9	J	746	ASN
9	J	772	ASN
9	J	1006	ASN
9	J	1015	ASN
9	J	1189	ASN
10	K	486	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

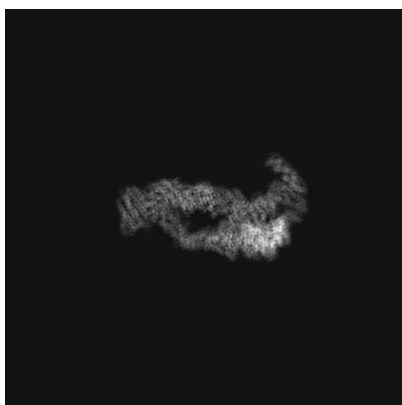
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30954. These allow visual inspection of the internal detail of the map and identification of artifacts.

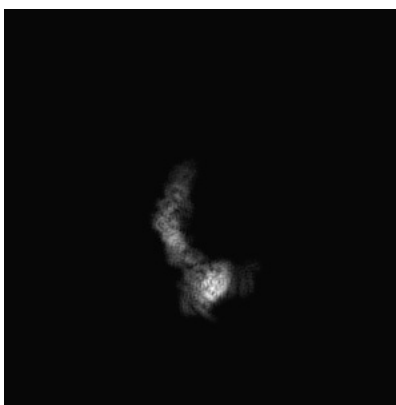
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

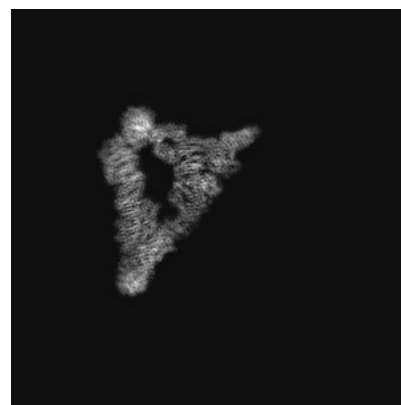
#### 6.1.1 Primary map



X



Y

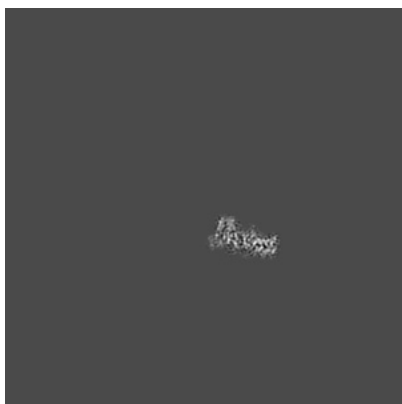


Z

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

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

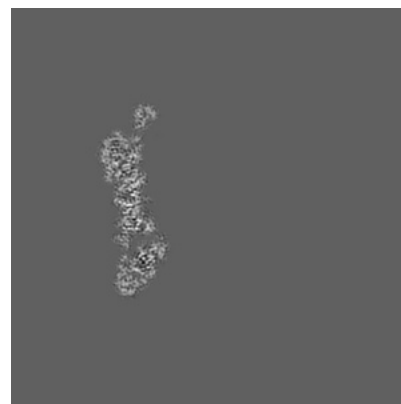
#### 6.2.1 Primary map



X Index: 240



Y Index: 240

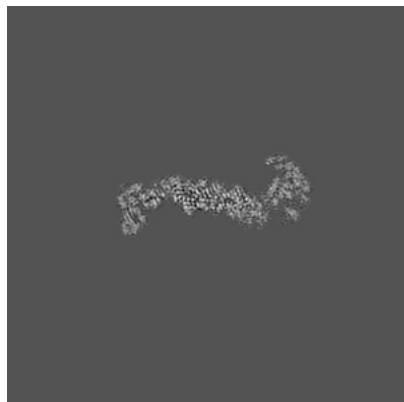


Z Index: 240

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: 147



Y Index: 322

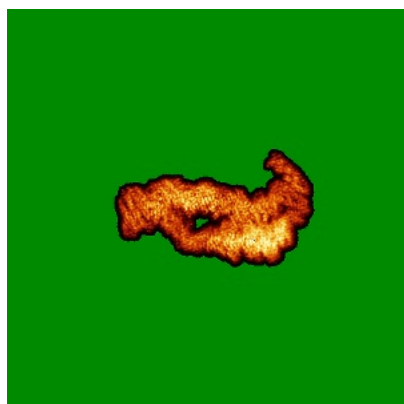


Z Index: 201

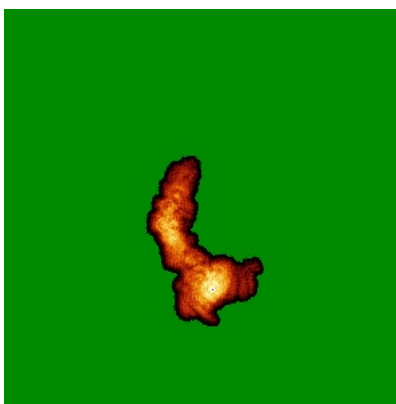
The images above show the largest variance slices of the map in three orthogonal directions.

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

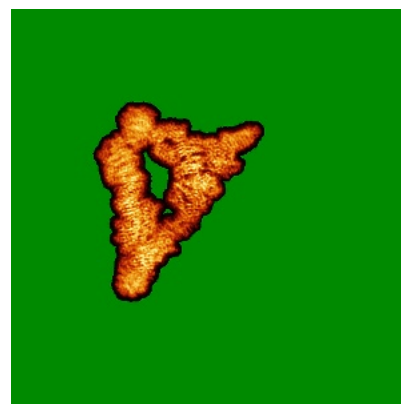
### 6.4.1 Primary map



X



Y

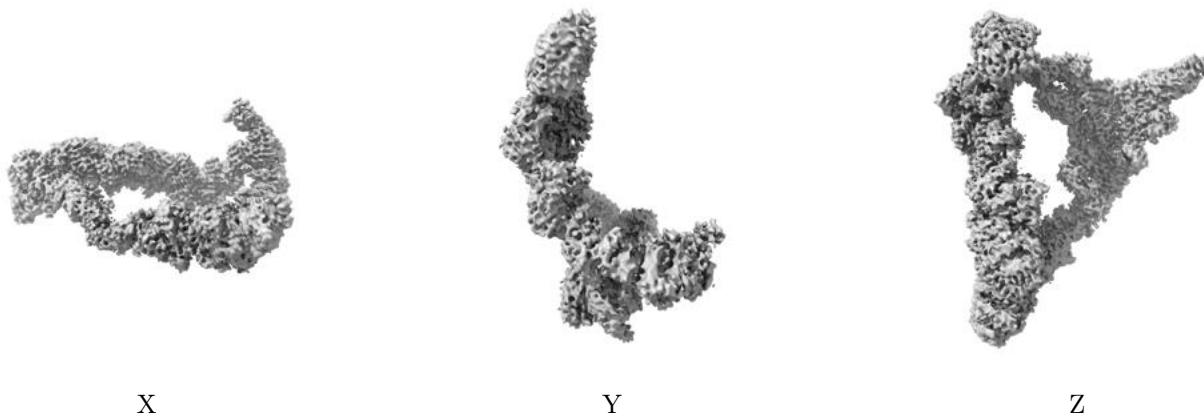


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

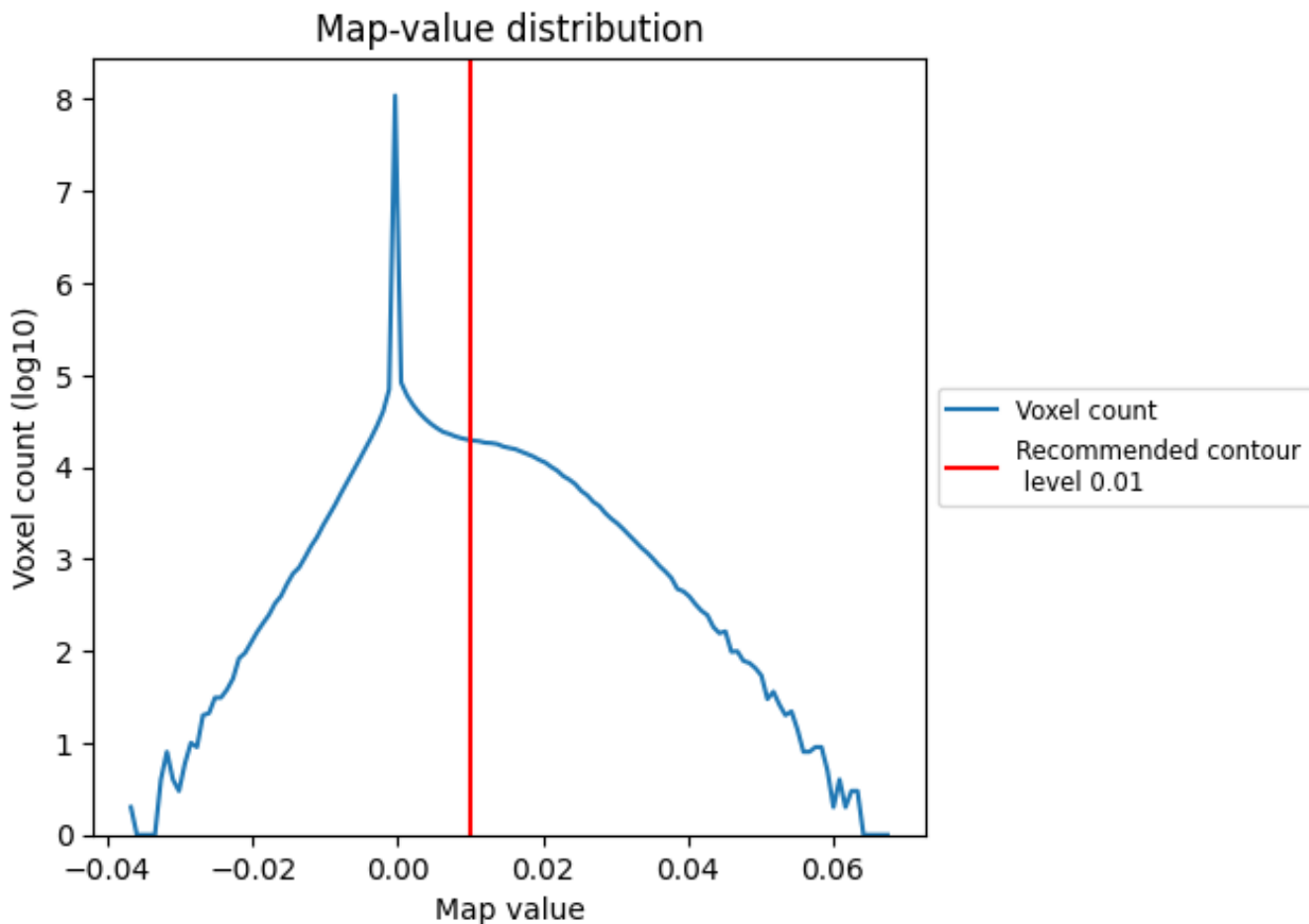
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

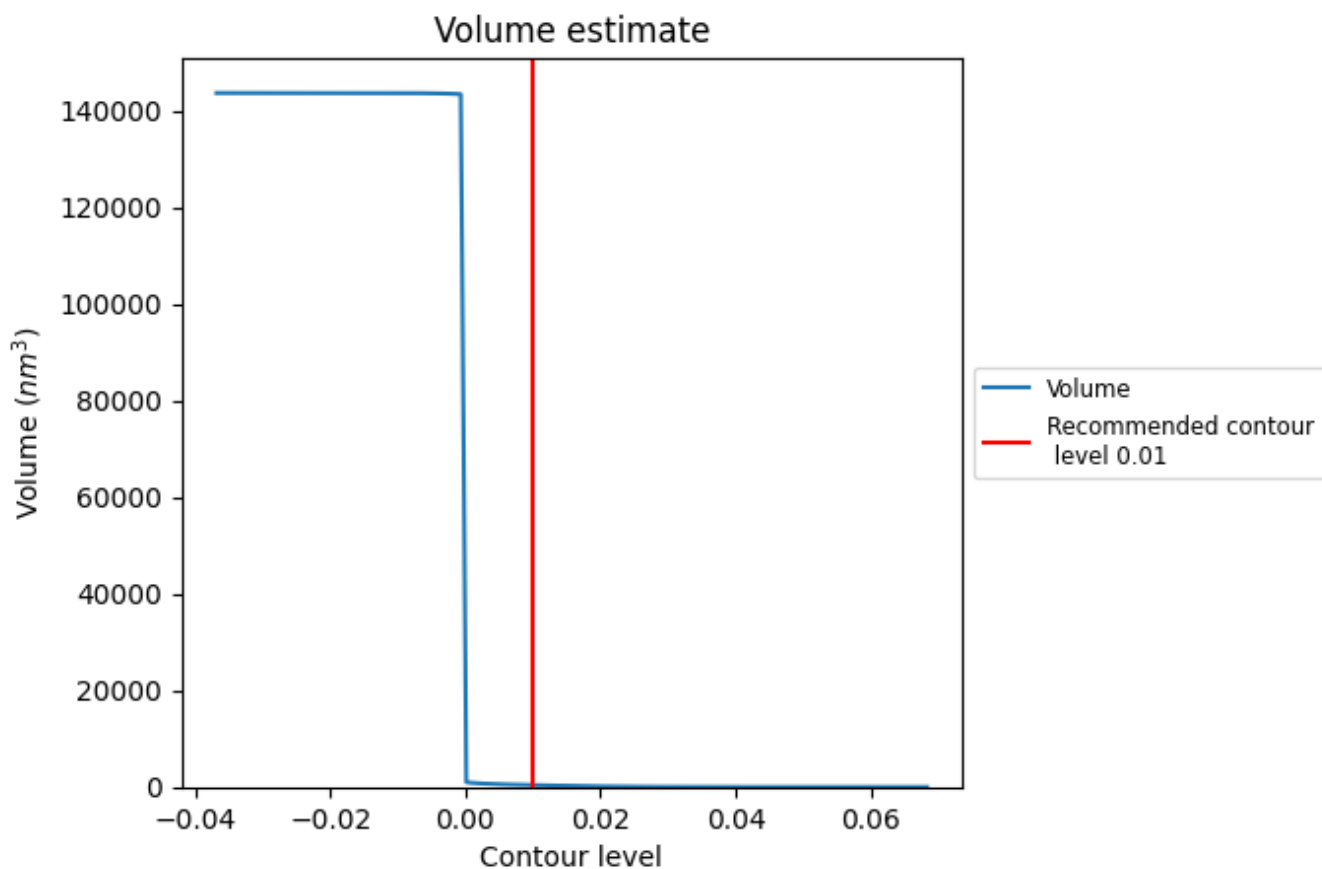
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

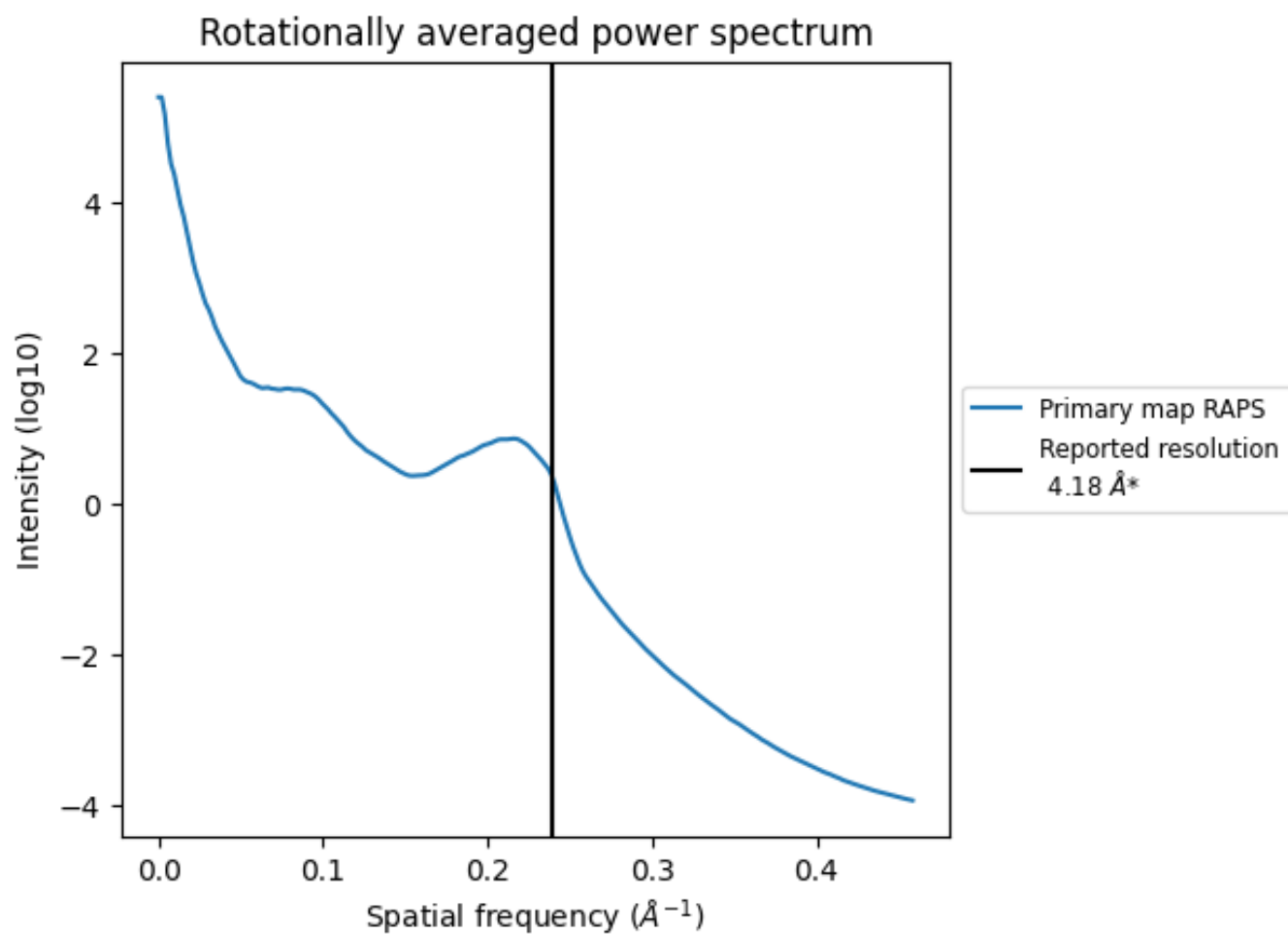
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 386 nm<sup>3</sup>; this corresponds to an approximate mass of 349 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 0.239 Å<sup>-1</sup>

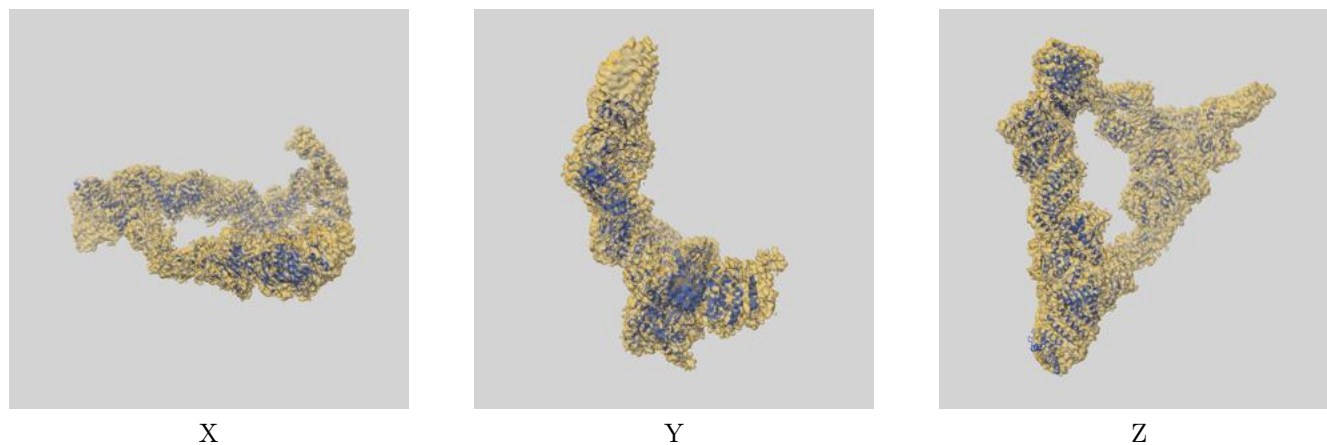
## 8 Fourier-Shell correlation

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

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

This section contains information regarding the fit between EMDB map EMD-30954 and PDB model 7E2C. Per-residue inclusion information can be found in section 3 on page 6.

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



The images above show the 3D surface view of the map at the recommended contour level 0.01 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](#)



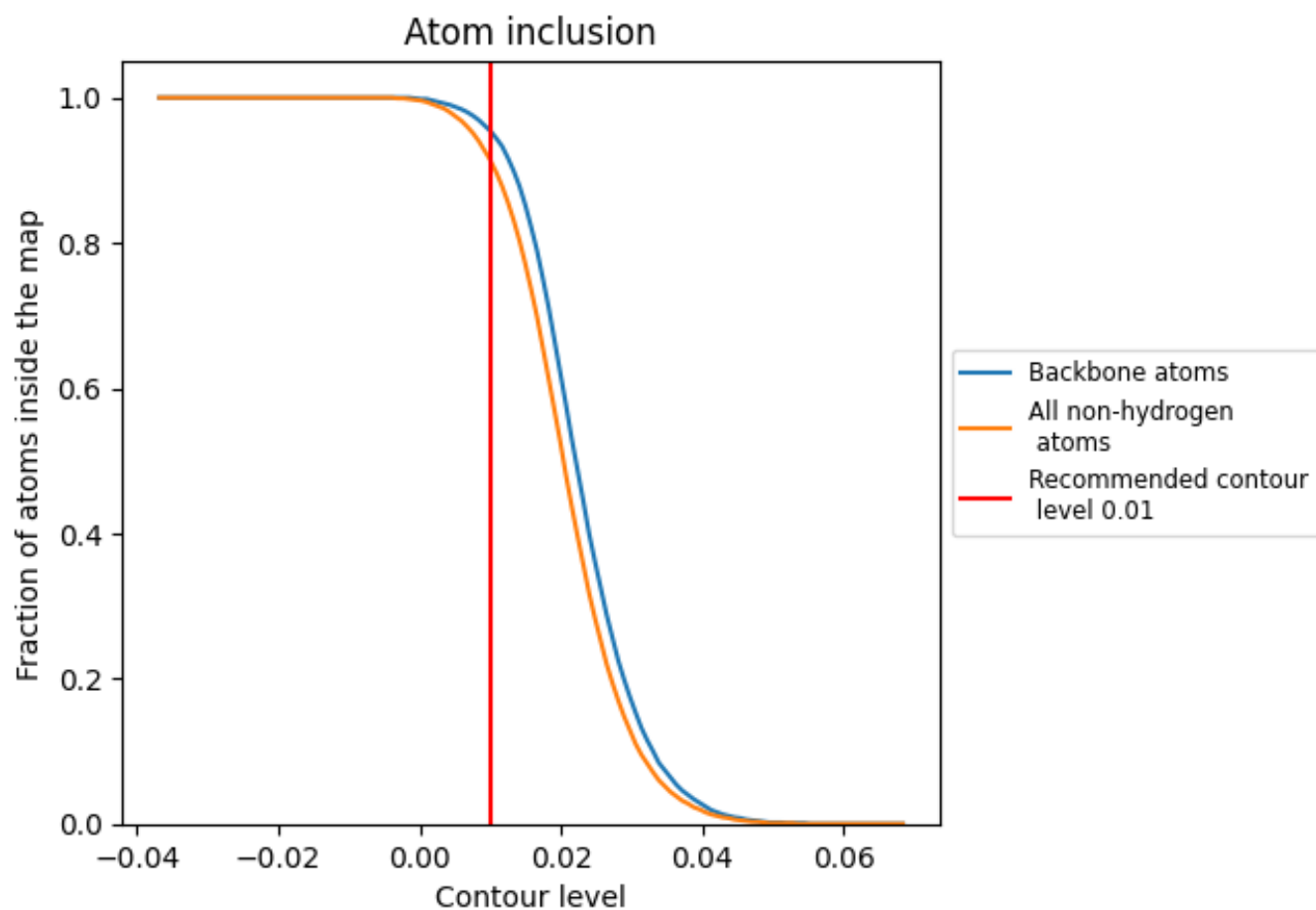
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

























## 9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 91% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9140	 0.3570
A	 0.7570	 0.2690
B	 0.8820	 0.2850
C	 0.8210	 0.2630
D	 0.9300	 0.3600
E	 0.9150	 0.3770
F	 0.9140	 0.3540
G	 0.9190	 0.3750
H	 0.9050	 0.3620
I	 0.9610	 0.3870
J	 0.9250	 0.3850
K	 0.9610	 0.3490

