



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 05:18 AM UTC

PDB ID : 5FJB / pdb_00005fjb
EMDB ID : EMD-3076
Title : Cyclophilin A Stabilize HIV-1 Capsid through a Novel Non- canonical Binding Site
Authors : Liu, C.; Perilla, J.R.; Ning, J.; Lu, M.; Hou, G.; Ramalhu, R.; Bedwell, G.J.; Ahn, J.; Shi, J.; Gronenborn, A.M.; Prevelige Jr, P.E.; Rouso, I.; Aiken, C.; Polenova, T.; Schulten, K.; Zhang, P.
Deposited on : 2015-10-07
Resolution : 9.00 Å(reported)
Based on initial model : 3J4F

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
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

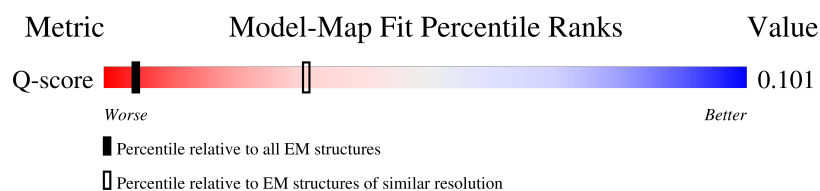
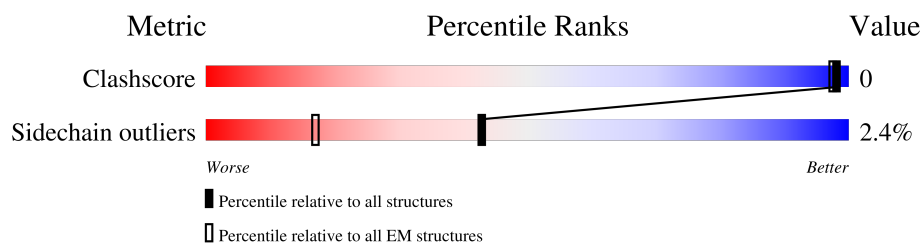
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.00 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	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	361 (7.50 - 8.50)

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

Mol	Chain	Length	Quality of chain
1	A	218	39% 43% 51% 5%
1	B	218	37% 44% 55% .
2	C	164	98% 54% 41% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4664 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 GAG POLYPROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	218	Total	C	N	O	S	0	0
			1703	1074	296	320	13		
1	B	218	Total	C	N	O	S	0	0
			1703	1074	296	320	13		

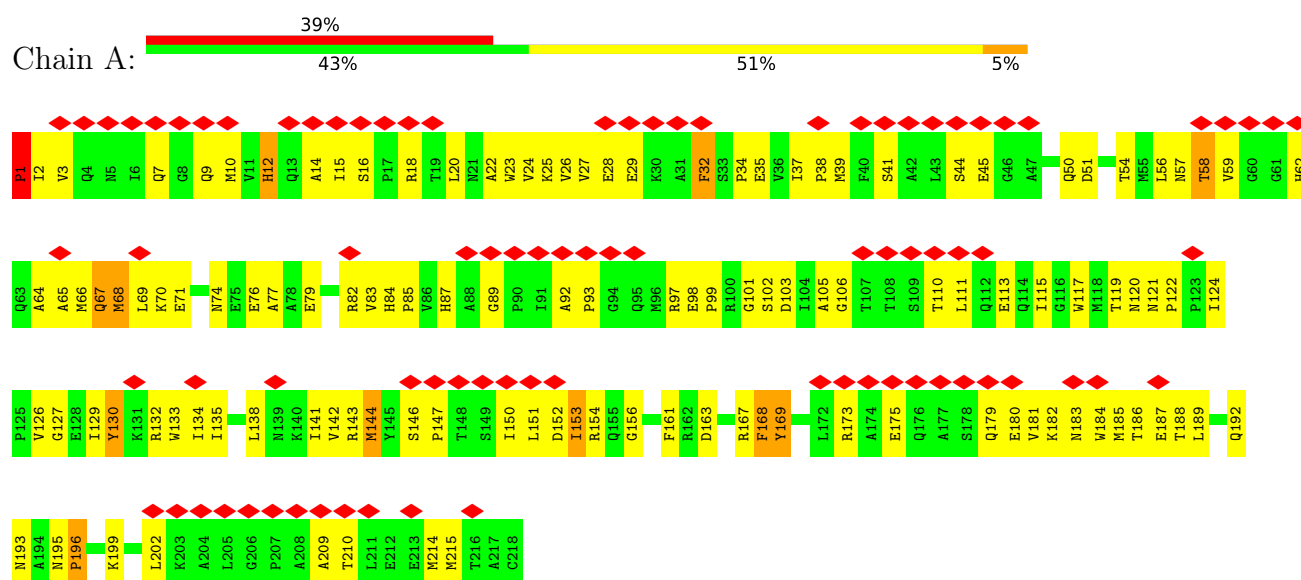
- Molecule 2 is a protein called PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	164	Total	C	N	O	S	0	0
			1258	797	217	236	8		

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.

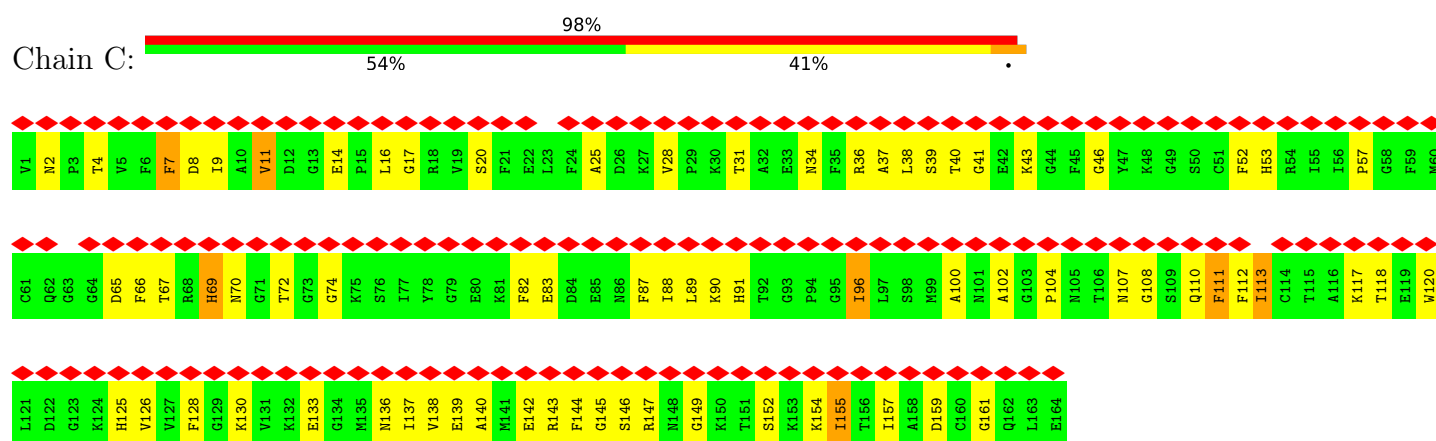
• Molecule 1: GAG POLYPROTEIN



• Molecule 1: GAG POLYPROTEIN



• Molecule 2: PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A



4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=Not provided°, rise=Not provided Å, axial sym=Not provided	Depositor
Number of segments used	Not provided	
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	15	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	59000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	57.381	Depositor
Minimum map value	-44.915	Depositor
Average map value	0.244	Depositor
Map value standard deviation	11.385	Depositor
Recommended contour level	20	Depositor
Map size (Å)	462.15997, 462.15997, 275.59998	wwPDB
Map dimensions	436, 436, 260	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

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	2.25	61/1741 (3.5%)	2.63	148/2368 (6.2%)
1	B	2.16	53/1741 (3.0%)	2.59	147/2368 (6.2%)
2	C	2.18	46/1286 (3.6%)	2.37	72/1723 (4.2%)
All	All	2.20	160/4768 (3.4%)	2.55	367/6459 (5.7%)

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	A	0	7
1	B	0	2
2	C	0	2
All	All	0	11

All (160) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	37	ILE	CA-C	11.27	1.64	1.52
1	B	65	ALA	N-CA	-10.65	1.33	1.46
1	B	178	SER	C-N	9.57	1.45	1.33
1	A	28	GLU	CA-C	-9.39	1.40	1.52
2	C	154	LYS	CA-CB	9.27	1.64	1.53
1	B	125	PRO	CA-CB	9.08	1.62	1.53
1	A	50	GLN	CA-CB	8.78	1.67	1.53
1	B	95	GLN	CA-C	-8.50	1.42	1.52
1	A	12	HIS	CG-CD2	-8.25	1.26	1.35
1	B	31	ALA	N-CA	8.08	1.58	1.46
1	B	133	TRP	CA-CB	8.08	1.66	1.53
1	A	106	GLY	CA-C	-8.05	1.40	1.51
1	A	70	LYS	N-CA	-8.03	1.36	1.46
1	A	188	THR	CA-C	-8.01	1.46	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	84	HIS	ND1-CE1	8.01	1.40	1.32
2	C	70	ASN	CA-C	-7.86	1.42	1.52
1	B	190	LEU	CA-CB	7.70	1.65	1.53
2	C	155	ILE	CA-C	-7.62	1.43	1.52
1	A	142	VAL	CA-C	-7.43	1.43	1.52
2	C	159	ASP	N-CA	-7.43	1.36	1.46
1	A	22	ALA	C-N	7.39	1.43	1.33
1	B	128	GLU	N-CA	7.35	1.54	1.46
1	B	125	PRO	C-N	7.32	1.42	1.33
2	C	43	LYS	CA-CB	7.29	1.65	1.53
1	A	26	VAL	C-N	7.29	1.42	1.33
1	B	205	LEU	C-N	7.18	1.44	1.33
1	B	183	ASN	C-N	7.14	1.43	1.33
1	B	188	THR	CA-C	7.06	1.61	1.52
1	A	199	LYS	C-N	6.98	1.42	1.33
2	C	36	ARG	CD-NE	6.94	1.55	1.46
1	B	84	HIS	CA-C	6.85	1.62	1.52
2	C	108	GLY	CA-C	6.83	1.56	1.51
2	C	17	GLY	N-CA	6.82	1.53	1.44
1	B	86	VAL	N-CA	6.75	1.54	1.46
2	C	138	VAL	CA-C	6.70	1.62	1.52
1	B	172	LEU	N-CA	-6.58	1.38	1.46
1	A	147	PRO	CA-CB	6.56	1.62	1.53
2	C	155	ILE	CA-CB	6.56	1.62	1.54
1	A	87	HIS	CE1-NE2	6.55	1.39	1.32
2	C	70	ASN	CA-CB	6.52	1.64	1.53
2	C	117	LYS	CA-CB	6.50	1.61	1.53
1	A	98	GLU	CA-C	6.50	1.59	1.52
1	B	207	PRO	N-CA	-6.50	1.39	1.47
1	A	57	ASN	N-CA	-6.38	1.38	1.46
1	B	87	HIS	CA-C	6.37	1.61	1.52
1	B	38	PRO	CA-CB	6.37	1.63	1.53
1	A	62	HIS	CB-CG	6.31	1.58	1.50
2	C	28	VAL	CA-C	6.28	1.59	1.52
1	A	189	LEU	CA-C	-6.27	1.44	1.52
1	B	16	SER	CA-CB	6.26	1.63	1.53
1	B	120	ASN	N-CA	-6.19	1.37	1.45
1	A	83	VAL	CA-CB	-6.15	1.46	1.54
1	B	144	MET	N-CA	-6.15	1.39	1.46
2	C	147	ARG	CD-NE	6.13	1.54	1.46
2	C	16	LEU	CA-C	-6.12	1.43	1.52
1	A	161	PHE	N-CA	-6.11	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	119	THR	N-CA	-6.11	1.39	1.46
2	C	11	VAL	CA-C	-6.09	1.44	1.52
1	A	23	TRP	C-N	6.08	1.41	1.33
1	A	120	ASN	CA-CB	6.06	1.62	1.53
1	A	143	ARG	CD-NE	6.04	1.54	1.46
1	B	43	LEU	CA-CB	6.04	1.62	1.53
1	A	130	TYR	CA-CB	6.03	1.63	1.53
1	A	133	TRP	NE1-CE2	-6.03	1.30	1.37
1	B	3	VAL	C-O	-6.02	1.17	1.24
1	A	185	MET	N-CA	-6.02	1.38	1.46
2	C	74	GLY	N-CA	6.02	1.54	1.45
1	A	105	ALA	CA-C	6.01	1.60	1.52
1	B	214	MET	C-N	5.94	1.42	1.33
2	C	2	ASN	CA-C	5.92	1.59	1.52
1	A	45	GLU	CA-CB	5.89	1.61	1.53
1	A	115	ILE	C-O	-5.89	1.17	1.24
1	B	13	GLN	C-N	5.84	1.41	1.33
1	A	79	GLU	CA-C	5.80	1.60	1.52
1	A	113	GLU	C-N	5.80	1.41	1.33
1	B	4	GLN	CA-CB	5.79	1.62	1.53
1	B	176	GLN	C-N	5.76	1.41	1.33
1	B	40	PHE	C-N	5.75	1.41	1.33
1	B	37	ILE	CA-CB	-5.75	1.51	1.54
1	B	187	GLU	CA-C	5.74	1.58	1.53
1	A	87	HIS	ND1-CE1	5.73	1.38	1.32
2	C	137	ILE	C-O	-5.72	1.17	1.24
2	C	20	SER	N-CA	5.72	1.53	1.46
1	A	102	SER	N-CA	-5.71	1.39	1.46
1	A	50	GLN	CA-C	5.68	1.60	1.52
2	C	83	GLU	C-O	5.67	1.30	1.23
2	C	83	GLU	C-N	5.65	1.41	1.33
1	B	88	ALA	CA-C	5.65	1.59	1.52
1	A	202	LEU	C-N	5.64	1.41	1.34
1	B	20	LEU	N-CA	-5.62	1.39	1.46
2	C	128	PHE	C-N	5.62	1.39	1.33
1	A	51	ASP	N-CA	5.61	1.53	1.46
2	C	100	ALA	N-CA	5.59	1.52	1.46
1	B	11	VAL	CA-C	5.58	1.59	1.52
1	B	67	GLN	CA-CB	5.57	1.62	1.53
2	C	142	GLU	C-N	5.55	1.41	1.33
1	B	13	GLN	N-CA	-5.55	1.39	1.46
1	A	59	VAL	CA-CB	-5.52	1.48	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	89	GLY	C-N	5.50	1.40	1.33
1	A	57	ASN	CA-CB	5.50	1.61	1.53
1	A	101	GLY	N-CA	5.49	1.52	1.45
2	C	157	ILE	CA-C	5.49	1.59	1.52
1	A	196	PRO	CA-C	5.47	1.60	1.52
1	A	111	LEU	C-O	-5.47	1.17	1.24
2	C	9	ILE	CA-C	-5.46	1.45	1.52
2	C	96	ILE	N-CA	-5.43	1.39	1.46
1	A	24	VAL	CA-CB	-5.43	1.47	1.54
1	A	92	ALA	C-N	-5.40	1.27	1.33
2	C	89	LEU	C-O	5.39	1.30	1.24
1	A	199	LYS	CA-C	-5.38	1.45	1.52
1	A	3	VAL	C-N	5.37	1.40	1.33
1	A	179	GLN	CA-CB	5.37	1.62	1.53
2	C	143	ARG	CA-CB	5.37	1.62	1.53
1	B	143	ARG	C-N	5.35	1.41	1.33
1	B	27	VAL	N-CA	5.34	1.53	1.46
1	A	181	VAL	C-N	-5.33	1.27	1.33
2	C	112	PHE	CA-C	5.33	1.58	1.52
2	C	146	SER	N-CA	5.33	1.52	1.45
1	B	75	GLU	CA-C	-5.32	1.46	1.52
1	A	199	LYS	N-CA	-5.32	1.39	1.46
2	C	149	GLY	C-O	-5.32	1.16	1.24
2	C	161	GLY	C-N	5.31	1.41	1.33
2	C	38	LEU	C-N	5.29	1.40	1.33
1	A	82	ARG	C-O	5.28	1.30	1.24
1	A	152	ASP	CA-CB	5.27	1.62	1.53
1	B	136	LEU	CA-C	5.26	1.59	1.52
1	A	193	ASN	C-N	5.26	1.40	1.33
1	B	200	THR	C-N	5.26	1.40	1.33
1	B	5	ASN	N-CA	-5.24	1.39	1.46
1	B	79	GLU	CA-C	-5.22	1.46	1.52
1	A	146	SER	CA-C	-5.22	1.46	1.52
2	C	8	ASP	CA-CB	5.21	1.61	1.53
1	A	169	TYR	CA-C	-5.20	1.46	1.52
1	B	165	VAL	C-N	5.20	1.40	1.33
1	A	76	GLU	C-N	5.20	1.40	1.33
1	B	65	ALA	CA-C	-5.19	1.46	1.52
2	C	72	THR	CA-CB	-5.19	1.45	1.53
2	C	4	THR	N-CA	5.18	1.52	1.46
1	B	200	THR	N-CA	5.18	1.52	1.46
1	B	143	ARG	CA-CB	5.18	1.61	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	97	ARG	NE-CZ	-5.17	1.27	1.33
1	B	51	ASP	CA-CB	5.16	1.61	1.53
1	B	172	LEU	C-N	5.13	1.40	1.33
1	A	14	ALA	N-CA	-5.12	1.39	1.46
1	A	79	GLU	C-N	5.12	1.40	1.33
2	C	139	GLU	CA-CB	5.11	1.61	1.53
2	C	144	PHE	N-CA	-5.10	1.39	1.46
2	C	126	VAL	N-CA	-5.10	1.39	1.46
1	A	24	VAL	C-N	5.09	1.40	1.33
1	A	9	GLN	N-CA	-5.09	1.39	1.46
1	B	94	GLY	N-CA	5.09	1.52	1.45
1	B	182	LYS	C-O	-5.08	1.18	1.24
1	A	54	THR	C-N	-5.07	1.27	1.33
2	C	89	LEU	CB-CG	5.07	1.63	1.53
2	C	90	LYS	N-CA	-5.07	1.39	1.45
1	A	59	VAL	CA-C	5.05	1.59	1.52
2	C	66	PHE	CA-CB	5.03	1.61	1.53
1	B	167	ARG	NE-CZ	5.01	1.38	1.33
2	C	111	PHE	C-N	5.00	1.40	1.33
2	C	96	ILE	CA-CB	-5.00	1.48	1.54

All (367) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	37	ILE	O-C-N	-12.07	112.70	120.42
1	B	67	GLN	OE1-CD-NE2	-11.73	110.87	122.60
1	B	10	MET	N-CA-C	11.55	127.40	111.92
1	A	32	PHE	CA-CB-CG	-11.41	102.39	113.80
1	A	187	GLU	N-CA-C	11.28	123.65	111.36
1	B	138	LEU	N-CA-C	10.43	123.70	111.71
1	A	154	ARG	NE-CZ-NH1	10.02	131.52	121.50
1	B	97	ARG	NE-CZ-NH2	-10.01	110.19	119.20
1	A	14	ALA	N-CA-C	9.52	123.29	110.35
1	A	185	MET	N-CA-C	9.46	122.59	111.71
2	C	70	ASN	OD1-CG-ND2	-9.44	113.16	122.60
1	A	84	HIS	CA-CB-CG	-9.43	104.37	113.80
1	A	124	ILE	N-CA-C	-9.33	97.61	107.60
2	C	37	ALA	O-C-N	-9.33	111.52	122.15
1	B	143	ARG	CA-C-N	9.25	132.68	120.28
1	B	143	ARG	C-N-CA	9.25	132.68	120.28
1	A	29	GLU	N-CA-C	9.13	120.84	111.07
1	A	65	ALA	CA-C-N	9.13	132.52	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	65	ALA	C-N-CA	9.13	132.52	120.28
2	C	36	ARG	N-CA-C	8.89	120.58	111.07
1	A	182	LYS	N-CA-C	8.79	120.47	111.07
1	A	64	ALA	CA-C-N	8.44	131.79	120.65
1	A	64	ALA	C-N-CA	8.44	131.79	120.65
1	B	204	ALA	CA-C-N	8.40	131.36	120.44
1	B	204	ALA	C-N-CA	8.40	131.36	120.44
2	C	88	ILE	N-CA-C	8.33	119.11	110.62
1	B	118	MET	CA-C-N	8.20	131.59	120.44
1	B	118	MET	C-N-CA	8.20	131.59	120.44
1	A	27	VAL	CA-C-N	8.18	131.08	120.44
1	A	27	VAL	C-N-CA	8.18	131.08	120.44
1	A	69	LEU	CA-C-N	8.15	131.87	120.29
1	A	69	LEU	C-N-CA	8.15	131.87	120.29
1	B	176	GLN	OE1-CD-NE2	-8.02	114.58	122.60
1	A	117	TRP	CA-C-N	8.00	131.00	120.28
1	A	117	TRP	C-N-CA	8.00	131.00	120.28
1	A	126	VAL	CA-C-N	7.99	128.81	119.94
1	A	126	VAL	C-N-CA	7.99	128.81	119.94
1	B	21	ASN	O-C-N	-7.98	113.66	122.12
1	B	120	ASN	N-CA-C	7.97	120.87	110.43
2	C	152	SER	CB-CA-C	-7.95	95.81	109.65
2	C	57	PRO	N-CA-C	7.95	124.22	111.26
2	C	107	ASN	OD1-CG-ND2	-7.89	114.71	122.60
1	A	15	ILE	O-C-N	7.88	131.09	122.66
1	A	124	ILE	O-C-N	-7.86	113.69	120.92
1	A	82	ARG	NE-CZ-NH1	7.85	129.35	121.50
1	B	181	VAL	N-CA-C	7.84	118.62	110.62
1	A	38	PRO	CA-C-N	7.82	130.76	120.28
1	A	38	PRO	C-N-CA	7.82	130.76	120.28
1	B	17	PRO	CA-C-N	7.79	131.05	120.38
1	B	17	PRO	C-N-CA	7.79	131.05	120.38
1	B	41	SER	N-CA-C	7.78	119.76	111.28
2	C	130	LYS	CA-C-N	7.77	130.96	120.63
2	C	130	LYS	C-N-CA	7.77	130.96	120.63
1	A	167	ARG	CA-C-N	7.69	131.48	120.79
1	A	167	ARG	C-N-CA	7.69	131.48	120.79
2	C	39	SER	N-CA-C	7.69	119.66	111.28
1	B	110	THR	CA-C-N	7.65	130.87	120.38
1	B	110	THR	C-N-CA	7.65	130.87	120.38
1	A	127	GLY	CA-C-N	7.62	130.49	120.28
1	A	127	GLY	C-N-CA	7.62	130.49	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	189	LEU	N-CA-C	7.58	120.20	111.11
1	A	10	MET	CA-C-N	7.54	131.40	120.91
1	A	10	MET	C-N-CA	7.54	131.40	120.91
1	B	54	THR	CA-C-N	7.54	130.25	120.44
1	B	54	THR	C-N-CA	7.54	130.25	120.44
2	C	87	PHE	CA-CB-CG	7.53	121.33	113.80
2	C	52	PHE	CA-CB-CG	-7.50	106.30	113.80
1	A	163	ASP	CA-CB-CG	7.50	120.10	112.60
2	C	53	HIS	CE1-NE2-CD2	-7.48	101.52	109.00
2	C	36	ARG	NH1-CZ-NH2	-7.48	109.58	119.30
2	C	14	GLU	O-C-N	-7.45	113.83	121.28
1	B	43	LEU	N-CA-C	7.44	119.39	111.28
1	A	180	GLU	N-CA-C	7.43	119.02	111.07
1	A	41	SER	N-CA-C	7.40	118.98	111.07
1	A	58	THR	N-CA-C	7.39	121.55	112.54
1	A	65	ALA	O-C-N	-7.38	114.36	122.03
1	B	22	ALA	N-CA-C	7.36	120.36	111.82
1	A	83	VAL	CB-CA-C	-7.32	102.43	112.24
1	A	153	ILE	N-CA-C	7.31	117.92	108.12
1	B	36	VAL	N-CA-CB	7.28	120.44	110.54
1	B	113	GLU	CA-C-N	7.28	129.91	120.44
1	B	113	GLU	C-N-CA	7.28	129.91	120.44
1	B	131	LYS	N-CA-C	7.23	120.20	111.82
1	A	26	VAL	CA-C-O	-7.21	112.68	120.47
2	C	125	HIS	CA-CB-CG	-7.17	106.63	113.80
1	B	140	LYS	N-CA-C	7.09	119.01	111.28
1	B	176	GLN	CA-C-N	7.09	132.06	120.94
1	B	176	GLN	C-N-CA	7.09	132.06	120.94
1	A	185	MET	CA-C-N	6.99	130.21	120.29
1	A	185	MET	C-N-CA	6.99	130.21	120.29
1	B	86	VAL	CA-C-N	6.98	130.67	120.82
1	B	86	VAL	C-N-CA	6.98	130.67	120.82
1	A	209	ALA	N-CA-C	6.95	120.30	110.50
1	B	210	THR	N-CA-CB	6.90	120.13	110.26
1	B	104	ILE	CA-C-O	6.89	127.69	120.25
1	B	112	GLN	CA-C-O	6.89	127.86	120.55
1	A	167	ARG	N-CA-C	6.88	118.78	111.28
1	A	87	HIS	CE1-NE2-CD2	-6.83	102.17	109.00
2	C	87	PHE	CA-C-N	6.82	129.81	120.46
2	C	87	PHE	C-N-CA	6.82	129.81	120.46
1	B	53	ASN	OD1-CG-ND2	-6.80	115.80	122.60
1	A	25	LYS	N-CA-C	6.79	118.34	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	115	ILE	CA-C-N	6.77	127.46	119.94
1	B	115	ILE	C-N-CA	6.77	127.46	119.94
1	B	103	ASP	CA-C-O	6.74	127.72	119.97
1	A	185	MET	CG-SD-CE	-6.63	86.31	100.90
1	A	193	ASN	OD1-CG-ND2	-6.62	115.98	122.60
1	B	132	ARG	N-CA-C	6.59	118.12	111.07
1	B	212	GLU	O-C-N	-6.58	115.29	122.07
1	A	115	ILE	O-C-N	-6.53	115.51	121.91
1	B	93	PRO	N-CA-C	6.53	125.92	112.47
1	B	35	GLU	CA-C-N	6.51	129.38	120.46
1	B	35	GLU	C-N-CA	6.51	129.38	120.46
1	A	130	TYR	CA-C-N	6.51	128.90	120.44
1	A	130	TYR	C-N-CA	6.51	128.90	120.44
1	B	132	ARG	NE-CZ-NH1	6.51	128.01	121.50
1	B	1	PRO	CA-C-N	6.50	132.21	122.91
1	B	1	PRO	C-N-CA	6.50	132.21	122.91
2	C	69	HIS	CE1-NE2-CD2	-6.50	102.50	109.00
1	A	215	MET	CA-C-O	6.49	127.30	120.42
2	C	70	ASN	CB-CG-ND2	6.47	126.11	116.40
1	A	68	MET	CA-C-N	6.47	128.95	120.28
1	A	68	MET	C-N-CA	6.47	128.95	120.28
1	B	21	ASN	OD1-CG-ND2	-6.45	116.15	122.60
2	C	102	ALA	N-CA-CB	-6.45	100.59	111.17
1	A	74	ASN	OD1-CG-ND2	-6.45	116.15	122.60
1	B	195	ASN	CB-CA-C	6.45	119.63	109.37
1	B	150	ILE	O-C-N	-6.45	115.61	121.87
1	B	97	ARG	NE-CZ-NH1	6.45	127.95	121.50
1	B	138	LEU	CA-C-N	6.44	128.81	120.44
1	B	138	LEU	C-N-CA	6.44	128.81	120.44
1	A	151	LEU	CA-C-O	6.41	127.25	119.31
1	B	195	ASN	OD1-CG-ND2	-6.40	116.20	122.60
1	B	153	ILE	O-C-N	-6.36	115.70	122.83
2	C	120	TRP	CB-CG-CD2	6.34	135.68	126.80
1	A	122	PRO	CA-C-N	6.33	126.09	119.76
1	A	122	PRO	C-N-CA	6.33	126.09	119.76
2	C	159	ASP	O-C-N	-6.32	116.66	123.42
2	C	133	GLU	N-CA-C	-6.30	99.49	109.07
1	A	175	GLU	CA-C-O	6.28	128.10	121.19
2	C	46	GLY	O-C-N	-6.25	118.61	123.80
1	B	166	ASP	CA-CB-CG	-6.25	106.35	112.60
2	C	110	GLN	N-CA-C	6.24	118.84	110.35
1	B	119	THR	CA-C-O	6.24	127.13	120.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	147	ARG	N-CA-C	6.21	118.05	111.28
1	A	58	THR	CA-C-N	6.16	128.33	120.56
1	A	58	THR	C-N-CA	6.16	128.33	120.56
2	C	39	SER	CA-C-N	6.15	129.03	120.29
2	C	39	SER	C-N-CA	6.15	129.03	120.29
1	A	9	GLN	OE1-CD-NE2	-6.13	116.47	122.60
1	A	120	ASN	O-C-N	-6.12	115.45	122.68
1	B	168	PHE	CA-C-N	6.12	128.48	120.28
1	B	168	PHE	C-N-CA	6.12	128.48	120.28
2	C	70	ASN	CA-CB-CG	6.11	118.71	112.60
1	B	135	ILE	CB-CA-C	6.10	120.64	112.22
2	C	125	HIS	CB-CG-CD2	-6.09	123.28	131.20
1	A	69	LEU	N-CA-C	6.08	117.90	111.28
2	C	67	THR	N-CA-CB	6.07	122.49	110.48
1	B	72	THR	N-CA-C	6.04	117.53	111.07
2	C	7	PHE	N-CA-CB	6.04	120.05	110.57
1	A	65	ALA	CA-C-O	6.03	127.33	121.00
1	B	189	LEU	CA-C-O	-6.03	114.44	120.90
2	C	34	ASN	N-CA-C	6.03	118.35	111.11
1	B	86	VAL	N-CA-C	6.03	121.87	109.34
1	B	121	ASN	CA-CB-CG	5.99	118.59	112.60
1	A	113	GLU	N-CA-C	5.99	117.47	111.07
2	C	36	ARG	NE-CZ-NH1	5.99	127.49	121.50
1	A	183	ASN	CB-CG-ND2	5.96	125.34	116.40
1	A	152	ASP	O-C-N	-5.96	114.89	122.34
1	A	195	ASN	CA-C-N	5.96	127.29	119.84
1	A	195	ASN	C-N-CA	5.96	127.29	119.84
1	B	78	ALA	CA-C-N	5.95	128.54	120.44
1	B	78	ALA	C-N-CA	5.95	128.54	120.44
1	B	198	CYS	N-CA-C	5.95	117.44	111.07
2	C	118	THR	OG1-CB-CG2	-5.94	97.42	109.30
1	A	196	PRO	N-CA-C	5.94	124.70	112.47
2	C	136	ASN	OD1-CG-ND2	-5.93	116.67	122.60
1	B	12	HIS	CA-CB-CG	5.92	119.72	113.80
1	A	28	GLU	CB-CG-CD	5.91	122.65	112.60
2	C	7	PHE	CB-CA-C	-5.91	99.49	109.72
1	A	102	SER	N-CA-C	5.91	118.67	111.82
1	B	55	MET	CA-C-N	5.91	128.19	120.28
1	B	55	MET	C-N-CA	5.91	128.19	120.28
1	B	99	PRO	N-CA-CB	-5.89	98.47	103.36
2	C	28	VAL	CA-C-N	-5.89	112.48	119.84
2	C	28	VAL	C-N-CA	-5.89	112.48	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	91	HIS	CE1-NE2-CD2	-5.88	103.12	109.00
1	B	164	TYR	O-C-N	-5.87	115.45	122.15
2	C	41	GLY	CA-C-N	5.87	128.73	120.28
2	C	41	GLY	C-N-CA	5.87	128.73	120.28
1	B	83	VAL	CB-CA-C	-5.87	104.22	112.14
1	B	73	ILE	CB-CA-C	-5.87	104.22	112.14
1	A	186	THR	CA-C-O	5.86	126.63	120.42
2	C	69	HIS	CG-CD2-NE2	5.86	113.06	107.20
1	A	56	LEU	CA-C-O	5.84	126.72	120.24
1	B	153	ILE	CA-CB-CG1	5.84	120.33	110.40
1	A	93	PRO	CA-C-O	-5.83	114.99	121.23
1	A	103	ASP	N-CA-C	5.83	117.30	111.07
1	B	150	ILE	N-CA-C	5.83	116.56	110.62
1	B	34	PRO	CA-C-N	5.82	132.65	121.54
1	B	34	PRO	C-N-CA	5.82	132.65	121.54
1	A	210	THR	N-CA-CB	5.81	119.12	110.29
2	C	157	ILE	O-C-N	-5.81	115.31	122.57
1	B	123	PRO	O-C-N	-5.80	116.14	123.10
1	A	20	LEU	N-CA-C	5.79	117.27	111.07
2	C	31	THR	CA-CB-OG1	5.75	118.23	109.60
1	B	89	GLY	CA-C-N	5.73	125.75	119.90
1	B	89	GLY	C-N-CA	5.73	125.75	119.90
1	A	62	HIS	CB-CA-C	5.71	119.83	111.73
1	B	152	ASP	N-CA-C	-5.71	106.32	113.28
1	A	168	PHE	CA-CB-CG	5.70	119.50	113.80
1	A	85	PRO	CA-C-O	-5.68	114.93	121.86
1	B	67	GLN	CG-CD-OE1	5.68	132.16	120.80
1	B	165	VAL	CA-C-N	5.68	128.69	120.79
1	B	165	VAL	C-N-CA	5.68	128.69	120.79
1	B	81	ASP	CA-CB-CG	-5.68	106.92	112.60
1	B	115	ILE	CB-CA-C	-5.67	104.48	112.14
1	B	23	TRP	N-CA-C	5.67	117.14	111.07
1	A	132	ARG	CA-C-N	5.67	127.88	120.28
1	A	132	ARG	C-N-CA	5.67	127.88	120.28
1	A	152	ASP	CA-C-O	5.65	125.97	119.35
2	C	145	GLY	CA-C-N	5.65	131.13	121.87
2	C	145	GLY	C-N-CA	5.65	131.13	121.87
1	A	195	ASN	O-C-N	-5.64	115.64	121.28
1	B	104	ILE	O-C-N	-5.64	114.09	121.82
1	B	115	ILE	N-CA-C	5.63	116.37	110.62
1	A	71	GLU	CB-CG-CD	5.63	122.17	112.60
1	A	66	MET	CG-SD-CE	-5.62	88.53	100.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	66	MET	O-C-N	-5.62	116.16	122.12
1	A	110	THR	CA-CB-CG2	-5.61	100.96	110.50
1	A	35	GLU	N-CA-CB	-5.61	101.66	110.30
1	B	52	LEU	CA-C-N	5.59	128.09	120.54
1	B	52	LEU	C-N-CA	5.59	128.09	120.54
1	B	211	LEU	CA-C-N	5.59	127.71	120.44
1	B	211	LEU	C-N-CA	5.59	127.71	120.44
1	B	179	GLN	N-CA-C	5.58	117.81	111.11
1	A	16	SER	O-C-N	-5.58	115.55	121.30
1	A	134	ILE	N-CA-C	5.58	115.78	110.42
1	A	181	VAL	CA-C-N	5.58	127.69	120.44
1	A	181	VAL	C-N-CA	5.58	127.69	120.44
1	B	3	VAL	CA-C-N	5.57	127.68	120.44
1	B	3	VAL	C-N-CA	5.57	127.68	120.44
1	A	54	THR	CA-C-O	-5.55	114.64	120.63
1	A	135	ILE	CA-C-N	5.55	127.72	120.28
1	A	135	ILE	C-N-CA	5.55	127.72	120.28
2	C	149	GLY	N-CA-C	-5.54	107.40	114.37
1	A	41	SER	CA-C-N	5.53	128.24	120.28
1	A	41	SER	C-N-CA	5.53	128.24	120.28
1	B	75	GLU	CA-C-N	5.52	128.23	120.28
1	B	75	GLU	C-N-CA	5.52	128.23	120.28
2	C	113	ILE	CA-C-N	5.51	128.59	120.82
2	C	113	ILE	C-N-CA	5.51	128.59	120.82
1	A	1	PRO	CA-C-N	5.51	128.57	120.91
1	A	1	PRO	C-N-CA	5.51	128.57	120.91
1	A	77	ALA	N-CA-C	-5.50	105.29	111.28
1	B	111	LEU	CA-C-N	5.50	127.65	120.28
1	B	111	LEU	C-N-CA	5.50	127.65	120.28
2	C	25	ALA	N-CA-C	5.48	118.01	111.71
1	A	129	ILE	CA-C-N	5.47	129.99	120.68
1	A	129	ILE	C-N-CA	5.47	129.99	120.68
1	B	65	ALA	CA-C-N	5.46	127.60	120.28
1	B	65	ALA	C-N-CA	5.46	127.60	120.28
2	C	125	HIS	ND1-CE1-NE2	5.46	113.86	108.40
1	A	184	TRP	O-C-N	-5.46	116.33	122.12
2	C	36	ARG	O-C-N	-5.45	116.45	122.07
1	B	180	GLU	N-CA-C	5.45	117.22	111.28
1	B	114	GLN	N-CA-CB	5.44	117.90	110.01
1	B	189	LEU	CA-C-N	5.43	127.88	120.54
1	B	189	LEU	C-N-CA	5.43	127.88	120.54
2	C	16	LEU	CA-C-O	5.42	125.84	119.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	186	THR	N-CA-CB	5.39	118.14	110.16
1	A	99	PRO	N-CA-C	5.39	118.93	110.80
1	A	124	ILE	CA-C-O	5.39	125.76	119.89
2	C	72	THR	CA-CB-OG1	5.38	117.68	109.60
1	B	23	TRP	CA-C-O	5.38	126.47	120.82
1	B	193	ASN	CA-CB-CG	-5.37	107.23	112.60
1	A	119	THR	CB-CA-C	-5.37	101.10	110.17
1	B	13	GLN	CA-C-N	5.36	128.71	121.05
1	B	13	GLN	C-N-CA	5.36	128.71	121.05
1	A	186	THR	O-C-N	-5.34	116.06	122.15
1	B	24	VAL	O-C-N	5.34	127.05	121.87
1	A	215	MET	CA-C-N	5.33	128.17	120.38
1	A	215	MET	C-N-CA	5.33	128.17	120.38
1	B	63	GLN	N-CA-CB	5.33	119.09	110.40
1	A	214	MET	CA-C-N	5.32	127.85	120.29
1	A	214	MET	C-N-CA	5.32	127.85	120.29
1	A	143	ARG	O-C-N	-5.32	116.48	122.12
2	C	152	SER	N-CA-CB	5.32	118.46	110.53
1	B	215	MET	CG-SD-CE	-5.31	89.22	100.90
2	C	39	SER	O-C-N	-5.31	116.49	122.12
1	B	147	PRO	CA-C-N	5.30	129.26	120.94
1	B	147	PRO	C-N-CA	5.30	129.26	120.94
1	A	144	MET	CG-SD-CE	-5.30	89.24	100.90
1	A	51	ASP	CB-CA-C	-5.29	102.58	110.88
1	B	96	MET	CA-C-N	5.28	128.27	120.82
1	B	96	MET	C-N-CA	5.28	128.27	120.82
1	A	138	LEU	CA-C-N	5.28	127.66	120.54
1	A	138	LEU	C-N-CA	5.28	127.66	120.54
2	C	37	ALA	CA-C-O	5.28	126.01	120.42
1	B	48	THR	CA-C-O	-5.27	115.02	120.87
2	C	82	PHE	N-CA-C	5.26	117.82	109.50
1	B	9	GLN	OE1-CD-NE2	-5.25	117.35	122.60
1	A	7	GLN	O-C-N	-5.25	115.89	122.35
1	A	122	PRO	N-CD-CG	5.25	110.10	103.80
1	A	183	ASN	OD1-CG-ND2	-5.25	117.35	122.60
1	A	51	ASP	N-CA-CB	5.24	117.61	110.01
1	A	215	MET	CA-CB-CG	5.24	124.58	114.10
1	B	170	LYS	N-CA-C	-5.24	105.57	111.28
1	A	156	GLY	O-C-N	-5.24	116.06	122.03
1	B	133	TRP	N-CA-C	5.23	116.98	111.28
2	C	104	PRO	N-CA-C	5.22	123.23	112.47
1	A	173	ARG	N-CA-C	5.22	116.97	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	196	PRO	CA-C-N	5.22	127.27	120.28
1	A	196	PRO	C-N-CA	5.22	127.27	120.28
1	B	41	SER	CA-C-O	-5.22	115.02	120.55
1	B	126	VAL	O-C-N	5.21	129.32	122.12
1	A	39	MET	CB-CA-C	5.20	119.43	110.79
1	B	192	GLN	OE1-CD-NE2	-5.19	117.41	122.60
1	A	120	ASN	CA-C-O	5.18	127.88	122.03
2	C	140	ALA	CA-C-N	5.17	127.17	120.44
2	C	140	ALA	C-N-CA	5.17	127.17	120.44
1	A	56	LEU	O-C-N	-5.17	115.51	122.23
1	A	195	ASN	CA-CB-CG	-5.17	107.43	112.60
1	A	142	VAL	N-CA-C	5.16	115.78	110.36
1	B	197	ASP	CA-CB-CG	-5.15	107.45	112.60
1	A	57	ASN	CB-CA-C	-5.14	102.26	110.79
1	A	117	TRP	N-CA-CB	5.13	117.45	110.01
1	B	190	LEU	N-CA-C	5.13	117.26	111.11
1	A	147	PRO	CA-C-N	5.12	128.34	120.82
1	A	147	PRO	C-N-CA	5.12	128.34	120.82
1	A	141	ILE	N-CA-CB	5.12	117.50	110.54
1	B	181	VAL	O-C-N	5.11	126.83	121.87
1	A	192	GLN	N-CA-C	-5.11	107.05	113.28
2	C	53	HIS	CB-CG-CD2	-5.11	124.56	131.20
1	B	184	TRP	O-C-N	-5.11	116.33	122.15
1	A	44	SER	CB-CA-C	-5.10	101.98	110.81
1	A	23	TRP	N-CA-C	5.10	116.53	111.07
1	B	9	GLN	CB-CA-C	5.10	118.66	110.29
2	C	146	SER	CA-C-N	5.10	127.11	120.28
2	C	146	SER	C-N-CA	5.10	127.11	120.28
1	B	119	THR	N-CA-CB	5.08	117.44	110.07
1	A	99	PRO	CA-C-O	-5.08	115.24	121.03
1	B	81	ASP	CA-C-N	5.08	127.34	120.44
1	B	81	ASP	C-N-CA	5.08	127.34	120.44
1	B	45	GLU	N-CA-C	5.08	117.66	110.10
1	A	67	GLN	CA-C-N	5.07	127.07	120.28
1	A	67	GLN	C-N-CA	5.07	127.07	120.28
1	B	98	GLU	CA-C-N	5.07	125.86	120.13
1	B	98	GLU	C-N-CA	5.07	125.86	120.13
1	B	115	ILE	CA-CB-CG2	5.07	119.12	110.50
1	A	34	PRO	N-CA-CB	5.07	108.40	102.88
2	C	43	LYS	N-CA-C	5.07	119.10	113.02
2	C	2	ASN	CA-C-O	-5.06	114.69	119.55
1	B	40	PHE	CA-CB-CG	-5.06	108.74	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	169	TYR	CA-C-N	5.05	127.05	120.28
1	B	169	TYR	C-N-CA	5.05	127.05	120.28
1	B	85	PRO	N-CA-CB	-5.05	97.95	103.25
1	A	111	LEU	CA-C-O	5.05	125.90	120.55
2	C	7	PHE	O-C-N	5.05	129.25	123.29
2	C	91	HIS	CG-CD2-NE2	5.04	112.24	107.20
2	C	87	PHE	N-CA-CB	-5.03	102.87	110.92
2	C	57	PRO	CA-C-O	5.03	126.80	121.32
1	B	130	TYR	O-C-N	-5.02	116.80	122.12
1	B	15	ILE	N-CA-C	5.01	115.46	108.84
1	B	120	ASN	OD1-CG-ND2	-5.01	117.59	122.60
1	A	215	MET	O-C-N	-5.01	116.44	122.15
1	B	178	SER	O-C-N	-5.00	116.86	122.97

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1	PRO	Peptide
1	A	121	ASN	Peptide
1	A	130	TYR	Sidechain
1	A	168	PHE	Sidechain
1	A	169	TYR	Sidechain
1	A	18	ARG	Sidechain
1	A	32	PHE	Sidechain
1	B	173	ARG	Sidechain
1	B	97	ARG	Sidechain
2	C	111	PHE	Sidechain
2	C	7	PHE	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1703	0	1704	2	0
1	B	1703	0	1704	0	0
2	C	1258	0	1228	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4664	0	4636	4	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 0.

All (4) 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:150:ILE:HD12	1:A:153:ILE:HG13	1.82	0.61
2:C:65:ASP:CG	2:C:69:HIS:H	2.27	0.43
2:C:11:VAL:HG22	2:C:155:ILE:HD12	2.03	0.41
1:A:68:MET:HE1	1:A:144:MET:HE1	2.03	0.41

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	186/186 (100%)	180 (97%)	6 (3%)	34	56
1	B	186/186 (100%)	183 (98%)	3 (2%)	55	70
2	C	132/132 (100%)	129 (98%)	3 (2%)	44	64
All	All	504/504 (100%)	492 (98%)	12 (2%)	43	64

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	PRO
1	A	2	ILE
1	A	12	HIS
1	A	58	THR
1	A	67	GLN
1	A	196	PRO
1	B	128	GLU
1	B	192	GLN
1	B	216	THR
2	C	40	THR
2	C	96	ILE
2	C	113	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	179	GLN
1	B	7	GLN
1	B	21	ASN
1	B	87	HIS

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.

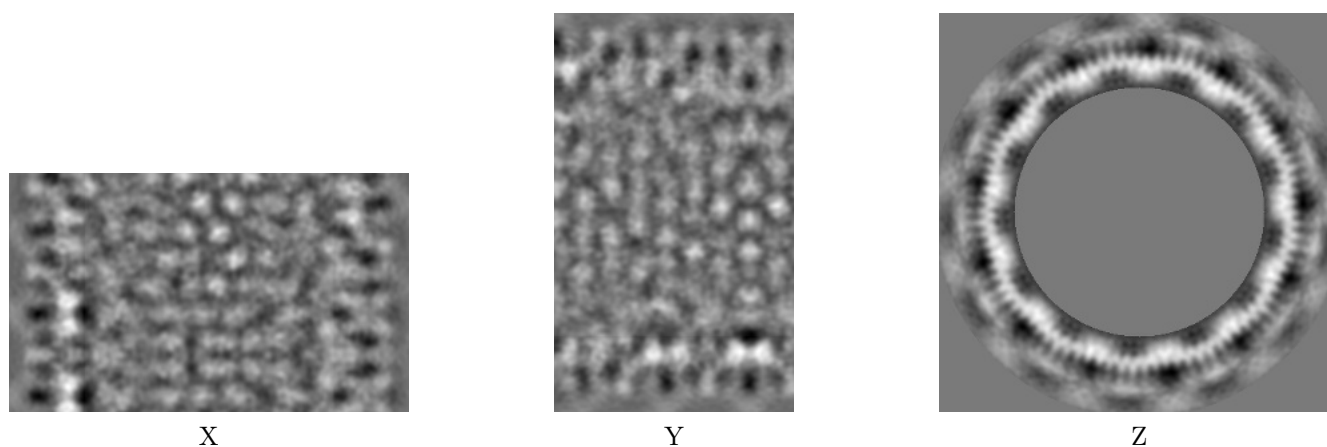
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3076. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

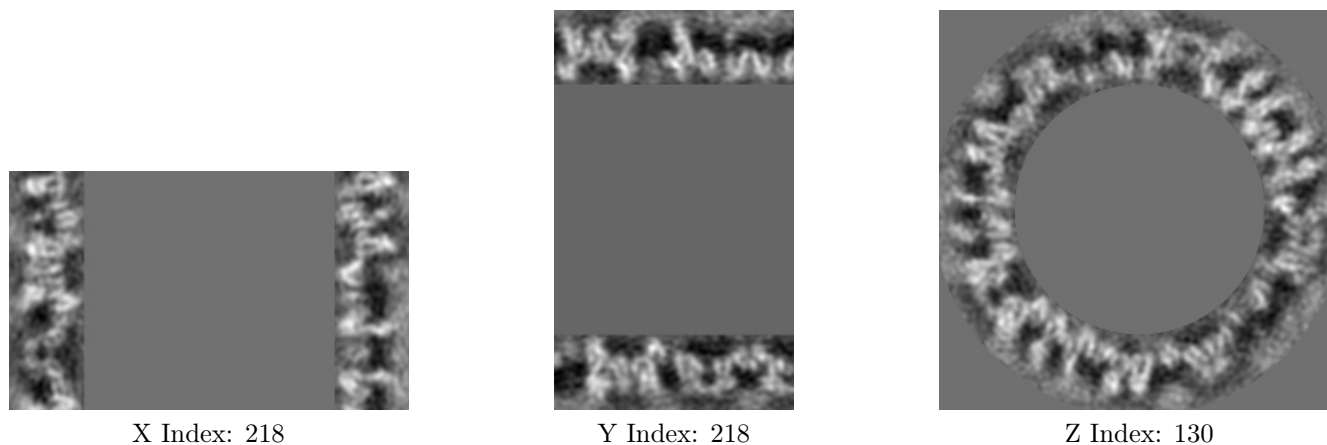
6.1.1 Primary map



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

6.2 Central slices [i](#)

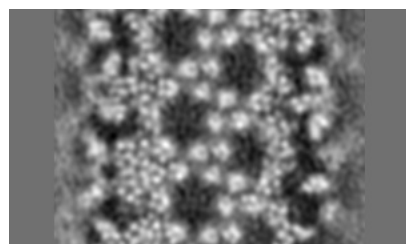
6.2.1 Primary map



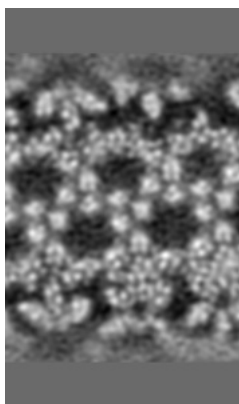
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

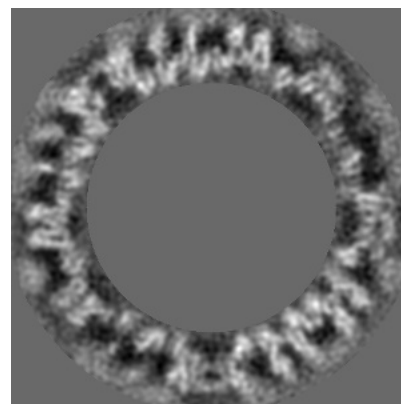
6.3.1 Primary map



X Index: 366



Y Index: 367

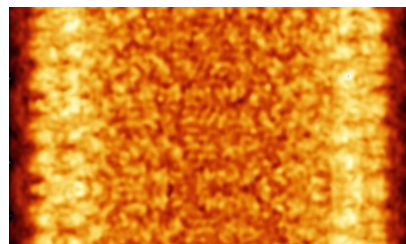


Z Index: 56

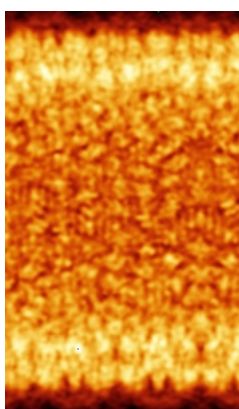
The images above show the largest variance slices of the map in three orthogonal directions.

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

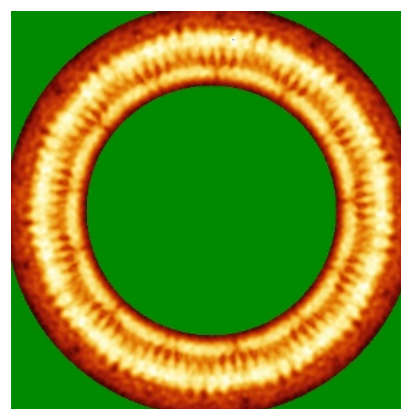
6.4.1 Primary map



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

This section was not generated.

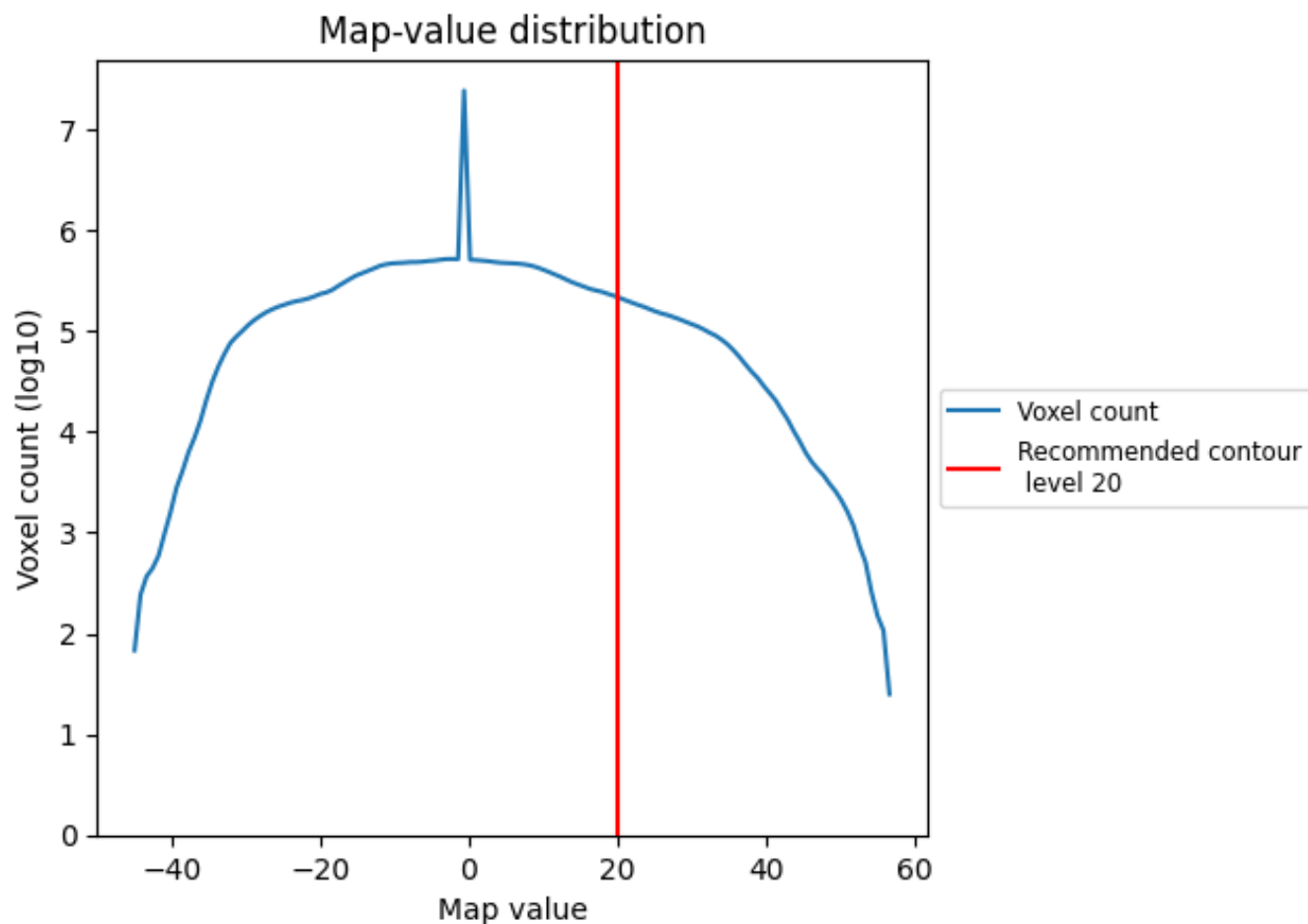
6.6 Mask visualisation

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

7 Map analysis [i](#)

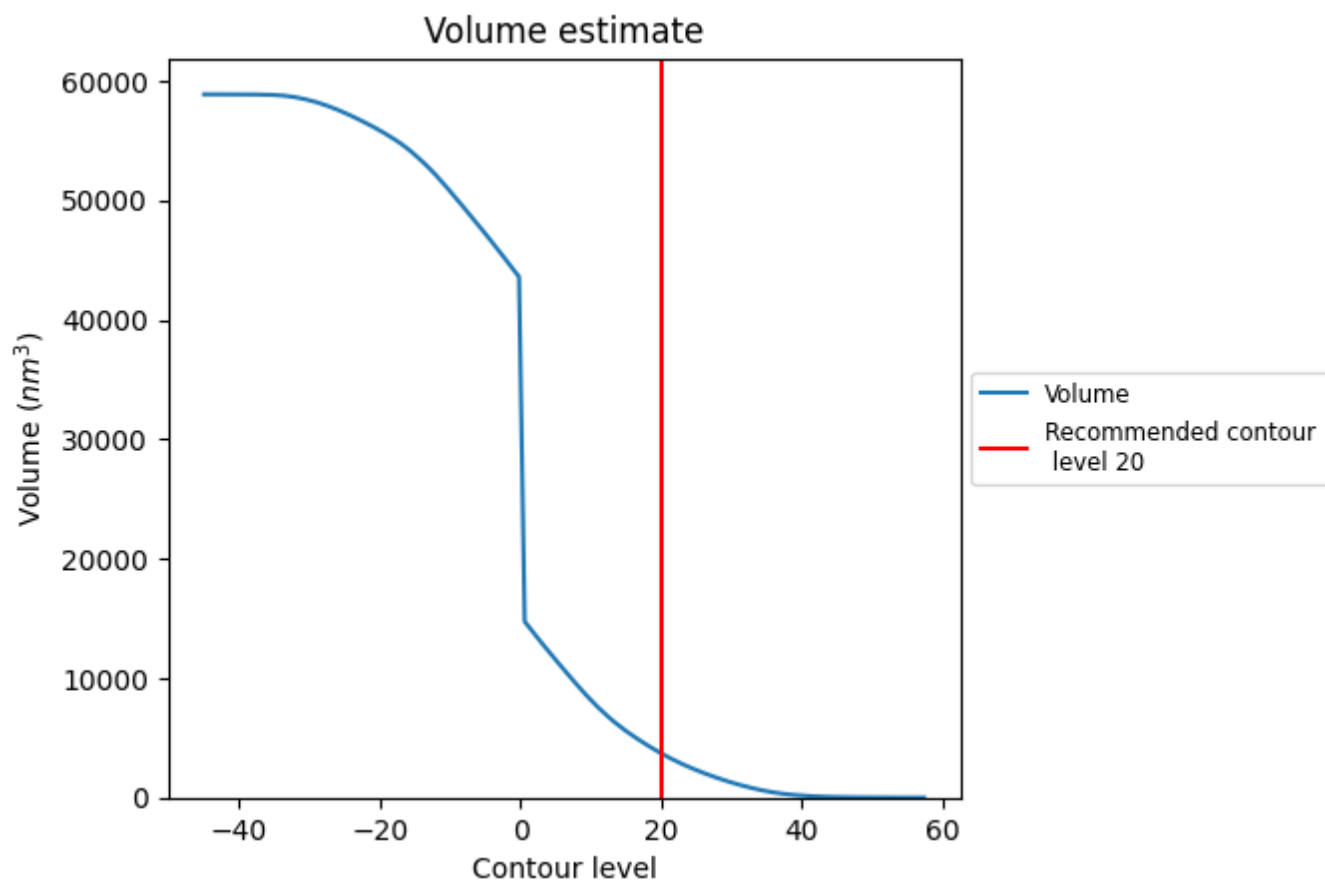
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3713 nm³; this corresponds to an approximate mass of 3354 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](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

8 Fourier-Shell correlation ⓘ

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

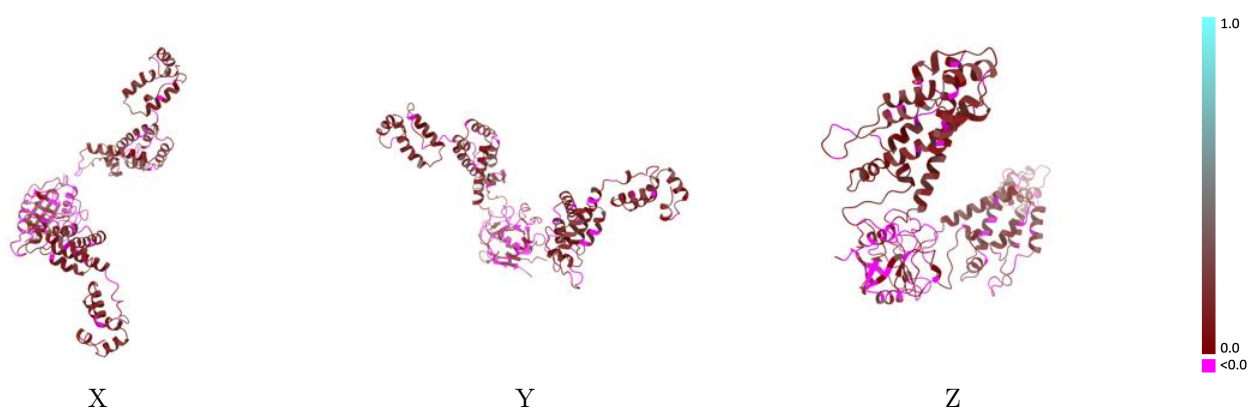
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3076 and PDB model 5FJB. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

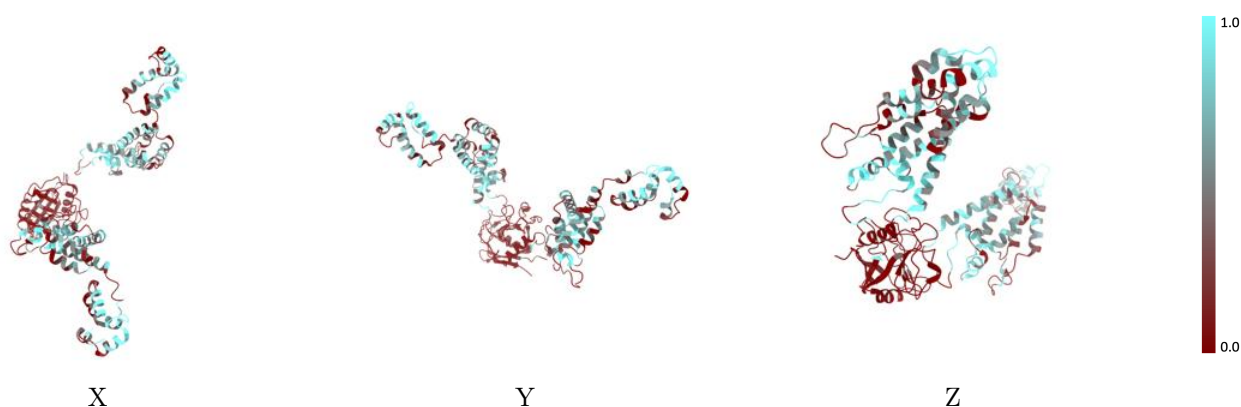
This section was not generated.

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



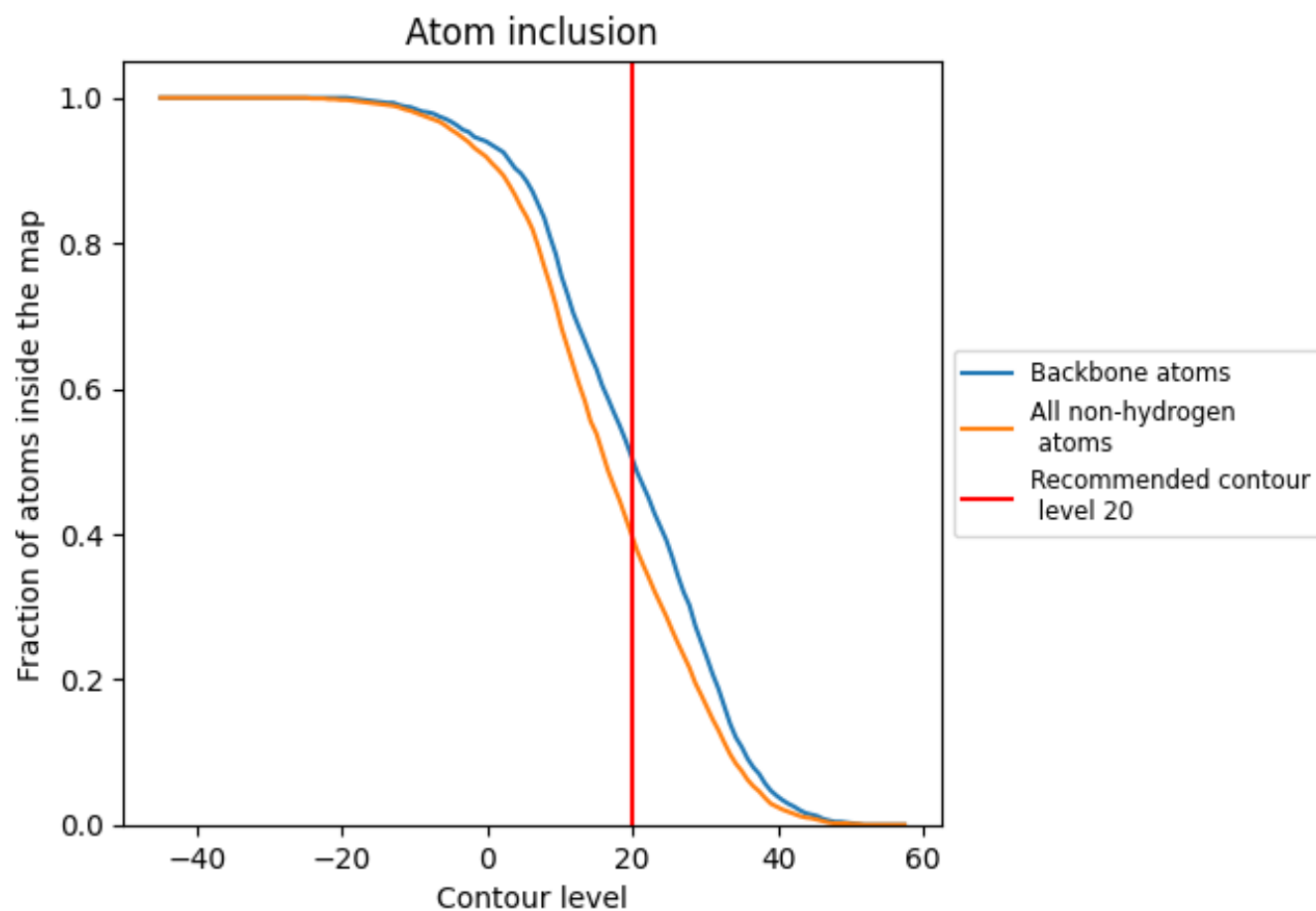
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (20).

9.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 39% 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 (20) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3940	0.1010
A	0.5270	0.1310
B	0.5350	0.1350
C	0.0260	0.0140

