



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 09:23 AM UTC

PDB ID : 4D1K / pdb_00004d1k
EMDB ID : EMD-2638
Title : Cryo-electron microscopy of tubular arrays of HIV-1 Gag resolves structures essential for immature virus assembly.
Authors : Bharat, T.A.M.; Castillo-Menendez, L.R.; Hagen, W.J.H.; Lux, V.; Igonet, S.; Schorb, M.; Schur, F.K.M.; Krauesslich, H.G.; Briggs, J.A.G.
Deposited on : 2014-05-02
Resolution : 9.40 Å (reported)
Based on initial model : 4COP

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:

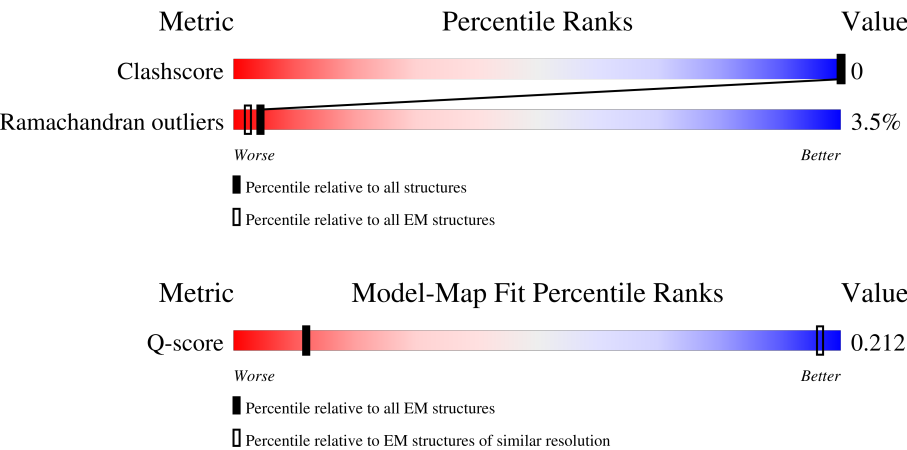
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 9.40 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	-
Q-score	-	25397	224 (8.90 - 9.90)

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	219	33% 65% 33% .
1	B	219	40% 72% 26% .
1	C	219	44% 72% 27% .
1	D	219	37% 70% 28% .
1	E	219	41% 68% 31% .

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Mol	Chain	Length	Quality of chain
1	F	219	42% 66% 32%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3942 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 PROTEIN.

Mol	Chain	Residues	Atoms			AltConf	Trace
1	A	219	Total 657	C 438	N 219	0	0
1	B	219	Total 657	C 438	N 219	0	0
1	C	219	Total 657	C 438	N 219	0	0
1	D	219	Total 657	C 438	N 219	0	0
1	E	219	Total 657	C 438	N 219	0	0
1	F	219	Total 657	C 438	N 219	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	15	ILE	LEU	variant	UNP Q5D0H3
A	87	HIS	GLN	variant	UNP Q5D0H3
A	120	HIS	SER	variant	UNP Q5D0H3
A	169	SER	TYR	engineered mutation	UNP Q5D0H3
B	15	ILE	LEU	variant	UNP Q5D0H3
B	87	HIS	GLN	variant	UNP Q5D0H3
B	120	HIS	SER	variant	UNP Q5D0H3
B	169	SER	TYR	engineered mutation	UNP Q5D0H3
C	15	ILE	LEU	variant	UNP Q5D0H3
C	87	HIS	GLN	variant	UNP Q5D0H3
C	120	HIS	SER	variant	UNP Q5D0H3
C	169	SER	TYR	engineered mutation	UNP Q5D0H3
D	15	ILE	LEU	variant	UNP Q5D0H3
D	87	HIS	GLN	variant	UNP Q5D0H3
D	120	HIS	SER	variant	UNP Q5D0H3
D	169	SER	TYR	engineered mutation	UNP Q5D0H3
E	15	ILE	LEU	variant	UNP Q5D0H3
E	87	HIS	GLN	variant	UNP Q5D0H3

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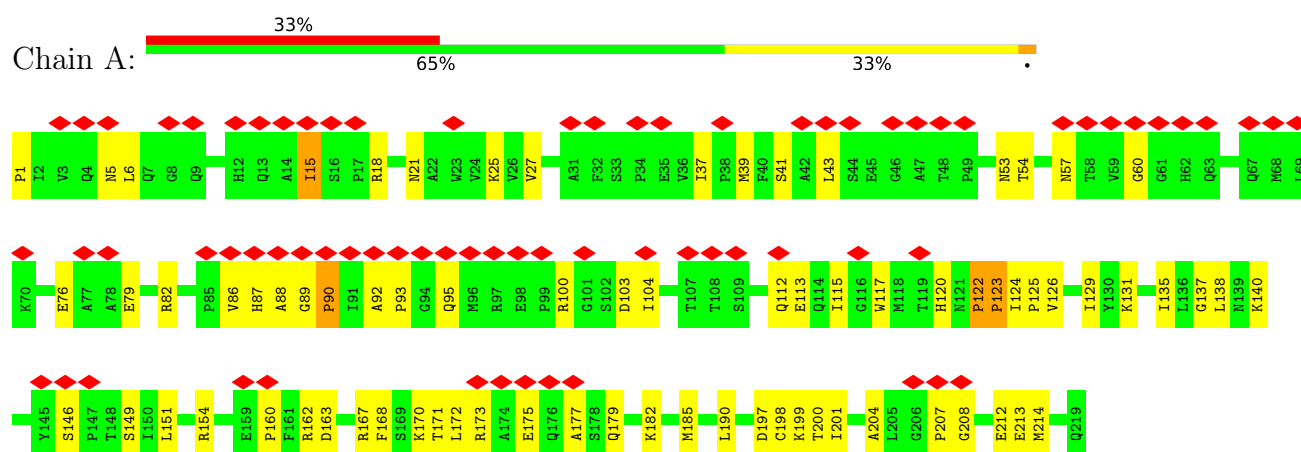
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Chain	Residue	Modelled	Actual	Comment	Reference
E	120	HIS	SER	variant	UNP Q5D0H3
E	169	SER	TYR	engineered mutation	UNP Q5D0H3
F	15	ILE	LEU	variant	UNP Q5D0H3
F	87	HIS	GLN	variant	UNP Q5D0H3
F	120	HIS	SER	variant	UNP Q5D0H3
F	169	SER	TYR	engineered mutation	UNP Q5D0H3

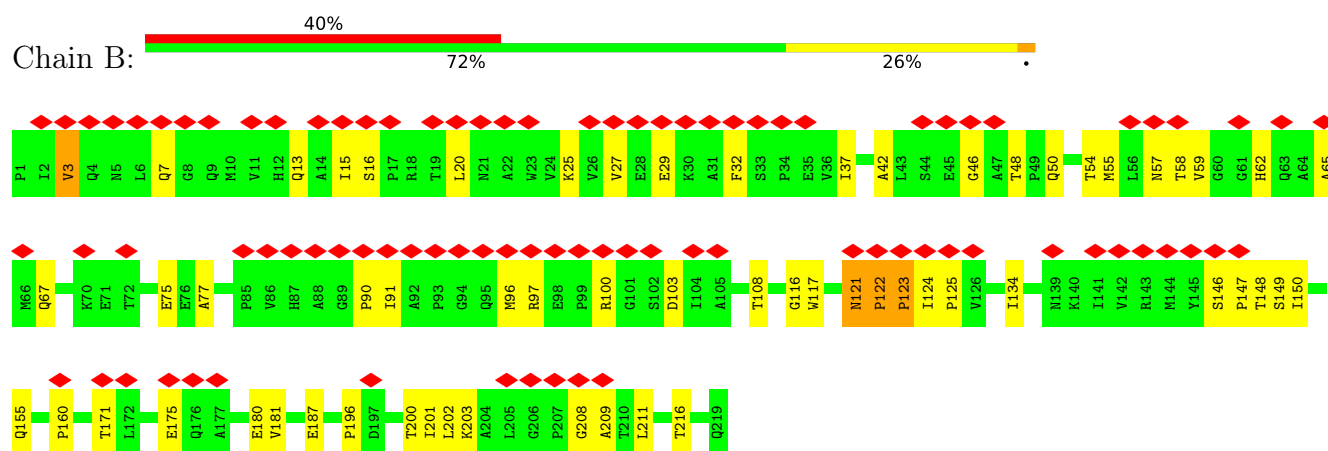
3 Residue-property plots

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.

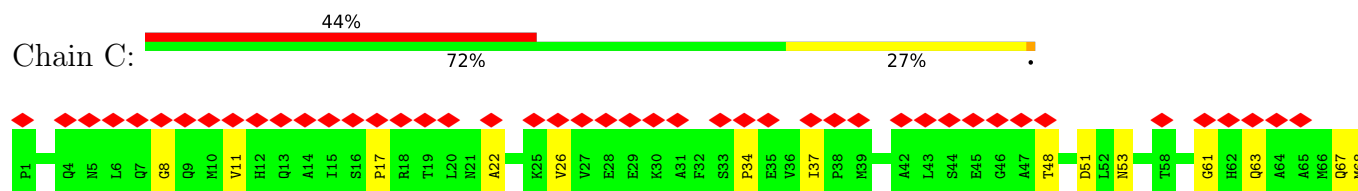
• Molecule 1: GAG PROTEIN

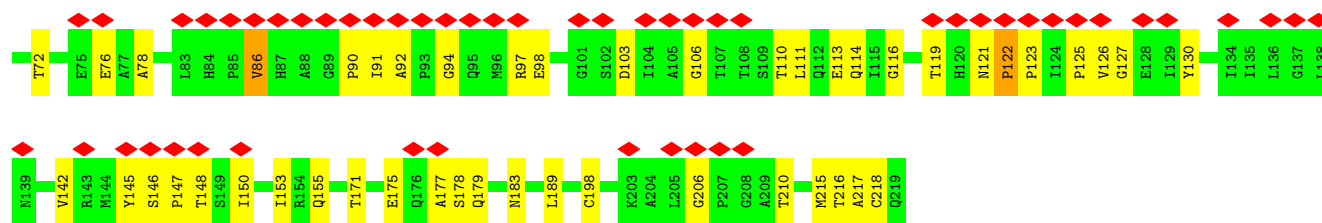


• Molecule 1: GAG PROTEIN

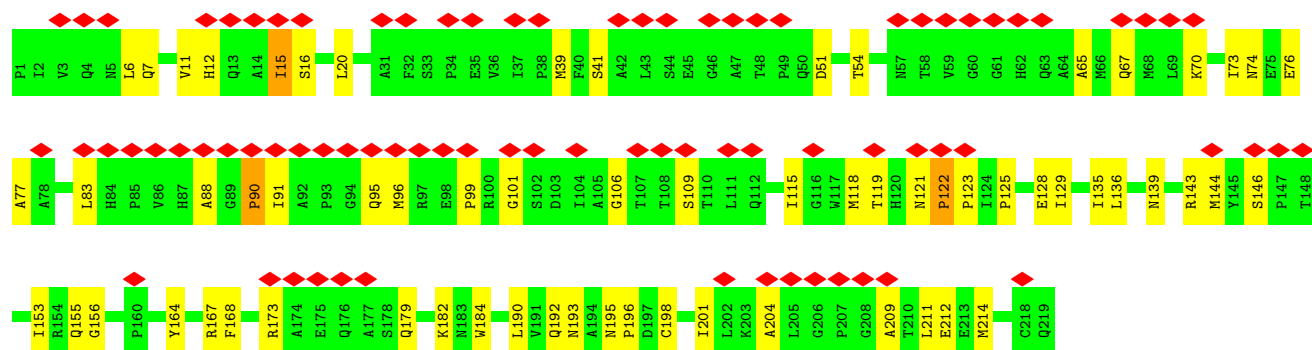


• Molecule 1: GAG PROTEIN

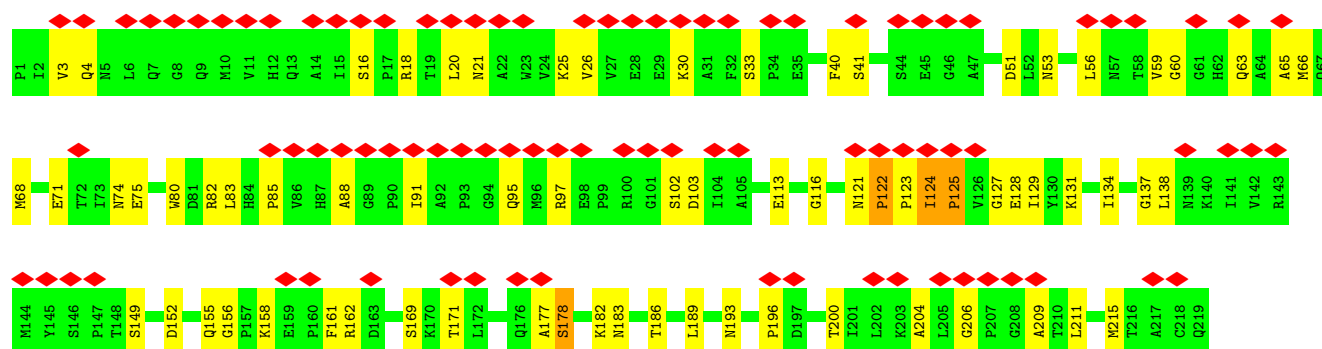
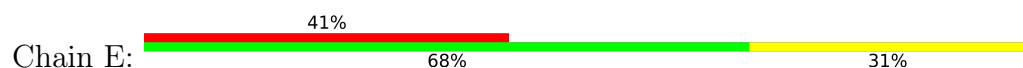




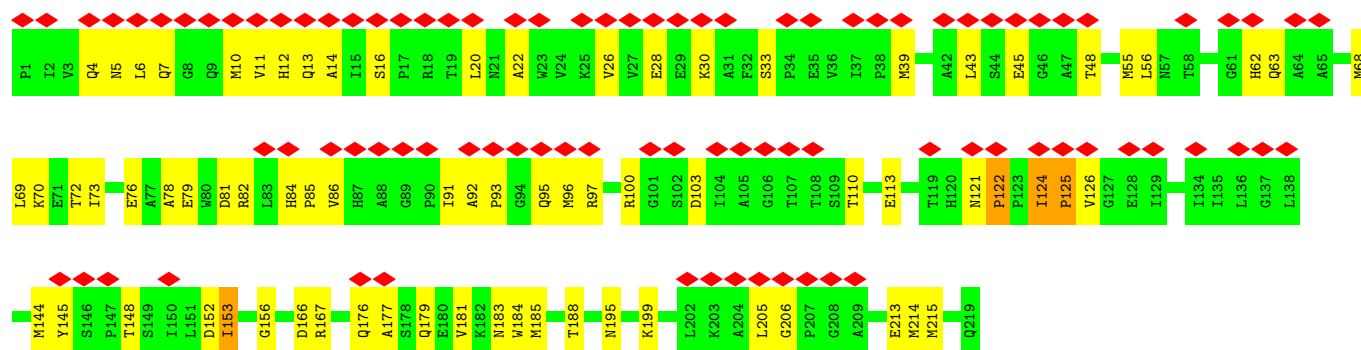
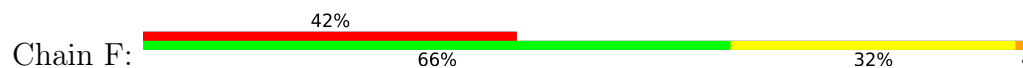
• Molecule 1: GAG PROTEIN



• Molecule 1: GAG PROTEIN



• Molecule 1: GAG PROTEIN



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 TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	23	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	Not provided	
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	86.177	Depositor
Minimum map value	-69.385	Depositor
Average map value	2.531	Depositor
Map value standard deviation	19.957	Depositor
Recommended contour level	27	Depositor
Map size (Å)	153.0, 153.0, 153.0	wwPDB
Map dimensions	100, 100, 100	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.53, 1.53, 1.53	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	2.53	36/656 (5.5%)	3.09	71/655 (10.8%)
1	B	2.48	28/656 (4.3%)	2.94	55/655 (8.4%)
1	C	2.45	24/656 (3.7%)	2.97	58/655 (8.9%)
1	D	2.49	31/656 (4.7%)	2.95	56/655 (8.5%)
1	E	2.53	29/656 (4.4%)	3.08	66/655 (10.1%)
1	F	2.40	28/656 (4.3%)	3.04	72/655 (11.0%)
All	All	2.48	176/3936 (4.5%)	3.01	378/3930 (9.6%)

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	1
1	B	0	2
1	D	0	1
1	E	0	2
1	F	0	2
All	All	0	8

All (176) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	185	MET	CA-C	9.56	1.65	1.52
1	A	154	ARG	CA-C	-9.30	1.41	1.52
1	F	103	ASP	CA-C	-8.72	1.41	1.52
1	A	37	ILE	C-N	8.72	1.44	1.34
1	D	122	PRO	CA-C	8.62	1.60	1.52
1	A	93	PRO	CA-C	8.58	1.64	1.52
1	F	85	PRO	CA-C	-8.57	1.41	1.52
1	B	124	ILE	CA-C	8.49	1.61	1.52
1	C	153	ILE	CA-C	-8.10	1.43	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	37	ILE	CA-C	-8.09	1.44	1.52
1	F	145	TYR	CA-C	8.09	1.63	1.52
1	D	65	ALA	N-CA	-8.06	1.36	1.46
1	C	210	THR	CA-C	-7.94	1.42	1.53
1	B	121	ASN	CA-C	7.69	1.61	1.52
1	D	196	PRO	C-N	7.65	1.43	1.33
1	A	82	ARG	CA-C	-7.58	1.43	1.52
1	E	66	MET	C-N	7.55	1.43	1.33
1	E	26	VAL	N-CA	7.54	1.55	1.46
1	D	76	GLU	C-N	7.49	1.43	1.33
1	D	118	MET	C-N	7.49	1.44	1.33
1	C	111	LEU	CA-C	-7.37	1.43	1.52
1	E	183	ASN	N-CA	-7.18	1.37	1.46
1	E	116	GLY	C-N	7.17	1.43	1.33
1	B	62	HIS	CA-C	-7.12	1.46	1.53
1	A	173	ARG	CA-C	7.09	1.61	1.52
1	B	116	GLY	C-N	7.06	1.43	1.33
1	C	92	ALA	CA-C	7.05	1.61	1.52
1	F	10	MET	CA-C	7.03	1.61	1.52
1	E	128	GLU	N-CA	-7.03	1.37	1.46
1	A	212	GLU	C-N	6.99	1.42	1.33
1	F	56	LEU	CA-C	-6.96	1.44	1.52
1	A	126	VAL	C-N	6.87	1.42	1.33
1	B	200	THR	N-CA	6.83	1.54	1.46
1	D	95	GLN	N-CA	-6.82	1.37	1.45
1	A	21	ASN	CA-C	-6.81	1.44	1.52
1	D	195	ASN	N-CA	6.79	1.53	1.45
1	B	103	ASP	CA-C	6.76	1.61	1.52
1	A	43	LEU	C-N	6.75	1.42	1.33
1	C	183	ASN	N-CA	6.74	1.54	1.46
1	D	173	ARG	N-CA	6.72	1.54	1.46
1	D	109	SER	CA-C	-6.70	1.44	1.52
1	A	113	GLU	C-N	6.68	1.42	1.33
1	E	200	THR	N-CA	6.62	1.54	1.46
1	C	103	ASP	CA-C	-6.60	1.44	1.52
1	B	103	ASP	C-N	6.58	1.42	1.33
1	F	91	ILE	N-CA	-6.57	1.38	1.46
1	A	151	LEU	C-N	6.53	1.42	1.33
1	E	21	ASN	N-CA	-6.43	1.38	1.46
1	B	96	MET	CA-C	6.42	1.60	1.52
1	F	93	PRO	N-CA	6.39	1.55	1.47
1	A	93	PRO	N-CA	-6.36	1.39	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	199	LYS	CA-C	-6.33	1.44	1.52
1	D	51	ASP	CA-C	-6.31	1.44	1.52
1	B	171	THR	C-N	6.30	1.42	1.34
1	A	82	ARG	N-CA	-6.30	1.38	1.46
1	F	43	LEU	C-N	6.24	1.42	1.33
1	C	98	GLU	CA-C	6.23	1.60	1.52
1	A	54	THR	CA-C	-6.18	1.44	1.52
1	C	216	THR	CA-C	-6.17	1.44	1.52
1	A	25	LYS	N-CA	-6.17	1.38	1.46
1	D	182	LYS	C-N	6.17	1.42	1.33
1	E	131	LYS	N-CA	-6.17	1.38	1.46
1	E	162	ARG	N-CA	-6.15	1.38	1.46
1	F	176	GLN	C-N	6.09	1.42	1.33
1	A	41	SER	N-CA	-6.05	1.39	1.46
1	A	170	LYS	C-N	6.02	1.41	1.33
1	F	166	ASP	CA-C	-6.00	1.45	1.52
1	A	88	ALA	N-CA	5.99	1.53	1.46
1	E	137	GLY	N-CA	5.99	1.53	1.45
1	E	137	GLY	CA-C	-5.92	1.45	1.52
1	F	84	HIS	C-N	5.92	1.40	1.33
1	C	217	ALA	N-CA	-5.90	1.38	1.46
1	D	155	GLN	N-CA	-5.89	1.39	1.45
1	D	168	PHE	N-CA	-5.87	1.39	1.46
1	F	113	GLU	N-CA	5.84	1.53	1.46
1	E	200	THR	CA-C	-5.84	1.45	1.52
1	A	86	VAL	C-N	5.84	1.41	1.33
1	B	196	PRO	N-CA	-5.84	1.40	1.47
1	B	181	VAL	CA-C	-5.83	1.45	1.52
1	A	131	LYS	N-CA	5.83	1.53	1.46
1	F	184	TRP	N-CA	-5.80	1.39	1.46
1	D	70	LYS	C-N	5.79	1.41	1.33
1	C	53	ASN	CA-C	-5.79	1.45	1.52
1	B	13	GLN	CA-C	5.76	1.59	1.52
1	B	65	ALA	C-N	5.75	1.41	1.33
1	E	51	ASP	N-CA	5.70	1.53	1.46
1	A	163	ASP	CA-C	-5.68	1.45	1.52
1	D	91	ILE	C-N	5.68	1.41	1.33
1	B	123	PRO	C-N	5.67	1.39	1.33
1	F	95	GLN	N-CA	5.64	1.53	1.46
1	F	153	ILE	N-CA	-5.64	1.39	1.46
1	C	127	GLY	CA-C	-5.64	1.45	1.52
1	C	53	ASN	N-CA	-5.62	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	25	LYS	C-N	5.61	1.40	1.33
1	A	100	ARG	CA-C	-5.61	1.45	1.53
1	E	4	GLN	C-N	5.61	1.40	1.33
1	C	61	GLY	N-CA	5.60	1.53	1.45
1	B	75	GLU	N-CA	5.59	1.53	1.46
1	C	113	GLU	C-N	5.58	1.41	1.33
1	D	12	HIS	C-N	5.58	1.40	1.33
1	E	3	VAL	C-N	5.56	1.41	1.33
1	F	81	ASP	N-CA	-5.55	1.39	1.46
1	E	182	LYS	N-CA	-5.55	1.39	1.46
1	E	138	LEU	CA-C	-5.54	1.45	1.52
1	C	189	LEU	CA-C	-5.54	1.45	1.52
1	D	106	GLY	N-CA	5.51	1.53	1.45
1	F	110	THR	C-N	5.51	1.41	1.33
1	D	11	VAL	CA-C	-5.51	1.45	1.52
1	A	115	ILE	CA-C	5.48	1.59	1.52
1	A	138	LEU	CA-C	5.47	1.59	1.52
1	D	54	THR	C-N	5.47	1.40	1.33
1	C	11	VAL	C-N	5.47	1.41	1.33
1	D	6	LEU	CA-C	-5.46	1.45	1.52
1	D	119	THR	N-CA	5.46	1.53	1.46
1	B	180	GLU	C-N	5.46	1.40	1.33
1	F	6	LEU	N-CA	-5.45	1.39	1.46
1	E	41	SER	CA-C	-5.43	1.46	1.52
1	B	121	ASN	C-N	5.43	1.39	1.33
1	B	108	THR	CA-C	-5.40	1.45	1.52
1	E	186	THR	C-N	5.38	1.41	1.34
1	E	26	VAL	CA-C	5.38	1.59	1.52
1	F	93	PRO	C-N	5.37	1.41	1.33
1	A	123	PRO	CA-C	-5.37	1.44	1.52
1	F	69	LEU	C-N	5.36	1.41	1.33
1	B	155	GLN	CA-C	5.36	1.58	1.52
1	C	178	SER	N-CA	5.33	1.52	1.45
1	D	193	ASN	CA-C	5.33	1.59	1.52
1	B	91	ILE	CA-C	5.32	1.59	1.52
1	D	179	GLN	C-N	5.30	1.41	1.33
1	B	203	LYS	C-N	5.29	1.40	1.33
1	E	83	LEU	CA-C	-5.29	1.45	1.52
1	C	175	GLU	N-CA	5.28	1.52	1.46
1	A	212	GLU	N-CA	-5.28	1.40	1.46
1	D	209	ALA	N-CA	-5.26	1.39	1.46
1	E	158	LYS	N-CA	-5.26	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	70	LYS	CA-C	5.26	1.59	1.52
1	B	37	ILE	CA-C	5.26	1.58	1.52
1	F	84	HIS	N-CA	5.25	1.52	1.46
1	F	124	ILE	CA-C	5.25	1.58	1.52
1	C	145	TYR	N-CA	-5.24	1.39	1.45
1	E	152	ASP	N-CA	5.23	1.52	1.46
1	A	163	ASP	N-CA	-5.23	1.39	1.46
1	F	195	ASN	C-N	-5.23	1.26	1.34
1	B	155	GLN	N-CA	-5.22	1.39	1.46
1	C	61	GLY	CA-C	5.22	1.58	1.51
1	D	201	ILE	C-N	-5.20	1.26	1.34
1	E	56	LEU	N-CA	5.20	1.52	1.46
1	D	7	GLN	C-N	5.19	1.39	1.32
1	F	30	LYS	CA-C	-5.19	1.46	1.52
1	A	95	GLN	CA-C	-5.19	1.47	1.52
1	D	211	LEU	N-CA	5.19	1.52	1.46
1	F	215	MET	N-CA	-5.19	1.40	1.46
1	D	129	ILE	CA-C	5.18	1.59	1.52
1	D	128	GLU	C-N	5.17	1.40	1.33
1	C	177	ALA	C-N	5.17	1.40	1.33
1	E	169	SER	CA-C	-5.16	1.46	1.52
1	A	6	LEU	C-N	5.16	1.41	1.33
1	C	155	GLN	N-CA	-5.16	1.39	1.46
1	A	1	PRO	N-CA	5.14	1.54	1.47
1	F	5	ASN	CA-C	-5.12	1.46	1.52
1	D	167	ARG	CA-C	5.11	1.59	1.52
1	B	29	GLU	CA-C	5.11	1.59	1.52
1	E	82	ARG	C-N	5.11	1.41	1.33
1	A	126	VAL	N-CA	-5.08	1.40	1.46
1	E	204	ALA	CA-C	-5.08	1.46	1.52
1	D	143	ARG	N-CA	-5.08	1.40	1.46
1	E	68	MET	C-N	-5.08	1.27	1.33
1	B	202	LEU	CA-C	-5.07	1.46	1.52
1	A	140	LYS	C-N	5.06	1.40	1.33
1	C	175	GLU	CA-C	5.06	1.59	1.52
1	A	160	PRO	N-CA	5.05	1.53	1.47
1	F	48	THR	C-N	5.04	1.41	1.33
1	B	77	ALA	CA-C	-5.04	1.46	1.52
1	B	57	ASN	N-CA	-5.04	1.40	1.46
1	E	211	LEU	CA-C	5.03	1.59	1.52
1	B	7	GLN	N-CA	5.00	1.52	1.46

All (378) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	122	PRO	N-CA-C	10.65	123.69	110.70
1	A	60	GLY	CA-C-N	10.46	131.51	120.00
1	A	60	GLY	C-N-CA	10.46	131.51	120.00
1	B	150	ILE	N-CA-C	10.27	123.89	111.05
1	A	122	PRO	N-CA-C	-9.82	98.71	110.70
1	D	212	GLU	N-CA-C	9.72	121.47	111.07
1	B	216	THR	N-CA-C	9.38	121.50	111.28
1	D	204	ALA	N-CA-C	9.21	120.92	111.07
1	D	190	LEU	N-CA-C	8.82	120.58	110.97
1	D	122	PRO	CA-C-N	8.76	130.78	119.84
1	D	122	PRO	C-N-CA	8.76	130.78	119.84
1	A	171	THR	CA-C-N	8.73	131.98	120.28
1	A	171	THR	C-N-CA	8.73	131.98	120.28
1	E	206	GLY	CA-C-N	8.60	128.25	119.56
1	E	206	GLY	C-N-CA	8.60	128.25	119.56
1	A	179	GLN	N-CA-C	8.58	120.71	111.36
1	E	204	ALA	N-CA-C	8.55	121.37	111.11
1	F	156	GLY	N-CA-C	8.52	122.23	112.00
1	A	213	GLU	N-CA-C	8.50	121.31	111.11
1	C	126	VAL	N-CA-C	8.45	119.24	110.62
1	D	41	SER	N-CA-C	8.41	120.07	111.07
1	E	156	GLY	CA-C-N	8.21	130.10	119.84
1	E	156	GLY	C-N-CA	8.21	130.10	119.84
1	D	156	GLY	CA-C-N	8.20	128.30	119.28
1	D	156	GLY	C-N-CA	8.20	128.30	119.28
1	C	150	ILE	N-CA-C	8.11	118.92	110.72
1	E	33	SER	CA-C-N	8.05	129.91	119.84
1	E	33	SER	C-N-CA	8.05	129.91	119.84
1	E	60	GLY	CA-C-N	8.04	130.47	120.34
1	E	60	GLY	C-N-CA	8.04	130.47	120.34
1	E	40	PHE	CA-C-N	8.02	130.87	120.44
1	E	40	PHE	C-N-CA	8.02	130.87	120.44
1	F	55	MET	CA-C-N	7.99	131.31	120.44
1	F	55	MET	C-N-CA	7.99	131.31	120.44
1	A	182	LYS	N-CA-C	7.97	119.97	111.28
1	A	89	GLY	N-CA-C	7.96	121.86	112.23
1	A	201	ILE	N-CA-C	7.96	118.06	110.42
1	E	91	ILE	N-CA-C	-7.95	101.15	112.35
1	F	20	LEU	N-CA-C	7.93	119.55	111.07
1	A	79	GLU	CA-C-N	7.88	131.18	120.54
1	A	79	GLU	C-N-CA	7.88	131.18	120.54
1	F	206	GLY	CA-C-N	7.83	127.90	119.28
1	F	206	GLY	C-N-CA	7.83	127.90	119.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	22	ALA	CA-C-N	7.83	130.61	120.44
1	F	22	ALA	C-N-CA	7.83	130.61	120.44
1	A	103	ASP	N-CA-C	-7.81	102.84	111.36
1	B	160	PRO	N-CA-C	7.70	122.88	111.03
1	E	171	THR	CA-C-N	7.65	131.29	120.28
1	E	171	THR	C-N-CA	7.65	131.29	120.28
1	A	27	VAL	CA-C-N	7.62	131.25	120.28
1	A	27	VAL	C-N-CA	7.62	131.25	120.28
1	C	198	CYS	CA-C-N	7.60	130.31	120.44
1	C	198	CYS	C-N-CA	7.60	130.31	120.44
1	F	152	ASP	N-CA-C	7.53	119.48	111.28
1	D	193	ASN	CA-C-N	7.50	132.07	120.75
1	D	193	ASN	C-N-CA	7.50	132.07	120.75
1	D	20	LEU	CA-C-N	7.45	130.12	120.44
1	D	20	LEU	C-N-CA	7.45	130.12	120.44
1	E	127	GLY	CA-C-N	7.45	130.86	120.29
1	E	127	GLY	C-N-CA	7.45	130.86	120.29
1	B	20	LEU	CA-C-N	7.43	130.09	120.44
1	B	20	LEU	C-N-CA	7.43	130.09	120.44
1	F	122	PRO	CA-C-N	7.38	129.07	119.84
1	F	122	PRO	C-N-CA	7.38	129.07	119.84
1	A	197	ASP	CA-C-N	7.34	129.99	120.44
1	A	197	ASP	C-N-CA	7.34	129.99	120.44
1	B	77	ALA	N-CA-C	7.34	119.28	111.28
1	A	92	ALA	CA-C-N	7.29	128.96	119.84
1	A	92	ALA	C-N-CA	7.29	128.96	119.84
1	D	184	TRP	CA-C-N	7.28	130.04	120.28
1	D	184	TRP	C-N-CA	7.28	130.04	120.28
1	C	48	THR	CA-C-N	7.28	127.62	119.32
1	C	48	THR	C-N-CA	7.28	127.62	119.32
1	C	91	ILE	CA-C-N	7.21	130.59	122.59
1	C	91	ILE	C-N-CA	7.21	130.59	122.59
1	F	213	GLU	N-CA-C	7.19	119.12	111.28
1	C	119	THR	N-CA-C	7.17	122.19	113.38
1	E	63	GLN	CA-C-N	7.14	130.43	120.29
1	E	63	GLN	C-N-CA	7.14	130.43	120.29
1	E	102	SER	N-CA-C	7.13	121.08	112.38
1	F	63	GLN	N-CA-C	7.12	119.90	111.71
1	D	67	GLN	CA-C-N	7.10	129.68	120.44
1	D	67	GLN	C-N-CA	7.10	129.68	120.44
1	B	42	ALA	N-CA-C	7.08	119.85	111.71
1	E	129	ILE	N-CA-C	7.03	117.17	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	83	LEU	N-CA-C	7.03	119.97	111.82
1	A	27	VAL	N-CA-C	6.93	117.72	110.72
1	B	122	PRO	N-CA-C	-6.87	102.31	110.70
1	D	164	TYR	N-CA-C	6.87	118.42	111.07
1	E	122	PRO	CA-C-N	6.85	128.40	119.84
1	E	122	PRO	C-N-CA	6.85	128.40	119.84
1	B	59	VAL	N-CA-C	-6.85	105.82	111.91
1	B	149	SER	N-CA-C	6.81	119.51	108.76
1	F	82	ARG	N-CA-C	-6.75	104.00	111.36
1	C	130	TYR	CA-C-N	6.74	129.31	120.28
1	C	130	TYR	C-N-CA	6.74	129.31	120.28
1	A	76	GLU	N-CA-C	6.73	118.70	111.36
1	E	193	ASN	N-CA-C	-6.71	104.67	112.92
1	D	91	ILE	N-CA-C	-6.71	103.95	110.72
1	F	167	ARG	N-CA-C	6.69	118.65	111.36
1	C	51	ASP	CA-C-N	6.68	129.78	120.29
1	C	51	ASP	C-N-CA	6.68	129.78	120.29
1	C	63	GLN	N-CA-C	6.67	119.38	111.71
1	D	90	PRO	CA-C-N	6.63	129.84	120.42
1	D	90	PRO	C-N-CA	6.63	129.84	120.42
1	E	161	PHE	N-CA-C	6.61	118.48	111.28
1	D	198	CYS	CA-C-N	6.60	129.12	120.28
1	D	198	CYS	C-N-CA	6.60	129.12	120.28
1	F	96	MET	N-CA-C	6.58	119.91	110.10
1	E	75	GLU	N-CA-C	6.54	118.07	111.07
1	C	17	PRO	CA-C-N	6.50	128.99	120.28
1	C	17	PRO	C-N-CA	6.50	128.99	120.28
1	F	45	GLU	N-CA-C	6.50	119.14	109.59
1	F	28	GLU	N-CA-C	6.49	119.17	111.71
1	F	16	SER	N-CA-C	6.48	117.05	109.60
1	A	151	LEU	N-CA-C	6.47	120.76	112.34
1	C	68	MET	N-CA-C	6.46	118.32	111.28
1	B	32	PHE	N-CA-C	-6.45	105.37	112.72
1	B	208	GLY	CA-C-N	6.44	129.96	120.95
1	B	208	GLY	C-N-CA	6.44	129.96	120.95
1	D	144	MET	N-CA-C	6.41	119.57	111.69
1	F	79	GLU	CA-C-N	6.36	128.71	120.44
1	F	79	GLU	C-N-CA	6.36	128.71	120.44
1	B	58	THR	N-CA-C	6.35	120.63	113.01
1	E	75	GLU	CA-C-N	6.34	129.30	120.29
1	E	75	GLU	C-N-CA	6.34	129.30	120.29
1	C	179	GLN	CA-C-N	6.32	128.75	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	179	GLN	C-N-CA	6.32	128.75	120.28
1	F	39	MET	CA-C-N	6.31	128.64	120.44
1	F	39	MET	C-N-CA	6.31	128.64	120.44
1	B	48	THR	CA-C-N	6.29	126.49	119.32
1	B	48	THR	C-N-CA	6.29	126.49	119.32
1	B	175	GLU	N-CA-C	6.29	118.87	109.25
1	C	179	GLN	N-CA-C	6.25	119.07	111.82
1	F	148	THR	N-CA-C	-6.24	99.82	109.24
1	E	30	LYS	CA-C-N	6.22	128.91	120.38
1	E	30	LYS	C-N-CA	6.22	128.91	120.38
1	A	82	ARG	N-CA-C	6.21	118.13	111.36
1	F	179	GLN	N-CA-C	6.20	119.02	111.82
1	C	171	THR	N-CA-C	6.20	118.04	111.28
1	B	67	GLN	N-CA-C	6.20	117.70	111.07
1	F	33	SER	CA-C-N	6.19	126.65	119.47
1	F	33	SER	C-N-CA	6.19	126.65	119.47
1	C	26	VAL	N-CA-C	6.19	116.36	110.42
1	B	25	LYS	CA-C-N	6.18	128.35	120.56
1	B	25	LYS	C-N-CA	6.18	128.35	120.56
1	A	162	ARG	CA-C-N	6.16	131.10	120.58
1	A	162	ARG	C-N-CA	6.16	131.10	120.58
1	F	100	ARG	CA-C-N	6.15	126.81	119.98
1	F	100	ARG	C-N-CA	6.15	126.81	119.98
1	B	54	THR	CA-C-N	6.14	128.42	120.44
1	B	54	THR	C-N-CA	6.14	128.42	120.44
1	B	7	GLN	N-CA-C	-6.14	105.95	113.50
1	F	185	MET	N-CA-C	6.14	117.97	111.28
1	B	100	ARG	CA-C-N	6.12	126.89	120.03
1	B	100	ARG	C-N-CA	6.12	126.89	120.03
1	A	175	GLU	N-CA-C	-6.10	99.30	109.24
1	D	135	ILE	N-CA-C	6.09	116.83	110.62
1	C	215	MET	CA-C-N	6.07	128.41	120.28
1	C	215	MET	C-N-CA	6.07	128.41	120.28
1	A	207	PRO	CA-C-N	6.05	126.83	119.99
1	A	207	PRO	C-N-CA	6.05	126.83	119.99
1	F	85	PRO	N-CA-C	-6.05	102.33	111.41
1	D	192	GLN	N-CA-C	6.05	117.95	111.36
1	F	125	PRO	CA-C-N	6.04	128.74	120.46
1	F	125	PRO	C-N-CA	6.04	128.74	120.46
1	C	121	ASN	CA-C-N	6.04	126.60	120.38
1	C	121	ASN	C-N-CA	6.04	126.60	120.38
1	E	18	ARG	CA-C-N	6.03	128.36	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	18	ARG	C-N-CA	6.03	128.36	120.28
1	F	14	ALA	N-CA-C	6.02	118.99	110.50
1	D	143	ARG	N-CA-C	6.02	117.84	111.28
1	C	116	GLY	CA-C-N	6.01	128.26	120.44
1	C	116	GLY	C-N-CA	6.01	128.26	120.44
1	C	114	GLN	CA-C-N	6.00	128.33	120.60
1	C	114	GLN	C-N-CA	6.00	128.33	120.60
1	A	208	GLY	N-CA-C	5.99	119.89	112.64
1	E	16	SER	N-CA-C	5.99	116.94	109.57
1	A	57	ASN	N-CA-C	5.98	118.59	111.71
1	B	55	MET	CA-C-N	5.97	128.77	120.29
1	B	55	MET	C-N-CA	5.97	128.77	120.29
1	F	78	ALA	CA-C-N	5.95	128.25	120.28
1	F	78	ALA	C-N-CA	5.95	128.25	120.28
1	D	77	ALA	N-CA-C	5.93	117.75	111.28
1	E	80	TRP	N-CA-C	-5.93	104.73	111.07
1	A	15	ILE	N-CA-C	5.90	121.61	109.34
1	B	103	ASP	CA-C-N	5.88	127.97	120.56
1	B	103	ASP	C-N-CA	5.88	127.97	120.56
1	F	11	VAL	CA-C-N	-5.88	112.72	120.95
1	F	11	VAL	C-N-CA	-5.88	112.72	120.95
1	A	5	ASN	CA-C-N	5.87	129.23	120.31
1	A	5	ASN	C-N-CA	5.87	129.23	120.31
1	D	39	MET	CA-C-N	5.87	128.07	120.44
1	D	39	MET	C-N-CA	5.87	128.07	120.44
1	A	190	LEU	N-CA-C	-5.84	104.91	111.28
1	D	73	ILE	CA-C-N	5.84	128.11	120.28
1	D	73	ILE	C-N-CA	5.84	128.11	120.28
1	D	201	ILE	CA-C-N	5.84	129.19	120.31
1	D	201	ILE	C-N-CA	5.84	129.19	120.31
1	A	160	PRO	N-CA-C	5.84	120.07	110.55
1	F	214	MET	CA-C-N	5.84	128.58	120.29
1	F	214	MET	C-N-CA	5.84	128.58	120.29
1	E	189	LEU	N-CA-C	-5.83	104.88	112.23
1	E	71	GLU	N-CA-C	5.83	117.64	111.28
1	C	86	VAL	CA-C-N	5.78	132.57	121.54
1	C	86	VAL	C-N-CA	5.78	132.57	121.54
1	F	13	GLN	N-CA-C	5.76	118.87	109.59
1	C	8	GLY	N-CA-C	-5.76	107.05	115.63
1	A	117	TRP	N-CA-C	5.75	117.22	111.07
1	E	134	ILE	CA-C-N	5.75	128.34	120.46
1	E	134	ILE	C-N-CA	5.75	128.34	120.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	204	ALA	N-CA-C	5.75	118.01	111.11
1	A	129	ILE	CA-C-N	5.74	128.44	120.29
1	A	129	ILE	C-N-CA	5.74	128.44	120.29
1	B	201	ILE	N-CA-C	5.74	116.39	110.36
1	C	94	GLY	CA-C-N	5.73	131.60	121.80
1	C	94	GLY	C-N-CA	5.73	131.60	121.80
1	A	112	GLN	N-CA-C	-5.73	105.03	111.28
1	C	78	ALA	CA-C-N	5.72	128.41	120.29
1	C	78	ALA	C-N-CA	5.72	128.41	120.29
1	B	16	SER	CA-C-N	5.72	125.84	119.32
1	B	16	SER	C-N-CA	5.72	125.84	119.32
1	F	33	SER	N-CA-C	-5.71	102.44	110.31
1	C	106	GLY	CA-C-N	5.70	128.19	120.44
1	C	106	GLY	C-N-CA	5.70	128.19	120.44
1	B	3	VAL	N-CA-C	5.70	118.04	108.81
1	F	68	MET	N-CA-C	5.70	117.95	111.11
1	A	18	ARG	CA-C-N	5.68	127.82	120.44
1	A	18	ARG	C-N-CA	5.68	127.82	120.44
1	B	27	VAL	N-CA-C	5.67	116.45	110.72
1	B	96	MET	N-CA-C	5.67	118.28	110.35
1	F	126	VAL	N-CA-C	5.66	116.39	110.62
1	F	76	GLU	CA-C-N	5.65	127.85	120.28
1	F	76	GLU	C-N-CA	5.65	127.85	120.28
1	C	217	ALA	N-CA-C	5.65	118.37	111.82
1	B	117	TRP	N-CA-C	5.64	117.51	111.36
1	D	136	LEU	CA-C-N	5.64	126.20	120.00
1	D	136	LEU	C-N-CA	5.64	126.20	120.00
1	F	199	LYS	CA-C-N	5.63	127.76	120.44
1	F	199	LYS	C-N-CA	5.63	127.76	120.44
1	E	125	PRO	N-CA-C	-5.63	100.87	112.47
1	D	16	SER	N-CA-C	5.63	118.40	109.40
1	D	15	ILE	N-CA-C	5.62	121.02	109.34
1	D	115	ILE	CA-C-N	5.61	126.33	119.99
1	D	115	ILE	C-N-CA	5.61	126.33	119.99
1	E	88	ALA	N-CA-C	5.60	117.83	111.11
1	E	113	GLU	N-CA-C	5.58	117.36	111.28
1	D	214	MET	N-CA-C	5.56	117.34	111.28
1	F	72	THR	N-CA-C	5.54	117.32	111.28
1	C	218	CYS	CA-C-N	5.54	131.67	121.70
1	C	218	CYS	C-N-CA	5.54	131.67	121.70
1	A	168	PHE	CA-C-N	5.53	127.96	120.44
1	A	168	PHE	C-N-CA	5.53	127.96	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	46	GLY	CA-C-N	5.53	129.20	121.24
1	B	46	GLY	C-N-CA	5.53	129.20	121.24
1	F	12	HIS	CA-C-N	5.52	130.93	122.93
1	F	12	HIS	C-N-CA	5.52	130.93	122.93
1	D	70	LYS	CA-C-N	5.51	127.66	120.28
1	D	70	LYS	C-N-CA	5.51	127.66	120.28
1	F	26	VAL	N-CA-C	5.50	115.70	110.42
1	B	134	ILE	CA-C-N	5.49	127.98	120.46
1	B	134	ILE	C-N-CA	5.49	127.98	120.46
1	C	76	GLU	N-CA-C	5.48	118.18	111.82
1	A	135	ILE	CA-C-N	5.48	127.62	120.28
1	A	135	ILE	C-N-CA	5.48	127.62	120.28
1	F	125	PRO	N-CA-C	-5.46	101.22	112.47
1	A	172	LEU	CA-C-N	5.44	128.01	120.29
1	A	172	LEU	C-N-CA	5.44	128.01	120.29
1	F	43	LEU	N-CA-C	5.43	119.54	113.02
1	E	74	ASN	N-CA-C	5.43	117.19	111.28
1	C	34	PRO	N-CA-C	5.42	121.68	113.81
1	C	22	ALA	N-CA-C	5.42	117.19	111.28
1	C	72	THR	CA-C-N	5.42	128.17	120.53
1	C	72	THR	C-N-CA	5.42	128.17	120.53
1	B	15	ILE	N-CA-C	5.37	120.51	109.34
1	E	155	GLN	CA-C-N	5.36	129.84	121.64
1	E	155	GLN	C-N-CA	5.36	129.84	121.64
1	C	110	THR	N-CA-C	-5.36	103.31	110.55
1	B	121	ASN	CA-C-N	-5.36	114.86	120.38
1	B	121	ASN	C-N-CA	-5.36	114.86	120.38
1	E	124	ILE	CA-C-N	5.35	126.53	119.84
1	E	124	ILE	C-N-CA	5.35	126.53	119.84
1	E	209	ALA	CA-C-N	5.34	131.21	122.07
1	E	209	ALA	C-N-CA	5.34	131.21	122.07
1	B	211	LEU	N-CA-C	-5.33	105.51	112.23
1	E	63	GLN	N-CA-C	5.33	117.78	111.33
1	F	121	ASN	CA-C-N	5.32	125.86	120.38
1	F	121	ASN	C-N-CA	5.32	125.86	120.38
1	D	195	ASN	CA-C-N	5.32	125.38	119.32
1	D	195	ASN	C-N-CA	5.32	125.38	119.32
1	E	53	ASN	N-CA-C	5.30	117.06	111.28
1	C	90	PRO	CA-C-N	5.30	127.34	120.56
1	C	90	PRO	C-N-CA	5.30	127.34	120.56
1	F	183	ASN	CA-C-N	5.29	127.32	120.44
1	F	183	ASN	C-N-CA	5.29	127.32	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	73	ILE	CA-C-N	5.29	127.37	120.28
1	F	73	ILE	C-N-CA	5.29	127.37	120.28
1	B	146	SER	N-CA-C	5.29	116.38	108.76
1	A	25	LYS	CA-C-N	5.27	127.20	120.56
1	A	25	LYS	C-N-CA	5.27	127.20	120.56
1	C	90	PRO	N-CA-C	5.27	119.48	110.95
1	A	90	PRO	N-CA-C	-5.26	101.63	112.47
1	E	196	PRO	CA-C-N	5.25	127.27	120.44
1	E	196	PRO	C-N-CA	5.25	127.27	120.44
1	D	88	ALA	N-CA-C	5.25	117.07	110.24
1	A	137	GLY	CA-C-N	5.24	127.30	120.28
1	A	137	GLY	C-N-CA	5.24	127.30	120.28
1	A	198	CYS	N-CA-C	5.24	116.67	111.07
1	E	65	ALA	N-CA-C	5.23	117.06	111.36
1	A	104	ILE	N-CA-C	5.23	115.95	110.62
1	B	209	ALA	N-CA-C	5.23	117.80	109.96
1	A	39	MET	N-CA-C	5.22	117.05	111.36
1	A	87	HIS	CA-C-N	5.22	127.27	120.28
1	A	87	HIS	C-N-CA	5.22	127.27	120.28
1	A	138	LEU	CA-C-N	5.21	127.21	120.44
1	A	138	LEU	C-N-CA	5.21	127.21	120.44
1	C	206	GLY	CA-C-N	5.19	125.27	119.87
1	C	206	GLY	C-N-CA	5.19	125.27	119.87
1	D	139	ASN	CA-C-N	5.17	127.47	120.38
1	D	139	ASN	C-N-CA	5.17	127.47	120.38
1	D	204	ALA	CA-C-N	5.17	127.21	120.28
1	D	204	ALA	C-N-CA	5.17	127.21	120.28
1	A	167	ARG	CA-C-N	5.16	127.15	120.44
1	A	167	ARG	C-N-CA	5.16	127.15	120.44
1	E	59	VAL	N-CA-C	-5.16	107.44	112.29
1	C	142	VAL	N-CA-C	5.16	115.93	110.72
1	E	25	LYS	CA-C-N	5.16	127.06	120.56
1	E	25	LYS	C-N-CA	5.16	127.06	120.56
1	B	187	GLU	N-CA-C	5.15	117.64	111.71
1	B	50	GLN	N-CA-C	5.15	116.97	111.36
1	E	162	ARG	N-CA-C	5.15	118.34	111.75
1	F	62	HIS	CA-C-N	5.15	127.69	120.28
1	F	62	HIS	C-N-CA	5.15	127.69	120.28
1	C	147	PRO	CA-C-N	5.14	131.36	121.54
1	C	147	PRO	C-N-CA	5.14	131.36	121.54
1	E	95	GLN	CA-C-N	5.13	128.14	120.95
1	E	95	GLN	C-N-CA	5.13	128.14	120.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	181	VAL	CA-C-N	5.13	127.16	120.28
1	F	181	VAL	C-N-CA	5.13	127.16	120.28
1	D	74	ASN	CA-C-N	5.13	127.10	120.44
1	D	74	ASN	C-N-CA	5.13	127.10	120.44
1	F	188	THR	CA-C-N	5.12	130.10	121.14
1	F	188	THR	C-N-CA	5.12	130.10	121.14
1	B	146	SER	CA-C-N	5.12	126.24	119.84
1	B	146	SER	C-N-CA	5.12	126.24	119.84
1	A	198	CYS	CA-C-N	5.12	127.14	120.28
1	A	198	CYS	C-N-CA	5.12	127.14	120.28
1	E	178	SER	CA-C-N	5.12	128.09	120.31
1	E	178	SER	C-N-CA	5.12	128.09	120.31
1	A	160	PRO	CA-C-N	5.11	127.13	120.28
1	A	160	PRO	C-N-CA	5.11	127.13	120.28
1	D	193	ASN	N-CA-C	-5.10	106.47	113.30
1	A	214	MET	CA-C-N	5.10	127.53	120.29
1	A	214	MET	C-N-CA	5.10	127.53	120.29
1	C	67	GLN	N-CA-C	5.09	116.52	111.07
1	A	53	ASN	CA-C-N	5.09	127.10	120.28
1	A	53	ASN	C-N-CA	5.09	127.10	120.28
1	E	103	ASP	CA-C-N	5.09	127.43	120.46
1	E	103	ASP	C-N-CA	5.09	127.43	120.46
1	E	215	MET	CA-C-N	5.08	127.09	120.28
1	E	215	MET	C-N-CA	5.08	127.09	120.28
1	B	90	PRO	CA-C-N	5.07	127.61	120.42
1	B	90	PRO	C-N-CA	5.07	127.61	120.42
1	B	171	THR	CA-C-N	5.07	127.57	120.28
1	B	171	THR	C-N-CA	5.07	127.57	120.28
1	E	209	ALA	N-CA-C	5.05	117.96	110.48
1	F	113	GLU	CA-C-N	5.04	126.99	120.44
1	F	113	GLU	C-N-CA	5.04	126.99	120.44
1	A	200	THR	N-CA-C	-5.03	105.69	111.07
1	F	144	MET	CA-C-N	5.03	128.83	120.94
1	F	144	MET	C-N-CA	5.03	128.83	120.94
1	B	97	ARG	N-CA-C	5.03	117.16	110.53
1	F	205	LEU	CA-C-N	5.03	129.76	121.87
1	F	205	LEU	C-N-CA	5.03	129.76	121.87
1	D	101	GLY	N-CA-C	5.02	118.95	112.83
1	E	20	LEU	N-CA-C	5.01	116.43	111.07
1	D	16	SER	CA-C-N	5.01	125.03	119.32
1	D	16	SER	C-N-CA	5.01	125.03	119.32

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	124	ILE	Peptide
1	B	121	ASN	Peptide
1	B	3	VAL	Peptide
1	D	121	ASN	Peptide
1	E	121	ASN	Peptide
1	E	124	ILE	Peptide
1	F	124	ILE	Peptide
1	F	4	GLN	Peptide

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	657	0	230	0	0
1	B	657	0	230	0	0
1	C	657	0	230	0	0
1	D	657	0	230	0	0
1	E	657	0	230	0	0
1	F	657	0	230	0	0
All	All	3942	0	1380	0	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.

There are no clashes within the asymmetric unit.

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	217/219 (99%)	200 (92%)	8 (4%)	9 (4%)	2	18
1	B	217/219 (99%)	205 (94%)	7 (3%)	5 (2%)	5	28
1	C	217/219 (99%)	202 (93%)	8 (4%)	7 (3%)	3	21
1	D	217/219 (99%)	202 (93%)	6 (3%)	9 (4%)	2	18
1	E	217/219 (99%)	205 (94%)	4 (2%)	8 (4%)	2	20
1	F	217/219 (99%)	201 (93%)	8 (4%)	8 (4%)	2	20
All	All	1302/1314 (99%)	1215 (93%)	41 (3%)	46 (4%)	4	20

All (46) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	90	PRO
1	A	120	HIS
1	A	122	PRO
1	A	123	PRO
1	A	146	SER
1	C	97	ARG
1	C	122	PRO
1	C	123	PRO
1	C	146	SER
1	D	15	ILE
1	D	122	PRO
1	D	123	PRO
1	D	125	PRO
1	E	123	PRO
1	F	97	ARG
1	F	122	PRO
1	A	15	ILE
1	A	177	ALA
1	C	148	THR
1	D	96	MET
1	D	146	SER
1	E	97	ARG
1	E	122	PRO
1	E	178	SER
1	F	125	PRO
1	F	177	ALA
1	A	125	PRO
1	B	122	PRO
1	B	147	PRO
1	E	125	PRO

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Mol	Chain	Res	Type
1	E	149	SER
1	E	177	ALA
1	F	7	GLN
1	A	149	SER
1	B	148	THR
1	C	125	PRO
1	E	85	PRO
1	D	99	PRO
1	F	92	ALA
1	B	123	PRO
1	D	90	PRO
1	C	86	VAL
1	F	86	VAL
1	B	125	PRO
1	F	153	ILE
1	D	153	ILE

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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.

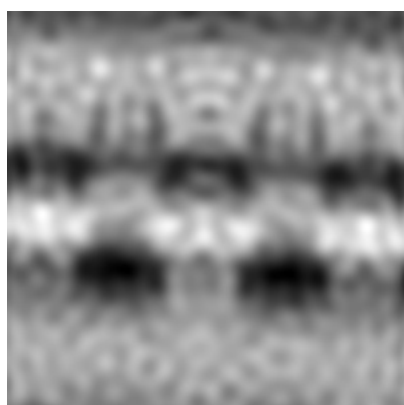
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2638. These allow visual inspection of the internal detail of the map and identification of artifacts.

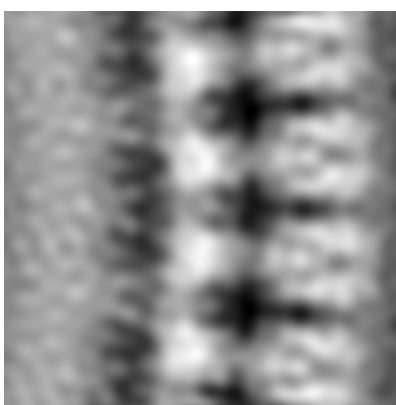
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

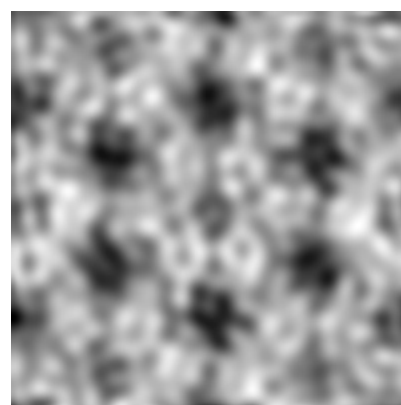
6.1.1 Primary map



X



Y



Z

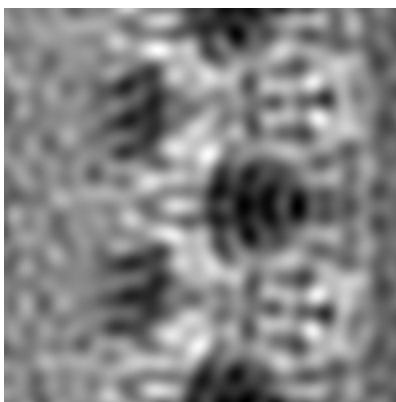
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

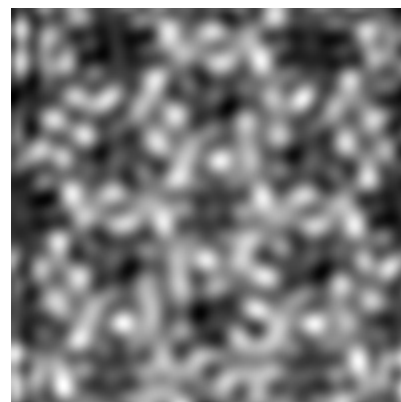
6.2.1 Primary map



X Index: 50



Y Index: 50

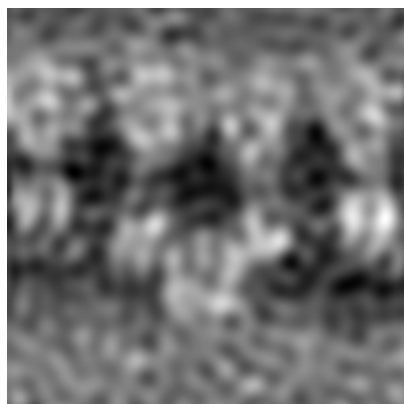


Z Index: 50

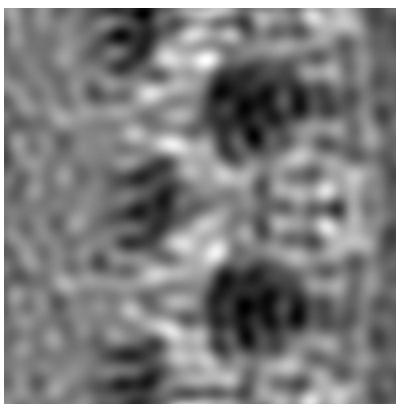
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

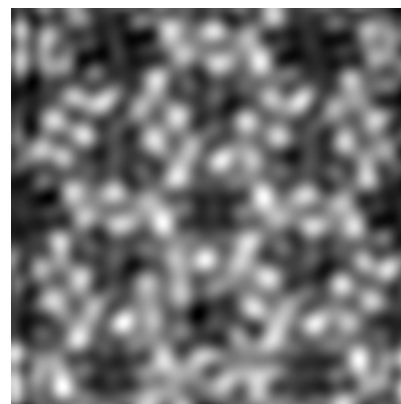
6.3.1 Primary map



X Index: 2



Y Index: 10

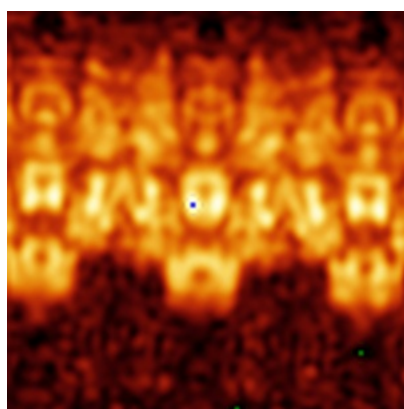


Z Index: 51

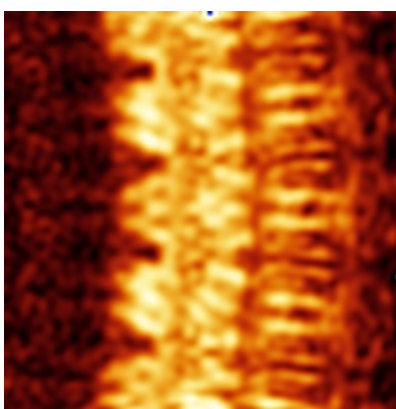
The images above show the largest variance slices of the map in three orthogonal directions.

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

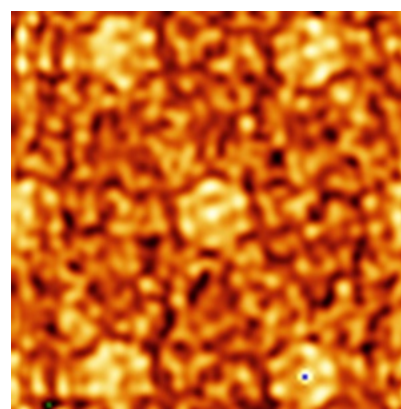
6.4.1 Primary map



X



Y

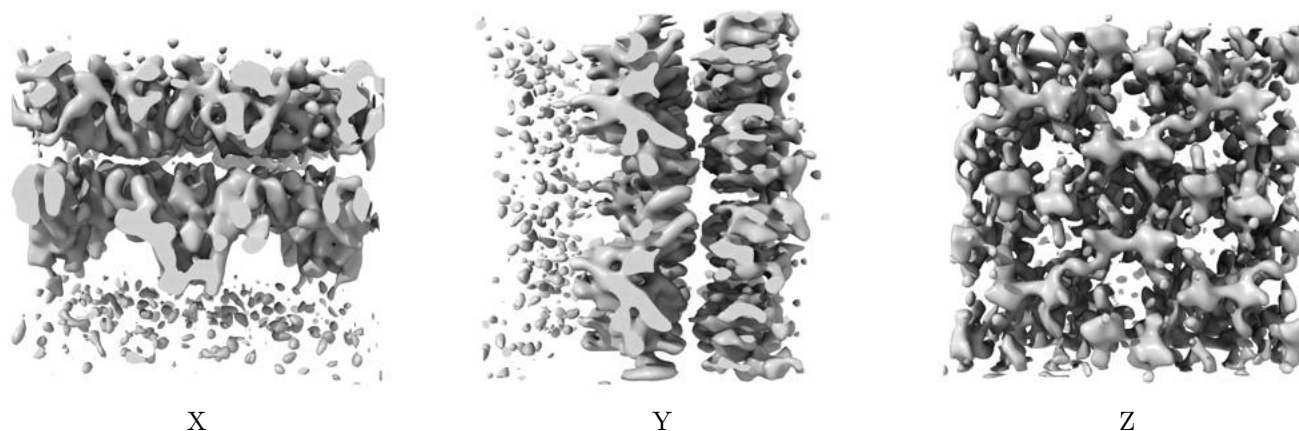


Z

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

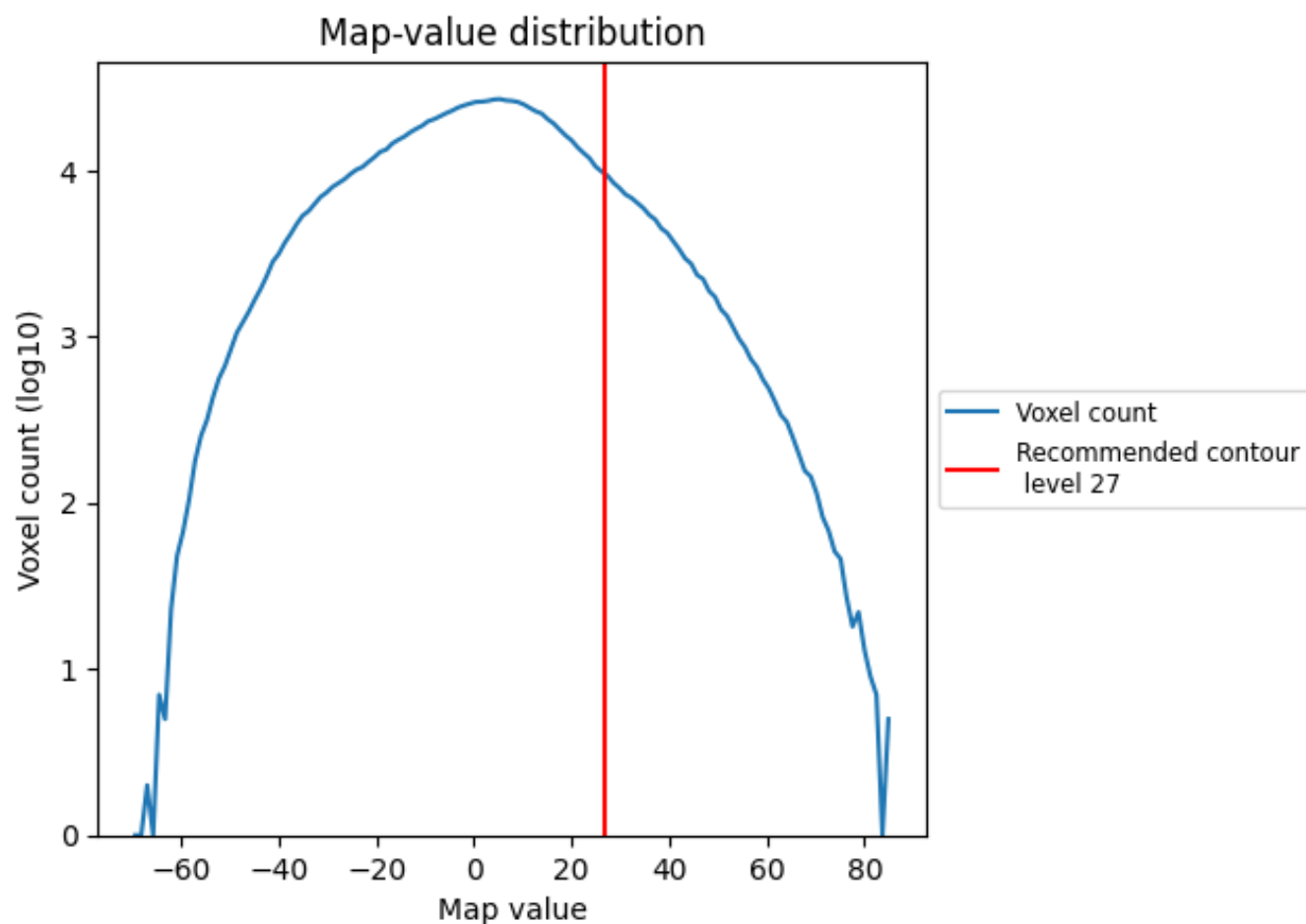
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

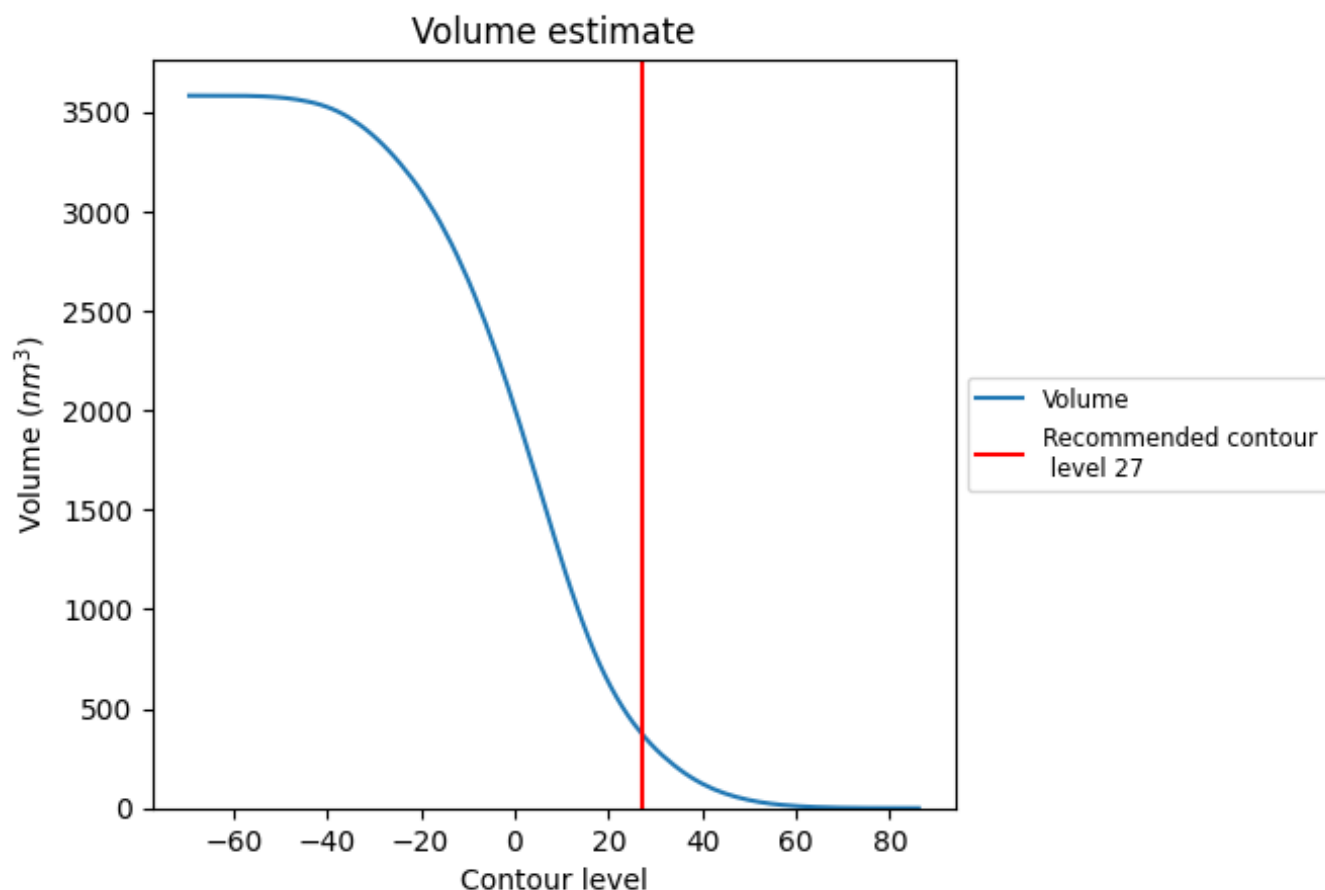
This section contains the results of statistical analysis of the map.

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.

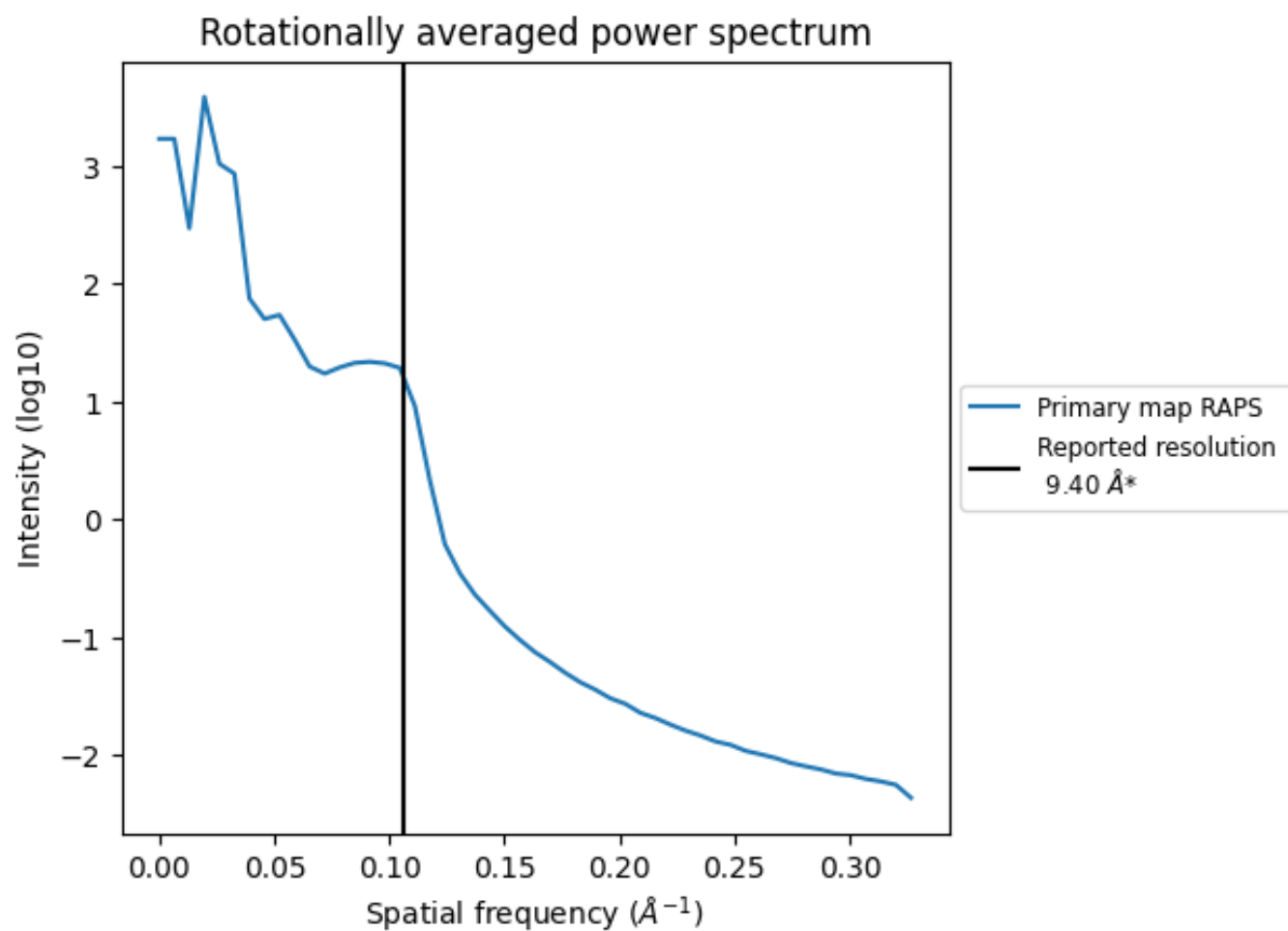
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 378 nm³; this corresponds to an approximate mass of 341 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 0.106 Å⁻¹

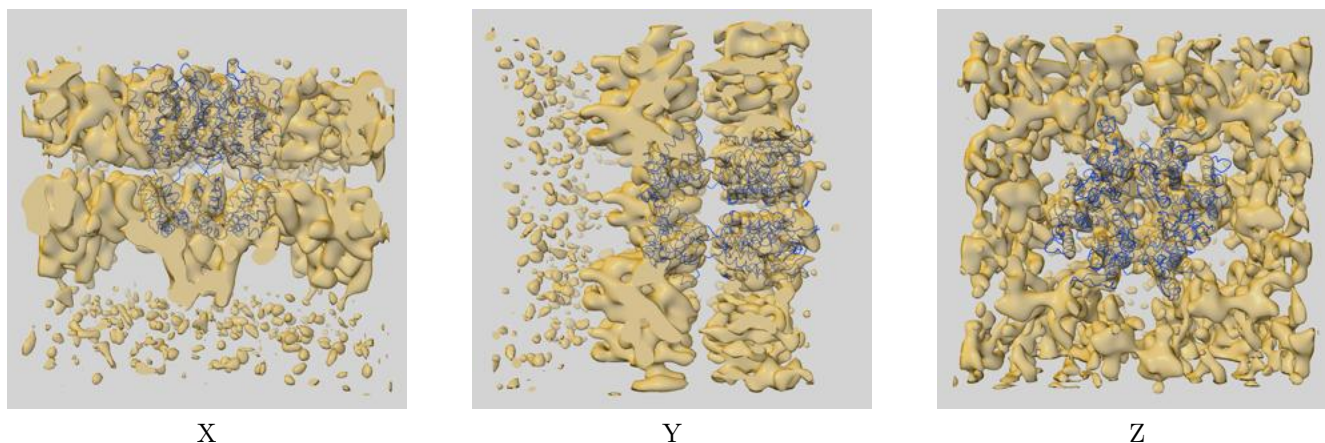
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

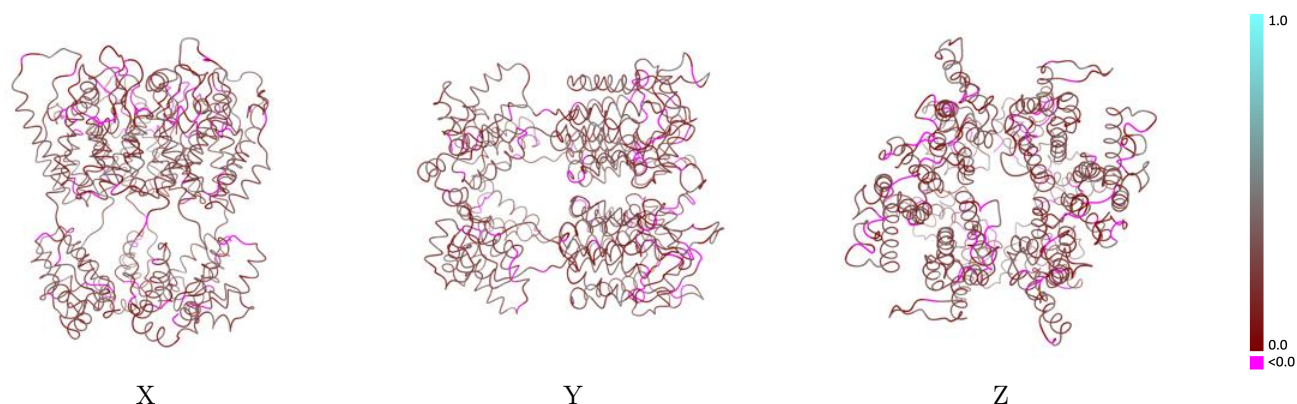
This section contains information regarding the fit between EMDB map EMD-2638 and PDB model 4D1K. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



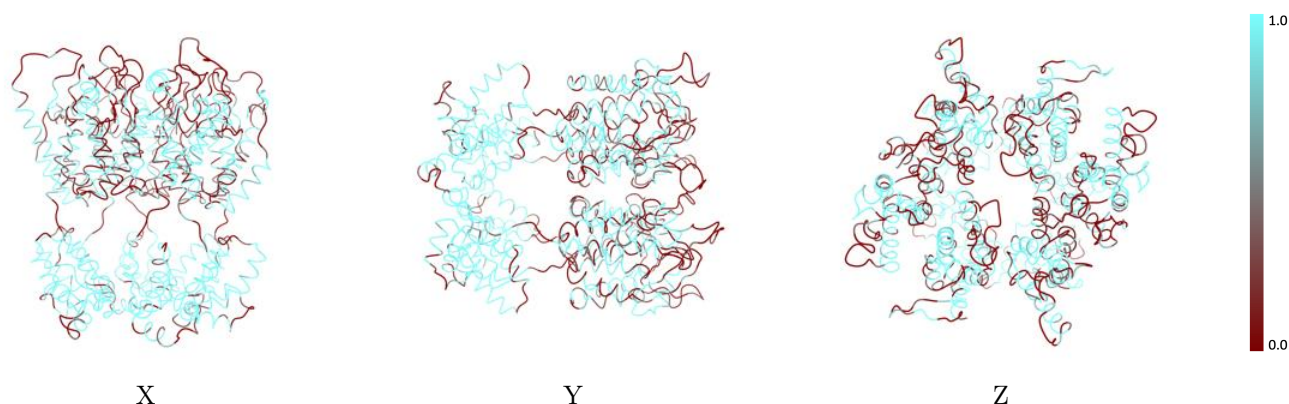
The images above show the 3D surface view of the map at the recommended contour level 27.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



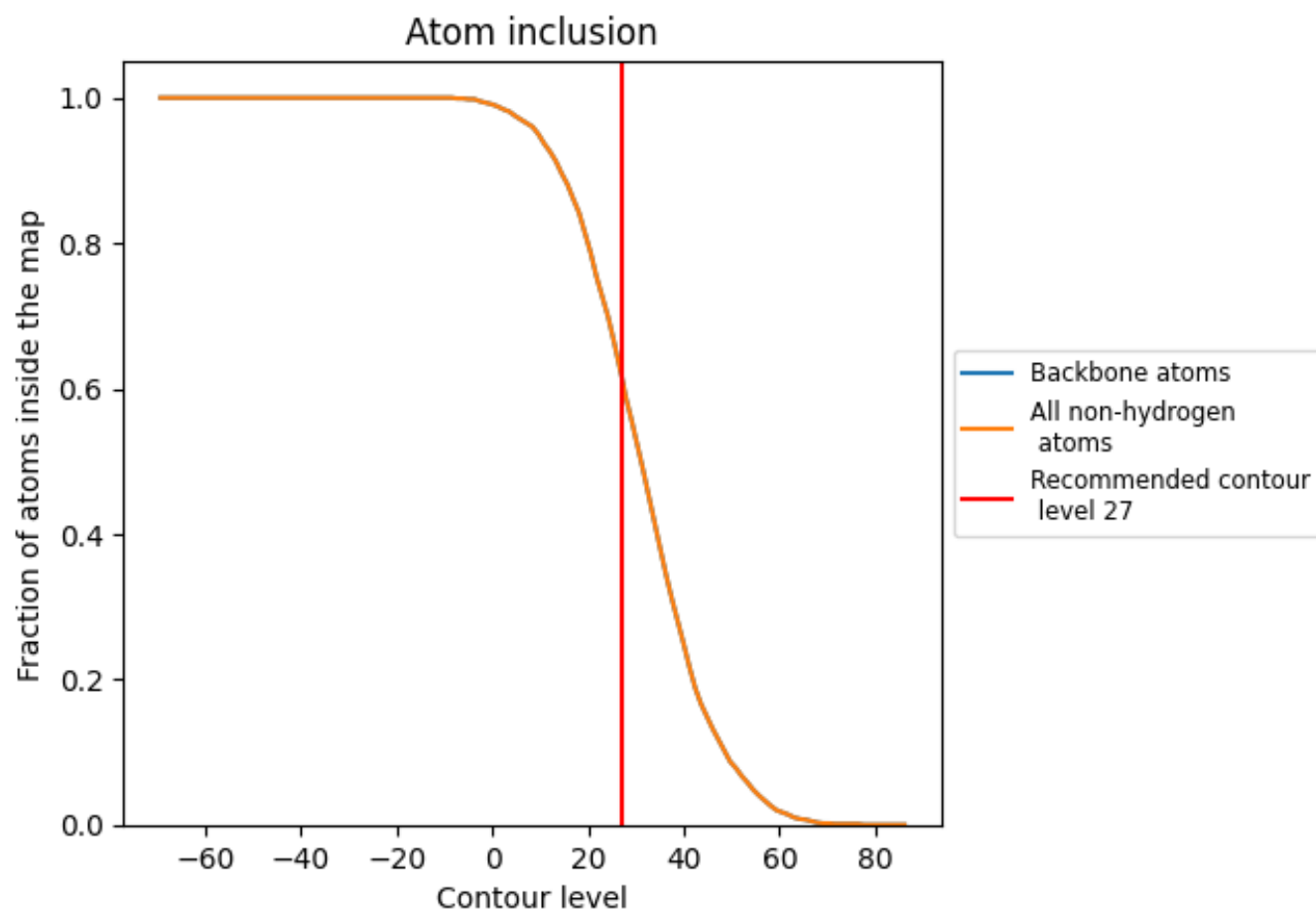
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (27).

9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 62% 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 (27) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6180	0.2120
A	0.6570	0.2200
B	0.6150	0.1990
C	0.5830	0.2160
D	0.6510	0.2160
E	0.6040	0.2080
F	0.5970	0.2130

1.0

0.0

<0.0