



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 05:03 PM UTC

PDB ID : 5VCA / pdb_00005vca
EMDB ID : EMD-8659
Title : VCP like ATPase from T. acidophilum (VAT)-Substrate bound conformation
Authors : Ripstein, Z.A.; Huang, R.; Augustyniak, R.; Kay, L.E.; Rubinstein, J.L.
Deposited on : 2017-03-31
Resolution : 4.80 Å(reported)
Based on initial model : 5VC7

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

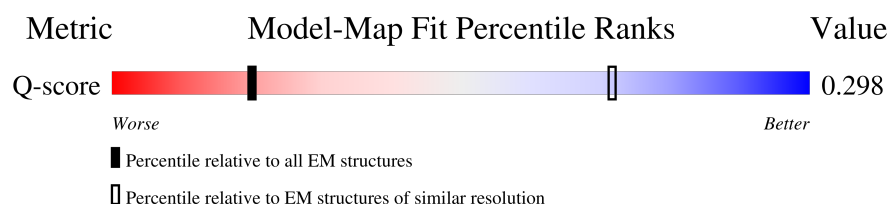
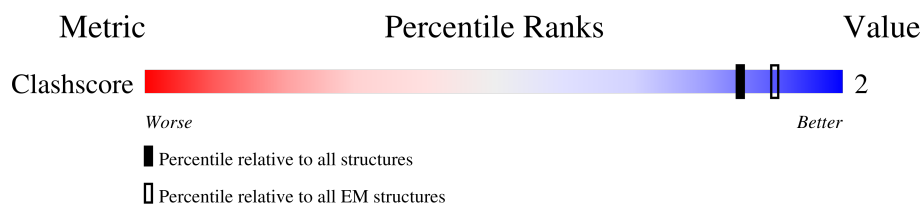
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

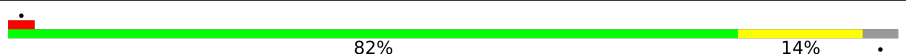
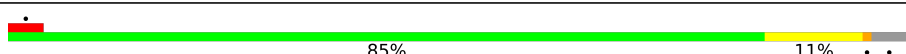
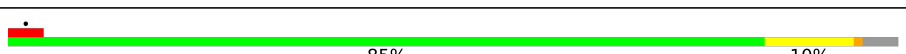
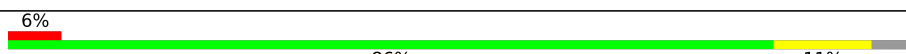
The reported resolution of this entry is 4.80 Å.

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	-
Q-score	-	25397	1575 (4.30 - 5.30)

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	M	564	 84% 12% .
1	N	564	 82% 14% .
1	O	564	 85% 11% . .
1	P	564	 7% 85% 10% . .
1	Q	564	 85% 10% . .
1	R	564	 6% 86% 11% .

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 16080 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 VCP-like ATPase.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	P	544	Total	C	N	O	0	0
			2680	1593	544	543		
1	M	544	Total	C	N	O	0	0
			2680	1593	544	543		
1	N	544	Total	C	N	O	0	0
			2680	1593	544	543		
1	O	544	Total	C	N	O	0	0
			2680	1593	544	543		
1	Q	544	Total	C	N	O	0	0
			2680	1593	544	543		
1	R	544	Total	C	N	O	0	0
			2680	1593	544	543		

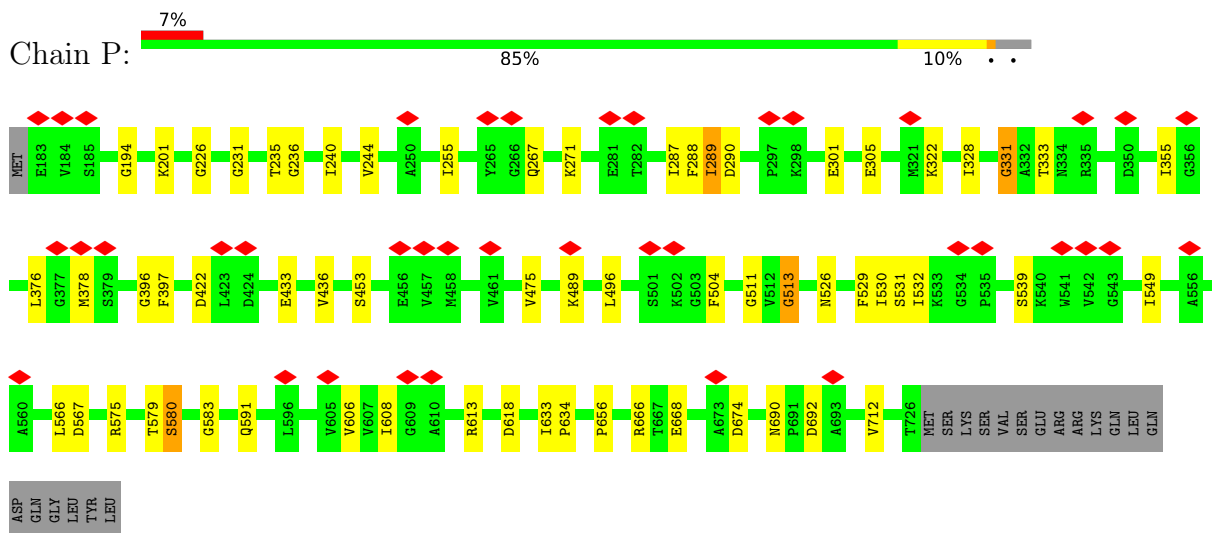
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	182	MET	-	expression tag	UNP O05209
M	182	MET	-	expression tag	UNP O05209
N	182	MET	-	expression tag	UNP O05209
O	182	MET	-	expression tag	UNP O05209
Q	182	MET	-	expression tag	UNP O05209
R	182	MET	-	expression tag	UNP O05209

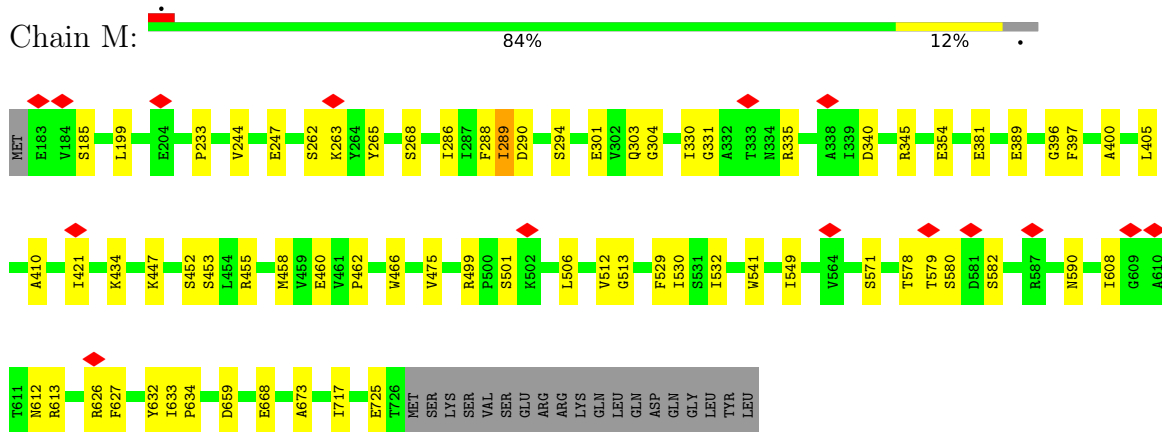
3 Residue-property plots

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.

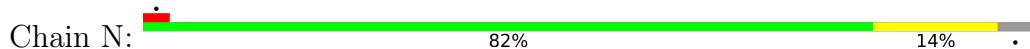
- Molecule 1: VCP-like ATPase

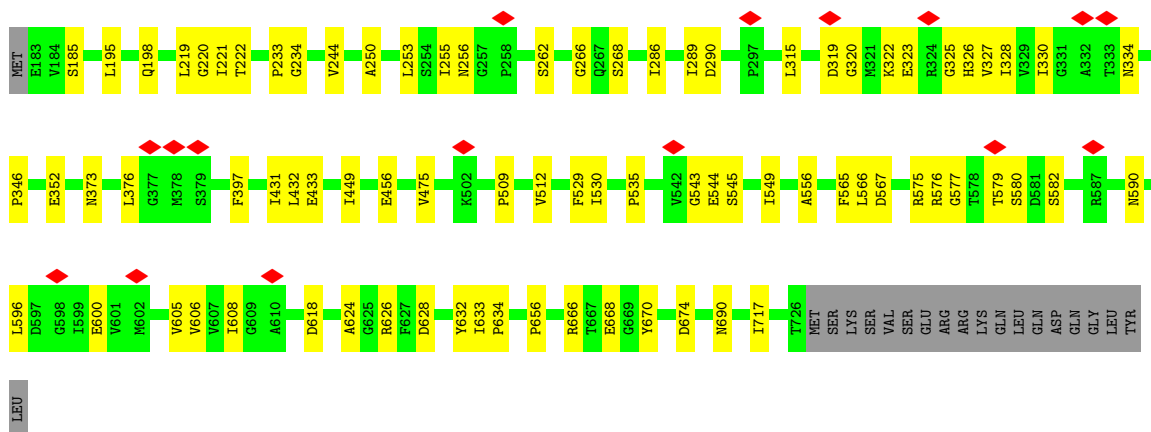


- Molecule 1: VCP-like ATPase

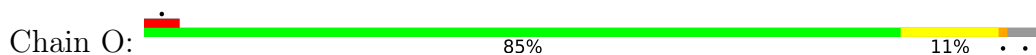


- Molecule 1: VCP-like ATPase

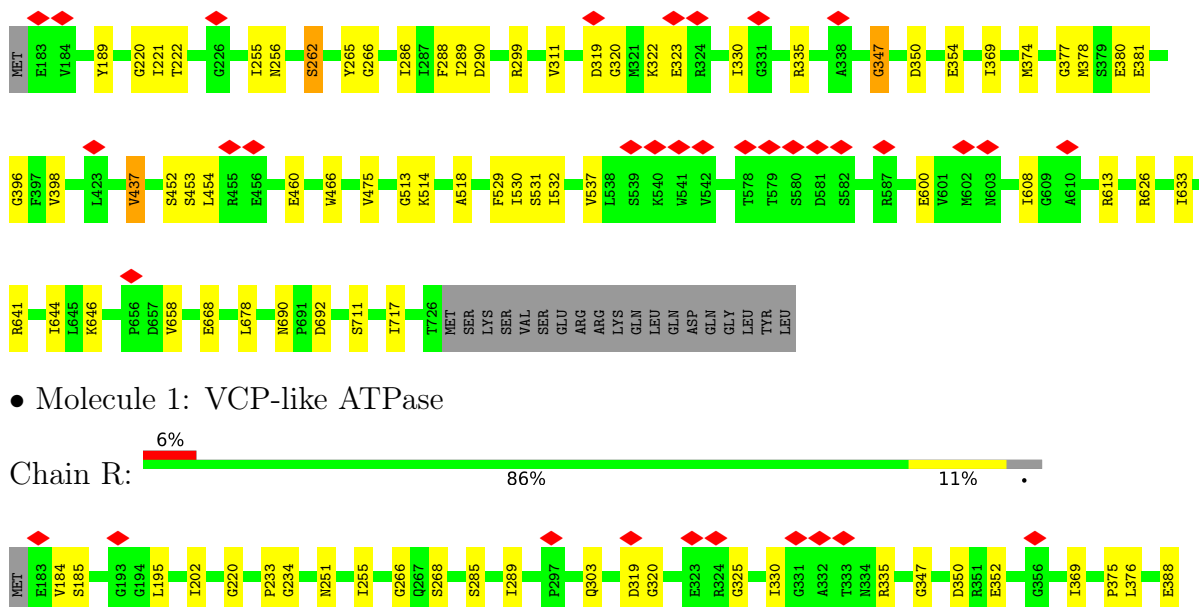
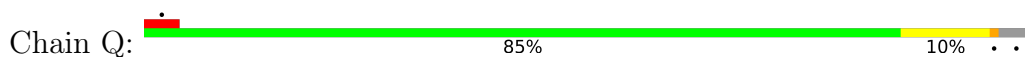


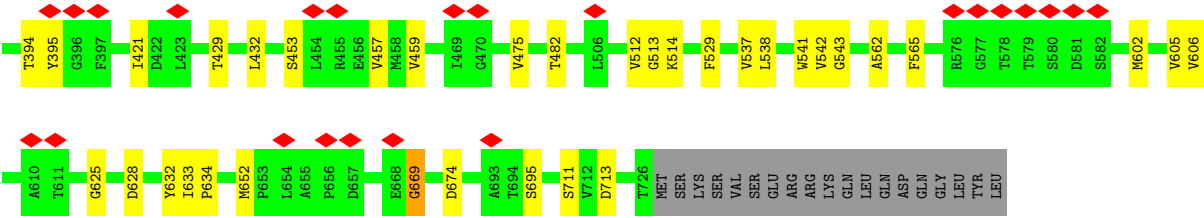


• Molecule 1: VCP-like ATPase



• Molecule 1: VCP-like ATPase





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	75205	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI 20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	1700	Depositor
Maximum defocus (nm)	2900	Depositor
Magnification	25000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.743	Depositor
Minimum map value	-0.411	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.137	Depositor
Map size (Å)	371.2, 371.2, 371.2	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.45, 1.45, 1.45	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	M	1.59	1/2679 (0.0%)	1.92	72/3726 (1.9%)
1	N	1.67	4/2679 (0.1%)	1.94	74/3726 (2.0%)
1	O	1.68	1/2679 (0.0%)	1.96	65/3726 (1.7%)
1	P	1.63	6/2679 (0.2%)	1.94	68/3726 (1.8%)
1	Q	1.65	2/2679 (0.1%)	1.92	73/3726 (2.0%)
1	R	1.65	1/2679 (0.0%)	1.92	67/3726 (1.8%)
All	All	1.65	15/16074 (0.1%)	1.93	419/22356 (1.9%)

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Q	531	SER	CA-C	-5.90	1.45	1.52
1	P	331	GLY	CA-C	-5.73	1.45	1.51
1	O	612	ASN	CA-C	-5.62	1.47	1.53
1	P	289	ILE	CA-C	-5.62	1.45	1.52
1	N	256	ASN	CA-C	-5.56	1.45	1.52
1	P	433	GLU	N-CA	-5.49	1.42	1.47
1	Q	530	ILE	CA-C	-5.39	1.46	1.52
1	N	690	ASN	CA-C	-5.39	1.48	1.52
1	R	289	ILE	CA-C	-5.23	1.46	1.52
1	N	219	LEU	CA-C	-5.21	1.46	1.52
1	N	253	LEU	CA-C	-5.17	1.47	1.53
1	P	240	ILE	CA-C	-5.12	1.46	1.52
1	P	532	ILE	CA-C	-5.11	1.46	1.52
1	P	633	ILE	CA-C	-5.07	1.49	1.52
1	M	447	LYS	CA-C	-5.06	1.47	1.53

All (419) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	O	319	ASP	N-CA-C	11.93	124.28	111.28
1	R	319	ASP	N-CA-C	10.05	122.23	111.28
1	P	376	LEU	N-CA-C	-9.56	102.70	114.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	R	633	ILE	N-CA-C	-9.32	98.92	108.15
1	P	513	GLY	N-CA-C	-9.22	99.96	115.08
1	O	289	ILE	N-CA-C	-8.96	96.53	108.35
1	Q	530	ILE	N-CA-C	-8.87	95.24	108.46
1	O	326	HIS	N-CA-C	-8.85	102.56	112.57
1	P	289	ILE	N-CA-C	-8.83	95.38	108.45
1	Q	322	LYS	N-CA-C	-8.70	95.59	109.59
1	O	628	ASP	N-CA-C	-8.62	103.61	114.56
1	R	394	THR	N-CA-C	-8.55	96.04	109.72
1	Q	255	ILE	N-CA-C	-8.52	96.24	108.42
1	N	530	ILE	N-CA-C	-8.36	96.01	108.46
1	N	255	ILE	N-CA-C	-8.35	95.49	108.44
1	Q	532	ILE	N-CA-C	-8.31	95.47	107.77
1	M	725	GLU	N-CA-C	-8.27	95.05	108.52
1	N	432	LEU	N-CA-C	-8.24	105.22	114.62
1	O	236	GLY	N-CA-C	-8.19	100.84	114.76
1	R	457	VAL	N-CA-C	-8.04	92.61	109.34
1	N	326	HIS	N-CA-C	-7.96	103.47	113.02
1	N	319	ASP	N-CA-C	7.92	119.91	111.28
1	N	475	VAL	N-CA-CB	7.92	119.82	110.55
1	P	475	VAL	N-CA-CB	7.90	119.80	110.55
1	R	606	VAL	N-CA-C	-7.83	96.86	108.45
1	P	255	ILE	N-CA-C	-7.81	97.25	108.42
1	M	512	VAL	N-CA-C	-7.81	103.62	113.22
1	N	289	ILE	N-CA-C	-7.80	96.91	108.45
1	P	288	PHE	N-CA-C	-7.74	95.65	108.34
1	O	475	VAL	N-CA-CB	7.68	119.54	110.55
1	N	600	GLU	N-CA-C	-7.65	97.66	109.52
1	P	532	ILE	N-CA-C	-7.64	96.46	107.77
1	Q	299	ARG	N-CA-C	-7.62	104.12	113.50
1	O	606	VAL	N-CA-C	-7.59	97.22	108.45
1	P	530	ILE	N-CA-C	-7.58	97.17	108.46
1	N	628	ASP	N-CA-C	-7.54	103.93	113.43
1	R	453	SER	N-CA-C	-7.51	105.28	114.75
1	O	576	ARG	N-CA-C	-7.47	103.76	113.17
1	Q	633	ILE	N-CA-C	-7.42	99.66	107.60
1	N	529	PHE	N-CA-C	-7.40	98.19	109.95
1	M	717	ILE	N-CA-CB	7.39	120.59	110.54
1	P	301	GLU	N-CA-C	-7.37	104.29	113.28
1	N	449	ILE	N-CA-C	-7.35	96.82	108.95
1	O	244	VAL	N-CA-C	-7.35	98.34	106.21
1	R	195	LEU	N-CA-C	-7.35	104.20	113.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	R	330	ILE	N-CA-C	-7.28	97.83	108.89
1	Q	514	LYS	CA-C-N	7.27	130.99	120.38
1	Q	514	LYS	C-N-CA	7.27	130.99	120.38
1	R	320	GLY	CA-C-N	7.21	135.32	121.54
1	R	320	GLY	C-N-CA	7.21	135.32	121.54
1	R	475	VAL	N-CA-CB	7.18	118.95	110.55
1	M	447	LYS	N-CA-C	-7.17	98.18	108.07
1	P	236	GLY	N-CA-C	-7.16	96.22	113.18
1	N	244	VAL	N-CA-C	-7.12	102.31	112.35
1	O	320	GLY	CA-C-N	7.12	135.15	121.54
1	O	320	GLY	C-N-CA	7.12	135.15	121.54
1	M	453	SER	N-CA-C	-7.12	103.15	112.41
1	M	612	ASN	N-CA-C	-7.12	104.22	113.12
1	M	475	VAL	N-CA-CB	7.08	118.83	110.55
1	Q	626	ARG	N-CA-C	-7.06	103.67	111.36
1	R	185	SER	N-CA-C	-7.03	98.49	109.25
1	P	433	GLU	N-CA-C	-7.03	103.37	113.21
1	P	397	PHE	N-CA-C	-7.02	97.97	108.99
1	M	396	GLY	N-CA-C	-6.97	96.65	113.18
1	M	421	ILE	N-CA-C	6.97	117.73	110.62
1	O	600	GLU	N-CA-C	-6.96	98.60	109.25
1	Q	289	ILE	N-CA-C	-6.96	98.47	108.42
1	M	513	GLY	N-CA-C	-6.94	96.72	113.18
1	P	436	VAL	N-CA-C	-6.94	94.90	109.34
1	N	456	GLU	N-CA-C	-6.91	104.32	112.89
1	Q	475	VAL	N-CA-CB	6.90	118.62	110.55
1	P	529	PHE	N-CA-C	-6.87	99.03	109.95
1	M	532	ILE	N-CA-C	-6.87	97.60	107.77
1	O	717	ILE	N-CA-CB	6.83	119.83	110.54
1	M	294	SER	N-CA-C	-6.82	103.64	112.23
1	Q	466	TRP	CB-CA-C	-6.80	99.49	110.79
1	R	432	LEU	N-CA-C	-6.80	103.57	112.41
1	P	322	LYS	N-CA-C	-6.74	97.92	108.90
1	O	453	SER	N-CA-C	-6.72	103.95	111.28
1	Q	335	ARG	CA-C-N	6.72	129.26	120.60
1	Q	335	ARG	C-N-CA	6.72	129.26	120.60
1	O	512	VAL	N-CA-C	-6.69	106.21	112.83
1	Q	452	SER	N-CA-C	-6.69	97.31	108.75
1	R	255	ILE	N-CA-C	-6.67	98.88	108.42
1	P	567	ASP	N-CA-C	-6.67	98.86	109.59
1	N	352	GLU	N-CA-C	-6.66	97.74	109.06
1	N	397	PHE	N-CA-C	-6.65	99.40	108.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Q	513	GLY	CA-C-N	6.65	129.51	120.54
1	Q	513	GLY	C-N-CA	6.65	129.51	120.54
1	R	347	GLY	CA-C-N	6.63	134.20	121.54
1	R	347	GLY	C-N-CA	6.63	134.20	121.54
1	Q	717	ILE	N-CA-CB	6.62	119.55	110.54
1	R	234	GLY	CA-C-N	6.61	129.13	120.28
1	R	234	GLY	C-N-CA	6.61	129.13	120.28
1	N	512	VAL	N-CA-C	-6.60	105.21	112.80
1	O	449	ILE	N-CA-C	-6.59	98.88	108.71
1	N	717	ILE	N-CA-CB	6.59	119.50	110.54
1	O	322	LYS	N-CA-C	-6.59	98.16	108.90
1	M	455	ARG	CA-C-N	6.58	134.12	121.54
1	M	455	ARG	C-N-CA	6.58	134.12	121.54
1	M	530	ILE	N-CA-C	-6.56	98.69	108.46
1	N	256	ASN	N-CA-C	-6.55	99.08	109.23
1	M	247	GLU	N-CA-C	-6.54	105.05	113.16
1	M	541	TRP	N-CA-C	-6.50	102.74	110.41
1	O	255	ILE	N-CA-C	-6.50	98.37	108.44
1	Q	460	GLU	N-CA-C	-6.50	99.61	108.38
1	N	220	GLY	CA-C-N	6.49	133.66	121.97
1	N	220	GLY	C-N-CA	6.49	133.66	121.97
1	Q	600	GLU	N-CA-C	-6.46	97.89	108.41
1	P	531	SER	N-CA-C	-6.44	97.77	108.34
1	N	634	PRO	N-CA-C	-6.39	102.90	110.70
1	O	530	ILE	N-CA-C	-6.38	98.96	108.46
1	N	323	GLU	CA-C-N	6.36	128.80	120.28
1	N	323	GLU	C-N-CA	6.36	128.80	120.28
1	M	529	PHE	N-CA-C	-6.36	99.84	109.95
1	O	381	GLU	CA-C-N	6.33	128.66	120.44
1	O	381	GLU	C-N-CA	6.33	128.66	120.44
1	N	606	VAL	N-CA-C	-6.33	99.09	108.45
1	R	350	ASP	N-CA-CB	6.33	119.52	110.16
1	M	354	GLU	N-CA-C	-6.32	99.41	109.59
1	Q	690	ASN	CA-C-N	6.32	125.82	119.24
1	Q	690	ASN	C-N-CA	6.32	125.82	119.24
1	M	263	LYS	N-CA-C	6.32	119.39	110.23
1	O	347	GLY	N-CA-C	-6.29	98.26	113.18
1	O	633	ILE	N-CA-C	-6.28	100.88	107.60
1	R	289	ILE	N-CA-C	-6.28	98.64	108.81
1	P	583	GLY	CA-C-N	6.27	128.69	120.60
1	P	583	GLY	C-N-CA	6.27	128.69	120.60
1	M	668	GLU	N-CA-C	-6.27	105.21	112.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	433	GLU	N-CA-C	-6.26	102.91	112.99
1	O	369	ILE	N-CA-CB	6.24	117.85	110.55
1	P	271	LYS	CB-CA-C	-6.23	101.37	110.96
1	O	220	GLY	CA-C-N	6.23	133.18	121.97
1	O	220	GLY	C-N-CA	6.23	133.18	121.97
1	R	634	PRO	N-CA-C	-6.21	103.12	110.70
1	N	322	LYS	N-CA-C	-6.21	99.27	109.40
1	M	633	ILE	N-CA-C	-6.20	100.97	107.60
1	P	692	ASP	N-CA-C	-6.19	99.63	109.59
1	Q	222	THR	N-CA-C	-6.19	100.98	110.32
1	N	222	THR	N-CA-C	-6.18	101.86	109.65
1	Q	668	GLU	N-CA-C	-6.18	105.39	113.17
1	N	608	ILE	N-CA-C	-6.17	97.47	107.28
1	N	632	TYR	N-CA-C	-6.17	100.45	110.20
1	N	195	LEU	N-CA-C	-6.16	105.63	113.02
1	R	669	GLY	CA-C-N	6.15	131.16	121.56
1	R	669	GLY	C-N-CA	6.15	131.16	121.56
1	R	541	TRP	N-CA-C	-6.15	101.27	110.06
1	N	250	ALA	N-CA-C	-6.13	99.21	108.96
1	R	537	VAL	N-CA-C	6.13	116.87	110.62
1	Q	380	GLU	N-CA-C	-6.12	99.67	108.60
1	M	549	ILE	N-CA-CB	6.10	117.68	110.55
1	P	244	VAL	N-CA-C	-6.09	103.76	112.35
1	N	549	ILE	N-CA-CB	6.08	117.67	110.55
1	Q	437	VAL	N-CA-C	-6.08	99.73	108.48
1	O	288	PHE	N-CA-C	-6.07	98.39	108.34
1	N	656	PRO	N-CA-C	-6.06	106.09	114.27
1	P	267	GLN	N-CA-C	-6.06	105.93	113.38
1	M	263	LYS	CA-C-N	6.04	133.08	121.54
1	M	263	LYS	C-N-CA	6.04	133.08	121.54
1	R	352	GLU	N-CA-C	-6.04	98.42	108.75
1	O	397	PHE	N-CA-C	-6.03	100.62	109.18
1	P	194	GLY	N-CA-C	-6.02	107.10	114.92
1	N	576	ARG	N-CA-C	-6.01	105.71	113.16
1	R	303	GLN	N-CA-C	-5.98	103.31	111.56
1	P	422	ASP	CA-C-N	5.98	128.29	120.28
1	P	422	ASP	C-N-CA	5.98	128.29	120.28
1	M	288	PHE	N-CA-C	-5.96	98.57	108.34
1	P	668	GLU	N-CA-C	-5.96	105.60	112.92
1	O	268	SER	N-CA-C	-5.95	104.37	111.69
1	P	328	ILE	N-CA-C	-5.94	100.13	108.80
1	M	634	PRO	N-CA-C	-5.93	103.46	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	596	LEU	N-CA-C	-5.90	104.93	111.36
1	R	268	SER	N-CA-C	-5.89	104.44	111.69
1	M	405	LEU	N-CA-CB	5.88	118.54	110.01
1	Q	262	SER	N-CA-C	5.87	117.76	111.36
1	O	395	TYR	N-CA-C	-5.87	106.08	113.18
1	O	383	LYS	N-CA-CB	5.86	118.51	110.01
1	N	315	LEU	N-CA-CB	5.86	118.85	110.06
1	O	632	TYR	N-CA-C	-5.82	101.00	110.20
1	N	544	GLU	N-CA-C	-5.81	104.13	111.92
1	R	513	GLY	N-CA-C	-5.81	99.42	113.18
1	P	201	LYS	CA-C-N	5.80	128.09	120.60
1	P	201	LYS	C-N-CA	5.80	128.09	120.60
1	N	376	LEU	N-CA-C	-5.79	106.26	113.38
1	M	582	SER	N-CA-C	-5.78	98.49	110.80
1	P	355	ILE	N-CA-C	-5.77	99.75	108.17
1	N	268	SER	N-CA-C	-5.76	104.60	111.69
1	M	265	TYR	N-CA-C	5.75	119.16	110.64
1	Q	330	ILE	N-CA-C	-5.74	100.17	108.89
1	M	290	ASP	N-CA-C	-5.74	100.59	109.14
1	Q	323	GLU	CA-C-N	5.74	127.97	120.28
1	Q	323	GLU	C-N-CA	5.74	127.97	120.28
1	R	202	ILE	CA-C-N	5.72	128.74	120.79
1	R	202	ILE	C-N-CA	5.72	128.74	120.79
1	R	429	THR	N-CA-C	-5.70	106.37	113.38
1	N	320	GLY	CA-C-N	5.70	132.43	121.54
1	N	320	GLY	C-N-CA	5.70	132.43	121.54
1	Q	220	GLY	CA-C-N	5.70	132.23	121.97
1	Q	220	GLY	C-N-CA	5.70	132.23	121.97
1	R	632	TYR	N-CA-C	-5.70	101.19	110.20
1	N	290	ASP	N-CA-C	-5.69	100.70	109.52
1	P	633	ILE	N-CA-C	-5.68	100.85	107.61
1	R	514	LYS	CA-C-N	5.68	128.67	120.38
1	R	514	LYS	C-N-CA	5.68	128.67	120.38
1	N	577	GLY	N-CA-C	-5.68	107.89	115.32
1	N	579	THR	N-CA-C	-5.67	104.11	111.71
1	Q	644	ILE	N-CA-C	5.67	116.41	110.62
1	O	596	LEU	N-CA-C	-5.67	105.18	111.36
1	Q	330	ILE	CA-C-N	5.67	126.85	121.46
1	Q	330	ILE	C-N-CA	5.67	126.85	121.46
1	P	666	ARG	N-CA-C	-5.67	104.72	111.69
1	M	335	ARG	CA-C-N	5.67	127.70	120.56
1	M	335	ARG	C-N-CA	5.67	127.70	120.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Q	290	ASP	N-CA-C	-5.67	100.68	109.24
1	Q	678	LEU	N-CA-CB	5.66	118.17	109.91
1	R	625	GLY	N-CA-C	-5.65	107.57	114.92
1	P	333	THR	N-CA-C	-5.64	100.16	108.79
1	P	566	LEU	N-CA-C	-5.64	99.09	108.34
1	M	303	GLN	N-CA-C	-5.64	100.72	109.24
1	O	645	LEU	N-CA-C	-5.64	105.21	111.36
1	P	613	ARG	CA-C-N	5.64	125.31	119.05
1	P	613	ARG	C-N-CA	5.64	125.31	119.05
1	Q	531	SER	N-CA-C	-5.63	99.10	108.34
1	N	198	GLN	CA-C-N	5.63	127.83	120.28
1	N	198	GLN	C-N-CA	5.63	127.83	120.28
1	Q	658	VAL	N-CA-C	-5.63	100.37	108.48
1	N	219	LEU	N-CA-C	-5.62	98.47	108.13
1	M	608	ILE	N-CA-C	-5.62	98.35	107.28
1	N	674	ASP	N-CA-CB	5.61	118.21	110.07
1	M	286	ILE	CA-C-N	5.61	129.65	121.80
1	M	286	ILE	C-N-CA	5.61	129.65	121.80
1	R	233	PRO	CA-C-N	5.61	131.86	122.16
1	R	233	PRO	C-N-CA	5.61	131.86	122.16
1	P	606	VAL	N-CA-C	-5.60	100.17	108.45
1	R	184	VAL	N-CA-C	-5.59	97.70	109.34
1	R	695	SER	N-CA-C	-5.59	96.44	107.69
1	O	567	ASP	N-CA-C	-5.59	100.59	109.59
1	P	549	ILE	N-CA-CB	5.57	117.07	110.55
1	R	602	MET	N-CA-C	-5.57	106.70	112.93
1	O	725	GLU	N-CA-C	-5.55	105.31	111.36
1	Q	692	ASP	N-CA-C	-5.54	100.85	109.72
1	R	512	VAL	N-CA-C	-5.54	106.43	112.80
1	M	289	ILE	N-CA-C	-5.54	100.50	108.42
1	M	475	VAL	N-CA-C	-5.53	105.11	110.42
1	O	355	ILE	N-CA-C	-5.52	100.39	108.11
1	O	577	GLY	N-CA-C	-5.52	106.96	115.73
1	Q	641	ARG	N-CA-CB	5.52	118.33	110.06
1	P	608	ILE	N-CA-C	-5.51	98.51	107.28
1	M	244	VAL	N-CA-C	-5.51	97.88	109.34
1	R	538	LEU	N-CA-C	5.51	119.26	112.54
1	O	318	MET	CA-C-N	5.50	127.66	120.28
1	O	318	MET	C-N-CA	5.50	127.66	120.28
1	R	513	GLY	CA-C-N	5.50	127.96	120.54
1	R	513	GLY	C-N-CA	5.50	127.96	120.54
1	N	605	VAL	N-CA-C	-5.50	101.74	109.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Q	286	ILE	CA-C-N	5.50	129.49	121.80
1	Q	286	ILE	C-N-CA	5.50	129.49	121.80
1	O	335	ARG	CA-C-N	5.49	127.48	120.56
1	O	335	ARG	C-N-CA	5.49	127.48	120.56
1	Q	354	GLU	N-CA-C	-5.49	100.75	109.59
1	M	462	PRO	N-CA-C	-5.49	101.16	112.47
1	O	532	ILE	N-CA-C	-5.49	99.65	107.77
1	Q	378	MET	N-CA-CB	5.48	119.75	110.49
1	O	641	ARG	N-CA-CB	5.47	118.17	110.12
1	O	454	LEU	CA-C-N	5.47	131.99	121.54
1	O	454	LEU	C-N-CA	5.47	131.99	121.54
1	O	198	GLN	CA-C-N	5.47	127.61	120.28
1	O	198	GLN	C-N-CA	5.47	127.61	120.28
1	R	330	ILE	CA-C-N	5.47	126.66	121.46
1	R	330	ILE	C-N-CA	5.47	126.66	121.46
1	R	713	ASP	N-CA-C	-5.47	100.39	109.46
1	P	290	ASP	N-CA-C	-5.46	101.00	109.14
1	M	185	SER	N-CA-C	-5.46	100.40	109.46
1	N	566	LEU	N-CA-C	-5.46	99.39	108.34
1	Q	529	PHE	N-CA-C	-5.45	101.28	109.95
1	P	396	GLY	CA-C-N	5.45	131.50	121.85
1	P	396	GLY	C-N-CA	5.45	131.50	121.85
1	O	287	ILE	N-CA-CB	5.45	117.05	110.95
1	M	397	PHE	N-CA-C	-5.45	100.79	109.23
1	O	566	LEU	N-CA-C	-5.45	99.41	108.34
1	Q	319	ASP	N-CA-C	5.44	117.21	111.28
1	Q	454	LEU	CA-C-N	5.44	131.93	121.54
1	Q	454	LEU	C-N-CA	5.44	131.93	121.54
1	M	613	ARG	CA-C-N	5.44	125.09	119.05
1	M	613	ARG	C-N-CA	5.44	125.09	119.05
1	Q	369	ILE	N-CA-CB	5.44	116.91	110.55
1	M	330	ILE	N-CA-C	-5.44	100.63	108.89
1	O	354	GLU	N-CA-C	-5.43	100.84	109.59
1	N	509	PRO	N-CA-C	-5.43	104.08	110.70
1	P	504	PHE	CA-C-N	5.43	131.34	122.81
1	P	504	PHE	C-N-CA	5.43	131.34	122.81
1	O	456	GLU	N-CA-C	-5.43	106.16	112.89
1	M	199	LEU	CA-C-N	5.42	126.92	120.14
1	M	199	LEU	C-N-CA	5.42	126.92	120.14
1	P	634	PRO	N-CA-C	-5.41	104.09	110.70
1	P	453	SER	N-CA-C	-5.40	104.29	112.99
1	N	668	GLU	N-CA-C	-5.40	107.95	114.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	286	ILE	N-CA-CB	5.38	118.06	111.60
1	N	666	ARG	N-CA-CB	5.38	118.22	110.20
1	Q	608	ILE	N-CA-C	-5.38	98.72	107.28
1	M	460	GLU	CA-C-N	5.38	132.07	122.13
1	M	460	GLU	C-N-CA	5.38	132.07	122.13
1	N	670	TYR	N-CA-C	-5.38	100.54	109.46
1	O	301	GLU	N-CA-C	-5.36	106.51	113.16
1	Q	347	GLY	N-CA-C	-5.36	100.48	113.18
1	P	226	GLY	N-CA-C	-5.36	100.49	113.18
1	M	506	LEU	N-CA-C	-5.34	100.47	109.07
1	M	233	PRO	N-CA-C	5.34	119.57	111.19
1	O	262	SER	N-CA-C	5.33	117.17	111.36
1	R	376	LEU	CB-CA-C	-5.32	102.53	110.88
1	R	543	GLY	N-CA-C	-5.32	108.28	115.36
1	P	489	LYS	CB-CA-C	-5.32	104.56	111.15
1	N	233	PRO	N-CA-C	5.30	119.51	111.19
1	N	626	ARG	N-CA-C	-5.30	106.59	113.16
1	N	328	ILE	N-CA-C	-5.29	102.24	109.55
1	N	234	GLY	CA-C-N	5.28	127.89	120.28
1	N	234	GLY	C-N-CA	5.28	127.89	120.28
1	M	499	ARG	N-CA-C	-5.28	99.90	109.09
1	M	626	ARG	N-CA-C	-5.28	105.12	112.30
1	R	628	ASP	N-CA-C	-5.28	104.44	112.04
1	N	543	GLY	N-CA-C	-5.26	100.70	113.18
1	M	632	TYR	N-CA-C	-5.26	101.89	110.20
1	M	381	GLU	CA-C-N	5.26	127.28	120.44
1	M	381	GLU	C-N-CA	5.26	127.28	120.44
1	O	371	THR	N-CA-C	5.25	118.95	112.54
1	P	231	GLY	CA-C-N	5.24	125.78	120.38
1	P	231	GLY	C-N-CA	5.24	125.78	120.38
1	P	580	SER	N-CA-C	-5.24	105.64	111.36
1	N	580	SER	N-CA-C	-5.24	102.32	109.71
1	M	340	ASP	N-CA-C	-5.24	101.67	109.42
1	O	605	VAL	N-CA-C	-5.23	102.33	109.55
1	R	388	GLU	N-CA-C	5.23	117.38	111.11
1	N	334	ASN	N-CA-C	-5.22	106.30	113.30
1	N	330	ILE	N-CA-C	-5.21	100.96	108.89
1	R	432	LEU	CA-C-N	5.21	131.49	121.54
1	R	432	LEU	C-N-CA	5.21	131.49	121.54
1	Q	311	VAL	N-CA-CB	5.21	117.62	110.54
1	P	378	MET	CA-C-N	5.20	127.50	120.38
1	P	378	MET	C-N-CA	5.20	127.50	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	R	369	ILE	N-CA-CB	5.20	116.63	110.55
1	Q	613	ARG	CA-C-N	5.19	124.81	119.05
1	Q	613	ARG	C-N-CA	5.19	124.81	119.05
1	Q	189	TYR	CB-CA-C	-5.18	102.52	110.81
1	Q	288	PHE	N-CA-C	-5.18	99.84	108.34
1	Q	396	GLY	N-CA-C	-5.18	100.90	113.18
1	M	434	LYS	N-CA-C	-5.18	106.81	112.72
1	N	475	VAL	N-CA-C	-5.18	105.45	110.42
1	N	633	ILE	N-CA-C	-5.18	101.97	107.77
1	R	395	TYR	N-CA-C	-5.18	106.81	113.02
1	Q	381	GLU	CA-C-N	5.18	127.17	120.44
1	Q	381	GLU	C-N-CA	5.18	127.17	120.44
1	M	466	TRP	CB-CA-C	-5.17	102.21	110.79
1	M	389	GLU	CA-C-N	5.17	127.46	120.38
1	M	389	GLU	C-N-CA	5.17	127.46	120.38
1	N	567	ASP	N-CA-C	-5.16	101.28	109.59
1	O	291	GLU	N-CA-C	-5.16	104.30	111.52
1	R	335	ARG	CA-C-N	5.16	127.15	120.70
1	R	335	ARG	C-N-CA	5.16	127.15	120.70
1	P	690	ASN	CA-C-N	5.16	126.29	119.84
1	P	690	ASN	C-N-CA	5.16	126.29	119.84
1	M	627	PHE	N-CA-CB	5.15	119.20	110.49
1	O	373	ASN	N-CA-C	-5.15	106.54	114.16
1	P	674	ASP	N-CA-CB	5.15	117.54	110.07
1	Q	221	ILE	N-CA-C	5.15	120.05	109.34
1	R	482	THR	N-CA-CB	5.15	117.53	110.07
1	O	431	ILE	N-CA-C	-5.14	100.48	107.99
1	O	329	VAL	N-CA-C	-5.13	100.17	107.77
1	R	325	GLY	N-CA-C	-5.13	101.01	113.18
1	Q	711	SER	N-CA-C	-5.13	106.70	113.12
1	M	304	GLY	N-CA-C	-5.13	101.02	113.18
1	M	345	ARG	CA-C-N	5.13	125.12	119.89
1	M	345	ARG	C-N-CA	5.13	125.12	119.89
1	N	545	SER	CA-C-N	5.13	130.53	120.99
1	N	545	SER	C-N-CA	5.13	130.53	120.99
1	P	235	THR	N-CA-C	-5.12	99.89	110.80
1	P	656	PRO	CA-C-N	5.12	127.14	120.28
1	P	656	PRO	C-N-CA	5.12	127.14	120.28
1	N	556	ALA	N-CA-C	-5.11	105.62	111.14
1	P	526	ASN	CA-C-N	5.11	131.30	121.54
1	P	526	ASN	C-N-CA	5.11	131.30	121.54
1	M	301	GLU	N-CA-C	-5.10	105.80	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	452	SER	N-CA-CB	5.09	117.69	110.46
1	Q	256	ASN	CA-C-N	5.09	124.85	121.13
1	Q	256	ASN	C-N-CA	5.09	124.85	121.13
1	R	674	ASP	N-CA-CB	5.09	117.70	110.16
1	R	565	PHE	N-CA-C	-5.09	100.16	108.76
1	M	458	MET	N-CA-C	-5.08	100.00	108.34
1	Q	537	VAL	N-CA-C	5.08	115.80	110.62
1	N	185	SER	CA-C-N	5.08	131.24	121.54
1	N	185	SER	C-N-CA	5.08	131.24	121.54
1	R	421	ILE	N-CA-C	-5.08	105.59	113.16
1	O	560	ALA	CA-C-O	-5.07	114.96	120.69
1	R	375	PRO	CA-C-N	5.07	127.03	120.44
1	R	375	PRO	C-N-CA	5.07	127.03	120.44
1	M	659	ASP	N-CA-C	-5.05	97.69	107.44
1	O	323	GLU	N-CA-C	-5.05	106.38	112.54
1	O	612	ASN	N-CA-C	-5.05	104.84	111.96
1	P	591	GLN	CA-C-N	5.05	127.35	120.54
1	P	591	GLN	C-N-CA	5.05	127.35	120.54
1	P	287	ILE	N-CA-CB	5.05	116.60	110.95
1	R	529	PHE	N-CA-C	-5.04	101.93	109.95
1	P	712	VAL	N-CA-CB	5.04	119.54	111.23
1	Q	320	GLY	CA-C-N	5.04	129.42	121.56
1	Q	320	GLY	C-N-CA	5.04	129.42	121.56
1	M	501	SER	N-CA-C	-5.04	100.07	110.80
1	N	565	PHE	N-CA-C	-5.04	100.69	108.90
1	R	459	VAL	N-CA-C	-5.03	100.60	107.75
1	O	613	ARG	CA-C-N	5.03	124.63	119.05
1	O	613	ARG	C-N-CA	5.03	124.63	119.05
1	Q	453	SER	CA-C-N	5.03	131.14	121.54
1	Q	453	SER	C-N-CA	5.03	131.14	121.54
1	M	268	SER	N-CA-C	-5.02	105.52	111.69
1	P	305	GLU	CA-C-N	5.02	127.61	120.53
1	P	305	GLU	C-N-CA	5.02	127.61	120.53
1	N	431	ILE	N-CA-C	-5.02	99.30	107.28
1	Q	398	VAL	N-CA-C	-5.01	101.45	109.17
1	Q	518	ALA	N-CA-C	5.00	117.11	111.11
1	Q	646	LYS	CA-C-N	5.00	127.31	120.46
1	Q	646	LYS	C-N-CA	5.00	127.31	120.46

There are no chirality outliers.

There are no planarity outliers.

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	M	2680	0	1205	17	0
1	N	2680	0	1205	15	0
1	O	2680	0	1205	12	0
1	P	2680	0	1205	17	0
1	Q	2680	0	1205	11	0
1	R	2680	0	1205	15	0
All	All	16080	0	7230	51	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 2.

All (51) 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:N:262:SER:CB	1:O:266:GLY:O	1.66	1.43
1:P:579:THR:CB	1:R:542:VAL:CB	1.98	1.39
1:O:262:SER:CA	1:Q:266:GLY:HA3	1.66	1.26
1:O:262:SER:HA	1:Q:266:GLY:CA	1.62	1.25
1:P:579:THR:CB	1:R:542:VAL:HA	1.84	1.07
1:P:579:THR:CB	1:R:542:VAL:CA	2.33	1.06
1:P:539:SER:CB	1:M:590:ASN:CB	2.37	1.03
1:Q:262:SER:CB	1:R:266:GLY:O	2.08	1.02
1:Q:262:SER:HA	1:R:266:GLY:HA3	1.40	1.01
1:P:580:SER:HA	1:M:579:THR:HA	1.42	0.99
1:P:496:LEU:O	1:R:652:MET:HA	1.69	0.92
1:M:580:SER:O	1:N:582:SER:CB	2.13	0.87
1:P:580:SER:CB	1:M:578:THR:O	2.24	0.86
1:Q:262:SER:HA	1:R:266:GLY:CA	2.07	0.84
1:O:262:SER:O	1:Q:265:TYR:O	1.97	0.81
1:M:400:ALA:HB1	1:N:346:PRO:O	1.79	0.81
1:M:673:ALA:CB	1:N:624:ALA:HB3	2.16	0.75
1:P:579:THR:CA	1:R:542:VAL:CB	2.67	0.72
1:M:673:ALA:HB1	1:N:624:ALA:HB3	1.76	0.66
1:P:580:SER:HA	1:M:579:THR:CA	2.21	0.64
1:M:673:ALA:HB3	1:N:624:ALA:HB3	1.81	0.61

Continued on next page...

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:535:PRO:CB	1:O:591:GLN:CB	2.84	0.56
1:P:579:THR:HA	1:R:542:VAL:CB	2.37	0.55
1:O:262:SER:HA	1:Q:266:GLY:HA3	0.71	0.54
1:P:289:ILE:O	1:P:331:GLY:HA2	2.07	0.54
1:N:575:ARG:HA	1:N:618:ASP:HA	1.90	0.53
1:Q:347:GLY:H	1:Q:350:ASP:HA	1.75	0.51
1:Q:377:GLY:HA3	1:Q:437:VAL:H	1.75	0.51
1:M:262:SER:CB	1:N:266:GLY:O	2.59	0.51
1:M:289:ILE:O	1:M:331:GLY:HA2	2.13	0.48
1:N:262:SER:HA	1:O:266:GLY:HA3	1.97	0.47
1:Q:262:SER:CA	1:R:266:GLY:O	2.62	0.47
1:P:496:LEU:O	1:R:652:MET:CA	2.54	0.46
1:O:325:GLY:C	1:O:327:VAL:H	2.24	0.46
1:P:511:GLY:C	1:P:513:GLY:H	2.25	0.44
1:P:580:SER:HA	1:M:579:THR:CB	2.47	0.44
1:M:571:SER:CB	1:N:590:ASN:CB	2.95	0.44
1:P:575:ARG:HA	1:P:618:ASP:HA	2.00	0.44
1:M:410:ALA:CB	1:N:221:ILE:CB	2.95	0.44
1:O:234:GLY:C	1:O:236:GLY:H	2.26	0.44
1:R:562:ALA:O	1:R:605:VAL:HA	2.18	0.44
1:Q:374:MET:CB	1:R:220:GLY:HA2	2.48	0.43
1:O:289:ILE:O	1:O:331:GLY:HA2	2.18	0.43
1:R:669:GLY:C	1:R:711:SER:H	2.26	0.43
1:M:673:ALA:HB1	1:N:624:ALA:CB	2.47	0.42
1:N:373:ASN:O	1:O:220:GLY:HA2	2.19	0.42
1:R:251:ASN:H	1:R:285:SER:HA	1.86	0.41
1:P:539:SER:CB	1:M:590:ASN:C	2.94	0.41
1:O:575:ARG:HA	1:O:618:ASP:HA	2.03	0.41
1:P:579:THR:C	1:M:579:THR:CB	2.95	0.40
1:N:325:GLY:C	1:N:327:VAL:H	2.30	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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.

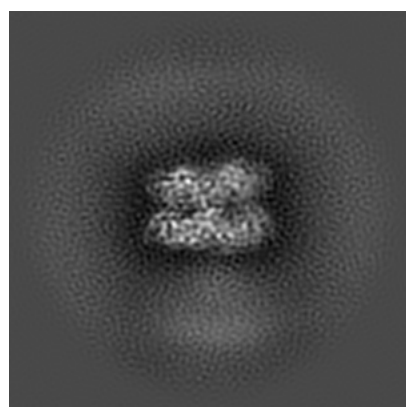
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8659. These allow visual inspection of the internal detail of the map and identification of artifacts.

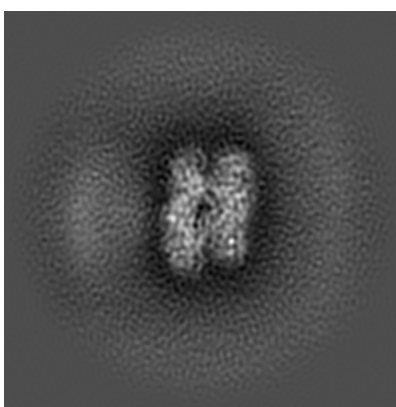
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

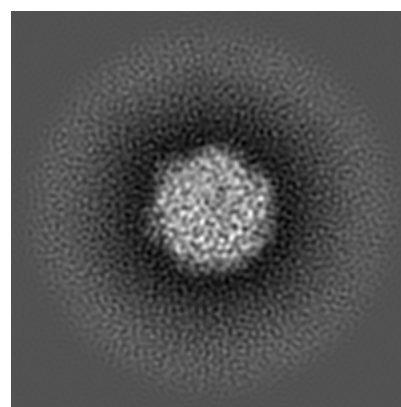
6.1.1 Primary map



X



Y

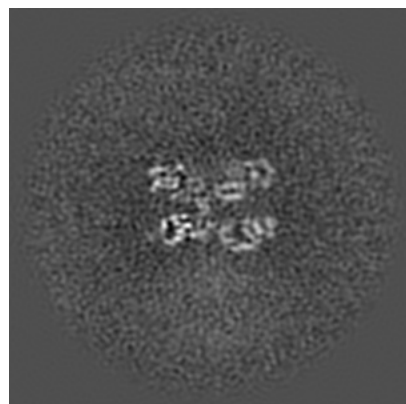


Z

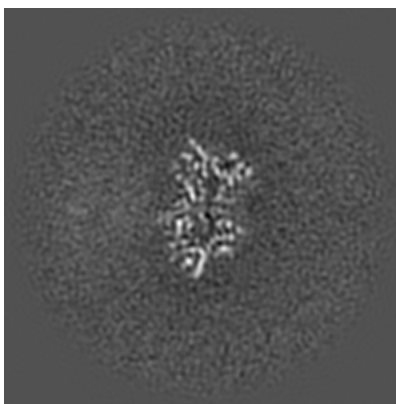
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

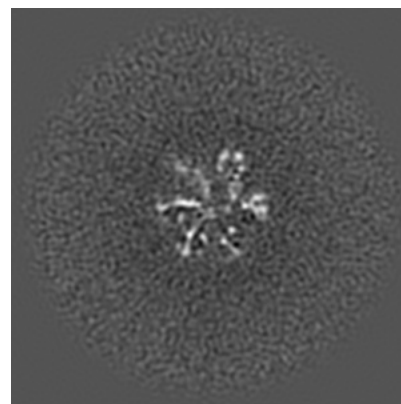
6.2.1 Primary map



X Index: 128



Y Index: 128

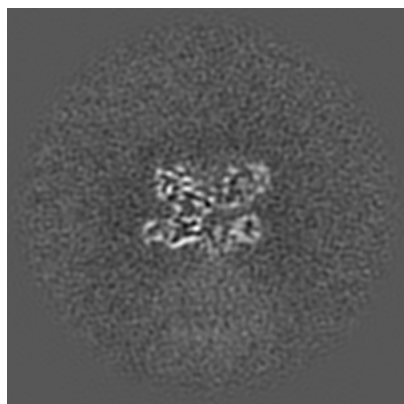


Z Index: 128

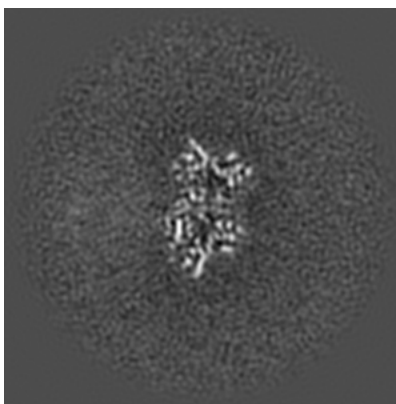
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

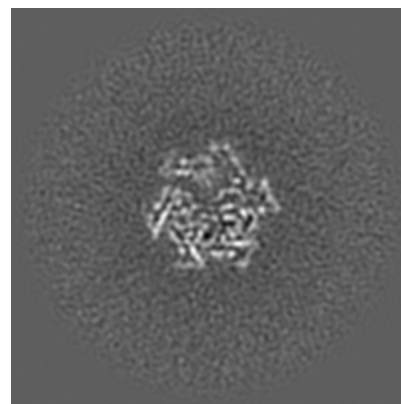
6.3.1 Primary map



X Index: 123



Y Index: 127

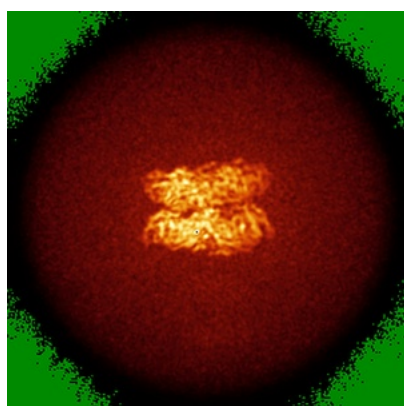


Z Index: 119

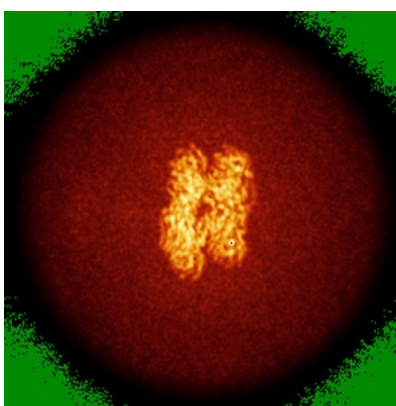
The images above show the largest variance slices of the map in three orthogonal directions.

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

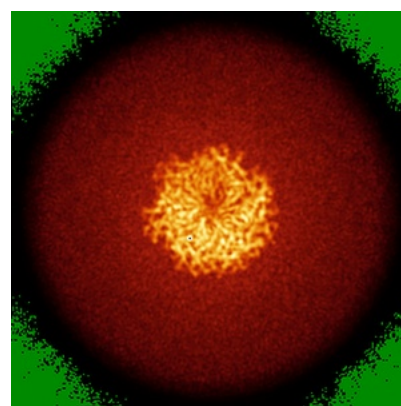
6.4.1 Primary map



X



Y

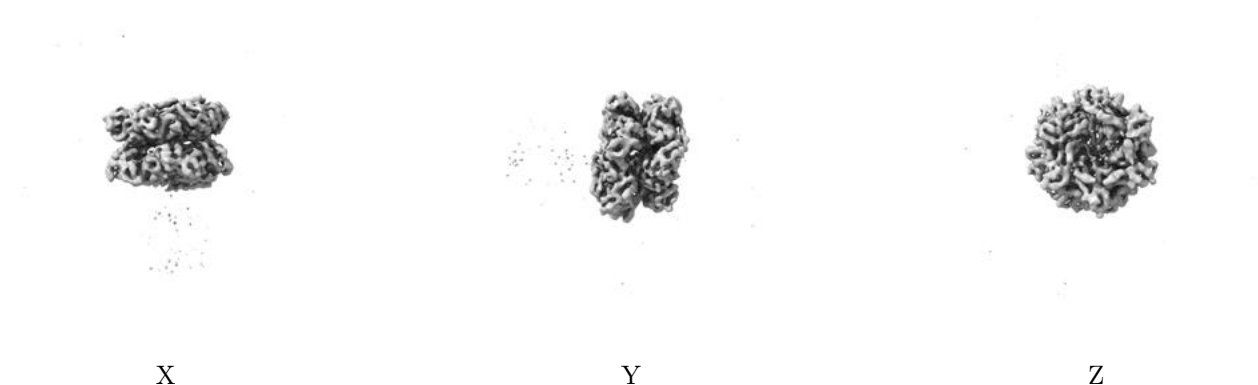


Z

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

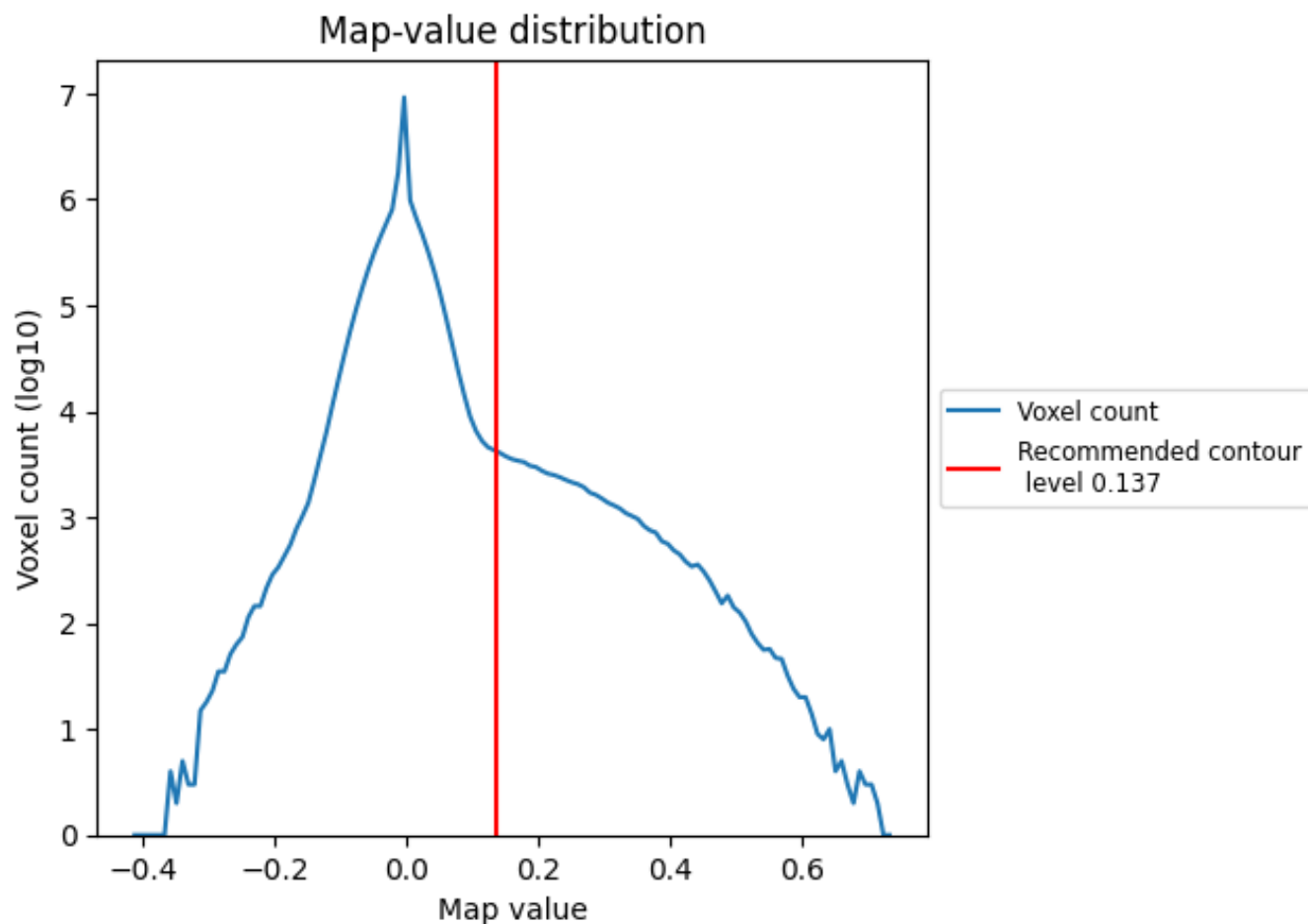
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

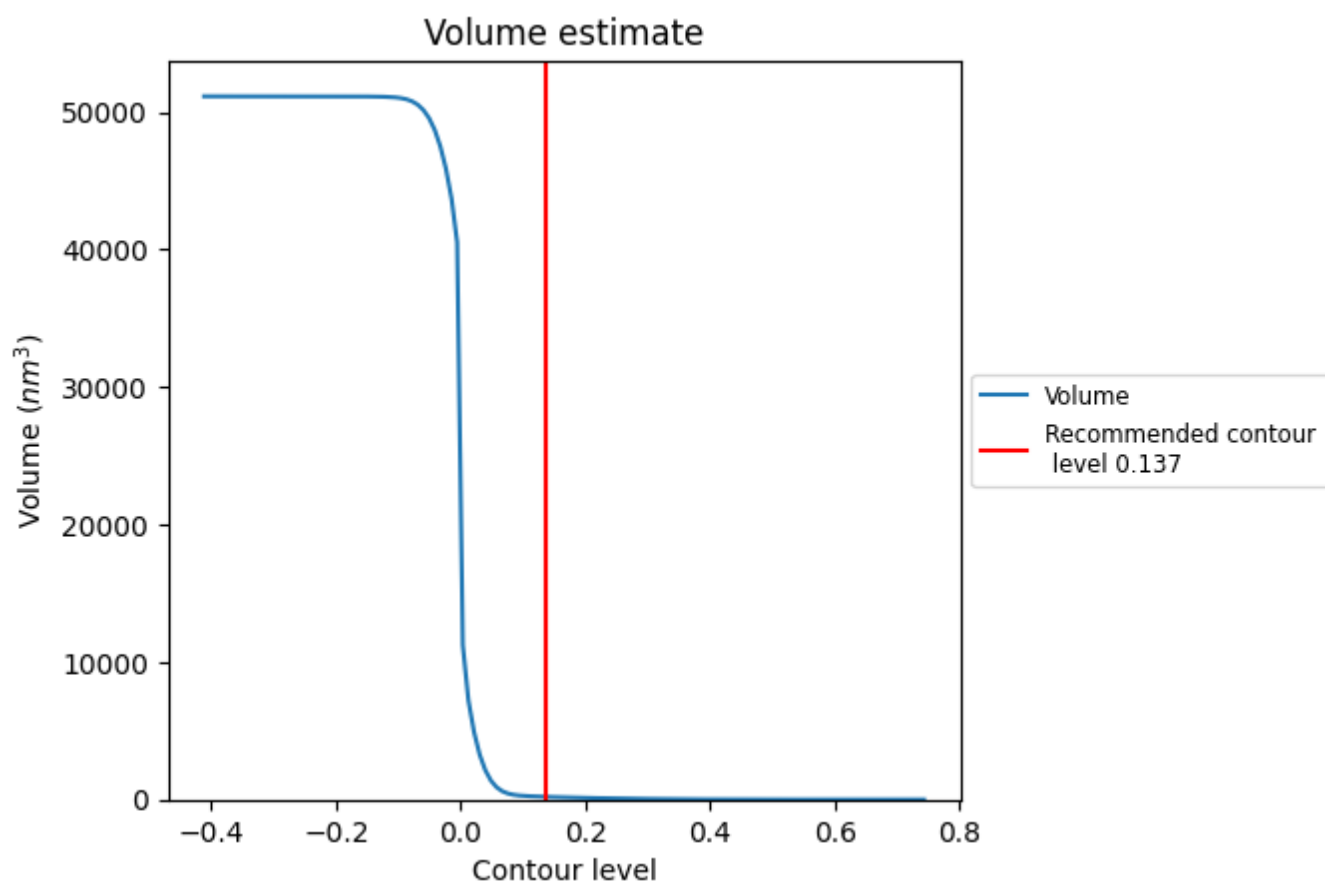
This section contains the results of statistical analysis of the map.

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.

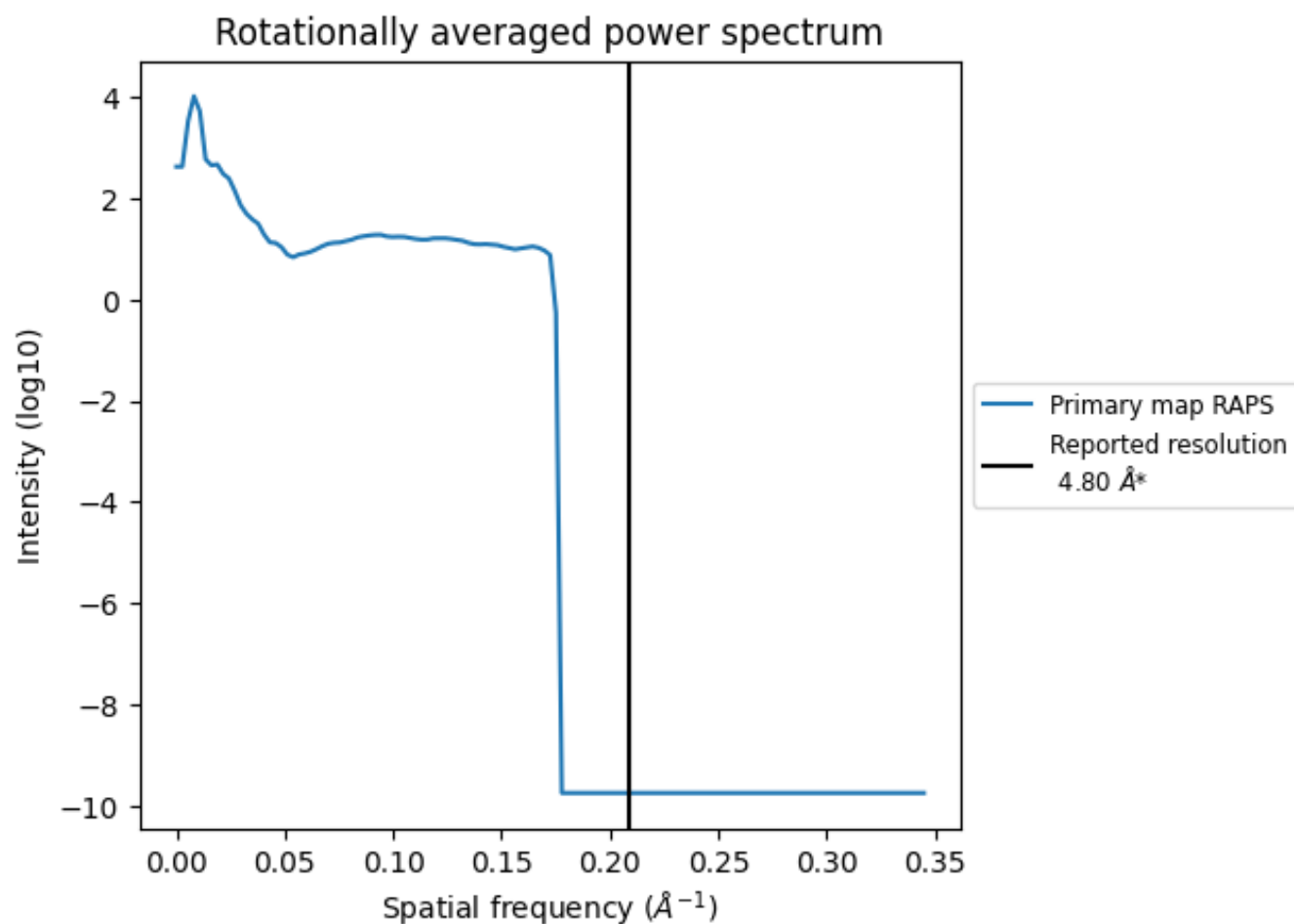
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 197 nm³; this corresponds to an approximate mass of 178 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 0.208 $\text{\AA}^{-1}$

8 Fourier-Shell correlation

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

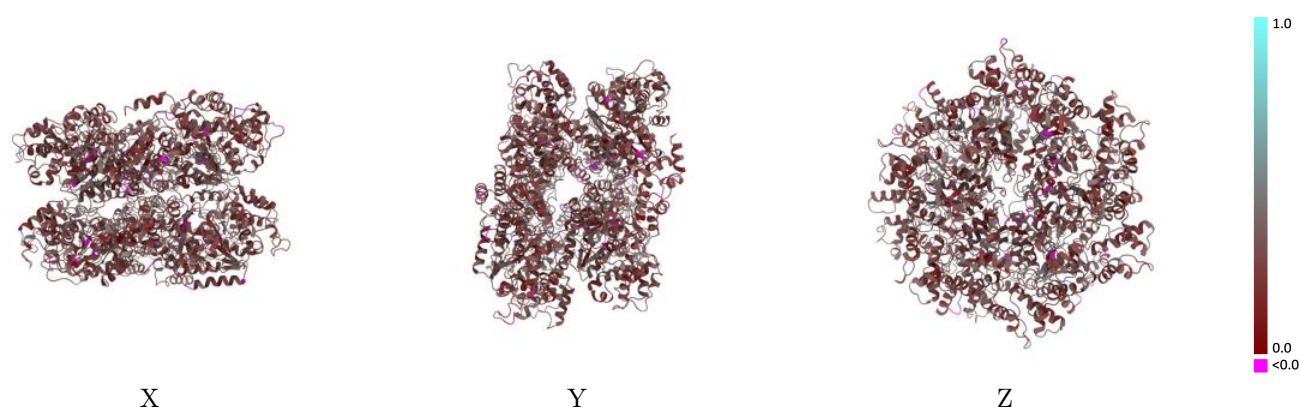
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8659 and PDB model 5VCA. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

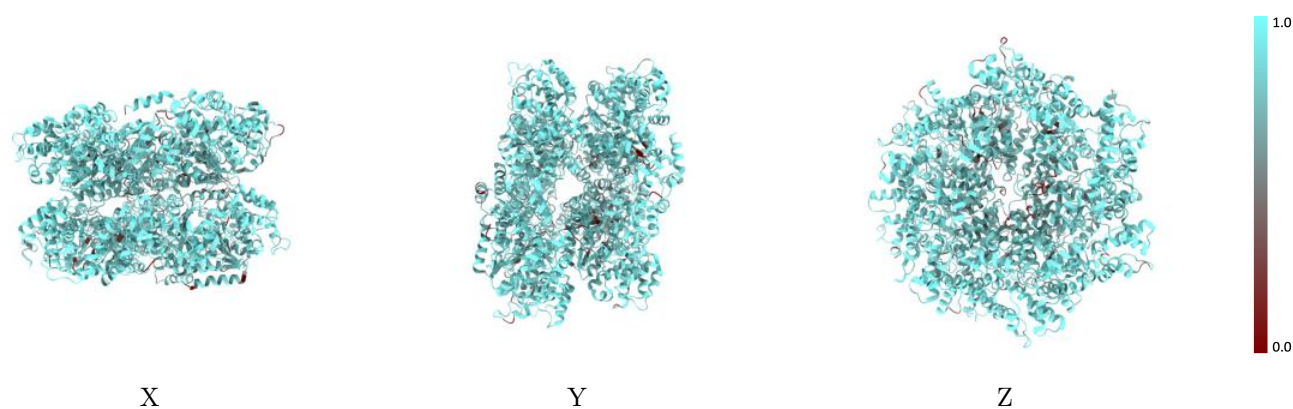
This section was not generated.

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



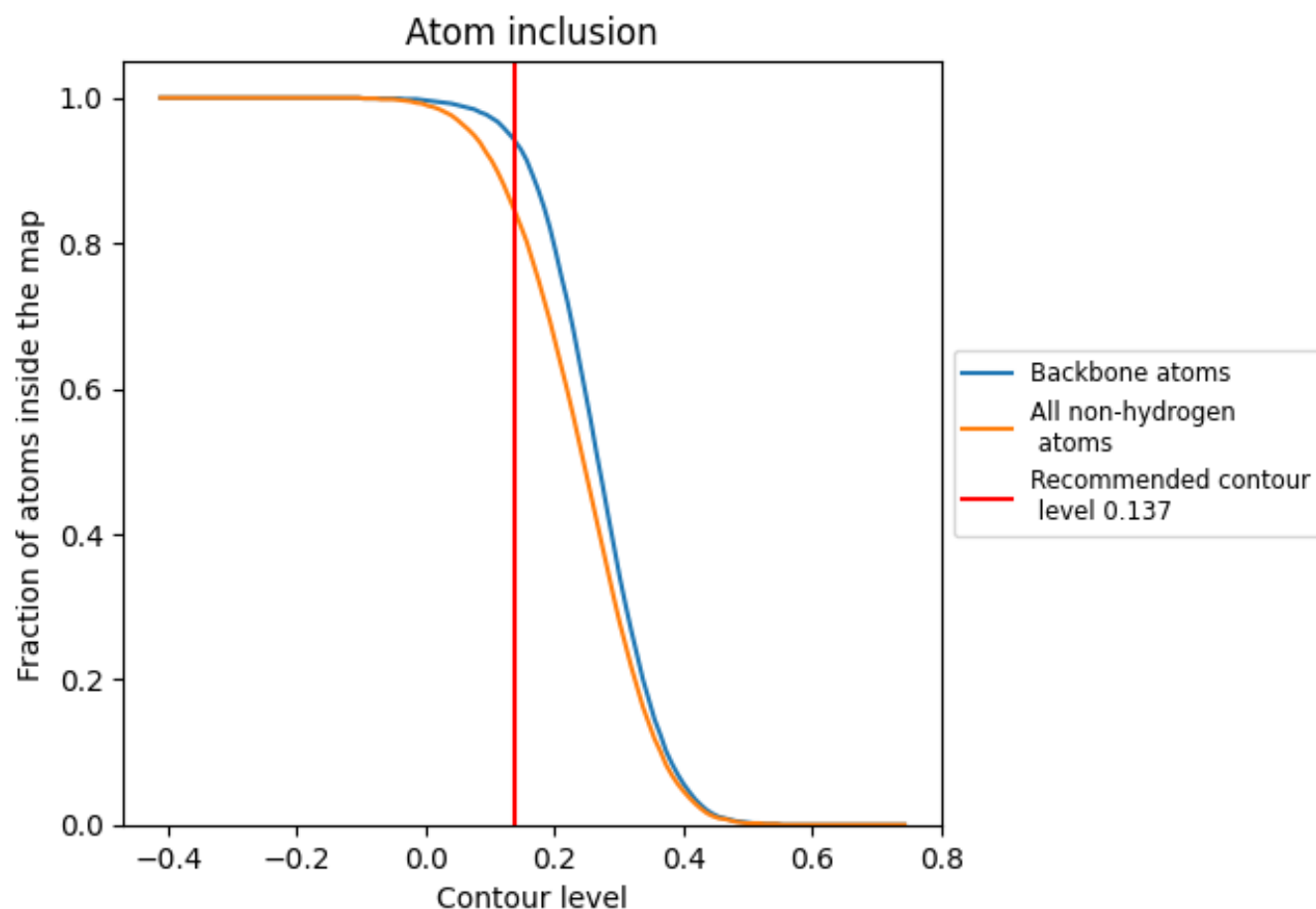
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.137).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 85% 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 (0.137) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8470	0.2980
M	0.8610	0.3030
N	0.8690	0.3040
O	0.8620	0.3020
P	0.8110	0.2890
Q	0.8500	0.2990
R	0.8290	0.2900

1.0

0.0

<0.0