



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 02:38 AM UTC

PDB ID : 3J02 / pdb_00003j02
EMDB ID : EMD-5258
Title : Lidless D386A Mm-cpn in the pre-hydrolysis ATP-bound state
Authors : Zhang, J.; Ma, B.; DiMaio, F.; Douglas, N.R.; Joachimiak, L.; Baker, D.;
Frydman, J.; Levitt, M.; Chiu, W.
Deposited on : 2011-02-10
Resolution : 8.00 Å(reported)

This is a wwPDB EM Validation Summary 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:

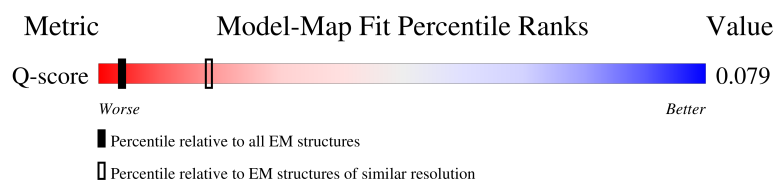
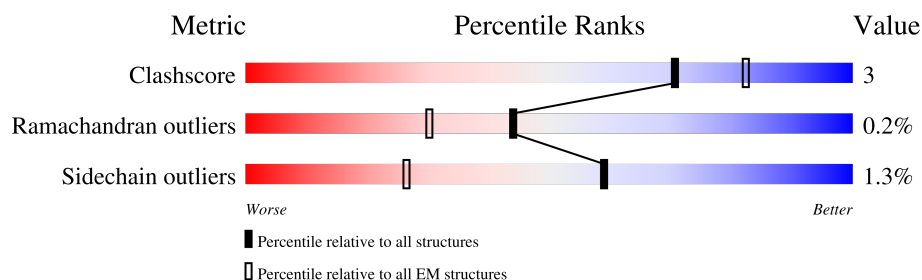
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 8.00 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.



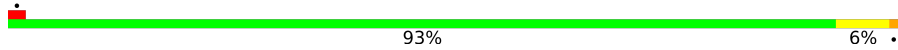
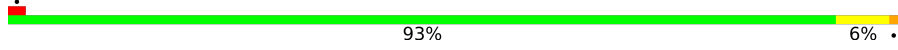
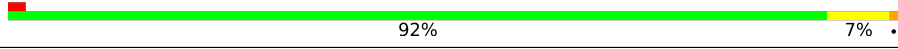
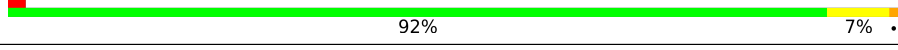
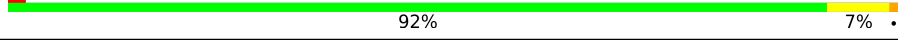
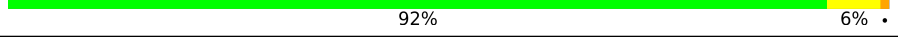
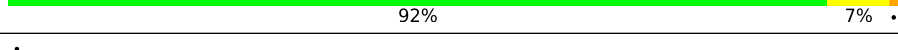
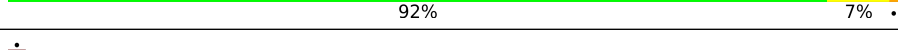
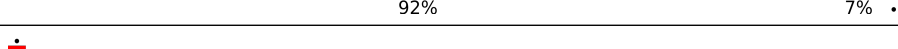
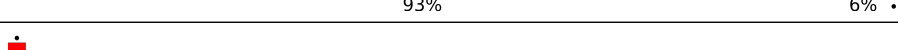
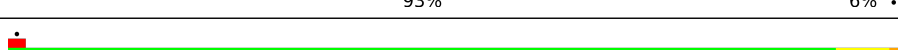
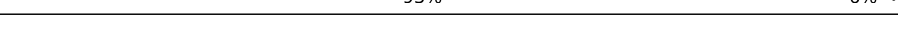
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	361 (7.50 - 8.50)

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	491	
1	B	491	
1	C	491	
1	D	491	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	E	491	 93% 6% .
1	F	491	 93% 6% .
1	G	491	 92% 7% .
1	H	491	 92% 7% .
1	I	491	 92% 7% .
1	J	491	 92% 6% .
1	K	491	 92% 7% .
1	L	491	 92% 7% .
1	M	491	 92% 7% .
1	N	491	 93% 6% .
1	O	491	 93% 6% .
1	P	491	 93% 6% .

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 58591 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 Lidless D386A Mm-cpn variant.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	491	Total	C	N	O	S	0	0
			3661	2271	634	732	24		
1	B	491	Total	C	N	O	S	0	0
			3662	2271	635	732	24		
1	C	491	Total	C	N	O	S	0	0
			3662	2271	635	732	24		
1	D	491	Total	C	N	O	S	0	0
			3662	2271	635	732	24		
1	E	491	Total	C	N	O	S	0	0
			3662	2271	635	732	24		
1	F	491	Total	C	N	O	S	0	0
			3662	2271	635	732	24		
1	G	491	Total	C	N	O	S	0	0
			3662	2271	635	732	24		
1	H	491	Total	C	N	O	S	0	0
			3662	2271	635	732	24		
1	I	491	Total	C	N	O	S	0	0
			3662	2271	635	732	24		
1	J	491	Total	C	N	O	S	0	0
			3662	2271	635	732	24		
1	K	491	Total	C	N	O	S	0	0
			3662	2271	635	732	24		
1	L	491	Total	C	N	O	S	0	0
			3662	2271	635	732	24		
1	M	491	Total	C	N	O	S	0	0
			3662	2271	635	732	24		
1	N	491	Total	C	N	O	S	0	0
			3662	2271	635	732	24		
1	O	491	Total	C	N	O	S	0	0
			3662	2271	635	732	24		
1	P	491	Total	C	N	O	S	0	0
			3662	2271	635	732	24		

There are 112 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	235	GLU	-	linker	UNP Q877G8
A	236	THR	-	linker	UNP Q877G8
A	237	ALA	-	linker	UNP Q877G8
A	238	SER	-	linker	UNP Q877G8
A	239	GLU	-	linker	UNP Q877G8
A	240	MET	-	linker	UNP Q877G8
A	358	ALA	ASP	engineered mutation	UNP Q877G8
B	726	GLU	-	linker	UNP Q877G8
B	727	THR	-	linker	UNP Q877G8
B	728	ALA	-	linker	UNP Q877G8
B	729	SER	-	linker	UNP Q877G8
B	730	GLU	-	linker	UNP Q877G8
B	731	MET	-	linker	UNP Q877G8
B	849	ALA	ASP	engineered mutation	UNP Q877G8
C	1217	GLU	-	linker	UNP Q877G8
C	1218	THR	-	linker	UNP Q877G8
C	1219	ALA	-	linker	UNP Q877G8
C	1220	SER	-	linker	UNP Q877G8
C	1221	GLU	-	linker	UNP Q877G8
C	1222	MET	-	linker	UNP Q877G8
C	1340	ALA	ASP	engineered mutation	UNP Q877G8
D	1708	GLU	-	linker	UNP Q877G8
D	1709	THR	-	linker	UNP Q877G8
D	1710	ALA	-	linker	UNP Q877G8
D	1711	SER	-	linker	UNP Q877G8
D	1712	GLU	-	linker	UNP Q877G8
D	1713	MET	-	linker	UNP Q877G8
D	1831	ALA	ASP	engineered mutation	UNP Q877G8
E	2199	GLU	-	linker	UNP Q877G8
E	2200	THR	-	linker	UNP Q877G8
E	2201	ALA	-	linker	UNP Q877G8
E	2202	SER	-	linker	UNP Q877G8
E	2203	GLU	-	linker	UNP Q877G8
E	2204	MET	-	linker	UNP Q877G8
E	2322	ALA	ASP	engineered mutation	UNP Q877G8
F	2690	GLU	-	linker	UNP Q877G8
F	2691	THR	-	linker	UNP Q877G8
F	2692	ALA	-	linker	UNP Q877G8
F	2693	SER	-	linker	UNP Q877G8
F	2694	GLU	-	linker	UNP Q877G8
F	2695	MET	-	linker	UNP Q877G8
F	2813	ALA	ASP	engineered mutation	UNP Q877G8
G	3181	GLU	-	linker	UNP Q877G8

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
G	3182	THR	-	linker	UNP Q877G8
G	3183	ALA	-	linker	UNP Q877G8
G	3184	SER	-	linker	UNP Q877G8
G	3185	GLU	-	linker	UNP Q877G8
G	3186	MET	-	linker	UNP Q877G8
G	3304	ALA	ASP	engineered mutation	UNP Q877G8
H	3672	GLU	-	linker	UNP Q877G8
H	3673	THR	-	linker	UNP Q877G8
H	3674	ALA	-	linker	UNP Q877G8
H	3675	SER	-	linker	UNP Q877G8
H	3676	GLU	-	linker	UNP Q877G8
H	3677	MET	-	linker	UNP Q877G8
H	3795	ALA	ASP	engineered mutation	UNP Q877G8
I	4163	GLU	-	linker	UNP Q877G8
I	4164	THR	-	linker	UNP Q877G8
I	4165	ALA	-	linker	UNP Q877G8
I	4166	SER	-	linker	UNP Q877G8
I	4167	GLU	-	linker	UNP Q877G8
I	4168	MET	-	linker	UNP Q877G8
I	4286	ALA	ASP	engineered mutation	UNP Q877G8
J	4654	GLU	-	linker	UNP Q877G8
J	4655	THR	-	linker	UNP Q877G8
J	4656	ALA	-	linker	UNP Q877G8
J	4657	SER	-	linker	UNP Q877G8
J	4658	GLU	-	linker	UNP Q877G8
J	4659	MET	-	linker	UNP Q877G8
J	4777	ALA	ASP	engineered mutation	UNP Q877G8
K	5145	GLU	-	linker	UNP Q877G8
K	5146	THR	-	linker	UNP Q877G8
K	5147	ALA	-	linker	UNP Q877G8
K	5148	SER	-	linker	UNP Q877G8
K	5149	GLU	-	linker	UNP Q877G8
K	5150	MET	-	linker	UNP Q877G8
K	5268	ALA	ASP	engineered mutation	UNP Q877G8
L	5636	GLU	-	linker	UNP Q877G8
L	5637	THR	-	linker	UNP Q877G8
L	5638	ALA	-	linker	UNP Q877G8
L	5639	SER	-	linker	UNP Q877G8
L	5640	GLU	-	linker	UNP Q877G8
L	5641	MET	-	linker	UNP Q877G8
L	5759	ALA	ASP	engineered mutation	UNP Q877G8
M	6127	GLU	-	linker	UNP Q877G8

Continued on next page...

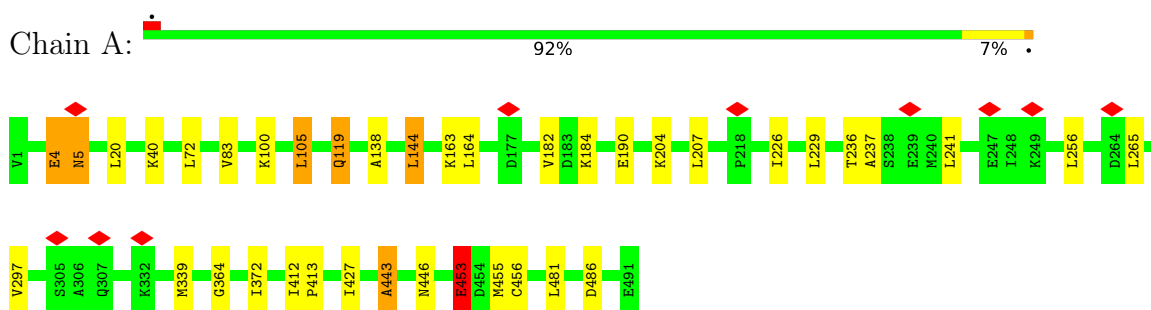
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
M	6128	THR	-	linker	UNP Q877G8
M	6129	ALA	-	linker	UNP Q877G8
M	6130	SER	-	linker	UNP Q877G8
M	6131	GLU	-	linker	UNP Q877G8
M	6132	MET	-	linker	UNP Q877G8
M	6250	ALA	ASP	engineered mutation	UNP Q877G8
N	6618	GLU	-	linker	UNP Q877G8
N	6619	THR	-	linker	UNP Q877G8
N	6620	ALA	-	linker	UNP Q877G8
N	6621	SER	-	linker	UNP Q877G8
N	6622	GLU	-	linker	UNP Q877G8
N	6623	MET	-	linker	UNP Q877G8
N	6741	ALA	ASP	engineered mutation	UNP Q877G8
O	7109	GLU	-	linker	UNP Q877G8
O	7110	THR	-	linker	UNP Q877G8
O	7111	ALA	-	linker	UNP Q877G8
O	7112	SER	-	linker	UNP Q877G8
O	7113	GLU	-	linker	UNP Q877G8
O	7114	MET	-	linker	UNP Q877G8
O	7232	ALA	ASP	engineered mutation	UNP Q877G8
P	7600	GLU	-	linker	UNP Q877G8
P	7601	THR	-	linker	UNP Q877G8
P	7602	ALA	-	linker	UNP Q877G8
P	7603	SER	-	linker	UNP Q877G8
P	7604	GLU	-	linker	UNP Q877G8
P	7605	MET	-	linker	UNP Q877G8
P	7723	ALA	ASP	engineered mutation	UNP Q877G8

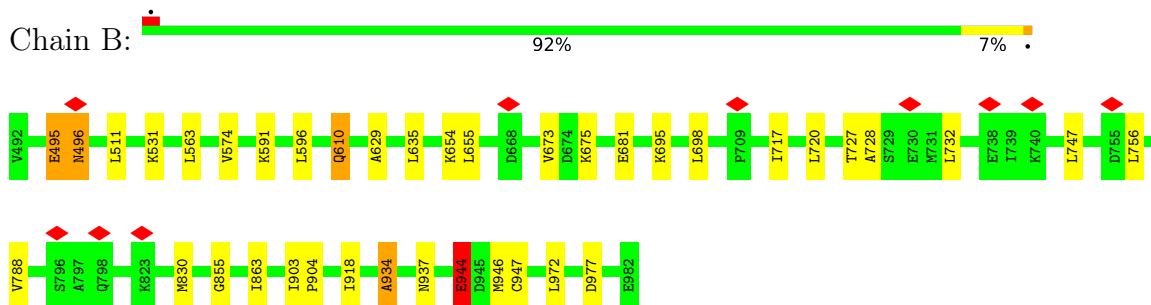
3 Residue-property plots

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.

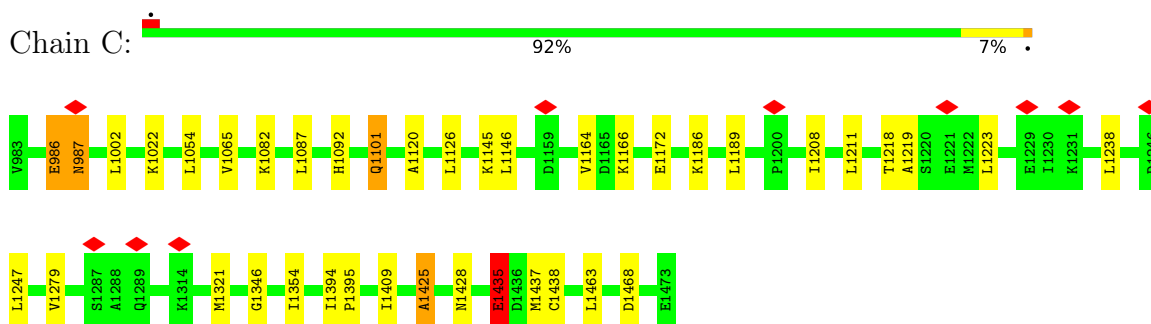
- Molecule 1: Lidless D386A Mm-cpn variant



- Molecule 1: Lidless D386A Mm-cpn variant

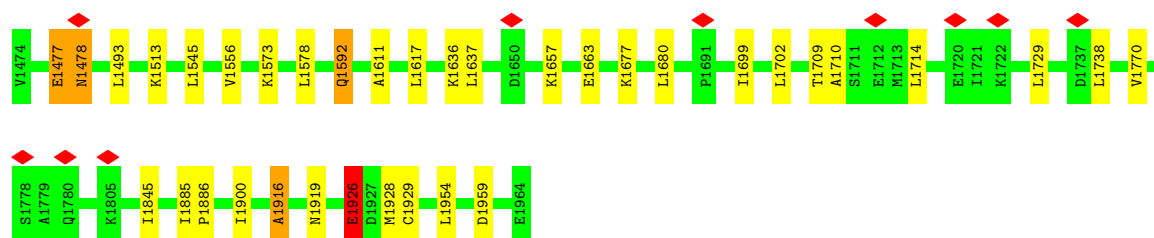


- Molecule 1: Lidless D386A Mm-cpn variant

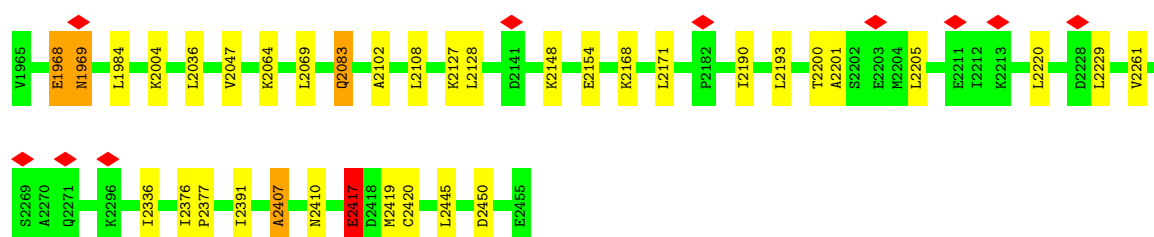


- Molecule 1: Lidless D386A Mm-cpn variant

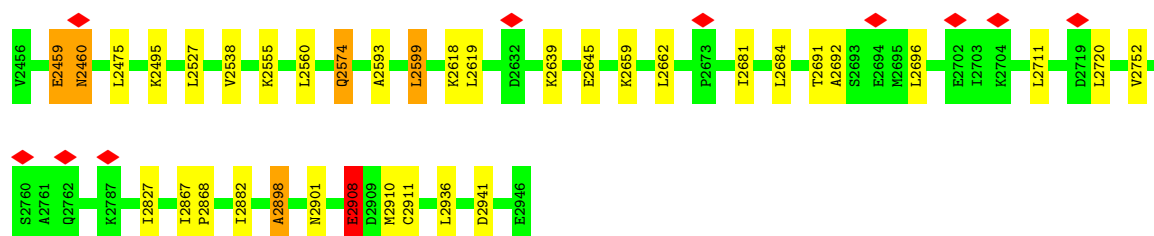




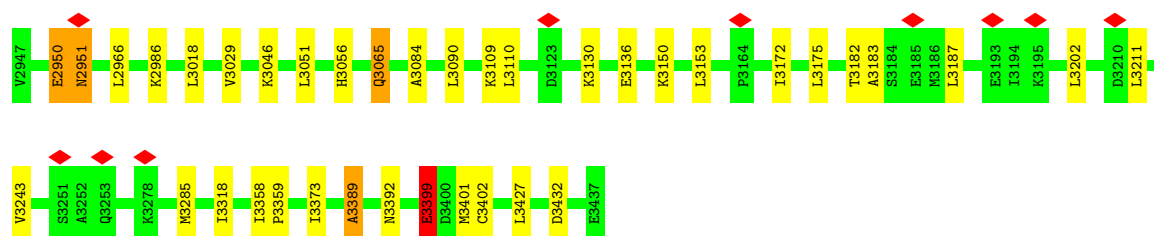
- Molecule 1: Lidless D386A Mm-cpn variant



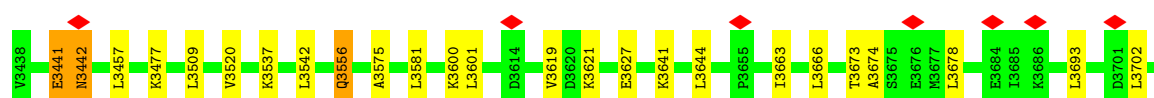
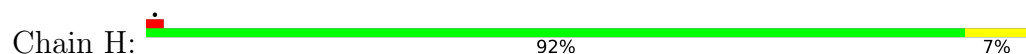
- Molecule 1: Lidless D386A Mm-cpn variant



- Molecule 1: Lidless D386A Mm-cpn variant

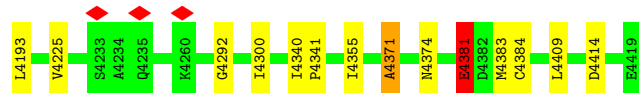
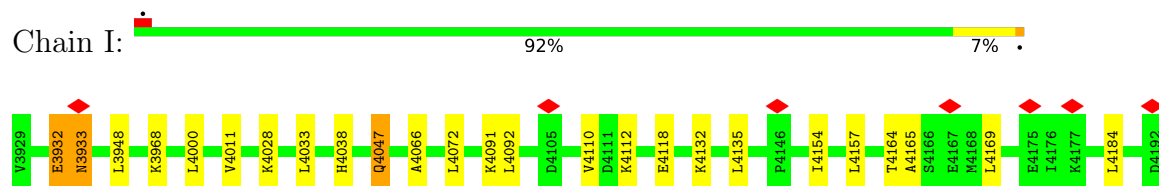


- Molecule 1: Lidless D386A Mm-cpn variant

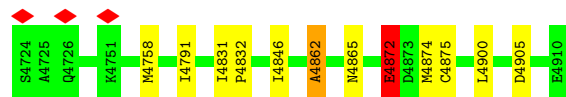
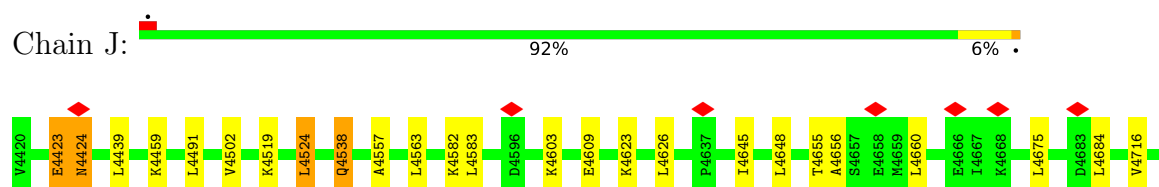




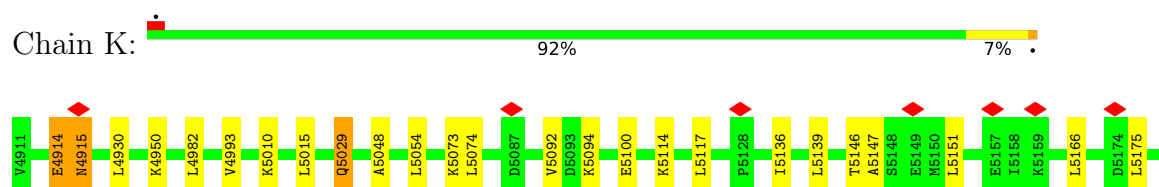
- Molecule 1: Lidless D386A Mm-cpn variant



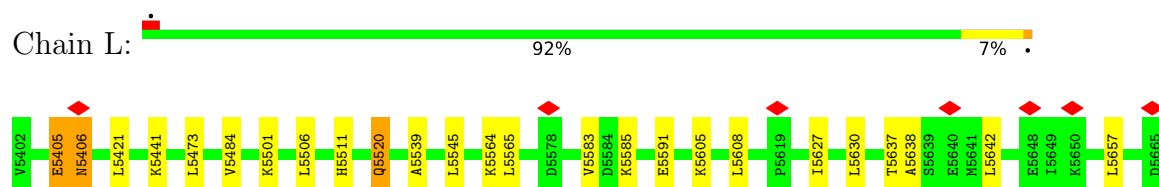
- Molecule 1: Lidless D386A Mm-cpn variant



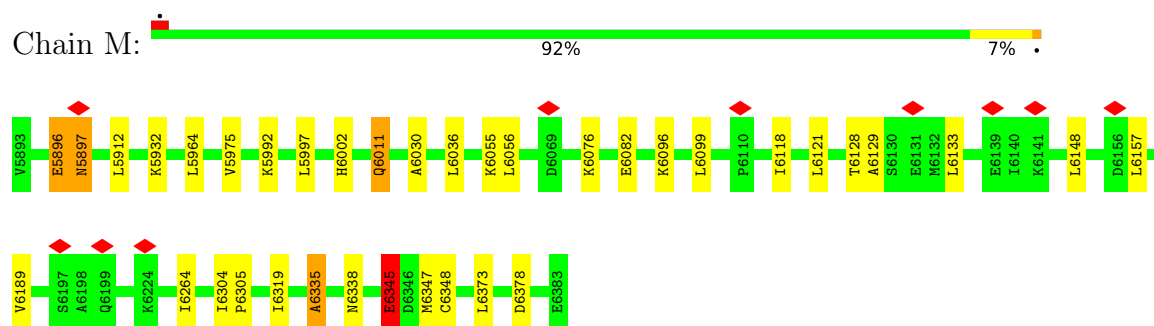
- Molecule 1: Lidless D386A Mm-cpn variant



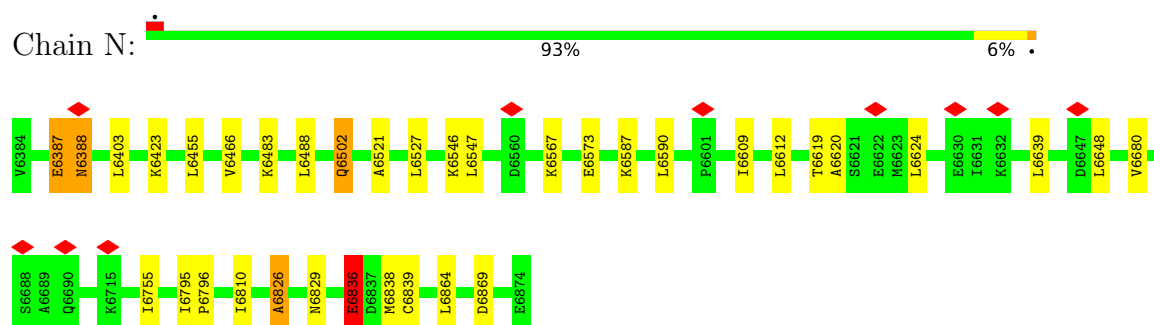
- Molecule 1: Lidless D386A Mm-cpn variant



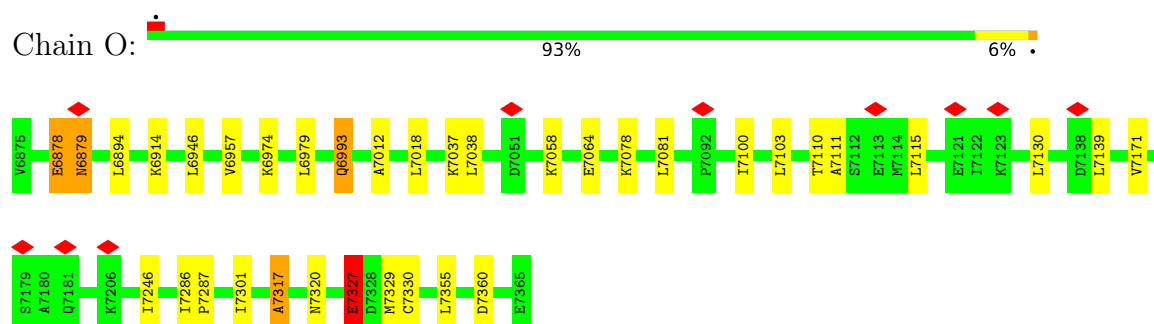
● Molecule 1: Lidless D386A Mm-cpn variant



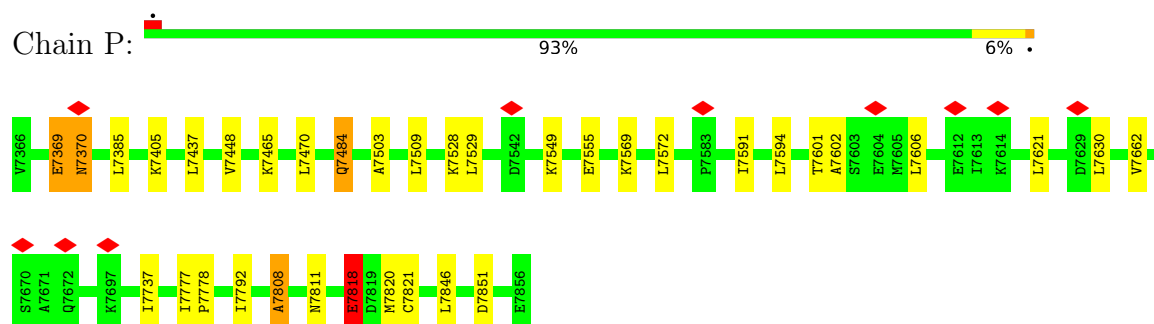
● Molecule 1: Lidless D386A Mm-cpn variant



● Molecule 1: Lidless D386A Mm-cpn variant



● Molecule 1: Lidless D386A Mm-cpn variant



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D8	Depositor
Number of particles used	12761	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Each CCD image	Depositor
Microscope	JEOL 2200FS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	112000	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor
Maximum map value	0.232	Depositor
Minimum map value	-0.122	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.02	Depositor
Map size ($\text{\AA}$)	340.8, 340.8, 340.8	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.42, 1.42, 1.42	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	0.92	3/3682 (0.1%)	1.07	9/4955 (0.2%)
1	B	0.92	3/3683 (0.1%)	1.07	9/4957 (0.2%)
1	C	0.92	4/3683 (0.1%)	1.07	9/4957 (0.2%)
1	D	0.92	3/3683 (0.1%)	1.07	9/4957 (0.2%)
1	E	0.92	3/3683 (0.1%)	1.07	9/4957 (0.2%)
1	F	0.92	3/3683 (0.1%)	1.07	9/4957 (0.2%)
1	G	0.92	4/3683 (0.1%)	1.07	9/4957 (0.2%)
1	H	0.92	3/3683 (0.1%)	1.07	9/4957 (0.2%)
1	I	0.92	4/3683 (0.1%)	1.07	9/4957 (0.2%)
1	J	0.92	3/3683 (0.1%)	1.07	9/4957 (0.2%)
1	K	0.92	3/3683 (0.1%)	1.07	9/4957 (0.2%)
1	L	0.92	4/3683 (0.1%)	1.07	9/4957 (0.2%)
1	M	0.92	4/3683 (0.1%)	1.07	9/4957 (0.2%)
1	N	0.92	3/3683 (0.1%)	1.07	9/4957 (0.2%)
1	O	0.92	3/3683 (0.1%)	1.07	9/4957 (0.2%)
1	P	0.92	3/3683 (0.1%)	1.07	9/4957 (0.2%)
All	All	0.92	53/58927 (0.1%)	1.07	144/79310 (0.2%)

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	3
1	B	0	3
1	C	0	3
1	D	0	3
1	E	0	3
1	F	0	3
1	G	0	3
1	H	0	3
1	I	0	3

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
1	J	0	3
1	K	0	3
1	L	0	3
1	M	0	3
1	N	0	3
1	O	0	3
1	P	0	3
All	All	0	48

The worst 5 of 53 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	443	ALA	C-O	7.14	1.32	1.24
1	C	1425	ALA	C-O	7.10	1.32	1.24
1	E	2407	ALA	C-O	7.10	1.32	1.24
1	G	3389	ALA	C-O	7.10	1.32	1.24
1	H	3880	ALA	C-O	7.10	1.32	1.24

The worst 5 of 144 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	O	6878	GLU	CA-C-O	-12.62	106.18	120.70
1	D	1477	GLU	CA-C-O	-12.62	106.19	120.70
1	M	5896	GLU	CA-C-O	-12.62	106.19	120.70
1	F	2459	GLU	CA-C-O	-12.61	106.19	120.70
1	P	7369	GLU	CA-C-O	-12.61	106.20	120.70

There are no chirality outliers.

5 of 48 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	119	GLN	Mainchain
1	A	138	ALA	Mainchain
1	A	453	GLU	Mainchain
1	B	610	GLN	Mainchain
1	B	629	ALA	Mainchain

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	3661	0	3801	31	0
1	B	3662	0	3802	29	0
1	C	3662	0	3802	29	0
1	D	3662	0	3802	27	0
1	E	3662	0	3802	27	0
1	F	3662	0	3802	28	0
1	G	3662	0	3802	27	0
1	H	3662	0	3802	27	0
1	I	3662	0	3802	27	0
1	J	3662	0	3802	29	0
1	K	3662	0	3802	29	0
1	L	3662	0	3802	28	0
1	M	3662	0	3802	27	0
1	N	3662	0	3802	27	0
1	O	3662	0	3802	27	0
1	P	3662	0	3802	26	0
All	All	58591	0	60831	415	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 3.

The worst 5 of 415 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:L:5585:LYS:H	1:L:5585:LYS:HD2	1.31	0.96
1:C:1166:LYS:H	1:C:1166:LYS:HD2	1.31	0.96
1:D:1657:LYS:H	1:D:1657:LYS:HD2	1.31	0.95
1:M:6076:LYS:H	1:M:6076:LYS:HD2	1.31	0.95
1:H:3621:LYS:HD2	1:H:3621:LYS:H	1.31	0.95

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	489/491 (100%)	472 (96%)	16 (3%)	1 (0%)	43	78
1	B	489/491 (100%)	472 (96%)	16 (3%)	1 (0%)	43	78
1	C	489/491 (100%)	472 (96%)	16 (3%)	1 (0%)	43	78
1	D	489/491 (100%)	472 (96%)	16 (3%)	1 (0%)	43	78
1	E	489/491 (100%)	472 (96%)	16 (3%)	1 (0%)	43	78
1	F	489/491 (100%)	472 (96%)	16 (3%)	1 (0%)	43	78
1	G	489/491 (100%)	472 (96%)	16 (3%)	1 (0%)	43	78
1	H	489/491 (100%)	472 (96%)	16 (3%)	1 (0%)	43	78
1	I	489/491 (100%)	472 (96%)	16 (3%)	1 (0%)	43	78
1	J	489/491 (100%)	472 (96%)	16 (3%)	1 (0%)	43	78
1	K	489/491 (100%)	472 (96%)	16 (3%)	1 (0%)	43	78
1	L	489/491 (100%)	472 (96%)	16 (3%)	1 (0%)	43	78
1	M	489/491 (100%)	472 (96%)	16 (3%)	1 (0%)	43	78
1	N	489/491 (100%)	472 (96%)	16 (3%)	1 (0%)	43	78
1	O	489/491 (100%)	472 (96%)	16 (3%)	1 (0%)	43	78
1	P	489/491 (100%)	472 (96%)	16 (3%)	1 (0%)	43	78
All	All	7824/7856 (100%)	7552 (96%)	256 (3%)	16 (0%)	44	78

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	ASN
1	B	496	ASN
1	C	987	ASN
1	D	1478	ASN
1	E	1969	ASN

5.3.2 Protein sidechains ⓘ

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	391/392 (100%)	386 (99%)	5 (1%)	61	74
1	B	392/392 (100%)	387 (99%)	5 (1%)	61	74
1	C	392/392 (100%)	387 (99%)	5 (1%)	61	74
1	D	392/392 (100%)	387 (99%)	5 (1%)	61	74
1	E	392/392 (100%)	387 (99%)	5 (1%)	61	74
1	F	392/392 (100%)	387 (99%)	5 (1%)	61	74
1	G	392/392 (100%)	387 (99%)	5 (1%)	61	74
1	H	392/392 (100%)	387 (99%)	5 (1%)	61	74
1	I	392/392 (100%)	387 (99%)	5 (1%)	61	74
1	J	392/392 (100%)	387 (99%)	5 (1%)	61	74
1	K	392/392 (100%)	387 (99%)	5 (1%)	61	74
1	L	392/392 (100%)	387 (99%)	5 (1%)	61	74
1	M	392/392 (100%)	387 (99%)	5 (1%)	61	74
1	N	392/392 (100%)	387 (99%)	5 (1%)	61	74
1	O	392/392 (100%)	387 (99%)	5 (1%)	61	74
1	P	392/392 (100%)	387 (99%)	5 (1%)	61	74
All	All	6271/6272 (100%)	6191 (99%)	80 (1%)	59	74

5 of 80 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	5506	LEU
1	O	6974	LYS
1	L	5666	LEU
1	N	6403	LEU
1	P	7385	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	4368	ASN
1	L	5847	ASN
1	P	7811	ASN
1	O	7314	ASN
1	I	4374	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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.

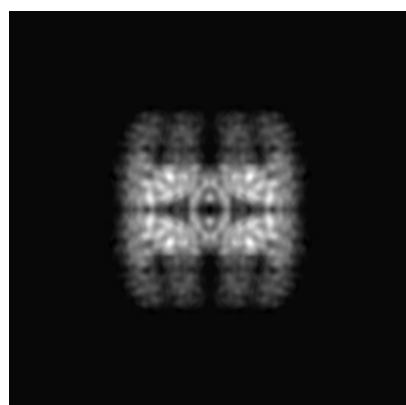
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5258. These allow visual inspection of the internal detail of the map and identification of artifacts.

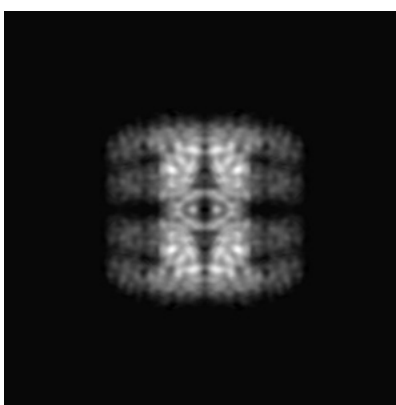
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

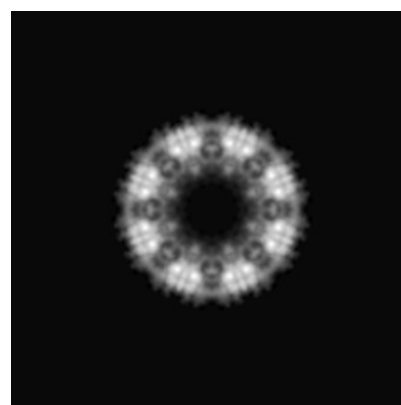
6.1.1 Primary map



X



Y

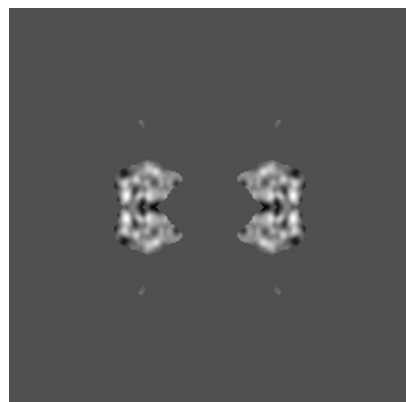


Z

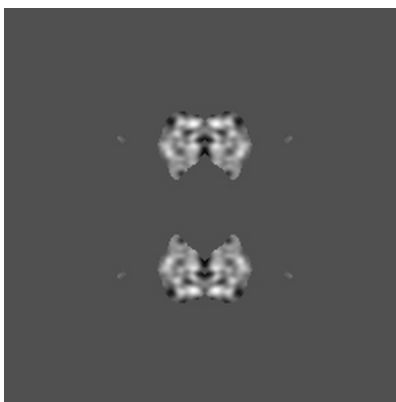
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

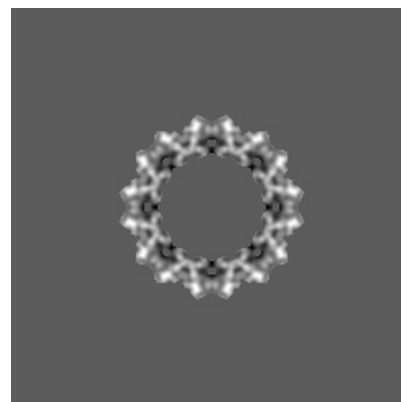
6.2.1 Primary map



X Index: 120



Y Index: 120

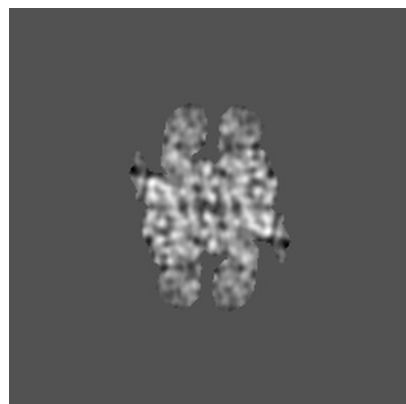


Z Index: 120

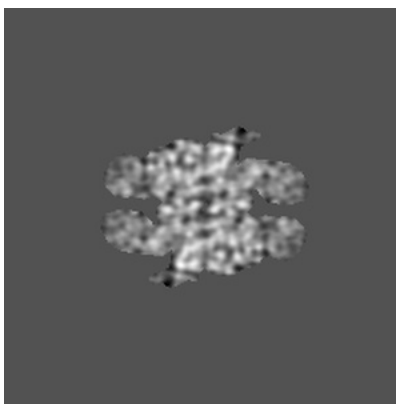
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 83



Y Index: 83

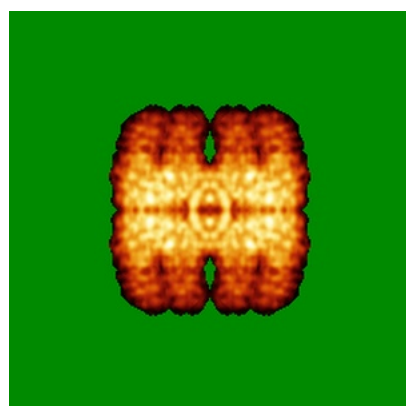


Z Index: 112

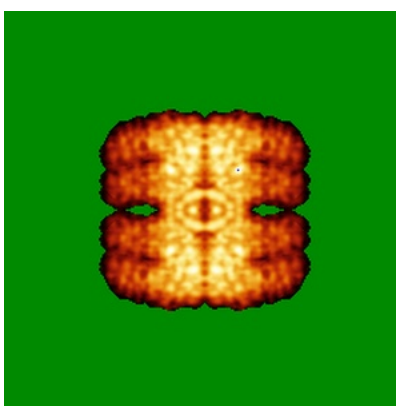
The images above show the largest variance slices of the map in three orthogonal directions.

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

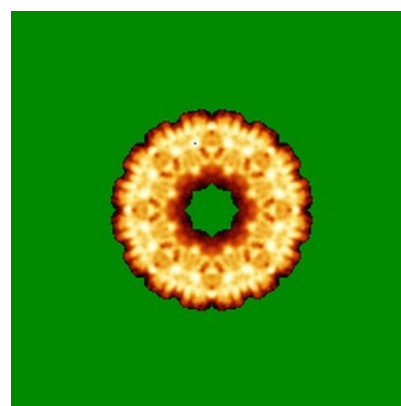
6.4.1 Primary map



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.

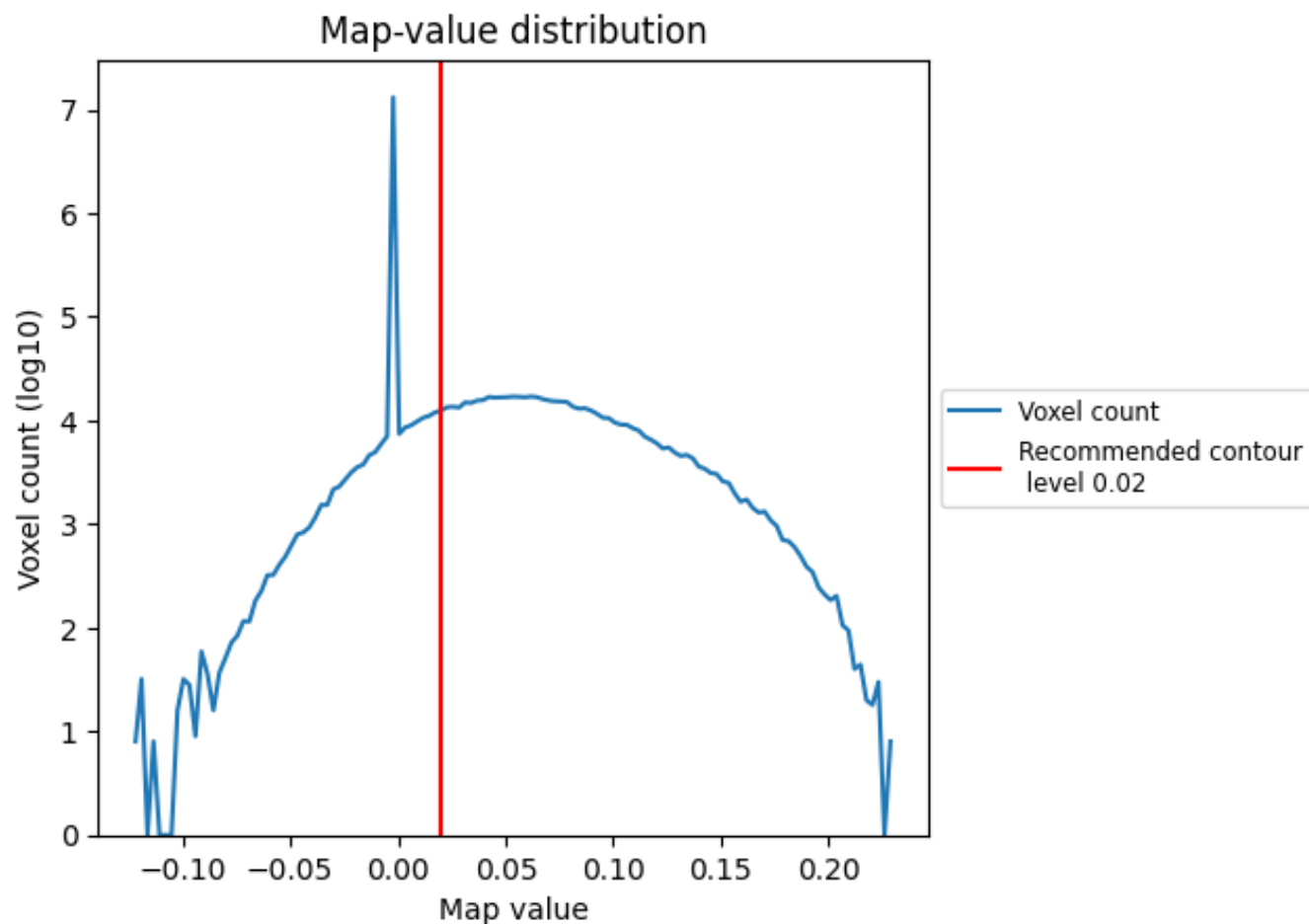
6.6 Mask visualisation

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

7 Map analysis [i](#)

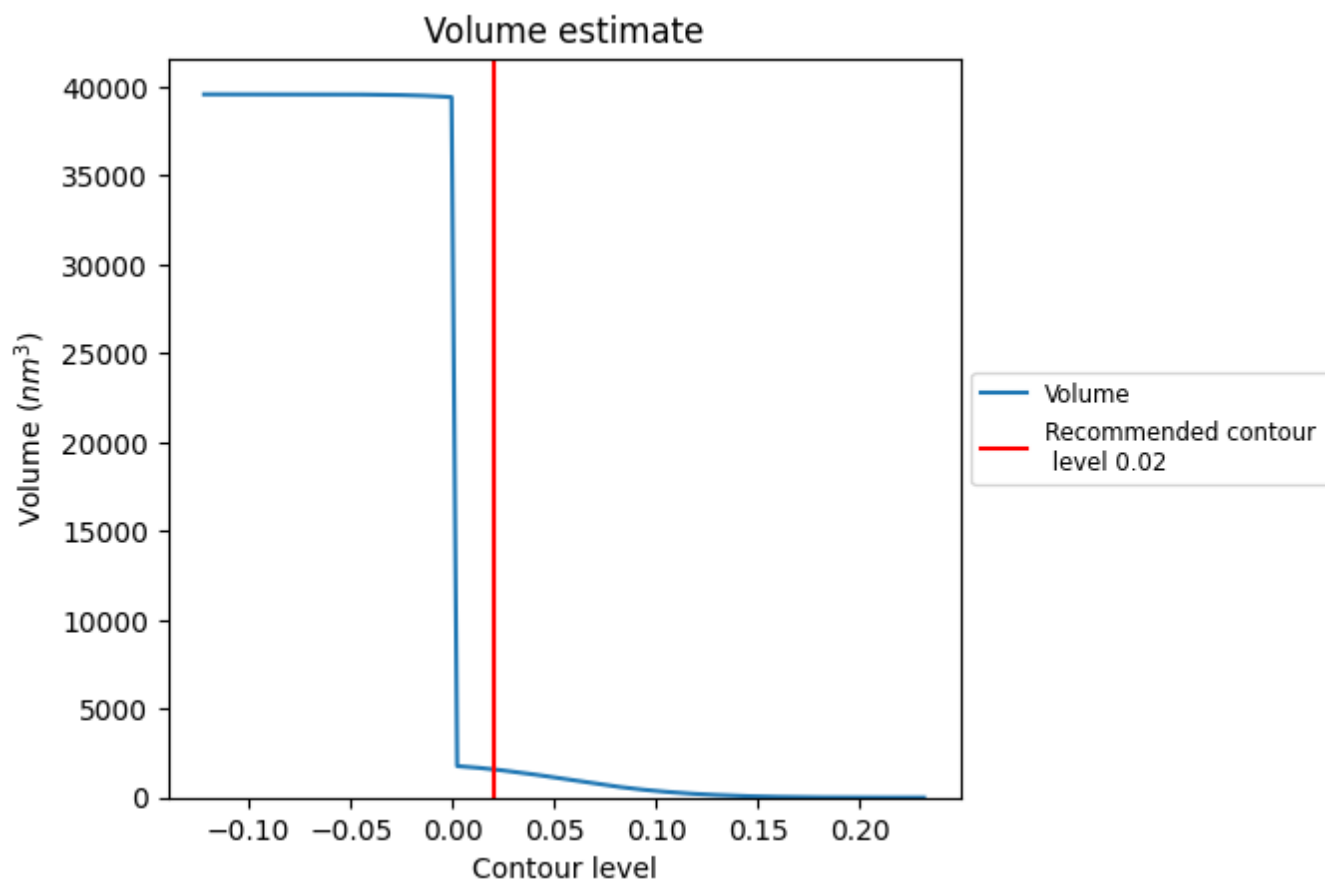
This section contains the results of statistical analysis of the map.

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.

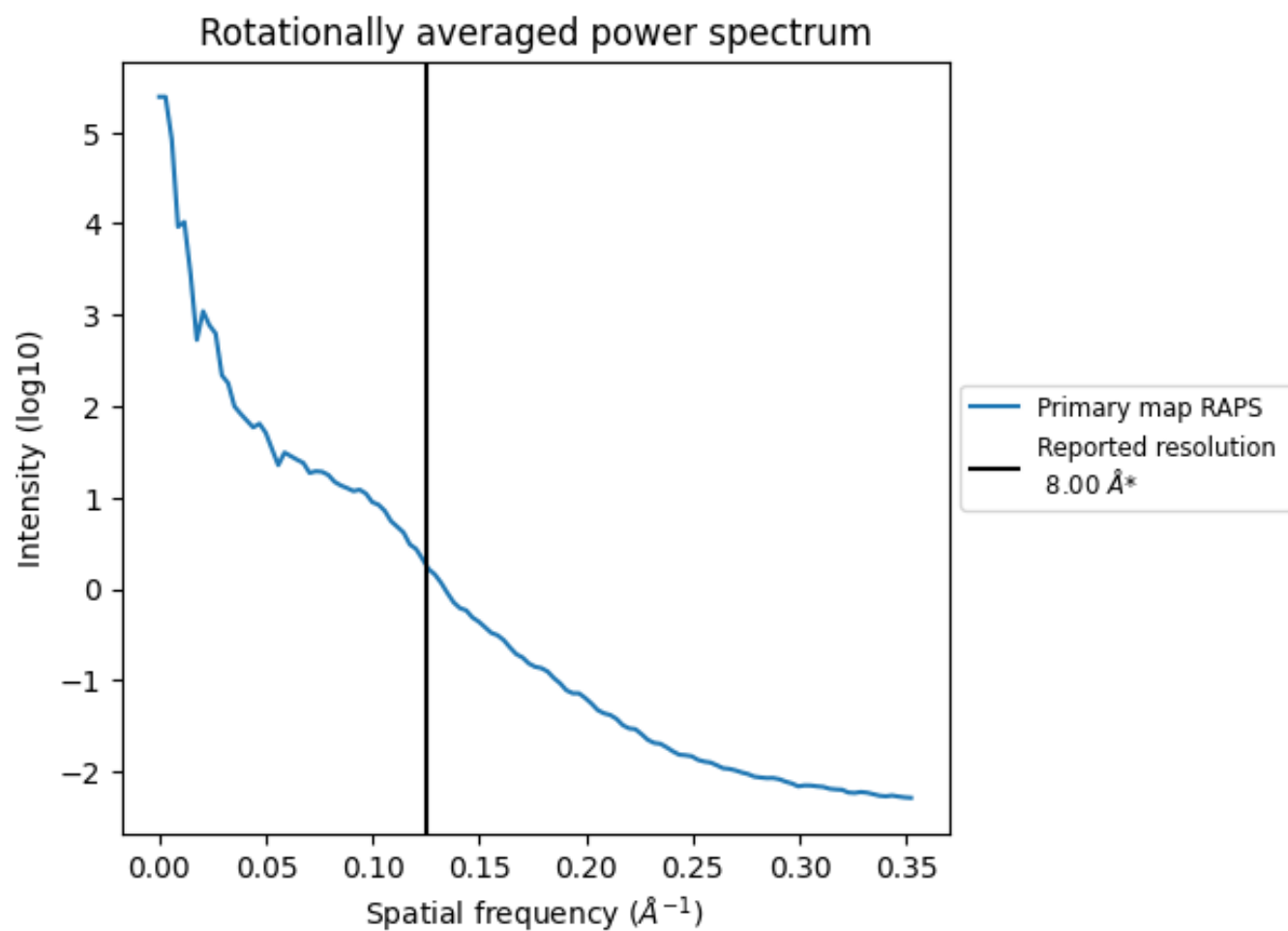
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1590 nm³; this corresponds to an approximate mass of 1437 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 0.125 Å⁻¹

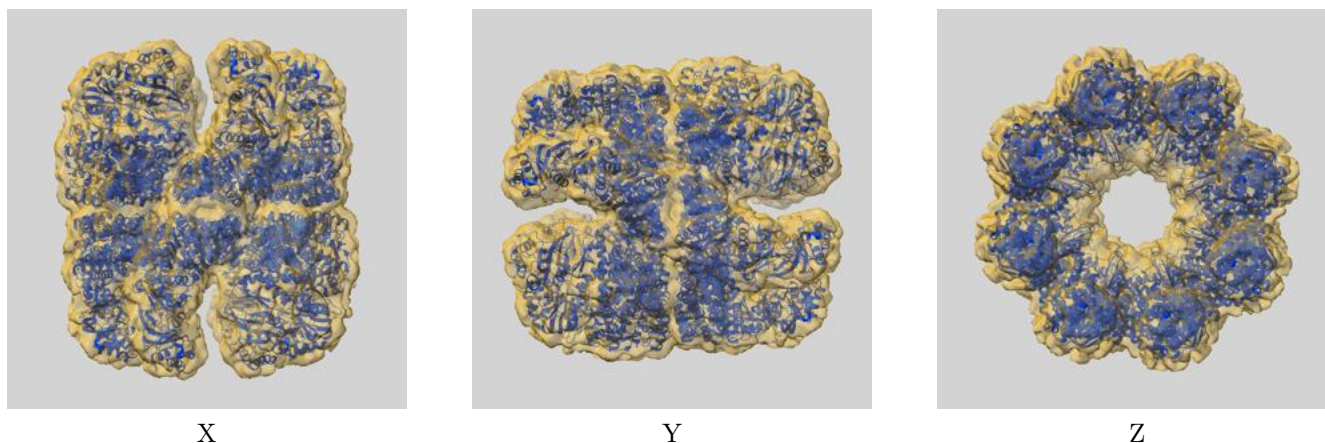
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

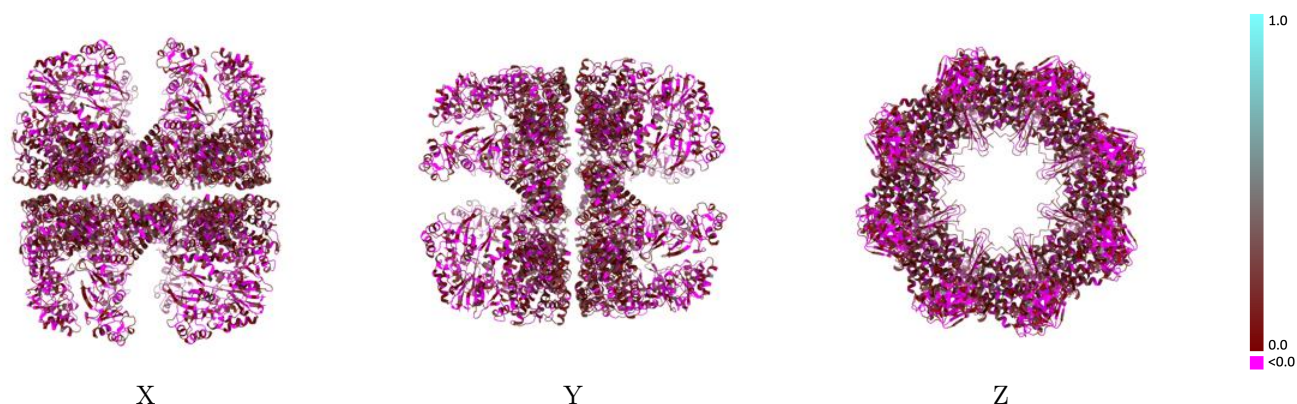
This section contains information regarding the fit between EMDB map EMD-5258 and PDB model 3J02. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.02 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](#)

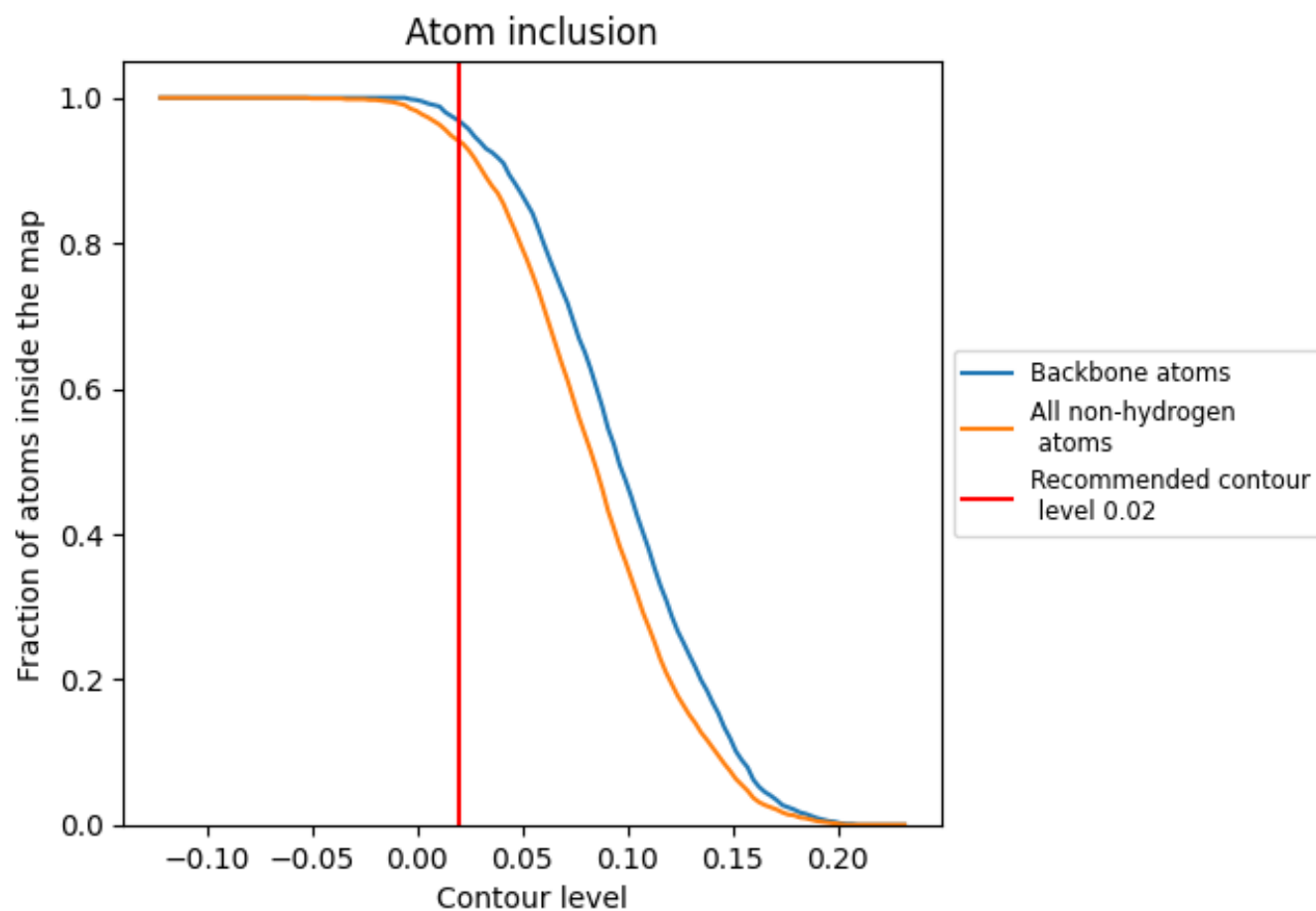


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 94% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9400	0.0790
A	0.9400	0.0790
B	0.9410	0.0790
C	0.9400	0.0790
D	0.9410	0.0790
E	0.9390	0.0800
F	0.9410	0.0790
G	0.9390	0.0800
H	0.9410	0.0790
I	0.9400	0.0780
J	0.9390	0.0780
K	0.9400	0.0790
L	0.9390	0.0790
M	0.9410	0.0790
N	0.9390	0.0790
O	0.9410	0.0790
P	0.9400	0.0780

1.0

0.0

<0.0