



wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Mar 2, 2017 – 11:25 am GMT

PDB ID : 3IZM
EMDB ID: : EMD-5249
Title : Mm-cpn wildtype with ATP
Authors : Douglas, N.R.; Reissmann, S.; Zhang, J.; Chen, B.; Jakana, J.; Kumar, R.;
Chiu, W.; Frydman, J.
Deposited on : 2010-10-30
Resolution : 7.20 Å(reported)

This is a wwPDB/EMDatabank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : recalc29047

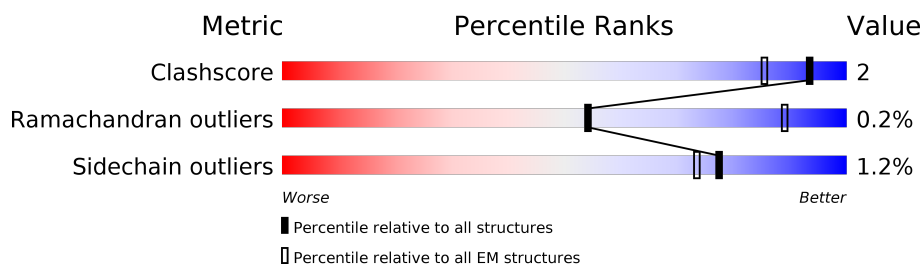
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.20 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)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	513	95% . .
1	B	513	95% . .
1	C	513	95% . .
1	D	513	96% . .
1	E	513	95% . .
1	F	513	96% . .
1	G	513	95% . .
1	H	513	95% . .
1	I	513	95% . .

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Mol	Chain	Length	Quality of chain
1	J	513	<div><div></div><div>95%</div><div></div></div> <div><div></div><div></div></div>
1	K	513	<div><div></div><div>95%</div><div></div></div> <div><div></div><div></div></div>
1	L	513	<div><div></div><div>95%</div><div></div></div> <div><div></div><div></div></div>
1	M	513	<div><div></div><div>95%</div><div></div></div> <div><div></div><div></div></div>
1	N	513	<div><div></div><div>96%</div><div></div></div> <div><div></div><div></div></div>
1	O	513	<div><div></div><div>95%</div><div></div></div> <div><div></div><div></div></div>
1	P	513	<div><div></div><div>96%</div><div></div></div> <div><div></div><div></div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 61632 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 Chaperonin.

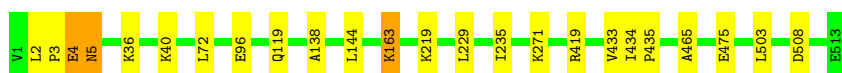
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	B	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	C	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	D	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	E	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	F	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	G	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	H	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	I	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	J	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	K	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	L	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	M	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	N	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	O	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	P	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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. 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. 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.

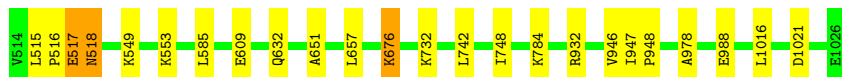
- Molecule 1: Chaperonin

Chain A: 



- Molecule 1: Chaperonin

Chain B: 



- Molecule 1: Chaperonin

Chain C: 



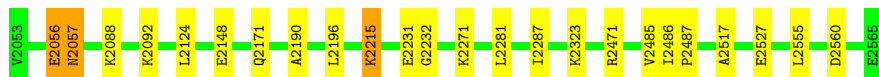
- Molecule 1: Chaperonin

Chain D: 



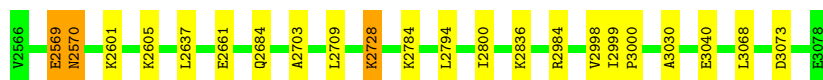
- Molecule 1: Chaperonin

Chain E: 



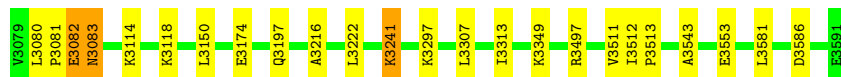
- Molecule 1: Chaperonin

Chain F: 



- Molecule 1: Chaperonin

Chain G: 95% ..



- Molecule 1: Chaperonin

Chain H: 95% ..



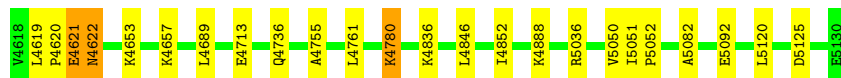
- Molecule 1: Chaperonin

Chain I: 95% ..



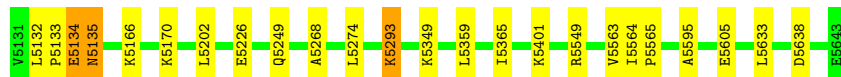
- Molecule 1: Chaperonin

Chain J: 95% ..



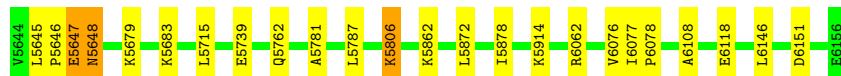
- Molecule 1: Chaperonin

Chain K: 95% ..



- Molecule 1: Chaperonin

Chain L: 95% ..



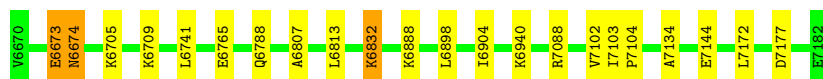
- Molecule 1: Chaperonin

Chain M: 95% ..



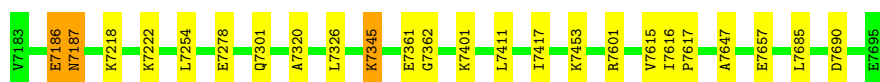
- Molecule 1: Chaperonin

Chain N:  96%



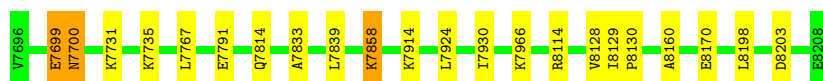
- Molecule 1: Chaperonin

Chain O:  95%



- Molecule 1: Chaperonin

Chain P:  96%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D	Depositor
Number of particles used	Not provided	Depositor
Resolution determination method	FSC at 0.5 cut-off	Depositor
CTF correction method	Not provided	Depositor
Microscope	JEM3200FSC	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Gatan 4Kx4K CCD camera	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 2$	RMSZ	$\# Z > 2$
1	A	0.88	2/3875 (0.1%)	0.78	2/5214 (0.0%)
1	B	0.88	2/3875 (0.1%)	0.78	2/5214 (0.0%)
1	C	0.88	2/3875 (0.1%)	0.78	2/5214 (0.0%)
1	D	0.88	2/3875 (0.1%)	0.78	2/5214 (0.0%)
1	E	0.88	2/3875 (0.1%)	0.78	2/5214 (0.0%)
1	F	0.88	2/3875 (0.1%)	0.78	2/5214 (0.0%)
1	G	0.88	2/3875 (0.1%)	0.78	2/5214 (0.0%)
1	H	0.88	2/3875 (0.1%)	0.78	2/5214 (0.0%)
1	I	0.88	2/3875 (0.1%)	0.78	2/5214 (0.0%)
1	J	0.88	2/3875 (0.1%)	0.78	2/5214 (0.0%)
1	K	0.88	2/3875 (0.1%)	0.78	2/5214 (0.0%)
1	L	0.88	2/3875 (0.1%)	0.78	2/5214 (0.0%)
1	M	0.88	2/3875 (0.1%)	0.78	2/5214 (0.0%)
1	N	0.88	2/3875 (0.1%)	0.78	2/5214 (0.0%)
1	O	0.88	2/3875 (0.1%)	0.78	2/5214 (0.0%)
1	P	0.88	2/3875 (0.1%)	0.78	2/5214 (0.0%)
All	All	0.88	32/62000 (0.1%)	0.78	32/83424 (0.0%)

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

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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 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	M	6160	GLU	C-O	-5.76	1.12	1.23
1	O	7186	GLU	C-O	-5.75	1.12	1.23
1	A	4	GLU	C-O	-5.72	1.12	1.23
1	C	1030	GLU	C-O	-5.72	1.12	1.23
1	E	2056	GLU	C-O	-5.72	1.12	1.23

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	229	LEU	CB-CG-CD2	-5.21	102.13	111.00
1	C	1255	LEU	CB-CG-CD2	-5.21	102.13	111.00
1	E	2281	LEU	CB-CG-CD2	-5.21	102.13	111.00
1	G	3307	LEU	CB-CG-CD2	-5.21	102.13	111.00
1	I	4333	LEU	CB-CG-CD2	-5.21	102.13	111.00

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	475	GLU	Mainchain
1	B	632	GLN	Mainchain
1	B	651	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	3852	0	3996	13	0
1	B	3852	0	3993	13	0
1	C	3852	0	3993	13	0
1	D	3852	0	3993	12	0
1	E	3852	0	3993	13	0
1	F	3852	0	3993	12	0
1	G	3852	0	3993	13	0
1	H	3852	0	3993	13	0
1	I	3852	0	3993	14	0
1	J	3852	0	3993	13	0
1	K	3852	0	3993	13	0
1	L	3852	0	3993	13	0
1	M	3852	0	3993	13	0
1	N	3852	0	3993	12	0
1	O	3852	0	3993	13	0
1	P	3852	0	3993	12	0
All	All	61632	0	63891	189	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.

The worst 5 of 189 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4:GLU:O	1:A:5:ASN:HB2	1.96	0.65
1:B:517:GLU:O	1:B:518:ASN:HB2	1.96	0.65
1:K:5134:GLU:O	1:K:5135:ASN:HB2	1.96	0.65
1:L:5647:GLU:O	1:L:5648:ASN:HB2	1.96	0.65
1:C:1030:GLU:O	1:C:1031:ASN:HB2	1.96	0.65

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	511/513 (100%)	497 (97%)	13 (2%)	1 (0%)	51	84
1	B	511/513 (100%)	497 (97%)	13 (2%)	1 (0%)	51	84
1	C	511/513 (100%)	497 (97%)	13 (2%)	1 (0%)	51	84
1	D	511/513 (100%)	497 (97%)	13 (2%)	1 (0%)	51	84
1	E	511/513 (100%)	497 (97%)	13 (2%)	1 (0%)	51	84
1	F	511/513 (100%)	497 (97%)	13 (2%)	1 (0%)	51	84
1	G	511/513 (100%)	497 (97%)	13 (2%)	1 (0%)	51	84
1	H	511/513 (100%)	497 (97%)	13 (2%)	1 (0%)	51	84
1	I	511/513 (100%)	497 (97%)	13 (2%)	1 (0%)	51	84
1	J	511/513 (100%)	497 (97%)	13 (2%)	1 (0%)	51	84
1	K	511/513 (100%)	497 (97%)	13 (2%)	1 (0%)	51	84
1	L	511/513 (100%)	497 (97%)	13 (2%)	1 (0%)	51	84
1	M	511/513 (100%)	497 (97%)	13 (2%)	1 (0%)	51	84
1	N	511/513 (100%)	497 (97%)	13 (2%)	1 (0%)	51	84
1	O	511/513 (100%)	497 (97%)	13 (2%)	1 (0%)	51	84
1	P	511/513 (100%)	497 (97%)	13 (2%)	1 (0%)	51	84
All	All	8176/8208 (100%)	7952 (97%)	208 (2%)	16 (0%)	54	84

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	ASN
1	B	518	ASN
1	C	1031	ASN
1	D	1544	ASN
1	E	2057	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	414/414 (100%)	409 (99%)	5 (1%)	75	88
1	B	414/414 (100%)	409 (99%)	5 (1%)	75	88
1	C	414/414 (100%)	409 (99%)	5 (1%)	75	88
1	D	414/414 (100%)	409 (99%)	5 (1%)	75	88
1	E	414/414 (100%)	409 (99%)	5 (1%)	75	88
1	F	414/414 (100%)	409 (99%)	5 (1%)	75	88
1	G	414/414 (100%)	409 (99%)	5 (1%)	75	88
1	H	414/414 (100%)	409 (99%)	5 (1%)	75	88
1	I	414/414 (100%)	409 (99%)	5 (1%)	75	88
1	J	414/414 (100%)	409 (99%)	5 (1%)	75	88
1	K	414/414 (100%)	409 (99%)	5 (1%)	75	88
1	L	414/414 (100%)	409 (99%)	5 (1%)	75	88
1	M	414/414 (100%)	409 (99%)	5 (1%)	75	88
1	N	414/414 (100%)	409 (99%)	5 (1%)	75	88
1	O	414/414 (100%)	409 (99%)	5 (1%)	75	88
1	P	414/414 (100%)	409 (99%)	5 (1%)	75	88
All	All	6624/6624 (100%)	6544 (99%)	80 (1%)	77	88

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

Mol	Chain	Res	Type
1	H	3663	LEU
1	I	4523	ARG
1	O	7345	LYS
1	H	3735	LEU
1	I	4140	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	3609	ASN
1	J	4635	ASN
1	O	7261	GLN
1	H	3670	GLN
1	I	4122	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.