wwPDB EM Map/Model Validation Report (i)

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PDB ID	:	3C9V
EMDB ID:	:	EMD-5002
Title	:	C7 Symmetrized Structure of Unliganded GroEL at 4.7 Angstrom Resolution from CryoEM
Authors	:	Ludtke, S.J.; Baker, M.L.; Chen, D.H.; Song, J.L.; Chuang, D.; Chiu, W.
Deposited on	:	2008-02-18
Resolution	:	4.70 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could
stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/EMValidationReportHelp

MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk27241

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 4.70 Å.

There are no percentiles available for this entry.

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	526	100%
1	B	526	100%
1	C	526	100%
1	D	526	100%
1	E	526	100%
1	F	526	100%
1	G	526	100%
1	H	526	100%
1	I	526	100%
1	J	526	100%
1	K	526	100%
1	L	526	100%
1	M	526	100%
1	N	526	100%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 7364 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 60 kDa chaperonin.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
1	A	526	526	526	0	526
1	B	526	526	526	0	526
1	C	526	526	526	0	526
1	D	526	526	526	0	526
1	E	526	526	526	0	526
1	F	526	526	526	0	526
1	G	526	526	526	0	526
1	H	526	526	526	0	526
1	I	526	526	526	0	526
1	J	526	526	526	0	526
1	K	526	526	526	0	526
1	L	526	526	526	0	526
1	M	526	526	526	0	526
1	N	526	526	526	0	526

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: 60 kDa chaperonin

Chain A: 100%

There are no outlier residues recorded for this chain.

- Molecule 1: 60 kDa chaperonin

Chain B: 100%

There are no outlier residues recorded for this chain.

- Molecule 1: 60 kDa chaperonin

Chain C: 100%

There are no outlier residues recorded for this chain.

- Molecule 1: 60 kDa chaperonin

Chain D: 100%

There are no outlier residues recorded for this chain.

- Molecule 1: 60 kDa chaperonin

Chain E: 100%

There are no outlier residues recorded for this chain.

- Molecule 1: 60 kDa chaperonin

Chain F: 100%

There are no outlier residues recorded for this chain.

- Molecule 1: 60 kDa chaperonin

Chain G: 100%

There are no outlier residues recorded for this chain.

- Molecule 1: 60 kDa chaperonin

Chain H: 100%

There are no outlier residues recorded for this chain.

- Molecule 1: 60 kDa chaperonin

Chain I: 100%

There are no outlier residues recorded for this chain.

- Molecule 1: 60 kDa chaperonin

Chain J: 100%

There are no outlier residues recorded for this chain.

- Molecule 1: 60 kDa chaperonin

Chain K: 100%

There are no outlier residues recorded for this chain.

- Molecule 1: 60 kDa chaperonin

Chain L: 100%

There are no outlier residues recorded for this chain.

- Molecule 1: 60 kDa chaperonin

Chain M: 100%

There are no outlier residues recorded for this chain.

- Molecule 1: 60 kDa chaperonin

Chain N: 100%

There are no outlier residues recorded for this chain.

4 Experimental information (i)

Property	Value	Source
Reconstruction method	Not provided	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	per micrograph	Depositor
Microscope	JEOL 3200SFF	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	36	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	60000	Depositor
Image detector	Kodak SO163 film	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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	526	0	0	0	0
1	B	526	0	0	0	0
1	C	526	0	0	0	0
1	D	526	0	0	0	0
1	E	526	0	0	0	0
1	F	526	0	0	0	0
1	G	526	0	0	0	0
1	H	526	0	0	0	0
1	I	526	0	0	0	0
1	J	526	0	0	0	0
1	K	526	0	0	0	0
1	L	526	0	0	0	0
1	M	526	0	0	0	0
1	N	526	0	0	0	0
All	All	7364	0	0	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

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)

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 carbohydrates 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.