wwPDB EM Map/Model Validation Report (i)

Apr 10, 2016 – 01:48 PM BST

PDB ID	:	3J4A
EMDB ID:	:	EMD-5690
Title	:	Structure of gp8 connector protein
Authors	:	Cuervo, A.; Pulido-Cid, M.; Chagoyen, M.; Arranz, R.; Gonzalez-Garcia, V.A.; Garcia-Doval, C.; Caston, J.R.; Valpuesta, J.M.; van Raaij, M.J.; Martin-Benito, J.; Carrascosa, J.L.
Deposited on	:	2013-07-09
Resolution	:	12.00 Å(reported)
Based on PDB ID	:	3LJ5

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

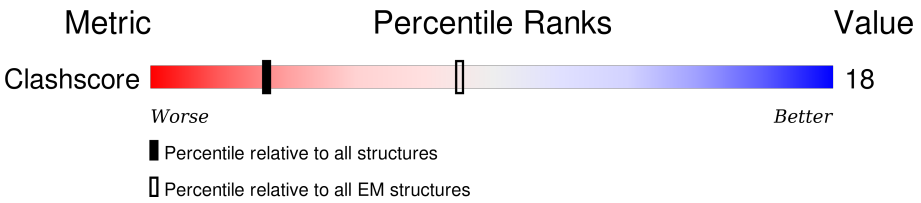
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk27241

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 12.00 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)
Clashscore	114402	924

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	497	97% .
1	B	497	97% .
1	C	497	97% .
1	D	497	97% .
1	E	497	97% .
1	F	497	97% .
1	G	497	97% .
1	H	497	97% .
1	I	497	97% .
1	J	497	97% .
1	K	497	97% .

Continued on next page...

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Mol	Chain	Length	Quality of chain
1	L	497	97%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 5964 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 Head-to-tail joining protein.

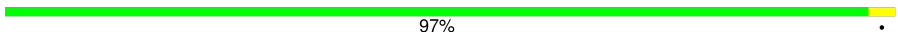
Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
1	A	497	497	497	0	497
1	J	497	497	497	0	497
1	K	497	497	497	0	497
1	L	497	497	497	0	497
1	B	497	497	497	0	497
1	C	497	497	497	0	497
1	D	497	497	497	0	497
1	E	497	497	497	0	497
1	F	497	497	497	0	497
1	G	497	497	497	0	497
1	H	497	497	497	0	497
1	I	497	497	497	0	497

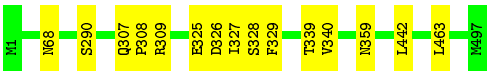
3 Residue-property plots (i)

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: Head-to-tail joining protein

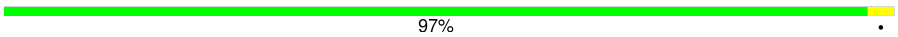
Chain A:

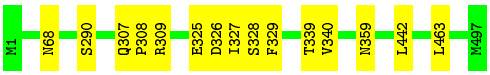




- Molecule 1: Head-to-tail joining protein

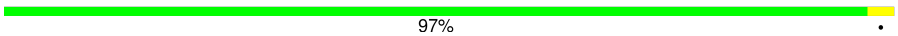
Chain J:





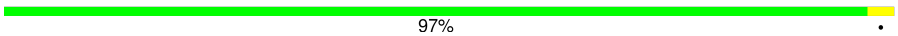
- Molecule 1: Head-to-tail joining protein

Chain K:



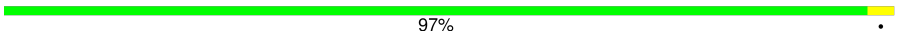
- Molecule 1: Head-to-tail joining protein

Chain L:



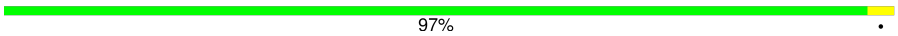
- Molecule 1: Head-to-tail joining protein

Chain B:



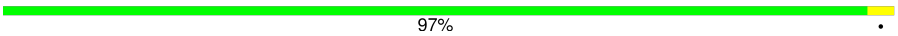
- Molecule 1: Head-to-tail joining protein

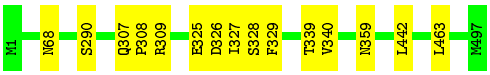
Chain C:



- Molecule 1: Head-to-tail joining protein

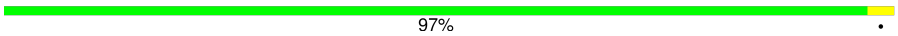
Chain D:

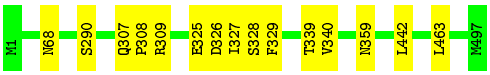




- Molecule 1: Head-to-tail joining protein

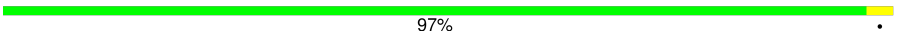
Chain E:

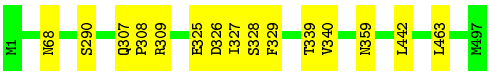




- Molecule 1: Head-to-tail joining protein

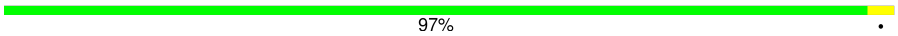
Chain F:

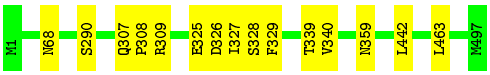




- Molecule 1: Head-to-tail joining protein

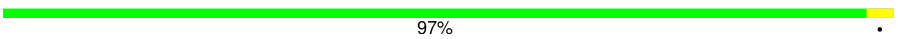
Chain G:

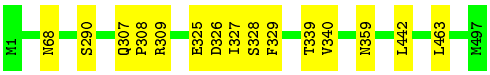




- Molecule 1: Head-to-tail joining protein

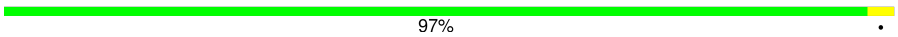
Chain H:

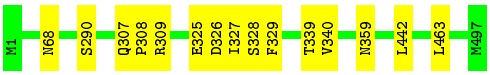




- Molecule 1: Head-to-tail joining protein

Chain I:





4 Experimental information (i)

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	1820	Depositor
Resolution determination method	FSC at 0.3 cut-off.	Depositor
CTF correction method	each micrograph	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	10	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	108696	Depositor
Image detector	4kx4k Eagle CCD camera (Gatan Inc.)	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	497	0	0	18	0
1	B	497	0	0	18	0
1	C	497	0	0	18	0
1	D	497	0	0	18	0
1	E	497	0	0	18	0
1	F	497	0	0	18	0
1	G	497	0	0	18	0
1	H	497	0	0	18	0
1	I	497	0	0	18	0
1	J	497	0	0	18	0
1	K	497	0	0	18	0
1	L	497	0	0	18	0
All	All	5964	0	0	108	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 18.

The worst 5 of 108 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:C:307:GLN:CA	1:D:326:ASP:CA	1.84	1.55
1:B:307:GLN:CA	1:C:326:ASP:CA	1.84	1.55
1:A:307:GLN:CA	1:B:326:ASP:CA	1.84	1.55
1:D:307:GLN:CA	1:E:326:ASP:CA	1.84	1.55
1:E:307:GLN:CA	1:F:326:ASP:CA	1.84	1.54

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.