



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Jan 1, 2018 – 11:52 AM EST

PDB ID : 4CC8
EMDB ID: : EMD-2484
Title : Pre-fusion structure of trimeric HIV-1 envelope glycoprotein determined by
cryo-electron microscopy
Authors : Bartesaghi, A.; Merk, A.; Borgnia, M.J.; Milne, J.L.S.; Subramaniam, S.
Deposited on : 2013-10-18
Resolution : 6.00 Å(reported)
Based on PDB ID : 3HMG, 3SE8

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) : rb-20030736

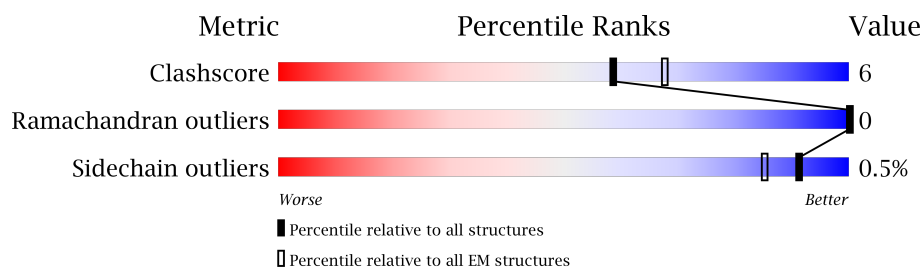
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.00 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	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	31	100%
1	B	31	100%
1	C	31	100%
2	D	344	91% 9%
2	E	344	91% 9%
2	G	344	90% 10%
3	F	233	85% 12% .
3	H	233	85% 12% .
3	I	233	85% 12% .

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Mol	Chain	Length	Quality of chain
4	J	209	<div><div></div><div>96%</div><div>.</div></div>
4	K	209	<div><div></div><div>95%</div><div>5%</div></div>
4	L	209	<div><div></div><div>95%</div><div>5%</div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 36195 atoms, of which 17649 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 GP41.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	31	Total	C	N	O	0	0
			124	62	31	31		
1	B	31	Total	C	N	O	0	0
			124	62	31	31		
1	C	31	Total	C	N	O	0	0
			124	62	31	31		

- Molecule 2 is a protein called GP120.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	D	344	Total	C	H	N	O	S	0	0
			5310	1689	2617	469	512	23		
2	E	344	Total	C	H	N	O	S	0	0
			5310	1689	2617	469	512	23		
2	G	344	Total	C	H	N	O	S	0	0
			5310	1689	2617	469	512	23		

- Molecule 3 is a protein called MONOCLONAL ANTIBODY VRC03 FAB HEAVY CHAIN.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	F	227	Total	C	H	N	O	S	0	0
			3423	1109	1686	292	328	8		
3	H	227	Total	C	H	N	O	S	0	0
			3423	1109	1686	292	328	8		
3	I	227	Total	C	H	N	O	S	0	0
			3423	1109	1686	292	328	8		

- Molecule 4 is a protein called MONOCLONAL ANTIBODY VRC03 FAB LIGHT CHAIN.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	J	208	Total	C	H	N	O	S	1	0
			3208	1026	1580	276	321	5		

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Mol	Chain	Residues	Atoms						AltConf	Trace
4	K	208	Total	C	H	N	O	S	1	0
			3208	1026	1580	276	321	5		
4	L	208	Total	C	H	N	O	S	1	0
			3208	1026	1580	276	321	5		

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: GP41

Chain A:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: GP41

Chain B:  100%

There are no outlier residues recorded for this chain.

- Molecule 1: GP41

Chain C:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: GP120

Chain D:  91% 9%



- Molecule 2: GP120

Chain E:  91% 9%




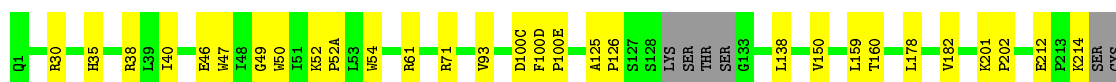
- Molecule 2: GP120

Chain G:  90% 10%



- Molecule 3: MONOCLONAL ANTIBODY VRC03 FAB HEAVY CHAIN

Chain F:  85% 12%



- Molecule 3: MONOCLONAL ANTIBODY VRC03 FAB HEAVY CHAIN

Chain H: 85% 12%



- Molecule 3: MONOCLONAL ANTIBODY VRC03 FAB HEAVY CHAIN

Chain I: 85% 12%



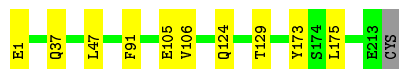
- Molecule 4: MONOCLONAL ANTIBODY VRC03 FAB LIGHT CHAIN

Chain J: 96%



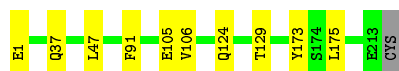
- Molecule 4: MONOCLONAL ANTIBODY VRC03 FAB LIGHT CHAIN

Chain K: 95% 5%



- Molecule 4: MONOCLONAL ANTIBODY VRC03 FAB LIGHT CHAIN

Chain L: 95% 5%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	88125	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	80	Depositor
Electron dose ($e^-/\text{\AA}^2$)	10	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	75000	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	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 >2	RMSZ	# Z >2
3	F	0.33	0/1788	0.52	0/2441
3	H	0.32	0/1788	0.52	0/2441
3	I	0.33	0/1788	0.52	0/2441
4	J	0.34	0/1669	0.51	0/2260
4	K	0.34	0/1669	0.51	0/2260
4	L	0.34	0/1669	0.51	0/2260
All	All	0.33	0/10371	0.51	0/14103

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

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	124	0	2	0	0
1	B	124	0	2	0	0
1	C	124	0	2	0	0
2	D	2693	2617	916	36	0
2	E	2693	2617	916	36	0
2	G	2693	2617	916	38	0
3	F	1737	1686	1682	30	0
3	H	1737	1686	1682	29	0
3	I	1737	1686	1682	31	0
4	J	1628	1580	1577	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	K	1628	1580	1577	12	0
4	L	1628	1580	1577	12	0
All	All	18546	17649	12531	174	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 6.

The worst 5 of 174 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)
2:D:279:UNK:ND2	3:F:100(C):ASP:OD2	1.65	1.27
2:E:279:UNK:ND2	3:H:100(C):ASP:OD2	1.66	1.26
2:G:279:UNK:ND2	3:I:100(C):ASP:OD2	1.67	1.24
2:D:280:UNK:OD1	3:F:50:TRP:NE1	1.85	1.09
2:E:280:UNK:OD1	3:H:50:TRP:NE1	1.87	1.05

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	
3	F	223/233 (96%)	219 (98%)	4 (2%)	0	100	100
3	H	223/233 (96%)	220 (99%)	3 (1%)	0	100	100
3	I	223/233 (96%)	219 (98%)	4 (2%)	0	100	100
4	J	207/209 (99%)	202 (98%)	5 (2%)	0	100	100
4	K	207/209 (99%)	202 (98%)	5 (2%)	0	100	100
4	L	207/209 (99%)	202 (98%)	5 (2%)	0	100	100
All	All	1290/1326 (97%)	1264 (98%)	26 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	
3	F	193/200 (96%)	191 (99%)	2 (1%)	80	90
3	H	193/200 (96%)	191 (99%)	2 (1%)	80	90
3	I	193/200 (96%)	191 (99%)	2 (1%)	80	90
4	J	182/182 (100%)	182 (100%)	0	100	100
4	K	182/182 (100%)	182 (100%)	0	100	100
4	L	182/182 (100%)	182 (100%)	0	100	100
All	All	1125/1146 (98%)	1119 (100%)	6 (0%)	91	95

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	H	71	ARG
3	I	212	GLU
3	H	212	GLU
3	F	212	GLU
3	I	71	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
4	J	90	GLN
4	K	90	GLN
4	L	90	GLN

5.3.3 RNA ⓘ

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	G	2
2	D	2
2	E	2

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	301:UNK	C	325:UNK	N	5.84
1	E	301:UNK	C	325:UNK	N	5.84
1	G	301:UNK	C	325:UNK	N	5.84
1	D	398:UNK	C	407:UNK	N	4.22
1	E	398:UNK	C	407:UNK	N	4.22