



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Jun 26, 2017 – 08:42 PM EDT

PDB ID : 5XJY
EMDB ID: : EMD-6724
Title : Cryo-EM structure of human ABCA1
Authors : Qian, H.W.; Yan, N.; Gong, X.
Deposited on : 2017-05-04
Resolution : 4.10 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
Mogul : 1.7.2 (RC1), CSD as538be (2017)
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-20029077

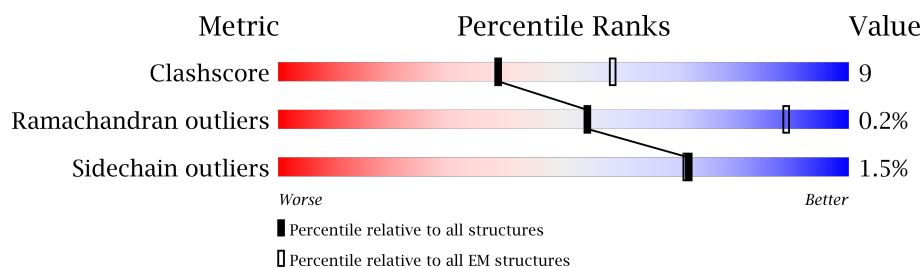
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.10 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	2305	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12785 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 ATP-binding cassette sub-family A member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1901	Total	C	N	O	S	0	0
			12626	8005	2236	2328	57		

There are 44 discrepancies between the modelled and reference sequences:

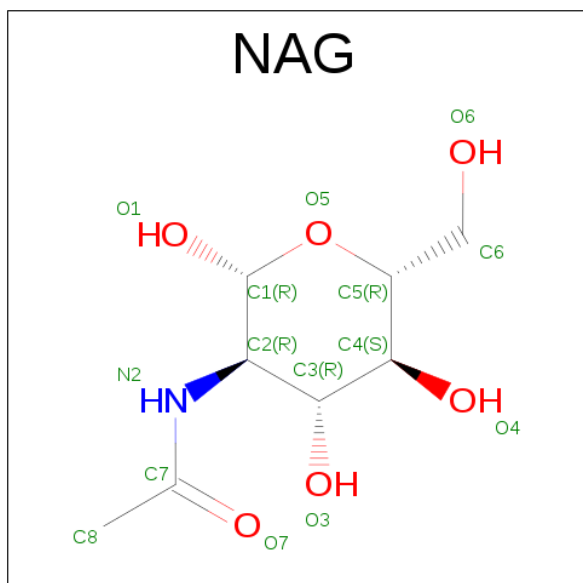
Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	expression tag	UNP O95477
A	-19	ALA	-	expression tag	UNP O95477
A	-18	ASP	-	expression tag	UNP O95477
A	-17	TYR	-	expression tag	UNP O95477
A	-16	LYS	-	expression tag	UNP O95477
A	-15	ASP	-	expression tag	UNP O95477
A	-14	ASP	-	expression tag	UNP O95477
A	-13	ASP	-	expression tag	UNP O95477
A	-12	ASP	-	expression tag	UNP O95477
A	-11	LYS	-	expression tag	UNP O95477
A	-10	SER	-	expression tag	UNP O95477
A	-9	GLY	-	expression tag	UNP O95477
A	-8	PRO	-	expression tag	UNP O95477
A	-7	ASP	-	expression tag	UNP O95477
A	-6	GLU	-	expression tag	UNP O95477
A	-5	VAL	-	expression tag	UNP O95477
A	-4	ASP	-	expression tag	UNP O95477
A	-3	ALA	-	expression tag	UNP O95477
A	-2	SER	-	expression tag	UNP O95477
A	-1	GLY	-	expression tag	UNP O95477
A	0	ARG	-	expression tag	UNP O95477
A	2262	LEU	-	expression tag	UNP O95477
A	2263	GLU	-	expression tag	UNP O95477
A	2264	GLY	-	expression tag	UNP O95477
A	2265	SER	-	expression tag	UNP O95477
A	2266	ASP	-	expression tag	UNP O95477
A	2267	GLU	-	expression tag	UNP O95477
A	2268	VAL	-	expression tag	UNP O95477

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Chain	Residue	Modelled	Actual	Comment	Reference
A	2269	ASP	-	expression tag	UNP O95477
A	2270	ALA	-	expression tag	UNP O95477
A	2271	VAL	-	expression tag	UNP O95477
A	2272	GLU	-	expression tag	UNP O95477
A	2273	GLY	-	expression tag	UNP O95477
A	2274	SER	-	expression tag	UNP O95477
A	2275	HIS	-	expression tag	UNP O95477
A	2276	HIS	-	expression tag	UNP O95477
A	2277	HIS	-	expression tag	UNP O95477
A	2278	HIS	-	expression tag	UNP O95477
A	2279	HIS	-	expression tag	UNP O95477
A	2280	HIS	-	expression tag	UNP O95477
A	2281	HIS	-	expression tag	UNP O95477
A	2282	HIS	-	expression tag	UNP O95477
A	2283	HIS	-	expression tag	UNP O95477
A	2284	HIS	-	expression tag	UNP O95477

- Molecule 2 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



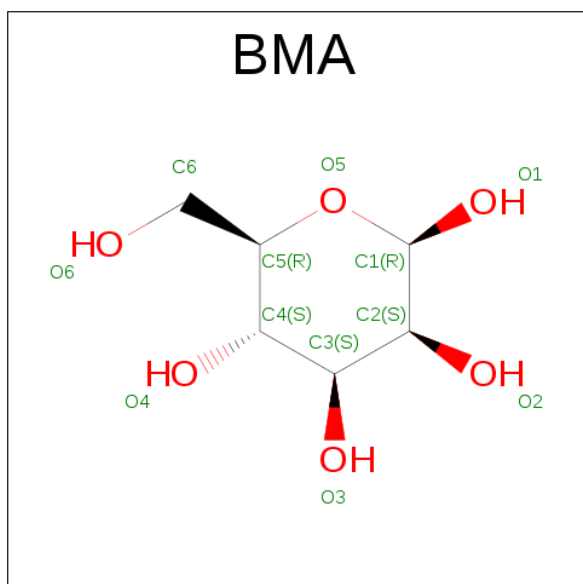
Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	N	O	0
			126	72	9	45	
2	A	1	Total	C	N	O	0
			126	72	9	45	
2	A	1	Total	C	N	O	0
			126	72	9	45	

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Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	N	O	0
			126	72	9	45	
2	A	1	Total	C	N	O	0
			126	72	9	45	
2	A	1	Total	C	N	O	0
			126	72	9	45	
2	A	1	Total	C	N	O	0
			126	72	9	45	
2	A	1	Total	C	N	O	0
			126	72	9	45	

- Molecule 3 is BETA-D-MANNOSE (three-letter code: BMA) (formula: $C_6H_{12}O_6$).

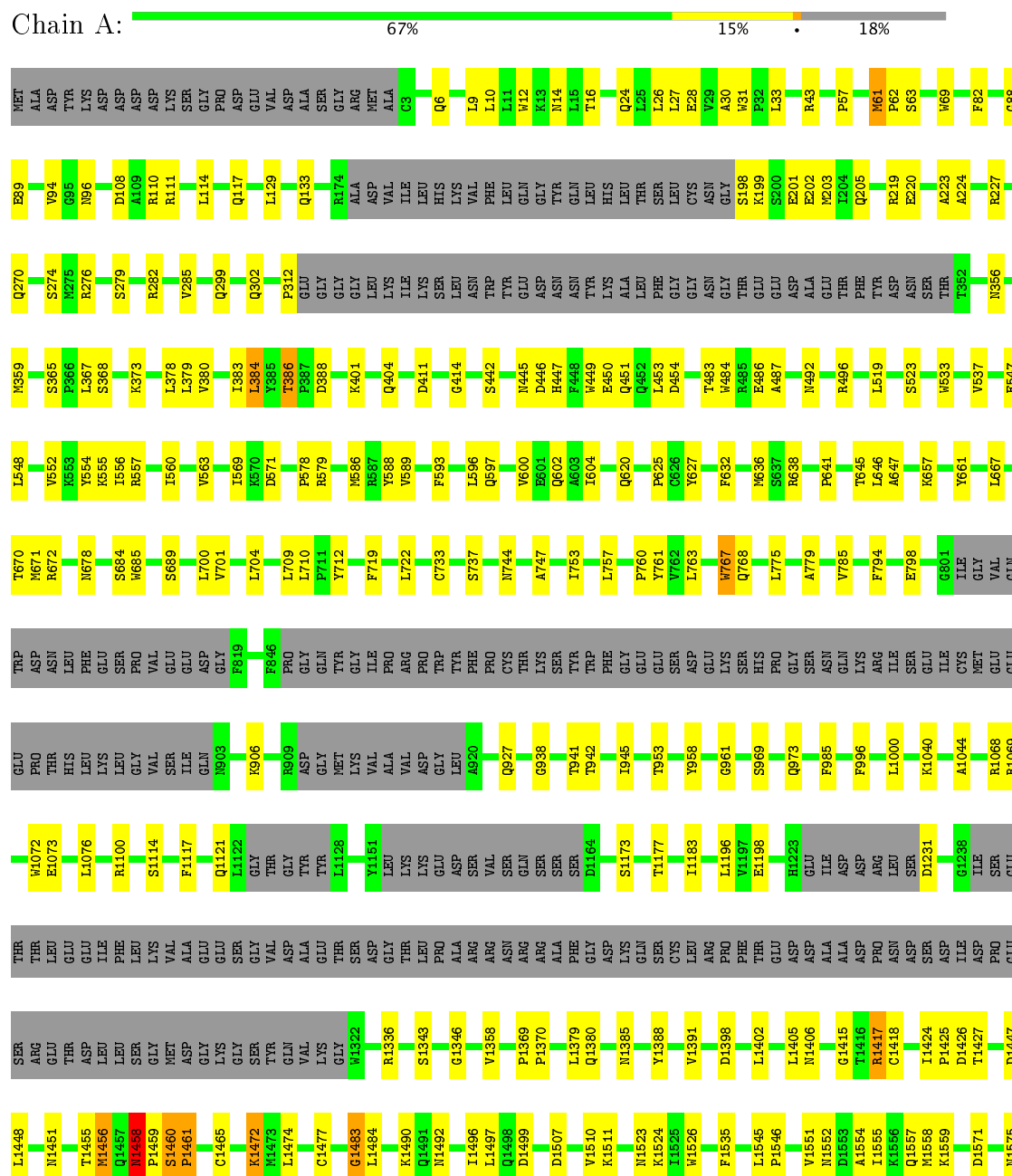


Mol	Chain	Residues	Atoms			AltConf
3	A	1	Total	C	O	0
			33	18	15	
3	A	1	Total	C	O	0
			33	18	15	
3	A	1	Total	C	O	0
			33	18	15	

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: ATP-binding cassette sub-family A member 1






4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	790156	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	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	Not provided	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, NAG

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	0.49	0/12840	0.69	9/17577 (0.1%)

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	15

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	1636	LEU	CA-CB-CG	8.43	134.69	115.30
1	A	367	LEU	CA-CB-CG	6.60	130.48	115.30
1	A	1497	LEU	CA-CB-CG	5.95	128.99	115.30
1	A	569	ILE	CG1-CB-CG2	-5.88	98.46	111.40
1	A	1815	LEU	CA-CB-CG	5.63	128.25	115.30

There are no chirality outliers.

5 of 15 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	384	LEU	Peptide
1	A	386	THR	Peptide
1	A	586	MET	Peptide
1	A	589	VAL	Peptide
1	A	94	VAL	Peptide

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	12626	0	10430	213	0
2	A	126	0	114	0	0
3	A	33	0	28	0	0
All	All	12785	0	10572	213	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 9.

The worst 5 of 213 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:1817:ARG:O	1:A:1821:ASP:HB2	1.80	0.81
1:A:1816:GLY:O	1:A:1820:ILE:HB	1.83	0.79
1:A:1402:LEU:O	1:A:1406:ASN:HB2	1.86	0.76
1:A:1685:LYS:O	1:A:1689:PHE:HB2	1.86	0.75
1:A:1461:PRO:HB3	1:A:1483:GLY:H	1.53	0.73

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	1869/2305 (81%)	1603 (86%)	263 (14%)	3 (0%)	51 84

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2017	PRO
1	A	1461	PRO
1	A	1459	PRO

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	943/2027 (46%)	929 (98%)	14 (2%)	70 86

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	638	ARG
1	A	767	TRP
1	A	1472	LYS
1	A	533	TRP
1	A	1458	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1458	ASN
1	A	1523	ASN
1	A	1610	ASN
1	A	1450	GLN
1	A	1607	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 ⓘ

12 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	A	2301	1	14,14,15	0.48	0	15,19,21	0.77	1 (6%)
2	NAG	A	2302	1	14,14,15	0.24	0	15,19,21	0.54	0
2	NAG	A	2303	1	14,14,15	0.24	0	15,19,21	0.41	0
2	NAG	A	2304	1	14,14,15	0.30	0	15,19,21	0.49	0
2	NAG	A	2305	1	14,14,15	0.82	2 (14%)	15,19,21	0.87	1 (6%)
2	NAG	A	2306	1,2	14,14,15	0.82	1 (7%)	15,19,21	0.70	0
2	NAG	A	2307	3,2	14,14,15	0.71	1 (7%)	15,19,21	1.21	2 (13%)
3	BMA	A	2308	3,2	11,11,12	0.61	0	13,15,17	0.83	1 (7%)
3	BMA	A	2309	3	11,11,12	0.70	0	13,15,17	0.86	0
3	BMA	A	2310	3	11,11,12	0.90	0	13,15,17	1.00	0
2	NAG	A	2311	1,2	14,14,15	0.37	0	15,19,21	0.83	0
2	NAG	A	2312	2	14,14,15	0.64	0	15,19,21	1.28	1 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	2301	1	-	0/6/23/26	0/1/1/1
2	NAG	A	2302	1	-	0/6/23/26	0/1/1/1
2	NAG	A	2303	1	-	0/6/23/26	0/1/1/1
2	NAG	A	2304	1	-	0/6/23/26	0/1/1/1
2	NAG	A	2305	1	-	0/6/23/26	0/1/1/1
2	NAG	A	2306	1,2	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	2307	3,2	-	0/6/23/26	0/1/1/1
3	BMA	A	2308	3,2	-	0/2/19/22	0/1/1/1
3	BMA	A	2309	3	-	0/2/19/22	0/1/1/1
3	BMA	A	2310	3	-	0/2/19/22	0/1/1/1
2	NAG	A	2311	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	2312	2	-	0/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2306	NAG	O5-C1	-2.90	1.39	1.43
2	A	2307	NAG	O5-C1	-2.39	1.39	1.43
2	A	2305	NAG	C1-C2	2.12	1.55	1.52
2	A	2305	NAG	O5-C1	2.16	1.47	1.43

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2308	BMA	O2-C2-C3	-2.18	105.89	110.17
2	A	2301	NAG	C1-O5-C5	2.64	115.81	112.17
2	A	2305	NAG	C1-O5-C5	2.76	115.97	112.17
2	A	2307	NAG	C1-O5-C5	2.88	116.13	112.17
2	A	2307	NAG	C2-N2-C7	2.88	127.14	122.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.