



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 13, 2017 – 04:58 am GMT

PDB ID : 2ELB
Title : Crystal Structure of the BAR-PH domain of human APPL1
Authors : Li, J.; Mao, X.; Dong, L.Q.; Liu, F.; Tong, L.
Deposited on : 2007-03-27
Resolution : 2.60 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

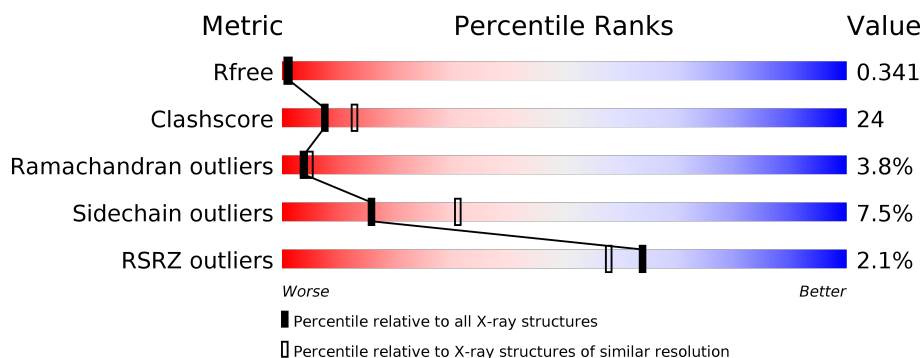
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	2542 (2.60-2.60)
Clashscore	112137	2895 (2.60-2.60)
Ramachandran outliers	110173	2848 (2.60-2.60)
Sidechain outliers	110143	2848 (2.60-2.60)
RSRZ outliers	101464	2550 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	396	<div> <div>2%</div> <div> <div></div> <div>49%</div> <div>33%</div> <div>6%</div> <div>11%</div> </div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2834 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Adapter protein containing PH domain, PTB domain and leucine zipper motif 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	351	Total	C	N	O	S	Se	0	0	0
			2834	1773	480	561	6	14			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MSE	-	CLONING ARTIFACT	UNP Q9UKG1
A	-18	GLY	-	CLONING ARTIFACT	UNP Q9UKG1
A	-17	SER	-	CLONING ARTIFACT	UNP Q9UKG1
A	-16	SER	-	CLONING ARTIFACT	UNP Q9UKG1
A	-15	HIS	-	CLONING ARTIFACT	UNP Q9UKG1
A	-14	HIS	-	CLONING ARTIFACT	UNP Q9UKG1
A	-13	HIS	-	CLONING ARTIFACT	UNP Q9UKG1
A	-12	HIS	-	CLONING ARTIFACT	UNP Q9UKG1
A	-11	HIS	-	CLONING ARTIFACT	UNP Q9UKG1
A	-10	HIS	-	CLONING ARTIFACT	UNP Q9UKG1
A	-9	SER	-	CLONING ARTIFACT	UNP Q9UKG1
A	-8	SER	-	CLONING ARTIFACT	UNP Q9UKG1
A	-7	GLY	-	CLONING ARTIFACT	UNP Q9UKG1
A	-6	LEU	-	CLONING ARTIFACT	UNP Q9UKG1
A	-5	VAL	-	CLONING ARTIFACT	UNP Q9UKG1
A	-4	PRO	-	CLONING ARTIFACT	UNP Q9UKG1
A	-3	ARG	-	CLONING ARTIFACT	UNP Q9UKG1
A	-2	GLY	-	CLONING ARTIFACT	UNP Q9UKG1
A	-1	SER	-	CLONING ARTIFACT	UNP Q9UKG1
A	0	HIS	-	CLONING ARTIFACT	UNP Q9UKG1
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q9UKG1
A	37	MSE	MET	MODIFIED RESIDUE	UNP Q9UKG1
A	44	MSE	MET	MODIFIED RESIDUE	UNP Q9UKG1
A	82	MSE	MET	MODIFIED RESIDUE	UNP Q9UKG1
A	111	MSE	MET	MODIFIED RESIDUE	UNP Q9UKG1
A	112	MSE	MET	MODIFIED RESIDUE	UNP Q9UKG1

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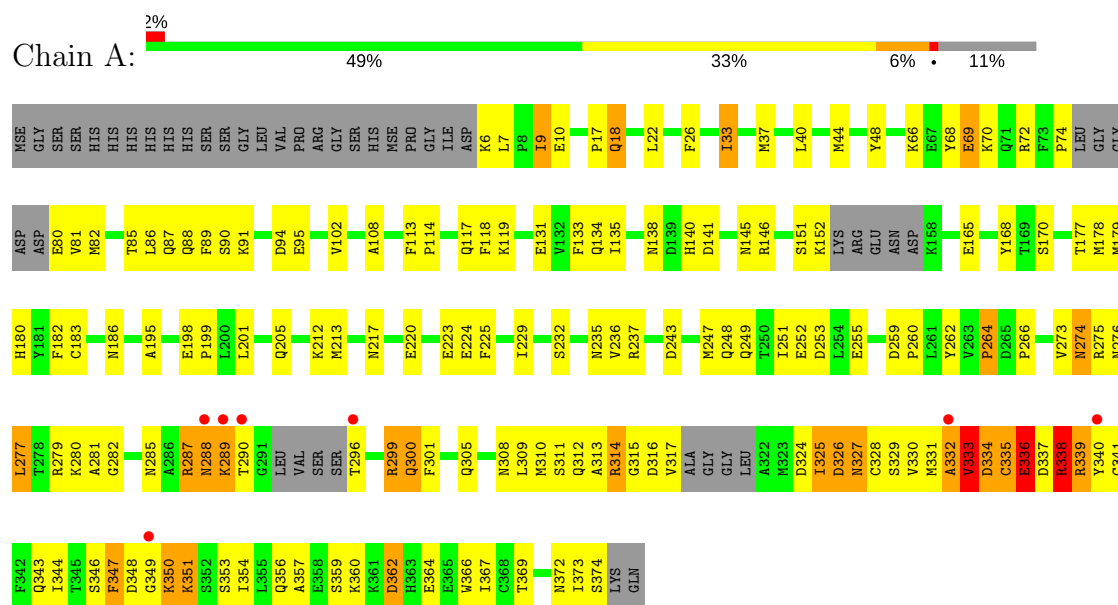
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Chain	Residue	Modelled	Actual	Comment	Reference
A	178	MSE	MET	MODIFIED RESIDUE	UNP Q9UKG1
A	179	MSE	MET	MODIFIED RESIDUE	UNP Q9UKG1
A	204	MSE	MET	MODIFIED RESIDUE	UNP Q9UKG1
A	213	MSE	MET	MODIFIED RESIDUE	UNP Q9UKG1
A	240	MSE	MET	MODIFIED RESIDUE	UNP Q9UKG1
A	247	MSE	MET	MODIFIED RESIDUE	UNP Q9UKG1
A	270	ASP	LYS	CONFLICT	UNP Q9UKG1
A	310	MSE	MET	MODIFIED RESIDUE	UNP Q9UKG1
A	323	MSE	MET	MODIFIED RESIDUE	UNP Q9UKG1
A	331	MSE	MET	MODIFIED RESIDUE	UNP Q9UKG1

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 the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: Adapter protein containing PH domain, PTB domain and leucine zipper motif 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	100.57Å 104.13Å 37.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.84 – 2.60 29.84 – 2.40	Depositor EDS
% Data completeness (in resolution range)	83.6 (29.84-2.60) 93.1 (29.84-2.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.16 (at 2.39Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.236 , 0.327 0.255 , 0.341	Depositor DCC
R_{free} test set	872 reflections (7.51%)	DCC
Wilson B-factor (Å ²)	38.6	Xtriage
Anisotropy	0.615	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 44.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.008 for k,h,-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	2834	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.41% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.45	0/2865	0.62	0/3835

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	2834	0	2768	137	0
All	All	2834	0	2768	137	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 24.

The worst 5 of 137 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:330:VAL:HB	1:A:348:ASP:HB2	1.24	1.15
1:A:347:PHE:HA	1:A:351:LYS:HA	1.62	0.81
1:A:18:GLN:HE21	1:A:18:GLN:HA	1.45	0.81
1:A:336:GLU:CD	1:A:337:ASP:H	1.84	0.79
1:A:290:THR:HA	1:A:296:THR:N	1.96	0.79

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 X-ray entries followed by that with respect to entries of similar resolution.

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	341/396 (86%)	291 (85%)	37 (11%)	13 (4%)	4 5

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	287	ARG
1	A	332	ALA
1	A	351	LYS
1	A	333	VAL
1	A	334	ASP

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	318/338 (94%)	294 (92%)	24 (8%)	16 31

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	299	ARG
1	A	316	ASP
1	A	353	SER
1	A	300	GLN

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Mol	Chain	Res	Type
1	A	314	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	221	GLN
1	A	248	GLN
1	A	327	ASN
1	A	217	ASN
1	A	343	GLN

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.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	337/396 (85%)	0.08	7 (2%) 64 58	20, 43, 69, 76	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	288	ASN	6.1
1	A	332	ALA	4.1
1	A	296	THR	3.6
1	A	289	LYS	2.7
1	A	349	GLY	2.5

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.