Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:45 AM GMT

PDB ID	:	2Y8D
Title	:	STRUCTURE OF DBL6 EPSILON DOMAIN FROM VAR2CSA STRAIN FCR3
Authors	:	Gangnard, S.; Ramboarina, S.; Lewit-Bentley, A.; Bentley, G.A.
Deposited on	:	2011-02-04
Resolution	:	1.84 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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:

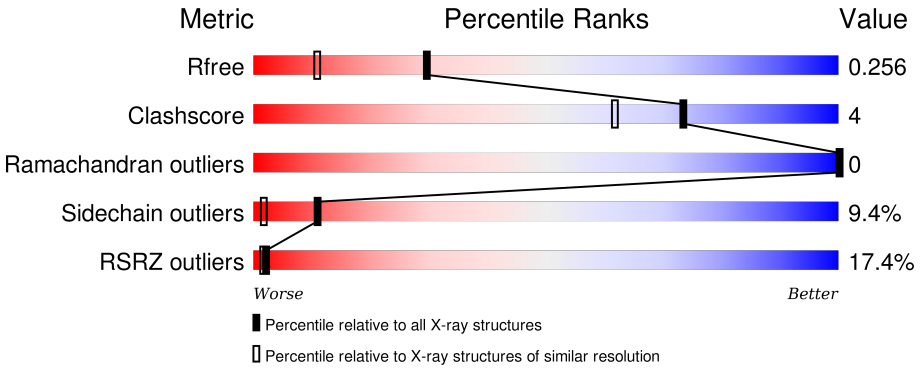
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.84 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}	91344	2634 (1.86-1.82)
Clashscore	102246	2862 (1.86-1.82)
Ramachandran outliers	100387	2831 (1.86-1.82)
Sidechain outliers	100360	2832 (1.86-1.82)
RSRZ outliers	91569	2639 (1.86-1.82)

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 <=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	306	16% 78% 12% • 8%

2 Entry composition

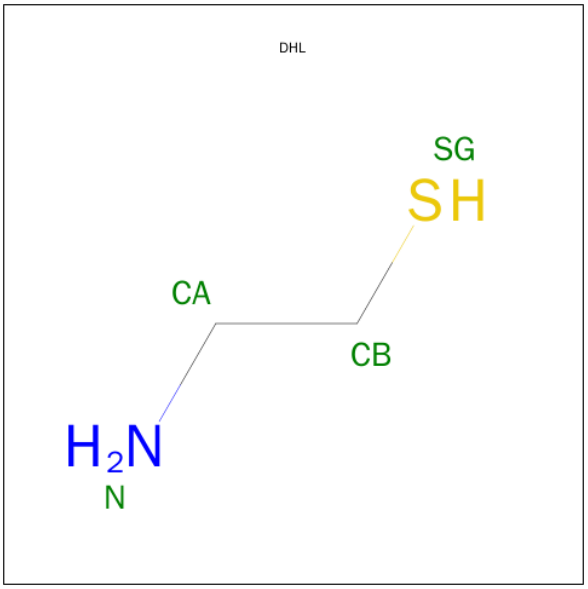
There are 4 unique types of molecules in this entry. The entry contains 2468 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ERYTHROCYTE MEMBRANE PROTEIN 1.

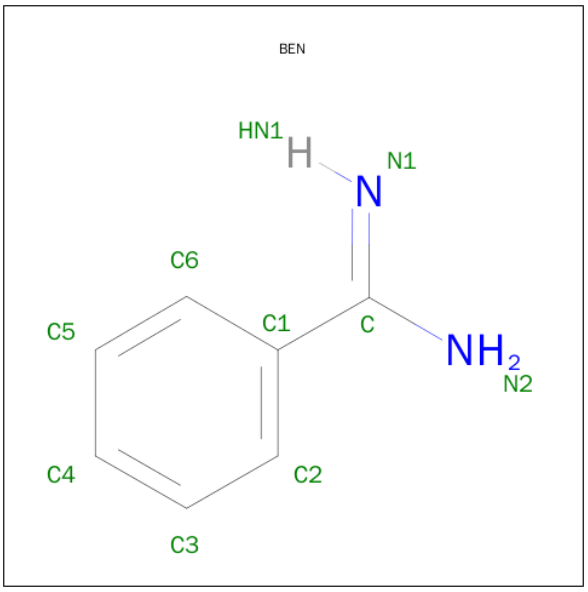
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	281	Total	C	N	O	S	0	4	0
			2339	1470	403	444	22			

- Molecule 2 is 2-AMINO-ETHANETHIOL (three-letter code: DHL) (formula: C_2H_7NS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	S	0	0
			4	2	1	1		
2	A	1	Total	C	N	S	0	0
			4	2	1	1		

- Molecule 3 is BENZAMIDINE (three-letter code: BEN) (formula: $C_7H_8N_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N 9 7 2	0	0

- Molecule 4 is water.

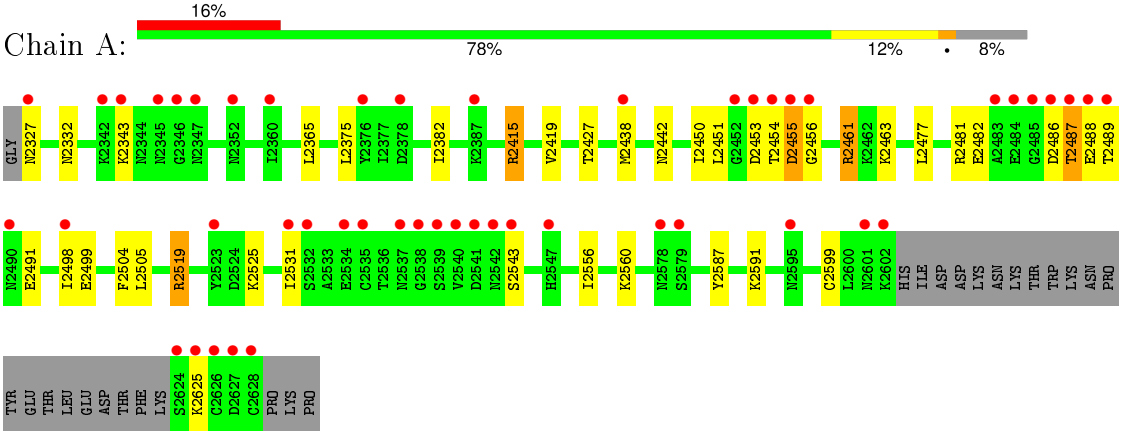
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	112	Total O 112 112	0	0

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 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: ERYTHROCYTE MEMBRANE PROTEIN 1

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	85.86Å 56.23Å 75.85Å 90.00° 123.09° 90.00°	Depositor
Resolution (Å)	43.92 – 1.84 35.18 – 1.84	Depositor EDS
% Data completeness (in resolution range)	93.5 (43.92-1.84) 93.6 (35.18-1.84)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.12 (at 1.84Å)	Xtriage
Refinement program	BUSTER 2.9.3	Depositor
R, R_{free}	0.203 , 0.235 0.218 , 0.256	Depositor DCC
R_{free} test set	1267 reflections (5.40%)	DCC
Wilson B-factor (Å^2)	36.6	Xtriage
Anisotropy	0.042	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 61.9	EDS
Estimated twinning fraction	0.016 for h,-k,-h-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 24727 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	2468	wwPDB-VP
Average B, all atoms (Å^2)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.56% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.54	0/2413	0.65	0/3236

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	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	2481	ARG	Sidechain

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	2339	0	2241	18	0
2	A	8	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	9	0	7	1	0
4	A	112	0	0	1	0
All	All	2468	0	2260	19	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 4.

All (19) 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:2415:ARG:HD3	1:A:2487:THR:HB	1.10	1.05
1:A:2415:ARG:HD3	1:A:2487:THR:CB	1.88	1.04
1:A:2415:ARG:CD	1:A:2487:THR:HB	1.96	0.95
1:A:2453:ASP:OD2	1:A:2461:ARG:HD3	1.95	0.66
1:A:2415:ARG:HD3	1:A:2487:THR:CG2	2.32	0.59
3:A:3629:BEN:N1	4:A:2113:HOH:O	2.33	0.56
1:A:2415:ARG:HB3	1:A:2489:THR:OG1	2.11	0.51
1:A:2438[C]:MET:HE1	1:A:2504:PHE:HB2	1.92	0.50
1:A:2415:ARG:CB	1:A:2489:THR:OG1	2.62	0.48
1:A:2486:ASP:OD1	1:A:2486:ASP:N	2.46	0.48
1:A:2427:THR:HG21	1:A:2498:ILE:HG23	1.95	0.48
1:A:2453:ASP:OD2	1:A:2461:ARG:CD	2.62	0.47
1:A:2419:VAL:HG11	1:A:2491:GLU:HB3	1.98	0.46
1:A:2427:THR:HG22	1:A:2499:GLU:HA	1.99	0.44
1:A:2587:TYR:CZ	1:A:2591:LYS:HG3	2.52	0.44
1:A:2455:ASP:HB3	1:A:2456:GLY:H	1.55	0.44
1:A:2415:ARG:H	1:A:2415:ARG:NE	2.19	0.40
1:A:2519:ARG:HG3	1:A:2556:ILE:HD11	2.02	0.40
1:A:2382:ILE:HG23	1:A:2450:ILE:HG13	2.03	0.40

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	282/306 (92%)	265 (94%)	17 (6%)	0	100 100

There are no Ramachandran outliers to report.

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	261/284 (92%)	237 (91%)	24 (9%)	11 2

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2327	ASN
1	A	2332	ASN
1	A	2343	LYS
1	A	2365	LEU
1	A	2375	LEU
1	A	2415	ARG
1	A	2442	ASN
1	A	2451	LEU
1	A	2454	THR
1	A	2455	ASP
1	A	2461	ARG
1	A	2463	LYS
1	A	2477	LEU
1	A	2482	GLU
1	A	2487	THR
1	A	2488	GLU
1	A	2505	LEU
1	A	2519	ARG
1	A	2525	LYS
1	A	2531	ILE
1	A	2543	SER

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Mol	Chain	Res	Type
1	A	2560	LYS
1	A	2599	CYS
1	A	2625	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2554	ASN
1	A	2572	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

3 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	$\#\|Z\| > 2$
3	BEN	A	3629	-	9,9,9	1.44	1 (11%)	9,11,11	3.78	7 (77%)
2	DHL	A	3630	1	3,3,3	0.36	0	2,2,2	0.40	0
2	DHL	A	3631	1	3,3,3	0.36	0	2,2,2	0.41	0

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
3	BEN	A	3629	-	-	0/4/4/4	0/1/1/1
2	DHL	A	3630	1	-	0/1/1/1	0/0/0/0
2	DHL	A	3631	1	-	0/1/1/1	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	3629	BEN	C1-C	-3.20	1.42	1.47

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	3629	BEN	C6-C1-C	-7.29	111.43	120.67
3	A	3629	BEN	C3-C2-C1	-3.61	115.80	120.33
3	A	3629	BEN	C5-C6-C1	-2.02	117.80	120.33
3	A	3629	BEN	C2-C1-C	2.46	123.79	120.67
3	A	3629	BEN	C5-C4-C3	3.03	125.24	119.93
3	A	3629	BEN	C6-C1-C2	4.16	124.78	118.60
3	A	3629	BEN	C1-C-N2	4.65	125.54	118.11

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	3629	BEN	1	0

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

6.1 Protein, DNA and RNA chains

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, 95^{th} 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	281/306 (91%)	0.98	49 (17%) 2 2	26, 50, 97, 114	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2487	THR	9.3
1	A	2486	ASP	8.5
1	A	2539	SER	8.2
1	A	2627	ASP	8.2
1	A	2624	SER	8.1
1	A	2628	CYS	7.7
1	A	2626	CYS	6.2
1	A	2488	GLU	5.8
1	A	2485	GLY	5.4
1	A	2532	SER	5.2
1	A	2537	ASN	4.9
1	A	2538	GLY	4.8
1	A	2541	ASP	4.5
1	A	2535	CYS	4.5
1	A	2542	ASN	4.5
1	A	2540	VAL	4.4
1	A	2343	LYS	4.4
1	A	2489	THR	4.4
1	A	2346	GLY	4.3
1	A	2455	ASP	4.3
1	A	2543	SER	4.2
1	A	2601	ASN	4.2
1	A	2625	LYS	4.0
1	A	2531	ILE	3.6
1	A	2454	THR	3.6
1	A	2523	TYR	3.5
1	A	2579	SER	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	2484	GLU	3.1
1	A	2387	LYS	3.0
1	A	2534	GLU	3.0
1	A	2376[A]	TYR	2.8
1	A	2595	ASN	2.7
1	A	2453	ASP	2.7
1	A	2602	LYS	2.6
1	A	2490	ASN	2.6
1	A	2347	ASN	2.6
1	A	2498	ILE	2.5
1	A	2578	ASN	2.4
1	A	2345	ASN	2.4
1	A	2352	ASN	2.3
1	A	2483	ALA	2.3
1	A	2438[A]	MET	2.3
1	A	2456	GLY	2.2
1	A	2547	HIS	2.2
1	A	2342	LYS	2.2
1	A	2378	ASP	2.1
1	A	2452	GLY	2.1
1	A	2327	ASN	2.0
1	A	2360	ILE	2.0

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)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
2	DHL	A	3630	4/4	0.95	0.26	1.13	56,64,64,67	0
3	BEN	A	3629	9/9	0.95	0.15	0.11	35,37,37,40	9
2	DHL	A	3631	4/4	0.89	0.36	-	74,74,75,78	0

6.5 Other polymers (i)

There are no such residues in this entry.