



wwPDB X-ray Structure Validation Summary Report i

Feb 27, 2014 – 11:38 PM GMT

PDB ID : 3DVU
Title : Crystal structure of the complex of murine gamma-herpesvirus 68 Bcl-2 homolog M11 and the Beclin 1 BH3 domain
Authors : Sinha, S.
Deposited on : 2008-07-20
Resolution : 2.50 Å (reported)

This is a wwPDB 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/ValidationPDFNotes.html>

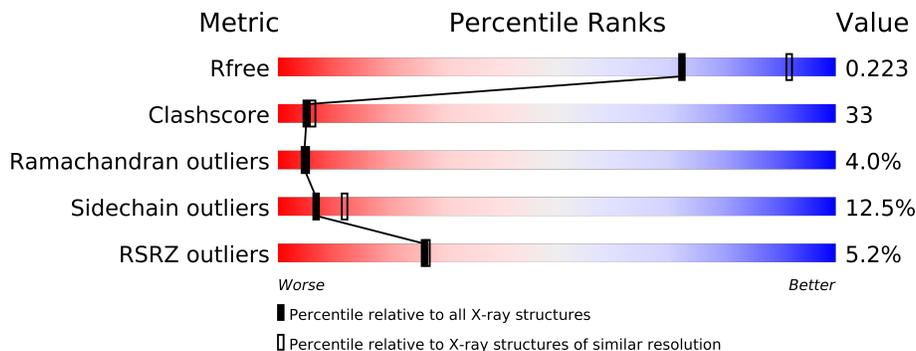
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **FAILED**
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.50 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}	66092	2784 (2.50-2.50)
Clashscore	79885	3562 (2.50-2.50)
Ramachandran outliers	78287	3480 (2.50-2.50)
Sidechain outliers	78261	3482 (2.50-2.50)
RSRZ outliers	66119	2785 (2.50-2.50)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	143	
1	B	143	
2	C	26	
2	D	26	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2578 atoms, of which 0 are hydrogen and 0 are deuterium.

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 V-bcl-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	130	1057	682	173	196	6	0	0	0
1	B	131	1066	687	174	199	6	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	INITIATING METHIONINE	UNP P89884
A	1	ALA	-	INSERTION	UNP P89884
A	137	HIS	-	EXPRESSION TAG	UNP P89884
A	138	HIS	-	EXPRESSION TAG	UNP P89884
A	139	HIS	-	EXPRESSION TAG	UNP P89884
A	140	HIS	-	EXPRESSION TAG	UNP P89884
A	141	HIS	-	EXPRESSION TAG	UNP P89884
A	142	HIS	-	EXPRESSION TAG	UNP P89884
B	0	MET	-	INITIATING METHIONINE	UNP P89884
B	1	ALA	-	INSERTION	UNP P89884
B	137	HIS	-	EXPRESSION TAG	UNP P89884
B	138	HIS	-	EXPRESSION TAG	UNP P89884
B	139	HIS	-	EXPRESSION TAG	UNP P89884
B	140	HIS	-	EXPRESSION TAG	UNP P89884
B	141	HIS	-	EXPRESSION TAG	UNP P89884
B	142	HIS	-	EXPRESSION TAG	UNP P89884

- Molecule 2 is a protein called Beclin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	24	181	110	33	36	2	0	0	0
2	D	24	180	109	32	37	2	0	0	0

- Molecule 3 is water.

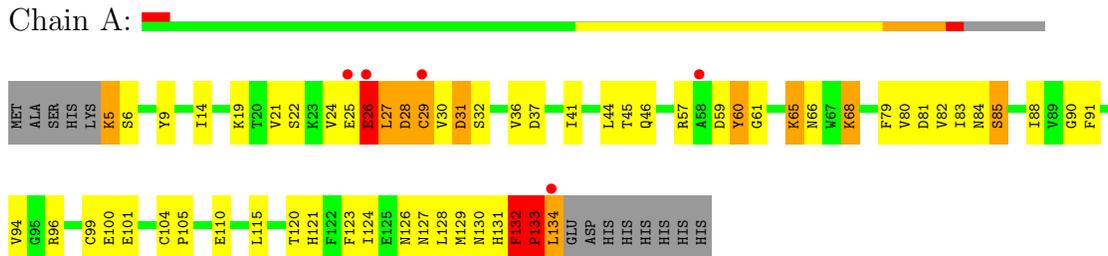
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	38	Total 38	O 38	0	0
3	B	41	Total 41	O 41	0	0
3	C	6	Total 6	O 6	0	0
3	D	9	Total 9	O 9	0	0

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 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.

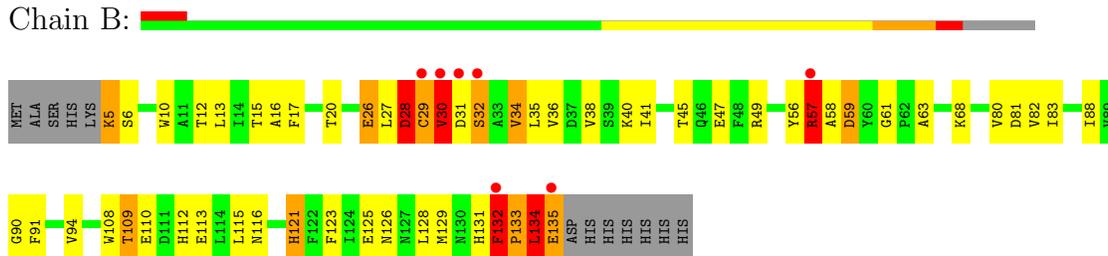
- Molecule 1: V-bcl-2

Chain A:



- Molecule 1: V-bcl-2

Chain B:



- Molecule 2: Beclin-1

Chain C:



- Molecule 2: Beclin-1

Chain D:



4 Data and refinement statistics

Xtrriage (Phenix) failed to run properly - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	44.42Å 53.13Å 64.06Å 90.00° 96.67° 90.00°	Depositor
Resolution (Å)	19.70 – 2.50 44.12 – 2.31	Depositor EDS
% Data completeness (in resolution range)	95.5 (19.70-2.50) 90.8 (44.12-2.31)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	0.16	Depositor
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.226 , 0.261 0.228 , 0.223	Depositor DCC
R_{free} test set	631 reflections (6.35%)	DCC
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 61.9	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2578	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

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	0.49	0/1083	0.81	3/1470 (0.2%)
1	B	0.52	0/1092	0.87	8/1482 (0.5%)
2	C	0.39	0/181	0.73	0/239
2	D	0.46	0/180	0.76	0/238
All	All	0.49	0/2536	0.83	11/3429 (0.3%)

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	32	SER	N-CA-C	-9.73	84.73	111.00
1	A	26	GLU	N-CA-C	-9.61	85.06	111.00
1	B	134	LEU	N-CA-C	-7.28	91.35	111.00
1	B	29	CYS	N-CA-C	-6.67	92.99	111.00
1	B	30	VAL	N-CA-C	-6.26	94.09	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1057	0	1031	64	0
1	B	1066	0	1037	80	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	181	0	182	10	0
2	D	180	0	178	12	0
3	A	38	0	0	21	0
3	B	41	0	0	8	0
3	C	6	0	0	3	0
3	D	9	0	0	3	0
All	All	2578	0	2428	164	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 33.

The worst 5 of 164 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:19:LYS:HA	3:A:159:HOH:O	1.71	0.90
1:A:79:PHE:HA	3:A:160:HOH:O	1.73	0.88
1:B:27:LEU:HD22	1:B:30:VAL:HG21	1.55	0.85
1:A:59:ASP:HB2	3:A:177:HOH:O	1.75	0.85
1:B:5:LYS:HB2	1:B:5:LYS:NZ	1.94	0.82

There are no symmetry-related clashes.

5.3 Torsion angles

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	128/143 (90%)	116 (91%)	7 (6%)	5 (4%)	5	5
1	B	129/143 (90%)	120 (93%)	5 (4%)	4 (3%)	7	8
2	C	22/26 (85%)	20 (91%)	1 (4%)	1 (4%)	4	4
2	D	22/26 (85%)	19 (86%)	1 (4%)	2 (9%)	1	1
All	All	301/338 (89%)	275 (91%)	14 (5%)	12 (4%)	5	5

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	27	LEU
1	A	29	CYS
1	A	61	GLY
1	B	61	GLY
2	C	124	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	119/131 (91%)	105 (88%)	14 (12%)	8 14
1	B	120/131 (92%)	106 (88%)	14 (12%)	8 14
2	C	20/22 (91%)	17 (85%)	3 (15%)	4 7
2	D	20/22 (91%)	16 (80%)	4 (20%)	2 3
All	All	279/306 (91%)	244 (88%)	35 (12%)	7 12

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	26	GLU
1	B	57	ARG
2	D	114	ARG
1	B	28	ASP
1	B	30	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	GLN
1	A	130	ASN
1	B	46	GLN
1	B	116	ASN
2	C	111	ASN

5.3.3 RNA

There are no RNA chains 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

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	130/143 (90%)	0.03	5 (3%) 38 40	38, 62, 98, 117	0
1	B	131/143 (91%)	0.15	7 (5%) 25 26	39, 62, 94, 116	0
2	C	24/26 (92%)	0.17	1 (4%) 35 36	48, 71, 118, 124	0
2	D	24/26 (92%)	0.50	3 (12%) 5 4	47, 66, 109, 115	0
All	All	309/338 (91%)	0.13	16 (5%) 26 27	38, 62, 106, 124	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	31	ASP	5.3
1	A	25	GLU	4.8
1	A	58	ALA	4.5
1	A	26	GLU	3.6
2	D	127	SER	3.2

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

There are no such residues in this entry.