



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 12:40 AM GMT

PDB ID : 2BBZ  
Title : Crystal Structure of MC159 Reveals Molecular Mechanism of DISC Assembly and vFLIP Inhibition  
Authors : Yang, J.K.; Wang, L.; Zheng, L.; Wan, F.; Ahmed, M.; Lenardo, M.J.; Wu, H.  
Deposited on : 2005-10-18  
Resolution : 3.80 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](mailto: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.

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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

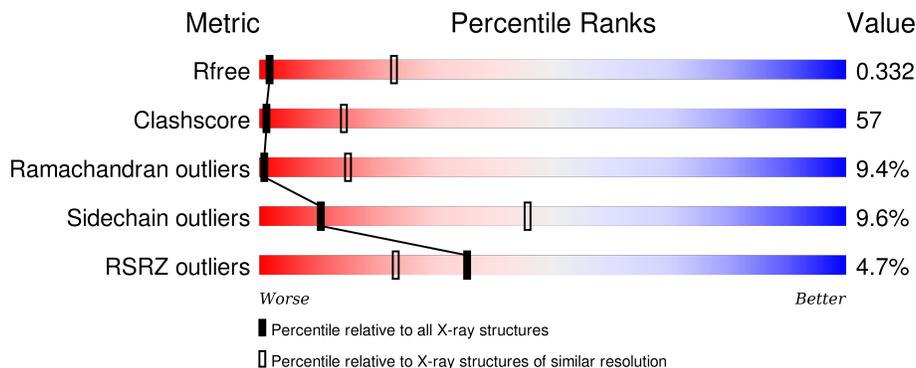
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.80 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	1317 (4.10-3.50)
Clashscore	102246	1458 (4.10-3.50)
Ramachandran outliers	100387	1397 (4.10-3.50)
Sidechain outliers	100360	1392 (4.10-3.50)
RSRZ outliers	91569	1325 (4.10-3.50)

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  $\geq 3$ , 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	249	 2% 24% 41% 10% • 24%
1	B	249	 6% 26% 40% 10% • 24%
1	C	249	 2% 24% 42% 10% • 24%
1	D	249	 5% 26% 40% 10% 24%

## 2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 6016 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 Viral CASP8 and FADD-like apoptosis regulator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	190	1491	937	256	287	11	0	0	0
1	B	190	1491	937	256	287	11	0	0	0
1	C	190	1491	937	256	287	11	0	0	0
1	D	190	1491	937	256	287	11	0	0	0

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	242	LEU	-	EXPRESSION TAG	UNP Q98325
A	243	GLU	-	EXPRESSION TAG	UNP Q98325
A	244	HIS	-	EXPRESSION TAG	UNP Q98325
A	245	HIS	-	EXPRESSION TAG	UNP Q98325
A	246	HIS	-	EXPRESSION TAG	UNP Q98325
A	247	HIS	-	EXPRESSION TAG	UNP Q98325
A	248	HIS	-	EXPRESSION TAG	UNP Q98325
A	249	HIS	-	EXPRESSION TAG	UNP Q98325
B	242	LEU	-	EXPRESSION TAG	UNP Q98325
B	243	GLU	-	EXPRESSION TAG	UNP Q98325
B	244	HIS	-	EXPRESSION TAG	UNP Q98325
B	245	HIS	-	EXPRESSION TAG	UNP Q98325
B	246	HIS	-	EXPRESSION TAG	UNP Q98325
B	247	HIS	-	EXPRESSION TAG	UNP Q98325
B	248	HIS	-	EXPRESSION TAG	UNP Q98325
B	249	HIS	-	EXPRESSION TAG	UNP Q98325
C	242	LEU	-	EXPRESSION TAG	UNP Q98325
C	243	GLU	-	EXPRESSION TAG	UNP Q98325
C	244	HIS	-	EXPRESSION TAG	UNP Q98325
C	245	HIS	-	EXPRESSION TAG	UNP Q98325
C	246	HIS	-	EXPRESSION TAG	UNP Q98325

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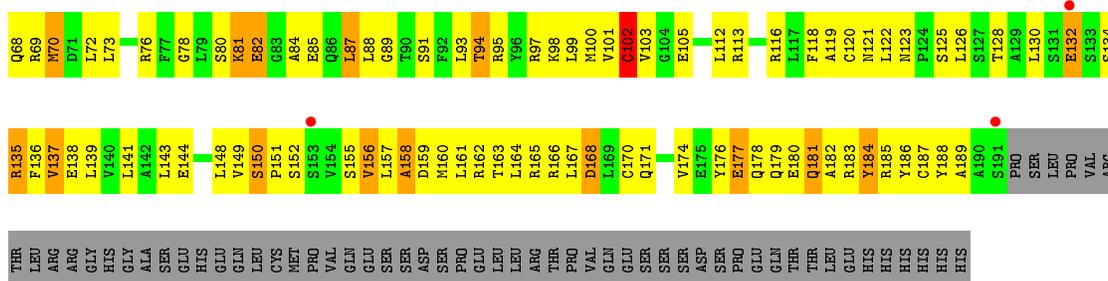
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Chain	Residue	Modelled	Actual	Comment	Reference
C	247	HIS	-	EXPRESSION TAG	UNP Q98325
C	248	HIS	-	EXPRESSION TAG	UNP Q98325
C	249	HIS	-	EXPRESSION TAG	UNP Q98325
D	242	LEU	-	EXPRESSION TAG	UNP Q98325
D	243	GLU	-	EXPRESSION TAG	UNP Q98325
D	244	HIS	-	EXPRESSION TAG	UNP Q98325
D	245	HIS	-	EXPRESSION TAG	UNP Q98325
D	246	HIS	-	EXPRESSION TAG	UNP Q98325
D	247	HIS	-	EXPRESSION TAG	UNP Q98325
D	248	HIS	-	EXPRESSION TAG	UNP Q98325
D	249	HIS	-	EXPRESSION TAG	UNP Q98325

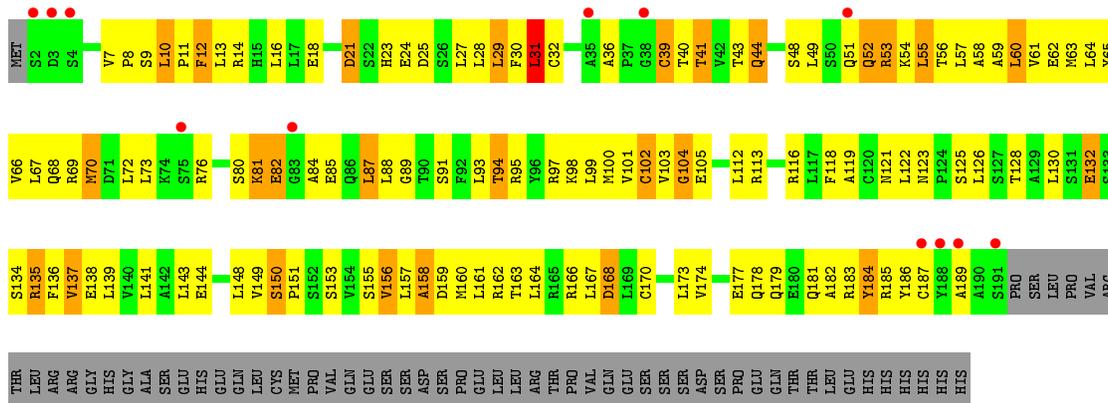
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	16	Total O 16 16	0	0
2	B	8	Total O 8 8	0	0
2	C	16	Total O 16 16	0	0
2	D	12	Total O 12 12	0	0





- Molecule 1: Viral CASP8 and FADD-like apoptosis regulator



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	83.86Å 108.06Å 142.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.80 29.76 – 3.79	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-3.80) 93.3 (29.76-3.79)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.04 (at 3.75Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.325 , 0.372 0.294 , 0.332	Depositor DCC
$R_{free}$ test set	1264 reflections (10.16%)	DCC
Wilson B-factor (Å <sup>2</sup> )	88.7	Xtrriage
Anisotropy	0.551	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 85.5	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Outliers	1 of 13293 reflections (0.008%)	Xtrriage
$F_o, F_c$ correlation	0.87	EDS
Total number of atoms	6016	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	67.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.03% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0/1510	0.65	0/2040
1	B	0.40	0/1510	0.62	0/2040
1	C	0.42	0/1510	0.63	0/2040
1	D	0.38	0/1510	0.62	0/2040
All	All	0.42	0/6040	0.63	0/8160

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	1491	0	1518	205	0
1	B	1491	0	1518	168	0
1	C	1491	0	1518	201	1
1	D	1491	0	1518	175	1
2	A	16	0	0	17	0
2	B	8	0	0	6	0
2	C	16	0	0	12	0
2	D	12	0	0	7	0
All	All	6016	0	6072	686	1

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 57.

The worst 5 of 686 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:181:GLN:HG2	1:C:165:ARG:HH22	1.17	1.01
1:D:177:GLU:HA	2:D:256:HOH:O	1.58	1.01
1:A:183:ARG:HG3	1:A:184:TYR:H	1.29	0.97
1:C:183:ARG:HG3	1:C:184:TYR:H	1.29	0.97
1:A:26:SER:HB3	2:A:259:HOH:O	1.64	0.97

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:123:ASN:ND2	1:D:51:GLN:OE1[4_546]	2.18	0.02

## 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	188/249 (76%)	123 (65%)	46 (24%)	19 (10%)	1	13
1	B	188/249 (76%)	121 (64%)	51 (27%)	16 (8%)	1	17
1	C	188/249 (76%)	123 (65%)	45 (24%)	20 (11%)	0	11
1	D	188/249 (76%)	123 (65%)	49 (26%)	16 (8%)	1	17
All	All	752/996 (76%)	490 (65%)	191 (25%)	71 (9%)	1	15

5 of 71 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	21	ASP
1	A	55	LEU
1	A	184	TYR
1	B	21	ASP

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Mol	Chain	Res	Type
1	B	55	LEU

### 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	170/226 (75%)	153 (90%)	17 (10%)	9 43
1	B	170/226 (75%)	154 (91%)	16 (9%)	11 47
1	C	170/226 (75%)	153 (90%)	17 (10%)	9 43
1	D	170/226 (75%)	155 (91%)	15 (9%)	12 50
All	All	680/904 (75%)	615 (90%)	65 (10%)	10 46

5 of 65 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	94	THR
1	C	29	LEU
1	D	85	GLU
1	B	102	CYS
1	C	12	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	15	HIS
1	C	123	ASN
1	D	123	ASN
1	B	178	GLN
1	D	171	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	190/249 (76%)	-0.09	4 (2%) 67 51	8, 43, 127, 162	0
1	B	190/249 (76%)	0.19	14 (7%) 17 11	8, 70, 144, 190	0
1	C	190/249 (76%)	-0.02	6 (3%) 51 35	8, 56, 140, 196	0
1	D	190/249 (76%)	0.21	12 (6%) 23 14	8, 86, 150, 185	0
All	All	760/996 (76%)	0.07	36 (4%) 35 23	8, 62, 141, 196	0

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	2	SER	7.9
1	B	187	CYS	5.7
1	A	2	SER	5.6
1	A	3	ASP	5.6
1	D	2	SER	5.1

### 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.