

wwPDB X-ray Structure Validation Summary Report (i)

May 13, 2020 – 07:40 am BST

PDB ID : 5IVN

> Title : BC2 nanobody in complex with the BC2 peptide tag

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2016-03-21 Deposited on

1.00 Å(reported) Resolution

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 https://www.wwpdb.org/validation/2017/XrayValidationReportHelp

with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity 4.02b-467

> 1.8.5 (274361), CSD as541be (2020) Mogul

Xtriage (Phenix) 1.13 EDS 2.11

Percentile statistics 20191225.v01 (using entries in the PDB archive December 25th 2019)

> Refmac 5.8.0158

CCP4 7.0.044 (Gargrove) Engh & Huber (2001)

Ideal geometry (proteins) Ideal geometry (DNA, RNA) Parkinson et al. (1996)

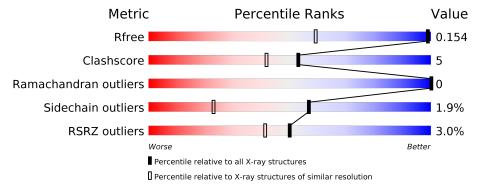
Validation Pipeline (wwPDB-VP) 2.11

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 1.00 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
R_{free}	130704	1050 (1.06-0.94)
Clashscore	141614	1117 (1.06-0.94)
Ramachandran outliers	138981	1043 (1.06-0.94)
Sidechain outliers	138945	1045 (1.06-0.94)
RSRZ outliers	127900	1023 (1.06-0.94)

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 respectively. 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	131	85%	8% • 6%
2	В	12	92%	8%



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1286 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 BC2-nanobody.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	123	Total	С	N	О	S	0	16	2
		-2-	1037	655	169	206	7			_

• Molecule 2 is a protein called Cadherin derived peptide.

\mathbf{Mol}	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	В	12	Total C N O 115 70 26 19	0	1	0

• Molecule 3 is water.

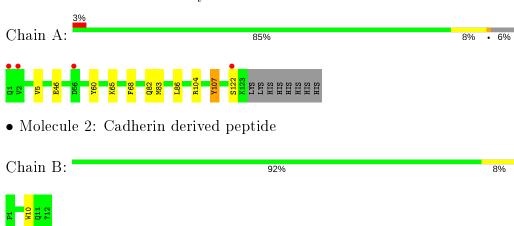
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	120	Total O 121 121	0	1
3	В	13	Total O 13 13	0	0



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 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: BC2-nanobody





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	106.01Å 31.53Å 35.88Å	Donogiton
a, b, c, α , β , γ	90.00° 107.54° 90.00°	Depositor
Resolution (Å)	50.55 - 1.00	Depositor
Resolution (A)	30.10 - 1.00	EDS
% Data completeness	99.7 (50.55-1.00)	Depositor
(in resolution range)	99.7 (30.10-1.00)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.17 (at 1.00Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
D D.	0.128 , 0.150	Depositor
R, R_{free}	0.134 , 0.154	DCC
R_{free} test set	3058 reflections $(5.00%)$	wwPDB-VP
Wilson B-factor (Å ²)	8.5	Xtriage
Anisotropy	0.314	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.38 , 58.1	EDS
L-test for twinning ²	$< L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	0.028 for -h-2*l,-k,l	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	1286	wwPDB-VP
Average B, all atoms (Å ²)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 13.06% of the height of the origin peak. No significant pseudotranslation is detected.

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



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 6E4, N7P

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	Boı	nd lengths	Bond angles		
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z >5	
1	A	1.10	5/1085~(0.5%)	0.81	0/1468	
2	В	0.85	0/97	0.68	0/129	
All	All	1.08	5/1182 (0.4%)	0.80	0/1597	

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(\mathbf{\mathring{A}})$	$\operatorname{Ideal}(\text{\AA})$
1	A	107[A]	TYR	CB-CG	-8.95	1.38	1.51
1	A	107[B]	TYR	CB-CG	-8.95	1.38	1.51
1	A	122	SER	CB-OG	-5.23	1.35	1.42
1	A	107[A]	TYR	CA-CB	-5.09	1.42	1.53
1	A	107[B]	TYR	CA-CB	-5.09	1.42	1.53

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	1037	0	985	12	0
2	В	115	0	91	0	0
3	A	121	0	0	7	0
3	В	13	0	0	0	0

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N.	Iol	Chain	Non-H	$\mathbf{H}(\mathbf{model})$	H(added)	Clashes	Symm-Clashes
A	All	All	1286	0	1076	12	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 5.

The worst 5 of 12 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{aligned} ext{Interatomic} \ ext{distance} \ (ext{Å}) \end{aligned}$	$egin{array}{c} ext{Clash} \ ext{overlap } (ext{Å}) \end{array}$
1:A:65[B]:LYS:NZ	3:A:203:HOH:O	1.70	1.20
1:A:46[A]:GLU:OE1	3:A:204:HOH:O	1.75	1.04
1:A:60:TYR:HB2	1:A:65[B]:LYS:HE2	1.38	1.02
1:A:65[B]:LYS:HE3	3:A:214:HOH:O	1.79	0.81
1:A:65[B]:LYS:CE	3:A:214:HOH:O	2.47	0.54

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	Perce	$\mathbf{entiles}$
1	A	137/131 (105%)	134 (98%)	3 (2%)	0	100	100
2	В	10/12 (83%)	10 (100%)	0	0	100	100
All	All	147/143 (103%)	144 (98%)	3 (2%)	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	112/110 (102%)	111 (99%)	1 (1%)	78 51		
2	В	9/8 (112%)	8 (89%)	1 (11%)	6 0		
All	All	121/118 (102%)	119 (98%)	2 (2%)	57 27		

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	104	ARG
2	В	10	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	Α	53	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains i

2 non-standard protein/DNA/RNA residues 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	Chain	Res	Res Link	Bond lengths			Bond angles		
10101	Moi Type Chain Ke	nes	es Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
2	6E4	В	12	2	9,9,9	1.27	1 (11%)	10,11,11	1.05	1 (10%)
2	N7P	В	1	2	9,10,11	1.70	2 (22%)	9,13,15	1.44	1 (11%)

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	${f Res}$	Link	Chirals	Torsions	Rings
2	6E4	В	12	2	-	2/9/9/9	-
2	N7P	В	1	2	-	0/4/16/18	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(ext{\AA})$
2	В	1	N7P	C1-N	-3.70	1.30	1.35
2	В	1	N7P	CA-N	-2.37	1.46	1.48
2	В	12	6E4	C05-C06	-2.24	1.48	1.53

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^o)$
2	В	1	N7P	O1-C1-N	-3.13	117.24	120.64
2	В	12	6E4	O10-C08-N09	-2.28	119.03	123.00

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	12	6E4	N07-C06-C08-N09
2	В	12	6E4	N07-C06-C08-O10

There are no ring outliers.

No monomer is involved in short contacts.

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^{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 $>$	$\#\mathrm{RSRZ}{>}2$	$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q < 0.9
1	A	123/131 (93%)	0.75	4 (3%) 46 37	5, 8, 27, 97	2 (1%)
2	В	10/12~(83%)	0.52	0 100 100	8, 10, 19, 40	0
All	All	133/143 (93%)	0.73	4 (3%) 50 41	5, 9, 29, 97	2 (1%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	VAL	4.3
1	A	1	GLN	3.5
1	A	122	SER	2.4
1	A	56	ASP	2.3

6.2 Non-standard residues in protein, DNA, RNA chains (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. 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	${f B-factors}({f A}^2)$	Q<0.9
2	6E4	В	12	10/10	0.95	0.09	9,14,17,24	0
2	N7P	В	1	10/11	0.96	0.08	8,10,15,16	0

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.

