

Full wwPDB X-ray Structure Validation Report (i)

Jan 25, 2023 – 12:21 pm GMT

PDB ID : 6Y14

Title : Bicyclic peptide bp65 crystallized as racemic mixture at 0.9 Angstrom resolu-

tion

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Deposited on : 2020-02-11

Resolution : 0.90 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

https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

Mol Probity : 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.31.3

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

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

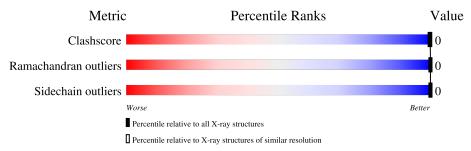
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\ DIFFRACTION$

The reported resolution of this entry is 0.90 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
Clashscore	141614	1132 (1.04-0.76)
Ramachandran outliers	138981	1055 (1.04-0.76)
Sidechain outliers	138945	1056 (1.04-0.76)

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 of 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%

Mol	Chain	Length	Quality of chain
1	A	13	100%
1	В	13	100%



2 Entry composition (i)

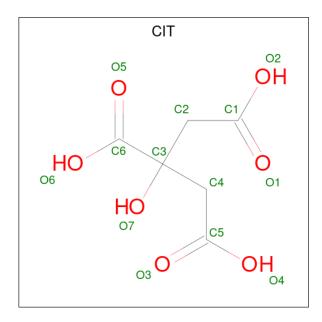
There are 3 unique types of molecules in this entry. The entry contains 477 atoms, of which 244 are hydrogens and 0 are deuteriums.

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 bp65.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
1	1 A	A 13		С	Н	N	О	S	0	0	1
1		10	214	68	117	15	12	2	0		1
1	D	13	Total	С	Н	N	О	S	0	0	1
1	Б	10	214	68	117	15	12	2	0	U	1

• Molecule 2 is CITRIC ACID (three-letter code: CIT) (formula: C₆H₈O₇).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C H O 18 6 5 7	0	0
2	В	1	Total C H O 18 6 5 7	0	0

• Molecule 3 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	8	Total O 8 8	0	0
3	В	5	Total O 5 5	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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. 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. 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: bp65
Chain A:

100%

There are no outlier residues recorded for this chain.
Molecule 1: bp65

Chain B:

100%

There are no outlier residues recorded for this chain.



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P -1	Depositor
Cell constants	16.48Å 26.21Å 29.91Å	Donogitor
a, b, c, α , β , γ	111.28° 92.26° 101.96°	Depositor
Resolution (Å)	27.70 - 0.90	Depositor
Resolution (A)	27.65 - 1.00	EDS
% Data completeness	87.7 (27.70-0.90)	Depositor
(in resolution range)	81.8 (27.65-1.00)	EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$	-	Xtriage
Refinement program	SHELX	Depositor
D D	0.126 , (Not available)	Depositor
R, R_{free}	(Not available) , (Not available)	DCC
R_{free} test set	3575 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	(Not available)	Xtriage
Anisotropy	(Not available)	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.48, 45.9	EDS
L-test for twinning ¹	$ < L >=$ (Not available), $ =$ (Not available)	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	477	wwPDB-VP
Average B, all atoms $(Å^2)$	3.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: (Not available)

Theoretical 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.



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: NH2, CIT, O65

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	0.66	0/84	0.74	0/109	
1	В	0.93	0/84	0.81	0/109	
All	All	0.81	0/168	0.78	0/218	

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	97	117	105	0	0
1	В	97	117	105	0	0
2	A	13	5	5	0	0
2	В	13	5	5	0	0
3	A	8	0	0	0	0
3	В	5	0	0	0	0
All	All	233	244	220	0	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 0.

There are no clashes within the asymmetric unit.



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	10/13 (77%)	10 (100%)	0	0	100	100
1	В	10/13 (77%)	10 (100%)	0	0	100	100
All	All	20/26 (77%)	20 (100%)	0	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	Analysed Rotameric		Perce	ntiles
1	A	10/11 (91%)	10 (100%)	0	100	100
1	В	10/11 (91%)	10 (100%)	0	100	100
All	All	20/22 (91%)	20 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

2 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		Des	T inle	Bo	ond leng	ths	Bond angles		
IVIOI	туре	Chain	Res	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	CIT	В	201	-	12,12,12	2.09	3 (25%)	17,17,17	1.97	7 (41%)
2	CIT	A	201	-	12,12,12	1.65	2 (16%)	17,17,17	1.73	3 (17%)

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
2	CIT	В	201	-	-	0/16/16/16	-
2	CIT	A	201	-	-	0/16/16/16	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(A)
2	В	201	CIT	C4-C3	4.57	1.59	1.53
2	A	201	CIT	C3-C6	4.14	1.57	1.53
2	В	201	CIT	C2-C3	3.47	1.58	1.53
2	В	201	CIT	O2-C1	-2.70	1.21	1.30
2	A	201	CIT	C4-C3	-2.06	1.51	1.53



All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
2	A	201	CIT	O7-C3-C6	-5.27	101.46	108.86
2	В	201	CIT	O5-C6-C3	4.30	128.35	122.25
2	В	201	CIT	C3-C4-C5	-3.06	106.40	113.81
2	В	201	CIT	O1-C1-C2	-2.80	114.77	122.94
2	В	201	CIT	O7-C3-C6	-2.72	105.04	108.86
2	В	201	CIT	O6-C6-C3	-2.56	108.60	113.05
2	A	201	CIT	C2-C3-C6	-2.48	104.78	110.11
2	В	201	CIT	C2-C3-C6	-2.24	105.30	110.11
2	В	201	CIT	O2-C1-C2	2.21	121.44	114.35
2	A	201	CIT	O1-C1-C2	-2.07	116.90	122.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

