



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2020 – 07:58 PM BST

PDB ID : 2F78
Title : BenM effector binding domain with its effector benzoate
Authors : Clark, T.; Haddad, S.; Ezezika, O.; Neidle, E.; Momany, C.
Deposited on : 2005-11-30
Resolution : 2.05 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 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) : 2.13.1

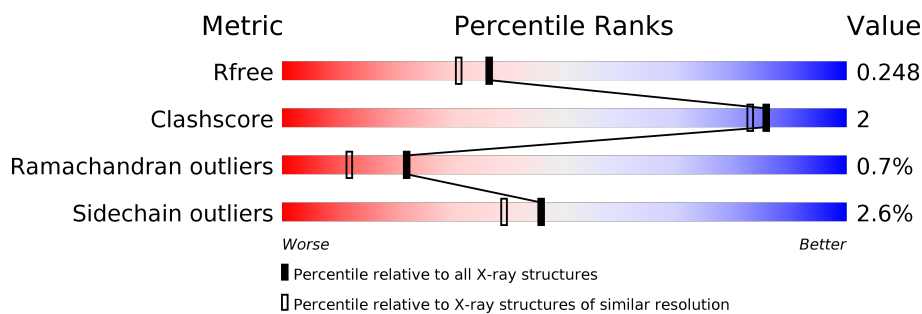
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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}	130704	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	232	
1	B	232	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4189 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.

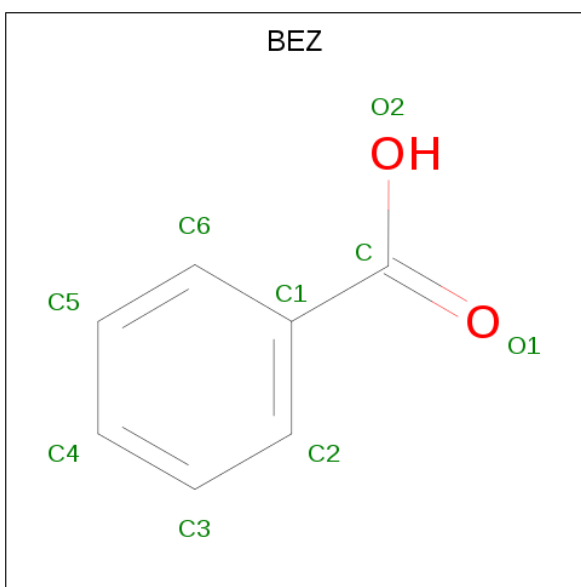
- Molecule 1 is a protein called HTH-type transcriptional regulator benM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	222	Total	C	N	O	S	0	9	0
			1836	1183	319	329	5			
1	B	214	Total	C	N	O	S	0	3	0
			1720	1108	295	312	5			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	305	LEU	-	CLONING ARTIFACT	UNP O68014
A	306	GLU	-	CLONING ARTIFACT	UNP O68014
A	307	HIS	-	EXPRESSION TAG	UNP O68014
A	308	HIS	-	EXPRESSION TAG	UNP O68014
A	309	HIS	-	EXPRESSION TAG	UNP O68014
A	310	HIS	-	EXPRESSION TAG	UNP O68014
A	311	HIS	-	EXPRESSION TAG	UNP O68014
A	312	HIS	-	EXPRESSION TAG	UNP O68014
B	305	LEU	-	CLONING ARTIFACT	UNP O68014
B	306	GLU	-	CLONING ARTIFACT	UNP O68014
B	307	HIS	-	EXPRESSION TAG	UNP O68014
B	308	HIS	-	EXPRESSION TAG	UNP O68014
B	309	HIS	-	EXPRESSION TAG	UNP O68014
B	310	HIS	-	EXPRESSION TAG	UNP O68014
B	311	HIS	-	EXPRESSION TAG	UNP O68014
B	312	HIS	-	EXPRESSION TAG	UNP O68014

- Molecule 2 is BENZOIC ACID (three-letter code: BEZ) (formula: C₇H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			9	7	2		
2	A	1	Total	C	O	0	0
			9	7	2		
2	B	1	Total	C	O	0	0
			9	7	2		
2	B	1	Total	C	O	0	0
			9	7	2		
2	B	1	Total	C	O	0	0
			9	7	2		

- Molecule 3 is water.

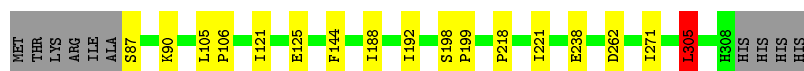
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	317	Total	O	0	0
			317	317		
3	B	271	Total	O	0	0
			271	271		

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: HTH-type transcriptional regulator benM

Chain A:  88% 7%



- Molecule 1: HTH-type transcriptional regulator benM

Chain B:  85% 6% 8%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	64.39 Å 69.51 Å 116.86 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.76 – 2.05 44.73 – 2.05	Depositor EDS
% Data completeness (in resolution range)	95.7 (59.76-2.05) 95.7 (44.73-2.05)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.35 (at 2.05 Å)	Xtriage
Refinement program	REFMAC refmac_5.2.0005	Depositor
R, R_{free}	0.180 , 0.242 0.192 , 0.248	Depositor DCC
R_{free} test set	1635 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	26.1	Xtriage
Anisotropy	0.086	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 34.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4189	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.60% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: BEZ

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	0.38	0/1898	0.58	1/2574 (0.0%)
1	B	0.36	0/1763	0.56	0/2392
All	All	0.37	0/3661	0.57	1/4966 (0.0%)

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	1	0
1	B	1	0
All	All	2	0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	305	LEU	N-CA-C	5.13	124.85	111.00

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	305	LEU	CA
1	B	275	ASN	CA

There are no planarity outliers.

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	1836	0	1891	9	0
1	B	1720	0	1769	8	0
2	A	18	0	10	0	0
2	B	27	0	15	0	0
3	A	317	0	0	1	0
3	B	271	0	0	2	0
All	All	4189	0	3685	16	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 2.

All (16) 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:188[B]:ILE:HD11	3:A:1060:HOH:O	1.97	0.64
1:B:226:GLU:HG2	1:B:229[B]:LEU:HD12	1.83	0.59
1:A:218:PRO:HB2	1:A:221:ILE:HD11	1.88	0.55
1:A:125:GLU:OE1	1:B:229[B]:LEU:HD11	2.09	0.53
1:B:192:ILE:HB	1:B:221[A]:ILE:HD13	1.92	0.50
1:A:105:LEU:HB3	1:A:106:PRO:HD3	1.94	0.48
1:A:144:PHE:CE1	1:A:271:ILE:HD12	2.49	0.48
1:B:206:HIS:HE1	1:B:266:ILE:O	1.98	0.47
1:B:192:ILE:HD12	1:B:218:PRO:HB3	1.98	0.46
1:B:91:THR:HG23	3:B:1138:HOH:O	2.16	0.44
1:B:147:LEU:HD21	3:B:1045:HOH:O	2.17	0.44
1:B:172:HIS:HD2	1:B:174:LEU:H	1.66	0.44
1:A:192:ILE:HB	1:A:221:ILE:HD13	2.00	0.44
1:A:198:SER:HB2	1:A:199:PRO:HD2	2.00	0.44

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	229/232 (99%)	226 (99%)	2 (1%)	1 (0%)	34	24
1	B	215/232 (93%)	212 (99%)	1 (0%)	2 (1%)	17	8
All	All	444/464 (96%)	438 (99%)	3 (1%)	3 (1%)	22	12

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	275	ASN
1	B	278	GLU
1	A	305	LEU

5.3.2 Protein sidechains

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	204/204 (100%)	199 (98%)	5 (2%)	47	40
1	B	190/204 (93%)	184 (97%)	6 (3%)	39	32
All	All	394/408 (97%)	383 (97%)	11 (3%)	46	37

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	87	SER
1	A	90	LYS
1	A	238	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	262	ASP
1	A	305	LEU
1	B	90	LYS
1	B	91	THR
1	B	188	ILE
1	B	274[A]	ARG
1	B	274[B]	ARG
1	B	275	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	161	ASN
1	B	172	HIS
1	B	206	HIS
1	B	291	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

5 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
2	BEZ	A	1001	-	7,9,9	0.78	0	8,11,11	0.94	0
2	BEZ	B	1002	-	7,9,9	1.06	1 (14%)	8,11,11	0.64	0
2	BEZ	B	1004	-	7,9,9	1.55	1 (14%)	8,11,11	0.40	0
2	BEZ	B	1005	-	7,9,9	1.48	1 (14%)	8,11,11	0.45	0
2	BEZ	A	1003	-	7,9,9	1.54	1 (14%)	8,11,11	0.35	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
2	BEZ	A	1001	-	-	0/0/4/4	0/1/1/1
2	BEZ	B	1002	-	-	0/0/4/4	0/1/1/1
2	BEZ	B	1004	-	-	0/0/4/4	0/1/1/1
2	BEZ	B	1005	-	-	0/0/4/4	0/1/1/1
2	BEZ	A	1003	-	-	0/0/4/4	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1003	BEZ	C1-C	3.81	1.51	1.47
2	B	1004	BEZ	C1-C	3.80	1.51	1.47
2	B	1005	BEZ	C1-C	3.73	1.51	1.47
2	B	1002	BEZ	C1-C	2.64	1.50	1.47

There are no bond angle outliers.

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 ⓘ

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

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

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

6.3 Carbohydrates ⓘ

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

6.4 Ligands ⓘ

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

6.5 Other polymers ⓘ

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