



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 01:07 pm BST

PDB ID : 2OJL
Title : Crystal structure of Q7WAF1_BORPA from Bordetella parapertussis. Northeast Structural Genomics target BpR68.
Authors : Benach, J.; Neely, H.; Seetharaman, J.; Wang, H.; Fang, Y.; Cunningham, K.; Ma, L.C.; Xiao, R.; Liu, J.; Baran, M.C.; Acton, T.B.; Rost, B.; Montelione, G.T.; Hunt, J.F.; Tong, L.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2007-01-12
Resolution : 2.10 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 : 2.11
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) : 2.11

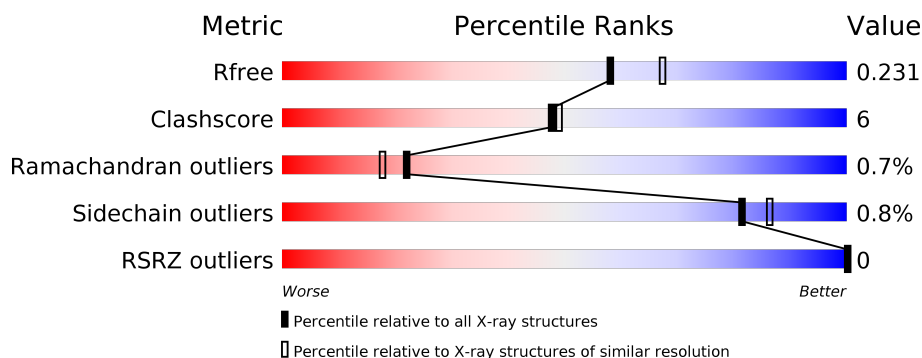
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 $\leq 5\%$. 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	108	 58% 15% 27%
1	B	108	 62% 7% 29%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1363 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 Hypothetical protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	79	Total	C	N	O	S	Se	0	0	0
			626	402	114	107	2	1			
1	B	77	Total	C	N	O	S	Se	0	0	0
			609	391	110	105	2	1			

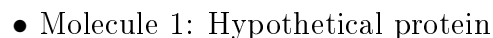
There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q7WAF1
A	28	MSE	MET	MODIFIED RESIDUE	UNP Q7WAF1
A	101	LEU	-	CLONING ARTIFACT	UNP Q7WAF1
A	102	GLU	-	CLONING ARTIFACT	UNP Q7WAF1
A	103	HIS	-	CLONING ARTIFACT	UNP Q7WAF1
A	104	HIS	-	CLONING ARTIFACT	UNP Q7WAF1
A	105	HIS	-	CLONING ARTIFACT	UNP Q7WAF1
A	106	HIS	-	CLONING ARTIFACT	UNP Q7WAF1
A	107	HIS	-	CLONING ARTIFACT	UNP Q7WAF1
A	108	HIS	-	CLONING ARTIFACT	UNP Q7WAF1
B	1	MSE	MET	MODIFIED RESIDUE	UNP Q7WAF1
B	28	MSE	MET	MODIFIED RESIDUE	UNP Q7WAF1
B	101	LEU	-	CLONING ARTIFACT	UNP Q7WAF1
B	102	GLU	-	CLONING ARTIFACT	UNP Q7WAF1
B	103	HIS	-	CLONING ARTIFACT	UNP Q7WAF1
B	104	HIS	-	CLONING ARTIFACT	UNP Q7WAF1
B	105	HIS	-	CLONING ARTIFACT	UNP Q7WAF1
B	106	HIS	-	CLONING ARTIFACT	UNP Q7WAF1
B	107	HIS	-	CLONING ARTIFACT	UNP Q7WAF1
B	108	HIS	-	CLONING ARTIFACT	UNP Q7WAF1

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	57	Total 57	O 57	0	0
2	B	71	Total 71	O 71	0	0

- Molecule 1: Hypothetical protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α , β , γ	65.67Å 65.67Å 76.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.10 39.73 – 2.10	Depositor EDS
% Data completeness (in resolution range)	92.8 (20.00-2.10) 97.2 (39.73-2.10)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.55 (at 2.10Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.198 , 0.218 0.214 , 0.231	Depositor DCC
R_{free} test set	1781 reflections (9.58%)	wwPDB-VP
Wilson B-factor (Å ²)	24.2	Xtriage
Anisotropy	0.374	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.5	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	0.94	EDS
Total number of atoms	1363	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.83% 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](#)

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	0.59	0/643	0.80	3/873 (0.3%)
1	B	0.57	0/624	0.89	4/845 (0.5%)
All	All	0.58	0/1267	0.85	7/1718 (0.4%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	54	ARG	NE-CZ-NH1	9.49	125.05	120.30
1	B	10	ARG	NE-CZ-NH2	7.31	123.96	120.30
1	A	54	ARG	NE-CZ-NH1	7.29	123.95	120.30
1	A	10	ARG	NE-CZ-NH2	6.47	123.54	120.30
1	B	10	ARG	NE-CZ-NH1	-5.72	117.44	120.30
1	B	66	GLU	OE1-CD-OE2	-5.35	116.89	123.30
1	A	66	GLU	OE1-CD-OE2	-5.29	116.95	123.30

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	626	0	613	7	0
1	B	609	0	600	9	0
2	A	57	0	0	0	0
2	B	71	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	1363	0	1213	15	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 6.

All (15) 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:B:9:PRO:HD2	2:B:3004:HOH:O	1.51	1.09
1:B:65:ARG:HB3	1:B:65:ARG:HH11	1.48	0.77
1:B:9:PRO:CD	2:B:3004:HOH:O	2.21	0.75
1:B:75:LYS:HG3	2:B:3033:HOH:O	1.95	0.65
1:B:75:LYS:O	1:B:79:GLN:HG3	2.07	0.54
1:B:65:ARG:HH11	1:B:65:ARG:CB	2.21	0.51
1:A:75:LYS:O	1:A:79:GLN:HG3	2.10	0.51
1:A:57:TYR:HB2	1:A:62:LEU:HD12	1.95	0.49
1:B:10:ARG:NH1	1:B:12:ALA:HB2	2.29	0.47
1:A:56:HIS:HD2	1:A:61:PRO:HA	1.79	0.46
1:A:47:PRO:HG3	1:B:33:LEU:HD22	1.97	0.46
1:B:9:PRO:HD3	2:B:3026:HOH:O	2.16	0.45
1:A:19:CYS:O	1:A:20:GLN:HB2	2.18	0.44
1:A:80:ARG:O	1:A:84:HIS:HD2	2.01	0.43
1:A:32:LEU:HD21	1:A:77:LEU:HG	2.03	0.40

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	77/108 (71%)	72 (94%)	5 (6%)	0	100	100
1	B	75/108 (69%)	71 (95%)	3 (4%)	1 (1%)	12	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	152/216 (70%)	143 (94%)	8 (5%)	1 (1%)	22 18

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	50	GLY

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	63/87 (72%)	63 (100%)	0	100 100
1	B	61/87 (70%)	60 (98%)	1 (2%)	62 69
All	All	124/174 (71%)	123 (99%)	1 (1%)	81 86

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	65	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	HIS
1	A	84	HIS
1	B	84	HIS

5.3.3 RNA ⓘ

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, 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	78/108 (72%)	0.04	0 100 100	12, 23, 40, 70	0
1	B	76/108 (70%)	0.17	0 100 100	13, 23, 40, 53	0
All	All	154/216 (71%)	0.11	0 100 100	12, 23, 40, 70	0

There are no RSRZ outliers to report.

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 [i](#)

There are no such residues in this entry.