



Full wwPDB X-ray Structure Validation Report ⓘ

May 28, 2020 – 09:54 pm BST

PDB ID : 2H5N
Title : Crystal Structure of Protein of Unknown Function PG1108 from Porphyromonas gingivalis W83
Authors : Nocek, B.; Bigelow, L.; Moy, S.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2006-05-26
Resolution : 2.01 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
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

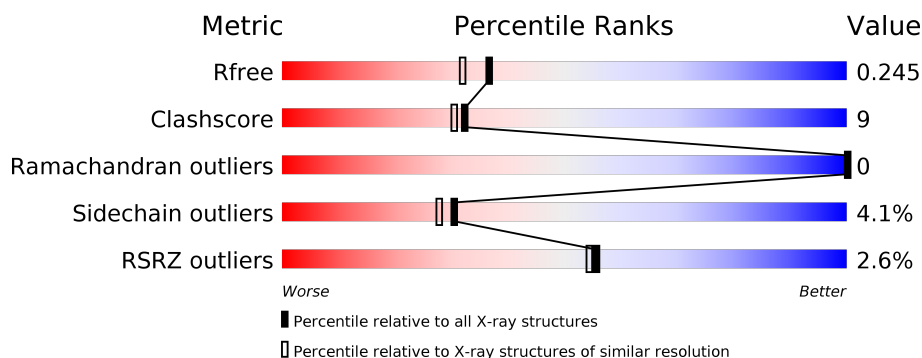
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.01 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	133	<div> <div>3%</div> <div> <div></div> <div>76%</div> <div>20%</div> <div>...</div> </div> </div>
1	B	133	<div> <div>%</div> <div> <div></div> <div>76%</div> <div>14%</div> <div>8%</div> </div> </div>
1	C	133	<div> <div>3%</div> <div> <div></div> <div>80%</div> <div>13%</div> <div>7%</div> </div> </div>
1	D	133	<div> <div>3%</div> <div> <div></div> <div>76%</div> <div>16%</div> <div>8%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4234 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 PG_1108.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	132	Total	C	N	O	S	4	1	0
			1014	637	168	196	13			
1	B	122	Total	C	N	O	S	0	4	0
			967	610	158	187	12			
1	C	124	Total	C	N	O	S	0	1	0
			955	604	154	184	13			
1	D	123	Total	C	N	O	S	0	3	0
			964	609	157	186	12			

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mg	0	0
			1	1		
2	A	1	Total	Mg	0	0
			1	1		
2	C	1	Total	Mg	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	78	Total	O	0	0
			78	78		
3	B	88	Total	O	0	0
			88	88		
3	C	83	Total	O	0	0
			83	83		
3	D	82	Total	O	0	0
			82	82		

● Molecule 1: Hypothetical protein PG 1108



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	79.96Å 84.83Å 164.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.01 37.70 – 2.01	Depositor EDS
% Data completeness (in resolution range)	99.5 (40.00-2.01) 99.5 (37.70-2.01)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.85 (at 2.01Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.188 , 0.244 0.189 , 0.245	Depositor DCC
R_{free} test set	1869 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	27.7	Xtriage
Anisotropy	0.601	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 43.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4234	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 4.83% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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	0.76	0/1022	0.84	2/1372 (0.1%)
1	B	0.79	0/975	0.77	0/1310
1	C	0.69	0/963	0.72	0/1294
1	D	0.84	1/972 (0.1%)	0.77	1/1307 (0.1%)
All	All	0.77	1/3932 (0.0%)	0.78	3/5283 (0.1%)

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	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	54	GLN	CG-CD	8.49	1.70	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4	GLY	N-CA-C	-7.19	95.13	113.10
1	D	54	GLN	OE1-CD-NE2	7.04	138.10	121.90
1	A	8	LEU	CA-CB-CG	5.14	127.13	115.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	132	ASN	CA

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	131	LYS	Peptide
1	A	3	LEU	Peptide

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	1014	0	1051	20	0
1	B	967	0	998	24	0
1	C	955	0	991	17	0
1	D	964	0	1001	15	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	78	0	0	3	0
3	B	88	0	0	1	3
3	C	83	0	0	3	0
3	D	82	0	0	4	3
All	All	4234	0	4041	70	3

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 9.

All (70) 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:132:ASN:ND2	3:A:1078:HOH:O	1.81	1.14
1:B:41:ALA:O	1:B:45[B]:ARG:HG2	1.61	0.96
1:B:58:ASP:OD2	3:B:1027:HOH:O	1.86	0.92
1:A:131:LYS:HG3	1:A:131:LYS:O	1.71	0.88
1:D:12:THR:O	1:D:83:ARG:NH1	2.12	0.82
1:B:106:LEU:O	1:B:110:THR:HG23	1.83	0.78
1:C:79:MET:HE3	1:C:83:ARG:HB3	1.74	0.70
1:C:80:ASP:OD1	1:C:83:ARG:HD3	1.93	0.68
1:A:26:LYS:O	1:A:30:MET:HG3	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:18:LEU:HD13	1:B:52:ILE:HD11	1.76	0.66
1:D:38:ALA:HB1	3:D:197:HOH:O	2.00	0.60
1:C:131:LYS:NZ	3:C:1077:HOH:O	2.34	0.60
1:A:30:MET:HG2	1:C:35:ILE:HD11	1.85	0.58
1:A:132:ASN:N	1:A:132:ASN:OD1	2.35	0.57
1:A:115:LEU:HD11	1:B:112:ILE:HG13	1.86	0.57
1:A:30:MET:HG2	1:C:35:ILE:CD1	2.35	0.56
1:B:102[A]:ASP:OD1	1:B:104:ASN:N	2.38	0.56
1:B:45[B]:ARG:HA	1:B:48:MET:HE3	1.86	0.56
1:A:49:ARG:NH1	3:A:1038:HOH:O	2.39	0.55
1:A:88:ALA:HB2	1:A:118:LEU:HB3	1.87	0.54
1:B:45[B]:ARG:HD3	1:B:48:MET:HE1	1.89	0.54
1:B:45[B]:ARG:HA	1:B:48:MET:CE	2.37	0.54
1:C:79:MET:CE	1:C:83:ARG:HB3	2.37	0.51
1:C:17:GLU:OE1	1:C:83:ARG:NH2	2.42	0.51
1:A:125:GLU:O	1:A:129:ASN:ND2	2.44	0.51
1:D:36[B]:LYS:O	1:D:40:ILE:HG12	2.11	0.50
1:C:79:MET:HE3	1:C:83:ARG:CB	2.39	0.50
1:C:99:GLY:HA2	1:C:127:ILE:HD11	1.94	0.50
1:D:35[B]:ILE:HD12	1:D:35[B]:ILE:N	2.27	0.50
1:B:48:MET:HA	1:B:52:ILE:O	2.12	0.49
1:B:45[A]:ARG:HA	1:B:48:MET:HE3	1.94	0.49
1:A:35:ILE:HG21	1:C:30[B]:MET:SD	2.53	0.49
1:D:102:ASP:OD1	1:D:104[A]:ASN:ND2	2.46	0.49
1:D:78:ARG:NH1	3:D:214:HOH:O	2.45	0.49
1:B:45[A]:ARG:HA	1:B:48:MET:CE	2.43	0.48
1:D:42:VAL:HG22	1:D:45:ARG:HH22	1.78	0.48
1:B:106:LEU:O	1:B:110:THR:CG2	2.58	0.48
1:C:11:MET:HE3	1:C:13:PHE:CE2	2.49	0.48
1:D:35[A]:ILE:C	1:D:36[A]:LYS:HG3	2.34	0.48
1:C:78:ARG:HG3	1:C:78:ARG:HH11	1.78	0.48
1:A:35:ILE:HD11	1:C:26:LYS:HG2	1.95	0.47
1:D:68:GLU:HB2	1:D:71:GLN:HG3	1.97	0.47
1:A:26:LYS:HE3	1:A:61:LEU:CD2	2.45	0.47
1:A:95:MET:HB3	1:A:105:GLU:HG2	1.98	0.46
1:B:76:ILE:HG23	1:B:79:MET:HE1	1.98	0.46
1:B:76:ILE:HG23	1:B:79:MET:CE	2.46	0.45
1:B:76:ILE:O	1:B:79:MET:HE2	2.16	0.45
1:D:95:MET:O	3:D:207:HOH:O	2.20	0.45
1:D:36[A]:LYS:HE2	1:D:36[A]:LYS:HB2	1.80	0.45
1:A:104:ASN:OD1	1:B:104:ASN:ND2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:LYS:HB3	1:A:62:LYS:NZ	2.32	0.44
1:D:24:MET:HG3	1:D:76:ILE:CD1	2.47	0.44
1:C:83:ARG:NH1	3:C:1054:HOH:O	2.51	0.44
1:A:79:MET:HE1	1:A:87:VAL:HG21	2.00	0.43
1:B:44:THR:O	1:B:48:MET:HG3	2.18	0.43
1:B:102[A]:ASP:OD1	1:B:105:GLU:OE2	2.35	0.43
1:B:24:MET:HG3	1:B:76:ILE:CD1	2.49	0.43
1:C:42:VAL:HG13	1:C:46:GLU:HG3	2.01	0.42
1:B:95:MET:HB3	1:B:105:GLU:HG2	2.00	0.42
1:D:78:ARG:HH11	1:D:78:ARG:HG3	1.84	0.42
1:C:26:LYS:HD2	1:C:61:LEU:HD23	2.01	0.42
1:A:90:TYR:CZ	1:A:94:ILE:HD11	2.55	0.42
1:B:131:LYS:HE2	1:B:131:LYS:HB3	1.72	0.41
1:A:99:GLY:HA2	1:A:127:ILE:CD1	2.50	0.41
1:B:102[A]:ASP:C	1:B:102[A]:ASP:OD1	2.59	0.41
1:A:104:ASN:HB3	3:A:1013:HOH:O	2.19	0.41
1:D:122:THR:OG1	1:D:125:GLU:HG3	2.21	0.41
1:B:71[A]:GLN:HE21	1:B:75:LEU:HG	1.87	0.40
1:C:78:ARG:NH1	3:C:1059:HOH:O	2.54	0.40
1:D:58:ASP:OD1	3:D:146:HOH:O	2.21	0.40

All (3) 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)
3:B:1026:HOH:O	3:D:197:HOH:O[5_445]	1.90	0.30
3:B:1027:HOH:O	3:D:210:HOH:O[5_445]	1.97	0.23
3:B:1072:HOH:O	3:D:197:HOH:O[5_445]	2.14	0.06

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	131/133 (98%)	131 (100%)	0	0	100	100
1	B	124/133 (93%)	124 (100%)	0	0	100	100
1	C	123/133 (92%)	123 (100%)	0	0	100	100
1	D	124/133 (93%)	123 (99%)	1 (1%)	0	100	100
All	All	502/532 (94%)	501 (100%)	1 (0%)	0	100	100

There are no Ramachandran outliers to report.

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	111/111 (100%)	101 (91%)	10 (9%)	9	6
1	B	106/111 (96%)	102 (96%)	4 (4%)	33	31
1	C	105/111 (95%)	104 (99%)	1 (1%)	76	81
1	D	106/111 (96%)	102 (96%)	4 (4%)	33	31
All	All	428/444 (96%)	409 (96%)	19 (4%)	30	25

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	5	ARG
1	A	8	LEU
1	A	52	ILE
1	A	53	LEU
1	A	62	LYS
1	A	82	GLU
1	A	120	THR
1	A	131	LYS
1	A	132	ASN
1	B	59	LEU
1	B	102[A]	ASP
1	B	102[B]	ASP

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Mol	Chain	Res	Type
1	B	110	THR
1	C	65	ASP
1	D	52	ILE
1	D	53	LEU
1	D	104[A]	ASN
1	D	104[B]	ASN

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

Mol	Chain	Res	Type
1	B	104	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](#)

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](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

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 ⓘ

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	132/133 (99%)	0.34	4 (3%) 50 49	16, 26, 35, 40	1 (0%)
1	B	122/133 (91%)	0.31	1 (0%) 86 85	15, 23, 34, 39	0
1	C	124/133 (93%)	0.21	4 (3%) 47 46	16, 25, 35, 40	0
1	D	123/133 (92%)	0.25	4 (3%) 46 45	15, 24, 36, 40	0
All	All	501/532 (94%)	0.28	13 (2%) 56 54	15, 24, 36, 40	1 (0%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	98	ASP	3.5
1	A	98	ASP	3.1
1	A	100	ASP	3.1
1	D	100	ASP	2.7
1	C	100	ASP	2.6
1	D	128	ASN	2.6
1	A	99	GLY	2.3
1	C	133	LEU	2.2
1	D	132	ASN	2.2
1	C	97	SER	2.2
1	D	35[A]	ILE	2.1
1	A	124	MET	2.1
1	B	40	ILE	2.0

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

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](#)

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, 95th 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	B-factors(\AA^2)	Q<0.9
2	MG	A	1001	1/1	0.93	0.13	47,47,47,47	0
2	MG	C	1001	1/1	0.95	0.15	31,31,31,31	0
2	MG	B	1001	1/1	0.99	0.10	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.