



# Full wwPDB X-ray Structure Validation Report

Jun 9, 2014 – 10:26 AM EDT

PDB ID : 4ON1  
Title : Crystal Structure of metalloproteinase-II from Bacteroides fragilis  
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Deposited on : 2014-01-28  
Resolution : 2.13 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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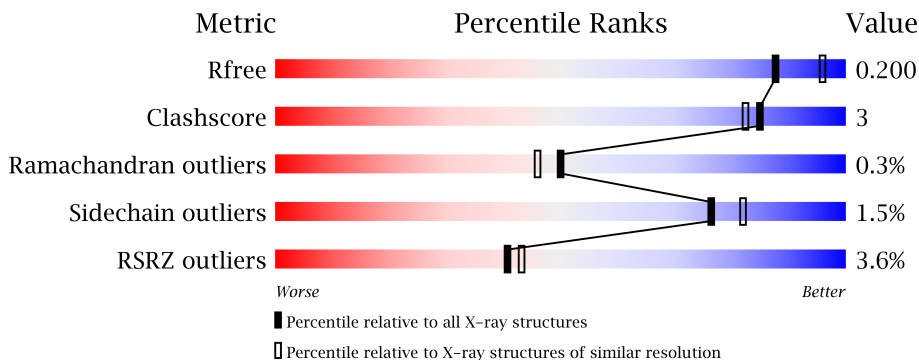
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : **FAILED**  
Xtriage (Phenix) : dev-1439  
EDS : stable23161  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable23161

# 1 Overall quality at a glance

The reported resolution of this entry is 2.13 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))
$R_{free}$	66092	1116 (2.16-2.12)
Clashscore	79885	1302 (2.16-2.12)
Ramachandran outliers	78287	1281 (2.16-2.12)
Sidechain outliers	78261	1281 (2.16-2.12)
RSRZ outliers	66119	1116 (2.16-2.12)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	379	
1	B	379	

## 2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 5735 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

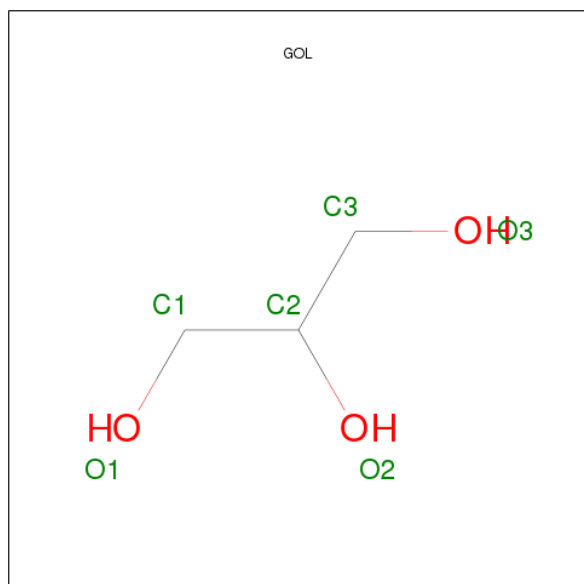
- Molecule 1 is a protein called Putative metalloprotease II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	334	Total	C	N	O	S	0	0	0
			2653	1679	444	522	8			
1	B	333	Total	C	N	O	S	0	0	0
			2645	1673	443	521	8			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is water.

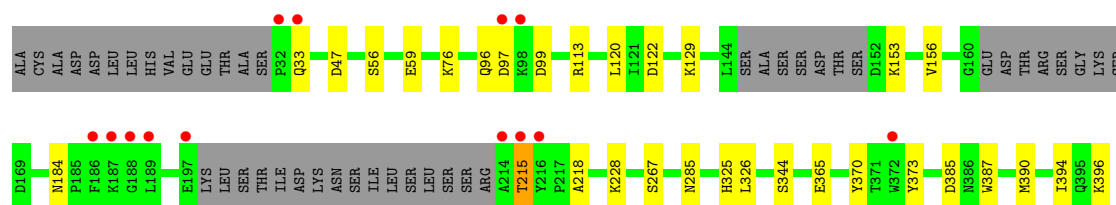
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	222	Total	O	0	0
			222	222		
4	B	207	Total	O	0	0
			207	207		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

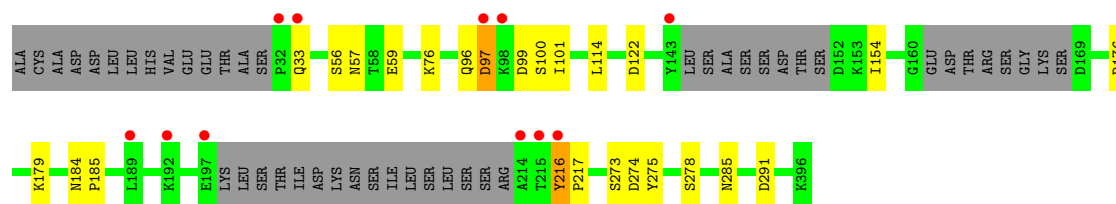
- Molecule 1: Putative metalloprotease II

Chain A: 



- Molecule 1: Putative metalloprotease II

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	44.42Å 114.39Å 140.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.32 – 2.13 44.32 – 2.12	Depositor EDS
% Data completeness (in resolution range)	99.8 (44.32-2.13) 99.8 (44.32-2.12)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.91 (at 2.12Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, $R_{free}$	0.159 , 0.200 0.158 , 0.200	Depositor DCC
$R_{free}$ test set	2062 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	26.9	Xtriage
Anisotropy	0.311	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 40.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 41245 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5735	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.30% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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	0.29	0/2708	0.47	0/3666
1	B	0.29	0/2700	0.48	0/3655
All	All	0.29	0/5408	0.47	0/7321

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	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	215	THR	Peptide

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2653	0	2582	17	0
1	B	2645	0	2571	13	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	B	6	0	8	1	0
4	A	222	0	0	2	0
4	B	207	0	0	2	0
All	All	5735	0	5161	29	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 3.

All (29) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:184:ASN:HD21	1:A:344:SER:HB3	1.49	0.76
1:B:291:ASP:OD1	4:B:685:HOH:O	2.15	0.65
1:B:285:ASN:OD1	4:B:696:HOH:O	2.17	0.60
1:A:184:ASN:ND2	1:A:373:TYR:OH	2.30	0.57
1:A:33:GLN:HA	1:B:33:GLN:OE1	2.09	0.53
1:A:113:ARG:HD3	1:A:120:LEU:HD21	1.92	0.52
1:B:76:LYS:HG2	1:B:96:GLN:OE1	2.10	0.52
1:A:76:LYS:HG2	1:A:96:GLN:OE1	2.11	0.50
1:B:216:TYR:H	1:B:217:PRO:HA	1.78	0.49
1:A:218:ALA:HB3	1:A:326:LEU:HD13	1.93	0.49
1:A:153:LYS:HD3	1:A:156:VAL:HG22	1.95	0.48
1:A:97:ASP:C	1:A:99:ASP:H	2.16	0.48
1:A:59:GLU:OE1	1:A:96:GLN:HG3	2.15	0.47
1:B:101:ILE:HD12	1:B:114:LEU:HD23	1.96	0.46
1:B:97:ASP:C	1:B:99:ASP:H	2.17	0.46
1:B:184:ASN:HA	1:B:185:PRO:HD3	1.79	0.46
1:B:275:TYR:HD2	1:B:278:SER:HG	1.63	0.45
1:B:154:ILE:HG12	1:B:179:LYS:HB3	1.98	0.45
1:A:387:TRP:HA	1:A:390:MET:HE3	2.00	0.43
1:A:365:GLU:HA	1:A:370:TYR:CG	2.54	0.42
1:A:285:ASN:ND2	4:A:600:HOH:O	2.45	0.42
1:B:273:SER:C	1:B:275:TYR:H	2.22	0.42
1:B:176:ASP:OD2	1:B:179:LYS:HD3	2.21	0.41
1:A:228:LYS:HD2	1:A:267:SER:HA	2.02	0.41
1:A:326:LEU:HG	1:A:394:ILE:HB	2.03	0.41
1:A:129:LYS:HG3	4:A:677:HOH:O	2.21	0.41
1:A:47:ASP:OD2	3:B:401:GOL:H11	2.20	0.41
1:B:59:GLU:OE1	1:B:96:GLN:HG3	2.21	0.40
1:A:325:HIS:HB3	1:A:396:LYS:O	2.22	0.40

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	326/379 (86%)	320 (98%)	6 (2%)	0	100	100
1	B	325/379 (86%)	318 (98%)	5 (2%)	2 (1%)	33	25
All	All	651/758 (86%)	638 (98%)	11 (2%)	2 (0%)	50	46

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	274	ASP
1	B	216	TYR

### 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	292/333 (88%)	288 (99%)	4 (1%)	78	84
1	B	291/333 (87%)	286 (98%)	5 (2%)	73	78
All	All	583/666 (88%)	574 (98%)	9 (2%)	76	82

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	SER
1	A	122	ASP
1	A	215	THR
1	A	385	ASP

*Continued on next page...*

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Mol	Chain	Res	Type
1	B	56	SER
1	B	57	ASN
1	B	97	ASP
1	B	100	SER
1	B	122	ASP

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	33	GLN
1	A	184	ASN
1	A	345	HIS

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

Mogul failed to run properly - this section will therefore be empty.

## 5.5 Carbohydrates ⓘ

Mogul failed to run properly - this section will therefore be empty.

## 5.6 Ligand geometry ⓘ

Mogul failed to run properly - this section will therefore be empty.

## 5.7 Other polymers ⓘ

Mogul failed to run properly - this section will therefore be empty.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	334/379 (88%)	-0.27	13 (3%) 37 40	12, 25, 67, 113	0
1	B	333/379 (87%)	-0.29	11 (3%) 44 47	13, 27, 65, 112	0
All	All	667/758 (87%)	-0.28	24 (3%) 41 43	12, 26, 65, 113	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	214	ALA	7.2
1	B	197	GLU	5.6
1	B	216	TYR	4.8
1	A	197	GLU	4.3
1	B	215	THR	4.0
1	A	97	ASP	3.8
1	B	97	ASP	3.8
1	B	32	PRO	3.4
1	B	214	ALA	3.1
1	A	215	THR	3.0
1	A	188	GLY	3.0
1	B	143	TYR	3.0
1	A	186	PHE	2.9
1	B	98	LYS	2.8
1	A	32	PRO	2.6
1	A	216	TYR	2.4
1	A	98	LYS	2.4
1	A	372	TRP	2.4
1	A	187	LYS	2.3
1	B	192	LYS	2.2
1	A	189	LEU	2.2
1	A	33	GLN	2.1
1	B	189	LEU	2.0
1	B	33	GLN	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

There are no carbohydrates in this entry.

## 6.4 Ligands

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	GOL	B	401	6/6	0.11	0.24	40,50,52,53	0
2	ZN	A	400	1/1	0.08	-0.28	19,19,19,19	0
2	ZN	B	400	1/1	0.08	-0.64	18,18,18,18	0

## 6.5 Other polymers

There are no such residues in this entry.