



# wwPDB X-ray Structure Validation Summary Report

Sep 13, 2020 – 09:21 PM BST

PDB ID : 5JWI  
Title : Crystal structure of Porphyromonas endodontalis DPP11 in complex with dipeptide Arg-Glu  
Authors : Bezerra, G.A.; Fedosyuk, S.; Ohara-Nemoto, Y.; Nemoto, T.K.; Djinovic-Carugo, K.  
Deposited on : 2016-05-12  
Resolution : 2.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

<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 : 2.14.4.dev1  
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) : 2.14.4.dev1

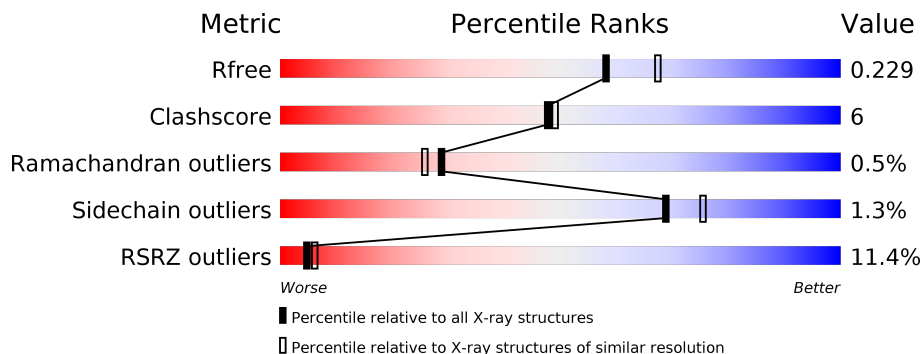
# 1 Overall quality at a glance

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  $\geq 3$ , 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	703	
1	B	703	

## 2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 11093 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.

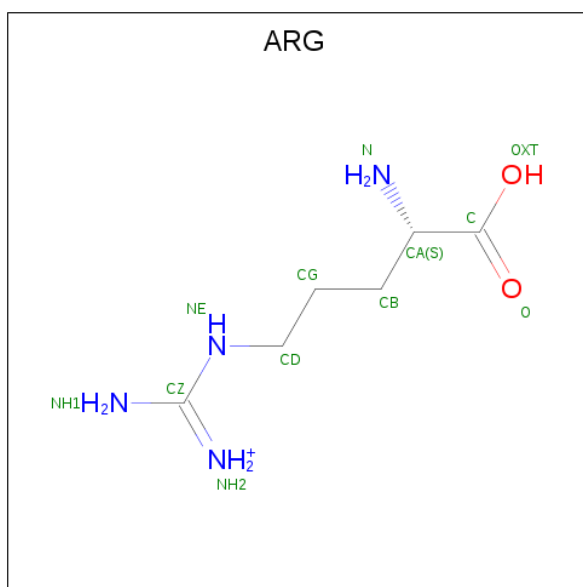
- Molecule 1 is a protein called Asp/Glu-specific dipeptidyl-peptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	697	5511	3493	955	1038	25	0	1	0
1	B	677	5038	3177	881	959	21	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

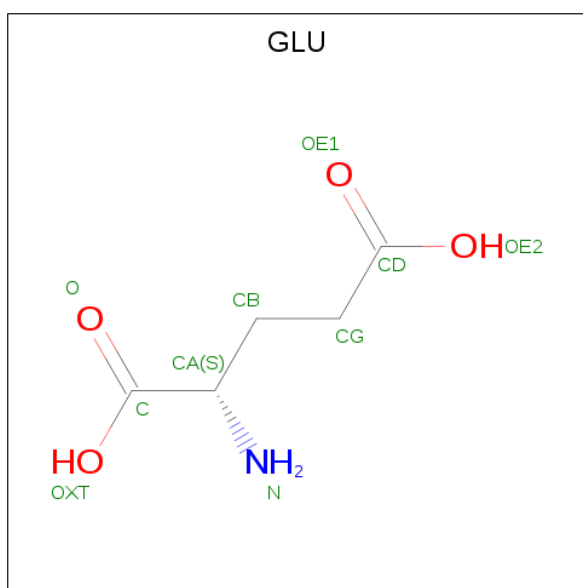
Chain	Residue	Modelled	Actual	Comment	Reference
A	21	MET	-	initiating methionine	UNP F8WQK8
A	652	ALA	SER	engineered mutation	UNP F8WQK8
A	718	HIS	-	expression tag	UNP F8WQK8
A	719	HIS	-	expression tag	UNP F8WQK8
A	720	HIS	-	expression tag	UNP F8WQK8
A	721	HIS	-	expression tag	UNP F8WQK8
A	722	HIS	-	expression tag	UNP F8WQK8
A	723	HIS	-	expression tag	UNP F8WQK8
B	21	MET	-	initiating methionine	UNP F8WQK8
B	652	ALA	SER	engineered mutation	UNP F8WQK8
B	718	HIS	-	expression tag	UNP F8WQK8
B	719	HIS	-	expression tag	UNP F8WQK8
B	720	HIS	-	expression tag	UNP F8WQK8
B	721	HIS	-	expression tag	UNP F8WQK8
B	722	HIS	-	expression tag	UNP F8WQK8
B	723	HIS	-	expression tag	UNP F8WQK8

- Molecule 2 is ARGinine (three-letter code: ARG) (formula: C<sub>6</sub>H<sub>15</sub>N<sub>4</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			11	6	4	1		
2	B	1	Total	C	N	O	0	0
			11	6	4	1		

- Molecule 3 is GLUTAMIC ACID (three-letter code: GLU) (formula: C<sub>5</sub>H<sub>9</sub>NO<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			10	5	1	4		
3	B	1	Total	C	N	O	0	0
			10	5	1	4		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	2	Total Cl 2 2	0	0

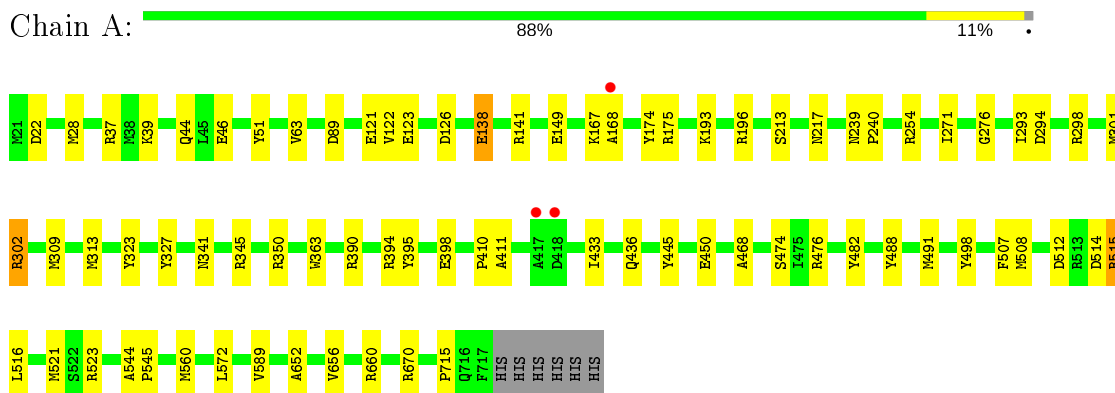
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	339	Total O 339 339	0	0
5	B	161	Total O 161 161	0	0

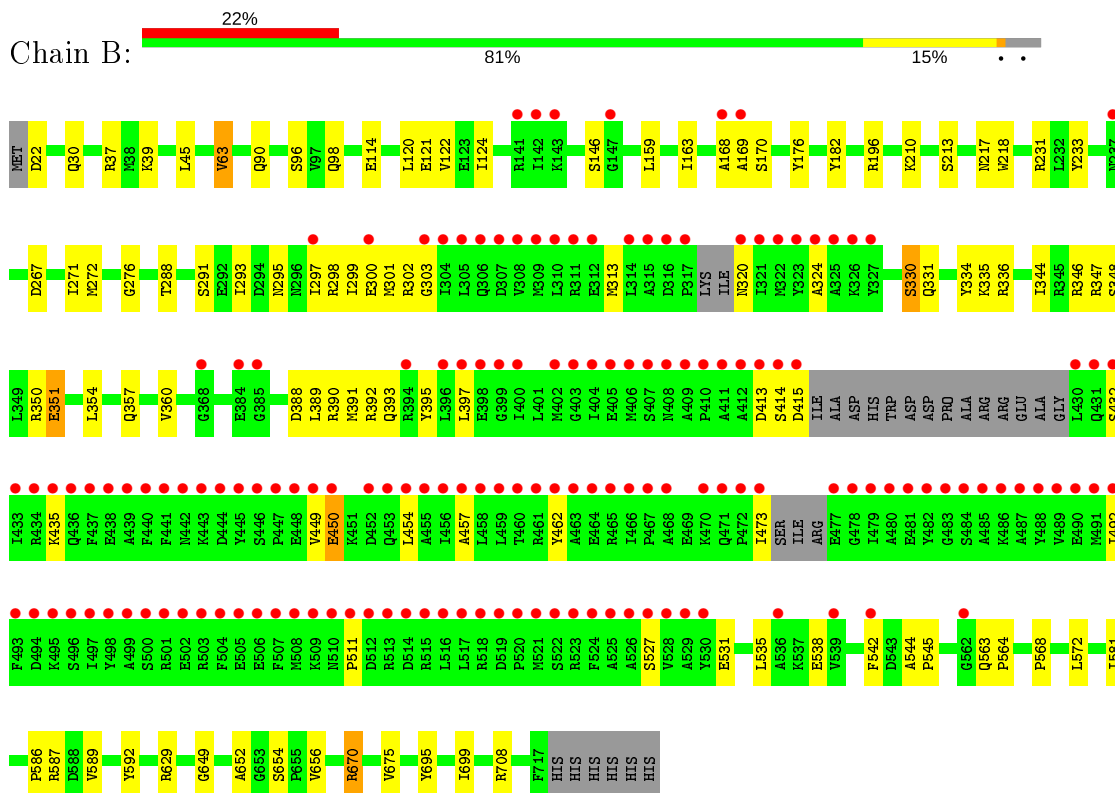
### 3 Residue-property plots

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 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: Asp/Glu-specific dipeptidyl-peptidase



- Molecule 1: Asp/Glu-specific dipeptidyl-peptidase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	111.44Å 112.53Å 148.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.57 – 2.10 47.57 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.8 (47.57-2.10) 98.8 (47.57-2.10)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.93 (at 2.10Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.189 , 0.229 0.191 , 0.229	Depositor DCC
$R_{free}$ test set	5385 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	40.3	Xtrriage
Anisotropy	0.233	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 50.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.023 for k,h,-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	11093	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.83% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical 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: CL

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	0.43	0/5636	0.55	2/7623 (0.0%)
1	B	0.38	0/5144	0.54	1/6990 (0.0%)
All	All	0.41	0/10780	0.55	3/14613 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	302	ARG	NE-CZ-NH2	-5.59	117.50	120.30
1	B	670	ARG	NE-CZ-NH2	-5.23	117.69	120.30
1	A	302	ARG	NE-CZ-NH1	5.09	122.85	120.30

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	5511	0	5354	57	0
1	B	5038	0	4631	69	0
2	A	11	0	12	0	0
2	B	11	0	12	0	0
3	A	10	0	6	2	0
3	B	10	0	6	1	0

*Continued on next page...*



Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	2	0	0	0	0
5	A	339	0	0	6	0
5	B	161	0	0	5	0
All	All	11093	0	10021	126	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.

The worst 5 of 126 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:298:ARG:HG3	1:A:302:ARG:HD3	1.59	0.84
1:B:182:TYR:OH	5:B:901:HOH:O	1.95	0.83
1:B:336:ARG:HH21	1:B:670:ARG:HH22	1.25	0.82
1:B:168:ALA:O	1:B:170:SER:N	2.17	0.78
1:A:254:ARG:NH1	5:A:901:HOH:O	2.12	0.77

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	696/703 (99%)	675 (97%)	20 (3%)	1 (0%)	51	54
1	B	669/703 (95%)	633 (95%)	30 (4%)	6 (1%)	17	12
All	All	1365/1406 (97%)	1308 (96%)	50 (4%)	7 (0%)	29	26

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	589	VAL

Continued on next page...

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	414	SER
1	B	589	VAL
1	B	146	SER
1	B	169	ALA

### 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	Rotameric	Outliers	Percentiles
1	A	563/583 (97%)	558 (99%)	5 (1%)	78 84
1	B	470/583 (81%)	462 (98%)	8 (2%)	60 67
All	All	1033/1166 (89%)	1020 (99%)	13 (1%)	69 75

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	63	VAL
1	B	330	SER
1	B	462	TYR
1	A	715	PRO
1	B	395	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	436	GLN
1	B	217	ASN
1	B	320	ASN
1	B	332	ASN
1	B	565	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 for Mogul analysis.

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	ARG	B	803	-	9,10,11	0.46	0	5,11,13	0.43	0
2	ARG	A	801	-	9,10,11	0.55	0	5,11,13	0.27	0
3	GLU	A	802	-	2,9,9	0.88	0	2,11,11	0.66	0
3	GLU	B	804	-	2,9,9	0.54	0	2,11,11	0.62	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	ARG	B	803	-	-	0/8/9/11	-
2	ARG	A	801	-	-	0/8/9/11	-
3	GLU	A	802	-	-	0/3/9/9	-
3	GLU	B	804	-	-	0/3/9/9	-

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.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	802	GLU	2	0
3	B	804	GLU	1	0

## 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, 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	697/703 (99%)	-0.16	3 (0%) 92 93	26, 41, 64, 84	0
1	B	677/703 (96%)	1.23	154 (22%) 0 0	28, 58, 157, 192	0
All	All	1374/1406 (97%)	0.52	157 (11%) 5 6	26, 47, 146, 192	0

The worst 5 of 157 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	323	TYR	10.9
1	B	517	LEU	10.9
1	B	169	ALA	10.4
1	B	439	ALA	10.3
1	B	489	VAL	10.1

### 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 monosaccharides 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, 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	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ARG	B	803	11/12	0.85	0.17	48,50,53,56	0
3	GLU	B	804	10/10	0.91	0.14	48,49,51,52	0
3	GLU	A	802	10/10	0.94	0.16	27,35,39,39	0
2	ARG	A	801	11/12	0.96	0.15	26,31,38,40	0
4	CL	B	801	1/1	0.98	0.12	56,56,56,56	0
4	CL	B	802	1/1	0.99	0.07	46,46,46,46	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.