



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2018 – 02:51 am GMT

PDB ID : 3E7M  
Title : Structure of murine iNOS oxygenase domain with inhibitor AR-C95791  
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Deposited on : 2008-08-18  
Resolution : 2.00 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.

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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 : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : trunk30967  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30967

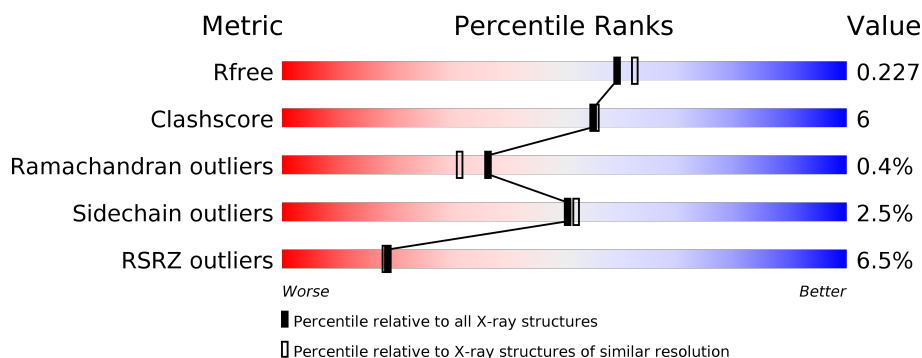
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
$R_{free}$	111664	7193 (2.00-2.00)
Clashscore	122126	8267 (2.00-2.00)
Ramachandran outliers	120053	8166 (2.00-2.00)
Sidechain outliers	120020	8165 (2.00-2.00)
RSRZ outliers	108989	7011 (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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	433	<div> <div>6%</div> <div> <div></div> <div>84%</div> <div>10%</div> <div>• •</div> </div> </div>
1	B	433	<div> <div>7%</div> <div> <div></div> <div>86%</div> <div>10%</div> <div>• •</div> </div> </div>



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.

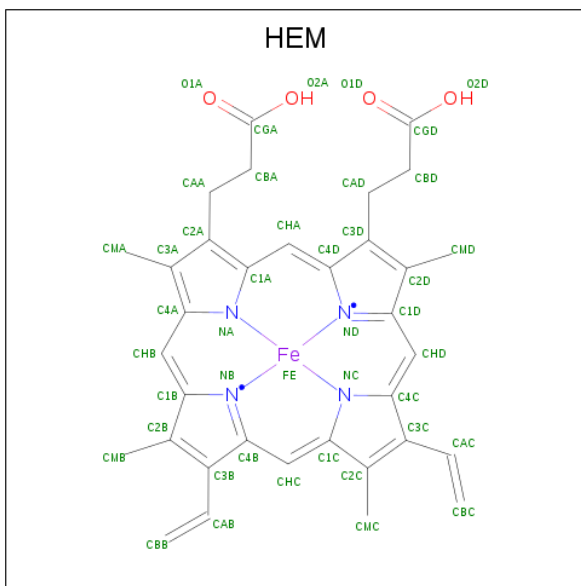
- Molecule 1 is a protein called Nitric oxide synthase, inducible.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	416	Total 3389	C 2174	N 583	O 612	S 20	0	0	0
1	B	421	Total 3421	C 2193	N 589	O 618	S 21	0	0	0

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

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

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).



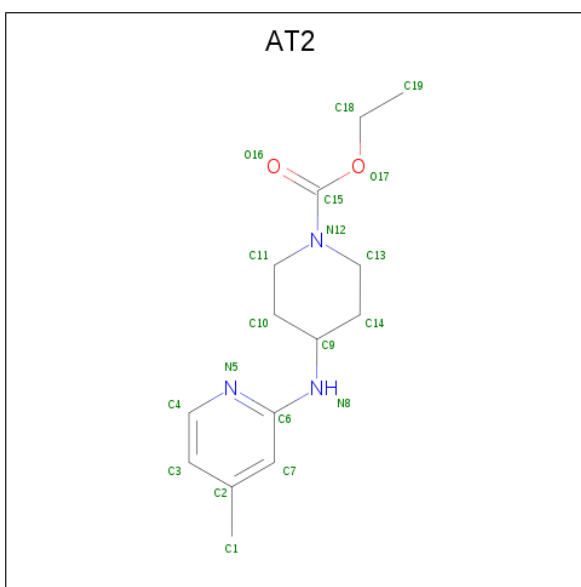
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 4 is 5,6,7,8-TETRAHYDROBIOPTERIN (three-letter code: H4B) (formula:  $C_9H_{15}N_5O_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			17	9	5	3		
4	B	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 5 is ETHYL 4-[(4-METHYLPYRIDIN-2-YL)AMINO]PIPERIDINE-1-CARBOXYLATE (three-letter code: AT2) (formula:  $C_{14}H_{21}N_3O_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			19	14	3	2		
5	B	1	Total	C	N	O	0	0
			19	14	3	2		

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



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

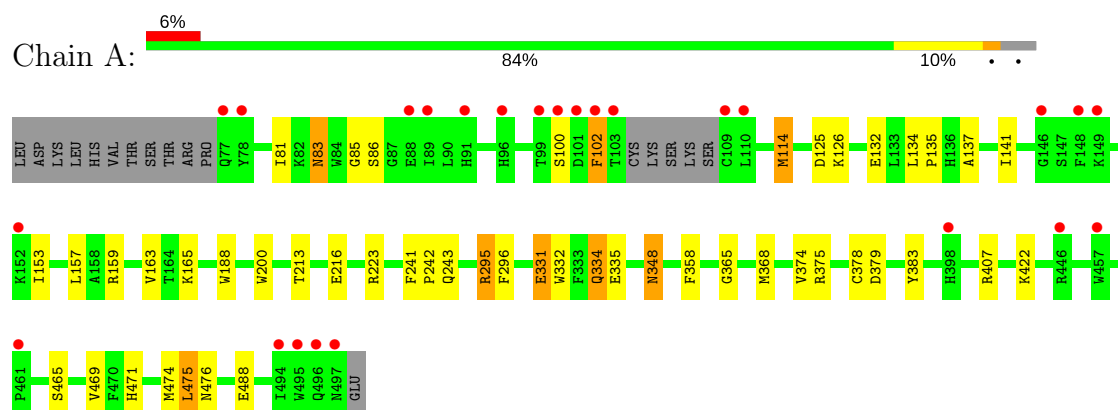
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	228	Total 228	O 228	0	0
7	B	278	Total 278	O 278	0	0

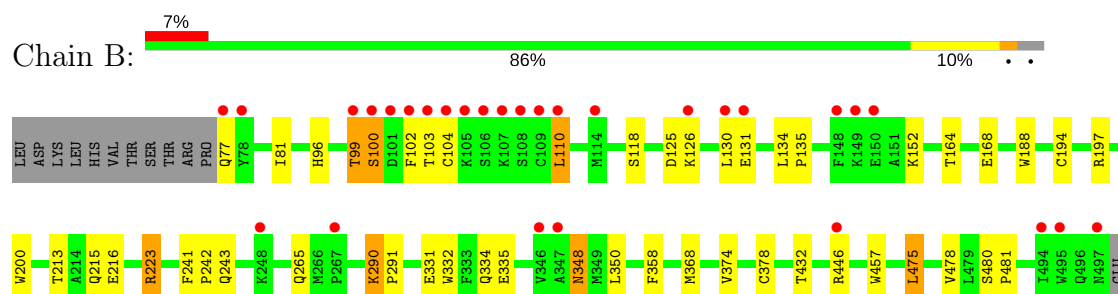
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Nitric oxide synthase, inducible



- Molecule 1: Nitric oxide synthase, inducible



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	213.85Å 213.85Å 116.64Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.96 – 2.00 39.41 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.7 (19.96-2.00) 98.7 (39.41-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.03	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.37 (at 2.00Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.223 , 0.237 0.214 , 0.227	Depositor DCC
$R_{free}$ test set	5249 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.3	Xtriage
Anisotropy	0.707	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 51.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7484	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.90% 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: HEM, ZN, AT2, H4B, EDO

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	0.33	0/3488	0.59	2/4743 (0.0%)
1	B	0.36	0/3521	0.63	1/4787 (0.0%)
All	All	0.34	0/7009	0.61	3/9530 (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	365	GLY	N-CA-C	-5.39	99.64	113.10
1	B	368	MET	N-CA-C	-5.19	96.98	111.00
1	A	368	MET	N-CA-C	-5.14	97.13	111.00

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	3389	0	3276	36	0
1	B	3421	0	3310	41	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	43	0	30	0	0
3	B	43	0	30	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	17	0	15	0	0
4	B	17	0	15	1	0
5	A	19	0	21	0	0
5	B	19	0	21	0	0
6	A	8	0	12	0	0
7	A	228	0	0	5	2
7	B	278	0	0	5	1
All	All	7484	0	6730	77	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 6.

The worst 5 of 77 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:103:THR:O	1:B:110:LEU:HD23	1.62	1.00
1:B:81:ILE:HD11	1:B:475:LEU:HD13	1.44	0.97
1:A:81:ILE:HD11	1:A:475:LEU:HD13	1.62	0.79
1:A:83:ASN:HD22	1:A:85:GLY:H	1.35	0.75
1:A:83:ASN:ND2	1:A:85:GLY:H	1.86	0.72

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)
7:A:1082:HOH:O	7:A:1082:HOH:O[11_655]	0.98	1.22
7:A:1376:HOH:O	7:A:1376:HOH:O[11_655]	1.19	1.01
7:B:1215:HOH:O	7:B:1303:HOH:O[9_766]	2.00	0.20

## 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	412/433 (95%)	393 (95%)	18 (4%)	1 (0%)	49	46
1	B	419/433 (97%)	402 (96%)	15 (4%)	2 (0%)	31	25
All	All	831/866 (96%)	795 (96%)	33 (4%)	3 (0%)	36	31

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	100	SER
1	B	100	SER
1	B	99	THR

### 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	362/381 (95%)	354 (98%)	8 (2%)	55	58
1	B	366/381 (96%)	356 (97%)	10 (3%)	48	49
All	All	728/762 (96%)	710 (98%)	18 (2%)	50	52

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	110	LEU
1	B	130	LEU
1	B	331	GLU
1	A	348	ASN
1	A	475	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	442	GLN
1	A	471	HIS
1	B	219	GLN

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Mol	Chain	Res	Type
1	A	421	GLN
1	B	215	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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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	$\# Z  > 2$
6	EDO	A	5001	-	3,3,3	0.60	0	2,2,2	0.60	0
6	EDO	A	5002	-	3,3,3	0.52	0	2,2,2	0.69	0
3	HEM	A	901	-	27,50,50	1.41	2 (7%)	17,82,82	1.09	1 (5%)
4	H4B	A	902	-	15,18,18	1.48	3 (20%)	11,26,26	1.95	4 (36%)
5	AT2	A	906	-	20,20,20	1.88	5 (25%)	26,26,26	1.44	4 (15%)
3	HEM	B	1901	-	27,50,50	1.45	3 (11%)	17,82,82	1.25	2 (11%)
4	H4B	B	1902	-	15,18,18	1.54	4 (26%)	11,26,26	1.85	3 (27%)
5	AT2	B	1906	-	20,20,20	1.81	5 (25%)	26,26,26	1.42	4 (15%)

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
6	EDO	A	5001	-	-	0/1/1/1	0/0/0/0
6	EDO	A	5002	-	-	0/1/1/1	0/0/0/0
3	HEM	A	901	-	-	0/6/54/54	0/0/8/8
4	H4B	A	902	-	-	0/8/17/17	0/2/2/2
5	AT2	A	906	-	-	0/11/21/21	0/2/2/2
3	HEM	B	1901	-	-	0/6/54/54	0/0/8/8
4	H4B	B	1902	-	-	0/8/17/17	0/2/2/2
5	AT2	B	1906	-	-	0/11/21/21	0/2/2/2

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	902	H4B	C7-C6	-3.91	1.48	1.52
3	A	901	HEM	C3B-CAB	-3.73	1.40	1.47
3	B	1901	HEM	C3B-CAB	-3.58	1.40	1.47
4	B	1902	H4B	C7-C6	-3.15	1.49	1.52
3	B	1901	HEM	C3C-CAC	-3.11	1.41	1.47

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	906	AT2	C3-C4-N5	-2.82	120.49	123.92
5	B	1906	AT2	C3-C4-N5	-2.67	120.67	123.92
4	A	902	H4B	N3-C2-N1	-2.65	121.21	125.43
4	B	1902	H4B	N3-C2-N1	-2.55	121.38	125.43
5	B	1906	AT2	O16-C15-N12	-2.36	120.25	124.36

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1902	H4B	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	416/433 (96%)	0.18	25 (6%)	22 21	23, 35, 51, 64	2 (0%)
1	B	421/433 (97%)	0.26	29 (6%)	17 16	22, 33, 50, 67	7 (1%)
All	All	837/866 (96%)	0.22	54 (6%)	19 18	22, 34, 50, 67	9 (1%)

The worst 5 of 54 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	102	PHE	12.2
1	B	100	SER	9.5
1	A	102	PHE	7.8
1	B	109	CYS	7.3
1	B	105	LYS	7.1

### 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 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, 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
6	EDO	A	5002	4/4	0.83	0.14	55,55,55,55	0
6	EDO	A	5001	4/4	0.85	0.10	52,54,55,55	0
2	ZN	A	900	1/1	0.90	0.15	45,45,45,45	1
4	H4B	B	1902	17/17	0.94	0.18	22,25,28,29	0
4	H4B	A	902	17/17	0.94	0.21	23,25,29,29	0
5	AT2	A	906	19/19	0.96	0.17	20,22,29,30	0
5	AT2	B	1906	19/19	0.96	0.20	18,22,28,30	0
2	ZN	B	1900	1/1	0.97	0.20	34,34,34,34	1
3	HEM	B	1901	43/43	0.98	0.18	18,22,25,26	0
3	HEM	A	901	43/43	0.98	0.16	21,24,26,29	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.