



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 11:50 am GMT

PDB ID : 1NDS  
Title : CRYSTALLOGRAPHIC STRUCTURE OF A SUBSTRATE BOUND BLUE COPPER NITRITE REDUCTASE FROM ALCALIGENES XYLOSOXIDANS  
Authors : Dodd, F.E.; Hasnain, S.S.; Abraham, Z.H.L.; Eady, R.R.; Smith, B.E.  
Deposited on : 1997-01-23  
Resolution : 2.80 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

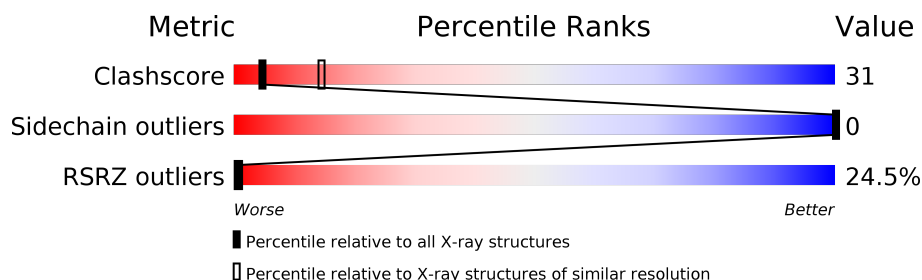
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
Clashscore	112137	3033 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (2.80-2.80)

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	330	<div> <div>25%</div> <div>94%</div> <div>6%</div> </div>
1	B	330	<div> <div>26%</div> <div>94%</div> <div>6%</div> </div>
1	C	330	<div> <div>23%</div> <div>94%</div> <div>6%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 1179 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 NITRITE REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	330	Total	C	N	O	S	0	0	323
			387	361	17	7	2			
1	B	330	Total	C	N	O	S	0	0	323
			387	361	17	7	2			
1	C	330	Total	C	N	O	S	0	0	323
			387	361	17	7	2			

There are 117 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	13	PRO	GLN	CONFLICT	UNP P81445
A	16	ALA	LYS	CONFLICT	UNP P81445
A	29	SER	GLU	CONFLICT	UNP P81445
A	32	ALA	VAL	CONFLICT	UNP P81445
A	33	ALA	SER	CONFLICT	UNP P81445
A	35	ALA	PRO	CONFLICT	UNP P81445
A	52	ALA	ILE	CONFLICT	UNP P81445
A	55	ASP	GLN	CONFLICT	UNP P81445
A	59	ALA	LEU	CONFLICT	UNP P81445
A	68	VAL	MET	CONFLICT	UNP P81445
A	120	ALA	VAL	CONFLICT	UNP P81445
A	139	ALA	GLN	CONFLICT	UNP P81445
A	165	ALA	PRO	CONFLICT	UNP P81445
A	166	ALA	GLN	CONFLICT	UNP P81445
A	168	ALA	LYS	CONFLICT	UNP P81445
A	169	ALA	LEU	CONFLICT	UNP P81445
A	171	ALA	HIS	CONFLICT	UNP P81445
A	185	VAL	ILE	CONFLICT	UNP P81445
A	188	ALA	ASP	CONFLICT	UNP P81445
A	189	ALA	LYS	CONFLICT	UNP P81445
A	192	ASN	HIS	CONFLICT	UNP P81445
A	194	SER	LYS	CONFLICT	UNP P81445
A	198	ALA	ASP	CONFLICT	UNP P81445

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Chain	Residue	Modelled	Actual	Comment	Reference
A	202	ALA	SER	CONFLICT	UNP P81445
A	204	ALA	GLN	CONFLICT	UNP P81445
A	207	VAL	ARG	CONFLICT	UNP P81445
A	218	ALA	VAL	CONFLICT	UNP P81445
A	223	ALA	ARG	CONFLICT	UNP P81445
A	235	ALA	SER	CONFLICT	UNP P81445
A	236	ALA	LYS	CONFLICT	UNP P81445
A	243	ILE	PHE	CONFLICT	UNP P81445
A	276	LEU	ARG	CONFLICT	UNP P81445
A	289	ALA	VAL	CONFLICT	UNP P81445
A	302	ALA	VAL	CONFLICT	UNP P81445
A	317	ALA	LEU	CONFLICT	UNP P81445
A	320	ALA	ILE	CONFLICT	UNP P81445
A	321	SER	LYS	CONFLICT	UNP P81445
A	333	SER	GLN	CONFLICT	UNP P81445
A	335	ALA	LYS	CONFLICT	UNP P81445
B	13	PRO	GLN	CONFLICT	UNP P81445
B	16	ALA	LYS	CONFLICT	UNP P81445
B	29	SER	GLU	CONFLICT	UNP P81445
B	32	ALA	VAL	CONFLICT	UNP P81445
B	33	ALA	SER	CONFLICT	UNP P81445
B	35	ALA	PRO	CONFLICT	UNP P81445
B	52	ALA	ILE	CONFLICT	UNP P81445
B	55	ASP	GLN	CONFLICT	UNP P81445
B	59	ALA	LEU	CONFLICT	UNP P81445
B	68	VAL	MET	CONFLICT	UNP P81445
B	120	ALA	VAL	CONFLICT	UNP P81445
B	139	ALA	GLN	CONFLICT	UNP P81445
B	165	ALA	PRO	CONFLICT	UNP P81445
B	166	ALA	GLN	CONFLICT	UNP P81445
B	168	ALA	LYS	CONFLICT	UNP P81445
B	169	ALA	LEU	CONFLICT	UNP P81445
B	171	ALA	HIS	CONFLICT	UNP P81445
B	185	VAL	ILE	CONFLICT	UNP P81445
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B	194	SER	LYS	CONFLICT	UNP P81445
B	198	ALA	ASP	CONFLICT	UNP P81445
B	202	ALA	SER	CONFLICT	UNP P81445
B	204	ALA	GLN	CONFLICT	UNP P81445
B	207	VAL	ARG	CONFLICT	UNP P81445

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Chain	Residue	Modelled	Actual	Comment	Reference
B	218	ALA	VAL	CONFLICT	UNP P81445
B	223	ALA	ARG	CONFLICT	UNP P81445
B	235	ALA	SER	CONFLICT	UNP P81445
B	236	ALA	LYS	CONFLICT	UNP P81445
B	243	ILE	PHE	CONFLICT	UNP P81445
B	276	LEU	ARG	CONFLICT	UNP P81445
B	289	ALA	VAL	CONFLICT	UNP P81445
B	302	ALA	VAL	CONFLICT	UNP P81445
B	317	ALA	LEU	CONFLICT	UNP P81445
B	320	ALA	ILE	CONFLICT	UNP P81445
B	321	SER	LYS	CONFLICT	UNP P81445
B	333	SER	GLN	CONFLICT	UNP P81445
B	335	ALA	LYS	CONFLICT	UNP P81445
C	13	PRO	GLN	CONFLICT	UNP P81445
C	16	ALA	LYS	CONFLICT	UNP P81445
C	29	SER	GLU	CONFLICT	UNP P81445
C	32	ALA	VAL	CONFLICT	UNP P81445
C	33	ALA	SER	CONFLICT	UNP P81445
C	35	ALA	PRO	CONFLICT	UNP P81445
C	52	ALA	ILE	CONFLICT	UNP P81445
C	55	ASP	GLN	CONFLICT	UNP P81445
C	59	ALA	LEU	CONFLICT	UNP P81445
C	68	VAL	MET	CONFLICT	UNP P81445
C	120	ALA	VAL	CONFLICT	UNP P81445
C	139	ALA	GLN	CONFLICT	UNP P81445
C	165	ALA	PRO	CONFLICT	UNP P81445
C	166	ALA	GLN	CONFLICT	UNP P81445
C	168	ALA	LYS	CONFLICT	UNP P81445
C	169	ALA	LEU	CONFLICT	UNP P81445
C	171	ALA	HIS	CONFLICT	UNP P81445
C	185	VAL	ILE	CONFLICT	UNP P81445
C	188	ALA	ASP	CONFLICT	UNP P81445
C	189	ALA	LYS	CONFLICT	UNP P81445
C	192	ASN	HIS	CONFLICT	UNP P81445
C	194	SER	LYS	CONFLICT	UNP P81445
C	198	ALA	ASP	CONFLICT	UNP P81445
C	202	ALA	SER	CONFLICT	UNP P81445
C	204	ALA	GLN	CONFLICT	UNP P81445
C	207	VAL	ARG	CONFLICT	UNP P81445
C	218	ALA	VAL	CONFLICT	UNP P81445
C	223	ALA	ARG	CONFLICT	UNP P81445
C	235	ALA	SER	CONFLICT	UNP P81445

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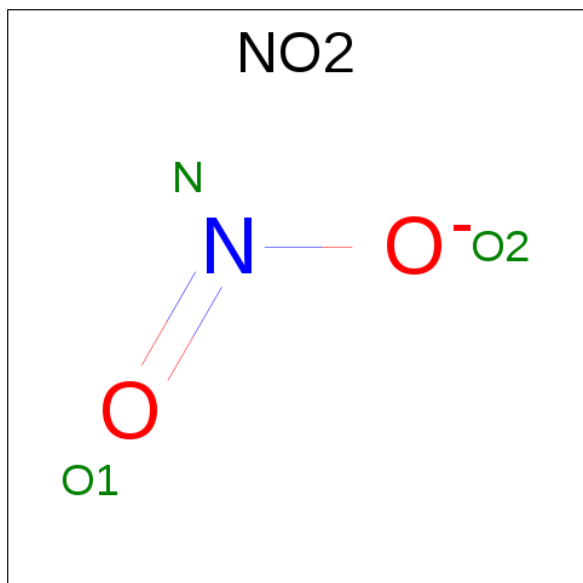
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Chain	Residue	Modelled	Actual	Comment	Reference
C	236	ALA	LYS	CONFLICT	UNP P81445
C	243	ILE	PHE	CONFLICT	UNP P81445
C	276	LEU	ARG	CONFLICT	UNP P81445
C	289	ALA	VAL	CONFLICT	UNP P81445
C	302	ALA	VAL	CONFLICT	UNP P81445
C	317	ALA	LEU	CONFLICT	UNP P81445
C	320	ALA	ILE	CONFLICT	UNP P81445
C	321	SER	LYS	CONFLICT	UNP P81445
C	333	SER	GLN	CONFLICT	UNP P81445
C	335	ALA	LYS	CONFLICT	UNP P81445

- Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

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

- Molecule 3 is NITRITE ION (three-letter code: NO2) (formula: NO<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total N O 3 1 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	N	O	0	0
			3	1	2		
3	C	1	Total	N	O	0	0
			3	1	2		

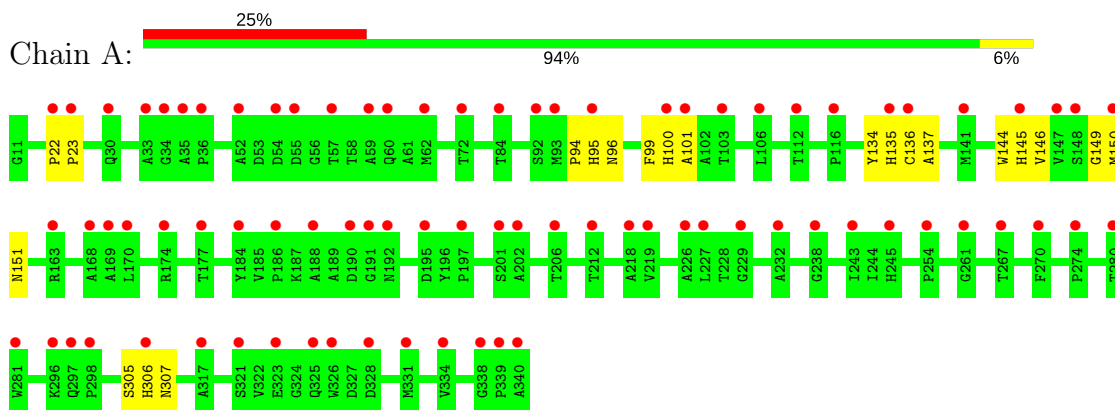
- Molecule 4 is water.

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

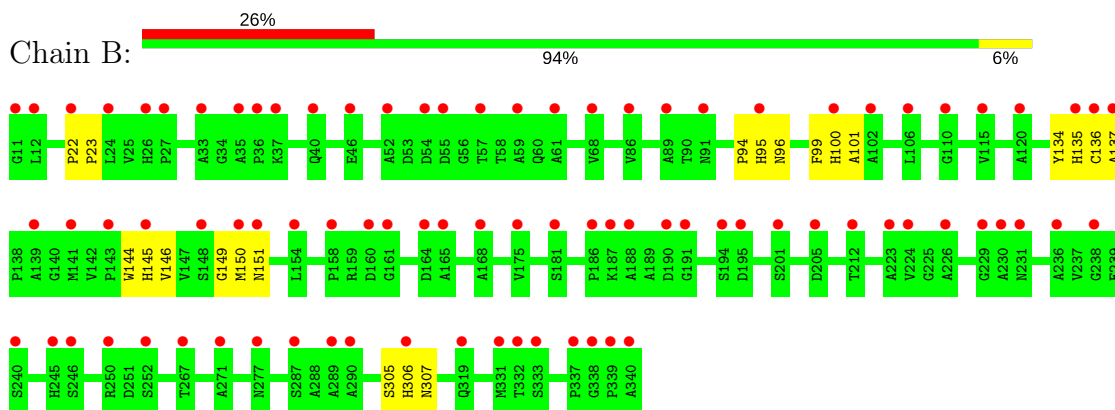
### 3 Residue-property plots [i](#)

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.

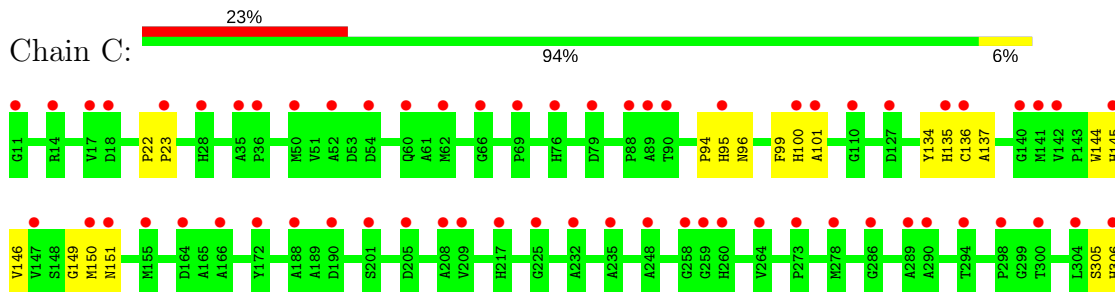
#### • Molecule 1: NITRITE REDUCTASE



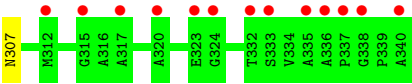
#### • Molecule 1: NITRITE REDUCTASE



#### • Molecule 1: NITRITE REDUCTASE







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.89Å 102.20Å 151.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.80 53.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	90.2 (8.00-2.80) 91.0 (53.00-2.80)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	8.90 (at 2.81Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, $R_{free}$	0.236 , 0.280 0.483 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	28.2	Xtriage
Anisotropy	0.257	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	1.22 , 639.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.41	EDS
Total number of atoms	1179	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	10.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.84% 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: NO2, CU

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	0.34	0/63	0.66	0/75
1	B	0.40	0/63	0.65	0/75
1	C	0.41	0/63	0.69	0/75
All	All	0.38	0/189	0.67	0/225

There are no bond length outliers.

There are no bond angle outliers.

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	387	0	42	14	0
1	B	387	0	42	13	0
1	C	387	0	42	13	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
3	A	3	0	0	1	0
3	B	3	0	0	0	0
3	C	3	0	0	0	0
4	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	1	0	0	0	0
4	C	1	0	0	0	0
All	All	1179	0	126	40	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 31.

All (40) 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:306:HIS:C	1:B:307:ASN:CA	2.40	0.90
1:C:136:CYS:C	1:C:137:ALA:CA	2.41	0.89
1:A:306:HIS:C	1:A:307:ASN:CA	2.41	0.89
1:A:136:CYS:C	1:A:137:ALA:CA	2.42	0.88
1:B:136:CYS:C	1:B:137:ALA:CA	2.41	0.88
1:C:150:MET:C	1:C:151:ASN:CA	2.42	0.88
1:C:145:HIS:C	1:C:146:VAL:CA	2.42	0.88
1:B:150:MET:C	1:B:151:ASN:CA	2.43	0.87
1:B:100:HIS:C	1:B:101:ALA:CA	2.43	0.87
1:C:306:HIS:C	1:C:307:ASN:CA	2.43	0.87
1:B:145:HIS:C	1:B:146:VAL:CA	2.44	0.86
1:A:150:MET:C	1:A:151:ASN:CA	2.45	0.85
1:C:100:HIS:C	1:C:101:ALA:CA	2.44	0.85
1:A:100:HIS:C	1:A:101:ALA:CA	2.44	0.85
1:A:145:HIS:C	1:A:146:VAL:CA	2.46	0.84
1:C:95:HIS:C	1:C:96:ASN:CA	2.47	0.83
1:A:99:PHE:CA	1:A:100:HIS:N	2.42	0.83
1:B:95:HIS:C	1:B:96:ASN:CA	2.47	0.83
1:C:99:PHE:CA	1:C:100:HIS:N	2.41	0.82
1:A:149:GLY:CA	1:A:150:MET:N	2.43	0.82
1:B:149:GLY:CA	1:B:150:MET:N	2.42	0.82
1:B:144:TRP:CA	1:B:145:HIS:N	2.43	0.81
1:A:95:HIS:C	1:A:96:ASN:CA	2.48	0.81
1:C:149:GLY:CA	1:C:150:MET:N	2.43	0.81
1:B:99:PHE:CA	1:B:100:HIS:N	2.43	0.80
1:A:134:TYR:CA	1:A:135:HIS:N	2.43	0.80
1:A:144:TRP:CA	1:A:145:HIS:N	2.44	0.80
1:A:305:SER:CA	1:A:306:HIS:N	2.45	0.80
1:B:94:PRO:CA	1:B:95:HIS:N	2.44	0.80
1:B:134:TYR:CA	1:B:135:HIS:N	2.45	0.80
1:C:144:TRP:CA	1:C:145:HIS:N	2.44	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:134:TYR:CA	1:C:135:HIS:N	2.46	0.78
1:A:94:PRO:CA	1:A:95:HIS:N	2.47	0.77
1:B:305:SER:CA	1:B:306:HIS:N	2.46	0.77
1:C:305:SER:CA	1:C:306:HIS:N	2.48	0.76
1:C:94:PRO:CA	1:C:95:HIS:N	2.48	0.76
1:C:22:PRO:CA	1:C:23:PRO:CA	2.95	0.44
1:A:22:PRO:CA	1:A:23:PRO:CA	2.97	0.43
1:B:22:PRO:CA	1:B:23:PRO:CA	2.97	0.42
1:A:135:HIS:CE1	3:A:503:NO2:O1	2.75	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

### 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	7/245 (3%)	7 (100%)	0	100	100
1	B	7/245 (3%)	7 (100%)	0	100	100
1	C	7/245 (3%)	7 (100%)	0	100	100
All	All	21/735 (3%)	21 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 9 ligands modelled in this entry, 6 are monoatomic - leaving 3 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	$\# Z  > 2$
3	NO2	A	503	2	1,2,2	1.00	0	0,1,1	0.00	-
3	NO2	B	503	2	1,2,2	0.99	0	0,1,1	0.00	-
3	NO2	C	503	2	1,2,2	0.99	0	0,1,1	0.00	-

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
3	NO2	A	503	2	-	0/0/0/0	0/0/0/0
3	NO2	B	503	2	-	0/0/0/0	0/0/0/0
3	NO2	C	503	2	-	0/0/0/0	0/0/0/0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	503	NO2	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

### 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	330/330 (100%)	1.42	81 (24%) <b>1</b> <b>1</b>	2, 8, 35, 71	0
1	B	330/330 (100%)	1.42	86 (26%) <b>1</b> <b>0</b>	2, 8, 35, 71	0
1	C	330/330 (100%)	1.43	76 (23%) <b>1</b> <b>1</b>	2, 8, 35, 71	0
All	All	990/990 (100%)	1.42	243 (24%) <b>1</b> <b>1</b>	2, 8, 36, 71	0

All (243) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	340	ALA	26.3
1	A	339	PRO	13.2
1	C	35	ALA	11.6
1	A	54	ASP	11.5
1	A	191	GLY	11.4
1	A	101	ALA	10.4
1	C	89	ALA	9.9
1	A	188	ALA	8.7
1	C	60	GLN	8.4
1	C	127	ASP	8.0
1	B	338	GLY	7.9
1	A	60	GLN	7.3
1	A	340	ALA	7.0
1	B	33	ALA	6.9
1	B	332	THR	6.9
1	B	188	ALA	6.8
1	B	55	ASP	6.7
1	C	304	LEU	6.7
1	A	36	PRO	6.6
1	C	151	ASN	6.5
1	C	286	GLY	6.1
1	A	296	LYS	6.0
1	C	136	CYS	5.9

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Mol	Chain	Res	Type	RSRZ
1	B	240	SER	5.6
1	B	137	ALA	5.6
1	C	205	ASP	5.3
1	B	35	ALA	5.1
1	C	298	PRO	5.1
1	C	18	ASP	5.1
1	B	37	LYS	5.0
1	B	136	CYS	5.0
1	A	243	ILE	5.0
1	B	339	PRO	5.0
1	B	331	MET	4.7
1	B	95	HIS	4.7
1	C	54	ASP	4.7
1	C	95	HIS	4.5
1	C	135	HIS	4.4
1	A	201	SER	4.4
1	B	143	PRO	4.4
1	B	135	HIS	4.4
1	B	250	ARG	4.4
1	B	187	LYS	4.4
1	A	135	HIS	4.3
1	A	270	PHE	4.2
1	B	141	MET	4.2
1	A	136	CYS	4.2
1	A	321	SER	4.1
1	B	27	PRO	4.1
1	B	161	GLY	4.1
1	B	168	ALA	4.1
1	C	217	HIS	4.0
1	A	261	GLY	4.0
1	C	150	MET	4.0
1	A	35	ALA	3.9
1	A	306	HIS	3.8
1	B	245	HIS	3.8
1	B	340	ALA	3.8
1	B	306	HIS	3.8
1	B	238	GLY	3.8
1	B	226	ALA	3.8
1	C	323	GLU	3.8
1	A	106	LEU	3.7
1	C	306	HIS	3.7
1	C	14	ARG	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	22	PRO	3.7
1	C	66	GLY	3.6
1	C	145	HIS	3.6
1	A	334	VAL	3.6
1	A	116	PRO	3.6
1	A	202	ALA	3.6
1	B	115	VAL	3.5
1	A	95	HIS	3.5
1	B	205	ASP	3.5
1	C	300	THR	3.5
1	C	17	VAL	3.5
1	B	54	ASP	3.5
1	B	194	SER	3.4
1	C	28	HIS	3.4
1	A	145	HIS	3.4
1	A	280	THR	3.4
1	C	88	PRO	3.3
1	A	59	ALA	3.3
1	A	212	THR	3.3
1	C	100	HIS	3.3
1	B	36	PRO	3.3
1	A	33	ALA	3.2
1	C	23	PRO	3.2
1	A	227	LEU	3.2
1	A	298	PRO	3.2
1	B	22	PRO	3.2
1	A	100	HIS	3.2
1	A	62	MET	3.2
1	B	106	LEU	3.2
1	C	332	THR	3.2
1	B	164	ASP	3.2
1	B	100	HIS	3.1
1	C	166	ALA	3.1
1	C	264	VAL	3.1
1	A	254	PRO	3.1
1	B	191	GLY	3.1
1	B	89	ALA	3.1
1	B	158	PRO	3.1
1	B	201	SER	3.0
1	B	229	GLY	3.0
1	A	170	LEU	3.0
1	A	184	TYR	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	145	HIS	3.0
1	A	30	GLN	3.0
1	A	163	ARG	3.0
1	A	232	ALA	3.0
1	A	93	MET	3.0
1	C	190	ASP	3.0
1	B	68	VAL	3.0
1	B	231	ASN	2.9
1	C	209	VAL	2.9
1	B	290	ALA	2.9
1	C	225	GLY	2.9
1	C	141	MET	2.9
1	C	248	ALA	2.9
1	B	150	MET	2.8
1	B	110	GLY	2.8
1	A	192	ASN	2.8
1	A	331	MET	2.8
1	B	165	ALA	2.8
1	C	208	ALA	2.8
1	B	57	THR	2.8
1	C	69	PRO	2.8
1	A	103	THR	2.8
1	C	201	SER	2.8
1	A	92	SER	2.8
1	C	101	ALA	2.8
1	B	151	ASN	2.7
1	B	61	ALA	2.7
1	A	197	PRO	2.7
1	B	271	ALA	2.7
1	B	277	ASN	2.7
1	B	12	LEU	2.7
1	C	147	VAL	2.7
1	A	325	GLN	2.7
1	B	289	ALA	2.7
1	C	232	ALA	2.7
1	C	336	ALA	2.7
1	B	139	ALA	2.7
1	B	160	ASP	2.7
1	B	287	SER	2.6
1	B	236	ALA	2.6
1	A	326	TRP	2.6
1	A	57	THR	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	320	ALA	2.6
1	B	267	THR	2.6
1	C	140	GLY	2.6
1	B	102	ALA	2.6
1	A	229	GLY	2.6
1	A	238	GLY	2.6
1	C	235	ALA	2.6
1	C	333	SER	2.5
1	A	84	THR	2.5
1	C	260	HIS	2.5
1	C	110	GLY	2.5
1	B	212	THR	2.5
1	A	174	ARG	2.5
1	C	36	PRO	2.5
1	A	226	ALA	2.5
1	B	40	GLN	2.5
1	C	50	MET	2.5
1	C	62	MET	2.5
1	A	186	PRO	2.4
1	B	337	PRO	2.4
1	A	52	ALA	2.4
1	B	11	GLY	2.4
1	C	11	GLY	2.4
1	C	278	MET	2.4
1	C	289	ALA	2.4
1	B	86	VAL	2.4
1	A	190	ASP	2.4
1	B	333	SER	2.4
1	C	312	MET	2.4
1	B	148	SER	2.4
1	A	168	ALA	2.3
1	C	337	PRO	2.3
1	B	224	VAL	2.3
1	A	112	THR	2.3
1	C	338	GLY	2.3
1	A	55	ASP	2.3
1	C	79	ASP	2.3
1	A	338	GLY	2.3
1	A	245	HIS	2.3
1	A	141	MET	2.3
1	B	120	ALA	2.3
1	C	155	MET	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	195	ASP	2.3
1	A	281	TRP	2.3
1	A	34	GLY	2.3
1	C	317	ALA	2.3
1	B	24	LEU	2.2
1	A	297	GLN	2.2
1	A	169	ALA	2.2
1	B	26	HIS	2.2
1	B	319	GLN	2.2
1	B	223	ALA	2.2
1	B	186	PRO	2.2
1	C	76	HIS	2.2
1	A	219	VAL	2.2
1	A	72	THR	2.2
1	B	175	VAL	2.2
1	A	148	SER	2.2
1	B	181	SER	2.2
1	C	290	ALA	2.2
1	A	150	MET	2.2
1	C	259	GLY	2.2
1	B	91	ASN	2.2
1	C	164	ASP	2.2
1	B	52	ALA	2.2
1	C	315	GLY	2.2
1	A	323	GLU	2.2
1	C	335	ALA	2.1
1	A	206	THR	2.1
1	A	177	THR	2.1
1	C	172	TYR	2.1
1	B	154	LEU	2.1
1	A	23	PRO	2.1
1	B	252	SER	2.1
1	B	46	GLU	2.1
1	C	52	ALA	2.1
1	B	246	SER	2.1
1	A	317	ALA	2.1
1	A	267	THR	2.1
1	B	190	ASP	2.1
1	C	273	PRO	2.1
1	B	195	ASP	2.1
1	A	274	PRO	2.1
1	A	328	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	218	ALA	2.0
1	C	258	GLY	2.0
1	C	188	ALA	2.0
1	C	324	GLY	2.0
1	A	147	VAL	2.0
1	B	59	ALA	2.0
1	B	230	ALA	2.0
1	C	90	THR	2.0
1	C	142	VAL	2.0
1	C	294	THR	2.0

## 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. 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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	NO2	B	503	3/3	0.91	0.55	-	29,29,29,29	0
3	NO2	A	503	3/3	0.89	0.61	-	29,29,29,29	0
3	NO2	C	503	3/3	0.92	0.43	-	29,29,29,29	0
2	CU	B	502	1/1	0.99	0.33	-	2,2,2,2	0
2	CU	B	501	1/1	0.98	0.40	-	10,10,10,10	0
2	CU	C	501	1/1	0.96	0.35	-	10,10,10,10	0
2	CU	A	501	1/1	0.94	0.27	-	10,10,10,10	0
2	CU	A	502	1/1	0.98	0.30	-	2,2,2,2	0
2	CU	C	502	1/1	0.98	0.28	-	2,2,2,2	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.