



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:04 PM 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
A user guide is available at
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

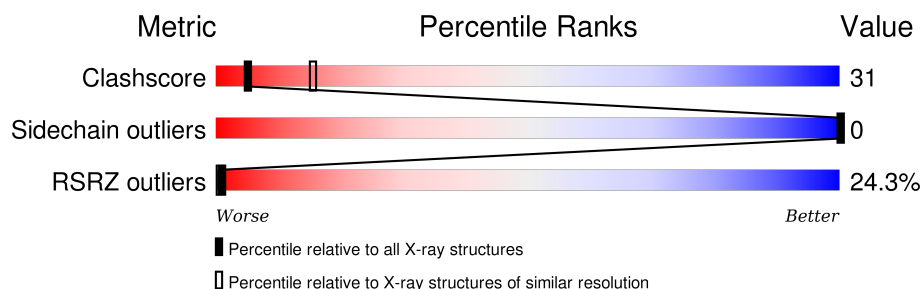
1 Overall quality at a glance

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	102246	2827 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (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 ≥ 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>22%</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
B	188	ALA	ASP	CONFLICT	UNP P81445
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B	192	ASN	HIS	CONFLICT	UNP P81445
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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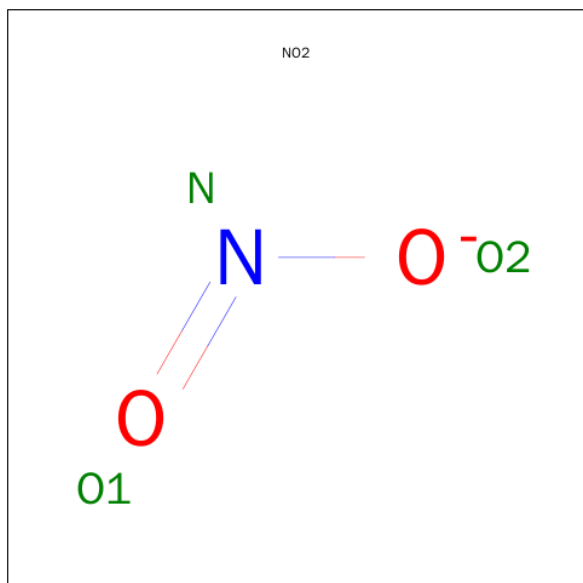
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Chain	Residue	Modelled	Actual	Comment	Reference
C	236	ALA	LYS	CONFLICT	UNP P81445
C	243	ILE	PHE	CONFLICT	UNP P81445
C	276	LEU	ARG	CONFLICT	UNP P81445
C	289	ALA	VAL	CONFLICT	UNP P81445
C	302	ALA	VAL	CONFLICT	UNP P81445
C	317	ALA	LEU	CONFLICT	UNP P81445
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: NO₂).



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		

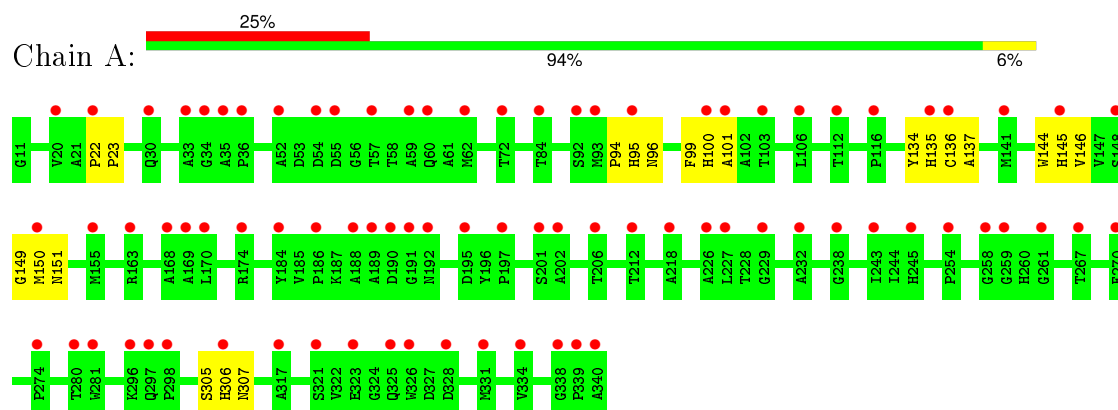
- Molecule 4 is water.

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		

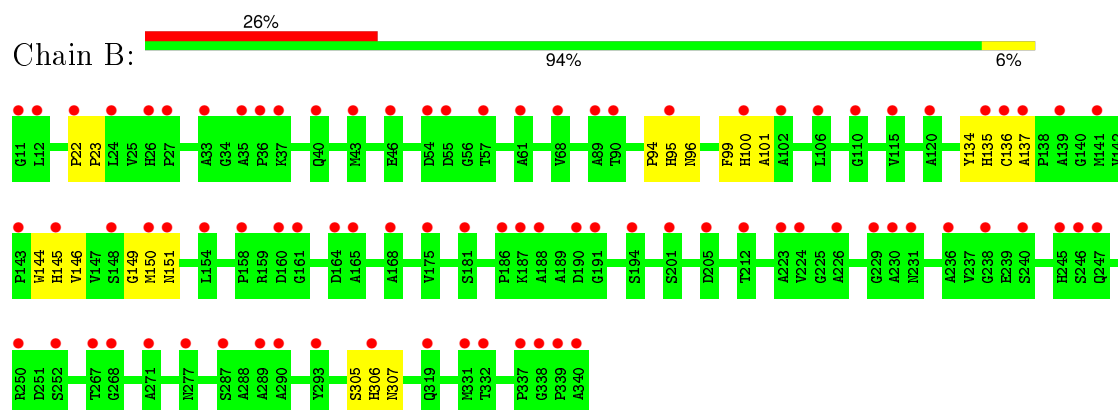
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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 ($\text{RSRZ} > 2$). 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.

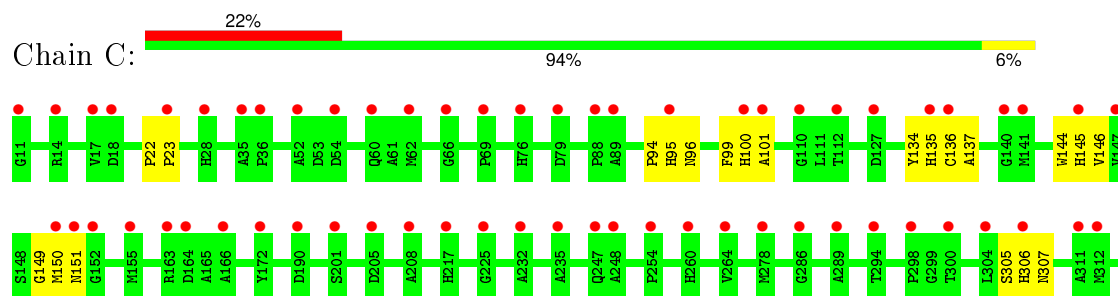
• Molecule 1: NITRITE REDUCTASE



• Molecule 1: NITRITE REDUCTASE



• Molecule 1: NITRITE REDUCTASE



G315	A316	A317	A320	S321	V322	E323	T332	S333	V334	A335	A336	P337	G338	P339	A340
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	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
$\langle I/\sigma(I) \rangle$ ¹	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 ²)	28.2	Xtriage
Anisotropy	0.257	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	1.25 , 650.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 24342 reflections (0.004%)	Xtriage
F_o, F_c correlation	0.41	EDS
Total number of atoms	1179	wwPDB-VP
Average B, all atoms (Å ²)	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.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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 ⓘ

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 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	2,2,2	0.38	0	1,1,1	0.31	0
3	NO2	B	503	2	2,2,2	0.38	0	1,1,1	0.33	0
3	NO2	C	503	2	2,2,2	0.37	0	1,1,1	0.30	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
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, 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	330/330 (100%)	1.41	82 (24%) 1 0	2, 8, 35, 71	0
1	B	330/330 (100%)	1.42	85 (25%) 1 0	2, 8, 35, 71	0
1	C	330/330 (100%)	1.45	74 (22%) 1 1	2, 8, 35, 71	0
All	All	990/990 (100%)	1.43	241 (24%) 1 0	2, 8, 36, 71	0

All (241) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	340	ALA	25.0
1	A	191	GLY	12.8
1	A	54	ASP	12.2
1	A	339	PRO	11.4
1	C	127	ASP	10.9
1	C	35	ALA	10.0
1	A	101	ALA	9.8
1	C	89	ALA	9.5
1	A	60	GLN	8.8
1	C	60	GLN	8.3
1	A	188	ALA	8.1
1	C	151	ASN	7.4
1	B	332	THR	7.4
1	B	338	GLY	7.3
1	A	36	PRO	7.0
1	B	35	ALA	7.0
1	C	304	LEU	6.7
1	B	33	ALA	6.5
1	B	188	ALA	6.4
1	C	136	CYS	6.2
1	A	340	ALA	6.2
1	C	298	PRO	6.1
1	C	286	GLY	6.0

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Mol	Chain	Res	Type	RSRZ
1	B	55	ASP	5.8
1	A	296	LYS	5.7
1	C	205	ASP	5.4
1	B	136	CYS	5.3
1	B	240	SER	5.3
1	B	36	PRO	5.1
1	B	331	MET	4.9
1	B	27	PRO	4.8
1	B	339	PRO	4.8
1	B	95	HIS	4.8
1	A	243	ILE	4.7
1	B	37	LYS	4.7
1	B	143	PRO	4.7
1	C	135	HIS	4.7
1	C	18	ASP	4.7
1	B	137	ALA	4.6
1	B	187	LYS	4.6
1	C	95	HIS	4.5
1	A	135	HIS	4.5
1	B	135	HIS	4.5
1	B	161	GLY	4.5
1	A	201	SER	4.4
1	C	54	ASP	4.4
1	A	270	PHE	4.4
1	A	136	CYS	4.4
1	A	321	SER	4.3
1	B	306	HIS	4.2
1	A	35	ALA	4.0
1	C	150	MET	4.0
1	A	306	HIS	4.0
1	C	306	HIS	4.0
1	B	340	ALA	3.9
1	A	261	GLY	3.9
1	C	217	HIS	3.9
1	A	202	ALA	3.9
1	B	277	ASN	3.8
1	B	250	ARG	3.8
1	A	334	VAL	3.8
1	C	190	ASP	3.8
1	A	106	LEU	3.7
1	A	298	PRO	3.7
1	C	36	PRO	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	245	HIS	3.6
1	C	323	GLU	3.6
1	C	145	HIS	3.6
1	B	115	VAL	3.6
1	C	66	GLY	3.6
1	C	225	GLY	3.6
1	A	95	HIS	3.5
1	A	59	ALA	3.5
1	B	54	ASP	3.5
1	B	238	GLY	3.5
1	C	300	THR	3.5
1	C	166	ALA	3.5
1	B	205	ASP	3.4
1	C	23	PRO	3.4
1	B	22	PRO	3.4
1	A	145	HIS	3.4
1	B	89	ALA	3.4
1	A	30	GLN	3.4
1	C	201	SER	3.3
1	A	168	ALA	3.3
1	B	226	ALA	3.3
1	C	332	THR	3.3
1	A	254	PRO	3.3
1	A	280	THR	3.3
1	A	22	PRO	3.3
1	B	337	PRO	3.3
1	C	100	HIS	3.2
1	B	106	LEU	3.2
1	A	116	PRO	3.2
1	B	158	PRO	3.2
1	A	100	HIS	3.2
1	B	141	MET	3.2
1	A	170	LEU	3.2
1	A	33	ALA	3.2
1	B	194	SER	3.2
1	C	14	ARG	3.1
1	C	28	HIS	3.1
1	B	100	HIS	3.1
1	B	145	HIS	3.1
1	C	69	PRO	3.1
1	A	232	ALA	3.1
1	B	151	ASN	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	17	VAL	3.0
1	C	264	VAL	3.0
1	C	336	ALA	3.0
1	C	88	PRO	3.0
1	B	165	ALA	3.0
1	A	326	TRP	3.0
1	A	62	MET	3.0
1	A	163	ARG	3.0
1	A	328	ASP	3.0
1	A	267	THR	3.0
1	B	150	MET	3.0
1	B	268	GLY	2.9
1	B	290	ALA	2.9
1	A	103	THR	2.9
1	B	164	ASP	2.9
1	C	141	MET	2.9
1	B	12	LEU	2.9
1	B	236	ALA	2.8
1	B	68	VAL	2.8
1	A	238	GLY	2.8
1	C	11	GLY	2.8
1	A	226	ALA	2.8
1	B	287	SER	2.8
1	B	175	VAL	2.8
1	C	147	VAL	2.8
1	B	110	GLY	2.7
1	B	168	ALA	2.7
1	C	232	ALA	2.7
1	B	267	THR	2.7
1	A	92	SER	2.7
1	A	192	ASN	2.7
1	B	212	THR	2.7
1	B	201	SER	2.7
1	C	248	ALA	2.7
1	A	331	MET	2.7
1	A	195	ASP	2.7
1	B	61	ALA	2.7
1	C	320	ALA	2.7
1	B	231	ASN	2.6
1	A	57	THR	2.6
1	B	191	GLY	2.6
1	C	208	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	227	LEU	2.6
1	A	93	MET	2.6
1	C	235	ALA	2.6
1	A	84	THR	2.6
1	A	325	GLN	2.6
1	A	297	GLN	2.5
1	A	229	GLY	2.5
1	B	289	ALA	2.5
1	B	181	SER	2.5
1	A	197	PRO	2.5
1	B	57	THR	2.5
1	C	76	HIS	2.5
1	C	278	MET	2.5
1	A	112	THR	2.5
1	A	34	GLY	2.5
1	A	52	ALA	2.5
1	C	260	HIS	2.5
1	A	190	ASP	2.5
1	A	259	GLY	2.5
1	B	90	THR	2.4
1	C	79	ASP	2.4
1	C	312	MET	2.4
1	C	338	GLY	2.4
1	B	139	ALA	2.4
1	A	212	THR	2.4
1	A	141	MET	2.4
1	C	62	MET	2.4
1	B	190	ASP	2.4
1	B	120	ALA	2.4
1	C	317	ALA	2.4
1	B	46	GLU	2.4
1	B	148	SER	2.4
1	A	206	THR	2.4
1	C	163	ARG	2.3
1	B	186	PRO	2.3
1	C	333	SER	2.3
1	C	337	PRO	2.3
1	B	24	LEU	2.3
1	B	154	LEU	2.3
1	B	160	ASP	2.3
1	C	155	MET	2.3
1	A	186	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	189	ALA	2.3
1	B	271	ALA	2.3
1	C	110	GLY	2.3
1	C	289	ALA	2.3
1	A	55	ASP	2.3
1	B	319	GLN	2.3
1	A	174	ARG	2.2
1	B	40	GLN	2.2
1	B	229	GLY	2.2
1	B	102	ALA	2.2
1	B	11	GLY	2.2
1	C	247	GLN	2.2
1	A	150	MET	2.2
1	B	223	ALA	2.2
1	A	72	THR	2.2
1	A	148	SER	2.2
1	C	322	VAL	2.2
1	C	164	ASP	2.2
1	C	311	ALA	2.2
1	A	184	TYR	2.2
1	B	247	GLN	2.2
1	C	52	ALA	2.2
1	C	140	GLY	2.2
1	C	294	THR	2.2
1	C	315	GLY	2.2
1	A	317	ALA	2.1
1	B	26	HIS	2.1
1	A	258	GLY	2.1
1	A	281	TRP	2.1
1	A	245	HIS	2.1
1	C	335	ALA	2.1
1	C	321	SER	2.1
1	C	254	PRO	2.1
1	A	155	MET	2.1
1	B	43	MET	2.1
1	C	172	TYR	2.1
1	A	20	VAL	2.1
1	B	293	TYR	2.1
1	C	112	THR	2.1
1	A	323	GLU	2.1
1	B	246	SER	2.1
1	B	252	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	274	PRO	2.1
1	A	169	ALA	2.1
1	A	218	ALA	2.1
1	B	224	VAL	2.0
1	A	338	GLY	2.0
1	C	101	ALA	2.0
1	B	230	ALA	2.0
1	C	152	GLY	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, 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	LLDF	B-factors(\AA^2)	Q<0.9
3	NO2	B	503	3/3	0.92	0.55	-	29,29,29,29	0
3	NO2	A	503	3/3	0.89	0.62	-	29,29,29,29	0
3	NO2	C	503	3/3	0.92	0.44	-	29,29,29,29	0
2	CU	B	502	1/1	0.99	0.32	-	2,2,2,2	0
2	CU	B	501	1/1	0.98	0.41	-	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	0.28	-	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	0.29	-	2,2,2,2	0

6.5 Other polymers [i](#)

There are no such residues in this entry.