



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 06:09 am GMT

PDB ID : 4GAE
Title : Crystal structure of plasmodium dxr in complex with a pyridine-containing inhibitor
Authors : Diao, J.; Xue, J.; Cai, G.; Deng, L.; Song, Y.
Deposited on : 2012-07-25
Resolution : 2.30 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

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 : 1.7.2 (RC1), CSD as538be (2017)
Xtrriage (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

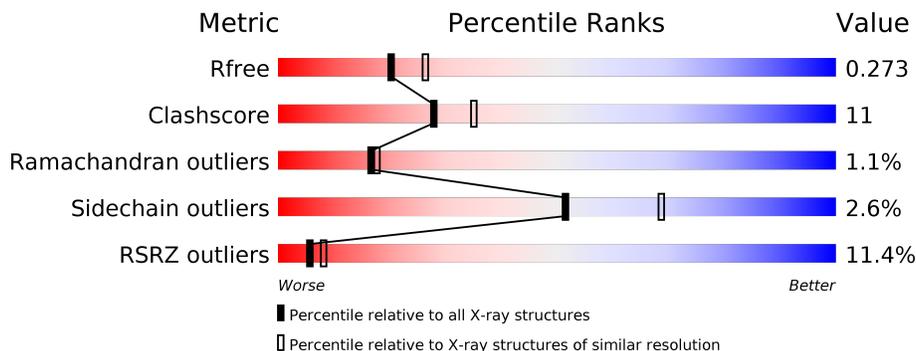
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	100719	4130 (2.30-2.30)
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (2.30-2.30)

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	426	
1	B	426	

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 6931 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 1-deoxy-D-xylulose 5-phosphate reductoisomerase, apicoplast.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	416	3324	2132	549	623	20	0	0	0
1	B	410	3276	2103	537	616	20	0	0	0

There are 26 discrepancies between the modelled and reference sequences:

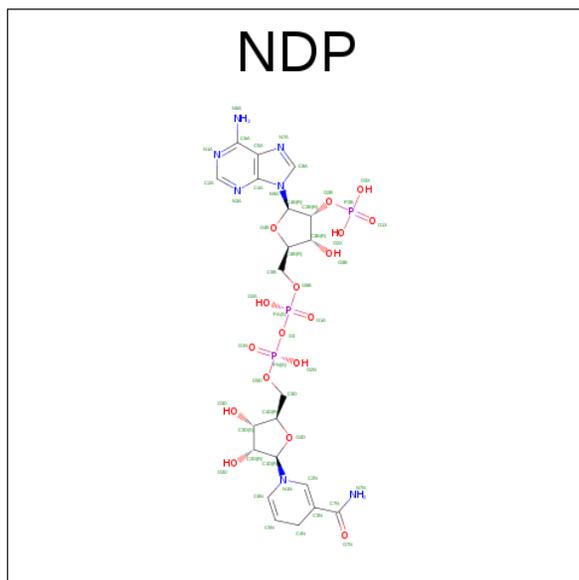
Chain	Residue	Modelled	Actual	Comment	Reference
A	63	MET	-	EXPRESSION TAG	UNP O96693
A	64	ARG	-	EXPRESSION TAG	UNP O96693
A	65	GLY	-	EXPRESSION TAG	UNP O96693
A	66	SER	-	EXPRESSION TAG	UNP O96693
A	67	HIS	-	EXPRESSION TAG	UNP O96693
A	68	HIS	-	EXPRESSION TAG	UNP O96693
A	69	HIS	-	EXPRESSION TAG	UNP O96693
A	70	HIS	-	EXPRESSION TAG	UNP O96693
A	71	HIS	-	EXPRESSION TAG	UNP O96693
A	72	HIS	-	EXPRESSION TAG	UNP O96693
A	73	GLY	-	EXPRESSION TAG	UNP O96693
A	74	SER	-	EXPRESSION TAG	UNP O96693
A	247	ILE	LEU	ENGINEERED MUTATION	UNP O96693
B	63	MET	-	EXPRESSION TAG	UNP O96693
B	64	ARG	-	EXPRESSION TAG	UNP O96693
B	65	GLY	-	EXPRESSION TAG	UNP O96693
B	66	SER	-	EXPRESSION TAG	UNP O96693
B	67	HIS	-	EXPRESSION TAG	UNP O96693
B	68	HIS	-	EXPRESSION TAG	UNP O96693
B	69	HIS	-	EXPRESSION TAG	UNP O96693
B	70	HIS	-	EXPRESSION TAG	UNP O96693
B	71	HIS	-	EXPRESSION TAG	UNP O96693
B	72	HIS	-	EXPRESSION TAG	UNP O96693
B	73	GLY	-	EXPRESSION TAG	UNP O96693
B	74	SER	-	EXPRESSION TAG	UNP O96693

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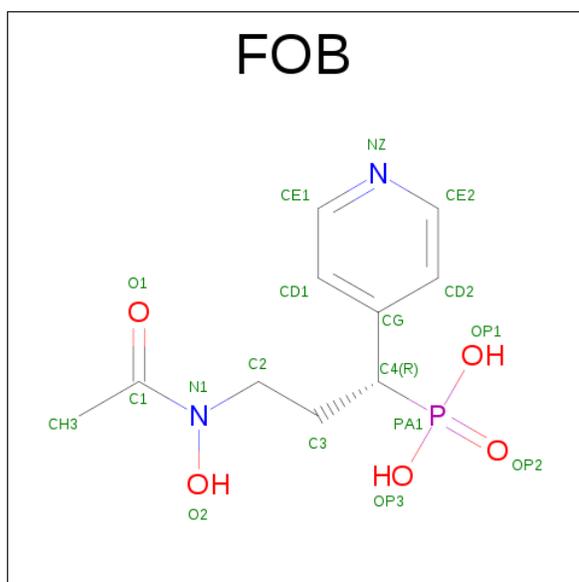
Chain	Residue	Modelled	Actual	Comment	Reference
B	247	ILE	LEU	ENGINEERED MUTATION	UNP O96693

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).



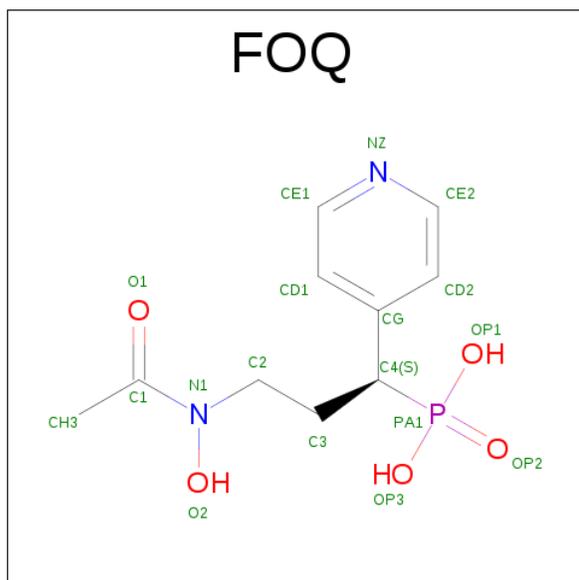
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 3 is [(1R)-3-[ACETYL(HYDROXY)AMINO]-1-(PYRIDIN-4-YL)PROPYL]PHOSPHONIC ACID (three-letter code: FOB) (formula: $C_{10}H_{15}N_2O_5P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	1
			18	10	2	5	1		
3	B	1	Total	C	N	O	P	0	1
			18	10	2	5	1		

- Molecule 4 is [(1S)-3-[ACETYL(HYDROXY)AMINO]-1-(PYRIDIN-4-YL)PROPYL]PHOSPHONIC ACID (three-letter code: FOQ) (formula: C₁₀H₁₅N₂O₅P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	1
			18	10	2	5	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	P	0	1
			18	10	2	5	1		

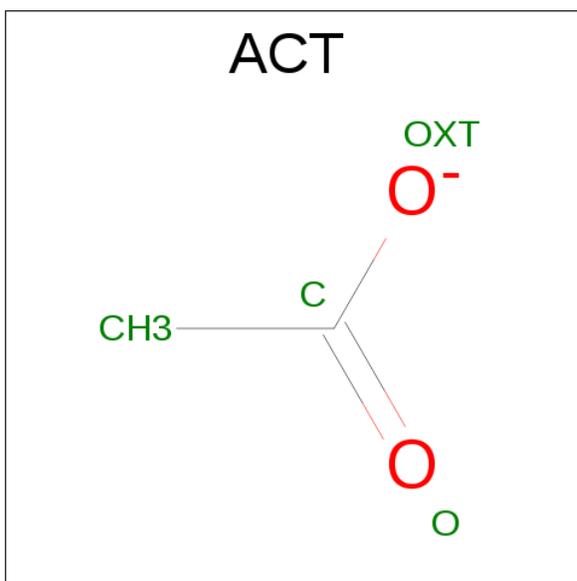
- Molecule 5 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	3	Total	Mn	0	0
			3	3		
5	A	1	Total	Mn	0	0
			1	1		

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

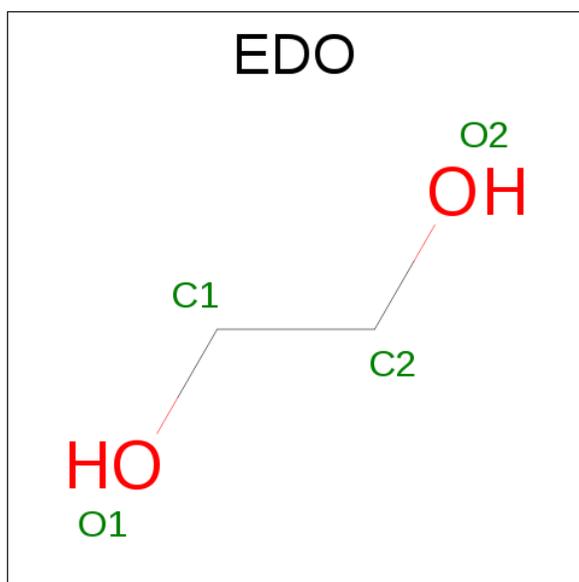
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Cl	0	0
			1	1		

- Molecule 7 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



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

- Molecule 8 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

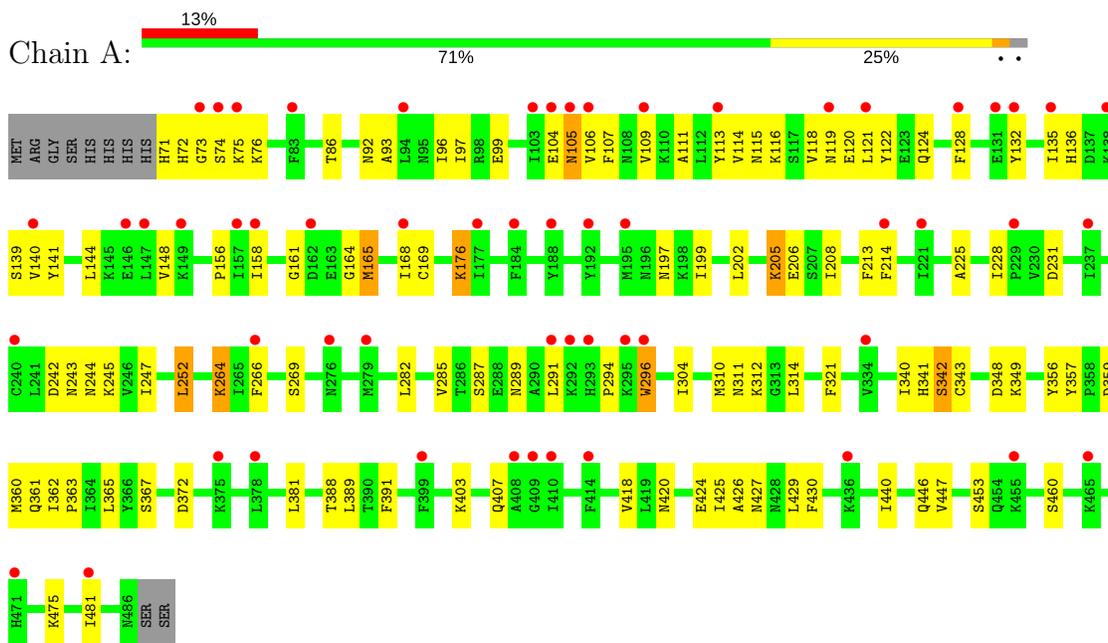
- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	67	Total O 67 67	0	0
9	B	71	Total O 71 71	0	0

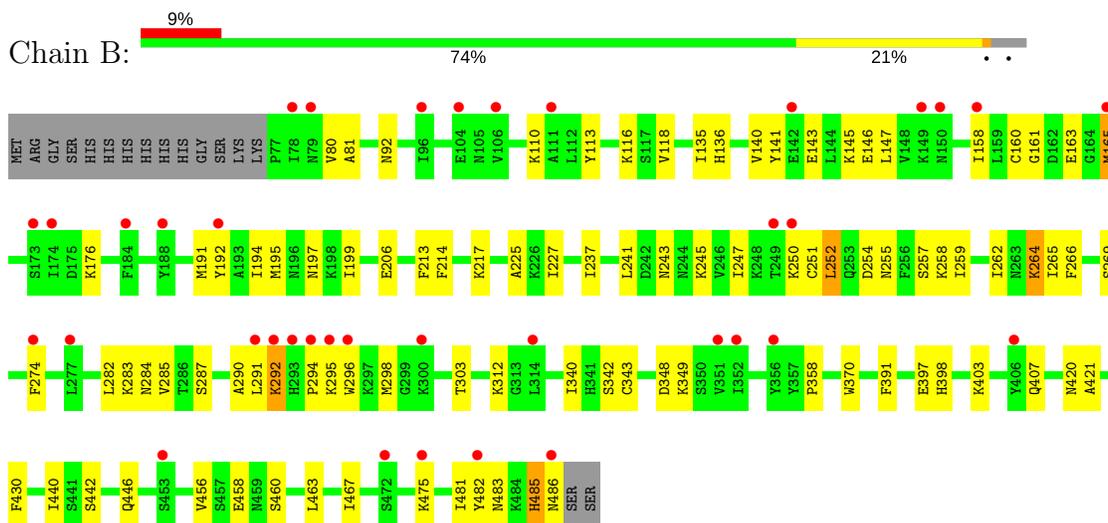
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: 1-deoxy-D-xylulose 5-phosphate reductoisomerase, apicoplast



- Molecule 1: 1-deoxy-D-xylulose 5-phosphate reductoisomerase, apicoplast



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	51.36Å 77.28Å 109.41Å 90.00° 91.50° 90.00°	Depositor
Resolution (Å)	44.64 – 2.30 44.64 – 2.30	Depositor EDS
% Data completeness (in resolution range)	89.0 (44.64-2.30) 89.1 (44.64-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.53 (at 2.29Å)	Xtrriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.230 , 0.273 0.230 , 0.273	Depositor DCC
R_{free} test set	1698 reflections (4.99%)	DCC
Wilson B-factor (Å ²)	30.3	Xtrriage
Anisotropy	0.170	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 30.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.037 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	6931	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.67% 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, 0.333 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: FOQ, CL, MN, EDO, FOB, ACT, NDP

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	0.35	0/3389	0.60	0/4575
1	B	0.38	0/3339	0.61	0/4509
All	All	0.37	0/6728	0.60	0/9084

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	3324	0	3369	88	0
1	B	3276	0	3322	67	0
2	A	48	0	26	2	0
2	B	48	0	26	0	0
3	A	18	0	12	1	0
3	B	18	0	12	0	0
4	A	18	0	12	0	0
4	B	18	0	12	0	0
5	A	1	0	0	0	0
5	B	3	0	0	0	0
6	A	1	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	4	0	3	0	0
7	B	4	0	3	0	0
8	A	4	0	6	0	0
8	B	8	0	12	0	0
9	A	67	0	0	0	0
9	B	71	0	0	3	0
All	All	6931	0	6815	153	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 11.

The worst 5 of 153 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:295:LYS:HD2	1:B:358:PRO:HG2	1.36	1.04
1:B:269:SER:HB2	1:B:312:LYS:HE3	1.50	0.92
1:A:156:PRO:HG2	1:A:158:ILE:HD11	1.65	0.79
1:B:295:LYS:CD	1:B:358:PRO:HG2	2.11	0.78
1:B:283:LYS:HB2	1:B:283:LYS:NZ	1.98	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	414/426 (97%)	385 (93%)	24 (6%)	5 (1%)	15	16
1	B	408/426 (96%)	386 (95%)	18 (4%)	4 (1%)	18	20
All	All	822/852 (96%)	771 (94%)	42 (5%)	9 (1%)	17	18

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	294	PRO
1	A	342	SER
1	A	453	SER
1	A	105	ASN
1	B	342	SER

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	382/391 (98%)	371 (97%)	11 (3%)	48	64
1	B	377/391 (96%)	368 (98%)	9 (2%)	54	72
All	All	759/782 (97%)	739 (97%)	20 (3%)	51	69

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	296	TRP
1	A	372	ASP
1	B	252	LEU
1	A	252	LEU
1	A	264	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	459	ASN
1	B	136	HIS
1	B	289	ASN
1	A	433	ASN
1	B	385	GLN

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 16 ligands modelled in this entry, 5 are monoatomic - leaving 11 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	NDP	A	501	-	43,52,52	1.47	4 (9%)	49,80,80	1.93	2 (4%)
3	FOB	A	502[A]	5	16,18,18	2.32	5 (31%)	13,25,25	1.47	4 (30%)
4	FOQ	A	503[B]	5	16,18,18	2.24	7 (43%)	13,25,25	1.46	3 (23%)
7	ACT	A	506	-	1,3,3	2.20	1 (100%)	0,3,3	0.00	-
8	EDO	A	507	-	3,3,3	0.52	0	2,2,2	0.34	0
2	NDP	B	501	-	43,52,52	1.54	4 (9%)	49,80,80	1.96	3 (6%)
3	FOB	B	502[A]	5	16,18,18	2.29	5 (31%)	13,25,25	1.30	1 (7%)
4	FOQ	B	503[B]	5	16,18,18	2.33	7 (43%)	13,25,25	1.30	1 (7%)
7	ACT	B	507	-	1,3,3	2.10	1 (100%)	0,3,3	0.00	-
8	EDO	B	508	-	3,3,3	0.52	0	2,2,2	0.33	0
8	EDO	B	509	-	3,3,3	0.56	0	2,2,2	0.29	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	NDP	A	501	-	-	0/30/77/77	0/5/5/5
3	FOB	A	502[A]	5	-	0/19/19/19	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	FOQ	A	503[B]	5	-	0/19/19/19	0/1/1/1
7	ACT	A	506	-	-	0/0/0/0	0/0/0/0
8	EDO	A	507	-	-	0/1/1/1	0/0/0/0
2	NDP	B	501	-	-	0/30/77/77	0/5/5/5
3	FOB	B	502[A]	5	-	0/19/19/19	0/1/1/1
4	FOQ	B	503[B]	5	-	0/19/19/19	0/1/1/1
7	ACT	B	507	-	-	0/0/0/0	0/0/0/0
8	EDO	B	508	-	-	0/1/1/1	0/0/0/0
8	EDO	B	509	-	-	0/1/1/1	0/0/0/0

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	502[A]	FOB	PA1-C4	-7.00	1.73	1.82
4	B	503[B]	FOQ	PA1-C4	-6.46	1.73	1.82
3	B	502[A]	FOB	PA1-C4	-6.28	1.74	1.82
4	A	503[B]	FOQ	PA1-C4	-6.22	1.74	1.82
4	A	503[B]	FOQ	PA1-OP1	-3.26	1.49	1.54

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	NDP	N3A-C2A-N1A	-12.04	118.37	128.86
2	A	501	NDP	N3A-C2A-N1A	-12.03	118.38	128.86
2	B	501	NDP	C1B-N9A-C4A	-3.44	120.69	126.64
2	A	501	NDP	C1B-N9A-C4A	-2.87	121.68	126.64
4	A	503[B]	FOQ	OP2-PA1-C4	-2.79	104.85	113.21

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
2	A	501	NDP	2	0
3	A	502[A]	FOB	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 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	416/426 (97%)	0.69	57 (13%) 3 5	21, 36, 71, 104	1 (0%)
1	B	410/426 (96%)	0.44	37 (9%) 10 14	18, 30, 54, 98	0
All	All	826/852 (96%)	0.57	94 (11%) 6 8	18, 33, 65, 104	1 (0%)

The worst 5 of 94 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	294	PRO	16.9
1	B	291	LEU	11.2
1	A	292	LYS	10.4
1	A	295	LYS	9.4
1	A	132	TYR	9.4

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
8	EDO	B	508	4/4	0.81	0.16	0.60	64,65,65,65	0
3	FOB	A	502[A]	18/18	0.91	0.20	0.13	28,35,38,39	18
3	FOB	B	502[A]	18/18	0.94	0.16	0.02	26,30,36,36	18
4	FOQ	A	503[B]	18/18	0.90	0.19	0.01	26,33,36,37	18
4	FOQ	B	503[B]	18/18	0.94	0.15	-0.08	20,24,31,31	18
5	MN	A	504	1/1	1.00	0.14	-0.63	26,26,26,26	0
2	NDP	B	501	48/48	0.95	0.10	-0.70	22,28,30,32	0
2	NDP	A	501	48/48	0.92	0.12	-0.79	30,38,42,42	0
6	CL	A	505	1/1	0.99	0.06	-1.94	45,45,45,45	0
5	MN	B	505	1/1	0.98	0.05	-2.15	40,40,40,40	0
5	MN	B	504	1/1	0.99	0.04	-2.23	24,24,24,24	0
5	MN	B	506	1/1	0.93	0.04	-3.16	49,49,49,49	0
8	EDO	B	509	4/4	0.80	0.37	-	78,79,79,79	0
8	EDO	A	507	4/4	0.80	0.35	-	78,79,80,80	0
7	ACT	A	506	4/4	0.74	0.32	-	93,93,94,94	0
7	ACT	B	507	4/4	0.90	0.28	-	65,67,67,67	0

6.5 Other polymers [i](#)

There are no such residues in this entry.