WORLDWIDE wwPDB PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 05:48 pm GMT

PDB ID	:	4KXM
Title	:	Crystal structure of DNPH1 (RCL) WITH N6-ISOPENTENYL-AMP
Authors	:	Padilla, A.; Labesse, G.; Kaminski, P.A.
Deposited on	:	2013-05-27
Resolution	:	2.24 Å(reported)

The following versions of software and data (see references ⓘ) were used in the production of this report:

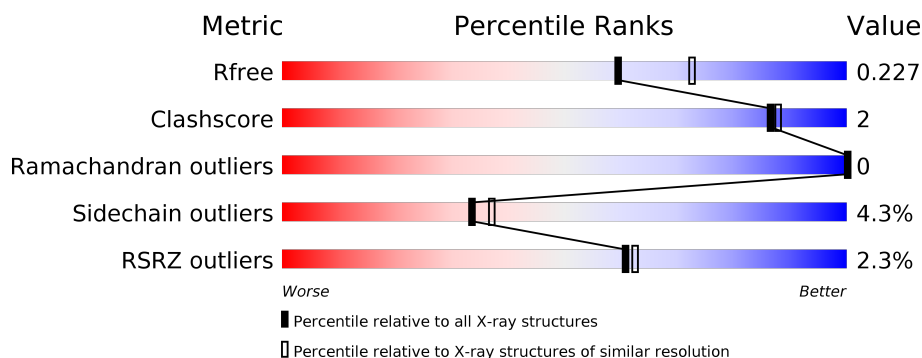|		
MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 2.24 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	Percentile Ranks	Value
Rfree		0.227
Clashscore		2
Ramachandran outliers		0
Sidechain outliers		4.3%
RSRZ outliers		2.3%

Worse   Better

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	1804 (2.26-2.22)
Clashscore	112137	1957 (2.26-2.22)
Ramachandran outliers	110173	1916 (2.26-2.22)
Sidechain outliers	110143	1917 (2.26-2.22)
RSRZ outliers	101464	1809 (2.26-2.22)

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 <=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	152	74% 11% • 14%
1	B	152	81% 5% • 13%
1	C	152	78% 7% • 14%
1	D	152	83% • • 13%

2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 4457 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 2'-deoxynucleoside 5'-phosphate N-hydrolase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	130	Total	C	N	O	S	0	2	0
			1035	654	186	191	4			
1	B	132	Total	C	N	O	S	0	1	0
			1048	662	189	193	4			
1	C	131	Total	C	N	O	S	0	1	0
			1037	656	188	189	4			
1	D	132	Total	C	N	O	S	0	2	0
			1042	659	190	189	4			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	8	MET	-	EXPRESSION TAG	UNP O35820
A	9	ARG	-	EXPRESSION TAG	UNP O35820
A	10	ARG	-	EXPRESSION TAG	UNP O35820
A	69	ASN	ASP	ENGINEERED MUTATION	UNP O35820
A	152	VAL	-	EXPRESSION TAG	UNP O35820
A	153	GLU	-	EXPRESSION TAG	UNP O35820
A	154	HIS	-	EXPRESSION TAG	UNP O35820
A	155	HIS	-	EXPRESSION TAG	UNP O35820
A	156	HIS	-	EXPRESSION TAG	UNP O35820
A	157	HIS	-	EXPRESSION TAG	UNP O35820
A	158	HIS	-	EXPRESSION TAG	UNP O35820
A	159	HIS	-	EXPRESSION TAG	UNP O35820
B	8	MET	-	EXPRESSION TAG	UNP O35820
B	9	ARG	-	EXPRESSION TAG	UNP O35820
B	10	ARG	-	EXPRESSION TAG	UNP O35820
B	69	ASN	ASP	ENGINEERED MUTATION	UNP O35820
B	152	VAL	-	EXPRESSION TAG	UNP O35820
B	153	GLU	-	EXPRESSION TAG	UNP O35820
B	154	HIS	-	EXPRESSION TAG	UNP O35820
B	155	HIS	-	EXPRESSION TAG	UNP O35820
B	156	HIS	-	EXPRESSION TAG	UNP O35820

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Chain	Residue	Modelled	Actual	Comment	Reference
B	157	HIS	-	EXPRESSION TAG	UNP O35820
B	158	HIS	-	EXPRESSION TAG	UNP O35820
B	159	HIS	-	EXPRESSION TAG	UNP O35820
C	8	MET	-	EXPRESSION TAG	UNP O35820
C	9	ARG	-	EXPRESSION TAG	UNP O35820
C	10	ARG	-	EXPRESSION TAG	UNP O35820
C	69	ASN	ASP	ENGINEERED MUTATION	UNP O35820
C	152	VAL	-	EXPRESSION TAG	UNP O35820
C	153	GLU	-	EXPRESSION TAG	UNP O35820
C	154	HIS	-	EXPRESSION TAG	UNP O35820
C	155	HIS	-	EXPRESSION TAG	UNP O35820
C	156	HIS	-	EXPRESSION TAG	UNP O35820
C	157	HIS	-	EXPRESSION TAG	UNP O35820
C	158	HIS	-	EXPRESSION TAG	UNP O35820
C	159	HIS	-	EXPRESSION TAG	UNP O35820
D	8	MET	-	EXPRESSION TAG	UNP O35820
D	9	ARG	-	EXPRESSION TAG	UNP O35820
D	10	ARG	-	EXPRESSION TAG	UNP O35820
D	69	ASN	ASP	ENGINEERED MUTATION	UNP O35820
D	152	VAL	-	EXPRESSION TAG	UNP O35820
D	153	GLU	-	EXPRESSION TAG	UNP O35820
D	154	HIS	-	EXPRESSION TAG	UNP O35820
D	155	HIS	-	EXPRESSION TAG	UNP O35820
D	156	HIS	-	EXPRESSION TAG	UNP O35820
D	157	HIS	-	EXPRESSION TAG	UNP O35820
D	158	HIS	-	EXPRESSION TAG	UNP O35820
D	159	HIS	-	EXPRESSION TAG	UNP O35820

- Molecule 2 is N6-ISOPENTENYL-ADENOSINE-5'-MONOPHOSPHATE (three-letter code: 6IA) (formula: $C_{15}H_{24}N_5O_7P$).
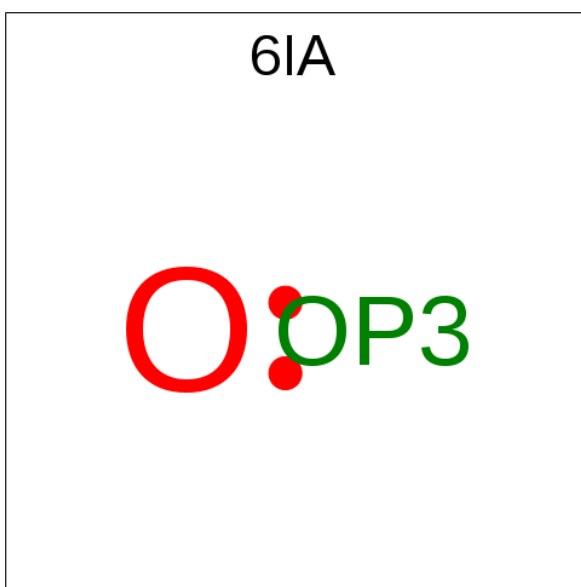
| Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			28	15	5	7	1		
2	B	1	Total	C	N	O	P	0	0
			28	15	5	7	1		
2	C	1	Total	C	N	O	P	0	0
			28	15	5	7	1		
2	D	1	Total	C	N	O	P	0	0
			28	15	5	7	1		

- Molecule 3 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	143	Total	O	0	0
			143	143		
3	B	17	Total	O	0	0
			17	17		
3	C	9	Total	O	0	0
			9	9		
3	D	14	Total	O	0	0
			14	14		

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.

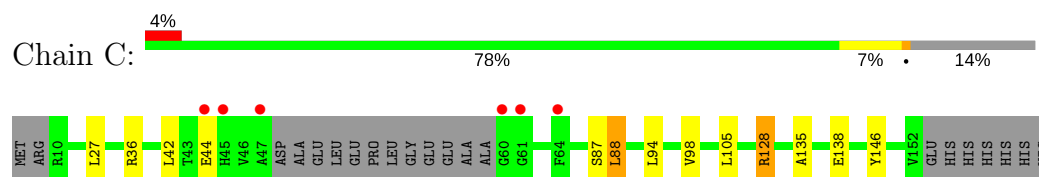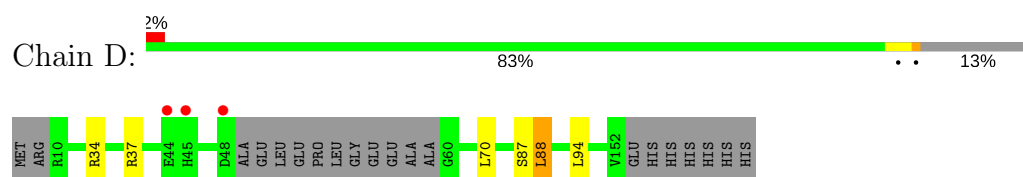• Molecule 1: 2'-deoxynucleoside 5'-phosphate N-hydrolase 1
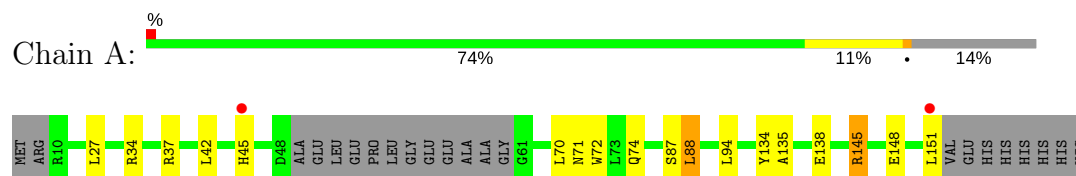
• Molecule 1: 2'-deoxynucleoside 5'-phosphate N-hydrolase 1
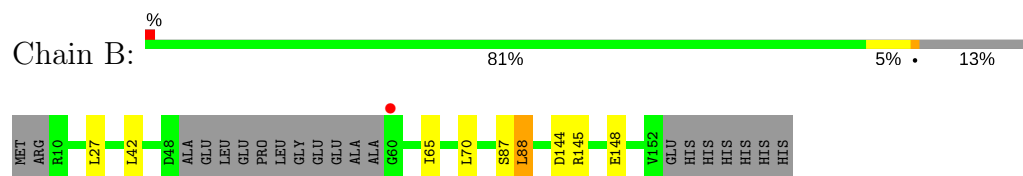
• Molecule 1: 2'-deoxynucleoside 5'-phosphate N-hydrolase 1

• Molecule 1: 2'-deoxynucleoside 5'-phosphate N-hydrolase 1

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	32.15Å 96.57Å 79.03Å 90.00° 101.58° 90.00°	Depositor
Resolution (Å)	38.71 – 2.24 38.71 – 2.24	Depositor EDS
% Data completeness (in resolution range)	92.0 (38.71-2.24) 92.0 (38.71-2.24)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	7.21 (at 2.24Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.174 , 0.227 0.173 , 0.227	Depositor DCC
R_{free} test set	1078 reflections (5.41%)	DCC
Wilson B-factor (Å^2)	16.4	Xtriage
Anisotropy	0.124	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 41.0	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.157 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4457	wwPDB-VP
Average B, all atoms (Å^2)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.98% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 6IA

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	0/1063	0.57	0/1435
1	B	0.44	0/1071	0.58	0/1445
1	C	0.43	0/1060	0.57	0/1430
1	D	0.39	0/1069	0.56	0/1443
All	All	0.42	0/4263	0.57	0/5753

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 ⓘ

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	1035	0	1009	10	0
1	B	1048	0	1026	4	0
1	C	1037	0	1021	6	1
1	D	1042	0	1021	3	0
2	A	28	0	21	1	0
2	B	28	0	21	1	0
2	C	28	0	21	0	0
2	D	28	0	21	1	0
3	A	143	0	0	0	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	17	0	0	0	0
3	C	9	0	0	0	0
3	D	14	0	0	0	0
All	All	4457	0	4161	21	1

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 2.

All (21) 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:145:ARG:NH2	1:A:148:GLU:OE1	2.26	0.69
1:D:34:ARG:HD2	1:D:37:ARG:HD2	1.85	0.58
1:A:45:HIS:HE1	1:A:72:TRP:HZ3	1.54	0.55
1:A:71:ASN:HA	1:A:74:GLN:HE21	1.69	0.55
1:A:87:SER:H	1:B:88:LEU:HD13	1.72	0.54
1:A:45:HIS:CE1	1:A:72:TRP:HZ3	2.25	0.54
1:A:88:LEU:HD13	1:B:87:SER:H	1.73	0.54
1:C:87:SER:H	1:D:88:LEU:HD13	1.73	0.53
1:C:135:ALA:O	1:C:138:GLU:HG2	2.08	0.53
1:C:36:ARG:HH22	1:C:44:GLU:CD	2.17	0.48
1:B:65:ILE:HD13	2:B:201:6IA:HN6	1.79	0.48
1:C:94:LEU:O	1:C:98:VAL:HG23	2.14	0.48
1:B:144:ASP:O	1:B:148:GLU:HB2	2.14	0.47
1:A:34:ARG:HD2	1:A:37:ARG:HD2	1.97	0.47
2:A:201:6IA:H152	2:A:201:6IA:N1	2.30	0.46
1:A:135:ALA:O	1:A:138:GLU:HG2	2.18	0.44
1:A:45:HIS:HE1	1:A:72:TRP:CZ3	2.34	0.44
1:C:88:LEU:HD13	1:D:87:SER:H	1.83	0.43
1:A:27:LEU:HD21	1:A:134:TYR:OH	2.19	0.43
1:C:105:LEU:HD22	1:C:146:TYR:CG	2.56	0.41
2:D:201:6IA:N1	2:D:201:6IA:H152	2.34	0.41

All (1) 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)
1:C:128:ARG:NH2	3:A:409:HOH:O[1_655]	1.95	0.25

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	128/152 (84%)	125 (98%)	3 (2%)	0	100	100
1	B	129/152 (85%)	125 (97%)	4 (3%)	0	100	100
1	C	128/152 (84%)	124 (97%)	4 (3%)	0	100	100
1	D	130/152 (86%)	127 (98%)	3 (2%)	0	100	100
All	All	515/608 (85%)	501 (97%)	14 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	106/122 (87%)	100 (94%)	6 (6%)	24	23
1	B	107/122 (88%)	102 (95%)	5 (5%)	30	32
1	C	106/122 (87%)	102 (96%)	4 (4%)	38	43
1	D	106/122 (87%)	103 (97%)	3 (3%)	49	57
All	All	425/488 (87%)	407 (96%)	18 (4%)	33	38

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	LEU
1	A	70	LEU

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Mol	Chain	Res	Type
1	A	88	LEU
1	A	94	LEU
1	A	145	ARG
1	A	151	LEU
1	B	27	LEU
1	B	42	LEU
1	B	70	LEU
1	B	88	LEU
1	B	145	ARG
1	C	27	LEU
1	C	42	LEU
1	C	88	LEU
1	C	128	ARG
1	D	70	LEU
1	D	88	LEU
1	D	94	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	45	HIS
1	A	71	ASN
1	A	74	GLN
1	A	85	GLN
1	B	71	ASN
1	B	74	GLN
1	B	75	GLN
1	B	85	GLN
1	C	85	GLN
1	D	71	ASN
1	D	74	GLN
1	D	85	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 ⓘ

4 ligands are modelled in this entry.

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	6IA	A	201	-	25,30,30	1.08	1 (4%)	28,44,44	2.39	4 (14%)
2	6IA	B	201	-	25,30,30	1.39	3 (12%)	28,44,44	2.34	5 (17%)
2	6IA	C	201	-	25,30,30	1.36	2 (8%)	28,44,44	2.36	4 (14%)
2	6IA	D	201	-	25,30,30	1.31	3 (12%)	28,44,44	2.65	2 (7%)

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	6IA	A	201	-	-	0/12/32/32	0/3/3/3
2	6IA	B	201	-	-	0/12/32/32	0/3/3/3
2	6IA	C	201	-	-	0/12/32/32	0/3/3/3
2	6IA	D	201	-	-	0/12/32/32	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	201	6IA	C13-C12	-3.12	1.39	1.52
2	C	201	6IA	C13-C12	-3.09	1.40	1.52
2	A	201	6IA	C13-C12	-3.01	1.40	1.52
2	D	201	6IA	C13-C12	-3.00	1.40	1.52
2	B	201	6IA	P-OP1	2.21	1.58	1.50
2	D	201	6IA	O4'-C1'	2.52	1.44	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	201	6IA	P-OP1	2.67	1.59	1.50
2	B	201	6IA	O4'-C1'	4.21	1.47	1.41
2	C	201	6IA	O4'-C1'	4.49	1.47	1.41

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	201	6IA	N3-C2-N1	-9.53	120.56	128.86
2	C	201	6IA	N3-C2-N1	-8.35	121.58	128.86
2	A	201	6IA	N3-C2-N1	-8.13	121.78	128.86
2	B	201	6IA	N3-C2-N1	-8.02	121.87	128.86
2	A	201	6IA	C4-C5-N7	-2.64	106.86	109.41
2	B	201	6IA	C5'-C4'-C3'	-2.60	105.36	115.29
2	B	201	6IA	C12-N6-C6	-2.19	120.44	123.26
2	A	201	6IA	O5'-P-OP1	2.08	112.31	106.47
2	C	201	6IA	N6-C6-N1	2.10	121.98	118.97
2	B	201	6IA	OP2-P-O5'	2.66	113.81	106.73
2	C	201	6IA	O5'-P-OP1	2.69	114.02	106.47
2	B	201	6IA	C2-N1-C6	6.64	120.86	116.53
2	C	201	6IA	C2-N1-C6	7.13	121.18	116.53
2	A	201	6IA	C2-N1-C6	7.41	121.36	116.53
2	D	201	6IA	C2-N1-C6	8.19	121.87	116.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	201	6IA	1	0
2	B	201	6IA	1	0
2	D	201	6IA	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	130/152 (85%)	-0.30	2 (1%)	74	75	5, 14, 27, 34	4 (3%)
1	B	132/152 (86%)	-0.35	1 (0%)	86	86	6, 12, 23, 29	10 (7%)
1	C	131/152 (86%)	-0.12	6 (4%)	33	33	6, 15, 29, 35	7 (5%)
1	D	132/152 (86%)	-0.24	3 (2%)	61	62	7, 15, 28, 36	11 (8%)
All	All	525/608 (86%)	-0.25	12 (2%)	61	62	5, 14, 28, 36	32 (6%)

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	60	GLY	4.9
1	D	45	HIS	4.4
1	C	45	HIS	3.6
1	D	48	ASP	3.3
1	A	151	LEU	2.8
1	A	45	HIS	2.5
1	C	44	GLU	2.4
1	C	64	PHE	2.3
1	C	61	GLY	2.3
1	B	60	GLY	2.1
1	C	47	ALA	2.1
1	D	44	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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(Å^2)	Q<0.9
2	6IA	B	201	28/28	0.94	0.14	0.94	9,19,25,27	5
2	6IA	A	201	28/28	0.95	0.13	0.34	8,14,22,23	5
2	6IA	C	201	28/28	0.97	0.14	0.16	12,19,33,35	5
2	6IA	D	201	28/28	0.97	0.11	-0.22	8,13,24,25	5

6.5 Other polymers ⓘ

There are no such residues in this entry.