



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 11:59 pm GMT

PDB ID : 5KR7
Title : KDM4C bound to pyrazolo-pyrimidine scaffold
Authors : Bellon, S.F.; Poy, F.; Setser, J.W.
Deposited on : 2016-07-07
Resolution : 1.90 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 : 1.7.2 (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

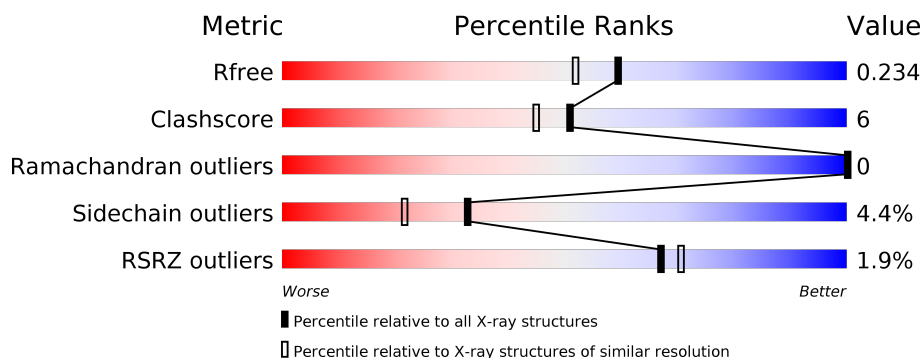
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	5047 (1.90-1.90)
Clashscore	112137	5731 (1.90-1.90)
Ramachandran outliers	110173	5669 (1.90-1.90)
Sidechain outliers	110143	5670 (1.90-1.90)
RSRZ outliers	101464	5100 (1.90-1.90)

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	367	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>10%</div> <div>7%</div> </div> </div>
1	B	367	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>9%</div> <div>8%</div> </div> </div>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 6018 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 Lysine-specific demethylase 4C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	340	Total	C	N	O	S	0	0	0
			2788	1802	463	504	19			
1	B	339	Total	C	N	O	S	0	0	0
			2777	1795	461	502	19			

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	GLY	-	expression tag	UNP Q9H3R0
A	-15	SER	-	expression tag	UNP Q9H3R0
A	-14	HIS	-	expression tag	UNP Q9H3R0
A	-13	MET	-	expression tag	UNP Q9H3R0
A	-12	ALA	-	expression tag	UNP Q9H3R0
A	-11	SER	-	expression tag	UNP Q9H3R0
A	-10	MET	-	expression tag	UNP Q9H3R0
A	-9	THR	-	expression tag	UNP Q9H3R0
A	-8	GLY	-	expression tag	UNP Q9H3R0
A	-7	GLY	-	expression tag	UNP Q9H3R0
A	-6	GLN	-	expression tag	UNP Q9H3R0
A	-5	GLN	-	expression tag	UNP Q9H3R0
A	-4	MET	-	expression tag	UNP Q9H3R0
A	-3	GLY	-	expression tag	UNP Q9H3R0
A	-2	ARG	-	expression tag	UNP Q9H3R0
A	-1	GLY	-	expression tag	UNP Q9H3R0
A	0	SER	-	expression tag	UNP Q9H3R0
B	-16	GLY	-	expression tag	UNP Q9H3R0
B	-15	SER	-	expression tag	UNP Q9H3R0
B	-14	HIS	-	expression tag	UNP Q9H3R0
B	-13	MET	-	expression tag	UNP Q9H3R0
B	-12	ALA	-	expression tag	UNP Q9H3R0
B	-11	SER	-	expression tag	UNP Q9H3R0
B	-10	MET	-	expression tag	UNP Q9H3R0
B	-9	THR	-	expression tag	UNP Q9H3R0

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	-8	GLY	-	expression tag	UNP Q9H3R0
B	-7	GLY	-	expression tag	UNP Q9H3R0
B	-6	GLN	-	expression tag	UNP Q9H3R0
B	-5	GLN	-	expression tag	UNP Q9H3R0
B	-4	MET	-	expression tag	UNP Q9H3R0
B	-3	GLY	-	expression tag	UNP Q9H3R0
B	-2	ARG	-	expression tag	UNP Q9H3R0
B	-1	GLY	-	expression tag	UNP Q9H3R0
B	0	SER	-	expression tag	UNP Q9H3R0

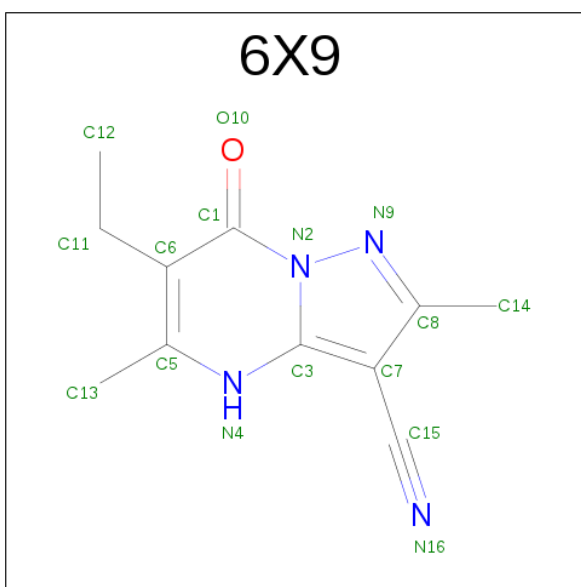
- Molecule 2 is FE (II) ION (three-letter code: FE2) (formula: Fe).

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

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 4 is 6-ethyl-2,5-dimethyl-7-oxidanylidene-4 {H}-pyrazolo[1,5-a]pyrimidine-3-carbonitrile (three-letter code: 6X9) (formula: C₁₁H₁₂N₄O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			16	11	4	1		
4	B	1	Total	C	N	O	0	0
			16	11	4	1		

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	208	Total	O	0	0
			208	208		
6	B	207	Total	O	0	0
			207	207		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	89.82Å 89.88Å 100.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	66.82 – 1.90 44.91 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.1 (66.82-1.90) 99.1 (44.91-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.32 (at 1.89Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.192 , 0.234 0.192 , 0.234	Depositor DCC
R_{free} test set	3241 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	19.6	Xtriage
Anisotropy	0.839	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 41.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for k,h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6018	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 50.08 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 6.8035e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 6X9, ZN, FE2, CL

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	0.61	0/2871	0.72	3/3885 (0.1%)
1	B	0.59	0/2860	0.71	1/3871 (0.0%)
All	All	0.60	0/5731	0.71	4/7756 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	1
All	All	0	3

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	329	ASP	CB-CG-OD1	7.21	124.79	118.30
1	A	330	ARG	NE-CZ-NH2	-6.09	117.25	120.30
1	A	329	ASP	CB-CG-OD1	5.92	123.62	118.30
1	A	330	ARG	NE-CZ-NH1	5.91	123.26	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	310	CYS	Mainchain
1	A	311	ARG	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
1	B	309	THR	Peptide

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	2788	0	2711	35	0
1	B	2777	0	2693	36	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	16	0	0	0	0
4	B	16	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	208	0	0	11	0
6	B	207	0	0	8	0
All	All	6018	0	5404	71	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 6.

All (71) 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:170:ILE:HD11	1:A:174:ASN:OD1	1.37	1.24
1:A:15:LYS:HE3	6:A:671:HOH:O	1.53	1.08
1:B:170:ILE:HD11	1:B:174:ASN:OD1	1.64	0.97
1:A:170:ILE:HD11	1:A:174:ASN:CG	1.89	0.92
1:B:170:ILE:HD11	1:B:174:ASN:CG	1.89	0.92
1:A:311:ARG:HB2	1:A:314:MET:CE	2.01	0.90
1:A:170:ILE:CD1	1:A:174:ASN:OD1	2.24	0.86
1:A:15:LYS:CD	6:A:671:HOH:O	2.23	0.86
1:A:310:CYS:HB2	1:A:311:ARG:HD2	1.57	0.85
1:B:331:TYR:CZ	1:B:335:LYS:HE3	2.16	0.79

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:311:ARG:HB2	1:A:314:MET:HE2	1.64	0.78
1:A:236:CYS:HB2	1:A:310:CYS:SG	2.24	0.78
1:A:170:ILE:CD1	1:A:174:ASN:CG	2.57	0.73
1:A:65:ASP:OD1	1:A:100:ARG:NH1	2.22	0.72
1:A:311:ARG:HB2	1:A:314:MET:HE3	1.70	0.72
1:B:65:ASP:OD1	1:B:100:ARG:NH1	2.24	0.69
1:B:28:GLU:HB3	6:B:686:HOH:O	1.93	0.68
1:A:15:LYS:CE	6:A:671:HOH:O	2.18	0.65
1:B:20:ARG:NH1	6:B:501:HOH:O	2.24	0.64
1:A:92:LYS:HG3	6:A:627:HOH:O	1.97	0.64
1:A:90:GLN:NE2	6:A:503:HOH:O	2.31	0.62
1:A:65:ASP:CG	1:A:100:ARG:HH12	2.03	0.61
1:A:92:LYS:CG	6:A:627:HOH:O	2.48	0.61
1:B:170:ILE:HD12	1:B:173:VAL:HG22	1.84	0.59
1:B:15:LYS:HD2	1:B:260:ASP:OD2	2.02	0.59
1:B:65:ASP:CG	1:B:100:ARG:HH12	2.06	0.59
1:A:310:CYS:CB	1:A:311:ARG:HD2	2.32	0.57
1:B:311:ARG:HB2	1:B:314:MET:CE	2.34	0.57
1:B:199:ILE:O	1:B:290:SER:HB2	2.05	0.57
1:B:311:ARG:HB2	1:B:314:MET:HE2	1.85	0.57
1:A:312:LYS:HB2	1:A:312:LYS:NZ	2.19	0.57
1:B:347:LYS:HD3	1:B:348:PRO:HD3	1.86	0.56
1:B:321:ILE:HG22	6:B:587:HOH:O	2.06	0.56
1:B:246:LEU:N	1:B:246:LEU:HD12	2.20	0.56
1:A:13:SER:OG	1:A:15:LYS:HG2	2.06	0.55
1:A:20:ARG:NE	6:A:502:HOH:O	2.26	0.54
1:A:157:THR:HB	1:A:294:ALA:O	2.07	0.54
1:B:331:TYR:OH	1:B:335:LYS:HE3	2.07	0.54
1:B:241:ARG:HG2	6:B:538:HOH:O	2.09	0.53
1:A:199:ILE:O	1:A:290:SER:HB2	2.09	0.52
1:B:312:LYS:HD3	1:B:313:ASP:H	1.74	0.52
1:B:145:GLU:OE1	1:B:145:GLU:HA	2.09	0.52
1:B:213:ILE:HD13	1:B:221:LEU:HB2	1.92	0.50
1:A:349:THR:HG21	6:A:630:HOH:O	2.10	0.50
1:A:64:ILE:HD13	1:A:142:ILE:HD12	1.93	0.50
1:B:157:THR:HB	1:B:294:ALA:O	2.14	0.48
1:B:312:LYS:O	1:B:313:ASP:HB2	2.13	0.47
1:B:224:LEU:HD11	1:B:228:PHE:HE2	1.79	0.47
1:B:170:ILE:CD1	1:B:174:ASN:CG	2.75	0.47
1:B:15:LYS:HA	1:B:15:LYS:HD3	1.40	0.47
1:B:224:LEU:HD11	1:B:228:PHE:CE2	2.49	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:246:LEU:HD12	1:A:246:LEU:N	2.30	0.46
1:B:347:LYS:HD3	1:B:348:PRO:CD	2.45	0.46
1:A:20:ARG:NH1	6:A:508:HOH:O	2.42	0.46
1:B:162:VAL:O	1:B:166:CYS:HB2	2.16	0.45
1:A:228:PHE:HZ	1:A:255:TYR:CE2	2.34	0.45
1:A:92:LYS:HG2	6:A:627:HOH:O	2.14	0.45
1:B:170:ILE:O	1:B:171:GLU:HB2	2.16	0.45
1:A:312:LYS:HZ2	1:A:312:LYS:H	1.64	0.44
1:B:20:ARG:NH2	6:B:505:HOH:O	2.31	0.44
1:B:100:ARG:NH1	6:B:503:HOH:O	2.28	0.44
1:A:15:LYS:HA	1:A:15:LYS:HD2	1.75	0.44
1:A:162:VAL:O	1:A:166:CYS:HB2	2.20	0.42
1:A:224:LEU:HD11	1:A:228:PHE:CE2	2.54	0.42
1:B:347:LYS:HD3	1:B:347:LYS:HA	1.28	0.42
1:B:231:SER:HB2	6:B:605:HOH:O	2.20	0.42
1:B:231:SER:CB	6:B:605:HOH:O	2.69	0.41
1:B:15:LYS:HZ2	1:B:15:LYS:HG2	1.76	0.41
1:B:312:LYS:HD3	1:B:313:ASP:N	2.34	0.41
1:A:321:ILE:HG22	6:A:584:HOH:O	2.21	0.41
1:A:58:ARG:HD3	1:A:61:TYR:CD1	2.56	0.41

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	338/367 (92%)	330 (98%)	8 (2%)	0	100	100
1	B	337/367 (92%)	331 (98%)	6 (2%)	0	100	100
All	All	675/734 (92%)	661 (98%)	14 (2%)	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	299/319 (94%)	286 (96%)	13 (4%)	33	22
1	B	297/319 (93%)	284 (96%)	13 (4%)	33	22
All	All	596/638 (93%)	570 (96%)	26 (4%)	33	22

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	GLU
1	A	67	LEU
1	A	80	GLN
1	A	81	SER
1	A	92	LYS
1	A	162	VAL
1	A	164	GLU
1	A	237	ASP
1	A	308	CYS
1	A	309	THR
1	A	311	ARG
1	A	312	LYS
1	A	316	LYS
1	B	10	LEU
1	B	15	LYS
1	B	24	GLU
1	B	114	LEU
1	B	145	GLU
1	B	164	GLU
1	B	253	LYS
1	B	311	ARG
1	B	312	LYS
1	B	329	ASP
1	B	333	LEU
1	B	335	LYS
1	B	347	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	226	GLN
1	B	74	GLN
1	B	226	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 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 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	$\# Z > 2$
4	6X9	A	403	2	12,17,17	1.51	2 (16%)	8,25,25	1.91	4 (50%)
4	6X9	B	403	2	12,17,17	1.53	4 (33%)	8,25,25	1.73	2 (25%)

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
4	6X9	A	403	2	-	0/2/4/4	0/2/2/2
4	6X9	B	403	2	-	0/2/4/4	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	403	6X9	C7-C3	-2.16	1.38	1.45
4	B	403	6X9	C6-C5	2.13	1.43	1.40
4	B	403	6X9	C5-N4	2.38	1.34	1.32
4	B	403	6X9	C13-C5	2.54	1.55	1.50
4	A	403	6X9	C13-C5	2.58	1.55	1.50
4	A	403	6X9	C5-N4	3.01	1.35	1.32

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	A	403	6X9	C12-C11-C6	-3.25	106.09	112.31
4	B	403	6X9	C8-C7-C15	-2.96	123.08	127.33
4	A	403	6X9	C8-C7-C15	-2.51	123.72	127.33
4	A	403	6X9	C5-N4-C3	2.00	120.43	117.69
4	A	403	6X9	C14-C8-N9	2.76	125.64	119.75
4	B	403	6X9	C14-C8-N9	3.18	126.52	119.75

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 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	340/367 (92%)	-0.08	7 (2%) 64 67	13, 23, 46, 102	0
1	B	339/367 (92%)	-0.11	6 (1%) 69 72	13, 23, 43, 90	0
All	All	679/734 (92%)	-0.10	13 (1%) 67 70	13, 23, 45, 102	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	313	ASP	5.3
1	A	10	LEU	4.1
1	A	312	LYS	3.4
1	B	312	LYS	3.4
1	B	309	THR	3.2
1	A	313	ASP	3.1
1	A	349	THR	2.8
1	B	10	LEU	2.8
1	A	346	THR	2.4
1	A	347	LYS	2.3
1	B	145	GLU	2.2
1	A	81	SER	2.1
1	B	170	ILE	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

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
4	6X9	A	403	16/16	0.97	0.08	-0.91	14,18,21,22	0
3	ZN	B	402	1/1	0.98	0.05	-1.19	26,26,26,26	0
3	ZN	A	402	1/1	0.99	0.06	-1.35	26,26,26,26	0
4	6X9	B	403	16/16	0.96	0.08	-1.89	16,19,22,24	0
5	CL	B	404	1/1	0.99	0.09	-2.95	18,18,18,18	0
5	CL	A	404	1/1	0.99	0.09	-3.30	18,18,18,18	0
2	FE2	A	401	1/1	1.00	0.06	-	15,15,15,15	0
2	FE2	B	401	1/1	0.99	0.06	-	14,14,14,14	0

6.5 Other polymers

There are no such residues in this entry.