WORLDWIDE PDB

PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Sep 26, 2014 – 04:41 PM EDT

PDB ID	:	4URL
Title	:	Crystal Structure of Staph ParE43kDa in complex with KBD
Authors	:	Lu, J.; Patel, S.; Sharma, N.; Soisson, S.; Kishii, R.; Takei, M.; Fukuda, Y.; Lumb, K.J.; Singh, S.B.
Deposited on	:	2014-06-30
Resolution	:	2.29 Å(reported)

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

MolProbity	:	4.02b-467
Mogul	:	1.16 November 2013
Xtriage (Phenix)	:	dev-1439
EDS	:	stable23828
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable23828

1 Overall quality at a glance ⓘ

The reported resolution of this entry is 2.29 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		0.254
Clashscore		4
Ramachandran outliers		0.6%
Sidechain outliers		3.8%
RSRZ outliers		3.0%

Worse   *Better*

▌Percentile relative to all X-ray structures

◻ Percentile relative to X-ray structures of similar resolution
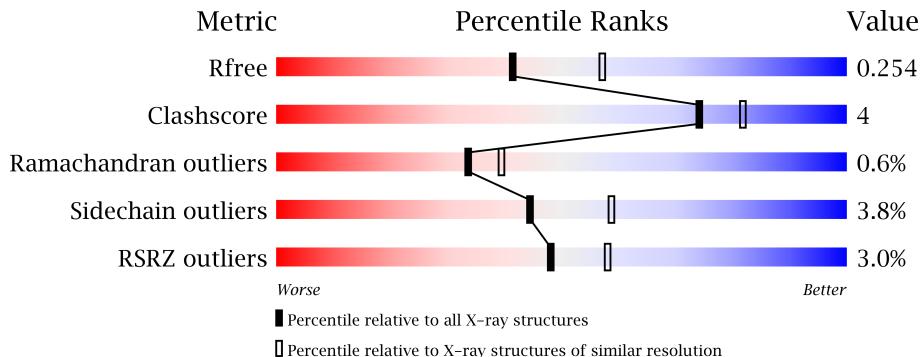
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	2929 (2.30-2.30)
Clashscore	79885	3679 (2.30-2.30)
Ramachandran outliers	78287	3642 (2.30-2.30)
Sidechain outliers	78261	3641 (2.30-2.30)
RSRZ outliers	66119	2930 (2.30-2.30)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	406	
1	B	406	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

| Mol	Type	Chain	Res	Geometry	Electron density
2	XAM	A	2000	-	X

2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 5748 atoms, of which 0 are hydrogen and 0 are deuterium.

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 DNA TOPOISOMERASE IV, B SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	364	Total	C	N	O	S	0	0	0
			2755	1718	485	550	2			
1	B	363	Total	C	N	O	S	0	1	0
			2759	1729	482	545	3			

- Molecule 2 is (1R,4AS,5S,6S,8AR)-5-{[(5S)-1-(3-O-ACETYL-4-O-CARBAMOYL-6-DEOXY-2-O-METHYL-ALPHA-L-TALOPYRANOSYL)-4-HYDROXY-2-OXO-5-(PROPAN-2-YL)-2,5-DIHYDRO-1H-PYRROL-3-YL]CARBONYL}-6-METHYL-4-METHYLIDENE-1,2,3,4,4A,5,6,8A-OCTAHYDRONAPHTHALEN-1-YL2,6-DIDEOXY-3-C-[(1S)-1-{[(3,4-DICHLORO-5-METHYL-1H-PYRROL-2-YL)CARBONYL]AMINO}ETHYL]-BETA-D-RIBO-HEXOPYRANOSIDE (three-letter code: XAM) (formula: $C_{44}H_{60}Cl_2N_4O_{14}$).
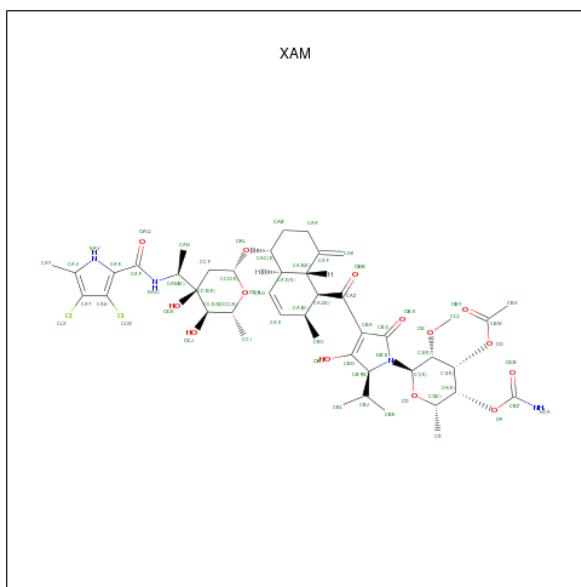
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	0	0
			64	44	2	4	14		
2	B	1	Total	C	Cl	N	O	0	0
			64	44	2	4	14		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	52	Total O 52 52	0	0
3	B	54	Total O 54 54	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 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 (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: DNA TOPOISOMERASE IV, B SUBUNIT

Chain A:
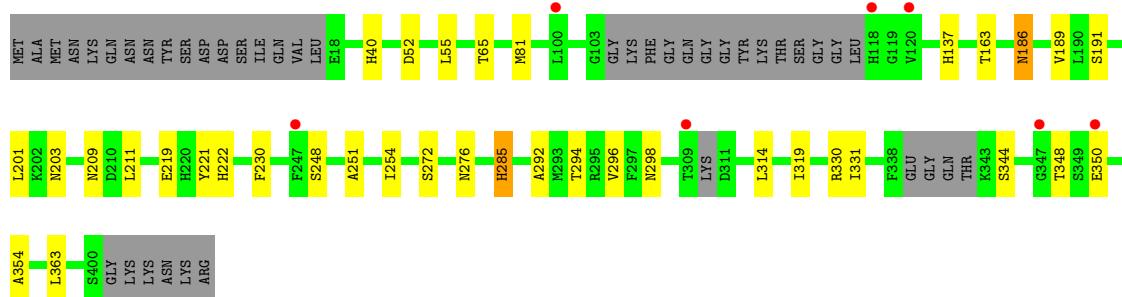
- Molecule 1: DNA TOPOISOMERASE IV, B SUBUNIT

Chain B:
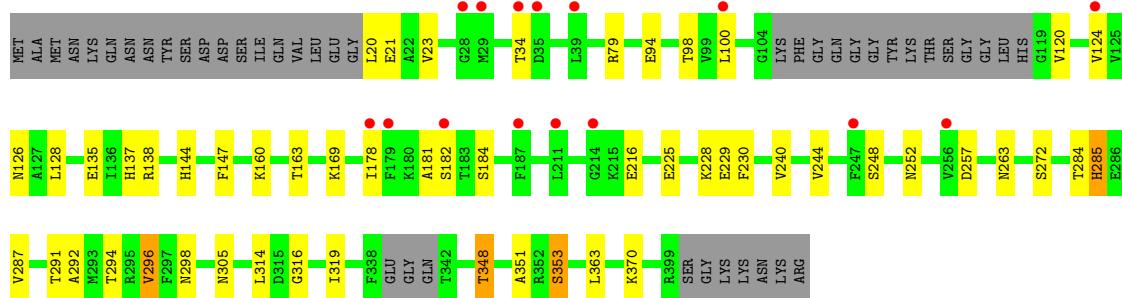
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	54.45Å 136.81Å 69.19Å 90.00° 111.92° 90.00°	Depositor
Resolution (Å)	49.73 – 2.29 49.73 – 2.29	Depositor EDS
% Data completeness (in resolution range)	98.8 (49.73-2.29) 99.2 (49.73-2.29)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.22 (at 2.29Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.217 , 0.252 0.220 , 0.254	Depositor DCC
R_{free} test set	1311 reflections (3.25%)	DCC
Wilson B-factor (Å^2)	44.1	Xtriage
Anisotropy	0.140	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 47.7	EDS
Estimated twinning fraction	0.027 for h,-k,-h-l	Xtriage
L-test for twinning	$< |L| > = 0.50, < L^2 > = 0.33$	Xtriage
Outliers	0 of 41708 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	5748	wwPDB-VP
Average B, all atoms (Å^2)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.54% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1] Intensities estimated from amplitudes.

5   Model quality ⓘ

5.1   Standard geometry ⓘ

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

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	0.50	0/2796	0.70	0/3778
1	B	0.52	0/2804	0.74	0/3785
All	All	0.51	0/5600	0.72	0/7563

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2   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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2755	0	2626	20	0
1	B	2759	0	2671	25	0
2	A	64	0	0	2	0
2	B	64	0	0	0	0
3	A	52	0	0	0	0
3	B	54	0	0	0	0
All	All	5748	0	5297	45	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 4.

All (45) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:94:GLU:O	1:B:98:THR:HB	1.62	0.99
1:A:298:ASN:HD21	1:A:314:LEU:H	1.15	0.93
1:A:296:VAL:HG11	1:A:363:LEU:HD23	1.64	0.79
1:A:292:ALA:O	1:A:296:VAL:HG12	1.86	0.76
1:B:298:ASN:HD21	1:B:314:LEU:H	1.34	0.73
1:A:40:HIS:CE1	1:A:186:ASN:H	2.10	0.69
1:B:284:THR:HG21	1:B:348:THR:O	1.95	0.67
1:B:252:ASN:HD21	1:B:353:SER:HB2	1.60	0.66
1:A:186:ASN:HD22	1:A:189:VAL:H	1.44	0.65
1:A:251:ALA:HB3	1:A:354:ALA:HA	1.80	0.64
1:B:128:LEU:HD22	1:B:178:ILE:HG21	1.80	0.63
1:A:40:HIS:HE1	1:A:186:ASN:H	1.48	0.59
1:A:81:MET:HE2	2:A:2000:XAM:CLW	2.39	0.59
1:B:296:VAL:HG22	1:B:363:LEU:HD23	1.85	0.59
1:A:65:THR:HG23	1:A:211:LEU:HD23	1.86	0.58
1:B:292:ALA:O	1:B:296:VAL:HG13	2.06	0.56
1:A:52:ASP:HA	1:A:55:LEU:HD12	1.88	0.55
1:A:296:VAL:CG1	1:A:363:LEU:HD23	2.38	0.52
1:B:294:THR:HA	1:B:319:ILE:HD13	1.93	0.51
1:A:272:SER:HB2	1:A:285:HIS:NE2	2.27	0.50
1:A:254:ILE:HG12	1:A:331:ILE:HG12	1.93	0.50
1:A:186:ASN:ND2	1:A:189:VAL:H	2.10	0.49
1:B:228:LYS:HG3	1:B:244:VAL:HB	1.93	0.49
1:B:144[B]:HIS:CD2	1:B:160:LYS:HG3	2.49	0.48
1:A:294:THR:HA	1:A:319:ILE:HD13	1.97	0.47
1:A:137:HIS:HD2	1:A:163:THR:OG1	1.98	0.46
1:B:137:HIS:HD2	1:B:163:THR:OG1	1.98	0.46
1:B:120:VAL:HB	1:B:124:VAL:HG21	1.97	0.46
1:B:135:GLU:HB2	1:B:169:LYS:HB3	1.98	0.46
1:B:20:LEU:HB2	1:B:21:GLU:H	1.53	0.45
1:B:294:THR:HG21	1:B:316:GLY:HA2	1.99	0.44
1:A:203:ASN:HA	1:A:222:HIS:HE2	1.83	0.43
1:B:23:VAL:HG21	1:B:124:VAL:HG22	2.00	0.43
1:A:81:MET:CE	2:A:2000:XAM:CLW	3.03	0.43
1:B:298:ASN:HD21	1:B:314:LEU:N	2.10	0.43
1:B:126:ASN:HD21	1:B:147:PHE:HB2	1.83	0.43
1:B:240:VAL:HA	1:B:263:ASN:HA	2.01	0.43
1:B:20:LEU:HG	1:B:100:LEU:HB2	2.00	0.42
1:A:191:SER:HB2	1:A:221:TYR:OH	2.19	0.42
1:B:79:ARG:O	1:B:138:ARG:HD2	2.20	0.42
1:B:284:THR:HG23	1:B:351:ALA:HB3	2.00	0.42
1:B:287:VAL:O	1:B:291:THR:HG23	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:225:GLU:HB2	1:B:229:GLU:HG3	2.02	0.42
1:B:272:SER:HB2	1:B:285:HIS:NE2	2.35	0.41
1:A:52:ASP:O	1:A:55:LEU:HB2	2.21	0.40

There are no symmetry-related clashes.

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	356/406 (88%)	341 (96%)	13 (4%)	2 (1%)	33	39
1	B	358/406 (88%)	343 (96%)	13 (4%)	2 (1%)	33	39
All	All	714/812 (88%)	684 (96%)	26 (4%)	4 (1%)	33	39

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	181	ALA
1	A	348	THR
1	A	344	SER
1	B	348	THR

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	287/343 (84%)	277 (96%)	10 (4%)	48	63
1	B	289/343 (84%)	277 (96%)	12 (4%)	40	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	576/686 (84%)	554 (96%)	22 (4%)	44 59

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	186	ASN
1	A	201	LEU
1	A	209	ASN
1	A	219	GLU
1	A	230	PHE
1	A	248	SER
1	A	276	ASN
1	A	285	HIS
1	A	330	ARG
1	A	350	GLU
1	B	34	THR
1	B	182	SER
1	B	184	SER
1	B	216	GLU
1	B	230	PHE
1	B	248	SER
1	B	257	ASP
1	B	285	HIS
1	B	296	VAL
1	B	305	ASN
1	B	353	SER
1	B	370	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	HIS
1	A	137	HIS
1	A	186	ASN
1	A	195	GLN
1	A	298	ASN
1	B	126	ASN
1	B	137	HIS
1	B	195	GLN
1	B	252	ASN
1	B	298	ASN

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Mol	Chain	Res	Type
1	B	386	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

2 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	XAM	A	2000	-	69,69,69	1.59	12 (17%)	106,106,106	1.72	18 (16%)
2	XAM	B	2000	-	69,69,69	1.60	10 (14%)	106,106,106	1.48	14 (13%)

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	XAM	A	2000	-	-	2/38/133/133	0/6/6/6
2	XAM	B	2000	-	-	0/38/133/133	0/6/6/6

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2000	XAM	OBB-CAZ	7.40	1.35	1.22
2	A	2000	XAM	OBB-CAZ	7.15	1.35	1.22
2	A	2000	XAM	CCE-CCD	4.70	1.62	1.54
2	B	2000	XAM	CBA-CAZ	-4.18	1.37	1.46
2	A	2000	XAM	CBA-CBG	4.05	1.46	1.36
2	B	2000	XAM	CBA-CBG	3.82	1.45	1.36
2	B	2000	XAM	C1-NBE	3.73	1.52	1.44
2	A	2000	XAM	CBA-CAZ	-3.70	1.38	1.46
2	B	2000	XAM	O4-CBZ	3.66	1.41	1.35
2	B	2000	XAM	OBI-CBG	-3.44	1.22	1.33
2	A	2000	XAM	OBI-CBG	-3.42	1.22	1.33
2	B	2000	XAM	CBF-CBG	3.41	1.57	1.51
2	B	2000	XAM	CBD-NBE	3.29	1.43	1.36
2	A	2000	XAM	CBD-NBE	3.26	1.43	1.36
2	A	2000	XAM	C1-NBE	3.24	1.51	1.44
2	B	2000	XAM	CCE-CCD	2.96	1.59	1.54
2	A	2000	XAM	CAS-CAT	2.86	1.45	1.36
2	A	2000	XAM	O4-CBZ	2.63	1.40	1.35
2	A	2000	XAM	CCE-CAM	2.35	1.62	1.55
2	A	2000	XAM	CAJ-CAZ	2.32	1.55	1.50
2	B	2000	XAM	CAJ-CAZ	2.10	1.55	1.50
2	A	2000	XAM	CBF-CBG	2.01	1.54	1.51

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2000	XAM	C5-O5-C1	6.88	121.65	112.53
2	B	2000	XAM	C5-O5-C1	5.98	120.46	112.53
2	B	2000	XAM	CCE-CAM-NAO	-5.53	106.74	111.35
2	A	2000	XAM	C4-O4-CBZ	5.31	124.60	117.03
2	A	2000	XAM	O4-CBZ-OCB	-4.75	119.80	124.26
2	B	2000	XAM	CAS-CAR-CAP	4.01	131.94	124.14
2	A	2000	XAM	CAU-CAT-CLX	3.98	130.69	125.90
2	A	2000	XAM	CBG-CBF-NBE	3.94	103.08	101.32
2	B	2000	XAM	CAU-CAT-CLX	3.84	130.53	125.90
2	A	2000	XAM	CAT-CAU-NAV	3.79	108.73	106.55
2	A	2000	XAM	OCK-CCE-CAM	-3.55	104.58	109.87
2	B	2000	XAM	C4-O4-CBZ	3.49	122.01	117.03
2	A	2000	XAM	C2-C1-NBE	3.15	117.70	113.61
2	B	2000	XAM	CAJ-CAE-CAF	3.15	123.42	114.74
2	A	2000	XAM	CCF-CCE-CAM	3.09	114.75	110.52
2	A	2000	XAM	CAS-CAR-CAP	2.91	129.80	124.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2000	XAM	CAS-CAT-CLX	-2.78	121.59	126.35
2	B	2000	XAM	O5-C1-NBE	-2.68	105.90	108.23
2	A	2000	XAM	CAE-CAD-CAG	2.67	112.08	108.25
2	A	2000	XAM	CBJ-CBF-CBG	2.59	115.14	111.52
2	A	2000	XAM	OBB-CAZ-CBA	-2.59	116.41	119.96
2	A	2000	XAM	CBF-CBG-CBA	-2.51	108.36	113.21
2	A	2000	XAM	O5-C1-NBE	-2.51	106.05	108.23
2	B	2000	XAM	CBF-CBG-CBA	-2.39	108.60	113.21
2	A	2000	XAM	CAJ-CAE-CAF	2.38	121.31	114.74
2	B	2000	XAM	CAE-CAD-CAG	2.28	111.53	108.25
2	B	2000	XAM	OBB-CAZ-CBA	-2.26	116.86	119.96
2	A	2000	XAM	O4-CBZ-NCA	2.23	114.53	110.55
2	A	2000	XAM	CAM-NAO-CAP	2.23	126.21	123.47
2	B	2000	XAM	OCK-CCE-CAM	-2.09	106.76	109.87
2	B	2000	XAM	CAN-CAM-CCE	2.01	115.72	113.43
2	B	2000	XAM	CBJ-CBF-NBE	2.01	117.41	113.72

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	2000	XAM	C4-O4-CBZ-NCA
2	A	2000	XAM	C4-O4-CBZ-OCB

There are no ring outliers.

5.7 Other polymers ⓘ

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 ⓘ

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	364/406 (89%)	0.39	7 (1%)	64 　 73	36, 52, 77, 94	0
1	B	363/406 (89%)	0.40	15 (4%)	35 　 46	32, 50, 78, 96	0
All	All	727/812 (89%)	0.40	22 (3%)	48 　 58	32, 51, 78, 96	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	179	PHE	3.9
1	B	182	SER	3.4
1	A	347	GLY	3.1
1	B	178	ILE	3.0
1	A	118	HIS	2.9
1	B	100	LEU	2.8
1	A	120	VAL	2.7
1	B	28	GLY	2.6
1	A	100	LEU	2.6
1	B	29	MET	2.5
1	B	124	VAL	2.5
1	B	35	ASP	2.5
1	A	247	PHE	2.4
1	B	211	LEU	2.3
1	B	187	PHE	2.3
1	B	214	GLY	2.3
1	A	309	THR	2.2
1	B	247	PHE	2.2
1	B	34	THR	2.1
1	B	39	LEU	2.1
1	B	256	VAL	2.1
1	A	350	GLU	2.1

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	RSR	LLDF	B-factors(Å^2)	Q<0.9
2	XAM	A	2000	64/64	0.24	2.04	48,68,83,88	0
2	XAM	B	2000	64/64	0.16	-0.09	40,61,85,90	0

6.5 Other polymers ⓘ

There are no such residues in this entry.