Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 08:33 AM GMT

PDB ID	:	3F69
Title	:	Crystal structure of the Mycobacterium tuberculosis PknB mutant kinase domain in complex with KT5720
Authors	:	Alber, T.; Mieczkowski, C.A.; TB Structural Genomics Consortium (TBSGC)
Deposited on	:	2008-11-05
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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

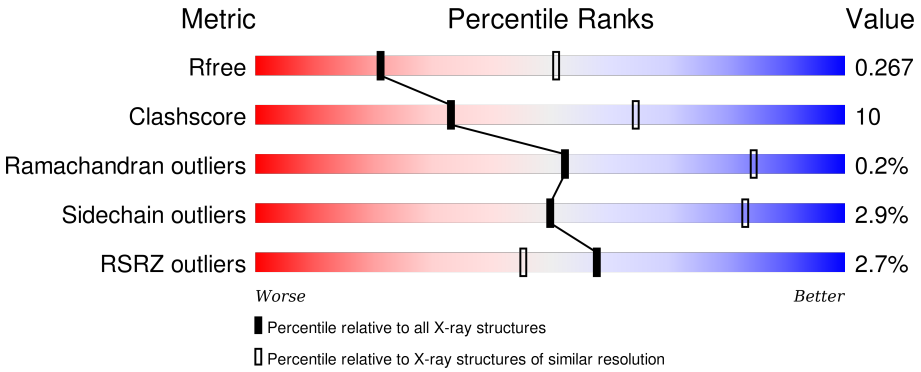
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

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))
R_{free}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (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 <=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	311	% 70% 15% • 13%
1	B	311	4% 71% 19% • 9%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4386 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.

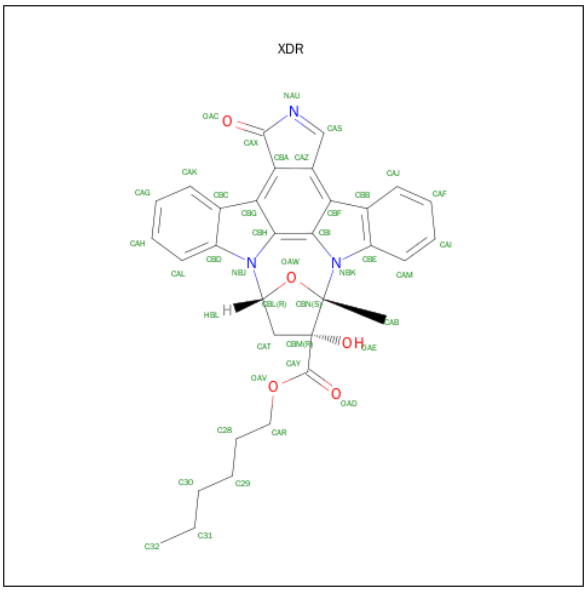
- Molecule 1 is a protein called Serine/threonine-protein kinase pknB.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	270	Total	C	N	O	S		62	2	0
			2094	1309	379	400	6				
1	B	283	Total	C	N	O	P	S	57	1	0
			2172	1352	391	422	1	6			

There are 12 discrepancies between the modelled and reference sequences:

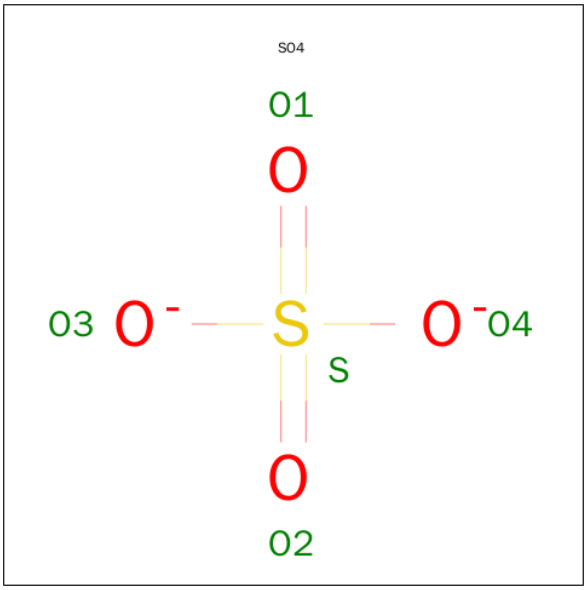
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P0A5S4
A	-1	SER	-	expression tag	UNP P0A5S4
A	0	HIS	-	expression tag	UNP P0A5S4
A	33	ASP	LEU	engineered	UNP P0A5S4
A	145	LEU	MET	engineered	UNP P0A5S4
A	155	VAL	MET	engineered	UNP P0A5S4
B	-2	GLY	-	expression tag	UNP P0A5S4
B	-1	SER	-	expression tag	UNP P0A5S4
B	0	HIS	-	expression tag	UNP P0A5S4
B	33	ASP	LEU	engineered	UNP P0A5S4
B	145	LEU	MET	engineered	UNP P0A5S4
B	155	VAL	MET	engineered	UNP P0A5S4

- Molecule 2 is HEXYL (5S,6R,8R)-6-HYDROXY-5-METHYL-13-OXO-5,6,7,8-TETRAHYDRO-13H-5,8-EPOXY-4B,8A,14-TRIAZADIBENZO[B,H]CYCLOOCTA[1,2,3,4-JKL]CYCLOPENTA[E]-AS-INDACENE-6-CARBOXYLATE (three-letter code: XDR) (formula: $C_{32}H_{29}N_3O_5$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C N O 35 27 3 5	0	0
2	B	1	Total C N O 35 27 3 5	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0

- Molecule 4 is water.

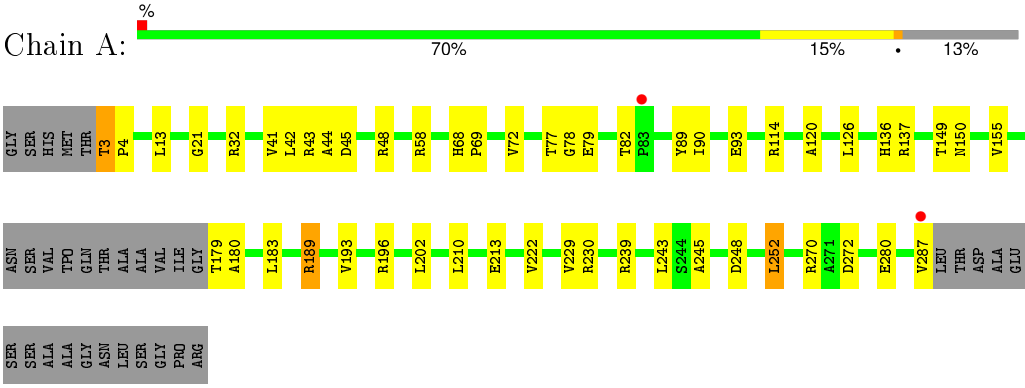
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	17	Total O 17 17	0	0
4	B	13	Total O 13 13	0	0

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 (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.

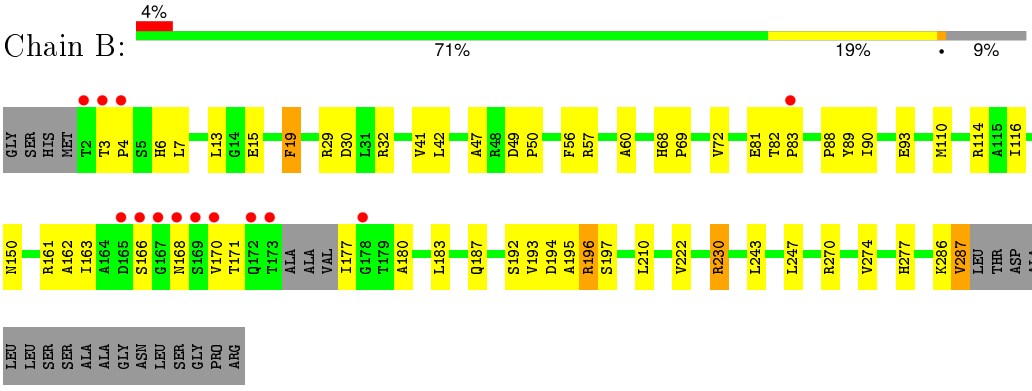
- Molecule 1: Serine/threonine-protein kinase pknB

Chain A:



- Molecule 1: Serine/threonine-protein kinase pknB

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	F 41 3 2	Depositor
Cell constants a, b, c, α, β, γ	297.56Å 297.56Å 297.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.78 – 2.80 39.76 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.2 (39.78-2.80) 99.2 (39.76-2.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.50 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.4.0077	Depositor
R, R_{free}	0.218 , 0.268 0.230 , 0.267	Depositor DCC
R_{free} test set	1419 reflections (5.33%)	DCC
Wilson B-factor (Å^2)	61.6	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 51.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.52$, $< L^2 > = 0.36$	Xtriage
Outliers	1 of 28056 reflections (0.004%)	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4386	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: TPO, SO4, XDR

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	1.11	9/2138 (0.4%)	0.77	9/2913 (0.3%)
1	B	0.62	4/2207 (0.2%)	0.71	7/3006 (0.2%)
All	All	0.90	13/4345 (0.3%)	0.74	16/5919 (0.3%)

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	B	0	1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	189	ARG	NE-CZ	-35.62	0.86	1.33
1	A	48	ARG	CG-CD	19.89	2.01	1.51
1	A	58	ARG	CD-NE	-11.52	1.26	1.46
1	A	280	GLU	CG-CD	-11.03	1.35	1.51
1	B	19	PHE	CG-CD1	9.47	1.52	1.38
1	B	230	ARG	CB-CG	-8.90	1.28	1.52
1	B	81	GLU	CB-CG	-8.46	1.36	1.52
1	B	177	ILE	CB-CG1	-7.89	1.31	1.54
1	A	43	ARG	CG-CD	-7.21	1.33	1.51
1	A	79	GLU	CB-CG	6.87	1.65	1.52
1	A	13	LEU	CG-CD1	-6.28	1.28	1.51
1	A	42	LEU	CG-CD1	-5.62	1.31	1.51
1	A	287	VAL	CB-CG1	-5.55	1.41	1.52

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	58	ARG	CD-NE-CZ	-11.02	108.17	123.60
1	B	19	PHE	CB-CG-CD2	10.95	128.47	120.80
1	A	189	ARG	CD-NE-CZ	10.23	137.92	123.60
1	A	48	ARG	CB-CG-CD	-8.10	90.55	111.60
1	A	48	ARG	CG-CD-NE	-7.49	96.08	111.80
1	B	19	PHE	CB-CG-CD1	-7.44	115.59	120.80
1	A	189	ARG	NE-CZ-NH1	-7.17	116.72	120.30
1	B	57	ARG	CG-CD-NE	-6.71	97.71	111.80
1	A	43	ARG	CB-CG-CD	6.58	128.71	111.60
1	A	287	VAL	CG1-CB-CG2	6.56	121.40	110.90
1	A	189	ARG	NE-CZ-NH2	6.06	123.33	120.30
1	B	230	ARG	CA-CB-CG	6.02	126.65	113.40
1	A	13	LEU	CB-CG-CD1	5.89	121.01	111.00
1	B	177	ILE	CA-CB-CG1	5.28	121.03	111.00
1	B	19	PHE	CD1-CG-CD2	-5.21	111.52	118.30
1	B	287	VAL	CA-CB-CG2	5.01	118.42	110.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	19	PHE	Sidechain

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	2094	0	2059	27	0
1	B	2172	0	2132	50	0
2	A	35	0	16	5	0
2	B	35	0	16	4	0
3	A	10	0	0	0	0
3	B	10	0	0	0	0
4	A	17	0	0	1	0
4	B	13	0	0	0	0
All	All	4386	0	4223	85	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 10.

All (85) 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:4:PRO:HG3	1:A:82:THR:HG22	1.30	1.10
2:A:309:XDR:HABA	2:A:309:XDR:HAM	1.36	1.04
2:B:309:XDR:HABA	2:B:309:XDR:HAM	1.43	0.98
1:B:3:THR:HB	1:B:4:PRO:HD2	1.61	0.80
1:A:126:LEU:HD12	1:A:202:LEU:HD22	1.63	0.79
1:B:32:ARG:HH11	1:B:32:ARG:HG2	1.47	0.78
2:A:309:XDR:CAM	2:A:309:XDR:HABA	2.14	0.77
1:A:72:VAL:HG21	1:A:155:VAL:HG12	1.66	0.77
1:B:137[B]:ARG:NH1	1:B:161:ARG:HD2	2.00	0.76
1:A:4:PRO:HG3	1:A:82:THR:CG2	2.13	0.75
1:B:7:LEU:HD11	1:B:13:LEU:HD11	1.69	0.73
2:A:309:XDR:HAM	2:A:309:XDR:CAB	2.17	0.69
1:B:194:ASP:OD2	1:B:196:ARG:NH1	2.26	0.68
1:B:32:ARG:HG2	1:B:32:ARG:NH1	2.08	0.68
1:B:163:ILE:HG23	1:B:168:ASN:O	1.92	0.68
2:B:309:XDR:CAB	2:B:309:XDR:HAM	2.22	0.67
1:B:171:TPO:CG2	1:B:171:TPO:O1P	2.41	0.67
1:B:286:LYS:O	1:B:287:VAL:HB	1.94	0.67
1:B:193:VAL:HG13	1:B:197:SER:OG	1.96	0.66
1:B:7:LEU:CD1	1:B:13:LEU:HD11	2.26	0.66
2:A:309:XDR:CAM	2:A:309:XDR:CAB	2.72	0.65
2:B:309:XDR:CAB	2:B:309:XDR:CAM	2.75	0.65
1:A:136:HIS:O	1:A:137:ARG:HB2	1.97	0.63
1:A:213:GLU:HB3	1:A:239:ARG:NH2	2.14	0.63
1:B:136:HIS:O	1:B:137[A]:ARG:HB2	1.98	0.62
1:B:110:MET:SD	1:B:114:ARG:HD3	2.40	0.62
1:B:171:TPO:HG21	1:B:171:TPO:O1P	1.99	0.61
1:B:194:ASP:C	1:B:194:ASP:OD1	2.35	0.61
1:B:82:THR:HB	1:B:83:PRO:CD	2.32	0.60
2:B:309:XDR:HABA	2:B:309:XDR:CAM	2.19	0.60
1:B:193:VAL:HG13	1:B:197:SER:CB	2.34	0.57
1:A:137:ARG:NH1	1:A:193:VAL:HG22	2.20	0.57
1:B:149:THR:O	1:B:150:ASN:HB2	2.03	0.57
1:B:166:SER:HB3	1:B:168:ASN:ND2	2.20	0.56
1:B:243:LEU:HD22	1:B:247:LEU:HD23	1.85	0.56
1:B:137[A]:ARG:CZ	1:B:161:ARG:NE	2.69	0.56
1:B:60:ALA:HA	1:B:90:ILE:HD11	1.88	0.56
1:B:194:ASP:OD1	1:B:196:ARG:N	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:180:ALA:HA	1:A:183:LEU:HG	1.88	0.55
1:A:72:VAL:HG13	1:A:93:GLU:HB3	1.88	0.55
1:B:168:ASN:HB3	1:B:192:SER:HB2	1.88	0.55
1:A:45:ASP:OD1	1:A:45:ASP:N	2.38	0.54
1:A:72:VAL:HG21	1:A:155:VAL:CG1	2.36	0.54
1:A:126:LEU:CD1	1:A:202:LEU:HD22	2.34	0.54
1:B:56:PHE:HE2	1:B:88:PRO:O	1.91	0.54
1:B:162:ALA:O	1:B:170:VAL:HG23	2.07	0.54
1:A:222:VAL:HG11	1:B:180:ALA:HB2	1.89	0.54
1:B:183:LEU:HD22	1:B:187:GLN:HB3	1.90	0.53
1:A:72:VAL:CG2	1:A:155:VAL:HG12	2.36	0.53
1:B:29:ARG:HD3	1:B:30:ASP:N	2.24	0.52
1:B:3:THR:HB	1:B:4:PRO:CD	2.37	0.52
1:B:41:VAL:HG12	1:B:89:TYR:HB3	1.92	0.51
1:B:116:ILE:HG21	1:B:277:HIS:HB2	1.92	0.50
1:B:136:HIS:O	1:B:137[B]:ARG:HB2	2.11	0.50
1:B:82:THR:HB	1:B:83:PRO:HD2	1.93	0.50
1:B:137[A]:ARG:NH1	1:B:161:ARG:HD2	2.28	0.49
1:B:183:LEU:HD22	1:B:187:GLN:CB	2.42	0.49
1:A:149:THR:O	1:A:150:ASN:CB	2.61	0.49
1:A:179:THR:O	1:A:180:ALA:HB3	2.12	0.49
1:B:137[A]:ARG:CZ	1:B:161:ARG:HE	2.27	0.48
1:A:78:GLY:HA3	1:A:89:TYR:CZ	2.50	0.47
1:A:179:THR:HA	4:A:312:HOH:O	2.15	0.47
1:B:68:HIS:CG	1:B:69:PRO:HD2	2.50	0.46
1:A:229:VAL:HG12	1:A:230:ARG:HG2	1.98	0.46
1:A:137:ARG:NH1	1:A:193:VAL:CG2	2.79	0.46
1:B:166:SER:CB	1:B:168:ASN:HD22	2.30	0.45
1:A:120:ALA:HB1	1:A:270:ARG:HG3	1.98	0.45
1:B:270:ARG:O	1:B:274:VAL:HG23	2.17	0.45
2:A:309:XDR:HATA	2:A:309:XDR:CBI	2.45	0.45
1:B:6:HIS:C	1:B:7:LEU:HD12	2.37	0.45
1:B:194:ASP:OD1	1:B:195:ALA:N	2.50	0.45
1:A:245:ALA:O	1:A:248:ASP:HB2	2.17	0.45
1:A:77:THR:HG22	1:A:90:ILE:HG23	1.99	0.45
1:B:7:LEU:HD13	1:B:13:LEU:HD21	1.99	0.44
1:B:137[B]:ARG:HE	1:B:193:VAL:HB	1.82	0.44
1:B:49:ASP:HA	1:B:50:PRO:HD3	1.83	0.44
1:A:3:THR:HG22	1:A:44:ALA:HB2	2.01	0.43
1:A:252:LEU:HD12	1:A:252:LEU:HA	1.68	0.43
1:A:68:HIS:CG	1:A:69:PRO:HD2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:210:LEU:HD22	1:B:243:LEU:HD21	2.01	0.43
1:B:171:TPO:O1P	1:B:171:TPO:HG22	2.19	0.43
1:B:42:LEU:HD21	1:B:47:ALA:HA	2.02	0.41
1:B:72:VAL:HG13	1:B:93:GLU:HB3	2.01	0.41
1:B:166:SER:CB	1:B:168:ASN:ND2	2.83	0.41
1:A:210:LEU:HA	1:A:210:LEU:HD23	1.88	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	268/311 (86%)	259 (97%)	8 (3%)	1 (0%)	39 74
1	B	279/311 (90%)	267 (96%)	12 (4%)	0	100 100
All	All	547/622 (88%)	526 (96%)	20 (4%)	1 (0%)	52 84

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	21	GLY

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	222/249 (89%)	213 (96%)	9 (4%)	37 72
1	B	230/249 (92%)	226 (98%)	4 (2%)	68 92
All	All	452/498 (91%)	439 (97%)	13 (3%)	50 83

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	THR
1	A	32	ARG
1	A	41	VAL
1	A	114	ARG
1	A	189	ARG
1	A	196	ARG
1	A	243	LEU
1	A	252	LEU
1	A	272	ASP
1	B	15	GLU
1	B	196	ARG
1	B	222	VAL
1	B	230	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	127	ASN
1	A	132	ASN
1	B	6	HIS
1	B	34	HIS
1	B	261	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

1 non-standard protein/DNA/RNA residue is 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	$\#\|Z\| > 2$
1	TPO	B	171	1	8,10,11	1.18	1 (12%)	7,14,16	1.01	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
1	TPO	B	171	1	-	0/8/11/13	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	171	TPO	P-O2P	2.17	1.62	1.54

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 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	171	TPO	3	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

6 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	XDR	A	309	-	32,42,47	2.14	5 (15%)	33,70,75	2.14	9 (27%)
3	SO4	A	310	-	4,4,4	0.17	0	6,6,6	0.13	0
3	SO4	A	311	-	4,4,4	0.17	0	6,6,6	0.32	0
2	XDR	B	309	-	32,42,47	2.30	8 (25%)	33,70,75	2.34	7 (21%)
3	SO4	B	310	-	4,4,4	0.20	0	6,6,6	0.15	0
3	SO4	B	311	-	4,4,4	0.19	0	6,6,6	0.22	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	XDR	A	309	-	-	0/8/46/51	0/0/8/8
3	SO4	A	310	-	-	0/0/0/0	0/0/0/0
3	SO4	A	311	-	-	0/0/0/0	0/0/0/0
2	XDR	B	309	-	-	0/8/46/51	0/0/8/8
3	SO4	B	310	-	-	0/0/0/0	0/0/0/0
3	SO4	B	311	-	-	0/0/0/0	0/0/0/0

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	309	XDR	CBM-CAY	-3.82	1.50	1.54
2	B	309	XDR	CBF-CBI	-3.40	1.38	1.42
2	A	309	XDR	CBF-CBI	-2.73	1.39	1.42
2	B	309	XDR	CBG-CBH	-2.58	1.39	1.42
2	A	309	XDR	CBM-CAY	-2.41	1.51	1.54
2	B	309	XDR	CBA-CBG	-2.26	1.39	1.43
2	B	309	XDR	CAZ-CBF	-2.26	1.40	1.43
2	A	309	XDR	OAV-CAY	2.10	1.37	1.33
2	B	309	XDR	OAV-CAY	2.21	1.37	1.33
2	B	309	XDR	CAS-NAU	4.09	1.46	1.33
2	A	309	XDR	CAS-NAU	4.14	1.46	1.33
2	B	309	XDR	CAZ-CAS	8.62	1.52	1.41
2	A	309	XDR	CAZ-CAS	8.67	1.52	1.41

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	309	XDR	CAZ-CAS-NAU	-4.71	102.04	111.09
2	B	309	XDR	CAZ-CAS-NAU	-4.68	102.09	111.09
2	B	309	XDR	OAD-CAY-CBM	-4.17	116.72	124.08
2	B	309	XDR	OAW-CBN-CAB	-3.83	102.52	108.49
2	A	309	XDR	OAD-CAY-CBM	-2.32	119.99	124.08
2	A	309	XDR	OAW-CBN-CAB	-2.22	105.03	108.49
2	A	309	XDR	CAR-OAV-CAY	2.02	119.56	116.00
2	A	309	XDR	OAC-CAX-CBA	3.81	126.65	122.68
2	A	309	XDR	OAE-CBM-CAT	4.03	122.52	111.06
2	A	309	XDR	OAV-CAY-CBM	4.04	118.55	111.62
2	A	309	XDR	OAW-CBN-CBM	4.09	107.28	100.22
2	B	309	XDR	OAE-CBM-CAT	4.47	123.76	111.06
2	B	309	XDR	OAW-CBN-CBM	5.27	109.33	100.22
2	B	309	XDR	OAE-CBM-CAY	5.39	117.60	109.40
2	A	309	XDR	OAE-CBM-CAY	5.42	117.65	109.40
2	B	309	XDR	OAV-CAY-CBM	5.69	121.38	111.62

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	309	XDR	5	0
2	B	309	XDR	4	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, 95^{th} 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	270/311 (86%)	-0.26	2 (0%) 89 84	15, 26, 36, 46	20 (7%)
1	B	282/311 (90%)	-0.00	13 (4%) 36 25	12, 25, 41, 56	16 (5%)
All	All	552/622 (88%)	-0.13	15 (2%) 58 45	12, 25, 39, 56	36 (6%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	2	THR	3.9
1	B	166	SER	3.7
1	B	168	ASN	3.7
1	B	167	GLY	3.0
1	B	83	PRO	3.0
1	B	165	ASP	2.9
1	B	169	SER	2.9
1	B	178	GLY	2.8
1	B	4	PRO	2.7
1	B	172	GLN	2.6
1	A	287	VAL	2.5
1	A	83	PRO	2.5
1	B	170	VAL	2.2
1	B	173	THR	2.2
1	B	3	THR	2.1

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

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, 95^{th} 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
1	TPO	B	171	11/12	0.93	0.20	-	50,51,52,52	0

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, 95^{th} 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	XDR	B	309	35/40	0.97	0.16	-0.25	13,18,22,22	0
2	XDR	A	309	35/40	0.96	0.15	-0.46	17,20,21,22	0
3	SO4	A	310	5/5	0.92	0.32	-	94,94,94,95	0
3	SO4	B	310	5/5	0.92	0.32	-	81,81,81,81	0
3	SO4	A	311	5/5	0.91	0.34	-	63,63,64,64	0
3	SO4	B	311	5/5	0.90	0.43	-	72,72,72,73	0

6.5 Other polymers (i)

There are no such residues in this entry.