



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 08:52 am GMT

PDB ID : 3UPP  
Title : Structure of penicillin-binding protein A from M. tuberculosis: ceftriaxone acyl-enzyme complex  
Authors : Davies, C.; Fedorovich, A.  
Deposited on : 2011-11-18  
Resolution : 2.40 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](mailto: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.

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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

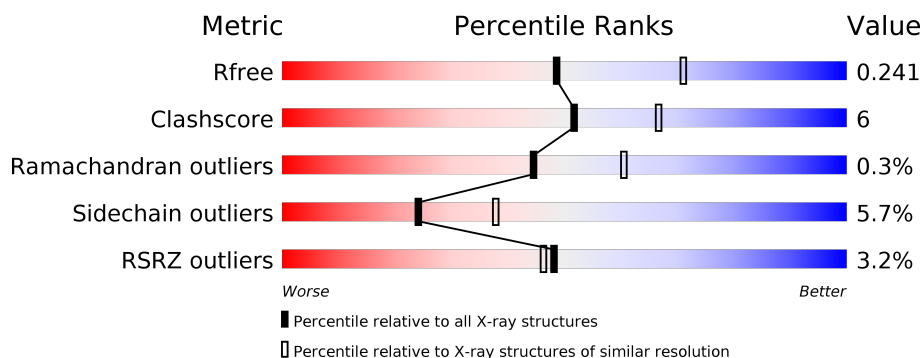
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	3166 (2.40-2.40)
Clashscore	112137	3674 (2.40-2.40)
Ramachandran outliers	110173	3616 (2.40-2.40)
Sidechain outliers	110143	3617 (2.40-2.40)
RSRZ outliers	101464	3195 (2.40-2.40)

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  $\geq 3$ , 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	462	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>13%</div> <div>• •</div> </div> </div>
1	B	462	<div> <div>4%</div> <div> <div></div> <div>79%</div> <div>15%</div> <div>• 5%</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6590 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.

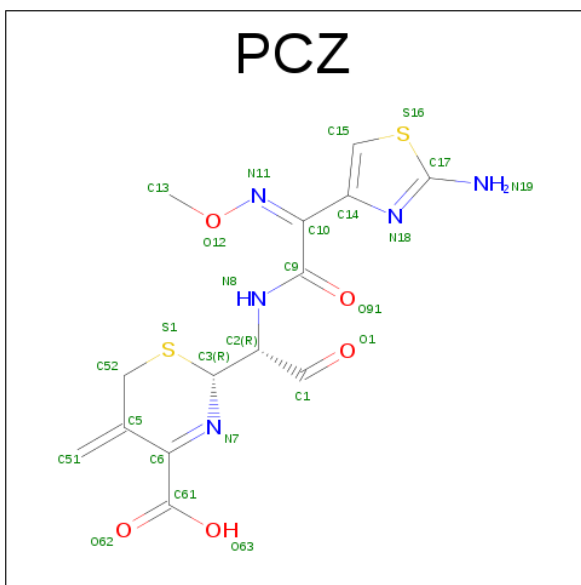
- Molecule 1 is a protein called Penicillin-binding protein A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	445	Total	C	N	O	S	0	0	0
			3284	2056	588	631	9			
1	B	439	Total	C	N	O	S	0	0	0
			3233	2023	582	619	9			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	30	GLY	-	EXPRESSION TAG	UNP P71586
A	31	ALA	-	EXPRESSION TAG	UNP P71586
A	32	MET	-	EXPRESSION TAG	UNP P71586
A	33	GLY	-	EXPRESSION TAG	UNP P71586
A	34	SER	-	EXPRESSION TAG	UNP P71586
A	384	ARG	GLY	SEE REMARK 999	UNP P71586
B	30	GLY	-	EXPRESSION TAG	UNP P71586
B	31	ALA	-	EXPRESSION TAG	UNP P71586
B	32	MET	-	EXPRESSION TAG	UNP P71586
B	33	GLY	-	EXPRESSION TAG	UNP P71586
B	34	SER	-	EXPRESSION TAG	UNP P71586
B	384	ARG	GLY	SEE REMARK 999	UNP P71586

- Molecule 2 is (2R)-2-[(1R)-1-{[(2Z)-2-(2-AMINO-1,3-THIAZOL-4-YL)-2-(METHOXYIMINO)ACETYL]AMINO}-2-OXOETHYL]-5-METHYLIDENE-5,6-DIHYDRO-2H-1,3-THIAZINE-4-CARBOXYLIC ACID (three-letter code: PCZ) (formula: C<sub>14</sub>H<sub>15</sub>N<sub>5</sub>O<sub>5</sub>S<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			26	14	5	5	2		
2	B	1	Total	C	N	O	S	0	0
			26	14	5	5	2		

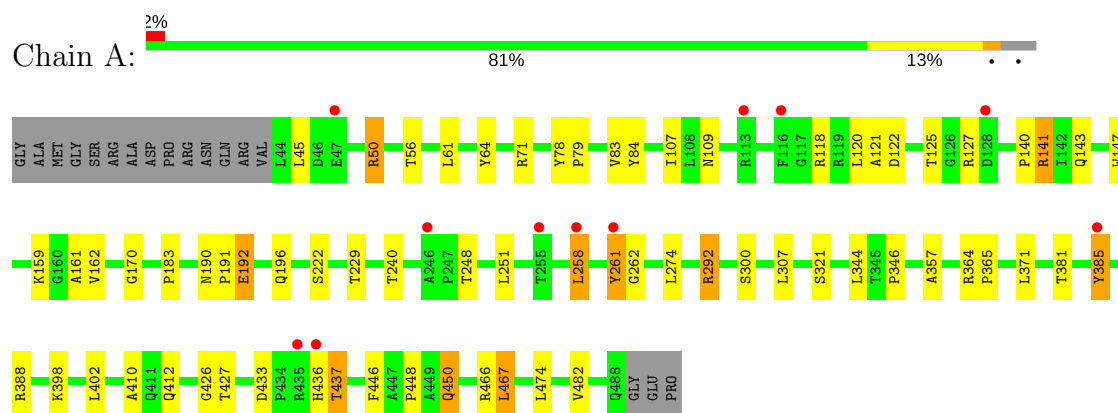
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	9	Total	O	0	0
			9	9		
3	B	12	Total	O	0	0
			12	12		

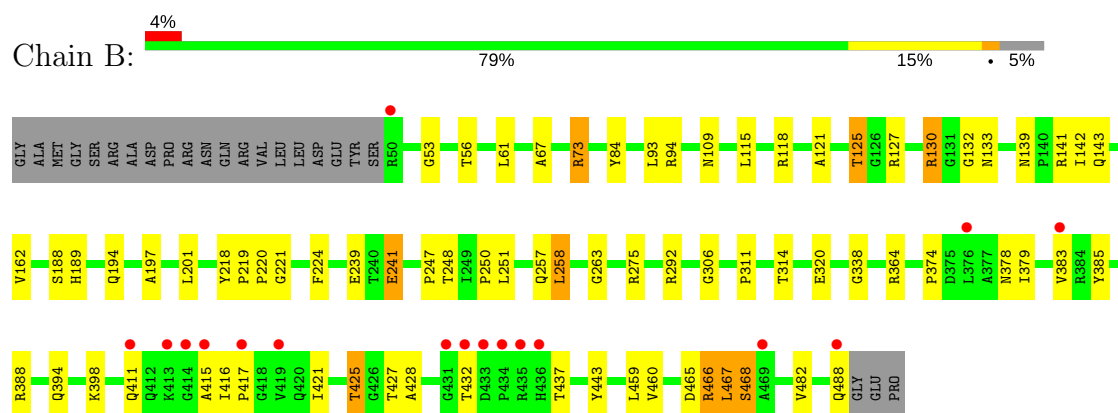
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Penicillin-binding protein A



#### • Molecule 1: Penicillin-binding protein A



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	123.08Å 123.08Å 101.28Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.29 – 2.40 40.29 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.8 (40.29-2.40) 98.6 (40.29-2.40)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.64 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.201 , 0.247 0.198 , 0.241	Depositor DCC
$R_{free}$ test set	1709 reflections (5.34%)	DCC
Wilson B-factor (Å <sup>2</sup> )	52.2	Xtriage
Anisotropy	0.421	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 30.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.042 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6590	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.50% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: PCZ

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	0/3354	0.61	0/4582
1	B	0.49	0/3302	0.63	0/4511
All	All	0.50	0/6656	0.62	0/9093

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	127	ARG	Peptide

### 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	3284	0	3276	38	0
1	B	3233	0	3230	45	0
2	A	26	0	13	4	0
2	B	26	0	13	0	0
3	A	9	0	0	0	0
3	B	12	0	0	0	0
All	All	6590	0	6532	84	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 (84) 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)
2:A:800:PCZ:N11	2:A:800:PCZ:O12	1.64	1.28
1:A:292:ARG:HG3	1:A:292:ARG:HH11	1.27	0.96
1:B:425:THR:HG22	1:B:443:TYR:HD1	1.53	0.73
1:B:115:LEU:HD21	1:B:379:ILE:HD11	1.70	0.72
1:A:292:ARG:NH1	1:A:292:ARG:HG3	2.01	0.69
1:B:306:GLY:HA2	1:B:388:ARG:NH1	2.08	0.69
2:A:800:PCZ:C13	2:A:800:PCZ:N11	2.58	0.66
1:A:84:TYR:CE2	1:A:143:GLN:HG2	2.36	0.60
1:A:364:ARG:HD2	1:A:385:TYR:CE1	2.36	0.60
1:B:84:TYR:CE2	1:B:143:GLN:HG2	2.37	0.60
1:B:306:GLY:HA2	1:B:388:ARG:HH12	1.67	0.59
1:A:64:TYR:HE1	1:A:79:PRO:HG3	1.68	0.59
1:B:239:GLU:HG2	1:B:275:ARG:HB2	1.85	0.59
1:B:94:ARG:HH11	1:B:194:GLN:HE22	1.51	0.58
1:A:251:LEU:HD21	1:A:258:LEU:HD22	1.86	0.58
1:A:222:SER:HB2	1:A:426:GLY:HA2	1.87	0.57
1:B:251:LEU:HD21	1:B:258:LEU:HD22	1.86	0.57
1:B:121:ALA:O	1:B:125:THR:HB	2.04	0.57
1:A:121:ALA:O	1:A:125:THR:HG22	2.05	0.56
1:A:45:LEU:HD21	1:A:71:ARG:HG2	1.88	0.56
1:B:239:GLU:HB2	1:B:398:LYS:NZ	2.21	0.56
1:B:437:THR:O	1:B:466:ARG:NH1	2.38	0.56
1:A:467:LEU:HD12	1:B:467:LEU:HD22	1.87	0.56
1:B:218:TYR:CE2	1:B:459:LEU:HD22	2.42	0.55
1:B:247:PRO:HB3	1:B:263:GLY:O	2.06	0.55
1:A:84:TYR:OH	1:A:140:PRO:HA	2.07	0.54
1:B:425:THR:HG22	1:B:443:TYR:CD1	2.38	0.53
1:A:192:GLU:O	1:A:196:GLN:HB2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:221:GLY:O	1:B:338:GLY:HA3	2.11	0.51
1:B:241:GLU:HG2	1:B:292:ARG:HH22	1.75	0.51
1:A:125:THR:HG21	1:A:127:ARG:CZ	2.41	0.50
1:B:219:PRO:HB2	1:B:428:ALA:HB1	1.93	0.50
1:A:410:ALA:O	1:A:412:GLN:NE2	2.43	0.50
1:A:107:ILE:HG13	1:A:371:LEU:HD13	1.94	0.50
1:A:56:THR:HG22	1:A:61:LEU:HD23	1.94	0.49
1:B:364:ARG:HD3	1:B:385:TYR:CZ	2.46	0.49
1:B:465:ASP:HB3	1:B:468:SER:HB3	1.94	0.49
1:B:197:ALA:O	1:B:201:LEU:HG	2.13	0.48
1:B:218:TYR:CD2	1:B:459:LEU:HD22	2.49	0.47
1:A:261:TYR:CD2	2:A:800:PCZ:H522	2.50	0.47
1:B:139:ASN:HB3	1:B:142:ILE:HD12	1.96	0.47
1:A:170:GLY:O	1:A:365:PRO:HA	2.15	0.47
1:B:459:LEU:HG	1:B:460:VAL:N	2.28	0.47
1:B:56:THR:HG22	1:B:61:LEU:HD23	1.96	0.47
1:B:311:PRO:HD3	1:B:320:GLU:HG3	1.97	0.47
1:A:292:ARG:CG	1:A:292:ARG:HH11	2.12	0.46
1:A:448:PRO:HB2	1:A:450:GLN:HG3	1.98	0.46
1:A:50:ARG:HD2	1:A:109:ASN:O	2.16	0.46
1:B:130:ARG:HB3	1:B:374:PRO:HB3	1.97	0.45
1:B:364:ARG:NH1	1:B:385:TYR:CD1	2.84	0.45
1:A:78:TYR:CD1	1:A:183:PRO:HB2	2.51	0.45
1:A:321:SER:HB3	1:A:344:LEU:HA	1.98	0.45
1:B:115:LEU:CD2	1:B:379:ILE:HD11	2.42	0.44
1:A:261:TYR:HA	1:A:262:GLY:HA2	1.76	0.44
1:A:83:VAL:HG22	1:A:147:TRP:CD1	2.53	0.44
1:A:398:LYS:O	1:A:402:LEU:HG	2.17	0.44
1:B:162:VAL:HG11	1:B:482:VAL:HG21	1.99	0.44
1:A:433:ASP:O	1:A:437:THR:OG1	2.34	0.44
1:A:192:GLU:HG2	1:A:192:GLU:H	1.55	0.44
2:A:800:PCZ:C9	2:A:800:PCZ:H133	2.48	0.44
1:B:53:GLY:HA3	1:B:132:GLY:O	2.19	0.42
1:A:357:ALA:HB2	1:A:446:PHE:CG	2.54	0.42
1:A:122:ASP:OD1	1:A:127:ARG:NH1	2.52	0.42
1:B:416:ILE:HD12	1:B:421:ILE:HD11	2.01	0.42
1:A:436:HIS:CD2	1:A:436:HIS:N	2.88	0.42
1:A:466:ARG:HG2	1:B:468:SER:HB2	2.02	0.42
1:B:239:GLU:HB2	1:B:398:LYS:CE	2.49	0.42
1:A:190:ASN:HA	1:A:191:PRO:HD3	1.85	0.42
1:B:130:ARG:NH2	1:B:133:ASN:OD1	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:ALA:HB3	1:A:346:PRO:HG2	2.02	0.41
1:A:83:VAL:HG22	1:A:147:TRP:CG	2.55	0.41
1:B:188:SER:O	1:B:194:GLN:NE2	2.53	0.41
1:B:364:ARG:NH1	1:B:364:ARG:HB3	2.36	0.41
1:B:250:PRO:HA	1:B:257:GLN:HG2	2.02	0.41
1:B:94:ARG:HH11	1:B:194:GLN:NE2	2.17	0.41
1:B:141:ARG:NH1	1:B:488:GLN:OE1	2.54	0.41
1:B:109:ASN:C	1:B:109:ASN:OD1	2.60	0.41
1:B:364:ARG:HD3	1:B:385:TYR:CE1	2.56	0.40
1:B:67:ALA:HB1	1:B:73:ARG:NH1	2.35	0.40
1:A:141:ARG:HD3	1:A:141:ARG:HA	1.68	0.40
1:A:162:VAL:HG11	1:A:482:VAL:HG21	2.03	0.40
1:A:229:THR:HG23	1:A:274:LEU:HD21	2.03	0.40
1:B:220:PRO:HG2	1:B:224:PHE:HB2	2.04	0.40
1:B:93:LEU:HD11	1:B:189:HIS:CD2	2.57	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	443/462 (96%)	427 (96%)	16 (4%)	0	100	100
1	B	437/462 (95%)	423 (97%)	11 (2%)	3 (1%)	25	37
All	All	880/924 (95%)	850 (97%)	27 (3%)	3 (0%)	44	60

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	417	PRO
1	B	415	ALA
1	B	314	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	338/350 (97%)	317 (94%)	21 (6%)	21	34
1	B	332/350 (95%)	315 (95%)	17 (5%)	28	44
All	All	670/700 (96%)	632 (94%)	38 (6%)	24	38

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	ARG
1	A	118	ARG
1	A	120	LEU
1	A	141	ARG
1	A	159	LYS
1	A	192	GLU
1	A	240	THR
1	A	248	THR
1	A	258	LEU
1	A	261	TYR
1	A	292	ARG
1	A	300	SER
1	A	307	LEU
1	A	381	THR
1	A	385	TYR
1	A	388	ARG
1	A	427	THR
1	A	437	THR
1	A	450	GLN
1	A	467	LEU
1	A	474	LEU
1	B	73	ARG
1	B	118	ARG
1	B	125	THR
1	B	130	ARG
1	B	241	GLU
1	B	248	THR

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Mol	Chain	Res	Type
1	B	258	LEU
1	B	378	ASN
1	B	383	VAL
1	B	394	GLN
1	B	411	GLN
1	B	425	THR
1	B	427	THR
1	B	432	THR
1	B	466	ARG
1	B	467	LEU
1	B	468	SER

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	242	GLN
1	A	257	GLN
1	A	378	ASN
1	A	394	GLN
1	A	436	HIS
1	A	450	GLN
1	B	189	HIS
1	B	194	GLN
1	B	242	GLN
1	B	378	ASN
1	B	394	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

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	PCZ	A	800	1	18,27,27	4.16	7 (38%)	11,37,37	3.20	4 (36%)
2	PCZ	B	800	1	18,27,27	3.35	5 (27%)	11,37,37	3.05	5 (45%)

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	PCZ	A	800	1	-	1/11/38/38	0/1/2/2
2	PCZ	B	800	1	-	0/11/38/38	0/1/2/2

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	800	PCZ	C14-C10	-8.79	1.33	1.48
2	B	800	PCZ	C14-C10	-8.73	1.33	1.48
2	B	800	PCZ	C61-C6	-7.29	1.40	1.52
2	A	800	PCZ	C61-C6	-7.23	1.40	1.52
2	A	800	PCZ	C15-S16	-2.81	1.66	1.70
2	A	800	PCZ	C2-C1	2.26	1.53	1.50
2	B	800	PCZ	C10-N11	3.24	1.34	1.29
2	A	800	PCZ	C51-C5	3.25	1.39	1.32
2	B	800	PCZ	C51-C5	3.28	1.40	1.32
2	A	800	PCZ	C10-N11	4.08	1.35	1.29
2	B	800	PCZ	O12-N11	6.46	1.53	1.40
2	A	800	PCZ	O12-N11	11.63	1.64	1.40

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	800	PCZ	C14-C15-S16	-6.00	104.42	111.79
2	A	800	PCZ	C14-C15-S16	-5.39	105.17	111.79
2	A	800	PCZ	N19-C17-N18	2.07	125.82	123.06
2	B	800	PCZ	C5-C52-S1	2.52	116.84	111.65
2	B	800	PCZ	N19-C17-N18	2.63	126.56	123.06
2	B	800	PCZ	C52-S1-C3	4.12	102.69	94.48
2	A	800	PCZ	C13-O12-N11	4.96	113.85	108.48
2	B	800	PCZ	O12-N11-C10	5.49	117.66	111.23
2	A	800	PCZ	O12-N11-C10	6.88	119.27	111.23

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	800	PCZ	C13-O12-N11-C10

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	800	PCZ	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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	445/462 (96%)	-0.02	11 (2%) 58 55	38, 52, 75, 82	0
1	B	439/462 (95%)	-0.04	17 (3%) 40 39	37, 52, 74, 85	0
All	All	884/924 (95%)	-0.03	28 (3%) 48 46	37, 52, 75, 85	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	415	ALA	5.0
1	B	417	PRO	5.0
1	A	255	THR	4.9
1	A	261	TYR	4.8
1	B	435	ARG	3.9
1	B	383	VAL	3.6
1	A	435	ARG	3.5
1	B	414	GLY	3.4
1	B	434	PRO	3.4
1	B	413	LYS	3.0
1	A	116	PHE	2.9
1	B	411	GLN	2.9
1	A	436	HIS	2.8
1	B	488	GLN	2.7
1	B	419	VAL	2.5
1	A	113	ARG	2.4
1	A	47	GLU	2.3
1	B	432	THR	2.3
1	B	50	ARG	2.3
1	B	376	LEU	2.3
1	A	246	ALA	2.2
1	A	128	ASP	2.2
1	A	258	LEU	2.2
1	B	433	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	469	ALA	2.1
1	B	436	HIS	2.1
1	A	385	TYR	2.1
1	B	431	GLY	2.1

## 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
2	PCZ	A	800	26/26	0.88	0.17	0.16	63,66,76,77	0
2	PCZ	B	800	26/26	0.93	0.18	0.02	53,58,62,66	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.