



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 03:27 pm GMT

PDB ID : 3U17  
Title : Structure of BasE N-terminal domain from *Acinetobacter baumannii* bound to 6-(p-benzoyl)phenyl-1-(pyridin-4-ylmethyl)-1H-pyrazolo[3,4-b]pyridine-4-carboxylic acid  
Authors : Gulick, A.M.; Drake, E.J.; Aldrich, C.C.; Neres, J.  
Deposited on : 2011-09-29  
Resolution : 2.10 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

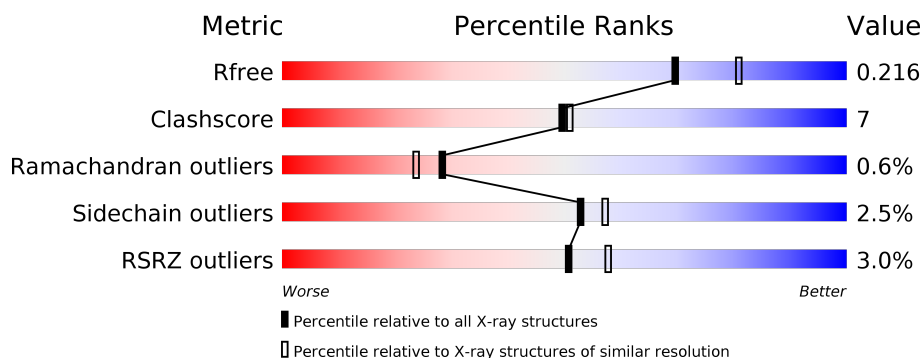
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	4243 (2.10-2.10)
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (2.10-2.10)

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	544	<div> <div>3%</div> <div> <div></div> <div>68%</div> <div>10%</div> <div>20%</div> </div> </div>
1	B	544	<div> <div>2%</div> <div> <div></div> <div>67%</div> <div>12%</div> <div>20%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	MPD	A	548	-	-	-	X
5	MRD	B	547	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7241 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.

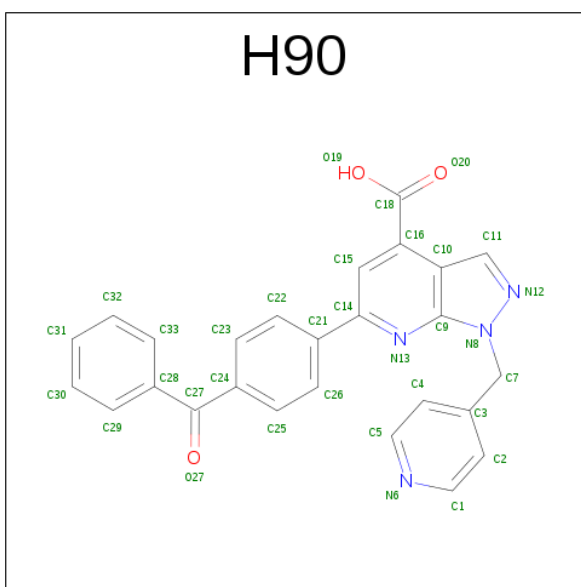
- Molecule 1 is a protein called Peptide arylation enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	433	Total	C	N	O	S	0	2	0
			3382	2152	581	634	15			
1	B	436	Total	C	N	O	S	0	1	0
			3389	2160	574	640	15			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP B2HVG8
A	0	HIS	-	EXPRESSION TAG	UNP B2HVG8
A	45	LEU	PRO	SEE REMARK 999	UNP B2HVG8
A	68	THR	SER	SEE REMARK 999	UNP B2HVG8
A	149	ASP	GLU	SEE REMARK 999	UNP B2HVG8
A	180	PHE	LEU	SEE REMARK 999	UNP B2HVG8
A	226	GLY	ASP	SEE REMARK 999	UNP B2HVG8
A	329	LEU	ILE	SEE REMARK 999	UNP B2HVG8
A	378	ARG	LYS	SEE REMARK 999	UNP B2HVG8
B	-1	GLY	-	EXPRESSION TAG	UNP B2HVG8
B	0	HIS	-	EXPRESSION TAG	UNP B2HVG8
B	45	LEU	PRO	SEE REMARK 999	UNP B2HVG8
B	68	THR	SER	SEE REMARK 999	UNP B2HVG8
B	149	ASP	GLU	SEE REMARK 999	UNP B2HVG8
B	180	PHE	LEU	SEE REMARK 999	UNP B2HVG8
B	226	GLY	ASP	SEE REMARK 999	UNP B2HVG8
B	329	LEU	ILE	SEE REMARK 999	UNP B2HVG8
B	378	ARG	LYS	SEE REMARK 999	UNP B2HVG8

- Molecule 2 is 6-(4-BENZOYLPHENYL)-1-(PYRIDIN-4-YLMETHYL)-1H-PYRAZOLO[3,4-B]PYRIDINE-4-CARBOXYLIC ACID (three-letter code: H90) (formula: C<sub>26</sub>H<sub>18</sub>N<sub>4</sub>O<sub>3</sub>).

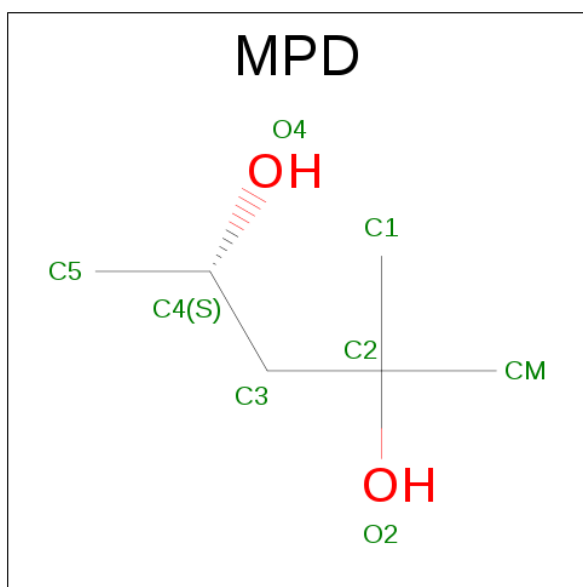


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			33	26	4	3		
2	B	1	Total	C	N	O	0	0
			33	26	4	3		

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

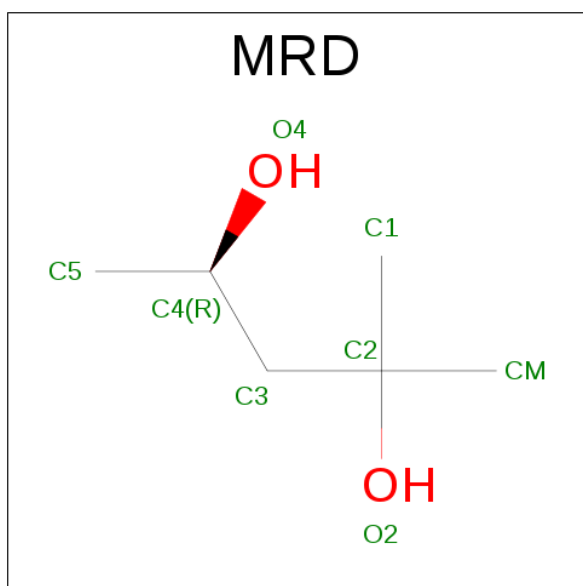
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	3	Total	Ca	0	0
			3	3		
3	A	4	Total	Ca	0	0
			4	4		

- Molecule 4 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			8	6	2		

- Molecule 5 is (4R)-2-METHYLPENTANE-2,4-DIOL (three-letter code: MRD) (formula:  $C_6H_{14}O_2$ ).



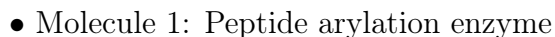
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			8	6	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	184	Total 184	O 184	0	0
6	B	197	Total 197	O 197	0	0



- Molecule 1: Peptide arylation enzyme





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	65.37Å 144.23Å 148.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.10 45.75 – 2.10	Depositor EDS
% Data completeness (in resolution range)	90.1 (40.00-2.10) 90.1 (45.75-2.10)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.51 (at 2.10Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, $R_{free}$	0.189 , 0.221 0.183 , 0.216	Depositor DCC
$R_{free}$ test set	3724 reflections (4.99%)	DCC
Wilson B-factor (Å <sup>2</sup> )	31.9	Xtriage
Anisotropy	0.729	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 45.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.009 for -h,l,k	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7241	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.85% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: H90, MRD, CA, MPD

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	0.37	0/3461	0.52	0/4711
1	B	0.37	0/3471	0.51	0/4728
All	All	0.37	0/6932	0.51	0/9439

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	3382	0	3302	45	0
1	B	3389	0	3292	44	0
2	A	33	0	17	3	0
2	B	33	0	17	2	0
3	A	4	0	0	0	0
3	B	3	0	0	0	0
4	A	8	0	14	1	0
5	B	8	0	14	0	0
6	A	184	0	0	3	0
6	B	197	0	0	1	0
All	All	7241	0	6656	91	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 7.

All (91) 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:305[A]:GLN:HE22	1:A:330:ASN:HD22	1.11	0.94
1:A:401:GLN:HG2	6:A:585:HOH:O	1.72	0.88
1:A:106:LEU:HD11	1:A:196:LEU:HD21	1.63	0.81
1:B:269:LEU:H	1:B:269:LEU:HD12	1.48	0.79
1:A:228:ASN:HD22	1:A:230:ASN:H	1.30	0.78
1:A:352:SER:H	1:A:355:GLN:HE21	1.31	0.78
1:B:248:PRO:HD3	1:B:311:GLN:HE22	1.50	0.77
1:B:248:PRO:HD3	1:B:311:GLN:NE2	2.04	0.72
1:B:213:ASP:HB2	1:B:394:TYR:HA	1.72	0.71
1:A:228:ASN:ND2	1:A:230:ASN:H	1.90	0.68
1:A:235[B]:CYS:SG	1:A:260:VAL:HG13	2.33	0.67
1:A:195:GLN:HE21	1:A:196:LEU:H	1.44	0.66
1:B:235[B]:CYS:SG	1:B:260:VAL:HG13	2.38	0.62
1:A:213:ASP:HB2	1:A:394:TYR:HA	1.82	0.61
1:B:90:GLU:OE2	1:B:170:LEU:HD21	2.00	0.61
1:B:269:LEU:H	1:B:269:LEU:CD1	2.14	0.61
1:B:133:ARG:HG3	1:B:163:GLN:HG2	1.84	0.60
1:B:200:SER:HB3	6:B:584:HOH:O	1.99	0.60
1:B:225:CYS:SG	1:B:248:PRO:HG3	2.45	0.57
1:B:174:GLU:HG2	1:B:175:THR:HG23	1.87	0.56
1:A:15:ARG:HD2	1:A:19:TYR:OH	2.06	0.55
1:A:228:ASN:HD22	1:A:228:ASN:C	2.10	0.55
1:B:269:LEU:HD12	1:B:269:LEU:N	2.20	0.55
1:A:64:THR:O	1:A:68:THR:HG23	2.07	0.53
1:B:38:VAL:O	1:B:42:PRO:HG3	2.08	0.53
2:A:543:H90:C9	2:A:543:H90:H2	2.37	0.53
1:B:72:GLU:OE1	1:B:177:ALA:HB1	2.08	0.53
1:B:265:ASN:HB2	1:B:266:PRO:CD	2.38	0.52
1:A:352:SER:H	1:A:355:GLN:NE2	2.04	0.52
1:B:348:ARG:HG2	1:B:362:ARG:NH2	2.26	0.51
1:B:314:GLY:HA2	2:B:543:H90:C10	2.40	0.51
1:B:437:LYS:N	1:B:437:LYS:HD3	2.26	0.51
1:B:65:ASN:O	1:B:69:ARG:HG2	2.11	0.50
2:B:543:H90:C9	2:B:543:H90:H2	2.41	0.50
1:B:135:HIS:CE1	1:B:137:VAL:HG23	2.47	0.50
1:A:115:TYR:OH	1:B:291:ILE:HG22	2.12	0.50
1:B:267:GLU:HB3	1:B:269:LEU:HD13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:GLN:O	1:A:166:ASP:HB2	2.12	0.49
1:A:144:ILE:HG12	6:A:715:HOH:O	2.12	0.49
1:A:291:ILE:O	1:A:295:GLU:HG2	2.13	0.49
1:B:235[B]:CYS:SG	1:B:260:VAL:CG1	3.01	0.49
1:B:266:PRO:HA	1:B:271:CYS:SG	2.53	0.48
1:A:228:ASN:HD22	1:A:230:ASN:N	2.05	0.48
1:A:305[A]:GLN:NE2	1:A:330:ASN:HD22	1.94	0.47
1:A:248:PRO:HD3	1:A:311:GLN:NE2	2.30	0.47
1:A:118:ASN:ND2	1:A:143:PHE:HE1	2.13	0.47
1:B:233:LEU:HB3	1:B:253:VAL:HG21	1.96	0.47
1:B:135:HIS:HE1	1:B:137:VAL:HG23	1.80	0.47
1:B:234:LEU:HB2	1:B:280:VAL:HG11	1.97	0.47
1:A:235[B]:CYS:SG	1:A:260:VAL:CG1	3.04	0.46
1:A:38:VAL:O	1:A:42:PRO:HG3	2.16	0.45
1:B:369:GLU:OE1	1:B:391:ARG:HD2	2.16	0.45
1:B:199:GLY:O	1:B:200:SER:O	2.35	0.45
1:A:175:THR:HA	1:A:176:PRO:HD3	1.81	0.45
4:A:548:MPD:HM2	4:A:548:MPD:H4	1.74	0.44
1:B:62:LEU:HD22	1:B:173:ILE:HG22	1.98	0.44
1:B:215:ASP:O	1:B:219:ARG:HG3	2.17	0.44
1:A:66:LEU:O	1:A:70:LEU:HG	2.18	0.44
1:B:65:ASN:OD1	1:B:176:PRO:HG3	2.18	0.44
1:A:133:ARG:HB2	1:A:161:ASN:O	2.18	0.44
1:B:105:VAL:O	1:B:193:PHE:HB2	2.18	0.43
1:A:195:GLN:NE2	1:A:196:LEU:H	2.15	0.43
1:A:314:GLY:HA2	2:A:543:H90:C10	2.49	0.43
1:A:342:GLY:HA3	1:A:395:THR:HA	1.99	0.43
1:B:195:GLN:HE21	1:B:196:LEU:H	1.66	0.43
1:B:342:GLY:HA3	1:B:395:THR:HA	2.01	0.43
1:A:265:ASN:HB2	1:A:266:PRO:CD	2.49	0.43
1:B:371:LYS:HE2	1:B:415:TYR:CG	2.54	0.43
1:A:73:LYS:HG2	1:A:156:ILE:HD11	2.01	0.43
1:B:162:HIS:HB2	1:B:166:ASP:HB2	2.01	0.43
1:B:404:GLU:O	1:B:408:GLN:HG2	2.19	0.43
1:A:75:LEU:HD11	1:A:156:ILE:HD12	2.01	0.42
1:A:248:PRO:HD3	1:A:311:GLN:HE22	1.83	0.42
1:B:227:LEU:HD11	1:B:248:PRO:HB2	2.01	0.42
1:A:314:GLY:HA2	2:A:543:H90:C16	2.50	0.42
1:B:425:THR:HB	1:B:426:PRO:HD2	2.01	0.42
1:A:135:HIS:HE1	1:A:137:VAL:HG23	1.86	0.41
1:A:362:ARG:NE	6:A:578:HOH:O	2.27	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:77:LYS:HE3	1:B:185:SER:O	2.20	0.41
1:A:27:ASP:HA	1:A:212:ASN:OD1	2.21	0.41
1:A:239:ALA:N	1:A:240:PRO:CD	2.83	0.41
1:A:267:GLU:HA	1:A:268:PRO:HD3	1.89	0.41
1:A:41:HIS:HB2	1:A:44:SER:OG	2.21	0.41
1:A:162:HIS:HB2	1:A:166:ASP:HB2	2.02	0.41
1:A:114:GLN:O	1:A:118:ASN:HB2	2.21	0.41
1:B:69:ARG:H	1:B:69:ARG:HG2	1.56	0.41
1:B:98:LEU:HD13	1:B:105:VAL:HB	2.02	0.41
1:B:27:ASP:HA	1:B:212:ASN:OD1	2.21	0.40
1:A:402:SER:N	1:A:403:PRO:HD3	2.36	0.40
1:A:118:ASN:HD22	1:A:143:PHE:HE1	1.67	0.40
1:A:305[A]:GLN:HE22	1:A:330:ASN:ND2	1.95	0.40

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	431/544 (79%)	420 (97%)	10 (2%)	1 (0%)	51	52
1	B	435/544 (80%)	422 (97%)	9 (2%)	4 (1%)	20	14
All	All	866/1088 (80%)	842 (97%)	19 (2%)	5 (1%)	28	24

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	200	SER
1	B	315	ALA
1	B	269	LEU
1	B	270	ASN
1	A	203	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	366/472 (78%)	357 (98%)	9 (2%)	53	57
1	B	366/472 (78%)	357 (98%)	9 (2%)	53	57
All	All	732/944 (78%)	714 (98%)	18 (2%)	53	57

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

Mol	Chain	Res	Type
1	A	114	GLN
1	A	118	ASN
1	A	125	GLN
1	A	175	THR
1	A	195	GLN
1	A	213	ASP
1	A	223	GLU
1	A	228	ASN
1	A	396	PHE
1	B	44	SER
1	B	52	ARG
1	B	69	ARG
1	B	201	THR
1	B	213	ASP
1	B	295	GLU
1	B	391	ARG
1	B	396	PHE
1	B	433	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	GLN
1	A	21	ASN
1	A	118	ASN
1	A	195	GLN

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Mol	Chain	Res	Type
1	A	228	ASN
1	A	230	ASN
1	A	270	ASN
1	A	355	GLN
1	B	17	GLN
1	B	18	HIS
1	B	21	ASN
1	B	53	GLN
1	B	142	GLN
1	B	195	GLN
1	B	230	ASN
1	B	276	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 11 ligands modelled in this entry, 7 are monoatomic - leaving 4 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	$\# Z  > 2$
2	H90	A	543	-	32,37,37	0.79	0	41,52,52	1.86	6 (14%)
4	MPD	A	548	-	7,7,7	0.33	0	9,10,10	0.53	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	H90	B	543	-	32,37,37	0.82	1 (3%)	41,52,52	1.84	9 (21%)
5	MRD	B	547	-	7,7,7	0.32	0	9,10,10	0.49	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	H90	A	543	-	-	0/16/20/20	0/5/5/5
4	MPD	A	548	-	-	0/5/5/5	0/0/0/0
2	H90	B	543	-	-	0/16/20/20	0/5/5/5
5	MRD	B	547	-	-	0/5/5/5	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	543	H90	C10-C9	-2.14	1.37	1.43

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	543	H90	C3-C7-N8	-6.01	103.98	112.58
2	B	543	H90	C3-C7-N8	-4.83	105.67	112.58
2	B	543	H90	C16-C15-C14	-3.42	119.32	121.16
2	A	543	H90	C16-C15-C14	-3.02	119.54	121.16
2	A	543	H90	C10-C11-N12	-2.94	104.55	110.70
2	A	543	H90	C18-C16-C10	-2.81	120.08	123.47
2	B	543	H90	C10-C11-N12	-2.78	104.90	110.70
2	B	543	H90	O27-C27-C24	-2.72	115.83	120.14
2	B	543	H90	C25-C24-C23	2.02	121.37	118.58
2	B	543	H90	C28-C27-C24	2.13	123.95	120.25
2	B	543	H90	C22-C21-C26	2.21	121.99	117.59
2	B	543	H90	C11-N12-N8	2.92	107.20	104.22
2	A	543	H90	C11-N12-N8	3.29	107.58	104.22
2	B	543	H90	C11-C10-C9	5.81	110.57	105.20
2	A	543	H90	C11-C10-C9	6.14	110.88	105.20

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.



3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	543	H90	3	0
4	A	548	MPD	1	0
2	B	543	H90	2	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	433/544 (79%)	-0.03	16 (3%) 42 49	27, 37, 67, 84	0
1	B	436/544 (80%)	-0.16	10 (2%) 61 66	27, 39, 59, 76	0
All	All	869/1088 (79%)	-0.10	26 (2%) 51 58	27, 38, 64, 84	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	269	LEU	3.6
1	A	143	PHE	3.5
1	A	150	VAL	3.4
1	B	180	PHE	3.2
1	A	164	ALA	3.1
1	A	181	VAL	3.1
1	A	201	THR	2.9
1	A	179	THR	2.8
1	A	165	THR	2.7
1	A	426	PRO	2.7
1	B	148	HIS	2.7
1	A	167	PHE	2.6
1	B	149	ASP	2.4
1	B	150	VAL	2.4
1	A	376	GLN	2.4
1	B	201	THR	2.3
1	A	177	ALA	2.3
1	B	39	GLN	2.3
1	A	166	ASP	2.2
1	A	151	ASN	2.2
1	A	139	SER	2.2
1	B	382	GLU	2.1
1	B	179	THR	2.1
1	A	149	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	426	PRO	2.1
1	A	152	LEU	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 [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(Å <sup>2</sup> )	Q<0.9
4	MPD	A	548	8/8	0.94	0.18	5.56	33,45,50,54	0
5	MRD	B	547	8/8	0.94	0.16	2.79	43,48,57,60	0
2	H90	A	543	33/33	0.96	0.14	0.64	22,33,46,48	0
2	H90	B	543	33/33	0.97	0.12	0.32	25,32,41,46	0
3	CA	B	544	1/1	0.97	0.10	-0.03	48,48,48,48	0
3	CA	A	544	1/1	0.96	0.10	-0.29	42,42,42,42	0
3	CA	A	546	1/1	0.98	0.10	-0.45	35,35,35,35	0
3	CA	A	545	1/1	0.99	0.08	-1.15	40,40,40,40	0
3	CA	B	546	1/1	0.86	0.06	-	69,69,69,69	0
3	CA	A	547	1/1	0.88	0.16	-	73,73,73,73	0
3	CA	B	545	1/1	0.88	0.07	-	77,77,77,77	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.