



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:44 PM GMT

PDB ID : 4JBF  
Title : Crystal structure of peptidoglycan glycosyltransferase from *Atopobium parvulum* DSM 20469.  
Authors : Filippova, E.V.; Wawrzak, Z.; Minasov, G.; Shuvalova, L.; Kiryukhina, O.; G.Babnigg; E.Rubin; J.Sacchettini; A.Joachimciak; W.F.Anderson; Midwest Center for Structural Genomics (MCSG); Structures of Mtb Proteins Confering Susceptibility to Known Mtb Inhibitors (MTBI)  
Deposited on : 2013-02-19  
Resolution : 1.92 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 (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

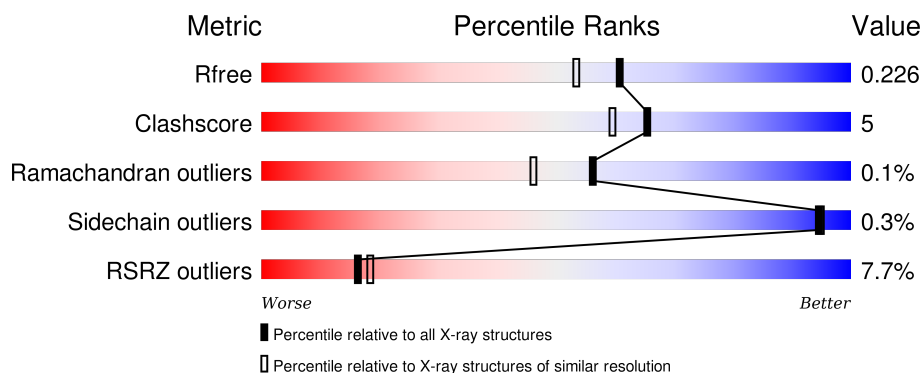
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.92 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	5832 (1.94-1.90)
Clashscore	102246	6540 (1.94-1.90)
Ramachandran outliers	100387	6464 (1.94-1.90)
Sidechain outliers	100360	6465 (1.94-1.90)
RSRZ outliers	91569	5846 (1.94-1.90)

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  $\geq 3$ , 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	482	<div> <div>6%</div> <div> <div></div> <div>78%</div> <div>7%</div> <div>15%</div> </div> </div>
1	B	482	<div> <div>7%</div> <div> <div></div> <div>77%</div> <div>8%</div> <div>•</div> <div>15%</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6378 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 Peptidoglycan glycosyltransferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	410	Total	C	N	O	S	Se	0	1	0
			2948	1833	499	601	2	13			
1	B	410	Total	C	N	O	S	Se	0	2	0
			2953	1832	501	605	2	13			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	473	MSE	-	EXPRESSION TAG	UNP C8W8H7
A	474	HIS	-	EXPRESSION TAG	UNP C8W8H7
A	475	HIS	-	EXPRESSION TAG	UNP C8W8H7
A	476	HIS	-	EXPRESSION TAG	UNP C8W8H7
A	477	HIS	-	EXPRESSION TAG	UNP C8W8H7
A	478	HIS	-	EXPRESSION TAG	UNP C8W8H7
A	479	HIS	-	EXPRESSION TAG	UNP C8W8H7
A	480	SER	-	EXPRESSION TAG	UNP C8W8H7
A	481	SER	-	EXPRESSION TAG	UNP C8W8H7
A	482	GLY	-	EXPRESSION TAG	UNP C8W8H7
A	483	VAL	-	EXPRESSION TAG	UNP C8W8H7
A	484	ASP	-	EXPRESSION TAG	UNP C8W8H7
A	485	LEU	-	EXPRESSION TAG	UNP C8W8H7
A	486	TRP	-	EXPRESSION TAG	UNP C8W8H7
A	487	SER	-	EXPRESSION TAG	UNP C8W8H7
A	488	HIS	-	EXPRESSION TAG	UNP C8W8H7
A	489	PRO	-	EXPRESSION TAG	UNP C8W8H7
A	490	GLN	-	EXPRESSION TAG	UNP C8W8H7
A	491	PHE	-	EXPRESSION TAG	UNP C8W8H7
A	492	GLU	-	EXPRESSION TAG	UNP C8W8H7
A	493	LYS	-	EXPRESSION TAG	UNP C8W8H7
A	494	GLY	-	EXPRESSION TAG	UNP C8W8H7
A	495	THR	-	EXPRESSION TAG	UNP C8W8H7
A	496	GLU	-	EXPRESSION TAG	UNP C8W8H7
A	497	ASN	-	EXPRESSION TAG	UNP C8W8H7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	498	LEU	-	EXPRESSION TAG	UNP C8W8H7
A	499	TYR	-	EXPRESSION TAG	UNP C8W8H7
A	500	PHE	-	EXPRESSION TAG	UNP C8W8H7
A	501	GLN	-	EXPRESSION TAG	UNP C8W8H7
A	502	SER	-	EXPRESSION TAG	UNP C8W8H7
A	503	ASN	-	EXPRESSION TAG	UNP C8W8H7
A	504	ALA	-	EXPRESSION TAG	UNP C8W8H7
B	473	MSE	-	EXPRESSION TAG	UNP C8W8H7
B	474	HIS	-	EXPRESSION TAG	UNP C8W8H7
B	475	HIS	-	EXPRESSION TAG	UNP C8W8H7
B	476	HIS	-	EXPRESSION TAG	UNP C8W8H7
B	477	HIS	-	EXPRESSION TAG	UNP C8W8H7
B	478	HIS	-	EXPRESSION TAG	UNP C8W8H7
B	479	HIS	-	EXPRESSION TAG	UNP C8W8H7
B	480	SER	-	EXPRESSION TAG	UNP C8W8H7
B	481	SER	-	EXPRESSION TAG	UNP C8W8H7
B	482	GLY	-	EXPRESSION TAG	UNP C8W8H7
B	483	VAL	-	EXPRESSION TAG	UNP C8W8H7
B	484	ASP	-	EXPRESSION TAG	UNP C8W8H7
B	485	LEU	-	EXPRESSION TAG	UNP C8W8H7
B	486	TRP	-	EXPRESSION TAG	UNP C8W8H7
B	487	SER	-	EXPRESSION TAG	UNP C8W8H7
B	488	HIS	-	EXPRESSION TAG	UNP C8W8H7
B	489	PRO	-	EXPRESSION TAG	UNP C8W8H7
B	490	GLN	-	EXPRESSION TAG	UNP C8W8H7
B	491	PHE	-	EXPRESSION TAG	UNP C8W8H7
B	492	GLU	-	EXPRESSION TAG	UNP C8W8H7
B	493	LYS	-	EXPRESSION TAG	UNP C8W8H7
B	494	GLY	-	EXPRESSION TAG	UNP C8W8H7
B	495	THR	-	EXPRESSION TAG	UNP C8W8H7
B	496	GLU	-	EXPRESSION TAG	UNP C8W8H7
B	497	ASN	-	EXPRESSION TAG	UNP C8W8H7
B	498	LEU	-	EXPRESSION TAG	UNP C8W8H7
B	499	TYR	-	EXPRESSION TAG	UNP C8W8H7
B	500	PHE	-	EXPRESSION TAG	UNP C8W8H7
B	501	GLN	-	EXPRESSION TAG	UNP C8W8H7
B	502	SER	-	EXPRESSION TAG	UNP C8W8H7
B	503	ASN	-	EXPRESSION TAG	UNP C8W8H7
B	504	ALA	-	EXPRESSION TAG	UNP C8W8H7

- Molecule 2 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C<sub>8</sub>H<sub>18</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			7	4	3		

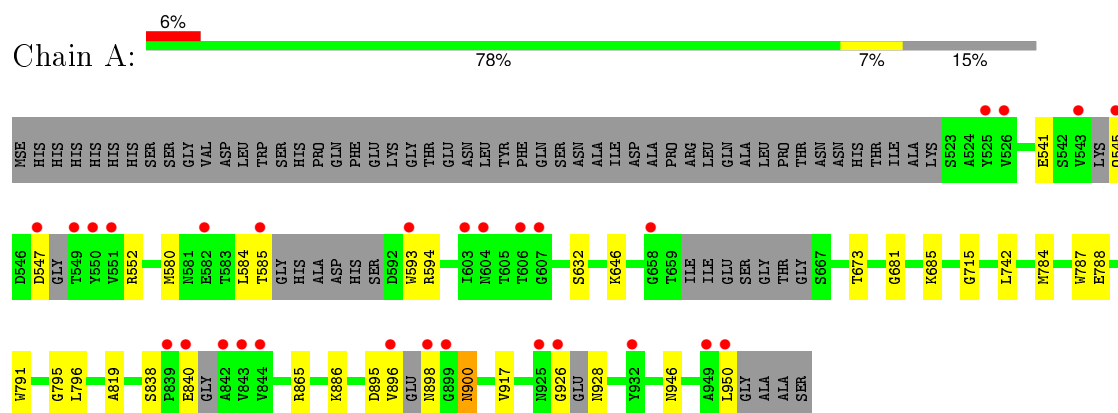
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	218	Total	O	0	4
			222	222		
3	B	247	Total	O	0	1
			248	248		

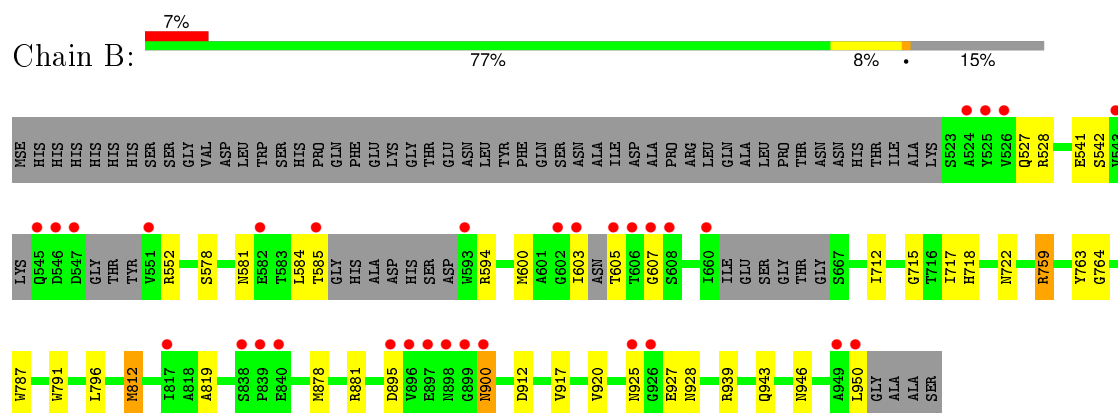
### 3 Residue-property plots

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: Peptidoglycan glycosyltransferase



#### • Molecule 1: Peptidoglycan glycosyltransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	66.93Å 70.17Å 114.82Å 90.00° 97.35° 90.00°	Depositor
Resolution (Å)	29.48 – 1.92 29.48 – 1.92	Depositor EDS
% Data completeness (in resolution range)	98.5 (29.48-1.92) 98.4 (29.48-1.92)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.43 (at 1.92Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.195 , 0.237 0.192 , 0.226	Depositor DCC
$R_{free}$ test set	4802 reflections (6.33%)	DCC
Wilson B-factor (Å <sup>2</sup> )	27.4	Xtriage
Anisotropy	0.413	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 56.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 79987 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	6378	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 4.73% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: PG4

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	0.74	0/2982	0.88	1/4044 (0.0%)
1	B	0.81	1/2985 (0.0%)	0.91	3/4047 (0.1%)
All	All	0.78	1/5967 (0.0%)	0.89	4/8091 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	812	MSE	N-CA	5.59	1.57	1.46

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	759[B]	ARG	NE-CZ-NH1	5.96	123.28	120.30
1	B	759[C]	ARG	NE-CZ-NH1	5.96	123.28	120.30
1	B	920	VAL	CB-CA-C	-5.59	100.77	111.40
1	A	865	ARG	NE-CZ-NH1	5.59	123.09	120.30

There are no chirality outliers.

There are no planarity outliers.

### 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	2948	0	2863	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2953	0	2874	36	0
2	B	7	0	9	0	0
3	A	222	0	0	4	0
3	B	248	0	0	3	0
All	All	6378	0	5746	58	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 5.

All (58) 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:B:759[C]:ARG:HG2	1:B:759[C]:ARG:HH21	1.27	0.98
1:B:878:MSE:CE	1:B:881:ARG:HH11	1.90	0.84
1:B:759[C]:ARG:HH21	1:B:759[C]:ARG:CG	1.90	0.84
1:B:878:MSE:HE2	1:B:881:ARG:HH11	1.45	0.80
1:A:545:GLN:HA	3:A:1146:HOH:O	1.83	0.77
1:B:759[C]:ARG:NH2	1:B:759[C]:ARG:HG2	2.04	0.69
1:B:912:ASP:HB2	3:B:1288:HOH:O	1.93	0.69
1:A:547:ASP:HB2	3:A:1145:HOH:O	1.93	0.68
1:A:946:ASN:O	1:A:950:LEU:HD13	1.93	0.68
1:B:759[C]:ARG:NH2	1:B:763:TYR:HB3	2.08	0.67
1:B:878:MSE:CE	1:B:881:ARG:NH1	2.58	0.66
1:A:545:GLN:N	3:A:1146:HOH:O	2.27	0.66
1:B:541:GLU:O	1:B:552:ARG:NH1	2.27	0.65
1:A:715:GLY:HA3	1:A:787:TRP:CD1	2.34	0.62
1:A:886:LYS:NZ	3:A:1078:HOH:O	2.33	0.61
1:B:715:GLY:HA3	1:B:787:TRP:CD1	2.35	0.60
1:B:939:ARG:HD3	3:B:1319:HOH:O	2.01	0.59
1:A:632:SER:HB2	1:A:673:THR:HG22	1.85	0.58
1:A:681:GLY:O	1:A:795:GLY:HA3	2.04	0.58
1:B:878:MSE:HE3	1:B:881:ARG:NH1	2.19	0.57
1:B:878:MSE:HE3	1:B:881:ARG:HH11	1.67	0.56
1:B:878:MSE:HE2	1:B:881:ARG:NH1	2.18	0.56
1:B:895:ASP:OD1	1:B:900:ASN:ND2	2.41	0.52
1:B:946:ASN:O	1:B:950:LEU:HD13	2.08	0.52
1:A:646:LYS:HE2	1:A:673:THR:OG1	2.11	0.51
1:B:759[C]:ARG:HH22	1:B:763:TYR:HB3	1.75	0.50
1:B:594:ARG:HB3	1:B:600:MSE:HE3	1.94	0.49
1:B:541:GLU:O	1:B:552:ARG:HD2	2.13	0.49
1:A:541:GLU:O	1:A:552:ARG:HD2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:578:SER:O	1:B:581:ASN:HB2	2.13	0.48
1:B:759[C]:ARG:NH2	1:B:763:TYR:C	2.67	0.48
1:A:791:TRP:CE3	1:A:796:LEU:HD12	2.49	0.47
1:A:593:TRP:CE2	1:A:594:ARG:CG	2.98	0.47
1:B:927:GLU:HG2	1:B:928:ASN:O	2.15	0.46
1:A:819:ALA:HA	1:A:917:VAL:HG21	1.97	0.46
1:B:819:ALA:HA	1:B:917:VAL:HG21	1.97	0.46
1:B:528:ARG:HA	1:B:584:LEU:O	2.16	0.45
1:A:900:ASN:O	1:A:900:ASN:ND2	2.50	0.45
1:B:759[C]:ARG:HH22	1:B:764:GLY:N	2.14	0.44
1:A:926:GLY:O	1:A:928:ASN:N	2.51	0.44
1:B:585:THR:O	1:B:607:GLY:HA2	2.18	0.44
1:A:685:LYS:HD3	1:A:742:LEU:HG	2.00	0.44
1:A:895:ASP:OD1	1:A:900:ASN:ND2	2.51	0.43
1:A:580:MSE:O	1:A:584:LEU:HG	2.19	0.43
1:B:791:TRP:CE3	1:B:796:LEU:HD12	2.54	0.42
1:B:943:GLN:NE2	3:B:1242:HOH:O	2.52	0.42
1:B:718:HIS:HB2	1:B:722:ASN:HD22	1.85	0.42
1:B:541:GLU:HB3	1:B:542:SER:H	1.64	0.42
1:A:584:LEU:O	1:A:585:THR:C	2.58	0.42
1:A:838:SER:C	1:A:840:GLU:N	2.72	0.42
1:A:896:VAL:O	1:A:898:ASN:N	2.53	0.42
1:B:812:MSE:HE2	1:B:812:MSE:HB2	1.92	0.42
1:B:718:HIS:HB2	1:B:722:ASN:ND2	2.35	0.41
1:B:527:GLN:CG	1:B:528:ARG:N	2.84	0.41
1:B:759[C]:ARG:NH2	1:B:764:GLY:N	2.69	0.41
1:A:784:MSE:HA	1:A:788:GLU:OE1	2.20	0.41
1:B:712:ILE:HD12	1:B:717:ILE:HG13	2.03	0.40
1:B:603:ILE:O	1:B:605:THR:N	2.55	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	395/482 (82%)	385 (98%)	10 (2%)	0	100	100
1	B	400/482 (83%)	384 (96%)	15 (4%)	1 (0%)	46	34
All	All	795/964 (82%)	769 (97%)	25 (3%)	1 (0%)	56	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	925	ASN

### 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	311/356 (87%)	310 (100%)	1 (0%)	94	95
1	B	311/356 (87%)	310 (100%)	1 (0%)	94	95
All	All	622/712 (87%)	620 (100%)	2 (0%)	94	95

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	900	ASN
1	B	900	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	527	GLN
1	A	570	GLN
1	A	722	ASN
1	A	925	ASN
1	B	527	GLN
1	B	570	GLN
1	B	722	ASN
1	B	753	ASN

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Mol	Chain	Res	Type
1	B	925	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](#)

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](#)

1 ligand 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	$\# Z  > 2$
2	PG4	B	1001	-	6,6,12	0.51	0	5,5,11	0.77	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	PG4	B	1001	-	-	0/4/4/10	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

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

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, 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	397/482 (82%)	0.26	29 (7%) 18 20	21, 37, 81, 125	0
1	B	397/482 (82%)	0.17	32 (8%) 15 17	21, 34, 77, 97	0
All	All	794/964 (82%)	0.21	61 (7%) 16 18	21, 35, 79, 125	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	603	ILE	6.0
1	B	525	TYR	5.7
1	A	898	ASN	5.5
1	A	551	VAL	5.3
1	A	926	GLY	5.2
1	B	898	ASN	5.2
1	A	925	ASN	4.8
1	B	899	GLY	4.6
1	A	525	TYR	4.5
1	B	605	THR	4.4
1	B	526	VAL	4.3
1	A	899	GLY	4.3
1	A	603	ILE	4.3
1	B	660	ILE	4.0
1	A	844	VAL	4.0
1	B	551	VAL	3.9
1	B	950	LEU	3.9
1	A	606	THR	3.8
1	B	897	GLU	3.8
1	A	549	THR	3.7
1	B	524	ALA	3.7
1	A	842	ALA	3.7
1	A	607	GLY	3.6
1	A	543	VAL	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	843	VAL	3.6
1	A	604	ASN	3.6
1	B	607	GLY	3.5
1	B	896	VAL	3.4
1	B	546	ASP	3.3
1	A	550	TYR	3.2
1	A	840	GLU	3.2
1	A	545	GLN	3.2
1	A	896	VAL	3.2
1	B	545	GLN	3.2
1	B	925	ASN	3.2
1	B	593	TRP	3.2
1	B	839	PRO	3.1
1	B	602	GLY	3.0
1	B	547	ASP	3.0
1	A	658	GLY	2.9
1	A	950	LEU	2.8
1	B	606	THR	2.7
1	A	585	THR	2.7
1	A	839	PRO	2.7
1	A	932	TYR	2.6
1	A	593	TRP	2.6
1	B	543	VAL	2.6
1	B	926	GLY	2.6
1	B	900	ASN	2.6
1	A	526	VAL	2.5
1	B	585	THR	2.4
1	A	547	ASP	2.4
1	B	608	SER	2.3
1	B	840	GLU	2.3
1	A	582	GLU	2.2
1	B	895	ASP	2.2
1	B	582	GLU	2.1
1	A	949	ALA	2.0
1	B	838	SER	2.0
1	B	949	ALA	2.0
1	B	817	ILE	2.0

## 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 [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	PG4	B	1001	7/13	0.86	0.13	1.27	42,44,49,50	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.