



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 26, 2019 – 02:21 AM EDT

PDB ID : 5G2B  
Title : Crystal structure of T. brucei PDE-B1 catalytic domain with inhibitor NPD-008  
Authors : Singh, A.K.; Anthonyrajah, E.S.; Brown, D.G.  
Deposited on : 2016-04-07  
Resolution : 1.83 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.0 (224370), CSD as540be (2019)  
Xtriage (Phenix) : 1.13  
EDS : rb-20031633  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20031633

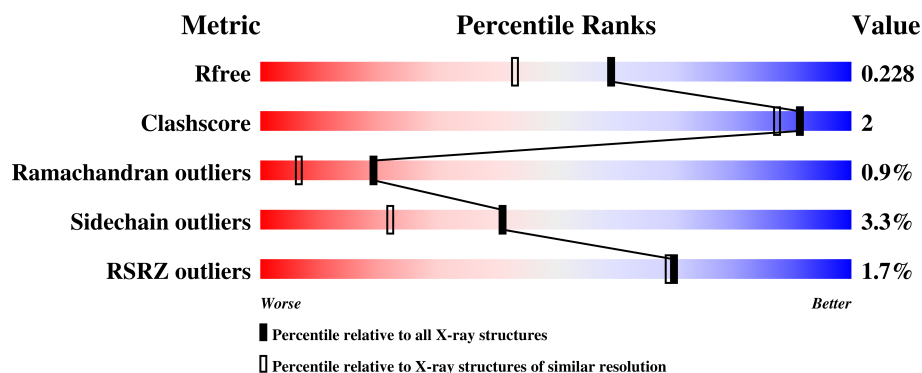
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.83 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))
$R_{free}$	111664	3313 (1.86-1.82)
Clashscore	122126	3530 (1.86-1.82)
Ramachandran outliers	120053	3495 (1.86-1.82)
Sidechain outliers	120020	3496 (1.86-1.82)
RSRZ outliers	108989	3265 (1.86-1.82)

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	360	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%; height: 1px; background-color: red;"></div> <div style="position: absolute; bottom: 0; left: 0; width: 100%; height: 10px; background-color: green;"></div> <div style="position: absolute; bottom: 0; left: 87%; width: 13%; height: 10px; background-color: yellow;"></div> <div style="position: absolute; bottom: 0; left: 99%; width: 1%; height: 10px; background-color: orange;"></div> <div style="position: absolute; bottom: 0; left: 100%; width: 1%; height: 10px; background-color: grey;"></div> </div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> <span>%</span> <span>87%</span> <span>5% • 8%</span> </div> </div>
1	B	360	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%; height: 1px; background-color: red;"></div> <div style="position: absolute; bottom: 0; left: 0; width: 100%; height: 10px; background-color: green;"></div> <div style="position: absolute; bottom: 0; left: 84%; width: 16%; height: 10px; background-color: yellow;"></div> <div style="position: absolute; bottom: 0; left: 99%; width: 1%; height: 10px; background-color: orange;"></div> <div style="position: absolute; bottom: 0; left: 100%; width: 1%; height: 10px; background-color: grey;"></div> </div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> <span>2%</span> <span>84%</span> <span>7% • 8%</span> </div> </div>

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 5752 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 CLASS 1 PHOSPHODIESTERASE PDEB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	333	Total	C	N	O	S	0	0	0
			2636	1673	445	500	18			
1	B	332	Total	C	N	O	S	0	0	0
			2624	1667	441	498	18			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	559	GLY	-	expression tag	UNP Q8WQX9
A	560	SER	-	expression tag	UNP Q8WQX9
A	561	HIS	-	expression tag	UNP Q8WQX9
A	562	MET	-	expression tag	UNP Q8WQX9
A	563	ALA	-	expression tag	UNP Q8WQX9
A	564	SER	-	expression tag	UNP Q8WQX9
B	559	GLY	-	expression tag	UNP Q8WQX9
B	560	SER	-	expression tag	UNP Q8WQX9
B	561	HIS	-	expression tag	UNP Q8WQX9
B	562	MET	-	expression tag	UNP Q8WQX9
B	563	ALA	-	expression tag	UNP Q8WQX9
B	564	SER	-	expression tag	UNP Q8WQX9

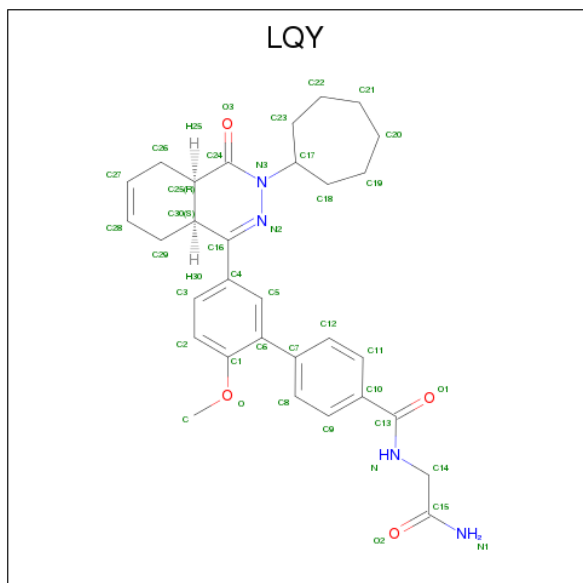
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

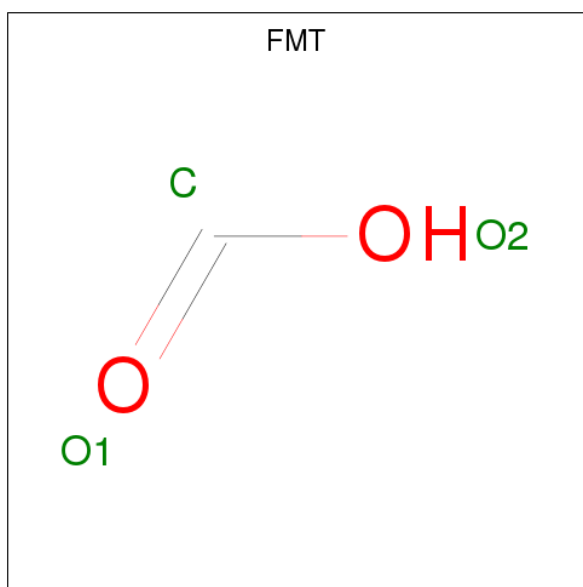
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is N-(2-amino-2-oxoethyl)-5'-[(4aR,8aS)-3-cycloheptyl-4-oxo-3,4,4a,5,8,8a-hexahydrophthalazin-1-yl]-2'-methoxy[1,1'-biphenyl]-4-carboxamide (three-letter code: LQY) (formula: C<sub>31</sub>H<sub>36</sub>N<sub>4</sub>O<sub>4</sub>).



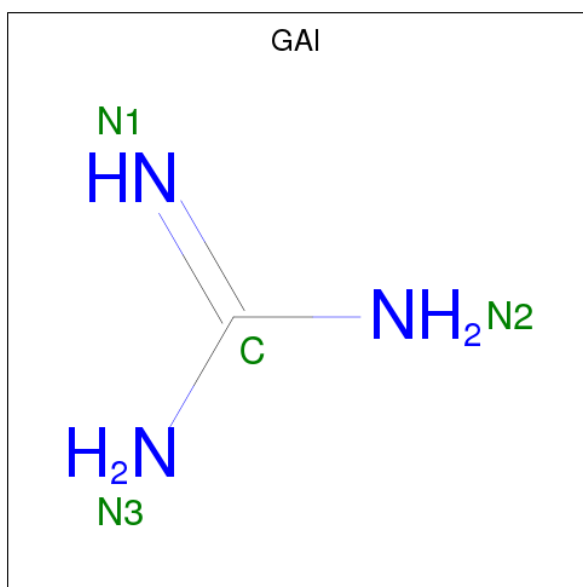
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			39	31	4	4		
4	B	1	Total	C	N	O	0	0
			39	31	4	4		

- Molecule 5 is FORMIC ACID (three-letter code: FMT) (formula: CH<sub>2</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			3	1	2		
5	A	1	Total	C	O	0	0
			3	1	2		
5	A	1	Total	C	O	0	0
			3	1	2		

- Molecule 6 is GUANIDINE (three-letter code: GAI) (formula:  $\text{CH}_5\text{N}_3$ ).



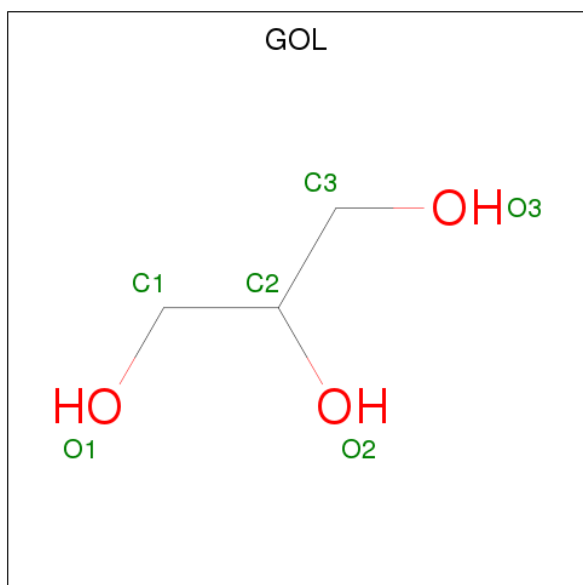
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	N	0	0
			4	1	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	N	0	0
			4	1	3		
6	B	1	Total	C	N	0	0
			4	1	3		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			6	3	3		

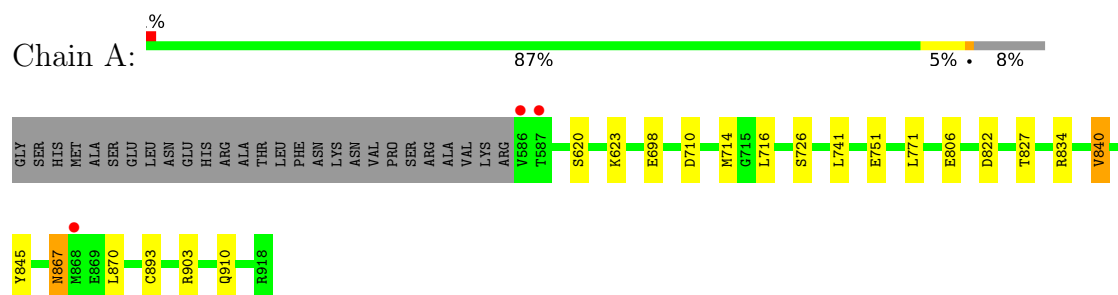
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	213	Total	O	0	0
			213	213		
8	B	170	Total	O	0	0
			170	170		

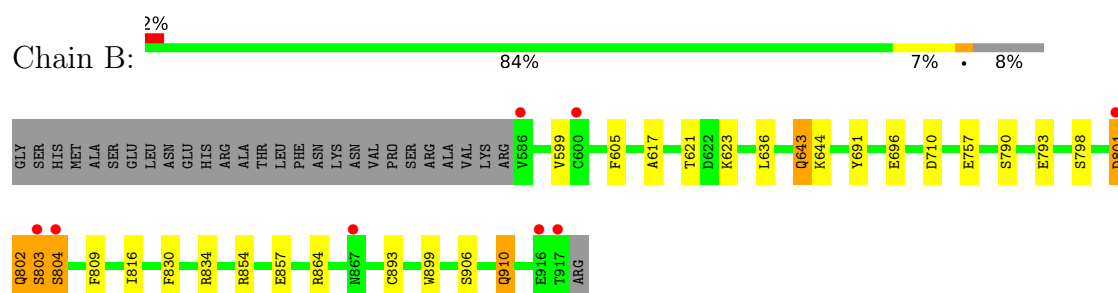
### 3 Residue-property plots [i](#)

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: CLASS 1 PHOSPHODIESTERASE PDEB1



#### • Molecule 1: CLASS 1 PHOSPHODIESTERASE PDEB1



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	114.36Å 115.74Å 68.41Å 90.00° 108.70° 90.00°	Depositor
Resolution (Å)	64.80 – 1.83 64.80 – 1.83	Depositor EDS
% Data completeness (in resolution range)	98.0 (64.80-1.83) 98.0 (64.80-1.83)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.46 (at 1.83Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, $R_{free}$	0.183 , 0.221 0.192 , 0.228	Depositor DCC
$R_{free}$ test set	3552 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.1	Xtriage
Anisotropy	0.624	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 46.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	5752	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.68% 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: GOL, ZN, LQY, FMT, MG, GAI

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	0.85	1/2687 (0.0%)	0.92	6/3634 (0.2%)
1	B	0.82	0/2675	0.88	2/3620 (0.1%)
All	All	0.83	1/5362 (0.0%)	0.90	8/7254 (0.1%)

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 (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	806	GLU	CG-CD	6.43	1.61	1.51

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	710	ASP	CB-CG-OD1	9.35	126.72	118.30
1	A	834	ARG	NE-CZ-NH2	-7.47	116.56	120.30
1	A	822	ASP	CB-CG-OD2	-6.23	112.69	118.30
1	A	710	ASP	CB-CG-OD1	5.84	123.56	118.30
1	A	714	MET	CB-CG-SD	5.65	129.35	112.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	803	SER	Peptide

## 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	2636	0	2598	6	0
1	B	2624	0	2585	13	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	39	0	0	1	0
4	B	39	0	0	0	0
5	A	9	0	3	0	0
6	A	8	0	8	0	0
6	B	4	0	4	0	0
7	B	6	0	8	1	0
8	A	213	0	0	3	0
8	B	170	0	0	3	0
All	All	5752	0	5206	19	1

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 2.

The worst 5 of 19 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:643:GLN:H	1:B:643:GLN:HE21	1.25	0.83
1:B:910:GLN:HG3	8:B:2168:HOH:O	1.90	0.70
8:A:2208:HOH:O	1:B:854:ARG:NH1	2.30	0.64
1:A:698:GLU:OE2	8:A:2069:HOH:O	2.16	0.57
1:B:834:ARG:HD2	8:B:2143:HOH:O	2.07	0.55

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:790:SER:OG	1:B:793:GLU:OE1[2_656]	2.08	0.12

## 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	331/360 (92%)	320 (97%)	9 (3%)	2 (1%)	27	13
1	B	330/360 (92%)	319 (97%)	7 (2%)	4 (1%)	14	4
All	All	661/720 (92%)	639 (97%)	16 (2%)	6 (1%)	19	6

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	804	SER
1	B	893	CYS
1	A	893	CYS
1	B	802	GLN
1	B	801	ASP

### 5.3.2 Protein sidechains [i](#)

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	288/311 (93%)	281 (98%)	7 (2%)	52	35
1	B	287/311 (92%)	275 (96%)	12 (4%)	32	14
All	All	575/622 (92%)	556 (97%)	19 (3%)	41	22

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	636	LEU
1	B	757	GLU
1	B	864	ARG
1	B	599	VAL
1	B	899	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	643	GLN
1	B	887	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 13 ligands modelled in this entry, 4 are monoatomic - leaving 9 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	$\# Z  > 2$
4	LQY	A	1003	-	43,43,43	0.74	2 (4%)	50,60,60	0.70	2 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	FMT	A	1004	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	A	1005	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	A	1006	-	0,2,2	0.00	-	0,1,1	0.00	-
6	GAI	A	1007	-	3,3,3	1.35	0	3,3,3	1.68	1 (33%)
6	GAI	A	1008	-	3,3,3	0.95	0	3,3,3	1.68	1 (33%)
4	LQY	B	1003	-	43,43,43	0.64	2 (4%)	50,60,60	0.72	1 (2%)
6	GAI	B	1004	-	3,3,3	1.69	0	3,3,3	1.06	0
7	GOL	B	1005	-	5,5,5	1.52	1 (20%)	5,5,5	2.95	2 (40%)

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
4	LQY	A	1003	-	-	0/21/59/59	0/5/5/5
5	FMT	A	1004	-	-	0/0/0/0	0/0/0/0
5	FMT	A	1005	-	-	0/0/0/0	0/0/0/0
5	FMT	A	1006	-	-	0/0/0/0	0/0/0/0
6	GAI	A	1007	-	-	0/0/0/0	0/0/0/0
6	GAI	A	1008	-	-	0/0/0/0	0/0/0/0
4	LQY	B	1003	-	-	0/21/59/59	0/5/5/5
6	GAI	B	1004	-	-	0/0/0/0	0/0/0/0
7	GOL	B	1005	-	-	0/4/4/4	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1003	LQY	C29-C28	2.31	1.54	1.49
4	B	1003	LQY	C23-C17	2.35	1.59	1.53
4	A	1003	LQY	C18-C17	2.60	1.60	1.53
7	B	1005	GOL	O3-C3	2.87	1.54	1.42
4	A	1003	LQY	C23-C17	3.10	1.61	1.53

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1007	GAI	N2-C-N1	-2.12	115.92	121.92
4	A	1003	LQY	C26-C25-C24	2.35	117.39	110.44
6	A	1008	GAI	N3-C-N2	2.51	122.11	116.13
4	B	1003	LQY	O3-C24-N3	2.77	125.01	121.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1003	LQY	O3-C24-N3	3.00	125.29	121.64

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1003	LQY	1	0
7	B	1005	GOL	1	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	333/360 (92%)	-0.42	3 (0%) 84 84	25, 37, 63, 88	0
1	B	332/360 (92%)	-0.25	8 (2%) 59 56	23, 36, 65, 101	0
All	All	665/720 (92%)	-0.33	11 (1%) 70 69	23, 36, 63, 101	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	586	VAL	6.4
1	A	586	VAL	5.0
1	B	917	THR	4.4
1	B	803	SER	3.7
1	B	801	ASP	3.3

### 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. 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	B-factors( $\text{\AA}^2$ )	Q<0.9
6	GAI	A	1008	4/4	0.64	0.16	50,55,59,63	0
5	FMT	A	1005	3/3	0.77	0.16	57,57,69,71	0
6	GAI	B	1004	4/4	0.81	0.13	52,53,55,58	0
4	LQY	A	1003	39/39	0.85	0.15	36,52,65,78	0
7	GOL	B	1005	6/6	0.86	0.12	36,38,43,47	0
5	FMT	A	1004	3/3	0.86	0.09	53,53,57,58	0
4	LQY	B	1003	39/39	0.89	0.12	34,40,51,55	0
5	FMT	A	1006	3/3	0.96	0.07	51,51,51,53	0
6	GAI	A	1007	4/4	0.97	0.08	31,34,37,38	0
3	MG	A	1002	1/1	0.99	0.13	14,14,14,14	0
2	ZN	A	1001	1/1	0.99	0.09	33,33,33,33	0
3	MG	B	1002	1/1	0.99	0.15	11,11,11,11	0
2	ZN	B	1001	1/1	0.99	0.10	30,30,30,30	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.