



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2023 – 12:32 AM EDT

PDB ID : 7LU4  
Title : Crystal structure of bacterial glycyl tRNA synthetase in complex with glycine  
Authors : Torres-Larios, A.  
Deposited on : 2021-02-20  
Resolution : 2.50 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35.1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35.1

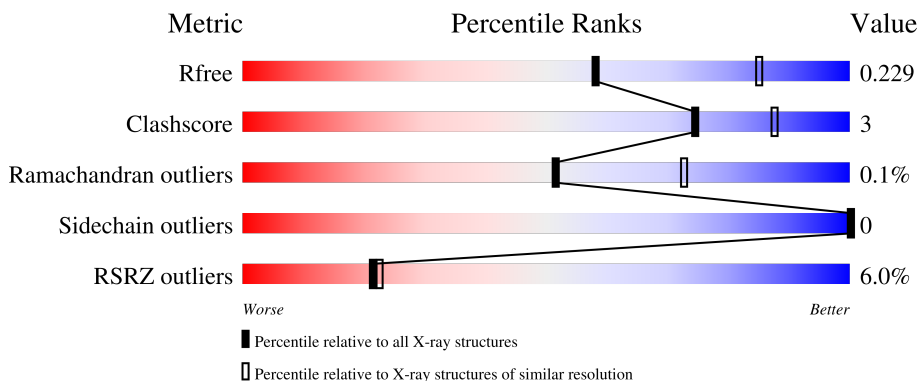
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*



The reported resolution of this entry is 2.50 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))
$R_{free}$	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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	1011	
1	B	1011	

## 2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 14715 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 Multifunctional fusion protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	978	7533	4815	1334	1366	18	0	0	0
1	B	977	7177	4526	1302	1332	17	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

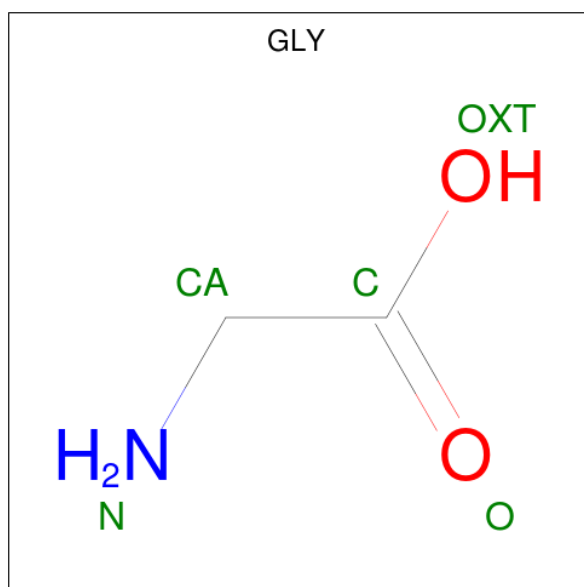
Chain	Residue	Modelled	Actual	Comment	Reference
A	23	SER	CYS	engineered mutation	UNP A0A0P6Y0P9
A	243	SER	CYS	engineered mutation	UNP A0A0P6Y0P9
A	706	SER	CYS	engineered mutation	UNP A0A0P6Y0P9
A	836	SER	CYS	engineered mutation	UNP A0A0P6Y0P9
A	898	SER	CYS	engineered mutation	UNP A0A0P6Y0P9
A	999	GLU	-	expression tag	UNP A0A0P6Y0P9
A	1000	ASN	-	expression tag	UNP A0A0P6Y0P9
A	1001	LEU	-	expression tag	UNP A0A0P6Y0P9
A	1002	TYR	-	expression tag	UNP A0A0P6Y0P9
A	1003	PHE	-	expression tag	UNP A0A0P6Y0P9
A	1004	GLN	-	expression tag	UNP A0A0P6Y0P9
A	1005	GLY	-	expression tag	UNP A0A0P6Y0P9
A	1006	HIS	-	expression tag	UNP A0A0P6Y0P9
A	1007	HIS	-	expression tag	UNP A0A0P6Y0P9
A	1008	HIS	-	expression tag	UNP A0A0P6Y0P9
A	1009	HIS	-	expression tag	UNP A0A0P6Y0P9
A	1010	HIS	-	expression tag	UNP A0A0P6Y0P9
A	1011	HIS	-	expression tag	UNP A0A0P6Y0P9
B	23	SER	CYS	engineered mutation	UNP A0A0P6Y0P9
B	243	SER	CYS	engineered mutation	UNP A0A0P6Y0P9
B	706	SER	CYS	engineered mutation	UNP A0A0P6Y0P9
B	836	SER	CYS	engineered mutation	UNP A0A0P6Y0P9
B	898	SER	CYS	engineered mutation	UNP A0A0P6Y0P9
B	999	GLU	-	expression tag	UNP A0A0P6Y0P9
B	1000	ASN	-	expression tag	UNP A0A0P6Y0P9

*Continued on next page...*

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	1001	LEU	-	expression tag	UNP A0A0P6Y0P9
B	1002	TYR	-	expression tag	UNP A0A0P6Y0P9
B	1003	PHE	-	expression tag	UNP A0A0P6Y0P9
B	1004	GLN	-	expression tag	UNP A0A0P6Y0P9
B	1005	GLY	-	expression tag	UNP A0A0P6Y0P9
B	1006	HIS	-	expression tag	UNP A0A0P6Y0P9
B	1007	HIS	-	expression tag	UNP A0A0P6Y0P9
B	1008	HIS	-	expression tag	UNP A0A0P6Y0P9
B	1009	HIS	-	expression tag	UNP A0A0P6Y0P9
B	1010	HIS	-	expression tag	UNP A0A0P6Y0P9
B	1011	HIS	-	expression tag	UNP A0A0P6Y0P9

- Molecule 2 is GLYCINE (three-letter code: GLY) (formula:  $C_2H_5NO_2$ ) (labeled as "Ligand of Interest" by depositor).

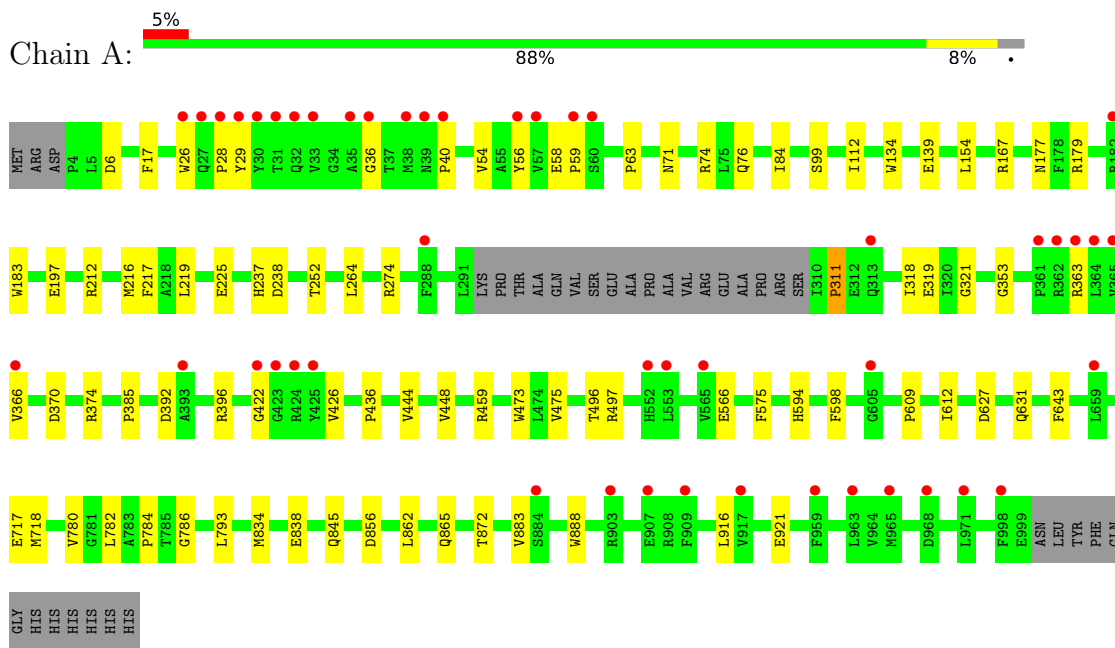


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	B	1	5	2	1	2	0	0

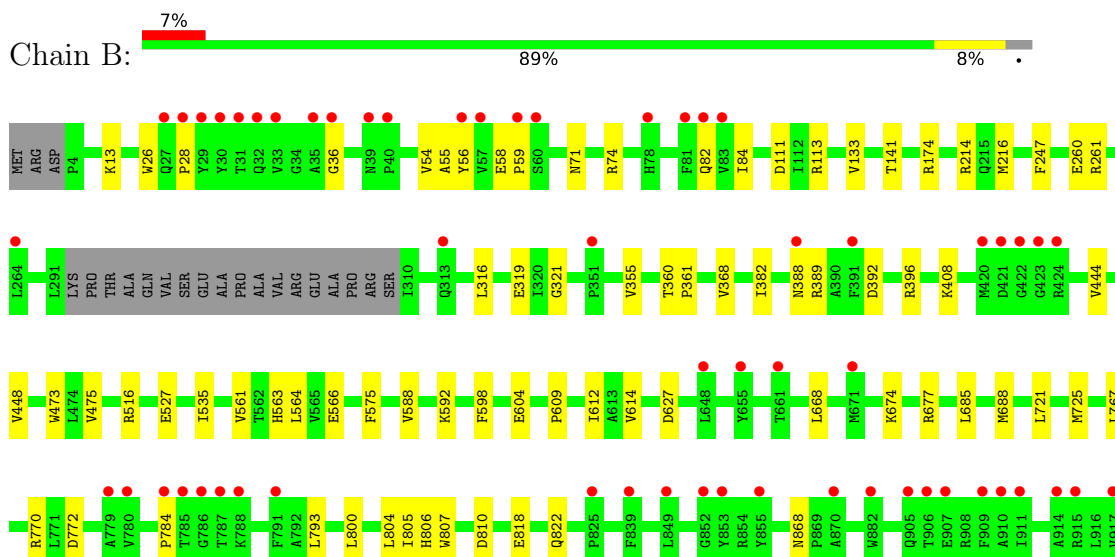
### 3 Residue-property plots [i](#)

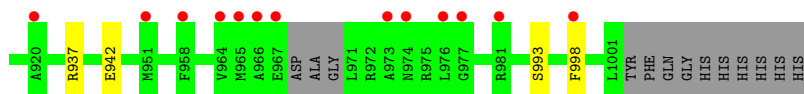
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Multifunctional fusion protein



- Molecule 1: Multifunctional fusion protein





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	238.58Å 127.86Å 133.06Å 90.00° 103.61° 90.00°	Depositor
Resolution (Å)	35.74 – 2.50 35.74 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.2 (35.74-2.50) 99.2 (35.74-2.50)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.53 (at 2.51Å)	Xtrriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, $R_{free}$	0.207 , 0.228 0.208 , 0.229	Depositor DCC
$R_{free}$ test set	6485 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	72.9	Xtrriage
Anisotropy	0.359	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 53.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	14715	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	81.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.06% 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](#)

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	0.27	0/7713	0.44	1/10501 (0.0%)
1	B	0.27	0/7349	0.44	0/9968
All	All	0.27	0/15062	0.44	1/20469 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	311	PRO	N-CA-CB	7.32	112.08	103.30

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	7533	0	7322	46	1
1	B	7177	0	6506	45	1
2	B	5	0	2	0	0
All	All	14715	0	13830	90	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 3.

All (90) 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:363:ARG:NH2	1:A:497:ARG:O	2.13	0.82
1:B:516:ARG:NH2	1:B:527:GLU:OE2	2.23	0.71
1:A:363:ARG:NH1	1:A:566:GLU:OE2	2.25	0.69
1:A:598:PHE:HB2	1:A:612:ILE:HB	1.78	0.66
1:B:111:ASP:OD2	1:B:113:ARG:NH2	2.29	0.65
1:A:26:TRP:HB3	1:A:56:TYR:HB3	1.79	0.65
1:B:382:ILE:HG21	1:B:408:LYS:HE2	1.78	0.65
1:A:784:PRO:HD3	1:A:793:LEU:HD12	1.80	0.63
1:A:154:LEU:O	1:A:459:ARG:NH2	2.35	0.59
1:A:916:LEU:HD22	1:A:921:GLU:HB3	1.83	0.59
1:B:598:PHE:HB2	1:B:612:ILE:HB	1.85	0.57
1:A:780:VAL:HG23	1:A:782:LEU:HD23	1.87	0.57
1:B:54:VAL:HG12	1:B:84:ILE:HB	1.87	0.56
1:A:54:VAL:HG12	1:A:84:ILE:HB	1.88	0.56
1:B:174:ARG:NH1	1:B:627:ASP:OD2	2.38	0.55
1:B:28:PRO:HB3	1:B:59:PRO:HD2	1.90	0.54
1:B:604:GLU:N	1:B:604:GLU:OE2	2.41	0.53
1:B:685:LEU:HA	1:B:688:MET:HE3	1.91	0.53
1:A:643:PHE:CE2	1:A:717:GLU:HG3	2.45	0.51
1:A:865:GLN:O	1:A:872:THR:OG1	2.30	0.50
1:B:993:SER:HA	1:B:998:PHE:CD1	2.47	0.50
1:B:805:ILE:C	1:B:807:TRP:H	2.15	0.50
1:A:76:GLN:HG3	1:A:197:GLU:OE1	2.13	0.49
1:A:319:GLU:OE1	1:A:496:THR:OG1	2.21	0.49
1:A:883:VAL:HG12	1:A:888:TRP:CE2	2.48	0.49
1:B:674:LYS:NZ	1:B:772:ASP:OD2	2.43	0.49
1:A:29:TYR:OH	1:A:238:ASP:OD1	2.21	0.49
1:A:225:GLU:OE2	1:A:274:ARG:NH2	2.37	0.49
1:B:767:LEU:HD11	1:B:804:LEU:HD21	1.93	0.49
1:B:818:GLU:O	1:B:822:GLN:OE1	2.32	0.48
1:A:318:ILE:HB	1:A:366:VAL:HB	1.96	0.48
1:B:214:ARG:NH1	1:B:260:GLU:OE2	2.37	0.47
1:B:784:PRO:HD3	1:B:793:LEU:HD12	1.95	0.47
1:A:177:ASN:HD21	1:A:179:ARG:NE	2.13	0.47
1:B:321:GLY:HA3	1:B:473:TRP:CD2	2.49	0.47
1:A:28:PRO:HB3	1:A:59:PRO:HD2	1.96	0.47
1:B:319:GLU:HB3	1:B:475:VAL:HB	1.96	0.47
1:B:360:THR:HB	1:B:566:GLU:HG2	1.95	0.47
1:A:392:ASP:OD1	1:A:396:ARG:N	2.48	0.47
1:A:575:PHE:CZ	1:A:609:PRO:HA	2.50	0.46
1:B:36:GLY:HA2	1:B:58:GLU:HG2	1.98	0.46
1:B:133:VAL:HB	1:B:141:THR:HB	1.98	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:845:GLN:HB3	1:A:862:LEU:HD11	1.97	0.45
1:B:810:ASP:HB3	1:B:868:ASN:HD21	1.81	0.45
1:B:247:PHE:HZ	1:B:261:ARG:HG3	1.82	0.45
1:A:219:LEU:HD13	1:B:216:MET:HG3	1.99	0.45
1:B:26:TRP:HB3	1:B:56:TYR:HB3	1.99	0.45
1:A:36:GLY:HA2	1:A:58:GLU:HG2	1.99	0.45
1:B:535:ILE:HD13	1:B:561:VAL:HG12	1.98	0.45
1:A:321:GLY:HA3	1:A:473:TRP:CD2	2.52	0.44
1:A:834:MET:O	1:A:838:GLU:HG3	2.16	0.44
1:B:355:VAL:HG22	1:B:368:VAL:HG22	1.99	0.44
1:A:112:ILE:HA	1:A:134:TRP:O	2.18	0.44
1:A:6:ASP:HB3	1:A:183:TRP:O	2.18	0.44
1:A:385:PRO:O	1:A:426:VAL:HG12	2.18	0.44
1:A:217:PHE:CE2	1:A:264:LEU:HD22	2.53	0.43
1:B:444:VAL:O	1:B:448:VAL:HG23	2.18	0.43
1:A:74:ARG:NH2	1:A:717:GLU:OE1	2.51	0.43
1:A:856:ASP:OD1	1:A:856:ASP:N	2.50	0.43
1:A:177:ASN:HD21	1:A:179:ARG:CZ	2.31	0.43
1:B:721:LEU:HB3	1:B:725:MET:HG2	2.00	0.42
1:B:805:ILE:O	1:B:806:HIS:HB3	2.18	0.42
1:B:937:ARG:HE	1:B:937:ARG:HB2	1.68	0.42
1:A:319:GLU:HB3	1:A:475:VAL:HB	2.00	0.42
1:B:668:LEU:O	1:B:677:ARG:NH2	2.53	0.42
1:A:40:PRO:HG3	1:A:237:HIS:CD2	2.54	0.42
1:B:388:ASN:OD1	1:B:389:ARG:N	2.53	0.42
1:B:55:ALA:HA	1:B:82:GLN:O	2.20	0.42
1:B:316:LEU:HB3	1:B:368:VAL:HB	2.02	0.42
1:A:71:ASN:HB3	1:A:74:ARG:HB2	2.01	0.42
1:A:353:GLY:N	1:A:370:ASP:O	2.44	0.42
1:A:444:VAL:O	1:A:448:VAL:HG23	2.20	0.42
1:A:627:ASP:O	1:A:631:GLN:HG2	2.20	0.42
1:B:561:VAL:HG11	1:B:614:VAL:HG21	2.01	0.42
1:A:177:ASN:ND2	1:A:179:ARG:HB2	2.35	0.41
1:A:374:ARG:HA	1:A:436:PRO:HA	2.03	0.41
1:B:321:GLY:HA3	1:B:473:TRP:CE2	2.55	0.41
1:A:139:GLU:O	1:A:167:ARG:HD3	2.21	0.41
1:B:392:ASP:OD1	1:B:396:ARG:N	2.52	0.41
1:A:212:ARG:O	1:A:216:MET:HG3	2.21	0.41
1:B:575:PHE:CZ	1:B:609:PRO:HA	2.56	0.40
1:B:113:ARG:HD3	1:B:564:LEU:O	2.20	0.40
1:B:588:VAL:HG13	1:B:592:LYS:HD3	2.03	0.40

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:770:ARG:HD3	1:B:800:LEU:HB2	2.03	0.40
1:A:63:PRO:HB2	1:A:252:THR:HG21	2.02	0.40
1:B:13:LYS:HD2	1:B:13:LYS:HA	1.95	0.40
1:A:17:PHE:CE2	1:A:99:SER:HB3	2.57	0.40
1:A:594:HIS:NE2	1:A:718:MET:SD	2.94	0.40
1:B:71:ASN:OD1	1:B:74:ARG:N	2.50	0.40
1:B:361:PRO:HG3	1:B:563:HIS:O	2.21	0.40

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:A:786:GLY:N	1:B:942:GLU:OE1[4_556]	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	974/1011 (96%)	954 (98%)	18 (2%)	2 (0%)	47	68
1	B	971/1011 (96%)	936 (96%)	35 (4%)	0	100	100
All	All	1945/2022 (96%)	1890 (97%)	53 (3%)	2 (0%)	51	73

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	311	PRO
1	A	422	GLY

### 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	749/827 (91%)	749 (100%)	0	100	100
1	B	659/827 (80%)	659 (100%)	0	100	100
All	All	1408/1654 (85%)	1408 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 monosaccharides 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	GLY	B	1101	-	4,4,4	1.12	1 (25%)	3,4,4	1.58	1 (33%)

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	GLY	B	1101	-	-	0/2/2/2	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1101	GLY	OXT-C	-2.10	1.23	1.30

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1101	GLY	OXT-C-O	-2.06	118.16	123.30

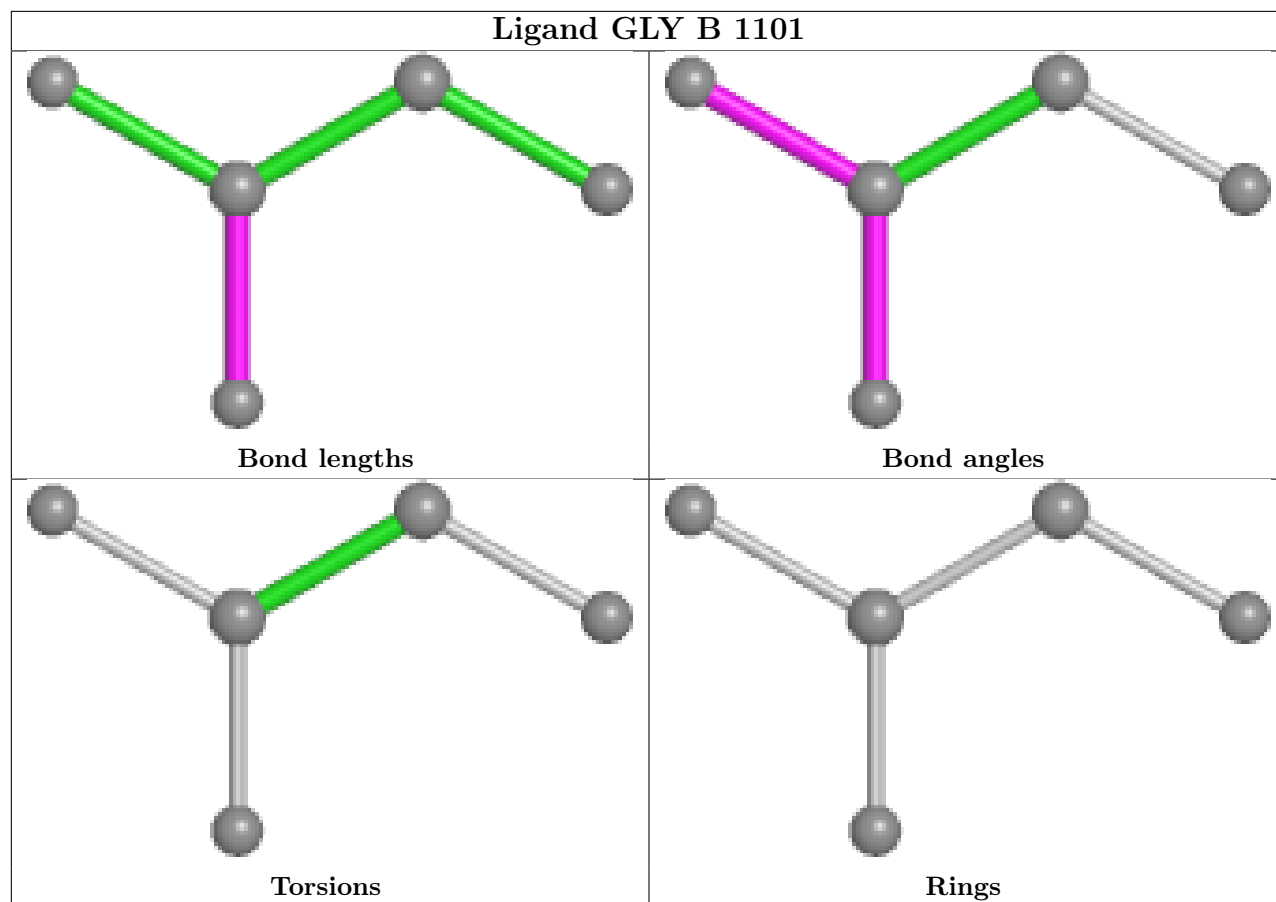
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 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	978/1011 (96%)	0.28	47 (4%) 30 32	50, 78, 105, 139	0
1	B	977/1011 (96%)	0.37	71 (7%) 15 15	50, 85, 122, 140	0
All	All	1955/2022 (96%)	0.32	118 (6%) 21 22	50, 80, 115, 140	0

All (118) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	30	TYR	5.0
1	B	786	GLY	4.8
1	A	30	TYR	4.6
1	B	958	PHE	4.6
1	A	26	TRP	4.6
1	A	29	TYR	4.5
1	A	31	THR	4.5
1	B	977	GLY	4.4
1	A	565	VAL	4.2
1	B	965	MET	4.2
1	B	31	THR	4.2
1	B	785	THR	4.1
1	A	28	PRO	4.1
1	B	855	TYR	4.0
1	B	60	SER	3.9
1	B	28	PRO	3.8
1	A	423	GLY	3.7
1	B	422	GLY	3.6
1	A	552	HIS	3.6
1	B	981	ARG	3.6
1	A	32	GLN	3.6
1	A	425	TYR	3.5
1	B	974	ASN	3.5
1	A	59	PRO	3.5

*Continued on next page...*

*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	424	ARG	3.5
1	B	29	TYR	3.4
1	B	839	PHE	3.4
1	A	965	MET	3.3
1	B	852	GLY	3.3
1	B	791	PHE	3.3
1	B	36	GLY	3.3
1	B	420	MET	3.3
1	B	966	ALA	3.2
1	B	32	GLN	3.2
1	B	967	GLU	3.2
1	B	787	THR	3.1
1	B	905	GLN	3.1
1	A	963	LEU	3.1
1	B	853	TYR	3.1
1	A	33	VAL	3.1
1	B	911	ILE	3.1
1	A	909	PHE	3.0
1	B	59	PRO	3.0
1	B	882	TRP	3.0
1	B	56	TYR	3.0
1	B	907	GLU	2.9
1	A	27	GLN	2.9
1	B	964	VAL	2.8
1	B	81	PHE	2.8
1	B	33	VAL	2.8
1	B	909	PHE	2.7
1	A	35	ALA	2.7
1	B	391	PHE	2.7
1	B	906	THR	2.7
1	A	36	GLY	2.7
1	A	968	ASP	2.7
1	B	915	ARG	2.7
1	B	976	LEU	2.7
1	A	903	ARG	2.6
1	B	973	ALA	2.6
1	A	39	ASN	2.6
1	A	363	ARG	2.6
1	A	365	VAL	2.6
1	B	914	ALA	2.6
1	A	422	GLY	2.6
1	B	264	LEU	2.6

*Continued on next page...*



*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	788	LYS	2.6
1	B	39	ASN	2.6
1	B	655	TYR	2.6
1	B	35	ALA	2.5
1	A	57	VAL	2.5
1	B	57	VAL	2.5
1	A	907	GLU	2.5
1	B	917	VAL	2.5
1	A	366	VAL	2.5
1	B	998	PHE	2.5
1	B	780	VAL	2.4
1	A	60	SER	2.4
1	A	313	GLN	2.4
1	A	424	ARG	2.4
1	B	910	ALA	2.4
1	B	951	MET	2.4
1	A	553	LEU	2.4
1	B	648	LEU	2.3
1	B	423	GLY	2.3
1	A	971	LEU	2.3
1	A	959	PHE	2.3
1	A	998	PHE	2.3
1	B	388	ASN	2.3
1	A	40	PRO	2.3
1	A	364	LEU	2.3
1	B	661	THR	2.2
1	B	849	LEU	2.2
1	B	671	MET	2.2
1	B	83	VAL	2.2
1	B	27	GLN	2.2
1	B	78	HIS	2.2
1	A	659	LEU	2.2
1	B	313	GLN	2.2
1	B	825	PRO	2.2
1	A	362	ARG	2.2
1	A	884	SER	2.2
1	B	870	ALA	2.2
1	A	38	MET	2.1
1	A	605	GLY	2.1
1	A	182	ARG	2.1
1	A	917	VAL	2.1
1	B	779	ALA	2.1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	56	TYR	2.1
1	A	288	PHE	2.1
1	B	82	GLN	2.1
1	A	361	PRO	2.0
1	B	40	PRO	2.0
1	B	920	ALA	2.0
1	B	421	ASP	2.0
1	A	393	ALA	2.0
1	B	351	PRO	2.0
1	B	784	PRO	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](#)

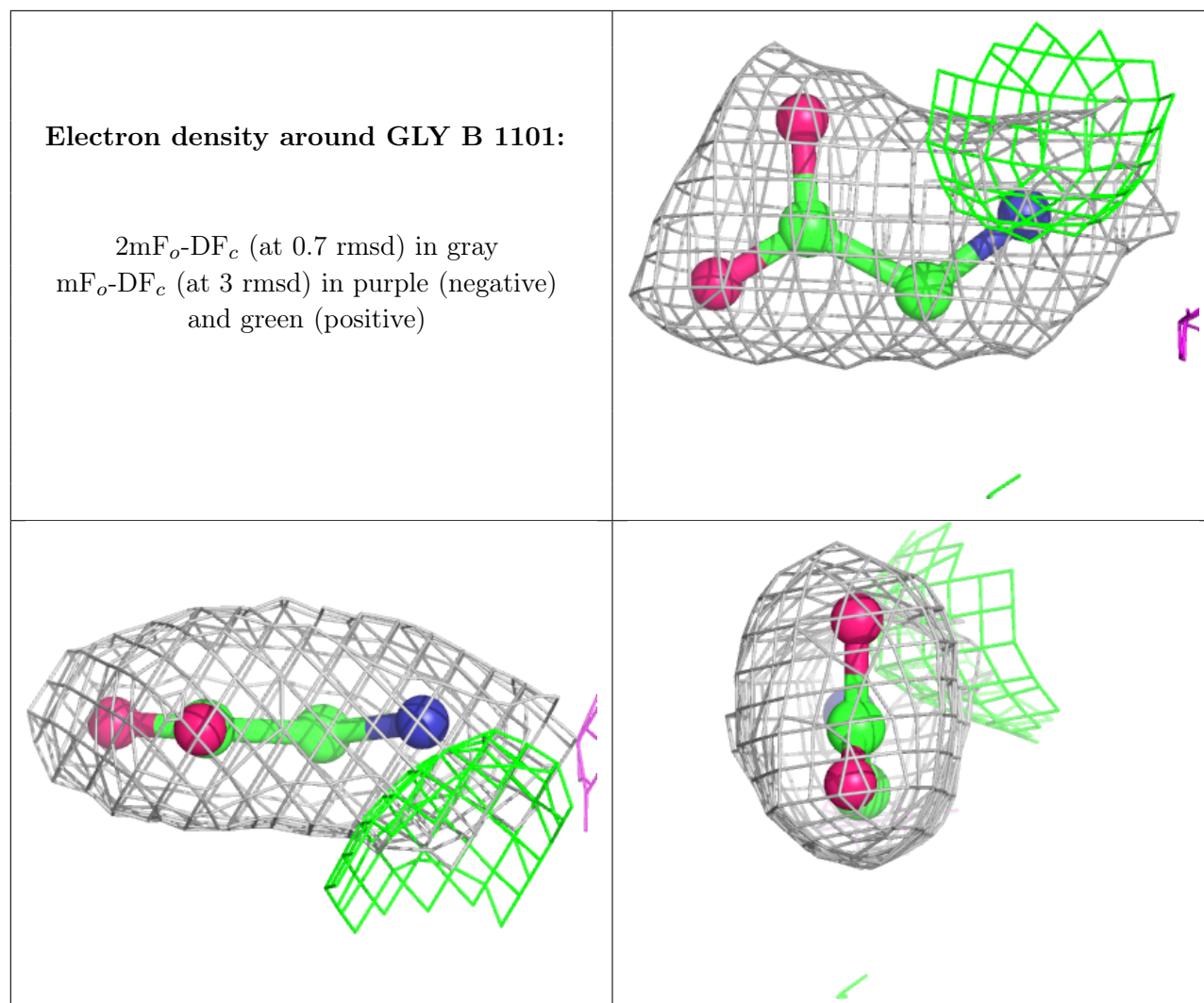
There are no monosaccharides in this entry.

## 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(Å <sup>2</sup> )	Q<0.9
2	GLY	B	1101	5/5	0.93	0.26	67,72,84,84	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



## 6.5 Other polymers [i](#)

There are no such residues in this entry.