



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 06:24 AM UTC

PDB ID : 5IFU / pdb_00005ifu
Title : Crystal Structure of Prolyl-tRNA synthetase (ProRS, Proline-tRNA ligase) from Plasmodium falciparum in complex with Glyburide
Authors : Dranow, D.M.; Hewitt, S.N.; Abendroth, J.; Structural Genomics Consortium (SGC)
Deposited on : 2016-02-26
Resolution : 2.45 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

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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

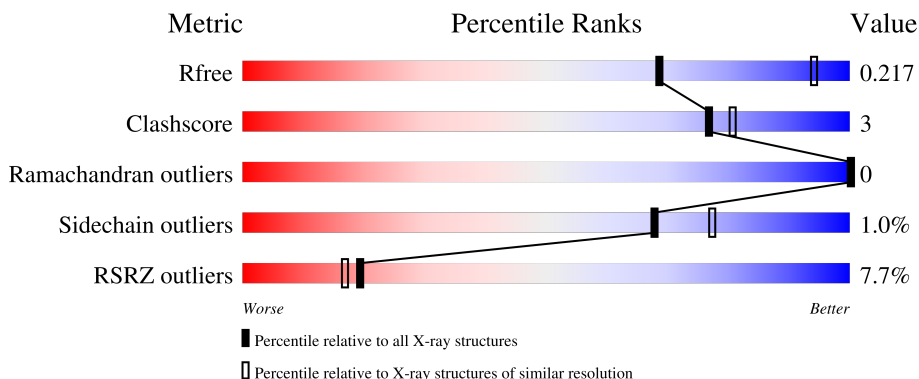
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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}	180053	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

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 ≥ 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	506	4% 81% 6% 13%
1	B	506	10% 78% 9% 12%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7313 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.

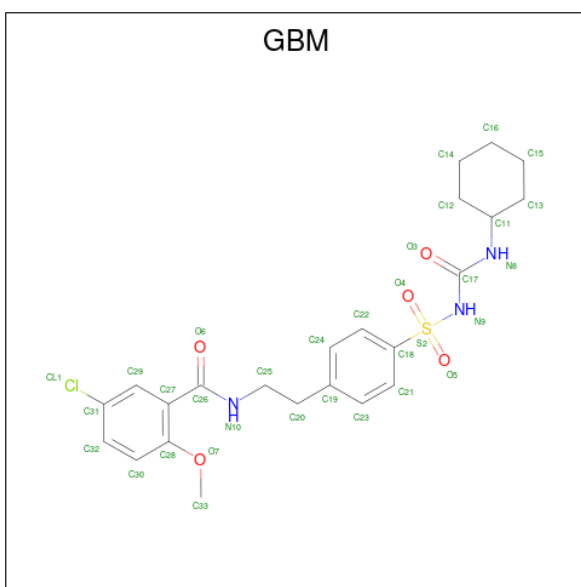
- Molecule 1 is a protein called Proline-tRNA ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	438	Total	C	N	O	S	0	4	0
			3528	2273	585	648	22			
1	B	445	Total	C	N	O	S	0	0	0
			3438	2214	573	631	20			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	241	MET	-	expression tag	UNP Q8I5R7
A	242	ALA	-	expression tag	UNP Q8I5R7
A	243	HIS	-	expression tag	UNP Q8I5R7
A	244	HIS	-	expression tag	UNP Q8I5R7
A	245	HIS	-	expression tag	UNP Q8I5R7
A	246	HIS	-	expression tag	UNP Q8I5R7
A	247	HIS	-	expression tag	UNP Q8I5R7
A	248	HIS	-	expression tag	UNP Q8I5R7
B	241	MET	-	expression tag	UNP Q8I5R7
B	242	ALA	-	expression tag	UNP Q8I5R7
B	243	HIS	-	expression tag	UNP Q8I5R7
B	244	HIS	-	expression tag	UNP Q8I5R7
B	245	HIS	-	expression tag	UNP Q8I5R7
B	246	HIS	-	expression tag	UNP Q8I5R7
B	247	HIS	-	expression tag	UNP Q8I5R7
B	248	HIS	-	expression tag	UNP Q8I5R7

- Molecule 2 is 5-chloro-N-(2-{4-[(cyclohexylcarbamoyl)sulfamoyl]phenyl}ethyl)-2-methoxybenzamide (CCD ID: GBM) (formula: C₂₃H₂₈ClN₃O₅S).

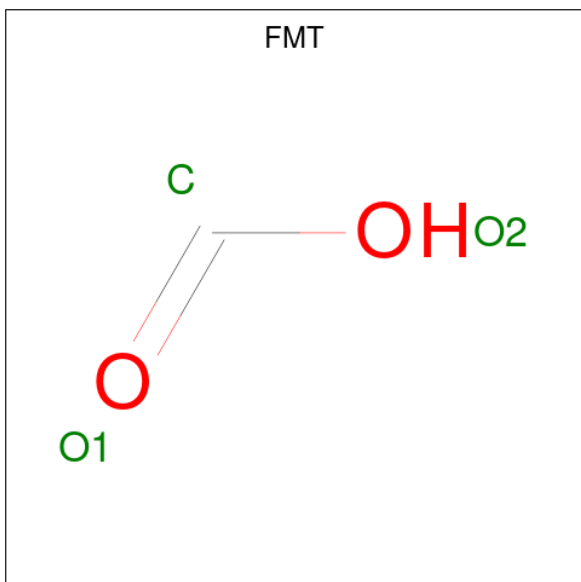


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	S	0	0
			33	23	1	3	5	1		
2	B	1	Total	C	N	O	S	0	0	
			20	14	2	3	1			

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total	Cl	0
			1	1	

- Molecule 4 is FORMIC ACID (CCD ID: FMT) (formula: CH₂O₂).



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

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		

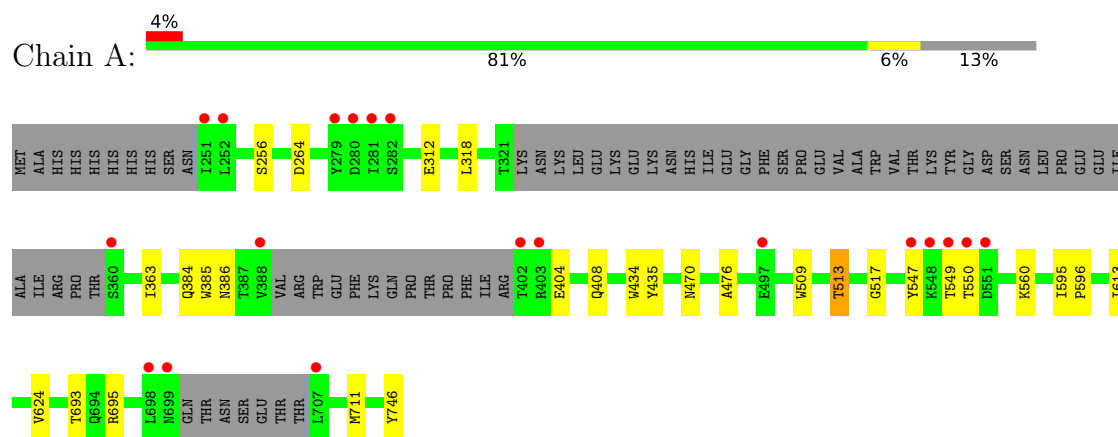
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	191	Total	O	0	0
			191	191		
6	B	52	Total	O	0	0
			52	52		

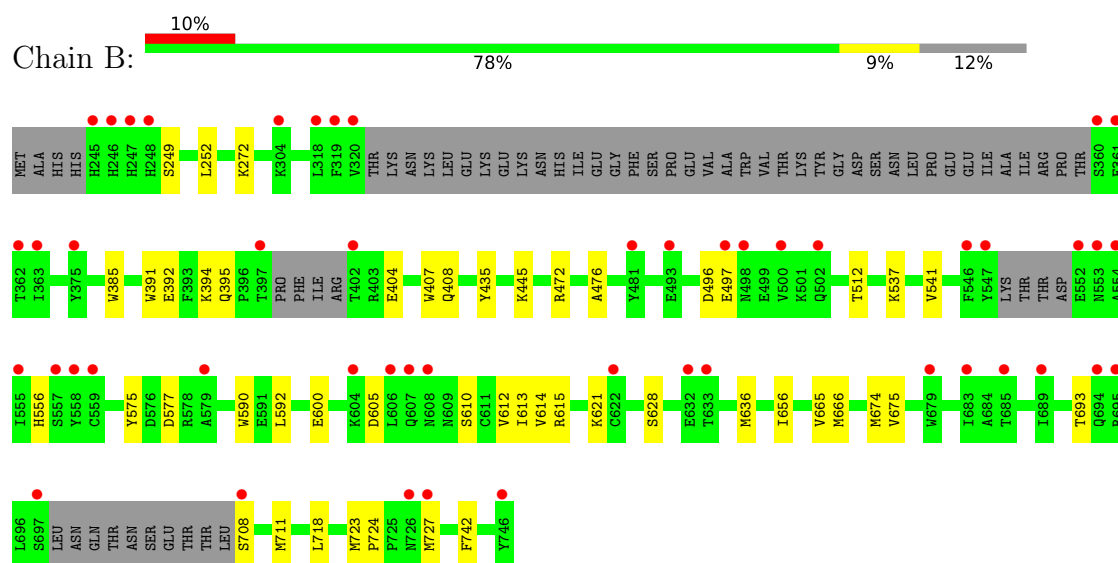
3 Residue-property plots [i](#)

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: Proline-tRNA ligase



• Molecule 1: Proline-tRNA ligase



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	138.31Å 138.31Å 156.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.74 – 2.45 43.74 – 2.45	Depositor EDS
% Data completeness (in resolution range)	99.5 (43.74-2.45) 96.5 (43.74-2.45)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.60 (at 2.45Å)	Xtriage
Refinement program	PHENIX dev_1819	Depositor
R, R_{free}	0.185 , 0.213 0.189 , 0.217	Depositor DCC
R_{free} test set	2752 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	45.6	Xtriage
Anisotropy	0.270	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 51.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7313	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.81% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: FMT, GBM, EDO, CL

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	0.29	0/3623	0.68	0/4906
1	B	0.27	0/3525	0.70	4/4795 (0.1%)
All	All	0.28	0/7148	0.69	4/9701 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	723	MET	CA-C-N	5.58	123.74	119.66
1	B	723	MET	C-N-CA	5.58	123.74	119.66
1	B	395	GLN	CA-C-N	5.03	124.47	119.24
1	B	395	GLN	C-N-CA	5.03	124.47	119.24

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	3528	0	3429	14	0
1	B	3438	0	3188	27	0
2	A	33	0	28	1	0
2	B	20	0	17	1	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	30	0	10	0	0
4	B	12	0	4	0	0
5	A	4	0	6	0	0
5	B	4	0	6	0	0
6	A	191	0	0	1	0
6	B	52	0	0	1	0
All	All	7313	0	6688	40	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 3.

All (40) 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:272:LYS:HB3	1:B:592:LEU:HD21	1.76	0.66
1:B:392:GLU:O	6:B:901:HOH:O	2.14	0.65
1:B:615:ARG:HB3	1:B:636:MET:HE3	1.80	0.62
1:B:693:THR:HG21	1:B:711:MET:HG2	1.84	0.60
1:B:496:ASP:OD1	1:B:497:GLU:N	2.36	0.59
1:B:435:TYR:CZ	1:B:476:ALA:HB1	2.39	0.58
1:A:312:GLU:OE2	1:B:537:LYS:NZ	2.32	0.57
1:B:407:TRP:HB2	1:B:512:THR:HG22	1.87	0.56
1:B:404:GLU:OE2	2:B:801:GBM:N9	2.33	0.56
1:A:256:SER:OG	1:A:264:ASP:OD2	2.23	0.54
1:A:385:TRP:CZ3	1:A:408:GLN:HB2	2.44	0.53
1:B:613:ILE:HG22	1:B:636:MET:HE1	1.92	0.52
1:A:693:THR:HG21	1:A:711:MET:HG2	1.93	0.51
1:B:600:GLU:HB2	1:B:612:VAL:HB	1.92	0.51
1:B:249:SER:HB2	1:B:252:LEU:HG	1.94	0.49
1:A:318:LEU:HG	1:A:363:ILE:HD12	1.94	0.48
1:A:695:ARG:NH2	6:A:904:HOH:O	2.47	0.48
1:A:547:TYR:C	1:A:549:THR:H	2.22	0.48
1:B:614:VAL:HG22	1:B:621:LYS:HG2	1.97	0.47
1:A:435:TYR:CZ	1:A:476:ALA:HB1	2.50	0.47
1:A:517:GLY:HA3	2:A:801:GBM:O3	2.15	0.47
1:B:249:SER:H	1:B:252:LEU:HD12	1.79	0.46
1:B:541:VAL:HG21	1:B:590:TRP:CD1	2.51	0.46
1:B:665:VAL:HG12	1:B:666:MET:HE2	1.98	0.46
1:A:404:GLU:HG3	1:A:513:THR:OG1	2.16	0.46
1:B:385:TRP:CZ3	1:B:408:GLN:HB2	2.52	0.45
1:B:445:LYS:HB3	1:B:718:LEU:HD12	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:472:ARG:NH2	1:B:708:SER:O	2.50	0.44
1:A:384[B]:GLN:NE2	1:A:386:ASN:OD1	2.45	0.44
1:B:656:ILE:HG12	1:B:674:MET:HE3	2.01	0.43
1:B:391:TRP:HB3	1:B:394:LYS:HE3	2.00	0.43
1:B:724:PRO:HB2	1:B:727:MET:HB2	2.00	0.42
1:B:675:VAL:HG23	1:B:742:PHE:HB2	2.01	0.42
1:A:613:ILE:HD12	1:A:624:VAL:HG21	2.01	0.42
1:A:595:ILE:HA	1:A:596:PRO:HD3	1.85	0.42
1:B:249:SER:N	1:B:252:LEU:HD12	2.35	0.41
1:B:666:MET:HE1	1:B:693:THR:HG22	2.02	0.41
1:B:575:TYR:CE2	1:B:577:ASP:HB3	2.56	0.41
1:A:470:ASN:ND2	1:A:746:TYR:OH	2.49	0.40
1:B:605:ASP:HB3	1:B:610:SER:O	2.20	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	434/506 (86%)	421 (97%)	13 (3%)	0	100	100
1	B	435/506 (86%)	425 (98%)	10 (2%)	0	100	100
All	All	869/1012 (86%)	846 (97%)	23 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	379/460 (82%)	374 (99%)	5 (1%)	61	73
1	B	345/460 (75%)	343 (99%)	2 (1%)	78	86
All	All	724/920 (79%)	717 (99%)	7 (1%)	68	77

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	434	TRP
1	A	509	TRP
1	A	513	THR
1	A	550	THR
1	A	560	LYS
1	B	556	HIS
1	B	628	SER

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

Mol	Chain	Res	Type
1	A	475	GLN
1	A	608	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 1 is monoatomic - leaving 18 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	FMT	A	805	-	2,2,2	0.73	0	1,1,1	0.22	0
2	GBM	B	801	-	21,21,35	1.79	7 (33%)	29,29,48	3.13	4 (13%)
4	FMT	A	807	-	2,2,2	0.73	0	1,1,1	0.23	0
4	FMT	A	804	-	2,2,2	0.73	0	1,1,1	0.21	0
4	FMT	A	806	-	2,2,2	0.72	0	1,1,1	0.22	0
4	FMT	B	802	-	2,2,2	0.72	0	1,1,1	0.21	0
2	GBM	A	801	-	35,35,35	1.83	10 (28%)	48,48,48	2.69	10 (20%)
4	FMT	B	804	-	2,2,2	0.73	0	1,1,1	0.22	0
4	FMT	B	803	-	2,2,2	0.73	0	1,1,1	0.22	0
5	EDO	A	813	-	3,3,3	0.44	0	2,2,2	0.29	0
4	FMT	A	812	-	2,2,2	0.74	0	1,1,1	0.24	0
4	FMT	A	810	-	2,2,2	0.75	0	1,1,1	0.25	0
4	FMT	B	805	-	2,2,2	0.73	0	1,1,1	0.21	0
5	EDO	B	806	-	3,3,3	0.44	0	2,2,2	0.25	0
4	FMT	A	809	-	2,2,2	0.72	0	1,1,1	0.21	0
4	FMT	A	811	-	2,2,2	0.71	0	1,1,1	0.22	0
4	FMT	A	808	-	2,2,2	0.73	0	1,1,1	0.23	0
4	FMT	A	803	-	2,2,2	0.70	0	1,1,1	0.18	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	GBM	B	801	-	-	1/15/23/35	0/2/2/3
2	GBM	A	801	-	-	10/27/35/35	0/3/3/3
5	EDO	A	813	-	-	0/1/1/1	-
5	EDO	B	806	-	-	0/1/1/1	-

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	GBM	C26-N10	5.45	1.45	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	GBM	C17-N8	3.75	1.45	1.35
2	B	801	GBM	C18-S2	3.72	1.82	1.76
2	B	801	GBM	C17-N8	3.68	1.45	1.35
2	A	801	GBM	C18-S2	3.58	1.82	1.76
2	A	801	GBM	S2-N9	3.36	1.72	1.64
2	B	801	GBM	S2-N9	3.04	1.71	1.64
2	A	801	GBM	C17-N9	3.00	1.46	1.39
2	A	801	GBM	O5-S2	2.93	1.46	1.43
2	B	801	GBM	O5-S2	2.93	1.46	1.43
2	B	801	GBM	O4-S2	2.80	1.46	1.43
2	B	801	GBM	C17-N9	2.73	1.45	1.39
2	A	801	GBM	O4-S2	2.69	1.46	1.43
2	A	801	GBM	O3-C17	-2.43	1.18	1.23
2	B	801	GBM	O3-C17	-2.27	1.18	1.23
2	A	801	GBM	O7-C28	2.12	1.40	1.37
2	A	801	GBM	O6-C26	-2.06	1.18	1.23

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	GBM	O5-S2-O4	-15.86	100.26	119.52
2	B	801	GBM	O5-S2-O4	-15.25	101.00	119.52
2	B	801	GBM	C18-S2-N9	3.53	111.69	106.06
2	A	801	GBM	C28-C27-C26	-3.21	120.44	126.24
2	B	801	GBM	O5-S2-C18	3.14	111.94	107.98
2	A	801	GBM	O5-S2-C18	2.99	111.75	107.98
2	A	801	GBM	C18-S2-N9	2.68	110.33	106.06
2	A	801	GBM	O7-C28-C30	-2.58	119.96	124.30
2	A	801	GBM	O7-C28-C27	2.55	120.26	116.55
2	A	801	GBM	N9-C17-N8	2.48	123.21	115.06
2	A	801	GBM	C11-N8-C17	-2.26	118.05	122.92
2	B	801	GBM	O4-S2-C18	2.18	110.73	107.98
2	A	801	GBM	O3-C17-N8	-2.10	118.19	122.67
2	A	801	GBM	C33-O7-C28	-2.00	114.57	117.51

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	GBM	O6-C26-C27-C28
2	A	801	GBM	N10-C26-C27-C28
2	A	801	GBM	C30-C28-O7-C33

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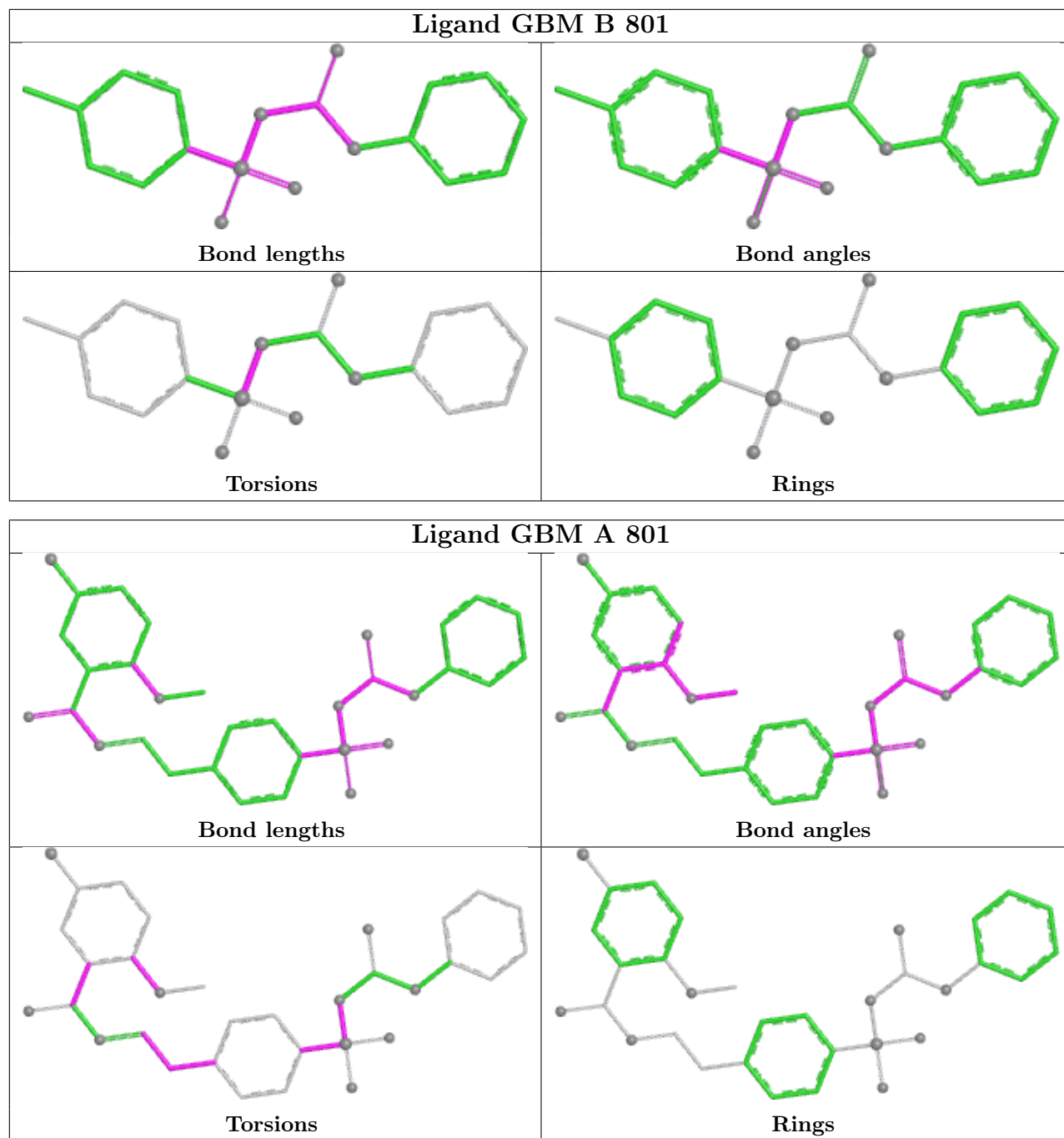
Mol	Chain	Res	Type	Atoms
2	A	801	GBM	C19-C20-C25-N10
2	A	801	GBM	C27-C28-O7-C33
2	A	801	GBM	C23-C19-C20-C25
2	A	801	GBM	C24-C19-C20-C25
2	B	801	GBM	C17-N9-S2-O5
2	A	801	GBM	C17-N9-S2-O5
2	A	801	GBM	C22-C18-S2-O5
2	A	801	GBM	C21-C18-S2-O5

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	801	GBM	1	0
2	A	801	GBM	1	0

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, 95th 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 ²)	Q<0.9
1	A	438/506 (86%)	-0.20	19 (4%) 40 39	16, 43, 79, 141	4 (0%)
1	B	445/506 (87%)	0.74	49 (11%) 10 8	35, 74, 116, 135	0
All	All	883/1012 (87%)	0.28	68 (7%) 19 17	16, 55, 111, 141	4 (0%)

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	547	TYR	7.3
1	B	360	SER	6.5
1	A	550	THR	6.0
1	B	247	HIS	5.1
1	B	607	GLN	5.1
1	A	251	ILE	4.9
1	B	402	THR	4.7
1	B	397	THR	4.7
1	A	707	LEU	4.5
1	B	697	SER	4.4
1	A	403	ARG	4.3
1	A	699	ASN	4.3
1	B	320	VAL	4.2
1	A	547	TYR	4.1
1	B	552	GLU	4.1
1	B	708	SER	4.0
1	B	683	ILE	3.9
1	B	694	GLN	3.9
1	B	632	GLU	3.7
1	B	726	ASN	3.7
1	A	252	LEU	3.7
1	B	319	PHE	3.6
1	A	402	THR	3.5
1	B	502	GLN	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	546	PHE	3.5
1	A	360	SER	3.4
1	A	388	VAL	3.3
1	B	245	HIS	3.3
1	A	548	LYS	3.3
1	A	280	ASP	3.3
1	B	608	ASN	3.2
1	B	746	TYR	3.2
1	B	557	SER	3.1
1	B	555	ILE	3.1
1	B	689	ILE	3.0
1	B	363	ILE	2.9
1	B	361	GLU	2.9
1	A	279	TYR	2.9
1	B	318	LEU	2.9
1	B	498	ASN	2.9
1	B	606	LEU	2.8
1	A	281	ILE	2.8
1	A	698	LEU	2.7
1	B	246	HIS	2.7
1	B	695	ARG	2.7
1	B	248	HIS	2.7
1	B	633	THR	2.7
1	A	282	SER	2.6
1	B	497	GLU	2.6
1	B	685	THR	2.6
1	B	375	TYR	2.6
1	B	554	ALA	2.6
1	A	549	THR	2.5
1	B	500	VAL	2.4
1	B	579	ALA	2.4
1	A	551	ASP	2.4
1	B	553	ASN	2.4
1	B	493	GLU	2.4
1	B	622	CYS	2.3
1	B	604	LYS	2.3
1	B	362	THR	2.2
1	B	679	TRP	2.2
1	B	304	LYS	2.2
1	B	559	CYS	2.1
1	B	727	MET	2.1
1	A	497	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	558	TYR	2.0
1	B	481	TYR	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 oligosaccharides 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, 95th 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.

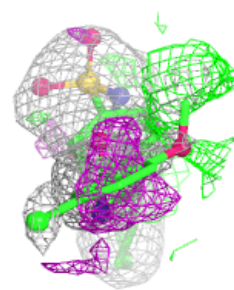
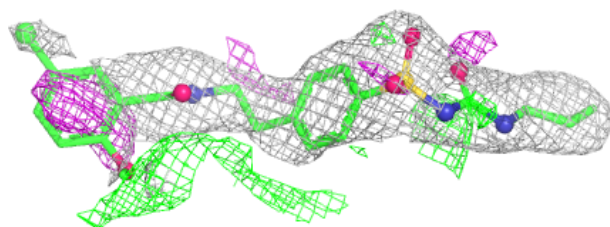
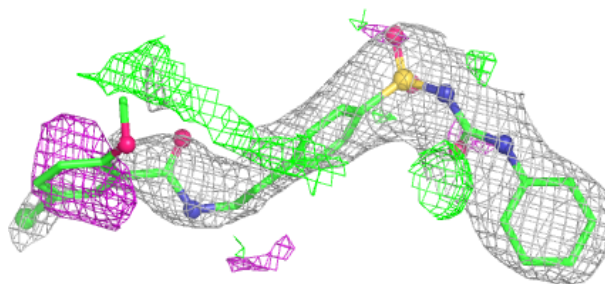
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	EDO	B	806	4/4	0.75	0.31	75,79,80,83	0
4	FMT	A	807	3/3	0.76	0.26	74,74,79,80	0
4	FMT	A	806	3/3	0.80	0.29	76,76,77,78	0
4	FMT	A	804	3/3	0.81	0.34	80,80,80,81	0
4	FMT	A	808	3/3	0.81	0.23	81,81,82,82	0
4	FMT	A	803	3/3	0.81	0.27	55,55,58,59	0
4	FMT	B	805	3/3	0.84	0.20	74,74,75,76	0
2	GBM	A	801	33/33	0.84	0.23	53,84,128,129	0
4	FMT	A	810	3/3	0.85	0.18	78,78,81,82	0
4	FMT	A	811	3/3	0.86	0.27	67,67,70,70	0
5	EDO	A	813	4/4	0.88	0.28	78,78,78,79	0
4	FMT	B	804	3/3	0.88	0.21	82,82,84,84	0
4	FMT	A	812	3/3	0.91	0.22	84,84,85,86	0
4	FMT	B	802	3/3	0.91	0.20	64,64,66,67	0
4	FMT	A	809	3/3	0.91	0.14	57,57,61,64	0
2	GBM	B	801	20/33	0.92	0.13	44,57,66,67	0
4	FMT	A	805	3/3	0.94	0.11	70,70,71,71	0
4	FMT	B	803	3/3	0.96	0.10	67,67,68,68	0
3	CL	A	802	1/1	0.99	0.05	39,39,39,39	0

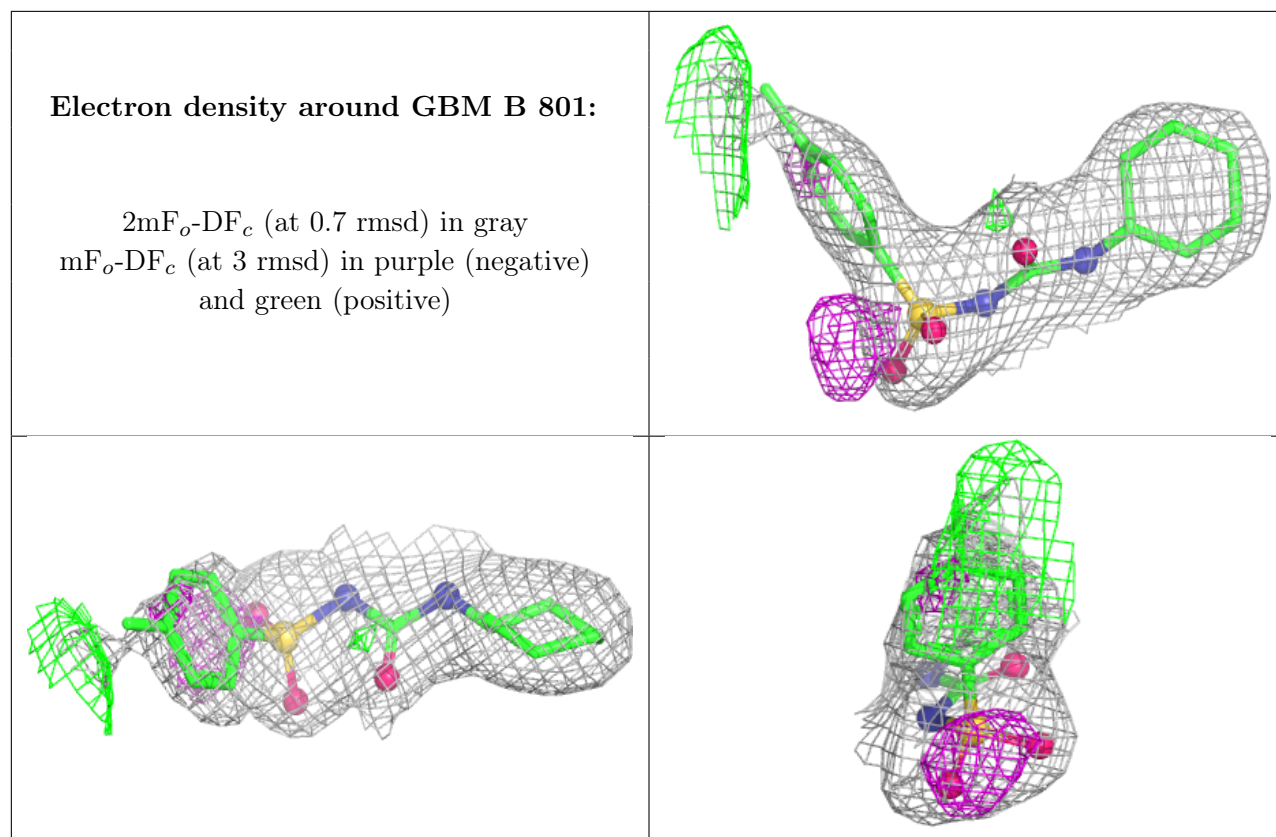
The following is a graphical depiction of the model fit to experimental electron density of all

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.

Electron density around GBM A 801:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers [i](#)

There are no such residues in this entry.