



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 01:59 am BST

PDB ID : 4N1X
Title : Structure of a putative peptidoglycan glycosyltransferase from *Atopobium parvulum* in complex with penicillin G
Authors : Filippova, E.V.; Minasov, G.; Shuvalova, L.; Kiryukhina, O.; Babnigg, G.; Rubin, E.; Sacchettini, J.; Joachimiak, A.; Anderson, W.F.; Midwest Center for Structural Genomics (MCSG); Structures of Mtb Proteins Conferring Susceptibility to Known Mtb Inhibitors (MTBI)
Deposited on : 2013-10-04
Resolution : 2.00 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 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	:	2.11
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)	:	2.11

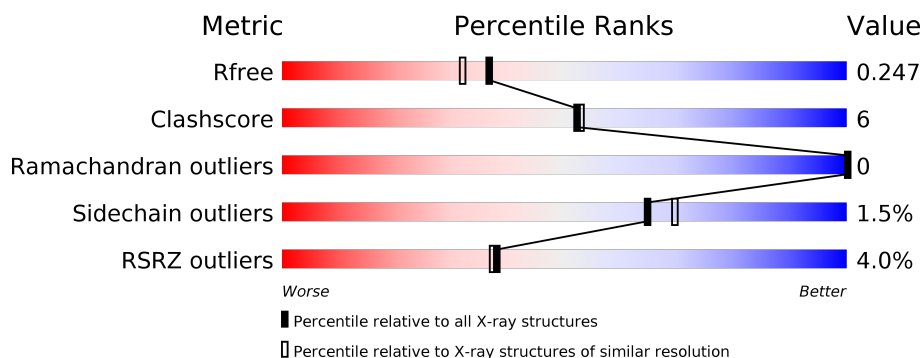
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 ≥ 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	472	<div> <div>3%</div> <div> <div></div> <div>78%</div> <div>9%</div> <div>12%</div> </div> </div>
1	B	472	<div> <div>4%</div> <div> <div></div> <div>78%</div> <div>9%</div> <div>13%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6813 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	414	Total	C	N	O	S	Se	0	0	0
			2975	1848	505	607	2	13			
1	B	412	Total	C	N	O	S	Se	0	3	0
			2976	1851	505	605	2	13			

There are 64 discrepancies between the modelled and reference sequences:

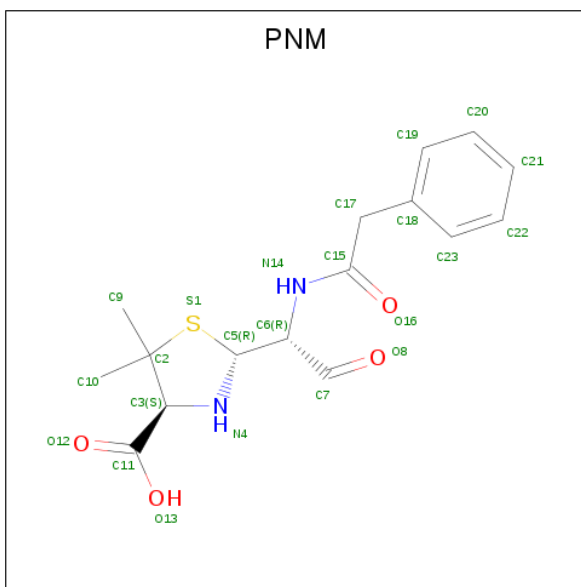
Chain	Residue	Modelled	Actual	Comment	Reference
A	483	MSE	-	EXPRESSION TAG	UNP C8W8H7
A	484	HIS	-	EXPRESSION TAG	UNP C8W8H7
A	485	HIS	-	EXPRESSION TAG	UNP C8W8H7
A	486	HIS	-	EXPRESSION TAG	UNP C8W8H7
A	487	HIS	-	EXPRESSION TAG	UNP C8W8H7
A	488	HIS	-	EXPRESSION TAG	UNP C8W8H7
A	489	HIS	-	EXPRESSION TAG	UNP C8W8H7
A	490	SER	-	EXPRESSION TAG	UNP C8W8H7
A	491	SER	-	EXPRESSION TAG	UNP C8W8H7
A	492	GLY	-	EXPRESSION TAG	UNP C8W8H7
A	493	VAL	-	EXPRESSION TAG	UNP C8W8H7
A	494	ASP	-	EXPRESSION TAG	UNP C8W8H7
A	495	LEU	-	EXPRESSION TAG	UNP C8W8H7
A	496	TRP	-	EXPRESSION TAG	UNP C8W8H7
A	497	SER	-	EXPRESSION TAG	UNP C8W8H7
A	498	HIS	-	EXPRESSION TAG	UNP C8W8H7
A	499	PRO	-	EXPRESSION TAG	UNP C8W8H7
A	500	GLN	-	EXPRESSION TAG	UNP C8W8H7
A	501	PHE	-	EXPRESSION TAG	UNP C8W8H7
A	502	GLU	-	EXPRESSION TAG	UNP C8W8H7
A	503	LYS	-	EXPRESSION TAG	UNP C8W8H7
A	504	GLY	-	EXPRESSION TAG	UNP C8W8H7
A	505	THR	-	EXPRESSION TAG	UNP C8W8H7
A	506	GLU	-	EXPRESSION TAG	UNP C8W8H7
A	507	ASN	-	EXPRESSION TAG	UNP C8W8H7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	508	LEU	-	EXPRESSION TAG	UNP C8W8H7
A	509	TYR	-	EXPRESSION TAG	UNP C8W8H7
A	510	PHE	-	EXPRESSION TAG	UNP C8W8H7
A	511	GLN	-	EXPRESSION TAG	UNP C8W8H7
A	512	SER	-	EXPRESSION TAG	UNP C8W8H7
A	513	ASN	-	EXPRESSION TAG	UNP C8W8H7
A	514	ALA	-	EXPRESSION TAG	UNP C8W8H7
B	483	MSE	-	EXPRESSION TAG	UNP C8W8H7
B	484	HIS	-	EXPRESSION TAG	UNP C8W8H7
B	485	HIS	-	EXPRESSION TAG	UNP C8W8H7
B	486	HIS	-	EXPRESSION TAG	UNP C8W8H7
B	487	HIS	-	EXPRESSION TAG	UNP C8W8H7
B	488	HIS	-	EXPRESSION TAG	UNP C8W8H7
B	489	HIS	-	EXPRESSION TAG	UNP C8W8H7
B	490	SER	-	EXPRESSION TAG	UNP C8W8H7
B	491	SER	-	EXPRESSION TAG	UNP C8W8H7
B	492	GLY	-	EXPRESSION TAG	UNP C8W8H7
B	493	VAL	-	EXPRESSION TAG	UNP C8W8H7
B	494	ASP	-	EXPRESSION TAG	UNP C8W8H7
B	495	LEU	-	EXPRESSION TAG	UNP C8W8H7
B	496	TRP	-	EXPRESSION TAG	UNP C8W8H7
B	497	SER	-	EXPRESSION TAG	UNP C8W8H7
B	498	HIS	-	EXPRESSION TAG	UNP C8W8H7
B	499	PRO	-	EXPRESSION TAG	UNP C8W8H7
B	500	GLN	-	EXPRESSION TAG	UNP C8W8H7
B	501	PHE	-	EXPRESSION TAG	UNP C8W8H7
B	502	GLU	-	EXPRESSION TAG	UNP C8W8H7
B	503	LYS	-	EXPRESSION TAG	UNP C8W8H7
B	504	GLY	-	EXPRESSION TAG	UNP C8W8H7
B	505	THR	-	EXPRESSION TAG	UNP C8W8H7
B	506	GLU	-	EXPRESSION TAG	UNP C8W8H7
B	507	ASN	-	EXPRESSION TAG	UNP C8W8H7
B	508	LEU	-	EXPRESSION TAG	UNP C8W8H7
B	509	TYR	-	EXPRESSION TAG	UNP C8W8H7
B	510	PHE	-	EXPRESSION TAG	UNP C8W8H7
B	511	GLN	-	EXPRESSION TAG	UNP C8W8H7
B	512	SER	-	EXPRESSION TAG	UNP C8W8H7
B	513	ASN	-	EXPRESSION TAG	UNP C8W8H7
B	514	ALA	-	EXPRESSION TAG	UNP C8W8H7

- Molecule 2 is OPEN FORM - PENICILLIN G (three-letter code: PNM) (formula: C₁₆H₂₀N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 23	C 16	N 2	O 4	S 1	0	0
2	B	1	Total 23	C 16	N 2	O 4	S 1	0	0

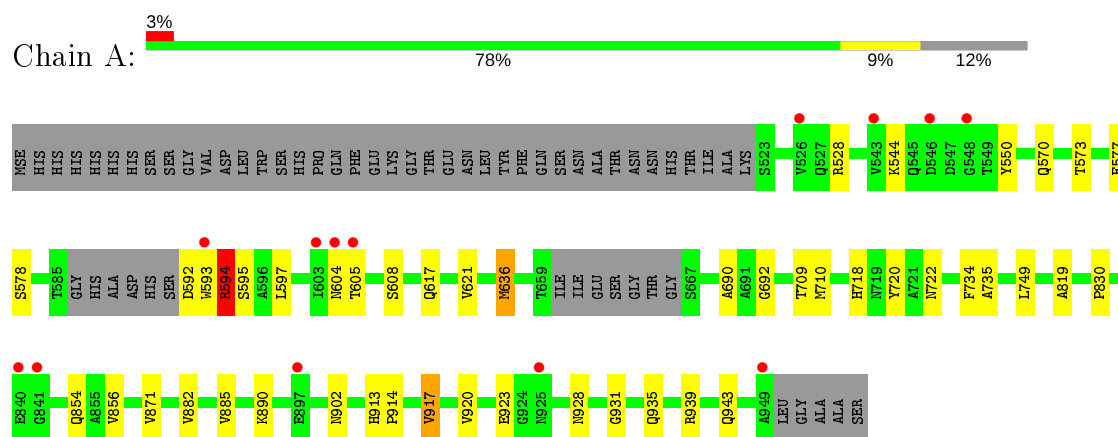
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	425	Total O 435 435	0	10
3	B	375	Total O 381 381	0	6

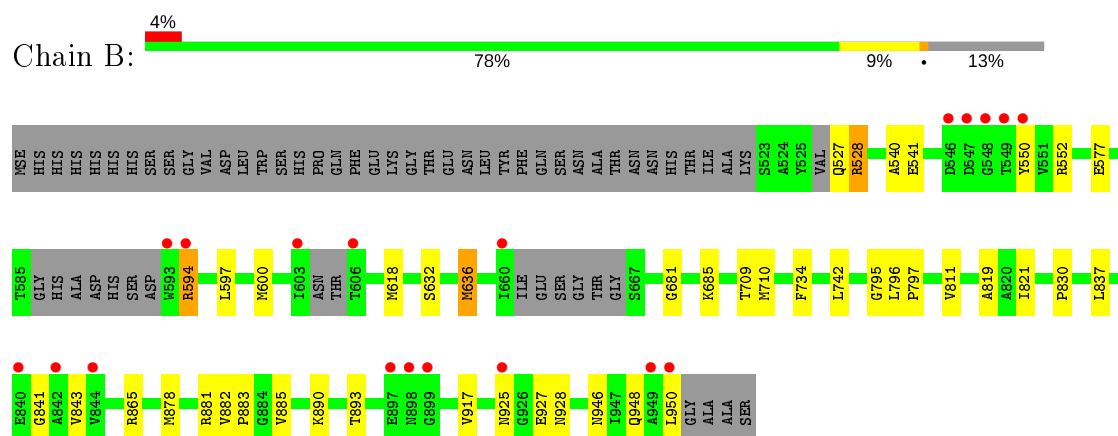
3 Residue-property plots [i](#)

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: 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, α , β , γ	68.62Å 70.14Å 115.34Å 90.00° 96.39° 90.00°	Depositor
Resolution (Å)	29.93 – 2.00 29.71 – 2.00	Depositor EDS
% Data completeness (in resolution range)	95.9 (29.93-2.00) 96.0 (29.71-2.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.68 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.200 , 0.237 0.214 , 0.247	Depositor DCC
R_{free} test set	3549 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	22.1	Xtriage
Anisotropy	0.052	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 53.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6813	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.02% 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: PNM

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	0.82	0/3014	0.96	2/4091 (0.0%)
1	B	0.75	0/3013	0.91	2/4087 (0.0%)
All	All	0.78	0/6027	0.94	4/8178 (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	636	MSE	N-CA-CB	-5.75	100.24	110.60
1	A	594	ARG	CB-CA-C	-5.74	98.91	110.40
1	B	925	ASN	N-CA-C	5.38	125.53	111.00
1	A	920	VAL	CB-CA-C	-5.06	101.78	111.40

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	2975	0	2885	32	0
1	B	2976	0	2894	33	0
2	A	23	0	18	1	0
2	B	23	0	18	1	0
3	A	435	0	0	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	381	0	0	3	0
All	All	6813	0	5815	65	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 6.

All (65) 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:594:ARG:HD3	1:B:594:ARG:H	1.20	1.06
1:A:605:THR:HB	3:A:1370:HOH:O	1.77	0.85
1:B:594:ARG:N	1:B:594:ARG:HD3	1.97	0.80
1:A:593:TRP:HB2	3:A:1215:HOH:O	1.83	0.79
1:A:592:ASP:OD1	1:A:593:TRP:N	2.21	0.73
1:B:878:MSE:HE2	1:B:881:ARG:CZ	2.22	0.70
1:B:878:MSE:HE2	1:B:881:ARG:NH1	2.08	0.68
1:B:528:ARG:NH1	1:B:577:GLU:O	2.27	0.68
1:B:528:ARG:HG2	1:B:552:ARG:NH1	2.11	0.66
1:B:841:GLY:HA2	3:B:1204:HOH:O	1.95	0.66
1:B:528:ARG:HG2	1:B:552:ARG:CZ	2.27	0.65
1:A:720:TYR:HB2	2:A:1001:PNM:S1	2.40	0.61
1:B:597:LEU:HD22	1:B:600:MSE:HE2	1.82	0.61
1:A:528:ARG:NH1	1:A:577:GLU:O	2.34	0.60
1:A:939:ARG:HG3	1:A:943:GLN:HE21	1.67	0.59
1:A:544:LYS:HB2	1:A:550:TYR:CE2	2.38	0.58
1:A:570:GLN:HG3	3:A:1246:HOH:O	2.03	0.58
1:A:939:ARG:NH2	3:A:1390:HOH:O	2.37	0.58
1:B:946:ASN:O	1:B:950:LEU:HD13	2.04	0.58
1:A:718:HIS:HB2	1:A:722:ASN:ND2	2.19	0.56
1:A:597:LEU:HD12	1:A:597:LEU:N	2.21	0.56
1:B:597:LEU:HB2	1:B:600:MSE:HE2	1.88	0.56
1:A:636:MSE:HE1	1:A:830:PRO:HB3	1.89	0.54
1:B:948:GLN:HG2	3:B:1463:HOH:O	2.07	0.54
1:A:854:GLN:HG2	3:A:1282:HOH:O	2.09	0.52
1:A:573:THR:HB	1:A:578:SER:HB2	1.92	0.51
1:A:734:PHE:CZ	1:A:890:LYS:HD3	2.45	0.51
1:A:605:THR:CB	3:A:1370:HOH:O	2.45	0.51
1:A:819:ALA:HA	1:A:917:VAL:HG21	1.91	0.50
1:B:882:VAL:HB	1:B:885:VAL:HG13	1.94	0.50
1:B:681:GLY:O	1:B:795:GLY:HA3	2.11	0.50
1:A:735:ALA:HA	1:A:871:VAL:HG22	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:597:LEU:CD1	1:A:597:LEU:N	2.76	0.49
1:B:618:MSE:HE1	1:B:948:GLN:HG3	1.95	0.49
1:A:636:MSE:CE	1:A:830:PRO:HB3	2.43	0.48
1:B:685:LYS:HD3	1:B:742:LEU:HG	1.94	0.48
3:A:1369:HOH:O	1:B:883:PRO:HG3	2.13	0.48
1:A:718:HIS:CE1	3:A:1124:HOH:O	2.66	0.47
1:B:636:MSE:HE2	1:B:830:PRO:HB3	1.96	0.47
1:B:734:PHE:CZ	1:B:890:LYS:HD3	2.49	0.47
1:B:594:ARG:HB2	1:B:600:MSE:CE	2.44	0.47
1:B:893:THR:HG22	2:B:1001:PNM:C22	2.44	0.47
1:B:819:ALA:HA	1:B:917:VAL:HG21	1.95	0.47
1:B:837:LEU:HD23	1:B:843:VAL:HA	1.98	0.46
1:B:594:ARG:HB2	1:B:600:MSE:HE1	1.98	0.45
1:B:527:GLN:HB2	1:B:550:TYR:CZ	2.52	0.45
1:A:594:ARG:HG2	1:A:595:SER:N	2.31	0.45
1:A:913:HIS:N	1:A:914:PRO:CD	2.80	0.45
1:A:928:ASN:OD1	1:A:928:ASN:C	2.54	0.44
1:B:540:ALA:O	1:B:541:GLU:HB2	2.18	0.44
1:A:617:GLN:O	1:A:621:VAL:HG23	2.18	0.43
1:B:710:MSE:HE2	3:B:1449:HOH:O	2.19	0.42
1:B:632:SER:OG	1:B:811:VAL:HG21	2.19	0.42
1:B:540:ALA:O	1:B:541:GLU:CB	2.67	0.42
1:B:597:LEU:N	1:B:597:LEU:HD12	2.35	0.41
1:A:902:ASN:OD1	1:A:923:GLU:HA	2.20	0.41
1:B:821:ILE:HG22	1:B:865:ARG:HG2	2.02	0.41
1:A:913:HIS:N	1:A:914:PRO:HD3	2.36	0.41
1:A:690:ALA:HB1	1:A:856:VAL:HG11	2.03	0.41
1:A:882:VAL:HB	1:A:885:VAL:CG1	2.50	0.41
1:A:931:GLY:O	1:A:935:GLN:HG3	2.20	0.41
1:B:796[B]:LEU:HA	1:B:797:PRO:HD2	1.90	0.41
1:A:692:GLY:HA2	1:A:749:LEU:HD21	2.04	0.40
1:A:594:ARG:HD2	1:A:604:ASN:ND2	2.35	0.40
1:B:927:GLU:HG2	1:B:928:ASN:N	2.36	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	408/472 (86%)	398 (98%)	10 (2%)	0	100	100
1	B	405/472 (86%)	392 (97%)	13 (3%)	0	100	100
All	All	813/944 (86%)	790 (97%)	23 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	312/348 (90%)	306 (98%)	6 (2%)	57	61
1	B	311/348 (89%)	308 (99%)	3 (1%)	76	81
All	All	623/696 (90%)	614 (99%)	9 (1%)	65	72

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	594	ARG
1	A	608	SER
1	A	636	MSE
1	A	709	THR
1	A	710	MSE
1	A	917	VAL
1	B	528	ARG
1	B	594	ARG

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Mol	Chain	Res	Type
1	B	709	THR

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	722	ASN
1	A	900	ASN
1	A	943	GLN
1	B	527	GLN
1	B	627	GLN
1	B	718	HIS
1	B	722	ASN
1	B	900	ASN
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](#)

2 ligands are 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	PNM	B	1001	1	17,24,24	1.18	2 (11%)	22,34,34	1.54	3 (13%)
2	PNM	A	1001	1	17,24,24	0.87	0	22,34,34	1.45	4 (18%)

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	PNM	B	1001	1	-	4/8/33/33	0/2/2/2
2	PNM	A	1001	1	-	4/8/33/33	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1001	PNM	C2-S1	-2.57	1.80	1.85
2	B	1001	PNM	O8-C7	2.27	1.29	1.19

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1001	PNM	C10-C2-S1	3.88	115.72	109.21
2	B	1001	PNM	C9-C2-C10	-3.84	104.53	110.78
2	A	1001	PNM	C6-N14-C15	-3.68	119.19	123.13
2	A	1001	PNM	C5-C6-N14	2.91	116.33	109.98
2	A	1001	PNM	C17-C15-N14	2.53	119.95	115.88
2	B	1001	PNM	C5-C6-N14	2.38	115.16	109.98
2	A	1001	PNM	O8-C7-C6	-2.01	119.22	124.83

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1001	PNM	C15-C17-C18-C19
2	A	1001	PNM	C15-C17-C18-C23
2	B	1001	PNM	O16-C15-C17-C18
2	B	1001	PNM	C15-C17-C18-C23
2	B	1001	PNM	C15-C17-C18-C19
2	B	1001	PNM	N14-C15-C17-C18
2	A	1001	PNM	O16-C15-C17-C18

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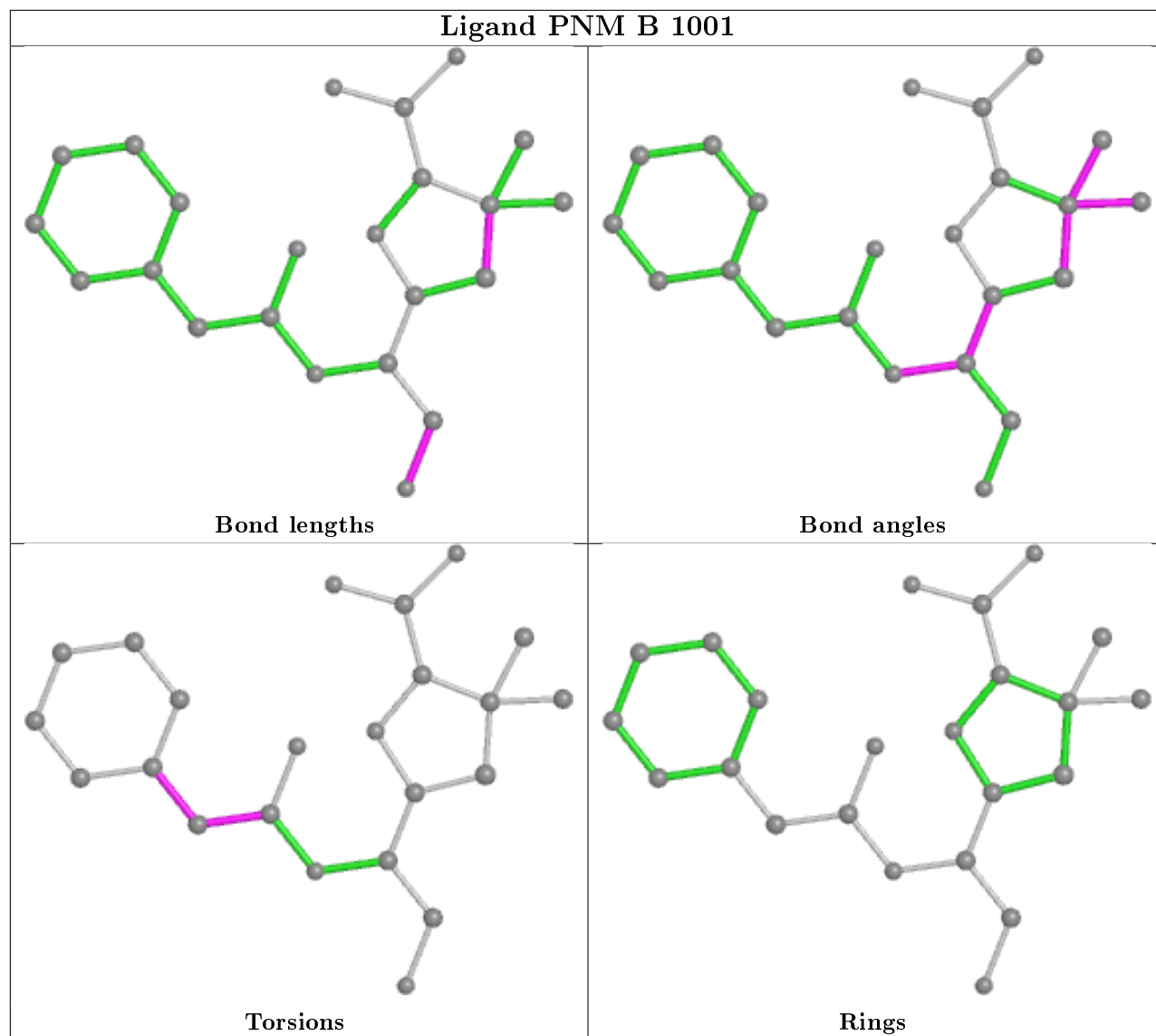
Mol	Chain	Res	Type	Atoms
2	A	1001	PNM	N14-C15-C17-C18

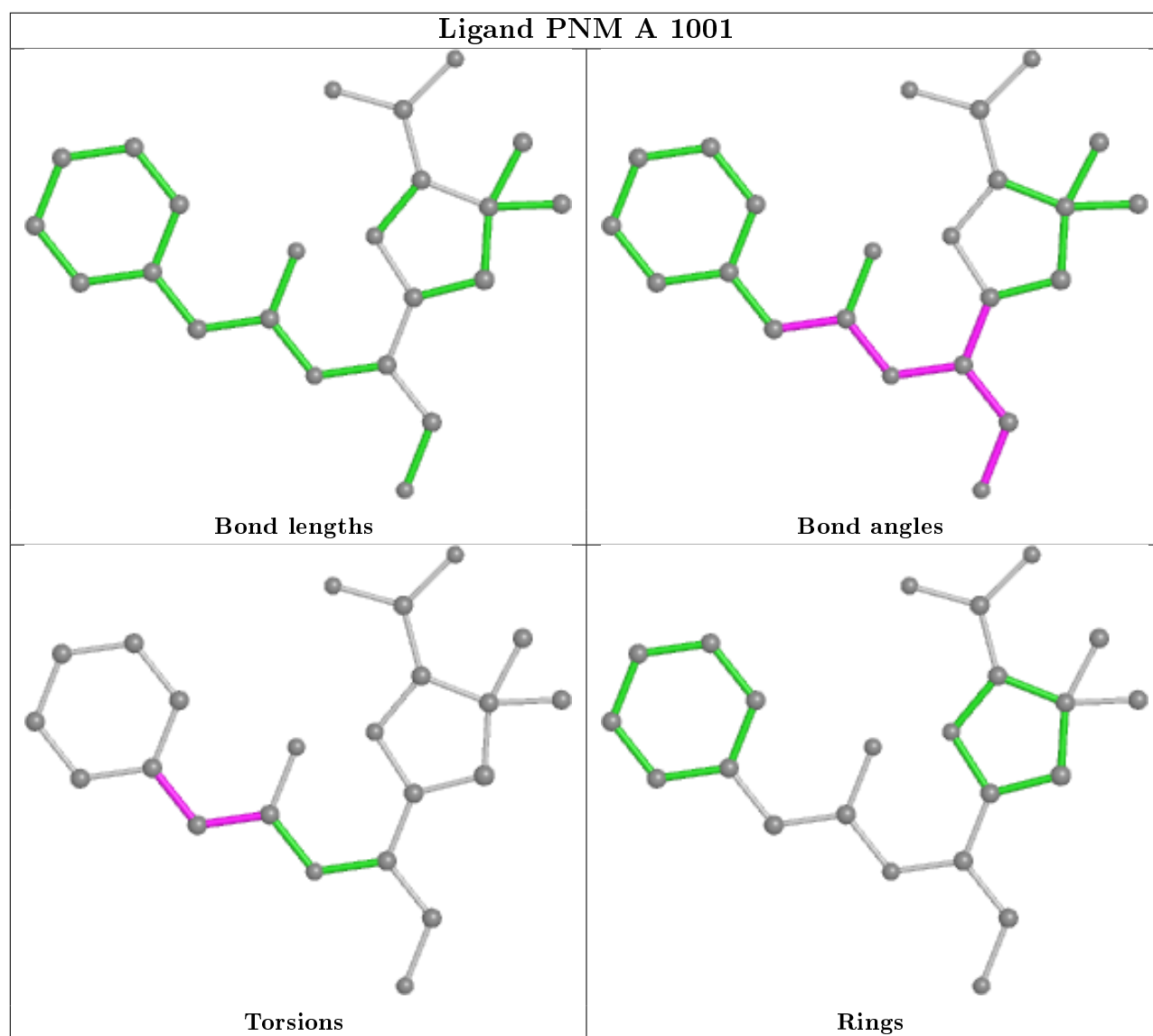
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1001	PNM	1	0
2	A	1001	PNM	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	401/472 (84%)	0.04	13 (3%) 47 46	11, 23, 59, 93	0
1	B	399/472 (84%)	0.07	19 (4%) 30 29	13, 24, 61, 77	0
All	All	800/944 (84%)	0.06	32 (4%) 38 37	11, 23, 59, 93	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	949	ALA	5.9
1	B	593	TRP	4.9
1	B	898	ASN	4.8
1	B	842	ALA	4.3
1	B	925	ASN	4.1
1	A	897	GLU	3.7
1	B	897	GLU	3.7
1	A	949	ALA	3.6
1	A	605	THR	3.6
1	B	606	THR	3.4
1	A	603	ILE	3.4
1	B	950	LEU	3.4
1	B	840	GLU	3.2
1	B	548	GLY	3.2
1	B	550	TYR	3.1
1	B	660	ILE	3.1
1	A	543	VAL	3.1
1	B	899	GLY	3.0
1	A	548	GLY	3.0
1	A	925	ASN	3.0
1	A	526	VAL	2.9
1	A	593	TRP	2.9
1	A	841	GLY	2.8
1	A	546	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	594	ARG	2.3
1	A	604	ASN	2.3
1	A	840	GLU	2.3
1	B	547	ASP	2.2
1	B	844	VAL	2.1
1	B	546	ASP	2.1
1	B	549	THR	2.1
1	B	603	ILE	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](#)

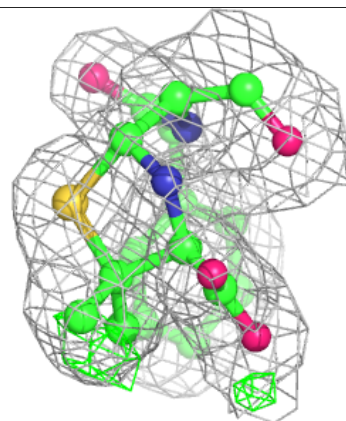
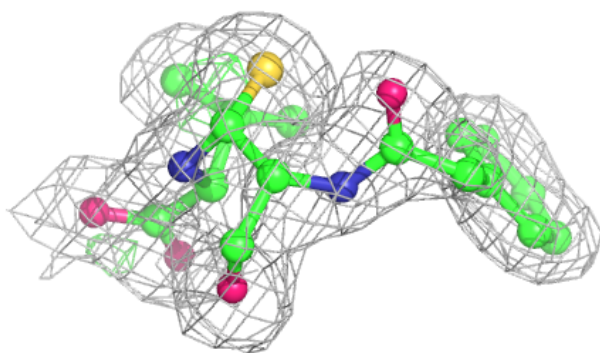
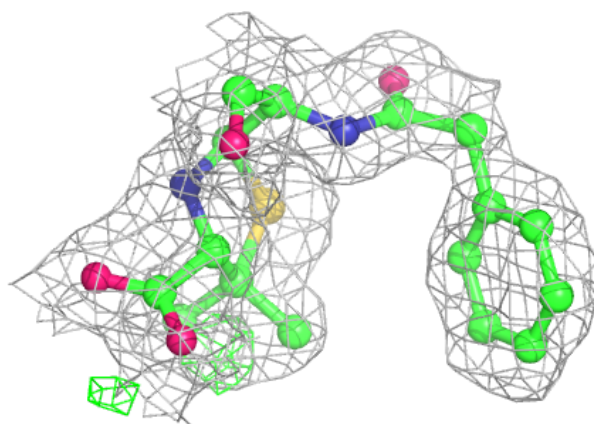
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	PNM	B	1001	23/23	0.92	0.10	17,26,33,36	0
2	PNM	A	1001	23/23	0.93	0.11	15,28,30,30	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.

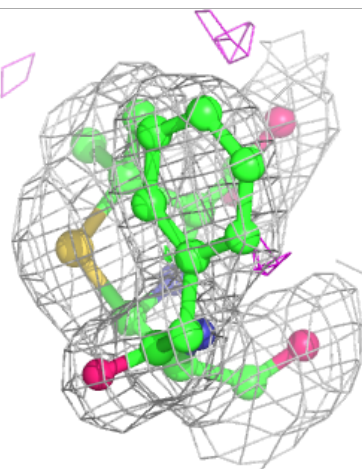
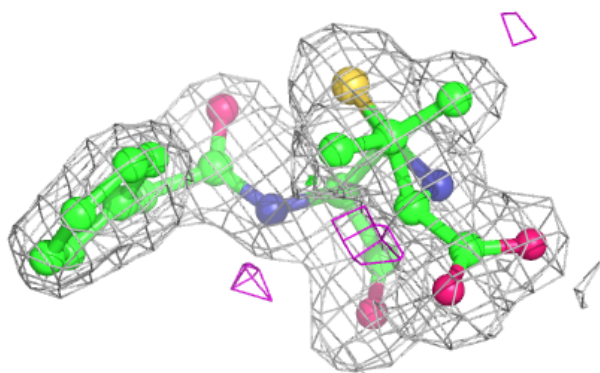
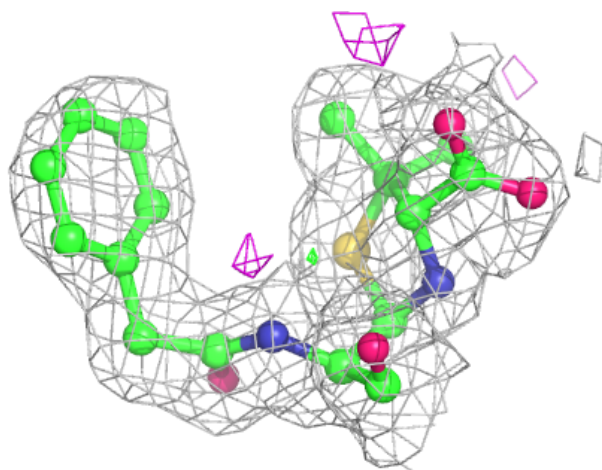
Electron density around PNM B 1001:

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



Electron density around PNM A 1001:

$2mF_o-DF_c$ (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.