



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:52 PM UTC

PDB ID : 9MKC / pdb_00009mkc
Title : Crystal structure of MALT1 in complex with an allosteric inhibitor
Authors : Bell, J.A.
Deposited on : 2024-12-17
Resolution : 2.80 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

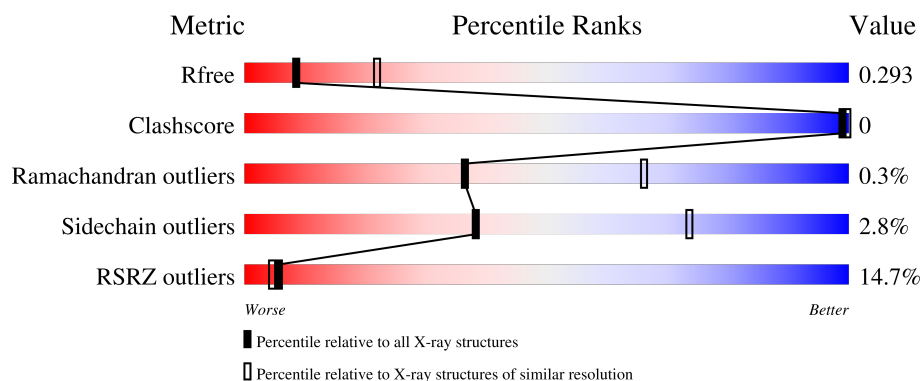
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	386	13% 85% 7% • 8%
1	B	386	14% 87% 5% • 8%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 11449 atoms, of which 5716 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.

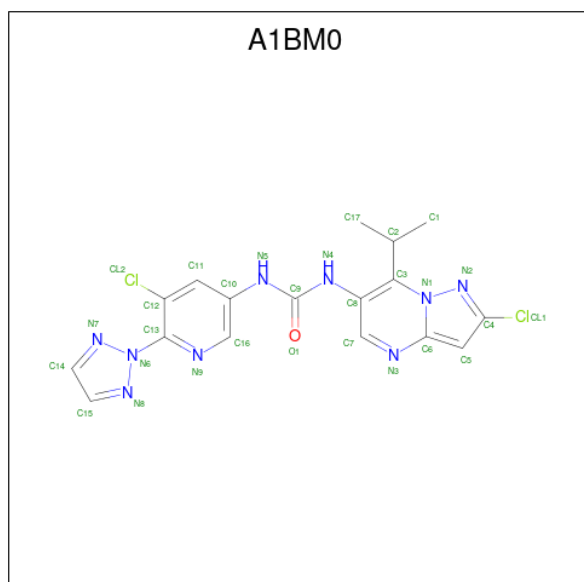
- Molecule 1 is a protein called Mucosa-associated lymphoid tissue lymphoma translocation protein 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	356	Total	C	H	N	O	S	0	0	0
			5669	1812	2839	460	538	20			
1	B	357	Total	C	H	N	O	S	0	0	0
			5684	1817	2847	461	539	20			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	Ca	0	0
			4	4		
2	B	4	Total	Ca	0	0
			4	4		

- Molecule 3 is N-[(8R)-2-chloro-7-(propan-2-yl)pyrazolo[1,5-a]pyrimidin-6-yl]-N'-[5-chloro-6-(2H-1,2,3-triazol-2-yl)pyridin-3-yl]urea (CCD ID: A1BM0) (formula: C₁₇H₁₅Cl₂N₉O) (labeled as "Ligand of Interest" by depositor).

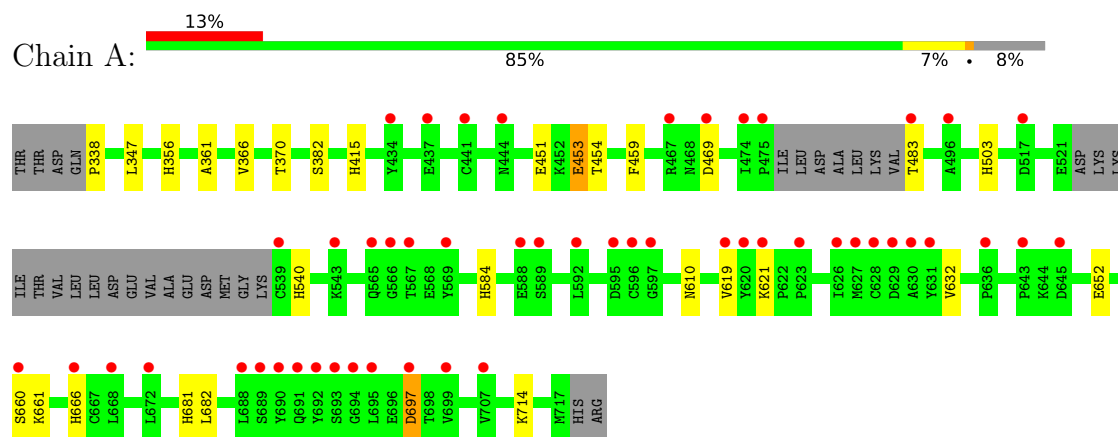


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	Cl	H	N	O	0	0
			44	17	2	15	9	1		
3	B	1	Total	C	Cl	H	N	O	0	0
			44	17	2	15	9	1		

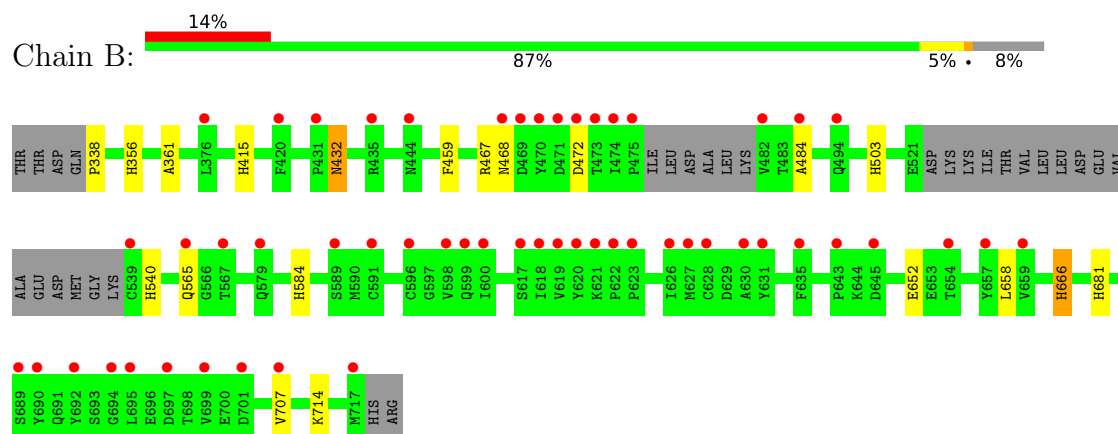
3 Residue-property plots [i](#)

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: Mucosa-associated lymphoid tissue lymphoma translocation protein 1



- Molecule 1: Mucosa-associated lymphoid tissue lymphoma translocation protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	72.66Å 77.15Å 92.47Å 90.00° 93.59° 90.00°	Depositor
Resolution (Å)	34.10 – 2.80 34.10 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (34.10-2.80) 99.9 (34.10-2.80)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 2.68Å)	Xtriage
Refinement program	PRIME-X	Depositor
R, R_{free}	0.281 , 0.305 0.273 , 0.293	Depositor DCC
R_{free} test set	1335 reflections (4.73%)	wwPDB-VP
Wilson B-factor (Å ²)	59.2	Xtriage
Anisotropy	0.549	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 35.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	11449	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.84% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, A1BM0

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	0.59	1/2884 (0.0%)	1.14	14/3899 (0.4%)
1	B	0.59	1/2891 (0.0%)	1.13	13/3909 (0.3%)
All	All	0.59	2/5775 (0.0%)	1.13	27/7808 (0.3%)

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 (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	503	HIS	CG-CD2	5.27	1.41	1.35
1	A	503	HIS	CG-CD2	5.01	1.41	1.35

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	472	ASP	N-CA-C	6.98	118.97	111.36
1	A	469	ASP	CA-CB-CG	6.74	119.34	112.60
1	A	459	PHE	CA-CB-CG	6.40	120.20	113.80
1	B	472	ASP	CA-CB-CG	6.00	118.60	112.60
1	A	584	HIS	ND1-CE1-NE2	5.99	114.39	108.40
1	B	584	HIS	ND1-CE1-NE2	5.89	114.29	108.40
1	A	356	HIS	ND1-CE1-NE2	5.81	114.21	108.40
1	B	540	HIS	ND1-CE1-NE2	5.80	114.20	108.40
1	A	540	HIS	ND1-CE1-NE2	5.77	114.17	108.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	361	ALA	N-CA-C	5.75	121.36	113.77
1	A	666	HIS	ND1-CE1-NE2	5.74	114.14	108.40
1	A	681	HIS	ND1-CE1-NE2	5.74	114.14	108.40
1	B	356	HIS	ND1-CE1-NE2	5.74	114.14	108.40
1	B	681	HIS	ND1-CE1-NE2	5.74	114.14	108.40
1	B	415	HIS	ND1-CE1-NE2	5.71	114.11	108.40
1	B	666	HIS	ND1-CE1-NE2	5.71	114.11	108.40
1	B	459	PHE	CA-CB-CG	5.71	119.51	113.80
1	A	415	HIS	ND1-CE1-NE2	5.68	114.08	108.40
1	B	468	ASN	CA-CB-CG	5.51	118.11	112.60
1	A	453	GLU	CB-CA-C	5.45	121.04	111.06
1	B	338	PRO	CA-N-CD	-5.27	104.63	112.00
1	A	361	ALA	N-CA-C	5.20	120.54	113.16
1	A	338	PRO	CA-N-CD	-5.16	104.78	112.00
1	B	432	ASN	CA-CB-CG	5.11	117.70	112.60
1	A	610	ASN	CA-CB-CG	5.10	117.70	112.60
1	A	661	LYS	CB-CA-C	5.07	118.95	110.44
1	A	697	ASP	CA-CB-CG	5.03	117.63	112.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	484	ALA	Peptide

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	2830	2839	2833	3	0
1	B	2837	2847	2842	0	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0
3	A	29	15	0	1	0
3	B	29	15	0	1	0
All	All	5733	5716	5675	5	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 0.

All (5) 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:366:VAL:O	1:A:370:THR:HG23	2.11	0.50
1:A:370:THR:HG21	1:A:382:SER:HB3	1.93	0.49
3:B:1005:A1BM0:CL2	3:B:1005:A1BM0:N8	2.88	0.44
3:A:1005:A1BM0:CL2	3:A:1005:A1BM0:N8	2.89	0.42
1:A:347:LEU:HD13	1:A:370:THR:HG22	2.02	0.41

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	350/386 (91%)	335 (96%)	14 (4%)	1 (0%)	36	66
1	B	351/386 (91%)	333 (95%)	17 (5%)	1 (0%)	36	66
All	All	701/772 (91%)	668 (95%)	31 (4%)	2 (0%)	36	66

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	660	SER
1	B	666	HIS

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	316/343 (92%)	305 (96%)	11 (4%)	32	67
1	B	317/343 (92%)	310 (98%)	7 (2%)	45	78
All	All	633/686 (92%)	615 (97%)	18 (3%)	38	73

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	451	GLU
1	A	453	GLU
1	A	454	THR
1	A	483	THR
1	A	619	VAL
1	A	621	LYS
1	A	632	VAL
1	A	652	GLU
1	A	682	LEU
1	A	697	ASP
1	A	714	LYS
1	B	432	ASN
1	B	467	ARG
1	B	565	GLN
1	B	652	GLU
1	B	658	LEU
1	B	707	VAL
1	B	714	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	371	ASN
1	A	375	GLN
1	A	579	GLN
1	B	375	GLN
1	B	419	ASN
1	B	432	ASN
1	B	450	GLN
1	B	457	ASN
1	B	508	ASN
1	B	546	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 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	$\# Z > 2$
3	A1BM0	A	1005	-	31,32,32	1.77	7 (22%)	38,46,46	1.10	2 (5%)
3	A1BM0	B	1005	-	31,32,32	1.80	7 (22%)	38,46,46	1.24	5 (13%)

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
3	A1BM0	A	1005	-	-	4/15/16/16	0/4/4/4
3	A1BM0	B	1005	-	-	6/15/16/16	0/4/4/4

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1005	A1BM0	N6-N7	4.65	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1005	A1BM0	N6-N7	4.42	1.39	1.33
3	B	1005	A1BM0	C12-C13	3.90	1.44	1.39
3	A	1005	A1BM0	N6-N8	3.70	1.38	1.33
3	A	1005	A1BM0	C12-C13	3.58	1.43	1.39
3	B	1005	A1BM0	N6-N8	3.53	1.38	1.33
3	B	1005	A1BM0	C6-N1	2.90	1.43	1.39
3	B	1005	A1BM0	C5-C6	-2.70	1.35	1.38
3	B	1005	A1BM0	C2-C3	2.54	1.54	1.51
3	A	1005	A1BM0	C6-N1	2.51	1.43	1.39
3	A	1005	A1BM0	C2-C3	2.46	1.54	1.51
3	A	1005	A1BM0	C5-C6	-2.39	1.35	1.38
3	B	1005	A1BM0	C4-CL1	-2.27	1.68	1.73
3	A	1005	A1BM0	C4-CL1	-2.22	1.68	1.73

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1005	A1BM0	C14-N7-N6	-2.34	100.21	103.42
3	B	1005	A1BM0	C5-C4-CL1	-2.28	123.42	126.64
3	A	1005	A1BM0	C14-N7-N6	-2.25	100.34	103.42
3	B	1005	A1BM0	C4-N2-N1	-2.07	102.26	104.66
3	A	1005	A1BM0	C5-C4-CL1	-2.04	123.76	126.64
3	B	1005	A1BM0	C15-C14-N7	2.01	111.74	109.06
3	B	1005	A1BM0	C8-N4-C9	-2.01	123.26	124.85

There are no chirality outliers.

All (10) torsion outliers are listed below:

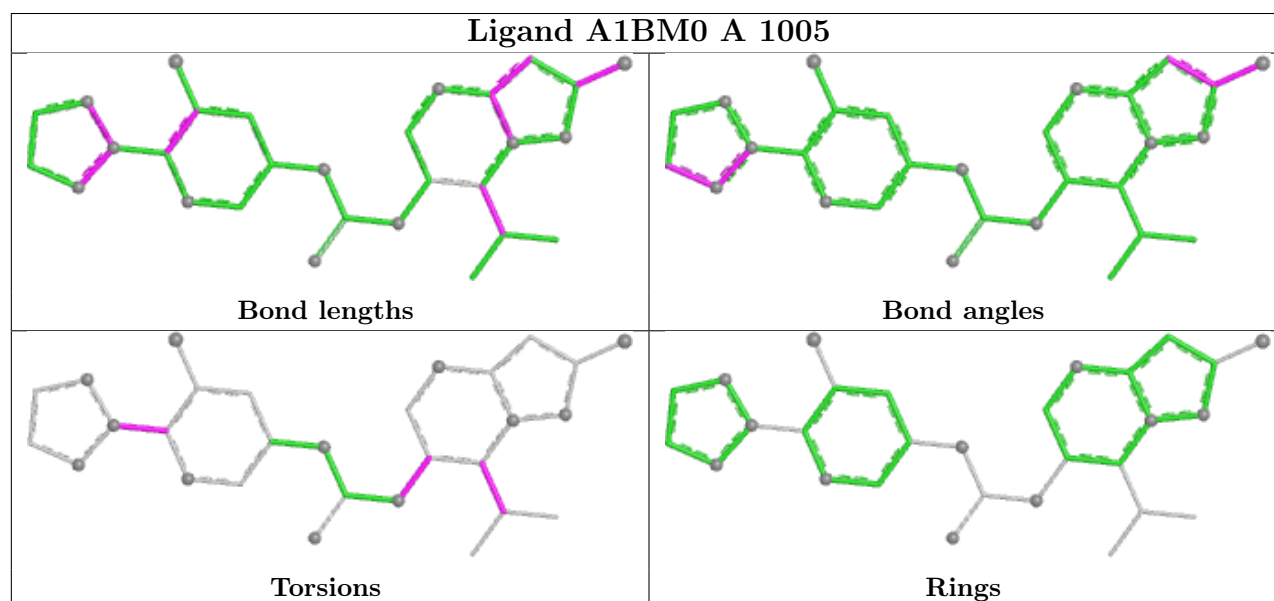
Mol	Chain	Res	Type	Atoms
3	A	1005	A1BM0	C12-C13-N6-N7
3	B	1005	A1BM0	C12-C13-N6-N7
3	A	1005	A1BM0	N9-C13-N6-N7
3	B	1005	A1BM0	N9-C13-N6-N7
3	B	1005	A1BM0	C12-C13-N6-N8
3	B	1005	A1BM0	C1-C2-C3-C8
3	A	1005	A1BM0	C3-C8-N4-C9
3	B	1005	A1BM0	C3-C8-N4-C9
3	A	1005	A1BM0	C1-C2-C3-C8
3	B	1005	A1BM0	C17-C2-C3-N1

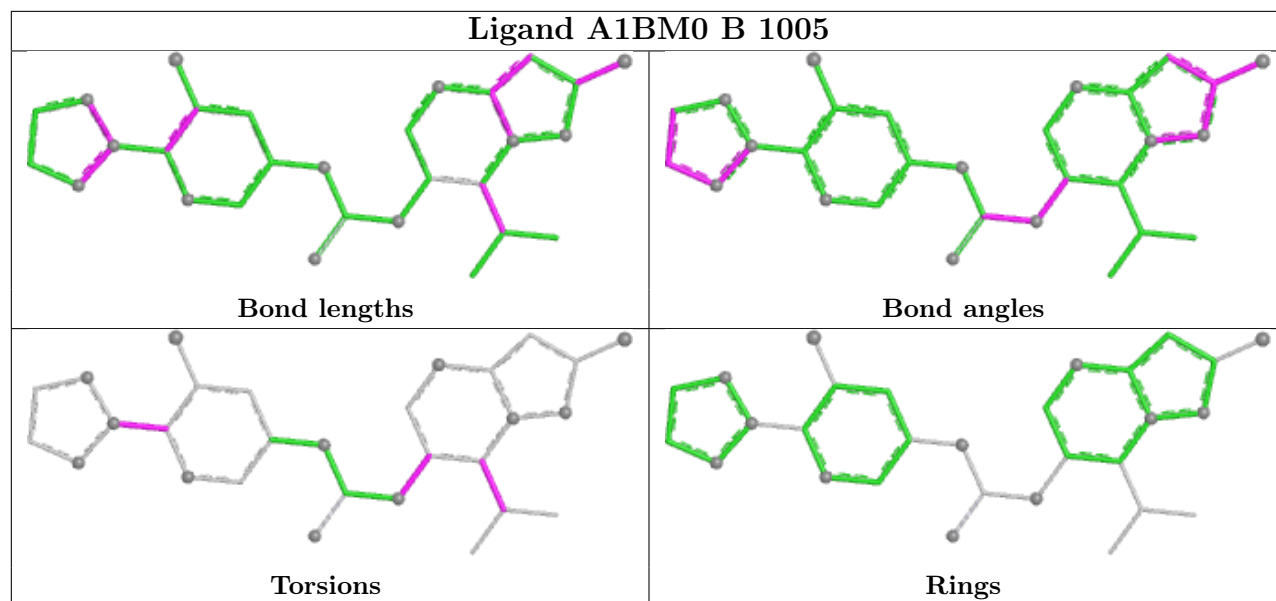
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1005	A1BM0	1	0
3	B	1005	A1BM0	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	356/386 (92%)	0.90	51 (14%) 6 5	35, 64, 136, 179	0
1	B	357/386 (92%)	0.95	54 (15%) 5 4	35, 64, 151, 179	0
All	All	713/772 (92%)	0.92	105 (14%) 6 4	35, 64, 148, 179	0

All (105) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	475	PRO	6.8
1	B	474	ILE	6.5
1	B	471	ASP	5.1
1	B	619	VAL	4.8
1	B	472	ASP	4.7
1	B	539	CYS	4.6
1	B	482	VAL	3.9
1	B	596	CYS	3.8
1	A	539	CYS	3.7
1	A	483	THR	3.7
1	B	473	THR	3.6
1	B	699	VAL	3.5
1	A	567	THR	3.5
1	B	717	MET	3.4
1	A	596	CYS	3.4
1	B	468	ASN	3.4
1	B	620	TYR	3.4
1	A	689	SER	3.4
1	B	692	TYR	3.2
1	A	597	GLY	3.2
1	B	690	TYR	3.2
1	A	668	LEU	3.2
1	B	627	MET	3.2
1	A	697	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	437	GLU	3.1
1	A	690	TYR	3.1
1	A	691	GLN	3.1
1	A	474	ILE	3.1
1	B	470	TYR	3.1
1	B	697	ASP	3.1
1	A	707	VAL	3.0
1	B	695	LEU	3.0
1	B	420	PHE	3.0
1	A	467	ARG	3.0
1	B	689	SER	2.9
1	B	444	ASN	2.8
1	B	654	THR	2.8
1	B	623	PRO	2.8
1	A	699	VAL	2.8
1	A	629	ASP	2.8
1	A	565	GLN	2.7
1	B	618	ILE	2.7
1	B	598	VAL	2.7
1	A	569	TYR	2.7
1	A	588	GLU	2.7
1	A	695	LEU	2.7
1	B	631	TYR	2.7
1	A	688	LEU	2.7
1	A	623	PRO	2.6
1	B	565	GLN	2.6
1	B	626	ILE	2.6
1	B	469	ASP	2.6
1	A	693	SER	2.5
1	B	645	ASP	2.5
1	A	660	SER	2.5
1	A	692	TYR	2.5
1	A	628	CYS	2.4
1	A	694	GLY	2.4
1	B	484	ALA	2.4
1	A	620	TYR	2.4
1	A	592	LEU	2.4
1	A	475	PRO	2.4
1	B	701	ASP	2.3
1	A	621	LYS	2.3
1	A	645	ASP	2.3
1	B	657	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	622	PRO	2.3
1	A	444	ASN	2.3
1	A	630	ALA	2.3
1	A	469	ASP	2.3
1	A	589	SER	2.3
1	A	543	LYS	2.3
1	B	591	CYS	2.3
1	B	628	CYS	2.3
1	A	631	TYR	2.3
1	B	635	PHE	2.2
1	B	707	VAL	2.2
1	B	494	GLN	2.2
1	A	666	HIS	2.2
1	A	434	TYR	2.2
1	B	589	SER	2.2
1	B	579	GLN	2.2
1	B	600	ILE	2.2
1	A	636	PRO	2.2
1	B	694	GLY	2.2
1	B	376	LEU	2.2
1	B	599	GLN	2.1
1	A	595	ASP	2.1
1	A	619	VAL	2.1
1	B	621	LYS	2.1
1	A	517	ASP	2.1
1	A	566	GLY	2.1
1	A	496	ALA	2.1
1	B	630	ALA	2.1
1	B	617	SER	2.1
1	A	627	MET	2.1
1	B	431	PRO	2.1
1	A	672	LEU	2.0
1	A	626	ILE	2.0
1	A	441	CYS	2.0
1	A	643	PRO	2.0
1	B	643	PRO	2.0
1	B	435	ARG	2.0
1	B	567	THR	2.0
1	B	659	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

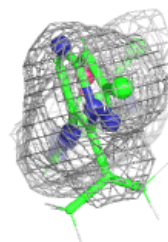
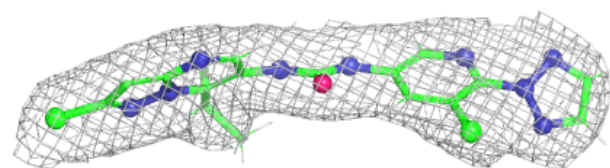
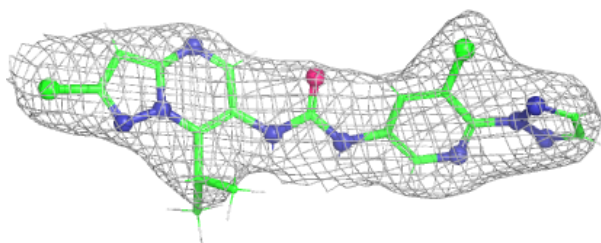
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	CA	B	1003	1/1	-0.18	0.11	153,153,153,153	0
2	CA	A	1004	1/1	0.44	0.15	160,160,160,160	0
2	CA	B	1004	1/1	0.73	0.20	154,154,154,154	0
2	CA	B	1002	1/1	0.79	0.17	68,68,68,68	0
2	CA	A	1003	1/1	0.80	0.11	75,75,75,75	0
2	CA	B	1001	1/1	0.83	0.28	75,75,75,75	0
2	CA	A	1001	1/1	0.87	0.27	66,66,66,66	0
3	A1BM0	B	1005	29/29	0.92	0.11	47,55,60,68	0
3	A1BM0	A	1005	29/29	0.93	0.12	40,51,57,62	0
2	CA	A	1002	1/1	0.96	0.10	77,77,77,77	0

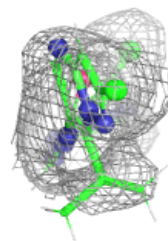
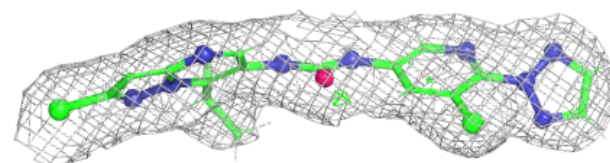
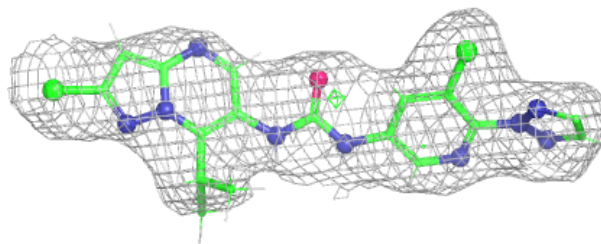
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around A1BM0 B 1005:

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

**Electron density around A1BM0 A 1005:**

$2mF_o-DF_c$ (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.