



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:03 PM UTC

PDB ID : 7PAW / pdb_00007paw
Title : MALT1 in complex with compound 1
Authors : Kack, H.; Oster, L.
Deposited on : 2021-07-30
Resolution : 2.19 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

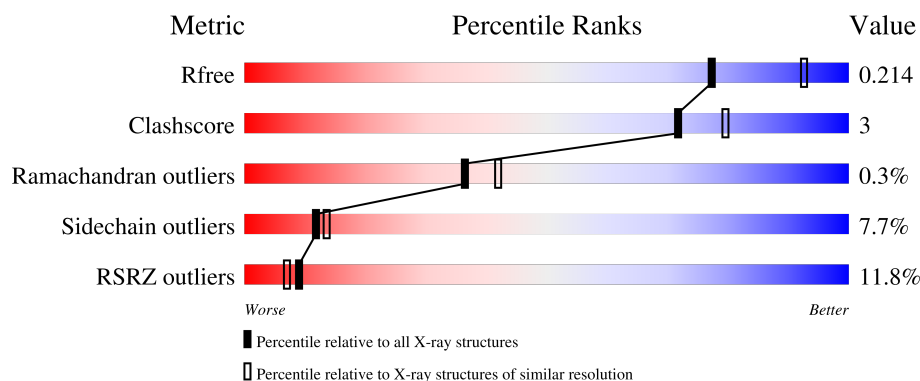
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.19 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	388	6% 74% 14% • 11%
1	B	388	15% 77% 16% • 5%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5724 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 Mucosa-associated lymphoid tissue lymphoma translocation protein 1.

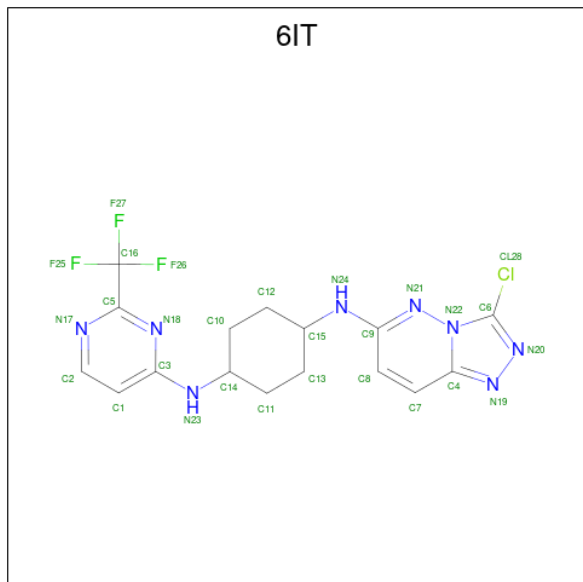
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	346	Total	C	N	O	S	0	1	0
			2748	1756	451	520	21			
1	B	367	Total	C	N	O	S	0	1	0
			2898	1859	470	546	23			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	338	MET	-	initiating methionine	UNP Q9UDY8
A	595	LYS	ASP	engineered mutation	UNP Q9UDY8
A	617	LYS	SER	engineered mutation	UNP Q9UDY8
A	666	ALA	HIS	engineered mutation	UNP Q9UDY8
A	681	GLU	HIS	engineered mutation	UNP Q9UDY8
A	720	HIS	-	expression tag	UNP Q9UDY8
A	721	HIS	-	expression tag	UNP Q9UDY8
A	722	HIS	-	expression tag	UNP Q9UDY8
A	723	HIS	-	expression tag	UNP Q9UDY8
A	724	HIS	-	expression tag	UNP Q9UDY8
A	725	HIS	-	expression tag	UNP Q9UDY8
B	338	MET	-	initiating methionine	UNP Q9UDY8
B	595	LYS	ASP	engineered mutation	UNP Q9UDY8
B	617	LYS	SER	engineered mutation	UNP Q9UDY8
B	666	ALA	HIS	engineered mutation	UNP Q9UDY8
B	681	GLU	HIS	engineered mutation	UNP Q9UDY8
B	720	HIS	-	expression tag	UNP Q9UDY8
B	721	HIS	-	expression tag	UNP Q9UDY8
B	722	HIS	-	expression tag	UNP Q9UDY8
B	723	HIS	-	expression tag	UNP Q9UDY8
B	724	HIS	-	expression tag	UNP Q9UDY8
B	725	HIS	-	expression tag	UNP Q9UDY8

- Molecule 2 is {N}1-(3-chloranyl-[1,2,4]triazolo[4,3-b]pyridazin-6-yl)-{N}4-[2-(trifluoro

methyl)pyrimidin-4-yl]cyclohexane-1,4-diamine (CCD ID: 6IT) (formula: $C_{16}H_{16}ClF_3N_8$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	Cl	F	N	0	0
			28	16	1	3	8		

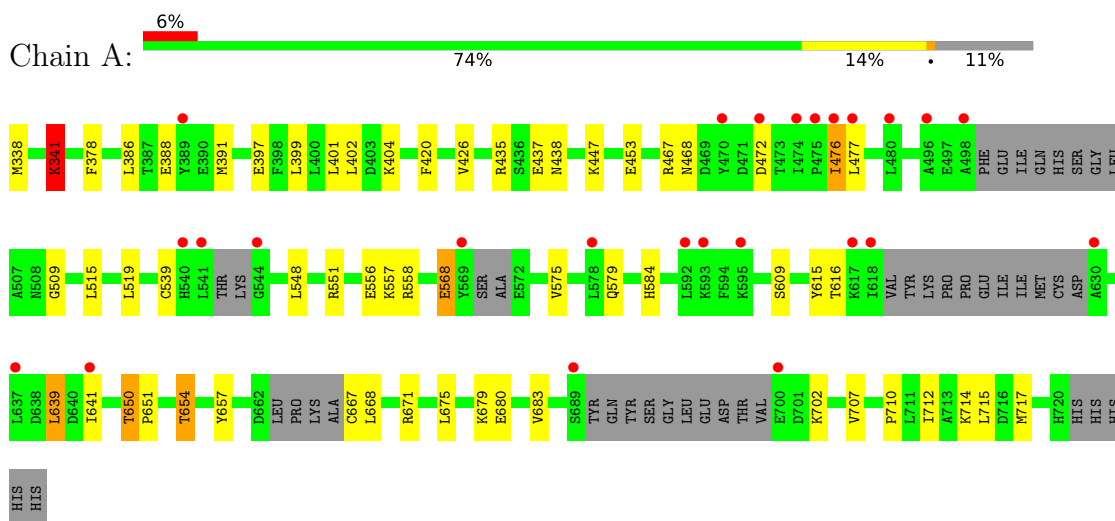
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	26	Total	O	0	0
			26	26		
3	B	24	Total	O	0	0
			24	24		

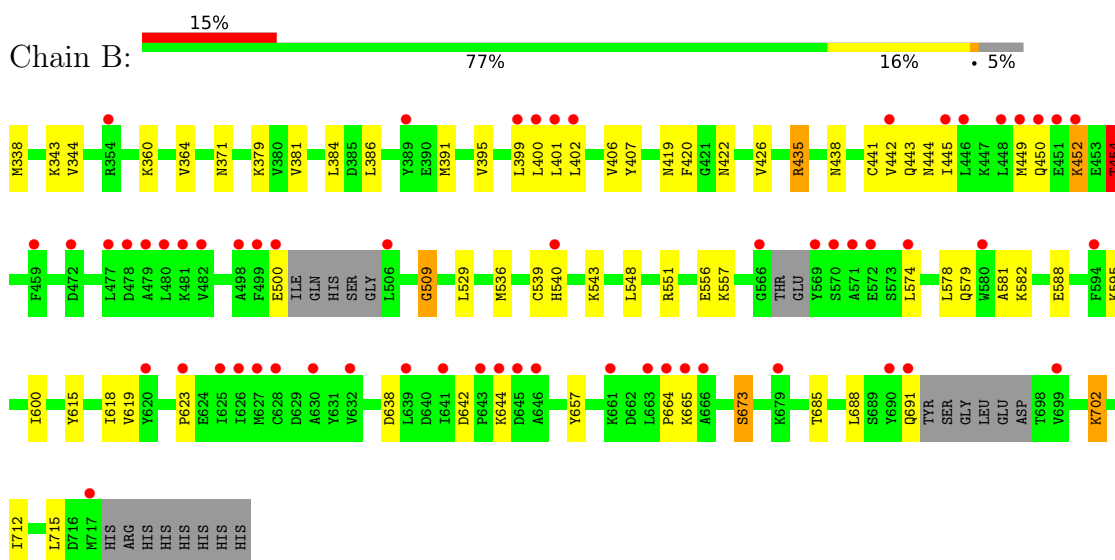
3 Residue-property plots [i](#)

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	52.45Å 74.97Å 106.87Å 90.00° 93.87° 90.00°	Depositor
Resolution (Å)	53.31 – 2.19 53.31 – 2.19	Depositor EDS
% Data completeness (in resolution range)	71.9 (53.31-2.19) 71.9 (53.31-2.19)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.21 (at 2.20Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.200 , 0.235 0.215 , 0.214	Depositor DCC
R_{free} test set	1479 reflections (3.48%)	wwPDB-VP
Wilson B-factor (Å ²)	39.9	Xtriage
Anisotropy	0.095	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 49.3	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	0.94	EDS
Total number of atoms	5724	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.02% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 6IT

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	0.86	1/2792 (0.0%)	1.30	14/3761 (0.4%)
1	B	0.82	0/2947	1.32	28/3977 (0.7%)
All	All	0.84	1/5739 (0.0%)	1.31	42/7738 (0.5%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	426	VAL	CA-C	5.35	1.57	1.53

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	638	ASP	CA-CB-CG	5.95	118.55	112.60
1	B	582	LYS	CA-C-N	5.90	129.00	120.38
1	B	582	LYS	C-N-CA	5.90	129.00	120.38
1	B	657	TYR	N-CA-C	-5.88	104.82	112.23
1	B	449	MET	CA-C-N	5.88	128.08	120.44
1	B	449	MET	C-N-CA	5.88	128.08	120.44
1	B	623	PRO	CA-C-N	5.85	128.44	120.54
1	B	623	PRO	C-N-CA	5.85	128.44	120.54
1	A	657	TYR	N-CA-C	-5.82	104.54	111.69
1	B	673	SER	N-CA-C	-5.77	101.42	110.36
1	B	665	LYS	CA-C-N	5.76	130.83	122.36
1	B	665	LYS	C-N-CA	5.76	130.83	122.36
1	B	426	VAL	N-CA-C	5.75	112.80	107.56
1	A	515	LEU	CA-C-N	5.73	128.22	120.38
1	A	515	LEU	C-N-CA	5.73	128.22	120.38
1	B	581	ALA	CA-C-N	5.58	127.75	120.28
1	B	581	ALA	C-N-CA	5.58	127.75	120.28
1	A	509	GLY	N-CA-C	-5.57	105.41	112.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	539	CYS	CA-C-N	5.56	127.99	120.38
1	B	539	CYS	C-N-CA	5.56	127.99	120.38
1	B	540	HIS	CA-C-N	5.54	127.70	120.28
1	B	540	HIS	C-N-CA	5.54	127.70	120.28
1	A	650	THR	CB-CA-C	5.48	117.92	109.15
1	B	400	LEU	CA-C-N	5.47	128.37	120.38
1	B	400	LEU	C-N-CA	5.47	128.37	120.38
1	B	509	GLY	N-CA-C	-5.38	105.40	112.82
1	B	360	LYS	CA-C-N	5.36	126.79	120.09
1	B	360	LYS	C-N-CA	5.36	126.79	120.09
1	A	378	PHE	CA-CB-CG	5.30	119.10	113.80
1	B	379	LYS	N-CA-C	-5.17	101.34	109.25
1	B	529	LEU	CA-C-N	5.15	127.19	120.28
1	B	529	LEU	C-N-CA	5.15	127.19	120.28
1	A	539	CYS	CA-C-N	5.10	127.07	120.44
1	A	539	CYS	C-N-CA	5.10	127.07	120.44
1	A	341	LYS	N-CA-C	-5.09	105.81	111.36
1	B	644	LYS	CA-C-N	5.09	128.72	120.23
1	B	644	LYS	C-N-CA	5.09	128.72	120.23
1	A	468	ASN	CA-CB-CG	5.04	117.64	112.60
1	A	388	GLU	CA-C-N	5.02	127.01	120.28
1	A	388	GLU	C-N-CA	5.02	127.01	120.28
1	A	575	VAL	CA-C-N	5.02	127.00	120.28
1	A	575	VAL	C-N-CA	5.02	127.00	120.28

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	2748	0	2770	18	0
1	B	2898	0	2951	21	0
2	B	28	0	0	1	0
3	A	26	0	0	0	0
3	B	24	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5724	0	5721	37	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 (37) 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:397:GLU:HG3	1:A:717:MET:HG2	1.41	0.97
1:A:435:ARG:H	1:A:438:ASN:HD22	1.33	0.77
1:B:435:ARG:H	1:B:438:ASN:HD22	1.36	0.73
1:A:616:THR:O	1:A:667:CYS:HB2	1.91	0.70
1:B:395:VAL:HG11	1:B:445:ILE:HG12	1.74	0.70
1:A:551:ARG:HG2	1:B:551:ARG:HG2	1.74	0.70
1:B:600:ILE:HD11	1:B:688:LEU:HD13	1.75	0.67
1:B:441:CYS:HB3	1:B:444:ASN:HD22	1.60	0.65
1:B:402:LEU:HB3	1:B:454:THR:HG23	1.79	0.63
1:A:338:MET:HE2	1:A:556:GLU:HB3	1.83	0.61
1:A:386:LEU:HB2	1:A:391:MET:HG3	1.84	0.59
1:B:442:VAL:HA	1:B:445:ILE:HD12	1.89	0.55
1:B:343:LYS:HG2	1:B:407:TYR:HB2	1.90	0.53
1:A:420:PHE:HB3	1:B:420:PHE:HB3	1.91	0.51
1:A:654:THR:HG23	1:A:671:ARG:HB2	1.93	0.50
1:A:341:LYS:HE2	1:A:568:GLU:HB2	1.94	0.50
1:B:500:GLU:HA	1:B:509:GLY:HA2	1.95	0.49
1:A:639:LEU:HB3	1:A:641:ILE:HG12	1.95	0.49
1:A:399:LEU:HD23	1:A:402:LEU:HD12	1.95	0.48
1:A:615:TYR:HA	1:A:668:LEU:O	2.15	0.47
1:B:422:ASN:HD22	1:B:443:GLN:HG2	1.80	0.47
1:B:344:VAL:HG13	2:B:801:6IT:CL28	2.52	0.45
1:A:584:HIS:HE1	1:A:609:SER:OG	1.98	0.45
1:B:386:LEU:HB2	1:B:391:MET:HG3	1.99	0.45
1:A:404:LYS:HA	1:A:453:GLU:O	2.17	0.45
1:B:402:LEU:O	1:B:452:LYS:HB3	2.17	0.44
1:B:600:ILE:HG12	1:B:618:ILE:HD13	1.98	0.44
1:B:406:VAL:O	1:B:454:THR:HG22	2.18	0.43
1:B:685:THR:HG21	1:B:702:LYS:HD3	2.01	0.43
1:B:615:TYR:CZ	1:B:664:PRO:HG2	2.53	0.43
1:A:651:PRO:O	1:A:654:THR:HG22	2.18	0.43
1:B:338:MET:HE2	1:B:556:GLU:HB3	2.00	0.43
1:A:675:LEU:HD22	1:A:710:PRO:HG2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:338:MET:HE3	1:A:558:ARG:CZ	2.49	0.42
1:A:476:ILE:H	1:A:476:ILE:HG13	1.65	0.42
1:B:536:MET:HE2	1:B:536:MET:HB3	1.90	0.42
1:B:399:LEU:HD21	1:B:445:ILE:HG23	2.03	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	333/388 (86%)	320 (96%)	12 (4%)	1 (0%)	36	42
1	B	360/388 (93%)	341 (95%)	18 (5%)	1 (0%)	36	42
All	All	693/776 (89%)	661 (95%)	30 (4%)	2 (0%)	36	42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	477	LEU
1	B	454	THR

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	305/344 (89%)	282 (92%)	23 (8%)	12	14
1	B	323/344 (94%)	298 (92%)	25 (8%)	12	13
All	All	628/688 (91%)	580 (92%)	48 (8%)	12	14

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	341	LYS
1	A	401	LEU
1	A	437	GLU
1	A	447	LYS
1	A	467	ARG
1	A	472	ASP
1	A	476	ILE
1	A	519	LEU
1	A	548	LEU
1	A	557	LYS
1	A	568	GLU
1	A	579	GLN
1	A	639	LEU
1	A	650	THR
1	A	654	THR
1	A	679	LYS
1	A	680	GLU
1	A	683	VAL
1	A	702	LYS
1	A	707	VAL
1	A	712	ILE
1	A	714	LYS
1	A	715	LEU
1	B	364	VAL
1	B	371	ASN
1	B	381	VAL
1	B	384	LEU
1	B	401	LEU
1	B	419	ASN
1	B	435	ARG
1	B	450	GLN
1	B	452	LYS

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Mol	Chain	Res	Type
1	B	454	THR
1	B	543	LYS
1	B	548	LEU
1	B	557	LYS
1	B	574	LEU
1	B	578	LEU
1	B	579	GLN
1	B	588	GLU
1	B	595	LYS
1	B	619	VAL
1	B	642	ASP
1	B	673	SER
1	B	691	GLN
1	B	702	LYS
1	B	712	ILE
1	B	715	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	422	ASN
1	A	438	ASN
1	A	494	GLN
1	A	577	ASN
1	A	584	HIS
1	A	718	HIS
1	B	352	ASN
1	B	371	ASN
1	B	422	ASN
1	B	438	ASN
1	B	444	ASN
1	B	579	GLN
1	B	584	HIS
1	B	601	GLN
1	B	703	GLN

5.3.3 RNA ⓘ

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](#)

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	6IT	B	801	-	28,31,31	1.06	2 (7%)	36,45,45	1.64	7 (19%)

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	6IT	B	801	-	-	0/14/24/24	0/4/4/4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	6IT	C8-C9	3.73	1.49	1.41
2	B	801	6IT	C3-N23	2.09	1.41	1.37

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	6IT	C6-N22-C4	-4.11	104.08	105.72
2	B	801	6IT	N23-C3-N18	4.02	122.85	117.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	6IT	C8-C9-N24	-3.66	114.35	122.40
2	B	801	6IT	N24-C9-N21	3.04	122.87	118.95
2	B	801	6IT	C16-C5-N17	2.60	119.15	115.12
2	B	801	6IT	C2-N17-C5	-2.39	113.67	115.63
2	B	801	6IT	C1-C3-N23	-2.20	116.73	120.77

There are no chirality outliers.

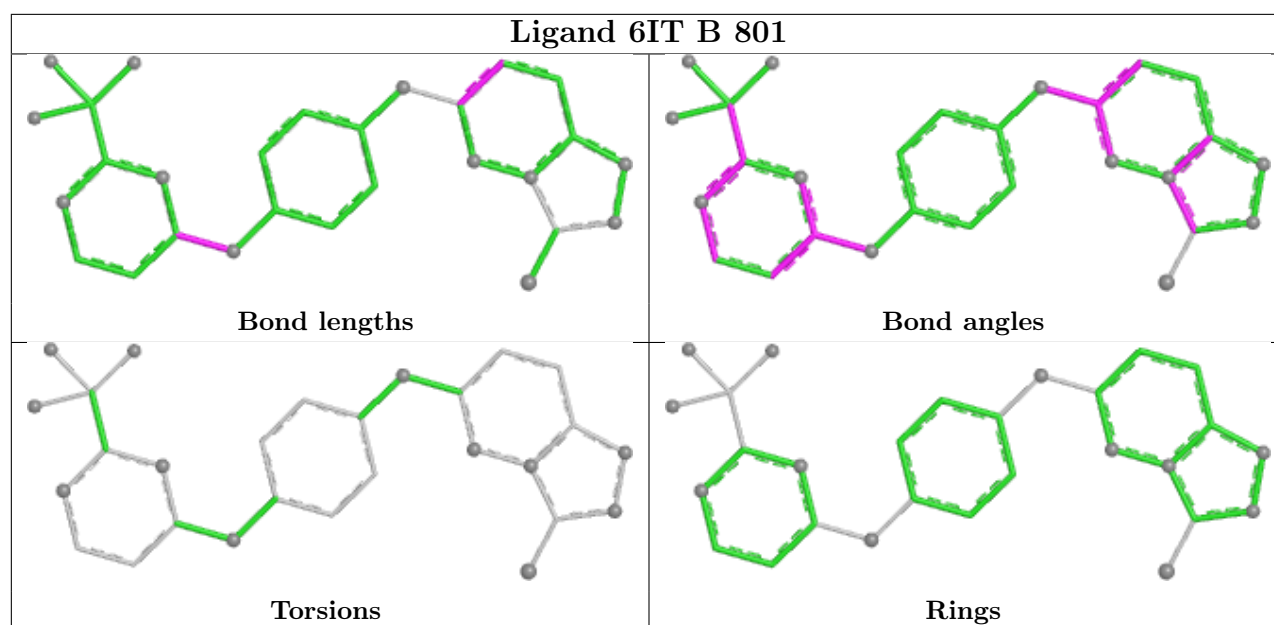
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	801	6IT	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	346/388 (89%)	0.50	25 (7%) 21 18	23, 50, 93, 119	1 (0%)
1	B	367/388 (94%)	0.75	59 (16%) 4 3	22, 52, 96, 138	1 (0%)
All	All	713/776 (91%)	0.63	84 (11%) 9 7	22, 51, 96, 138	2 (0%)

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	480	LEU	6.3
1	A	544	GLY	5.8
1	A	477	LEU	5.8
1	B	569	TYR	5.0
1	B	566	GLY	4.9
1	B	449	MET	4.7
1	A	689	SER	4.7
1	B	479	ALA	4.7
1	B	626	ILE	4.5
1	B	445	ILE	4.4
1	B	666	ALA	4.2
1	B	627	MET	4.0
1	B	482	VAL	3.8
1	A	476	ILE	3.7
1	B	499	PHE	3.6
1	B	500	GLU	3.5
1	B	623	PRO	3.5
1	A	618	ILE	3.4
1	B	451	GLU	3.4
1	B	448	LEU	3.4
1	B	401	LEU	3.3
1	B	690	TYR	3.3
1	A	498	ALA	3.3
1	B	646	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	571	ALA	3.1
1	A	541	LEU	3.1
1	B	402	LEU	3.1
1	B	628	CYS	3.1
1	B	472	ASP	3.1
1	B	663	LEU	3.1
1	B	644	LYS	3.0
1	B	478	ASP	3.0
1	B	442	VAL	3.0
1	A	617	LYS	3.0
1	A	480	LEU	2.9
1	B	643	PRO	2.9
1	B	498	ALA	2.9
1	A	474	ILE	2.9
1	B	639	LEU	2.8
1	B	691	GLN	2.8
1	B	717	MET	2.8
1	A	578	LEU	2.8
1	B	665	LYS	2.8
1	B	661	LYS	2.8
1	A	569	TYR	2.7
1	B	570	SER	2.6
1	B	399	LEU	2.6
1	A	389	TYR	2.6
1	B	450	GLN	2.6
1	B	625	ILE	2.6
1	B	354	ARG	2.5
1	A	637	LEU	2.5
1	B	481	LYS	2.5
1	A	475	PRO	2.5
1	B	459	PHE	2.5
1	B	540	HIS	2.5
1	B	699	VAL	2.4
1	B	620	TYR	2.4
1	B	446	LEU	2.4
1	B	594	PHE	2.4
1	B	580	TRP	2.4
1	A	470	TYR	2.4
1	A	540	HIS	2.4
1	B	641	ILE	2.4
1	B	679	LYS	2.4
1	A	630	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	389	TYR	2.3
1	B	506	LEU	2.3
1	A	472	ASP	2.3
1	B	645	ASP	2.3
1	B	452	LYS	2.3
1	A	595	LYS	2.3
1	A	641	ILE	2.2
1	A	592	LEU	2.2
1	A	496	ALA	2.1
1	B	630	ALA	2.1
1	B	400	LEU	2.1
1	B	572	GLU	2.1
1	A	700	GLU	2.1
1	B	664	PRO	2.1
1	B	632	VAL	2.1
1	B	477	LEU	2.1
1	A	593	LYS	2.1
1	B	574	LEU	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](#)

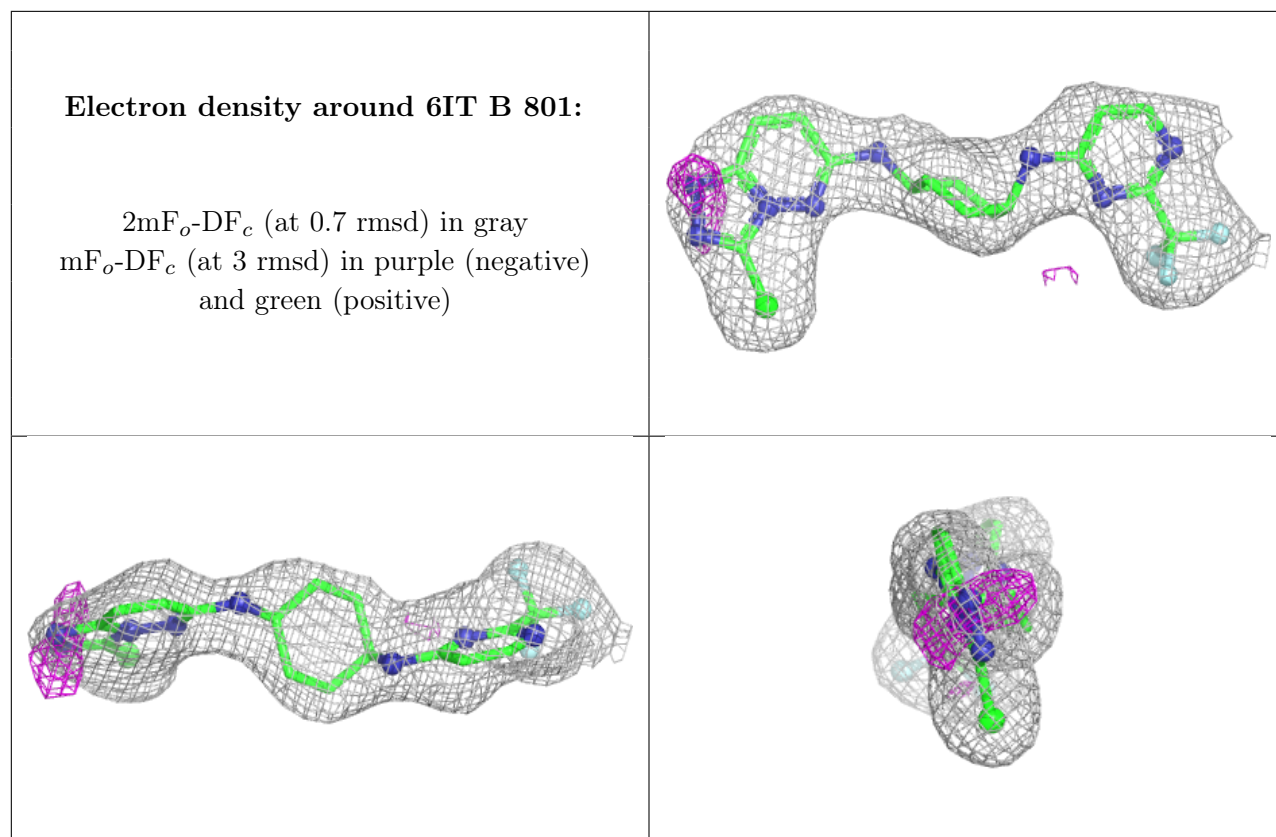
There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
2	6IT	B	801	28/28	0.93	0.10	47,53,56,57	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.