



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 02:58 PM EDT

PDB ID : 4BBX / pdb_00004bbx
Title : Discovery of a potent, selective and orally active PDE10A inhibitor for the treatment of schizophrenia
Authors : Bartolome-Nebreda, J.M.; Conde-Ceide, S.; Delgado, F.; Martin, M.L.; Martinez-Vituro, C.M.; Pastor, J.; Tong, H.M.; Iturrino, L.; Macdonald, G.J.; Sanderson, W.; Megens, A.; Langlois, X.; Somers, M.; Vanhoof, G.
Deposited on : 2012-09-28
Resolution : 2.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

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](#) ①) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtrriage (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

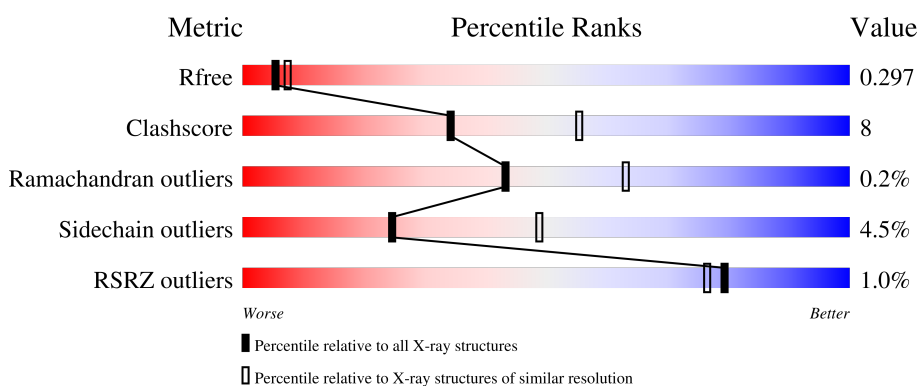
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	336	
1	B	336	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	LKF	A	1760	-	-	X	-

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 5131 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.

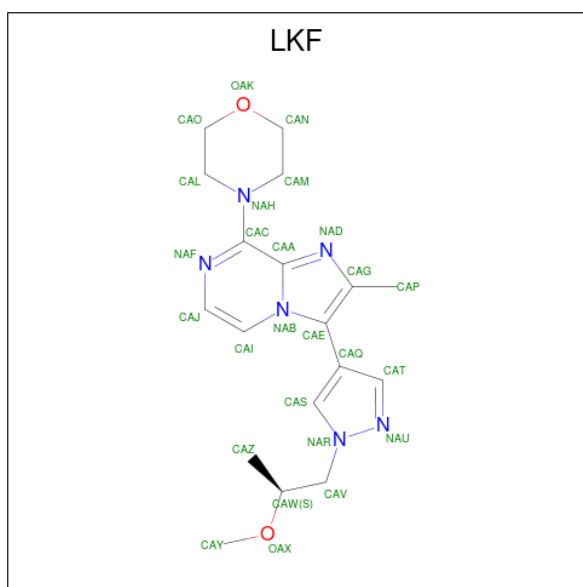
- Molecule 1 is a protein called CAMP AND CAMP-INHIBITED CGMP 3', 5'-CYCLIC PHOSPHODIESTERASE 10A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	312	2511	1606	425	457	23	0	0	0
1	B	312	2511	1606	425	457	23	0	0	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	441	MET	-	expression tag	UNP Q9Y233
A	442	GLY	-	expression tag	UNP Q9Y233
A	770	ARG	-	expression tag	UNP Q9Y233
A	771	HIS	-	expression tag	UNP Q9Y233
A	772	HIS	-	expression tag	UNP Q9Y233
A	773	HIS	-	expression tag	UNP Q9Y233
A	774	HIS	-	expression tag	UNP Q9Y233
A	775	HIS	-	expression tag	UNP Q9Y233
A	776	HIS	-	expression tag	UNP Q9Y233
B	441	MET	-	expression tag	UNP Q9Y233
B	442	GLY	-	expression tag	UNP Q9Y233
B	770	ARG	-	expression tag	UNP Q9Y233
B	771	HIS	-	expression tag	UNP Q9Y233
B	772	HIS	-	expression tag	UNP Q9Y233
B	773	HIS	-	expression tag	UNP Q9Y233
B	774	HIS	-	expression tag	UNP Q9Y233
B	775	HIS	-	expression tag	UNP Q9Y233
B	776	HIS	-	expression tag	UNP Q9Y233

- Molecule 2 is 4-[3-[1-[(2S)-2-methoxypropyl]pyrazol-4-yl]-2-methyl-imidazo[1,2-a]pyrazin-8-yl]morpholine (CCD ID: LKF) (formula: C₁₈H₂₄N₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			26	18	6	2		
2	B	1	Total	C	N	O	0	0
			26	18	6	2		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		
3	B	1	Total	Zn	0	0
			1	1		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		
4	B	1	Total	Mg	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	26	Total	O	0	0
			26	26		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	27	Total	O	0	0
			27	27		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	49.29Å 81.28Å 158.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	79.31 – 2.50 79.31 – 2.50	Depositor EDS
% Data completeness (in resolution range)	96.6 (79.31-2.50) 96.6 (79.31-2.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 2.51Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.234 , 0.293 0.242 , 0.297	Depositor DCC
R_{free} test set	1168 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	51.6	Xtrriage
Anisotropy	0.112	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 37.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5131	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.12% 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: LKF, ZN, MG

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	0.79	9/2573 (0.3%)	0.93	5/3488 (0.1%)
1	B	0.77	10/2573 (0.4%)	0.91	8/3488 (0.2%)
All	All	0.78	19/5146 (0.4%)	0.92	13/6976 (0.2%)

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	640	GLN	CD-OE1	5.63	1.34	1.23
1	A	508	ASN	CG-OD1	5.48	1.33	1.23
1	A	634	GLN	CD-OE1	5.46	1.33	1.23
1	B	634	GLN	CD-OE1	5.42	1.33	1.23
1	B	451	GLN	CD-OE1	5.41	1.33	1.23
1	A	733	GLN	CD-OE1	5.39	1.33	1.23
1	B	474	ASN	CG-OD1	5.29	1.33	1.23
1	A	474	ASN	CG-ND2	-5.24	1.22	1.33
1	A	714	GLN	CD-OE1	5.19	1.33	1.23
1	B	485	HIS	ND1-CE1	5.17	1.37	1.32
1	B	585	HIS	ND1-CE1	5.13	1.37	1.32
1	A	645	ASN	CG-OD1	5.12	1.33	1.23
1	A	585	HIS	ND1-CE1	5.12	1.37	1.32
1	B	466	HIS	ND1-CE1	5.11	1.37	1.32
1	A	485	HIS	ND1-CE1	5.10	1.37	1.32
1	B	748	ASN	CG-OD1	5.09	1.33	1.23
1	B	647	ASN	CG-OD1	5.08	1.33	1.23
1	B	714	GLN	CD-OE1	5.07	1.33	1.23
1	A	647	ASN	CG-OD1	5.04	1.33	1.23

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	585	HIS	CB-CG-CD2	-6.60	122.61	131.20
1	B	466	HIS	CB-CG-CD2	-6.57	122.66	131.20
1	A	485	HIS	CB-CG-CD2	-6.53	122.71	131.20
1	B	485	HIS	CB-CG-CD2	-6.50	122.75	131.20
1	B	585	HIS	CB-CG-CD2	-6.32	122.98	131.20
1	B	540	ASP	CA-CB-CG	5.88	118.48	112.60
1	B	466	HIS	CB-CG-ND1	5.66	131.18	122.70
1	A	585	HIS	CB-CG-ND1	5.62	131.12	122.70
1	A	485	HIS	CB-CG-ND1	5.59	131.09	122.70
1	B	485	HIS	CB-CG-ND1	5.55	131.02	122.70
1	B	585	HIS	CB-CG-ND1	5.50	130.95	122.70
1	A	624	ASP	N-CA-C	-5.24	101.60	109.15
1	B	712	VAL	CB-CA-C	-5.08	108.96	114.35

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2511	0	2461	41	0
1	B	2511	0	2461	34	0
2	A	26	0	24	10	0
2	B	26	0	24	3	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	26	0	0	0	0
5	B	27	0	0	2	0
All	All	5131	0	4970	76	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 8.

All (76) 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:703:MET:HE1	2:A:1760:LKF:HAW	1.49	0.93
1:A:625:LEU:HD23	2:A:1760:LKF:HAT	1.55	0.88
1:A:682:ILE:CD1	2:A:1760:LKF:HAN1	2.05	0.86
1:B:536:THR:HG23	1:B:537:LEU:HD23	1.58	0.84
1:A:682:ILE:HD11	2:A:1760:LKF:HAN1	1.63	0.81
1:B:624:ASP:HB3	1:B:627:LEU:HD12	1.72	0.70
1:A:682:ILE:HD13	2:A:1760:LKF:HAO1	1.73	0.70
1:A:704:MET:HE3	2:A:1760:LKF:HAY3	1.78	0.66
1:A:682:ILE:HD13	2:A:1760:LKF:HAN1	1.79	0.64
1:A:704:MET:CE	2:A:1760:LKF:HAY3	2.30	0.61
1:B:754:LYS:CG	5:B:2024:HOH:O	2.48	0.60
1:A:571:PRO:O	1:A:574:ALA:HB3	2.01	0.59
1:B:703:MET:HE3	1:B:704:MET:HE2	1.84	0.59
1:A:488:CYS:HB3	1:A:492:CYS:SG	2.42	0.58
1:A:462:ILE:HD11	1:A:483:MET:HG3	1.86	0.58
1:B:509:TYR:CE2	1:B:555:LEU:HD13	2.41	0.56
1:A:514:TYR:CD2	1:A:682:ILE:HG22	2.40	0.56
1:A:703:MET:HE2	1:A:704:MET:HG3	1.88	0.56
1:A:473:GLU:HA	1:A:476:TRP:CE2	2.43	0.54
1:A:629:PHE:CE1	1:A:723:VAL:HG22	2.43	0.53
1:B:698:ILE:N	1:B:698:ILE:HD13	2.24	0.52
1:A:514:TYR:CG	1:A:682:ILE:HG22	2.44	0.52
1:B:749:LEU:HD12	1:B:749:LEU:O	2.10	0.52
1:A:463:GLU:OE2	1:A:528:TYR:OH	2.24	0.51
1:A:690:GLY:HA3	1:A:704:MET:O	2.11	0.51
1:B:667:SER:OG	1:B:678:THR:HG21	2.10	0.51
1:B:665:LEU:O	1:B:668:VAL:HG22	2.11	0.51
1:A:523:VAL:HG13	1:A:663:CYS:HB3	1.93	0.50
1:A:480:PHE:CE2	1:A:551:LEU:HD22	2.46	0.50
1:B:473:GLU:HA	1:B:476:TRP:CE2	2.47	0.50
1:B:523:VAL:HG21	1:B:553:HIS:CE1	2.47	0.49
1:A:508:ASN:OD1	1:A:592:ILE:HD11	2.12	0.49
1:A:581:MET:HE3	1:A:585:HIS:CE1	2.47	0.49
1:B:703:MET:HE1	2:B:1760:LKF:NAU	2.27	0.49
1:B:751:GLN:O	1:B:755:VAL:HG23	2.12	0.49
1:B:705:ASP:OD2	1:B:708:LYS:NZ	2.36	0.49
1:A:629:PHE:HE1	1:A:723:VAL:HG22	1.77	0.48
1:B:485:HIS:HB3	1:B:490:THR:HG22	1.95	0.48
1:B:714:GLN:HA	1:B:756:ILE:HD11	1.95	0.48
1:B:757:ARG:NH2	1:B:759:GLU:OE2	2.46	0.48
1:A:583:GLN:HG2	1:A:621:ILE:HD11	1.95	0.47
1:B:693:MET:HE1	1:B:700:PRO:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:493:PHE:CD1	1:B:600:ILE:HB	2.50	0.47
1:B:646:LEU:N	1:B:646:LEU:HD22	2.29	0.47
1:A:592:ILE:HA	1:A:595:LEU:HD12	1.95	0.47
1:A:725:ILE:HB	1:A:726:PRO:HD3	1.97	0.47
1:B:619:ALA:O	1:B:660:MET:HE2	2.16	0.46
1:A:734:ILE:O	1:A:735:LEU:HD23	2.16	0.45
1:B:720:TYR:HA	1:B:724:ALA:HB3	1.98	0.45
1:A:586:PHE:O	1:A:590:VAL:HG23	2.16	0.45
1:A:581:MET:HE3	1:A:585:HIS:HE1	1.82	0.45
1:A:646:LEU:HD22	1:A:646:LEU:H	1.81	0.45
1:B:739:GLU:N	1:B:740:PRO:CD	2.80	0.44
1:B:453:THR:O	1:B:453:THR:HG23	2.17	0.44
1:A:655:VAL:HG22	1:A:734:ILE:HD13	2.00	0.44
1:A:560:PHE:HA	1:A:689:GLU:OE1	2.18	0.43
1:A:734:ILE:HG22	1:A:735:LEU:CD2	2.49	0.43
1:B:617:ARG:HD2	5:B:2016:HOH:O	2.16	0.43
1:A:501:PHE:CD1	1:A:592:ILE:HG22	2.54	0.43
1:A:717:LEU:CD2	1:A:749:LEU:HD11	2.48	0.43
1:A:480:PHE:CD1	1:A:551:LEU:HD13	2.53	0.43
1:A:704:MET:HE3	2:A:1760:LKF:CAY	2.45	0.43
1:A:462:ILE:HD11	1:A:483:MET:CG	2.49	0.43
1:B:525:HIS:O	1:B:528:TYR:HB3	2.19	0.43
1:B:734:ILE:HG22	1:B:735:LEU:HD23	2.00	0.42
1:B:476:TRP:HB3	1:B:521:VAL:HG21	2.02	0.42
1:B:623:THR:CG2	1:B:660:MET:HE3	2.49	0.42
1:A:677:LEU:HD21	1:B:722:ALA:HB2	2.02	0.42
1:B:629:PHE:HE2	2:B:1760:LKF:HAY1	1.85	0.41
1:B:712:VAL:N	1:B:713:PRO:CD	2.83	0.41
2:A:1760:LKF:HAM1	2:A:1760:LKF:NAD	2.35	0.41
1:A:496:GLU:O	1:A:500:ARG:HB2	2.20	0.40
1:B:582:GLU:HA	1:B:585:HIS:CD2	2.56	0.40
2:B:1760:LKF:NAD	2:B:1760:LKF:HAM1	2.36	0.40
1:A:476:TRP:HB3	1:A:521:VAL:HG21	2.03	0.40
1:B:646:LEU:CD1	1:B:655:VAL:HG21	2.51	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	310/336 (92%)	292 (94%)	18 (6%)	0	100	100
1	B	310/336 (92%)	296 (96%)	13 (4%)	1 (0%)	36	55
All	All	620/672 (92%)	588 (95%)	31 (5%)	1 (0%)	43	63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	599	ASN

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	277/303 (91%)	266 (96%)	11 (4%)	28	54
1	B	277/303 (91%)	263 (95%)	14 (5%)	21	43
All	All	554/606 (91%)	529 (96%)	25 (4%)	24	49

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	451	GLN
1	A	453	THR
1	A	464	LEU
1	A	555	LEU
1	A	563	SER

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Mol	Chain	Res	Type
1	A	578	THR
1	A	604	LEU
1	A	635	LEU
1	A	655	VAL
1	A	676	LYS
1	A	677	LEU
1	B	449	LEU
1	B	456	VAL
1	B	460	LYS
1	B	555	LEU
1	B	572	LEU
1	B	587	SER
1	B	612	VAL
1	B	635	LEU
1	B	676	LYS
1	B	677	LEU
1	B	698	ILE
1	B	717	LEU
1	B	739	GLU
1	B	753	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	451	GLN
1	A	570	HIS
1	A	611	GLN
1	A	748	ASN
1	B	585	HIS
1	B	611	GLN
1	B	640	GLN
1	B	649	GLN
1	B	714	GLN

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 6 ligands modelled in this entry, 4 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
2	LKF	B	1760	-	28,29,29	0.90	1 (3%)	26,41,41	1.38	2 (7%)
2	LKF	A	1760	-	28,29,29	0.88	1 (3%)	26,41,41	1.35	3 (11%)

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	LKF	B	1760	-	-	4/14/22/22	0/4/4/4
2	LKF	A	1760	-	-	3/14/22/22	0/4/4/4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1760	LKF	CAQ-CAE	-2.94	1.42	1.47
2	A	1760	LKF	CAQ-CAE	-2.87	1.43	1.47

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1760	LKF	CAQ-CAE-NAB	4.19	127.79	121.49
2	A	1760	LKF	CAQ-CAE-NAB	3.69	127.04	121.49
2	B	1760	LKF	CAG-CAE-NAB	2.90	106.49	104.67
2	A	1760	LKF	CAG-CAE-NAB	2.80	106.43	104.67
2	A	1760	LKF	CAQ-CAS-NAR	-2.22	105.00	106.78

There are no chirality outliers.

All (7) torsion outliers are listed below:

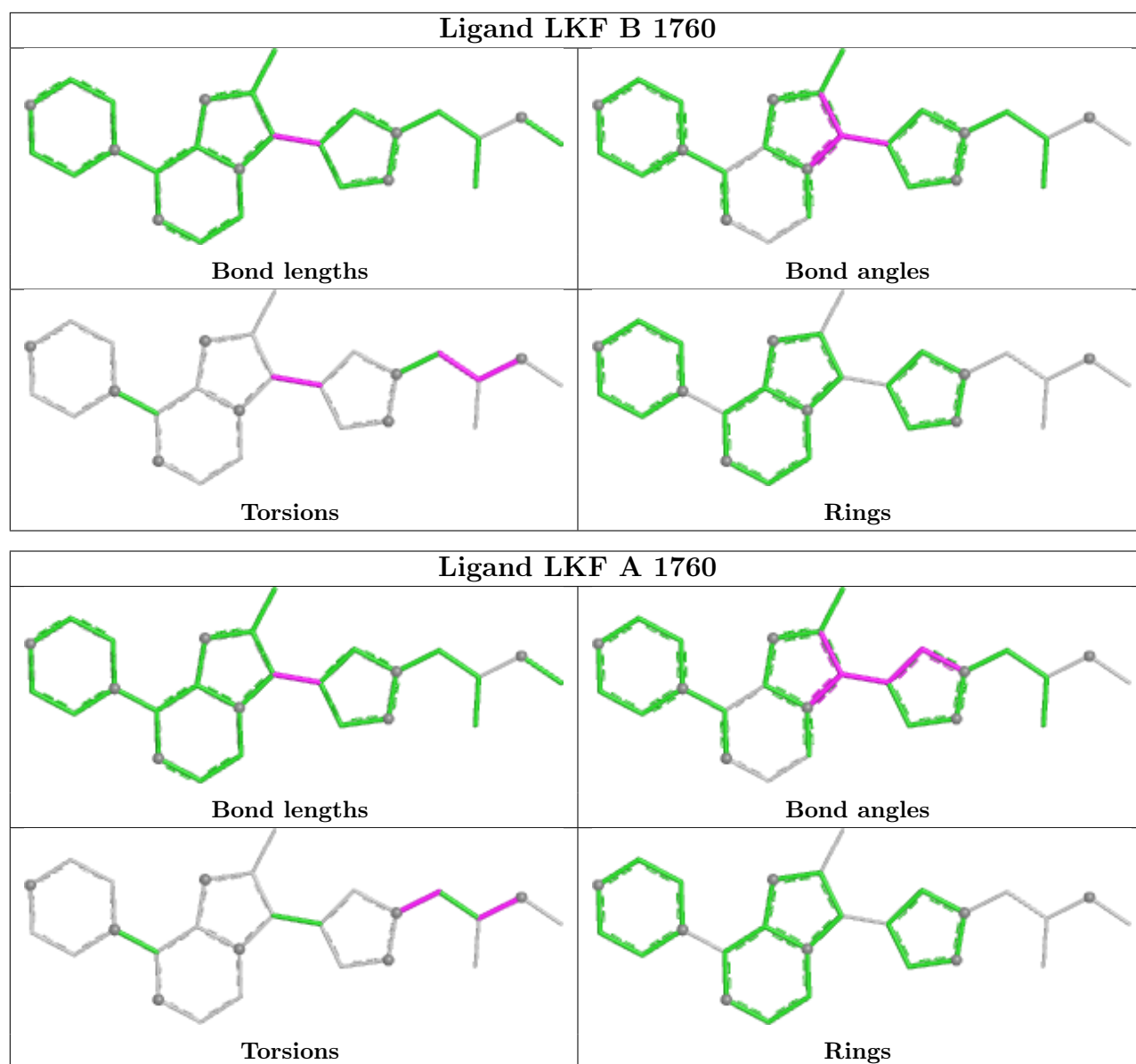
Mol	Chain	Res	Type	Atoms
2	A	1760	LKF	CAZ-CAW-OAX-CAY
2	B	1760	LKF	NAR-CAV-CAW-CAZ
2	B	1760	LKF	CAZ-CAW-OAX-CAY
2	B	1760	LKF	CAG-CAE-CAQ-CAS
2	A	1760	LKF	CAW-CAV-NAR-CAS
2	B	1760	LKF	NAB-CAE-CAQ-CAS
2	A	1760	LKF	CAV-CAW-OAX-CAY

There are no ring outliers.

2 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1760	LKF	3	0
2	A	1760	LKF	10	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	312/336 (92%)	0.23	5 (1%) 70 67	41, 57, 72, 81	0
1	B	312/336 (92%)	0.25	1 (0%) 90 87	41, 56, 74, 78	0
All	All	624/672 (92%)	0.24	6 (0%) 79 76	41, 56, 73, 81	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	568	PHE	4.3
1	B	448	GLY	2.9
1	A	450	MET	2.6
1	A	575	LEU	2.3
1	A	495	LEU	2.2
1	A	448	GLY	2.1

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](#)

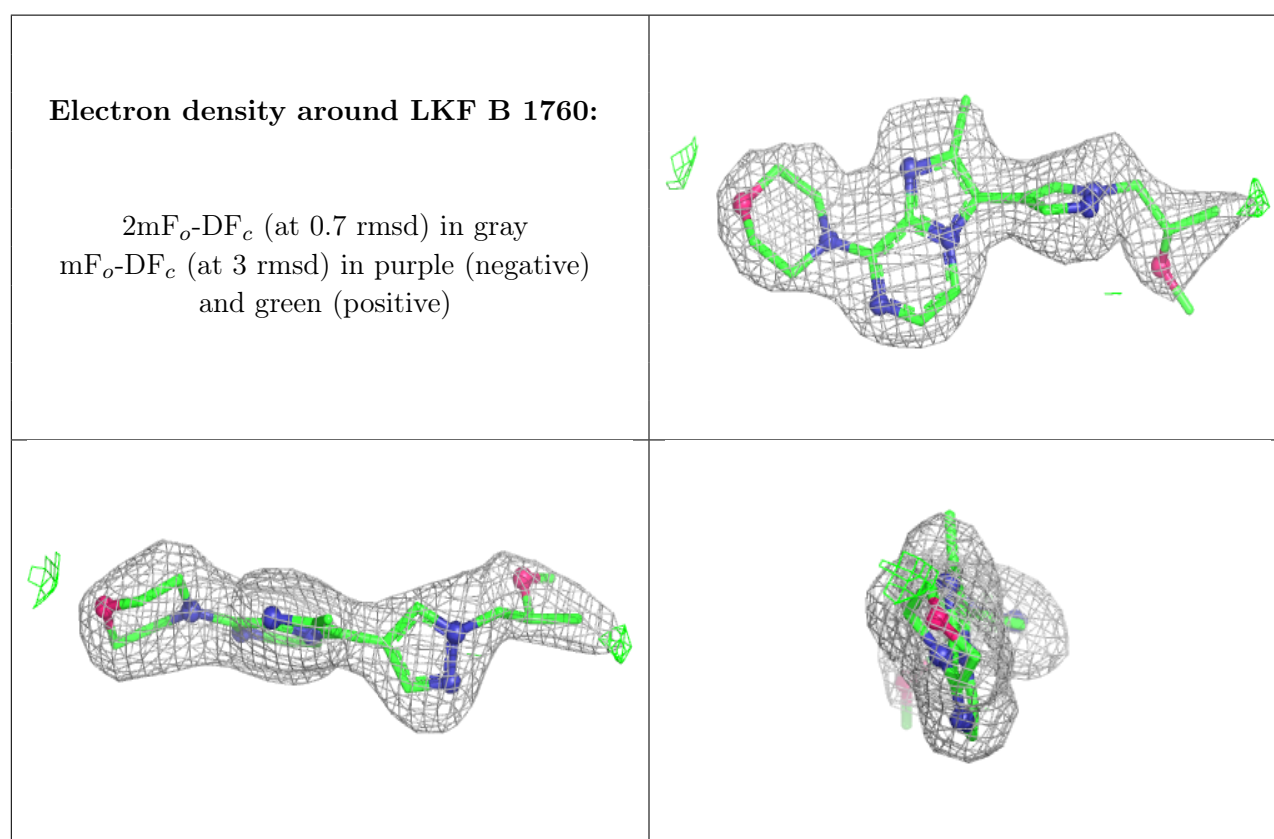
There are no oligosaccharides in this entry.

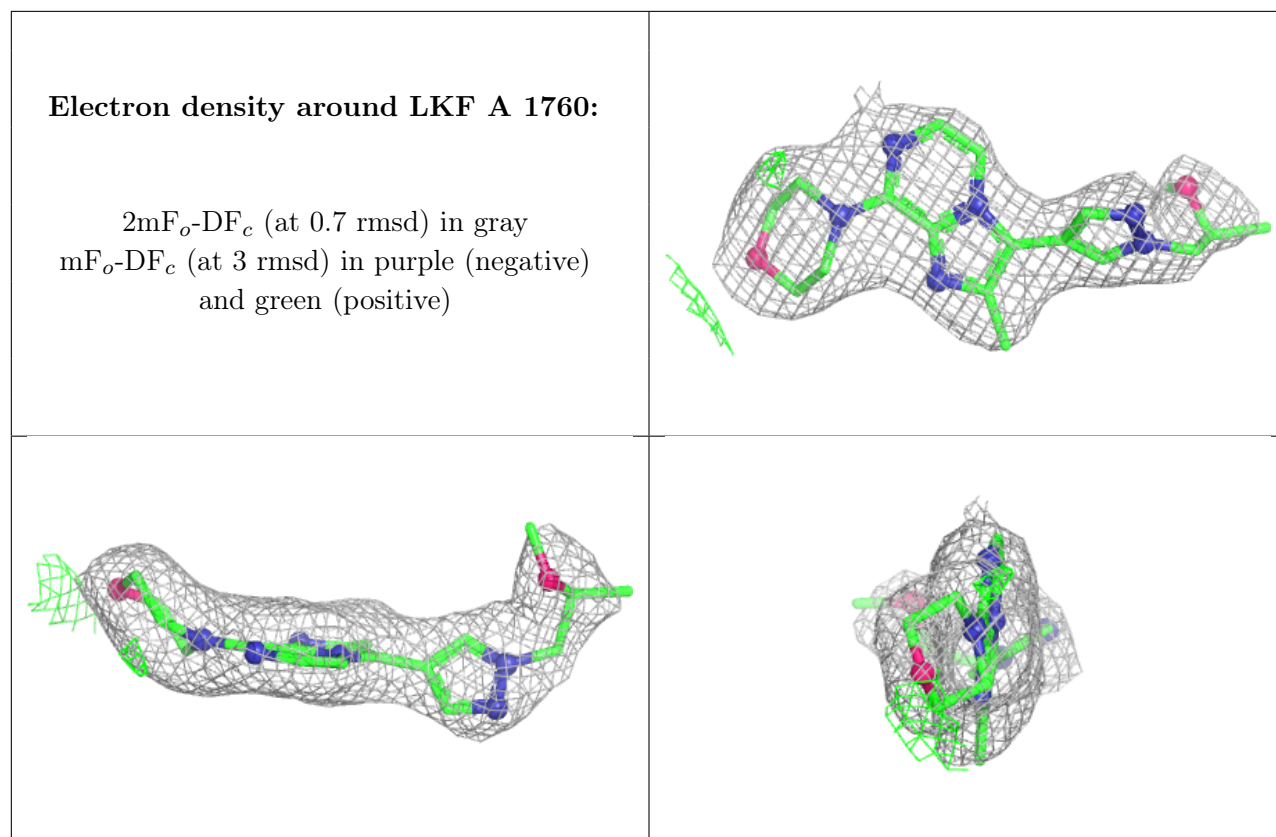
6.4 Ligands [i](#)

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(\AA^2)	Q<0.9
2	LKF	B	1760	26/26	0.86	0.12	49,51,57,58	0
2	LKF	A	1760	26/26	0.90	0.10	60,61,63,63	0
3	ZN	A	1761	1/1	1.00	0.02	47,47,47,47	0
3	ZN	B	1761	1/1	1.00	0.03	50,50,50,50	0
4	MG	A	1762	1/1	1.00	0.02	29,29,29,29	0
4	MG	B	1762	1/1	1.00	0.04	29,29,29,29	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.