



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 08:38 am BST

PDB ID : 4YBI
Title : Crystal structure of BACE with amino thiazine inhibitor LY2811376
Authors : Timm, D.E.
Deposited on : 2015-02-18
Resolution : 1.84 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

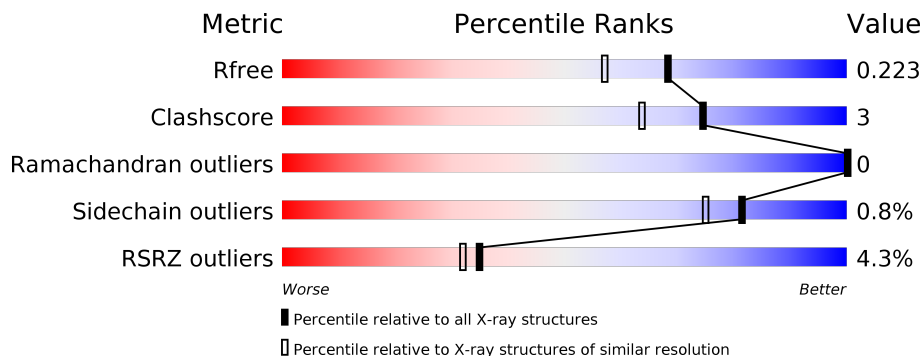
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.84 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	4003 (1.86-1.82)
Clashscore	141614	4233 (1.86-1.82)
Ramachandran outliers	138981	4185 (1.86-1.82)
Sidechain outliers	138945	4186 (1.86-1.82)
RSRZ outliers	127900	3957 (1.86-1.82)

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	442	 4% 81% 6% 12%
1	B	442	 4% 82% 5% 12%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6994 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.

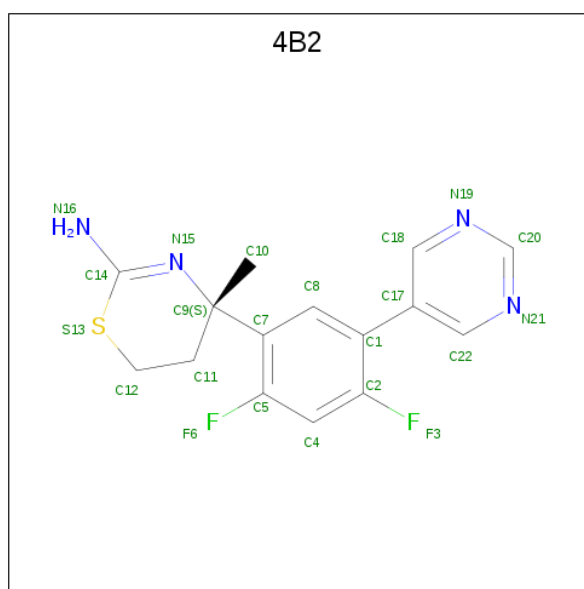
- Molecule 1 is a protein called Beta-secretase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	388	Total 3081	C 1978	N 507	O 582	S 14	0	7	0
1	B	388	Total 3091	C 1987	N 507	O 583	S 14	0	9	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-48	MET	-	initiating methionine	UNP P56817
B	-48	MET	-	initiating methionine	UNP P56817

- Molecule 2 is (4S)-4-[2,4-difluoro-5-(pyrimidin-5-yl)phenyl]-4-methyl-5,6-dihydro-4H-1,3-thiazin-2-amine (three-letter code: 4B2) (formula: C₁₅H₁₄F₂N₄S).



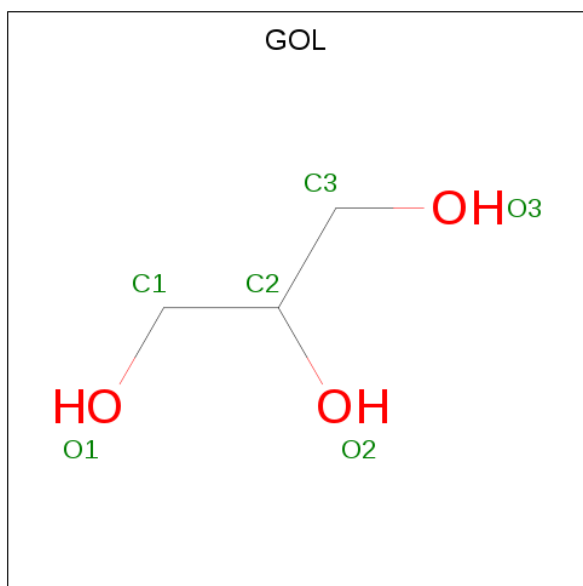
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	F	N	S		
2	A	1	Total 22	C 15	F 2	N 4	S 1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	F	N	S		
2	B	1	22	15	2	4	1	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	6	3	3	0	0
3	A	1	6	3	3	0	0
3	B	1	6	3	3	0	0
3	B	1	6	3	3	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	379	379	379	0	0
4	B	375	375	375	0	0

4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	86.77Å 90.79Å 131.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	23.30 – 1.84 22.87 – 1.84	Depositor EDS
% Data completeness (in resolution range)	99.9 (23.30-1.84) 99.9 (22.87-1.84)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.13 (at 1.84Å)	Xtrriage
Refinement program	REFMAC 5.8.0069	Depositor
R, R_{free}	0.179 , 0.223 0.180 , 0.223	Depositor DCC
R_{free} test set	1058 reflections (1.17%)	wwPDB-VP
Wilson B-factor (Å ²)	19.2	Xtrriage
Anisotropy	0.746	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 56.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.000 for k,h,-l	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6994	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 45.69 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.2739e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: GOL, 4B2

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	0/3179	0.69	0/4321
1	B	0.55	0/3196	0.67	0/4346
All	All	0.57	0/6375	0.68	0/8667

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	197	TRP	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	3081	0	3012	20	0
1	B	3091	0	3030	18	0
2	A	22	0	14	0	0
2	B	22	0	14	2	0
3	A	12	0	16	0	0
3	B	12	0	16	0	0
4	A	379	0	0	2	0
4	B	375	0	0	5	0
All	All	6994	0	6102	39	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 (39) 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:364[A]:GLU:HG3	4:A:535:HOH:O	1.75	0.87
1:B:300:ILE:HD13	1:B:337[A]:ILE:HD12	1.55	0.87
1:A:234:LEU:HD13	1:A:337:ILE:HD11	1.64	0.79
1:B:364[B]:GLU:HG3	4:B:523:HOH:O	1.86	0.74
1:A:-3:GLY:HA2	1:A:181:HIS:HD2	1.52	0.74
1:B:71:TYR:HE1	4:B:738:HOH:O	1.74	0.70
1:A:163:GLN:O	1:A:167:LEU:HG	1.94	0.67
1:A:-3:GLY:HA2	1:A:181:HIS:CD2	2.31	0.66
1:B:118[B]:ILE:CD1	2:B:401:4B2:H4	2.30	0.61
1:A:234:LEU:HD13	1:A:337:ILE:CD1	2.31	0.60
1:B:71:TYR:CE1	4:B:738:HOH:O	2.52	0.59
1:B:288:MET:HE2	1:B:379:MET:HB3	1.88	0.55
1:B:267:LEU:HD13	1:B:269:CYS:SG	2.46	0.55
1:A:125:GLU:CD	1:A:195:ARG:HH21	2.10	0.54
1:A:364[B]:GLU:HG2	4:A:879:HOH:O	2.09	0.52
1:B:30[A]:LEU:HD23	1:B:118[A]:ILE:HG12	1.92	0.51
1:A:267:LEU:HD13	1:A:269:CYS:SG	2.50	0.51
1:B:73:GLN:HB3	4:B:730:HOH:O	2.12	0.49
2:B:401:4B2:F6	2:B:401:4B2:H5	2.04	0.48
1:A:125:GLU:OE2	1:A:195:ARG:NH2	2.43	0.47
1:B:222:TYR:HA	1:B:223:ASP:HA	1.74	0.46
1:B:2:MET:HG2	1:B:90:GLY:HA2	1.96	0.46
1:A:199:TYR:HB3	1:A:352[B]:ILE:HD11	1.97	0.46
1:B:149[B]:LEU:HD23	4:B:844:HOH:O	2.17	0.45
1:B:300:ILE:HD13	1:B:337[A]:ILE:CD1	2.38	0.44
1:A:1[A]:GLU:HG2	1:A:2:MET:HG3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:PRO:CB	1:A:310:GLU:HG3	2.48	0.44
1:A:165:GLU:O	1:A:169:SER:HB3	2.19	0.42
1:A:2:MET:HG2	1:A:90:GLY:HA2	2.00	0.42
1:A:222:TYR:HA	1:A:223:ASP:HA	1.77	0.42
1:B:205:ARG:HB3	1:B:286:TYR:HB2	2.02	0.42
1:B:125:GLU:CD	1:B:195:ARG:HH21	2.23	0.41
1:A:163:GLN:HA	1:A:166:VAL:HG22	2.03	0.41
1:A:160:PRO:HB2	1:A:310:GLU:HG3	2.03	0.41
1:B:30[A]:LEU:HB3	1:B:118[A]:ILE:HG12	2.02	0.40
1:A:30:LEU:HD23	1:A:118[B]:ILE:HG22	2.03	0.40
1:A:65:LYS:HE3	1:A:80:LEU:HD12	2.03	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	391/442 (88%)	385 (98%)	6 (2%)	0	100	100
1	B	395/442 (89%)	389 (98%)	6 (2%)	0	100	100
All	All	786/884 (89%)	774 (98%)	12 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	337/373 (90%)	336 (100%)	1 (0%)	92	90
1	B	339/373 (91%)	335 (99%)	4 (1%)	71	61
All	All	676/746 (91%)	671 (99%)	5 (1%)	81	78

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	197	TRP
1	B	72	THR
1	B	75	LYS
1	B	169	SER
1	B	197	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	114	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](#)

6 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	4B2	A	401	-	22,24,24	0.74	1 (4%)	24,35,35	1.71	3 (12%)
3	GOL	A	402	-	5,5,5	0.36	0	5,5,5	0.48	0
3	GOL	B	403	-	5,5,5	0.15	0	5,5,5	0.50	0
3	GOL	A	403	-	5,5,5	0.19	0	5,5,5	0.71	0
2	4B2	B	401	-	22,24,24	0.76	1 (4%)	24,35,35	1.41	1 (4%)
3	GOL	B	402	-	5,5,5	0.42	0	5,5,5	0.48	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	4B2	A	401	-	-	0/10/22/22	0/3/3/3
3	GOL	A	402	-	-	2/4/4/4	-
3	GOL	B	403	-	-	2/4/4/4	-
3	GOL	A	403	-	-	0/4/4/4	-
2	4B2	B	401	-	-	0/10/22/22	0/3/3/3
3	GOL	B	402	-	-	2/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	4B2	C14-N16	2.14	1.39	1.34
2	A	401	4B2	C14-N16	2.07	1.38	1.34

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	4B2	C10-C9-N15	-7.14	98.28	108.24
2	B	401	4B2	C10-C9-N15	-4.96	101.32	108.24
2	A	401	4B2	C12-C11-C9	-2.10	111.20	114.50
2	A	401	4B2	C18-C17-C1	2.05	125.04	121.45

There are no chirality outliers.

All (6) torsion outliers are listed below:

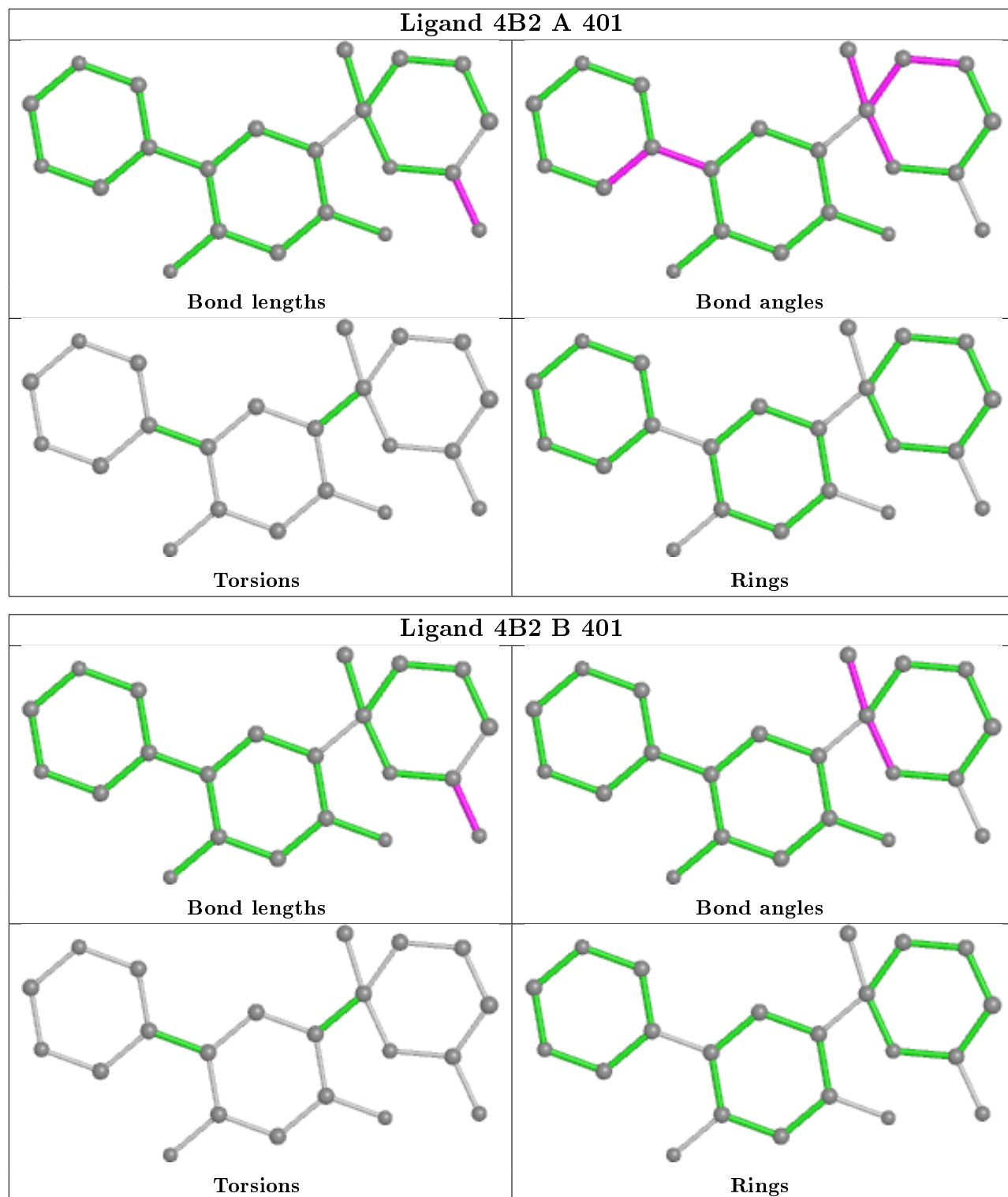
Mol	Chain	Res	Type	Atoms
3	B	403	GOL	C1-C2-C3-O3
3	B	403	GOL	O2-C2-C3-O3
3	A	402	GOL	O1-C1-C2-C3
3	B	402	GOL	O1-C1-C2-C3
3	A	402	GOL	O1-C1-C2-O2
3	B	402	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	4B2	2	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

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	388/442 (87%)	-0.05	16 (4%) 37 34	12, 21, 42, 66	0
1	B	388/442 (87%)	-0.02	17 (4%) 34 31	14, 22, 44, 81	0
All	All	776/884 (87%)	-0.03	33 (4%) 35 32	12, 22, 43, 81	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	312	VAL	6.9
1	B	312	VAL	6.2
1	B	314	THR	6.1
1	B	-2	SER	5.8
1	B	72	THR	4.4
1	B	73	GLN	4.3
1	B	163	GLN	4.2
1	B	313	ALA	3.7
1	A	313	ALA	3.5
1	B	74	GLY	3.4
1	A	72	THR	3.2
1	A	73	GLN	3.2
1	A	163	GLN	3.0
1	B	380	GLU	2.9
1	A	68	TYR	2.8
1	A	380	GLU	2.6
1	B	259	ASP	2.6
1	B	0	VAL	2.6
1	B	381	ASP	2.4
1	B	384	TYR	2.3
1	B	145	HIS	2.3
1	A	49	HIS	2.3
1	A	145	HIS	2.2
1	B	49	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	378	ASP	2.2
1	A	111	ASN	2.1
1	A	118[A]	ILE	2.1
1	A	378	ASP	2.1
1	A	381	ASP	2.1
1	B	216	ASP	2.1
1	A	164	SER	2.1
1	A	39	ALA	2.1
1	A	47	PHE	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](#)

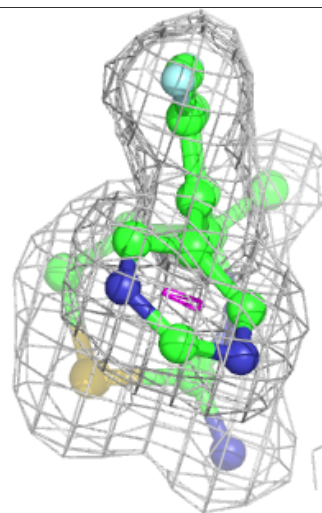
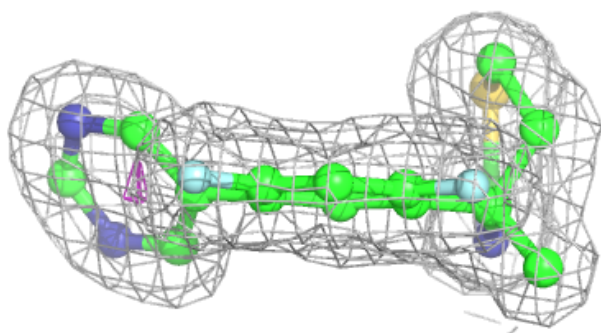
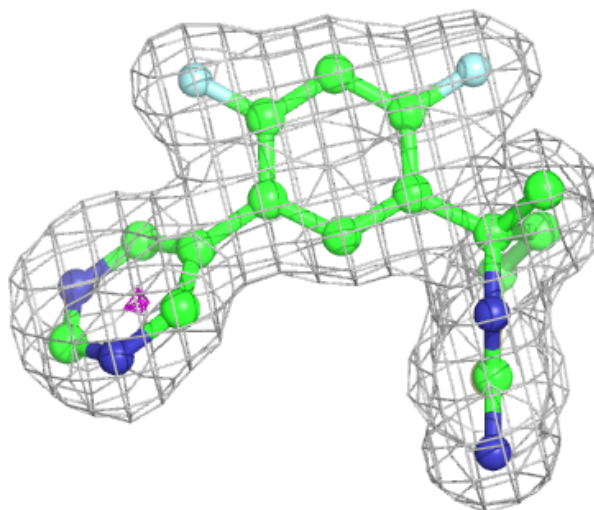
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	GOL	B	403	6/6	0.79	0.22	57,62,67,68	0
3	GOL	A	403	6/6	0.90	0.18	44,49,54,59	0
3	GOL	B	402	6/6	0.92	0.12	31,33,35,36	0
3	GOL	A	402	6/6	0.93	0.12	34,35,41,41	0
2	4B2	B	401	22/22	0.95	0.07	22,25,28,28	0
2	4B2	A	401	22/22	0.97	0.09	22,24,29,30	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.

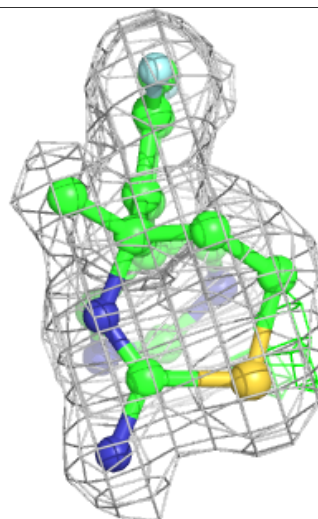
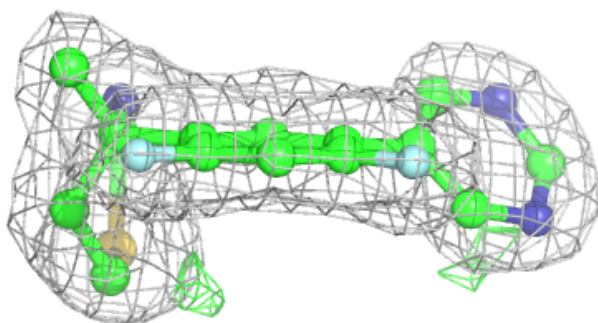
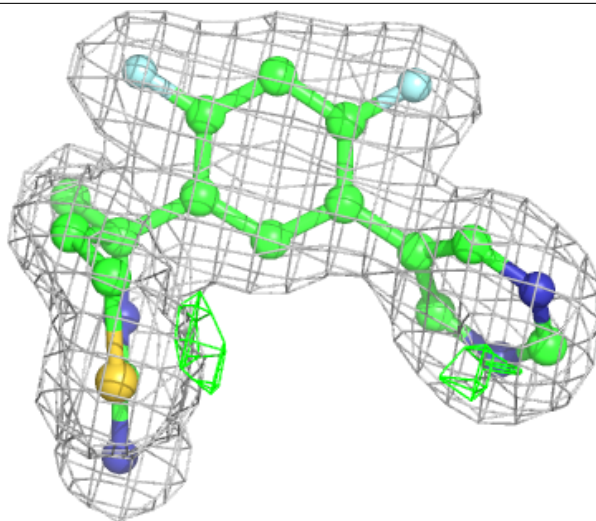
Electron density around 4B2 B 401:

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



Electron density around 4B2 A 401:

$2mF_o-DF_c$ (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.