



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 02:48 PM UTC

PDB ID : 9FHE / pdb_00009fhe
Title : hKHK-C in complex with BI-9787 (pH 5.5)
Authors : Ebenhoch, R.; Pautsch, A.
Deposited on : 2024-05-27
Resolution : 2.31 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

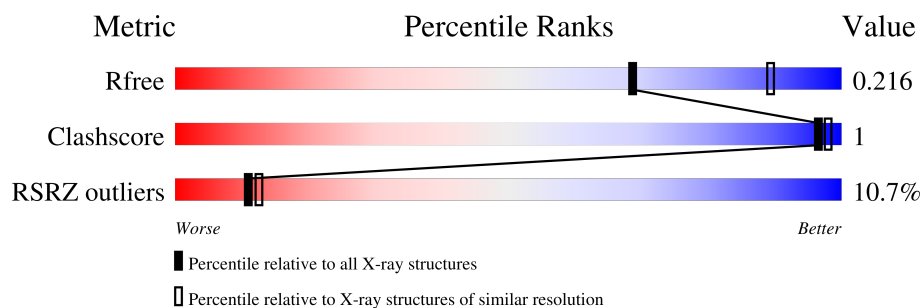
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.31 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	7754 (2.34-2.30)
Clashscore	190562	8383 (2.34-2.30)
RSRZ outliers	180081	7760 (2.34-2.30)

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	313	14% 90% 5% 5%
1	B	313	6% 95% • •

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9477 atoms, of which 4575 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 Ketohexokinase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	296	Total	C	H	N	O	S	2237	0	0
			4496	1414	2237	405	428	12			
1	B	301	Total	C	H	N	O	S	2280	0	0
			4576	1438	2280	413	433	12			

There are 38 discrepancies between the modelled and reference sequences:

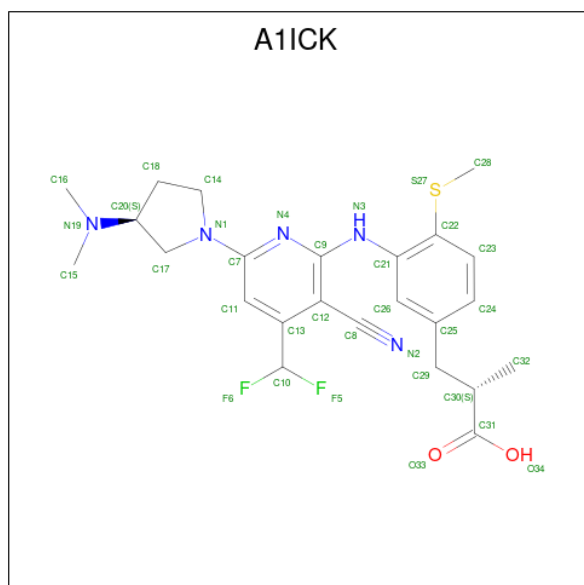
Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	MET	-	initiating methionine	UNP P50053
A	-13	GLY	-	expression tag	UNP P50053
A	-12	SER	-	expression tag	UNP P50053
A	-11	SER	-	expression tag	UNP P50053
A	-10	HIS	-	expression tag	UNP P50053
A	-9	HIS	-	expression tag	UNP P50053
A	-8	HIS	-	expression tag	UNP P50053
A	-7	HIS	-	expression tag	UNP P50053
A	-6	HIS	-	expression tag	UNP P50053
A	-5	HIS	-	expression tag	UNP P50053
A	-4	SER	-	expression tag	UNP P50053
A	-3	SER	-	expression tag	UNP P50053
A	-2	GLY	-	expression tag	UNP P50053
A	-1	LEU	-	expression tag	UNP P50053
A	0	VAL	-	expression tag	UNP P50053
A	1	PRO	-	expression tag	UNP P50053
A	2	ARG	-	expression tag	UNP P50053
A	3	GLY	-	expression tag	UNP P50053
A	4	SER	-	expression tag	UNP P50053
B	-14	MET	-	initiating methionine	UNP P50053
B	-13	GLY	-	expression tag	UNP P50053
B	-12	SER	-	expression tag	UNP P50053
B	-11	SER	-	expression tag	UNP P50053
B	-10	HIS	-	expression tag	UNP P50053
B	-9	HIS	-	expression tag	UNP P50053

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-8	HIS	-	expression tag	UNP P50053
B	-7	HIS	-	expression tag	UNP P50053
B	-6	HIS	-	expression tag	UNP P50053
B	-5	HIS	-	expression tag	UNP P50053
B	-4	SER	-	expression tag	UNP P50053
B	-3	SER	-	expression tag	UNP P50053
B	-2	GLY	-	expression tag	UNP P50053
B	-1	LEU	-	expression tag	UNP P50053
B	0	VAL	-	expression tag	UNP P50053
B	1	PRO	-	expression tag	UNP P50053
B	2	ARG	-	expression tag	UNP P50053
B	3	GLY	-	expression tag	UNP P50053
B	4	SER	-	expression tag	UNP P50053

- Molecule 2 is (2 {S})-3-[3-[[4-[bis(fluoranyl)methyl]-3-cyano-6-[(3 {S})-3-(dimethylamino)pyrrolidin-1-yl]pyridin-2-yl]amino]-4-methylsulfanyl-phenyl]-2-methyl-propanoic acid (CCD ID: A1ICK) (formula: C₂₄H₂₉F₂N₅O₂S) (labeled as "Ligand of Interest" by depositor).

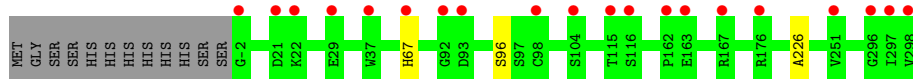


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	F	H	N	O	S	
			63	24	2	29	5	2	1	29
2	B	1	Total	C	F	H	N	O	S	
			63	24	2	29	5	2	1	29

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	118	Total 118	O 118	0	0
3	B	161	Total 161	O 161	0	0

- Molecule 1: Ketohexokinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	81.66Å 83.12Å 146.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	72.30 – 2.31 72.30 – 2.31	Depositor EDS
% Data completeness (in resolution range)	70.3 (72.30-2.31) 70.3 (72.30-2.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 2.32Å)	Xtriage
Refinement program	BUSTER 2.11.8	Depositor
R, R_{free}	0.218 , 0.235 (Not available) , 0.216	Depositor DCC
R_{free} test set	1519 reflections (3.43%)	wwPDB-VP
Wilson B-factor (Å ²)	59.2	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 44.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.000 for k,h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9477	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.30% 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: A1ICK

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	0.75	1/2301 (0.0%)	0.96	0/3111
1	B	0.74	1/2339 (0.0%)	0.97	0/3163
All	All	0.74	2/4640 (0.0%)	0.96	0/6274

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	226	ALA	CA-C	6.34	1.61	1.52
1	B	226	ALA	CA-C	5.67	1.60	1.52

There are no bond angle outliers.

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	2259	2237	2237	9	0
1	B	2296	2280	2283	2	0
2	A	34	29	0	1	0
2	B	34	29	0	0	0
3	A	118	0	0	0	0
3	B	161	0	0	0	0
All	All	4902	4575	4520	9	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 1.

All (9) 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:113:HIS:CE1	1:A:115:THR:HG22	2.39	0.58
1:A:242:SER:OG	1:A:279:ARG:HD2	2.10	0.52
1:A:101:ILE:HD13	1:A:252:ASP:OD1	2.14	0.47
1:A:35:GLN:NE2	1:B:96:SER:OG	2.48	0.41
1:A:247:PRO:HD2	2:A:301:A1ICK:F5	2.11	0.41
1:A:156:HIS:O	1:A:160:GLN:HG2	2.21	0.41
1:A:245:PHE:CE1	1:A:279:ARG:NH2	2.89	0.40
1:A:37:TRP:CZ3	1:B:67:HIS:HB3	2.56	0.40
1:A:193:LYS:HE2	1:A:225:TRP:NE1	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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

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	A1ICK	B	301	-	34,36,36	0.49	0	40,51,51	0.67	1 (2%)
2	A1ICK	A	301	-	34,36,36	0.50	0	40,51,51	0.96	4 (10%)

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	A1ICK	B	301	-	-	6/27/37/37	0/3/3/3
2	A1ICK	A	301	-	-	5/27/37/37	0/3/3/3

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	A1ICK	C21-N3-C9	2.81	137.51	129.28
2	A	301	A1ICK	C29-C30-C31	2.32	114.88	110.18
2	A	301	A1ICK	C15-N19-C20	2.15	116.09	112.39
2	A	301	A1ICK	C32-C30-C31	-2.09	103.66	109.16
2	B	301	A1ICK	C15-N19-C20	2.03	115.89	112.39

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	A1ICK	C18-C20-N19-C16
2	B	301	A1ICK	C18-C20-N19-C16
2	A	301	A1ICK	C23-C22-S27-C28

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Mol	Chain	Res	Type	Atoms
2	A	301	A1ICK	C21-C22-S27-C28
2	B	301	A1ICK	C23-C22-S27-C28
2	A	301	A1ICK	C24-C25-C29-C30
2	B	301	A1ICK	C21-C22-S27-C28
2	A	301	A1ICK	C26-C25-C29-C30
2	B	301	A1ICK	C32-C30-C31-O33
2	B	301	A1ICK	C32-C30-C31-O34
2	B	301	A1ICK	C29-C30-C31-O34

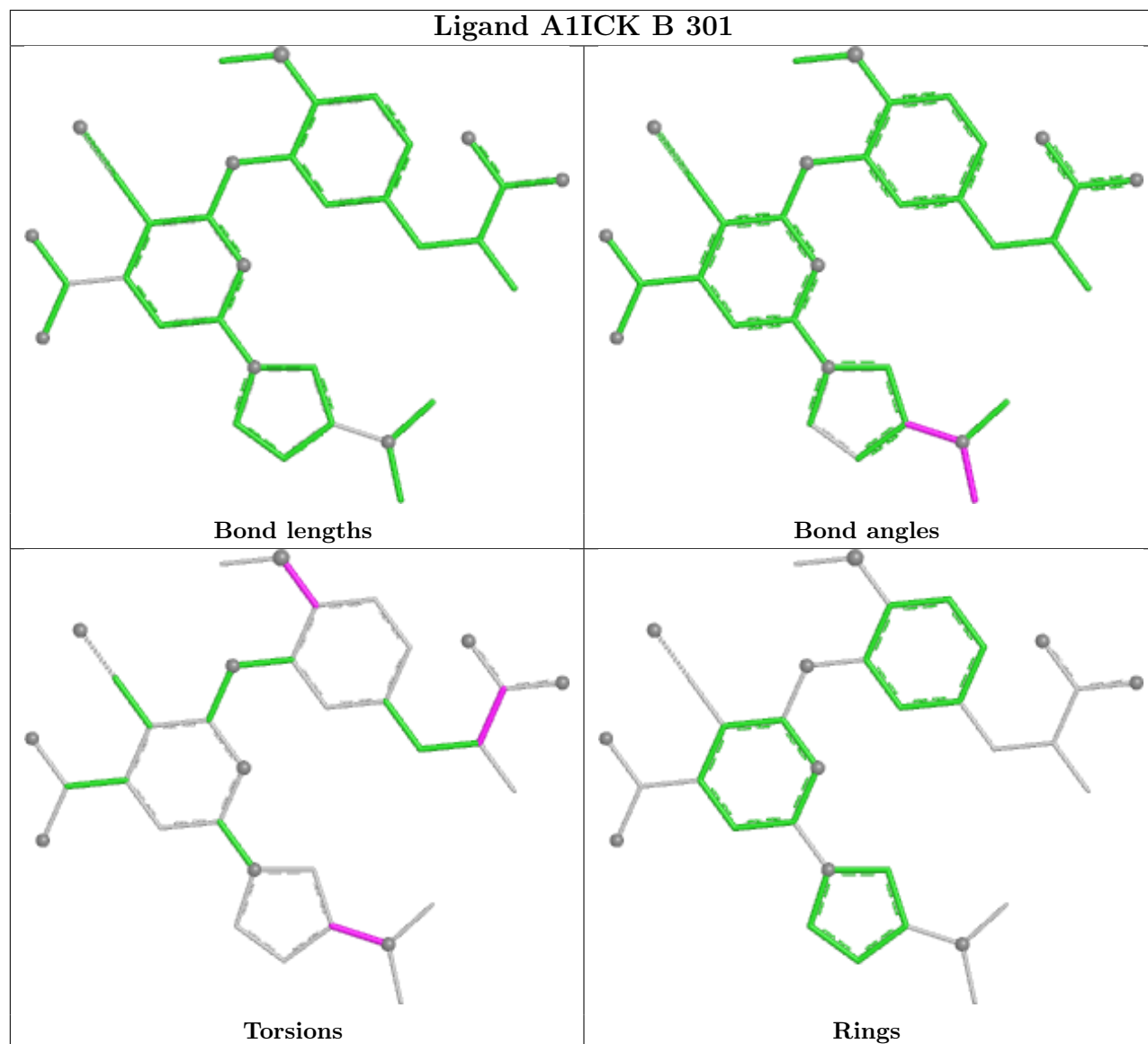
There are no ring outliers.

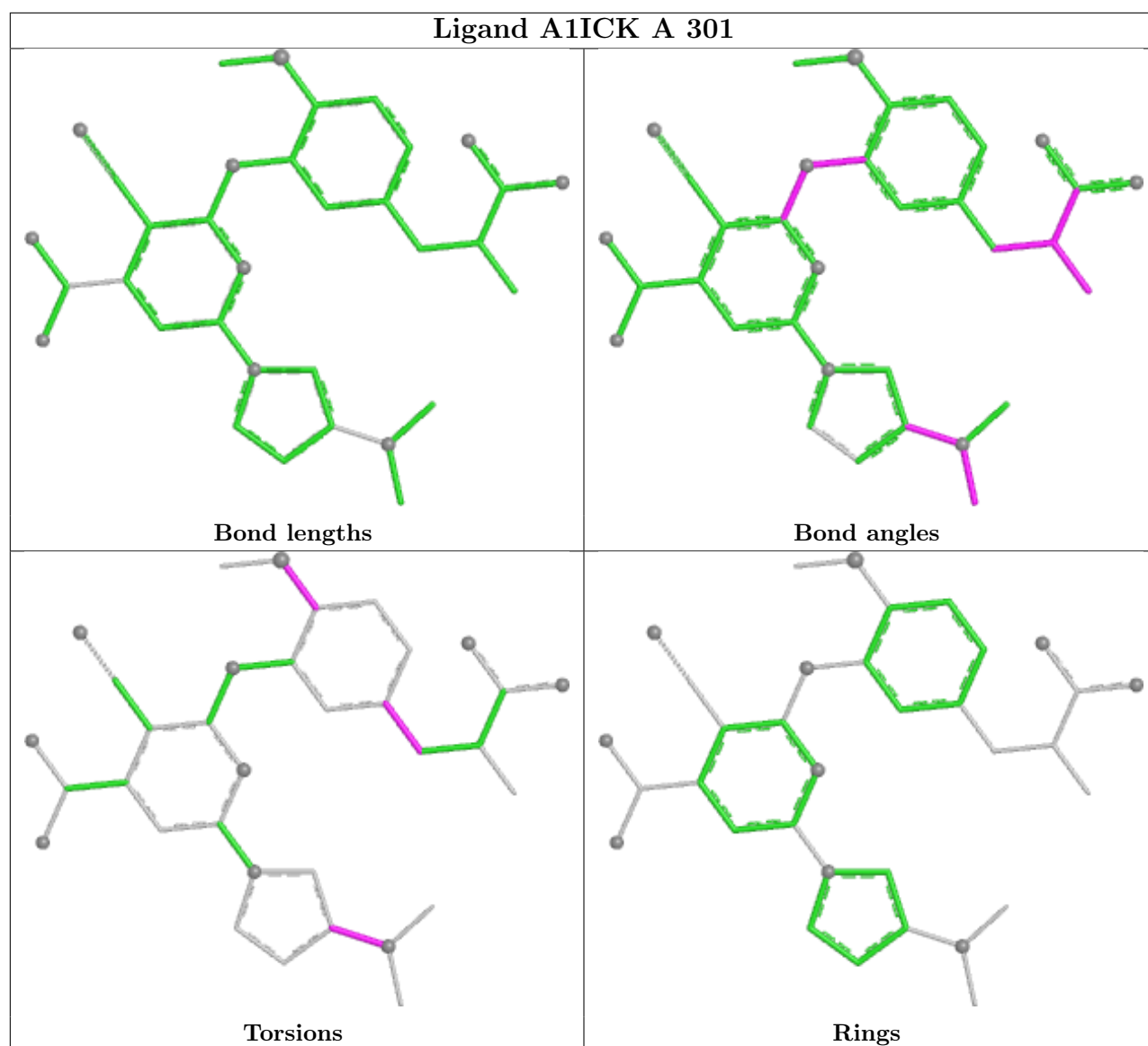
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	A1ICK	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.

Ligand A1ICK B 301





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	296/313 (94%)	1.08	44 (14%) 5 6	21, 37, 56, 67	0
1	B	301/313 (96%)	0.53	20 (6%) 24 27	18, 29, 45, 55	0
All	All	597/626 (95%)	0.80	64 (10%) 11 12	18, 32, 52, 67	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	298	VAL	6.1
1	A	90	SER	4.8
1	A	295	ASP	4.7
1	A	91	LYS	4.7
1	A	67	HIS	4.6
1	A	115	THR	4.6
1	B	298	VAL	4.1
1	A	92	GLY	3.9
1	B	163	GLU	3.7
1	A	116	SER	3.5
1	A	78	ARG	3.5
1	A	162	PRO	3.5
1	B	296	GLY	3.4
1	A	161	PRO	3.3
1	A	93	ASP	3.2
1	B	37	TRP	3.1
1	A	88	TRP	3.1
1	B	297	ILE	3.0
1	A	165	LYS	3.0
1	B	162	PRO	3.0
1	A	120	VAL	3.0
1	A	61	GLY	3.0
1	A	79	ARG	3.0
1	A	164	GLN	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	114	ASP	2.9
1	A	3	GLY	2.8
1	A	159	ARG	2.8
1	A	158	THR	2.8
1	A	180	PHE	2.8
1	A	296	GLY	2.7
1	A	182	LEU	2.7
1	B	251	VAL	2.7
1	B	21	ASP	2.7
1	A	205	GLU	2.7
1	B	115	THR	2.6
1	B	176	ARG	2.6
1	B	92	GLY	2.5
1	A	127	LYS	2.5
1	A	297	ILE	2.5
1	B	116	SER	2.4
1	A	209	ARG	2.4
1	B	104	SER	2.4
1	A	11	LEU	2.4
1	A	21	ASP	2.3
1	A	166	ILE	2.3
1	A	70	ASP	2.3
1	A	94	THR	2.3
1	A	129	ASP	2.3
1	B	29	GLU	2.3
1	A	37	TRP	2.3
1	A	71	PHE	2.2
1	B	93	ASP	2.2
1	A	198	HIS	2.2
1	A	35	GLN	2.2
1	A	117	LEU	2.2
1	B	98	CYS	2.2
1	A	123	THR	2.1
1	B	22	LYS	2.1
1	A	163	GLU	2.1
1	B	-2	GLY	2.1
1	B	67	HIS	2.0
1	A	124	ASP	2.0
1	A	176	ARG	2.0
1	B	167	ARG	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](#)

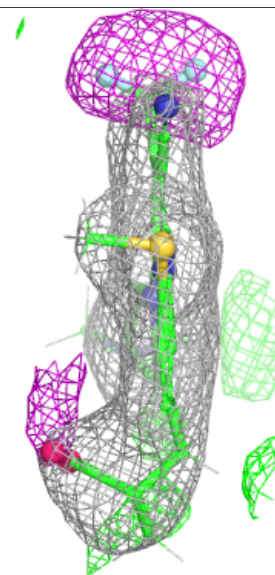
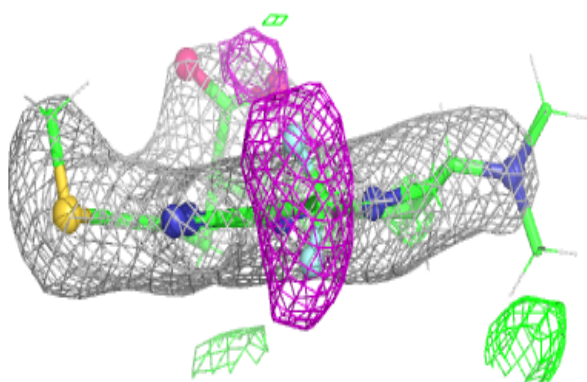
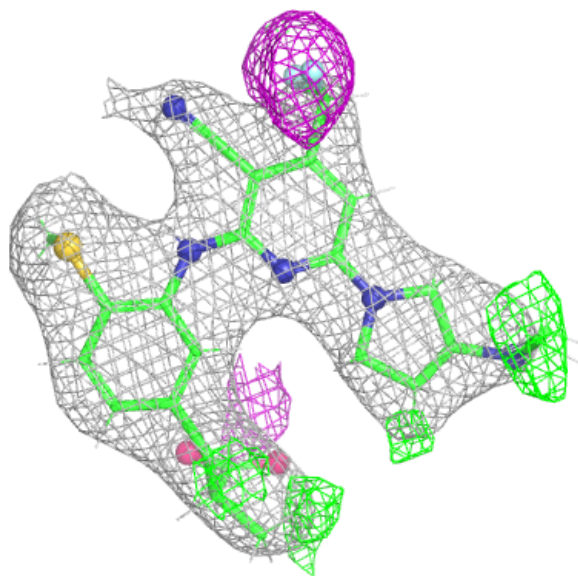
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	A1ICK	B	301	34/34	0.86	0.19	57,66,69,70	63
2	A1ICK	A	301	34/34	0.88	0.17	54,60,62,64	63

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.

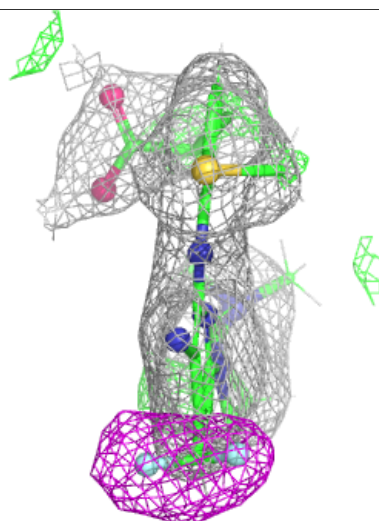
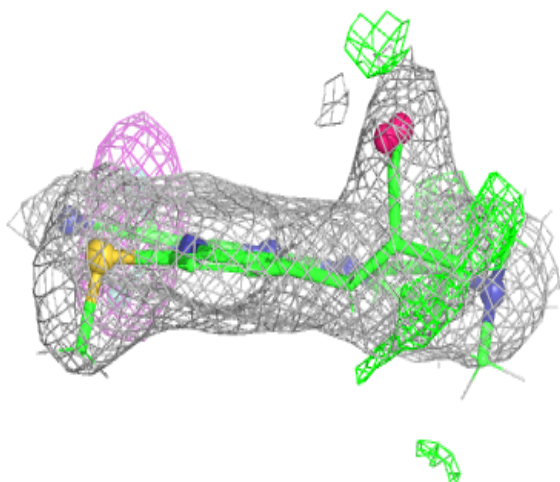
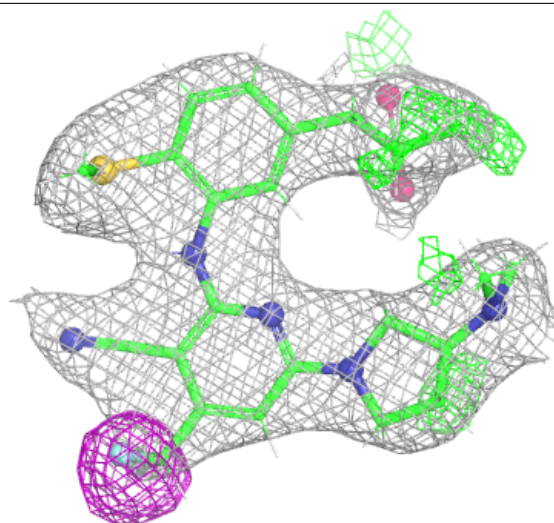
Electron density around A1ICK B 301:

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



Electron density around A1ICK A 301:

$2mF_o-DF_c$ (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.