



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 09:52 PM UTC

PDB ID : 10SL / pdb\_000010sl  
Title : Crystal Structure of serine/threonine-protein kinase (AEK1) from Trypanosoma cruzi in complex with Hesperadin  
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)  
Deposited on : 2026-02-05  
Resolution : 2.72 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](mailto: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>.

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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

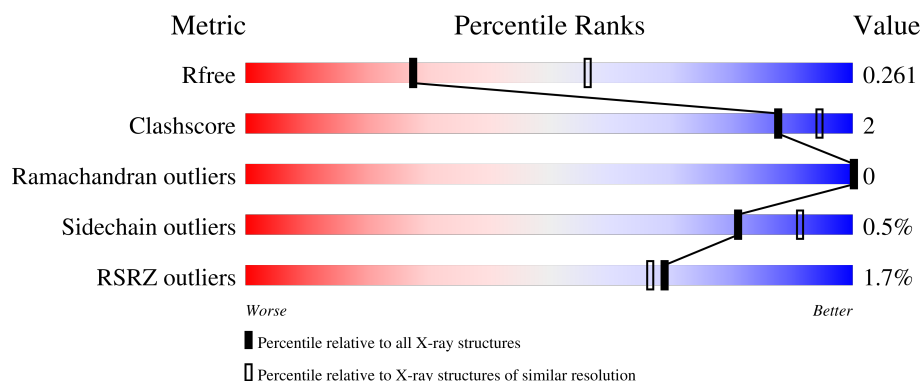
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.72 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	4348 (2.74-2.70)
Clashscore	190562	4665 (2.74-2.70)
Ramachandran outliers	187476	4584 (2.74-2.70)
Sidechain outliers	187428	4585 (2.74-2.70)
RSRZ outliers	180081	4348 (2.74-2.70)

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  $\geq 3$ , 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	361	<div> <div>%</div> <div> <div></div> <div>90%</div> <div>6%</div> </div> </div>
1	B	361	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>7%</div> <div>10%</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5417 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 Putative rac serine-threonine kinase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	338	Total	C	N	O	P	S	0	0	0
			2711	1741	457	498	3	12			
1	B	325	Total	C	N	O	P	S	0	0	0
			2614	1683	440	477	2	12			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	122	MET	-	initiating methionine	UNP Q4E2L0
A	185	ILE	THR	engineered mutation	UNP Q4E2L0
A	227	PHE	VAL	engineered mutation	UNP Q4E2L0
A	314	SER	ASN	engineered mutation	UNP Q4E2L0
A	475	LEU	-	expression tag	UNP Q4E2L0
A	476	GLU	-	expression tag	UNP Q4E2L0
A	477	HIS	-	expression tag	UNP Q4E2L0
A	478	HIS	-	expression tag	UNP Q4E2L0
A	479	HIS	-	expression tag	UNP Q4E2L0
A	480	HIS	-	expression tag	UNP Q4E2L0
A	481	HIS	-	expression tag	UNP Q4E2L0
A	482	HIS	-	expression tag	UNP Q4E2L0
B	122	MET	-	initiating methionine	UNP Q4E2L0
B	185	ILE	THR	engineered mutation	UNP Q4E2L0
B	227	PHE	VAL	engineered mutation	UNP Q4E2L0
B	314	SER	ASN	engineered mutation	UNP Q4E2L0
B	475	LEU	-	expression tag	UNP Q4E2L0
B	476	GLU	-	expression tag	UNP Q4E2L0
B	477	HIS	-	expression tag	UNP Q4E2L0
B	478	HIS	-	expression tag	UNP Q4E2L0
B	479	HIS	-	expression tag	UNP Q4E2L0
B	480	HIS	-	expression tag	UNP Q4E2L0
B	481	HIS	-	expression tag	UNP Q4E2L0
B	482	HIS	-	expression tag	UNP Q4E2L0

- # H1N

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 37	C 29	N 4	O 3	S 1	0	0
2	B	1	Total 37	C 29	N 4	O 3	S 1	0	0

- MLI
- 
- Chemical structure of Malic acid (MLI) is shown. The structure consists of a central carbon atom (C1) bonded to a carboxylate group (C2=O6, C2-O7<sup>-</sup>), a hydroxyl group (C1-O8), and a carboxymethyl group (C3-COO<sup>-</sup>, where C3 is bonded to O9<sup>-</sup> and O8). The atoms are labeled with green text: C1, C2, C3, O6, O7, O8, O9. The oxygen atoms are shown in red with negative charges.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			7	3	4		

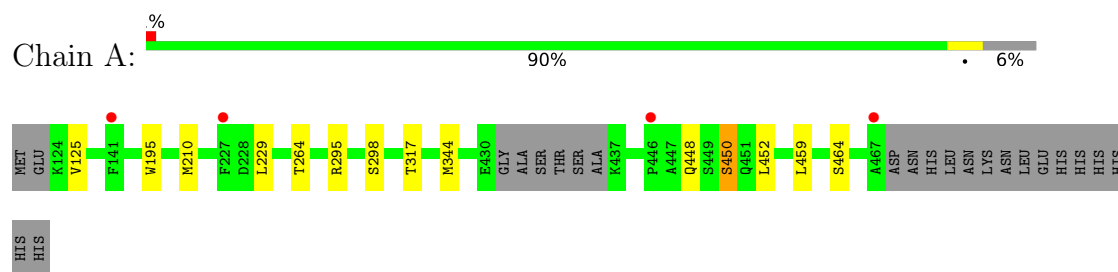
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	7	Total	O	0	0
			7	7		
4	B	4	Total	O	0	0
			4	4		

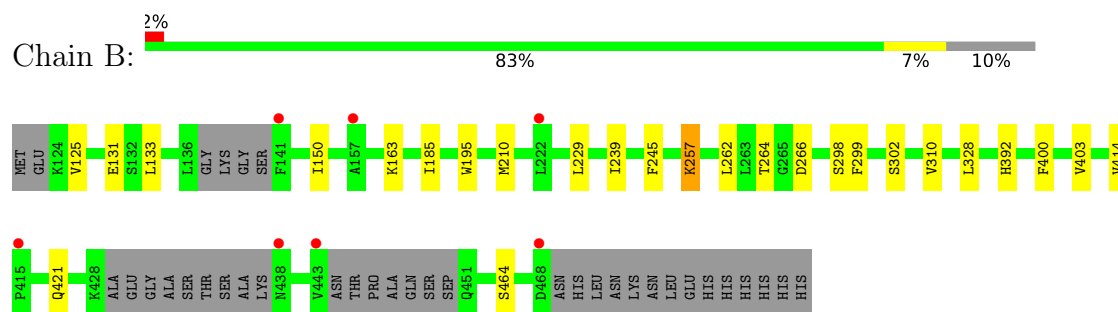
### 3 Residue-property plots

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: Putative rac serine-threonine kinase



- Molecule 1: Putative rac serine-threonine kinase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	86.52Å 86.52Å 193.04Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.82 – 2.72 48.82 – 2.72	Depositor EDS
% Data completeness (in resolution range)	99.6 (48.82-2.72) 99.9 (48.82-2.72)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.18 (at 2.73Å)	Xtriage
Refinement program	PHENIX (2.0_5936: ???)	Depositor
R, $R_{free}$	0.223 , 0.269 0.224 , 0.261	Depositor DCC
$R_{free}$ test set	1131 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	69.1	Xtriage
Anisotropy	0.582	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 67.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.020 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5417	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 39.28 % 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 3.2501e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: SEP, MLI, H1N

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	0.10	0/2746	0.29	0/3714
1	B	0.09	0/2656	0.28	0/3594
All	All	0.10	0/5402	0.28	0/7308

There are no bond length outliers.

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	2711	0	2637	7	0
1	B	2614	0	2538	15	0
2	A	37	0	31	0	0
2	B	37	0	31	2	0
3	B	7	0	2	1	0
4	A	7	0	0	0	0
4	B	4	0	0	0	0
All	All	5417	0	5239	21	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 2.



All (21) 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:B:239:ILE:HD13	1:B:328:LEU:HD21	1.86	0.57
1:B:131:GLU:HB2	1:B:150:ILE:HD11	1.92	0.52
1:B:210:MET:HE1	1:B:264:THR:HG22	1.92	0.51
1:A:344:MET:HE3	1:A:459:LEU:HB3	1.93	0.49
1:A:125:VAL:HG21	1:A:195:TRP:CG	2.47	0.49
1:B:414:VAL:HG23	1:B:414:VAL:O	2.14	0.47
1:B:400:PHE:HA	1:B:403:VAL:HG12	1.97	0.47
1:A:295:ARG:HH11	1:A:317:THR:HG22	1.80	0.46
1:B:229:LEU:C	1:B:229:LEU:HD23	2.41	0.46
1:B:185:ILE:HG23	1:B:245:PHE:HE2	1.79	0.46
1:A:210:MET:HE1	1:A:264:THR:HG22	1.99	0.44
1:A:229:LEU:C	1:A:229:LEU:HD13	2.43	0.44
1:A:448:GLN:O	1:A:450:SEP:N	2.52	0.43
1:B:210:MET:O	2:B:501:H1N:HAR	2.19	0.42
1:A:452:LEU:HD11	1:B:163:LYS:HB3	2.02	0.41
1:B:257:LYS:HD3	1:B:302:SER:OG	2.20	0.41
1:B:262:LEU:HD11	2:B:501:H1N:HAX2	2.03	0.41
1:B:125:VAL:HG21	1:B:195:TRP:CD1	2.56	0.41
1:B:299:PHE:CD2	1:B:310:VAL:HG12	2.55	0.41
1:B:131:GLU:O	1:B:133:LEU:HD12	2.20	0.40
1:B:392:HIS:NE2	3:B:502:MLI:H12	2.37	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	331/361 (92%)	322 (97%)	9 (3%)	0	100	100
1	B	315/361 (87%)	306 (97%)	9 (3%)	0	100	100
All	All	646/722 (90%)	628 (97%)	18 (3%)	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	286/317 (90%)	286 (100%)	0	100	100
1	B	277/317 (87%)	274 (99%)	3 (1%)	65	84
All	All	563/634 (89%)	560 (100%)	3 (0%)	81	91

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	257	LYS
1	B	266	ASP
1	B	421	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	162	ASN
1	A	381	ASN
1	A	441	GLN
1	A	456	GLN
1	B	421	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](#)

5 non-standard protein/DNA/RNA residues 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
1	SEP	A	298	1	8,9,10	1.62	1 (12%)	7,12,14	1.51	1 (14%)
1	SEP	A	450	1	8,9,10	1.63	1 (12%)	7,12,14	1.71	1 (14%)
1	SEP	A	464	1	8,9,10	1.63	1 (12%)	7,12,14	1.45	1 (14%)
1	SEP	B	464	1	8,9,10	1.60	1 (12%)	7,12,14	1.34	1 (14%)
1	SEP	B	298	1	8,9,10	1.59	1 (12%)	7,12,14	1.19	1 (14%)

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
1	SEP	A	298	1	-	0/6/8/10	-
1	SEP	A	450	1	-	1/6/8/10	-
1	SEP	A	464	1	-	1/6/8/10	-
1	SEP	B	464	1	-	0/6/8/10	-
1	SEP	B	298	1	-	0/6/8/10	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	450	SEP	P-O1P	3.56	1.61	1.50
1	A	298	SEP	P-O1P	3.54	1.61	1.50
1	A	464	SEP	P-O1P	3.54	1.61	1.50
1	B	464	SEP	P-O1P	3.52	1.61	1.50
1	B	298	SEP	P-O1P	3.46	1.61	1.50

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	450	SEP	OG-CB-CA	3.96	111.99	108.14
1	A	298	SEP	OG-CB-CA	3.55	111.60	108.14
1	A	464	SEP	OG-CB-CA	3.27	111.33	108.14
1	B	464	SEP	OG-CB-CA	3.01	111.08	108.14
1	B	298	SEP	OG-CB-CA	2.56	110.64	108.14

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	450	SEP	CB-OG-P-O2P
1	A	464	SEP	CB-OG-P-O2P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	450	SEP	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

3 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	H1N	A	501	-	39,41,41	1.40	3 (7%)	50,58,58	1.77	4 (8%)
2	H1N	B	501	-	39,41,41	1.46	3 (7%)	50,58,58	1.64	4 (8%)
3	MLI	B	502	-	6,6,6	1.53	1 (16%)	7,7,7	1.26	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	H1N	A	501	-	-	8/23/57/57	0/5/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	H1N	B	501	-	-	3/23/57/57	0/5/5/5
3	MLI	B	502	-	-	0/4/4/4	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	H1N	CBD-CBJ	-7.22	1.47	1.54
2	A	501	H1N	CBD-CBJ	-6.96	1.48	1.54
2	B	501	H1N	CBC-CBD	-4.54	1.45	1.51
2	A	501	H1N	CBC-CBD	-4.24	1.46	1.51
2	A	501	H1N	CAH-NAI	2.16	1.51	1.47
2	B	501	H1N	CAH-NAI	2.16	1.51	1.47
3	B	502	MLI	C1-C3	2.11	1.54	1.51

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	H1N	CAQ-NAP-CAO	10.69	135.74	120.63
2	B	501	H1N	CAQ-NAP-CAO	9.68	134.31	120.63
2	A	501	H1N	CBB-CBC-CBD	3.78	134.61	130.57
2	B	501	H1N	CBB-CBC-CBD	3.61	134.43	130.57
2	A	501	H1N	OBK-CBJ-CBD	3.31	127.80	126.39
2	B	501	H1N	OBK-CBJ-CBD	3.19	127.75	126.39
2	A	501	H1N	CBB-CBC-CBH	-2.73	118.63	120.48
2	B	501	H1N	CBB-CBC-CBH	-2.54	118.77	120.48

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	H1N	CAN-CAO-CBD-CBC
2	A	501	H1N	CBA-NAZ-SAY-OBE
2	A	501	H1N	CBA-NAZ-SAY-CAX
2	B	501	H1N	CAN-CAO-CBD-CBC
2	A	501	H1N	CAG-CAH-NAI-CAJ
2	B	501	H1N	CBA-NAZ-SAY-OAU
2	A	501	H1N	CAE-CAQ-NAP-CAO
2	A	501	H1N	CAT-CAX-SAY-NAZ
2	B	501	H1N	CBA-NAZ-SAY-CAX
2	A	501	H1N	CAT-CAX-SAY-OAU
2	A	501	H1N	CAR-CAQ-NAP-CAO

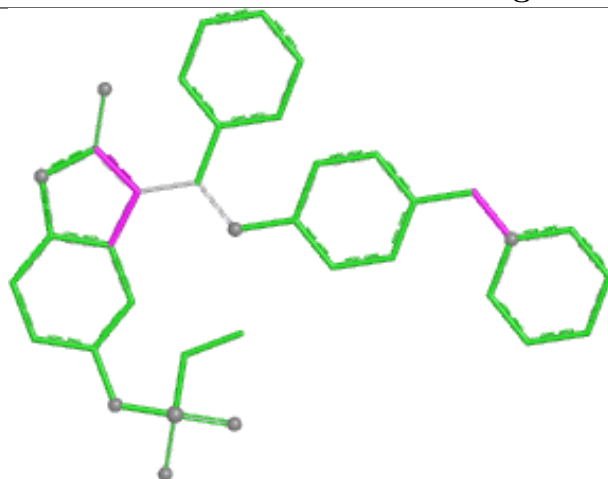
There are no ring outliers.

2 monomers are involved in 3 short contacts:

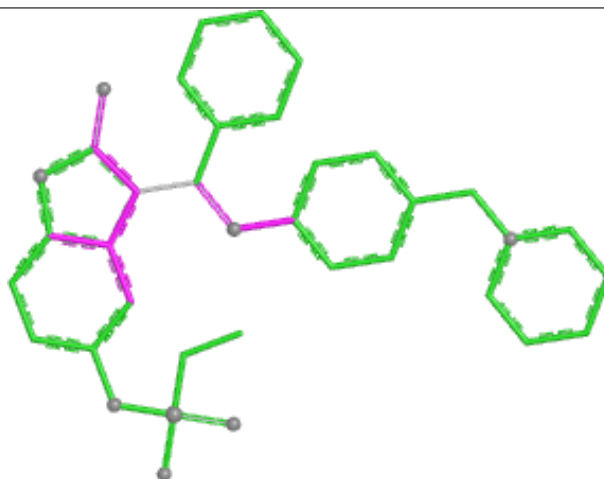
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	H1N	2	0
3	B	502	MLI	1	0

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.

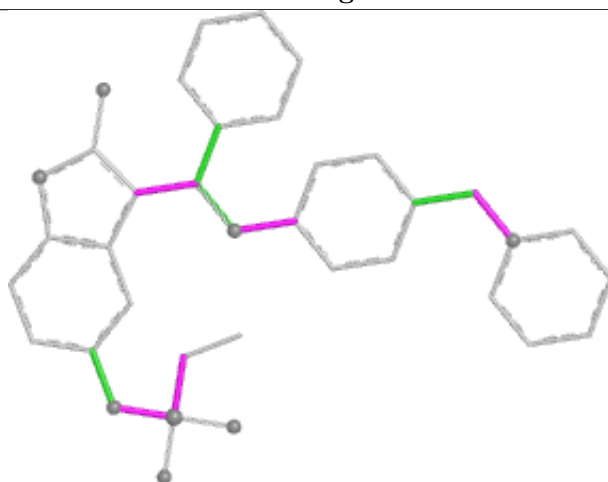
## Ligand H1N A 501



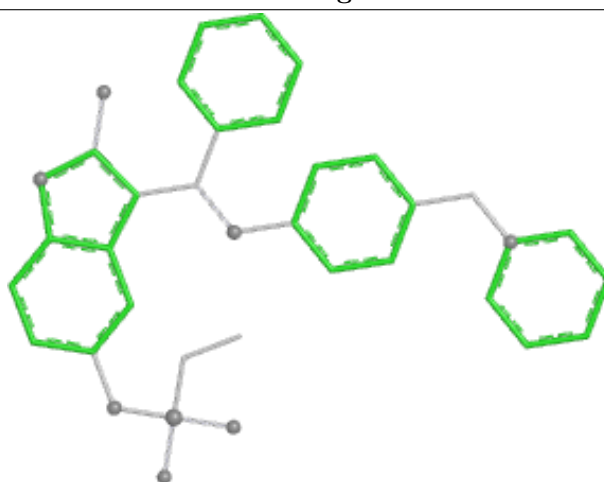
Bond lengths



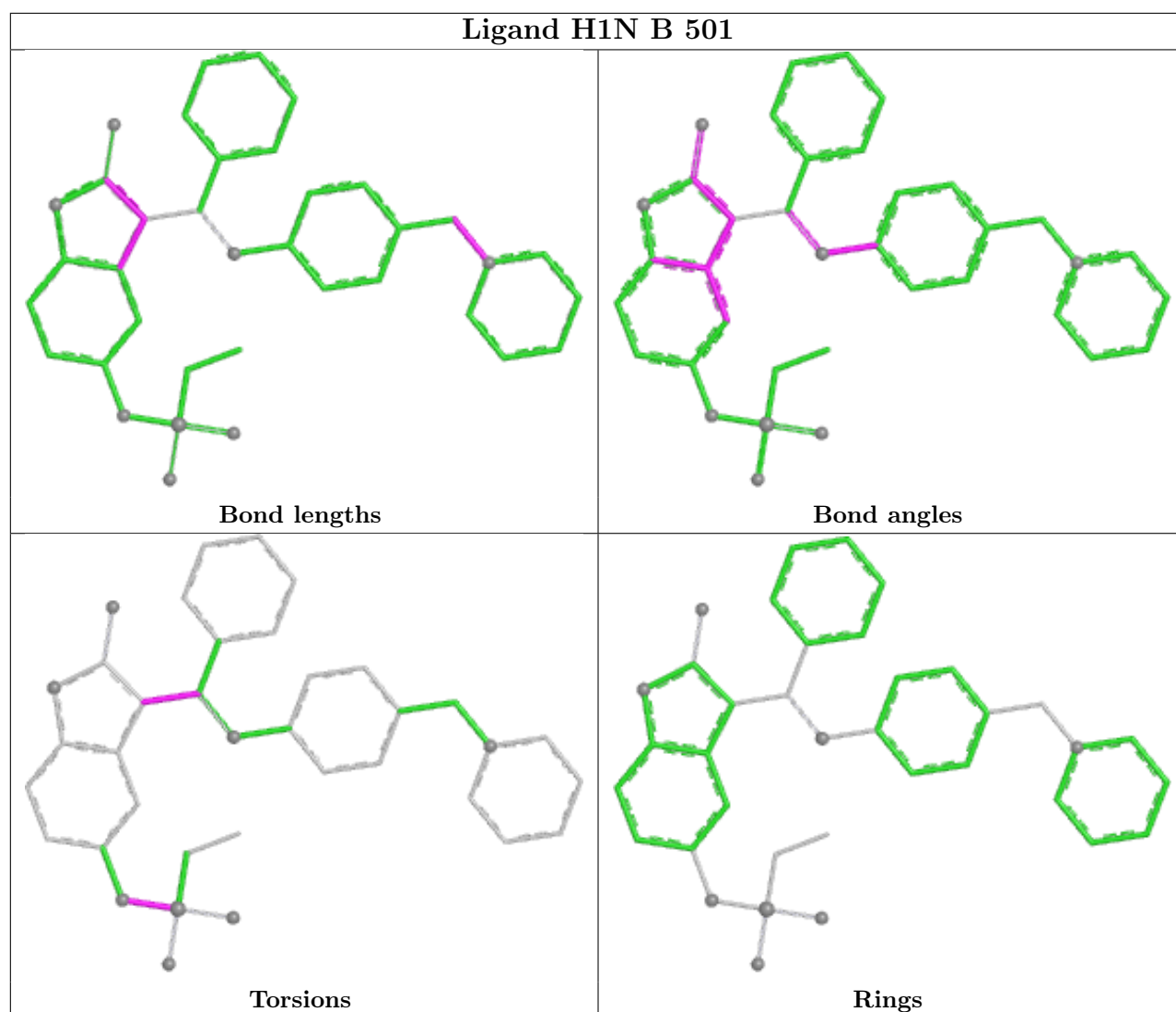
Bond angles



Torsions



Rings



## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	335/361 (92%)	0.20	4 (1%) 76 75	59, 86, 122, 141	0
1	B	323/361 (89%)	0.25	7 (2%) 62 59	50, 89, 128, 147	0
All	All	658/722 (91%)	0.22	11 (1%) 69 66	50, 88, 125, 147	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	438	ASN	3.1
1	B	141	PHE	2.9
1	A	227	PHE	2.6
1	A	141	PHE	2.5
1	B	443	VAL	2.4
1	B	222	LEU	2.3
1	A	467	ALA	2.2
1	B	157	ALA	2.1
1	A	446	PRO	2.1
1	B	415	PRO	2.1
1	B	468	ASP	2.1

### 6.2 Non-standard residues in protein, DNA, RNA chains [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	SEP	A	450	10/11	0.67	0.12	123,134,151,151	0
1	SEP	A	464	10/11	0.93	0.07	85,93,117,125	0
1	SEP	B	464	10/11	0.93	0.09	62,72,95,97	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
1	SEP	B	298	10/11	0.94	0.08	61,73,83,83	0
1	SEP	A	298	10/11	0.95	0.07	66,79,85,93	0

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 6.4 Ligands [i](#)

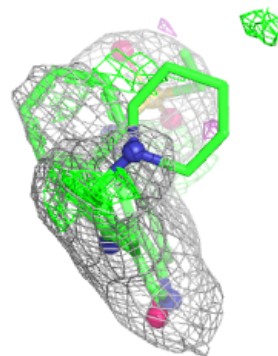
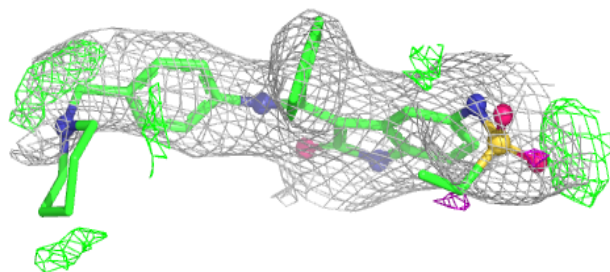
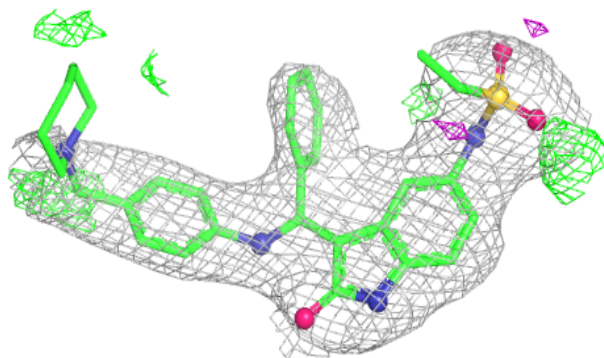
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
3	MLI	B	502	7/7	0.71	0.21	65,68,83,93	0
2	H1N	B	501	37/37	0.85	0.17	71,91,136,141	0
2	H1N	A	501	37/37	0.91	0.12	60,74,99,103	0

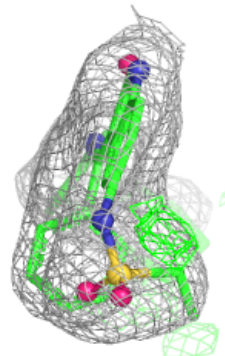
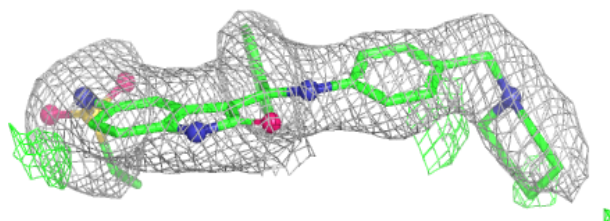
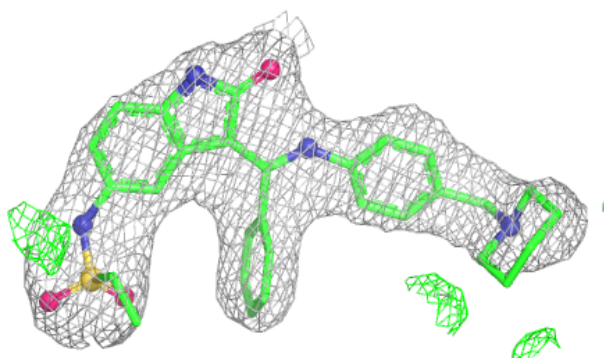
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around H1N B 501:**

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

**Electron density around H1N A 501:**

$2mF_o-DF_c$  (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.