



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 15, 2026 – 02:19 AM UTC

PDB ID : 9IX3 / pdb_00009ix3
Title : Crystal structure of the mouse RIP3 kinase domain in complexed with compound 18
Authors : Xie, H.; Su, H.X.; Li, M.J.; Xu, Y.C.
Deposited on : 2024-07-26
Resolution : 2.07 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

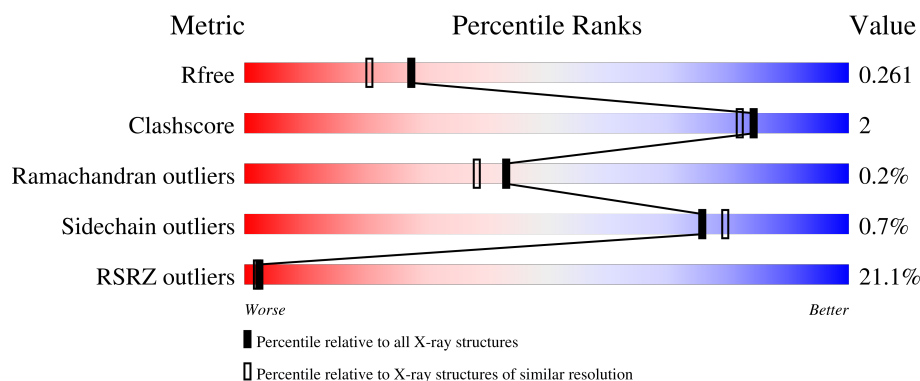
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.07 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	3774 (2.08-2.04)
Clashscore	190562	3883 (2.08-2.04)
Ramachandran outliers	187476	3860 (2.08-2.04)
Sidechain outliers	187428	3860 (2.08-2.04)
RSRZ outliers	180081	3775 (2.08-2.04)

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	325	12% 75% 5% 20%
1	B	325	21% 73% 5% 22%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4042 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 Receptor-interacting serine/threonine-protein kinase 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	260	Total	C	N	O	S	0	0	0
			1990	1280	341	361	8			
1	B	253	Total	C	N	O	S	0	0	0
			1911	1232	331	340	8			

There are 30 discrepancies between the modelled and reference sequences:

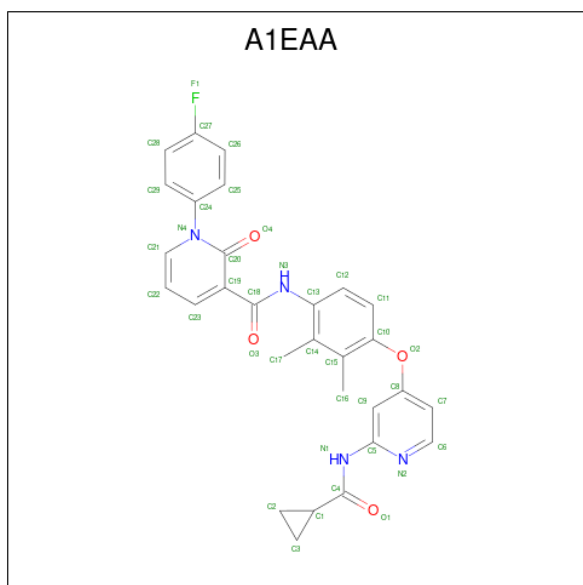
Chain	Residue	Modelled	Actual	Comment	Reference
A	111	ALA	CYS	conflict	UNP Q9QZL0
A	136	ASP	ASN	conflict	UNP Q9QZL0
A	198	LYS	ASP	conflict	UNP Q9QZL0
A	314	LEU	-	expression tag	UNP Q9QZL0
A	315	GLU	-	expression tag	UNP Q9QZL0
A	316	HIS	-	expression tag	UNP Q9QZL0
A	317	HIS	-	expression tag	UNP Q9QZL0
A	318	HIS	-	expression tag	UNP Q9QZL0
A	319	HIS	-	expression tag	UNP Q9QZL0
A	320	HIS	-	expression tag	UNP Q9QZL0
A	321	HIS	-	expression tag	UNP Q9QZL0
A	322	HIS	-	expression tag	UNP Q9QZL0
A	323	HIS	-	expression tag	UNP Q9QZL0
A	324	HIS	-	expression tag	UNP Q9QZL0
A	325	HIS	-	expression tag	UNP Q9QZL0
B	111	ALA	CYS	conflict	UNP Q9QZL0
B	136	ASP	ASN	conflict	UNP Q9QZL0
B	198	LYS	ASP	conflict	UNP Q9QZL0
B	314	LEU	-	expression tag	UNP Q9QZL0
B	315	GLU	-	expression tag	UNP Q9QZL0
B	316	HIS	-	expression tag	UNP Q9QZL0
B	317	HIS	-	expression tag	UNP Q9QZL0
B	318	HIS	-	expression tag	UNP Q9QZL0
B	319	HIS	-	expression tag	UNP Q9QZL0
B	320	HIS	-	expression tag	UNP Q9QZL0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	321	HIS	-	expression tag	UNP Q9QZL0
B	322	HIS	-	expression tag	UNP Q9QZL0
B	323	HIS	-	expression tag	UNP Q9QZL0
B	324	HIS	-	expression tag	UNP Q9QZL0
B	325	HIS	-	expression tag	UNP Q9QZL0

- Molecule 2 is {N}-[4-[2-(cyclopropylcarbonylamino)pyridin-4-yl]oxy-2,3-dimethyl-phenyl]-1-(4-fluorophenyl)-2-oxidanylidene-pyridine-3-carboxamide (CCD ID: A1EAA) (formula: C₂₉H₂₅FN₄O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			38	29	1	4	4		
2	B	1	Total	C	F	N	O	0	0
			38	29	1	4	4		

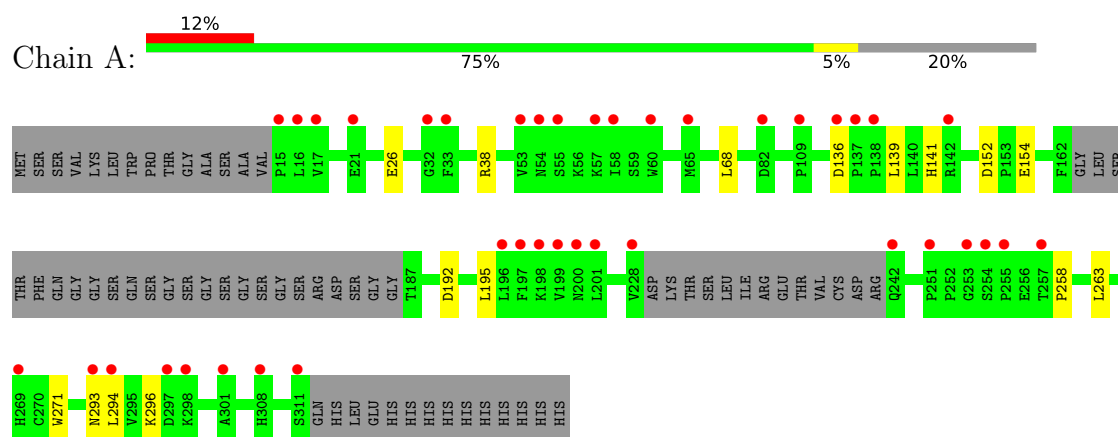
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	41	Total	O	0	0
			41	41		
3	B	24	Total	O	0	0
			24	24		

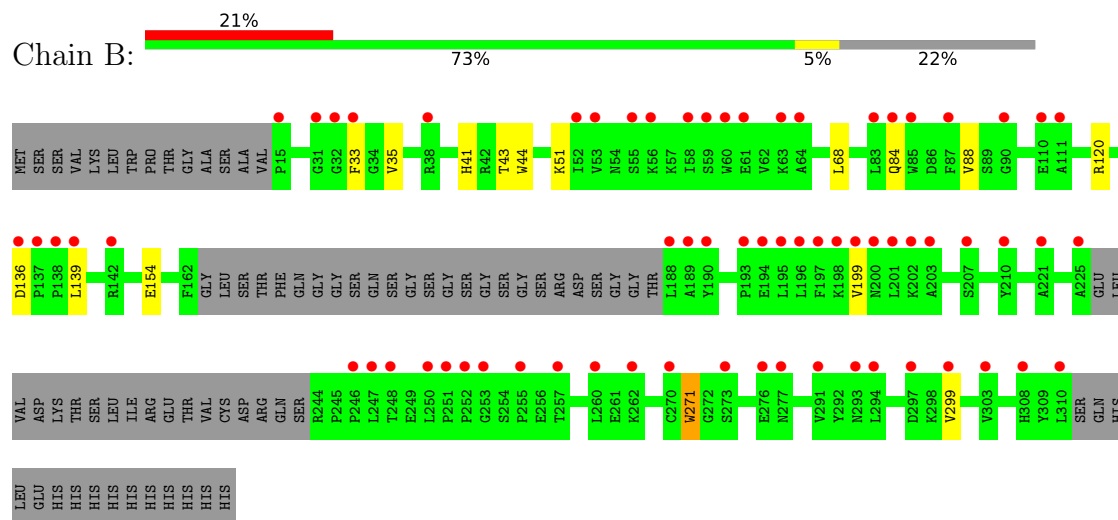
3 Residue-property plots [i](#)

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: Receptor-interacting serine/threonine-protein kinase 3



- Molecule 1: Receptor-interacting serine/threonine-protein kinase 3



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	144.20Å 54.16Å 104.03Å 90.00° 130.99° 90.00°	Depositor
Resolution (Å)	54.42 – 2.07 54.42 – 2.07	Depositor EDS
% Data completeness (in resolution range)	99.8 (54.42-2.07) 99.8 (54.42-2.07)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 2.07Å)	Xtriage
Refinement program	PHENIX (1.17.1_3660: ???)	Depositor
R, R_{free}	0.228 , 0.260 0.229 , 0.261	Depositor DCC
R_{free} test set	1701 reflections (4.57%)	wwPDB-VP
Wilson B-factor (Å ²)	34.7	Xtriage
Anisotropy	0.868	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 45.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.005 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4042	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.18% 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: A1EAA

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	0.16	0/2038	0.40	2/2774 (0.1%)
1	B	0.15	0/1957	0.33	0/2666
All	All	0.15	0/3995	0.37	2/5440 (0.0%)

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	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	141	HIS	CA-C-N	5.56	132.16	121.54
1	A	141	HIS	C-N-CA	5.56	132.16	121.54

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	136	ASP	Peptide
1	B	136	ASP	Peptide

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	1990	0	1961	7	0
1	B	1911	0	1873	10	0
2	A	38	0	0	1	0
2	B	38	0	0	1	0
3	A	41	0	0	0	0
3	B	24	0	0	0	0
All	All	4042	0	3834	18	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 (18) 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:154:GLU:HG3	1:B:154:GLU:HG3	1.70	0.71
1:B:35:VAL:HG21	1:B:88:VAL:HG21	1.81	0.62
1:B:41:HIS:CD2	1:B:44:TRP:H	2.21	0.59
1:B:120:ARG:HD3	1:B:299:VAL:HG21	1.87	0.57
1:A:26:GLU:OE2	1:A:38:ARG:NH2	2.40	0.55
1:A:258:PRO:HB2	1:A:294:LEU:HD23	1.91	0.53
1:B:41:HIS:HD2	1:B:43:THR:H	1.58	0.51
1:B:41:HIS:HD2	1:B:44:TRP:H	1.59	0.49
2:B:401:A1EAA:O4	2:B:401:A1EAA:N3	2.47	0.48
1:B:68:LEU:HD21	1:B:139:LEU:HD13	1.95	0.47
1:B:33:PHE:HD2	1:B:51:LYS:HE3	1.81	0.46
2:A:401:A1EAA:O4	2:A:401:A1EAA:N3	2.49	0.45
1:B:271:TRP:CD1	1:B:271:TRP:C	2.94	0.45
1:A:68:LEU:HD21	1:A:139:LEU:HD13	1.98	0.44
1:A:293:ASN:HA	1:A:296:LYS:HE3	2.00	0.44
1:A:271:TRP:CD1	1:A:271:TRP:C	2.97	0.42
1:A:192:ASP:HB3	1:A:195:LEU:HG	2.02	0.41
1:B:84:GLN:HA	1:B:88:VAL:O	2.21	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	254/325 (78%)	247 (97%)	7 (3%)	0	100	100
1	B	247/325 (76%)	241 (98%)	5 (2%)	1 (0%)	30	23
All	All	501/650 (77%)	488 (97%)	12 (2%)	1 (0%)	43	38

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	199	VAL

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	213/283 (75%)	211 (99%)	2 (1%)	70	74
1	B	199/283 (70%)	198 (100%)	1 (0%)	81	85
All	All	412/566 (73%)	409 (99%)	3 (1%)	76	79

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

Mol	Chain	Res	Type
1	A	152	ASP
1	A	263	LEU
1	B	271	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are

no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

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	A1EAA	A	401	-	42,42,42	0.64	2 (4%)	59,60,60	0.92	2 (3%)
2	A1EAA	B	401	-	42,42,42	0.65	2 (4%)	59,60,60	1.01	3 (5%)

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	A1EAA	A	401	-	-	1/24/26/26	0/5/5/5
2	A1EAA	B	401	-	-	0/24/26/26	0/5/5/5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	A1EAA	C1-C4	-2.37	1.47	1.51
2	A	401	A1EAA	C1-C4	-2.34	1.47	1.51
2	A	401	A1EAA	C19-C20	-2.22	1.39	1.45
2	B	401	A1EAA	C19-C20	-2.21	1.40	1.45

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	A1EAA	C23-C19-C18	4.83	121.62	117.94
2	B	401	A1EAA	C19-C20-N4	4.09	119.15	113.17
2	A	401	A1EAA	C19-C20-N4	4.02	119.06	113.17
2	A	401	A1EAA	C23-C19-C18	3.81	120.84	117.94
2	B	401	A1EAA	C20-C19-C18	-2.31	118.90	121.52

There are no chirality outliers.

All (1) torsion outliers are listed below:

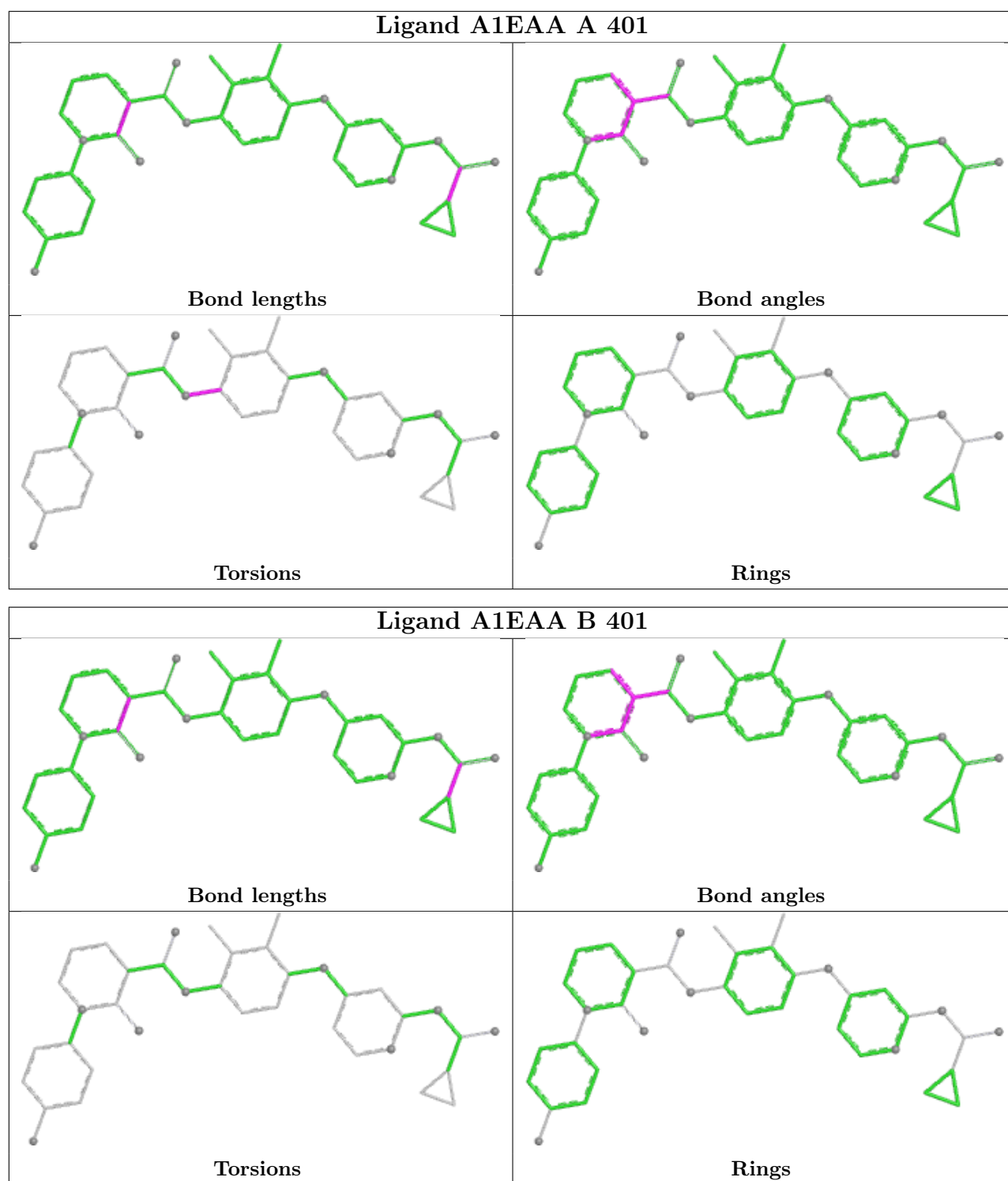
Mol	Chain	Res	Type	Atoms
2	A	401	A1EAA	C14-C13-N3-C18

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	A1EAA	1	0
2	B	401	A1EAA	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 ⓘ

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	260/325 (80%)	1.06	40 (15%) 5 5	26, 40, 64, 77	0
1	B	253/325 (77%)	1.51	68 (26%) 1 1	30, 48, 73, 87	0
All	All	513/650 (78%)	1.28	108 (21%) 2 2	26, 44, 72, 87	0

All (108) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	199	VAL	6.2
1	A	255	PRO	5.3
1	B	33	PHE	5.1
1	A	136	ASP	5.1
1	B	200	ASN	5.0
1	B	196	LEU	4.7
1	A	57	LYS	4.6
1	B	199	VAL	4.5
1	A	60	TRP	4.4
1	A	253	GLY	4.3
1	B	253	GLY	4.1
1	A	311	SER	4.1
1	B	201	LEU	3.9
1	A	15	PRO	3.8
1	B	15	PRO	3.8
1	B	225	ALA	3.7
1	B	203	ALA	3.7
1	B	136	ASP	3.5
1	A	228	VAL	3.5
1	B	202	LYS	3.5
1	B	87	PHE	3.4
1	B	248	THR	3.3
1	B	193	PRO	3.3
1	B	138	PRO	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	255	PRO	3.2
1	A	82	ASP	3.1
1	A	197	PHE	3.1
1	B	58	ILE	3.1
1	B	53	VAL	3.1
1	B	139	LEU	3.1
1	B	59	SER	3.1
1	A	200	ASN	3.0
1	A	257	THR	3.0
1	B	197	PHE	3.0
1	B	247	LEU	3.0
1	B	32	GLY	3.0
1	B	189	ALA	3.0
1	B	221	ALA	2.9
1	A	32	GLY	2.9
1	B	310	LEU	2.9
1	B	294	LEU	2.8
1	B	188	LEU	2.8
1	B	195	LEU	2.8
1	A	254	SER	2.8
1	B	64	ALA	2.8
1	A	58	ILE	2.8
1	B	297	ASP	2.7
1	B	260	LEU	2.7
1	A	109	PRO	2.7
1	A	308	HIS	2.7
1	B	207	SER	2.7
1	B	84	GLN	2.7
1	B	137	PRO	2.7
1	B	257	THR	2.6
1	A	251	PRO	2.6
1	B	56	LYS	2.6
1	B	299	VAL	2.6
1	A	137	PRO	2.6
1	B	246	PRO	2.6
1	A	269	HIS	2.6
1	B	273	SER	2.6
1	B	293	ASN	2.5
1	B	250	LEU	2.5
1	B	142	ARG	2.5
1	B	308	HIS	2.4
1	B	194	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	196	LEU	2.3
1	B	252	PRO	2.3
1	B	60	TRP	2.3
1	B	85	TRP	2.3
1	A	21	GLU	2.3
1	A	198	LYS	2.3
1	A	301	ALA	2.3
1	B	63	LYS	2.3
1	A	55	SER	2.2
1	B	198	LYS	2.2
1	A	297	ASP	2.2
1	A	201	LEU	2.2
1	B	83	LEU	2.2
1	A	17	VAL	2.2
1	B	291	VAL	2.2
1	B	270	CYS	2.2
1	B	210	TYR	2.2
1	A	54	ASN	2.2
1	B	262	LYS	2.2
1	B	61	GLU	2.1
1	A	16	LEU	2.1
1	A	294	LEU	2.1
1	B	55	SER	2.1
1	B	277	ASN	2.1
1	B	110	GLU	2.1
1	A	242	GLN	2.1
1	B	303	VAL	2.1
1	A	298	LYS	2.1
1	B	111	ALA	2.1
1	A	65	MET	2.1
1	B	276	GLU	2.1
1	B	38	ARG	2.1
1	B	31	GLY	2.1
1	A	142	ARG	2.0
1	B	251	PRO	2.0
1	B	190	TYR	2.0
1	B	52	ILE	2.0
1	A	33	PHE	2.0
1	A	53	VAL	2.0
1	A	293	ASN	2.0
1	A	138	PRO	2.0
1	B	90	GLY	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](#)

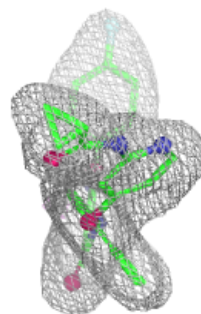
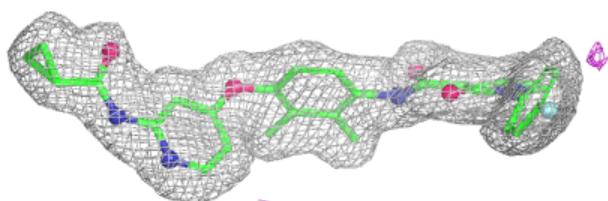
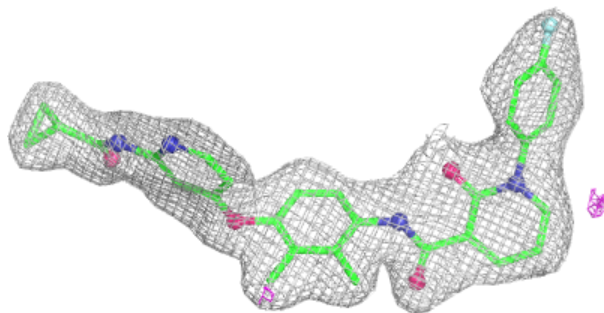
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	A1EAA	B	401	38/38	0.92	0.10	30,37,46,54	0
2	A1EAA	A	401	38/38	0.95	0.09	24,33,40,49	0

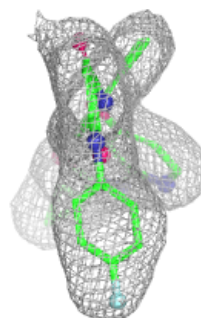
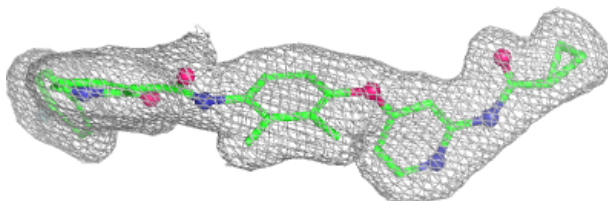
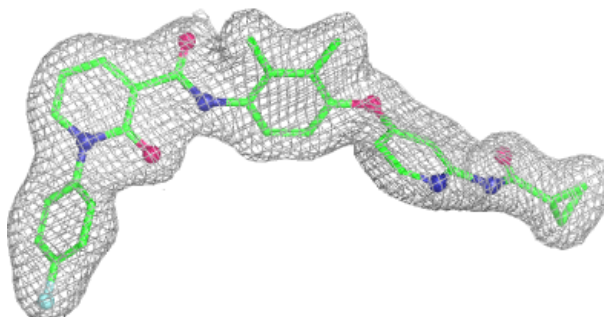
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around A1EAA 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 A1EAA 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.