



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:52 PM UTC

PDB ID : 6VRV / pdb_00006vrv
Title : Discovery of SARxxxx92, a pan-PIM kinase inhibitor, efficacious in a KG1 tumor model
Authors : Barberis, C.E.; Batchelor, J.D.; Liu, J.
Deposited on : 2020-02-10
Resolution : 1.74 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

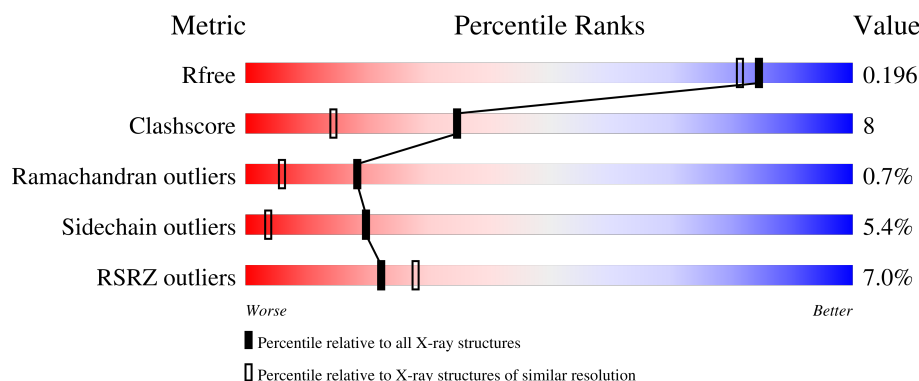
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.74 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	1187 (1.74-1.74)
Clashscore	190562	1207 (1.74-1.74)
Ramachandran outliers	187476	1200 (1.74-1.74)
Sidechain outliers	187428	1200 (1.74-1.74)
RSRZ outliers	180081	1188 (1.74-1.74)

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	274	7% 73% 20% 5% ..

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
3	GOL	A	402	-	X	-	-

2 Entry composition [i](#)

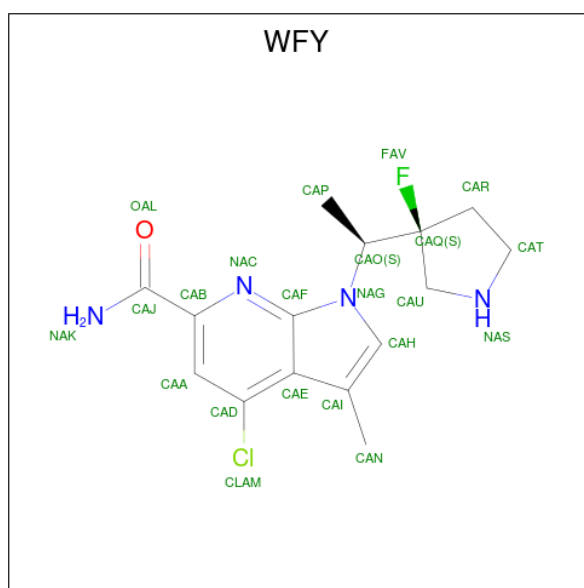
There are 4 unique types of molecules in this entry. The entry contains 2481 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Serine/threonine-protein kinase pim-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	271	2209	1412	387	402	8	0	0	0

- Molecule 2 is 4-chloro-1-{(1S)-1-[(3S)-3-fluoropyrrolidin-3-yl]ethyl}-3-methyl-1H-pyrrolo[2,3-b]pyridine-6-carboxamide (CCD ID: WFY) (formula: C₁₅H₁₈ClFN₄O) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

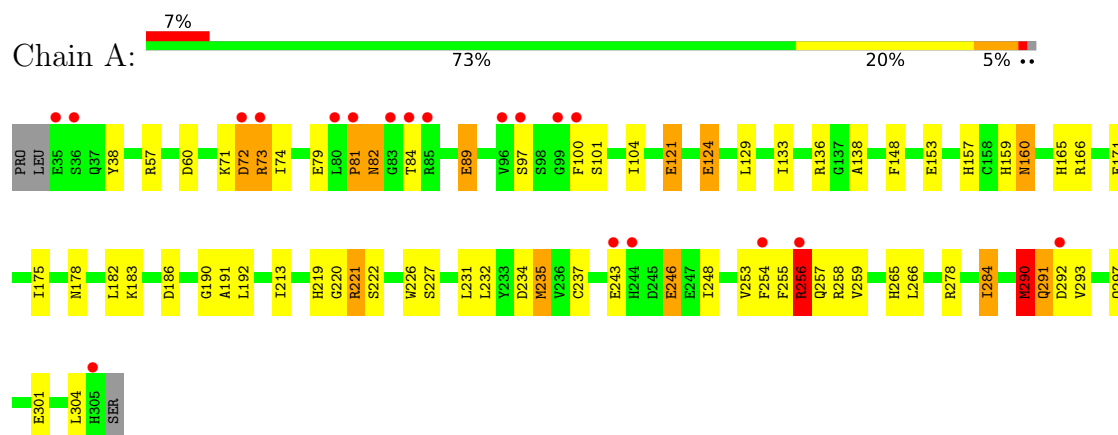
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	244	Total	O	0	0
			244	244		

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: Serine/threonine-protein kinase pim-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	98.80Å 98.80Å 81.19Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	85.57 – 1.74 85.57 – 1.74	Depositor EDS
% Data completeness (in resolution range)	100.0 (85.57-1.74) 100.0 (85.57-1.74)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.14 (at 1.74Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.172 , 0.197 0.171 , 0.196	Depositor DCC
R_{free} test set	2342 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	26.4	Xtriage
Anisotropy	0.116	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 38.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.036 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	2481	wwPDB-VP
Average B, all atoms (Å ²)	32.0	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: GOL, WFY

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	1.98	47/2268 (2.1%)	1.56	15/3078 (0.5%)

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

All (47) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	290	MET	SD-CE	-12.95	1.47	1.79
1	A	258	ARG	CZ-NH1	12.72	1.50	1.32
1	A	159	HIS	CG-CD2	9.46	1.46	1.35
1	A	89	GLU	CD-OE1	9.12	1.42	1.25
1	A	157	HIS	ND1-CE1	9.08	1.41	1.32
1	A	253	VAL	CA-CB	8.30	1.64	1.54
1	A	165	HIS	ND1-CE1	7.93	1.40	1.32
1	A	256	ARG	CZ-NH2	7.76	1.43	1.33
1	A	159	HIS	ND1-CE1	7.30	1.39	1.32
1	A	284	ILE	N-CA	7.18	1.54	1.46
1	A	104	ILE	C-O	6.84	1.30	1.24
1	A	265	HIS	CE1-NE2	6.83	1.39	1.32
1	A	138	ALA	C-O	6.67	1.31	1.23
1	A	278	ARG	C-O	6.59	1.32	1.23
1	A	291	GLN	CD-NE2	6.55	1.47	1.33
1	A	265	HIS	CG-CD2	6.53	1.43	1.35
1	A	258	ARG	CZ-NH2	6.38	1.41	1.33
1	A	266	LEU	N-CA	6.35	1.53	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	227	SER	N-CA	6.27	1.54	1.46
1	A	182	LEU	C-O	6.17	1.31	1.23
1	A	191	ALA	N-CA	6.10	1.53	1.45
1	A	153	GLU	N-CA	6.09	1.53	1.46
1	A	220	GLY	N-CA	5.93	1.53	1.45
1	A	255	PHE	N-CA	5.80	1.53	1.46
1	A	171	GLU	N-CA	5.73	1.53	1.46
1	A	258	ARG	CD-NE	5.71	1.54	1.46
1	A	254	PHE	N-CA	5.58	1.52	1.45
1	A	226	TRP	CD2-CE2	5.53	1.50	1.41
1	A	175	ILE	N-CA	5.51	1.53	1.46
1	A	235	MET	CG-SD	5.50	1.94	1.80
1	A	129	LEU	CA-CB	5.49	1.62	1.53
1	A	213	ILE	N-CA	5.49	1.52	1.46
1	A	235	MET	C-O	-5.48	1.17	1.24
1	A	222	SER	CA-CB	5.47	1.62	1.53
1	A	259	VAL	N-CA	5.34	1.52	1.46
1	A	213	ILE	CA-CB	5.32	1.60	1.54
1	A	278	ARG	CZ-NH1	5.28	1.40	1.32
1	A	256	ARG	CD-NE	5.27	1.53	1.46
1	A	159	HIS	CB-CG	5.11	1.57	1.50
1	A	190	GLY	C-O	5.10	1.29	1.23
1	A	192	LEU	C-O	5.09	1.30	1.23
1	A	133	ILE	N-CA	5.09	1.52	1.46
1	A	166	ARG	CA-CB	5.07	1.60	1.53
1	A	219	HIS	CE1-NE2	5.06	1.37	1.32
1	A	227	SER	CA-CB	5.02	1.61	1.53
1	A	160	ASN	CB-CG	-5.02	1.39	1.52
1	A	248	ILE	N-CA	5.01	1.52	1.46

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	256	ARG	NE-CZ-NH1	-8.83	112.67	121.50
1	A	256	ARG	NE-CZ-NH2	8.12	126.51	119.20
1	A	89	GLU	CG-CD-OE2	-7.42	101.33	118.40
1	A	89	GLU	N-CA-CB	-6.78	99.88	110.06
1	A	259	VAL	N-CA-C	-6.16	99.33	108.45
1	A	72	ASP	N-CA-C	5.59	119.20	112.38
1	A	293	VAL	CG1-CB-CG2	-5.43	98.86	110.80
1	A	258	ARG	NH1-CZ-NH2	5.41	126.33	119.30
1	A	104	ILE	CB-CG1-CD1	-5.40	102.46	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	221	ARG	CA-CB-CG	-5.38	103.34	114.10
1	A	258	ARG	NE-CZ-NH2	-5.32	114.42	119.20
1	A	186	ASP	CA-CB-CG	-5.22	107.38	112.60
1	A	234	ASP	N-CA-CB	-5.19	102.49	110.12
1	A	121	GLU	N-CA-CB	-5.16	101.66	109.92
1	A	265	HIS	O-C-N	5.01	127.23	122.07

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	304	LEU	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	2209	0	2151	32	0
2	A	22	0	0	0	0
3	A	6	0	8	1	0
4	A	244	0	0	10	1
All	All	2481	0	2159	33	1

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 (33) 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:256:ARG:H	1:A:256:ARG:HD2	1.37	0.87
1:A:256:ARG:HG3	1:A:256:ARG:NH1	1.91	0.81
1:A:256:ARG:HG3	1:A:256:ARG:HH11	1.45	0.81
1:A:178:ASN:OD1	4:A:501:HOH:O	2.01	0.78
1:A:121:GLU:OE2	1:A:183:LYS:HE2	1.85	0.76
1:A:256:ARG:H	1:A:256:ARG:CD	1.95	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:GLU:HG2	4:A:563:HOH:O	1.87	0.74
1:A:246:GLU:HG2	4:A:618:HOH:O	1.87	0.73
1:A:256:ARG:HG2	1:A:257:GLN:HG2	1.73	0.70
1:A:100:PHE:HD2	4:A:508:HOH:O	1.73	0.70
1:A:231:LEU:HG	1:A:235:MET:HE2	1.80	0.62
1:A:121:GLU:CD	1:A:183:LYS:HE2	2.25	0.62
1:A:232:LEU:HA	1:A:235:MET:HE3	1.82	0.61
1:A:89:GLU:HB2	4:A:549:HOH:O	2.03	0.58
1:A:221:ARG:HG2	4:A:520:HOH:O	2.02	0.58
1:A:100:PHE:CD2	4:A:508:HOH:O	2.53	0.54
1:A:291:GLN:O	1:A:292:ASP:HB3	2.06	0.54
1:A:73:ARG:NH2	4:A:506:HOH:O	2.40	0.53
1:A:256:ARG:HH11	1:A:256:ARG:CG	2.11	0.52
1:A:256:ARG:HD2	1:A:256:ARG:N	2.17	0.50
1:A:81:PRO:O	1:A:82:ASN:HB3	2.13	0.48
1:A:57:ARG:NH1	1:A:60:ASP:OD2	2.49	0.45
1:A:71:LYS:HA	1:A:74:ILE:HD12	1.98	0.45
1:A:81:PRO:O	1:A:82:ASN:CB	2.65	0.45
1:A:221:ARG:HD2	4:A:638:HOH:O	2.17	0.44
1:A:148:PHE:CD1	1:A:235:MET:HE1	2.53	0.44
3:A:402:GOL:H32	4:A:600:HOH:O	2.17	0.43
1:A:284:ILE:O	1:A:290:MET:HG3	2.19	0.43
1:A:38:TYR:CE1	1:A:57:ARG:HG3	2.55	0.41
1:A:297:GLN:O	1:A:301:GLU:HG3	2.21	0.41
1:A:237:CYS:HB3	1:A:256:ARG:HD3	2.02	0.41
1:A:148:PHE:HD1	1:A:235:MET:HE1	1.86	0.40
1:A:57:ARG:HH11	1:A:60:ASP:CG	2.30	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:528:HOH:O	4:A:658:HOH:O[3_665]	2.17	0.03

5.3 Torsion angles

5.3.1 Protein backbone

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	269/274 (98%)	262 (97%)	5 (2%)	2 (1%)	18 6

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	ASN
1	A	81	PRO

5.3.2 Protein sidechains ⓘ

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	242/245 (99%)	229 (95%)	13 (5%)	20 4

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	ASP
1	A	73	ARG
1	A	79	GLU
1	A	84	THR
1	A	97	SER
1	A	101	SER
1	A	124	GLU
1	A	136	ARG
1	A	160	ASN
1	A	243	GLU
1	A	246	GLU
1	A	256	ARG
1	A	290	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	252	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](#)

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	$\# Z > 2$
3	GOL	A	402	-	5,5,5	0.41	0	5,5,5	3.00	2 (40%)
2	WFY	A	401	-	19,24,24	4.12	12 (63%)	26,37,37	3.65	15 (57%)

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
3	GOL	A	402	-	-	4/4/4/4	-
2	WFY	A	401	-	-	0/8/23/23	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	WFY	CAE-CAF	-9.11	1.28	1.40
2	A	401	WFY	CAB-CAJ	-6.83	1.42	1.50
2	A	401	WFY	CAR-CAT	6.32	1.61	1.53
2	A	401	WFY	CAF-NAC	6.06	1.42	1.34
2	A	401	WFY	CAP-CAO	5.43	1.64	1.52
2	A	401	WFY	CAH-NAG	-5.30	1.29	1.38
2	A	401	WFY	CAA-CAD	4.58	1.46	1.38
2	A	401	WFY	CAB-NAC	2.74	1.38	1.34
2	A	401	WFY	CAE-CAI	-2.42	1.41	1.45
2	A	401	WFY	CAF-NAG	2.23	1.42	1.37
2	A	401	WFY	CAE-CAD	-2.11	1.36	1.39
2	A	401	WFY	CAN-CAI	-2.07	1.46	1.50

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	WFY	CAF-NAG-CAH	9.53	112.02	108.08
2	A	401	WFY	CAE-CAI-CAH	6.82	114.08	106.70
3	A	402	GOL	O3-C3-C2	-6.16	82.63	110.38
2	A	401	WFY	CAN-CAI-CAH	-5.83	120.19	127.10
2	A	401	WFY	CAP-CAO-CAQ	-5.77	108.64	114.66
2	A	401	WFY	OAL-CAJ-CAB	4.89	123.75	119.65
2	A	401	WFY	CAB-CAA-CAD	4.85	121.78	118.13
2	A	401	WFY	CAE-CAD-CLAM	3.96	124.72	119.62
2	A	401	WFY	CAA-CAD-CAE	-3.88	118.18	122.17
2	A	401	WFY	CAA-CAB-NAC	-3.69	117.01	123.41
2	A	401	WFY	OAL-CAJ-NAK	-3.18	118.03	122.62
2	A	401	WFY	CAF-CAE-CAI	-3.07	102.87	106.69
2	A	401	WFY	CAA-CAB-CAJ	2.57	127.06	118.79
3	A	402	GOL	O2-C2-C1	2.37	119.01	109.18
2	A	401	WFY	NAC-CAF-NAG	-2.13	124.29	126.99
2	A	401	WFY	CAN-CAI-CAE	-2.13	125.73	128.58
2	A	401	WFY	CAR-CAT-NAS	-2.07	100.86	105.62

There are no chirality outliers.

All (4) torsion outliers are listed below:

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

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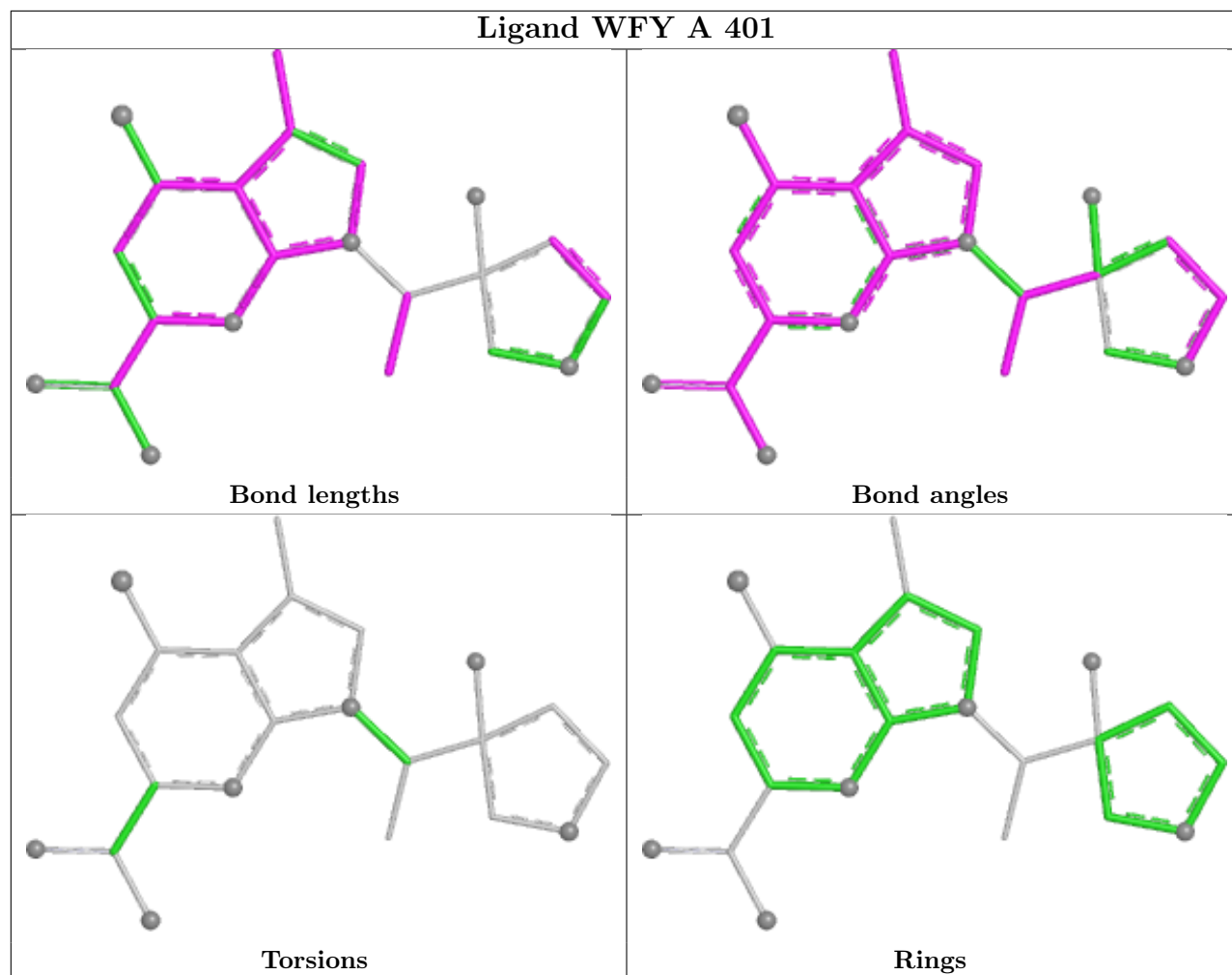
Mol	Chain	Res	Type	Atoms
3	A	402	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	402	GOL	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 [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	271/274 (98%)	0.11	19 (7%)	22 28	16, 26, 64, 84	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	305	HIS	5.0
1	A	100	PHE	4.1
1	A	81	PRO	3.9
1	A	84	THR	3.5
1	A	80	LEU	3.4
1	A	83	GLY	3.3
1	A	99	GLY	3.0
1	A	97	SER	2.9
1	A	292	ASP	2.5
1	A	36	SER	2.5
1	A	256	ARG	2.4
1	A	254	PHE	2.4
1	A	96	VAL	2.4
1	A	85	ARG	2.3
1	A	243	GLU	2.3
1	A	72	ASP	2.3
1	A	244	HIS	2.2
1	A	73	ARG	2.2
1	A	35	GLU	2.1

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

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](#)

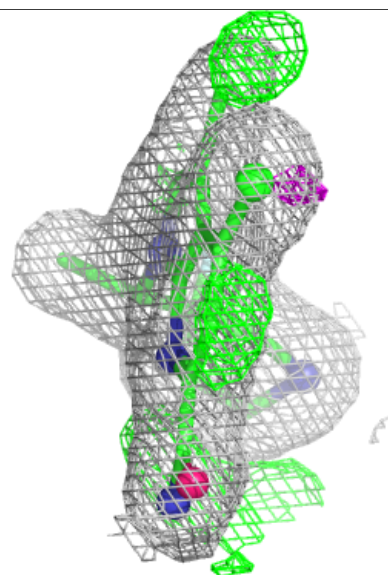
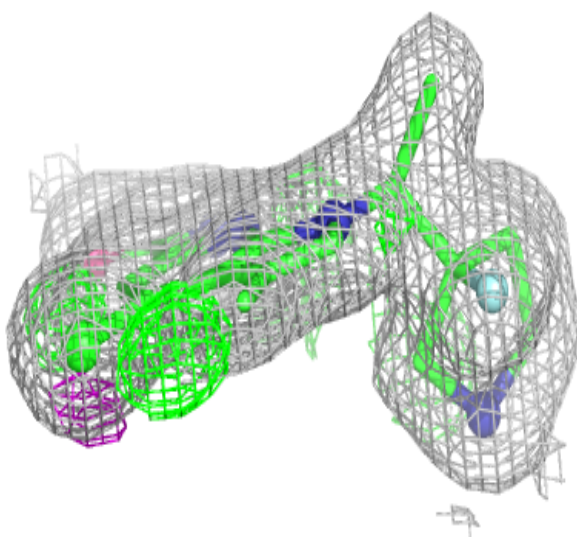
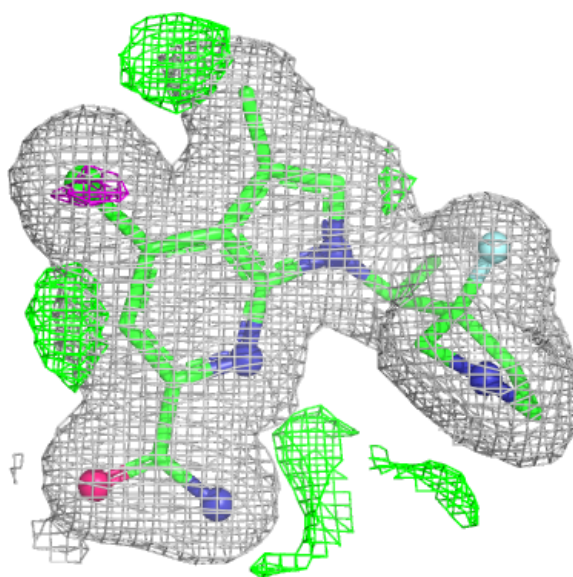
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
3	GOL	A	402	6/6	0.93	0.10	27,45,51,55	0
2	WFY	A	401	22/22	0.96	0.07	20,23,28,31	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 WFY 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 ⓘ

There are no such residues in this entry.