



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 29, 2020 – 12:19 PM EST

PDB ID : 7K6O
Title : Crystal structure of PI3Kalpha inhibitor 10-5429
Authors : Chen, P.; Brooun, A.; Deng, Y.L.; Grodsky, N.; Kaiser, S.E.
Deposited on : 2020-09-21
Resolution : 2.74 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 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 : 2.16
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) : 2.16

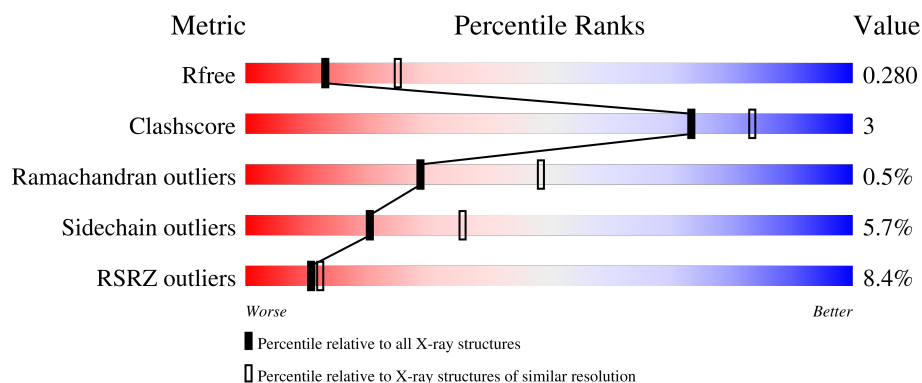
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


The reported resolution of this entry is 2.74 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}	130704	1271 (2.76-2.72)
Clashscore	141614	1322 (2.76-2.72)
Ramachandran outliers	138981	1297 (2.76-2.72)
Sidechain outliers	138945	1298 (2.76-2.72)
RSRZ outliers	127900	1243 (2.76-2.72)

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	946	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6469 atoms, of which 27 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.

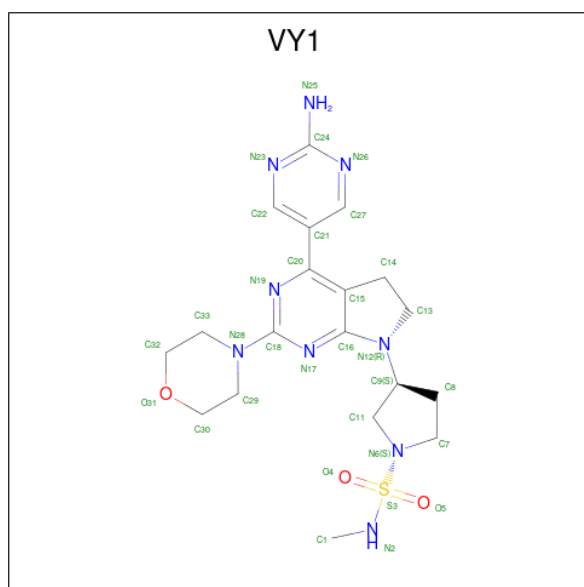
- Molecule 1 is a protein called Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic sub-unit alpha isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	852	6339	4043	1071	1175	50	38	1	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	103	GLY	-	expression tag	UNP P42336
A	104	SER	-	expression tag	UNP P42336

- Molecule 2 is (3S)-3-[4-(2-aminopyrimidin-5-yl)-2-(morpholin-4-yl)-5,6-dihydro-7H-pyrrolo[2,3-d]pyrimidin-7-yl]-N-methylpyrrolidine-1-sulfonamide (three-letter code: VY1) (formula: C₁₉H₂₇N₉O₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	H	N	O	S		
2	A	1	59	19	27	9	3	1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	71	Total	O	0	0
			71	71		

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: Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit alpha isoform



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.92Å 135.78Å 141.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	97.84 – 2.74 97.85 – 2.74	Depositor EDS
% Data completeness (in resolution range)	99.9 (97.84-2.74) 99.9 (97.85-2.74)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.40 (at 2.73Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.231 , 0.262 0.248 , 0.280	Depositor DCC
R_{free} test set	1525 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	73.9	Xtriage
Anisotropy	0.312	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 80.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.023 for -h,l,k	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6469	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.13% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: VY1

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	0.42	0/6477	0.57	0/8836

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 [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	6339	0	5741	40	0
2	A	32	27	0	0	0
3	A	71	0	0	0	0
All	All	6442	27	5741	40	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 (40) 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:749:GLN:HE21	1:A:764:LEU:H	1.27	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:405:SER:HB2	1:A:456:LEU:HD23	1.79	0.64
1:A:741:ARG:HH21	1:A:744:PHE:HE2	1.48	0.61
1:A:335:ARG:HG3	1:A:386:TRP:CE3	2.38	0.58
1:A:495:HIS:NE2	1:A:578:ASP:OD1	2.34	0.58
1:A:973:LYS:HA	1:A:977:PHE:CB	2.34	0.58
1:A:916:ARG:HE	1:A:931:HIS:HD2	1.52	0.57
1:A:665:HIS:HE1	1:A:754:PRO:O	1.87	0.56
1:A:124:PRO:HG2	1:A:127:GLU:HG3	1.88	0.55
1:A:198:VAL:O	1:A:199:SER:O	2.24	0.55
1:A:596:GLU:HB3	1:A:997:LEU:HD13	1.88	0.54
1:A:137:GLN:HE22	1:A:140:ARG:HH11	1.54	0.53
1:A:267:LEU:HG	1:A:273:ILE:HG13	1.90	0.53
1:A:764:LEU:HB3	1:A:766:LEU:HD23	1.90	0.53
1:A:807:LEU:HD12	1:A:846:GLY:HA3	1.91	0.52
1:A:620:GLU:HG2	1:A:652:PHE:CD1	2.45	0.51
1:A:333:ALA:HA	1:A:392:TYR:HA	1.93	0.50
1:A:713:ILE:HG12	1:A:845:VAL:HG11	1.94	0.49
1:A:192:VAL:HG12	1:A:283:PRO:HG2	1.95	0.49
1:A:328:TRP:CE2	1:A:577:ARG:HD2	2.49	0.48
1:A:213:HIS:HD2	1:A:268:SER:OG	1.96	0.48
1:A:197:ILE:HD11	1:A:789:MET:HE2	1.94	0.47
1:A:345:ASN:O	1:A:378:CYS:SG	2.72	0.47
1:A:371:VAL:HG12	1:A:387:LEU:HG	1.96	0.47
1:A:378:CYS:O	1:A:381:PRO:HD3	2.14	0.47
1:A:640:LYS:HE2	1:A:680:VAL:HG11	1.97	0.47
1:A:749:GLN:HE21	1:A:764:LEU:N	2.06	0.46
1:A:376:VAL:HG21	1:A:381:PRO:HB3	1.96	0.46
1:A:402:LEU:HD23	1:A:427:ILE:HD12	1.98	0.45
1:A:376:VAL:CG2	1:A:381:PRO:HB3	2.47	0.45
1:A:428:ASN:ND2	1:A:643:GLN:HE21	2.16	0.44
1:A:916:ARG:HE	1:A:931:HIS:CD2	2.34	0.44
1:A:562:PRO:HG3	1:A:591:PRO:HG2	1.99	0.43
1:A:358:THR:HG22	1:A:404:LEU:HD23	2.01	0.43
1:A:354:ILE:HG21	1:A:381:PRO:HG3	2.01	0.43
1:A:344:VAL:HG23	1:A:381:PRO:HD2	2.01	0.42
1:A:198:VAL:HG22	1:A:203:ASP:HB2	2.03	0.41
1:A:764:LEU:HB3	1:A:766:LEU:CD2	2.49	0.41
1:A:1038:TYR:O	1:A:1042:GLN:HG2	2.21	0.41
1:A:120:ALA:HB2	1:A:703:ASN:HD21	1.85	0.41

There are no symmetry-related clashes.

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	835/946 (88%)	803 (96%)	28 (3%)	4 (0%)	29	48

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	199	SER
1	A	378	CYS
1	A	973	LYS
1	A	933	ASP

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	617/860 (72%)	582 (94%)	35 (6%)	20	36

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	109	GLU
1	A	156	LEU
1	A	251	ILE
1	A	290	LYS
1	A	292	SER
1	A	335	ARG
1	A	354	ILE

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Mol	Chain	Res	Type
1	A	374	GLN
1	A	380	ASN
1	A	387	LEU
1	A	401	ARG
1	A	461	VAL
1	A	462	THR
1	A	488	ASP
1	A	559	VAL
1	A	561	ILE
1	A	596	GLU
1	A	632	LEU
1	A	648	LEU
1	A	655	LYS
1	A	656	LYS
1	A	681	SER
1	A	766	LEU
1	A	770	ARG
1	A	779	LEU
1	A	790	SER
1	A	791	GLU
1	A	797	ASN
1	A	805	ASP
1	A	834	LEU
1	A	845	VAL
1	A	916	ARG
1	A	937	PHE
1	A	1006	LEU
1	A	1017	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	137	GLN
1	A	157	ASN
1	A	180	HIS
1	A	213	HIS
1	A	269	GLN
1	A	384	ASN
1	A	428	ASN
1	A	637	GLN
1	A	665	HIS
1	A	703	ASN

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Mol	Chain	Res	Type
1	A	749	GLN
1	A	760	GLN
1	A	763	ASN
1	A	826	ASN
1	A	931	HIS
1	A	994	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	VY1	A	9001	-	36,36,36	1.64	10 (27%)	41,53,53	1.32	4 (9%)

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	VY1	A	9001	-	-	4/18/47/47	0/5/5/5

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	9001	VY1	C18-N17	3.38	1.40	1.34
2	A	9001	VY1	C24-N26	3.23	1.40	1.35
2	A	9001	VY1	C24-N23	3.21	1.39	1.35
2	A	9001	VY1	S3-N2	3.06	1.65	1.61
2	A	9001	VY1	C21-C20	-2.92	1.45	1.49
2	A	9001	VY1	S3-N6	2.50	1.68	1.62
2	A	9001	VY1	C18-N19	2.37	1.38	1.34
2	A	9001	VY1	C16-N12	2.21	1.42	1.38
2	A	9001	VY1	C18-N28	2.18	1.39	1.35
2	A	9001	VY1	C13-N12	2.17	1.50	1.46

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	9001	VY1	C16-N12-C9	-4.19	116.79	125.39
2	A	9001	VY1	C13-N12-C9	-3.62	116.94	123.35
2	A	9001	VY1	C1-N2-S3	2.67	124.21	119.51
2	A	9001	VY1	C9-C11-N6	2.02	106.56	102.57

There are no chirality outliers.

All (4) torsion outliers are listed below:

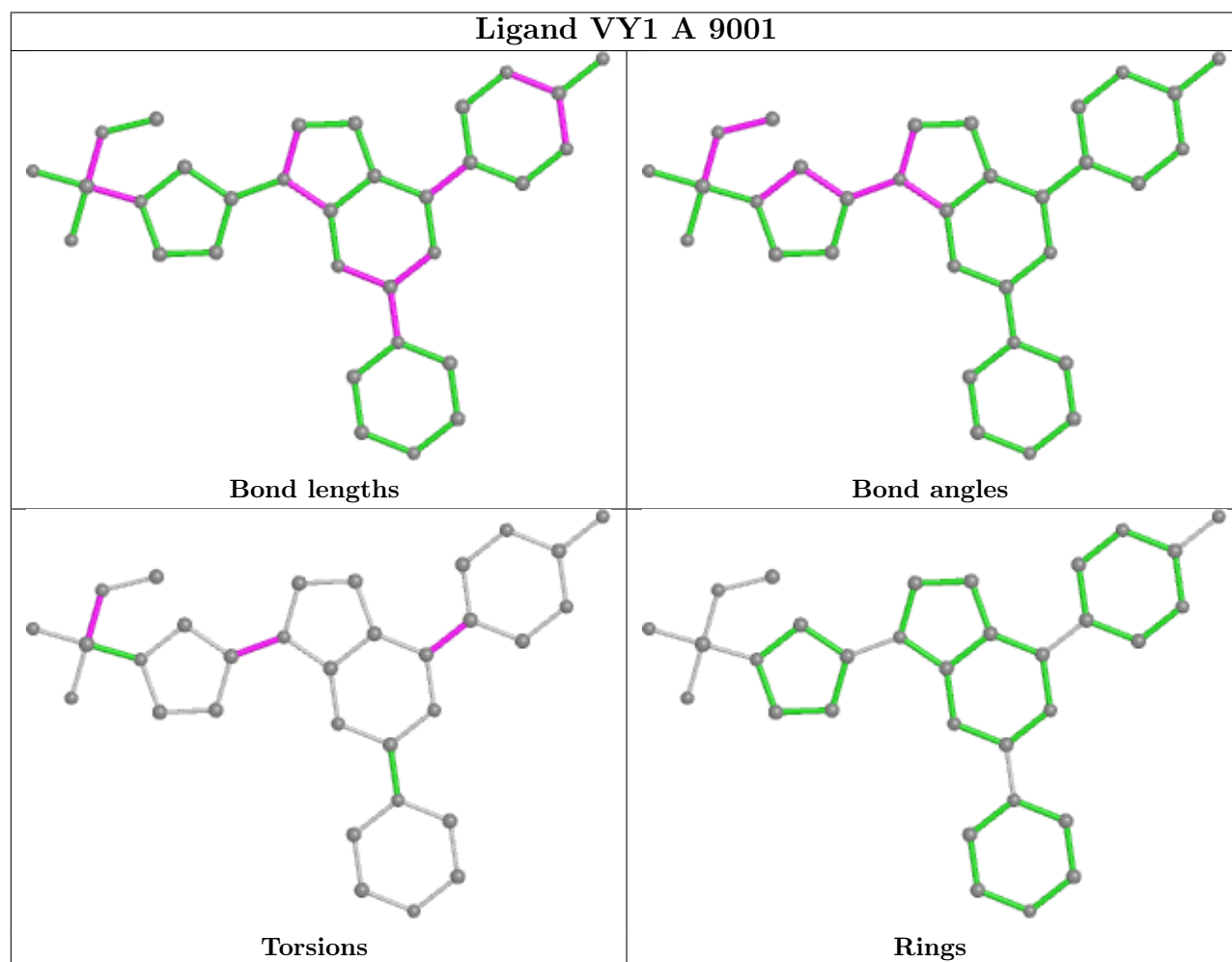
Mol	Chain	Res	Type	Atoms
2	A	9001	VY1	C1-N2-S3-O4
2	A	9001	VY1	C1-N2-S3-O5
2	A	9001	VY1	C8-C9-N12-C16
2	A	9001	VY1	N19-C20-C21-C27

There are no ring outliers.

No monomer is involved in short contacts.

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	844/946 (89%)	0.66	71 (8%) 11 12	45, 80, 131, 153	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	307	TYR	4.9
1	A	1016	PHE	4.2
1	A	180	HIS	4.0
1	A	570	LEU	3.8
1	A	739	MET	3.7
1	A	735	LEU	3.7
1	A	719	LEU	3.6
1	A	1038	TYR	3.5
1	A	988	TYR	3.5
1	A	961	LEU	3.5
1	A	715	LEU	3.4
1	A	857	ILE	3.4
1	A	1022	ILE	3.3
1	A	881	LEU	3.2
1	A	131	VAL	3.2
1	A	213	HIS	3.1
1	A	554	HIS	3.1
1	A	299	MET	3.1
1	A	744	PHE	3.1
1	A	775	ALA	3.1
1	A	556	HIS	3.0
1	A	601	LEU	2.9
1	A	308	SER	2.8
1	A	304	MET	2.8
1	A	576	SER	2.8
1	A	209	LEU	2.7
1	A	862	CYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	287	LEU	2.7
1	A	934	PHE	2.6
1	A	331	ASN	2.6
1	A	622	TYR	2.6
1	A	832	ARG	2.6
1	A	864	GLY	2.5
1	A	285	LEU	2.5
1	A	330	ILE	2.5
1	A	306	SER	2.5
1	A	297	LEU	2.4
1	A	936	HIS	2.4
1	A	561	ILE	2.4
1	A	874	SER	2.4
1	A	593	ILE	2.4
1	A	817	ILE	2.4
1	A	411	GLY	2.4
1	A	543	ILE	2.4
1	A	396	LEU	2.4
1	A	250	TYR	2.3
1	A	938	LEU	2.3
1	A	262	LEU	2.3
1	A	1021	TYR	2.3
1	A	871	GLN	2.3
1	A	329	VAL	2.3
1	A	910	ILE	2.3
1	A	1019	ILE	2.2
1	A	909	PHE	2.2
1	A	998	PHE	2.2
1	A	1026	LEU	2.2
1	A	974	THR	2.2
1	A	920	ASN	2.2
1	A	328	TRP	2.2
1	A	908	THR	2.1
1	A	191	ILE	2.1
1	A	905	CYS	2.1
1	A	448	VAL	2.1
1	A	220	VAL	2.0
1	A	848	ILE	2.0
1	A	156	LEU	2.0
1	A	766	LEU	2.0
1	A	708	ALA	2.0
1	A	278	MET	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	334	LEU	2.0
1	A	224	ALA	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](#)

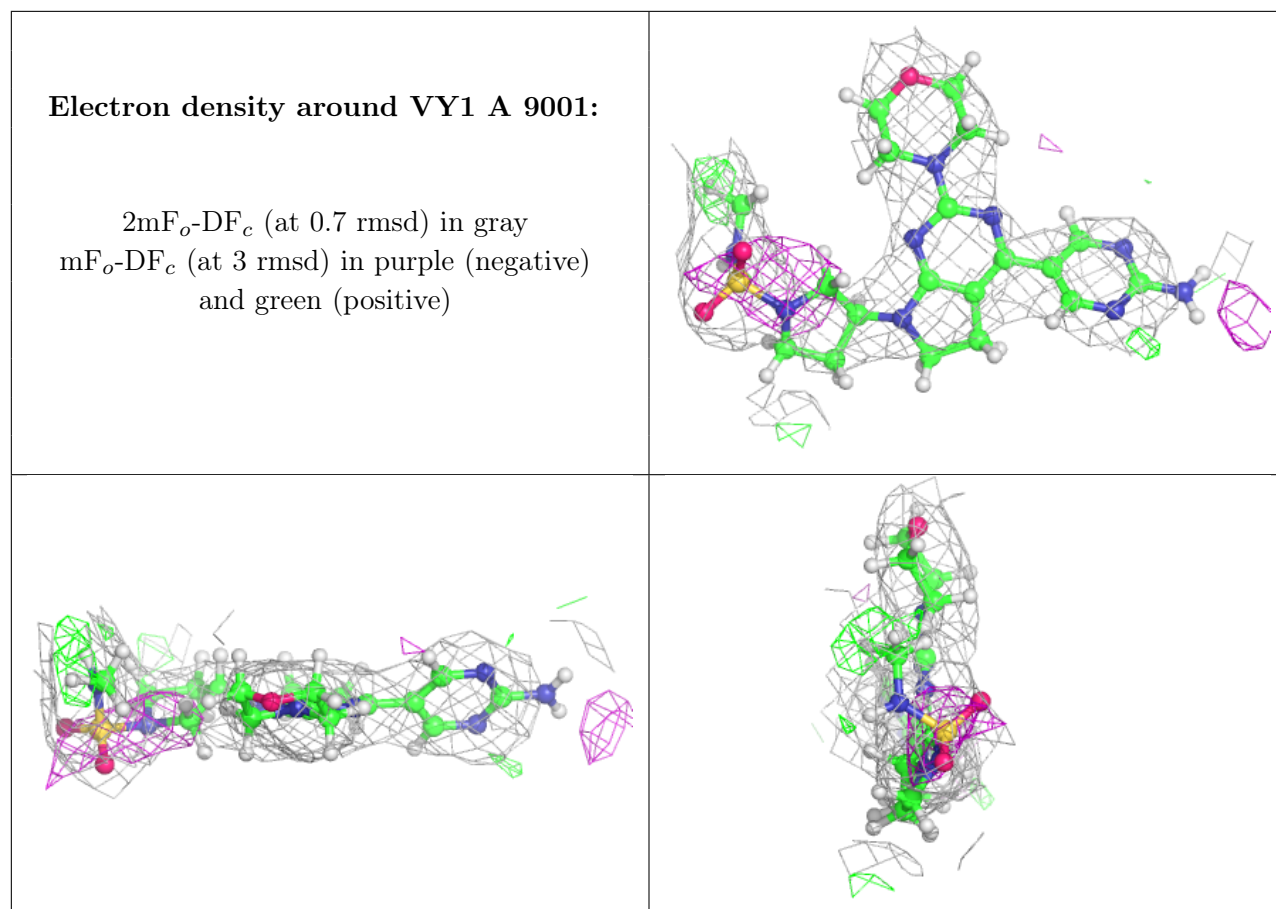
There are no monosaccharides in this entry.

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(\AA^2)	Q<0.9
2	VY1	A	9001	32/32	0.82	0.29	97,107,128,128	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.



6.5 Other polymers ⓘ

There are no such residues in this entry.