



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 28, 2025 – 10:17 AM EDT

PDB ID : 8V65 / pdb\_00008v65  
Title : Nanorana parkeri saxiphilin:dcGTX2 (co-crystal)  
Authors : Zakrzewska, S.; Minor, D.L.  
Deposited on : 2023-12-01  
Resolution : 1.80 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>.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0rc1  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

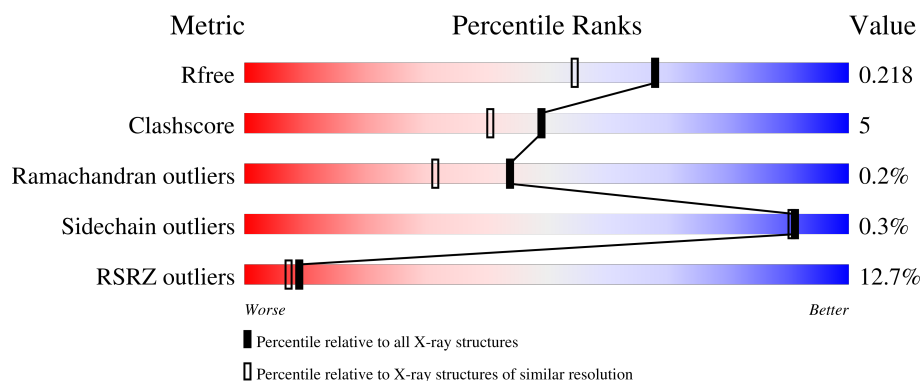
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


The reported resolution of this entry is 1.80 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))
$R_{free}$	164625	7108 (1.80-1.80)
Clashscore	180529	8162 (1.80-1.80)
Ramachandran outliers	177936	8077 (1.80-1.80)
Sidechain outliers	177891	8076 (1.80-1.80)
RSRZ outliers	164620	7108 (1.80-1.80)

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	854	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6840 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 Saxiphilin.

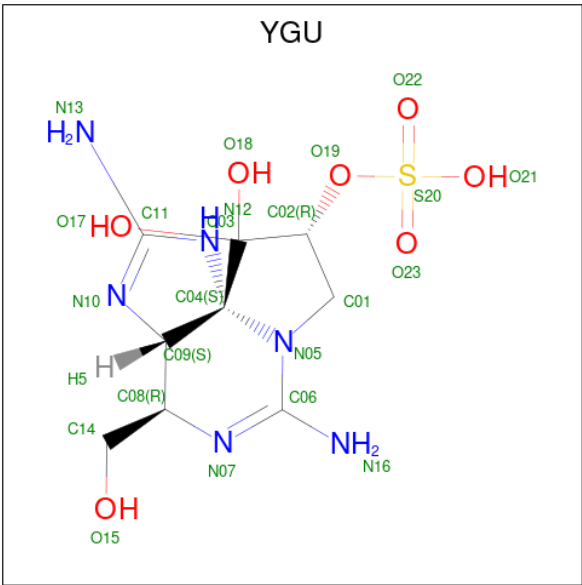
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	821	6373	3989	1102	1223	59	0	1	0

- Molecule 2 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula:  $C_{10}H_{22}O_6$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	16	10	6	0	0

- Molecule 3 is (3a*S*,4*R*,7*R*,9*R*,10a*S*)-2,6-diamino-10,10-dihydroxy-4-(hydroxymethyl)-3a,4,9,10-tetrahydro-1*H*,8*H*-pyrrolo[1,2-*c*]purin-9-yl hydrogen sulfate (CCD ID: YGU) (formula:  $C_9H_{16}N_6O_7S$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
3	A	1	23	9	6	7	1	0	0

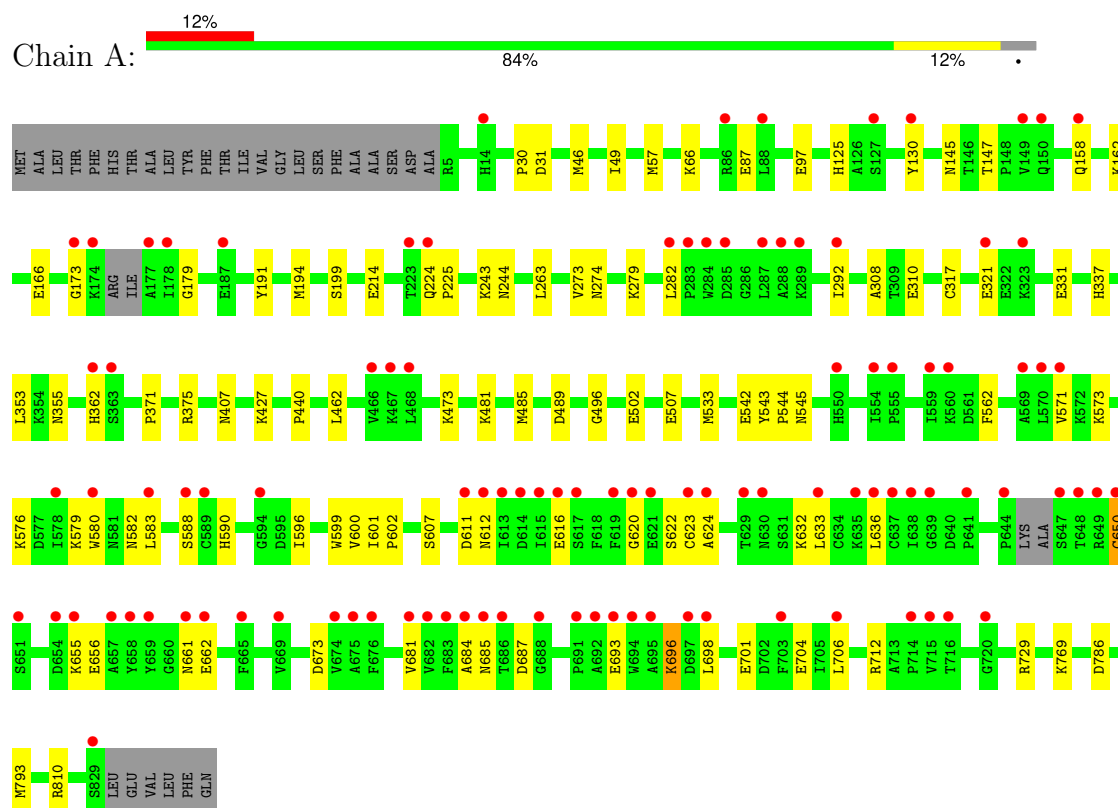
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	428	Total	O	0	0
			428	428		

### 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: Saxiphilin



## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	229.67Å 229.67Å 67.71Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.31 – 1.80 50.31 – 1.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (50.31-1.80) 100.0 (50.31-1.80)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.05 (at 1.79Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, $R_{free}$	0.199 , 0.218 0.199 , 0.218	Depositor DCC
$R_{free}$ test set	121417 reflections (1.62%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.1	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 42.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.011 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	6840	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.36% of the height of the origin peak. No significant pseudotranslation is detected.*

<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: YGU, 1PE

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	0.18	0/6518	0.38	0/8815

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	6373	0	6164	67	0
2	A	16	0	22	1	0
3	A	23	0	0	0	0
4	A	428	0	0	11	0
All	All	6840	0	6186	67	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 5.

All (67) 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:310:GLU:OE1	4:A:1001:HOH:O	1.81	0.97
1:A:489:ASP:OD2	4:A:1002:HOH:O	1.85	0.94
1:A:274:ASN:HB3	2:A:901:1PE:H131	1.68	0.76
1:A:786:ASP:OD2	4:A:1003:HOH:O	2.04	0.75
1:A:87:GLU:OE1	4:A:1004:HOH:O	2.05	0.74
1:A:97:GLU:OE1	4:A:1005:HOH:O	2.09	0.70
1:A:225:PRO:HG3	1:A:362:HIS:CD2	2.28	0.67
1:A:145:ASN:ND2	4:A:1020:HOH:O	2.35	0.60
1:A:579:LYS:HE2	1:A:582:ASN:HD22	1.68	0.59
1:A:292:ILE:HD12	1:A:462:LEU:HD22	1.87	0.57
1:A:507:GLU:OE2	4:A:1007:HOH:O	2.18	0.57
1:A:687:ASP:N	1:A:698:LEU:O	2.33	0.56
1:A:46:MET:HE1	1:A:66:LYS:HG2	1.88	0.54
1:A:485:MET:HE3	1:A:769:LYS:HD3	1.91	0.53
1:A:588:SER:OG	1:A:622:SER:OG	2.18	0.53
1:A:706:LEU:HD23	1:A:712:ARG:HG2	1.92	0.52
1:A:810:ARG:NH2	4:A:1009:HOH:O	2.24	0.52
1:A:321:GLU:HA	1:A:321:GLU:OE1	2.10	0.51
1:A:244:ASN:ND2	4:A:1025:HOH:O	2.42	0.50
1:A:786:ASP:OD1	1:A:786:ASP:N	2.40	0.50
1:A:473:LYS:HE2	1:A:496:GLY:O	2.12	0.50
1:A:49:ILE:CD1	1:A:57:MET:HG2	2.42	0.49
1:A:542:GLU:OE1	1:A:729:ARG:HD3	2.12	0.49
1:A:616:GLU:HA	1:A:633:LEU:HD21	1.94	0.48
1:A:481:LYS:HD3	1:A:502:GLU:OE2	2.12	0.48
1:A:607:SER:HB2	1:A:612:ASN:HA	1.95	0.48
1:A:693:GLU:HB2	1:A:696:LYS:HE3	1.96	0.48
1:A:292:ILE:CD1	1:A:462:LEU:HD22	2.44	0.47
1:A:661:ASN:HB3	1:A:681:VAL:HG22	1.95	0.47
1:A:130:TYR:CZ	1:A:147:THR:HG22	2.50	0.47
1:A:162:LYS:NZ	4:A:1037:HOH:O	2.48	0.47
1:A:243:LYS:O	1:A:375:ARG:NH2	2.48	0.47
1:A:158:GLN:HG2	4:A:1235:HOH:O	2.15	0.46
1:A:576:LYS:HE2	1:A:576:LYS:HB3	1.64	0.46
1:A:125:HIS:ND1	1:A:611:ASP:OD1	2.39	0.46
1:A:407:ASN:OD1	1:A:440:PRO:HB3	2.16	0.45
1:A:279:LYS:HE3	1:A:371:PRO:O	2.16	0.45
1:A:194:MET:SD	1:A:224:GLN:NE2	2.89	0.45
1:A:214:GLU:HG2	1:A:355:ASN:O	2.17	0.45
1:A:571:VAL:HG12	1:A:673:ASP:O	2.17	0.45
1:A:693:GLU:HA	1:A:696:LYS:HG3	1.98	0.45
1:A:263:LEU:HD22	1:A:308:ALA:HA	1.98	0.44

Continued on next page...



Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:704:GLU:OE2	1:A:712:ARG:NH2	2.31	0.44
1:A:632:LYS:HB3	1:A:632:LYS:HE2	1.82	0.44
1:A:655:LYS:HD2	1:A:655:LYS:HA	1.80	0.44
1:A:662:GLU:HG3	1:A:685:ASN:OD1	2.17	0.43
1:A:650:CYS:N	1:A:656:GLU:OE1	2.47	0.43
1:A:30:PRO:O	1:A:31:ASP:HB2	2.18	0.43
1:A:166:GLU:OE1	1:A:191:TYR:OH	2.22	0.43
1:A:317:CYS:HB3	1:A:331:GLU:OE1	2.19	0.43
1:A:596:ILE:HA	1:A:600:VAL:HB	2.01	0.43
1:A:599:TRP:C	1:A:602:PRO:HD2	2.44	0.43
1:A:533:MET:HE3	1:A:533:MET:HB3	1.81	0.43
1:A:273:VAL:HG11	1:A:292:ILE:HG21	2.01	0.42
1:A:337[B]:HIS:CD2	1:A:427:LYS:HD2	2.54	0.42
1:A:590:HIS:CD2	1:A:624:ALA:HB2	2.54	0.42
1:A:533:MET:HG2	1:A:793:MET:CE	2.50	0.42
1:A:620:GLY:O	1:A:632:LYS:HE2	2.20	0.42
1:A:179:GLY:HA2	1:A:199:SER:OG	2.21	0.41
1:A:580:TRP:CE3	1:A:583:LEU:HD11	2.56	0.41
1:A:601:ILE:HB	1:A:602:PRO:HD3	2.02	0.41
1:A:684:ALA:C	1:A:685:ASN:HD22	2.28	0.41
1:A:623:CYS:HB2	1:A:636:LEU:HB3	2.02	0.41
1:A:282:LEU:HD12	1:A:282:LEU:HA	1.85	0.41
1:A:544:PRO:HD2	1:A:562:PHE:O	2.20	0.41
1:A:543:TYR:CZ	1:A:545:ASN:HB3	2.55	0.41
1:A:573:LYS:NZ	1:A:701:GLU:O	2.39	0.41

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	816/854 (96%)	791 (97%)	23 (3%)	2 (0%)	44	31

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	696	LYS
1	A	173	GLY

### 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	706/731 (97%)	704 (100%)	2 (0%)	<a href="#">91</a> <a href="#">90</a>

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	353	LEU
1	A	650	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	120	HIS
1	A	249	GLN
1	A	316	GLN
1	A	362	HIS
1	A	512	GLN
1	A	608	ASN

### 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	$\# Z  > 2$
2	1PE	A	901	-	15,15,15	0.14	0	14,14,14	0.07	0
3	YGU	A	902	-	20,25,25	0.66	0	13,42,42	1.34	1 (7%)

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	1PE	A	901	-	-	8/13/13/13	-
3	YGU	A	902	-	-	1/7/59/59	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	902	YGU	N05-C06-N07	-3.42	120.66	125.42

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	901	1PE	OH6-C15-C25-OH5
2	A	901	1PE	OH2-C12-C22-OH3
2	A	901	1PE	C12-C22-OH3-C23

*Continued on next page...*

*Continued from previous page...*

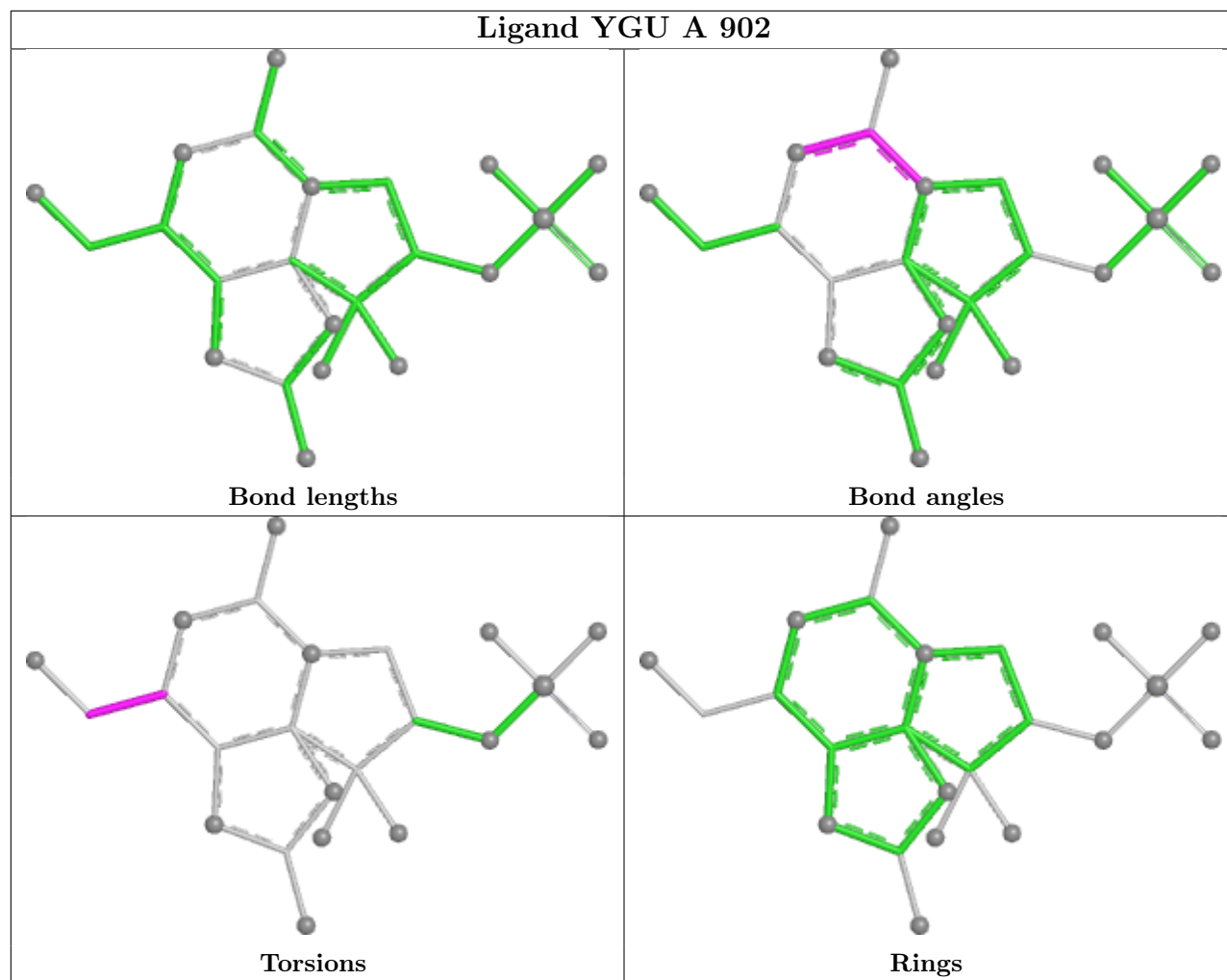
Mol	Chain	Res	Type	Atoms
2	A	901	1PE	OH4-C13-C23-OH3
3	A	902	YGU	N07-C08-C14-O15
2	A	901	1PE	C25-C15-OH6-C26
2	A	901	1PE	C15-C25-OH5-C14
2	A	901	1PE	C16-C26-OH6-C15
2	A	901	1PE	OH5-C14-C24-OH4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	901	1PE	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, 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	821/854 (96%)	0.78	104 (12%) 9 7	22, 52, 103, 134	2 (0%)

All (104) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	613	ILE	5.9
1	A	638	ILE	4.7
1	A	641	PRO	4.6
1	A	698	LEU	4.4
1	A	635	LYS	4.4
1	A	695	ALA	4.3
1	A	284	TRP	4.1
1	A	177	ALA	4.1
1	A	174	LYS	4.0
1	A	466	VAL	4.0
1	A	173	GLY	3.9
1	A	224	GLN	3.8
1	A	292	ILE	3.8
1	A	694	TRP	3.8
1	A	644	PRO	3.7
1	A	697	ASP	3.6
1	A	665	PHE	3.6
1	A	658	TYR	3.5
1	A	648	THR	3.5
1	A	571	VAL	3.4
1	A	681	VAL	3.4
1	A	639	GLY	3.4
1	A	570	LEU	3.3
1	A	692	ALA	3.2
1	A	682	VAL	3.2
1	A	468	LEU	3.2
1	A	620	GLY	3.1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	283	PRO	3.1
1	A	554	ILE	3.0
1	A	691	PRO	3.0
1	A	714	PRO	3.0
1	A	289	LYS	3.0
1	A	569	ALA	3.0
1	A	633	LEU	3.0
1	A	178	ILE	3.0
1	A	688	GLY	2.9
1	A	647	SER	2.9
1	A	615	ILE	2.9
1	A	614	ASP	2.9
1	A	624	ALA	2.9
1	A	223	THR	2.8
1	A	362	HIS	2.8
1	A	559	ILE	2.8
1	A	676	PHE	2.7
1	A	149	VAL	2.7
1	A	616	GLU	2.7
1	A	588	SER	2.7
1	A	720	GLY	2.7
1	A	703	PHE	2.7
1	A	589	CYS	2.7
1	A	363	SER	2.7
1	A	321	GLU	2.6
1	A	130	TYR	2.6
1	A	662	GLU	2.6
1	A	657	ALA	2.6
1	A	669	VAL	2.5
1	A	683	PHE	2.5
1	A	580	TRP	2.5
1	A	661	ASN	2.5
1	A	684	ALA	2.5
1	A	693	GLU	2.5
1	A	623	CYS	2.4
1	A	675	ALA	2.4
1	A	187	GLU	2.4
1	A	612	ASN	2.4
1	A	829	SER	2.4
1	A	650	CYS	2.4
1	A	659	TYR	2.4
1	A	629	THR	2.4

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	287	LEU	2.4
1	A	636	LEU	2.4
1	A	467	LYS	2.4
1	A	637	CYS	2.4
1	A	630	ASN	2.3
1	A	649	ARG	2.3
1	A	88	LEU	2.3
1	A	715	VAL	2.3
1	A	651	SER	2.3
1	A	86	ARG	2.3
1	A	560	LYS	2.3
1	A	686	THR	2.2
1	A	611	ASP	2.2
1	A	674	VAL	2.2
1	A	288	ALA	2.2
1	A	323	LYS	2.2
1	A	621	GLU	2.2
1	A	555	PRO	2.2
1	A	150	GLN	2.1
1	A	619	PHE	2.1
1	A	14	HIS	2.1
1	A	285	ASP	2.1
1	A	654	ASP	2.1
1	A	282	LEU	2.1
1	A	127	SER	2.1
1	A	594	GLY	2.1
1	A	583	LEU	2.0
1	A	578	ILE	2.0
1	A	716	THR	2.0
1	A	550	HIS	2.0
1	A	158	GLN	2.0
1	A	655	LYS	2.0
1	A	617	SER	2.0
1	A	706	LEU	2.0
1	A	685	ASN	2.0

## 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](#)

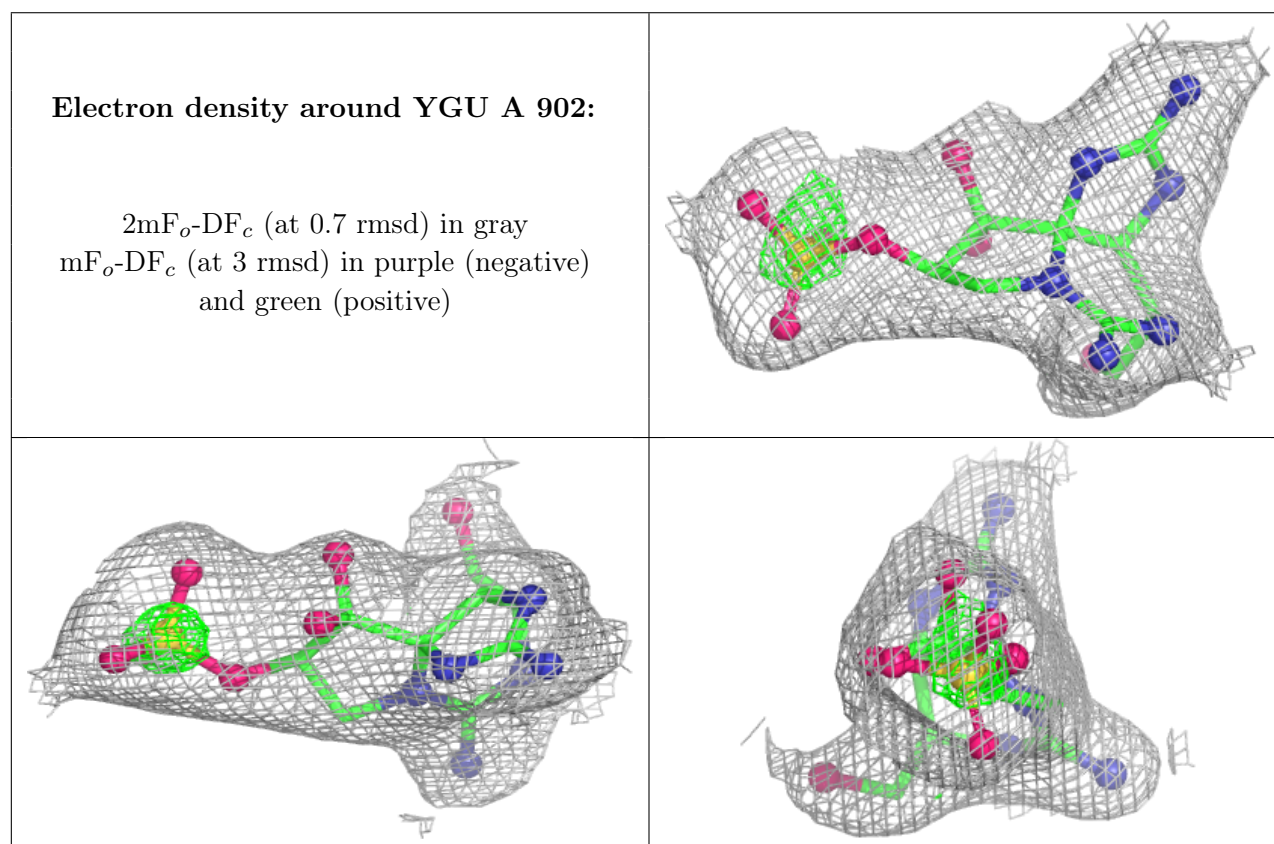
There are no monosaccharides in this entry.

## 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, 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
2	1PE	A	901	16/16	0.82	0.21	66,76,87,94	0
3	YGU	A	902	23/23	0.92	0.09	47,69,83,176	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 [i](#)

There are no such residues in this entry.