



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 12:36 AM UTC

PDB ID : 6YVE / pdb_00006yve
Title : Glycogen phosphorylase b in complex with pelargonidin 3-O-beta-D-glucoside
Authors : Drakou, C.E.; Gardeli, C.; Tsialtas, I.; Alexopoulos, S.; Mallouchos, A.; Koulas, S.; Tsagkarakou, A.; Asimakopoulos, D.; Leonidas, D.D.; Psarra, A.M.; Skamnaki, V.T.
Deposited on : 2020-04-28
Resolution : 2.10 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

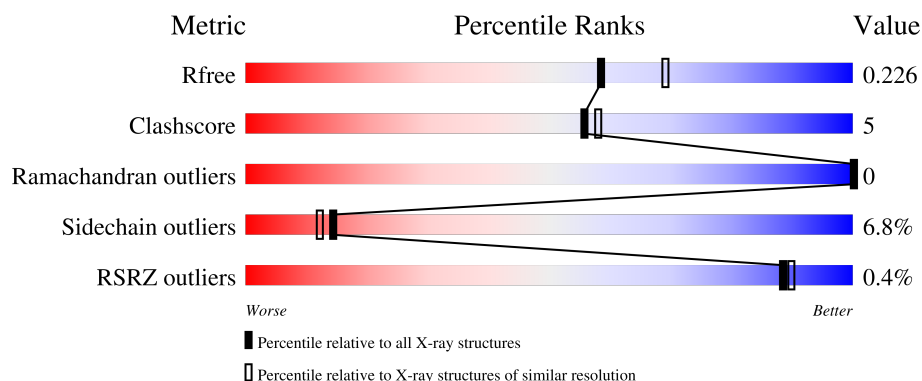
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	AAA	843	

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
4	PUQ	AAA	903	X	-	-	-

2 Entry composition [i](#)

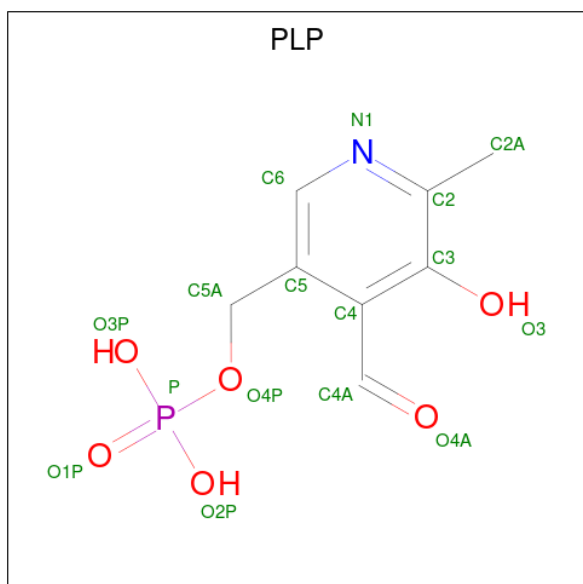
There are 5 unique types of molecules in this entry. The entry contains 14057 atoms, of which 6805 are hydrogens and 0 are deuteriums.

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 Glycogen phosphorylase, muscle form.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	AAA	811	Total	C	H	N	O	S	306	21	0
			13544	4321	6770	1196	1225	32			

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (CCD ID: PLP) (formula: $C_8H_{10}NO_6P$).



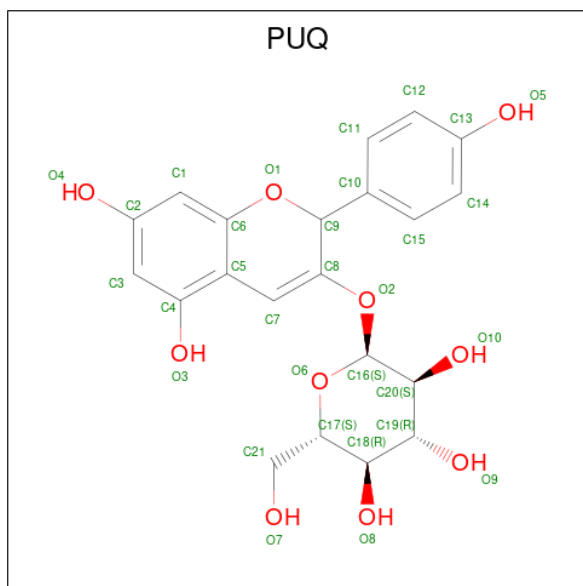
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	AAA	1	Total	C	H	N	O	P	1	0
			23	8	8	1	5	1		

- Molecule 3 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	AAA	1	Total	C	H	O	S	0	0
			10	2	6	1	1		

- Molecule 4 is pelargonidin 3-O-beta-D-glucoside (CCD ID: PUQ) (formula: $C_{21}H_{22}O_{10}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	AAA	1	Total	C	H	O	6	0
			52	21	21	10		

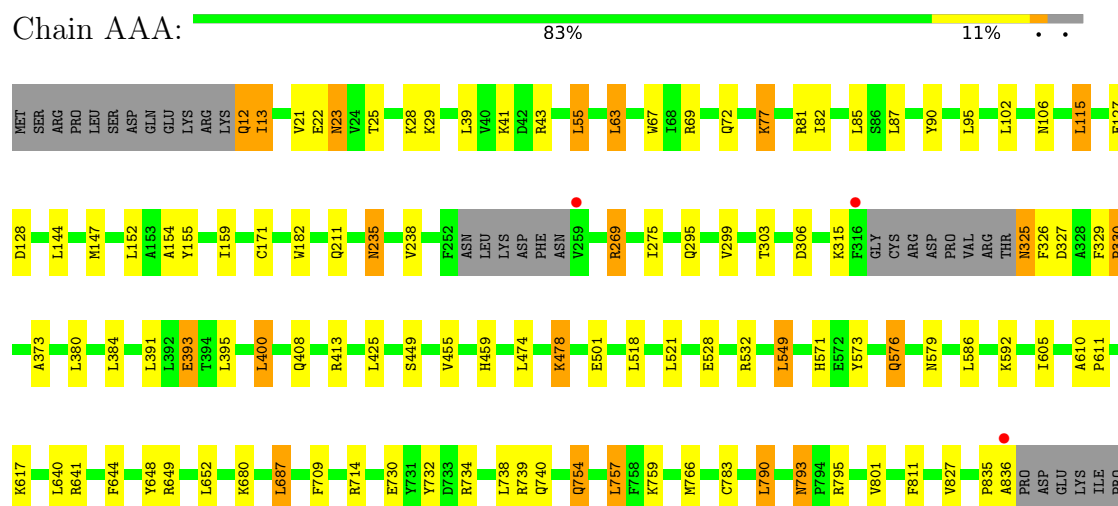
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	AAA	428	Total 428	O 428	0	0

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: Glycogen phosphorylase, muscle form



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	126.15Å 126.15Å 115.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	126.15 – 2.10 89.20 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (126.15-2.10) 99.9 (89.20-2.10)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.69 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.169 , 0.226 0.169 , 0.226	Depositor DCC
R_{free} test set	2646 reflections (4.68%)	wwPDB-VP
Wilson B-factor (Å ²)	37.8	Xtriage
Anisotropy	0.019	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 32.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	14057	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.97% 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: DMS, PLP, PUQ

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	AAA	1.04	1/6923 (0.0%)	1.35	3/9366 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AAA	330	PRO	C-O	-5.32	1.17	1.24

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AAA	269	ARG	CA-C-N	5.06	127.31	120.38
1	AAA	269	ARG	C-N-CA	5.06	127.31	120.38
1	AAA	811	PHE	CA-CB-CG	-5.03	108.77	113.80

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	AAA	6774	6770	6724	63	1
2	AAA	15	8	6	4	0
3	AAA	4	6	6	0	0
4	AAA	31	21	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	AAA	428	0	0	8	1
All	All	7252	6805	6736	64	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 5.

All (64) 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:AAA:680:LYS:NZ	2:AAA:901:PLP:C4A	1.77	1.44
1:AAA:680:LYS:HZ2	2:AAA:901:PLP:C4A	1.40	1.23
1:AAA:680:LYS:HZ1	2:AAA:901:PLP:C4A	1.56	0.97
1:AAA:680:LYS:CE	2:AAA:901:PLP:C4A	2.63	0.76
1:AAA:269:ARG:NH1	5:AAA:1001:HOH:O	2.22	0.72
1:AAA:127:GLU:HG2	1:AAA:182:TRP:HA	1.77	0.67
1:AAA:730:GLU:O	1:AAA:734:ARG:HG3	1.99	0.63
1:AAA:518[A]:LEU:O	1:AAA:521[A]:LEU:HB2	1.99	0.62
1:AAA:82:ILE:HD11	1:AAA:827[A]:VAL:HG11	1.81	0.62
1:AAA:766[A]:MET:HE2	5:AAA:1408:HOH:O	2.01	0.60
1:AAA:81[A]:ARG:NH1	1:AAA:155:TYR:OH	2.35	0.59
1:AAA:611:PRO:O	1:AAA:617:LYS:HE3	2.03	0.59
1:AAA:455:VAL:H	1:AAA:459:HIS:HD2	1.51	0.58
1:AAA:413:ARG:NH2	5:AAA:1008:HOH:O	2.36	0.57
1:AAA:159:ILE:CG1	1:AAA:299[B]:VAL:CG2	2.83	0.57
1:AAA:393:GLU:HG2	1:AAA:400:LEU:HD12	1.87	0.56
1:AAA:28:LYS:HD2	1:AAA:115:LEU:HD13	1.86	0.56
1:AAA:85[B]:LEU:HD21	1:AAA:303:THR:HG21	1.87	0.56
1:AAA:159:ILE:HG13	1:AAA:299[B]:VAL:CG2	2.36	0.56
1:AAA:611:PRO:O	1:AAA:617:LYS:CE	2.54	0.56
1:AAA:740:GLN:NE2	5:AAA:1010:HOH:O	2.38	0.56
1:AAA:687:LEU:HD13	1:AAA:801:VAL:HG22	1.89	0.55
1:AAA:13:ILE:HD12	1:AAA:501:GLU:HG2	1.88	0.54
1:AAA:85[A]:LEU:HD21	1:AAA:303:THR:HG21	1.88	0.54
1:AAA:449:SER:O	1:AAA:478:LYS:HD2	2.07	0.54
1:AAA:77:LYS:NZ	5:AAA:1016:HOH:O	2.42	0.52
1:AAA:85[A]:LEU:CD2	1:AAA:303:THR:HG21	2.40	0.51
1:AAA:605:ILE:O	1:AAA:644:PHE:HA	2.12	0.50
1:AAA:592:LYS:NZ	1:AAA:740:GLN:HE22	2.09	0.50
1:AAA:21:VAL:O	1:AAA:25[A]:THR:HG23	2.12	0.50
1:AAA:63:LEU:HD13	1:AAA:102:LEU:HD11	1.92	0.50
1:AAA:325:ASN:HD22	1:AAA:326:PHE:N	2.10	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:23:ASN:HB2	5:AAA:1058:HOH:O	2.12	0.49
1:AAA:732:TYR:CZ	1:AAA:739:ARG:HG3	2.48	0.49
4:AAA:903:PUQ:O6	4:AAA:903:PUQ:C7	2.62	0.47
1:AAA:55:LEU:HD13	1:AAA:95:LEU:HD21	1.97	0.47
1:AAA:235:ASN:HD22	1:AAA:235:ASN:H	1.64	0.46
1:AAA:373:ALA:HA	1:AAA:449:SER:HB3	1.99	0.45
1:AAA:793:ASN:C	1:AAA:793:ASN:HD22	2.23	0.45
1:AAA:67:TRP:HA	1:AAA:238:VAL:HB	1.97	0.45
1:AAA:147[A]:MET:HE2	1:AAA:154:ALA:HB1	2.00	0.44
1:AAA:325:ASN:HD22	1:AAA:326:PHE:H	1.64	0.44
1:AAA:87[A]:LEU:CD1	1:AAA:299[A]:VAL:HG11	2.48	0.44
1:AAA:835:PRO:O	1:AAA:836:ALA:HB2	2.17	0.44
1:AAA:790[A]:LEU:HD22	1:AAA:790[A]:LEU:O	2.17	0.44
1:AAA:87[A]:LEU:HD11	1:AAA:299[A]:VAL:HG11	2.00	0.44
1:AAA:159:ILE:CG1	1:AAA:299[B]:VAL:HG22	2.47	0.43
1:AAA:610:ALA:CB	4:AAA:903:PUQ:C1	2.97	0.43
1:AAA:275:ILE:O	1:AAA:295:GLN:HG2	2.19	0.42
1:AAA:754[A]:GLN:O	1:AAA:757:LEU:HB2	2.18	0.42
1:AAA:147[A]:MET:HE2	1:AAA:154:ALA:CB	2.49	0.42
1:AAA:754[B]:GLN:O	1:AAA:757:LEU:HB2	2.19	0.42
1:AAA:69:ARG:HA	1:AAA:72:GLN:HG2	2.00	0.42
1:AAA:549:LEU:HD12	1:AAA:549:LEU:HA	1.94	0.42
1:AAA:571:HIS:H	1:AAA:576:GLN:HE22	1.68	0.41
1:AAA:329:PHE:N	1:AAA:330:PRO:CD	2.83	0.41
1:AAA:528:GLU:OE1	1:AAA:795:ARG:NH1	2.52	0.41
1:AAA:159:ILE:HG12	1:AAA:299[B]:VAL:HG22	2.01	0.41
1:AAA:25[A]:THR:HG22	5:AAA:1349:HOH:O	2.21	0.41
1:AAA:576:GLN:HE21	1:AAA:576:GLN:HB2	1.61	0.41
1:AAA:12:GLN:NE2	1:AAA:106:ASN:OD1	2.54	0.40
1:AAA:709:PHE:HB3	1:AAA:783:CYS:SG	2.61	0.40
1:AAA:408:GLN:HG3	5:AAA:1197:HOH:O	2.21	0.40
1:AAA:648:TYR:HA	1:AAA:652:LEU:HD23	2.04	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)
1:AAA:171[A]:CYS:HG	5:AAA:1338:HOH:O[5_544]	1.41	0.19

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	AAA	826/843 (98%)	804 (97%)	22 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	AAA	722/732 (99%)	670 (93%)	52 (7%)	13	11

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	12	GLN
1	AAA	13	ILE
1	AAA	22	GLU
1	AAA	23	ASN
1	AAA	29	LYS
1	AAA	39	LEU
1	AAA	41	LYS
1	AAA	43	ARG
1	AAA	55	LEU
1	AAA	63	LEU
1	AAA	77	LYS
1	AAA	90	TYR
1	AAA	115	LEU

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Mol	Chain	Res	Type
1	AAA	128	ASP
1	AAA	144	LEU
1	AAA	152	LEU
1	AAA	211	GLN
1	AAA	235	ASN
1	AAA	306	ASP
1	AAA	315	LYS
1	AAA	325	ASN
1	AAA	327	ASP
1	AAA	380	LEU
1	AAA	384	LEU
1	AAA	391	LEU
1	AAA	393	GLU
1	AAA	395	LEU
1	AAA	400	LEU
1	AAA	425	LEU
1	AAA	474	LEU
1	AAA	478	LYS
1	AAA	532	ARG
1	AAA	549	LEU
1	AAA	573	TYR
1	AAA	576	GLN
1	AAA	579	ASN
1	AAA	586	LEU
1	AAA	640	LEU
1	AAA	641	ARG
1	AAA	649[A]	ARG
1	AAA	649[B]	ARG
1	AAA	687	LEU
1	AAA	714	ARG
1	AAA	738[A]	LEU
1	AAA	738[B]	LEU
1	AAA	754[A]	GLN
1	AAA	754[B]	GLN
1	AAA	757	LEU
1	AAA	759	LYS
1	AAA	790[A]	LEU
1	AAA	790[B]	LEU
1	AAA	793	ASN

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 ⓘ

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	PLP	AAA	901	-	15,15,16	0.87	1 (6%)	21,22,23	0.73	0
4	PUQ	AAA	903	-	33,34,34	1.44	3 (9%)	44,50,50	3.12	7 (15%)
3	DMS	AAA	902	-	3,3,3	0.47	0	3,3,3	0.18	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	PLP	AAA	901	-	-	2/6/6/8	0/1/1/1
4	PUQ	AAA	903	-	1/1/8/8	5/9/42/42	0/4/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	AAA	903	PUQ	O1-C9	-4.58	1.39	1.45
4	AAA	903	PUQ	C9-C8	-3.85	1.42	1.50
4	AAA	903	PUQ	O5-C13	-3.05	1.30	1.37
2	AAA	901	PLP	C4A-C4	-2.66	1.46	1.51

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	AAA	903	PUQ	O2-C8-C9	14.06	127.75	110.27
4	AAA	903	PUQ	O2-C8-C7	-12.43	114.94	126.02
4	AAA	903	PUQ	O1-C9-C10	4.67	115.95	109.33
4	AAA	903	PUQ	O6-C17-C18	3.04	115.18	109.70
4	AAA	903	PUQ	C19-C18-C17	2.75	115.21	110.23
4	AAA	903	PUQ	C12-C11-C10	-2.06	119.13	121.18
4	AAA	903	PUQ	O6-C16-O2	2.05	113.34	107.90

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	AAA	903	PUQ	C9

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	AAA	903	PUQ	C15-C10-C9-O1
2	AAA	901	PLP	C4-C5-C5A-O4P
4	AAA	903	PUQ	C11-C10-C9-O1
4	AAA	903	PUQ	C9-C8-O2-C16
2	AAA	901	PLP	C6-C5-C5A-O4P
4	AAA	903	PUQ	O6-C16-O2-C8
4	AAA	903	PUQ	C11-C10-C9-C8

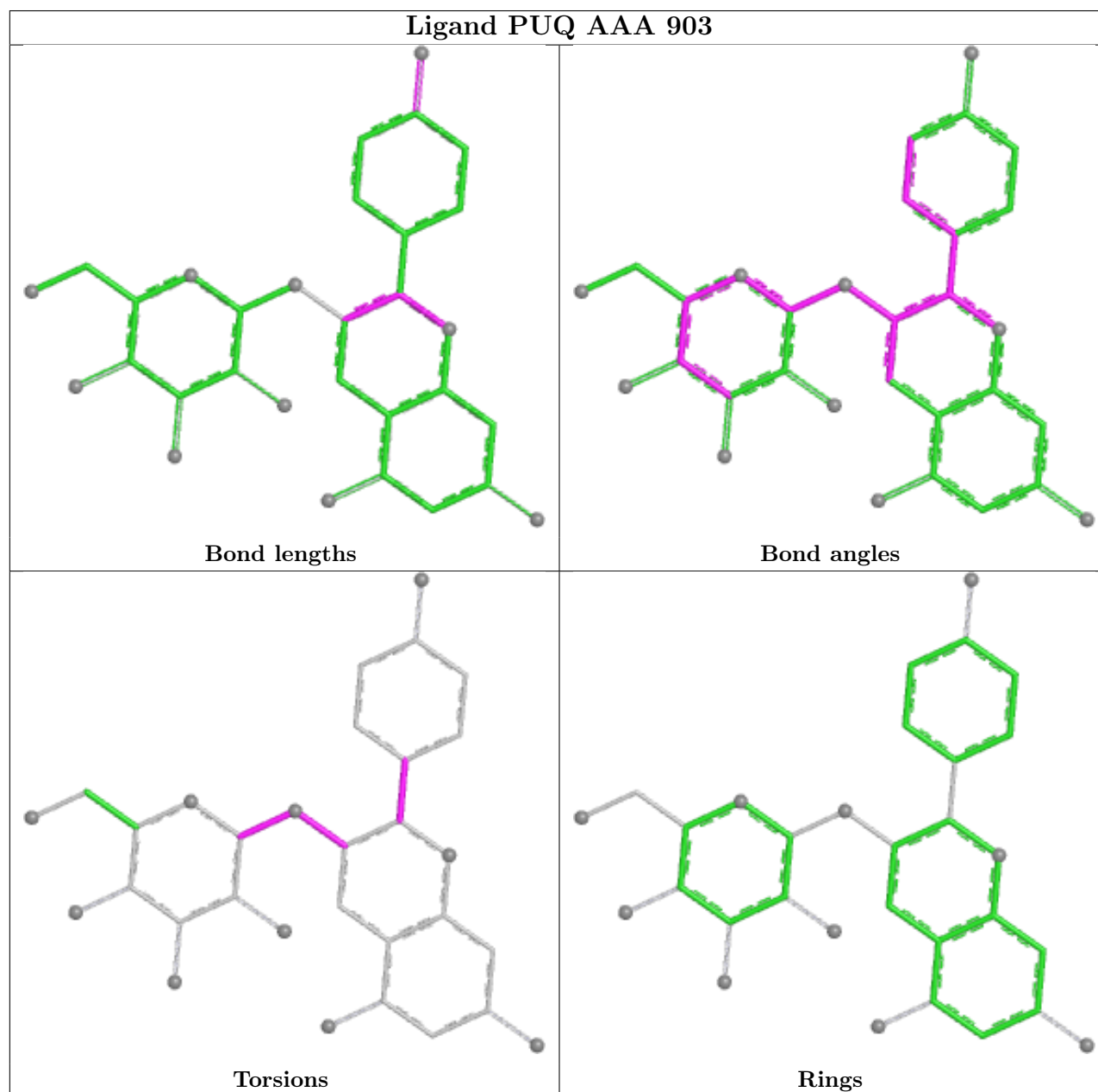
There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	AAA	901	PLP	4	0
4	AAA	903	PUQ	2	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 ⓘ

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 [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, 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	AAA	811/843 (96%)	-0.42	3 (0%) 88 90	16, 39, 64, 108	21 (2%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	836	ALA	4.4
1	AAA	316	PHE	3.9
1	AAA	259	VAL	2.9

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.

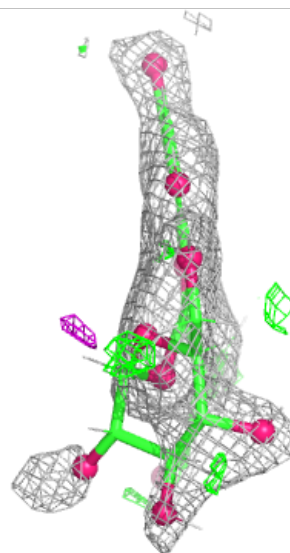
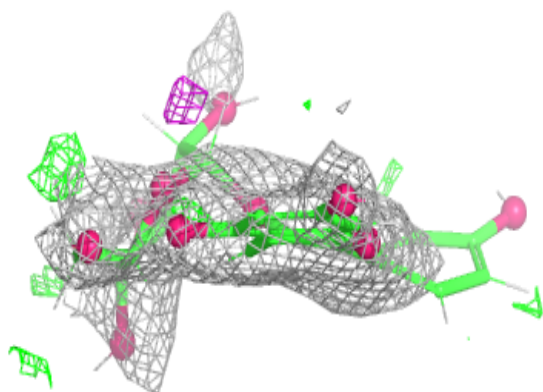
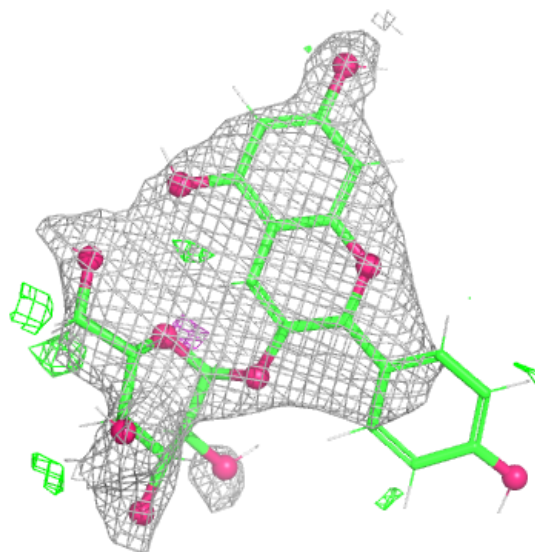
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	PUQ	AAA	903	31/31	0.75	0.16	48,80,91,93	52
3	DMS	AAA	902	4/4	0.90	0.14	46,59,66,72	0
2	PLP	AAA	901	15/16	0.99	0.04	30,33,37,37	1

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 PUQ AAA 903:

$2mF_o-DF_c$ (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.