



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 16, 2024 – 01:45 AM EDT

PDB ID : 2AMV
Title : THE STRUCTURE OF GLYCOGEN PHOSPHORYLASE B WITH AN AL
KYL-DIHYDROPYRIDINE-DICARBOXYLIC ACID
Authors : Zographos, S.E.; Oikonomakos, N.G.; Johnson, L.N.
Deposited on : 1998-10-13
Resolution : 2.30 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

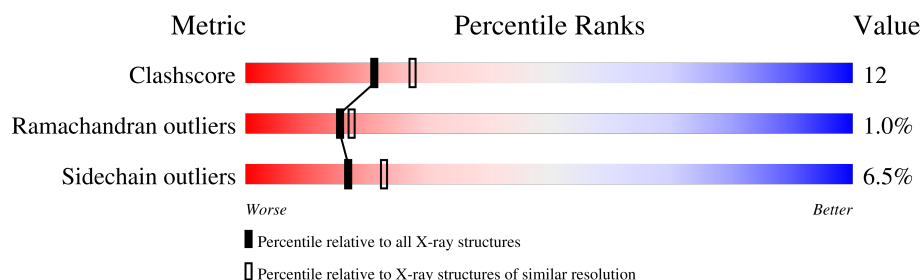
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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))
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	842	70%25%••

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7350 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.

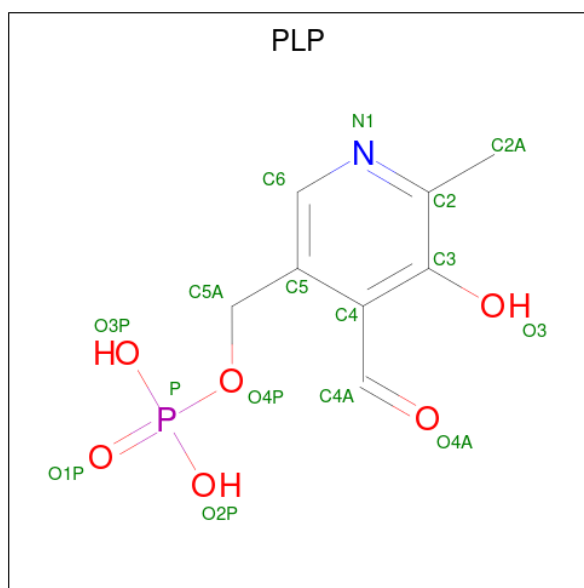
- Molecule 1 is a protein called PROTEIN (GLYCOGEN PHOSPHORYLASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	829	6742	4298	1188	1226	30	0	0	0

There is a discrepancy between the modelled and reference sequences:

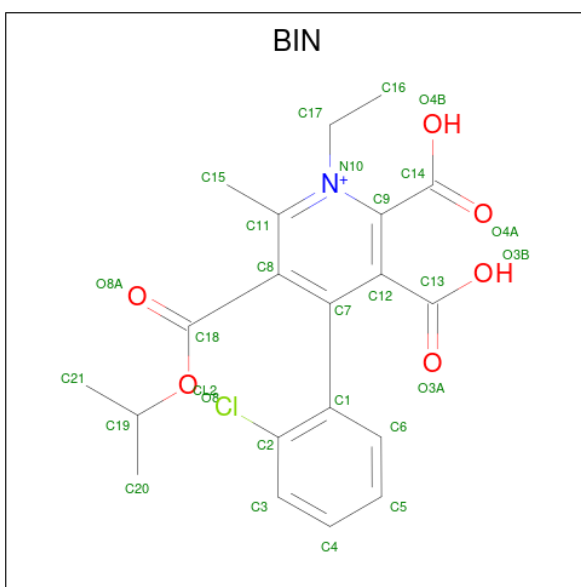
Chain	Residue	Modelled	Actual	Comment	Reference
A	609	ALA	PRO	SEE REMARK 999	UNP P00489

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



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	15	8	1	5	1	0	0

- Molecule 3 is 2,3-DICARBOXY-4-(2-CHLORO-PHENYL)-1-ETHYL-5-ISOPROPOXYCARBONYL-6-METHYL-PYRIDINIUM (three-letter code: BIN) (formula: $C_{20}H_{21}ClNO_6$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	O	0	0
			28	20	1	1	6		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 5 is water.

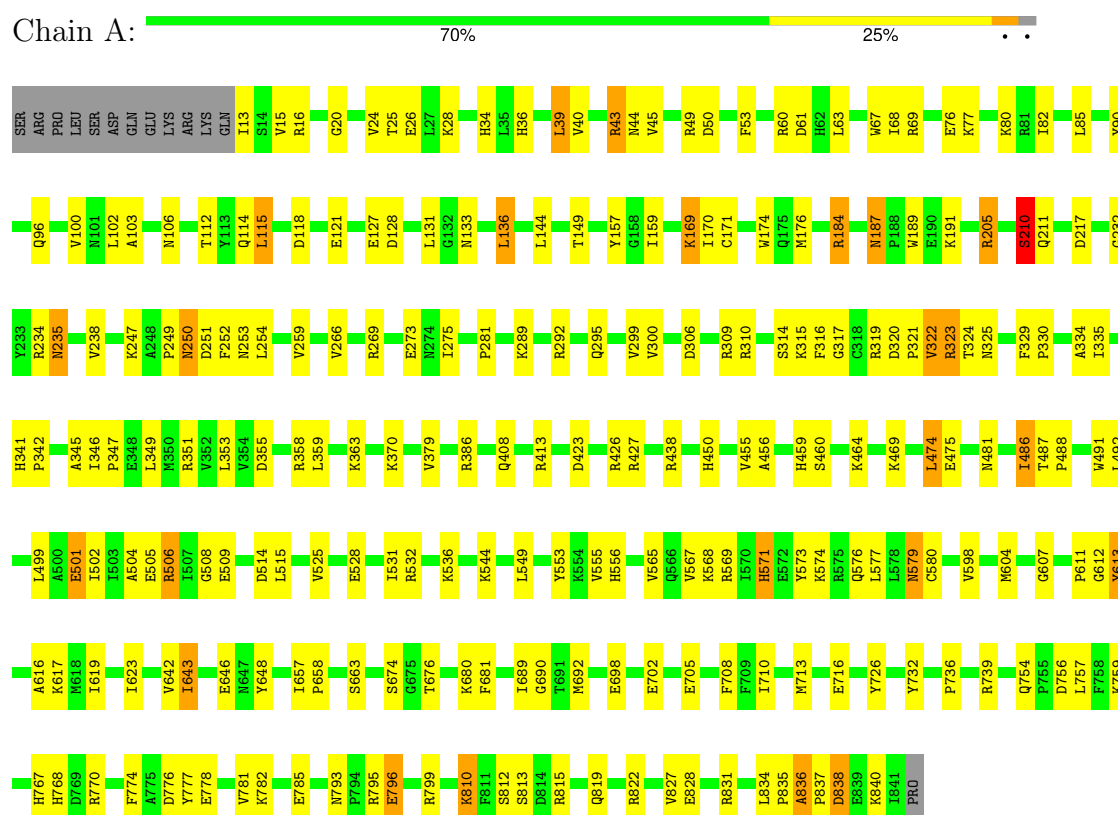
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	559	Total 559	O 559	0	0

3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

• Molecule 1: PROTEIN (GLYCOGEN PHOSPHORYLASE)



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	127.11Å 127.11Å 115.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.30	Depositor
% Data completeness (in resolution range)	94.0 (30.00-2.30)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.201 , 0.282	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7350	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

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: BIN, GOL, PLP

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	0.41	0/6895	0.64	2/9332 (0.0%)

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	136	LEU	CA-CB-CG	7.23	131.92	115.30
1	A	317	GLY	N-CA-C	-5.12	100.30	113.10

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	6742	0	6688	164	0
2	A	15	0	7	0	0
3	A	28	0	19	1	0
4	A	6	0	8	0	0
5	A	559	0	0	20	1
All	All	7350	0	6722	164	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 12.

All (164) 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:571:HIS:HB2	1:A:574:LYS:HD2	1.48	0.93
1:A:235:ASN:H	1:A:235:ASN:HD22	1.27	0.81
1:A:250:ASN:N	1:A:250:ASN:HD22	1.78	0.79
1:A:159:ILE:HG13	1:A:299:VAL:CG2	2.13	0.79
1:A:250:ASN:ND2	1:A:250:ASN:H	1.80	0.78
1:A:506:ARG:HG2	1:A:506:ARG:HH11	1.49	0.78
1:A:171:CYS:HB2	5:A:1435:HOH:O	1.83	0.78
1:A:321:PRO:O	1:A:322:VAL:HB	1.84	0.77
1:A:247:LYS:HG3	5:A:1400:HOH:O	1.87	0.75
1:A:612:GLY:H	1:A:617:LYS:NZ	1.85	0.74
1:A:85:LEU:HD13	1:A:335:ILE:HG23	1.68	0.73
1:A:320:ASP:HB2	1:A:321:PRO:HD3	1.69	0.73
1:A:13:ILE:CG2	1:A:15:VAL:HG22	2.20	0.71
1:A:250:ASN:N	1:A:250:ASN:ND2	2.39	0.69
1:A:306:ASP:OD1	1:A:309:ARG:NH1	2.26	0.69
1:A:793:ASN:ND2	1:A:796:GLU:HB2	2.07	0.69
1:A:604:MET:HG2	1:A:643:ILE:HG22	1.75	0.68
1:A:26:GLU:HG2	5:A:1535:HOH:O	1.98	0.62
1:A:82:ILE:HD11	1:A:827:VAL:HG21	1.81	0.62
1:A:793:ASN:ND2	1:A:796:GLU:HG2	2.14	0.62
1:A:159:ILE:HG13	1:A:299:VAL:HG23	1.82	0.61
1:A:211:GLN:HG3	1:A:358:ARG:HH12	1.63	0.61
1:A:322:VAL:O	1:A:323:ARG:HB3	2.00	0.61
1:A:486:ILE:HD11	1:A:680:LYS:HE3	1.83	0.61
1:A:544:LYS:HE3	5:A:1548:HOH:O	2.00	0.61
1:A:486:ILE:CD1	1:A:676:THR:HB	2.31	0.61
1:A:157:TYR:OH	1:A:310:ARG:NH2	2.35	0.60
1:A:254:LEU:HD21	1:A:266:VAL:HG22	1.84	0.59
1:A:69:ARG:HE	1:A:836:ALA:CB	2.15	0.59
1:A:28:LYS:HD2	1:A:115:LEU:HD13	1.83	0.58
1:A:250:ASN:HD22	1:A:250:ASN:H	1.40	0.58
1:A:555:VAL:O	1:A:556:HIS:HB3	2.04	0.58
1:A:341:HIS:HB2	1:A:342:PRO:HD3	1.86	0.57
1:A:423:ASP:O	1:A:427:ARG:HG3	2.04	0.57
1:A:13:ILE:HG22	1:A:15:VAL:HG22	1.84	0.57
1:A:34:HIS:HE1	1:A:61:ASP:OD2	1.87	0.57
1:A:612:GLY:H	1:A:617:LYS:HZ3	1.52	0.57
1:A:501:GLU:O	1:A:505:GLU:HG3	2.06	0.56
1:A:732:TYR:CZ	1:A:739:ARG:HG3	2.40	0.56
1:A:756:ASP:HB3	5:A:1044:HOH:O	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:319:ARG:CZ	1:A:325:ASN:HB2	2.36	0.56
1:A:171:CYS:HB3	1:A:176:MET:HG3	1.88	0.56
1:A:726:TYR:OH	1:A:774:PHE:HB2	2.05	0.56
1:A:456:ALA:HB2	1:A:674:SER:HB2	1.88	0.56
1:A:211:GLN:HG3	1:A:358:ARG:NH1	2.21	0.55
1:A:486:ILE:HD11	1:A:680:LYS:CE	2.36	0.55
1:A:506:ARG:HH11	1:A:506:ARG:CG	2.19	0.55
1:A:612:GLY:H	1:A:617:LYS:HZ1	1.53	0.55
1:A:60:ARG:HA	1:A:63:LEU:HD12	1.89	0.55
1:A:487:THR:O	1:A:491:TRP:HB2	2.05	0.55
1:A:269:ARG:O	1:A:273:GLU:HG3	2.07	0.55
1:A:732:TYR:CE1	1:A:739:ARG:HG3	2.41	0.54
1:A:736:PRO:HD2	5:A:1476:HOH:O	2.07	0.54
1:A:705:GLU:HG3	5:A:1057:HOH:O	2.06	0.54
1:A:275:ILE:O	1:A:295:GLN:HG2	2.07	0.54
1:A:346:ILE:HB	1:A:347:PRO:CD	2.38	0.53
1:A:259:VAL:HG13	1:A:259:VAL:O	2.08	0.53
1:A:713:MET:HG3	1:A:776:ASP:OD1	2.08	0.53
1:A:795:ARG:O	1:A:799:ARG:HG3	2.08	0.53
1:A:235:ASN:HD22	1:A:235:ASN:N	1.96	0.52
1:A:379:VAL:HG22	5:A:1217:HOH:O	2.08	0.52
1:A:118:ASP:OD2	1:A:121:GLU:HG3	2.09	0.52
1:A:351:ARG:O	1:A:355:ASP:HB2	2.10	0.52
1:A:499:LEU:HD12	1:A:502:ILE:HD11	1.92	0.52
1:A:782:LYS:O	1:A:785:GLU:HB2	2.09	0.51
1:A:210:SER:OG	1:A:211:GLN:N	2.41	0.51
1:A:815:ARG:O	1:A:819:GLN:HG3	2.10	0.51
1:A:346:ILE:HB	1:A:347:PRO:HD3	1.91	0.51
1:A:488:PRO:O	1:A:492:LEU:HB3	2.10	0.51
1:A:25:THR:HG23	5:A:1414:HOH:O	2.10	0.51
1:A:777:TYR:O	1:A:781:VAL:HG23	2.11	0.51
1:A:43:ARG:HG3	1:A:44:ASN:N	2.26	0.51
1:A:49:ARG:O	1:A:53:PHE:HD2	1.94	0.50
1:A:834:LEU:HG	1:A:835:PRO:HD2	1.93	0.50
1:A:455:VAL:H	1:A:459:HIS:HD2	1.60	0.50
1:A:532:ARG:HB2	5:A:1501:HOH:O	2.12	0.50
1:A:68:ILE:HG12	3:A:930:BIN:H19	1.93	0.49
1:A:553:TYR:HB2	1:A:555:VAL:HG23	1.94	0.49
1:A:20:GLY:O	1:A:24:VAL:HG23	2.12	0.49
1:A:460:SER:O	1:A:464:LYS:HG3	2.12	0.49
1:A:579:ASN:C	1:A:579:ASN:HD22	2.15	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:663:SER:HB2	1:A:681:PHE:CG	2.48	0.48
1:A:314:SER:HB2	5:A:1406:HOH:O	2.12	0.48
1:A:149:THR:HG23	1:A:831:ARG:NH1	2.28	0.48
1:A:657:ILE:HB	1:A:658:PRO:HD3	1.94	0.48
1:A:184:ARG:HD2	5:A:1311:HOH:O	2.13	0.48
1:A:329:PHE:HB3	1:A:330:PRO:HD3	1.96	0.48
1:A:169:LYS:HA	1:A:646:GLU:OE1	2.13	0.48
1:A:39:LEU:HD22	1:A:50:ASP:OD1	2.14	0.48
1:A:506:ARG:CG	1:A:506:ARG:NH1	2.77	0.48
1:A:322:VAL:O	1:A:323:ARG:CB	2.61	0.47
1:A:689:ILE:HG23	1:A:689:ILE:O	2.13	0.47
1:A:102:LEU:O	1:A:103:ALA:HB3	2.15	0.47
1:A:159:ILE:CG1	1:A:299:VAL:HG23	2.45	0.47
1:A:28:LYS:HE2	1:A:114:GLN:OE1	2.14	0.47
1:A:474:LEU:HD22	1:A:474:LEU:O	2.15	0.47
1:A:567:VAL:HB	1:A:648:TYR:CE1	2.50	0.47
1:A:611:PRO:HA	1:A:617:LYS:NZ	2.30	0.47
1:A:69:ARG:HH22	1:A:838:ASP:CA	2.28	0.47
1:A:460:SER:OG	1:A:481:ASN:ND2	2.36	0.47
1:A:205:ARG:NH1	1:A:217:ASP:OD2	2.48	0.47
1:A:565:VAL:CG2	1:A:681:PHE:CE1	2.99	0.47
1:A:450:HIS:HE1	5:A:1271:HOH:O	1.98	0.46
1:A:604:MET:HG2	1:A:643:ILE:CG2	2.45	0.46
1:A:619:ILE:O	1:A:623:ILE:HG13	2.14	0.46
1:A:692:MET:HG2	1:A:710:ILE:HG21	1.96	0.46
1:A:617:LYS:HD2	5:A:1018:HOH:O	2.15	0.46
1:A:320:ASP:CB	1:A:321:PRO:HD3	2.43	0.46
1:A:330:PRO:HB3	1:A:370:LYS:HB3	1.97	0.46
1:A:793:ASN:HD21	1:A:796:GLU:HG2	1.78	0.46
1:A:187:ASN:ND2	1:A:189:TRP:H	2.14	0.45
1:A:67:TRP:HA	1:A:238:VAL:HB	1.99	0.45
1:A:319:ARG:NH1	1:A:325:ASN:HB2	2.32	0.45
1:A:754:GLN:HB3	1:A:757:LEU:HB2	1.99	0.44
1:A:770:ARG:HG3	5:A:1135:HOH:O	2.17	0.44
1:A:456:ALA:C	1:A:481:ASN:HD21	2.21	0.44
1:A:408:GLN:HG3	5:A:1396:HOH:O	2.17	0.44
1:A:793:ASN:HD22	1:A:796:GLU:HB2	1.77	0.44
1:A:69:ARG:HE	1:A:836:ALA:HA	1.82	0.44
1:A:323:ARG:HG3	1:A:324:THR:N	2.32	0.44
1:A:837:PRO:O	1:A:838:ASP:CB	2.65	0.44
1:A:36:HIS:O	1:A:40:VAL:HA	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:254:LEU:HB2	5:A:1355:HOH:O	2.18	0.43
1:A:778:GLU:HB3	5:A:1525:HOH:O	2.18	0.43
1:A:793:ASN:ND2	1:A:796:GLU:CB	2.80	0.43
1:A:726:TYR:HH	1:A:774:PHE:HB2	1.83	0.43
1:A:69:ARG:HE	1:A:836:ALA:CA	2.31	0.43
1:A:810:LYS:O	1:A:810:LYS:HG3	2.18	0.43
1:A:170:ILE:HA	1:A:174:TRP:O	2.19	0.43
1:A:569:ARG:HD2	1:A:569:ARG:HA	1.87	0.43
1:A:613:TYR:CD2	1:A:616:ALA:HB2	2.54	0.43
1:A:568:LYS:O	1:A:607:GLY:HA3	2.19	0.42
1:A:426:ARG:NH1	1:A:427:ARG:HG2	2.34	0.42
1:A:486:ILE:HG13	1:A:491:TRP:CD1	2.53	0.42
1:A:349:LEU:HD12	1:A:349:LEU:O	2.19	0.42
1:A:515:LEU:CD2	1:A:812:SER:HB2	2.49	0.42
1:A:16:ARG:HB2	1:A:106:ASN:OD1	2.19	0.42
1:A:319:ARG:NH2	1:A:325:ASN:HB2	2.33	0.42
1:A:486:ILE:HD13	1:A:676:THR:HB	2.01	0.42
1:A:822:ARG:NH1	1:A:828:GLU:OE2	2.53	0.42
1:A:767:HIS:HB2	1:A:768:HIS:CE1	2.55	0.42
1:A:571:HIS:CB	1:A:574:LYS:HD2	2.34	0.41
1:A:690:GLY:O	1:A:710:ILE:HA	2.20	0.41
1:A:133:ASN:OD1	1:A:281:PRO:HA	2.21	0.41
1:A:232:GLY:HA3	1:A:235:ASN:HD21	1.85	0.41
1:A:289:LYS:O	1:A:292:ARG:HB3	2.21	0.41
1:A:96:GLN:O	1:A:100:VAL:HG23	2.20	0.41
1:A:525:VAL:O	1:A:531:ILE:HD11	2.21	0.41
1:A:528:GLU:HB2	5:A:1072:HOH:O	2.20	0.41
1:A:455:VAL:H	1:A:459:HIS:CD2	2.39	0.41
1:A:15:VAL:HA	1:A:509:GLU:OE2	2.20	0.41
1:A:249:PRO:HG2	1:A:253:ASN:HB2	2.02	0.41
1:A:569:ARG:O	1:A:574:LYS:HD3	2.21	0.41
1:A:573:TYR:CZ	1:A:574:LYS:HE2	2.56	0.41
1:A:611:PRO:HA	1:A:617:LYS:HZ3	1.85	0.41
1:A:191:LYS:HA	1:A:191:LYS:HD2	1.87	0.40
1:A:504:ALA:HA	1:A:508:GLY:O	2.21	0.40
1:A:25:THR:HG22	5:A:1424:HOH:O	2.20	0.40
1:A:300:VAL:CG1	1:A:345:ALA:HA	2.51	0.40
1:A:698:GLU:O	1:A:702:GLU:HG2	2.21	0.40
1:A:413:ARG:HH22	1:A:475:GLU:CD	2.24	0.40
1:A:577:LEU:O	1:A:580:CYS:HB2	2.20	0.40
1:A:80:LYS:HE2	1:A:334:ALA:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:353:LEU:HD22	1:A:359:LEU:HD22	2.03	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)
5:A:1444:HOH:O	5:A:1444:HOH:O[7_555]	2.07	0.13

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	827/842 (98%)	774 (94%)	45 (5%)	8 (1%)	15 17

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	251	ASP
1	A	322	VAL
1	A	838	ASP
1	A	210	SER
1	A	323	ARG
1	A	234	ARG
1	A	514	ASP
1	A	836	ALA

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	718/731 (98%)	671 (94%)	47 (6%)	17	23

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	LEU
1	A	43	ARG
1	A	45	VAL
1	A	76	GLU
1	A	77	LYS
1	A	90	TYR
1	A	112	THR
1	A	115	LEU
1	A	127	GLU
1	A	128	ASP
1	A	131	LEU
1	A	136	LEU
1	A	144	LEU
1	A	169	LYS
1	A	184	ARG
1	A	187	ASN
1	A	205	ARG
1	A	210	SER
1	A	235	ASN
1	A	250	ASN
1	A	252	PHE
1	A	315	LYS
1	A	316	PHE
1	A	363	LYS
1	A	386	ARG
1	A	438	ARG
1	A	469	LYS
1	A	474	LEU
1	A	486	ILE
1	A	501	GLU
1	A	506	ARG
1	A	536	LYS
1	A	549	LEU
1	A	571	HIS
1	A	576	GLN

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Mol	Chain	Res	Type
1	A	579	ASN
1	A	598	VAL
1	A	613	TYR
1	A	642	VAL
1	A	643	ILE
1	A	708	PHE
1	A	716	GLU
1	A	759	LYS
1	A	796	GLU
1	A	810	LYS
1	A	813	SER
1	A	840	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	ASN
1	A	34	HIS
1	A	71	GLN
1	A	72	GLN
1	A	97	ASN
1	A	106	ASN
1	A	167	ASN
1	A	187	ASN
1	A	219	GLN
1	A	235	ASN
1	A	250	ASN
1	A	264	GLN
1	A	284	ASN
1	A	325	ASN
1	A	390	HIS
1	A	450	HIS
1	A	459	HIS
1	A	477	HIS
1	A	481	ASN
1	A	484	ASN
1	A	539	GLN
1	A	560	ASN
1	A	566	GLN
1	A	576	GLN
1	A	579	ASN
1	A	729	GLN

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Mol	Chain	Res	Type
1	A	793	ASN
1	A	832	GLN

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 ⓘ

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	A	999	1	15,15,16	1.30	1 (6%)	21,22,23	1.10	1 (4%)
4	GOL	A	998	-	5,5,5	0.28	0	5,5,5	0.35	0
3	BIN	A	930	-	25,29,29	5.09	14 (56%)	27,42,42	2.60	10 (37%)

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	A	999	1	-	1/6/6/8	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	A	998	-	-	4/4/4/4	-
3	BIN	A	930	-	-	9/18/22/22	0/2/2/2

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	930	BIN	C11-N10	11.93	1.55	1.36
3	A	930	BIN	C8-C7	11.02	1.66	1.42
3	A	930	BIN	C2-C1	9.34	1.58	1.41
3	A	930	BIN	C8-C11	7.49	1.44	1.36
3	A	930	BIN	C4-C3	6.72	1.50	1.38
3	A	930	BIN	C3-C2	6.67	1.51	1.36
3	A	930	BIN	O8-C19	5.71	1.60	1.47
3	A	930	BIN	C5-C6	5.01	1.47	1.36
3	A	930	BIN	C12-C7	4.75	1.52	1.42
3	A	930	BIN	C2-CL2	-4.29	1.63	1.74
3	A	930	BIN	C8-C18	3.81	1.58	1.50
3	A	930	BIN	C6-C1	3.80	1.49	1.42
2	A	999	PLP	C4A-C4	3.04	1.57	1.51
3	A	930	BIN	O3B-C13	-2.62	1.22	1.30
3	A	930	BIN	O3A-C13	2.22	1.29	1.22

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	930	BIN	C7-C8-C18	-5.49	116.02	122.13
3	A	930	BIN	C16-C17-N10	4.99	121.85	111.98
3	A	930	BIN	C1-C2-CL2	4.69	127.22	119.25
3	A	930	BIN	C17-N10-C9	-4.40	116.86	119.47
3	A	930	BIN	C7-C12-C13	-4.16	116.12	121.89
3	A	930	BIN	O4A-C14-C9	-3.87	116.08	121.17
3	A	930	BIN	O3B-C13-O3A	-3.36	116.13	123.35
3	A	930	BIN	C15-C11-C8	3.35	128.63	122.85
2	A	999	PLP	O2P-P-O1P	3.01	122.56	110.83
3	A	930	BIN	C15-C11-N10	-2.63	115.92	119.08
3	A	930	BIN	C12-C7-C8	-2.52	116.85	120.21

There are no chirality outliers.

All (14) torsion outliers are listed below:

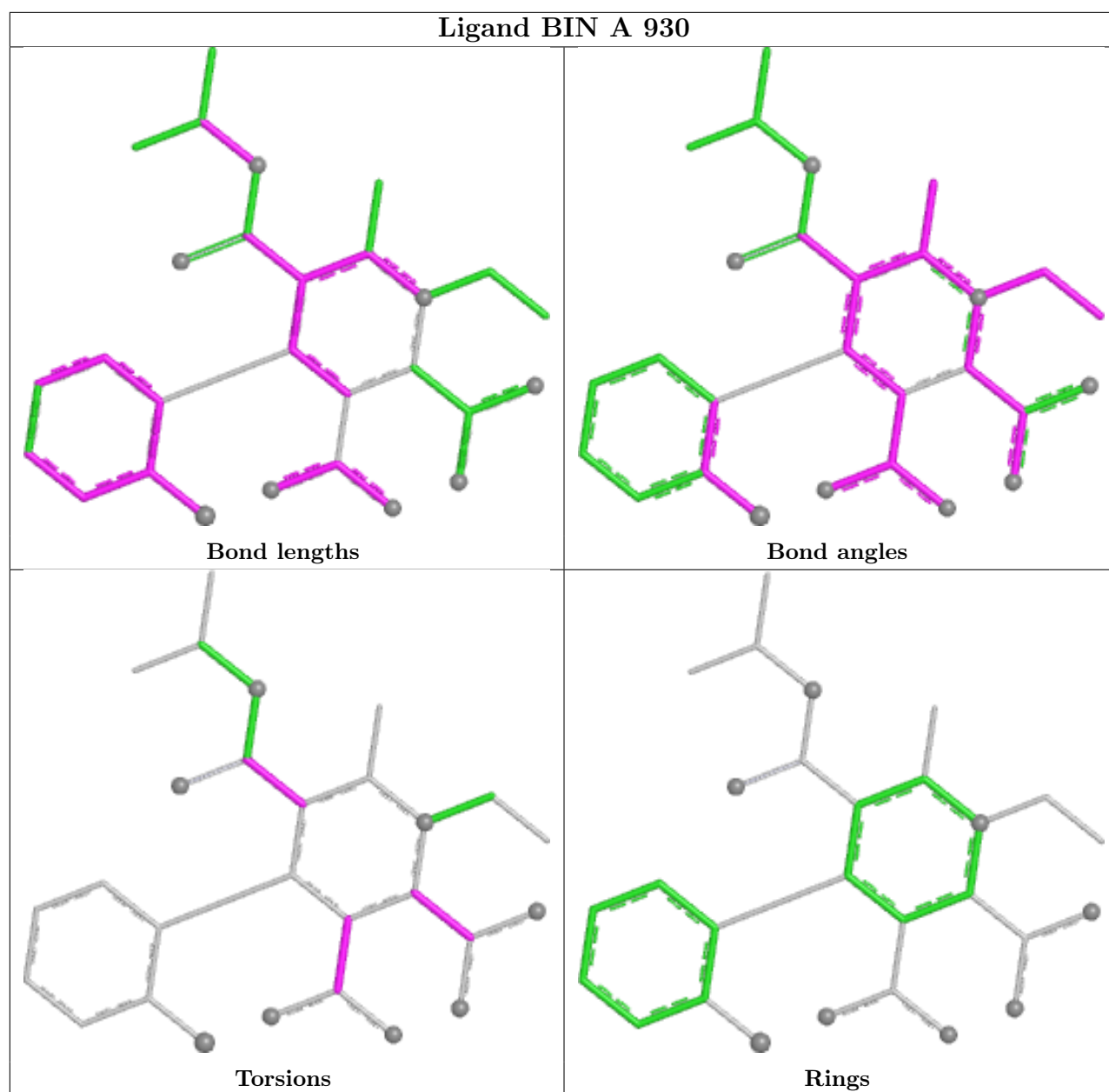
Mol	Chain	Res	Type	Atoms
3	A	930	BIN	O4A-C14-C9-N10
3	A	930	BIN	C7-C12-C13-O3A
3	A	930	BIN	C7-C12-C13-O3B
4	A	998	GOL	O1-C1-C2-C3
4	A	998	GOL	C1-C2-C3-O3
3	A	930	BIN	O8A-C18-C8-C7
2	A	999	PLP	C6-C5-C5A-O4P
3	A	930	BIN	O8-C18-C8-C7
4	A	998	GOL	O2-C2-C3-O3
3	A	930	BIN	C9-C12-C13-O3A
4	A	998	GOL	O1-C1-C2-O2
3	A	930	BIN	C9-C12-C13-O3B
3	A	930	BIN	O8-C18-C8-C11
3	A	930	BIN	O4B-C14-C9-N10

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	930	BIN	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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.