



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:05 PM UTC

PDB ID : 1H5U / pdb_00001h5u
Title : THE 1.76 Å RESOLUTION CRYSTAL STRUCTURE OF GLYCOGEN PHOSPHORYLASE B COMPLEXED WITH GLUCOSE AND CP320626, A POTENTIAL ANTIDIABETIC DRUG
Authors : Oikonomakos, N.G.; Zographos, S.E.; Skamnaki, V.T.; Archontis, G.
Deposited on : 2001-05-25
Resolution : 1.76 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)
Xtrriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

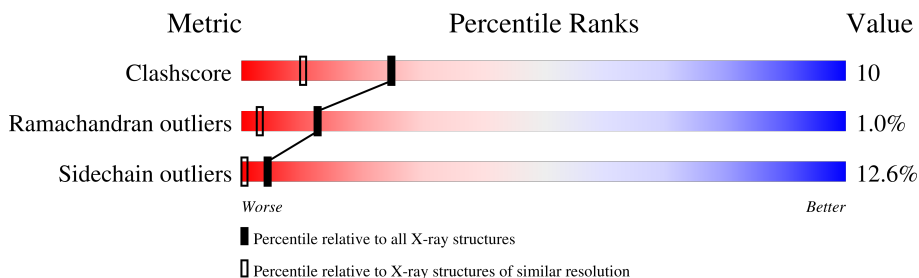
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.76 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	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)

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	 71% 20% 6% •

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7004 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.

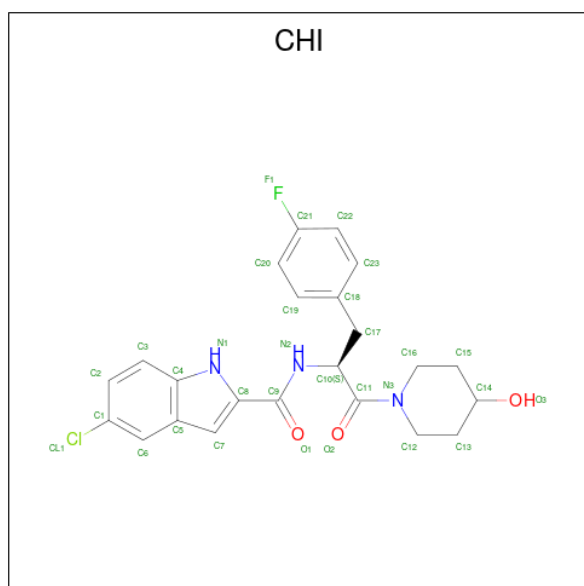
- Molecule 1 is a protein called GLYCOGEN PHOSPHORYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	811	Total	C	N	O	S	0	0	0
			6591	4203	1160	1199	29			

There is a discrepancy between the modelled and reference sequences:

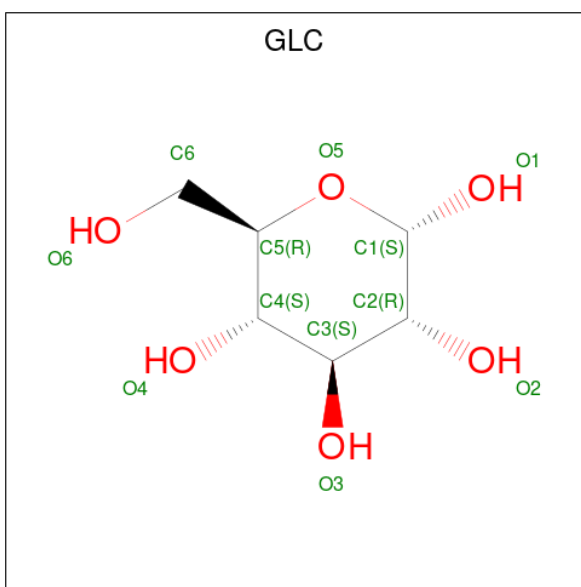
Chain	Residue	Modelled	Actual	Comment	Reference
A	380	ILE	LEU	conflict	UNP P00489

- Molecule 2 is 5-CHLORO-1H-INDOLE-2-CARBOXYLIC ACID [1-(4-FLUOROBENZYL)-2-(4-HYDROXYPIPERIDIN-1YL)-2-OXOETHYL]AMIDE (CCD ID: CHI) (formula: $C_{23}H_{23}ClFN_3O_3$).



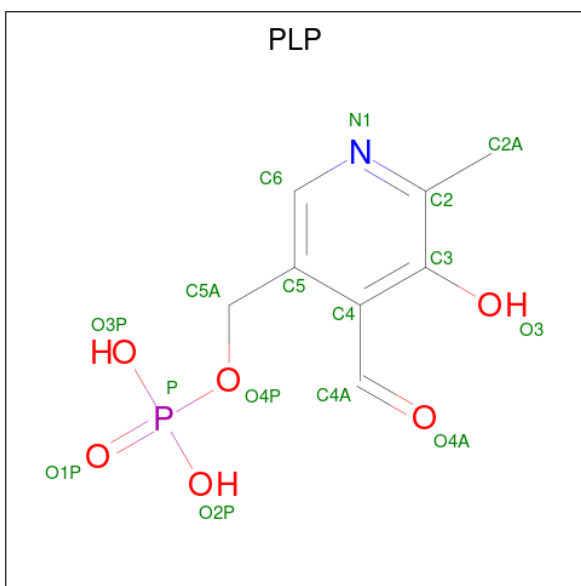
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Cl	F	N	O	0	0
			31	23	1	1	3	3		

- Molecule 3 is alpha-D-glucopyranose (CCD ID: GLC) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			12	6	6		

- Molecule 4 is PYRIDOXAL-5'-PHOSPHATE (CCD ID: PLP) (formula: $C_8H_{10}NO_6P$).



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

- Molecule 5 is water.

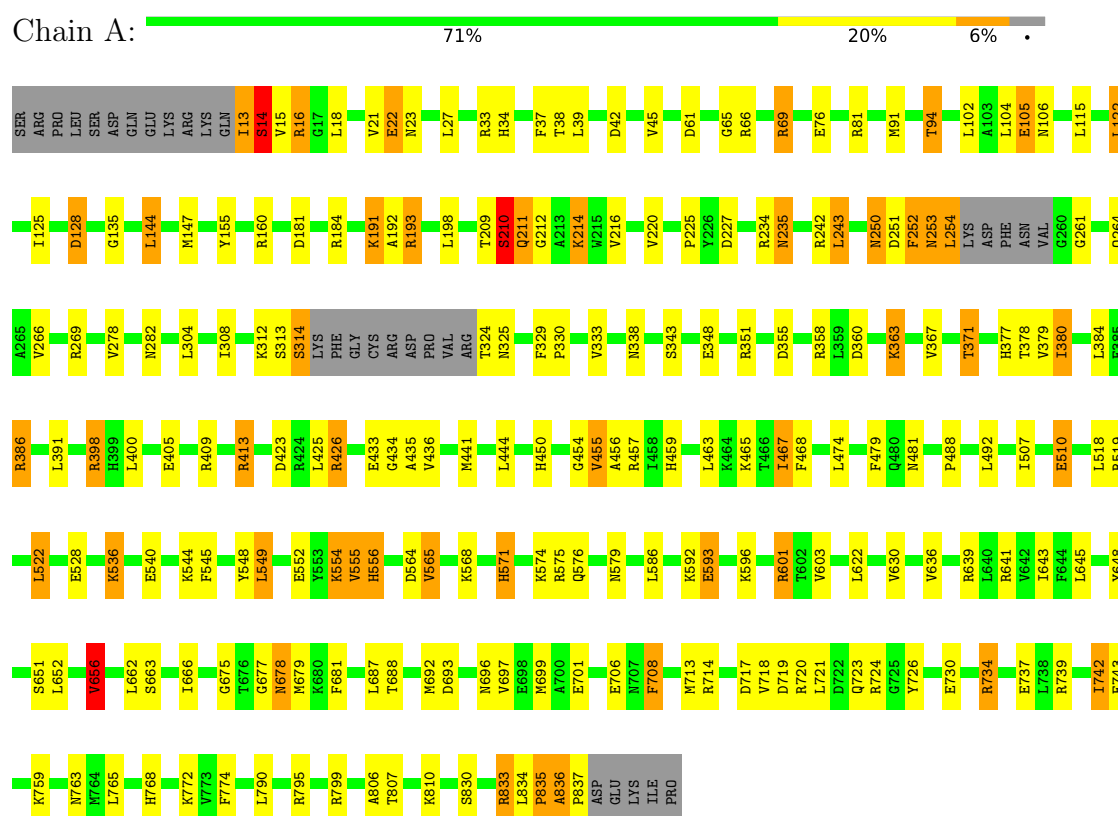
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	355	Total 355	O 355	0	0

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: 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	128.97Å 128.97Å 116.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	26.25 – 1.76	Depositor
% Data completeness (in resolution range)	95.8 (26.25-1.76)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.211 , 0.235	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7004	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GLC, PLP, CHI

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	0.44	0/6739	0.92	25/9121 (0.3%)

There are no bond length outliers.

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	16	ARG	N-CA-C	-8.21	102.82	112.92
1	A	576	GLN	N-CA-C	-7.77	102.90	112.38
1	A	565	VAL	N-CA-C	6.93	118.78	108.46
1	A	91	MET	N-CA-C	6.59	119.80	111.69
1	A	479	PHE	N-CA-C	6.59	120.24	109.76
1	A	656	VAL	CB-CA-C	-6.45	103.56	112.02
1	A	212	GLY	N-CA-C	6.18	119.81	112.33
1	A	105	GLU	N-CA-C	6.08	118.41	111.11
1	A	278	VAL	N-CA-C	6.00	116.99	108.42
1	A	675	GLY	N-CA-C	-5.85	105.40	112.48
1	A	454	GLY	N-CA-C	-5.59	102.95	112.51
1	A	507	ILE	N-CA-C	5.57	118.25	112.90
1	A	216	VAL	N-CA-C	5.56	116.86	108.96
1	A	630	VAL	N-CA-C	5.50	115.70	110.42
1	A	714	ARG	N-CA-C	-5.36	102.53	110.46
1	A	37	PHE	N-CA-C	5.34	118.02	111.82
1	A	220	VAL	N-CA-C	5.24	115.85	108.36
1	A	333	VAL	N-CA-C	5.21	115.62	108.12
1	A	677	GLY	N-CA-C	-5.18	106.51	112.73
1	A	135	GLY	N-CA-C	5.11	118.82	112.64
1	A	455	VAL	N-CA-C	5.08	117.00	112.17
1	A	666	ILE	N-CA-C	5.07	119.88	109.34
1	A	688	THR	N-CA-C	5.06	117.22	109.07
1	A	656	VAL	N-CA-C	5.01	115.24	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	575	ARG	N-CA-C	5.00	118.14	111.24

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	6591	0	6535	130	0
2	A	31	0	23	0	0
3	A	12	0	12	0	0
4	A	15	0	7	0	0
5	A	355	0	0	14	0
All	All	7004	0	6577	130	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 10.

All (130) 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:251:ASP:CG	1:A:252:PHE:H	1.57	1.09
1:A:519:ARG:HH22	1:A:807:THR:HG22	1.14	1.08
1:A:252:PHE:C	1:A:254:LEU:H	1.61	1.07
1:A:15:VAL:HG23	5:A:2002:HOH:O	1.64	0.97
1:A:252:PHE:O	1:A:254:LEU:N	1.96	0.96
1:A:225:PRO:HB2	1:A:242:ARG:HD2	1.52	0.89
1:A:252:PHE:C	1:A:254:LEU:N	2.30	0.85
1:A:227:ASP:OD2	1:A:242:ARG:HD3	1.75	0.85
1:A:519:ARG:NH2	1:A:807:THR:HG22	1.91	0.85
1:A:739:ARG:O	1:A:743:GLU:HG3	1.79	0.81
1:A:678:ASN:HD22	1:A:679:MET:H	1.27	0.80
1:A:225:PRO:CB	1:A:242:ARG:HD2	2.12	0.78
1:A:65:GLY:O	1:A:69:ARG:HG2	1.84	0.78
1:A:261:GLY:HA3	5:A:2122:HOH:O	1.85	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:VAL:CG2	5:A:2002:HOH:O	2.29	0.75
1:A:719:ASP:O	1:A:723:GLN:HG2	1.87	0.74
1:A:251:ASP:CG	1:A:252:PHE:N	2.32	0.74
1:A:455:VAL:H	1:A:459:HIS:HD2	1.35	0.74
1:A:795:ARG:O	1:A:799:ARG:HG3	1.89	0.72
1:A:545:PHE:CZ	1:A:656:VAL:HG13	2.25	0.70
1:A:13:ILE:O	1:A:14:SER:HB2	1.90	0.70
1:A:413:ARG:HG2	1:A:413:ARG:HH21	1.56	0.68
1:A:250:ASN:HA	1:A:269:ARG:HH21	1.58	0.67
1:A:266:VAL:O	1:A:269:ARG:HG3	1.95	0.67
1:A:713:MET:HB3	1:A:717:ASP:HB2	1.76	0.66
1:A:329:PHE:HB3	1:A:330:PRO:HD3	1.78	0.66
1:A:235:ASN:H	1:A:235:ASN:HD22	1.43	0.65
1:A:16:ARG:HD3	1:A:105:GLU:HG2	1.77	0.65
1:A:235:ASN:HA	1:A:833:ARG:HG3	1.77	0.65
1:A:678:ASN:HD22	1:A:679:MET:N	1.96	0.63
1:A:555:VAL:HG23	1:A:556:HIS:N	2.17	0.60
1:A:65:GLY:O	1:A:69:ARG:CG	2.51	0.59
1:A:592:LYS:HD2	1:A:592:LYS:O	2.03	0.59
1:A:730:GLU:O	1:A:734:ARG:HG2	2.02	0.59
1:A:34:HIS:HE1	1:A:61:ASP:OD1	1.85	0.58
1:A:379:VAL:HG22	5:A:2171:HOH:O	2.03	0.58
1:A:678:ASN:ND2	1:A:679:MET:H	1.99	0.58
1:A:16:ARG:HB3	1:A:105:GLU:HB3	1.87	0.56
1:A:160:ARG:HB2	1:A:243:LEU:HB3	1.86	0.56
1:A:367:VAL:O	1:A:371:THR:HG23	2.06	0.55
1:A:386:ARG:HH21	1:A:386:ARG:HB2	1.71	0.55
1:A:450:HIS:HE1	5:A:2169:HOH:O	1.91	0.54
1:A:413:ARG:HG2	1:A:413:ARG:NH2	2.22	0.54
1:A:718:VAL:HG13	1:A:772:LYS:HE2	1.90	0.54
1:A:343:SER:OG	1:A:441:MET:HE3	2.08	0.54
1:A:571:HIS:HB2	1:A:574:LYS:HG3	1.90	0.53
1:A:692:MET:HE3	1:A:697:VAL:HG22	1.90	0.53
1:A:360:ASP:OD1	1:A:363:LYS:HB2	2.09	0.53
1:A:699:MET:HE2	1:A:708:PHE:HZ	1.72	0.53
1:A:34:HIS:HD2	1:A:38:THR:OG1	1.93	0.52
1:A:313:SER:O	1:A:314:SER:C	2.54	0.51
1:A:463:LEU:HA	1:A:467:ILE:HG22	1.92	0.51
1:A:355:ASP:OD1	1:A:398:ARG:HD3	2.09	0.51
1:A:191:LYS:HG3	1:A:193:ARG:HE	1.75	0.51
1:A:94:THR:CG2	5:A:2036:HOH:O	2.60	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:726:TYR:OH	1:A:774:PHE:HB2	2.11	0.50
1:A:636:VAL:O	1:A:639:ARG:HD3	2.11	0.50
1:A:378:THR:OG1	1:A:380:ILE:HG12	2.11	0.50
1:A:835:PRO:O	1:A:836:ALA:O	2.30	0.50
1:A:836:ALA:HB1	1:A:837:PRO:CD	2.42	0.49
1:A:191:LYS:HG2	1:A:193:ARG:HH21	1.76	0.49
1:A:282:ASN:HB2	5:A:2134:HOH:O	2.12	0.49
1:A:555:VAL:CG2	1:A:556:HIS:N	2.75	0.49
1:A:386:ARG:HB2	1:A:386:ARG:NH2	2.27	0.49
1:A:122:LEU:HA	1:A:125:ILE:HD12	1.94	0.48
1:A:536:LYS:HE2	1:A:540:GLU:OE1	2.13	0.48
1:A:810:LYS:O	1:A:810:LYS:HG2	2.13	0.48
1:A:254:LEU:HD21	1:A:266:VAL:HG23	1.95	0.48
1:A:457:ARG:HH12	1:A:701:GLU:CD	2.21	0.48
1:A:564:ASP:OD1	1:A:601:ARG:NH1	2.47	0.48
1:A:191:LYS:HE2	1:A:192:ALA:O	2.14	0.48
1:A:251:ASP:O	1:A:254:LEU:CB	2.62	0.48
1:A:678:ASN:HD22	1:A:678:ASN:N	2.12	0.47
1:A:351:ARG:O	1:A:355:ASP:HB2	2.14	0.47
1:A:367:VAL:O	1:A:371:THR:CG2	2.63	0.47
1:A:81:ARG:HG2	1:A:155:TYR:HE2	1.79	0.47
1:A:251:ASP:O	1:A:254:LEU:HB3	2.16	0.46
1:A:214:LYS:HB3	1:A:214:LYS:HE2	1.72	0.46
1:A:742:ILE:HD11	1:A:774:PHE:CZ	2.51	0.46
1:A:510:GLU:HB2	5:A:2221:HOH:O	2.16	0.46
1:A:592:LYS:HD2	1:A:592:LYS:C	2.41	0.45
1:A:21:VAL:HG23	1:A:22:GLU:N	2.31	0.45
1:A:209:THR:O	1:A:211:GLN:N	2.49	0.45
1:A:144:LEU:HD12	1:A:147:MET:CE	2.46	0.45
1:A:308:ILE:O	1:A:312:LYS:HG3	2.18	0.44
1:A:467:ILE:HG23	1:A:468:PHE:CG	2.53	0.44
1:A:678:ASN:ND2	1:A:679:MET:N	2.62	0.44
1:A:13:ILE:O	1:A:14:SER:CB	2.59	0.44
1:A:579:ASN:C	1:A:579:ASN:HD22	2.24	0.44
1:A:639:ARG:HG2	5:A:2262:HOH:O	2.18	0.44
1:A:81:ARG:HG2	1:A:155:TYR:CE2	2.54	0.43
1:A:519:ARG:HG2	1:A:519:ARG:HH21	1.83	0.43
1:A:488:PRO:O	1:A:492:LEU:HB3	2.18	0.43
1:A:128:ASP:OD2	1:A:651:SER:HB3	2.19	0.43
1:A:209:THR:O	1:A:210:SER:C	2.62	0.43
1:A:304:LEU:HD12	1:A:348:GLU:CG	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:391:LEU:HD12	1:A:391:LEU:HA	1.86	0.43
1:A:648:TYR:HA	1:A:652:LEU:HD23	2.01	0.42
1:A:519:ARG:NH2	1:A:519:ARG:HG2	2.34	0.42
1:A:21:VAL:CG2	1:A:22:GLU:N	2.82	0.42
1:A:456:ALA:C	1:A:481:ASN:HD21	2.27	0.42
1:A:42:ASP:OD2	1:A:45:VAL:HG22	2.19	0.42
1:A:737:GLU:HG3	5:A:2302:HOH:O	2.18	0.42
1:A:423:ASP:O	1:A:426:ARG:HG3	2.19	0.42
1:A:338:ASN:OD1	1:A:377:HIS:NE2	2.53	0.42
1:A:663:SER:HB2	1:A:681:PHE:CG	2.55	0.42
1:A:678:ASN:ND2	1:A:678:ASN:N	2.66	0.42
1:A:836:ALA:HB1	1:A:837:PRO:HD2	2.00	0.42
1:A:181:ASP:OD2	1:A:184:ARG:CZ	2.68	0.41
1:A:641:ARG:HG3	5:A:2249:HOH:O	2.18	0.41
1:A:522:LEU:HD12	1:A:522:LEU:HA	1.84	0.41
1:A:834:LEU:O	1:A:836:ALA:N	2.54	0.41
1:A:363:LYS:O	1:A:367:VAL:HG23	2.20	0.41
1:A:519:ARG:O	1:A:522:LEU:HB2	2.20	0.41
1:A:66:ARG:NH2	1:A:837:PRO:HG3	2.35	0.41
1:A:234:ARG:NH1	5:A:2112:HOH:O	2.32	0.41
1:A:522:LEU:HD13	1:A:806:ALA:CB	2.50	0.41
1:A:571:HIS:ND1	5:A:2232:HOH:O	2.37	0.41
1:A:16:ARG:HB2	1:A:106:ASN:CG	2.46	0.41
1:A:405:GLU:O	1:A:409:ARG:HG3	2.21	0.41
1:A:693:ASP:O	1:A:696:ASN:HB2	2.21	0.41
1:A:225:PRO:HB3	1:A:242:ARG:HD2	1.98	0.41
1:A:592:LYS:HG3	1:A:593:GLU:HG2	2.02	0.41
1:A:834:LEU:HA	1:A:834:LEU:HD12	1.78	0.41
1:A:380:ILE:HG12	1:A:380:ILE:H	1.68	0.40
1:A:548:TYR:CD1	1:A:548:TYR:C	2.98	0.40
1:A:549:LEU:HA	1:A:549:LEU:HD12	1.79	0.40
1:A:94:THR:HG22	5:A:2036:HOH:O	2.19	0.40
1:A:434:GLY:O	1:A:435:ALA:C	2.64	0.40
1:A:601:ARG:HH11	1:A:601:ARG:HD3	1.76	0.40

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	805/842 (96%)	765 (95%)	32 (4%)	8 (1%)	12 3

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	14	SER
1	A	210	SER
1	A	253	ASN
1	A	836	ALA
1	A	554	LYS
1	A	835	PRO
1	A	555	VAL
1	A	556	HIS

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	701/731 (96%)	613 (87%)	88 (13%)	4 0

All (88) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ILE
1	A	14	SER
1	A	18	LEU

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Mol	Chain	Res	Type
1	A	22	GLU
1	A	23	ASN
1	A	27	LEU
1	A	33	ARG
1	A	39	LEU
1	A	69	ARG
1	A	76	GLU
1	A	94	THR
1	A	102	LEU
1	A	104	LEU
1	A	115	LEU
1	A	122	LEU
1	A	128	ASP
1	A	144	LEU
1	A	191	LYS
1	A	193	ARG
1	A	198	LEU
1	A	210	SER
1	A	211	GLN
1	A	214	LYS
1	A	235	ASN
1	A	243	LEU
1	A	250	ASN
1	A	252	PHE
1	A	253	ASN
1	A	254	LEU
1	A	264	GLN
1	A	314	SER
1	A	324	THR
1	A	325	ASN
1	A	358	ARG
1	A	363	LYS
1	A	371	THR
1	A	380	ILE
1	A	384	LEU
1	A	386	ARG
1	A	398	ARG
1	A	400	LEU
1	A	413	ARG
1	A	425	LEU
1	A	426	ARG
1	A	433	GLU

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Mol	Chain	Res	Type
1	A	436	VAL
1	A	444	LEU
1	A	465	LYS
1	A	467	ILE
1	A	474	LEU
1	A	510	GLU
1	A	518	LEU
1	A	522	LEU
1	A	528	GLU
1	A	536	LYS
1	A	544	LYS
1	A	549	LEU
1	A	552	GLU
1	A	554	LYS
1	A	565	VAL
1	A	568	LYS
1	A	571	HIS
1	A	586	LEU
1	A	593	GLU
1	A	596	LYS
1	A	601	ARG
1	A	603	VAL
1	A	622	LEU
1	A	643	ILE
1	A	645	LEU
1	A	656	VAL
1	A	662	LEU
1	A	678	ASN
1	A	687	LEU
1	A	706	GLU
1	A	708	PHE
1	A	720	ARG
1	A	721	LEU
1	A	724	ARG
1	A	734	ARG
1	A	742	ILE
1	A	759	LYS
1	A	763	ASN
1	A	765	LEU
1	A	768	HIS
1	A	790	LEU
1	A	830	SER

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Mol	Chain	Res	Type
1	A	833	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	HIS
1	A	36	HIS
1	A	72	GLN
1	A	208	HIS
1	A	235	ASN
1	A	253	ASN
1	A	412	ASN
1	A	450	HIS
1	A	459	HIS
1	A	481	ASN
1	A	484	ASN
1	A	560	ASN
1	A	566	GLN
1	A	579	ASN
1	A	614	HIS
1	A	678	ASN
1	A	763	ASN
1	A	832	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](#)

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	$\# Z > 2$
3	GLC	A	998	-	12,12,12	1.45	3 (25%)	17,17,17	0.70	0
4	PLP	A	999	1	15,15,16	1.41	2 (13%)	21,22,23	1.15	2 (9%)
2	CHI	A	920	-	34,34,34	2.55	17 (50%)	48,48,48	1.63	10 (20%)

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	GLC	A	998	-	-	0/2/22/22	0/1/1/1
4	PLP	A	999	1	-	2/6/6/8	0/1/1/1
2	CHI	A	920	-	-	0/20/30/30	0/4/4/4

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	920	CHI	C11-N3	5.62	1.43	1.35
2	A	920	CHI	C20-C21	4.50	1.46	1.37
2	A	920	CHI	C3-C4	3.85	1.45	1.39
2	A	920	CHI	C3-C2	3.80	1.45	1.38
2	A	920	CHI	C2-C1	3.60	1.44	1.38
2	A	920	CHI	C23-C18	3.47	1.45	1.38
2	A	920	CHI	C20-C19	3.44	1.44	1.38
2	A	920	CHI	C6-C1	3.40	1.43	1.38
2	A	920	CHI	C8-N1	-3.40	1.33	1.38
2	A	920	CHI	C22-C21	3.16	1.43	1.37
4	A	999	PLP	C3-C2	-3.14	1.37	1.41
2	A	920	CHI	C19-C18	3.10	1.45	1.38
2	A	920	CHI	C4-N1	-2.89	1.33	1.38
3	A	998	GLC	C1-C2	2.87	1.58	1.52
2	A	920	CHI	C15-C14	2.72	1.57	1.51
4	A	999	PLP	C5A-C5	2.59	1.57	1.50
2	A	920	CHI	C10-C11	2.55	1.58	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	920	CHI	C23-C22	2.54	1.42	1.38
3	A	998	GLC	C3-C2	2.48	1.58	1.52
3	A	998	GLC	C4-C5	2.38	1.58	1.53
2	A	920	CHI	C17-C10	2.29	1.59	1.54
2	A	920	CHI	C13-C14	2.19	1.56	1.51

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	920	CHI	C4-C5-C7	-4.17	103.38	106.80
2	A	920	CHI	C6-C5-C4	4.04	121.63	119.13
2	A	920	CHI	O1-C9-C8	-3.16	117.01	121.09
2	A	920	CHI	C16-N3-C12	2.73	118.26	112.68
2	A	920	CHI	C8-C9-N2	2.71	120.47	116.86
2	A	920	CHI	C4-N1-C8	2.66	111.86	109.01
2	A	920	CHI	C10-C11-N3	2.65	122.84	118.85
4	A	999	PLP	C5-C6-N1	-2.58	119.64	123.83
2	A	920	CHI	C5-C6-C1	-2.57	117.31	120.40
4	A	999	PLP	O3P-P-O1P	2.22	119.48	110.83
2	A	920	CHI	C16-C15-C14	2.20	113.58	111.14
2	A	920	CHI	C23-C22-C21	2.05	120.48	118.38

There are no chirality outliers.

All (2) torsion outliers are listed below:

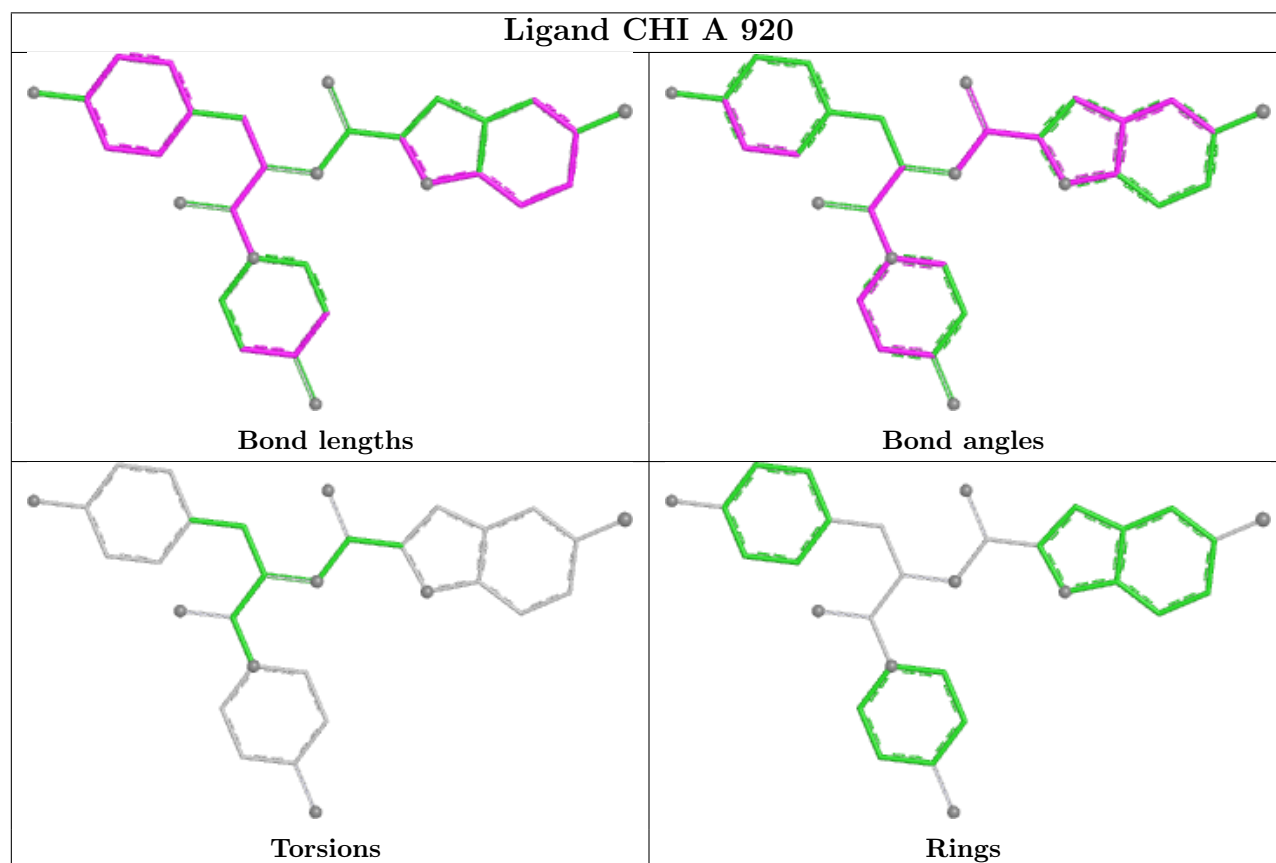
Mol	Chain	Res	Type	Atoms
4	A	999	PLP	C6-C5-C5A-O4P
4	A	999	PLP	C4-C5-C5A-O4P

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

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.