



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 05:22 AM UTC

PDB ID : 1NOI / pdb_00001noi
Title : COMPLEX OF GLYCOGEN PHOSPHORYLASE WITH A TRANSITION
STATE ANALOGUE NOJIRIMYCIN TETRAZOLE AND PHOSPHATE IN
THE T AND R STATES
Authors : Johnson, L.N.; Mitchell, E.P.
Deposited on : 1996-03-12
Resolution : 2.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
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

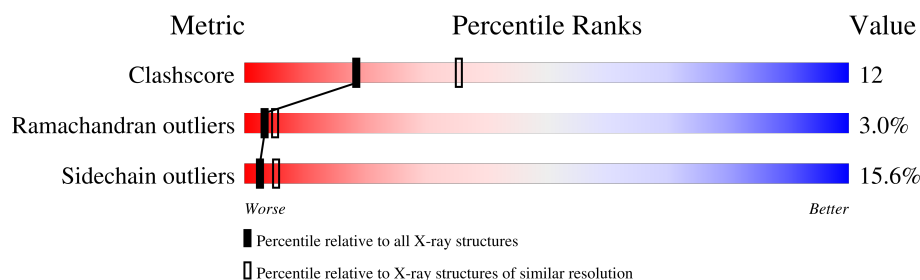
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)

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	
1	B	842	
1	C	842	
1	D	842	

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
2	PO4	A	997	-	X	-	-
2	PO4	B	997	-	X	-	-
2	PO4	C	997	-	X	-	-
2	PO4	D	997	-	X	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 27788 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.

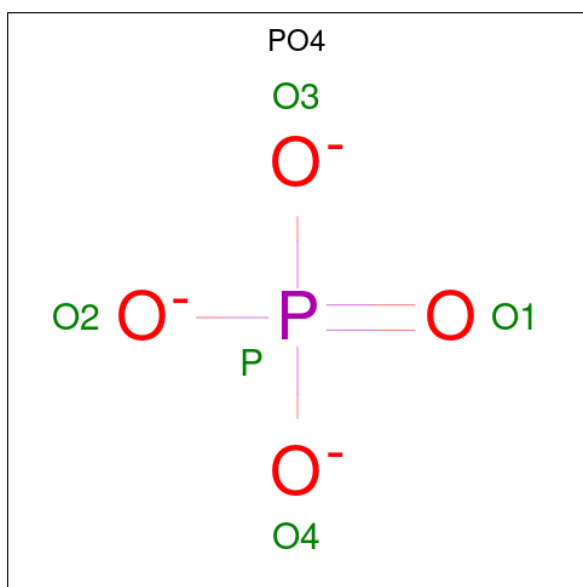
- Molecule 1 is a protein called GLYCOGEN PHOSPHORYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	824	Total	C	N	O	S	0	0	1
			6692	4264	1185	1213	30			
1	B	824	Total	C	N	O	S	0	0	1
			6692	4264	1185	1213	30			
1	C	824	Total	C	N	O	S	0	0	1
			6692	4264	1185	1213	30			
1	D	824	Total	C	N	O	S	0	0	1
			6692	4264	1185	1213	30			

There are 8 discrepancies between the modelled and reference sequences:

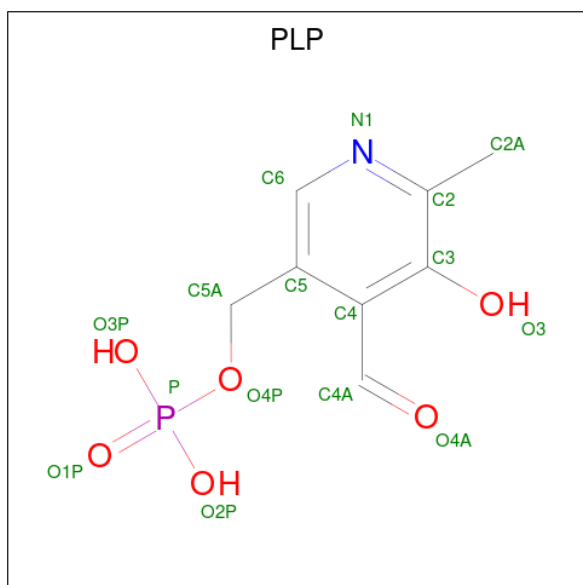
Chain	Residue	Modelled	Actual	Comment	Reference
A	380	ILE	LEU	conflict	UNP P00489
A	609	PRO	ALA	conflict	UNP P00489
B	380	ILE	LEU	conflict	UNP P00489
B	609	PRO	ALA	conflict	UNP P00489
C	380	ILE	LEU	conflict	UNP P00489
C	609	PRO	ALA	conflict	UNP P00489
D	380	ILE	LEU	conflict	UNP P00489
D	609	PRO	ALA	conflict	UNP P00489

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



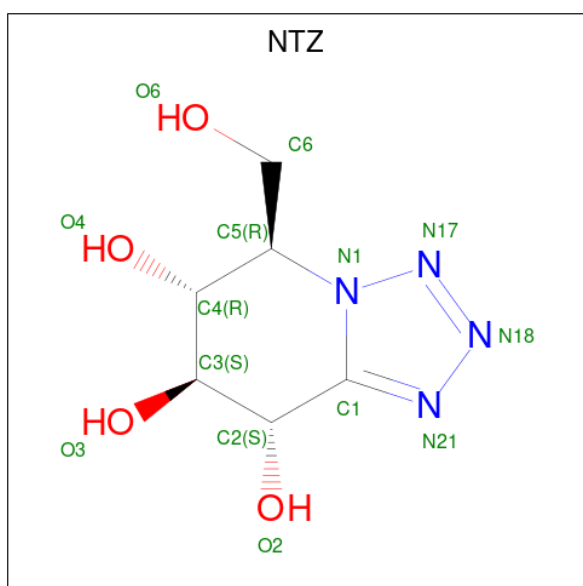
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is PYRIDOXAL-5'-PHOSPHATE (CCD ID: PLP) (formula: C₈H₁₀NO₆P).



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

- Molecule 4 is NOJIRIMYCINE TETRAZOLE (CCD ID: NTZ) (formula: $C_6H_{10}N_4O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	6	4	4		
4	B	1	Total	C	N	O	0	0
			14	6	4	4		
4	C	1	Total	C	N	O	0	0
			14	6	4	4		
4	D	1	Total	C	N	O	0	0
			14	6	4	4		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	223	Total	O	0	0
			223	223		
5	B	222	Total	O	0	0
			222	222		

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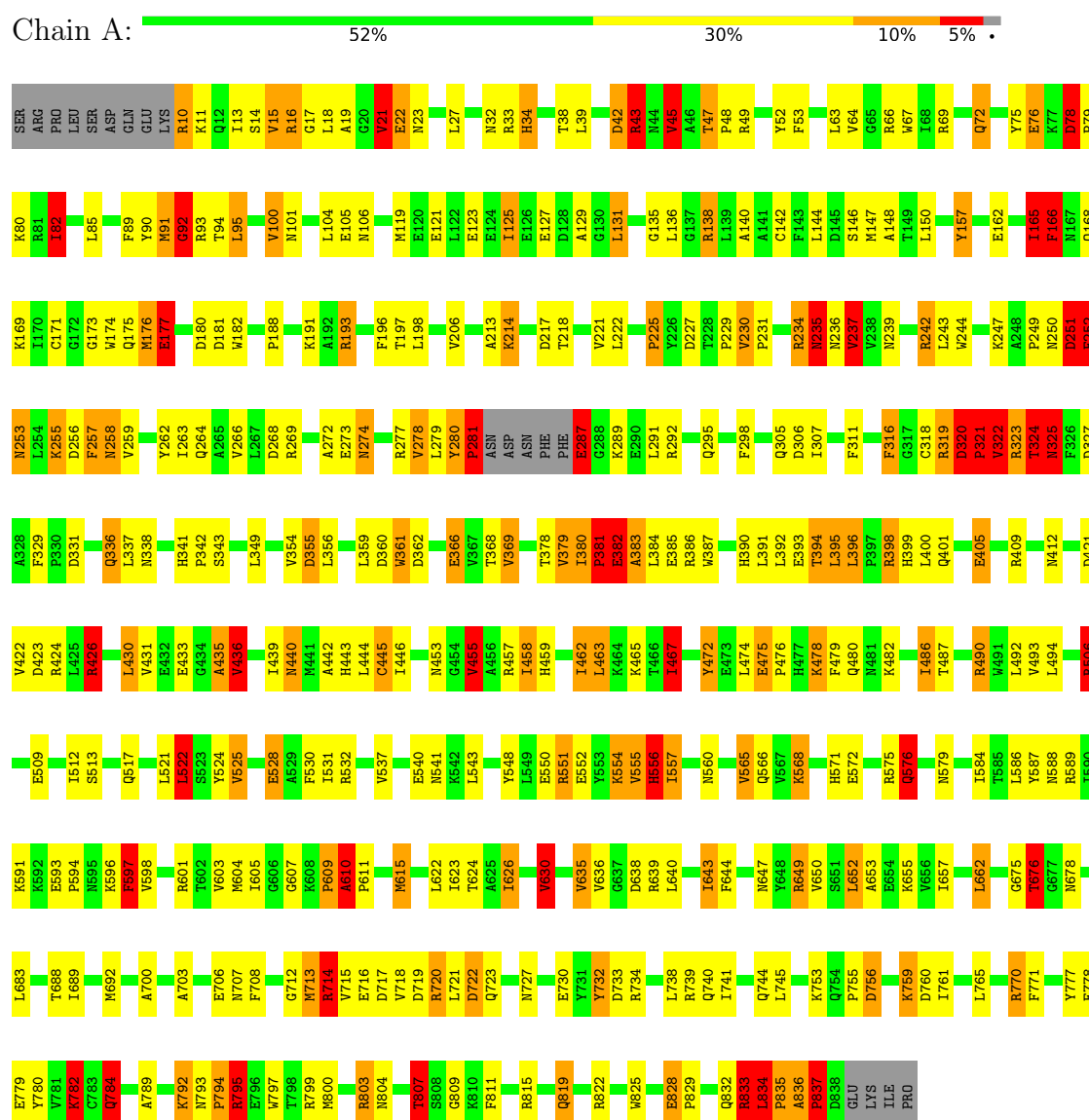
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	218	Total 218	O 218	0	0
5	D	221	Total 221	O 221	0	0

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.

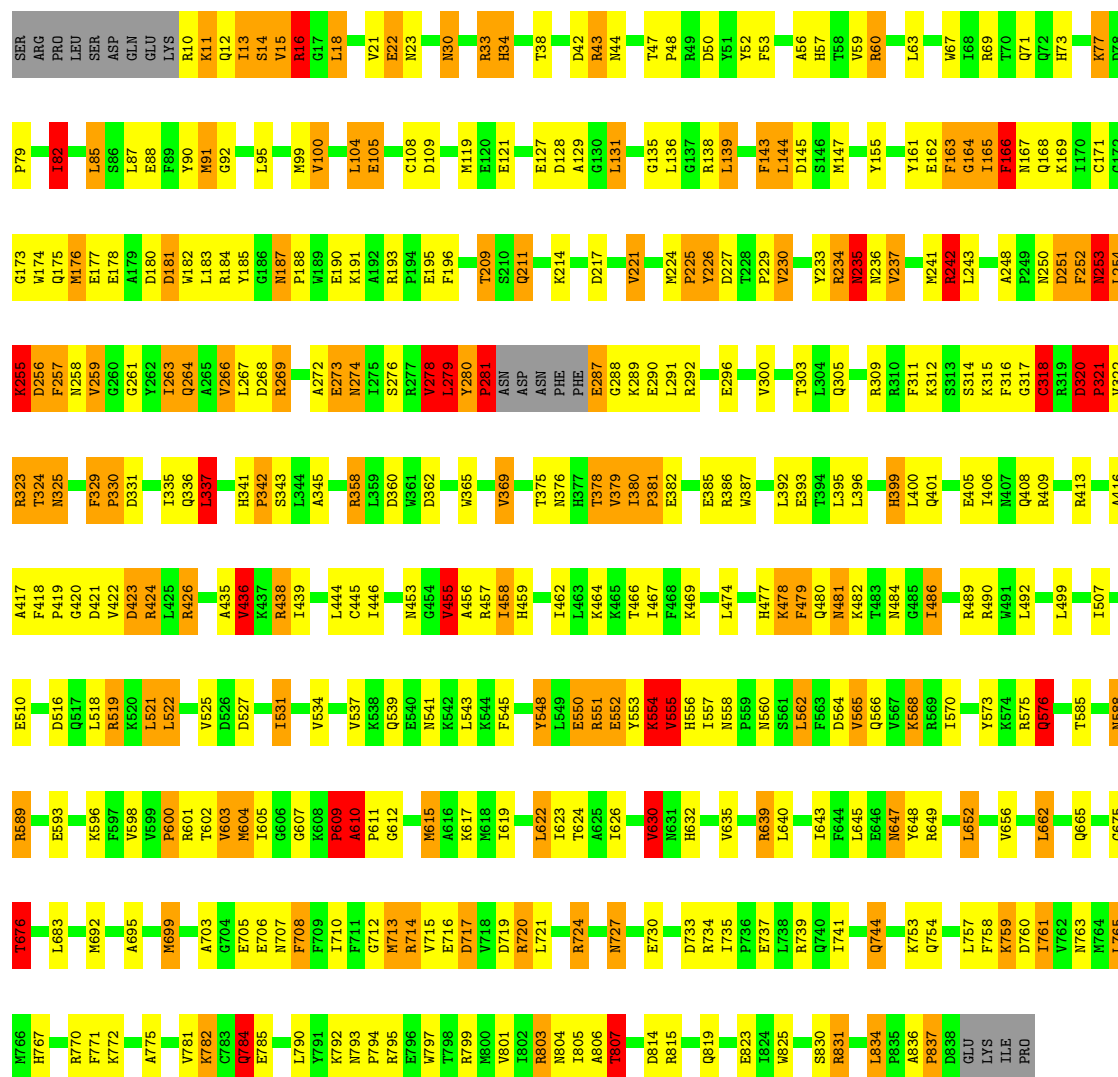
Note EDS was not executed.

• Molecule 1: GLYCOGEN PHOSPHORYLASE



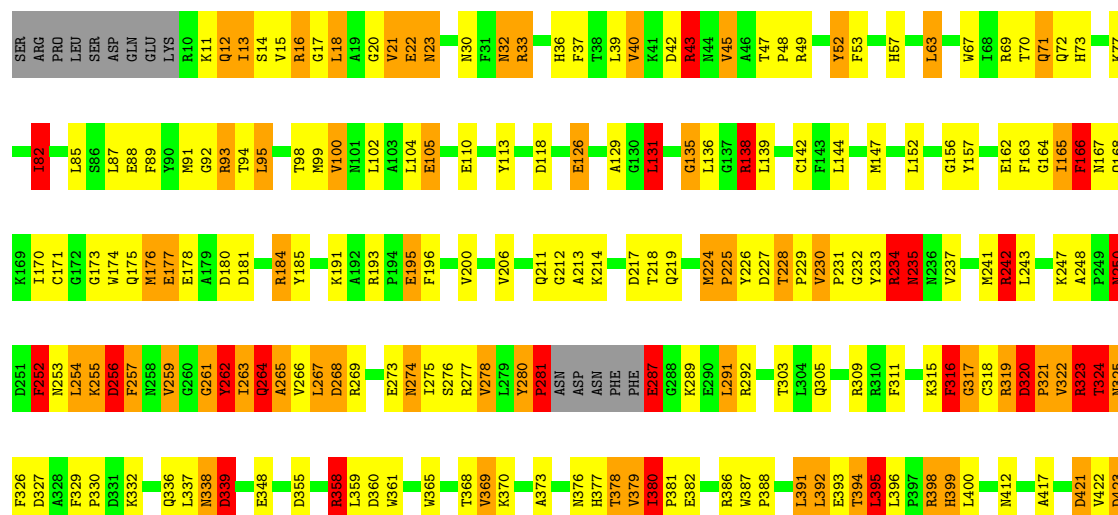
• Molecule 1: GLYCOGEN PHOSPHORYLASE

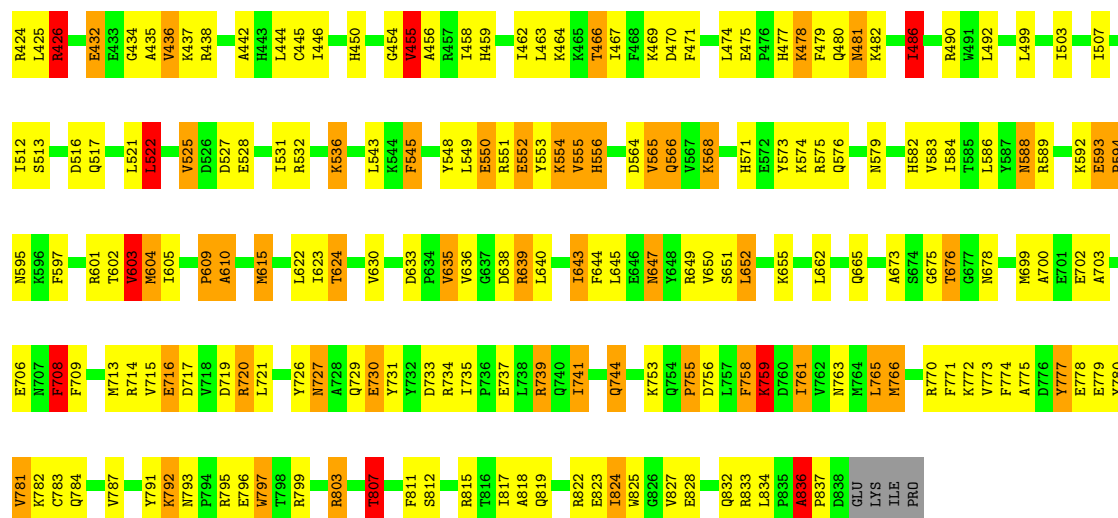




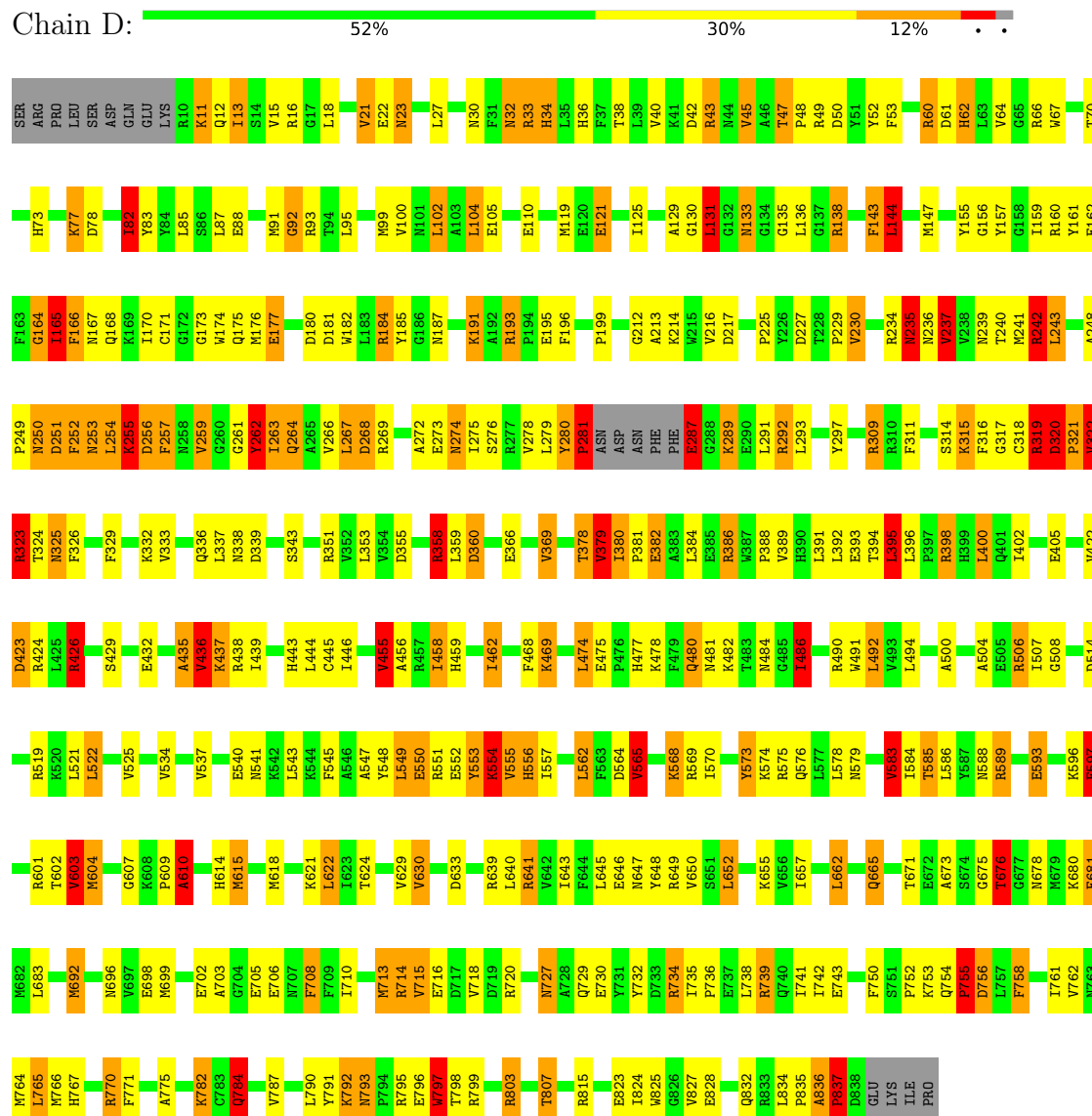
Molecule 1: GLYCOGEN PHOSPHORYLASE

Chain C: 50% 31% 13%





• 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 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	119.00Å 190.00Å 88.20Å 90.00° 109.35° 90.00°	Depositor
Resolution (Å)	8.00 – 2.50	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.50)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.171 , 0.273	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	27788	wwPDB-VP
Average B, all atoms (Å ²)	34.0	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: PLP, NTZ, PO4

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	1.18	25/6843 (0.4%)	2.16	279/9261 (3.0%)
1	B	1.14	23/6843 (0.3%)	2.14	292/9261 (3.2%)
1	C	1.15	18/6843 (0.3%)	2.10	281/9261 (3.0%)
1	D	1.19	28/6843 (0.4%)	2.15	300/9261 (3.2%)
All	All	1.16	94/27372 (0.3%)	2.14	1152/37044 (3.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	9
1	B	0	4
1	C	0	7
1	D	0	6
All	All	0	26

The worst 5 of 94 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	322	VAL	CA-CB	12.51	1.71	1.54
1	C	82	ILE	CA-CB	11.17	1.68	1.54
1	D	230	VAL	CA-CB	10.57	1.63	1.54
1	B	100	VAL	CA-CB	9.90	1.67	1.54
1	D	237	VAL	CA-CB	9.86	1.67	1.54

The worst 5 of 1152 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	280	TYR	N-CA-C	16.72	123.27	108.22
1	A	455	VAL	N-CA-CB	-15.27	92.57	112.26
1	B	266	VAL	N-CA-C	-14.40	96.85	110.82
1	D	325	ASN	CA-CB-CG	14.37	126.97	112.60
1	C	455	VAL	N-CA-CB	-14.37	93.48	112.16

There are no chirality outliers.

5 of 26 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	157	TYR	Sidechain
1	A	252	PHE	Sidechain
1	A	262	TYR	Sidechain
1	A	472	TYR	Sidechain
1	A	52	TYR	Sidechain

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	6692	0	6650	149	0
1	B	6692	0	6650	166	1
1	C	6692	0	6650	188	0
1	D	6692	0	6650	167	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	1	0
2	D	5	0	0	0	0
3	A	15	0	7	0	0
3	B	15	0	6	1	0
3	C	15	0	7	0	0
3	D	15	0	6	0	0
4	A	14	0	10	0	0
4	B	14	0	10	0	0
4	C	14	0	10	0	0
4	D	14	0	10	0	0
5	A	223	0	0	14	1
5	B	222	0	0	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	218	0	0	16	1
5	D	221	0	0	16	1
All	All	27788	0	26666	644	2

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.

The worst 5 of 644 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:D:322:VAL:HG13	1:D:325:ASN:HB3	1.43	0.98
1:C:171:CYS:SG	1:C:176:MET:HG3	2.09	0.92
1:B:85:LEU:HD21	1:B:303:THR:HG21	1.54	0.90
1:A:615:MET:HE1	1:A:761:ILE:HG12	1.57	0.86
1:D:225:PRO:HB2	1:D:242:ARG:HD2	1.58	0.86

All (2) 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:1030:HOH:O	5:D:1049:HOH:O[2_646]	1.46	0.74
1:B:550:GLU:OE2	5:C:1030:HOH:O[2_746]	2.04	0.16

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	822/842 (98%)	741 (90%)	52 (6%)	29 (4%)	3 4
1	B	822/842 (98%)	743 (90%)	59 (7%)	20 (2%)	4 8
1	C	822/842 (98%)	751 (91%)	46 (6%)	25 (3%)	3 5

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	D	822/842 (98%)	746 (91%)	51 (6%)	25 (3%)	3 5
All	All	3288/3368 (98%)	2981 (91%)	208 (6%)	99 (3%)	3 5

5 of 99 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	16	ARG
1	A	19	ALA
1	A	22	GLU
1	A	166	PHE
1	A	253	ASN

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	712/732 (97%)	590 (83%)	122 (17%)	2 4
1	B	712/732 (97%)	613 (86%)	99 (14%)	3 7
1	C	712/732 (97%)	607 (85%)	105 (15%)	3 6
1	D	712/732 (97%)	594 (83%)	118 (17%)	2 4
All	All	2848/2928 (97%)	2404 (84%)	444 (16%)	2 5

5 of 444 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	95	LEU
1	D	837	PRO
1	C	492	LEU
1	D	792	LYS
1	D	486	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 95 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	517	GLN
1	D	12	GLN
1	C	566	GLN
1	C	744	GLN
1	D	168	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

12 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	PLP	A	999	1	15,15,16	1.05	1 (6%)	21,22,23	1.28	2 (9%)
4	NTZ	B	998	-	13,15,15	2.59	6 (46%)	14,22,22	3.60	5 (35%)
3	PLP	D	999	1	15,15,16	1.54	2 (13%)	21,22,23	1.14	1 (4%)
4	NTZ	C	998	-	13,15,15	3.68	5 (38%)	14,22,22	3.53	4 (28%)
2	PO4	D	997	-	4,4,4	3.62	3 (75%)	6,6,6	2.39	4 (66%)
4	NTZ	A	998	-	13,15,15	2.06	3 (23%)	14,22,22	3.92	3 (21%)
2	PO4	B	997	-	4,4,4	3.80	4 (100%)	6,6,6	2.23	2 (33%)
4	NTZ	D	998	-	13,15,15	3.07	5 (38%)	14,22,22	4.36	5 (35%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PO4	C	997	-	4,4,4	3.92	4 (100%)	6,6,6	2.56	4 (66%)
3	PLP	B	999	1	15,15,16	1.46	3 (20%)	21,22,23	1.12	1 (4%)
2	PO4	A	997	-	4,4,4	3.57	4 (100%)	6,6,6	2.78	4 (66%)
3	PLP	C	999	1	15,15,16	1.73	3 (20%)	21,22,23	1.19	2 (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
3	PLP	A	999	1	-	1/6/6/8	0/1/1/1
4	NTZ	B	998	-	-	0/2/22/22	0/2/2/2
3	PLP	D	999	1	-	1/6/6/8	0/1/1/1
4	NTZ	C	998	-	-	1/2/22/22	0/2/2/2
4	NTZ	A	998	-	-	1/2/22/22	0/2/2/2
4	NTZ	D	998	-	-	0/2/22/22	0/2/2/2
3	PLP	B	999	1	-	1/6/6/8	0/1/1/1
3	PLP	C	999	1	-	1/6/6/8	0/1/1/1

The worst 5 of 43 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	998	NTZ	C1-N21	8.26	1.40	1.32
4	D	998	NTZ	C1-N21	7.94	1.40	1.32
4	C	998	NTZ	C1-N1	7.35	1.40	1.34
4	B	998	NTZ	C1-N1	6.03	1.39	1.34
4	A	998	NTZ	C1-N1	5.07	1.38	1.34

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	998	NTZ	N1-N17-N18	9.81	113.51	106.00
4	A	998	NTZ	C1-N1-N17	-9.67	102.05	108.47
4	B	998	NTZ	N1-C1-N21	9.63	113.11	108.45
4	C	998	NTZ	N1-C1-N21	8.75	112.68	108.45
4	D	998	NTZ	C1-N1-N17	-8.69	102.70	108.47

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	999	PLP	C4-C5-C5A-O4P
3	D	999	PLP	C4-C5-C5A-O4P
4	A	998	NTZ	C4-C5-C6-O6
4	C	998	NTZ	C4-C5-C6-O6
3	A	999	PLP	C6-C5-C5A-O4P

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	997	PO4	1	0
3	B	999	PLP	1	0

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.