



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 07:09 AM UTC

PDB ID : 6D23 / pdb_00006d23
Title : GLUCOSE-6-P DEHYDROGENASE (APO FORM) FROM TRY-
PANOSOMA CRUZI
Authors : Botti, H.; Ortiz, C.; Comini, M.A.; Larrieux, N.; Buschiazzo, A.
Deposited on : 2018-04-12
Resolution : 2.85 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)
Xtrriage (Phenix) : 2.0
EDS : 3.0
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

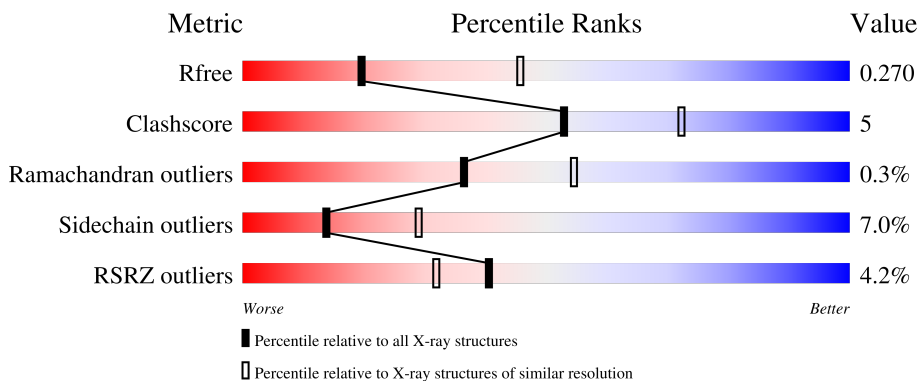
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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	A	541	 4% 72% 16% • 10%
1	B	541	 3% 74% 16% • 9%
1	C	541	 4% 74% 16% • 9%
1	D	541	 4% 74% 16% • 9%

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 15846 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 Glucose-6-phosphate 1-dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	487	3858	2446	684	713	15	0	3	0
1	B	490	3857	2445	675	722	15	0	1	0
1	C	494	3900	2472	686	726	16	0	3	0
1	D	494	3893	2468	684	725	16	0	2	0

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	15	MET	-	expression tag	UNP Q1WBU6
A	16	GLY	-	expression tag	UNP Q1WBU6
A	17	SER	-	expression tag	UNP Q1WBU6
A	18	SER	-	expression tag	UNP Q1WBU6
A	19	HIS	-	expression tag	UNP Q1WBU6
A	20	HIS	-	expression tag	UNP Q1WBU6
A	21	HIS	-	expression tag	UNP Q1WBU6
A	22	HIS	-	expression tag	UNP Q1WBU6
A	23	HIS	-	expression tag	UNP Q1WBU6
A	24	HIS	-	expression tag	UNP Q1WBU6
A	25	SER	-	expression tag	UNP Q1WBU6
A	26	SER	-	expression tag	UNP Q1WBU6
A	27	GLY	-	expression tag	UNP Q1WBU6
A	28	LEU	-	expression tag	UNP Q1WBU6
A	29	VAL	-	expression tag	UNP Q1WBU6
A	30	PRO	-	expression tag	UNP Q1WBU6
A	31	ARG	-	expression tag	UNP Q1WBU6
A	32	GLY	-	expression tag	UNP Q1WBU6
A	33	SER	-	expression tag	UNP Q1WBU6
A	34	HIS	-	expression tag	UNP Q1WBU6
A	35	MET	-	expression tag	UNP Q1WBU6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	36	ALA	-	expression tag	UNP Q1WBU6
A	37	SER	-	expression tag	UNP Q1WBU6
A	290	GLU	ALA	conflict	UNP Q1WBU6
B	15	MET	-	expression tag	UNP Q1WBU6
B	16	GLY	-	expression tag	UNP Q1WBU6
B	17	SER	-	expression tag	UNP Q1WBU6
B	18	SER	-	expression tag	UNP Q1WBU6
B	19	HIS	-	expression tag	UNP Q1WBU6
B	20	HIS	-	expression tag	UNP Q1WBU6
B	21	HIS	-	expression tag	UNP Q1WBU6
B	22	HIS	-	expression tag	UNP Q1WBU6
B	23	HIS	-	expression tag	UNP Q1WBU6
B	24	HIS	-	expression tag	UNP Q1WBU6
B	25	SER	-	expression tag	UNP Q1WBU6
B	26	SER	-	expression tag	UNP Q1WBU6
B	27	GLY	-	expression tag	UNP Q1WBU6
B	28	LEU	-	expression tag	UNP Q1WBU6
B	29	VAL	-	expression tag	UNP Q1WBU6
B	30	PRO	-	expression tag	UNP Q1WBU6
B	31	ARG	-	expression tag	UNP Q1WBU6
B	32	GLY	-	expression tag	UNP Q1WBU6
B	33	SER	-	expression tag	UNP Q1WBU6
B	34	HIS	-	expression tag	UNP Q1WBU6
B	35	MET	-	expression tag	UNP Q1WBU6
B	36	ALA	-	expression tag	UNP Q1WBU6
B	37	SER	-	expression tag	UNP Q1WBU6
B	290	GLU	ALA	conflict	UNP Q1WBU6
C	15	MET	-	expression tag	UNP Q1WBU6
C	16	GLY	-	expression tag	UNP Q1WBU6
C	17	SER	-	expression tag	UNP Q1WBU6
C	18	SER	-	expression tag	UNP Q1WBU6
C	19	HIS	-	expression tag	UNP Q1WBU6
C	20	HIS	-	expression tag	UNP Q1WBU6
C	21	HIS	-	expression tag	UNP Q1WBU6
C	22	HIS	-	expression tag	UNP Q1WBU6
C	23	HIS	-	expression tag	UNP Q1WBU6
C	24	HIS	-	expression tag	UNP Q1WBU6
C	25	SER	-	expression tag	UNP Q1WBU6
C	26	SER	-	expression tag	UNP Q1WBU6
C	27	GLY	-	expression tag	UNP Q1WBU6
C	28	LEU	-	expression tag	UNP Q1WBU6
C	29	VAL	-	expression tag	UNP Q1WBU6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	30	PRO	-	expression tag	UNP Q1WBU6
C	31	ARG	-	expression tag	UNP Q1WBU6
C	32	GLY	-	expression tag	UNP Q1WBU6
C	33	SER	-	expression tag	UNP Q1WBU6
C	34	HIS	-	expression tag	UNP Q1WBU6
C	35	MET	-	expression tag	UNP Q1WBU6
C	36	ALA	-	expression tag	UNP Q1WBU6
C	37	SER	-	expression tag	UNP Q1WBU6
C	290	GLU	ALA	conflict	UNP Q1WBU6
D	15	MET	-	expression tag	UNP Q1WBU6
D	16	GLY	-	expression tag	UNP Q1WBU6
D	17	SER	-	expression tag	UNP Q1WBU6
D	18	SER	-	expression tag	UNP Q1WBU6
D	19	HIS	-	expression tag	UNP Q1WBU6
D	20	HIS	-	expression tag	UNP Q1WBU6
D	21	HIS	-	expression tag	UNP Q1WBU6
D	22	HIS	-	expression tag	UNP Q1WBU6
D	23	HIS	-	expression tag	UNP Q1WBU6
D	24	HIS	-	expression tag	UNP Q1WBU6
D	25	SER	-	expression tag	UNP Q1WBU6
D	26	SER	-	expression tag	UNP Q1WBU6
D	27	GLY	-	expression tag	UNP Q1WBU6
D	28	LEU	-	expression tag	UNP Q1WBU6
D	29	VAL	-	expression tag	UNP Q1WBU6
D	30	PRO	-	expression tag	UNP Q1WBU6
D	31	ARG	-	expression tag	UNP Q1WBU6
D	32	GLY	-	expression tag	UNP Q1WBU6
D	33	SER	-	expression tag	UNP Q1WBU6
D	34	HIS	-	expression tag	UNP Q1WBU6
D	35	MET	-	expression tag	UNP Q1WBU6
D	36	ALA	-	expression tag	UNP Q1WBU6
D	37	SER	-	expression tag	UNP Q1WBU6
D	290	GLU	ALA	conflict	UNP Q1WBU6

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



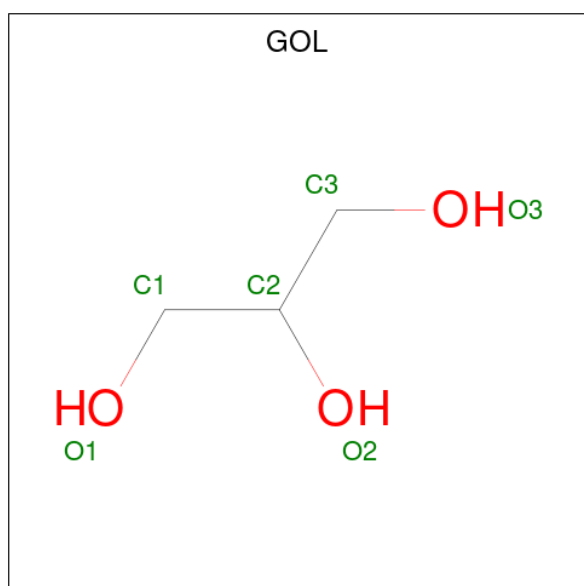
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

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

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	5	Total Cl 5 5	0	0
4	B	4	Total Cl 4 4	0	0
4	C	9	Total Cl 9 9	0	0
4	D	5	Total Cl 5 5	0	0

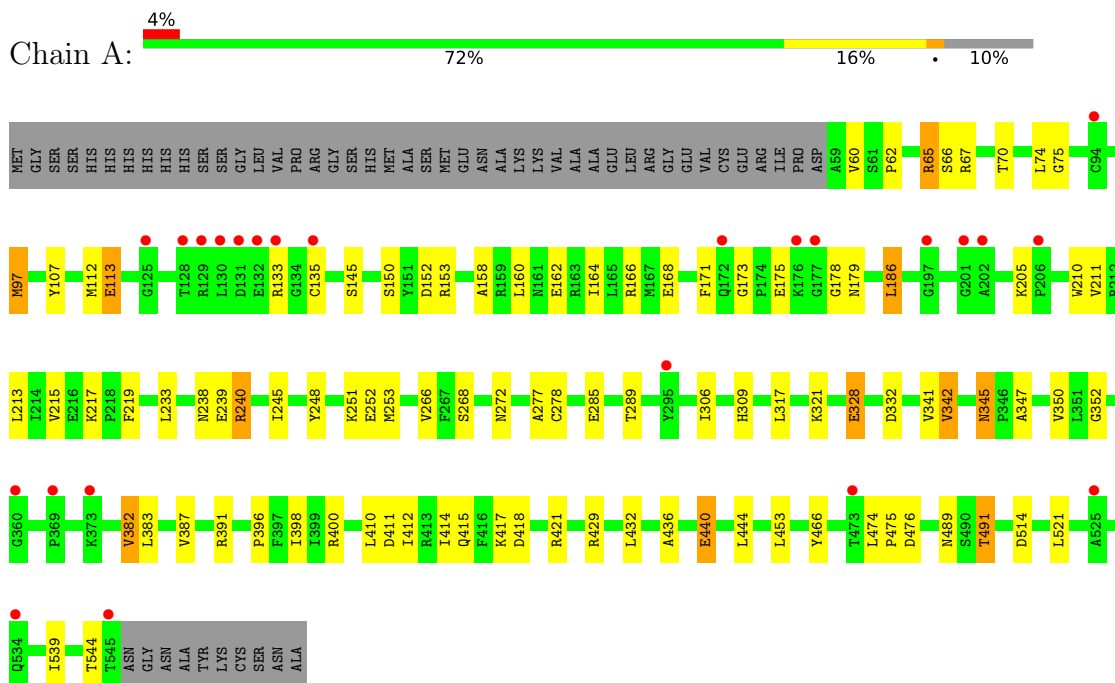
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	16	Total O 16 16	0	0
5	B	8	Total O 8 8	0	0
5	C	22	Total O 22 22	0	0
5	D	29	Total O 29 29	0	0

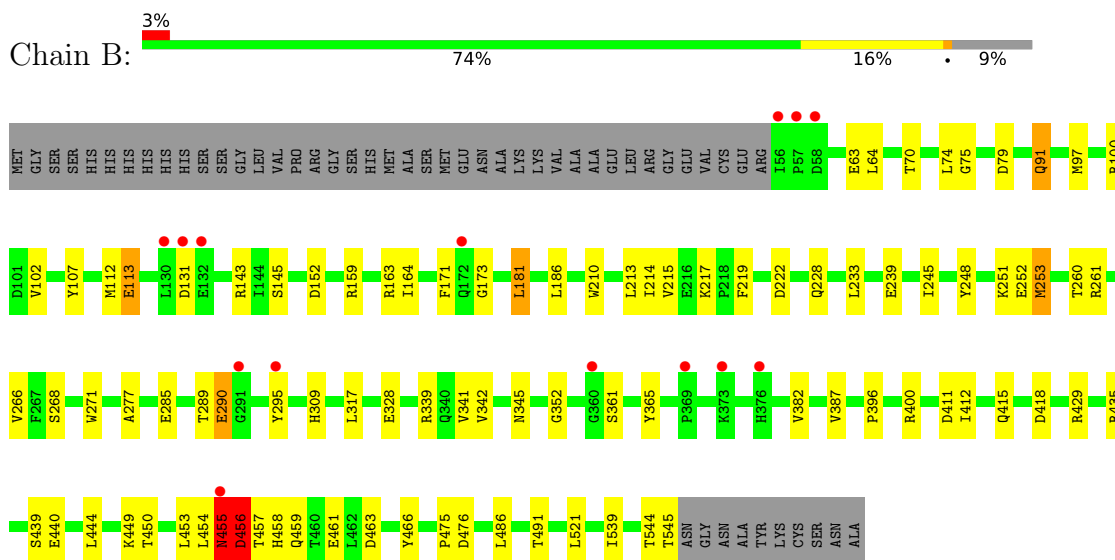
3 Residue-property plots [i](#)

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.

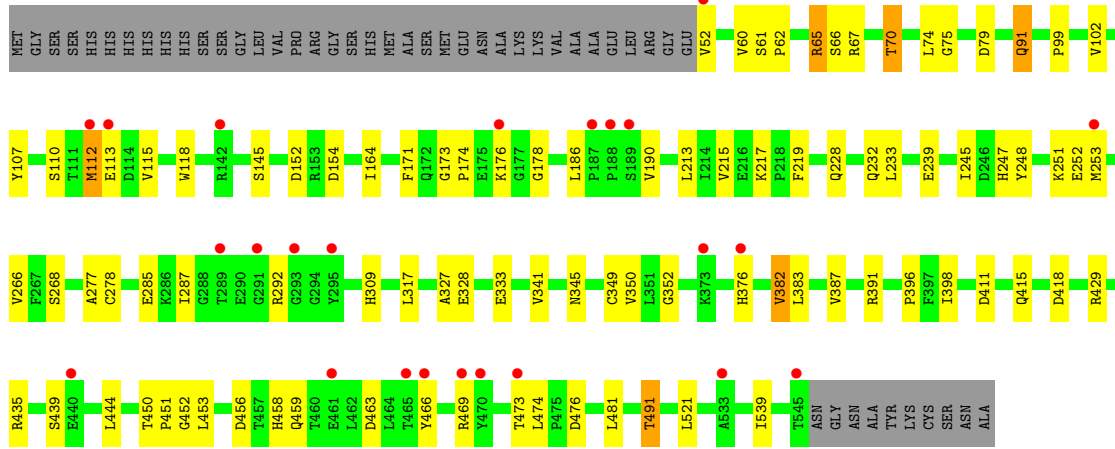
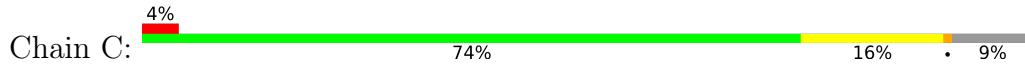
- Molecule 1: Glucose-6-phosphate 1-dehydrogenase



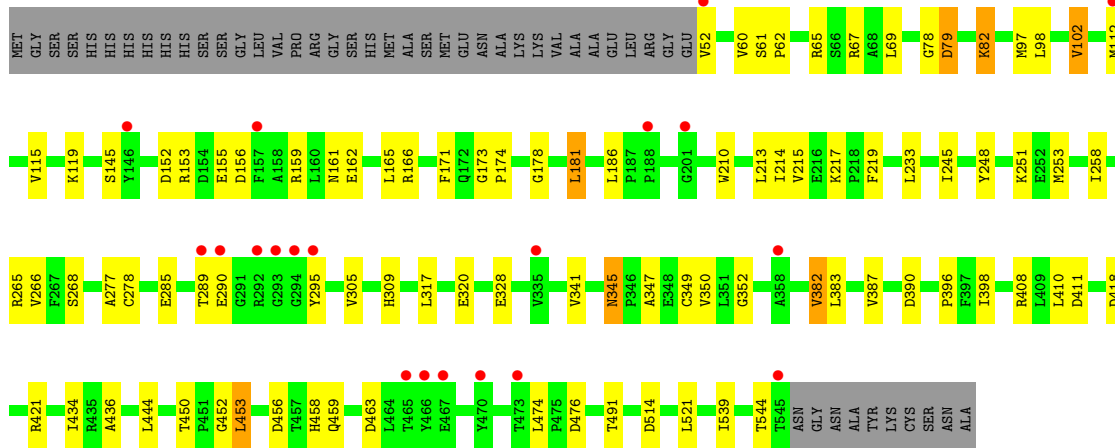
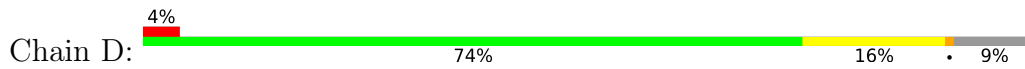
- Molecule 1: Glucose-6-phosphate 1-dehydrogenase



• Molecule 1: Glucose-6-phosphate 1-dehydrogenase



• Molecule 1: Glucose-6-phosphate 1-dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	96.61Å 132.96Å 107.83Å 90.00° 100.11° 90.00°	Depositor
Resolution (Å)	29.63 – 2.85 29.63 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.0 (29.63-2.85) 98.9 (29.63-2.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.24 (at 2.85Å)	Xtrriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.204 , 0.249 0.219 , 0.270	Depositor DCC
R_{free} test set	1257 reflections (2.03%)	wwPDB-VP
Wilson B-factor (Å ²)	39.4	Xtrriage
Anisotropy	0.340	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 59.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	15846	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 24.71 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.6399e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: SO4, CL, GOL

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	0.85	0/3945	1.36	19/5344 (0.4%)
1	B	0.87	1/3938 (0.0%)	1.39	20/5342 (0.4%)
1	C	0.89	1/3988 (0.0%)	1.37	19/5407 (0.4%)
1	D	0.88	0/3977	1.36	13/5393 (0.2%)
All	All	0.88	2/15848 (0.0%)	1.37	71/21486 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	253	MET	SD-CE	-5.67	1.65	1.79
1	C	217	LYS	CA-C	5.10	1.59	1.53

The worst 5 of 71 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	455[A]	ASN	CA-C-N	8.30	136.64	121.70
1	B	455[A]	ASN	C-N-CA	8.30	136.64	121.70
1	B	455[B]	ASN	CA-C-N	8.30	136.64	121.70
1	B	455[B]	ASN	C-N-CA	8.30	136.64	121.70
1	C	154	ASP	CA-C-N	7.90	132.66	120.82

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	3858	0	3834	50	0
1	B	3857	0	3804	42	0
1	C	3900	0	3855	35	0
1	D	3893	0	3848	40	0
2	A	30	0	0	0	0
2	B	30	0	0	1	0
2	C	20	0	0	0	0
2	D	40	0	0	0	0
3	A	30	0	40	8	0
3	B	30	0	40	5	0
3	C	36	0	48	0	0
3	D	24	0	32	5	0
4	A	5	0	0	0	0
4	B	4	0	0	0	0
4	C	9	0	0	0	0
4	D	5	0	0	1	0
5	A	16	0	0	0	0
5	B	8	0	0	0	0
5	C	22	0	0	1	0
5	D	29	0	0	0	0
All	All	15846	0	15501	155	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.

The worst 5 of 155 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:215:VAL:HG12	1:D:219:PHE:HE1	1.46	0.79
1:C:215:VAL:HG12	1:C:219:PHE:HE1	1.48	0.78
1:B:215:VAL:HG12	1:B:219:PHE:HE1	1.47	0.78
1:A:215:VAL:HG12	1:A:219:PHE:HE1	1.49	0.77
1:B:251:LYS:HG2	3:B:608:GOL:H12	1.74	0.68

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	488/541 (90%)	462 (95%)	25 (5%)	1 (0%)	43	62
1	B	489/541 (90%)	456 (93%)	30 (6%)	3 (1%)	21	38
1	C	495/541 (92%)	469 (95%)	25 (5%)	1 (0%)	43	62
1	D	494/541 (91%)	469 (95%)	24 (5%)	1 (0%)	43	62
All	All	1966/2164 (91%)	1856 (94%)	104 (5%)	6 (0%)	36	54

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	440	GLU
1	B	290	GLU
1	B	440	GLU
1	B	456	ASP
1	C	174	PRO

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	412/462 (89%)	387 (94%)	25 (6%)	17	35
1	B	412/462 (89%)	381 (92%)	31 (8%)	12	26
1	C	417/462 (90%)	384 (92%)	33 (8%)	11	24
1	D	416/462 (90%)	384 (92%)	32 (8%)	12	25
All	All	1657/1848 (90%)	1536 (93%)	121 (7%)	14	27

5 of 121 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	70	THR
1	D	345	ASN
1	C	233	LEU
1	D	328	GLU
1	D	491	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	492	ASN
1	C	232	GLN
1	C	172	GLN
1	C	241	GLN
1	B	91	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](#)

Of 67 ligands modelled in this entry, 23 are monoatomic - leaving 44 for Mogul analysis.

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	GOL	B	607	-	5,5,5	0.21	0	5,5,5	0.44	0
3	GOL	B	615	-	5,5,5	0.24	0	5,5,5	0.22	0
3	GOL	C	611	-	5,5,5	0.14	0	5,5,5	0.26	0
3	GOL	C	602	-	5,5,5	0.18	0	5,5,5	0.37	0
2	SO4	D	604	-	4,4,4	0.21	0	6,6,6	0.21	0
3	GOL	B	614	-	5,5,5	0.19	0	5,5,5	0.24	0
2	SO4	A	603	-	4,4,4	0.20	0	6,6,6	0.32	0
2	SO4	A	605	-	4,4,4	0.24	0	6,6,6	0.15	0
3	GOL	C	601	-	5,5,5	0.14	0	5,5,5	0.25	0
2	SO4	C	606	-	4,4,4	0.51	0	6,6,6	0.32	0
2	SO4	D	602	-	4,4,4	0.30	0	6,6,6	0.22	0
3	GOL	A	609	-	5,5,5	0.12	0	5,5,5	0.25	0
2	SO4	C	605	-	4,4,4	0.33	0	6,6,6	0.20	0
2	SO4	D	601	-	4,4,4	0.35	0	6,6,6	0.31	0
3	GOL	B	609	-	5,5,5	0.15	0	5,5,5	0.28	0
3	GOL	C	610	-	5,5,5	0.30	0	5,5,5	0.34	0
3	GOL	A	607	-	5,5,5	0.20	0	5,5,5	0.84	0
2	SO4	D	603	-	4,4,4	0.30	0	6,6,6	0.29	0
2	SO4	D	605	-	4,4,4	0.29	0	6,6,6	0.12	0
2	SO4	C	604	-	4,4,4	0.34	0	6,6,6	0.49	0
2	SO4	C	607	-	4,4,4	0.25	0	6,6,6	0.13	0
2	SO4	B	606	-	4,4,4	0.28	0	6,6,6	0.19	0
2	SO4	A	604	-	4,4,4	0.32	0	6,6,6	0.14	0
3	GOL	C	609	-	5,5,5	0.16	0	5,5,5	0.31	0
2	SO4	D	606	-	4,4,4	0.27	0	6,6,6	0.13	0
3	GOL	C	608	-	5,5,5	0.11	0	5,5,5	0.40	0
2	SO4	B	601	-	4,4,4	0.25	0	6,6,6	0.51	0
2	SO4	D	607	-	4,4,4	0.27	0	6,6,6	0.22	0
2	SO4	B	604	-	4,4,4	0.48	0	6,6,6	0.29	0
3	GOL	D	611	-	5,5,5	0.22	0	5,5,5	0.23	0
2	SO4	A	601	-	4,4,4	0.31	0	6,6,6	0.38	0
3	GOL	A	610	-	5,5,5	0.13	0	5,5,5	0.99	0
3	GOL	D	609	-	5,5,5	0.20	0	5,5,5	0.50	0
2	SO4	A	602	-	4,4,4	0.40	0	6,6,6	0.32	0
2	SO4	B	602	-	4,4,4	0.37	0	6,6,6	0.35	0
3	GOL	A	611	-	5,5,5	0.11	0	5,5,5	0.41	0
2	SO4	B	605	-	4,4,4	0.23	0	6,6,6	0.24	0
2	SO4	D	608	-	4,4,4	0.36	0	6,6,6	0.17	0
2	SO4	A	606	-	4,4,4	0.31	0	6,6,6	0.25	0
2	SO4	B	603	-	4,4,4	0.26	0	6,6,6	0.18	0
3	GOL	A	608	-	5,5,5	0.15	0	5,5,5	0.38	0
3	GOL	D	610	-	5,5,5	0.21	0	5,5,5	0.59	0
3	GOL	D	612	-	5,5,5	0.13	0	5,5,5	0.21	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	B	608	-	5,5,5	0.20	0	5,5,5	0.30	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
3	GOL	B	607	-	-	1/4/4/4	-
3	GOL	B	615	-	-	2/4/4/4	-
3	GOL	C	611	-	-	0/4/4/4	-
3	GOL	C	602	-	-	0/4/4/4	-
3	GOL	B	614	-	-	2/4/4/4	-
3	GOL	C	601	-	-	0/4/4/4	-
3	GOL	A	609	-	-	2/4/4/4	-
3	GOL	B	609	-	-	0/4/4/4	-
3	GOL	C	610	-	-	0/4/4/4	-
3	GOL	A	607	-	-	0/4/4/4	-
3	GOL	C	609	-	-	0/4/4/4	-
3	GOL	C	608	-	-	1/4/4/4	-
3	GOL	B	608	-	-	2/4/4/4	-
3	GOL	D	609	-	-	0/4/4/4	-
3	GOL	A	610	-	-	2/4/4/4	-
3	GOL	A	611	-	-	0/4/4/4	-
3	GOL	A	608	-	-	2/4/4/4	-
3	GOL	D	610	-	-	2/4/4/4	-
3	GOL	D	612	-	-	2/4/4/4	-
3	GOL	D	611	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	609	GOL	O1-C1-C2-C3
3	B	608	GOL	C1-C2-C3-O3
3	B	615	GOL	O1-C1-C2-C3
3	D	610	GOL	C1-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
3	D	611	GOL	O1-C1-C2-O2

There are no ring outliers.

13 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	607	GOL	1	0
3	B	614	GOL	1	0
3	A	609	GOL	3	0
3	B	609	GOL	1	0
3	A	607	GOL	1	0
2	B	604	SO4	1	0
3	A	610	GOL	3	0
3	D	609	GOL	1	0
3	A	611	GOL	1	0
3	A	608	GOL	1	0
3	D	610	GOL	2	0
3	D	612	GOL	2	0
3	B	608	GOL	2	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 [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	A	487/541 (90%)	0.37	24 (4%) 35 27	7, 44, 82, 106	3 (0%)
1	B	490/541 (90%)	0.25	14 (2%) 53 45	14, 41, 78, 99	1 (0%)
1	C	494/541 (91%)	0.40	24 (4%) 35 27	13, 41, 78, 98	3 (0%)
1	D	494/541 (91%)	0.30	20 (4%) 42 33	13, 41, 75, 99	2 (0%)
All	All	1965/2164 (90%)	0.33	82 (4%) 40 32	7, 42, 79, 106	9 (0%)

The worst 5 of 82 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	295	TYR	5.3
1	D	295	TYR	4.5
1	C	52	VAL	4.4
1	D	146	TYR	4.3
1	B	295	TYR	3.9

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
3	GOL	B	609	6/6	0.58	0.25	72,78,82,84	0
2	SO4	D	604	5/5	0.61	0.23	90,92,92,94	0
2	SO4	A	605	5/5	0.66	0.23	106,107,107,108	0
4	CL	B	611	1/1	0.66	0.16	94,94,94,94	0
2	SO4	B	603	5/5	0.67	0.24	121,121,122,123	0
3	GOL	C	611	6/6	0.68	0.18	56,60,61,64	0
3	GOL	A	610	6/6	0.68	0.26	51,54,55,56	0
3	GOL	A	608	6/6	0.71	0.19	55,57,58,59	0
3	GOL	D	612	6/6	0.72	0.18	59,62,63,64	0
2	SO4	D	608	5/5	0.72	0.19	104,105,106,108	0
3	GOL	D	610	6/6	0.74	0.21	37,53,55,55	0
3	GOL	A	607	6/6	0.75	0.19	38,43,46,46	0
2	SO4	D	603	5/5	0.75	0.20	72,72,74,77	0
3	GOL	B	615	6/6	0.76	0.18	40,48,49,49	0
3	GOL	C	610	6/6	0.76	0.15	46,51,52,52	0
2	SO4	C	607	5/5	0.76	0.15	105,105,106,107	0
3	GOL	C	601	6/6	0.77	0.26	73,75,77,77	0
2	SO4	D	605	5/5	0.78	0.16	123,123,123,123	0
3	GOL	D	609	6/6	0.79	0.20	51,56,58,59	0
4	CL	D	615	1/1	0.80	0.18	77,77,77,77	0
3	GOL	B	608	6/6	0.81	0.15	50,56,58,59	0
2	SO4	C	606	5/5	0.83	0.18	69,75,75,76	0
3	GOL	A	611	6/6	0.83	0.14	53,56,61,62	0
3	GOL	B	607	6/6	0.83	0.15	43,45,47,47	0
3	GOL	C	602	6/6	0.83	0.15	42,42,43,44	0
3	GOL	C	609	6/6	0.83	0.13	42,46,49,49	0
4	CL	C	603	1/1	0.83	0.16	79,79,79,79	0
3	GOL	A	609	6/6	0.83	0.19	55,60,60,61	0
4	CL	A	615	1/1	0.84	0.12	68,68,68,68	0
2	SO4	D	607	5/5	0.85	0.22	107,108,108,109	0
3	GOL	C	608	6/6	0.85	0.12	44,45,45,47	0
4	CL	D	616	1/1	0.85	0.12	82,82,82,82	0
4	CL	B	612	1/1	0.86	0.13	67,67,67,67	0
2	SO4	D	602	5/5	0.86	0.15	79,80,83,83	0
4	CL	C	614	1/1	0.87	0.12	68,68,68,68	0
2	SO4	A	603	5/5	0.88	0.11	69,72,72,74	0
4	CL	C	615	1/1	0.88	0.10	68,68,68,68	0
4	CL	D	617	1/1	0.88	0.10	66,66,66,66	0
2	SO4	A	604	5/5	0.89	0.15	67,68,68,70	0
3	GOL	D	611	6/6	0.89	0.11	31,34,39,45	0
2	SO4	B	604	5/5	0.89	0.09	59,62,64,65	0
2	SO4	C	605	5/5	0.89	0.15	70,71,72,72	0
2	SO4	B	602	5/5	0.90	0.11	68,68,70,70	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	CL	A	616	1/1	0.90	0.10	59,59,59,59	0
4	CL	C	618	1/1	0.90	0.13	57,57,57,57	0
2	SO4	B	606	5/5	0.90	0.31	106,107,107,109	0
2	SO4	A	602	5/5	0.90	0.11	68,69,69,71	0
4	CL	A	614	1/1	0.90	0.12	74,74,74,74	0
4	CL	C	619	1/1	0.91	0.11	67,67,67,67	0
4	CL	A	612	1/1	0.91	0.10	58,58,58,58	0
4	CL	C	616	1/1	0.91	0.13	80,80,80,80	0
2	SO4	B	601	5/5	0.91	0.10	49,50,52,57	0
2	SO4	A	601	5/5	0.93	0.09	55,56,57,62	0
3	GOL	B	614	6/6	0.93	0.10	23,29,33,37	0
4	CL	C	612	1/1	0.94	0.06	48,48,48,48	0
4	CL	C	613	1/1	0.94	0.12	64,64,64,64	0
4	CL	C	617	1/1	0.94	0.21	67,67,67,67	0
2	SO4	D	606	5/5	0.94	0.27	130,131,131,132	0
4	CL	D	614	1/1	0.95	0.07	69,69,69,69	0
4	CL	B	610	1/1	0.95	0.10	60,60,60,60	0
2	SO4	D	601	5/5	0.95	0.08	40,43,45,46	0
4	CL	D	613	1/1	0.95	0.09	67,67,67,67	0
2	SO4	C	604	5/5	0.96	0.07	42,43,44,46	0
4	CL	A	613	1/1	0.97	0.05	41,41,41,41	0
4	CL	B	613	1/1	0.97	0.08	47,47,47,47	0
2	SO4	A	606	5/5	0.97	0.07	44,45,48,52	0
2	SO4	B	605	5/5	0.97	0.07	43,44,49,50	0

6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.