



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 07:39 PM GMT

PDB ID : 4PIW  
Title : Crystal structure of sugar aminotransferase WecE from Escherichia coli K-12  
Authors : Wang, F.; Xu, W.; Helmich, K.E.; Singh, S.; Yennamalli, R.M.; Miller, M.D.;  
Bingman, C.A.; Thorson, J.S.; Phillips Jr., G.N.; Enzyme Discovery for Nat-  
ural Product Biosynthesis (NatPro)  
Deposited on : 2014-05-09  
Resolution : 2.70 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

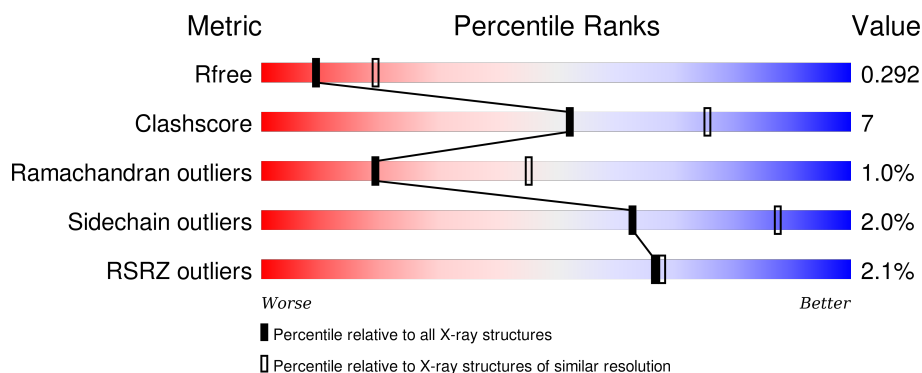
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	396	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 16%, green 74%, grey 9%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>74%</span> <span>16%</span> <span>• 9%</span> </div> </div>
1	B	396	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 75%, yellow 16%, orange 1%, grey 9%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span></span> <span>75%</span> <span>16%</span> <span>• 9%</span> </div> </div>
1	C	396	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 17%, green 73%, grey 9%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>73%</span> <span>17%</span> <span>• 9%</span> </div> </div>
1	D	396	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 73%, yellow 17%, orange 1%, grey 9%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span></span> <span>73%</span> <span>17%</span> <span>• 9%</span> </div> </div>
1	E	396	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 15%, green 76%, grey 9%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>76%</span> <span>15%</span> <span>• 9%</span> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	396	<div><div></div><div>7%</div><div></div><div>73%</div><div></div><div>17%</div><div></div><div>•</div><div>9%</div></div>
1	G	396	<div><div></div><div>2%</div><div></div><div>74%</div><div></div><div>16%</div><div></div><div>•</div><div>9%</div></div>
1	H	396	<div><div></div><div>3%</div><div></div><div>75%</div><div></div><div>16%</div><div></div><div>•</div><div>9%</div></div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 22917 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 TDP-4-keto-6-deoxy-D-glucose transaminase family protein.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
1	A	360	Total	C	N	O	P	S	Se	0	0	0
			2823	1796	481	527	1	7	11			
1	B	362	Total	C	N	O	P	S	Se	0	0	0
			2839	1807	483	529	1	7	12			
1	C	362	Total	C	N	O	P	S	Se	0	0	0
			2838	1805	483	531	1	7	11			
1	D	361	Total	C	N	O	P	S	Se	0	0	0
			2831	1802	482	528	1	7	11			
1	E	362	Total	C	N	O	P	S	Se	0	0	0
			2839	1807	483	529	1	7	12			
1	F	359	Total	C	N	O	P	S	Se	0	0	0
			2809	1785	479	526	1	7	11			
1	G	361	Total	C	N	O	P	S	Se	0	0	0
			2825	1796	481	528	1	7	12			
1	H	361	Total	C	N	O	P	S	Se	0	0	0
			2825	1796	481	528	1	7	12			

There are 160 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MSE	-	expression tag	UNP N2U028
A	-18	GLY	-	expression tag	UNP N2U028
A	-17	SER	-	expression tag	UNP N2U028
A	-16	SER	-	expression tag	UNP N2U028
A	-15	HIS	-	expression tag	UNP N2U028
A	-14	HIS	-	expression tag	UNP N2U028
A	-13	HIS	-	expression tag	UNP N2U028
A	-12	HIS	-	expression tag	UNP N2U028
A	-11	HIS	-	expression tag	UNP N2U028
A	-10	HIS	-	expression tag	UNP N2U028
A	-9	SER	-	expression tag	UNP N2U028
A	-8	SER	-	expression tag	UNP N2U028
A	-7	GLY	-	expression tag	UNP N2U028

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	LEU	-	expression tag	UNP N2U028
A	-5	VAL	-	expression tag	UNP N2U028
A	-4	PRO	-	expression tag	UNP N2U028
A	-3	ARG	-	expression tag	UNP N2U028
A	-2	GLY	-	expression tag	UNP N2U028
A	-1	SER	-	expression tag	UNP N2U028
A	0	HIS	-	expression tag	UNP N2U028
B	-19	MSE	-	expression tag	UNP N2U028
B	-18	GLY	-	expression tag	UNP N2U028
B	-17	SER	-	expression tag	UNP N2U028
B	-16	SER	-	expression tag	UNP N2U028
B	-15	HIS	-	expression tag	UNP N2U028
B	-14	HIS	-	expression tag	UNP N2U028
B	-13	HIS	-	expression tag	UNP N2U028
B	-12	HIS	-	expression tag	UNP N2U028
B	-11	HIS	-	expression tag	UNP N2U028
B	-10	HIS	-	expression tag	UNP N2U028
B	-9	SER	-	expression tag	UNP N2U028
B	-8	SER	-	expression tag	UNP N2U028
B	-7	GLY	-	expression tag	UNP N2U028
B	-6	LEU	-	expression tag	UNP N2U028
B	-5	VAL	-	expression tag	UNP N2U028
B	-4	PRO	-	expression tag	UNP N2U028
B	-3	ARG	-	expression tag	UNP N2U028
B	-2	GLY	-	expression tag	UNP N2U028
B	-1	SER	-	expression tag	UNP N2U028
B	0	HIS	-	expression tag	UNP N2U028
C	-19	MSE	-	expression tag	UNP N2U028
C	-18	GLY	-	expression tag	UNP N2U028
C	-17	SER	-	expression tag	UNP N2U028
C	-16	SER	-	expression tag	UNP N2U028
C	-15	HIS	-	expression tag	UNP N2U028
C	-14	HIS	-	expression tag	UNP N2U028
C	-13	HIS	-	expression tag	UNP N2U028
C	-12	HIS	-	expression tag	UNP N2U028
C	-11	HIS	-	expression tag	UNP N2U028
C	-10	HIS	-	expression tag	UNP N2U028
C	-9	SER	-	expression tag	UNP N2U028
C	-8	SER	-	expression tag	UNP N2U028
C	-7	GLY	-	expression tag	UNP N2U028
C	-6	LEU	-	expression tag	UNP N2U028
C	-5	VAL	-	expression tag	UNP N2U028

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	PRO	-	expression tag	UNP N2U028
C	-3	ARG	-	expression tag	UNP N2U028
C	-2	GLY	-	expression tag	UNP N2U028
C	-1	SER	-	expression tag	UNP N2U028
C	0	HIS	-	expression tag	UNP N2U028
D	-19	MSE	-	expression tag	UNP N2U028
D	-18	GLY	-	expression tag	UNP N2U028
D	-17	SER	-	expression tag	UNP N2U028
D	-16	SER	-	expression tag	UNP N2U028
D	-15	HIS	-	expression tag	UNP N2U028
D	-14	HIS	-	expression tag	UNP N2U028
D	-13	HIS	-	expression tag	UNP N2U028
D	-12	HIS	-	expression tag	UNP N2U028
D	-11	HIS	-	expression tag	UNP N2U028
D	-10	HIS	-	expression tag	UNP N2U028
D	-9	SER	-	expression tag	UNP N2U028
D	-8	SER	-	expression tag	UNP N2U028
D	-7	GLY	-	expression tag	UNP N2U028
D	-6	LEU	-	expression tag	UNP N2U028
D	-5	VAL	-	expression tag	UNP N2U028
D	-4	PRO	-	expression tag	UNP N2U028
D	-3	ARG	-	expression tag	UNP N2U028
D	-2	GLY	-	expression tag	UNP N2U028
D	-1	SER	-	expression tag	UNP N2U028
D	0	HIS	-	expression tag	UNP N2U028
E	-19	MSE	-	expression tag	UNP N2U028
E	-18	GLY	-	expression tag	UNP N2U028
E	-17	SER	-	expression tag	UNP N2U028
E	-16	SER	-	expression tag	UNP N2U028
E	-15	HIS	-	expression tag	UNP N2U028
E	-14	HIS	-	expression tag	UNP N2U028
E	-13	HIS	-	expression tag	UNP N2U028
E	-12	HIS	-	expression tag	UNP N2U028
E	-11	HIS	-	expression tag	UNP N2U028
E	-10	HIS	-	expression tag	UNP N2U028
E	-9	SER	-	expression tag	UNP N2U028
E	-8	SER	-	expression tag	UNP N2U028
E	-7	GLY	-	expression tag	UNP N2U028
E	-6	LEU	-	expression tag	UNP N2U028
E	-5	VAL	-	expression tag	UNP N2U028
E	-4	PRO	-	expression tag	UNP N2U028
E	-3	ARG	-	expression tag	UNP N2U028

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-2	GLY	-	expression tag	UNP N2U028
E	-1	SER	-	expression tag	UNP N2U028
E	0	HIS	-	expression tag	UNP N2U028
F	-19	MSE	-	expression tag	UNP N2U028
F	-18	GLY	-	expression tag	UNP N2U028
F	-17	SER	-	expression tag	UNP N2U028
F	-16	SER	-	expression tag	UNP N2U028
F	-15	HIS	-	expression tag	UNP N2U028
F	-14	HIS	-	expression tag	UNP N2U028
F	-13	HIS	-	expression tag	UNP N2U028
F	-12	HIS	-	expression tag	UNP N2U028
F	-11	HIS	-	expression tag	UNP N2U028
F	-10	HIS	-	expression tag	UNP N2U028
F	-9	SER	-	expression tag	UNP N2U028
F	-8	SER	-	expression tag	UNP N2U028
F	-7	GLY	-	expression tag	UNP N2U028
F	-6	LEU	-	expression tag	UNP N2U028
F	-5	VAL	-	expression tag	UNP N2U028
F	-4	PRO	-	expression tag	UNP N2U028
F	-3	ARG	-	expression tag	UNP N2U028
F	-2	GLY	-	expression tag	UNP N2U028
F	-1	SER	-	expression tag	UNP N2U028
F	0	HIS	-	expression tag	UNP N2U028
G	-19	MSE	-	expression tag	UNP N2U028
G	-18	GLY	-	expression tag	UNP N2U028
G	-17	SER	-	expression tag	UNP N2U028
G	-16	SER	-	expression tag	UNP N2U028
G	-15	HIS	-	expression tag	UNP N2U028
G	-14	HIS	-	expression tag	UNP N2U028
G	-13	HIS	-	expression tag	UNP N2U028
G	-12	HIS	-	expression tag	UNP N2U028
G	-11	HIS	-	expression tag	UNP N2U028
G	-10	HIS	-	expression tag	UNP N2U028
G	-9	SER	-	expression tag	UNP N2U028
G	-8	SER	-	expression tag	UNP N2U028
G	-7	GLY	-	expression tag	UNP N2U028
G	-6	LEU	-	expression tag	UNP N2U028
G	-5	VAL	-	expression tag	UNP N2U028
G	-4	PRO	-	expression tag	UNP N2U028
G	-3	ARG	-	expression tag	UNP N2U028
G	-2	GLY	-	expression tag	UNP N2U028
G	-1	SER	-	expression tag	UNP N2U028

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Chain	Residue	Modelled	Actual	Comment	Reference
G	0	HIS	-	expression tag	UNP N2U028
H	-19	MSE	-	expression tag	UNP N2U028
H	-18	GLY	-	expression tag	UNP N2U028
H	-17	SER	-	expression tag	UNP N2U028
H	-16	SER	-	expression tag	UNP N2U028
H	-15	HIS	-	expression tag	UNP N2U028
H	-14	HIS	-	expression tag	UNP N2U028
H	-13	HIS	-	expression tag	UNP N2U028
H	-12	HIS	-	expression tag	UNP N2U028
H	-11	HIS	-	expression tag	UNP N2U028
H	-10	HIS	-	expression tag	UNP N2U028
H	-9	SER	-	expression tag	UNP N2U028
H	-8	SER	-	expression tag	UNP N2U028
H	-7	GLY	-	expression tag	UNP N2U028
H	-6	LEU	-	expression tag	UNP N2U028
H	-5	VAL	-	expression tag	UNP N2U028
H	-4	PRO	-	expression tag	UNP N2U028
H	-3	ARG	-	expression tag	UNP N2U028
H	-2	GLY	-	expression tag	UNP N2U028
H	-1	SER	-	expression tag	UNP N2U028
H	0	HIS	-	expression tag	UNP N2U028

- Molecule 2 is water.

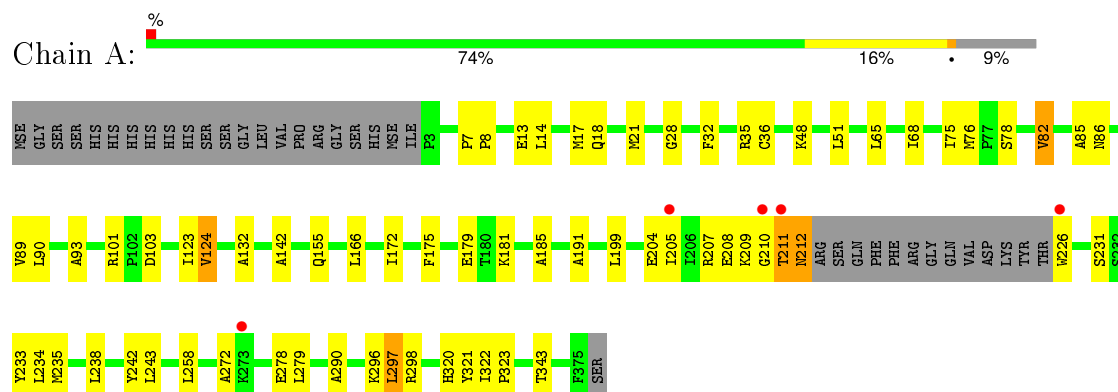
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	27	Total O 27 27	0	0
2	B	27	Total O 27 27	0	0
2	C	37	Total O 37 37	0	0
2	D	32	Total O 32 32	0	0
2	E	26	Total O 26 26	0	0
2	F	22	Total O 22 22	0	0
2	G	50	Total O 50 50	0	0
2	H	67	Total O 67 67	0	0



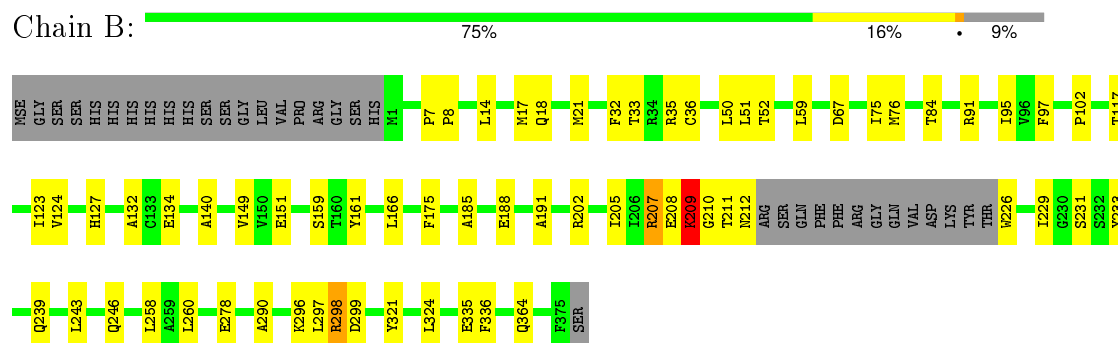
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

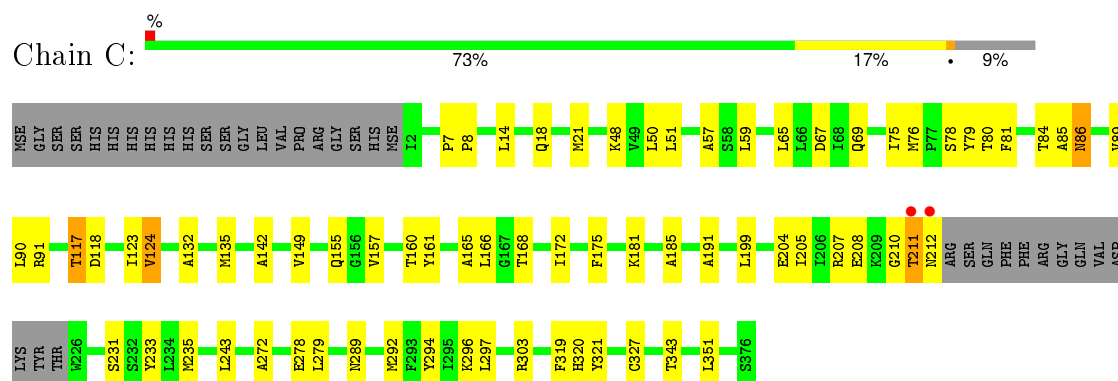
- Molecule 1: TDP-4-keto-6-deoxy-D-glucose transaminase family protein



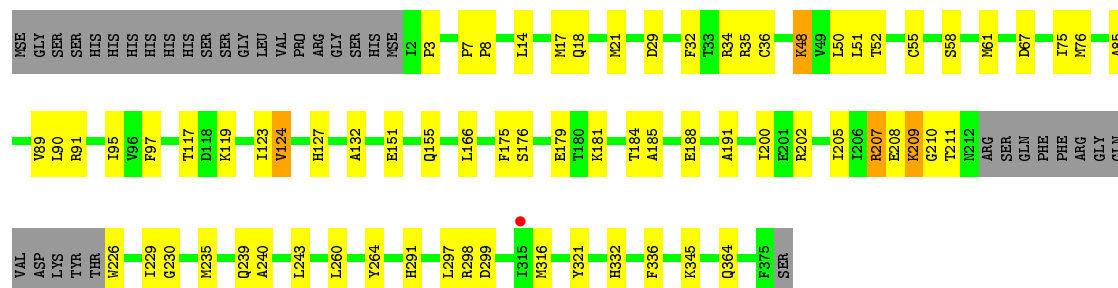
- Molecule 1: TDP-4-keto-6-deoxy-D-glucose transaminase family protein

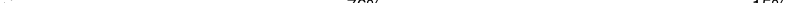


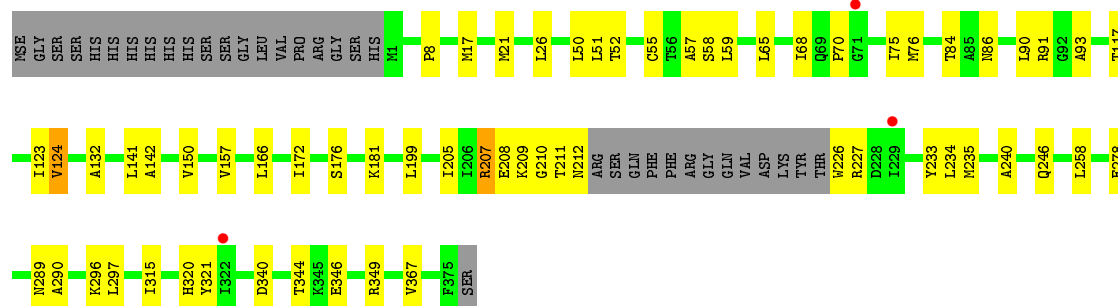
- Molecule 1: TDP-4-keto-6-deoxy-D-glucose transaminase family protein



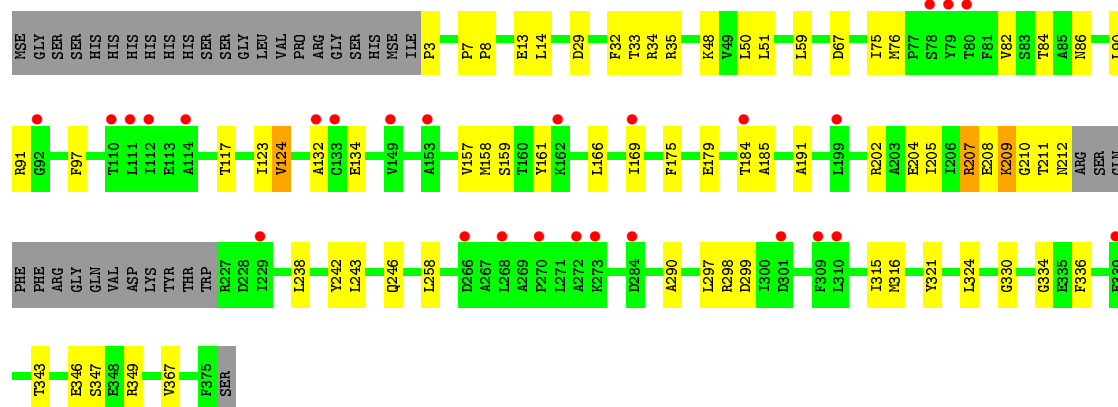
- Chain D:  73% 17% • 9%



- Chain E:  76% 15% 9%

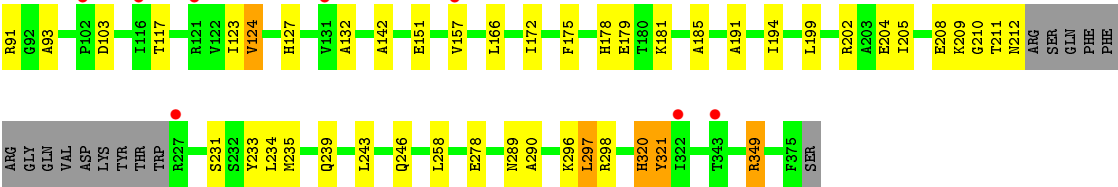


- Chain F:  7% 73% 17% 9%

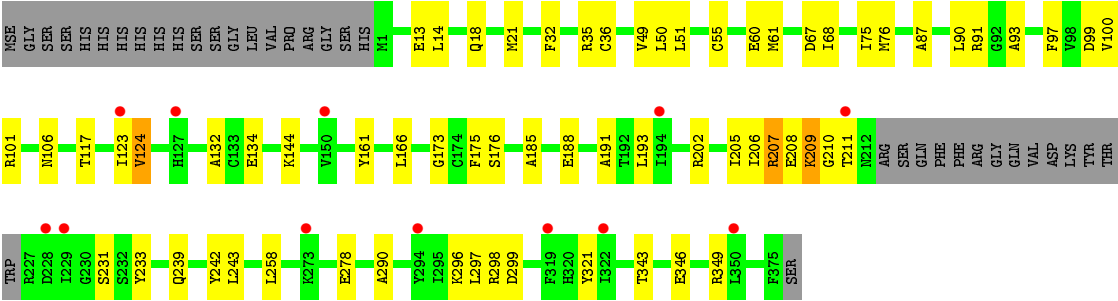


- Chain G:  2% 74% 16% 9%





● Molecule 1: TDP-4-keto-6-deoxy-D-glucose transaminase family protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	125.34Å 87.48Å 161.55Å 90.00° 91.10° 90.00°	Depositor
Resolution (Å)	48.80 – 2.70 48.37 – 2.60	Depositor EDS
% Data completeness (in resolution range)	89.8 (48.80-2.70) 70.3 (48.37-2.60)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.99 (at 2.61Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1678)	Depositor
R, $R_{free}$	0.236 , 0.275 0.256 , 0.292	Depositor DCC
$R_{free}$ test set	2985 reflections (1.85%)	DCC
Wilson B-factor (Å <sup>2</sup> )	32.3	Xtriage
Anisotropy	0.853	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.150 for h,-k,-l 0.126 for h,-k,-l	Xtriage
Reported twinning fraction	0.150 for h,-k,-l	Depositor
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	0 of 86071 reflections	Xtriage
$F_o, F_c$ correlation	0.87	EDS
Total number of atoms	22917	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.85% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: LLP

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	0.21	0/2847	0.36	0/3840
1	B	0.21	0/2863	0.36	0/3862
1	C	0.20	0/2862	0.36	0/3860
1	D	0.21	0/2855	0.36	0/3852
1	E	0.20	0/2863	0.36	0/3862
1	F	0.20	0/2831	0.35	0/3817
1	G	0.20	0/2847	0.36	0/3839
1	H	0.20	0/2847	0.36	0/3839
All	All	0.20	0/22815	0.36	0/30771

There are no bond length outliers.

There are no bond angle outliers.

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	2823	0	2784	42	0
1	B	2839	0	2806	41	0
1	C	2838	0	2799	44	0
1	D	2831	0	2794	49	0
1	E	2839	0	2806	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	2809	0	2774	37	0
1	G	2825	0	2796	40	0
1	H	2825	0	2796	37	0
2	A	27	0	0	0	0
2	B	27	0	0	1	0
2	C	37	0	0	1	0
2	D	32	0	0	1	0
2	E	26	0	0	0	0
2	F	22	0	0	2	0
2	G	50	0	0	3	0
2	H	67	0	0	5	0
All	All	22917	0	22355	300	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 7.

The worst 5 of 300 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:B:67:ASP:HB2	1:B:202:ARG:HH12	1.45	0.82
1:H:67:ASP:HB2	1:H:202:ARG:HH12	1.45	0.81
1:A:207:ARG:HG3	1:A:233:TYR:HB2	1.65	0.76
1:D:67:ASP:HB2	1:D:202:ARG:HH12	1.50	0.75
1:G:278:GLU:HB2	1:G:296:LYS:HB2	1.67	0.74

There are no symmetry-related clashes.

## 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	A	355/396 (90%)	338 (95%)	14 (4%)	3 (1%)	24 51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	357/396 (90%)	332 (93%)	21 (6%)	4 (1%)	17	42
1	C	357/396 (90%)	339 (95%)	16 (4%)	2 (1%)	30	59
1	D	356/396 (90%)	341 (96%)	11 (3%)	4 (1%)	17	42
1	E	357/396 (90%)	340 (95%)	13 (4%)	4 (1%)	17	42
1	F	354/396 (89%)	332 (94%)	17 (5%)	5 (1%)	14	35
1	G	356/396 (90%)	337 (95%)	16 (4%)	3 (1%)	24	51
1	H	356/396 (90%)	341 (96%)	11 (3%)	4 (1%)	17	42
All	All	2848/3168 (90%)	2700 (95%)	119 (4%)	29 (1%)	19	45

5 of 29 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	209	LYS
1	D	298	ARG
1	E	297	LEU
1	F	298	ARG
1	H	298	ARG

### 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	294/313 (94%)	288 (98%)	6 (2%)	63	87
1	B	296/313 (95%)	290 (98%)	6 (2%)	63	87
1	C	296/313 (95%)	291 (98%)	5 (2%)	68	90
1	D	295/313 (94%)	290 (98%)	5 (2%)	68	90
1	E	296/313 (95%)	287 (97%)	9 (3%)	48	79
1	F	293/313 (94%)	289 (99%)	4 (1%)	74	92
1	G	295/313 (94%)	288 (98%)	7 (2%)	57	85
1	H	295/313 (94%)	290 (98%)	5 (2%)	68	90
All	All	2360/2504 (94%)	2313 (98%)	47 (2%)	63	87

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	332	HIS
1	E	207	ARG
1	H	117	THR
1	E	117	THR
1	E	212	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	239	GLN
1	F	239	GLN
1	H	212	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

8 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
1	LLP	A	181	1	23,24,25	2.79	8 (34%)	28,32,34	1.28	5 (17%)
1	LLP	B	181	1	23,24,25	2.81	8 (34%)	28,32,34	1.35	4 (14%)
1	LLP	C	181	1	23,24,25	2.84	8 (34%)	28,32,34	1.14	4 (14%)
1	LLP	D	181	1	23,24,25	2.82	8 (34%)	28,32,34	1.29	4 (14%)
1	LLP	E	181	1	23,24,25	2.81	7 (30%)	28,32,34	1.24	4 (14%)
1	LLP	F	181	1	23,24,25	2.80	8 (34%)	28,32,34	1.28	5 (17%)
1	LLP	G	181	1	23,24,25	2.80	8 (34%)	28,32,34	1.25	4 (14%)
1	LLP	H	181	1	23,24,25	2.81	7 (30%)	28,32,34	1.25	5 (17%)



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
1	LLP	A	181	1	-	0/15/17/19	0/1/1/1
1	LLP	B	181	1	-	0/15/17/19	0/1/1/1
1	LLP	C	181	1	-	1/15/17/19	0/1/1/1
1	LLP	D	181	1	-	0/15/17/19	0/1/1/1
1	LLP	E	181	1	-	1/15/17/19	0/1/1/1
1	LLP	F	181	1	-	0/15/17/19	0/1/1/1
1	LLP	G	181	1	-	0/15/17/19	0/1/1/1
1	LLP	H	181	1	-	0/15/17/19	0/1/1/1

The worst 5 of 62 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	181	LLP	C4-C5	-3.94	1.36	1.42
1	B	181	LLP	C4-C5	-3.94	1.36	1.42
1	A	181	LLP	C4-C5	-3.89	1.36	1.42
1	F	181	LLP	C4-C5	-3.89	1.36	1.42
1	G	181	LLP	C4-C5	-3.86	1.36	1.42

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	181	LLP	CE-NZ-C4'	-3.41	109.11	118.97
1	G	181	LLP	CE-NZ-C4'	-3.24	109.62	118.97
1	H	181	LLP	CE-NZ-C4'	-3.11	109.97	118.97
1	D	181	LLP	CE-NZ-C4'	-3.11	109.98	118.97
1	A	181	LLP	C4-C4'-NZ	-2.99	108.43	125.06

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	E	181	LLP	C4-C4'-NZ-CE
1	C	181	LLP	C4-C4'-NZ-CE

There are no ring outliers.

5 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	181	LLP	1	0
1	C	181	LLP	1	0
1	D	181	LLP	5	0
1	E	181	LLP	1	0
1	G	181	LLP	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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 ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	348/396 (87%)	-0.07	5 (1%) 78 77	21, 30, 44, 66	0
1	B	349/396 (88%)	-0.06	0 100 100	23, 35, 47, 58	0
1	C	350/396 (88%)	-0.06	2 (0%) 90 91	19, 32, 45, 64	0
1	D	349/396 (88%)	-0.02	1 (0%) 94 95	20, 34, 50, 64	0
1	E	349/396 (88%)	0.09	3 (0%) 85 86	24, 39, 58, 77	0
1	F	347/396 (87%)	0.61	27 (7%) 16 14	33, 57, 76, 90	0
1	G	348/396 (87%)	0.31	8 (2%) 64 64	26, 48, 65, 81	0
1	H	348/396 (87%)	0.39	12 (3%) 49 49	27, 48, 64, 76	0
All	All	2788/3168 (88%)	0.15	58 (2%) 67 68	19, 38, 65, 90	0

The worst 5 of 58 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	268	LEU	5.3
1	F	272	ALA	4.7
1	G	227	ARG	4.3
1	F	153	ALA	4.2
1	F	310	LEU	3.7

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

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
1	LLP	G	181	24/25	0.94	0.19	-	32,42,48,52	0
1	LLP	H	181	24/25	0.93	0.18	-	32,40,50,53	0
1	LLP	A	181	24/25	0.92	0.19	-	21,30,37,40	0
1	LLP	B	181	24/25	0.92	0.18	-	22,30,41,41	0
1	LLP	C	181	24/25	0.92	0.21	-	21,29,38,43	0
1	LLP	D	181	24/25	0.94	0.18	-	24,30,38,41	0
1	LLP	E	181	24/25	0.89	0.21	-	25,32,42,46	0
1	LLP	F	181	24/25	0.87	0.23	-	40,51,65,68	0

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

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

There are no such residues in this entry.