



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 10:51 PM GMT

PDB ID : 4ZAH  
Title : Crystal structure of sugar aminotransferase WecE with External Aldimine VII from Escherichia coli K-12  
Authors : Wang, F.; Singh, S.; Cao, H.; Xu, W.; Miller, M.D.; Thorson, J.S.; Phillips Jr., G.N.; Enzyme Discovery for Natural Product Biosynthesis (NatPro)  
Deposited on : 2015-04-13  
Resolution : 2.24 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

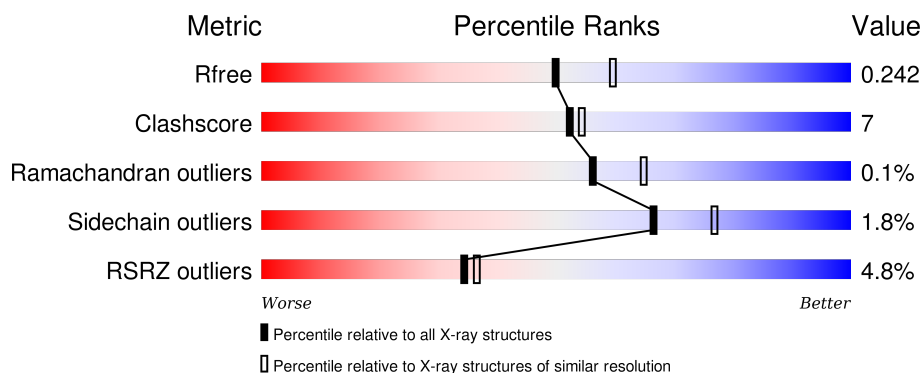
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.24 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	1611 (2.26-2.22)
Clashscore	102246	1764 (2.26-2.22)
Ramachandran outliers	100387	1724 (2.26-2.22)
Sidechain outliers	100360	1724 (2.26-2.22)
RSRZ outliers	91569	1616 (2.26-2.22)

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>80%</div> <div>13%</div> <div>7%</div> </div>
1	B	396	<div> <div>84%</div> <div>9%</div> <div>7%</div> </div>
1	C	396	<div> <div>82%</div> <div>10%</div> <div>7%</div> </div>
1	D	396	<div> <div>3%</div> <div>84%</div> <div>9%</div> <div>7%</div> </div>
1	E	396	<div> <div>81%</div> <div>11%</div> <div>7%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	396	
1	G	396	
1	H	396	

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	T5K	A	500[A]	X	-	-	-
2	T5K	B	500[A]	X	-	-	-
2	T5K	C	500[A]	X	-	-	-
2	T5K	D	500[A]	X	-	-	-
2	T5K	E	500[A]	X	-	-	-
2	T5K	E	500[B]	-	-	-	X
2	T5K	F	500[A]	X	-	-	X
2	T5K	F	500[B]	-	-	-	X
2	T5K	G	500[A]	X	-	-	X
2	T5K	G	500[B]	-	-	-	X
2	T5K	H	500[A]	X	-	-	X
2	T5K	H	500[B]	-	-	-	X

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 24368 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 dTDP-4-amino-4,6-dideoxygalactose transaminase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	370	Total	C	N	O	S	0	4	0
			2931	1864	505	543	19			
1	B	370	Total	C	N	O	S	0	1	0
			2902	1846	498	539	19			
1	C	368	Total	C	N	O	S	0	3	0
			2904	1848	499	538	19			
1	D	369	Total	C	N	O	S	0	3	0
			2917	1853	505	540	19			
1	E	367	Total	C	N	O	S	0	1	0
			2882	1833	496	534	19			
1	F	367	Total	C	N	O	S	0	0	0
			2871	1827	492	533	19			
1	G	367	Total	C	N	O	S	0	0	0
			2871	1827	492	533	19			
1	H	368	Total	C	N	O	S	0	0	0
			2877	1830	493	535	19			

There are 160 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP P27833
A	-18	GLY	-	expression tag	UNP P27833
A	-17	SER	-	expression tag	UNP P27833
A	-16	SER	-	expression tag	UNP P27833
A	-15	HIS	-	expression tag	UNP P27833
A	-14	HIS	-	expression tag	UNP P27833
A	-13	HIS	-	expression tag	UNP P27833
A	-12	HIS	-	expression tag	UNP P27833
A	-11	HIS	-	expression tag	UNP P27833
A	-10	HIS	-	expression tag	UNP P27833
A	-9	SER	-	expression tag	UNP P27833
A	-8	SER	-	expression tag	UNP P27833
A	-7	GLY	-	expression tag	UNP P27833

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	LEU	-	expression tag	UNP P27833
A	-5	VAL	-	expression tag	UNP P27833
A	-4	PRO	-	expression tag	UNP P27833
A	-3	ARG	-	expression tag	UNP P27833
A	-2	GLY	-	expression tag	UNP P27833
A	-1	SER	-	expression tag	UNP P27833
A	0	HIS	-	expression tag	UNP P27833
B	-19	MET	-	initiating methionine	UNP P27833
B	-18	GLY	-	expression tag	UNP P27833
B	-17	SER	-	expression tag	UNP P27833
B	-16	SER	-	expression tag	UNP P27833
B	-15	HIS	-	expression tag	UNP P27833
B	-14	HIS	-	expression tag	UNP P27833
B	-13	HIS	-	expression tag	UNP P27833
B	-12	HIS	-	expression tag	UNP P27833
B	-11	HIS	-	expression tag	UNP P27833
B	-10	HIS	-	expression tag	UNP P27833
B	-9	SER	-	expression tag	UNP P27833
B	-8	SER	-	expression tag	UNP P27833
B	-7	GLY	-	expression tag	UNP P27833
B	-6	LEU	-	expression tag	UNP P27833
B	-5	VAL	-	expression tag	UNP P27833
B	-4	PRO	-	expression tag	UNP P27833
B	-3	ARG	-	expression tag	UNP P27833
B	-2	GLY	-	expression tag	UNP P27833
B	-1	SER	-	expression tag	UNP P27833
B	0	HIS	-	expression tag	UNP P27833
C	-19	MET	-	initiating methionine	UNP P27833
C	-18	GLY	-	expression tag	UNP P27833
C	-17	SER	-	expression tag	UNP P27833
C	-16	SER	-	expression tag	UNP P27833
C	-15	HIS	-	expression tag	UNP P27833
C	-14	HIS	-	expression tag	UNP P27833
C	-13	HIS	-	expression tag	UNP P27833
C	-12	HIS	-	expression tag	UNP P27833
C	-11	HIS	-	expression tag	UNP P27833
C	-10	HIS	-	expression tag	UNP P27833
C	-9	SER	-	expression tag	UNP P27833
C	-8	SER	-	expression tag	UNP P27833
C	-7	GLY	-	expression tag	UNP P27833
C	-6	LEU	-	expression tag	UNP P27833
C	-5	VAL	-	expression tag	UNP P27833

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	PRO	-	expression tag	UNP P27833
C	-3	ARG	-	expression tag	UNP P27833
C	-2	GLY	-	expression tag	UNP P27833
C	-1	SER	-	expression tag	UNP P27833
C	0	HIS	-	expression tag	UNP P27833
D	-19	MET	-	initiating methionine	UNP P27833
D	-18	GLY	-	expression tag	UNP P27833
D	-17	SER	-	expression tag	UNP P27833
D	-16	SER	-	expression tag	UNP P27833
D	-15	HIS	-	expression tag	UNP P27833
D	-14	HIS	-	expression tag	UNP P27833
D	-13	HIS	-	expression tag	UNP P27833
D	-12	HIS	-	expression tag	UNP P27833
D	-11	HIS	-	expression tag	UNP P27833
D	-10	HIS	-	expression tag	UNP P27833
D	-9	SER	-	expression tag	UNP P27833
D	-8	SER	-	expression tag	UNP P27833
D	-7	GLY	-	expression tag	UNP P27833
D	-6	LEU	-	expression tag	UNP P27833
D	-5	VAL	-	expression tag	UNP P27833
D	-4	PRO	-	expression tag	UNP P27833
D	-3	ARG	-	expression tag	UNP P27833
D	-2	GLY	-	expression tag	UNP P27833
D	-1	SER	-	expression tag	UNP P27833
D	0	HIS	-	expression tag	UNP P27833
E	-19	MET	-	initiating methionine	UNP P27833
E	-18	GLY	-	expression tag	UNP P27833
E	-17	SER	-	expression tag	UNP P27833
E	-16	SER	-	expression tag	UNP P27833
E	-15	HIS	-	expression tag	UNP P27833
E	-14	HIS	-	expression tag	UNP P27833
E	-13	HIS	-	expression tag	UNP P27833
E	-12	HIS	-	expression tag	UNP P27833
E	-11	HIS	-	expression tag	UNP P27833
E	-10	HIS	-	expression tag	UNP P27833
E	-9	SER	-	expression tag	UNP P27833
E	-8	SER	-	expression tag	UNP P27833
E	-7	GLY	-	expression tag	UNP P27833
E	-6	LEU	-	expression tag	UNP P27833
E	-5	VAL	-	expression tag	UNP P27833
E	-4	PRO	-	expression tag	UNP P27833
E	-3	ARG	-	expression tag	UNP P27833

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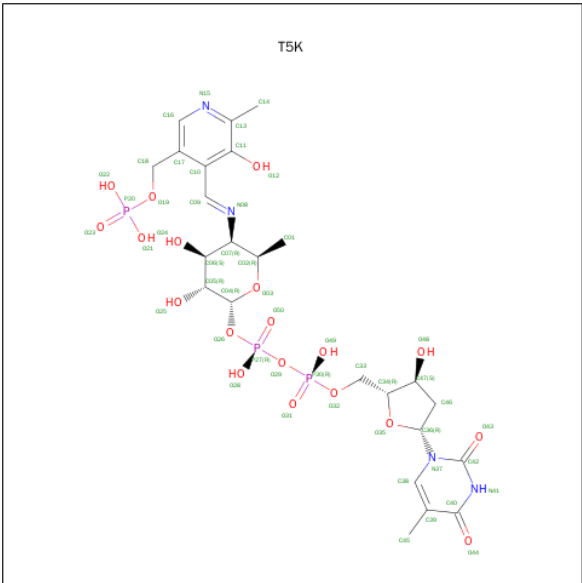
Chain	Residue	Modelled	Actual	Comment	Reference
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E	-1	SER	-	expression tag	UNP P27833
E	0	HIS	-	expression tag	UNP P27833
F	-19	MET	-	initiating methionine	UNP P27833
F	-18	GLY	-	expression tag	UNP P27833
F	-17	SER	-	expression tag	UNP P27833
F	-16	SER	-	expression tag	UNP P27833
F	-15	HIS	-	expression tag	UNP P27833
F	-14	HIS	-	expression tag	UNP P27833
F	-13	HIS	-	expression tag	UNP P27833
F	-12	HIS	-	expression tag	UNP P27833
F	-11	HIS	-	expression tag	UNP P27833
F	-10	HIS	-	expression tag	UNP P27833
F	-9	SER	-	expression tag	UNP P27833
F	-8	SER	-	expression tag	UNP P27833
F	-7	GLY	-	expression tag	UNP P27833
F	-6	LEU	-	expression tag	UNP P27833
F	-5	VAL	-	expression tag	UNP P27833
F	-4	PRO	-	expression tag	UNP P27833
F	-3	ARG	-	expression tag	UNP P27833
F	-2	GLY	-	expression tag	UNP P27833
F	-1	SER	-	expression tag	UNP P27833
F	0	HIS	-	expression tag	UNP P27833
G	-19	MET	-	initiating methionine	UNP P27833
G	-18	GLY	-	expression tag	UNP P27833
G	-17	SER	-	expression tag	UNP P27833
G	-16	SER	-	expression tag	UNP P27833
G	-15	HIS	-	expression tag	UNP P27833
G	-14	HIS	-	expression tag	UNP P27833
G	-13	HIS	-	expression tag	UNP P27833
G	-12	HIS	-	expression tag	UNP P27833
G	-11	HIS	-	expression tag	UNP P27833
G	-10	HIS	-	expression tag	UNP P27833
G	-9	SER	-	expression tag	UNP P27833
G	-8	SER	-	expression tag	UNP P27833
G	-7	GLY	-	expression tag	UNP P27833
G	-6	LEU	-	expression tag	UNP P27833
G	-5	VAL	-	expression tag	UNP P27833
G	-4	PRO	-	expression tag	UNP P27833
G	-3	ARG	-	expression tag	UNP P27833
G	-2	GLY	-	expression tag	UNP P27833
G	-1	SER	-	expression tag	UNP P27833

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Chain	Residue	Modelled	Actual	Comment	Reference
G	0	HIS	-	expression tag	UNP P27833
H	-19	MET	-	initiating methionine	UNP P27833
H	-18	GLY	-	expression tag	UNP P27833
H	-17	SER	-	expression tag	UNP P27833
H	-16	SER	-	expression tag	UNP P27833
H	-15	HIS	-	expression tag	UNP P27833
H	-14	HIS	-	expression tag	UNP P27833
H	-13	HIS	-	expression tag	UNP P27833
H	-12	HIS	-	expression tag	UNP P27833
H	-11	HIS	-	expression tag	UNP P27833
H	-10	HIS	-	expression tag	UNP P27833
H	-9	SER	-	expression tag	UNP P27833
H	-8	SER	-	expression tag	UNP P27833
H	-7	GLY	-	expression tag	UNP P27833
H	-6	LEU	-	expression tag	UNP P27833
H	-5	VAL	-	expression tag	UNP P27833
H	-4	PRO	-	expression tag	UNP P27833
H	-3	ARG	-	expression tag	UNP P27833
H	-2	GLY	-	expression tag	UNP P27833
H	-1	SER	-	expression tag	UNP P27833
H	0	HIS	-	expression tag	UNP P27833

- Molecule 2 is [[(2R,3S,5R)-5-[5-methyl-2,4-bis(oxidanylidene)pyrimidin-1-yl]-3-oxidanyl-oxolan-2-yl]methoxy-oxidanyl-phosphoryl] [(2R,3R,4S,5R,6R)-6-methyl-5-[(E)-[2-methyl-3-oxidanyl-5-(phosphonooxymethyl)pyridin-4-yl]methylideneamino]-3,4-bis(oxidanyl)oxan-2-yl] hydrogen phosphate (three-letter code: T5K) (formula: C<sub>24</sub>H<sub>35</sub>N<sub>4</sub>O<sub>19</sub>P<sub>3</sub>).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	1
			66	32	6	24	4		
2	B	1	Total	C	N	O	P	0	1
			66	32	6	24	4		
2	C	1	Total	C	N	O	P	0	1
			66	32	6	24	4		
2	D	1	Total	C	N	O	P	0	1
			66	32	6	24	4		
2	E	1	Total	C	N	O	P	0	1
			66	32	6	24	4		
2	F	1	Total	C	N	O	P	0	1
			66	32	6	24	4		
2	G	1	Total	C	N	O	P	0	1
			66	32	6	24	4		
2	H	1	Total	C	N	O	P	0	1
			66	32	6	24	4		

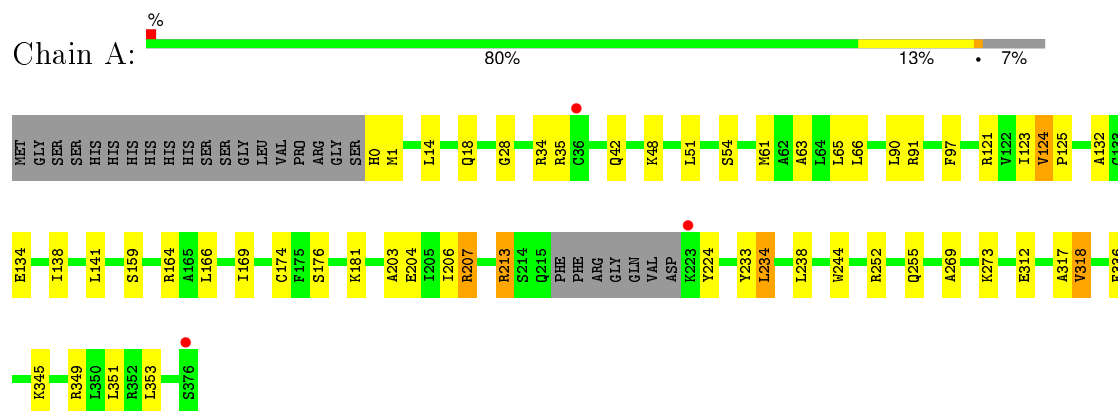
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	173	Total	O	0	0
			173	173		
3	B	128	Total	O	0	0
			128	128		
3	C	113	Total	O	0	0
			113	113		
3	D	92	Total	O	0	0
			92	92		
3	E	90	Total	O	0	0
			90	90		
3	F	32	Total	O	0	0
			32	32		
3	G	30	Total	O	0	0
			30	30		
3	H	27	Total	O	0	0
			27	27		

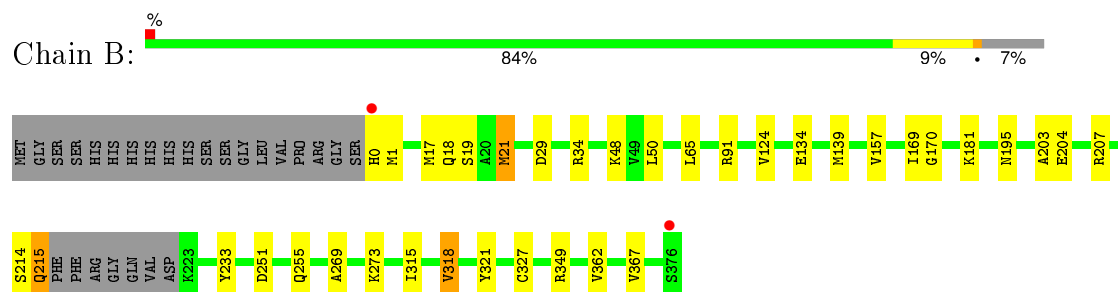
### 3 Residue-property plots [i](#)

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.

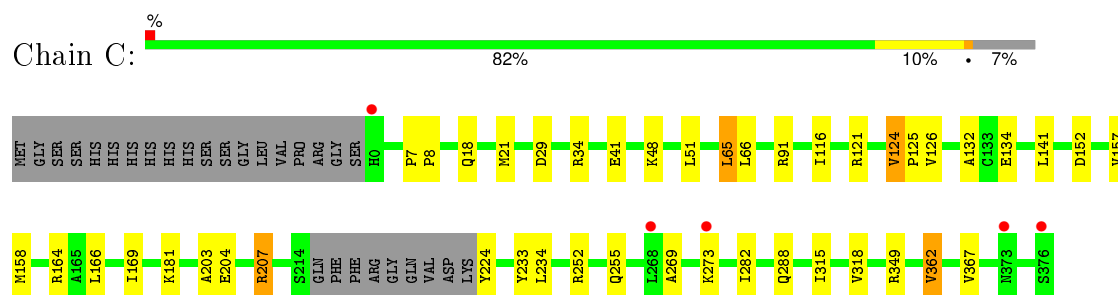
- Molecule 1: dTDP-4-amino-4,6-dideoxygalactose transaminase



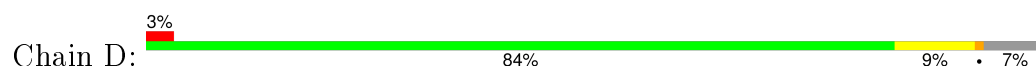
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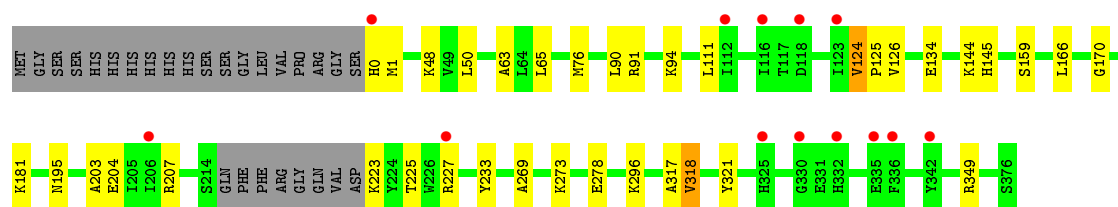


- Molecule 1: dTDP-4-amino-4,6-dideoxygalactose transaminase

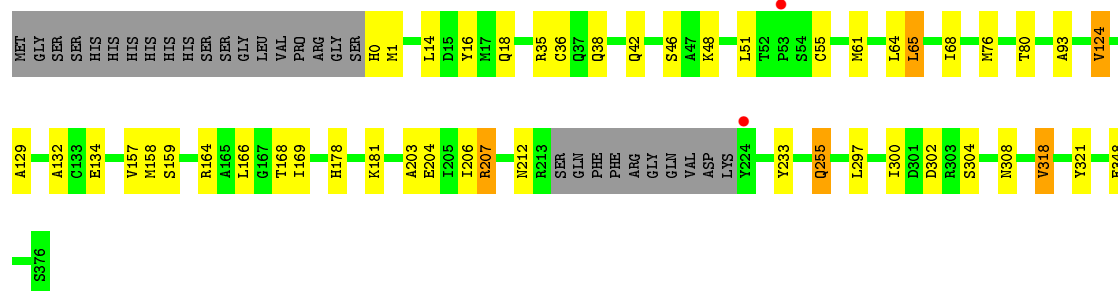
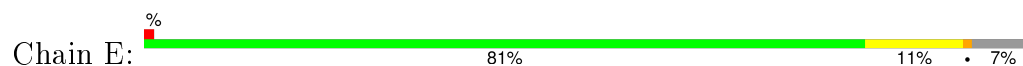


- Molecule 1: dTDP-4-amino-4,6-dideoxygalactose transaminase

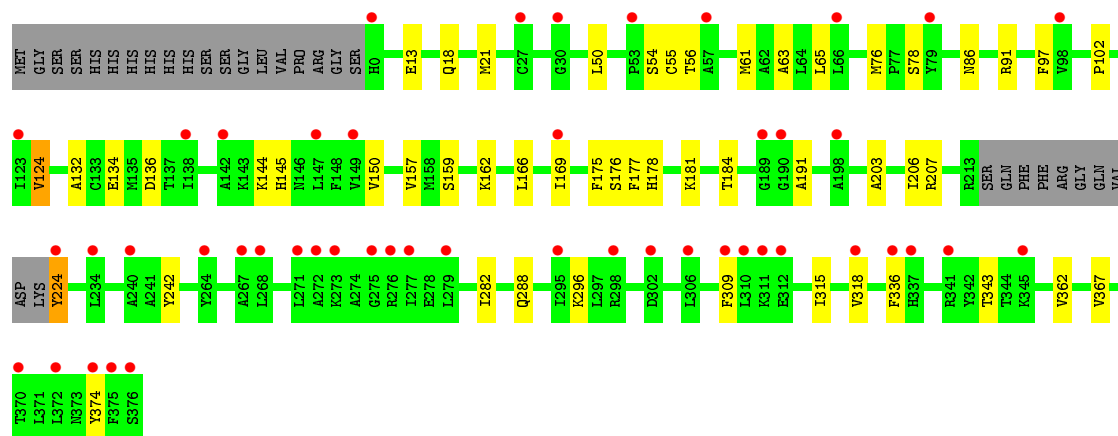
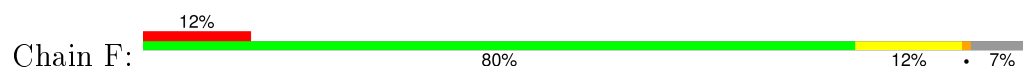




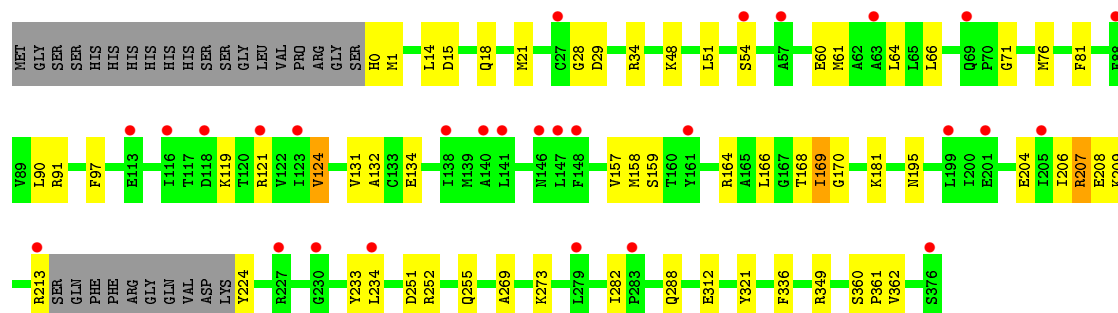
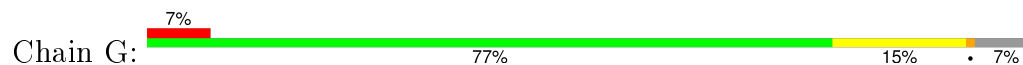
- Molecule 1: dTDP-4-amino-4,6-dideoxygalactose transaminase



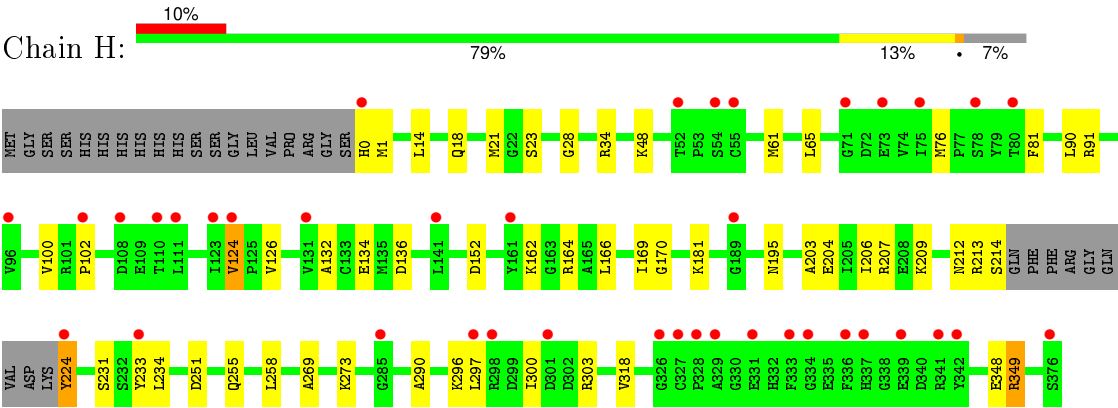
- Molecule 1: dTDP-4-amino-4,6-dideoxygalactose transaminase



- Molecule 1: dTDP-4-amino-4,6-dideoxygalactose transaminase



● Molecule 1: dTDP-4-amino-4,6-dideoxygalactose transaminase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	88.07Å 103.94Å 109.39Å 72.10° 73.55° 74.08°	Depositor
Resolution (Å)	48.21 – 2.24 49.12 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.21-2.24) 77.3 (49.12-2.00)	Depositor EDS
$R_{merge}$	0.25	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.35 (at 2.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1951)	Depositor
R, $R_{free}$	0.203 , 0.246 0.203 , 0.242	Depositor DCC
$R_{free}$ test set	2001 reflections (1.34%)	DCC
Wilson B-factor (Å <sup>2</sup> )	26.1	Xtriage
Anisotropy	0.380	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 45.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 232741 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	24368	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.41% 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: T5K

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	0.62	2/2993 (0.1%)	0.72	3/4053 (0.1%)
1	B	0.60	2/2964 (0.1%)	0.68	1/4015 (0.0%)
1	C	0.51	0/2966	0.64	1/4018 (0.0%)
1	D	0.52	1/2979 (0.0%)	0.64	0/4033
1	E	0.51	1/2944 (0.0%)	0.64	0/3988
1	F	0.46	0/2933	0.60	0/3974
1	G	0.41	0/2933	0.55	0/3974
1	H	0.39	0/2939	0.57	0/3982
All	All	0.51	6/23651 (0.0%)	0.63	5/32037 (0.0%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	318	VAL	CB-CG2	-7.73	1.36	1.52
1	D	318	VAL	CB-CG2	-7.71	1.36	1.52
1	E	318	VAL	CB-CG2	-7.64	1.36	1.52
1	A	174	CYS	CB-SG	5.98	1.92	1.82
1	A	318	VAL	CB-CG2	-5.28	1.41	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	213	ARG	NE-CZ-NH1	-8.73	115.94	120.30
1	A	141	LEU	CA-CB-CG	8.14	134.03	115.30
1	B	21	MET	CG-SD-CE	-6.45	89.88	100.20
1	C	234	LEU	CA-CB-CG	5.73	128.48	115.30
1	A	234	LEU	CA-CB-CG	5.23	127.32	115.30

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	2931	0	2906	46	0
1	B	2902	0	2875	35	0
1	C	2904	0	2878	29	0
1	D	2917	0	2890	29	0
1	E	2882	0	2853	43	0
1	F	2871	0	2841	49	0
1	G	2871	0	2841	47	0
1	H	2877	0	2846	37	0
2	A	66	0	38	10	0
2	B	66	0	39	15	0
2	C	66	0	39	6	0
2	D	66	0	39	7	0
2	E	66	0	39	14	0
2	F	66	0	39	22	0
2	G	66	0	39	7	0
2	H	66	0	39	5	0
3	A	173	0	0	8	0
3	B	128	0	0	7	0
3	C	113	0	0	5	0
3	D	92	0	0	6	0
3	E	90	0	0	5	0
3	F	32	0	0	1	0
3	G	30	0	0	3	0
3	H	27	0	0	3	0
All	All	24368	0	23241	314	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 314 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)
2:F:500[A]:T5K:C34	2:F:500[A]:T5K:O35	1.66	1.30
2:E:500[A]:T5K:C34	2:E:500[A]:T5K:O35	1.67	1.27
2:D:500[A]:T5K:O35	2:D:500[A]:T5K:C34	1.65	1.24

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:500[A]:T5K:C34	2:A:500[A]:T5K:O35	1.65	1.22
2:G:500[A]:T5K:O35	2:G:500[A]:T5K:C34	1.67	1.20

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	370/396 (93%)	361 (98%)	9 (2%)	0	100	100
1	B	367/396 (93%)	357 (97%)	10 (3%)	0	100	100
1	C	367/396 (93%)	360 (98%)	7 (2%)	0	100	100
1	D	368/396 (93%)	359 (98%)	9 (2%)	0	100	100
1	E	364/396 (92%)	356 (98%)	8 (2%)	0	100	100
1	F	363/396 (92%)	356 (98%)	7 (2%)	0	100	100
1	G	363/396 (92%)	355 (98%)	7 (2%)	1 (0%)	46	51
1	H	364/396 (92%)	354 (97%)	9 (2%)	1 (0%)	46	51
All	All	2926/3168 (92%)	2858 (98%)	66 (2%)	2 (0%)	56	65

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	213	ARG
1	G	169	ILE

### 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	309/327 (94%)	304 (98%)	5 (2%)	70	80
1	B	306/327 (94%)	302 (99%)	4 (1%)	76	85
1	C	306/327 (94%)	298 (97%)	8 (3%)	54	64
1	D	307/327 (94%)	302 (98%)	5 (2%)	70	80
1	E	303/327 (93%)	298 (98%)	5 (2%)	68	78
1	F	302/327 (92%)	297 (98%)	5 (2%)	68	78
1	G	302/327 (92%)	296 (98%)	6 (2%)	63	73
1	H	303/327 (93%)	298 (98%)	5 (2%)	68	78
All	All	2438/2616 (93%)	2395 (98%)	43 (2%)	66	77

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	134	GLU
1	E	134	GLU
1	H	134	GLU
1	D	223	LYS
1	D	349	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	F	145	HIS

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry

16 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	T5K	A	500[A]	-	45,53,53	3.43	19 (42%)	60,81,81	1.80	10 (16%)
2	T5K	A	500[B]	-	15,16,53	2.65	9 (60%)	21,23,81	1.68	6 (28%)
2	T5K	B	500[A]	-	45,53,53	3.51	20 (44%)	60,81,81	1.71	13 (21%)
2	T5K	B	500[B]	-	15,16,53	2.46	8 (53%)	21,23,81	1.14	3 (14%)
2	T5K	C	500[A]	-	45,53,53	3.41	18 (40%)	60,81,81	1.92	11 (18%)
2	T5K	C	500[B]	-	15,16,53	2.12	4 (26%)	21,23,81	1.02	0
2	T5K	D	500[A]	-	45,53,53	3.46	16 (35%)	60,81,81	1.70	8 (13%)
2	T5K	D	500[B]	-	15,16,53	2.63	7 (46%)	21,23,81	1.32	3 (14%)
2	T5K	E	500[A]	-	45,53,53	3.16	17 (37%)	60,81,81	2.36	17 (28%)
2	T5K	E	500[B]	-	15,16,53	2.60	7 (46%)	21,23,81	1.53	4 (19%)
2	T5K	F	500[A]	-	45,53,53	3.17	19 (42%)	60,81,81	1.99	16 (26%)
2	T5K	F	500[B]	-	15,16,53	2.28	6 (40%)	21,23,81	1.23	3 (14%)
2	T5K	G	500[A]	-	45,53,53	3.39	17 (37%)	60,81,81	1.66	6 (10%)
2	T5K	G	500[B]	-	15,16,53	2.61	4 (26%)	21,23,81	1.47	4 (19%)
2	T5K	H	500[A]	-	45,53,53	3.37	19 (42%)	60,81,81	1.77	8 (13%)
2	T5K	H	500[B]	-	15,16,53	2.16	3 (20%)	21,23,81	0.91	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
2	T5K	A	500[A]	-	1/1/11/12	0/28/64/64	0/4/4/4
2	T5K	A	500[B]	-	-	0/8/8/64	0/1/1/4
2	T5K	B	500[A]	-	1/1/11/12	0/28/64/64	0/4/4/4
2	T5K	B	500[B]	-	-	0/8/8/64	0/1/1/4
2	T5K	C	500[A]	-	1/1/11/12	0/28/64/64	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	T5K	C	500[B]	-	-	0/8/8/64	0/1/1/4
2	T5K	D	500[A]	-	1/1/11/12	0/28/64/64	0/4/4/4
2	T5K	D	500[B]	-	-	0/8/8/64	0/1/1/4
2	T5K	E	500[A]	-	1/1/11/12	0/28/64/64	0/4/4/4
2	T5K	E	500[B]	-	-	0/8/8/64	0/1/1/4
2	T5K	F	500[A]	-	1/1/11/12	0/28/64/64	0/4/4/4
2	T5K	F	500[B]	-	-	2/8/8/64	0/1/1/4
2	T5K	G	500[A]	-	1/1/11/12	0/28/64/64	0/4/4/4
2	T5K	G	500[B]	-	-	0/8/8/64	0/1/1/4
2	T5K	H	500[A]	-	1/1/11/12	0/28/64/64	0/4/4/4
2	T5K	H	500[B]	-	-	0/8/8/64	0/1/1/4

The worst 5 of 193 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	500[A]	T5K	O35-C36	-6.45	1.27	1.42
2	E	500[A]	T5K	C47-C34	-6.37	1.35	1.53
2	A	500[A]	T5K	C47-C34	-6.35	1.35	1.53
2	B	500[A]	T5K	C47-C34	-6.34	1.35	1.53
2	D	500[A]	T5K	C47-C34	-6.27	1.35	1.53

The worst 5 of 112 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	500[A]	T5K	P27-O29-P30	-6.97	113.15	132.73
2	E	500[A]	T5K	O03-C04-O26	-6.68	102.56	111.36
2	E	500[A]	T5K	C07-N08-C09	-6.31	110.05	118.70
2	C	500[A]	T5K	O03-C04-O26	-5.26	104.42	111.36
2	H	500[A]	T5K	P27-O29-P30	-4.83	119.16	132.73

5 of 8 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	D	500[A]	T5K	C02
2	B	500[A]	T5K	C02
2	H	500[A]	T5K	C02
2	F	500[A]	T5K	C02
2	C	500[A]	T5K	C02

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	500[B]	T5K	C11-C10-C09-N08
2	F	500[B]	T5K	C17-C10-C09-N08

There are no ring outliers.

13 monomers are involved in 86 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500[A]	T5K	8	0
2	A	500[B]	T5K	2	0
2	B	500[A]	T5K	10	0
2	B	500[B]	T5K	5	0
2	C	500[A]	T5K	6	0
2	D	500[A]	T5K	6	0
2	D	500[B]	T5K	1	0
2	E	500[A]	T5K	14	0
2	F	500[A]	T5K	14	0
2	F	500[B]	T5K	8	0
2	G	500[A]	T5K	4	0
2	G	500[B]	T5K	3	0
2	H	500[A]	T5K	5	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 ⓘ

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	370/396 (93%)	-0.20	3 (0%) 87 87	26, 40, 61, 85	0
1	B	370/396 (93%)	-0.22	2 (0%) 91 92	29, 46, 66, 90	0
1	C	368/396 (92%)	-0.15	5 (1%) 78 80	28, 47, 70, 97	0
1	D	369/396 (93%)	0.11	13 (3%) 48 50	29, 52, 78, 91	0
1	E	367/396 (92%)	0.00	2 (0%) 91 92	51, 61, 75, 91	0
1	F	367/396 (92%)	0.73	48 (13%) 5 4	60, 79, 96, 108	0
1	G	367/396 (92%)	0.57	28 (7%) 17 17	46, 77, 105, 126	0
1	H	368/396 (92%)	0.74	39 (10%) 8 8	53, 85, 108, 127	0
All	All	2946/3168 (92%)	0.20	140 (4%) 34 36	26, 60, 97, 127	0

The worst 5 of 140 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	337	HIS	5.7
1	G	376	SER	5.3
1	F	375	PHE	5.0
1	F	374	TYR	4.8
1	F	123	ILE	4.7

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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(Å <sup>2</sup> )	Q<0.9
2	T5K	H	500[A]	50/50	0.75	0.34	3.10	96,104,110,112	50
2	T5K	H	500[B]	16/50	0.75	0.34	2.92	96,99,102,103	16
2	T5K	F	500[B]	16/50	0.63	0.29	2.82	110,115,118,120	16
2	T5K	G	500[B]	16/50	0.75	0.30	2.72	102,106,111,112	16
2	T5K	G	500[A]	50/50	0.75	0.30	2.45	95,104,110,112	50
2	T5K	F	500[A]	50/50	0.63	0.29	2.45	97,109,117,124	50
2	T5K	E	500[B]	16/50	0.82	0.23	2.06	100,103,108,111	16
2	T5K	C	500[B]	16/50	0.91	0.20	2.00	34,42,49,50	16
2	T5K	E	500[A]	50/50	0.82	0.23	1.74	100,111,118,120	0
2	T5K	C	500[A]	50/50	0.91	0.20	1.57	28,52,65,69	50
2	T5K	D	500[B]	16/50	0.93	0.16	0.60	38,41,47,50	16
2	T5K	B	500[B]	16/50	0.94	0.14	0.50	34,43,49,51	16
2	T5K	D	500[A]	50/50	0.93	0.16	0.37	37,49,64,65	50
2	T5K	A	500[A]	50/50	0.95	0.14	0.07	27,44,52,54	50
2	T5K	B	500[A]	50/50	0.94	0.14	-0.02	33,50,60,67	50
2	T5K	A	500[B]	16/50	0.95	0.14	-0.14	32,39,47,49	16

## 6.5 Other polymers ⓘ

There are no such residues in this entry.