



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 07:52 AM GMT

PDB ID : 3TXV
Title : Crystal structure of a probable tagatose 6 phosphate kinase from Sinorhizobium meliloti 1021
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Deposited on : 2011-09-23
Resolution : 2.80 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

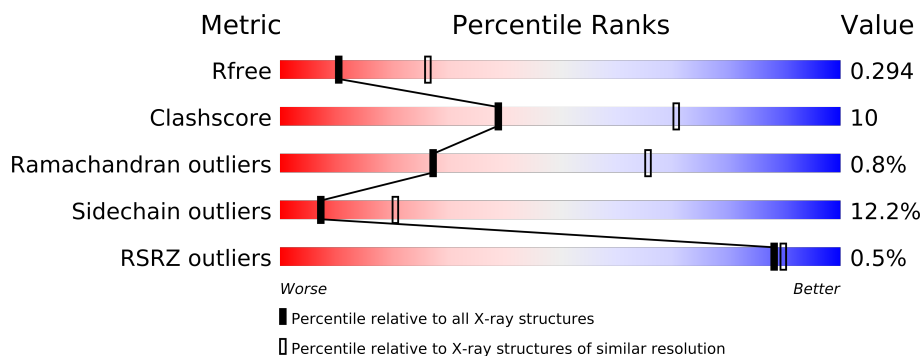
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance


The reported resolution of this entry is 2.80 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}	66092	1799 (2.80-2.80)
Clashscore	79885	2295 (2.80-2.80)
Ramachandran outliers	78287	2252 (2.80-2.80)
Sidechain outliers	78261	2254 (2.80-2.80)
RSRZ outliers	66119	1802 (2.80-2.80)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	450	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2878 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Probable tagatose 6-phosphate kinase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	387	2847	1811	486	538	4	8	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	EXPRESSION TAG	UNP Q92UY3
A	2	VAL	-	EXPRESSION TAG	UNP Q92UY3
A	429	ALA	-	EXPRESSION TAG	UNP Q92UY3
A	430	GLU	-	EXPRESSION TAG	UNP Q92UY3
A	431	ASN	-	EXPRESSION TAG	UNP Q92UY3
A	432	LEU	-	EXPRESSION TAG	UNP Q92UY3
A	433	TYR	-	EXPRESSION TAG	UNP Q92UY3
A	434	PHE	-	EXPRESSION TAG	UNP Q92UY3
A	435	GLN	-	EXPRESSION TAG	UNP Q92UY3
A	436	SER	-	EXPRESSION TAG	UNP Q92UY3
A	437	HIS	-	EXPRESSION TAG	UNP Q92UY3
A	438	HIS	-	EXPRESSION TAG	UNP Q92UY3
A	439	HIS	-	EXPRESSION TAG	UNP Q92UY3
A	440	HIS	-	EXPRESSION TAG	UNP Q92UY3
A	441	HIS	-	EXPRESSION TAG	UNP Q92UY3
A	442	HIS	-	EXPRESSION TAG	UNP Q92UY3
A	443	TRP	-	EXPRESSION TAG	UNP Q92UY3
A	444	SER	-	EXPRESSION TAG	UNP Q92UY3
A	445	HIS	-	EXPRESSION TAG	UNP Q92UY3
A	446	PRO	-	EXPRESSION TAG	UNP Q92UY3
A	447	GLN	-	EXPRESSION TAG	UNP Q92UY3
A	448	PHE	-	EXPRESSION TAG	UNP Q92UY3
A	449	GLU	-	EXPRESSION TAG	UNP Q92UY3
A	450	LYS	-	EXPRESSION TAG	UNP Q92UY3

- Molecule 2 is water.

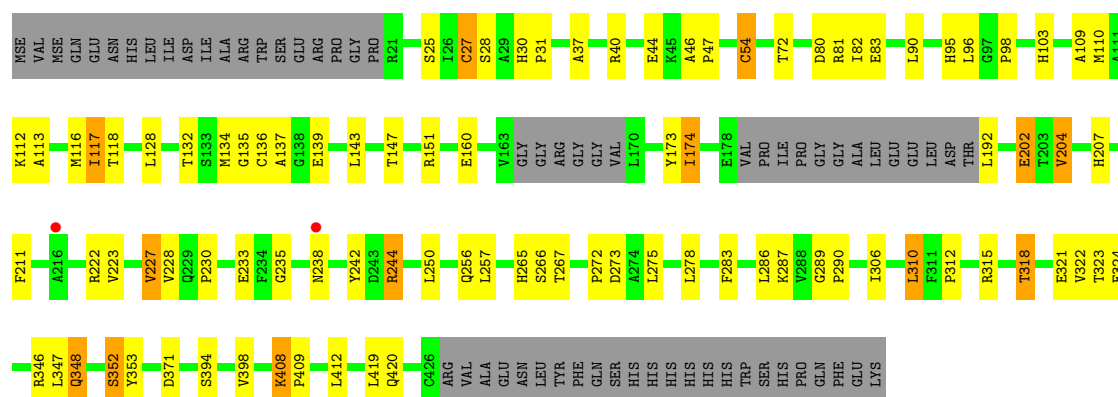
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	31	Total 31	O 31	0	0

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: Probable tagatose 6-phosphate kinase

Chain A:



4 Data and refinement statistics

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, α , β , γ	140.00Å 140.00Å 97.36Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.68 – 2.80 48.68 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.2 (48.68-2.80) 99.1 (48.68-2.80)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.43 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.240 , 0.293 0.245 , 0.294	Depositor DCC
R_{free} test set	716 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	54.7	Xtriage
Anisotropy	0.107	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 20.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 14238 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	2878	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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	0.88	3/2903 (0.1%)	0.82	1/3946 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	233	GLU	CG-CD	5.64	1.60	1.51
1	A	54	CYS	CB-SG	5.57	1.91	1.82
1	A	27	CYS	CB-SG	-5.49	1.72	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	44	GLU	N-CA-C	5.30	125.31	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2847	0	2716	54	0
2	A	31	0	0	3	0
All	All	2878	0	2716	54	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including

hydrogens) of the entry. The overall clashscore for this entry is 10.

All (54) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:318:THR:HG22	1:A:321:GLU:H	1.12	1.11
1:A:174:ILE:HD11	1:A:227:VAL:HG22	1.43	1.00
1:A:46:ALA:HB1	1:A:47:PRO:CD	1.94	0.97
1:A:46:ALA:HB1	1:A:47:PRO:HD2	1.44	0.96
1:A:202:GLU:HG2	2:A:474:HOH:O	1.69	0.90
1:A:204:VAL:HG11	1:A:257:LEU:HD21	1.52	0.90
1:A:318:THR:HG22	1:A:321:GLU:N	1.91	0.84
1:A:116:MSE:HG3	1:A:117:ILE:N	1.97	0.80
1:A:136:CYS:O	1:A:139:GLU:HG3	1.82	0.78
1:A:348:GLN:HG3	1:A:352:SER:HB2	1.71	0.72
1:A:40:ARG:NH2	1:A:420:GLN:HG3	2.05	0.71
1:A:394:SER:O	1:A:398:VAL:HG23	1.93	0.68
1:A:204:VAL:HG11	1:A:257:LEU:CD2	2.25	0.64
1:A:116:MSE:HG3	1:A:117:ILE:H	1.64	0.60
1:A:204:VAL:CG1	1:A:257:LEU:HD21	2.29	0.60
1:A:113:ALA:O	1:A:116:MSE:HG3	2.02	0.59
1:A:137:ALA:HB2	2:A:459:HOH:O	2.03	0.58
1:A:37:ALA:HA	1:A:419:LEU:CD1	2.34	0.57
1:A:134:MSE:SE	1:A:134:MSE:H	2.38	0.56
1:A:135:GLY:HA2	1:A:143:LEU:HD11	1.88	0.55
1:A:230:PRO:HB3	1:A:283:PHE:CE1	2.42	0.55
1:A:207:HIS:O	1:A:211:PHE:HD1	1.91	0.54
1:A:173:TYR:HB2	1:A:223:VAL:HG22	1.90	0.54
1:A:265:HIS:NE2	1:A:287:LYS:HD2	2.23	0.54
1:A:348:GLN:HG3	1:A:352:SER:CB	2.36	0.53
1:A:408:LYS:HB3	1:A:409:PRO:HD3	1.89	0.53
1:A:290:PRO:HD3	2:A:468:HOH:O	2.10	0.50
1:A:25:SER:HB3	1:A:287:LYS:HA	1.93	0.50
1:A:116:MSE:CG	1:A:117:ILE:N	2.73	0.50
1:A:147:THR:O	1:A:151:ARG:HG3	2.12	0.50
1:A:324:GLU:OE1	1:A:346:ARG:HG3	2.12	0.49
1:A:174:ILE:HD11	1:A:227:VAL:CG2	2.29	0.49
1:A:265:HIS:CD2	1:A:287:LYS:HD2	2.47	0.49
1:A:37:ALA:HA	1:A:419:LEU:HD11	1.94	0.48
1:A:46:ALA:CB	1:A:47:PRO:CD	2.74	0.48
1:A:109:ALA:CB	1:A:136:CYS:SG	3.03	0.47
1:A:135:GLY:HA2	1:A:143:LEU:CD1	2.45	0.47
1:A:244:ARG:HH11	1:A:244:ARG:CG	2.27	0.47
1:A:80:ASP:O	1:A:82:ILE:N	2.48	0.46
1:A:318:THR:O	1:A:322:VAL:HG23	2.15	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:228:VAL:O	1:A:230:PRO:HD3	2.16	0.46
1:A:98:PRO:HG3	1:A:110:MSE:SE	2.67	0.45
1:A:103:HIS:H	1:A:103:HIS:CD2	2.33	0.45
1:A:346:ARG:O	1:A:347:LEU:C	2.55	0.45
1:A:160:GLU:CD	1:A:222:ARG:HH21	2.21	0.43
1:A:160:GLU:OE1	1:A:222:ARG:NH2	2.52	0.43
1:A:267:THR:HG21	1:A:286:LEU:CD2	2.48	0.42
1:A:306:ILE:HG23	1:A:310:LEU:HD22	2.01	0.42
1:A:346:ARG:HB3	1:A:346:ARG:HH11	1.84	0.42
1:A:242:TYR:CD2	1:A:278:LEU:HG	2.56	0.41
1:A:54:CYS:HA	1:A:116:MSE:HE1	2.03	0.41
1:A:235:GLY:O	1:A:353:TYR:HB2	2.21	0.40
1:A:30:HIS:HA	1:A:31:PRO:HD2	1.80	0.40
1:A:54:CYS:HB3	1:A:95:HIS:O	2.22	0.40

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	381/450 (85%)	362 (95%)	16 (4%)	3 (1%)	27 65

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	81	ARG
1	A	289	GLY
1	A	272	PRO

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	270/332 (81%)	237 (88%)	33 (12%)	7 20

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	CYS
1	A	28	SER
1	A	72	THR
1	A	83	GLU
1	A	90	LEU
1	A	96	LEU
1	A	112	LYS
1	A	117	ILE
1	A	118	THR
1	A	128	LEU
1	A	132	THR
1	A	174	ILE
1	A	192	LEU
1	A	202	GLU
1	A	204	VAL
1	A	227	VAL
1	A	238	ASN
1	A	244	ARG
1	A	250	LEU
1	A	256	GLN
1	A	266	SER
1	A	273	ASP
1	A	275	LEU
1	A	310	LEU
1	A	312	PRO
1	A	315	ARG
1	A	318	THR
1	A	323	THR
1	A	348	GLN
1	A	352	SER
1	A	371	ASP
1	A	408	LYS
1	A	412	LEU

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

Mol	Chain	Res	Type
1	A	56	GLN
1	A	103	HIS
1	A	238	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 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	387/450 (86%)	-0.30	2 (0%) 88 90	24, 45, 62, 73	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	216	ALA	2.3
1	A	238	ASN	2.1

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 ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.