



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 11:32 PM GMT

PDB ID : 1R2T
Title : CRYSTAL STRUCTURE OF RABBIT MUSCLE TRIOSEPHOSPHATE ISOMERASE
Authors : Aparicio, R.; Ferreira, S.T.; Polikarpov, I.
Deposited on : 2003-09-29
Resolution : 2.25 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>

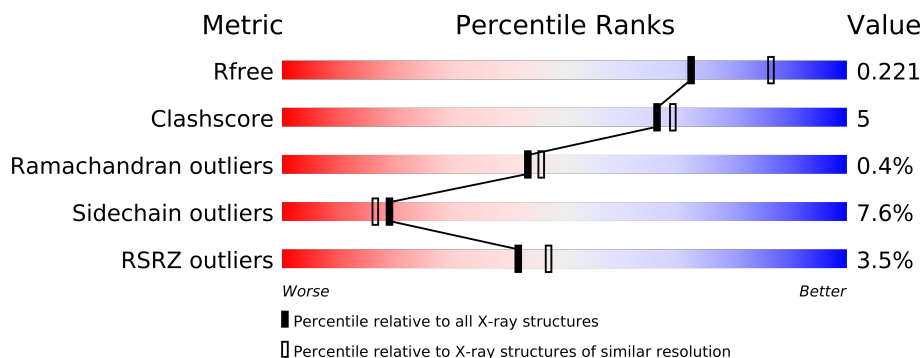
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.25 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	1108 (2.28-2.24)
Clashscore	79885	1326 (2.28-2.24)
Ramachandran outliers	78287	1291 (2.28-2.24)
Sidechain outliers	78261	1291 (2.28-2.24)
RSRZ outliers	66119	1110 (2.28-2.24)

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	248	
1	B	248	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4090 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 Triosephosphate isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	246	Total	C	N	O	S	8	4	0
			1874	1183	324	360	7			
1	B	247	Total	C	N	O	S	14	3	0
			1881	1192	324	358	7			

- Molecule 2 is water.

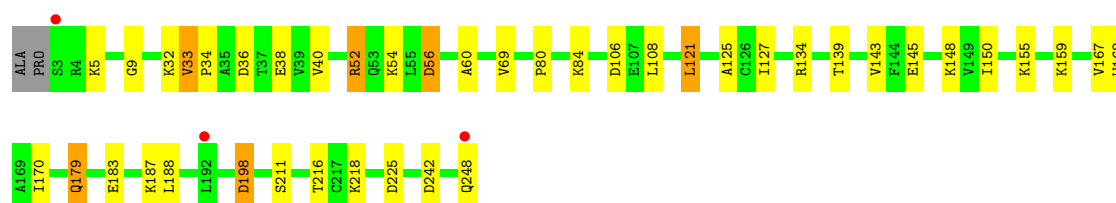
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	166	Total	O	0	0
			166	166		
2	B	169	Total	O	0	0
			169	169		

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.

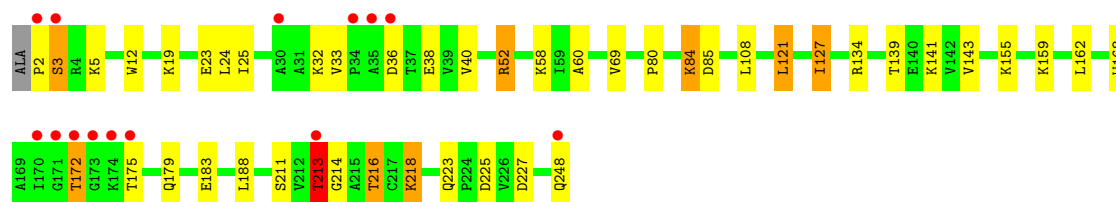
- Molecule 1: Triosephosphate isomerase

Chain A: 



- Molecule 1: Triosephosphate isomerase

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.16Å 72.03Å 93.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.54 – 2.25 15.19 – 2.25	Depositor EDS
% Data completeness (in resolution range)	97.5 (15.54-2.25) 97.5 (15.19-2.25)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 2.25Å)	Xtriage
Refinement program	REFMAC 5.1.19	Depositor
R, R_{free}	0.182 , 0.220 0.179 , 0.221	Depositor DCC
R_{free} test set	1032 reflections (5.22%)	DCC
Wilson B-factor (Å ²)	30.9	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 40.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 20816 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4090	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.11% 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	0.99	4/1928 (0.2%)	0.84	13/2609 (0.5%)
1	B	0.70	3/1929 (0.2%)	0.89	10/2611 (0.4%)
All	All	0.86	7/3857 (0.2%)	0.87	23/5220 (0.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	179	GLN	CG-CD	-24.86	0.93	1.51
1	A	145	GLU	CD-OE1	-22.32	1.01	1.25
1	B	32	LYS	CB-CG	-15.13	1.11	1.52
1	A	145	GLU	CD-OE2	14.65	1.41	1.25
1	B	214	GLY	C-N	-10.20	1.10	1.34
1	B	141	LYS	CD-CE	-8.44	1.30	1.51
1	A	187	LYS	CD-CE	5.92	1.66	1.51

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	32	LYS	CA-CB-CG	14.58	145.47	113.40
1	A	145	GLU	CG-CD-OE2	-10.15	97.99	118.30
1	B	32	LYS	CB-CG-CD	9.33	135.85	111.60
1	A	145	GLU	OE1-CD-OE2	8.04	132.95	123.30
1	A	179	GLN	CB-CG-CD	7.51	131.12	111.60
1	A	145	GLU	CB-CG-CD	7.03	133.19	114.20
1	B	141	LYS	CD-CE-NZ	-6.91	95.81	111.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	56[A]	ASP	CB-CG-OD2	6.31	123.98	118.30
1	A	56[B]	ASP	CB-CG-OD2	6.31	123.98	118.30
1	B	213	THR	CA-C-N	-6.23	103.74	116.20
1	A	106	ASP	CB-CG-OD2	6.13	123.82	118.30
1	B	227	ASP	CB-CG-OD2	5.87	123.58	118.30
1	B	216	THR	OG1-CB-CG2	-5.79	96.68	110.00
1	A	198	ASP	CB-CG-OD2	5.66	123.39	118.30
1	B	36	ASP	CB-CG-OD2	5.61	123.35	118.30
1	B	225	ASP	CB-CG-OD2	5.44	123.19	118.30
1	A	54	LYS	CD-CE-NZ	5.36	124.04	111.70
1	A	36	ASP	CB-CG-OD2	5.34	123.11	118.30
1	B	58	LYS	CA-CB-CG	5.31	125.09	113.40
1	A	225	ASP	CB-CG-OD2	5.14	122.92	118.30
1	A	242	ASP	CB-CG-OD2	5.11	122.90	118.30
1	B	85	ASP	CB-CG-OD2	5.10	122.89	118.30
1	A	216	THR	OG1-CB-CG2	-5.09	98.29	110.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	213	THR	Mainchain

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	1874	0	1886	16	0
1	B	1881	0	1897	22	0
2	A	166	0	0	4	1
2	B	169	0	0	4	1
All	All	4090	0	3783	38	1

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 5.

All (38) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:218:LYS:NZ	1:B:248:GLN:O	1.88	1.06
1:A:56[B]:ASP:OD1	2:A:313:HOH:O	1.77	1.01
1:A:52:ARG:O	1:A:52:ARG:HD3	1.74	0.87
1:B:52:ARG:HD3	1:B:52:ARG:O	1.79	0.82
1:A:56[B]:ASP:CG	2:A:313:HOH:O	2.18	0.79
1:B:2:PRO:HB3	2:B:417:HOH:O	1.84	0.78
1:B:213:THR:OG1	1:B:216:THR:HG22	1.86	0.75
1:B:143:VAL:HG13	1:B:188:LEU:HD21	1.68	0.74
1:A:143:VAL:HG13	1:A:188:LEU:HD21	1.76	0.67
1:A:56[B]:ASP:OD2	2:A:313:HOH:O	2.14	0.65
1:B:2:PRO:HA	1:B:3:SER:O	2.01	0.60
1:B:223:GLN:O	2:B:396:HOH:O	2.17	0.59
1:A:148:LYS:NZ	2:A:371:HOH:O	2.22	0.59
1:A:167:VAL:HA	1:A:170:ILE:HD12	1.86	0.57
1:A:134:ARG:HD3	1:A:168:TRP:CD2	2.39	0.57
1:A:52:ARG:C	1:A:52:ARG:HD3	2.24	0.57
1:B:40:VAL:HG22	1:B:60:ALA:HB3	1.87	0.56
1:B:127:ILE:HD12	1:B:162[B]:LEU:HD12	1.86	0.56
1:B:134:ARG:HD3	1:B:168:TRP:CD2	2.41	0.56
1:B:12:TRP:CZ2	1:B:24[B]:LEU:HD21	2.43	0.54
1:A:80:PRO:HB3	1:A:121:LEU:HD22	1.91	0.53
1:B:80:PRO:HB3	1:B:121:LEU:HD22	1.91	0.52
1:B:84:LYS:HG2	1:B:121:LEU:HD13	1.93	0.51
1:B:52:ARG:HD3	1:B:52:ARG:C	2.24	0.50
1:B:175:THR:HG23	2:B:315:HOH:O	2.11	0.50
1:A:40:VAL:HG22	1:A:60:ALA:HB3	1.96	0.48
1:A:139:THR:O	1:A:143:VAL:HB	2.17	0.45
1:B:24[B]:LEU:HD23	1:B:25:ILE:N	2.32	0.43
1:A:5:LYS:HE2	1:A:38:GLU:HB2	1.99	0.43
1:B:139:THR:O	1:B:143:VAL:HB	2.19	0.42
1:B:5:LYS:HE2	1:B:38:GLU:HB2	2.01	0.42
1:A:9:GLY:HA2	1:A:40:VAL:O	2.20	0.42
1:A:33:VAL:HA	1:A:34:PRO:HD3	1.96	0.41
1:B:179:GLN:NE2	1:B:179:GLN:H	2.17	0.41
1:B:19:LYS:HE2	2:B:385:HOH:O	2.19	0.41
1:A:125:ALA:HB1	1:A:150:ILE:HD13	2.02	0.41
1:B:127:ILE:HD12	1:B:162[B]:LEU:CD1	2.51	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:323:HOH:O	2:B:341:HOH:O[2_564]	2.18	0.02

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	248/248 (100%)	242 (98%)	6 (2%)	0	100	100
1	B	248/248 (100%)	237 (96%)	9 (4%)	2 (1%)	27	24
All	All	496/496 (100%)	479 (97%)	15 (3%)	2 (0%)	43	46

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	172	THR
1	B	3	SER

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	200/197 (102%)	182 (91%)	18 (9%)	14	11
1	B	200/197 (102%)	186 (93%)	14 (7%)	21	19
All	All	400/394 (102%)	368 (92%)	32 (8%)	19	14

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	LYS
1	A	33	VAL
1	A	52	ARG

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Mol	Chain	Res	Type
1	A	69	VAL
1	A	84	LYS
1	A	108	LEU
1	A	121	LEU
1	A	127	ILE
1	A	155[A]	LYS
1	A	155[B]	LYS
1	A	159	LYS
1	A	179	GLN
1	A	183[A]	GLU
1	A	183[B]	GLU
1	A	198	ASP
1	A	211	SER
1	A	218	LYS
1	A	248	GLN
1	B	23	GLU
1	B	33	VAL
1	B	52	ARG
1	B	69	VAL
1	B	84	LYS
1	B	108	LEU
1	B	121	LEU
1	B	127	ILE
1	B	155	LYS
1	B	159	LYS
1	B	172	THR
1	B	183	GLU
1	B	211	SER
1	B	218	LYS

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	248	GLN
1	B	179	GLN
1	B	195	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	246/248 (99%)	-0.31	3 (1%) 75 81	9, 17, 28, 38	3 (1%)
1	B	246/248 (99%)	-0.08	14 (5%) 23 27	8, 17, 30, 39	3 (1%)
All	All	492/496 (99%)	-0.20	17 (3%) 42 47	8, 17, 30, 39	6 (1%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	172	THR	6.9
1	B	2	PRO	6.1
1	B	248	GLN	5.9
1	A	248	GLN	5.6
1	B	173	GLY	5.2
1	B	171	GLY	5.0
1	B	175	THR	4.3
1	B	170	ILE	3.4
1	B	174	LYS	3.3
1	B	35	ALA	3.0
1	B	30	ALA	2.5
1	B	34	PRO	2.4
1	B	36	ASP	2.4
1	A	192	LEU	2.3
1	B	3	SER	2.3
1	A	3	SER	2.2
1	B	213	THR	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.