Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 04:08 pm BST

PDB ID	:	2X16
Title	:	Crystallographic binding studies with an engineered monomeric variant of triosephosphate isomerase
Authors	:	Salin, M.; Kapetaniou, E.G.; Vaismaa, M.; Lajunen, M.; Casteleijn, M.G.; Neubauer, P.; Salmon, L.; Wierenga, R.
Deposited on	:	2009-12-21
Resolution	:	2.13 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 following versions of software and data (see references ①) were used in the production of this report:

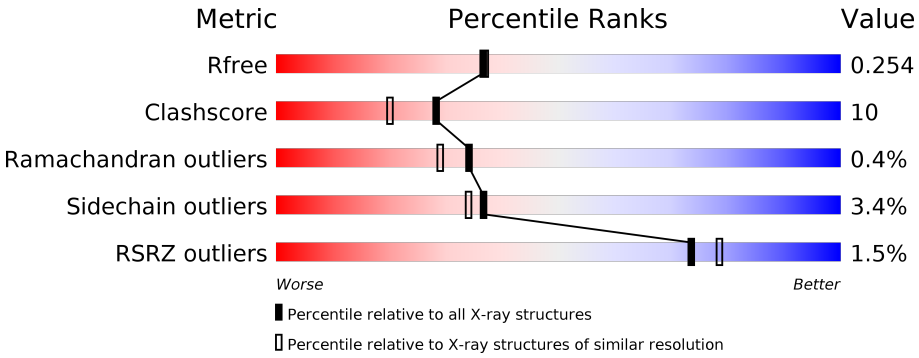
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

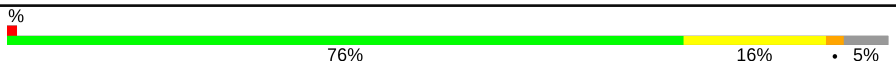
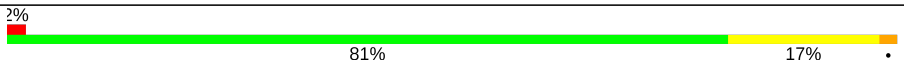
The reported resolution of this entry is 2.13 Å.

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}	130704	2523 (2.16-2.12)
Clashscore	141614	2653 (2.16-2.12)
Ramachandran outliers	138981	2618 (2.16-2.12)
Sidechain outliers	138945	2617 (2.16-2.12)
RSRZ outliers	127900	2485 (2.16-2.12)

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 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 <=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	238	
1	B	238	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3909 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 TRIOSEPHOSPHATE ISOMERASE, GLYCOSOMAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	225	Total	C	N	O	S	0	1	0
			1708	1088	300	316	4			
1	B	237	Total	C	N	O	S	0	1	0
			1801	1145	316	336	4			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	15	SER	ASN	engineered mutation	UNP P04789
A	18	PRO	GLN	engineered mutation	UNP P04789
A	19	ASP	GLN	engineered mutation	UNP P04789
A	68	GLY	ILE	engineered mutation	UNP P04789
A	69	ASN	ALA	engineered mutation	UNP P04789
A	70	ALA	LYS	engineered mutation	UNP P04789
A	71	ASP	SER	engineered mutation	UNP P04789
A	72	ALA	GLY	engineered mutation	UNP P04789
A	81	ALA	PRO	engineered mutation	UNP P04789
A	82	SER	ILE	engineered mutation	UNP P04789
A	100	TRP	ALA	engineered mutation	UNP P04789
A	233	ALA	VAL	engineered mutation	UNP P04789
B	15	SER	ASN	engineered mutation	UNP P04789
B	18	PRO	GLN	engineered mutation	UNP P04789
B	19	ASP	GLN	engineered mutation	UNP P04789
B	68	GLY	ILE	engineered mutation	UNP P04789
B	69	ASN	ALA	engineered mutation	UNP P04789
B	70	ALA	LYS	engineered mutation	UNP P04789
B	71	ASP	SER	engineered mutation	UNP P04789
B	72	ALA	GLY	engineered mutation	UNP P04789
B	81	ALA	PRO	engineered mutation	UNP P04789
B	82	SER	ILE	engineered mutation	UNP P04789
B	100	TRP	ALA	engineered mutation	UNP P04789
B	233	ALA	VAL	engineered mutation	UNP P04789

- Molecule 2 is water.

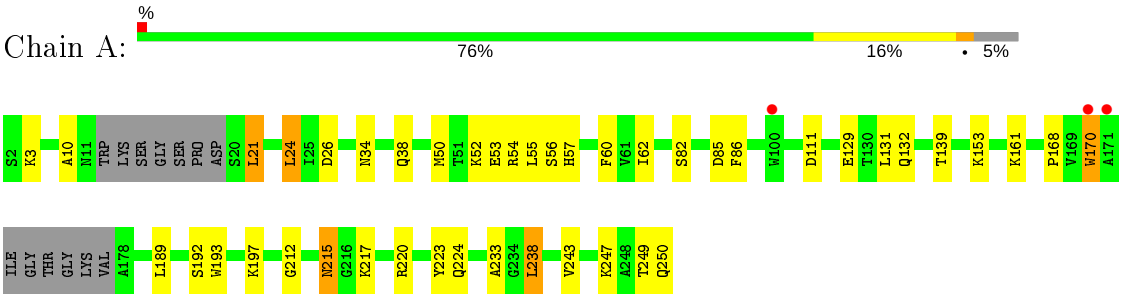
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	172	Total O 172 172	0	0
2	B	228	Total O 228 228	0	0

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 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.

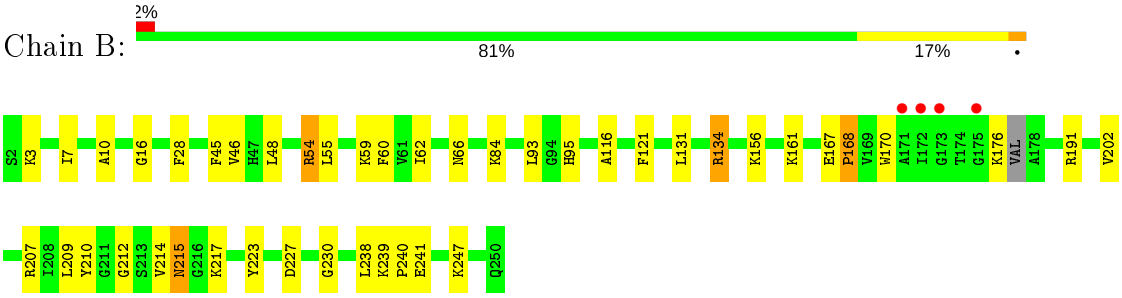
- Molecule 1: TRIOSEPHOSPHATE ISOMERASE, GLYCOSOMAL

Chain A:



- Molecule 1: TRIOSEPHOSPHATE ISOMERASE, GLYCOSOMAL

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	45.49Å 85.30Å 55.88Å 90.00° 98.60° 90.00°	Depositor
Resolution (Å)	44.98 – 2.13 44.98 – 2.13	Depositor EDS
% Data completeness (in resolution range)	98.4 (44.98-2.13) 98.4 (44.98-2.13)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.21 (at 2.14Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.180 , 0.261 0.174 , 0.254	Depositor DCC
R_{free} test set	1162 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	27.3	Xtriage
Anisotropy	0.386	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 48.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	3909	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.39% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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	0.36	0/1741	0.53	0/2363
1	B	0.39	0/1838	0.54	0/2494
All	All	0.38	0/3579	0.53	0/4857

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

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	1708	0	1718	31	0
1	B	1801	0	1811	39	0
2	A	172	0	0	4	0
2	B	228	0	0	5	0
All	All	3909	0	3529	69	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 10.

All (69) 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:54:ARG:HG3	1:B:54:ARG:HH11	1.39	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:54:ARG:CG	1:B:54:ARG:HH11	1.93	0.82
1:A:132:GLN:HG3	2:A:2105:HOH:O	1.82	0.79
1:A:111:ASP:OD1	1:A:153:LYS:HE2	1.87	0.73
1:A:220:ARG:O	1:A:224:GLN:HG2	1.91	0.69
1:A:215:ASN:HD22	1:A:217:LYS:H	1.41	0.67
1:B:54:ARG:HG3	1:B:54:ARG:NH1	2.08	0.67
1:B:215:ASN:HD22	1:B:215:ASN:C	2.00	0.65
1:A:50:MET:O	1:A:53:GLU:HG2	1.97	0.65
1:A:215:ASN:ND2	1:A:217:LYS:H	1.95	0.64
1:B:176:LYS:HG3	2:B:2176:HOH:O	2.03	0.57
1:B:54:ARG:CB	1:B:54:ARG:HH11	2.17	0.56
1:B:131:LEU:HD22	2:B:2176:HOH:O	2.06	0.55
1:A:215:ASN:HD22	1:A:215:ASN:C	2.10	0.54
1:B:3:LYS:NZ	1:B:223:TYR:O	2.41	0.54
1:A:52:LYS:HD2	1:A:86:PHE:CE2	2.43	0.53
1:A:131:LEU:HA	1:A:170:TRP:HB2	1.88	0.53
1:A:131:LEU:HA	1:A:170:TRP:CB	2.39	0.53
1:B:168:PRO:HB3	1:B:170:TRP:NE1	2.24	0.53
1:B:241:GLU:O	1:B:241:GLU:HG3	2.10	0.52
1:B:54:ARG:HH11	1:B:54:ARG:HB3	1.75	0.52
1:A:168:PRO:HD2	1:A:212:GLY:CA	2.40	0.51
1:B:116:ALA:O	1:B:121:PHE:HB2	2.10	0.51
1:A:243:VAL:HG12	1:A:247:LYS:HE2	1.94	0.50
1:B:55:LEU:HD21	1:B:60:PHE:HB3	1.93	0.50
1:A:53:GLU:HG3	1:A:54:ARG:HG2	1.94	0.49
1:A:56:SER:O	1:B:59:LYS:HE3	2.12	0.48
1:A:215:ASN:HD22	1:A:217:LYS:N	2.10	0.47
1:B:16:GLY:HA2	2:B:2020:HOH:O	2.15	0.47
1:B:28:PHE:HE2	1:B:238:LEU:HD11	1.78	0.47
1:B:212:GLY:O	1:B:214:VAL:HG23	2.15	0.47
1:A:26:ASP:OD1	1:A:54:ARG:NH2	2.43	0.46
1:B:156:LYS:HE3	1:B:202:VAL:HG23	1.97	0.46
1:B:54:ARG:NH1	1:B:54:ARG:HB3	2.31	0.46
1:A:3:LYS:NZ	1:A:223:TYR:O	2.49	0.45
1:B:84:LYS:HG2	1:B:121:PHE:CE1	2.51	0.45
1:A:57:HIS:HB3	1:A:60:PHE:CD1	2.52	0.45
1:B:210:TYR:CZ	1:B:212:GLY:HA3	2.51	0.45
1:A:10:ALA:HA	1:A:233:ALA:O	2.16	0.45
1:B:7:ILE:HB	1:B:209:LEU:HD21	1.99	0.45
1:B:191:ARG:NE	1:B:227:ASP:OD2	2.47	0.44
1:B:95:HIS:NE2	1:B:167:GLU:OE2	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:249:THR:O	1:A:250:GLN:HB2	2.18	0.44
1:A:193:TRP:CE2	1:A:197:LYS:HG3	2.53	0.43
1:A:24:LEU:HD23	1:A:24:LEU:HA	1.69	0.43
1:B:45:PHE:HA	1:B:48:LEU:HD12	2.01	0.43
1:B:7:ILE:O	1:B:230:GLY:HA3	2.18	0.43
1:B:215:ASN:HD21	1:B:217:LYS:HB2	1.84	0.43
1:A:52:LYS:NZ	2:A:2042:HOH:O	2.52	0.43
1:B:10:ALA:HB1	1:B:238:LEU:HD13	2.01	0.42
1:B:54:ARG:HA	1:B:54:ARG:HD2	1.78	0.42
1:A:21:LEU:HD21	1:A:238:LEU:HD21	2.02	0.42
1:B:134:ARG:HE	1:B:134:ARG:HB2	1.76	0.41
1:B:247:LYS:NZ	1:B:247:LYS:HB2	2.36	0.41
1:A:243:VAL:O	1:A:247:LYS:HG3	2.21	0.41
1:B:239:LYS:HB2	1:B:240:PRO:CD	2.50	0.41
1:B:215:ASN:C	1:B:215:ASN:ND2	2.71	0.41
1:B:66:ASN:HA	1:B:93:LEU:HD23	2.02	0.41
1:A:129:GLU:CD	1:A:139:THR:HG23	2.42	0.41
1:A:52:LYS:NZ	2:A:2044:HOH:O	2.54	0.41
1:B:10:ALA:CB	1:B:238:LEU:HD13	2.51	0.41
1:A:34:ASN:OD1	1:A:34:ASN:N	2.53	0.41
1:A:38:GLN:NE2	2:A:2029:HOH:O	2.50	0.41
1:B:176:LYS:CG	2:B:2176:HOH:O	2.65	0.41
1:B:46:VAL:HG13	2:B:2060:HOH:O	2.21	0.40
1:B:48:LEU:HD23	1:B:62:ILE:HD11	2.03	0.40
1:A:161:LYS:HA	1:A:161:LYS:HD2	1.94	0.40
1:A:55:LEU:HD23	1:A:62:ILE:HD11	2.04	0.40
1:B:161:LYS:HD2	1:B:161:LYS:HA	1.81	0.40

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	220/238 (92%)	212 (96%)	6 (3%)	2 (1%)	17 10
1	B	234/238 (98%)	229 (98%)	5 (2%)	0	100 100
All	All	454/476 (95%)	441 (97%)	11 (2%)	2 (0%)	34 29

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	170	TRP
1	A	238	LEU

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	175/187 (94%)	168 (96%)	7 (4%)	31 28
1	B	185/187 (99%)	180 (97%)	5 (3%)	44 43
All	All	360/374 (96%)	348 (97%)	12 (3%)	37 35

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	LEU
1	A	24	LEU
1	A	82	SER
1	A	85	ASP
1	A	189	LEU
1	A	192	SER
1	A	215	ASN
1	B	54	ARG
1	B	134	ARG
1	B	168	PRO
1	B	207	ARG
1	B	215	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	89	ASN
1	A	215	ASN
1	A	224	GLN
1	B	38	GLN
1	B	65	GLN
1	B	89	ASN
1	B	215	ASN
1	B	224	GLN
1	B	250	GLN

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

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, 95^{th} 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	225/238 (94%)	-0.16	3 (1%)	77	81	16, 29, 48, 67	0
1	B	237/238 (99%)	-0.21	4 (1%)	70	75	15, 25, 45, 67	0
All	All	462/476 (97%)	-0.18	7 (1%)	73	78	15, 26, 47, 67	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	172	ILE	4.6
1	B	175	GLY	4.3
1	B	173	GLY	3.4
1	A	100	TRP	2.5
1	A	170	TRP	2.4
1	A	171	ALA	2.3
1	B	171	ALA	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 (i)

There are no such residues in this entry.