Full wwPDB X-ray Structure Validation Report (i)

Feb 5, 2024 – 08:38 AM EST

PDB ID	:	1TPU
Title	:	S96P CHANGE IS A SECOND-SITE SUPPRESSOR FOR H95N SLUGGISH MUTANT TRIOSEPHOSPHATE ISOMERASE
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Deposited on	:	1994-11-07
Resolution	:	1.90 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

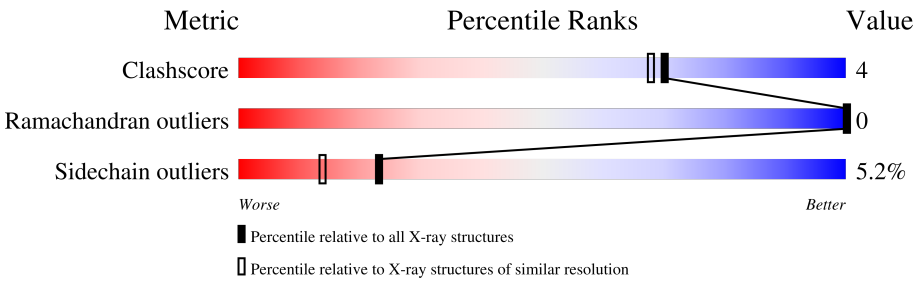
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.90 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))
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)

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 of 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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	247	85% 13% ••
1	B	247	88% 9% ••

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4014 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.

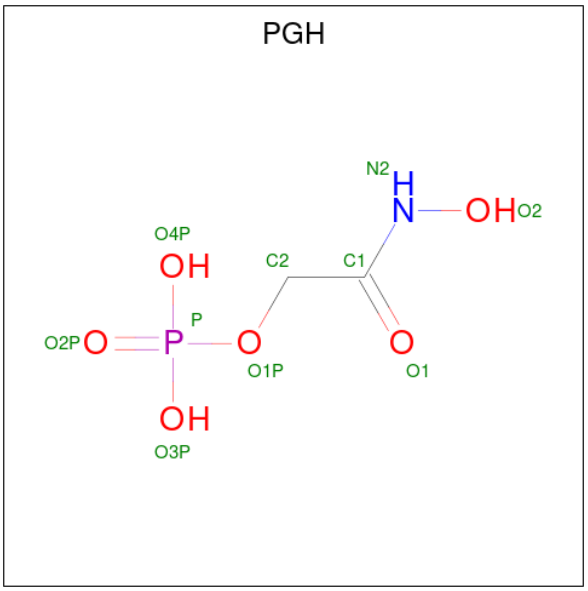
- Molecule 1 is a protein called TRIOSEPHOSPHATE ISOMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	245	1854	1174	324	350	6	0	0	0
1	B	245	1854	1174	324	350	6	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	95	ASN	HIS	engineered mutation	UNP P00940
A	194	THR	SER	conflict	UNP P00940
B	95	ASN	HIS	engineered mutation	UNP P00940
B	194	THR	SER	conflict	UNP P00940

- Molecule 2 is PHOSPHOGLYCOLOHYDROXAMIC ACID (three-letter code: PGH) (formula: $C_2H_6NO_6P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	10	2	1	6	1	0	0
			Total	C	N	O	P		
2	B	1	10	2	1	6	1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	142	142	142	0	0
			Total	O		
3	B	144	144	144	0	0

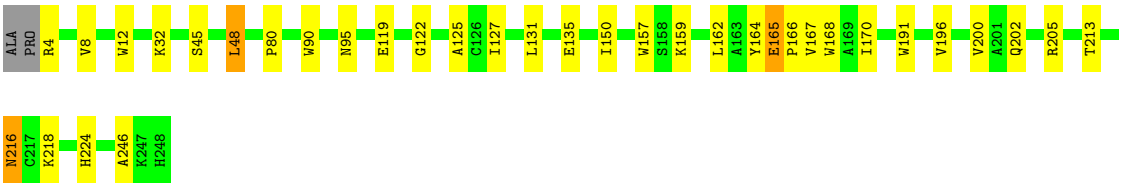
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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. 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. 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.

Note EDS was not executed.

• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain A:



• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain B:

4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	136.30Å 74.10Å 57.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 1.90	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-1.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.176 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4014	wwPDB-VP
Average B, all atoms ($Å^2$)	16.0	wwPDB-VP

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: PGH

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	0.83	0/1888	1.34	16/2548 (0.6%)
1	B	0.80	0/1888	1.34	15/2548 (0.6%)
All	All	0.82	0/3776	1.34	31/5096 (0.6%)

There are no bond length outliers.

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	157	TRP	CD1-CG-CD2	8.64	113.21	106.30
1	A	90	TRP	CD1-CG-CD2	8.57	113.16	106.30
1	B	90	TRP	CD1-CG-CD2	7.87	112.59	106.30
1	B	168	TRP	CD1-CG-CD2	7.71	112.47	106.30
1	A	157	TRP	CD1-CG-CD2	7.70	112.46	106.30
1	A	168	TRP	CD1-CG-CD2	7.70	112.46	106.30
1	A	12	TRP	CD1-CG-CD2	7.45	112.26	106.30
1	B	90	TRP	CE2-CD2-CG	-7.38	101.40	107.30
1	A	168	TRP	CE2-CD2-CG	-7.36	101.41	107.30
1	A	90	TRP	CE2-CD2-CG	-7.35	101.42	107.30
1	A	157	TRP	CE2-CD2-CG	-7.30	101.46	107.30
1	B	157	TRP	CE2-CD2-CG	-7.10	101.62	107.30
1	B	191	TRP	CD1-CG-CD2	7.08	111.97	106.30
1	B	12	TRP	CD1-CG-CD2	7.00	111.90	106.30
1	B	12	TRP	CE2-CD2-CG	-6.71	101.93	107.30
1	B	191	TRP	CE2-CD2-CG	-6.69	101.95	107.30
1	A	12	TRP	CE2-CD2-CG	-6.64	101.99	107.30
1	A	157	TRP	CG-CD2-CE3	6.53	139.77	133.90
1	B	52	ARG	NE-CZ-NH2	-6.47	117.06	120.30
1	B	168	TRP	CE2-CD2-CG	-6.38	102.20	107.30
1	A	191	TRP	CE2-CD2-CG	-6.33	102.24	107.30
1	B	52	ARG	NE-CZ-NH1	6.23	123.42	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	191	TRP	CD1-CG-CD2	6.18	111.25	106.30
1	B	98	ARG	NE-CZ-NH1	6.18	123.39	120.30
1	B	157	TRP	CG-CD1-NE1	-5.81	104.29	110.10
1	A	90	TRP	CG-CD1-NE1	-5.65	104.45	110.10
1	A	168	TRP	CB-CG-CD1	-5.36	120.03	127.00
1	A	12	TRP	CG-CD1-NE1	-5.27	104.83	110.10
1	A	157	TRP	CG-CD1-NE1	-5.20	104.90	110.10
1	B	168	TRP	CG-CD1-NE1	-5.16	104.94	110.10
1	A	168	TRP	CG-CD2-CE3	5.03	138.43	133.90

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	1854	0	1862	14	0
1	B	1854	0	1862	13	0
2	A	10	0	4	0	0
2	B	10	0	4	3	0
3	A	142	0	0	1	0
3	B	144	0	0	1	0
All	All	4014	0	3732	27	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 4.

All (27) 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:127:ILE:HD11	1:B:188:LEU:HD21	1.74	0.69
1:A:45:SER:HA	1:A:48:LEU:HD22	1.73	0.68
1:A:213:THR:H	1:A:216:ASN:HD21	1.48	0.60
1:B:25:ILE:HG21	1:B:54:LYS:HB3	1.84	0.60
1:B:165:GLU:HB2	1:B:170:ILE:HD11	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:131:LEU:O	1:A:135:GLU:HG2	2.04	0.58
1:A:213:THR:H	1:A:216:ASN:ND2	2.03	0.55
1:A:218:LYS:HG3	1:A:246:ALA:O	2.07	0.54
1:A:167:VAL:HA	1:A:170:ILE:HD12	1.89	0.53
1:B:213:THR:H	1:B:216:ASN:HD21	1.56	0.51
1:B:213:THR:H	1:B:216:ASN:ND2	2.09	0.50
1:B:232:GLY:HA3	2:B:250:PGH:H21	1.93	0.49
1:A:80:PRO:HB2	1:A:119:GLU:HG3	1.95	0.49
1:B:236:LEU:O	1:B:237:LYS:HE3	2.14	0.48
1:A:4:ARG:HD3	1:A:202:GLN:O	2.16	0.46
1:B:193:LYS:HD3	3:B:623:HOH:O	2.16	0.45
1:A:196:VAL:HG11	1:A:200:VAL:HG11	1.99	0.44
1:B:232:GLY:CA	2:B:250:PGH:H21	2.47	0.44
1:A:165:GLU:HB2	1:A:170:ILE:HD11	1.99	0.44
1:B:232:GLY:N	2:B:250:PGH:H21	2.31	0.44
1:A:125:ALA:HB1	1:A:150:ILE:HD13	2.00	0.44
1:B:216:ASN:HD22	1:B:216:ASN:C	2.21	0.44
1:A:135:GLU:HG3	3:A:736:HOH:O	2.18	0.43
1:A:122:GLY:HA2	1:A:159:LYS:HB3	2.02	0.42
1:B:84:LYS:HG3	1:B:121:LEU:HD21	2.02	0.41
1:A:164:TYR:CE2	1:A:166:PRO:HD3	2.55	0.41
1:B:148:LYS:HA	1:B:148:LYS:HE3	2.01	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	243/247 (98%)	237 (98%)	6 (2%)	0	100	100
1	B	243/247 (98%)	238 (98%)	5 (2%)	0	100	100
All	All	486/494 (98%)	475 (98%)	11 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	191/192 (100%)	181 (95%)	10 (5%)	23 14
1	B	191/192 (100%)	181 (95%)	10 (5%)	23 14
All	All	382/384 (100%)	362 (95%)	20 (5%)	23 14

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	VAL
1	A	32	LYS
1	A	48	LEU
1	A	95	ASN
1	A	127	ILE
1	A	162	LEU
1	A	165	GLU
1	A	205	ARG
1	A	216	ASN
1	A	224	HIS
1	B	40	VAL
1	B	86	ILE
1	B	95	ASN
1	B	130	LYS
1	B	141	LYS
1	B	148	LYS
1	B	165	GLU
1	B	188	LEU
1	B	216	ASN
1	B	237	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	65	ASN
1	A	100	HIS
1	A	111	GLN
1	A	115	HIS
1	A	179	GLN
1	A	216	ASN
1	A	248	HIS
1	B	100	HIS
1	B	115	HIS
1	B	179	GLN
1	B	216	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

2 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	PGH	A	250	-	9,9,9	1.13	1 (11%)	10,12,12	1.15	0
2	PGH	B	250	-	9,9,9	0.99	1 (11%)	10,12,12	1.59	2 (20%)

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	PGH	A	250	-	-	3/8/8/8	-
2	PGH	B	250	-	-	7/8/8/8	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	250	PGH	P-O4P	-2.09	1.46	1.54
2	A	250	PGH	P-O1P	-2.02	1.53	1.60

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	250	PGH	C2-C1-N2	-3.14	110.91	116.37
2	B	250	PGH	O1-C1-N2	2.17	125.94	123.27

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	250	PGH	N2-C1-C2-O1P
2	A	250	PGH	C2-C1-N2-O2
2	A	250	PGH	O1-C1-N2-O2
2	B	250	PGH	N2-C1-C2-O1P
2	B	250	PGH	C2-C1-N2-O2
2	B	250	PGH	O1-C1-N2-O2
2	B	250	PGH	C2-O1P-P-O4P
2	B	250	PGH	C2-O1P-P-O2P
2	B	250	PGH	C2-O1P-P-O3P
2	B	250	PGH	O1-C1-C2-O1P

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	250	PGH	3	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 (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.