



# wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 11:18 PM GMT

PDB ID : 2V4M  
Title : THE ISOMERASE DOMAIN OF HUMAN GLUTAMINE-FRUCTOSE-6-PHOSPHATETRANSAMINASE 1 (GFPT1) IN COMPLEX WITH FRUCTOSE 6-PHOSPHATE  
Authors : Moche, M.; Lehtio, L.; Andersson, J.; Arrowsmith, C.H.; Berglund, H.; Collins, R.; Dahlgren, L.G.; Edwards, A.M.; Flodin, S.; Flores, A.; Graslund, S.; Hammarstrom, M.; Johansson, A.; Johansson, I.; Karlberg, T.; Kotenyova, T.; Nilsson, M.E.; Nyman, T.; Persson, C.; Sagemark, J.; Svensson, S.; Schueler, H.; Thorsell, A.G.; Tresaugues, L.; Uppenberg, J.; Van Den Berg, S.; Welin, M.; Wisniewska, M.; Weigelt, J.; Nordlund, P.; Wikstrom, M.  
Deposited on : 2008-09-26  
Resolution : 2.29 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

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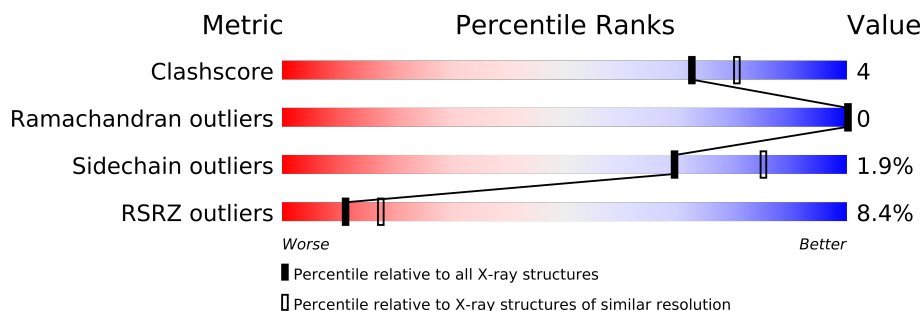
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 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 2.29 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	79885	3679 (2.30-2.30)
Ramachandran outliers	78287	3642 (2.30-2.30)
Sidechain outliers	78261	3641 (2.30-2.30)
RSRZ outliers	66119	2930 (2.30-2.30)

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. 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	376	
1	B	376	
1	C	376	
1	D	376	

## 2 Entry composition i

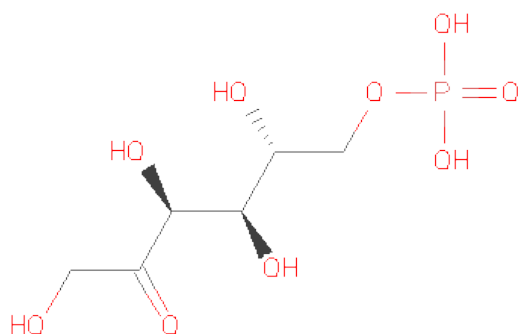
There are 4 unique types of molecules in this entry. The entry contains 11333 atoms, of which 0 are hydrogen and 0 are deuterium.

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 GLUCOSAMINE--FRUCTOSE-6-PHOSPHATEAMINO-TRANSFERASE [ISOMERIZING] 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	352	Total	C	N	O	S	0	3	0
			2775	1747	482	518	28			
1	B	351	Total	C	N	O	S	0	2	0
			2762	1739	481	516	26			
1	C	352	Total	C	N	O	S	0	4	0
			2794	1760	488	519	27			
1	D	350	Total	C	N	O	S	0	4	0
			2773	1745	483	518	27			

- Molecule 2 is FRUCTOSE -6-PHOSPHATE (three-letter code: F6R) (formula: C<sub>6</sub>H<sub>13</sub>O<sub>9</sub>P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			16	6	9	1		
2	B	1	Total	C	O	P	0	0
			16	6	9	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	C	1	Total	C	O	P	0	0
			16	6	9	1		
2	D	1	Total	C	O	P	0	0
			16	6	9	1		

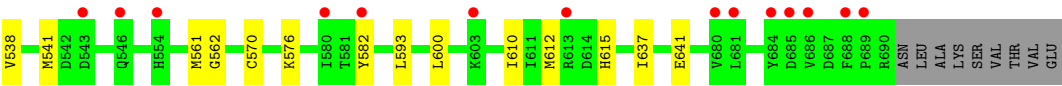
- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	1	Total	Cl	0	0
			1	1		

- Molecule 4 is water.

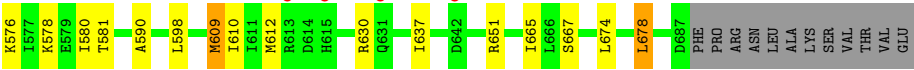
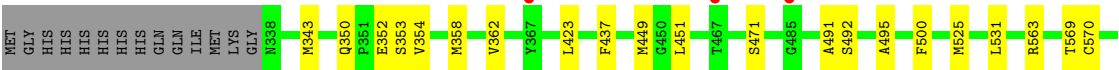
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	35	Total	O	0	0
			35	35		
4	B	14	Total	O	0	0
			14	14		
4	C	50	Total	O	0	0
			50	50		
4	D	65	Total	O	0	0
			65	65		





● Molecule 1: GLUCOSAMINE--FRUCTOSE-6-PHOSPHATEAMINOTRANSFERASE [ISOMERIZING] 1

Chain D: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	178.82Å 178.82Å 157.11Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	54.89 – 2.29 54.85 – 2.29	Depositor EDS
% Data completeness (in resolution range)	99.2 (54.89-2.29) 96.8 (54.85-2.29)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.17 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.5.0035	Depositor
R, $R_{free}$	0.167 , 0.185 0.218 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	40.7	Xtriage
Anisotropy	0.073	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 29.6	EDS
Estimated twinning fraction	0.679 for H, K, L 0.321 for -H-K, K, -L 0.000 for h,-h-k,-l	Xtriage
Reported twinning fraction	0.679 for H, K, L 0.321 for -H-K, K, -L	Depositor
L-test for twinning	$\langle  L  \rangle = 0.54$ , $\langle L^2 \rangle = 0.38$	Xtriage
Outliers	0 of 81887 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	11333	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.54% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: F6R, CL

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	0.41	0/2815	0.56	0/3794
1	B	0.37	0/2803	0.52	0/3780
1	C	0.45	0/2836	0.59	0/3824
1	D	0.47	0/2813	0.60	0/3792
All	All	0.43	0/11267	0.57	0/15190

There are no bond length outliers.

There are no bond angle outliers.

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	2775	0	2833	19	0
1	B	2762	0	2814	41	0
1	C	2794	0	2849	19	0
1	D	2773	0	2829	20	0
2	A	16	0	11	0	0
2	B	16	0	11	1	0
2	C	16	0	11	0	0
2	D	16	0	11	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	1	0	0	0	0
4	A	35	0	0	0	0
4	B	14	0	0	0	0
4	C	50	0	0	0	0
4	D	65	0	0	0	0
All	All	11333	0	11369	97	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 4.

The worst 5 of 97 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:563:ARG:HG3	1:D:590:ALA:HB3	1.40	1.01
1:B:548:LEU:HD22	1:B:653:ILE:HD11	1.63	0.81
1:D:612:MET:CE	1:D:637:ILE:HG22	2.17	0.74
1:D:491:ALA:HB1	1:D:576:LYS:HE3	1.71	0.73
1:C:508:LEU:O	1:C:521[A]:ARG:NH1	2.23	0.71

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	353/376 (94%)	342 (97%)	11 (3%)	0	100	100
1	B	351/376 (93%)	344 (98%)	7 (2%)	0	100	100
1	C	354/376 (94%)	349 (99%)	5 (1%)	0	100	100
1	D	352/376 (94%)	346 (98%)	6 (2%)	0	100	100
All	All	1410/1504 (94%)	1381 (98%)	29 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	311/330 (94%)	309 (99%)	2 (1%)	92	97
1	B	309/330 (94%)	302 (98%)	7 (2%)	63	80
1	C	313/330 (95%)	306 (98%)	7 (2%)	64	81
1	D	311/330 (94%)	304 (98%)	7 (2%)	63	80
All	All	1244/1320 (94%)	1221 (98%)	23 (2%)	69	86

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	457	ARG
1	C	525	MET
1	D	651	ARG
1	C	500	PHE
1	C	582	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	622	ASN
1	B	382	GLN

### 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

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 for Mogul analysis.

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	F6R	A	800	-	15,15,15	0.67	0	21,21,21	1.21	2 (9%)
2	F6R	B	800	-	15,15,15	0.56	0	21,21,21	0.93	1 (4%)
2	F6R	C	800	-	15,15,15	0.62	0	21,21,21	1.19	2 (9%)
2	F6R	D	800	-	15,15,15	0.77	0	21,21,21	1.06	1 (4%)

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	F6R	A	800	-	-	0/20/20/20	0/0/0/0
2	F6R	B	800	-	-	0/20/20/20	0/0/0/0
2	F6R	C	800	-	-	0/20/20/20	0/0/0/0
2	F6R	D	800	-	-	0/20/20/20	0/0/0/0

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	800	F6R	C4-C3-C2	2.89	114.50	110.77
2	A	800	F6R	O3-C3-C2	-2.79	106.61	111.16
2	C	800	F6R	O3-C3-C2	-2.26	107.47	111.16
2	C	800	F6R	O2P-P-O3P	2.12	117.37	110.44
2	D	800	F6R	C1-C2-C3	2.07	120.18	116.26

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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<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	352/376 (93%)	0.59	38 (10%) 6 10	28, 44, 69, 76	0
1	B	351/376 (93%)	0.94	56 (15%) 3 4	34, 59, 79, 85	0
1	C	352/376 (93%)	0.33	18 (5%) 27 37	22, 37, 58, 66	0
1	D	350/376 (93%)	0.16	7 (2%) 62 72	20, 33, 51, 55	0
All	All	1405/1504 (93%)	0.50	119 (8%) 11 17	20, 41, 73, 85	0

The worst 5 of 119 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	490	VAL	8.9
1	A	685	ASP	5.9
1	C	688	PHE	5.9
1	A	613	ARG	5.5
1	A	628	VAL	5.3

### 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	F6R	C	800	16/16	0.14	-0.06	29,31,33,34	0
2	F6R	B	800	16/16	0.17	-0.17	44,48,51,52	0
2	F6R	D	800	16/16	0.13	-0.23	28,30,32,33	0
2	F6R	A	800	16/16	0.13	-0.32	38,40,41,41	0
3	CL	C	1691	1/1	0.07	-2.07	45,45,45,45	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.