

# Full wwPDB X-ray Structure Validation Report (i)

#### Mar 5, 2024 - 09:05 AM EST

PDB ID	:	2RI0
Title	:	Crystal Structure of glucosamine 6-phosphate deaminase (NagB) from S. mu-
		tans
Authors	:	Li, D.; Liu, C.; Li, L.F.; Su, X.D.
Deposited on	:	2007-10-10
Resolution	:	1.60  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 (1)) were used in the production of this report:

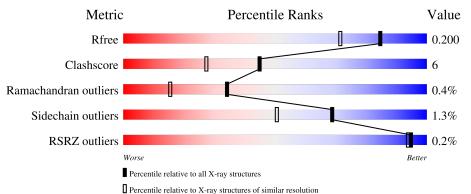
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

The reported resolution of this entry is 1.60 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	3398 (1.60-1.60)
Clashscore	141614	3665(1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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% 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	А	234	90%	9%		
1	В	234	91%	7% •		



# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4338 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.

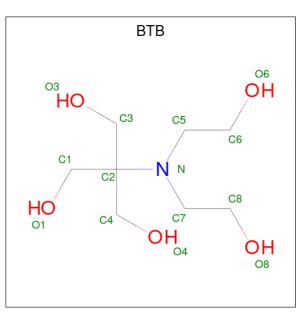
• Molecule 1 is a protein called Glucosamine-6-phosphate deaminase.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Δ	234	Total	С	Ν	0	S	0	0	0
	A	204	1809	1165	287	348	9	0	0	0
1	Р	234	Total	С	Ν	0	S	0	0	0
	D	234	1836	1177	295	355	9	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	0	SER	-	expression tag	UNP Q8DV70
В	0	SER	-	expression tag	UNP Q8DV70

• Molecule 2 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPAN E-1,3-DIOL (three-letter code: BTB) (formula: C<sub>8</sub>H<sub>19</sub>NO<sub>5</sub>).



Ι	Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
	2	А	1	Total 14	C 8	N 1	O 5	0	0

Continued on next page...



Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	В	1	Total 14	C 8	N 1	O 5	0	0

• Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	2	Total Na 2 2	0	0

• Molecule 4 is water.

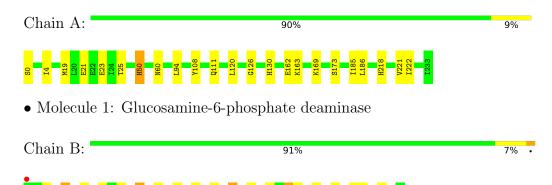
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	311	Total O 311 311	0	0
4	В	352	Total O 352 352	0	0



# 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 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: Glucosamine-6-phosphate deaminase





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	54.00Å 82.17Å 134.91Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	45.13 - 1.60	Depositor
Resolution (A)	45.13 - 1.60	EDS
% Data completeness	96.7 (45.13-1.60)	Depositor
(in resolution range)	96.7 (45.13 - 1.60)	EDS
R <sub>merge</sub>	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.15 (at 1.60 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
D D.	0.177 , $0.199$	Depositor
$R, R_{free}$	0.176 , $0.200$	DCC
$R_{free}$ test set	3865 reflections $(5.04%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	17.2	Xtriage
Anisotropy	0.154	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.36,46.1	EDS
L-test for twinning <sup>2</sup>	$ < 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	4338	wwPDB-VP
Average B, all atoms $(Å^2)$	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.74% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: NA, BTB

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	Mol Chain		lengths	Bond angles		
	Unain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.53	0/1866	0.64	0/2521	
1	В	0.61	0/1892	0.71	1/2551~(0.0%)	
All	All	0.57	0/3758	0.68	1/5072~(0.0%)	

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	В	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
1	В	123	LEU	CA-CB-CG	5.67	128.33	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	В	161	PHE	Peptide

## 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



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	1809	0	1834	19	0
1	В	1836	0	1881	23	0
2	А	14	0	19	4	0
2	В	14	0	19	4	0
3	В	2	0	0	0	0
4	А	311	0	0	5	0
4	В	352	0	0	7	0
All	All	4338	0	3753	48	0

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

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 6.

All (48) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:4:ILE:HD11	1:A:19:MET:HE1	1.62	0.79
1:B:159[B]:ARG:HD2	4:B:722:HOH:O	1.84	0.76
1:B:150:THR:HG22	1:B:153:THR:H	1.53	0.74
1:A:169:LYS:HE3	4:A:529:HOH:O	1.87	0.74
1:A:4:ILE:HD11	1:A:19:MET:CE	2.21	0.70
2:B:236:BTB:C3	2:B:236:BTB:H81	2.23	0.69
1:B:159[B]:ARG:CD	4:B:722:HOH:O	2.40	0.68
1:B:162:GLU:HB3	4:B:745:HOH:O	1.93	0.68
1:A:4:ILE:CD1	1:A:19:MET:CE	2.72	0.67
1:B:21:GLU:OE2	1:B:50:HIS:HE1	1.78	0.67
1:B:161:PHE:HA	1:B:162:GLU:HG3	1.78	0.66
1:A:23:GLU:OE2	2:A:234:BTB:H11	1.97	0.65
1:B:162:GLU:CB	4:B:745:HOH:O	2.44	0.64
1:A:21:GLU:OE2	1:A:50[A]:HIS:HE1	1.81	0.64
1:B:107:GLU:HG3	1:B:111[B]:GLN:HE21	1.64	0.62
1:A:120:LEU:HD11	1:A:186[B]:LEU:HG	1.81	0.62
1:A:4:ILE:CD1	1:A:19:MET:HE1	2.28	0.60
1:A:173[A]:SER:OG	4:A:244:HOH:O	2.17	0.60
2:A:234:BTB:O8	2:A:234:BTB:H41	2.02	0.59
1:A:25[A]:THR:HG21	4:A:540:HOH:O	2.03	0.59
1:B:8:ASN:ND2	1:B:11[A]:GLU:H	2.00	0.58
1:B:8:ASN:ND2	1:B:11[B]:GLU:H	2.01	0.58
1:A:4:ILE:CD1	1:A:19:MET:HE3	2.34	0.58
2:B:236:BTB:H81	2:B:236:BTB:H32	1.86	0.57
1:B:150:THR:HG21	4:B:689:HOH:O	2.05	0.56

Continued on next page...



Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:189:ALA:HB3	1:B:225:VAL:HG12	1.86	0.56
2:B:236:BTB:H81	2:B:236:BTB:H31	1.89	0.54
1:A:0:SER:N	4:A:466:HOH:O	2.42	0.51
1:A:218:HIS:HB3	1:A:221:VAL:HG23	1.92	0.51
1:B:8:ASN:C	1:B:8:ASN:HD22	2.14	0.50
2:A:234:BTB:O6	2:A:234:BTB:H82	2.13	0.48
2:A:234:BTB:H41	2:A:234:BTB:C8	2.44	0.47
1:B:162:GLU:HB2	4:B:745:HOH:O	2.11	0.47
1:B:159[B]:ARG:HE	1:B:159[B]:ARG:HB2	1.49	0.46
1:B:150:THR:CG2	1:B:153:THR:H	2.26	0.45
1:A:185:ILE:HB	1:A:221:VAL:HG22	1.98	0.45
1:B:19:MET:HE1	1:B:222:ILE:HG13	1.98	0.44
1:B:161:PHE:HA	1:B:162:GLU:CG	2.48	0.43
2:B:236:BTB:H12	2:B:236:BTB:H52	1.88	0.42
1:A:126:GLY:HA3	1:A:130:HIS:CE1	2.54	0.42
1:B:218:HIS:HB3	1:B:221:VAL:HG23	2.02	0.42
1:A:108:TYR:CE1	1:B:159[B]:ARG:HD3	2.55	0.41
1:B:8:ASN:HD22	1:B:11[A]:GLU:H	1.68	0.41
1:A:186[B]:LEU:HD23	1:A:222:ILE:HB	2.03	0.41
1:B:8:ASN:HD22	1:B:11[B]:GLU:H	1.68	0.41
1:A:60:ASN:HB2	1:A:94:LEU:HG	2.02	0.40
1:A:111[B]:GLN:HB2	4:A:377:HOH:O	2.21	0.40
1:B:80:LYS:HD3	4:B:646:HOH:O	2.21	0.40

Continued from previous page...

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	Percentil	$\mathbf{es}$
1	А	240/234~(103%)	234~(98%)	4(2%)	2(1%)	19 6	
1	В	240/234~(103%)	235~(98%)	5(2%)	0	100 100	0

Continued on next page...



Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	480/468~(103%)	469 (98%)	9(2%)	2~(0%)	34 15

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	163	LYS
1	А	162	GLU

#### 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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	193/192~(100%)	191~(99%)	2(1%)	76 61
1	В	200/192~(104%)	196 (98%)	4 (2%)	55 31
All	All	393/384~(102%)	387~(98%)	6 (2%)	69 44

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	50[A]	HIS
1	А	50[B]	HIS
1	В	2	LYS
1	В	8	ASN
1	В	50	HIS
1	В	150	THR

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

Mol	Chain	Res	Type
1	В	8	ASN
1	В	50	HIS



#### 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)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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		
			nes	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	BTB	В	236	3	13,13,13	0.47	0	7,16,16	0.79	0
2	BTB	А	234	-	13,13,13	0.40	0	7,16,16	0.50	0

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	BTB	В	236	3	-	3/21/21/21	-
2	BTB	А	234	-	-	8/21/21/21	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.



Mol	Chain	Res	Type	Atoms
2	А	234	BTB	O1-C1-C2-C3
2	А	234	BTB	O1-C1-C2-C4
2	А	234	BTB	O1-C1-C2-N
2	А	234	BTB	C1-C2-C4-O4
2	А	234	BTB	C3-C2-C4-O4
2	А	234	BTB	N-C2-C4-O4
2	В	236	BTB	C3-C2-N-C7
2	В	236	BTB	C4-C2-N-C7
2	А	234	BTB	N-C7-C8-O8
2	В	236	BTB	C8-C7-N-C2
2	А	234	BTB	C3-C2-N-C5

All (11) torsion outliers are listed below:

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	236	BTB	4	0
2	А	234	BTB	4	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)

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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q < 0.9
1	А	234/234~(100%)	-0.33	0 100 100	4, 10, 19, 24	0
1	В	234/234~(100%)	-0.16	1 (0%) 92 92	3, 8, 17, 23	0
All	All	468/468 (100%)	-0.24	1 (0%) 95 94	3, 9, 18, 24	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	0	SER	2.1

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

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

## 6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

#### 6.4 Ligands (i)

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. The B-factors column lists the minimum, median,  $95^{th}$  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	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q < 0.9
2	BTB	А	234	14/14	0.72	0.28	41,45,46,48	0
2	BTB	В	236	14/14	0.90	0.13	9,19,24,25	0
3	NA	В	234	1/1	0.98	0.04	22,22,22,22	0
3	NA	В	235	1/1	0.99	0.04	16,16,16,16	0



## 6.5 Other polymers (i)

There are no such residues in this entry.

