

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

#### Aug 27, 2023 – 07:17 PM EDT

PDB ID	:	3HVU
Title	:	1.95 Angstrom Crystal Structure of Complex of Hypoxanthine-Guanine Phos
		phoribosyltransferase from Bacillus anthracis with 2-(N-morpholino)ethanesu
		lfonic acid (MES)
Authors	:	Minasov, G.; Halavaty, A.; Shuvalova, L.; Dubrovska, I.; Winsor, J.; Papazisi,
		L.; Anderson, W.F.; Center for Structural Genomics of Infectious Diseases
		(CSGID)
Deposited on	:	2009-06-16
Resolution	:	1.95 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

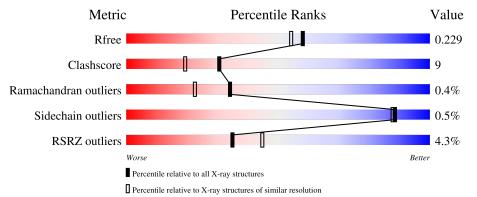
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)

# 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 1.95 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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	204	76% 1	.4%	9%
1	В	204	73% 17'	%	9%
1	С	204	78%	12%	9%
1	D	204	75% 15	5%	9%

Validation Pipeline (wwPDB-VP) : 2.35



#### 3HVU

# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6662 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.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	А	185	Total	С	Ν	Ο	$\mathbf{S}$	0	8	0
	Π	100	1528	985	241	295	7	0	0	0
1	В	185	Total	С	Ν	Ο	$\mathbf{S}$	0	10	0
		105	1547	994	243	303	7	0	10	0
1	С	185	Total	С	Ν	Ο	$\mathbf{S}$	0	8	0
	165	1532	987	242	296	7	0	8	0	
1	Л	185	Total	С	Ν	0	S	0	5	0
	180	1501	969	234	291	$\overline{7}$		5	0	

• Molecule 1 is a protein called Hypoxanthine phosphoribosyltransferase.

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	-23	MET	-	insertion	UNP Q81VX6
А	-22	HIS	-	insertion	UNP Q81VX6
А	-21	HIS	-	insertion	UNP Q81VX6
А	-20	HIS	-	insertion	UNP Q81VX6
А	-19	HIS	-	insertion	UNP Q81VX6
А	-18	HIS	-	insertion	UNP Q81VX6
А	-17	HIS	-	insertion	UNP Q81VX6
А	-16	SER	-	insertion	UNP Q81VX6
A	-15	SER	-	insertion	UNP Q81VX6
А	-14	GLY	-	insertion	UNP Q81VX6
A	-13	VAL	-	insertion	UNP Q81VX6
А	-12	ASP	-	insertion	UNP Q81VX6
А	-11	LEU	-	insertion	UNP Q81VX6
A	-10	GLY	-	insertion	UNP Q81VX6
А	-9	THR	-	insertion	UNP Q81VX6
А	-8	GLU	-	insertion	UNP Q81VX6
А	-7	ASN	-	insertion	UNP Q81VX6
А	-6	LEU	-	insertion	UNP Q81VX6
А	-5	TYR	-	insertion	UNP Q81VX6
А	-4	PHE	-	insertion	UNP Q81VX6
А	-3	GLN	-	insertion	UNP Q81VX6



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A-1ASN-insertionUNP Q81V.A0ALA-insertionUNP Q81V.B-23MET-insertionUNP Q81V.B-22HIS-insertionUNP Q81V.B-21HIS-insertionUNP Q81V.B-20HIS-insertionUNP Q81V.B-19HIS-insertionUNP Q81V.B-19HIS-insertionUNP Q81V.B-11HIS-insertionUNP Q81V.B-16SER-insertionUNP Q81V.B-16SER-insertionUNP Q81V.B-15SER-insertionUNP Q81V.B-14GLY-insertionUNP Q81V.B-13VAL-insertionUNP Q81V.B-11LEU-insertionUNP Q81V.B-11LEU-insertionUNP Q81V.B-10GLY-insertionUNP Q81V.B-6LEU-insertionUNP Q81V.B-7ASN-insertionUNP Q81V.B-3GLN-insertionUNP Q81V.B-3GLN-insertionUNP Q81V.B-2SER-insertionUNP Q81V.B-3GLN-insertionUNP Q81V. <th>Chain</th> <th>Residue</th> <th>Modelled</th> <th>Actual</th> <th>Comment</th> <th>Reference</th>	Chain	Residue	Modelled	Actual	Comment	Reference
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $				-		UNP Q81VX6
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$				-		UNP Q81VX6
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $				-		UNP Q81VX6
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B $-20$ HIS $-$ insertionUNP Q81V.B $-19$ HIS $-$ insertionUNP Q81V.B $-18$ HIS $-$ insertionUNP Q81V.B $-17$ HIS $-$ insertionUNP Q81V.B $-16$ SER $-$ insertionUNP Q81V.B $-16$ SER $-$ insertionUNP Q81V.B $-16$ SER $-$ insertionUNP Q81V.B $-13$ VAL $-$ insertionUNP Q81V.B $-12$ ASP $-$ insertionUNP Q81V.B $-11$ LEU $-$ insertionUNP Q81V.B $-10$ GLY $-$ insertionUNP Q81V.B $-10$ GLY $-$ insertionUNP Q81V.B $-9$ THR $-$ insertionUNP Q81V.B $-6$ LEU $-$ insertionUNP Q81V.B $-6$ LEU $-$ insertionUNP Q81V.B $-6$ LEU $-$ insertionUNP Q81V.B $-3$ GLN $-$ insertionUNP Q81V.B $-2$ SER $-$ insertionUNP Q81V.B $-1$ ASN $-$ insertionUNP Q81V.B $-1$ ASN $-$ insertionUNP Q81V.B $-1$ ASN $-$ insertionUNP Q81V.C $-23$ MET $-$ insertionUNP Q81V.				-		UNP Q81VX6
B-19HIS-insertionUNP Q81V.B-18HIS-insertionUNP Q81V.B-17HIS-insertionUNP Q81V.B-16SER-insertionUNP Q81V.B-15SER-insertionUNP Q81V.B-14GLY-insertionUNP Q81V.B-13VAL-insertionUNP Q81V.B-12ASP-insertionUNP Q81V.B-11LEU-insertionUNP Q81V.B-10GLY-insertionUNP Q81V.B-9THR-insertionUNP Q81V.B-9THR-insertionUNP Q81V.B-7ASN-insertionUNP Q81V.B-6LEU-insertionUNP Q81V.B-5TYR-insertionUNP Q81V.B-3GLN-insertionUNP Q81V.B-2SER-insertionUNP Q81V.B0ALA-insertionUNP Q81V.C-23MET-insertionUNP Q81V.C-20HIS-insertionUNP Q81V.C-18HIS-insertionUNP Q81V.C-18HIS-insertionUNP Q81V.C-16SER-insertionUNP Q81V. <td></td> <td></td> <td></td> <td>-</td> <td></td> <td>UNP Q81VX6</td>				-		UNP Q81VX6
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B-13VAL-insertionUNP Q81V.B-12ASP-insertionUNP Q81V.B-11LEU-insertionUNP Q81V.B-10GLY-insertionUNP Q81V.B-9THR-insertionUNP Q81V.B-9THR-insertionUNP Q81V.B-9THR-insertionUNP Q81V.B-8GLU-insertionUNP Q81V.B-7ASN-insertionUNP Q81V.B-6LEU-insertionUNP Q81V.B-5TYR-insertionUNP Q81V.B-4PHE-insertionUNP Q81V.B-3GLN-insertionUNP Q81V.B-1ASN-insertionUNP Q81V.B-1ASN-insertionUNP Q81V.B0ALA-insertionUNP Q81V.C-23MET-insertionUNP Q81V.C-20HIS-insertionUNP Q81V.C-19HIS-insertionUNP Q81V.C-18HIS-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-14GLY-insertionUNP Q81V.	В	-15	SER	-	insertion	UNP Q81VX6
B-12ASP-insertionUNP Q81V.B-11LEU-insertionUNP Q81V.B-10GLY-insertionUNP Q81V.B-9THR-insertionUNP Q81V.B-9THR-insertionUNP Q81V.B-9THR-insertionUNP Q81V.B-8GLU-insertionUNP Q81V.B-7ASN-insertionUNP Q81V.B-6LEU-insertionUNP Q81V.B-5TYR-insertionUNP Q81V.B-4PHE-insertionUNP Q81V.B-3GLN-insertionUNP Q81V.B-2SER-insertionUNP Q81V.B0ALA-insertionUNP Q81V.B0ALA-insertionUNP Q81V.C-23MET-insertionUNP Q81V.C-21HIS-insertionUNP Q81V.C-19HIS-insertionUNP Q81V.C-18HIS-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-14GLY-insertionUNP Q81V.	В	-14	GLY	-	insertion	UNP Q81VX6
B-11LEU-insertionUNP Q81VB-10GLY-insertionUNP Q81VB-9THR-insertionUNP Q81VB-8GLU-insertionUNP Q81VB-7ASN-insertionUNP Q81VB-6LEU-insertionUNP Q81VB-6LEU-insertionUNP Q81VB-5TYR-insertionUNP Q81VB-4PHE-insertionUNP Q81VB-3GLN-insertionUNP Q81VB-2SER-insertionUNP Q81VB-1ASN-insertionUNP Q81VB0ALA-insertionUNP Q81VC-23MET-insertionUNP Q81VC-20HIS-insertionUNP Q81VC-19HIS-insertionUNP Q81VC-18HIS-insertionUNP Q81VC-16SER-insertionUNP Q81VC-15SER-insertionUNP Q81VC-14GLY-insertionUNP Q81V	В	-13	VAL	-	insertion	UNP Q81VX6
B-10GLY-insertionUNP Q81V.B-9THR-insertionUNP Q81V.B-8GLU-insertionUNP Q81V.B-7ASN-insertionUNP Q81V.B-6LEU-insertionUNP Q81V.B-6LEU-insertionUNP Q81V.B-5TYR-insertionUNP Q81V.B-3GLN-insertionUNP Q81V.B-2SER-insertionUNP Q81V.B-1ASN-insertionUNP Q81V.B0ALA-insertionUNP Q81V.B0ALA-insertionUNP Q81V.C-23MET-insertionUNP Q81V.C-20HIS-insertionUNP Q81V.C-19HIS-insertionUNP Q81V.C-18HIS-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-14GLY-insertionUNP Q81V.	В	-12	ASP	-	insertion	UNP Q81VX6
B-9THR-insertionUNP Q81V.B-8GLU-insertionUNP Q81V.B-7ASN-insertionUNP Q81V.B-6LEU-insertionUNP Q81V.B-5TYR-insertionUNP Q81V.B-4PHE-insertionUNP Q81V.B-3GLN-insertionUNP Q81V.B-2SER-insertionUNP Q81V.B-1ASN-insertionUNP Q81V.B0ALA-insertionUNP Q81V.C-23MET-insertionUNP Q81V.C-21HIS-insertionUNP Q81V.C-20HIS-insertionUNP Q81V.C-18HIS-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-14GLY-insertionUNP Q81V.		-11		-	insertion	UNP Q81VX6
B-8GLU-insertionUNP Q81V.B-7ASN-insertionUNP Q81V.B-6LEU-insertionUNP Q81V.B-5TYR-insertionUNP Q81V.B-5TYR-insertionUNP Q81V.B-4PHE-insertionUNP Q81V.B-3GLN-insertionUNP Q81V.B-2SER-insertionUNP Q81V.B-1ASN-insertionUNP Q81V.B0ALA-insertionUNP Q81V.C-23MET-insertionUNP Q81V.C-22HIS-insertionUNP Q81V.C-21HIS-insertionUNP Q81V.C-19HIS-insertionUNP Q81V.C-18HIS-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-14GLY-insertionUNP Q81V.	В	-10	GLY	-	insertion	UNP Q81VX6
B-7ASN-insertionUNP Q81V.B-6LEU-insertionUNP Q81V.B-5TYR-insertionUNP Q81V.B-5TYR-insertionUNP Q81V.B-4PHE-insertionUNP Q81V.B-3GLN-insertionUNP Q81V.B-2SER-insertionUNP Q81V.B-1ASN-insertionUNP Q81V.B0ALA-insertionUNP Q81V.C-23MET-insertionUNP Q81V.C-22HIS-insertionUNP Q81V.C-21HIS-insertionUNP Q81V.C-20HIS-insertionUNP Q81V.C-19HIS-insertionUNP Q81V.C-18HIS-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-14GLY-insertionUNP Q81V.	В	-9	THR	-	insertion	UNP Q81VX6
B-6LEU-insertionUNP Q81VB-5TYR-insertionUNP Q81VB-4PHE-insertionUNP Q81VB-3GLN-insertionUNP Q81VB-2SER-insertionUNP Q81VB-1ASN-insertionUNP Q81VB0ALA-insertionUNP Q81VC-23MET-insertionUNP Q81VC-22HIS-insertionUNP Q81VC-21HIS-insertionUNP Q81VC-20HIS-insertionUNP Q81VC-18HIS-insertionUNP Q81VC-16SER-insertionUNP Q81VC-16SER-insertionUNP Q81VC-14GLY-insertionUNP Q81V	В	-8	GLU	-	insertion	UNP Q81VX6
B-5TYR-insertionUNP Q81V.B-4PHE-insertionUNP Q81V.B-3GLN-insertionUNP Q81V.B-2SER-insertionUNP Q81V.B-1ASN-insertionUNP Q81V.B0ALA-insertionUNP Q81V.C-23MET-insertionUNP Q81V.C-22HIS-insertionUNP Q81V.C-22HIS-insertionUNP Q81V.C-20HIS-insertionUNP Q81V.C-19HIS-insertionUNP Q81V.C-18HIS-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-14GLY-insertionUNP Q81V.	В	-7	ASN	-	insertion	UNP Q81VX6
B-4PHE-insertionUNP Q81V.B-3GLN-insertionUNP Q81V.B-2SER-insertionUNP Q81V.B-1ASN-insertionUNP Q81V.B0ALA-insertionUNP Q81V.C-23MET-insertionUNP Q81V.C-22HIS-insertionUNP Q81V.C-22HIS-insertionUNP Q81V.C-21HIS-insertionUNP Q81V.C-20HIS-insertionUNP Q81V.C-19HIS-insertionUNP Q81V.C-18HIS-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-14GLY-insertionUNP Q81V.	В			-	insertion	UNP Q81VX6
B-3GLN-insertionUNP Q81V.B-2SER-insertionUNP Q81V.B-1ASN-insertionUNP Q81V.B0ALA-insertionUNP Q81V.C-23MET-insertionUNP Q81V.C-22HIS-insertionUNP Q81V.C-22HIS-insertionUNP Q81V.C-21HIS-insertionUNP Q81V.C-20HIS-insertionUNP Q81V.C-19HIS-insertionUNP Q81V.C-18HIS-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-14GLY-insertionUNP Q81V.	В	-5		-	insertion	UNP Q81VX6
B-2SER-insertionUNP Q81V.B-1ASN-insertionUNP Q81V.B0ALA-insertionUNP Q81V.C-23MET-insertionUNP Q81V.C-22HIS-insertionUNP Q81V.C-22HIS-insertionUNP Q81V.C-21HIS-insertionUNP Q81V.C-20HIS-insertionUNP Q81V.C-19HIS-insertionUNP Q81V.C-18HIS-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-14GLY-insertionUNP Q81V.				-	insertion	UNP Q81VX6
B-1ASN-insertionUNP Q81V.B0ALA-insertionUNP Q81V.C-23MET-insertionUNP Q81V.C-22HIS-insertionUNP Q81V.C-22HIS-insertionUNP Q81V.C-21HIS-insertionUNP Q81V.C-20HIS-insertionUNP Q81V.C-19HIS-insertionUNP Q81V.C-18HIS-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-14GLY-insertionUNP Q81V.				-	insertion	UNP Q81VX6
B0ALA-insertionUNP Q81V.C-23MET-insertionUNP Q81V.C-22HIS-insertionUNP Q81V.C-21HIS-insertionUNP Q81V.C-20HIS-insertionUNP Q81V.C-19HIS-insertionUNP Q81V.C-18HIS-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-14GLY-insertionUNP Q81V.	В	-2	SER	-		UNP Q81VX6
C-23MET-insertionUNP Q81V.C-22HIS-insertionUNP Q81V.C-21HIS-insertionUNP Q81V.C-20HIS-insertionUNP Q81V.C-19HIS-insertionUNP Q81V.C-18HIS-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-14GLY-insertionUNP Q81V.				-		UNP Q81VX6
C-22HIS-insertionUNP Q81VC-21HIS-insertionUNP Q81VC-20HIS-insertionUNP Q81VC-19HIS-insertionUNP Q81VC-18HIS-insertionUNP Q81VC-17HIS-insertionUNP Q81VC-16SER-insertionUNP Q81VC-15SER-insertionUNP Q81VC-14GLY-insertionUNP Q81V	В	0	ALA	-	insertion	UNP Q81VX6
C-21HIS-insertionUNP Q81VC-20HIS-insertionUNP Q81VC-19HIS-insertionUNP Q81VC-18HIS-insertionUNP Q81VC-17HIS-insertionUNP Q81VC-16SER-insertionUNP Q81VC-15SER-insertionUNP Q81VC-14GLY-insertionUNP Q81V	$\mathbf{C}$			-	insertion	UNP Q81VX6
C-20HIS-insertionUNP Q81VC-19HIS-insertionUNP Q81VC-18HIS-insertionUNP Q81VC-17HIS-insertionUNP Q81VC-16SER-insertionUNP Q81VC-15SER-insertionUNP Q81VC-14GLY-insertionUNP Q81V	С	-22	HIS	-	insertion	UNP Q81VX6
C-19HIS-insertionUNP Q81V.C-18HIS-insertionUNP Q81V.C-17HIS-insertionUNP Q81V.C-16SER-insertionUNP Q81V.C-15SER-insertionUNP Q81V.C-14GLY-insertionUNP Q81V.	С	-21	HIS	-	insertion	UNP Q81VX6
C-18HIS-insertionUNP Q81VC-17HIS-insertionUNP Q81VC-16SER-insertionUNP Q81VC-15SER-insertionUNP Q81VC-14GLY-insertionUNP Q81V		-20		-		UNP Q81VX6
C-17HIS-insertionUNP Q81VC-16SER-insertionUNP Q81VC-15SER-insertionUNP Q81VC-14GLY-insertionUNP Q81V	С	-19	HIS	-	insertion	UNP Q81VX6
C-16SER-insertionUNP Q81VC-15SER-insertionUNP Q81VC-14GLY-insertionUNP Q81V	С	-18	HIS	-	insertion	UNP Q81VX6
C-15SER-insertionUNP Q81VC-14GLY-insertionUNP Q81V	С	-17	HIS	-	insertion	UNP Q81VX6
C -14 GLY - insertion UNP Q81V		-16	SER	-	insertion	UNP Q81VX6
		-15	SER	-		UNP Q81VX6
	С	-14	GLY	-	insertion	UNP Q81VX6
C $ $ -13 $ $ VAL $ $ - $ $ insertion $ $ UNP Q81V.	С	-13	VAL	-	insertion	UNP Q81VX6
		-12	ASP	-	insertion	UNP Q81VX6
		-11	LEU	-	insertion	UNP Q81VX6
C -10 GLY - insertion UNP Q81V.	С	-10	GLY	-	insertion	UNP Q81VX6
C -9 THR - insertion UNP Q81V.	С	-9	THR	-	insertion	UNP Q81VX6

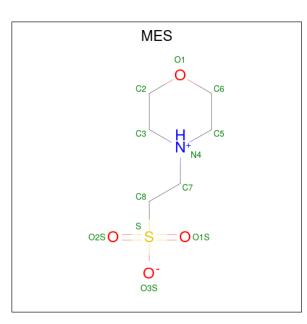


Chain	Residue	vious page         Modelled	Actual	Comment	Reference
С	-8	GLU	_	insertion	UNP Q81VX6
С	-7	ASN	_	insertion	UNP Q81VX6
С	-6	LEU	_	insertion	UNP Q81VX6
С	-5	TYR	-	insertion	UNP Q81VX6
С	-4	PHE	-	insertion	UNP Q81VX6
С	-3	GLN	-	insertion	UNP Q81VX6
С	-2	SER	-	insertion	UNP Q81VX6
С	-1	ASN	-	insertion	UNP Q81VX6
С	0	ALA	-	insertion	UNP Q81VX6
D	-23	MET	-	insertion	UNP Q81VX6
D	-22	HIS	-	insertion	UNP Q81VX6
D	-21	HIS	-	insertion	UNP Q81VX6
D	-20	HIS	-	insertion	UNP Q81VX6
D	-19	HIS	-	insertion	UNP Q81VX6
D	-18	HIS	-	insertion	UNP Q81VX6
D	-17	HIS	-	insertion	UNP Q81VX6
D	-16	SER	-	insertion	UNP Q81VX6
D	-15	SER	-	insertion	UNP Q81VX6
D	-14	GLY	-	insertion	UNP Q81VX6
D	-13	VAL	-	insertion	UNP Q81VX6
D	-12	ASP	-	insertion	UNP Q81VX6
D	-11	LEU	-	insertion	UNP Q81VX6
D	-10	GLY	-	insertion	UNP Q81VX6
D	-9	THR	-	insertion	UNP Q81VX6
D	-8	GLU	-	insertion	UNP Q81VX6
D	-7	ASN	-	insertion	UNP Q81VX6
D	-6	LEU	-	insertion	UNP Q81VX6
D	-5	TYR	-	insertion	UNP Q81VX6
D	-4	PHE	-	insertion	UNP Q81VX6
D	-3	GLN	-	insertion	UNP Q81VX6
D	-2	SER	-	insertion	UNP Q81VX6
D	-1	ASN	-	insertion	UNP Q81VX6
D	0	ALA	-	insertion	UNP Q81VX6

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• Molecule 2 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula:  $C_6H_{13}NO_4S$ ).





Mol	Chain	Residues		Ato	oms			ZeroOcc	AltConf	
2	Δ	1	Total	С	Ν	0	S	0	0	
2		1	12	6	1	4	1	0	U	
2	В	1	Total	С	Ν	Ο	$\mathbf{S}$	0	0	
	2 D	T	12	6	1	4	1	0	0	
2	С	1	Total	С	Ν	Ο	$\mathbf{S}$	0	0	
	1	12	6	1	4	1	0	0		
2	Л	1	Total	С	Ν	0	S	0	0	
	2 D	1	12	6	1	4	1	0	0	

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	Total Na 1 1	0	0
3	В	1	Total Na 1 1	0	0
3	С	1	Total Na 1 1	0	0
3	D	1	Total Na 1 1	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	119	Total O 119 119	0	1



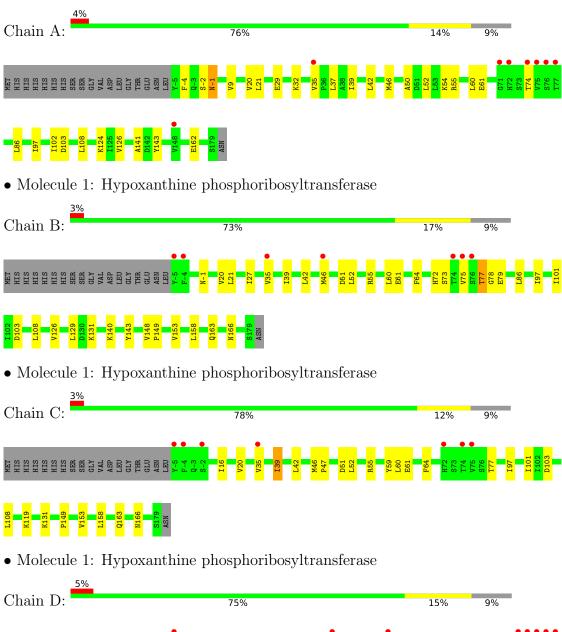
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	128	Total O 128 128	0	0
4	С	127	Total O 130 130	0	3
4	D	124	Total O 125 125	0	1



# 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: Hypoxanthine phosphoribosyltransferase





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	52.71Å 93.38Å 94.90Å	Deperitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.03^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	29.96 - 1.95	Depositor
Resolution (A)	28.15 - 1.95	EDS
% Data completeness	98.1 (29.96-1.95)	Depositor
(in resolution range)	97.9(28.15-1.95)	EDS
R <sub>merge</sub>	0.05	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.29 (at 1.95 Å)	Xtriage
Refinement program	REFMAC 5.5.0044	Depositor
D D.	0.192 , $0.232$	Depositor
$R, R_{free}$	0.205 , $0.229$	DCC
$R_{free}$ test set	3338 reflections $(5.08\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	34.0	Xtriage
Anisotropy	0.774	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.31 , 30.0	EDS
L-test for twinning <sup>2</sup>	$<  L  > = 0.50, < L^2 > = 0.34$	Xtriage
	0.001 for -h,l,k	
Estimated twinning fraction	0.005 for -h,-l,-k	Xtriage
	0.467 for h,-k,-l	
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	6662	wwPDB-VP
Average B, all atoms $(Å^2)$	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 57.36 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.3929e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

<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: MES, NA

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	
MOI	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.56	0/1554	0.79	0/2101
1	В	0.58	0/1573	0.80	0/2127
1	С	0.58	0/1558	0.77	0/2105
1	D	0.58	0/1526	0.79	0/2064
All	All	0.57	0/6211	0.79	0/8397

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 (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	А	1528	0	1553	38	0
1	В	1547	0	1560	38	0
1	С	1532	0	1558	32	0
1	D	1501	0	1530	31	0
2	А	12	0	13	0	0
2	В	12	0	13	1	0
2	С	12	0	13	1	0
2	D	12	0	13	0	0
3	А	1	0	0	0	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	В	1	0	0	0	0
3	С	1	0	0	0	0
3	D	1	0	0	0	0
4	А	119	0	0	2	0
4	В	128	0	0	3	0
4	С	130	0	0	2	0
4	D	125	0	0	1	0
All	All	6662	0	6253	114	0

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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 9.

The worst 5 of 114 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:77:THR:HG21	4:B:490:HOH:O	1.81	0.80
1:B:73:SER:O	1:B:77:THR:CG2	2.30	0.79
1:A:50:ALA:HB2	1:C:46[B]:MET:SD	2.26	0.75
1:A:20:VAL:HG13	1:A:52:LEU:HA	1.75	0.69
1:B:72[B]:HIS:CE1	1:B:75:VAL:HG21	2.28	0.68

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	А	191/204~(94%)	185~(97%)	6 (3%)	0	100 100
1	В	193/204~(95%)	186 (96%)	5(3%)	2(1%)	15 6
1	С	191/204 (94%)	185 (97%)	5(3%)	1 (0%)	29 17
1	D	188/204~(92%)	181 (96%)	7 (4%)	0	100 100



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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	763/816~(94%)	737~(97%)	23 (3%)	3~(0%)	34 22

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	77	THR
1	С	149	PRO
1	В	149	PRO

#### 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	А	172/181~(95%)	170 (99%)	2(1%)	71 68
1	В	174/181~(96%)	174 (100%)	0	100 100
1	С	172/181~(95%)	171 (99%)	1 (1%)	86 85
1	D	169/181~(93%)	168 (99%)	1 (1%)	86 85
All	All	687/724~(95%)	683~(99%)	4 (1%)	88 85

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	-1[A]	ASN
1	А	-1[B]	ASN
1	С	39	ILE
1	D	138	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	С	-1	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)

Of 8 ligands modelled in this entry, 4 are 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	Dec	es Link	Bond lengths			Bond angles		
	туре		nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	MES	А	181	-	12,12,12	2.07	1 (8%)	14,16,16	1.00	0
2	MES	С	181	-	12,12,12	2.33	1 (8%)	14,16,16	1.47	2 (14%)
2	MES	D	181	-	12,12,12	2.24	1 (8%)	14,16,16	1.32	1 (7%)
2	MES	В	181	-	12,12,12	2.14	1 (8%)	14,16,16	1.50	4 (28%)

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	MES	А	181	-	-	2/6/14/14	0/1/1/1
2	MES	С	181	-	-	2/6/14/14	0/1/1/1
2	MES	D	181	-	-	2/6/14/14	0/1/1/1
2	MES	В	181	-	-	2/6/14/14	0/1/1/1



Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
2	С	181	MES	C8-S	-7.72	1.66	1.77
2	D	181	MES	C8-S	-7.42	1.67	1.77
2	В	181	MES	C8-S	-7.09	1.67	1.77
2	А	181	MES	C8-S	-7.03	1.67	1.77

All (4) bond length outliers are listed below:

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	D	181	MES	O3S-S-C8	3.84	111.98	105.77
2	С	181	MES	O3S-S-C8	3.55	111.51	105.77
2	В	181	MES	O3S-S-C8	3.02	110.65	105.77
2	В	181	MES	C5-N4-C3	2.40	114.23	108.83
2	В	181	MES	C6-C5-N4	2.30	113.58	110.10

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	С	181	MES	C8-C7-N4-C3
2	С	181	MES	C8-C7-N4-C5
2	D	181	MES	C8-C7-N4-C3
2	D	181	MES	C8-C7-N4-C5
2	А	181	MES	C8-C7-N4-C3

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	С	181	MES	1	0
2	В	181	MES	1	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	185/204~(90%)	0.27	8 (4%) 35 45	20, 28, 37, 52	0
1	В	185/204~(90%)	0.27	7 (3%) 40 50	18, 27, 35, 53	0
1	С	185/204~(90%)	0.31	7 (3%) 40 50	22, 28, 41, 55	0
1	D	185/204~(90%)	0.31	10 (5%) 25 34	20, 27, 38, 55	0
All	All	740/816~(90%)	0.29	32 (4%) 35 45	18, 27, 39, 55	0

The worst 5 of 32 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	74	THR	5.0
1	А	35	VAL	4.6
1	С	74	THR	4.5
1	D	72	HIS	4.3
1	А	72[A]	HIS	4.3

## 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
3	NA	С	182	1/1	0.80	0.16	$57,\!57,\!57,\!57$	0
3	NA	А	182	1/1	0.81	0.14	$51,\!51,\!51,\!51$	0
3	NA	D	182	1/1	0.92	0.12	$57,\!57,\!57,\!57$	0
2	MES	С	181	12/12	0.93	0.16	41,57,66,67	0
3	NA	В	182	1/1	0.94	0.07	60,60,60,60	0
2	MES	В	181	12/12	0.96	0.15	46,52,64,64	0
2	MES	D	181	12/12	0.96	0.17	41,55,65,66	0
2	MES	А	181	12/12	0.97	0.12	43,56,63,64	0

## 6.5 Other polymers (i)

There are no such residues in this entry.

