

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

#### May 13, 2020 – 03:32 pm BST

PDB ID	:	5L4Z
$\operatorname{Title}$	:	Crystal structure of enzyme in purine metabolism
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Deposited on	:	2016-05-27
$\operatorname{Resolution}$	:	1.84  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 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 as 541 be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
$\operatorname{Refmac}$	:	5.8.0158
$\operatorname{CCP4}$	:	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 (i)

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

The reported resolution of this entry is 1.84 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
$R_{free}$	130704	4003 (1.86-1.82)
Clash score	141614	4233 (1.86-1.82)
Ramachandran outliers	138981	4185 (1.86-1.82)
Sidechain outliers	138945	4186 (1.86-1.82)
RSRZ outliers	127900	3957 (1.86-1.82)

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				
			10%				
1	A	555	80%	5%	15%		

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GOL	А	609	-	-	-	Х
2	GOL	А	610	-	-	-	Х



## 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4224 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 Cytosolic purine 5'-nucleotidase.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	А	470	Total 3935	${ m C} 2555$	N 647	0 711	S 22	0	19	0

Chain	Residue	Modelled	Actual	Actual Comment	
А	-18	MET	-	initiating methionine	UNP P49902
A	-17	GLY	-	expression tag	UNP P49902
А	-16	SER	-	expression tag	UNP P49902
А	-15	SER	-	expression tag	UNP P49902
А	-14	HIS	-	expression tag	UNP P49902
А	-13	HIS	-	expression tag	UNP P49902
A	-12	HIS	-	expression tag	UNP P49902
А	-11	HIS	-	expression tag	UNP P49902
А	-10	HIS	-	expression tag	UNP P49902
А	-9	HIS	-	expression tag	UNP P49902
A	-8	SER	-	expression tag	UNP P49902
А	-7	SER	-	expression tag	UNP P49902
A	-6	GLY	-	expression tag	UNP P49902
А	-5	LEU	-	expression tag	UNP P49902
А	-4	VAL	-	expression tag	UNP P49902
A	-3	PRO	-	expression tag	UNP P49902
A	-2	ARG	-	expression tag	UNP P49902
A	-1	GLY	-	expression tag	UNP P49902
А	0	SER	-	expression tag	UNP P49902
А	238	TRP	ARG	engineered mutation	UNP P49902

There are 20 discrepancies between the modelled and reference sequences:

• Molecule 2 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 6  3  3 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 6  3  3 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 6  3  3 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 6  3  3 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} {\rm Total} & {\rm C} & {\rm O} \\ 6 & 3 & 3 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
2	А	1	Total C O 6 3 3	0	0
2	А	1	Total C O 6 3 3	0	0
2	А	1	Total C O 6 3 3	0	0
2	А	1	Total C O 6 3 3	0	0
2	А	1	TotalCO633	0	0
2	А	1	TotalCO633	0	0
2	А	1	$\begin{bmatrix} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{bmatrix}$	0	0

• Molecule 3 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	210	Total         O           211         211	0	1



## 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: Cytosolic purine 5'-nucleotidase



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants	91.32Å $126.50$ Å $130.51$ Å	Deperitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
$\mathbf{P}_{\text{assolution}}(\hat{\mathbf{A}})$	45.42 - 1.84	Depositor
Resolution (A)	45.42 - 1.84	$\mathrm{EDS}$
% Data completeness	99.4 (45.42-1.84)	Depositor
(in resolution range $)$	99.4(45.42 - 1.84)	EDS
R <sub>merge</sub>	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.31 (at 1.84 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.8.0131	Depositor
D D .	0.177 , $0.205$	Depositor
$\Pi, \Pi_{free}$	0.186 , $0.210$	DCC
$R_{free}$ test set	2101  reflections  (3.21%)	wwPDB-VP
Wilson B-factor $(Å^2)$	29.0	Xtriage
Anisotropy	0.135	Xtriage
Bulk solvent $k_{sol}(e/A^3), B_{sol}(A^2)$	0.38 , 50.5	EDS
L-test for twinning <sup>2</sup>	$< L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	0.012 for -h,-l,-k	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4224	wwPDB-VP
Average B, all atoms $(Å^2)$	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.11% 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.



 $<sup>^1 {\</sup>rm Intensities}$  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: GOL

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).

Mal	Chain	Bond	lengths	Bond angles		
		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.66	0/4093	0.78	2/5528~(0.0%)	

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	277	ARG	NE-CZ-NH2	-8.43	116.09	120.30
1	А	54	ASP	CB-CG-OD1	5.26	123.04	118.30

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	3935	0	3913	14	0
2	А	78	0	104	0	0
3	А	211	0	0	0	0
All	All	4224	0	4017	14	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 2.

All (14) close contacts within the same asymmetric unit are listed below, sorted by their clash



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:232[A]:LEU:HD12	1:A:236[A]:LEU:HD13	1.64	0.79
1:A:232[A]:LEU:CD1	1:A:236[A]:LEU:HD13	2.20	0.71
1:A:154[A]:ASN:ND2	1:A:354[A]:PHE:CD1	2.70	0.60
1:A:353:ILE:HD13	1:A:370:LEU:HD22	1.87	0.57
1:A:322:GLN:O	1:A:325:ILE:HG22	2.06	0.55
1:A:398:PHE:O	1:A:399:LEU:HD12	2.13	0.48
1:A:232[A]:LEU:HD13	1:A:465:PHE:HZ	1.79	0.47
1:A:395:LEU:HD21	1:A:422:ARG:HG3	1.97	0.46
1:A:358:LEU:HD23	1:A:358:LEU:C	2.40	0.41
1:A:32:TYR:CZ	1:A:380[A]:HIS:CE1	3.07	0.41
1:A:50:GLY:HA3	1:A:246:PHE:CZ	2.55	0.41
1:A:453[A]:GLN:HA	1:A:453[A]:GLN:OE1	2.21	0.40
1:A:354[B]:PHE:CZ	1:A:359:LYS:HE2	2.56	0.40
1:A:321:LEU:HA	1:A:327:TYR:OH	2.22	0.40

magnitude.

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	Perce	$\mathbf{ntiles}$
1	А	485/555 (87%)	472 (97%)	12 (2%)	1 (0%)	47	33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	419	ILE



#### 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	435/497~(88%)	433~(100%)	2~(0%)	88 85	

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	27	TYR
1	А	425	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

#### 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 carbohydrates in this entry.

#### 5.6 Ligand geometry (i)

13 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



Mal	True	Chain	Dec	Tinl	B	ond leng	gths	E	Bond ang	gles
	mor Type	Chain	nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	GOL	А	610	-	5,5,5	0.43	0	$5,\!5,\!5$	0.33	0
2	GOL	А	604	-	5,5,5	0.31	0	$5,\!5,\!5$	0.32	0
2	GOL	A	603	-	5,5,5	0.38	0	5,5,5	0.32	0
2	GOL	А	607	-	5,5,5	0.10	0	5,5,5	1.04	0
2	GOL	A	609	-	5,5,5	0.45	0	$5,\!5,\!5$	0.76	0
2	GOL	А	611	-	5,5,5	0.37	0	5,5,5	0.36	0
2	GOL	А	612	-	5,5,5	0.39	0	5,5,5	0.31	0
2	GOL	A	602	-	5,5,5	0.22	0	5,5,5	0.31	0
2	GOL	А	601	-	5,5,5	0.16	0	5,5,5	0.52	0
2	GOL	A	606	-	5,5,5	0.52	0	$5,\!5,\!5$	0.52	0
2	GOL	A	608	-	5,5,5	0.50	0	5,5,5	0.59	0
2	GOL	A	605	-	5,5,5	0.47	0	5,5,5	0.48	0
2	GOL	A	613	-	5,5,5	0.37	0	5,5,5	0.50	0

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).

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	GOL	А	610	-	-	2/4/4/4	-
2	GOL	А	604	-	-	0/4/4/4	-
2	GOL	А	603	-	-	0/4/4/4	-
2	GOL	А	607	-	-	2/4/4/4	-
2	GOL	А	609	-	-	3/4/4/4	-
2	GOL	А	611	-	-	2/4/4/4	-
2	GOL	А	612	-	-	2/4/4/4	-
2	GOL	А	602	-	-	2/4/4/4	-
2	GOL	А	601	-	-	0/4/4/4	-
2	GOL	А	606	-	-	2/4/4/4	-
2	GOL	A	608	-	-	2/4/4/4	-
2	GOL	A	605	-	-	4/4/4/4	-
2	GOL	A	613	-	-	2/4/4/4	_

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.



Mol	Chain	Res	Type	Atoms
2	А	611	GOL	O1-C1-C2-C3
2	А	612	GOL	O1-C1-C2-C3
2	А	606	GOL	C1-C2-C3-O3
2	А	608	GOL	O1-C1-C2-C3
2	А	605	GOL	C1-C2-C3-O3
2	А	609	GOL	O2-C2-C3-O3
2	А	608	GOL	O1-C1-C2-O2
2	А	605	GOL	O1-C1-C2-O2
2	А	605	GOL	O2-C2-C3-O3
2	А	610	GOL	O1-C1-C2-C3
2	А	607	GOL	O1-C1-C2-C3
2	А	609	GOL	C1-C2-C3-O3
2	А	602	GOL	C1-C2-C3-O3
2	А	605	GOL	O1-C1-C2-C3
2	А	612	GOL	O1-C1-C2-O2
2	А	602	GOL	O2-C2-C3-O3
2	А	606	GOL	O2-C2-C3-O3
2	А	611	GOL	O1-C1-C2-O2
2	A	610	GOL	O1-C1-C2-O2
2	A	613	GOL	O2-C2-C3-O3
2	A	609	GOL	O1-C1-C2-C3
2	A	613	GOL	C1-C2-C3-O3
2	A	607	GOL	O1-C1-C2-O2

All (23) torsion outliers are listed below:

There are no ring outliers.

No monomer is involved in short contacts.

### 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<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	< <b>RSRZ</b> >	#RSRZ $>$ 2	$OWAB( m A^2)$	Q<0.9
1	А	470/555~(84%)	0.43	57 (12%) 4 3	20, 31, 83, 112	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	398	PHE	10.5
1	А	397	ILE	8.2
1	А	419	ILE	8.2
1	А	421	ARG	8.0
1	А	15	MET	6.4
1	А	29	ARG	6.2
1	А	395	LEU	6.1
1	А	23	ALA	6.0
1	А	399	LEU	5.9
1	А	388	LEU	5.4
1	А	27	TYR	5.3
1	А	423	ILE	5.0
1	А	22	HIS	5.0
1	А	418	SER	4.9
1	А	396	ASP	4.7
1	А	387	SER	4.3
1	А	394	SER	4.3
1	А	392	LEU	4.1
1	А	420	GLN	4.0
1	А	32	TYR	4.0
1	А	18	ASN	3.9
1	А	16	PRO	3.8
1	А	19	MET	3.8
1	А	3	THR	3.7
1	А	13	ALA	3.5
1	А	390	GLU	3.5
1	А	354[A]	PHE	3.5

Continued on next page...



Mol	Chain	$\mathbf{Res}$	Type	RSRZ
1	А	26	LYS	3.4
1	А	393	GLN	3.4
1	А	11	ASN	3.3
1	А	319	GLY	3.3
1	А	422	ARG	3.2
1	А	210	TYR	3.1
1	А	383	THR	3.1
1	А	12	ALA	3.1
1	А	391	GLU	3.1
1	А	14	ASP	3.0
1	А	386	SER	3.0
1	А	25	LYS	2.9
1	А	400	ALA	2.9
1	А	426	VAL	2.8
1	А	389	PHE	2.7
1	А	320	PRO	2.7
1	А	21	LYS	2.7
1	А	384	ASP	2.6
1	А	9	LEU	2.6
1	А	17	ALA	2.6
1	А	24	LEU	2.6
1	А	308	LYS	2.6
1	А	30	GLU	2.4
1	A	129	ARG	2.4
1	A	20	ASP	2.3
1	A	424	LYS	2.2
1	A	401	GLU	2.2
1	A	5	TRP	2.1
1	A	323	HIS	2.1
1	A	322	GLN	2.1

Continued from previous page...

#### 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 carbohydrates 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	${f B} ext{-factors}({ m \AA}^2)$	Q<0.9
2	GOL	А	609	6/6	0.40	0.50	$64,\!73,\!76,\!81$	0
2	GOL	А	608	6/6	0.61	0.32	$48,\!53,\!58,\!68$	0
2	GOL	А	613	6/6	0.69	0.28	72,81,87,90	0
2	GOL	А	605	6/6	0.70	0.33	$56,\!58,\!61,\!66$	0
2	GOL	А	612	6/6	0.74	0.34	$32,\!50,\!50,\!50$	0
2	GOL	А	611	6/6	0.76	0.34	$71,\!73,\!74,\!75$	0
2	GOL	А	610	6/6	0.77	0.43	$67,\!70,\!72,\!76$	0
2	GOL	А	603	6/6	0.78	0.21	45,48,51,55	0
2	GOL	А	606	6/6	0.82	0.18	$50,\!55,\!58,\!59$	0
2	GOL	А	607	6/6	0.85	0.41	$41,\!56,\!59,\!68$	0
2	GOL	А	601	6/6	0.85	0.22	$52,\!53,\!56,\!57$	0
2	GOL	A	604	6/6	0.88	0.15	39,48,52,53	0
2	GOL	А	602	6/6	0.93	0.14	31,42,43,53	0

#### 6.5 Other polymers (i)

There are no such residues in this entry.

