Full wwPDB X-ray Structure Validation Report (i)

Oct 3, 2023 – 02:42 AM EDT

PDB ID	:	6OB6
Title	:	Human equilibrative nucleoside transporter-1, S-(4-nitrobenzyl)-6-thioinosine bound, merohedrally twinned
Authors	:	Wright, N.J.; Lee, S.-Y.
Deposited on	:	2019-03-19
Resolution	:	2.90 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 (1)) were used in the production of this report:

MolProbity	:	FAILED
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
buster-report	:	1.1.7 (2018)
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)	:	2.35.1

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 2.90 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 11026 atoms, of which 5514 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 Equilibrative nucleoside transporter 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	365	5536	1874	2770	416	454	22	0	0	0
1	B	357	5398	1823	2710	404	438	23	0	0	0

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP Q99808
A	1	ALA	-	expression tag	UNP Q99808
A	168	PHE	LEU	engineered mutation	UNP Q99808
A	175	ALA	PRO	engineered mutation	UNP Q99808
A	?	-	PRO	deletion	UNP Q99808
A	?	-	GLY	deletion	UNP Q99808
A	?	-	GLU	deletion	UNP Q99808
A	?	-	GLN	deletion	UNP Q99808
A	?	-	GLU	deletion	UNP Q99808
A	?	-	THR	deletion	UNP Q99808
A	?	-	LYS	deletion	UNP Q99808
A	?	-	LEU	deletion	UNP Q99808
A	?	-	ASP	deletion	UNP Q99808
A	?	-	LEU	deletion	UNP Q99808
A	?	-	ILE	deletion	UNP Q99808
A	?	-	SER	deletion	UNP Q99808
A	?	-	LYS	deletion	UNP Q99808
A	?	-	GLY	deletion	UNP Q99808
A	?	-	GLU	deletion	UNP Q99808
A	?	-	GLU	deletion	UNP Q99808
A	?	-	PRO	deletion	UNP Q99808
A	?	-	ARG	deletion	UNP Q99808
A	?	-	ALA	deletion	UNP Q99808
A	?	-	GLY	deletion	UNP Q99808
A	?	-	LYS	deletion	UNP Q99808

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLU	deletion	UNP Q99808
A	?	-	GLU	deletion	UNP Q99808
A	?	-	SER	deletion	UNP Q99808
A	?	-	GLY	deletion	UNP Q99808
A	?	-	VAL	deletion	UNP Q99808
A	?	-	SER	deletion	UNP Q99808
A	?	-	VAL	deletion	UNP Q99808
A	?	-	SER	deletion	UNP Q99808
A	?	-	ASN	deletion	UNP Q99808
A	?	-	SER	deletion	UNP Q99808
A	?	-	GLN	deletion	UNP Q99808
A	288	LYS	ASN	engineered mutation	UNP Q99808
A	457	GLY	-	expression tag	UNP Q99808
A	458	THR	-	expression tag	UNP Q99808
A	459	GLU	-	expression tag	UNP Q99808
A	460	LEU	-	expression tag	UNP Q99808
A	461	LEU	-	expression tag	UNP Q99808
A	462	GLN	-	expression tag	UNP Q99808
A	463	VAL	-	expression tag	UNP Q99808
A	464	ASP	-	expression tag	UNP Q99808
A	465	THR	-	expression tag	UNP Q99808
A	466	ASN	-	expression tag	UNP Q99808
A	467	SER	-	expression tag	UNP Q99808
A	468	LEU	-	expression tag	UNP Q99808
A	469	GLU	-	expression tag	UNP Q99808
A	470	VAL	-	expression tag	UNP Q99808
A	471	LEU	-	expression tag	UNP Q99808
A	472	PHE	-	expression tag	UNP Q99808
A	473	GLN	-	expression tag	UNP Q99808
B	0	MET	-	expression tag	UNP Q99808
B	1	ALA	-	expression tag	UNP Q99808
B	168	PHE	LEU	engineered mutation	UNP Q99808
B	175	ALA	PRO	engineered mutation	UNP Q99808
B	?	-	PRO	deletion	UNP Q99808
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B	?	-	GLU	deletion	UNP Q99808
B	?	-	GLN	deletion	UNP Q99808
B	?	-	GLU	deletion	UNP Q99808
B	?	-	THR	deletion	UNP Q99808
B	?	-	LYS	deletion	UNP Q99808
B	?	-	LEU	deletion	UNP Q99808
B	?	-	ASP	deletion	UNP Q99808

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	LEU	deletion	UNP Q99808
B	?	-	ILE	deletion	UNP Q99808
B	?	-	SER	deletion	UNP Q99808
B	?	-	LYS	deletion	UNP Q99808
B	?	-	GLY	deletion	UNP Q99808
B	?	-	GLU	deletion	UNP Q99808
B	?	-	GLU	deletion	UNP Q99808
B	?	-	PRO	deletion	UNP Q99808
B	?	-	ARG	deletion	UNP Q99808
B	?	-	ALA	deletion	UNP Q99808
B	?	-	GLY	deletion	UNP Q99808
B	?	-	LYS	deletion	UNP Q99808
B	?	-	GLU	deletion	UNP Q99808
B	?	-	GLU	deletion	UNP Q99808
B	?	-	SER	deletion	UNP Q99808
B	?	-	GLY	deletion	UNP Q99808
B	?	-	VAL	deletion	UNP Q99808
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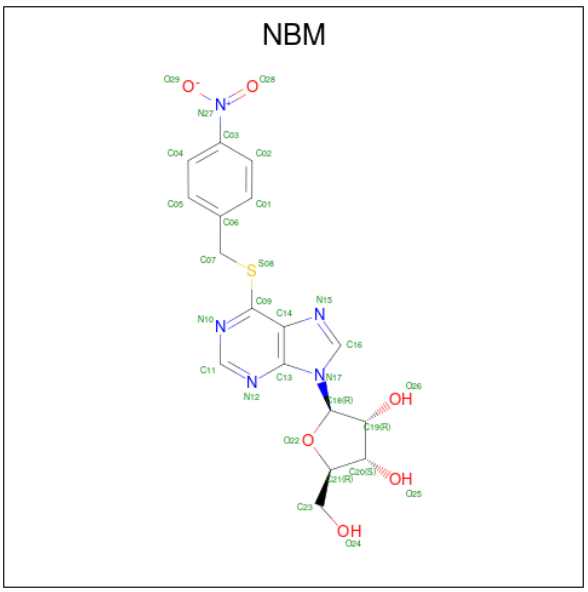
B	460	LEU	-	expression tag	UNP Q99808
B	461	LEU	-	expression tag	UNP Q99808
B	462	GLN	-	expression tag	UNP Q99808
B	463	VAL	-	expression tag	UNP Q99808
B	464	ASP	-	expression tag	UNP Q99808
B	465	THR	-	expression tag	UNP Q99808
B	466	ASN	-	expression tag	UNP Q99808
B	467	SER	-	expression tag	UNP Q99808
B	468	LEU	-	expression tag	UNP Q99808
B	469	GLU	-	expression tag	UNP Q99808
B	470	VAL	-	expression tag	UNP Q99808
B	471	LEU	-	expression tag	UNP Q99808
B	472	PHE	-	expression tag	UNP Q99808
B	473	GLN	-	expression tag	UNP Q99808

- Molecule 2 is 6-{[(4-nitrophenyl)methyl]sulfanyl}-9-beta-D-ribofuranosyl-9H-purine

(three-letter code: NBM) (formula: $C_{17}H_{17}N_5O_6S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	S	0	0
			46	17	17	5	6	1		
2	B	1	Total	C	H	N	O	S	0	0
			46	17	17	5	6	1		

MolProbity and EDS failed to run properly - this section is therefore empty.

3 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α, β, γ	72.53Å 72.53Å 335.46Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	62.81 – 2.90	Depositor
% Data completeness (in resolution range)	74.9 (62.81-2.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.51 (at 2.91Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.205 , 0.252	Depositor
Wilson B-factor (Å^2)	45.8	Xtriage
Anisotropy	0.060	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.36$, $< L^2 > = 0.19$	Xtriage
Estimated twinning fraction	0.377 for h,-h-k,-l	Xtriage
Total number of atoms	11026	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.33% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

4 Model quality (i)

4.1 Standard geometry (i)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts (i)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains (i)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA (i)

MolProbity failed to run properly - this section is therefore empty.

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

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

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 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	NBM	B	501	-	28,32,32	4.22	9 (32%)	31,46,46	1.47	4 (12%)
2	NBM	A	501	-	28,32,32	4.33	9 (32%)	31,46,46	1.67	5 (16%)

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	NBM	B	501	-	-	0/8/31/31	0/4/4/4
2	NBM	A	501	-	-	0/8/31/31	0/4/4/4

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	NBM	O22-C18	14.17	1.60	1.41
2	B	501	NBM	O22-C18	13.70	1.60	1.41
2	B	501	NBM	C19-C18	-12.95	1.34	1.53
2	A	501	NBM	C19-C18	-12.93	1.34	1.53
2	A	501	NBM	O22-C21	-7.85	1.27	1.45
2	B	501	NBM	O22-C21	-7.84	1.27	1.45
2	A	501	NBM	C09-S08	6.68	1.84	1.76
2	B	501	NBM	C09-S08	6.01	1.83	1.76
2	A	501	NBM	C07-C06	2.87	1.57	1.51
2	A	501	NBM	C01-C06	2.68	1.44	1.38
2	B	501	NBM	C07-C06	2.66	1.57	1.51
2	B	501	NBM	C01-C06	2.44	1.44	1.38
2	A	501	NBM	O26-C19	2.29	1.48	1.43
2	A	501	NBM	C20-C21	2.27	1.58	1.53
2	B	501	NBM	O25-C20	-2.17	1.37	1.43
2	A	501	NBM	O25-C20	-2.15	1.37	1.43
2	B	501	NBM	C20-C21	2.15	1.58	1.53
2	B	501	NBM	O26-C19	2.14	1.48	1.43

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	501	NBM	N12-C11-N10	-4.96	120.93	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	501	NBM	N12-C11-N10	-4.92	120.99	128.68
2	A	501	NBM	C07-S08-C09	4.81	108.06	101.52
2	B	501	NBM	C20-C19-C18	3.00	105.50	100.98
2	A	501	NBM	C20-C19-C18	2.89	105.33	100.98
2	A	501	NBM	C13-C14-N15	-2.77	106.52	109.40
2	B	501	NBM	C07-S08-C09	2.45	104.85	101.52
2	B	501	NBM	C06-C07-S08	2.08	118.80	110.62
2	A	501	NBM	C11-N10-C09	2.06	120.92	116.36

There are no chirality outliers.

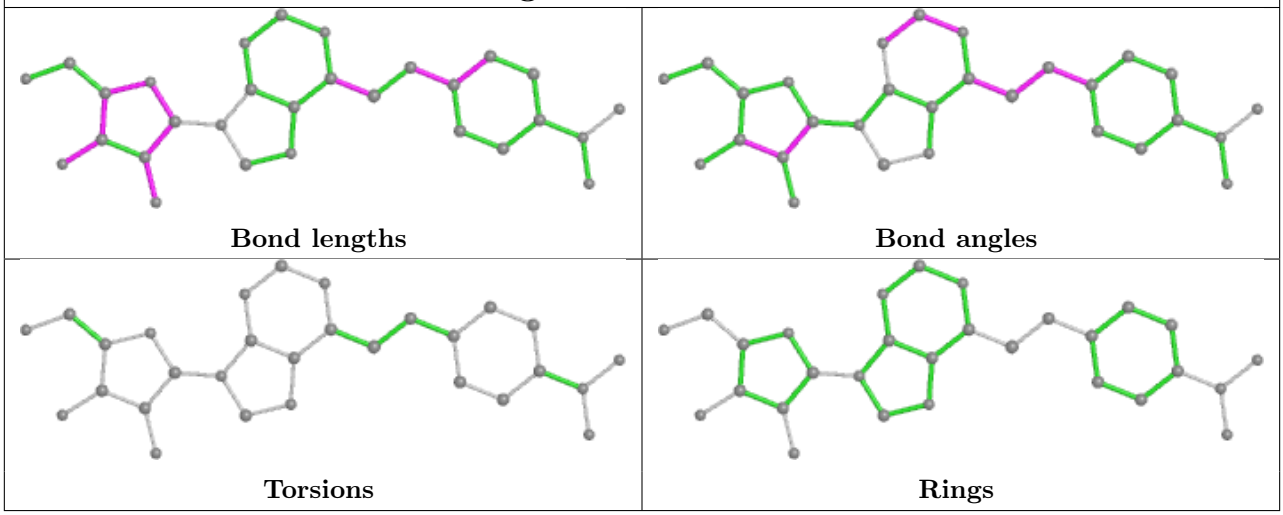
There are no torsion outliers.

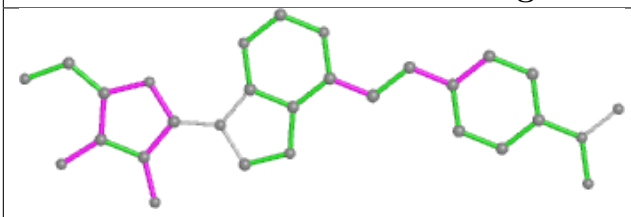
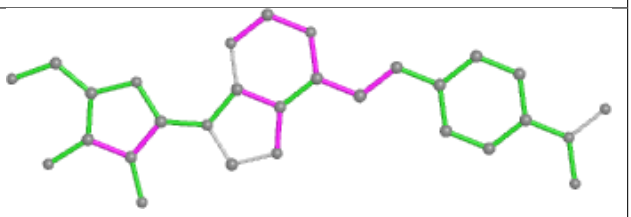
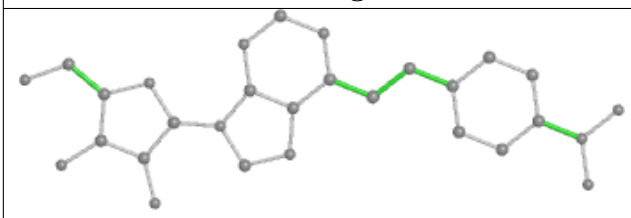
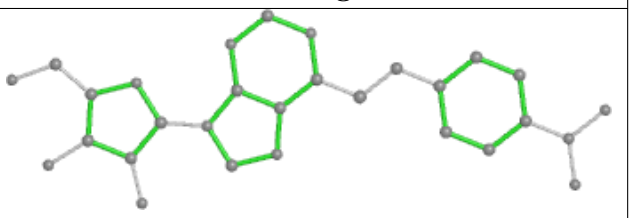
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand NBM B 501



Ligand NBM A 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

5 Fit of model and data (i)

5.1 Protein, DNA and RNA chains (i)

EDS failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates (i)

EDS failed to run properly - this section is therefore empty.

5.4 Ligands (i)

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers (i)

EDS failed to run properly - this section is therefore empty.