

Correction to “Substrate Dynamics Contribute to Enzymatic Specificity in Human and Bacterial Methionine Adenosyltransferases”

Madhuri Gade, Li Lynn Tan, Adam M. Damry, Mahakaran Sandhu, Joseph S. Brock, Andie Delaney, Alejandro Villar-Briones, Colin J. Jackson,* and Paola Laurino*

JACS Au 2021, 1 (12), 2349–2360. DOI: 10.1021/jacsau.1c00464



Cite This: JACS Au 2022, 2, 258–258



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There is an error in the k_{cat} unit conversion. The correct values in Table 1 should read as follows.

Table 1. Kinetic Parameters^a for SNM Analogue Formation by hMAT2A and eMAT

enzyme:substrate	k_{cat} (s ⁻¹)	K_{M} (mM)	$k_{\text{cat}}/K_{\text{M}}$ (M ⁻¹ s ⁻¹)
hMAT2A:ATP	0.21 ± 0.016	0.27 ± 0.07	777
hMAT2A:GTP	0.9 ± 0.166	1.26 ± 0.40	714
hMAT2A:CTP	0.027 ± 0.001	0.08 ± 0.02	337
hMAT2A:UTP	0.32 ± 0.038	0.97 ± 0.2	329
eMAT:ATP	0.018 ± 0.001	0.06 ± 0.02	300
eMAT:GTP	0.005 ± 0.001	0.97 ± 0.30	5
eMAT:CTP	0.046 ± 0.003	1.3 ± 0.25	35
eMAT:UTP	0.006 ± 0.001	2.90 ± 0.7	2

^aKinetic parameters for the SNM analogue formation by hMAT2A and eMAT using a concentration of ATP, GTP, CTP, and UTP in the range of 0.025–5 mM and a fixed saturating concentration of methionine (10 mM) in the presence of HEPES (100 mM), KCl (50 mM), and MgCl₂ (10 mM), pH 8, at 37 °C. [hMAT2A] was 0.5 μM and [eMAT] was 0.5 μM for ATP, 5 μM for GTP and CTP, and 10 μM for UTP. Product formation was analyzed by UPLC and data fitted to the Michaelis–Menten equation using GraphPad Prism 7.02 (Figure S1).

Published: January 7, 2022

