

Supplementary Tables

Collection of discrimination indices for metabolic enzymes that can act on two substrates having small and well-defined structural differences.

Supplementary Table 1 - Enzyme discrimination towards alternative substrates lacking a methyl group

Data for the present table were obtained by defining first a list of couples of common metabolites differing by just one methyl group (e.g., L-threonine/L-serine; 2-ketobutyrate/pyruvate; thymine/uracil and so forth). Then, for each pair of substrates, the BRENDA repository of enzyme data [1] was thoroughly searched using the following criteria

- 1) The enzyme must have been tested against the two substrates in the same study and the catalytic parameters for the two substrates must have been obtained under otherwise identical conditions.
- 2) The methyl group must not be directly involved in the reaction (e.g., in methyltransferases) nor change substantially the chemical properties of an adjacent group undergoing reaction (e.g., change an aldehyde into a ketone) .
- 3) Only cases where the methyl-containing substrate was preferred are included. When the kinetics of the enzyme under examination showed cooperativity, an approximate discrimination index was calculated based on the ratio of $k_{cat}/S_{0.5}$ values for the two substrates. If, in the same study, selectivity was assessed under more than one condition (e.g., at different pH values, using different, physiologically available cosubstrates etc) the table entry refers to the condition yielding the highest discrimination index.

The data list is ordered according to increasing substrate mass. Only the 25 cases with the highest discrimination index – indicated as $(k_{cat}/K_M)_{ps}/(k_{cat}/K_M)_{as}$ - are shown in Figure 1a.

Abbreviation	Enzyme	Preferred Substrate	Alternative substrate	$(k_{cat}/K_M)_{ps}/(k_{cat}/K_M)_{as}$	Ref.
		1-propanol	Ethanol		
ADH <i>A. pernix</i>	Alcohol dehydrogenase from <i>Aeropyrum pernix</i>	$k_{cat}/K_M=0.25 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0.017 \text{ mM}^{-1}\text{s}^{-1}$	14.7	[2]
ADH <i>S. solfa</i>	Alcohol dehydrogenase from <i>Sulfolobus solfataricus</i>	$k_{cat}/K_M=212 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=6.7 \text{ mM}^{-1}\text{s}^{-1}$	31.6	[3]
		2-ketobutyrate	Pyruvate		
AlaDH <i>A. fulgid</i>	Alanine dehydrogenase from <i>Archaeoglobus fulgidus</i>	$k_{cat}/K_M=739 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=298 \text{ mM}^{-1}\text{s}^{-1}$	2.5	[4]
		2-ketoisovalerate	2-ketobutyrate		
KADC <i>M. tuber</i>	α -ketoacid decarboxylase from <i>Mycobacterium tuberculosis</i>	$k_{cat}/K_M=1.16 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0.42 \text{ mM}^{-1}\text{s}^{-1}$	2.8	[5]

		L-valine	L-2-aminobutyrate		
ValDH <i>S. cinnam</i>	L-valine dehydrogenase from <i>Streptomyces cinnamomensis</i>	$k_{cat}/K_M=21,76 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=5,3 \text{ mM}^{-1}\text{s}^{-1}$	4.1	[6]
ValDH <i>S. fradiae</i>	L-valine dehydrogenase from <i>Streptomyces fradiae</i>	$V/K_M=897 \mu\text{kat}^{-1}\text{mg}^{-1} \text{ mM}^{-1}$	$V/K_M=239 \mu\text{kat}^{-1} \text{ mg}^{-1} \text{ mM}^{-1}$	3.8	[7]*
ValDH <i>S. aureof</i>	L-valine dehydrogenase from <i>Streptomyces aureofaciens</i>	$V/K_M=51 \mu\text{kat}^{-1} \text{ mg}^{-1} \text{ mM}^{-1}$	$V/K_M=2.8 \mu\text{kat}^{-1} \text{ mg}^{-1} \text{ mM}^{-1}$	18.1	[8]*
		L-threonine	L-serine		
ThrAL <i>E. histol</i>	L-threonine ammonia-lyase from <i>Entamoeba histolytica</i>	$V/K_M=0.7$ (units unspecified)	$V/K_M=0.2$ (units unspecified)	3.5	[9]
ThrAL <i>S. lycop</i>	L-threonine ammonia-lyase from <i>Solanum lycopersicum</i>	$V/K_M=83.3/2.3=36.2 \text{ U mg}^{-1} \text{ mM}^{-1}$	$V/K_M=55.5/3=18.5 \text{ U mg}^{-1} \text{ mM}^{-1}$	2	[10]
		L-isoleucine	L-valine		
IleMOX <i>L. japon</i>	L-isoleucine N-monooxygenase from <i>Lotus japonicus</i>	$k_{cat}/K_M=2.03 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0.31 \text{ mM}^{-1}\text{s}^{-1}$	6.4	[11]
BCAT <i>Thermo</i>	branched-chain-amino-acid transaminase from <i>Thermococcus sp. CKU-1</i>	$k_{cat}/K_M=350 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=38 \text{ mM}^{-1}\text{s}^{-1}$	9.2	[12]
BCAT <i>H. sapie</i>	Branched-chain-amino-acid transaminase from <i>Homo sapiens</i>	$k_{cat}/K_M=3359 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=618 \text{ mM}^{-1}\text{s}^{-1}$	5.4	[13]
		2-hydroxy-2-ethyl 3-ketobutyrate	Acetolactate		
KARI <i>E. coli</i>	Ketol-acid reductoisomerase (NADP+) from <i>Escherichia coli</i>	$k_{cat}/K_M=11.67 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=7.14 \text{ mM}^{-1}\text{s}^{-1}$	1.6	[14]
		Thymidine	Deoxyuridine		
TK <i>T. brucei</i>	Thymidine kinase from <i>Trypanosoma brucei</i>	$k_{cat}/K_M=400 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=63 \text{ mM}^{-1}\text{s}^{-1}$	6.4	[15]
TK <i>L. major</i>	Thymidine kinase from <i>Leishmania major</i>	$k_{cat}/K_M=2380 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=276 \text{ mM}^{-1}\text{s}^{-1}$	8.6	[16]
TK <i>C. parvum</i>	Thymidine kinase from <i>Cryptosporidium parvum</i>	$k_{cat}/K_M=6.7 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=4.5 \text{ mM}^{-1}\text{s}^{-1}$	1.5	[17]

		dTMP	dUMP		
dTMK <i>Y. pestis</i>	dTMP kinase from <i>Yersinia pestis</i>	$k_{cat}/K_M=214 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=2.22 \text{ mM}^{-1}\text{s}^{-1}$	97.3	[18]
dTMPK <i>E. coli</i>	dTMP kinase from <i>Escherichia coli</i>	$k_{cat}/K_M=1320 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=4.8 \text{ mM}^{-1}\text{s}^{-1}$	275	[18]
dTMPK <i>P. falcip</i>	dTMP kinase from <i>Plasmodium falciparum</i>	$k_{cat}/K_M=154.5 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=5.2 \text{ mM}^{-1}\text{s}^{-1}$	29.7	[19]
dTMPK <i>H. sapie</i>	dTMP kinase from <i>Homo sapiens</i>	$k_{cat}/K_M=150 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=28 \text{ mM}^{-1}\text{s}^{-1}$	5.4	[20]
		dTDP	dUDP		
NDPK <i>S. cerev</i>	Nucleotide diphosphate kinase from <i>Saccharomyces cerevisiae</i>	$V/K_M=794 \text{ min}^{-1}$	$V/K_M=405 \text{ min}^{-1}$	2	[21]
		Propionyl-CoA	Acetyl-CoA		
PrCoAS <i>S. chole</i>	Propionyl-CoA synthetase from <i>Salmonella choleraesuis</i>	$k_{cat}/K_M=15 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=2.5 \text{ mM}^{-1}\text{s}^{-1}$	6	[22]
PrCoAL <i>R. solan</i>	Propionyl-CoA synthetase from <i>Ralstonia solanacearum</i>	$k_{cat}/K_M=6.8 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=3.6 \text{ mM}^{-1}\text{s}^{-1}$	1.9	[22]
PrCoAC <i>L. interr</i>	Propionyl-CoA carboxylase from <i>Leptospira interrogans</i>	$k_{cat}/K_M=26 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0.144 \text{ mM}^{-1}\text{s}^{-1}$	181	[23]
PrCoAC <i>M. xant</i>	Propionyl-CoA carboxylase from <i>Myxococcus xanthus</i>	$V/K_M=6.56/0.032=205 \text{ U mg}^{-1} \text{ mM}^{-1}$	$V/K_M=0.94/0.25=3.76 \text{ U mg}^{-1} \text{ mM}^{-1}$	54.5	[24]
		Methylmalonyl-CoA	Malonyl-CoA		
MMCoAD <i>V. alcal</i>	(S)-methylmalonyl-CoA decarboxylase from <i>Veillonella alcalescens</i>	$V/K_M=V/0.007$ (units unspecified)	$V/K_M=V/0.035$ (units unspecified)	5	[25]*
MMCoAH <i>R. norveg</i>	(S)-methylmalonyl-CoA hydrolase from <i>Rattus norvegicus</i>	$k_{cat}/K_M=23,3/0.7=33.3 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=5,3/0.7=7.6 \text{ mM}^{-1}\text{s}^{-1}$	4.4	[26]

Supplementary Table 2 - Enzyme discrimination towards alternative substrates lacking a hydroxyl group

Data for the present table were obtained similarly to those in Supplementary Table 1. First a list of pairs of common metabolites (differing by just one hydroxyl group) was drawn, (e.g., L-threonine/2-aminobutyrate; ribose/deoxyribose; tyrosine/phenylalanine and so forth). Then, the scientific literature was thoroughly searched (using again the BRENDA repository as a starting point [1]) to identify enzymes known to react with both substrates in a pair.

Only cases where the OH-containing substrate was preferred are included.

When the kinetics of the enzyme under examination showed cooperativity, an approximate discrimination index was calculated based on the ratio of $k_{cat}/S_{0.5}$ values for the two substrates. If, in the same study, selectivity was assessed under more than one condition (e.g., at different pH values, using different, physiologically available cosubstrates etc) the table entry refers to the condition yielding the highest discrimination index (only the 25 enzymes in this table with the highest discrimination index are shown in Figure 1b).

Notably, for some enzymes, it was reported that an alternative substrate lacking a specific OH group is completely unreactive. Barring the trivial cases in which the hydroxyl group is directly involved in the reaction (either because it undergoes transformation or because it provides catalytic assistance during the transformation [27]) it is possible that the 'complete absence' of activity reflects a sensitivity limit of the assay used. For example Arivett et al [28] reported that an *E. coli* nucleoside hydrolase exhibited no activity against 2'-deoxynucleosides. However, this does not mean that the discrimination index of the hydrolase is infinite, but simply that reaction with the deoxy substrate was too slow to be detected under the conditions of the assay.

Abbreviation	Enzyme	Preferred Substrate	Alternative substrate	$(k_{cat}/K_M)_{ps}/(k_{cat}/K_M)_{as}$	Ref.
		Glycolaldehyde	Acetaldehyde		
HPAI <i>E. coli</i>	4-hydroxy-2-oxovalerate aldolase from <i>Escherichia coli</i>	$k_{cat}/K_M=5.27 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=3.3 \text{ mM}^{-1}\text{s}^{-1}$	1.6	[29]
		3-hydroxy propionaldehyde	propionaldehyde		
PDDH <i>K. pneu</i>	1,3-propanediol oxidoreductase from <i>Klebsiella pneumoniae</i>	$k_{cat}/K_M=76.6 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=1.1 \text{ mM}^{-1}\text{s}^{-1}$	69.6	[30]
		Glycerol	1,3-propanediol		
GK <i>C. mycod</i>	Glycerol kinase from <i>Candida mycoderma</i>	$V/K_M=0.5/0.044=11.4 \text{ U mM}^{-1}$	$V/K_M=0.0025/86=2.9 \times 10^{-5} \text{ U mM}^{-1}$	393000	[31]
GK <i>S. cerev</i>	Glycerol kinase from <i>Saccharomyces cerevisiae</i>	$V/K_M=0.203/0.041=5 \text{ U mM}^{-1}$	$V/K_M=0.002/51=3.9 \times 10^{-5} \text{ U mM}^{-1}$	125000	[31]
GK <i>E. coli</i>	Glycerol kinase from <i>Escherichia coli</i>	$V/K_M=0.823/0.042=19.6 \text{ U mM}^{-1}$	$V/K_M=0.004/21=2 \times 10^{-4} \text{ U mM}^{-1}$	100000	[31]
GK <i>B. stear</i>	Glycerol kinase from <i>Bacillus stearothermophilus</i>	$V/K_M=0.491/0.054=9.1 \text{ U mM}^{-1}$	$V/K_M=0.015/80=1.8 \times 10^{-4} \text{ U mM}^{-1}$	49400	[31]

		Hydroxypyruvate	Pyruvate		
GHPR <i>S. meli</i>	Glyoxylate-Hydroxypyruvate reductase from <i>Sinorhizobium meliloti</i>	$k_{cat}/K_M=1.2 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0.057 \text{ mM}^{-1}\text{s}^{-1}$	20.9	[32]
		L-serine	L-alanine		
SGAT <i>O. sati</i>	Serine:glyoxylate aminotransferase from <i>Oryza sativa</i>	$k_{cat}/K_M=19.82/2.41=8.22 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=8.56/52.5=0.16 \text{ mM}^{-1}\text{s}^{-1}$	51.4	[33]
		L-3-hydroxyproline	L-proline		
HProE <i>T. lito</i>	Hydroxyproline epimerase from <i>Thermococcus litoralis</i>	$k_{cat}/K_M=430 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=138 \text{ mM}^{-1}\text{s}^{-1}$	3.1	[34]
		Tyramine	Phenylethylamine		
AANAT <i>D. melan</i>	Arylalkylamine N-acetyltransferase from <i>Drosophila melanogaster</i>	$k_{cat}/K_M=1600 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=500 \text{ mM}^{-1}\text{s}^{-1}$	3.2	[35]
		5-hydroxy tryptamine (serotonin)	Tryptamine		
SHT <i>C. annu</i>	Hydroxycinnamoyl-CoA:Serotonin N-(Hydroxycinnamoyl)transferase from <i>Capsicum annuum</i>			15.1	[36]
SS <i>R. serp</i>	Strictosidine synthase from <i>Rauwolfia serpentina</i>	$k_{cat}/K_M=249.29 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=147.92 \text{ mM}^{-1}\text{s}^{-1}$	1.7	[37]
		4-hydroxy phenylpyruvate	Phenylpyruvate		
HPPR <i>W. fluor</i>	Hydroxyphenylpyruvate reductase in <i>Wickerhamia fluorescens</i>	$k_{cat}/K_M=150/0.4=375 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=73/0.64=114.06 \text{ mM}^{-1}\text{s}^{-1}$	3.3	[38]
		L-tyrosine	L-phenylalanine		
TMOX <i>H. sapi</i>	Tyrosine 3-monooxygenase in <i>Homo sapiens</i>	$k_{cat}/K_M=156.33 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=16 \text{ mM}^{-1}\text{s}^{-1}$	9.8	[39]
TAT <i>P. somni</i>	Tyrosine transaminase from <i>Papaver somniferum</i>	$k_{cat}/K_M=0.13 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0.01 \text{ mM}^{-1}\text{s}^{-1}$	13	[40]
TAT <i>M. muscu</i>	Tyrosine transaminase from <i>Mus musculus</i>	$k_{cat}/K_M=10,66 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=1,33 \text{ mM}^{-1}\text{s}^{-1}$	8	[41]
TAT <i>H. sapi</i>	Tyrosine transaminase from <i>Homo sapiens</i>	$k_{cat}/K_M=87 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0,0064 \text{ mM}^{-1}\text{s}^{-1}$	13593	[42]

YARS <i>E. coli</i>	tyrosyl-tRNA synthetase from <i>Escherichia coli</i>	$k_{cat}/K_M=7800 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0.059 \text{ mM}^{-1}\text{s}^{-1}$	132200	[43]
YARS <i>B. subti</i>	tyrosyl-tRNA synthetase from <i>Bacillus subtilis</i>	$k_{cat}/K_M=980 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0.0098 \text{ mM}^{-1}\text{s}^{-1}$	100000	[43]
		3,4 dihydroxy phenylalanine	L-tyrosine		
AAADC <i>P. somni</i>	Aromatic amino acid decarboxylase from <i>Papaver somniferum</i> (isozyme 2)	$V/K_M=0.21/1=0.21 \text{ fkat mg}^{-1} \text{ mM}^{-1}$	$V/K_M=0.12/1=0.12 \text{ fkat mg}^{-1} \text{ mM}^{-1}$	1.8	[44]
AAADC <i>S. scrofa</i>	Aromatic amino acid decarboxylase from <i>Sus scrofa</i>			6130	[45]
		D-ribose-5-P	2-deoxy-D-ribose-5-P		
TK <i>S. cerev</i>	Transketolase from <i>Saccharomyces cerevisiae</i>	$k_{cat}/K_M=310 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0.12 \text{ mM}^{-1}\text{s}^{-1}$	2580	[46]
		Inosine	2- Deoxyinosine		
PNP <i>P. yoelii</i>	Purine nucleoside phosphorylase from <i>Plasmodium yoelii</i>	$k_{cat}/K_M=400 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=15 \text{ mM}^{-1}\text{s}^{-1}$	26.7	[47]
PNP <i>P. falcip</i>	Purine nucleoside phosphorylase from <i>Plasmodium falciparum</i>	$k_{cat}/K_M=230 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=9.8 \text{ mM}^{-1}\text{s}^{-1}$	23.5	[47]
		AMP	2-deoxy-AMP		
ADK <i>E. coli</i>	Adenylate kinase from <i>Escherichia coli</i>	$V/K_M=1247/0.038=32815 \text{ U mg}^{-1} \text{ mM}^{-1}$	$V/K_M=875/0.85=2,38 \text{ U mg}^{-1} \text{ mM}^{-1}$	31.8	[48]
ADK <i>H. sapi</i>	Adenylate kinase (mitochondrial) from <i>Homo sapiens</i>	$V/K_M=17 \text{ U mg}^{-1} \text{ mM}^{-1}$	$V/K_M=0.17 \text{ U mg}^{-1} \text{ mM}^{-1}$	100	[49]
		UDP	2-deoxy-UDP		
NDPK <i>S. cerev</i>	Nucleotide diphosphate kinase from <i>Saccharomyces cerevisiae</i>	$V/K_M=473 \text{ min}^{-1}$	$V/K_M=405 \text{ min}^{-1}$	1.2	[21]
		ATP	2-deoxy-ATP		
PGK <i>H. sapi</i>	Phosphoglycerate kinase from <i>Homo sapiens</i>	$k_{cat}/K_M=1700 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=30 \text{ mM}^{-1}\text{s}^{-1}$	56.7	[50]
PRPPS <i>S. olea</i>	Phosphoribosyl diphosphate synthase from <i>Spinacia olearia</i>	$V/K_M=13.1/0.17=77 \text{ U mg}^{-1} \text{ mM}^{-1}$	$V/K_M=12.8/0.233=77 \text{ U mg}^{-1} \text{ mM}^{-1}$	1.4	[51]
ACoAS <i>B. japon</i>	Acetyl-CoA synthetase from <i>Bradyrhizobium japonicum</i>	$V/K_M=18/0.275=65.4 \text{ U mg}^{-1} \text{ mM}^{-1}$	$V/K_M=10.2/2.3=2,38 \text{ U mg}^{-1} \text{ mM}^{-1}$	14.7	[52]*
MAT <i>M. jann</i>	S-adenosyl	$V/K_M=V/0.26$ (units)	$V/K_M=0.81xV/0.42$	2	[53]

	methionine synthetase from <i>Methanococcus jannaschii</i>	unspecified)	(units unspecified)		
		GTP	2- deoxy-GTP		
PEPCK <i>A. suum</i>	Phosphoenol pyruvate carboxykinase (GTP-dependent) from <i>Ascaris suum</i>	$k_{cat}/K_M=272 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=3.2 \text{ mM}^{-1}\text{s}^{-1}$	84.1	[54]

Supplementary Table 3 - Enzyme discrimination towards alternative substrates longer by one methylene group

Data for the present table were obtained similarly to those in Supplementary Tables 1 and 2. In this case, the initial list of metabolite pairs was constituted of molecules with an approximately linear structure. The alternative substrate was longer by one methylene (-CH₂-) group with respect to the reference (preferred) substrate.

The data list is ordered according to increasing substrate mass. Only the 25 enzymes in this table with the highest discrimination index are shown in Figure 1c.

Abbreviation	Enzyme	Preferred Substrate	Alternative substrate	$k_{cat}/K_M)_{ps}/(k_{cat}/K_M)_{as}$	Ref.
		Acetate	Propionate		
AcCoAS <i>B. japon</i>	Acetyl-CoA synthetase from <i>Bradyrhizobium japonicum</i>	$k_{cat}/K_M=18/.05=360$ U mg ⁻¹ mM ⁻¹	$k_{cat}/K_M=2.5/0.2=12.5$ U mg ⁻¹ mM ⁻¹	28.8	[52]
		Pyruvate	α-ketobutyrate		
LLADH <i>P. falcip</i>	L-Lactate dehydrogenase from <i>Plasmodium falciparum</i>	$k_{cat}/K_M=96/0,055=1700$ mM ⁻¹ s ⁻¹	$k_{cat}/K_M=80/0,6=0,0026$ mM ⁻¹ s ⁻¹	130	[55]
LLADH <i>S. tuber</i>	L-Lactate dehydrogenase from <i>Solanum tuberosum</i>	$V/K_M=6.5/0,2=32.5$ U mg ⁻¹ mM ⁻¹	$V/K_M=5.1/0,2=0.066$ U mg ⁻¹ mM ⁻¹	1960	[2]
DLADH <i>P. aeru</i>	D-Lactate dehydrogenase from <i>Pseudomonas aeruginosa</i>	$k_{cat}/K_M=4000$ mM ⁻¹ s ⁻¹	$k_{cat}/K_M=150$ mM ⁻¹ s ⁻¹	26.7	[56]
DLDH <i>A. coli</i>	D-Lactate dehydrogenase from <i>Escherichia coli</i>	$k_{cat}/K_M=160$ mM ⁻¹ s ⁻¹	$k_{cat}/K_M=1$ mM ⁻¹ s ⁻¹	160	[56]
POR <i>M. marip</i>	Pyruvate oxidoreductase (pyruvate synthase) from <i>Methanococcus maripaludis</i>	$V/K_M=7.7/0,115=67$ U mg ⁻¹ mM ⁻¹	$V/K_M=3.6/0,205=17.6$ U mg ⁻¹ mM ⁻¹	3.8	[57]
		β-alanine	γ-aminobutyrate		
CS <i>H. sapi</i>	Carnosine synthase from <i>Homo sapiens</i>	$k_{cat}/K_M=1.28$ mM ⁻¹ s ⁻¹	$k_{cat}/K_M=0.05$ mM ⁻¹ s ⁻¹	25.6	[58]
CS <i>M. musc</i>	Carnosine synthase from <i>Mus musculus</i>	$k_{cat}/K_M=1.16$ mM ⁻¹ s ⁻¹	$k_{cat}/K_M=0.07$ mM ⁻¹ s ⁻¹	16.6	[58]
CS <i>G. gallus</i>	Carnosine synthase from <i>Gallus gallus</i>	$k_{cat}/K_M=6.03$ mM ⁻¹ s ⁻¹	$k_{cat}/K_M=0.44$ mM ⁻¹ s ⁻¹	13.7	[58]
		L-alanine	L-2-aminobutyrate		
AlaDH <i>B. subt</i>	Alanine dehydrogenase from <i>Bacillus subtilis</i>			765	[59]
AlaDH <i>B. sphae</i>	Alanine dehydrogenase from <i>Bacillus sphaericus</i>			801	[60]

		L-serine	L-homoserine		
SAT <i>S. laven</i>	L-serine O-acetyltransferase from <i>Streptomyces lavendulae</i>	$k_{cat}/K_M=0.317 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0.015 \text{ mM}^{-1}\text{s}^{-1}$	21.1	[61]
		L-valine	L-leucine		
ValDH <i>S. cinnam</i>	Valine dehydrogenase (NADP+) from <i>Streptomyces cinnamomensis</i>	$k_{cat}/K_M=28,3/1,3=21,7 \text{ mM}^{-1}\text{s}^{-1}$	$11,9/4=2,95 \text{ mM}^{-1}\text{s}^{-1}$	7.36	[6]
BCAT <i>S. lycop</i>	Branched-chain-amino-acid transaminase from <i>Solanum lycopersicum</i>	$k_{cat}/K_M=80 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=40 \text{ mM}^{-1}\text{s}^{-1}$	2	[62]
BCAT <i>S. penn</i>	Branched-chain-amino-acid transaminase from <i>Solanum pennellii</i>	$k_{cat}/K_M=70 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=61 \text{ mM}^{-1}\text{s}^{-1}$	1.15	[62]
DDAF <i>P. agglo</i>	3-[[[(2R,3R)-3-carboxyoxiran-2-yl]carbonyl]amino]-L-alanine-L-valine ligase from <i>Pantoea agglomerans</i>	$k_{cat}/K_M=0.52 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0,024 \text{ mM}^{-1}\text{s}^{-1}$	21.7	[63]
		L-asparagine	L-glutamine		
AsnH <i>T. gammat</i>	Asparaginase from <i>Thermococcus gammatolerans</i>	$k_{cat}/K_M=572.1 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=52.1 \text{ mM}^{-1}\text{s}^{-1}$	11	[64]
		L-ornithine	L-lysine		
OCCAT <i>P. savas</i>	Ornithine carbamoyltransferase from <i>Pseudomonas savastanoi</i>	$k_{cat}/K_M=49/1,1=44,5 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0,0036/25=0,00014 \text{ mM}^{-1}\text{s}^{-1}$	317860	[65]
OCCO <i>O. oeni</i>	Ornithine decarboxylase From <i>Oenococcus oeni</i>	$k_{cat}/K_M=9,2 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0,02 \text{ mM}^{-1}\text{s}^{-1}$	460	[66]
OCCO <i>L. brevis</i>	Ornithine decarboxylase From <i>Lactobacillus brevis</i>	$k_{cat}/K_M=4,7 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0,08 \text{ mM}^{-1}\text{s}^{-1}$	58.8	[66]
OCCO <i>N. glutin</i>	Ornithine decarboxylase from <i>Nicotiana glutinosa</i>	$k_{cat}/K_M=77,8/0,56=138,9 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0,24/1,59=0,15 \text{ mM}^{-1}\text{s}^{-1}$	926	[67]
		L-aspartate	L-glutamate		
AspNAT <i>H. sapi</i>	aspartate N-acetyltransferase from <i>Homo sapiens</i>	$k_{cat}/K_M=0,071/0,16=0,44 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0,023/8,6=0,0026 \text{ mM}^{-1}\text{s}^{-1}$	165	[68]
		D-aspartate	D-glutamate		
DAO <i>S. scrofa</i>	D-aspartate oxidase from <i>Sus scrofa</i>	$k_{cat}/K_M=14.9 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0.14 \text{ mM}^{-1}\text{s}^{-1}$	106	[69]
DAO <i>B. taurus</i>	D-aspartate oxidase from <i>Bos taurus</i>	$k_{cat}/K_M=6.1 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0.21 \text{ mM}^{-1}\text{s}^{-1}$	29	[69]

DAO <i>V. humic</i>	D-aspartate oxidase from <i>Vanrija humicola</i>	$k_{cat}/K_M=29.8 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0.024 \text{ mM}^{-1}\text{s}^{-1}$	1242	[70]
		α-ketoglutarate	α-keto adipate		
SDH <i>S. cerev</i>	Saccharopine dehydrogenase from <i>Saccharomyces cerevisiae</i>	$k_{cat}/K_M=280 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=0.86 \text{ mM}^{-1}\text{s}^{-1}$	326	[71]
		Nα-acetyl-L-ornithine	Nα-acetyl-L-lysine		
NAOD <i>E. coli</i>	N-Acetylornithine deacetylase from <i>Escherichia coli</i>	$k_{cat}/K_M=850 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=90 \text{ mM}^{-1}\text{s}^{-1}$	9.4	[72]
		Acetyl CoA	Propionyl CoA		
IPMS <i>C. necat</i>	Isopropylmaleate synthase from <i>Cupriavidus necator</i> (α -ketovalerate as co-substrate)			80	[73]
HSerTA <i>S. pombe</i>	Homoserine transacetylase from <i>Schizosaccharomyces pombe</i>	$k_{cat}/K_M=447 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=332 \text{ mM}^{-1}\text{s}^{-1}$	1.35	[74]
HSerTA <i>H. influ</i>	Homoserine transacetylase from <i>Haemophilus influenzae</i>	$k_{cat}/K_M=650 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=330 \text{ mM}^{-1}\text{s}^{-1}$	2	[75]
HSerTA <i>T. marit</i>	Homoserine transacetylase from <i>Thermotoga maritima</i>	$k_{cat}/K_M=110 \text{ mM}^{-1}\text{s}^{-1}$	$k_{cat}/K_M=59 \text{ mM}^{-1}\text{s}^{-1}$	1.9	[76]
		Propionyl CoA	Butyryl CoA		
PCC <i>R. etli</i>	Propionyl-CoA carboxylase from <i>Rhizobium etli</i>	$V/K_M=45,078 \text{ U mg}^{-1} \text{ mM}^{-1}$	$V/K_M=1.864 \text{ U mg}^{-1} \text{ mM}^{-1}$	24.2	[77]
PCC <i>S. coeli</i>	Propionyl-CoA carboxylase from <i>Streptomyces coelicolor</i>	$V/K_M=13.9 \text{ U mg}^{-1} \text{ mM}^{-1}$	$V/K_M=6.6 \text{ U mg}^{-1} \text{ mM}^{-1}$	2.1	[78]

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