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- Enzyme Nomenclature**
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## Information on EC 1.2.1.10 - acetaldehyde dehydrogenase (acetylating)

Word Map on EC 1.2.1.10



Specify your search results

Mark a special word or phrase in this record:

Search Reference ID:

Search UniProt Accession:

Select one or more organisms in this record:

All organisms

Acinetobacter sp. HBS-2  
Amoeba  
Chlorogonium elongatum  
Citrobacter sp.

The expected taxonomic range for this enzyme is: Bacteria, Eukaryota

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EC NUMBER ▲▼	COMMENTARY ▲▼ ×
1.2.1.10	-

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RECOMMENDED NAME ▲▼	GeneOntology No. ▲▼
acetaldehyde dehydrogenase (acetylating)	GO:0008774

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REACTION ▲▼	REACTION DIAGRAM	COMMENTARY ▲▼ ×	ORGANISM ▲▼	UNIPROT ▲▼	LITERATURE ▲▼
acetaldehyde + CoA + NAD+ = acetyl-CoA + NADH + H+		<a href="#">7 entries</a>			

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REACTION TYPE ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼ ×	LITERATURE ▲▼
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oxidation	+ 2 entries			
redox reaction	-	-	-	-
reduction	-	-	-	-

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PATHWAY ▲▼	BRENDA Link ▲▼	KEGG Link ▲▼	MetaCyc Link ▲▼
mixed acid fermentation	-	-	FERMENTATION-PWY
superpathway of fermentation (Chlamydomonas reinhardtii)	-	-	PWY4LZ-257
L-threonine degradation IV	-	-	PWY-5436
acetylene degradation	-	-	P161-PWY
pyruvate fermentation to ethanol III	-	-	PWY-6587
2-aminoethylphosphonate degradation I	-	-	PHOSPHONOTASE-PWY
2'-deoxy-alpha-D-ribose 1-phosphate degradation	-	-	PWY-7180
pyruvate fermentation to ethanol I	-	-	PWY-5480
2-oxopentenoate degradation	-	-	PWY-5162
ethanol degradation I	-	-	ETOH-ACETYLCOA-ANA-PWY
heterolactic fermentation	-	-	P122-PWY
triethylamine degradation	-	-	PWY-7085
3-phenylpropionate degradation	BRENDA pathway	-	-
ethanol fermentation	BRENDA pathway	-	-
threonine metabolism	BRENDA pathway	-	-
Phenylalanine metabolism	-	00360	-
Benzoate degradation	-	00362	-
Pyruvate metabolism	-	00620	-
Dioxin degradation	-	00621	-
Xylene degradation	-	00622	-
Butanoate metabolism	-	00650	-
Metabolic pathways	-	01100	-
Microbial metabolism in diverse environments	-	01120	-

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SYSTEMATIC NAME ▲▼	IUBMB Comments ▲▼
acetaldehyde:NAD <sup>+</sup> oxidoreductase (CoA-acetylating)	Also acts, more slowly, on glycolaldehyde, propanal and butanal. In several bacterial species this enzyme forms a bifunctional complex with EC 4.1.3.39, 4-hydroxy-2-oxovalerate aldolase. The enzymes from the bacteria Burkholderia xenovorans and Thermus thermophilus also perform the reaction of EC 1.2.1.87, propanal dehydrogenase (propanoylating). Involved in the meta-cleavage pathway for the degradation of phenols, methylphenols and catechols. NADP <sup>+</sup> can replace NAD <sup>+</sup> but the rate of reaction is much slower [3].



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+ Show Synonyms (47 entries)

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CAS REGISTRY NUMBER ▲▼	COMMENTARY ▲▼ ×
9028-91-5	-

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ORGANISM ▲▼	COMMENTARY ▲▼ ×	LITERATURE ▲▼	UNIPROT ▲▼	SEQUENCE DB ▲▼	SOURCE ▲▼
Acinetobacter sp. HBS-2	-	695594	A5JT11	UniProt	<a href="#">BRENDA</a>
Citrobacter sp.	-	738721	-	-	<a href="#">BRENDA</a>
Citrobacter sp. S-77	-	738721	-	-	<a href="#">BRENDA</a>
Clostridium beijerinckii	strain NRRL B592	390174	-	-	<a href="#">BRENDA</a>
Clostridium beijerinckii NRRL B592	strain NRRL B592	390174	-	-	<a href="#">BRENDA</a>
Clostridium kluyveri	-	286052, 390168, 390170, 390176	-	-	<a href="#">BRENDA</a>
Escherichia coli	+ 6 entries				
Escherichia coli XL2-Blue	strain XL2-Blue	690971	-	-	<a href="#">BRENDA</a>
Giardia intestinalis	strain WB	390177	-	-	<a href="#">BRENDA</a>
Giardia intestinalis WB	strain WB	390177	-	-	<a href="#">BRENDA</a>
Leuconostoc mesenteroides	+ 2 entries				
Leuconostoc mesenteroides LMC7	strain LMC7	672735	Q5RLY6	SwissProt	<a href="#">BRENDA</a>
Moorella sp.	-	735567	-	-	<a href="#">BRENDA</a>
Moorella sp. HUC22-1	-	735567	-	-	<a href="#">BRENDA</a>
Paraburkholderia xenovorans	-	724341	Q79AF6	UniProt	<a href="#">BRENDA</a>
Polytomella sp. Pringsheim 198.80	-	739328	Q70YJ9	UniProt	<a href="#">BRENDA</a>
Propionibacterium freudenreichii	-	390166	-	-	<a href="#">BRENDA</a>
Pseudomonas sp.	+ 3 entries				
Pseudomonas sp. CF600	+ 2 entries				
Pseudomonas sp. NCIMB9816	strain NCIMB9816	390179	-	-	<a href="#">BRENDA</a>
Ruminiclostridium thermocellum	+ 2 entries				
Thermoanaerobacter ethanolicus	+ 2 entries				
Thermoanaerobacter ethanolicus 39E	strain 39E	286197	-	-	<a href="#">BRENDA</a>
Thermoanaerobacter ethanolicus JW200	-	738990	C7IV28	UniProt	<a href="#">BRENDA</a>
Thermoanaerobacter sp.	-	735506	B0K315, B0K4A2	UniProt	<a href="#">BRENDA</a>
Thermoanaerobacter sp. X514	-	738990	B0K4A2	UniProt	<a href="#">BRENDA</a>
Thermoanaerobacterium saccharolyticum	+ 2 entries				
Thermoanaerobacterium saccharolyticum DSM 8691	-	736365	I3VSF1	UniProt	<a href="#">BRENDA</a>
Thermus thermophilus	-	736748	Q53WH9	UniProt	<a href="#">BRENDA</a>

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GENERAL INFORMATION ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼ ×	LITERATURE ▲▼
metabolism	+ 3 entries			
physiological function	+ 4 entries			

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SUBSTRATE ▲▼	PRODUCT ▲▼	REACTION DIAGRAM	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY (Substrate) ▲▼ ×	LITERATURE (Substrate) ▲▼	COMMENTARY (Product) ▲▼ ×	LITERATURE (Product) ▲▼	Reversibility r=reversible ir=irreversible ?=not specified ▲▼
acetaldehyde + CoA + NAD+	acetyl-CoA + NADH		+ 35 entries						
acetaldehyde + CoA + NAD+	acetyl-CoA + NADH + H+		+ 4 entries						
acetaldehyde + CoA + NAD+ + H+	acetyl-CoA + NADH		+ 2 entries						
acetaldehyde + NAD+	acetate + NADH + H+		Citrobacter sp.	-	-	738721	-	-	?
acetaldehyde + NAD+ + CoA	acetyl-CoA + NADH + H+		Moorella sp.	-	-	735567	-	-	r
acetaldehyde + NADP+ + CoA	acetyl-CoA + NADPH + H+		Moorella sp.	-	-	735567	-	-	r
acetyl-CoA + NADH	acetaldehyde + CoA + NAD+		Escherichia coli	-	-	390163, 390171	-	-	r
acetyl-CoA + NADH + H+	acetaldehyde + CoA + NAD+		+ 5 entries						
acetyl-CoA + NADH + H+	acetaldehyde + NAD+ + CoA		+ 4 entries						
acetyl-CoA + NADPH + H+	acetaldehyde + CoA + NADP+		+ 4 entries						
acetyl-CoA + NADPH + H+	acetaldehyde + NADP+ + CoA		Moorella sp.	-	-	735567	-	-	r
butylaldehyde + CoA + NAD+	butyl-CoA + NADH		Citrobacter sp.	-	21% of the activity with acetaldehyde	738721	-	-	?
butyraldehyde + CoA + NAD+	butyryl-CoA + NADH + H+		+ 2 entries						
butyryl-CoA + NADH + H+	butyraldehyde + CoA + NAD+		Thermoanaerobacter sp.	B0K315, B0K4A2	-	735506	-	-	r
caprylaldehyde + CoA + NAD+	caprylyl-CoA + NADH		Clostridium kluyveri	-	-	286052	-	-	?

formaldehyde + CoA + NAD+	formyl-CoA + NADH		+ 3 entries						
formaldehyde + CoA + NAD+	formyl-CoA + NADH + H+		Acinetobacter sp. HBS-2	A5JT11	-	695594	-	-	?
glutaraldehyde + CoA + NAD+	glutaryl-CoA + NADH		Propionibacterium freudenreichii	-	-	390166	-	-	?
glycolaldehyde + CoA + NAD+	hydroxyacetyl-CoA + NADH		Clostridium kluyveri	-	-	390168	-	-	?
glyoxal + CoA + NAD+	glyoxyl-CoA + NADH		Propionibacterium freudenreichii	-	-	390166	-	-	?
heptylaldehyde + CoA + NAD+	heptanoyl-CoA + NADH		+ 2 entries						
hexylaldehyde + CoA + NAD+	hexanoyl-CoA + NADH		+ 2 entries						
isobutyraldehyde + CoA + NAD+	isobutyryl-CoA + NADH		+ 6 entries						
n-butyraldehyde + CoA + NAD+	n-butyryl-CoA + NADH		+ 11 entries						
pentaldehyde + CoA + NAD+	pentyl-CoA + NADH + H+		Paraburkholderia xenovorans	Q79AF6	-	724341	-	-	r
picolinaldehyde + CoA + NAD+	picolinyl-CoA + NADH + H+		Paraburkholderia xenovorans	Q79AF6	-	724341	-	-	r
propanal + CoA + NAD+	propionyl-CoA + NADH		+ 8 entries						
propionaldehyde + CoA + NAD+	propionyl-CoA + NADH + H+		+ 2 entries						
propionaldehyde + CoA + NAD+	propyl-CoA + NADH		Citrobacter sp.	-	51.8% of the activity with acetaldehyde	738721	-	-	?
valeraldehyde + CoA + NAD+	valeryl-CoA + NADH		+ 4 entries						
additional information	?	-	+ 11 entries						

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NATURAL SUBSTRATES ▲ ▼	NATURAL PRODUCTS ▲ ▼	REACTION DIAGRAM	ORGANISM ▲ ▼	UNIPROT ▲ ▼	COMMENTARY (Substrate) ▲▼ ×	LITERATURE (Substrate) ▲ ▼	COMMENTARY (Product) ▲▼ ×	LITERATURE (Product) ▲▼	REVERSIBILITY r=reversible ir=irreversible ?=not specified ▲▼
acetaldehyde + CoA + NAD+	acetyl-CoA + NADH		+ 20 entries						
acetaldehyde + CoA + NAD+	acetyl-CoA + NADH + H+		+ 3 entries						
formaldehyde + CoA + NAD+	formyl-CoA + NADH + H+		Acinetobacter sp. HBS-2	A5JT11	-	695594	-	-	?

propanal + CoA + NAD+	propionyl-CoA + NADH		+ 3 entries						
propionaldehyde + CoA + NAD+	propionyl-CoA + NADH + H+		Acinetobacter sp. HBS-2	A5JT11	-	695594	-	-	?
additional information	?	-	+ 2 entries						

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COFACTOR ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼	×	LITERATURE ▲▼	IMAGE
CoA	+ 9 entries					
NAD+	+ 13 entries					
NADH	+ 8 entries					
NADP+	Citrobacter sp.	-	NAD+ is 57fold preferred over NADP+		738721	
NADPH	+ 3 entries					
additional information	Clostridium kluveri	-	enzyme is able to acetylate other thiols than CoA, e.g. pantetheine, 2-mercaptoethanol, dithioerythritol, glutathione, cysteamine		390176	-

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METALS and IONS ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼	×	LITERATURE ▲▼
Fe2+	Escherichia coli	-	3fold activation with 0.00003 mM, 5fold activation with 0.03 mM, activation only of NADH oxidation, not NAD+ reduction		390163
Mn2+	Acinetobacter sp. HBS-2	A5JT11	activity of the enzyme is elevated		695594

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INHIBITORS ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼	×	LITERATURE ▲▼	IMAGE
acetaldehyde	Escherichia coli	-	competitive inhibition		724721	
acetyl-CoA	Clostridium kluveri	-	competitive inhibitor with respect to NAD+; competitive to NAD+		390176	
ADP	Leuconostoc mesenteroides	-	1 mM 42% inhibition, competitive to NAD+		390167	
ADP-ribose	Escherichia coli	-	-		390164	
AgNO3	Leuconostoc mesenteroides	-	1 mM 20% inhibition		390167	
AMP	+ 2 entries					
ATP	Leuconostoc mesenteroides	-	1 mM 38% inhibition, competitive to NAD+		390167	

benzaldehyde	<i>Escherichia coli</i>	-	-	390164	
Ca2+	<i>Giardia intestinalis</i>	-	5 mM causes 51% inhibition	390177	
Chloroethanol	<i>Escherichia coli</i>	-	-	390171	
CuSO4	<i>Leuconostoc mesenteroides</i>	-	1 mM 49% inhibition	390167	
Disulfiram	<i>Giardia intestinalis</i>	-	0.01 mM causes 70% inhibition	390177	
HgCl2	<i>Leuconostoc mesenteroides</i>	-	1 mM 31% inhibition	390167	
iodoacetamide	<i>Giardia intestinalis</i>	-	1 mM causes 88-96% inhibition	390177	
iodoacetate	<i>Pseudomonas sp.</i>	-	-	657161	
Mg2+	<i>Giardia intestinalis</i>	-	5 mM causes 51% inhibition	390177	
Mn2+	<i>Giardia intestinalis</i>	-	5 mM causes 84% inhibition	390177	
Na2HAsO4	<i>Leuconostoc mesenteroides</i>	-	1 mM 100% inhibition, 0.1 mM 32% inhibition	390167	
NAD+	<i>Clostridium beijerinckii</i>	-	double competitive, NAD+/CoA ratio is kept at 1:0.24	390174	
NADH	<i>Clostridium kluyveri</i>	-	competitive inhibitor with respect to CoA; competitive to CoA	390176	
p-chloromercuribenzoate	<i>Giardia intestinalis</i>	-	0.01 mM causes 88-96% inhibition	390177	
Tris	<i>Escherichia coli</i>	-	rate of reaction falls off rapidly in Tris	390173	
Valproate	<i>Giardia intestinalis</i>	-	50 mM causes 20-46% inhibition	390177	
additional information	<i>Leuconostoc mesenteroides</i>	-	low ionic strength buffers, 0.2 M boric acid/Na2CO3, 0.2 M glycine/NaOH, 0.2 M NH4Cl/NH4OH, pH 8.0, not inhibitory at 1 mM: K+, Na+, Li+, Mg2+, Mn2+, Zn2+, Ca2+, Fe2+, Fe3+, EDTA, p-chloromercuribenzoate, iodoacetate, N3-, dipyriddy, lactic acid, acetic acid, ethanol, acetylphosphate, pyruvic acid, adenine, adenosine, guanine, guanosine, GMP, GDP, not inhibitory at 0.1 mM: NADP+, NADPH	390167	-

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ACTIVATING COMPOUND ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼	LITERATURE ▲▼	IMAGE ▲▼
2-mercaptoethanol	2 entries				
3-pyridinecarboxaldehyde adenine dinucleotide	<i>Escherichia coli</i>	-	NAD+ analogue, activates by binding strongly to activator site, binds weakly to catalytic site	390164	
dithiothreitol	<i>Escherichia coli</i>	-	does require dithiothreitol for optimum activity	390173	

GSH	Leuconostoc mesenteroides	-	7fold activation	390167	
NAD+	Escherichia coli	-	reduces lag phase before attainment of steady state rate in conjunction with 2-mercaptoethanol	390164	
sulfhydryl compound	+ 2 entries				

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KM VALUE [mM] ▲▼	SUBSTRATE ▲ ▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼	×	LITERATURE ▲▼	IMAGE ▲▼
22	2-mercaptoethanol	Clostridium kluveri	-	-		390176	
0.01518 - 133	acetaldehyde	+ 20 entries					
0.007 - 1.6	acetyl-CoA	+ 9 entries					
2.3 - 11	Butanal	+ 2 entries					
3.23 - 31.7	Butyraldehyde	+ 6 entries					
0.0057 - 0.0272	butyryl-CoA	+ 2 entries					
0.008 - 0.16	CoA	+ 10 entries					
0.00212	formaldehyde	Acinetobacter sp. HBS-2	A5JT11	-		695594	
20	glycolaldehyde	Clostridium kluveri	-	-		390168	
0.029 - 0.166	n-Butyryl-CoA	+ 3 entries					
0.05 - 0.44	NAD+	+ 9 entries					
0.0076 - 0.1	NADH	+ 6 entries					
0.0673 - 0.206	NADPH	+ 2 entries					
11	pantetheine	Clostridium kluveri	-	-		390176	
8.2	pentaldehyde	Paraburkholderia xenovorans	Q79AF6	mutant enzyme I195A, at 25°C in 100 mM HEPES buffer (pH 8.0)		724341	
3.2 - 18.2	picolinaldehyde	+ 4 entries					
0.603 - 6.9	propanal	+ 3 entries					
0.00049 - 79.5	propionaldehyde	+ 6 entries					
1.5	Valeraldehyde	Propionibacterium freudenreichii	-	-		390166	

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TURNOVER NUMBER [1/s] ▲▼	SUBSTRATE ▲ ▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼	×	LITERATURE ▲▼	IMAGE ▲▼
6.9 - 37.9	acetaldehyde	+ 9 entries					
7.1 - 16.7	Butyraldehyde	+ 4 entries					
13	pentaldehyde	Paraburkholderia xenovorans	Q79AF6	mutant enzyme I195A, at 25°C in 100 mM HEPES buffer (pH 8.0)		724341	
1.9 - 3.2	picolinaldehyde	+ 4 entries					
3.4 - 24.9	propionaldehyde	+ 6 entries					



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kcat/KM VALUE [1/mMs <sup>-1</sup> ]	SUBSTRATE	ORGANISM	UNIPROT	COMMENTARY	LITERATURE	IMAGE
0.147 - 2.224	acetaldehyde	<a href="#">9 entries</a>				
55.3 - 381	acetyl-CoA	<a href="#">2 entries</a>				
0.0433 - 7.11	Butyraldehyde	<a href="#">7 entries</a>				
394 - 833	butyryl-CoA	<a href="#">2 entries</a>				
0.0265 - 1.584	pentaldehyde	<a href="#">5 entries</a>				
0.00011 - 0.597	picolinaldehyde	<a href="#">6 entries</a>				
0.0425 - 1.219	propionaldehyde	<a href="#">6 entries</a>				

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Ki VALUE [mM]	INHIBITOR	ORGANISM	UNIPROT	COMMENTARY	LITERATURE	IMAGE
265	acetaldehyde	<i>Escherichia coli</i>	-	at 25°C in 50 mM Tris/HCl buffer, pH 8.0	<a href="#">724721</a>	
2.5	ADP	<i>Leuconostoc mesenteroides</i>	-	-	<a href="#">390167</a>	
0.75	AMP	<i>Leuconostoc mesenteroides</i>	-	-	<a href="#">390167</a>	
8.6	ATP	<i>Leuconostoc mesenteroides</i>	-	-	<a href="#">390167</a>	

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SPECIFIC ACTIVITY [μmol/min/mg]	ORGANISM	UNIPROT	COMMENTARY	LITERATURE
0.04	<i>Ruminiclostridium thermocellum</i>	<a href="#">A0A0H3W5U9, A3DCI2</a>	gene AdhE deletion mutant, cosubstrate NADH, pH 7.0, 55°C	<a href="#">736365</a>
0.05	<i>Thermoanaerobacterium saccharolyticum</i>	<a href="#">A0A0H3W5K4, I3VSF1</a>	wild-type, cosubstrate NADPH, pH 7.0, 55°C	<a href="#">736365</a>
0.09	<i>Thermoanaerobacterium saccharolyticum</i>	<a href="#">A0A0H3W5K4, I3VSF1</a>	gene AdhE deletion mutant, cosubstrate NADH, pH 7.0, 55°C; gene AdhE deletion mutant, cosubstrate NADPH, pH 7.0, 55°C; wild-type, cosubstrate NADH, pH 7.0, 55°C	<a href="#">736365</a>
0.1	<i>Ruminiclostridium thermocellum</i>	<a href="#">A0A0H3W5U9, A3DCI2</a>	gene AdhE deletion mutant, cosubstrate NADPH, pH 7.0, 55°C	<a href="#">736365</a>
0.11	<i>Citrobacter</i> sp.	-	cofactor NADP <sup>+</sup> , pH 7.0, 30°C	<a href="#">738721</a>
0.16	<i>Ruminiclostridium thermocellum</i>	<a href="#">A0A0H3W5U9, A3DCI2</a>	wild-type, cosubstrate NADPH, pH 7.0, 55°C	<a href="#">736365</a>
0.47	<i>Citrobacter</i> sp.	-	cofactor NADP <sup>+</sup> , presence of CoA, pH 7.0, 30°C	<a href="#">738721</a>
0.87	<i>Leuconostoc mesenteroides</i>	-	-	<a href="#">390167</a>
1.38	<i>Citrobacter</i> sp.	-	cofactor NAD <sup>+</sup> , pH 7.0, 30°C	<a href="#">738721</a>
1.6	<i>Leuconostoc mesenteroides</i>	<a href="#">Q5RLY6</a>	crude extracts from expression in <i>Escherichia coli</i> DH5alpha, one unit is defined as the amount of enzyme activity that catalysed the transformation of 1 micromol NADH per min	<a href="#">672735</a>
1.7	<i>Leuconostoc</i>	<a href="#">Q5RLY6</a>	crude extracts from expression in <i>Escherichia coli</i> BL21, one unit is defined as the	<a href="#">672735</a>

	mesenteroides		amount of enzyme activity that catalysed the transformation of 1 micromol NADH per min	
2	<i>Clostridium beijerinckii</i>	-	-	390174
2.18	<i>Ruminiclostridium thermocellum</i>	A0A0H3W5U9, A3DCI2	wild-type, cosubstrate NADH, pH 7.0, 55°C	736365
2.8	<i>Moorella</i> sp.	-	cleavage of thioester, cofactor NADPH, pH 8.0, 60°C	735567
3.11	<i>Escherichia coli</i>	-	-	390171
3.7	<i>Moorella</i> sp.	-	condensation of thioester, cofactor NADP+, pH 10.0, 60°C	735567
4.88	<i>Clostridium beijerinckii</i>	-	undialyzed, anaerobically purified	390174
7.36	<i>Citrobacter</i> sp.	-	cofactor NAD+, presence of CoA, pH 7.0, 30°C	738721
8.75	<i>Giardia intestinalis</i>	-	bifunctional fusion protein of aldehyde and alcohol dehydrogenase	390177
9.62	<i>Clostridium beijerinckii</i>	-	dialyzed, incubated with dithiothreitol and CoA	390174
14.1	<i>Escherichia coli</i>	-	-	390164
16	<i>Thermoanaerobacter ethanolicus</i>	-	-	286197
18.8	<i>Moorella</i> sp.	-	cleavage of thioester, cofactor NADH, pH 8.0, 60°C	735567
29.9	<i>Moorella</i> sp.	-	condensation of thioester, cofactor NAD+, pH 10.0, 60°C	735567
48.6	<i>Clostridium kluyveri</i>	-	-	390176
60.6	<i>Acinetobacter</i> sp. HBS-2	A5JT11	recombinant enzyme	695594
83.7	<i>Propionibacterium freudenreichii</i>	-	-	390166

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pH OPTIMUM ▲▼	ORGANISM ▲▼	UNIPROT ▲	COMMENTARY ▲▼	×	LITERATURE ▲▼
6.5	<i>Citrobacter</i> sp.	-	-		738721
6.8	<i>Clostridium kluyveri</i>	-	NADH oxidation; NADH oxidation, with potassium phosphate buffer		390176
7	+ 3 entries				
8	+ 2 entries				
8.5	+ 2 entries				
8.8	<i>Escherichia coli</i>	-	in cyclohexylaminoethanesulfonic acid or Tris-(hydroxymethyl)-methyl-amino-propanesulfonic acid buffer		390173
9	<i>Clostridium kluyveri</i>	-	NAD+ reduction		286052
9.1	<i>Clostridium kluyveri</i>	-	NAD+ reduction		390176
10	<i>Moorella</i> sp.	-	condensation of thioester		735567

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pH RANGE ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼	×	LITERATURE ▲▼
5 - 8	<i>Clostridium kluyveri</i>	-	less than 50% of maximal activity above and below		390176

5.5	<a href="#">Citrobacter sp.</a>	-	complete inactivation	738721
6 - 7	<a href="#">Clostridium beijerinckii</a>	-	NAD+ reduction	390174
6.2 - 7.4	<a href="#">Escherichia coli</a>	-	67% of maximal activity at pH 6.2, 79% of maximal activity at pH 7.4	390171
6.5 - 9.5	<a href="#">Clostridium beijerinckii</a>	-	activity of NADH oxidation increases between 6.5-9.5	390174
6.5 - 8.5	<a href="#">Pseudomonas sp.</a>	-	activity increases gradually over pH range from 6.5 to 8.5	390175
7 - 9.5	<a href="#">Propionibacterium freudenreichii</a>	-	30% of maximal activity at pH 7.0, 100% at pH 9.5	390166
8.2 - 9.5	<a href="#">Propionibacterium freudenreichii</a>	-	-	390166
8.5 - 10	<a href="#">Clostridium kluveri</a>	-	70% of maximal activity at pH 8.5, 80% of maximal activity at pH 10	286052

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TEMPERATURE OPTIMUM ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼ ×	LITERATURE ▲▼
30	<a href="#">Leuconostoc mesenteroides</a>	-	-	390167
40	<a href="#">Citrobacter sp.</a>	-	-	738721
45	<a href="#">Propionibacterium freudenreichii</a>	-	-	390166
60	<a href="#">Moorella sp.</a>	-	at pH 8.0	735567

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TEMPERATURE RANGE ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼ ×	LITERATURE ▲▼
20 - 60	<a href="#">Propionibacterium freudenreichii</a>	-	55% of maximal activity at 20°C, 60% at 60°C	390166
50	<a href="#">Moorella sp.</a>	-	71% of maximum activity	735567
70	<a href="#">Moorella sp.</a>	-	52% of maximum activity	735567

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pI VALUE ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼ ×	LITERATURE ▲▼
6.98	<a href="#">Polytomella sp. Pringsheim 198.80</a>	Q70YJ9	calculated from sequence	739328

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SOURCE TISSUE ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼ ×	LITERATURE ▲▼	SOURCE ▲▼
cell culture	<a href="#">+ 2 entries</a>				
culture condition:ethanol-grown cell	<a href="#">Polytomella sp. Pringsheim 198.80</a>	Q70YJ9	at pH 6.0 and pH 3.7	739328	<b>BRENDA</b>

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LOCALIZATION ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼ ×	GeneOntology No. ▲▼	LITERATURE ▲▼	SOURCE ▲▼
cytosol	<a href="#">+ 3 entries</a>					
membrane	<a href="#">+ 2 entries</a>					
mitochondrion	<a href="#">Polytomella sp. Pringsheim 198.80</a>	Q70YJ9	higher enzyme level in mitochondria from cells grown at pH 6.0 than in mitochondria from cells grown at pH 3.7	5739	739328	<b>BRENDA</b>
particle-bound	<a href="#">Clostridium kluveri</a>	-	-	-	286052,	<b>BRENDA</b>

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PDB ▲▼	SCOP	CATH	ORGANISM ▲▼	UNIPROT ▲▼
5j78, download, 3D-view	SCOPe (5j78)	CATH (5j78)	Geobacillus thermoglucosidasius (strain C56-YS93)	A0A0M1QQ83
5j7i, download, 3D-view	SCOPe (5j7i)	CATH (5j7i)	Geobacillus thermoglucosidasius (strain C56-YS93)	A0A0M1QQ83
4c3s, download, 3D-view	SCOPe (4c3s)	CATH (4c3s)	Lachnoclostridium phytofermentans (strain ATCC 700394 / DSM 18823 / ISDg)	A9KN57

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MOLECULAR WEIGHT ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼	LITERATURE ▲▼
32500	Pseudomonas sp.	-	2 * 32500 + 2 * 39000, determined by nucleotide sequence, SDS-PAGE, two subunits of aldehyde dehydrogenase (acylating) and two of 4-hydroxy-2-ketovalerate	390175
33344	Escherichia coli	-	1 * 33344, electrospray ionization mass spectrometry	724721
35300	Escherichia coli	-	gel filtration	724721
39000	Pseudomonas sp.	-	2 * 32500 + 2 * 39000, determined by nucleotide sequence, SDS-PAGE, two subunits of aldehyde dehydrogenase (acylating) and two of 4-hydroxy-2-ketovalerate	390175
48000	Propionibacterium freudenreichii	-	4 * 48000, SDS-PAGE	390166
51700	Thermoanaerobacter sp.	B0K315, B0K4A2	5 * 51700, calculated, 5 * 52400, SDS-PAGE	735506
52400	Thermoanaerobacter sp.	B0K315, B0K4A2	5 * 51700, calculated, 5 * 52400, SDS-PAGE	735506
55000	Clostridium beijerinckii	-	2 * 55000, SDS-PAGE	390174
57000	Acinetobacter sp. HBS-2	A5JT11	SDS-PAGE	695594
94900	Thermoanaerobacter sp.	B0K315, B0K4A2	6 * 97700, calculated, 6 * 94900, SDS-PAGE	735506
95000	Giardia intestinalis	-	x * 95000, SDS-PAGE, amino acid sequence	390177
96000	Escherichia coli	-	ca. 40 * 96000, pyruvate-formate-lyase-deactivase with alcohol and aldehyde dehydrogenase activity, nucleotide sequence	390163
96600	Leuconostoc mesenteroides	Q5RLY6	deduced from sequence	672735
97700	Thermoanaerobacter sp.	B0K315, B0K4A2	6 * 97700, calculated, 6 * 94900, SDS-PAGE	735506
100000	⊕ 2 entries			
120000	Escherichia coli	-	one of four isozymes, gel filtration	390162
140000	Pseudomonas sp.	-	-	657161
148000	Pseudomonas sp.	-	gel filtration, molecular mass of enzyme complex, occurs in complex with 4-hydroxy-2-ketovalerate	390175
188000	Propionibacterium freudenreichii	-	gel filtration	390166

265000	<a href="#">Thermoanaerobacter sp.</a>	<a href="#">BOK315, BOK4A2</a>	gel filtration	735506
290000	<a href="#">Clostridium kluyveri</a>	-	gel filtration and sedimentation coefficient	390176
360000	<a href="#">Thermoanaerobacter ethanolicus</a>	-	gel filtration	286197
370000	<a href="#">Escherichia coli</a>	-	one of four isozymes, gel filtration	390162
400000	<a href="#">Citrobacter sp.</a>	-	gel filtration	738721
520000	<a href="#">Escherichia coli</a>	-	one of four isozymes, gel filtration	390162
555000	<a href="#">Thermoanaerobacter sp.</a>	<a href="#">BOK315, BOK4A2</a>	gel filtration	735506
900000	<a href="#">Escherichia coli</a>	-	one of four isozymes, gel filtration	390162

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SUBUNITS <a href="#">▲▼</a>	ORGANISM <a href="#">▲▼</a>	UNIPROT <a href="#">▲</a>	COMMENTARY <a href="#">▲▼</a>	LITERATURE <a href="#">▲▼</a>
?	<a href="#">+ 4 entries</a>			
dimer	<a href="#">+ 2 entries</a>			
hexamer	<a href="#">Thermoanaerobacter sp.</a>	<a href="#">BOK315, BOK4A2</a>	6 * 97700, calculated, 6 * 94900, SDS-PAGE	735506
monomer	<a href="#">Escherichia coli</a>	-	1 * 33344, electrospray ionization mass spectrometry	724721
pentamer	<a href="#">Thermoanaerobacter sp.</a>	<a href="#">BOK315, BOK4A2</a>	5 * 51700, calculated, 5 * 52400, SDS-PAGE	735506
polymer	<a href="#">Escherichia coli</a>	-	ca. 40 * 96000, pyruvate-formate-lyase-deactivase with alcohol and aldehyde dehydrogenase activity, nucleotide sequence	390163
tetramer	<a href="#">+ 9 entries</a>			
<a href="#">additional information</a>	<a href="#">+ 2 entries</a>			

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Crystallization/COMMENTARY <a href="#">▲▼</a>	ORGANISM <a href="#">▲▼</a>	UNIPROT <a href="#">▲▼</a>	LITERATURE <a href="#">▲▼</a>
hanging drop vapor diffusion method, in the absence of cofactor or in the presence of either 5 mM NAD+ or CoA using 22% PEG 4000, 0.1 M HEPES/NaOH pH 7.5, 0.1 M sodium acetate	<a href="#">Escherichia coli</a>	-	724721
-	<a href="#">Pseudomonas sp.</a>	-	657161
hanging drop method, streak-seeding	<a href="#">Pseudomonas sp.</a>	-	390178

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pH STABILITY <a href="#">▲▼</a>	ORGANISM <a href="#">▲</a>	UNIPROT <a href="#">▲▼</a>	COMMENTARY <a href="#">▲▼</a>	LITERATURE <a href="#">▲▼</a>
5 - 8	<a href="#">Clostridium</a>	-	enzyme activity falls to 50% at pH 5 and pH 8	390176

	<a href="#">kluveri</a>			
7	<a href="#">Clostridium beijerinckii</a>	-	more stable at pH 7 than at pH 6, 8 or 9 in either Tris acetate or potassium phosphate test buffer, at the same pH more stable in Tris acetate test buffer	390174

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TEMPERATURE STABILITY ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼ ×	LITERATURE ▲▼
40	+ 2 entries			
45	<a href="#">Leuconostoc mesenteroides</a>	-	15 min, inactivation	390167
70	<a href="#">Propionibacterium freudenreichii</a>	-	3 min, inactivation above	390166

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GENERAL STABILITY ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	LITERATURE ▲▼
activity is highest in HEPES buffer and somewhat lower in phosphate buffer, activity in Tris buffer is about half the rate in HEPES buffer	<a href="#">Pseudomonas sp.</a>	-	390175
dithioerythritol stabilizes	<a href="#">Clostridium kluveri</a>	-	390176
extremely unstable in absence of 2-mercaptoethanol	<a href="#">Escherichia coli</a>	-	390171
labile during purification, stabilization by 2-hydroxyethylsulfide	<a href="#">Escherichia coli</a>	-	390164
no stabilization by detergents, acetone, ethanol, NAD <sup>+</sup> , glycerol, CoA, anaerobic conditions	<a href="#">Clostridium kluveri</a>	-	390176
sensitive to O <sub>2</sub> , can be protected against O <sub>2</sub> inactivation by dithiothreitol	<a href="#">Clostridium beijerinckii</a>	-	390174
with Tris acetate buffer at pH 7, less stable at higher buffer concentration between 10 and 150 mM	<a href="#">Clostridium beijerinckii</a>	-	390174

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STORAGE STABILITY ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	LITERATURE ▲▼
-60°C, 20 mM MOPS-KOH pH 7.6, 0.1 mM EDTA, up to one year	<a href="#">Escherichia coli</a>	-	390163
-70°C, 10 mM Tris-HCl buffer, pH 8, 3 mM dithioerythritol, 2 weeks, 15% loss of activity	<a href="#">Clostridium kluveri</a>	-	390176
-70°C, 3 mM dithioerythritol, 85% of enzymatic activity remains after 2 weeks	<a href="#">Clostridium kluveri</a>	-	390176
-80°C, 10 mM phosphate buffer, pH 7.5, 1 mM dithiothreitol	<a href="#">Pseudomonas sp.</a>	-	390175
3°C, ammonium sulfate step of purification, several months	<a href="#">Escherichia coli</a>	-	390171
4°C, anaerobically	<a href="#">Thermoanaerobacter ethanolicus</a>	-	286197
5 mM dithiothreitol protects enzyme in crude extracts from O <sub>2</sub> -inactivation for at least 2 hours	<a href="#">Clostridium beijerinckii</a>	-	390174
addition of 140 mM KCl to 10 mM Tris acetate stabilizes as no activity is lost after 3 days	<a href="#">Clostridium beijerinckii</a>	-	390174
CoA and dithiothreitol restore a higher activity than one of these compounds alone	<a href="#">Clostridium beijerinckii</a>	-	390174
glycerol at 20%, vol/vol, stabilizes in 50 mM Tris acetate buffer at pH 7, as no activity is lost after 3 days at 4°C under argon	<a href="#">Clostridium beijerinckii</a>	-	390174

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Purification/COMMENTARY ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	LITERATURE ▲▼
-	+ 4 entries		
ADHE cannot be solubilized from membrane with detergents such as 1% Triton X-100 or 1% sulfobetaine 3-12. The enzyme is easily dissociated from membrane by high-salt buffers containing either 1.0 M NaCl or (NH <sub>4</sub> ) <sub>2</sub> SO <sub>4</sub> without detergents	Citrobacter sp.	-	738721
by affinity chromatography by means of a Ni-Sepharose column	Acinetobacter sp. HBS-2	A5JT11	695594
from anaerobically grown cells, rod-shaped	Escherichia coli	-	390163
Ni-NTA column chromatography	Paraburkholderia xenovorans	Q79AF6	724341
on DEAE and NAD <sup>+</sup> -linked affinity columns, combined with an ammonium sulfate fractionation step	Escherichia coli	-	690971
partial	+ 3 entries		
Q-Sepharose column chromatography, phenyl Sepharose column chromatography, and Superdex 200 gel filtration	Escherichia coli	-	724721
under anaerobic conditions	Clostridium beijerinckii	-	390174

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Cloned/COMMENTARY ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	LITERATURE ▲▼
-	+ 2 entries		
Escherichia coli strain W1485	Escherichia coli	-	390173
expressed in Escherichia coli C41 (DE3) cells	Escherichia coli	-	724721
expression in Escherichia coli	+ 2 entries		
expression in Escherichia coli BL21 and DH5alpha	Leuconostoc mesenteroides	Q5RLY6	672735
expression in Escherichia coli; expression in Escherichia coli	Thermoanaerobacter sp.	B0K315, B0K4A2	735506
expression in Pyrococcus furiosus from which the native aldehyde oxidoreductase (AOR) gene is deleted. A strain containing the Thermoanaerobacter ethanolicus AdhE in a synthetic operon with AdhA is constructed. The AdhA gene is amplified from Thermoanaerobacter sp. X514. The amino acid sequence of AdhA from Thermoanaerobacter sp. X514 is identical to that of AdhA from Thermoanaerobacter ethanolicus. Of the bacterial strains expressing the various heterologous AdhE genes, only those containing AdhE and AdhA from Thermoanaerobacter sp. produced ethanol above background. The Thermoanaerobacter ethanolicus AdhEA strain containing both AdhE and AdhA produces the most ethanol (4.2 mM), followed by Thermoanaerobacter ethanolicus AdhE strain (2.6 mM), Thermoanaerobacter ethanolicus AdhA strain (1.8 mM) and Thermoanaerobacter sp. X514 AdhE strain (1.5 mM). Ethanol and acetate are the only major carbon end-products from glucose under these conditions. For these four strains, the amount of ethanol produced per estimated glucose consumed is increased from the background level to 1.2, 1.0, 0.8 and 0.7 respectively	Thermoanaerobacter ethanolicus	C7IV28	738990
expression of the enzyme from Thermoanaerobacter sp. X514 in Pyrococcus furiosus from which the native aldehyde oxidoreductase (AOR) gene is deleted. Ethanol and acetate are the only major carbon end-products from glucose under these conditions. The amount of ethanol produced per estimated glucose consumed is increased from the background level 0.7 respectively	Thermoanaerobacter sp. X514	B0K4A2	738990
gene adhE, pyruvate-formate-lyase-deactivase with alcohol and acetaldehyde dehydrogenase activity	Escherichia coli	-	390163

in Escherichia coli BL21 cells	Acinetobacter sp. HBS-2	A5JT11	695594
overexpression in Escherichia coli	Pseudomonas sp.	-	390175
pT7.5-dmpFG plasmid expressed in Escherichia coli C41(DE3)	Escherichia coli	-	690971

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EXPRESSION ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	LITERATURE ▲▼
expression is strongly influenced by the pH of the culture medium. Expression in cells grown on ethanol is higher at pH 6.0 than at pH 3.7	Polytomella sp. Pringsheim 198.80	Q70YJ9	739328

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ENGINEERING ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼	×	LITERATURE ▲▼
C131A	Paraburkholderia xenovorans	Q79AF6	inactive		724341
C131S	Paraburkholderia xenovorans	Q79AF6	inactive		724341
D208A	Paraburkholderia xenovorans	Q79AF6	the mutant shows reduced catalytic efficiency compared to the wild type enzyme		724341
I171A	Paraburkholderia xenovorans	Q79AF6	level of activation of BphI by the mutant enzyme are reduced by more than 3fold in the presence of NADH and more than 4.5fold when the enzyme is undergoing turnover. The mutation results in a 35% reduction in acetaldehyde channeling efficiency		724341
I171F	Paraburkholderia xenovorans	Q79AF6	the mutant shows strongly reduced catalytic efficiency compared to the wild type enzyme		724341
I195A	Paraburkholderia xenovorans	Q79AF6	the variant has a 20fold higher catalytic efficiency for butyraldehyde and pentaldehyde compared to the catalytic efficiency of the wild type toward its natural substrate acetaldehyde. The mutation results in a 35% reduction in acetaldehyde channeling efficiency		724341
I195F	Paraburkholderia xenovorans	Q79AF6	the mutant shows severely reduced catalytic efficiency compared to the wild type enzyme		724341
I195W	Paraburkholderia xenovorans	Q79AF6	the mutant shows strongly reduced catalytic efficiency compared to the wild type enzyme		724341
N170A	Paraburkholderia xenovorans	Q79AF6	the mutation does not substantially alter aldehyde channeling efficiencies. The level of activation of BphI by the mutant enzyme are reduced by more than 3fold in the presence of NADH and more than 4.5fold when the enzyme is undergoing turnover		724341
N170D	Paraburkholderia xenovorans	Q79AF6	level of activation of BphI by the mutant enzyme are reduced by more than 3fold in the presence of NADH and more than 4.5fold when the enzyme is undergoing turnover		724341
I159A	+ 2 entries				
additional information	+ 2 entries				

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APPLICATION ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼	×	LITERATURE ▲▼
biofuel production	+ 3 entries				



synthesis	+ 5 entries
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