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Show **abbreviated version** of the Enzyme Summary Page.

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Information on EC 1.2.1.10 - acetaldehyde dehydrogenase (acetylating)

Word Map on EC 1.2.1.10

Please wait a moment until all data is loaded. This message will disappear when all data is loaded.

Specify your search results

Mark a special word or phrase in this record: Mark!

Search Reference ID: Search

Search UniProt Accession: Search

Select one or more organisms in this record:

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

Submit

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+		+ 7 entries			

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REACTION TYPE	ORGANISM	UNIPROT	COMMENTARY	LITERATURE

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+ 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+ can replace NAD+ 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	BRENDA
Citrobacter sp.	-	738721	-	-	BRENDA
Citrobacter sp. S-77	-	738721	-	-	BRENDA
Clostridium beijerinckii	strain NRRL B592	390174	-	-	BRENDA
Clostridium beijerinckii NRRL B592	strain NRRL B592	390174	-	-	BRENDA
Clostridium kluyveri	-	286052, 390168, 390170, 390176	-	-	BRENDA
Escherichia coli	⊞ 6 entries				
Escherichia coli XL2-Blue	strain XL2-Blue	690971	-	-	BRENDA
Giardia intestinalis	srain WB	390177	-	-	BRENDA
Giardia intestinalis WB	srain WB	390177	-	-	BRENDA
Leuconostoc mesenteroides	⊞ 2 entries				
Leuconostoc mesenteroides LMC7	strain LMC7	672735	Q5RLY6	SwissProt	BRENDA
Moorella sp.	-	735567	-	-	BRENDA
Moorella sp. HUC22-1	-	735567	-	-	BRENDA
Paraburkholderia xenovorans	-	724341	Q79AF6	UniProt	BRENDA
Polytomella sp. Pringsheim 198.80	-	739328	Q70YJ9	UniProt	BRENDA
Propionibacterium freudenreichii	-	390166	-	-	BRENDA
Pseudomonas sp.	⊞ 3 entries				
Pseudomonas sp. CF600	⊞ 2 entries				
Pseudomonas sp. NCIMB9816	strain NCIMB9816	390179	-	-	BRENDA
Ruminiclostridium thermocellum	⊞ 2 entries				
Thermoanaerobacter ethanolicus	⊞ 2 entries				
Thermoanaerobacter ethanolicus 39E	strain 39E	286197	-	-	BRENDA
Thermoanaerobacter ethanolicus JW200	-	738990	C7IV28	UniProt	BRENDA
Thermoanaerobacter sp.	-	735506	B0K315, B0K4A2	UniProt	BRENDA
Thermoanaerobacter sp. X514	-	738990	B0K4A2	UniProt	BRENDA
Thermoanaerobacterium saccharolyticum	⊞ 2 entries				
Thermoanaerobacterium saccharolyticum DSM 8691	-	736365	I3VSF1	UniProt	BRENDA
Thermus thermophilus	-	736748	Q53WH9	UniProt	BRENDA

Thermus thermophilus DSM 579	-	736748	Q53WH9	UniProt	BRENDA

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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 kluyveri	-	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 kluyveri	-	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	Escherichia coli	-	-	390164	⌬
Ca2+	Giardia intestinalis	-	5 mM causes 51% inhibition	390177	⌬
Chloroethanol	Escherichia coli	-	-	390171	⌬
CuSO4	Leuconostoc mesenteroides	-	1 mM 49% inhibition	390167	⌬
Disulfiram	Giardia intestinalis	-	0.01 mM causes 70% inhibition	390177	⌬
HgCl2	Leuconostoc mesenteroides	-	1 mM 31% inhibition	390167	⌬
iodoacetamide	Giardia intestinalis	-	1 mM causes 88-96% inhibition	390177	⌬
iodoacetate	Pseudomonas sp.	-	-	657161	⌬
Mg2+	Giardia intestinalis	-	5 mM causes 51% inhibition	390177	⌬
Mn2+	Giardia intestinalis	-	5 mM causes 84% inhibition	390177	⌬
Na2HAsO4	Leuconostoc mesenteroides	-	1 mM 100% inhibition, 0.1 mM 32% inhibition	390167	⌬
NAD+	Clostridium beijerinckii	-	double competitive, NAD+/CoA ratio is kept at 1:0.24	390174	⌬
NADH	Clostridium kluyveri	-	competitive inhibitor with respect to CoA; competitive to CoA	390176	⌬
p-chloromercuribenzoate	Giardia intestinalis	-	0.01 mM causes 88-96% inhibition	390177	⌬
Tris	Escherichia coli	-	rate of reaction falls off rapidly in Tris	390173	⌬
Valproate	Giardia intestinalis	-	50 mM causes 20-46% inhibition	390177	⌬
additional information	Leuconostoc mesenteroides	-	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-, dipyridyl, 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	Escherichia coli	-	NAD+ analogue, activates by binding strongly to activator site, binds weakly to catalytic site	390164	⌬
dithiothreitol	Escherichia coli	-	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 kluyveri	-	-	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 kluyveri	-	-	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 kluyveri	-	-	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 [$1/mMs^{-1}$] ▲▼	SUBSTRATE ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼ ×	LITERATURE ▲▼	IMAGE ▲▼
0.147 - 2.224	acetaldehyde	⊞ 9 entries				⌬
55.3 - 381	acetyl-CoA	⊞ 2 entries				⌬
0.0433 - 7.11	Butyraldehyde	⊞ 7 entries				⌬
394 - 833	butyryl-CoA	⊞ 2 entries				⌬
0.0265 - 1.584	pentaldehyde	⊞ 5 entries				⌬
0.00011 - 0.597	picolinaldehyde	⊞ 6 entries				⌬
0.0425 - 1.219	propionaldehyde	⊞ 6 entries				⌬

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Ki VALUE [mM] ▲▼	INHIBITOR ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼ ×	LITERATURE ▲▼	IMAGE ▲▼
265	acetaldehyde	Escherichia coli	-	at 25�C in 50 mM Tris/HCl buffer, pH 8.0	724721	⌬
2.5	ADP	Leuconostoc mesenteroides	-	-	390167	⌬
0.75	AMP	Leuconostoc mesenteroides	-	-	390167	⌬
8.6	ATP	Leuconostoc mesenteroides	-	-	390167	⌬

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

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

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

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pH RANGE	ORGANISM	UNIPROT	COMMENTARY	LITERATURE
5 - 8	Clostridium kluyveri	-	less than 50% of maximal activity above and below	390176

5.5	Citrobacter sp.	-	complete inactivation	738721
6 - 7	Clostridium beijerinckii	-	NAD+ reduction	390174
6.2 - 7.4	Escherichia coli	-	67% of maximal activity at pH 6.2, 79% of maximal activity at pH 7.4	390171
6.5 - 9.5	Clostridium beijerinckii	-	activity of NADH oxidation increases between 6.5-9.5	390174
6.5 - 8.5	Pseudomonas sp.	-	activity increases gradually over pH range from 6.5 to 8.5	390175
7 - 9.5	Propionibacterium freudenreichii	-	30% of maximal activity at pH 7.0, 100% at pH 9.5	390166
8.2 - 9.5	Propionibacterium freudenreichii	-	-	390166
8.5 - 10	Clostridium kluyveri	-	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	Leuconostoc mesenteroides	-	-	390167
40	Citrobacter sp.	-	-	738721
45	Propionibacterium freudenreichii	-	-	390166
60	Moorella sp.	-	at pH 8.0	735567

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TEMPERATURE RANGE ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼ ✕	LITERATURE ▲▼
20 - 60	Propionibacterium freudenreichii	-	55% of maximal activity at 20�C, 60% at 60�C	390166
50	Moorella sp.	-	71% of maximum activity	735567
70	Moorella sp.	-	52% of maximum activity	735567

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pI VALUE ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼ ✕	LITERATURE ▲▼
6.98	Polytomella sp. Pringsheim 198.80	Q70YJ9	calculated from sequence	739328

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SOURCE TISSUE ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼ ✕	LITERATURE ▲▼	SOURCE ▲▼
cell culture	⊞ 2 entries				
culture condition:ethanol-grown cell	Polytomella sp. Pringsheim 198.80	Q70YJ9	at pH 6.0 and pH 3.7	739328	BRENDA

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LOCALIZATION ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼ ✕	GeneOntology No. ▲▼	LITERATURE ▲▼	SOURCE ▲▼
cytosol	⊞ 3 entries					
membrane	⊞ 2 entries					
mitochondrion	Polytomella sp. Pringsheim 198.80	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	BRENDA
particle-bound	Clostridium kluyveri	-	-	-	286052,	BRENDA

					390170	

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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	Thermoanaerobacter sp.	B0K315, B0K4A2	gel filtration	735506
290000	Clostridium kluyveri	-	gel filtration and sedimentation coefficient	390176
360000	Thermoanaerobacter ethanolicus	-	gel filtration	286197
370000	Escherichia coli	-	one of four isozymes, gel filtration	390162
400000	Citrobacter sp.	-	gel filtration	738721
520000	Escherichia coli	-	one of four isozymes, gel filtration	390162
555000	Thermoanaerobacter sp.	B0K315, B0K4A2	gel filtration	735506
900000	Escherichia coli	-	one of four isozymes, gel filtration	390162

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SUBUNITS ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼ ✕	LITERATURE ▲▼
?	⊞ 4 entries			
dimer	⊞ 2 entries			
hexamer	Thermoanaerobacter sp.	B0K315, B0K4A2	6 * 97700, calculated, 6 * 94900, SDS-PAGE	735506
monomer	Escherichia coli	-	1 * 33344, electrospray ionization mass spectrometry	724721
pentamer	Thermoanaerobacter sp.	B0K315, B0K4A2	5 * 51700, calculated, 5 * 52400, SDS-PAGE	735506
polymer	Escherichia coli	-	ca. 40 * 96000, pyruvate-formate-lyase-deactivase with alcohol and aldehyde dehydrogenase activity, nucleotide sequence	390163
tetramer	⊞ 9 entries			
additional information	⊞ 2 entries			

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Crystallization/COMMENTARY ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	LITERATURE ▲▼
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	Escherichia coli	-	724721
-	Pseudomonas sp.	-	657161
hanging drop method, streak-seeding	Pseudomonas sp.	-	390178

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pH STABILITY ▲▼	ORGANISM ▲▼	UNIPROT ▲▼	COMMENTARY ▲▼ ✕	LITERATURE ▲▼
5 - 8	Clostridium	-	enzyme activity falls to 50% at pH 5 and pH 8	390176

	kluyveri			
7	Clostridium beijerinckii	-	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	Leuconostoc mesenteroides	-	15 min, inactivation	390167
70	Propionibacterium freudenreichii	-	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	Pseudomonas sp.	-	390175
dithioerythritol stabilizes	Clostridium kluyveri	-	390176
extremely unstable in absence of 2-mercaptoethanol	Escherichia coli	-	390171
labile during purification, stabilization by 2-hydroxyethyldisulfide	Escherichia coli	-	390164
no stabilization by detergents, acetone, ethanol, NAD+, glycerol, CoA, anaerobic conditions	Clostridium kluyveri	-	390176
sensitive to O2, can be protected against O2 inactivation by dithiothreitol	Clostridium beijerinckii	-	390174
with Tris acetate buffer at pH 7, less stable at higher buffer concentration between 10 and 150 mM	Clostridium beijerinckii	-	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	Escherichia coli	-	390163
-70�C, 10 mM Tris-HCl buffer, pH 8, 3 mM dithioerythritol, 2 weeks, 15% loss of activity	Clostridium kluyveri	-	390176
-70�C, 3 mM dithioerythritol, 85% of enzymatic activity remains after 2 weeks	Clostridium kluyveri	-	390176
-80�C, 10 mM phosphate buffer, pH 7.5, 1 mM dithiothreitol	Pseudomonas sp.	-	390175
3�C, ammonium sulfate step of purification, several months	Escherichia coli	-	390171
4�C, anaerobically	Thermoanaerobacter ethanolicus	-	286197
5 mM dithiothreitol protects enzyme in crude extracts from O2-inactivation for at least 2 hours	Clostridium beijerinckii	-	390174
addition of 140 mM KCl to 10 mM Tris acetate stabilizes as no activity is lost after 3 days	Clostridium beijerinckii	-	390174
CoA and dithiothreitol restore a higher activity than one of these compounds alone	Clostridium beijerinckii	-	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	Clostridium beijerinckii	-	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 (NH4)2SO4 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+-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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UPDATE!
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BRENDA professional