https://jgi.doe.gov/why-sequence-actinotalea-fermentans/

http://www.uniprot.org/taxonomy/862422

https://link.springer.com/chapter/10.1007%2F978-3-642-86605-0\_102

https://en.wikipedia.org/wiki/2-isopropylmalate\_synthase

https://www.sciencedirect.com/science/article/pii/S0003986111003468

https://www.sciencedirect.com/science/article/pii/S0168165617315481

http://www.thelabrat.com/protocols/Bacterialspecies/Actinotaleafermentans.shtml

Why sequence Actinotalea fermentans?

*Actinotalea fermentans* is a bacterium isolated from a landfill and grows best in moderate temperature, where it ferments cellulose to acetate and ethanol aerobically. This organism was previously considered as a potential way to convert cellulose to ethanol for use as a fuel, but the fermentation reaction always led to reduced yields, reducing the bacterium’s usefulness.

Recently, scientists have engineered synthetic co-cultures of *A. fermentans* with yeast to produce useful chemicals and fuels directly from cellulose or agricultural feedstocks such as corn stover, switchgrass, poplar and sugarcane bagasse. This technique will allow *A. fermentans* to be used to convert cellulose to ethanol while allowing researchers to avoid the same problems encountered before.

Sequencing the bacterium will provide the biofuels research community with a valuable resource for understanding and engineering a cellulose-fermenting organism. Additionally, the *A. fermentans* genome will be of interest to those studying microbial energy utilization and physiology.

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| --- | --- |
| [Mnemonic i](http://www.uniprot.org/help/taxonomy#organism-code) | - |
| [Taxon identifier i](http://www.uniprot.org/help/taxonomy) | 862422 |
| [Scientific name i](http://www.uniprot.org/help/taxonomy#organism-denomination) | Actinotalea fermentans ATCC 43279 = JCM 9966 = DSM 3133 |
| Taxonomy navigation | Up› [Actinotalea fermentans](http://www.uniprot.org/taxonomy/43671)  DownTerminal (leaf) node. |
| [Common name i](http://www.uniprot.org/help/taxonomy) | - |
| [Synonym i](http://www.uniprot.org/help/taxonomy) | - |
| [Other names i](http://www.uniprot.org/help/taxonomy#other-names) | › Actinotalea fermentans ATCC 43279 › Actinotalea fermentans DSM 3133 › Actinotalea fermentans JCM 9966 |
| [Rank i](http://www.uniprot.org/help/taxonomy#lineage) | - |
| [Lineage i](http://www.uniprot.org/help/taxonomy#lineage) | › [cellular organisms](http://www.uniprot.org/taxonomy/131567)    › [Bacteria](http://www.uniprot.org/taxonomy/2)      › [Terrabacteria group](http://www.uniprot.org/taxonomy/1783272)        › [Actinobacteria](http://www.uniprot.org/taxonomy/201174)          › [Actinobacteria](http://www.uniprot.org/taxonomy/1760)            › [Micrococcales](http://www.uniprot.org/taxonomy/85006)              › [Cellulomonadaceae](http://www.uniprot.org/taxonomy/85016)                › [Actinotalea](http://www.uniprot.org/taxonomy/458839)                  › [Actinotalea fermentans](http://www.uniprot.org/taxonomy/43671) |
| See also | › [NCBI](http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?lvl=0&amp;id=862422) |

From Wikipedia, the free encyclopedia

[Jump to navigation](https://en.wikipedia.org/wiki/2-isopropylmalate_synthase#mw-head) [Jump to search](https://en.wikipedia.org/wiki/2-isopropylmalate_synthase#p-search) In [enzymology](https://en.wikipedia.org/wiki/Enzymology), a **2-isopropylmalate synthase** ([EC](https://en.wikipedia.org/wiki/Enzyme_Commission_number) [2.3.3.13](https://enzyme.expasy.org/EC/2.3.3.13)) is an [enzyme](https://en.wikipedia.org/wiki/Enzyme) that [catalyzes](https://en.wikipedia.org/wiki/Catalysis) the [chemical reaction](https://en.wikipedia.org/wiki/Chemical_reaction)

acetyl-CoA + 3-methyl-2-oxobutanoate + H2O ⇌ {\displaystyle \rightleftharpoons } (2S)-2-isopropylmalate + CoA

The three [substrates](https://en.wikipedia.org/wiki/Substrate_(biochemistry)) of this enzyme are [acetyl-CoA](https://en.wikipedia.org/wiki/Acetyl-CoA), [3-methyl-2-oxobutanoate](https://en.wikipedia.org/wiki/3-methyl-2-oxobutanoate), and [H2O](https://en.wikipedia.org/wiki/Water), and its [products](https://en.wikipedia.org/wiki/Product_(chemistry)) are [(2S)-2-isopropylmalate](https://en.wikipedia.org/wiki/(2S)-2-isopropylmalate) and [CoA](https://en.wikipedia.org/wiki/Coenzyme_A).

The enzyme belongs to the family of [transferases](https://en.wikipedia.org/wiki/Transferase), specifically those [acyltransferases](https://en.wikipedia.org/wiki/Acyltransferases) that convert acyl groups into alkyl groups on transfer. The [systematic name](https://en.wikipedia.org/wiki/List_of_enzymes) of this enzyme class is *acetyl-CoA:3-methyl-2-oxobutanoate C-acetyltransferase (thioester-hydrolysing, carboxymethyl-forming)*. Other names in common use include *3-carboxy-3-hydroxy-4-methylpentanoate 3-methyl-2-oxobutanoate-lyase*, *(CoA-acetylating)*, *alpha-isopropylmalate synthetase*, *alpha-isopropylmalate synthase*, *alpha-isopropylmalic synthetase*, *isopropylmalate synthase*, and *isopropylmalate synthetase*. This enzyme participates in biosynthesis of L-[leucine](https://en.wikipedia.org/wiki/Leucine) and [pyruvate metabolism](https://en.wikipedia.org/wiki/Pyruvate_metabolism). Monovalent and divalent cation activation have been reported for enzymes from different sources.[[1]](https://en.wikipedia.org/wiki/2-isopropylmalate_synthase#cite_note-1)[[2]](https://en.wikipedia.org/wiki/2-isopropylmalate_synthase#cite_note-2)[[3]](https://en.wikipedia.org/wiki/2-isopropylmalate_synthase#cite_note-3)

[*Mycobacterium tuberculosis*](https://en.wikipedia.org/wiki/Mycobacterium_tuberculosis) α-isopropylmalate synthase requires a divalent metal ion, of which Mg2+ and Mn2+ give highest activity, and a monovalent cation, with K+ as the best activator.[[4]](https://en.wikipedia.org/wiki/2-isopropylmalate_synthase#cite_note-4)[[5]](https://en.wikipedia.org/wiki/2-isopropylmalate_synthase#cite_note-5) Zn2+ was shown to be an inhibitor, contrary to what was assumed from the structural data. In addition to the complex requirements for a divalent metal and further activation by K+, *M. tuberculosis* α-isopropylmalate synthase follows a random kinetic mechanism for catalysis.[[*citation needed*](https://en.wikipedia.org/wiki/Wikipedia:Citation_needed)] Another feature of the *M. tuberculosis* homolog is that L-leucine, the feedback inhibitor, inhibits the enzyme in a time-dependent fashion. This was the first demonstration of a feedback inhibitor that displays slow-onset inhibition.[[6]](https://en.wikipedia.org/wiki/2-isopropylmalate_synthase#cite_note-6)