In general in comparison to (S)-selective ω-transaminases the number of available (R)-selective ω-transaminase is much more limited. This stands in sharp contrast to the high demand for (R)-selective ω-transaminases which are highly desirable for the asymmetric synthesis of (R)-enantiomers of various chiral-amines. Thus, there is still the need to provide further (R)-selective transaminases and means and methods to obtain them in order to produce R-enantiomers, in particular optically active amines, for instance for pharmaceutical or agrochemical applications, which are up to now either not available at all or not in an economically feasible process, preferably in industrial scale.

The present invention is therefore based on the technical problem to provide simple, fast and reliable means and methods to identify, characterize and obtain (R)-selective ω-transaminases, in particular for the production of desired (R)-enantiomers, preferably in optically pure form, which are preferably suitable for identification, characterization and preparation in an industrial scale.

The present invention solves its technical problem by the provision of the teaching of the independent claims, in particular the claimed process, the products and uses obtained thereby.

Summary

In one aspect, there is provided a process for the preparation of a (R)-selective ω-transaminase, comprising the following steps:

a) providing at least one query biomolecule sequence of at least one (R)-selective ω-transaminase and at least one biomolecule bank,

b) searching the biomolecule bank with the query biomolecule sequence to identify a group of first target biomolecule sequences, wherein the first target biomolecule sequences have a degree of sequence identity of at least 20% to the query biomolecule sequence, calculated on amino acid level,

c) selecting in the group of first target biomolecule sequences a group of second biomolecule target sequences, which do not comprise, on amino acid level, at least one of the following amino acid sequence motives c1) to c3) with

c1) at position 95 to 97 an amino acid sequence Tyr Xa1 Xa2, with Xa1 being an amino acid Ile, Val, Leu, Met, Phe, and Xa2 being an amino acid Arg or Lys or

c2) at position 97 to 99 an amino acid sequence Tyr Xaa Gln, with Xaa being an amino acid and in the region from position 105 to 111 an amino acid sequence Arg Xaa Xa3, Xa3 being an amino acid, preferably being His or

c3) at position 38 Thr, at position 97 Lys and at position 107 to 109 an amino acid sequence Arg Xa4 Xa5, Xa4 being an amino acid, preferably being Gly and Xa5 being an amino acid, preferably being Tyr

and which comprise

c4) at position 95 another amino acid than Tyr, Arg, Lys, or at position 95 Tyr, but at position 97 no Arg or Lys and

c5) at position 40 no Lys or Arg and

c6) in the region from position 161 to 165 at least one Lys

to identify a group of second target biomolecule sequences and

d) providing a biomolecule having the second target biomolecule sequence identified in step c) and being, or coding at least partially, a protein with the activity of a (R)-selective ω-transaminase.

Detailed Description

Thus, the present teaching provides in a particular embodiment a process for the preparation of a (R)-selective ω-transaminase (also called ω-TA), comprising the following steps:

a) providing at least one query biomolecule sequence of at least one transaminase or lyase, preferably a transaminase or lyase which belongs to fold-type IV of PLP-dependent enzymes, and at least one biomolecule bank,