# Engineering an Artificial Pathway to Improve the Bioconversion of Lysine into Chiral Amino Alcohol 2-Hydroxycadaverine using a Semi-Rational Design

**Jie Cheng [1,*,†], Shujian Xiao [1,†], Qing Luo [2], Bangxu Wang [1], Rumei Zeng [1], Liming Zhao [3] and Jiamin Zhang [1]**

[1] College of Food and Bioengineering, Chengdu University, Chengdu 610106, China; xiaoshujian1995@163.com (S.X.); wangbangxu@stu.cdu.edu.cn (B.W.); zengrumei@stu.cdu.edu.cn (R.Z.); zhangjiamin@cdu.edu.cn (J.Z.)
[2] Faculty of Applied Sciences, Macao Polytechnic University, Macao 999078, China; p2214931@mpu.mo
[3] State Key Laboratory of Bioreactor Engineering, East China University of Science and Technology, Shanghai 200237, China; zhaoliming@ecust.edu.cn
* Correspondence: author: chengjie@cdu.edu.cn
† These authors contributed equally to this work.

**Supplementary Data S1**:
The codon-optimized nucleotide sequence of lysine hydroxylase from *Kineococcus radiotolerans* ($KDO_{Kr}$)

ATGTCTAGCCTGTTCCTGGATTCCTCTGCGCACGTCCCTACCCTGTTCGAACTGCCGGCAC-
CGCAACGCGCGGCTCTGGCGGCTCTGGGTGCACGTCTGACCGCTGATCCGGTTACCGAGC
CGGATGCGTTCGGTCGTCAGGCTCGTCTGCTGGCGCGTGAACTGAGCGTGGAAGTTAC-
CGAGGCACTGTGGGCGTTCGAAGAACGTGGTTCCGACTCCGGTGTGCTGGTCCTGCGTGG
CCTGGAAGTGGGTGAACTGCCACCGACTCCGGCAGATAACACCGGTGG-
TATTGGTGGTCG-
TACCCTGCTGGCACGTCAGCAGGCAATCGTTTCCCACGCGCTGGGTCACATGGTCGGTTAT
GCCGCAGAAGGCCATGGTCACCTGCTGCAGGATATGGTTCCGAAC-
GCGCGTCTGGCTGCGACCCCTGCGCGCAATGCACGGCCGCTCTCCATTCGCGCCGCGTTTC
GATGGCACGGACCGTTTCATCAGCCGCGGCAACAGTCCCAGGGTTCCCGTGTTGAACTG-
GAA-
GCGCATACCGAACAGTGCTTCTCCGACCTGCGCCCGGATTATGTTGTGCTGGGTTGTCTGC
GTGGTGACGCCGACGCAGCAACCTATGCATTTCGTGCGCTGGATCTGCTGGCGCAC-
GTAGACCCGACCGACGTGATGGAGCTGTTTCGTCCGCTGTGGACCACCCTGGTGGACGAA
AGCTTTGCTGACTTCCTGGACACCCGTGAAGTGCGTGGCCCGTTCTC-
TATTCTGTCTGGCGACGTGGACGACCCGACCATGCTGGTTGATCAGGATCTGATGCATGGC
ATCACTAAACACGCTCAGGCGCTGCTGGAACGTGTTCTGGAAATCTATGTGG-
CACATCGTCACGCTGTTGTTCTGCAGCCAGGTGATGTGCTGCTGCTGGATAACTTCGTGGT
CCGCGATCTGCGTCGTTCTCGTTTCGCTCGTCCAGGCGGTAAC-
CGTGTCGTTCAGGCGTCTTTTTCTTAA

**Supplementary Data S2:**
The codon-optimized nucleotide sequence of pyridoxal phosphate-dependent decarboxylase from *Chitinophaga pinensis* ($DC_{Cp}$)

ATGAGCACCACCGCATTCGCTGGCTGGGAACAACCGCTGCAGGATATCGTACTGCCAG-
TGAAGGAAACCTACAAAGACATCTTCCACCAAGGTAGCGCTGCGGAATACGAAAACGCA
ATCAACGGTGCTCGCGAACTGGTAACCAACTTCCTGCACCG-
TAATCGTCAGCCTTTCTCCGGTGTTTCCTCTACTGCACTGCGCGCTGCATTCGCAGCGGTCG
ACTTCGACACCCCACTGCCAGATTACGAATCCCTGCTGCAGGAAGTACAGGAACTGTAC-
GTTAAACACGCAACCGCCTTTCACCTGCCTGCTTATATCGCGCACCTGAACTGTCCGGTTG
TAATCCCGGCAGTGGCAGCTGAAGTACTGATCGCCGCGATCAATTCCTCCCAGGACAC-
GTGG-
GACCAGTCTGCTGGTGGTACGCTGATGGAACAGCAGCTGATCTCTTGGACCGCACGTGAA
ATCGGCTTCGGCACCGTCGCGGATGGCGTTTTCACCGCTGGTGGTTCTCAGTCCAAC-
CTGATGGGCCTGCTGCTGGCTCGTGACCACTATGCAATTACCAACGGTGGTCATAACATCA
AAAAGCAGGGCCTGCCGGGTGATGCATCTCGTTACCGTATCTTTATTAGCGAAAAGGCG-
CAC-
TTCTCTAACCACAAAGGTGCAGCTCTGCTGGGTCTGGGCGAGCAAGCACTGGTTGAAATC
AAAACCGACGCACGCTTTCGTATGGACGCTGAACTGCTGGAAGAA-
GCGATCGCGCGCGAAATCCAACAGGGTAACATCCCGATCGCTGTTGTTGCGACTGCTGGC
ACCACCGATTTCGGTAATCTGGACCCGCTGGCGGATATCGGCCGCATCGCGGCAAAA-
TATAACCTGTGGTACCATATTGACGCCGCTTATGGTTGTGGTCTGCTGCTGACCGAGAAAT
ACCGCCACCTGCTGAACGGTATGGAAACTGCTCATTCTGTGACGATCGAT-
TATCACAAGTCCTTTTTCCAACCGATTTCTTCTAGCGCCTTCATCGTGAAGGACAAACAGT
ACCTGCGTCTGCTGCGCATGCACGTGGACTACCTGAACCCTAAGGACGAAGACTATGAC-
GAC-
CTGAACCAGATCAACAAGAGCATCATGCAGTCCACTCGTCGTTTCGATGCTCTGAAACTG
TGGTTCACGCTGCGTCTGATGGGTAAACAGAAACTGGGCGCGTACACCGAAAC-
CATCATCGAAACCGCCGAAAAGGCTGCAGAAGTAATTGGCCTGGATCCAGAACTGGAAC
TGCTGAGCTACTCCGACATTGGTGTGATCCTGTTCCGTTACGCCCCGGAGCAG-
TATAACCCGGCTGACCTGGATGCCCTGAACCAGTACATCAAAAAAACCATGTTTAACACT
GGCCTGGTTCTGGTTGCGTCTACCCGTGTTAACGGTAACTTCTAC-
CTGAAGTTTACTATGCTGAACCCGCTGACCACCCTGGATGACGTCCACTTCATTCTGAACA
CCATCAAAGAGACTGGCGCCGCATGGCGTCAGTAA

**Table S1.** The $OD_{600}$ value at specific times of strains ML101 and ML102.

| Time (h) | The $OD_{600}$ of ML101 | The $OD_{600}$ of ML102 |
|---|---|---|
| 0 | 0±0.00 | 0±0.00 |
| 2 | 0.41±0.03 | 0.38±0.02 |
| 3 | 0.82±0.04 | 0.84±0.05 |
| 6 | 2.13±0.11 | 2.24±0.12 |
| 12 | 5.36±0.42 | 5.57±0.44 |
| 24 | 5.78±0.46 | 5.84±0.43 |