

Supporting information

A multi-enzyme cascade with internal cofactor cycling for the green conversion of inert n-alkanes to α,ω -dicarboxylic acids

Zhijun Kong,^{*a} Weihan Sun,^a Wenjin Dong,^a Su Song,^a Li Ma,^{*a} Shengying Li^{*a,b} and Hui Chen^{*a}

^a State Key Laboratory of Microbial Technology, Shandong University, Qingdao 266237, China

^b Laboratory for Marine Biology and Biotechnology, Qingdao Marine Science and Technology Center,
Qingdao 266237, China

* Corresponding Author: Li Ma (maliqu@sdu.edu.cn)

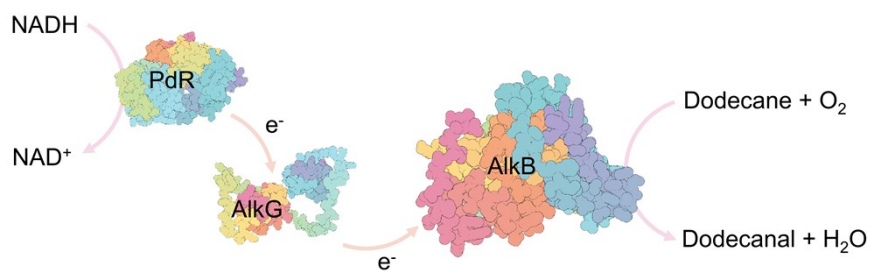
Shengying Li (lishengying@sdu.edu.cn)

Hui Chen (Chen.Hui@sdu.edu.cn)

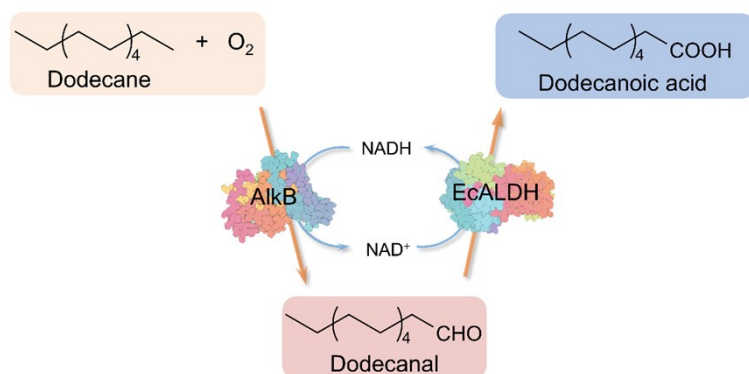
ORCID: Li Ma: 0000-0003-1601-7125

Shengying Li: 0000-0002-5244-870X

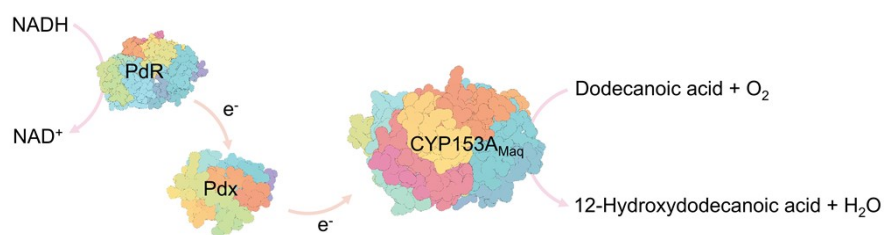
Hui Chen: 0000-0002-8944-0090



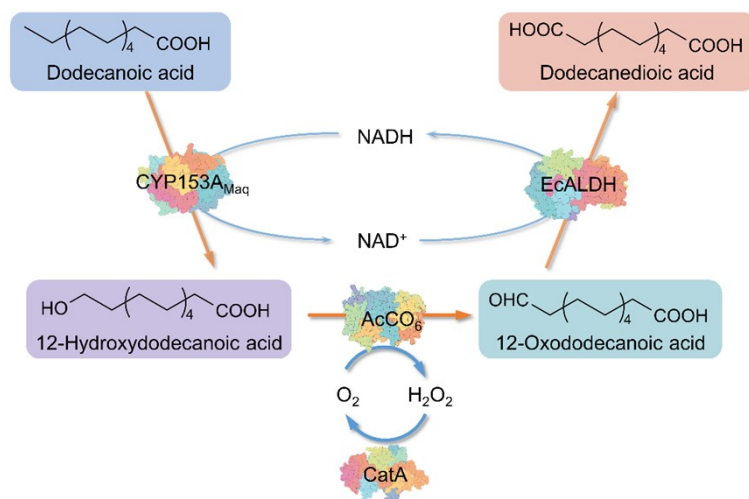
Scheme S1 The terminal C-H bond hydroxylation of dodecane catalyzed by AlkB. AlkB is a non-heme diiron monooxygenase. During the catalytic cycle, the diiron center activates molecular oxygen (O₂). One oxygen atom is inserted into the terminal C-H bond of the alkane substrate. Concurrently, the second oxygen atom acts as the terminal acceptor for the hydrogen atoms—specifically, the hydride equivalent derived from NADH (transferred via the PdR-AlkG electron cascade) and a proton—to ultimately generate a molecule of water (H₂O). Thus, the hydrogen atoms removed during this oxidation process are transferred to form H₂O.^{1,2}



Scheme S2 The scheme of multi-enzymatic conversion from dodecane to dodecanoic acid coupled with NADH regeneration.



Scheme S3 ω -hydroxylation of 12-hydroxydodecanoic acid catalyzed by CYP153A_{Maq}. CYP153A_{Maq} is a cytochrome P450 monooxygenase. In its catalytic cycle, the heme iron center activates O₂. One oxygen atom is incorporated into the ω -position of dodecanoic acid to form the hydroxyl group. The second oxygen atom serves as the terminal acceptor for the hydrogen atoms (the electron/hydride equivalents donated by NADH via the PdR-Pdx chain, along with a proton), yielding a molecule of H₂O.³



Scheme S4 A multi-enzyme cascade conversion scheme for the conversion of dodecanoic acid to dodecanedioic acid ingeniously integrates an internal NADH cycle regeneration system.

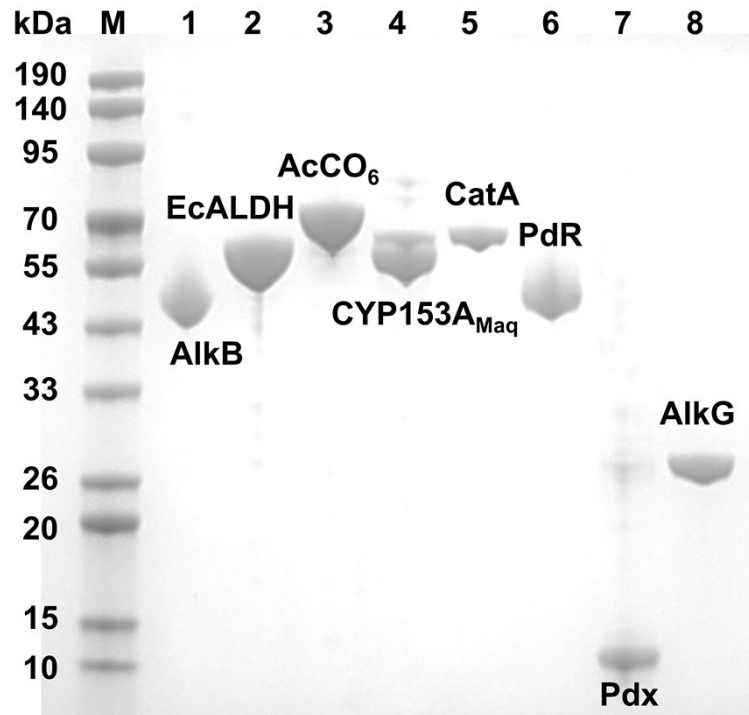


Fig. S1 SDS-PAGE analysis of purified enzymes used in this study. (a) Lane M: marker; Lane 1: AlkB (46.9 kDa); Lane 2: EcALDH (54.2 kDa); Lane 3: AcCO₆ (60.9 kDa); Lane 4: CYP153A_{Maq} (55.1 kDa); Lane 5: CatA (55.9 kDa); Lane 6: PdR (46.6 kDa); Lane 7: Pdx (12.6 kDa); Lane 8: AlkG (20.1 kDa).

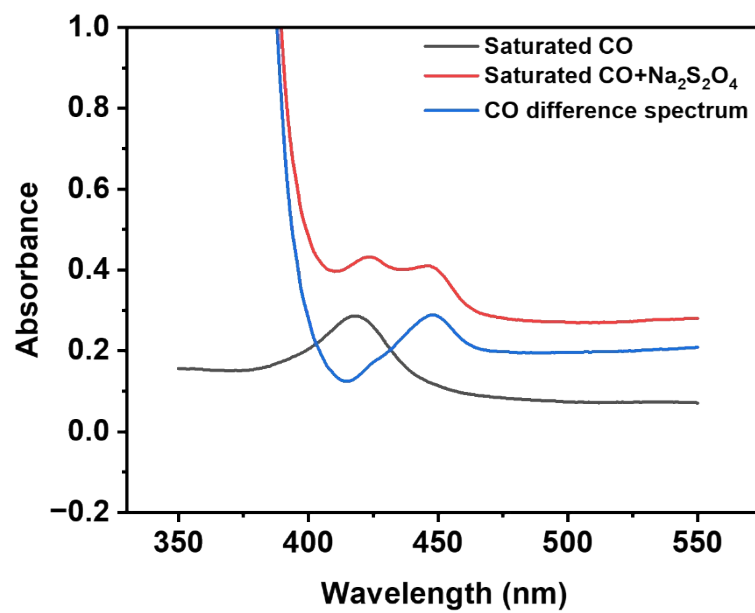


Fig. S2 CO difference spectra of purified CYP153A_{Maq}. Black curve: The CO staturated CYP153A_{Maq} sample; Red curve: Added Na₂S₂O₄ to the CO staturated CYP153A_{Maq} sample; Blue curve: CO difference spectra.

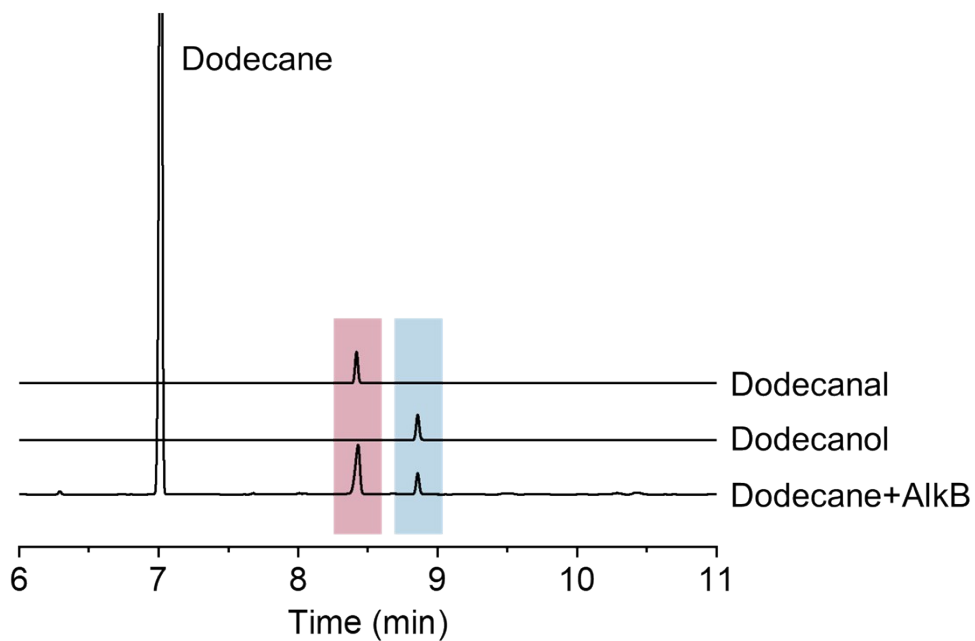


Fig. S3 GC analysis of the formation of dodecanol and dodecanal catalyzed by AlkB. The reactions were performed in a 7 mL sealed vial with magnetic string at room temperature. The 500 μ L reaction mixture contained 100 mM KPi buffer (pH=8.0), 10 μ M (0.06 U/mL) AlkB, 30 μ M AlkG, 60 μ M PdR (molar ratio of AlkB: AlkG: PdR=1:3:6), 4 mM NADH and 0.75% (v/v) dodecane as substrate. After the reactions were completed, the reaction mixtures were extracted with MTBE containing 0.5 mM n-eicosane as an internal standard.

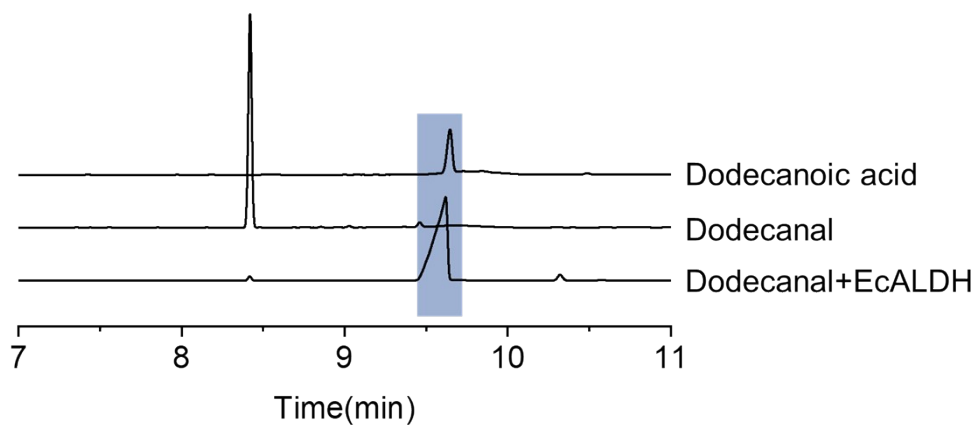


Fig. S4 GC analysis of the formation of dodecanoic acid catalyzed by EcALDH. The reactions were performed in a 7 mL sealed vial with magnetic string at room temperature. The 500 μ L reaction mixture contained 100 mM KPi buffer (pH=8.0), 10 μ M (0.20 U/mL) EcALDH, 4 mM NAD^+ and 2 mM dodecanal. After the reactions were completed, the reaction mixtures were extracted with MTBE containing 0.5 mM n-eicosane as an internal standard.

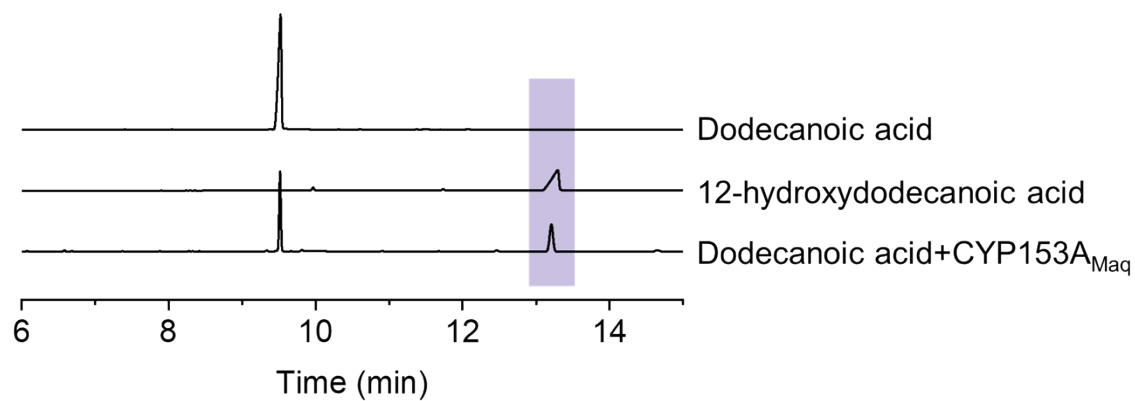


Fig. S5 GC analysis of the formation of 12-hydroxydodecanoic acid catalyzed by CYP153A_{Maq}. The reactions were performed in a 7 mL sealed vial with magnetic string at room temperature. The 500 μ L reaction mixture contained 100 mM KPi buffer (pH=8.0), 30 mM MgCl₂, 10 μ M (0.10 U/mL) CYP153A_{Maq}, 10 μ M PdR, 100 μ M Pdx (molar ratio of CYP153A_{Maq}: PdR: Pdx=1:1:10), 2 mM NADH and 2 mM dodecanoic acid. After the reaction was completed, the reaction mixture was first acidified with 10% (v/v) hydrochloric acid. Then, MTBE containing 0.5 mM n-eicosane as an internal standard was added for extraction.

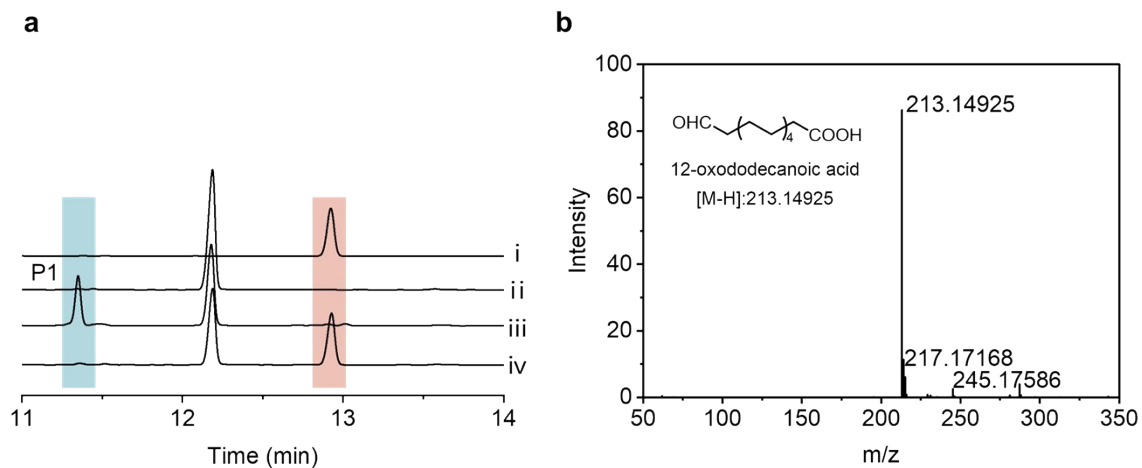


Fig. S6 a GC analysis of the formation of dodecanedioic acid catalyzed by AcCO_6 and EcALDH. (i) GC analysis of dodecanedioic acid standard. (ii) GC analysis of the negative control (without AcCO_6 and EcALDH) using 12-hydroxydodecanoic acid as the substrate. (iii) GC analysis of the conversion from 12-hydroxydodecanoic acid to 12-oxododecanoic acid catalyzed by AcCO_6 . (iv) GC analysis of the conversion from 12-hydroxydodecanoic acid to dodecanedioic acid catalyzed by AcCO_6 and EcALDH. AcCO_6 -catalyzed reactions were performed in a 7 mL sealed vial with magnetic string at room temperature. The 500 μL reaction mixture contained 100 mM KPi buffer (pH=8.0), 10 μM (0.003 U/mL) AcCO_6 and 2 mM 12-hydroxydodecanoic acid. Since 12-oxododecanoic acid standards were unavailable, we indirectly verified the aldehyde dehydrogenase activity of EcALDH by adding 10 μM (0.17 U/mL) EcALDH and 2 mM NAD^+ to the reaction mixture described above, thereby converting the intermediate 12-oxododecanoic acid into dodecanedioic acid. After the reactions were completed, the reaction mixtures were first acidified with 10% (v/v) hydrochloric acid. Then, MTBE containing 0.5 mM n-eicosane as an internal standard was added for extraction. The derivatization method reported by Slaughter et al.⁴ was used for sample processing. **b** When AcCO_6 catalyzed the conversion of 12-hydroxydodecanoic acid, a new product peak (labeled P1) was observed (**Figure S6a**). LC-MS analysis confirmed this product to be 12-oxododecanoic acid.

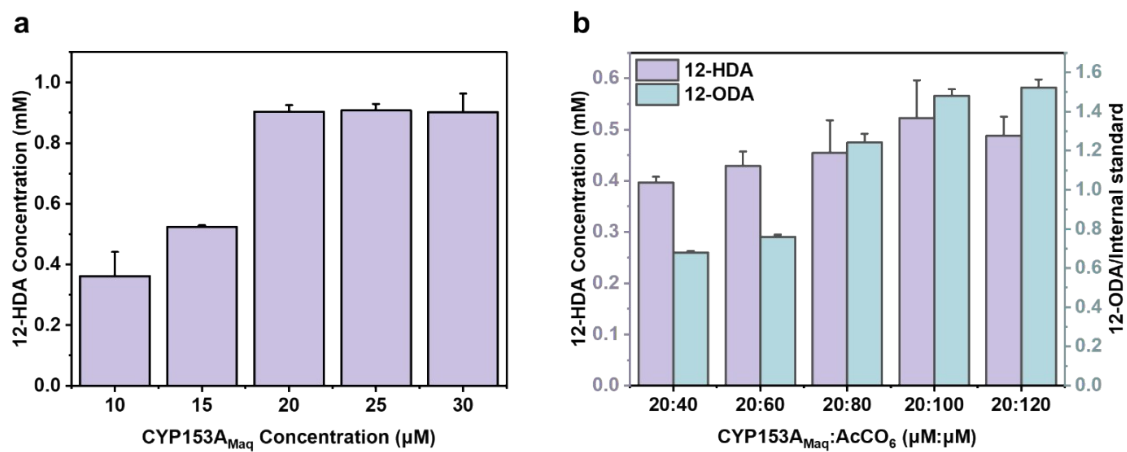


Fig. S7 Optimization of the enzyme ratio for CYP153A_{Maq} to AcCO₆. **a** The enzyme concentration of CYP153A_{Maq} was optimized. With the Mg²⁺ concentration fixed at 30 mM, CYP153A_{Maq} was added at varying concentrations. **b** The enzyme ratio of CYP153A_{Maq} to AcCO₆ was optimized. With CYP153A_{Maq} concentration fixed at 20 μM (0.19 U/mL), AcCO₆ was added at varying concentrations.

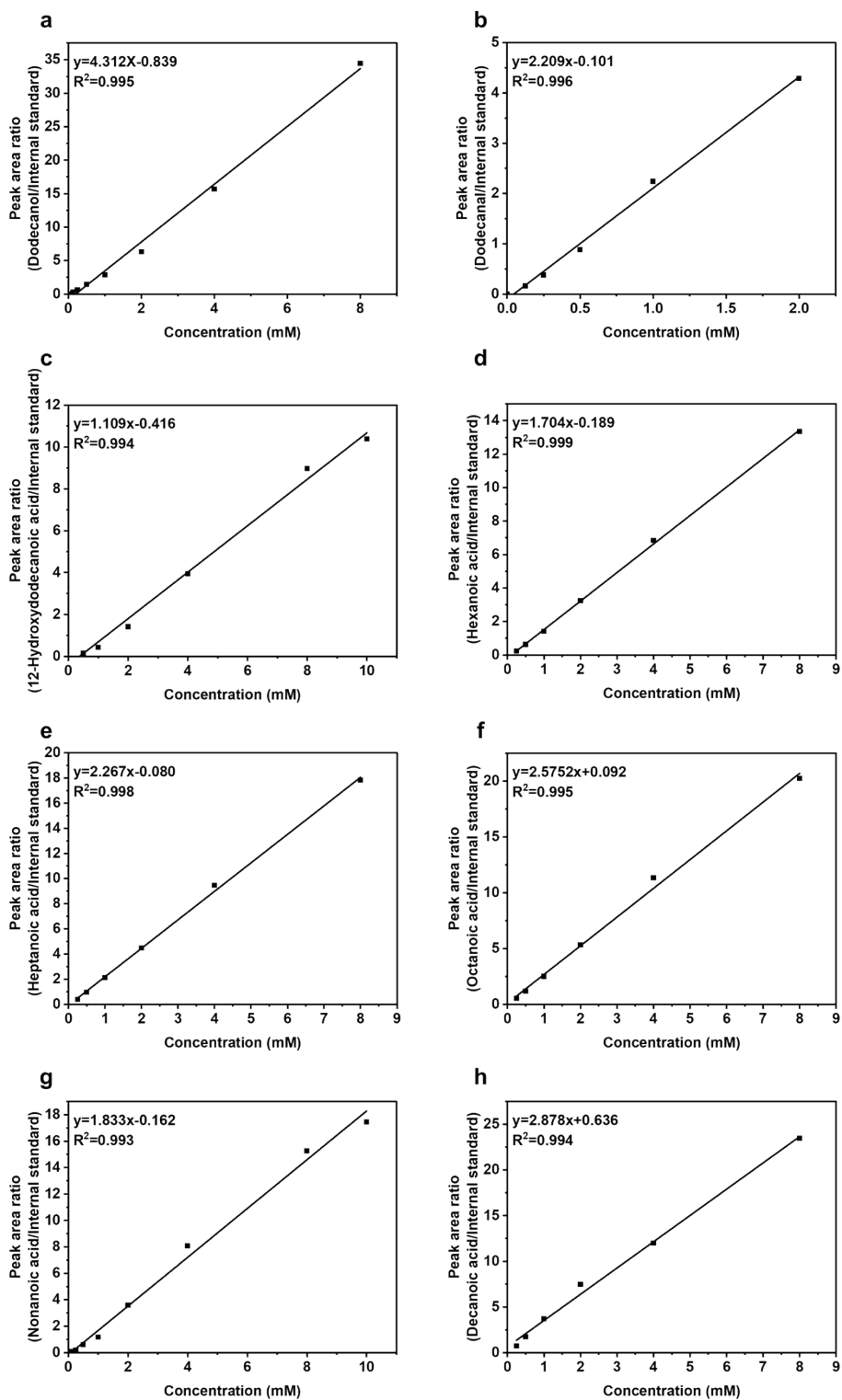


Fig. S8 GC calibration curve for the quantification analysis of dodecanol (a), dodecanol (b), 12-hydroxydodecanoic acid (c), hexanoic acid (d), heptanoic acid (e), octanoic acid (f), nonanoic acid (g) and decanoic acid (h).

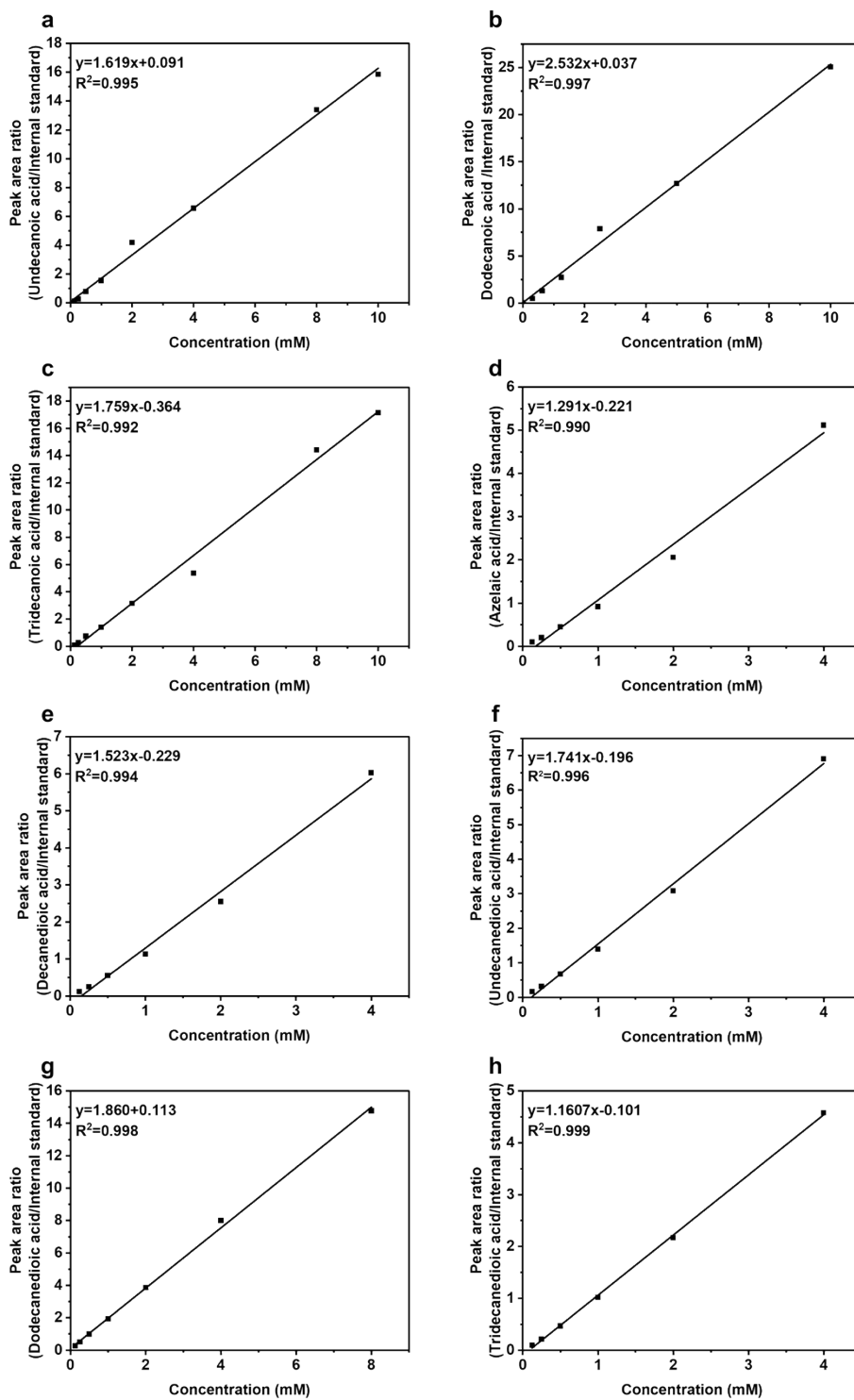


Fig. S9 GC calibration curve for the quantification analysis of undecanoic acid (a), dodecanoic acid (b), tridecanoic acid (c), azelaic acid (d), decanedioic acid (e), undecanedioic acid (f), dodecanedioic acid (g) and tridecanedioic acid (h).

Table S1. Comparison of key performance and sustainability metrics of the proposed multi-enzyme cascade system with established chemical oxidation and whole-cell fermentation methods.

Metrics	Typical process	Substrate	Reaction conditions	Catalyst	Oxidizing agent	Cofactor	Atom economy	Regional selectivity	Ref.
This Work	Multi-enzyme cascade reaction	Dodecane	Room temperature, room pressure	Enzymes	O ₂	Internal hydrogen-borrowing cycle	All substrate atoms enter the product	100% Terminal selectivity	
Chemical synthesis	Butadiene Trimerization Route	1,3-Butadiene	High temperature (>100 °C), high pressure	Precious metals (Pd, V, TiCl ₄)	HNO ₃	Consuming stoichio-metric ratio of oxidant	Produces large amounts of N ₂ O	Producing short -chain heteroacids	5
Microbial fermentation	Fermentation by engineered <i>C. viswanathii</i>	Dodecane	30 °C, room pressure	Cells	O ₂	Exogenous Glucose (NAD(P)H regeneration & Growth)	Fatty acid catabolism via β-oxidation	Few by-products	6
Microbial fermentation	Fermentation by engineered <i>Y. lipolytica</i>	Dodecane	28 °C, room pressure	Cells	O ₂	Exogenous Glucose (NAD(P)H regeneration & Growth)	Intermediate accumulation	Few by-products	7
Microbial fermentation	Fermentation by <i>C. viswanathii</i> <i>ipe-1</i>	Dodecane	30 °C, room pressure	Cells	O ₂	Exogenous Glucose & xylose (NAD(P)H regeneration & Growth)	Fatty acid catabolism via β-oxidation	Few by-products	8

DNA sequences and amino acid sequences of enzymes used in this stud

The AlkB gene, derived from *Pseudomonas putida* GPO1, has been codon-optimized for expression in *E. coli*. The gene sequence contains a 6×His tag, and the start and stop codons are indicated by lowercase letters and underscores.

atgCTTGAGAAACACAGAGTTCTGGATTCCGCTCCAGAGTACGTAGATAAAAAGAAATATCTCTGGATACTATCAACTTTGTG
GCCGGCTACTCCGATGATCGGAATCTGGCTTGCAAATGAAACTGGTTGGGGGATTTTTATGGGCTGGTATTGCTCGTATGG
TACGGCGCACTTCCATTGCTTGATGCGATGTTTGGTGAGGACTTTAATAATCCGCTGAAGAAGTGGTGCCGAACTAGAGA
AGGAGCGGTACTATCGAGTTTTGACATATCTAACAGTTCCTATGCATTACGCTGCATTAATTGTGTCAGCATGGTGGGTGCGGA
ACTCAGCCAATGTCTTGGCTTGAAATGGTGCGCTTGCCTTGTCACTGGGTATCGTGAACGGACTAGCGCTCAATACAGGAC
ACGAACTCGGTACAAGAAGGAGACTTTTGATCGTTGGATGGCCAAAATTGTGTTGGCTGTCGTAGGGTACGGTCACTTCTT
TATTGAGCATAATAAGGGTCATCACCGTATGTCGCTACACCGATGGATCCTGCAACATCCCGGATGGGAGAAAGCATTAT
AAGTTTTCAATCCGTGAGATCCAGGAGCATTATTCTGTGCTTGGGGCTTGAGGAACAACGCCTTTCGCGCCGTGGCCAAA
GCGTTTGGAGTTTCGATAATGAAATCTCCAACCAATGATCATCACAGTTATTCTTTACGCCGTTCTCCTTGCCTTGTGGAC
CTAAGATGCTGGTGTCTGCGGATTCAAATGGCTTTCGTTGGTGGCAGCTGACCAGTGCGAACTATATTGAACATTACGG
CTTGCTCCGTCAAAAAATGGAGGACGGTTCGATATGAGCATCAAAAGCCGCACCATTCTTGAATAGTAATCACATCGTCTCT
AATCTAGTGCTGTTCCACCTTCAGCGGCACTCGGATCACACGCGCATCCAACACGTTCTTATCAGTCACTTCGGGATTTTCCC
GGCCTGCCGGCTCTCCGACGGGTACCCTGGTGCATTTTTGATGGCGATGATTCCTCAGTGGTTTAGATCAGTTATGGATCC
CAAGGTAGTAGATTGGGCTGGTGGTGACCTTAATAAGATCCAAATTGATGATTCGATGCGAGAAACCTATTTGAAAAAATT
GGCACTAGTAGTGCTGGTCATAGTTCGAGTACCTCTGCGGTAGCATCGCACCACCACCACCACCtag

MLEKHRVLDSAPEYVDKKYLWILSTLWPATPMIGIWLANETGWGIFYGLVLLVWYGALPLLDAMFGEDFNNPPEEVVPKLEKER
YYRVLTYLTPMHYAALIVSAWWVGTQPMWLEIGALALSLGIVNGLALNTGHELGHKKETFDRWMAKIVLAVVGYGHFFIEHN
KGHHRDVATPMDPATSRMGESYKFSIREIPGAFIRAWGLEEQRLSRRGQSVWSFDNEILQPMIITVILYAVLLALFGPKMLVFLPI
QMAFGWWQLTSANYIEHYGLLRQKMEDGRYEHQKPHHSWNSNHIVSNLVLFLHQRHSDHHAHPTRSYQSLRDFPLPALPTG
YPGAFLMAMIPQWFRSVMDPKVVDWAGGDLNKIQIDDSMRETYLKKFGTSSAGHSSSTSAVASHHHHHH

The AlkG gene, derived from *Pseudomonas putida* GPO1, has been codon-optimized for expression in *E. coli*. The gene sequence has a 6×His tag, and the start and stop codons are marked with lowercase letters and underscores.

atgGCGAGCTACAAATGCCCGGATTGCAACTATGTTTATGACGAGAGCGCGGTAATGTTACGAAGTTTCAGCCCGGGCA
CCCCGTGGCACCTGATCCCGGAAGACTGGTGCTGCCCGATTGCGCGGTGCGTGACAAGCTGGATTCATGCTGATTGAGA
GCGGTGTGGGCGAAAAAGGTGTTACCAGCACCCACACCAGCCGAACCTGAGCGAGGTGAGCGGCACCAGCCTGACCGCG
GAAGCGGTGGTTGCGCCGACCAGCCTGGAGAAGCTGCCGAGCGCGGACGTTAAGGGTCAGGATCTGTACAAAACCAACC
GCCGCGTAGCGATGCGCAGGGTGGCAAGGCGTACCTGAAATGGATCTGCATTACCTGCGGTCACATCTATGACGAAGCGCT
GGGCGATGAGGCGGAAGTTTCACCCCGGCACCCGTTTTGAGGACATTCCGGATGACTGGTGCTGCCCGGACTGCGGTGC
GACCAAAGAAGATTATGTGCTGTATGAAGAGAAGCTCGAGCACCACCACCACCACCtaa

MASYKPCDCNYVYDESAGNVHEGFSPGTPWHLIPEDWCCPDCAVRDKLDFMLIESGVGEKGVSTHTSPNLSEVSGTSLTAEAV
VAPTSLEKLPSADVKGQDLYKTQPPRSDAQGGKAYLKWICITCGHIYDEALGDEAEGFTPGRFEDIPDDWCCPDCGATKEDYVLY
EEKLEHHHHHH

The PdR gene, derived from *Pseudomonas putida*, has been codon-optimized for expression in *E. coli*. The gene sequence contains a 6×His tag, and the start and stop codons are indicated by lowercase letters and underscores.

atgAACGCAAACGACAACGTGGTCATCGTCGGTACCGGACTGGCTGGCGTTGAGGTCGCCTTCGGCCTGCGGCCAGCGGCT
GGGAAGGCAATATCCGGTTGGTGGGGATGCGACGGTAATCCCCATCACCTACCACCGCTATCAAAGCTTACTTGGCCGG
CAAAGCCACAGCGGAAAGCCTGTACCTGAGAACCCAGATGCCTATGCAGCGCAGAACATCCAATACTCGGAGGCACACA
GGTAACGGCTATCAACCGCGACCGACAGCAAGTAATCTATCGGATGGCCGGGCACTGGATTACGACCGGCTGGTATTGGC
TACCGGAGGGCGTCCAAGACCCCTACCGGTGGCCAGTGGCGCAGTTGAAAGGCGAACTTTGATACCTGCGCACACT
CGAGGACGCCGAGTGCATTCGCCGGCAGCTGATTGCGGATAACCGTCTGGTGGTATTGGTGGCGGCTACATTGGCCTTGA
AGTGGCTGCCACCGCCATCAAGGCGAACATGCACGTCACCCTGCTTGATACGGCAGCCCGGGTCTGGAGCGGGTTACCGC
CCGCCCGGTATCGGCCTTTTACGAGCACCTACCCGCGAAGCCGGCGTTGACATACGAACCGGCACGCAGGTGTGCGGGTT
CGAGATGTCGACCGACCAACAGAAGGTTACCGCCGCTCTGCGAGGACGGCACAAGGCTGCCAGCGGATCTGGTAATCGC
CGGGATTGGCCTGATACCAAAGTTCGCGAGTTGGCCAGTGGCCGGCCTGCAGGTTGATAACGGCATCGTGATCAACGAACA
CATGCAGACCTCTGATCCCTTGATCATGGCCGTCGGCGACTGTGCCGATTTACAGTCAGCTCTATGACCGCTGGGTGCGTA
TCGAATCGGTGCCAATGCCTTGGAGCAGGCACGAAAGATCGCCGCCATCCTCTGTGGCAAGGTGCCACGCGATGAGGCGG
CGCCCTGGTTCTGGTCCGATCAGTATGAGATCGGATTGAAGATGGTTCGGACTGTCCGAAGGGTACGACCGGATCATTGTCC
GCGGCTCTTTGGCGCAACCCGACTTCAGCGTTTTCTACCTGCAGGGAGACCGGGTATTGGCGGTCGATACAGTGAACCGTCC
AGTGGAGTTCAACCGTCAAACAATAATCACGGATCGTTTCCCGGTTGAACCAAACCTACTCGGTGACGAAAGCGTGCCG
TTAAAGGAAATCATCGCCGCCGCAAAGCTGAACTGAGTAGTGCCACCACCACCACCACCActaa

MNANDNVVIVGTGLAGVEVAFGLRASGWEGNIRLVGDATVIPHLLPLSKAYLAGKATAESLYLRTPDAYAAQNIQLLGGTQVTA
INRDRQQVILSDGRALDYDRLVLATGGRPRPLPVASGAVGKANNFRYLRTLEDAECIRRLIADNRLVIGGGYIGLEVAATAIKAN
MHVTLTDAARVLERVTAPPVSIFYEHLHREAGVDIRTGTQVCGFEMSTDQQKVTAVLCEGTRLPADLVIAGIGLIPNCELASAA
GLQVDNGIVINEHMQTS DPLIMAVGDCARFHSQLYDRWVRIESVPNALEQARKIAAILCGKVPRDEAAPWFWSQYEIGLKMV
GLSEGYDRIIVRGS LAQPDFS VFY LQGDRVLAVDTVNRPV EFNQSKQIITDRLPVEPNLLGDES VPLKEIIAAKAELSS AHHHHHH

The EcALDH gene, derived from *Escherichia coli* K-12, has been codon-optimized for *E. coli* expression. The gene sequence contains a 6×His tag, and the start and stop codons are indicated by lowercase letters and underscores.

atgAATTTTCATCATCTGGCTTACTGGCAGGATAAAGCGTTAAGTCTCGCCATTGAAAACCGCTTATTTATTAACGGTGAATAT
ACTGCTGCGGCGGAAAATGAAACCTTTGAAACCGTTGATCCGGTCACCCAGGCACCGCTGGCGAAAATTGCCGCGGCAAG
AGCGTCGATATCGACCGTGCATGAGCGCAGCACGCGGCGTATTTGAACGCGGCGACTGGTCACTCTCTTCTCCGGCTAAAC
GTAAAGCGGTACTGAATAAACTCGCCGATTTAATGGAAGCCACGCCGAAGAGCTGGCACTGCTGAAAACCTCTGACACCG
GCAAACCGATTCTGTCACAGTCTGCGTGATGATATTCGCGGCGGCGCGGCCATTGCTGGTACGCCGAAGCGATCGACA
AAGTGATGGCGAAGTGGCGACCACAGTAGCCATGAGCTGGCGATGATCGTGCCTGAACCGTGGCGTGATTGCCGCCA
TCGTGCCGTGGAACCTCCCGCTGTTGCTGACTTCTGAAAACCTCGGCCCGGCGCTGGCGGCGGGAACAGCGTGATTCTAA
AACCGTCTGAAAAATCACCGCTCAGTGCATTCTGCTCGCGGGGCTGGCGAAAAGAAGCAGGCTTGCCGGATGGTGTGTTGA
ACGTGGTGACGGGTTTTGGTTCATGAAGCCGGGCGAGGCGCTGTCGCGTCATAACGATATCGACGCCATTGCCTTTACCGGTT
AACCCGTACCGGGAACAGCTGCTGAAAGATGCGGGGCGACAGCAACATGAAACGCGTCTGGCTGGAAGCGGGCGGCAAAA
GCGCCAACATCGTTTTGCTGACTGCCCGATTTGCAACAGGCGCAAGCGCCACCGCAGCAGGCATTTCTACAACAGGG
ACAGGTGTGCATCGCCGGAACGCGCCTGTTGCTGGAAGAGAGCATCGCCGATGAATTCTTAGCCCTGTTAAAACAGCAGGC
GCAAAACTGGCAGCCGGGCCATCCACTTGATCCCGCAACCACCATGGGCACCTTAATCGACTGCGCCCACGCCACTCGGTC
CATAGCTTTATTCGGGAAGGCGAAAAGCAAAGGGCAACTGTTGTTGGATGGCCGTAACGCCGGGCTGGCTGCCGCCATCGGC
CCGACCATCTTTGTGGATGTGGACCCGAATGCGTCTTAAGTCGCGAAGAGATTTTCGGTCCGGTGTGGTGGTACGCGTT
TCACATCAGAAGAACAGGCGCTACAGCTTGCCAACGACAGCCAGTACGGCCTTGGCGGCGCGGTATGGACGCGCGACCTCT
CCC GCGCGCACCCGATGAGCCGACGCTGAAAGCCGTTCCGTCTTCGTCAATAACTACAACGACGGCGATATGACCGTGCC
GTTTGGCGGCTATAAGCAGAGCGGCAACGGTTCGCGACAAATCCCTGCATGCCCTTGAAAAATTCCTGAACTGAAAACCATC
TGGATAAGCCTGGAGGCCACCACCACCACCACCActaa

MNFHHLAYWQDKALSLAIENRLFINGEYTA AENETFETVDPVTQAPLAKIARGKSV DIDRAMSAARGVFERGDWSLSSPAKRKA
VLNKLADLMEAHAEELALLELDTGKPIRHS LRDDIPGAARAIRWYAE AIDKVYGEVATTSHELAMIVREPVGVIAAIVPWNFPLLL
TCWKLGPALAAGNSVILKPSEKSPLSAIRLAGLAKEAGLPDGV LNVVTGFGHEAGQALSRHNDIDAI AFTGSTRTGKQLLDAGDS
NMKRVWLEAGGKSANIVFADCPDLQQAASATAAGIFYNQGVCIAGTR LLLLEESIADEF LALLKQQAQNWQPGHPLDPATTMG
TLIDCAHADSVHSFIREGESKGQLLLDGRNAGLAAAIGPTIFVDVDPNASLSREEIFGPVLV VTRFTSEEQALQLANDS QYGLGAAV
WTRDLSRAHRMSRRLKAGSVFVNNYNDGDMTPFGGYKQSGNGRDKSLH ALEKFTELKTIWISLEAHHHHHH

The CYP153A_{Maq} gene, derived from *Marinobacter aquaeole*, has been codon-optimized for expression in *E. coli*.

The gene sequence contains a 6×His tag, and the start and stop codons are indicated by lowercase letters and underscores.

atgCCA ACTCTACCCAGGACATTTGATGACATCCAGAGCCGCTTGATTAACGCAACCAGCCGTGTGGTCCGATGCAGCGCCA
AATCAAGGGTTGAAGTCTTGATGAGCGCGAAGCGCAAAACCTTTGGTCCGCGCCGTCCGATGCCGGAGTTCGTGGAGAC
GCCGATCCCGGATGTGAATACCTTAGCGCTGGAGGATATTGATGTGTCTAACCCGTTCTGTATCGCCAGGGCCAATGGCGT
GCGTACTTCAAACGCTTGAGAGACGAAGCACCGGTTCACTATCAGAAAACTCTCCGTTTGGTCCGTTTTGGTCCGTTACGCG
TTTCGAGGACATCCTGTTCTGTCGATAAGAGCCATGATTTGTTTTAGGTTGACCCGCTGAGG
GTCTTTCCCTGGAAATGTTTATCGCCATGGATCCACCGAAGCACGACGTTCAACGTAGCAGCGTCCAGGGTGTGGTGGCGCC
AAAGAACCTGAAGGAGATGGAAGGTCTAATCCGTTCCCGGACCGGCGACGTCCTGGACAGCTTACCGACTGATAAACCGTT
TAACTGGGTTCCGGCTGTGTCAAAGAAGTACGCGGCCGTATGCTGGCGACCCTGCTGGATTTCCGTACGAAGAGCGTAC
AAATTAGTAGAATGGTCGGATCGCATGGCAGGCGCAGCGAGCGGACTGGTGGTGGTTCGCGGACGAAAACGCCATGTT
TGACGACGCGCGGATATGGCGCGTAGCTTCAGCCGTCTGTGGCGTGACAAAGAGGCACGTCGTGCTGCGGGTGAAGAAC
CGGGTTTTGACCTGATCAGCCTGCTGCAGAGCAACAAAGAAACCAAGGACCTGATAAATCGGCCTATGGAATTCATCGGCAA
CCTGACCTTGCTGATCGTTGGTGGCAATGATACCACCCGTA ACTCTATGTCCGGTGGTCTGGTGGCCATGAATGAATCCCGC
GTGAATTCGAAAACTCAAGGCTAAGCCAGAGCTCATCCCGAATATGGTTAGCGAAATTATCCGTTGGCAGACCCCGCTGGC
GTACATGAGACGTATTGCCAAACAAGATGTGGAGCTGGGCGGACAAACCATCAAAAAAGGCGACCGCGTGGTGTATGTGGT
ATGCTAGCGGTAACCGCGATGAGCGCAAGTTCGACAATCCGGACCAGTTTATTATCGATCGTAAGGACGCTCGTAACCACAT
GTCGTTCCGGTACGGTGTGCATCGTTGCATGGGCAACCCGCTTGCTGAGCTGCAACTCCGTATTCTGTGGGAGGAGATCTTG
AAGCGCTTTGATAATATTGAAGTTGTTGAGGAGCCGGAGCGCGTCCAGTCGAACTTTGTTCTGGCTACAGCCGTCTGATGG
TTAAGTTGACGCCGAATCCCTCGAGCACCACCACCACCACCActg

MPTLPRTFDDIQSRLINATSRVPMQRQIQGLKFLMSAKRKTGPRRPMPEFVETPIPDVNTLALEDIDVSNPFLYRQQQWRAYF
KRLRDEAPVHYQKNSPFGPFWSVTRFEDILFVDKSHDLFSAEPRILGDPPEGLSLEMFIAMDPPKHDVQRSSVQGVVAPKNLKEM
EGLIRSRTGDVLDLPTDKPFNWVPAVSKELTGRMLATLLDFPYEERHKLVEWSDRMAGAASATGGEFADENAMFDDAADMAR
SFSRLWRDKEARRAAGEEPGFDLISLLQSNKETKDILNRPMEFIGNLTLIVGGNDTTRNSMSGGLVAMNEFPREFEKLKAKPELIP
NMVSEIIRWQTPLAYMRRIAKQDVELGGQTIKKGDRVVMWYASGNRDERKFDNPDQFIIDRKDARNHMSFGYGVHRCMGNRL
AELQLRILWEEILKRFDNIEVVEEPERVQSNFVRGYSRLMVKLTTPNSLEHHHHHH

The Pdx gene, derived from *Pseudomonas putida*, has been codon-optimized for expression in *E. coli*. The gene sequence contains a 6×His tag, and the start and stop codons are indicated by lowercase letters and underscores.

atgAGTAAAGTAGTCTATGTTTCACACGATGGTACTCGTCGCGAGCTGGACGTAGCCGATGGCGTGAGCCTGATGCAAGCGG
CGGTCTCCAACGGCATCTACGACATCGTGGGTGACTGTGGTGGTTCTGCGAGCTGCGCTACGTGCCACGTGTATGTTAACGA
GGCGTTCACCGATAAAGTCCGGCAGCTAATGAGCGCGAGATCGGCATGCTGGAATGCGTCACCGCAGAACTTAAGCCGAA
CAGCCGTCTGTGTGCCAGATTATTATGACCCCGAATTGGACGGCATTGTTGTTGATGTGCCAGATCGTCAGTGGCTCGAG
CACCACCACCACCACtga

MSKVYVSHDGRRELDVADGVSLMQAAVSNGIYDIVGDCGGSASCATCHVYVNEAFTDKVPAANEREIGMLECVTAELKPNRS
LCCQIIMTPELDGIVVDVPDRQWLEHHHHHH

The AcCO₆ gene, derived from *Arthrobacter cholorphenolicus*, has been codon-optimized for the *E. coli* expression system. The gene sequence contains a 9×His tag, and the start and stop codons are indicated by lowercase letters and underscores.

atgGGCAGCAGCCATCATCATCATCATCATCACAGCAGCGGCCTGGTGCCGCGCGGCAGCCATATTGATAACATTGA
AAACCTGAGCGATCGCGGCTTTGATTATGTGGTGATTGGCGGCGCAGCGGGGCGGGCGGTGGCGGCGCCTGAGCG
AAGATCCGGATGTGAGCGTGGCGCTGGTGAAGCGGGCCCGATGATCGCAACATCCGGAAATTCTGCAGCTGGATCGCT
GGATGAACTGCTGGAAAGCGGCTATGATTGGGATTATCCGATTGAACCGCAGGAAAACGGCAACAGCTTTATGCGCCATG
CGCGCGGAAAGTATGGGCGGCTGCAGCAGCCATAACGCGTGCAATTGCGTTTTGGGCGCCGCGAAGATCTGGATGAA
TGGGAAAGCAAATATGGCGGACCGGCTGGAACGCGGCGAACGCGTGCCGCTGTATAAACGCCTGGAAACCAACCAGGA
TGCGGGCCCGGATGCGCCGCATCATGGCGATAGCGGCCCGGTGCATCTGATGAACGTGCCGCCGGCGGATCCGAGCGGCG
TGGCGCTGCTGGATGCGTGCAAGAAGCGGGCATTCCGCGCGCGCTTTAACCCGGCACCACCGTGGTGAACGGCGCG
AACTTTTTTCAGATTAACCGCGCGGCGATGGCACCCGAGCAGCAGCAGCGTGAGCTATATTCATCCGATTATTGAACGCG
ATAACTTTACCTGCTGACCGGCTGCGCGCGGCCAGCTGGTGTGGATGCGGATAAACGCTGCACCGGCGTGGAAGTGG
TGGGCGGCGCGCGGCCACCCATCGCTGACCGCGGCCATGAAGTATTCTGAGCACCGGCGCGATTGATAGCCCGA
AACTGCTGATGCTGAGCGCATTGGCCCGGCGAACATCTGGCGCAGCATGGCATTGAAGTCTGGTGGATAGCCCGGGC
GTGGGCGAAAACCTGCAGGATCATCCGGAAGGCGTGGTGCAGTTGAAGCGAAACAGCCGATGGTGCAGACCAGCACCCA
GTGGTGGGAAATTGGCATTTTTACCCGACCGAAGATGGCCTGGATCGCCCGGATCTGATGATGCATTATGGCAGCACCCCG
CGGATCGCAACACCCTGCGCCATGGCTATCCGACCACCGAAAACGGCTTTAGCCTGACCCCGAACGTGACCCATGCGCGCA
GCCGCGGACCGTGCCTGCGCAGCCGCGATTTTCGCGATAAACCGATGGTGGATCCGCGCTATTTTACCGATCCGGAAG
GCCATGATGCGCGTATGGTGGCGGGCATTGCGAAAGCGCGGAAATTGCGGCGCAGCCGGCGATGAGCGCGTGGACC
GGCCGGAACCTGAGCCCGGCGTGGGCGCGCAGACCGATGAAGAAGTGCAGGATTATATTCGAAAACCCATAACACCGTG
TATCATCCGGTGGCACCGTGCATGGGCGCGGATGATGATGGCATGAGCCCGCTGGATGCGCGCCTGCGCGTGAAGG
CGTGACCGGCTGCGCGTGGCGGATGCGAGCGTATGCCGGAACATGTGACCGTGAACCCGAACATTACCGTATGATGAT
TGGCGAACGCTGCGCGGATCTGATTAAGCGGATTATGCGGGCGCGGATGCGCTGGAAGAAAAGAACTGACCACCAGCT
TTGCGtaa

MGSSHHHHHHHHSSGLVPRGSHIDNIENLSDRGFDYVVIGGGSAGAAVAARLSEDPDVSVALVEAGPDDRNIPILQLDRWM
ELLESGYDWDYPIEPQENGSFMRHARAKVMGGCSSHNACIAFWAPREDLEWESKYGATGWNAANAWPLYKRLETNQDAG
PDAPHHGDSGPVHLMNVPPADPSGVALLDACEEAGIPRARFNTGTTVVNGANFFQINRRGDGTRSSSSVSIHPIIERDNFTLLTG

LRARQLVFDADKRCTGVEVGGARGRTHRLTARHEVILSTGAIDSPKLLMLSGIGPAEHLAQHGIEVLVDSPGVGENLQDHPEGV
VQFEAKQPMVQTSTQWWEIGIFPTEDGLDRPDLMMHYGSTPRDRNTRLRHGYPTTENGFSLTPNVTHARSRGTVRLRSRDFRD
KPMVDPRYFTDPEGHDMRVMVAGIRKAREIAAQPAMSAWTGRELSPGVGAQTDEELQDYIRKTHNTVYHPVGTVRMGADDD
GMSPLDARLRVKGVTGLRVADASVMPEHVTV NPNITVMMIGERCADLIKADYAGADALEEKELTTSFA

The CatA gene, derived from *Bacillus subtilis*, has been codon-optimized for the *E. coli* expression system. The gene sequence contains a 9×His tag, and the start and stop codons are indicated by lowercase letters and underscores.

atgAGCAGCAATAAACTGACCACCAGCTGGGGTGCGCCGGTTGGCGATAATCAAATAGCATGACCGCGGTAGCCGTGGC
CCGACCCTGATTACAGACGTGCACCTGCTGGAAAAGCTGGCGCACTTCAACCGTGAGCGTGTCCGGAACGTGTTGTTTCATG
CGAAGGGTGCGGGTGCGCACGGCTATTTGAGGTGACCAACGATGTTACCAAGTACACCAAAGCGGCGTTTCTGAGCGAAG
TGGGCAAGCGTACCCCGCTGTTTCATCCGTTTTAGCACCGTTGCGGGTGAGCTGGGTAGCGCGGACACCGTGCCTGATCCGC
GTGGCTTCGCGGTTAAGTTTTATACCGAGGAAGGCAACTACGACATCGTGGTAACAACACCCCGTTTTCTTTATCCGTGAC
GCGATTAAATTCGGGATTTTATTCACACCCAGAAGCGTGACCCGAAAACCCACCTGAAGAACCCGACCGCGGTGTGGGATT
TTTGAGCCTGAGCCCGGAGAGCCTGCACCAAGTTACCATCCTGATGAGCGACCGTGGTATTCCGGCGACCTGCGTCACAT
GCACGGCTTCGGTAGCCACACCTTAAGTGGACCAACCGGAGCCGGAAGGCGTGTGGATCAAATATCACTTCAAGACCGA
ACAGGGTGTGAAGAACCTGGATGTTAACACCGCGGCGAAAATTGCGGGCGAGAACCCGGACTACCACACCGAGGACCTGTT
CAACGCGATCGAGAACGGTGACTATCCGGCGTGGAACTGTACGTGAGATTATGCCGCTGGAGGATGCGAACACCTATCG
TTTCGACCCGTTTGATGTGACCAAGGTTTGGAGCCAAAAGACTACCCGCTGATCGAAGTGGGCCGTATGGTTCTGGATCGT
AACCCGAAAACCTATTTGCGGAAAGTGAACAAGCGACCTTTAGCCCGGGCACCTGGTGCCGGGTATTGACGTTAGCCCG
GATAAGATGCTGCAGGGCCGCTGTTTCGCGTATCACGACGCGCACCGTTACCGTGTGGGTGCGAACCACCAAGCGCTGCCG
ATCAACCGTGCAGGTAACAAAGTTAACAACCTACCAGCGTGATGGTCAAATGCGTTTTGACGATAACGGTGCCGGTAGCGTG
TACTATGAACCGAACAGCTTTGGCGGTCCGAAGGAGAGCCCGAAGACAAACAGGCGGCGTATCCGGTGAAGGCATTGC
GGATAGCGTTAGCTACGACCACTATGATCACTACACCCAGGCGGGTGACCTGTACCGTCTGATGAGCGAGGATGAACGTAC
CCGTCTGGTGGAAAACATCGTTAACGCGATGAAACCGGTTGAGAAAGAGGAGATCAAACCTGCGTCAAATGAACACTTCTA
CAAAGCGGACCCGGAATACGGTAAACGTGTTGCGGAAGGTCTGGGCCTGCCGATTAAGAAGGACAGCCTCGAGCACACC
ACCACCACCta

MSSNKLTSWGAPVGDNQNSMTAGSRGPTLIQDVHLEKLAHFNRRVPERVVHAKGAGAHGYFEVNDVTKYKAFLSEVG
KRTPLFIRFSTVAGELGSADTVRDPGRFAVKFYTEEGNYDIVGNNTPVFFIRDAIKFPDFIHTQKRDPKTHLKNPTAVWDFWLSPE
SLHQVTILMSDRGIPATLRHMHGFGSHTFKWTNAEPEGVWIKYHFKTEQGVKNLDVNTAAKIAGENPDYHTEDLFNAIENGDP
AWKLYVQIMPLEDANTYRFPDFVTKVWSQKDYPLIEVGRMVLDNRPENYFAEVEQATFSPGTLVPGIDVSPDKMLQGRFAYH
DAHRYRVGANHQALPINRARNKVNYYQRDGMRFDDNGGGSVYYEPNSFGGPKESPEDKQAAYPVQGIADSVSYDHYDHYT
QAGDLYRLMSEDERTRLVENIVNAMKPVKEEIKLRQIEHFYKADPEYGKRVAE GLGLPIKDSLEHHHHHH

References

- 1 Y.-F. Tsai, W.-I. Luo, J.-L. Chang, C.-W. Chang, H.-C. Chuang, R. Ramu, G.-T. Wei, J.-M. Zen and S. S. F. Yu, *Sci. Rep.*, 2017, **7**, 8369.
- 2 Y. M. van Nuland, F. A. de Vogel, E. L. Scott, G. Eggink and R. A. Weusthuis, *Metab. Eng.*, 2017, **44**, 134–142.
- 3 S. Honda Malca, D. Scheps, L. Kühnel, E. Venegas-Venegas, A. Seifert, B. M. Nestl and B. Hauer, *Chem. Commun.*, 2012, **48**, 5115–5117.
- 4 E. Kühnel, D. D. P. Laffan, G. C. Lloyd-Jones, T. Martínez del Campo, I. R. Shepperson and J. L. Slaughter, *Angew. Chem. Int. Ed.*, 2007, **46**, 7075–7078.
- 5 *Eur Pat.*, 2407444A2, 2012.
- 6 N. N. Pham, C.-W. Chang, Y.-H. Chang, Y. Tu, J.-Y. Chou, H.-Y. Wang and Y.-C. Hu, *Metab. Eng.*, 2023, **77**, 76–88.
- 7 S. Lim, H.-w. Yoo, S. Sarak, B.-g. Kim and H. Yun, *J. Ind. Eng. Chem.*, 2021, **98**, 358–365.
- 8 W. Cao, B. Liu, J. Luo, J. Yin and Y. Wan, *Bioresour. Technol.*, 2017, **243**, 179–187.