

Table S1. List of Oligonucleotides used in this study

Oligonucleotides	Sequence 5'→3'
<i>ald_{BS}_RBS_fw</i>	CCGGAATTCGAAAGGAGGCCCTTCAGATGATCATAGGGGTTCTAA
<i>ald_{BS}_rv</i>	CCGGGAATTCCTAAGCACCCGCCACAGATG
<i>ilvE_{Ec}_RBS_fw</i>	CCGGCCGGCCGGAATTC AAGGAGATATAGATATGACCACGAAGAAAGCTGA
<i>ilvE_{Ec}_rv</i>	CCGGCCGGCCGGCCGAATTCCTATTGATTAACCTTGATCTA
<i>ilvE_{Sm}_RBS_fw</i>	CCCCCGCCGGCGAATTC AAGGAGATATAGATATGACAGTAGATTTAGATTG
<i>ilvE_{Sm}_rv</i>	CCGGCCGAATTCCTAGTCATCAACTTTATATA
<i>ta_{Cv}_fw</i>	TATATGAATTCATGCAGAAACAGCGTACC
<i>ta_{Cv}_rv</i>	TATAGTCGACTTAGGCCAGACCACGTG
<i>fdh_RBS_fw</i>	CCGGGAGCTCAAGGAGATATAGATATGAAAATCGTTCTCGTTTT
<i>fdh_rv</i>	CCGGTCTAGATTATGCGACCTTTTTGTCAT
<i>gdh_RBS_fw</i>	CCGGGAGCTCAAGGAGATATAGATATGTATAAAGATCTGGAAGG
<i>gdh_rv</i>	CCGGTCTAGATTATTAGCCACGACCCGCCT
<i>ptdh_RBS_fw</i>	CCGGGAGCTCAAGGAGATATAGATATGCTGCCGAAACTGGTCAT
<i>ptdh_rv</i>	CCGGTCTAGATTAGTCAGCCGAGGGTTGGCTT
pBAD28_fw	CTGACGCTTTTTATCGCAAC
pBAD28_rv	CAGACCGCTTCTGCGTTCTG
GA_ald_RBS_EcoRI_fw	GCCGGGAATTC AAGGAGATATAGATATGATCATAGGGGTTCTAA
GA_ald_rv	GCCCGAGCTCTTAAGCACCCGCCACAGATG
GA_avtA_RBS_fw	CCGGGAGCTCAAGGAGATATAGATATGACATTCTCCCTTTTGG
GA_avtA_rv	CCGGGGATCCTTAGTGACTTTCAGCCCAGG

GA_kan_EcoRI_fw	ATTCACACAGGAAACAGACCATGGTTGAGCGATTGTGTAGGCTG
GA_kan_rv	TGAATATCCTCCTTAGTTCCTCCGGGGATCCGTCGACCT
GA_trc_fw	GGAATAAGGAGGATATTCAGACATCATAACGGTTCTGGC
GA_trc_rv	TATCTATATCTCCTTGATCCCCGGGTACCGAGCTCGAATT
GA_ald_RBS_fw	GGATCCAAGGAGATATAGAT ATG ATCATAGGGGTTCTCTAA
GA_ald_EcoRI_rv	CCGGGTACCGAGCTCGAATTATGGGAATTAGCCATGGTCCT TA AGCACCCGCCACAG ATGATTC
GA_rocG_RBS_fw	GGATCCAAGGAGATATAGAT ATG AGCGCGAAACAGGTGAG
GA_rocG_EcoRI_rv	CCGGGTACCGAGCTCGAATTATGGGAATTAGCCATGGTCCT TA CACCCAGCCACGAA AAC
HS_araCB_fw	<u>ACTCTCTACTGTTTCTCATACCGTTTTTTTGGATGGAGTGAAACGATG</u> GTGTAGGC TGGAGCTGCTTC
HS_araD_rv	<u>GTTTGATTGGCTGTGGTTTTATACAGTCATTACTGCCGTAATATGCCTTATGGGAAT</u> TAGCCATGGTCC
araC_fw	ATTAGCGGATCCTACCTGAC
polB_rv	GCCTGGTTTCGTTTGATTGG
Kt_rv	GGCTGGGTGTGGCGGACCGC

Enzymatic restriction sites are underlined, homologous sequences of *E. coli* genome are scored, ribosomal binding sites are shown in italics, stop and start codons are highlighted in bold. Abbreviations: RBS: ribosomal binding site; GA: Gibson assembly, HS: homologous sequences

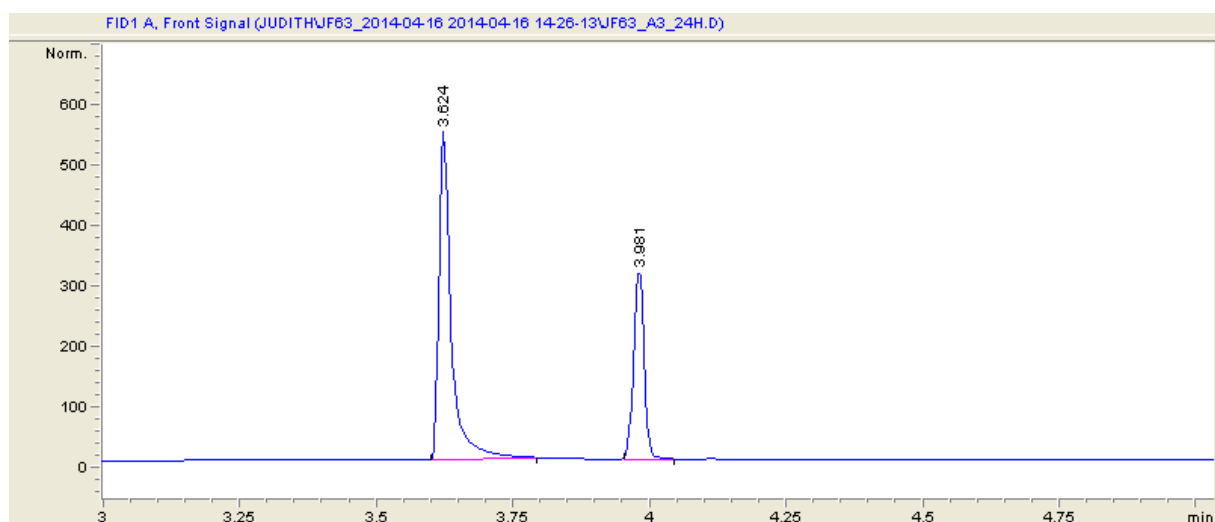


Figure S1. GC-chromatogram for determination of conversion in the reductive amination of 4-phenyl-2-butanone catalyzed by single-cell catalyst 6. The amine product was assigned by comparison of elution orders with commercially available reference material.

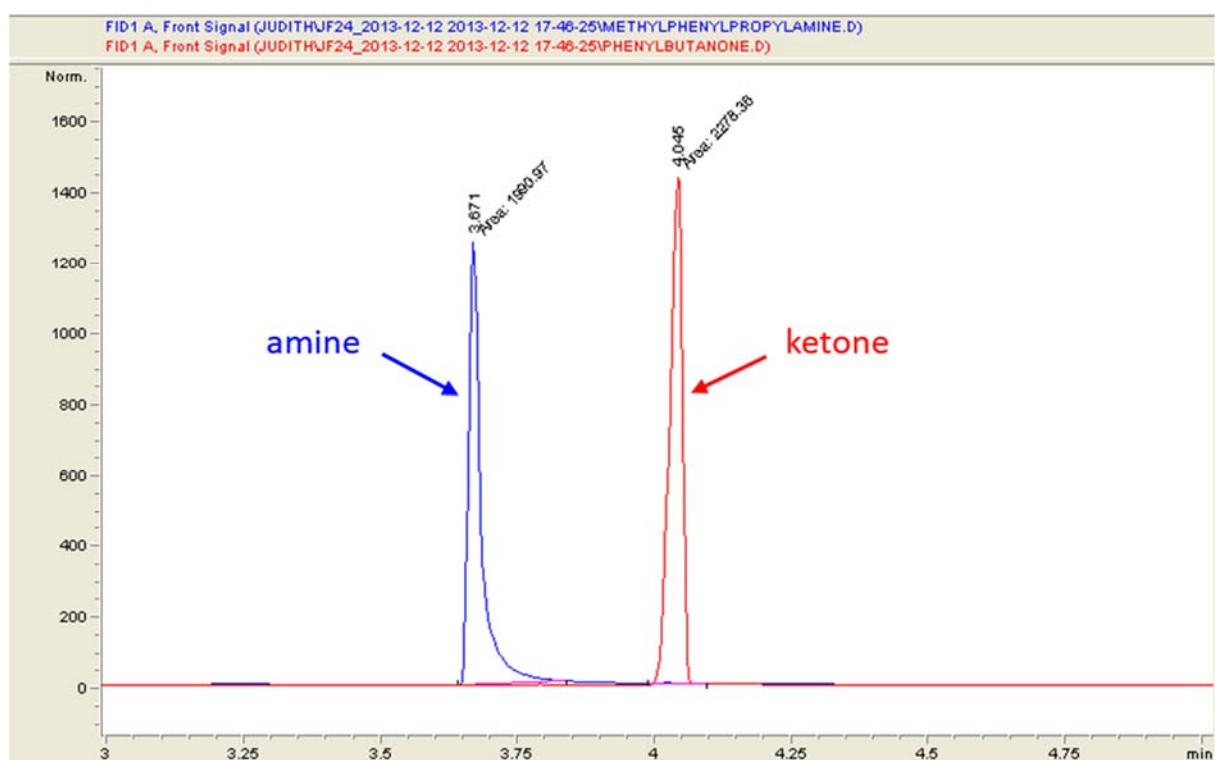


Figure S2. GC-chromatogram of reference compounds 4-phenyl-2-butanone and 1-methyl-3-phenylpropylamine.

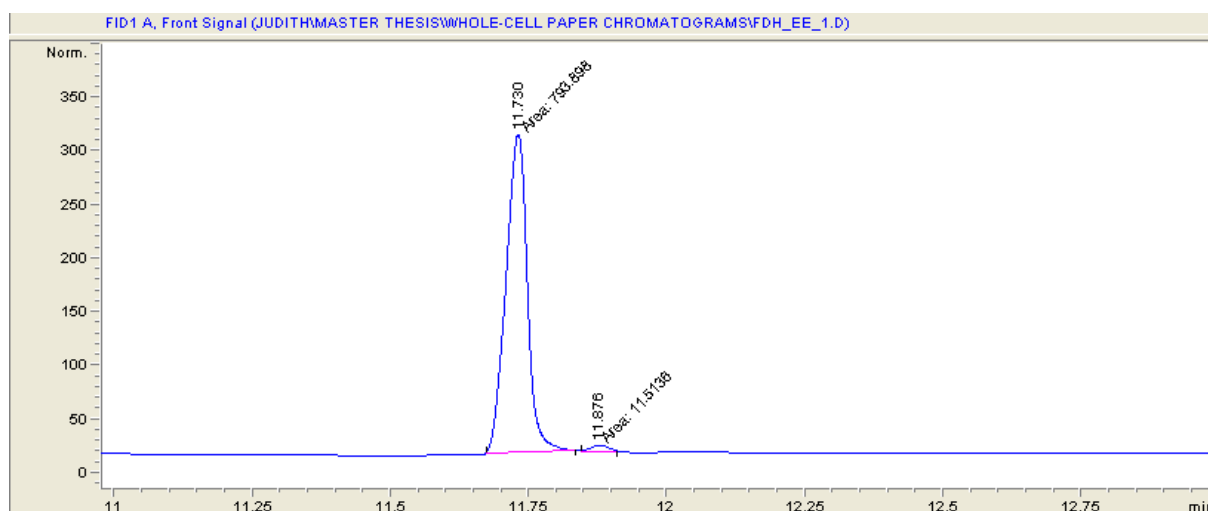


Figure S3. GC-chromatogram for determination of *enantiomeric excess* in the reductive amination of 4-phenyl-2-butanone catalyzed by single-cell catalyst 6. The absolute configuration was assigned by comparison of elution orders with commercially available optically pure amines.

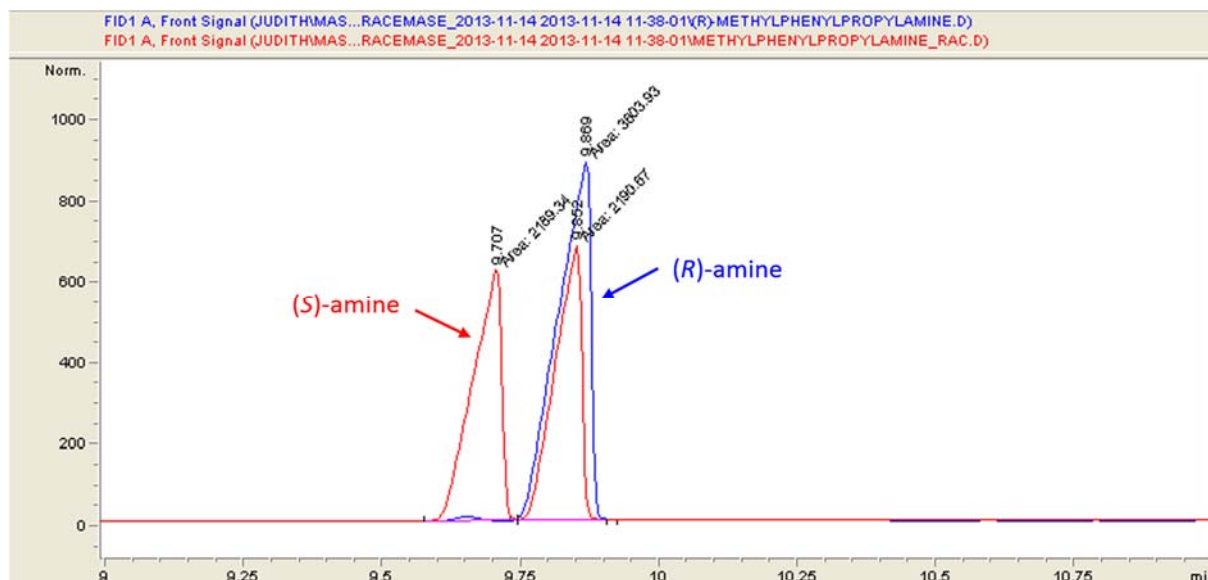


Figure S4. GC-chromatogram of racemic and optically pure reference compound (*R*)-1-methyl-3-phenylpropylamine.