

Is literature data useful for identifying enzyme catalysts for new substrates? -A case study on reduction of 1-aryl-2-alkanoates

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Table of Contents

1. List of enzyme catalysts	2
2. Experimental enantiomeric excess values	4
2.1 <i>para</i> -Substituted derivatives	4
2.2 Compounds 5i-5n	7
2.3 Compounds 1a-4a	9
3. Enantioselectivity: Pearson coefficients and correlation plots.....	12
3.1 <i>para</i> -Substituted derivatives	12
3.2 Compounds 5i-5k	13
3.3 Compounds 5l-n	15
3.4 Compounds 5a-8a	16
4. The use of model compounds to predict ee	19
5. Rates of reduction.....	22
5.1 Compounds 5a-h	22
5.2 Compounds 5i-n	27
5.3 Compounds 5a-8a	34
6. References	37

1. List of enzyme catalysts

Table S1. List of enzymes with references used in reactions with ketones **1a-n** and **6a-8a**.

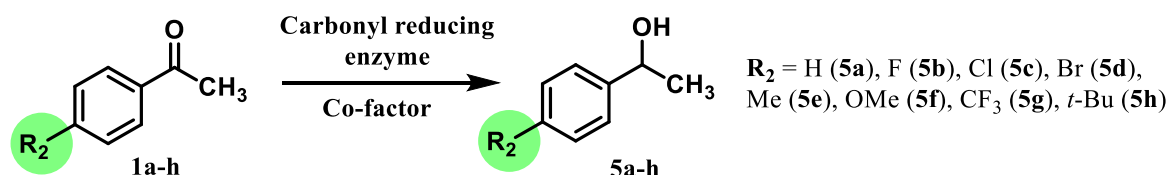
Abbreviation	Full description	Reference
CR <i>C. magnolia</i>	Carbonyl reductase from <i>Candida magnolia</i>	Zhu <i>et al.</i> 2006 [1]
KRED101-KRED128	Carbonyl reductases from Codexis (KRED)	Zhu <i>et al.</i> 2005 [2]; compound 6a : [3]
ADH <i>P. furiosus</i>	Alcohol dehydrogenase from <i>Pyrococcus furiosus</i> (PFADH)	Zhu <i>et al.</i> 2006 [4]
CR <i>S. salmonicolor</i>	Wild type and mutants carbonyl reductases from <i>Sporobolomyces salmonicolor</i>	Zhu <i>et al.</i> 2006 [5]; Zhu <i>et al.</i> 2008 [6]; Li <i>et al.</i> 2010 [7]
CR <i>K. thermotolerans</i>	Carbonyl reductase from <i>Kluyveromyces thermotolerans</i>	Xu <i>et al.</i> 2012 [8]
ADH <i>S. cerevisiae</i> (YMRC226c)	Alcohol dehydrogenase from <i>Saccharomyces cerevisiae</i> (YMRC226c)	Yang <i>et al.</i> 2007 [9]
PAR <i>Corynebacterium</i> strain (ST-10)	Phenylacetaldehyde oxidoreductase from <i>Corynebacterium</i> strain, ST-10	Itoh <i>et al.</i> 1999 [10]
ADH <i>Leifsonia</i> sp.	Alcohol dehydrogenase from <i>Leifsonia</i> sp.	Inoue <i>et al.</i> 2005 [11]
CR <i>S. coelicolor</i>	Carbonyl reductase from <i>Streptomyces coelicolor</i>	Wang <i>et al.</i> 2011 [12]
CR <i>P. guilliermondii</i> NRRL Y-324	Carbonyl reductase from <i>Pichia guilliermondii</i> NRRL Y-324 (PgCR)	Xu <i>et al.</i> 2013 [13]
CR <i>C. glabrata</i> (CgKR1, CgKR2)	Carbonyl reductases from <i>Candida glabrata</i>	Liang <i>et al.</i> 2013 [14]; Compound 8a : Ma <i>et al.</i> 2012 [15]
CR <i>C. parapsilosis</i>	Wild type and mutant carbonyl reductases from <i>Candida parapsilosis</i>	Wang <i>et al.</i> 2014 [16]
CR <i>C. parapsilosis</i> (CPAR1-CPAR8)	Additional carbonyl reductases from <i>Candida parapsilosis</i>	Guo <i>et al.</i> 2014 [17]
ADH <i>A. aromaticum</i>	(S)-1-Phenylethanol dehydrogenase from <i>Aromatoleum aromaticum</i>	Dudzik <i>et al.</i> 2015 [18]
ADH <i>K. capsulate</i>	Medium chain alcohol dehydrogenase from <i>Kuraishia capsulate</i> (CBS1993)	Wu <i>et al.</i> 2016 [19]
CR <i>P. pastoris</i>	Carbonyl reductase from <i>Pichia pastoris</i> , GS115	Li <i>et al.</i> 2013 [20]
ADH <i>B. gladioli</i> (BgADH1; BgADH2; BgADH1:)	Short chain alcohol dehydrogenases from <i>Burholderia gladioli</i>	Chen <i>et al.</i> 2015 [21]
KR <i>S. stipitis</i>	Ketoreductase from <i>Scheffersomyces stipitis</i> CBS 6045	Shang <i>et al.</i> 2017[22]
ADH <i>Chryseobacterium</i> sp CA49	Short chain alcohol dehydrogenases from <i>Chryseobacterium</i> sp CA49 (ChKRED20)	Tang <i>et al.</i> 2014 [23]
ADH <i>L. brevis</i>	Alcohol dehydrogenase from <i>Lactobacillus brevis</i>	Rodriguez <i>et al.</i> 2014 [24] Cacchi <i>et al.</i> 2009 [25]
CR <i>Bacillus</i> sp.	Carbonyl reductase from <i>Bacillus</i> sp ECU0013	Ni <i>et al.</i> 2011 [26]
ADH <i>T. Brockii</i>	Alcohol dehydrogenases from <i>Thermoanaerobacter Brockii</i> (WT and mutants)	Sun <i>et al.</i> 2016 [27]
ADH-R <i>L. kefir</i>	(R)-Specific alcohol dehydrogenase from <i>Lactobacillus kefir</i>	Weckbecher <i>et al.</i> 2006 [28]
ADH <i>Pseudomonas</i> sp ATCC 49794	Alcohol dehydrogenases from ADH <i>Pseudomonas</i> sp.	Bradshaw <i>et al.</i> 1992 [29]
ADH <i>T. thermophilus</i> (ADH1)	Alcohol dehydrogenases from <i>Thermus thermophilus</i> , isolate ADH1	Pennacchio <i>et al.</i> 2008 [30]
ADH <i>C. maris</i>	Alcohol dehydrogenases from <i>Candida maris</i>	Kawano <i>et al.</i> 2011 [31]
CR <i>A. baylyi</i> ATC 3305	Recombinant diketoreductase from <i>Acinetobacter baylyi</i> ATC 3305	Wu <i>et al.</i> 2009 [32]
CR <i>L. brevis</i> (LbCR)	Carbonyl reductase from <i>Lactobacillus brevis</i>	Gong <i>et al.</i> 2017 [33]
ADH evo-1.1.200	Recombinant alcohol dehydrogenase, ADH evo-1.1.200, from evocatol GmbH	Kara <i>et al.</i> 2014 [34]
Reductase <i>Bacillus</i> sp ECU0013 (FabG)	β -Ketoacetyl-APC reductase from <i>Bacillus</i> sp ECU0013 (FabG)	Ni <i>et al.</i> 2011 [35]
CR <i>Y. lipolytica</i> ACA-DC 50109	Carbonyl reductase from <i>Yarrowia lipolytica</i> ACA-DC 50109	Xu <i>et al.</i> 2015 [36]
AKR Ytbe, <i>Bacillus</i> sp. ECU0013	Aldo-keto reductase from <i>Bacillus</i> sp ECU0013 (Protein Ytbe)	Ni <i>et al.</i> 2011 [37]
Reductase <i>C. tenuis</i> (CtXR AKR2B5)	Xylose reductase from <i>Candida tenuis</i> (CtXR AKR2B5)	Vogl <i>et al.</i> 2011. [38]

Abbreviation	Full description	Reference
<i>ADH T. ethanolicus-I86A</i>	Mutant <i>I86A</i> of alcohol dehydrogenase from <i>Thermoanaerobacter ethanolicus</i>	Musa <i>et al.</i> 2009 [39]
<i>(S)</i> -ADH <i>R. erytropolis</i>	<i>(R)</i> -Specific alcohol dehydrogenase from <i>Rhodococcus erytropolis</i>	Hummel <i>et al.</i> 1997 [40] Gröger <i>et al.</i> 2004 [41]

2. Experimental enantiomeric excess values

2.1 *para*-Substituted derivatives

Table S2. Enantiomeric excess after reduction of **1a-h** using different enzymes. Anti-Prelog selectivity is shown as negative values.



Enzyme [Ref]	5a (H)	5b (<i>p</i> -F)	5c (<i>p</i> -Cl)	5d (<i>p</i> -Br)	5e (<i>p</i> -Me)	5f (<i>p</i> -OMe)	5g (<i>p</i> -CF ₃)	5h (<i>p</i> - <i>t</i> -Bu)
CR <i>C. magnolia</i> [1]	-99	-99	-99	-99	-99	-99	-99	-99
KRED101 [2]	-14	-18	-10	-20	-42	-40	14	12
KRED102 [2]	ND-LR ^{a)}	ND-LR ^{a)}	99	99	ND-LR ^{a)}	ND-LR ^{a)}	99	ND-LR ^{a)}
KRED103[2]	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}
KRED104 [2]	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}
KRED105 [2]	99	ND-LR ^{a)}	99	99	ND-LR ^{a)}	ND-LR ^{a)}	99	ND-LR ^{a)}
KRED106 [2]	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}
KRED107 [2]	-99	-99	-99	-99	-99	-99	-99	-99
KRED108 [2]	99	99	99	99	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}
KRED109 [2]	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}
KRED110 [2]	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}
KRED111 [2]	85	90	98	98	99	99	91	99
KRED113 [2]	0	-16	-28	-30	-44	-50	-28	12
KRED114 [2]	90	84	98	98	88	99	91	99
KRED115 [2]	85	82	98	98	84	99	90	99
KRED116 [2]	99	ND-LR ^{a)}	99	99	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}
KRED117 [2]	99	ND-LR ^{a)}	99	99	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}
KRED120 [2]	99	99	99	99	ND-LR ^{a)}	99	99	
KRED121 [2]	99	99	99	99	99	99	90	99
KRED123 [2]	88	95	99	99	77	89	93	99
KRED124 [2]	99	99	99	99	99	99	99	99
KRED125 [2]	99	ND-LR ^{a)}	99	99	99	99	99	99
KRED126 [2]	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	99	ND-LR ^{a)}
KRED127 [2]	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}
KRED128 [2]	60	16	40	56	86	10	99	99
ADH <i>P. furiosus</i> [4]	99	99	99	99	99		99	
CR <i>S. salmonicolor</i> -WT [5]	-42	-46	-14	-42	-59	-57	17	-31
CR <i>S. salmonicolor</i> -M242C [7]	13	54	27	-4	-38	-18	5	96

Enzyme [Ref]	5a (H)	5b (p-F)	5c (p-Cl)	5d (p-Br)	5e (p-Me)	5f (p-OMe)	5g (p-CF ₃)	5h (p-t-Bu)
CR <i>S. salmonicolor</i> -M242D [7]	82	90	77	61	43	39	37	99
CR <i>S. salmonicolor</i> -M242G [7]	54	70	62	52	4	-6	17	90
CR <i>S. salmonicolor</i> -M242Y [7]	12	41	36	22	-21	-7	28	93
CR <i>S. salmonicolor</i> -Q245H [6]	78	92	90	92	95	79	ND ^{b)}	96
CR <i>S. salmonicolor</i> -Q245L [6]	82	93	96	97	95	96	ND ^{b)}	99
CR <i>S. salmonicolor</i> -Q245P [6]	64	90	96	98	96	98	ND ^{b)}	99
CR <i>S. salmonicolor</i> -M242C/Q245L [7]	17	16	50	24	20	36	94	99
CR <i>S. salmonicolor</i> -M242F/ Q245T [7]	42	90	94	89	72	92	98	95
CR <i>S. salmonicolor</i> -M242L/ Q245P [7]	74	92	99	99	99	99	99	99
CR <i>S. salmonicolor</i> -M242L/ Q245T [7]	58	94	98	99	95	97	99	99
CR <i>K.thermotolerans</i> [8]	-99	ND ^{b)}	-99		-99	-99	-99	ND ^{b)}
ADH <i>S. cerevisiae</i> (YMRC226c) [9]	99	ND ^{b)}	99	99	99	99	98	ND ^{b)}
PAR <i>Corynebacterium</i> strain (ST-10) [10]	96	ND ^{b)}	99	99	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
ADH <i>Leifsonia</i> sp. [11]	-99	ND ^{b)}	-99	-99	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
CR <i>S. coelicolor</i> [12]	-96	ND ^{b)}	-99	-99	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
CR <i>P. guilliermondii</i> NRRL Y-324 [13]	-99	ND ^{b)}	-99	-99	-99	ND ^{b)}	ND ^{b)}	ND ^{b)}
CR <i>C. glabrata</i> (CgKR1) [14]	99	99	99	99	99	99	ND ^{b)}	ND ^{b)}
CR <i>C. glabrata</i> (CgKR2) [14]	99	97	99	98	97	99	ND ^{b)}	ND ^{b)}
CR <i>C. parapsilosis</i> -WT [16]	97	ND ^{b)}	ND ^{b)}	99	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
CR <i>C. parapsilosis</i> -F285A [16]	35	ND ^{b)}	ND ^{b)}	72	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
CR <i>C. parapsilosis</i> -W286A [16]	-57	ND ^{b)}	ND ^{b)}	65	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
CR <i>C. parapsilosis</i> -F285A/W286A [16]	-86	ND ^{b)}	ND ^{b)}	-22	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
CR <i>C. parapsilosis</i> (CPAR1) [17]	68	ND ^{b)}	99	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
CR <i>C. parapsilosis</i> (CPAR2) [17]	-62	ND ^{b)}	-83	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
CR <i>C. parapsilosis</i> (CPAR3) [17]	ND-LR ^{a)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
CR <i>C. parapsilosis</i> (CPAR4) [17]	99	ND ^{b)}	99	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
CR <i>C. parapsilosis</i> (CPAR5) [17]	75	ND ^{b)}	59	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
CR <i>C. parapsilosis</i> (CPAR6) [17]	-99	ND ^{b)}	-99	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
CR <i>C. parapsilosis</i> (CPAR7) [17]	ND-LR ^{a)}	ND ^{b)}	40	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
CR <i>C. parapsilosis</i> (CPAR8) [17]	ND-LR ^{a)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
ADH <i>A. aromaticum</i> [18]	99	99	ND ^{b)}	ND ^{b)}	ND ^{b)}	99	ND ^{b)}	ND ^{b)}
ADH <i>K. capsulate</i> [19]	99	99	99	99	99	99	ND ^{b)}	ND ^{b)}
CR <i>P. pastoris</i> [20]	99	ND ^{b)}	99	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
ADH <i>B. gladioli</i> (BgADH1) [21]	-99	-99	ND ^{b)}	ND ^{b)}	-99	-99	-99	ND ^{b)}
ADH <i>B. gladioli</i> (BgADH2) [21]	-99	-99	ND ^{b)}	ND ^{b)}	-99	-99	-99	ND ^{b)}

Enzyme [Ref]	5a (H)	5b (p-F)	5c (p-Cl)	5d (p-Br)	5e (p-Me)	5f (p-OMe)	5g (p-CF ₃)	5h (p-t-Bu)
ADH <i>B. gladioli</i> (BgADH5) [21]	-90	-99	ND ^b	ND ^b	-99	-95	-99	ND ^b
KR <i>S. stipos</i> [22]	71.9	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>Chryseobacterium sp CA49</i> [23]	-99	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	-99	ND ^b
ADH <i>L. brevis</i> [24]	-99	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
CR <i>Bacillus sp.</i> ECU0013 [26]	99	ND ^b	99	99	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -WT [27]	18	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -W110A [27]	91	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -W110M [27]	99	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -W110E [27]	99	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -I86L/L294N [27]	-97	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -A85V/I86N/C295N [27]	-72	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -I86N/L294N/C295V [27]	ND-LR ^a)	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -A85V/I86N/L294V/C295N [27]	-50	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -I86V/L294N [27]	-28	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -I86N/L294V/C295N [27]	-99	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -I86N/C295N [27]	99	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -W110S [27]	92	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -W110L [27]	99	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -I86A [27]	-98	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -I86V/W110L/L294Q [27]	93	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -I86Q [27]	-96	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -I86N [27]	-99	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -A85V/I86Q [27]	-56	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -I86V/W110V [27]	96	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -A85V/I86L/W110Q/L294Q [27]	-5	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -I86V/L294Q [27]	-10	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. Brockii</i> -I86L/W110Q/L294Q [27]	69	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH-R <i>L. kefir</i> (DSM 20587) [28]	-99	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>Pseudomonas sp</i> ATCC 49794 [29]	-99	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>T. thermophilus</i> (ADH1) [30]	99	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
ADH <i>C. maris</i> [31]	-99	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b
CR <i>A. baylyi</i> ATC 3305 [32]	-31	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b	ND ^b

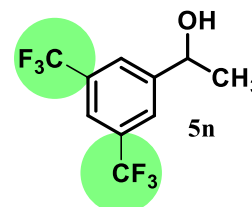
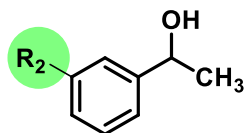
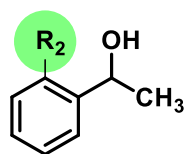
Enzyme [Ref]	5a (H)	5b (p-F)	5c (p-Cl)	5d (p-Br)	5e (p-Me)	5f (p-OMe)	5g (p-CF ₃)	5h (p-t-Bu)
CR <i>L. brevis</i> (LbCR) [33]	99	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
ADH evo-1.1.200 [34]	96.5	ND ^{b)}	98	ND ^{b)}	ND ^{b)}	98	ND ^{b)}	ND ^{b)}
Reductase <i>Bacillus</i> sp ECU0013 (FabG) [35]	65	ND ^{b)}	88	93	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
CR <i>Y. lipolytica</i> ACA-DC 50109 [36]	99	ND ^{b)}			ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
AKR Ytbe, <i>Bacillus</i> sp. ECU0013 [37]	99	ND ^{b)}	99	99	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
Reductase <i>C. tenuis</i> (CtXR AKR2B5) [38]	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
ADH <i>T. ethanolicus</i> -I86A [39]	99	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
(S)-ADH <i>R. erythropolis</i> [40]	99	99	99	99	99	99	ND ^{b)}	ND ^{b)}
(S)-ADH <i>R. erythropolis</i> [40]	ND ^{b)}	ND ^{b)}	99	97		ND ^{b)}	ND ^{b)}	ND ^{b)}
ADH <i>L. brevis</i> [25]	-98	-98	ND ^{b)}	ND ^{b)}	-99	ND ^{b)}	ND ^{b)}	ND ^{b)}

^{a)}ND-LR: not determined due to low reactivity

^{b)}ND: not determined.

2.2 Compounds 5i-5n

Table S3. Enantiomeric excess after reduction of **1a** and **1i-n** using different enzymes. Anti-Prelog selectivity is shown as negative values.



$R_2 =$ H (**5a**), Cl (**5i**), Me (**5j**), MeO (**5k**)

$R_2 =$ H (**5a**), Cl (**5l**), Me (**5m**),

Enzyme [Ref]	5a (H)	5i (o-Cl)	5j (o-Me)	5k (o-OMe)	5l (m-Cl)	5m (m-Me)	5n (3,5-di-CF ₃)
KRED101 [2]	-14	-18	-69	-99	-65	-88	99
KRED102 [2]	ND-LR ^{a)}	99	ND-LR ^{a)}	99	99	99	ND-LR ^{a)}
KRED103 [2]	ND-LR ^{a)}	99	99	99	99	99	ND-LR ^{a)}
KRED104 [2]	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	ND-LR ^{a)}	99	99	ND-LR ^{a)}
KRED105 [2]	99	99	99	99	99	99	ND-LR ^{a)}
KRED106 [2]	ND-LR ^{a)}	99	ND-LR ^{a)}	ND-LR ^{a)}	99	99	ND-LR ^{a)}
KRED107 [2]	-99	0	ND-LR ^{a)}	ND-LR ^{a)}	-86	-78	ND-LR ^{a)}
KRED108 [2]	99	99	ND-LR ^{a)}	99	99	99	ND-LR ^{a)}
KRED109 [2]	ND-LR ^{a)}	99	ND-LR ^{a)}	ND-LR ^{a)}	99	99	ND-LR ^{a)}
KRED110 [2]	ND-LR ^{a)}	99	ND-LR ^{a)}	99	99	99	99
KRED111 [2]	85	90	98	-48	40	-30	99
KRED113 [2]	0	32	-50	-99	-64	-84	99

Enzyme [Ref]	5a (H)	5i (o-Cl)	5j (o-Me)	5k (o- OMe)	5l (m-Cl)	5m (m-Me)	5n (3,5-di-CF ₃)
KRED114 [2]	90	83	77	-50	84	34	99
KRED115 [2]	85	89	75	-50	45	-23	99
KRED116 [2]	99	99	ND-LR ^{a)}	99	99	99	ND-LR ^{a)}
KRED117 [2]	99	99	ND-LR ^{a)}	99	99	99	ND-LR ^{a)}
KRED120 [2]	99	99	ND-LR ^{a)}	99	99	99	0
KRED121 [2]	99	76	ND-LR ^{a)}	-42	94	72	99
KRED123 [2]	88	82	ND-LR ^{a)}	-34	58	-26	99
KRED124 [2]	99	99	ND-LR ^{a)}	ND-LR ^{a)}	99	99	ND-LR ^{a)}
KRED125 [2]	99	99	ND-LR ^{a)}	ND-LR ^{a)}	98	99	ND-LR ^{a)}
KRED126 [2]	ND- LR ^{a)}	99	ND-LR ^{a)}	ND-LR ^{a)}	99	99	-92
KRED127 [2]	ND- LR ^{a)}	99	ND-LR ^{a)}	ND-LR ^{a)}	99	99	ND-LR ^{a)}
KRED128 [2]	60	84	ND-LR ^{a)}	ND-LR ^{a)}	82	78	90
ADH <i>P. furiosus</i> [4]	99	99	ND-LR ^{a)}	99	99	99	99
CR <i>S. salmonicolor</i> -WT [5]	-42	-15	-70	-99	-66	-92	-99
CR <i>K. thermotolerans</i> [8]	-99	-99	-99	-99	-99	-99	-99
ADH <i>S. cerevisiae</i> (YMRC226c) [9]	99	99	ND ^{b)}	ND ^{b)}	99	ND ^{b)}	ND ^{b)}
PAR <i>Corynebacterium</i> strain (ST-10) [10]	96	99	ND ^{b)}	ND ^{b)}	99	ND ^{b)}	ND ^{b)}
ADH <i>Leifsonia</i> sp. [11]	-99	ND ^{b)}	ND ^{b)}	ND ^{b)}	-99	ND ^{b)}	ND ^{b)}
CR <i>C. glabrata</i> (CgKR1) [14]	99	-96	99	99	99	96	ND ^{b)}
CR <i>C. glabrata</i> (CgKR2) [14]	99	-98	99	99	94	91	ND ^{b)}
CR <i>C. parapsilosis</i> -WT [16]	97	81	ND ^{b)}	ND ^{b)}	99	74	ND ^{b)}
CR <i>C. parapsilosis</i> -F285A [16]	35	49	ND ^{b)}	ND ^{b)}	72	24	ND ^{b)}
CR <i>C. parapsilosis</i> - W286A [16]	-57	-8	ND ^{b)}	ND ^{b)}	-52	23	ND ^{b)}
CR <i>C. parapsilosis</i> - F285A/W286A [16]	-86	-64	ND ^{b)}	ND ^{b)}	-76	-15	ND ^{b)}
CR <i>C. parapsilosis</i> (CPAR1) [17]	68	78	ND ^{b)}	ND ^{b)}	99	ND ^{b)}	ND ^{b)}
CR <i>C. parapsilosis</i> (CPAR2) [17]	-62	-68	ND ^{b)}	ND ^{b)}	-56	ND ^{b)}	ND ^{b)}
CR <i>C. parapsilosis</i> (CPAR3) [17]	ND- LR ^{a)}	40	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
CR <i>C. parapsilosis</i> (CPAR4) [17]	99	99	ND ^{b)}	ND ^{b)}	99	ND ^{b)}	ND ^{b)}
CR <i>C. parapsilosis</i> (CPAR5) [17]	75	69	ND ^{b)}	ND ^{b)}	63	ND ^{b)}	ND ^{b)}
CR <i>C. parapsilosis</i> (CPAR6) [17]	-99	-99	ND ^{b)}	ND ^{b)}	-99	ND ^{b)}	ND ^{b)}
CR <i>C. parapsilosis</i> (CPAR7) [17]	ND- LR ^{a)}	31	ND ^{b)}	ND ^{b)}	56	ND ^{b)}	ND ^{b)}
CR <i>C. parapsilosis</i> (CPAR8) [17]	ND- LR ^{a)}	ND-LR ^{a)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
ADH <i>A. aromaticum</i> [18]	99	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	99	ND ^{b)}
ADH <i>K. capsulate</i> [19]	99	99	99	ND ^{b)}	99	99	ND ^{b)}
CR <i>P. pastoris</i> [20]	99	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
ADH <i>B. gladioli</i> (BgADH1) [21]	-99	ND ^{b)}	ND ^{b)}	-93	ND ^{b)}	ND ^{b)}	-98
ADH <i>B. gladioli</i> (BgADH2) [21]	-99	ND ^{b)}	ND ^{b)}	-95	ND ^{b)}	ND ^{b)}	-99
ADH <i>B. gladioli</i> (BgADH5) [21]	-90	ND ^{b)}	ND ^{b)}	-90	ND ^{b)}	ND ^{b)}	-99
KR <i>S. stipos</i> [22]	71.9	90	73	ND ^{b)}	80	87	ND ^{b)}

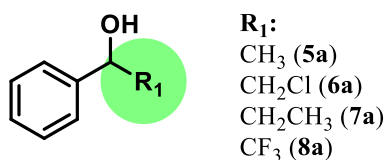
Enzyme [Ref]	5a (H)	5i (o-Cl)	5j (o-Me)	5k (o- OMe)	5l (m-Cl)	5m (m-Me)	5n (3,5-di-CF ₃)
ADH <i>Chryseobacterium</i> sp CA49 [23]	-99	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	-99
CR Y. <i>lipolytica</i> ACA-DC 50109 [36]	ND ^{b)}	99	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
Reductase <i>C. tenuis</i> (CtXR AKR2B5) [38]	ND ^{b)}	99	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}	ND ^{b)}
(S)-ADH <i>R. erythropolis</i> [40]	ND ^{b)}	99	ND ^{b)}	ND ^{b)}	99	ND ^{b)}	ND ^{b)}

^{a)}ND-LR: not determined due to low reactivity

^{b)}ND: not determined.

2.3 Compounds 1a-4a

Table S4. Enantiomeric excess after reduction of **1a-4a** using different enzymes. Anti-Prelog selectivity is shown as negative values.



Enzyme [Ref]	5a (CH ₃)	6a (CH ₂ Cl)	7a (Et)	8a (CF ₃)
CR <i>C. magnolia</i> [1]	-99	-99	ND	ND
KRED101 [2]	-14	-98 [3]	ND	ND
KRED102 [2]	ND-LR ^{a)}	NR-LR ^{a)}	ND	ND
KRED103[2]	ND-LR ^{a)}	NR-LR ^{a)}	ND	ND
KRED104 [2]	ND-LR ^{a)}	NR-LR ^{a)}	ND	ND
KRED105 [2]	99	NR-LR ^{a)}	ND	ND
KRED106 [2]	ND-LR ^{a)}	NR-LR ^{a)}	ND	ND
KRED107 [2]	-99	-98 [3]	ND	ND
KRED108 [2]	99	NR-LR ^{a)}	ND	ND
KRED109 [2]	ND-LR ^{a)}	NR-LR ^{a)}	ND	ND
KRED110 [2]	ND-LR ^{a)}	NR-LR ^{a)}	ND	ND
KRED111 [2]	85	-2 [3]	ND	ND
KRED113 [2]	0	-98 [3]	ND	ND
KRED114 [2]	90	42 [3]	ND	ND
KRED115 [2]	85	0 [3]	ND	ND
KRED116 [2]	99	NR-LR ^{a)}	ND	ND

Enzyme [Ref]	5a (CH ₃)	6a (CH ₂ Cl)	7a (Et)	8a (CF ₃)
KRED117 [2]	99	NR-LR ^{a)}	ND	ND
KRED120 [2]	99	NR-LR ^{a)}	ND	ND
KRED121 [2]	99	62 [3]	ND	ND
KRED123 [2]	88	-26 [3]	ND	ND
KRED124 [2]	99	NR-LR ^{a)}	ND	ND
KRED125 [2]	99	NR-LR ^{a)}	ND	ND
KRED126 [2]	ND-LR ^{a)}	-92 [3]	ND	ND
KRED127 [2]	ND-LR ^{a)}	NR-LR ^{a)}	ND	ND
KRED128 [2]	60	90 [3]	ND	ND
ADH <i>P. furiosus</i> [4]	99	99	ND	ND
CR <i>S. salmonicolor</i> -WT [5]	-42	-98	ND	ND
CR <i>K. termotolerans</i> [8]	-99	-99	-99	-99
ADH <i>S. cerevisiae</i> (YMRC226c) [9]	99	98	ND	ND
PAR <i>Corynebacterium</i> strain (ST-10) [10]	96	99	99	ND
ADH <i>Leifsonia</i> sp. [11]	-99	-99	-99	-99
CR <i>S. coelicolor</i> [12]	-96	-99	ND	-99
CR <i>P. guilliermondii</i> NRRL Y-324 [13]	-99	-99	ND	-99
CR <i>C. glabrata</i> (CgKR1) [14]	99	48	67	-63 [15]
CR <i>C. glabrata</i> (CgKR2) [14]	99	3	75	ND
ADH <i>A. aromaticum</i> [18]	99	99	99	ND
ADH <i>K. capsulate</i> [19]	99	99	ND	ND
CR <i>P. pastoris</i> [20]	99	99	ND	ND
KR <i>S. stipos</i> [22]	71.9	37	ND	50
ADH <i>Chryseobacterium</i> sp CA49 [23]	-99	-99	-99	-99
ADH <i>L. brevis</i> [24]	-99	-99	-99	-99
CR <i>Bacillus</i> sp. ECU0013 [26]	99	99	99	99
ADH <i>T. Brockii</i> -WT [27]	18	ND	45	ND
ADH <i>T. Brockii</i> -W110A [27]	91	ND	95	ND
ADH <i>T. Brockii</i> -W110M [27]	99	ND	98	ND
ADH <i>T. Brockii</i> -W110E [27]	99	ND	97	ND
ADH <i>T. Brockii</i> - I86L/L294N [27]	-97	ND	-93	ND
ADH <i>T. Brockii</i> - A85V/I86N/C295N [27]	-72	ND	ND-LR ^{a)}	ND
ADH <i>T. Brockii</i> - I86N/L294N/C295V [27]	ND-LR ^{a)}	ND	ND-LR ^{a)}	ND
ADH <i>T. Brockii</i> - A85V/I86N/L294V/C295N [27]	-50	ND	ND-LR ^{a)}	ND
ADH <i>T. Brockii</i> - I86V/L294N [27]	-28	ND	36	ND
ADH <i>T. Brockii</i> - I86N/L294V/C295N [27]	-99	ND	-98	ND

Enzyme [Ref]	5a (CH ₃)	6a (CH ₂ Cl)	7a (Et)	8a (CF ₃)
ADH <i>T. brockii</i> -I86N/C295N [27]	99	ND	-91	ND
ADH <i>T. brockii</i> -W110S [27]	92	ND	98	ND
ADH <i>T. brockii</i> -W110L [27]	99	ND	99	ND
ADH <i>T. brockii</i> -I86A [27]	-98	ND	-97	ND
ADH <i>T. brockii</i> -I86V/W110L/L294Q [27]	93	ND	-97	ND
ADH <i>T. brockii</i> -I86Q [27]	-96	ND	-97	ND
ADH <i>T. brockii</i> -I86N [27]	-99	ND	-98	ND
ADH <i>T. brockii</i> -A85V/I86Q [27]	-56	ND	-51	ND
ADH <i>T. brockii</i> -I86V/W110V [27]	96	ND	98	ND
ADH <i>T. brockii</i> -A85V/I86L/W110Q/L294Q [27]	-5	ND	-90	ND
ADH <i>T. brockii</i> -I86V/L294Q [27]	-10	ND	15	ND
ADH <i>T. brockii</i> -I86L/W110Q/L294Q [27]	69	ND	82	ND
ADH-R <i>L. kefir</i> (DSM 20587) [28]	-99	ND	-99	ND
ADH <i>Pseudomonas</i> sp ATCC 49794 [29]	-99	ND	ND	-99
ADH <i>T. thermophilus</i> (ADH1) [30]	99	ND	ND	93
ADH <i>C. maris</i> [31]	-99	ND	ND	-99
CR <i>A. baylyi</i> ATC 3305 [32]	-31	ND	0	ND
CR <i>L. brevis</i> (LbCR) [33]	99	98	ND	ND
ADH evo-1.1.200 [34]	96.5	100	ND	ND
Reductase <i>Bacillus</i> sp ECU0013 (FabG) [35]	65	89	98	ND
CR <i>Y. lipolytica</i> ACA-DC 50109 [36]	99	99	99	99
AKR Ytbe, <i>Bacillus</i> sp. ECU0013 [37]	99	99	ND	99

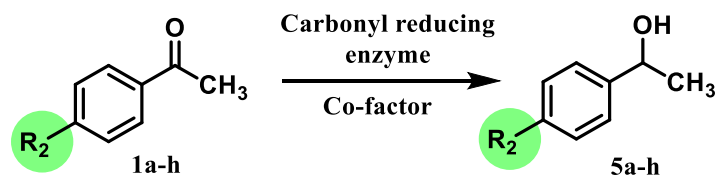
a)ND-LR: not determined due to low reactivity

b)ND: not determined.

3. Enantioselectivity: Pearson coefficients and correlation plots

3.1 *para*-Substituted derivatives

Table S5. Pearson correlation coefficient for ee-data of compounds **5a-h** different substituents. The number of enzymes included in the correlation is given in brackets.



Compound	5a (H)	5b (F)	5c (Cl)	5d (Br)	5e (Me)	5f (OMe)	5g (CF ₃)
5b (F)	0.973 (33)						
5c (Cl)	0.979 (46)	0.978 (29)					
5d (Br)	0.937 (43)	0.965 (29)	0.992 (40)				
5e (Me)	0.964 (34)	0.931 (30)	0.953 (31)	0.978 (30)			
5f (OMe)	0.953 (34)	0.952 (31)	0.966 (30)	0.975 (29)	0.980 (32)		
5g (CF ₃)	0.946 (30)	0.909 (25)	0.951 (27)	0.935 (26)	0.955 (27)	0.946 (27)	
5h (<i>t</i> -Bu)	0.909 (24)	0.926 (23)	0.929 (24)	0.897 (24)	0.829 (24)	0.831 (24)	0.875 (21)

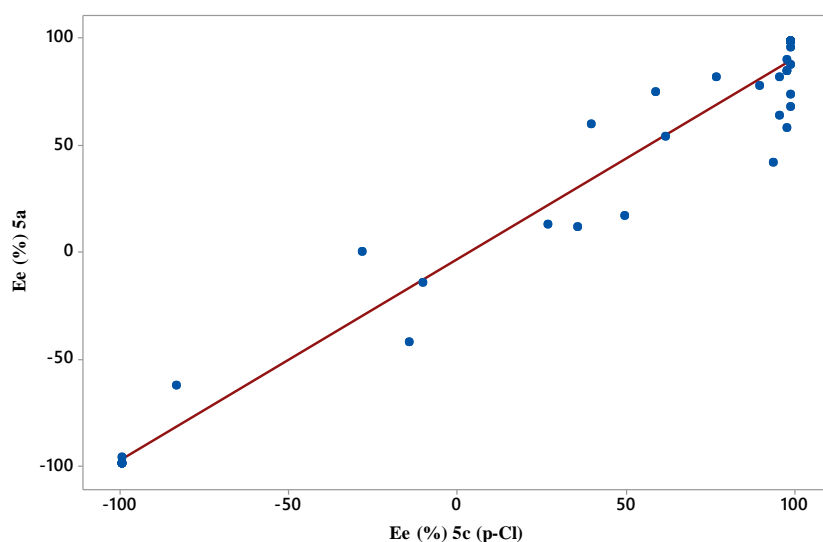


Figure S1. Scatterplot for ee data for compounds **5a** (H) and **5c** (*p*-Cl) based on 46 examples. Regression line: $Ee \text{ 5a} = -3.06 + 0.94 \times ee\text{-5c}$, $R^2 = 95.8$, $n = 46$.

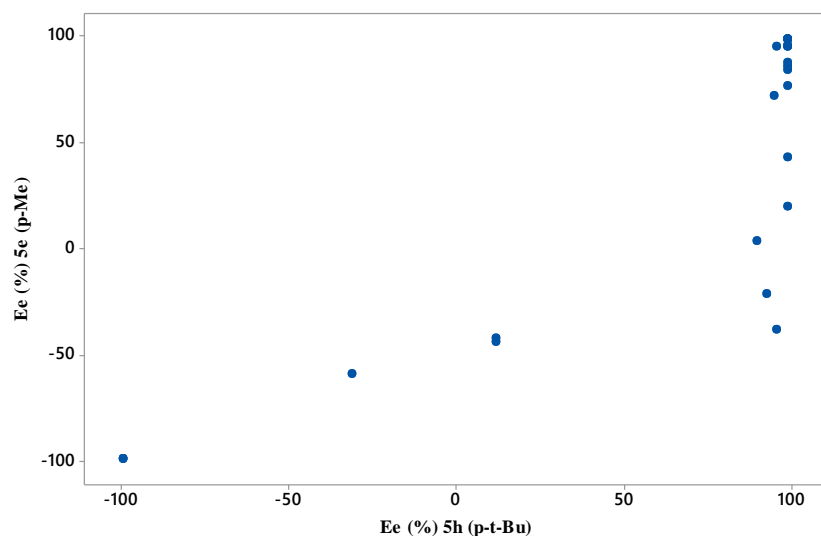
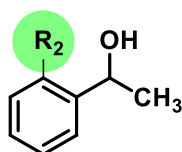


Figure S2. Scatterplot for ee data for compounds **5e** (*p*-Me) and **5h** (*p*-*t*-Bu) based on 24 examples.

3.2 Compounds 5i-5k

Table S6. Pearson correlation coefficient for ee-data of **5a** and **5i-5k**. The number of enzymes included in the correlation is given in brackets.



$R_2 =$ H (**5a**), Cl (**5i**), M (**5j**), MeO (**5k**)

	5a (H)	5i (o-Cl)	5j (o-Me)
5i (o-Cl)	0.725 (34) 0.957 (32) ^{a)}	*	*
5j (o-Me)	0.973 (12) 0.969 (10) ^{a)}	0.443 (13) 0.944 (11) ^{a)}	* *
5k (o-OMe)	0.753 (20)	0.296 (20)	0.783 (11)

^{a)}Removing data for two extreme outliers (two ketoreductases from *Candida glabrata* [14]).

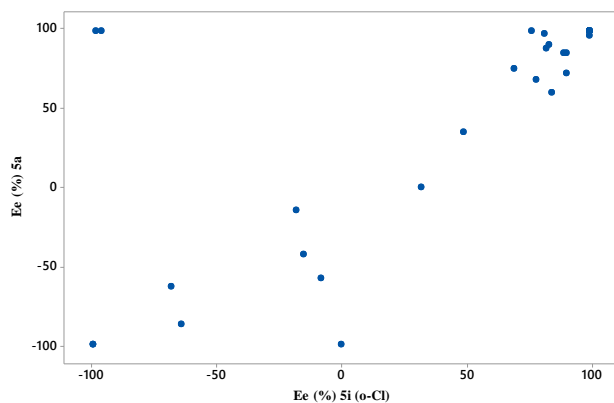


Figure S3. Scatterplot for ee data for compounds **5a** (H) and **5i** (*o*-Cl) based on 34 examples.

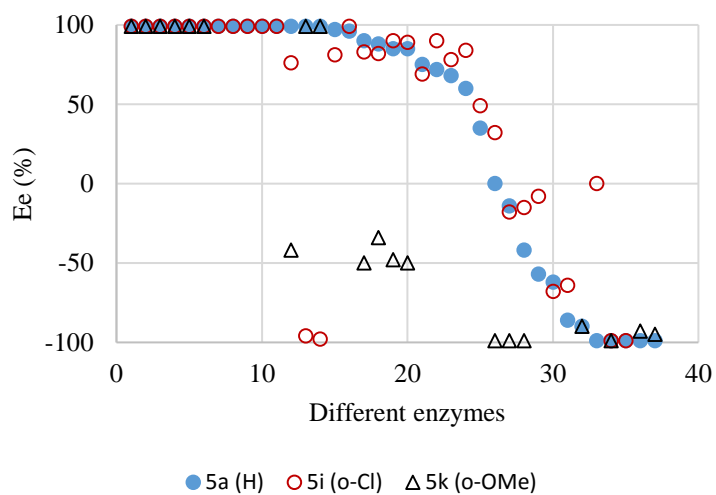
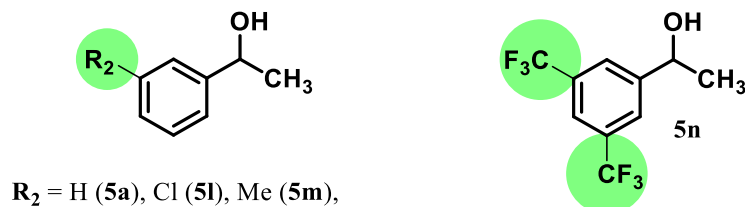


Figure S4. Comparison of ee data of **5a** (37 enzymes), **5i** (*o*-Cl, 34 enzymes) and **5k** (*o*-OMe, 19 enzymes). Interestingly, the presence of an *ortho*-methoxy substituent was found to favour anti-Prelog selectivity in a number of cases.

3.3 Compounds 5l-n

Table S7. Pearson correlation coefficient for ee-data of **5n-5n**. The number of enzymes included in the correlation is given in brackets.



	5l (m-Cl)	5m (m-Me)	5n (3,5-diCF3)
5a	0.963 (35)	0.775 (28)	0.861 (16)
5c (p-Cl)	0.953 (32)	0.793 (23)	0.615 (14)
5e (p-Me)	0.975 (18)	0.850 (17)	0.844 (14)
5g (p-CF3)	0.926 (19)	0.784 (18)	0.705 (17)
5i (o-Cl)	0.726 (42)	0.525 (34)	0.502 (14)
5j (o-Me)	0.973 (13)	0.872 (13)	0.639 (7)
5l (m-Cl)	*	*	*
5m (m-Me)	0.905 (28)	*	*
5n (3,5-diCF3)	0.348 (14)	0.17 (14)	*

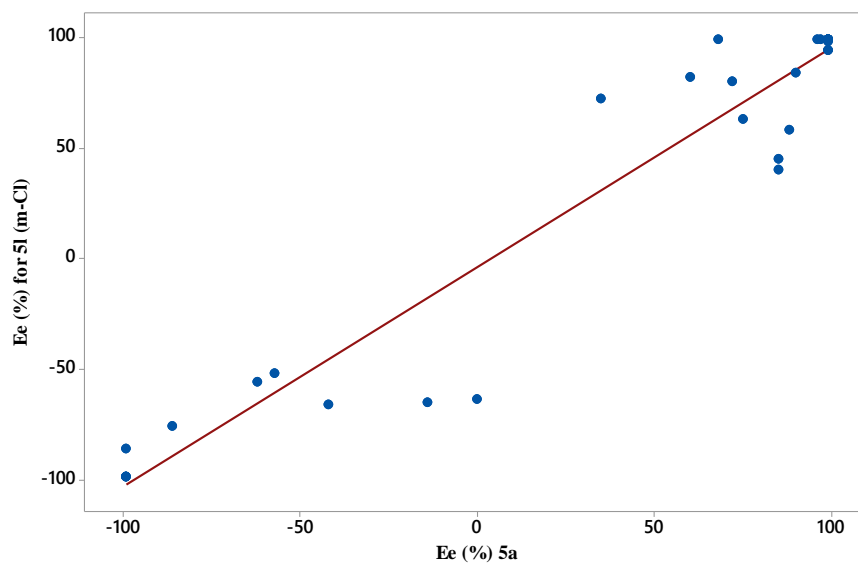


Figure S5. Scatterplot for ee data for compounds **5l (m-Cl)** and **5a (H)** based on 35 examples. Regression line: $E_e \mathbf{5l} = 3.908 + 0.994 \times ee\text{-}\mathbf{5a}$, $R^2 = 92.8$, $n = 35$.

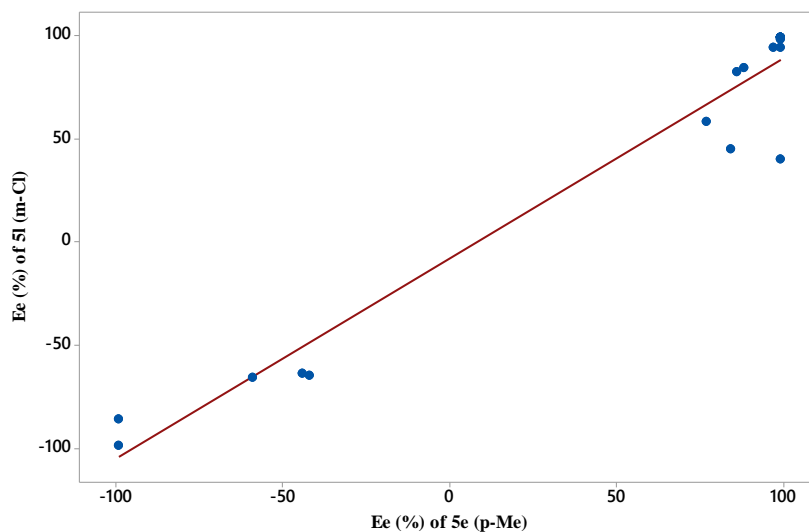
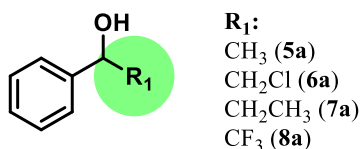


Figure S6. Scatterplot for ee data for compounds **5l** (*m*-Cl) and **5e** (*p*-Me) based on 18 examples. Regression line: $Ee\ 5l = -8.115 + 0.972 \times ee\ 5e$, $R^2 = 95.1$, $n = 18$.

3.4 Compounds 5a-8a

Table S8. Pearson correlation coefficient for ee data of **5a**, **6a**, **7a** and **8a**. The number of enzymes included in the correlation is given in brackets.



	5a (CH₃)	6a (CH₂Cl)	7a (Et)
6a (CH₂Cl)	0.892 (28)	*	
7a (Et)	0.809 (30)	0.970 (9)	*
8a (CF₃)	0.871 (12)	0.888 (9)	0.828 (6)

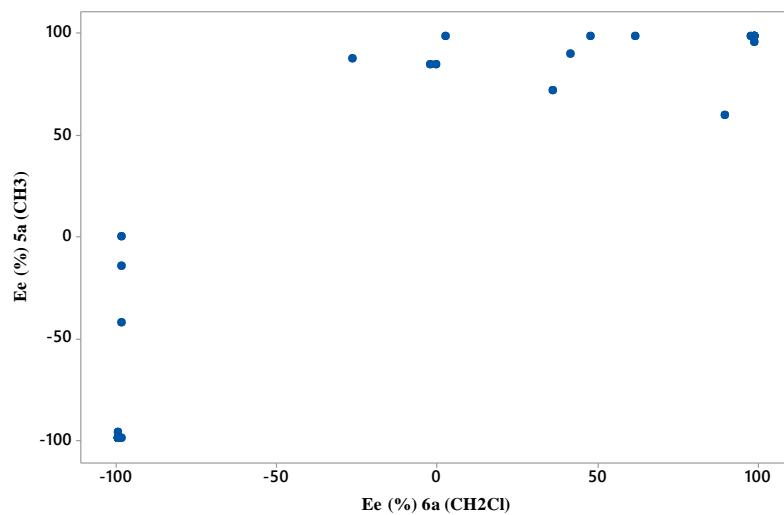


Figure S7. Scatterplot for ee data for compounds **5a** (CH₃) and **6a** (CH₂Cl) based on 28 examples.

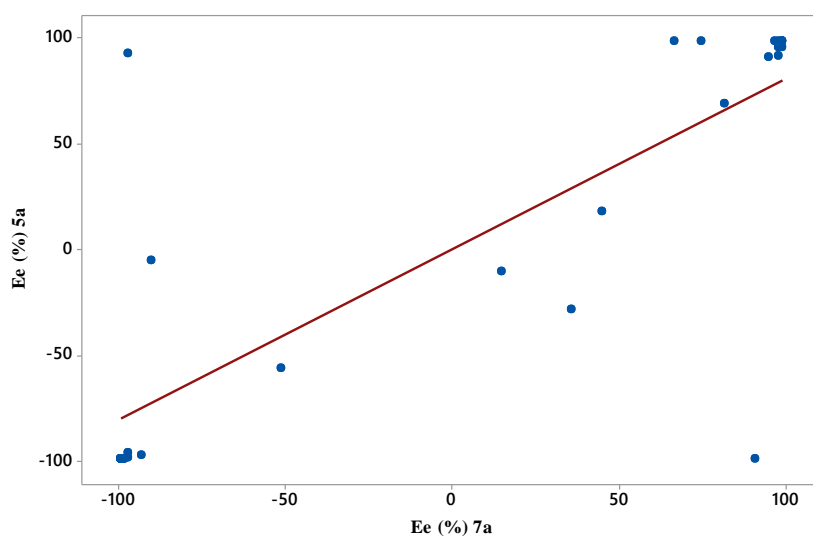


Figure S8. Scatterplot for ee data for compounds **5a** (CH₃) and **7a** (Et) based on 30 examples.

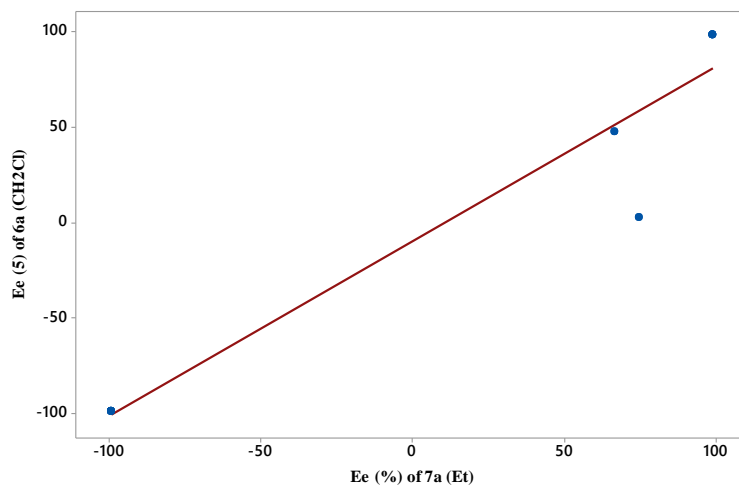


Figure S9. Scatterplot for ee data for compounds **6a** (CH₂Cl) and **7a** (Et) based on 9 examples. Regression line: Ee **6a** = $-9.732 + 0.9205 \times \text{ee-7a}$, $R^2 = 94.2$, $n = 9$.

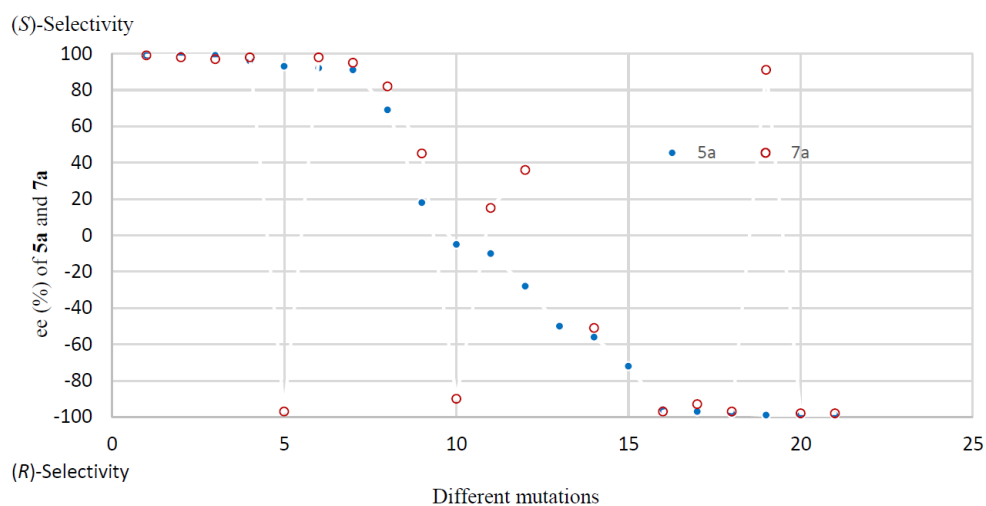


Figure S10. Effect of mutation on ee in ADH *T. Brockii* reductions leading to **5a** and **7a**. Data is taken from Reetz *et al.* [27].

4. The use of model compounds to predict ee

Table S9. Estimation of ee-values of processes towards **5a-f**, **5i** and **5l** using data for structurally related analogues as input in models.

Target	Model	Model ee (%)	GOF	Equation	Calc. ee (%)	Exp. Ee (%)	Ref
(R)-5a	5b	-98	94.6	$Ee = -1.85 + 0.93 \times ee-5b$	-93	-98	<i>ADH L. brevis</i> /[25]
(R)-5a	5b	99	94.6	$Ee = -1.85 + 0.93 \times ee-5b$	90	99	(S)-ADH <i>R. erytropolis</i> [40]
(S)-5a	5c	98	95.8	$Ee = -3.06 + 0.94 \times ee-5c$	89	97	ADH evo-1.1.200/[34]
(S)-5a	5c	99	95.8	$Ee = -3.06 + 0.94 \times ee-5c$	90	99	AKR Ytbe, <i>Bacillus sp.</i> ECU0013/[37]
(S)-5a	5c	88	95.8	$Ee = -3.06 + 0.94 \times ee-5c$	80	65	Reductase (FabG) <i>Bacillus sp.</i> / [35]
(S)-5a	5c	99	95.8	$Ee = -3.06 + 0.94 \times ee-5c$	90	99	(S)-ADH <i>R. erytropolis</i> [40]
(S)-5a	5d	99	87.9	$Ee = -6.07 + 0.95 \times ee-5d$	88	99	AKR Ytbe, <i>Bacillus sp.</i> ECU0013/[37]
(S)-5a	5d	93	87.9	$Ee = -6.07 + 0.95 \times ee-5d$	82	65	Reductase (FabG) <i>Bacillus sp.</i> / [35]
(S)-5a	5d	99	87.9	$Ee = -6.07 + 0.95 \times ee-5d$	88	99	(S)-ADH <i>R. erytropolis</i> [40]
(R)-5a	5e	-99	96.1	$Ee = 33.08 + (0.92 \times ee-5e) - (0.004 \times ee-5e^2)$	-97	-98	<i>ADH L. brevis</i> /[25]
(S)-5a	5e	99	96.1	$Ee = 33.08 + (0.92 \times ee-5e) - (0.004 \times ee-5e^2)$	85	99	(S)-ADH <i>R. erytropolis</i> [40]
(S)-5a	5f	98	94.8	$Ee = 33.73 + (0.93 \times ee-5f) - (0.004 \times ee-5f^2)$	86	97	ADH evo-1.1.200/[34]
(S)-5a	5f	99	94.8	$Ee = 33.73 + (0.93 \times ee-5f) - (0.004 \times ee-5f^2)$	87	99	(S)-ADH <i>R. erytropolis</i> [40]
(S)-5a	5i	99	91.6	$Ee = -12.55 + 1.10 \times 5i$	96	99	<i>CR Y. lipolytica</i> ACA-DC 50109/ [36]
(S)-5b	5a	99	94.6	$Ee = 4.36 + 1.02 \times ee-5a$	105	99	(S)-ADH <i>R. erytropolis</i> [40]
(R)-5b	5a	-98	94.6	$Ee = 4.36 + 1.02 \times ee-5a$	-96	-98	<i>ADH L. brevis</i> /[25]
(S)-5b	5c	99	95.7	$Ee = -3.17 + (0.996 \times ee-5c)$	95	99	(S)-ADH <i>R. erytropolis</i> [40]
(R)-5b	5e	-99	92.3	$Ee = 45.49 + (0.95 \times ee-5e) - (0.005 \times ee-5e^2)$	-98	-98	<i>ADH L. brevis</i> /[25]
(S)-5c	5a	65	95.8	$Ee = 5.18 + 1.02 \times ee-5a$	71	88	Reductase (FabG) <i>Bacillus sp.</i> / [35]
(S)-5c	5a	99	95.8	$Ee = 5.18 + 1.02 \times ee-5a$	106	99	AKR Ytbe, <i>Bacillus sp.</i> ECU0013/[37]
(S)-5c	5a	99	95.8	$Ee = 5.18 + 1.02 \times ee-5a$	106	99	(S)-ADH <i>R. erytropolis</i> [40]
(S)-5c	5a	97	95.8	$Ee = 5.18 + 1.02 \times ee-5a$	104	99	ADH evo-1.1.200/[34]
(S)-5c	5b	99	95.7	$Ee = 5.70 + (0.961 \times ee-5b)$	101	99	(S)-ADH <i>R. erytropolis</i> [40]
(S)-5c	5d	99	98.5	$Ee = 4.88 + 0.96 \times ee-5d$	100	99	ADH evo-1.1.200/[34]
(S)-5c	5d	97	98.5	$Ee = 4.88 + 0.96 \times ee-5d$	98	99	(S)-ADH <i>R. erytropolis</i> [41]
(S)-5c	5d	99	98.5	$Ee = 4.88 + 0.96 \times ee-5d$	100	99	(S)-ADH <i>R. erytropolis</i> [40]
(S)-5c	5d	93	98.5	$Ee = 4.88 + 0.96 \times ee-5d$	94	88	Reductase (FabG) <i>Bacillus sp.</i> / [35]

Target	Model	Model ee (%)	GOF	Equation	Calc. ee (%)	Exp. Ee (%)	Ref
(S)-5c	5f	98	98.6	$Ee=41.89+(0.99 \times ee-5f)-(0.004 \times ee-5f^2)$	100	98	ADH evo-1.1.200/[34]
(S)-5d	5a	65	87.9	$Ee=12.08+0.93 \times ee-5a$	73	93	Reductase (FabG) <i>Bacillus sp.</i> / [35]
(S)-5d	5c	88	98.5	$Ee=-4.16+1.02 \times ee-5c$	86	93	Reductase (FabG) <i>Bacillus sp.</i> / [35]
(S)-5d	5c	98	98.5	$Ee=-4.16+1.02 \times ee-5c$	96	97	(S)-ADH <i>R. erytropolis</i> [41]
(S)-5d	5c	99	98.5	$Ee=-4.16+1.02 \times ee-5c$	97	99	(S)-ADH <i>R. erytropolis</i> [40]
(S)-5d	5c	99	98.5	$Ee=-4.16+1.02 \times ee-5c$	97	99	AKR Ytbe, <i>Bacillus sp.</i> ECU0013/[37]
(R)-5e	5a	-98	93.5	$Ee=-14.99+(1.05 \times ee-5a)+(0.002 \times ee-5a^2)$	-99	-99	ADH <i>L. brevis</i> [25]
(S)-5e	5a	99	93.5	$Ee=-14.99+(1.05 \times ee-5a)+(0.002 \times ee-5a^2)$	109	99	(S)-ADH <i>R. erytropolis</i> [40]
(R)-5e	5b	-98	87.4	$Ee=-21.33+(0.95 \times ee-5b)+(0.002 \times ee-5b^2)$	-95	-99	ADH <i>L. brevis</i> [25]
(R)-5e	5b	99	87.4	$Ee=-21.33+(0.95 \times ee-5b)+(0.002 \times ee-5b^2)$	92	99	(S)-ADH <i>R. erytropolis</i> [40]
(R)-5e	5f	99	96.0	$Ee=0.19+0.982 \times ee-5f$	97	99	(S)-ADH <i>R. erytropolis</i> [40]
(S)-5f	5a	97	90.8	$Ee=-3.81+1.04 \times ee-5a$	97	98	ADH evo-1.1.200/[34]
(S)-5f	5a	99	90.8	$Ee=-3.81+1.04 \times ee-5a$	99	99	(S)-ADH <i>R. erytropolis</i> [40]
(S)-5f	5c	98	97.9	$Ee=-41.99+(0.98 \times ee-5c)+(0.004 \times ee-5c^2)$	92	98	ADH evo-1.1.200/[34]
(S)-5f	5c	99	97.9	$Ee=-41.99+(0.98 \times ee-5c)+(0.004 \times ee-5c^2)$	94	99	(S)-ADH <i>R. erytropolis</i> [40]
(S)-5i	5a	99	91.6	$Ee=15.01+0.84 \times ee-5a$	98	99	<i>CR Y. lipolytica</i> ACA-DC 50109/ [36]
(S)-5i	5a	99	91.6	$Ee=15.01+0.84 \times ee-5a$	98	99	(S)-ADH <i>R. erytropolis</i> [40]
(S)-5l	5a	99	93.3	$Ee=-16.64+(0.970 \times ee-5a)+(0.002 \times 5a^2)$	99	99	(S)-ADH <i>R. erytropolis</i> [40]
(S)-5l	5e	99	96.0	$Ee=-29.31+(0.919 \times ee-5e)+(0.003 \times ee-5e^2)$	91	99	(S)-ADH <i>R. erytropolis</i> [40]

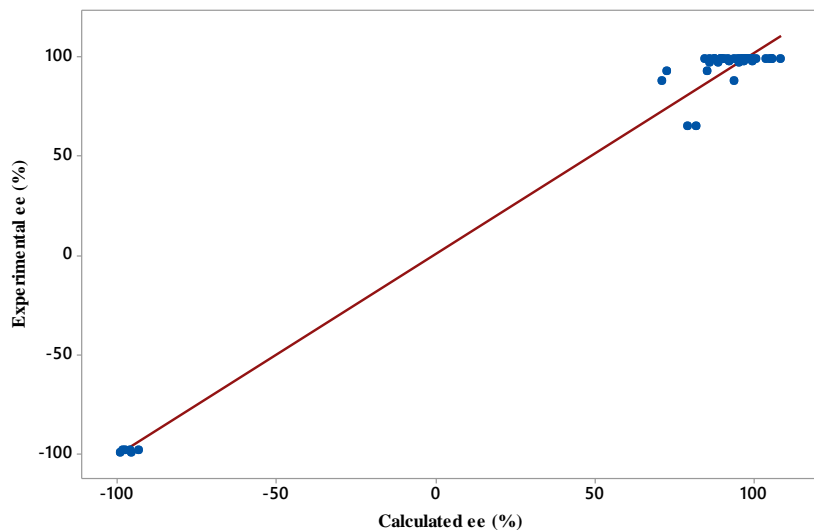


Figure S11: Experiment and computed ee-values for **5a-f**, **5i** and **5l**.

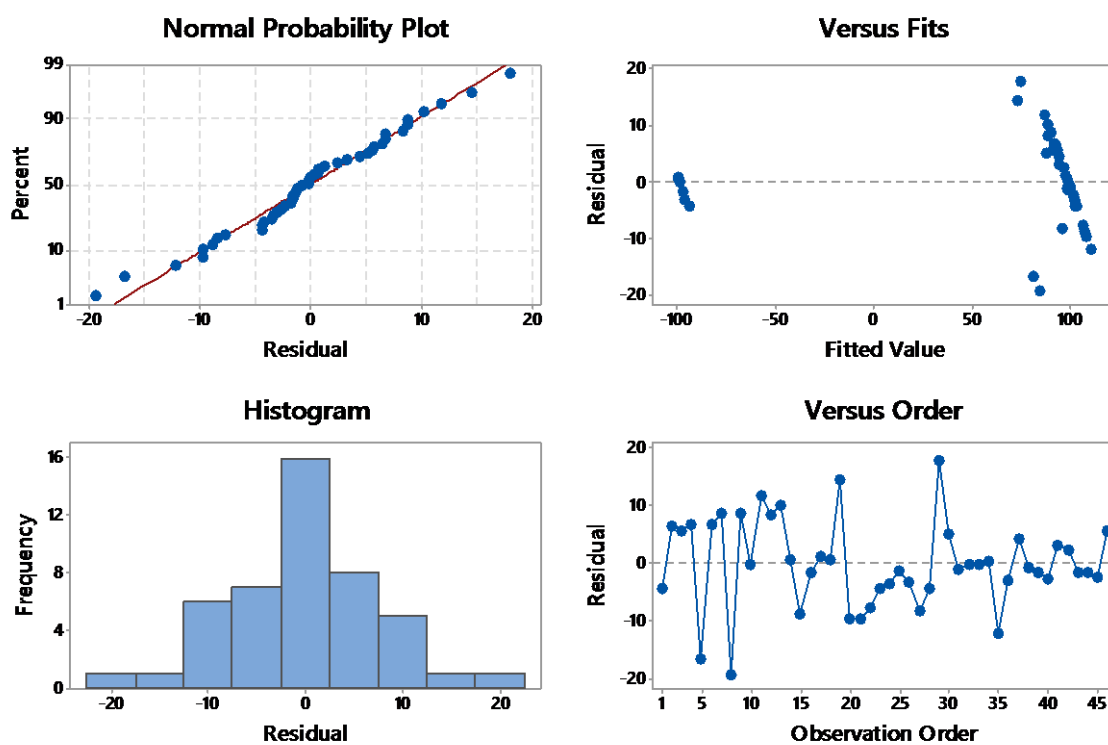
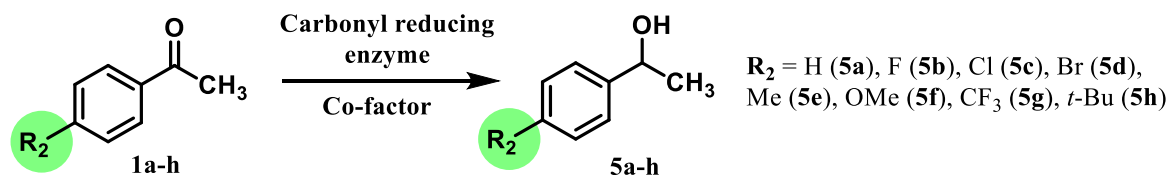


Figure S12: Residuals for computed ee-values for **5a-f**, **5i** and **5l**.

5. Rates of reduction

5.1 Compounds 5a-h

Table S10. Reported conversion/rates for compounds **5a-h**. ND = not determined. Some of the data is converted from relative activity using data in the articles.



Enzyme preparation	Unit	5a (H)	5b (p-F)	5c (p-Cl)	5d (p-Br)	5e (p-Me)	5f (p-OMe)	5g (p-CF ₃)	5h (p-t-Bu)
CR <i>C. magnolia</i>	μmol/min×mg	0.065	0.864	0.455	0.682	0.059	0.018	1.136	0.010
KRED 101	Rel. rate	380	138	250	290	116	28	460	24
KRED102	Rel. rate	2	1	25	38	1	<1	60	7
KRED103	Rel. rate	<1	<1	3	<1	<1	<1	5	0
KRED104	Rel. rate	<1	<1	4	4	<1	<1	6	0
KRED105	Rel. rate	11	8	28	15	5	<1	24	0
KRED106	Rel. rate	<1	<1	<1	<1	<1	<1	<1	0
KRED107	Rel. rate	142	516	>1000	>1000	570	61	>1000	97
KRED108	Rel. rate	22	14	28	14	<1	3	7	0
KRED109	Rel. rate	<1	<1	<1	<1	<1	<1	<1	<1
KRED110	Rel. rate	<1	<1	2	<1	0	0	<1	0
KRED 111	Rel. rate	495	730	532	582	678	562	468	57
KRED112		ND	ND	ND	ND	ND	ND	ND	ND
KRED113	Rel. rate	172	80	96	109	56	12	140	13
KRED114	Rel. rate	144	461	170	190	626	446	190	117
KRED115	Rel. rate	520	753	571	628	681	513	519	72
KRED116	Rel. rate	18	8	25	14	2	4	6	0
KRED117	Rel. rate	27	6	30	20	2	5	6	0
KRED118		ND	ND	ND	ND	ND	ND	ND	ND
KRED120	Rel. rate	49	32	55	40	7	11	16	0
KRED121	Rel. rate	352	23	550	734	38	17	672	130
KRED123	Rel. rate	351	573	606	623	145	42	458	34
KRED124	Rel. rate	50	100	438	389	10	33	274	10
KRED125	Rel. rate	14	6	167	256	10	2	650	70
KRED126	Rel. rate	1	1	5	6	1	<1	14	<1
KRED127	Rel. rate	1	1	4	5	0	0	8	<1
KRED128	Rel. rate	470	735	>1000	>1000	620	123	>1000	338
KRED130		ND	ND	ND	ND	ND	ND	ND	ND
KRED131		ND	ND	ND	ND	ND	ND	ND	ND
ADH <i>P. furiosus</i>	μmol/min×mg	0.013	0.021	0.017	0.010	0.014	0.000	0.019	0.000

Enzyme preparation	Unit	5a (H)	5b (p-F)	5c (p-Cl)	5d (p-Br)	5e (p-Me)	5f (p-OMe)	5g (p-CF ₃)	5h (p-t-Bu)
CR <i>S. salmonicolor</i> -WT	μmol/min×mg	0.028	0.014	0.020	0.013	0.011	0.020	0.092	0.011
CR <i>S. salmonicolor</i> -M242C	Kcat/KM, min ⁻¹ *mM ⁻¹	1.0	1.3	3.46	2.4	0.5	0.3	3.0	0.1
CR <i>S. salmonicolor</i> -M242D	Kcat/KM, min ⁻¹ *mM ⁻¹	0.2	0.2	0.10	0.1	0.1	0.1	0.3	0.1
CR <i>S. salmonicolor</i> -M242G	Kcat/KM, min ⁻¹ *mM ⁻¹	0.72	0.52	0.61	0.65	0.13	0.09	1.11	0.04
CR <i>S. salmonicolor</i> -M242Y	Kcat/KM, min ⁻¹ *mM ⁻¹	0.30	0.25	0.15	0.10	0.15	0.05	0.25	ND
CR <i>S. salmonicolor</i> -Q245H	μmol/min×mg	0.085	0.072	0.238	0.203	0.025	0.016	ND	0.032
CR <i>S. salmonicolor</i> -Q245L	μmol/min×mg	0.086	0.036	0.067	0.047	0.020	0.020	ND	0.009
CR <i>S. salmonicolor</i> -Q245P	μmol/min×mg	0.039	0.025	0.309	0.403	0.045	0.062	ND	0.084
CR <i>S. salmonicolor</i> -M242C/Q245L	Kcat/KM, min ⁻¹ *mM ⁻¹	<10	<10	38	42	<10	<10	178	<10
CR <i>S. salmonicolor</i> -M242F/ Q245T	Kcat/KM, min ⁻¹ *mM ⁻¹	50	127	375	360	28	33	167	<10
CR <i>S. salmonicolor</i> -M242L/ Q245P	Kcat/KM, min ⁻¹ *mM ⁻¹	<10	<10	66	122	<10	<10	23	<10
CR <i>S. salmonicolor</i> -M242L/ Q245T	Kcat/KM, min ⁻¹ *mM ⁻¹	34	70	370	459	34	34	689	<10
CR <i>K. thermotolerans</i>	μmol/min×mg	0.2	ND	3.9		1	0.1	1.0	ND
ADH <i>S. cerevisiae</i> (YMRC226c)	μmol/min×mg	0.020	ND	0.504	0.078	0.031	0.054	0.036	ND
PAR <i>Corynebacterium st.</i> (ST-10)	μmol/min×mg	0.35	ND	3.40	3.82	ND	ND	ND	ND
ADH <i>Leifsonia sp.</i>	μmol/min×mg	0.06	ND	0.6	0.77	ND	ND	ND	ND
CR <i>S. coelicolor</i>	Rel. activity	1	ND	6	8	ND	ND	ND	ND
CR <i>P. guilliermondii</i> NRRL Y-324	μmol/min×mg	0.23	ND	0.11	0.61	1.2	ND	ND	ND
CR <i>C. glabrata</i> (CgKR1)	Conv. (%)	46	94	98	99	98	94	ND	ND
CR <i>C. glabrata</i> (CgKR2)	Conv. (%)	2	15	17	66	4	6	ND	ND
CR <i>C. glabrata</i> (CgKR1)	μmol/min×mg	0.123	ND	0.195	0.182	ND	ND	ND	ND
CR <i>C. parapsilosis</i> -WT	K _{cat} /K _M , mM ⁻¹ *s ⁻¹	13.25	ND	ND	1.43	ND	ND	ND	ND
CR <i>C. parapsilosis</i> -F285A	K _{cat} /K _M ,	10.02	ND	ND	7.29	ND	ND	ND	ND
CR <i>C. parapsilosis</i> -W286A	mM ⁻¹ *s ⁻¹	11.59	ND	ND	7.47	ND	ND	ND	ND
CR <i>C. parapsilosis</i> -F285A/W286A	K _{cat} /K _M ,	10.19	ND	ND	8.58	ND	ND	ND	ND
CR <i>C. parapsilosis</i> (CPAR1)	μmol/min×mg	0.15	ND	0.39	ND	ND	ND	ND	ND
CR <i>C. parapsilosis</i> (CPAR2)	μmol/min×mg	0.87	ND	1.57	ND	ND	ND	ND	ND
CR <i>C. parapsilosis</i> (CPAR3)	μmol/min×mg	0	ND	0	ND	ND	ND	ND	ND
CR <i>C. parapsilosis</i> (CPAR4)	μmol/min×mg	0.67	ND	1.21	ND	ND	ND	ND	ND
CR <i>C. parapsilosis</i> (CPAR5)	μmol/min×mg	0.13	ND	0.24	ND	ND	ND	ND	ND
CR <i>C. parapsilosis</i> (CPAR6)	μmol/min×mg	0.02	ND	0.03	ND	ND	ND	ND	ND
CR <i>C. parapsilosis</i> (CPAR7)	μmol/min×mg	0	ND	0.03	ND	ND	ND	ND	ND
CR <i>C. parapsilosis</i> (CPAR8)	μmol/min×mg	0	ND	0	ND	ND	ND	ND	ND
ADH <i>A. aromaticum</i>		ND	ND	ND	ND	ND	ND	ND	ND
ADH <i>K. capsule</i>	μmol/min×mg	0.410	0.806	0.912	1.75	1.06	0.441	ND	ND
CR <i>P. pastoris</i>	μmol/min×mg	0.073	ND	0.074	ND	ND	ND	ND	ND

Enzyme preparation	Unit	5a (H)	5b (p-F)	5c (p-Cl)	5d (p-Br)	5e (p-Me)	5f (p-OMe)	5g (p-CF ₃)	5h (p-t-Bu)
ADH <i>B. gladioli</i> (BgADH1)	μmol/min×mg	6.13	6.28	ND	ND	5.49	6.29	6.44	ND
ADH <i>B. gladioli</i> (BgADH2)	μmol/min×mg	6.35	6.56	ND	ND	6.21	6.57	6.98	ND
ADH <i>B. gladioli</i> (BgADH5)	μmol/min×mg	4.51	4.66	ND	ND	4.39	4.63	5.35	ND
KR <i>S. stipos</i> CBS 6045	μmol/min×mg	4.95	ND	ND	ND	ND	ND	ND	ND
ADH <i>Chryseobacterium</i> sp. CA49	μmol/min×mg	1.41	ND	ND	ND	ND	ND	1.41	ND
ADH <i>L. brevis</i>	k _{cat} /K _M , M ⁻¹ ·s ⁻¹	16000	ND	ND	ND	ND	ND	ND	ND
CR BYueD <i>Bacillus</i> sp. ECU0013	μmol/min×mg	0.023	ND	0.01	0.014	ND	ND	ND	ND
ADH <i>T. Brockii</i> -WT	Conv. (%)	12	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -W110A	Conv. (%)	25	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -W110M	Conv. (%)	98	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -W110E	Conv. (%)	97	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -I86L/L294N	Conv. (%)	90	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -A85V/I86N/C295N	Conv. (%)	5	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -I86N/L294N/C295V	Conv. (%)	5	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -A85V/I86N/L294V/C295N	Conv. (%)	5	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -I86V/L294N	Conv. (%)	5	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -I86N/L294V/C295N	Conv. (%)	96	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -I86N/C295N	Conv. (%)	97	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -W110S	Conv. (%)	26	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -W110L	Conv. (%)	99	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -I86A	Conv. (%)	98	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -I86V/W110L/L294Q	Conv. (%)	71	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -I86Q	Conv. (%)	97	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -I86N	Conv. (%)	98	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -A85V/I86Q	Conv. (%)	6	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -I86V/W110V	Conv. (%)	95	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -A85V/I86L/W110Q/L294Q	Conv. (%)	5	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -I86V/L294Q	Conv. (%)	11	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. Brockii</i> -I86L/W110Q/L294Q	Conv. (%)	5	ND	ND	ND	ND	ND	ND	ND
ADH-R <i>L. kefir</i> (DSM 20587)	μmol/min×mg	558	ND	591	ND	ND	ND	ND	ND
ADH <i>Pseudomonas</i> sp. ATCC 49794	μmol/min×mg	2.1	ND	ND	ND	ND	ND	ND	ND
ADH <i>T. thermophilus</i> (ADH1)	K _{cat} /K _M , mM ⁻¹ ·s ⁻¹	Not reported	ND	ND	ND	ND	ND	ND	ND
ADH <i>C. maris</i>	μmol/min×mg	40.4	40.4	40.4	ND	ND	ND	ND	ND
CR <i>A. baylyi</i> ATC 3305	Conv. (%)	10.6	ND	ND	ND	ND	ND	ND	ND
CR <i>L. brevis</i> (LbCR)	μmol/min×mg	1.14	ND	ND	ND	ND	ND	ND	ND
ADH evo-1.1.200	Conv. (%), 14 days	41	ND	37	ND	ND	18	ND	ND

Enzyme preparation	Unit	5a (H)	5b (p-F)	5c (p-Cl)	5d (p-Br)	5e (p-Me)	5f (p-OMe)	5g (p-CF ₃)	5h (p-t-Bu)
Reductase (FabG) <i>Bacillus sp.</i>	μmol/min×mg	0.006	ND	0.011	0.052	ND	ND	ND	ND
CR <i>Y. lipolytica</i> ACA-DC 50109	μmol/min×mg	0.159	ND	ND	ND	ND	ND	ND	ND
AKR Ytbe, <i>Bacillus sp</i> ECU0013	Rel. activity	9	ND	64.2	32.8	ND	ND	ND	ND
Reductase <i>C. tenuis</i> (CtXR AKR2B5)	Cat _{eff} , M ⁻¹ *s ⁻¹	0.5	ND	6.6	ND	ND	ND	ND	ND
ADH <i>T. ethanolicus-I86A</i>	μmol/min×mg	18	ND	ND	ND	ND	ND	ND	ND
(S)-ADH <i>R. erythropolis</i>	μmol/min×mg	3.51	5.33	13	25.48	15.86	4.81	ND	ND
(S)-ADH <i>R. erythropolis</i>	μmol/min×mL	43	83.4	515	573	275	99.3	ND	ND
ADH <i>L. brevis</i>	Conv. (%)	76	86	ND	ND	76	ND	ND	ND

Table S11. Relative rates of selected enzymes based on values reported in Table S10. Values reported to >1000 was set to 1001 and values < 1 was set to 0.99.

Enzyme preparation	5a (H)	5b (p-F)	5c (p-Cl)	5d (p-Br)	5e (p-Me)	5f (p-Me)	5g (p-CF ₃)	5h (p-t-Bu)
<i>C. magnolia</i>	1.00	13.29	7.00	10.49	0.91	0.28	17.48	0.15
KRED101	1.00	0.36	0.66	0.76	0.31	0.07	1.21	0.06
KRED102	1.00	0.50	12.50	19.00	0.50	0.50	30.00	3.50
KRED103	1.00	1.00	3.03	1.00	1.00	1.00	5.05	0.10
KRED104	1.00	1.00	4.04	4.04	1.00	1.00	6.06	0.10
KRED105	1.00	0.73	2.55	1.36	0.45	0.09	2.18	0.01
KRED106	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.10
KRED107	1.00	3.49	6.76	6.76	3.85	0.41	6.76	0.66
KRED108	1.00	0.64	1.27	0.68	0.05	0.14	0.32	0.00
KRED109	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
KRED110	1.00	1.00	2.02	1.00	0.00	0.00	1.00	0.00
KRED111	1.00	1.47	1.09	1.18	1.37	1.14	0.95	2.59
KRED113	1.00	0.47	0.56	0.63	0.33	0.07	0.81	0.08
KRED114	1.00	3.20	1.18	1.32	4.35	3.10	1.32	0.81
KRED115	1.00	1.45	1.10	1.21	1.31	0.99	1.00	0.14
KRED116	1.00	0.01	1.39	0.78	0.11	0.22	0.33	0.00
KRED117	1.00	0.22	1.11	0.74	0.07	0.19	0.22	0.00
KRED120	1.00	0.65	1.12	0.82	0.14	0.22	0.33	0.00
KRED121	1.00	0.07	1.56	2.09	0.11	0.05	1.91	0.37
KRED123	1.00	1.63	1.73	1.77	0.41	0.12	1.30	0.10
KRED124	1.00	2.00	8.76	7.78	0.20	0.66	5.48	0.20
KRED125	1.00	0.43	11.93	18.29	0.71	0.14	46.43	5.00
KRED126	1.00	1.00	5.00	6.00	1.00	0.99	14.00	0.99
KRED127	1.00	1.00	4.00	5.00	0.00	0.00	8.00	0.99
KRED128	1.00	1.56	2.13	2.13	1.32	0.26	2.13	0.72
ADH <i>P. furiosus</i>	1.00	1.62	1.31	0.77	1.08	ND	1.46	ND

<i>CR S. salmonicolor</i> -WT	1.00	0.50	0.71	0.46	0.39	0.71	ND	0.39
<i>CR S. salmonicolor</i> -Q245P	1.00	0.64	7.92	10.33	0.64	1.59	ND	0.82
<i>CR S. salmonicolor</i> -Q245H	1.00	0.85	2.80	2.39	0.29	0.19	ND	0.38
<i>CR S. salmonicolor</i> -Q245L	1.00	0.42	0.78	0.55	0.23	0.23	ND	0.10
ADH <i>S. cerevisiae</i> (YMRC226c)	1.00	ND	25.20	3.90	1.55	2.70	ND	ND
ADH <i>K. capsulate</i>	1.00	1.96	2.22	4.26	2.59	1.07	ND	ND

Table S12. Statistic of conversion rates of **5b-h** relative to that of **5a**.

Parameter	5b (<i>p</i> -F)	5c (<i>p</i> -Cl)	5d (<i>p</i> -Br)	5e (<i>p</i> -Me)	5f (<i>p</i> -OMe)	5g (<i>p</i> -CF ₃)	5h (<i>p</i> - <i>t</i> -Bu)
Examples compared	31	32	32	32	31	26	29
Average relative rates as compared to 5a	1.5	3.9	3.7	0.9	0.7	6.1	0.7
# lower rate than 5a	14 (45.2%)	4 (12.5%)	9 (28.1%)	19 (59.4%)	22 (71.0%)	6 (23.1%)	25 (86.2%)

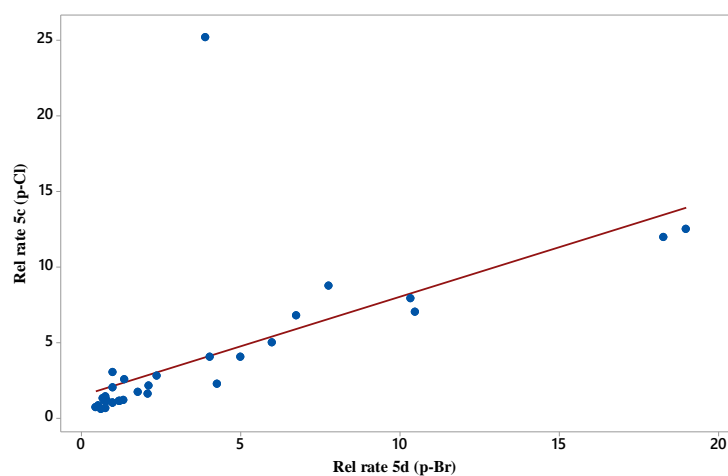


Figure S13. Relative rate for formation of **5c** (*p*-Cl) as a function of relative rate of **5d** (*p*-Br).

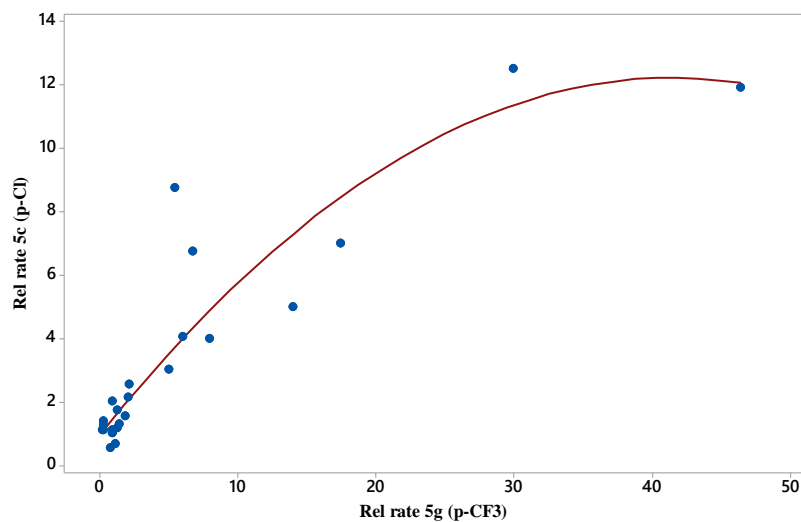
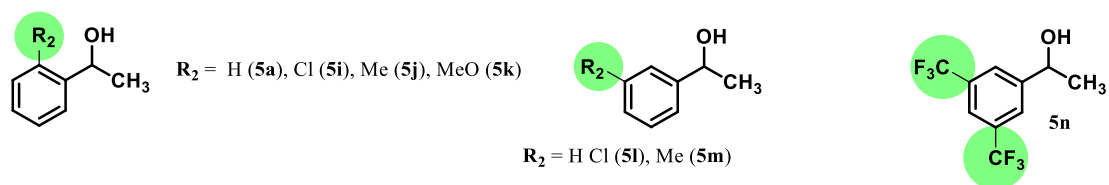


Figure S14. Relative rate for formation of **5c** (*p*-Cl) as a function of relative rate of **5g** (*p*-CF₃).

5.2 Compounds **5i-n**

Table S13. Reported conversion/rates for compounds **5i-n**.



Enzyme preparation	Unit	5a (H)	5i (<i>o</i> -Cl)	5j (<i>o</i> -Me)	5k (<i>o</i> -OMe)	5l (<i>m</i> -Cl)	5m (<i>m</i> -Me)	5n (3,5-diCF ₃)
KRED 101	Rel. rate	380	>1000	30	600	>1000	850	159
KRED102	Rel. rate	2	182	<1	50	42	15	2
KRED103	Rel. rate	<1	892	20	100	55	20	1
KRED104	Rel. rate	<1	<1	<1	<1	36	14	1
KRED105	Rel. rate	11	>1000	70	246	57	19	1
KRED106	Rel. rate	<1	143	0	5	58	24	<1
KRED107	Rel. rate	142	20	0	0	172	62	8
KRED108	Rel. rate	22	50	0	12	159	76	<1
KRED109	Rel. rate	<1	76	<1	5	26	10	<1
KRED110	Rel. rate	<1	96	0	13	36	14	<1
KRED 111	Rel. rate	495	>1000	37	125	977	366	789
KRED113	Rel. rate	172	>1000	16	585	>1000	714	164
KRED114	Rel. rate	144	899	18	119	>1000	307	862
KRED115	Rel. rate	520	982	64	238	918	257	831
KRED116	Rel. rate	18	46	0	14	120	21	3

Enzyme preparation	Unit	5a (H)	5i (o-Cl)	5j (o-Me)	5k (o-OMe)	5l (m-Cl)	5m (m-Me)	5n (3,5-diCF ₃)
KRED117	Rel. rate	27	55	0	23	140	23	3
KRED120	Rel. rate	49	93	0	42	181	122	3
KRED121	Rel. rate	352	547	5	32	906	77	682
KRED123	Rel. rate	351	958	2	63	893	296	792
KRED124	Rel. rate	50	39	0	0	179	30	3
KRED125	Rel. rate	14	153	4	5	94	25	4
KRED126	Rel. rate	1	34	0	1	42	15	21
KRED127	Rel. rate	1	30	0	1	36	14	2
KRED128	Rel. rate	470	401	<1	<1	933	186	85
ADH <i>P. furiosus</i>	$\mu\text{mol}/\text{min} \times \text{mg}$	0.013	0.030	0.000	0.020	0.037	0.020	0.017
CR <i>S. salmonicolor</i> -WT	$\mu\text{mol}/\text{min} \times \text{mg}$	0.028	0.078	0.014	0.024	0.280	0.064	0.120
CR <i>K. thermotolerans</i>	$\mu\text{mol}/\text{min} \times \text{mg}$	0.2	0.1	0.3	0.1	0.2	0.2	0.3
ADH <i>S. cerevisiae</i> (YMRC226c)	$\mu\text{mol}/\text{min} \times \text{mg}$	0.020	0.019			0.100	0.090	
PAR <i>Corynebacterium st.</i> (ST-10)	$\mu\text{mol}/\text{min} \times \text{mg}$	0.35	0.17			6.74		
ADH <i>Leifsonia sp.</i>	$\mu\text{mol}/\text{min} \times \text{mg}$	0.06				0.7		
CR <i>C. glabrata</i> (CgKR1)	Conv. (%)	46	43	21	15	99	57	
CR <i>C. glabrata</i> (CgKR2)	Conv. (%)	2	82	6	0.2	52	20	
CR <i>C. parapsilosis</i> -WT	$K_{\text{cat}}/K_M, \text{mM}^{-1} \cdot \text{s}^{-1}$	13.25	1.25			1.19	2.07	
CR <i>C. parapsilosis</i> -F285A	K_{cat}/K_M	10.02	4.78			3.78	2.05	
CR <i>C. parapsilosis</i> -W286A	$\text{mM}^{-1} \cdot \text{s}^{-1}$	11.59	5.78			2.15	2.58	
CR <i>C. parapsilosis</i> -F285A/W286A	K_{cat}/K_M	10.19	9.84			3.88	5.58	
CR <i>C. parapsilosis</i> (CPAR1)	$\mu\text{mol}/\text{min} \times \text{mg}$	0.15	0.35			0.12		
CR <i>C. parapsilosis</i> (CPAR2)	$\mu\text{mol}/\text{min} \times \text{mg}$	0.87	0.92			1.54		
CR <i>C. parapsilosis</i> (CPAR3)	$\mu\text{mol}/\text{min} \times \text{mg}$	0	0.04			0		
CR <i>C. parapsilosis</i> (CPAR4)	$\mu\text{mol}/\text{min} \times \text{mg}$	0.67	1.35			1.88		
CR <i>C. parapsilosis</i> (CPAR5)	$\mu\text{mol}/\text{min} \times \text{mg}$	0.13	0.19			0.27		
CR <i>C. parapsilosis</i> (CPAR6)	$\mu\text{mol}/\text{min} \times \text{mg}$	0.02	0.05			0.04		
CR <i>C. parapsilosis</i> (CPAR7)	$\mu\text{mol}/\text{min} \times \text{mg}$	0	0.05			0.06		
CR <i>C. parapsilosis</i> (CPAR8)	$\mu\text{mol}/\text{min} \times \text{mg}$	0	0			0		
ADH <i>A. aromaticum</i>	Not given							
ADH <i>K. capsulate</i>	$\mu\text{mol}/\text{min} \times \text{mg}$	0.410	0.342	0.152		0.76		
CR <i>P. pastoris</i>	$\mu\text{mol}/\text{min} \times \text{mg}$	0.073						
ADH <i>B. gladioli</i> (BgADH1)	$\mu\text{mol}/\text{min} \times \text{mg}$	6.13			4.18			5.67
ADH <i>B. gladioli</i> (BgADH2)	$\mu\text{mol}/\text{min} \times \text{mg}$	6.35			4.83			6.13
ADH <i>B. gladioli</i> (BgADH5)	$\mu\text{mol}/\text{min} \times \text{mg}$	4.51			3.64			4.05
KR <i>S. stipos</i> CBS 6045	$\mu\text{mol}/\text{min} \times \text{mg}$	4.95	3.78	1.37		16.4	7.3	
ADH <i>Chryseobacterium sp.</i> CA49	$\mu\text{mol}/\text{min} \times \text{mg}$	1.41						1
ADH <i>C. maris</i>	$\mu\text{mol}/\text{min} \times \text{mg}$	40.4	4.131			55.08		

Enzyme preparation	Unit	5a (H)	5i (o-Cl)	5j (o-Me)	5k (o-OMe)	5l (m-Cl)	5m (m-Me)	5n (3,5-diCF ₃)
CR <i>Y. lipolytica</i> ACA-DC 50109	$\mu\text{mol}/\text{min} \times \text{mg}$	0.159	ND					
Reductase <i>C. tenuis</i> (CtXR AKR2B5)	$\text{Cat}_{\text{eff}}, \text{M}^{-1}\text{s}^{-1}$	0.5	340.3			0.8		
(S)-ADH <i>R. erythropolis</i>	$\mu\text{mol}/\text{min} \times \text{mg}$	3.51	1.56			38.22		

Table S14. Relative rates of selected enzymes based on values reported in Table S13. Values reported to >1000 was set to 1001 and values < 1 was set to 0.99.

Enzyme preparation	5a (H)	5i (o-Cl)	5j (o-Me)	5k (o-Ome)
KRED101	1.0	2.6	0.1	1.6
KRED102	1.0	91.0	0.5	25.0
KRED103	1.0	901.0	20.2	101.0
KRED104	1.0	1.0	1.0	1.0
KRED105	1.0	91.0	6.4	22.4
KRED106	1.0	144.4	0.0	5.1
KRED107	1.0	0.1	0.0	0.0
KRED108	1.0	2.3	0.0	0.5
KRED109	1.0	76.8	1.0	5.1
KRED110	1.0	97.0	0.0	13.1
KRED 111	1.0	2.0	0.1	0.3
KRED113	1.0	5.8	0.1	3.4
KRED114	1.0	6.2	0.1	0.8
KRED115	1.0	1.9	0.1	0.5
KRED116	1.0	2.6	0.0	0.8
KRED117	1.0	2.0	0.0	0.9
KRED120	1.0	1.9	0.0	0.9
KRED121	1.0	1.6	0.0	0.1
KRED123	1.0	2.7	0.0	0.2
KRED124	1.0	0.8	0.0	0.0
KRED125	1.0	10.9	0.3	0.4
KRED126	1.0	34.0	0.0	1.0
KRED127	1.0	30.0	0.0	1.0
KRED128	1.0	0.9	0.0	0.0
ADH <i>P. furiosus</i>	1.0	2.3	ND	1.6
CR <i>S. salmonicolor</i> -WT	1.0	2.8	0.5	0.9
CR <i>K. termotolerans</i>	1.0	0.5	1.5	0.3
ADH <i>S. cerevisiae</i> (YMRC226c)	1.0	1.0	ND	ND
CR <i>C. glabrata</i> (CgKR1)	1.0	0.9	0.5	0.3
CR <i>C. glabrata</i> (CgKR2)	1.0	41.0	3.0	0.1
CR <i>C. parapsilosis</i> -WT	1.0	0.1	ND	ND
CR <i>C. parapsilosis</i> -F285A	1.0	0.5	ND	ND
CR <i>C. parapsilosis</i> -W286A	1.0	0.5	ND	ND

Enzyme preparation	5a (H)	5i (o-Cl)	5j (o-Me)	5k (o-Ome)
CR <i>C. parapsilosis</i> -F285A/W286A	1.0	1.0	ND	ND
CR <i>C. parapsilosis</i> (CPAR1)	1.0	2.3	ND	ND
CR <i>C. parapsilosis</i> (CPAR2)	1.0	1.1	ND	ND
CR <i>C. parapsilosis</i> (CPAR4)	1.0	2.0	ND	ND
CR <i>C. parapsilosis</i> (CPAR5)	1.0	1.5	ND	ND
CR <i>C. parapsilosis</i> (CPAR6)	1.0	2.5	ND	ND
ADH <i>K. caosulate</i>	1.0	0.8	0.4	ND
ADH <i>B. gladioli</i> (BgADH1)	1.0	ND	ND	0.7
ADH <i>B. gladioli</i> (BgADH2)	1.0	ND	ND	0.8
ADH <i>B. gladioli</i> (BgADH5)	1.0	ND	ND	0.8
KR <i>S. stipos</i> CBS 6045	1.0	0.8	0.3	ND

Table S15. Statistic of conversion rates of **5i-k** relative to that of **5a**.

Parameter	5i (o-Cl)	5j (o-Me)	5k (o-OMe)
Examples compared	41	30	32
Average relative rates as compared to 5a	38.5	1.2	5.9
# lower rate than 5a	10 (24.4%)	23 (76.7%)	20 (62.5%)

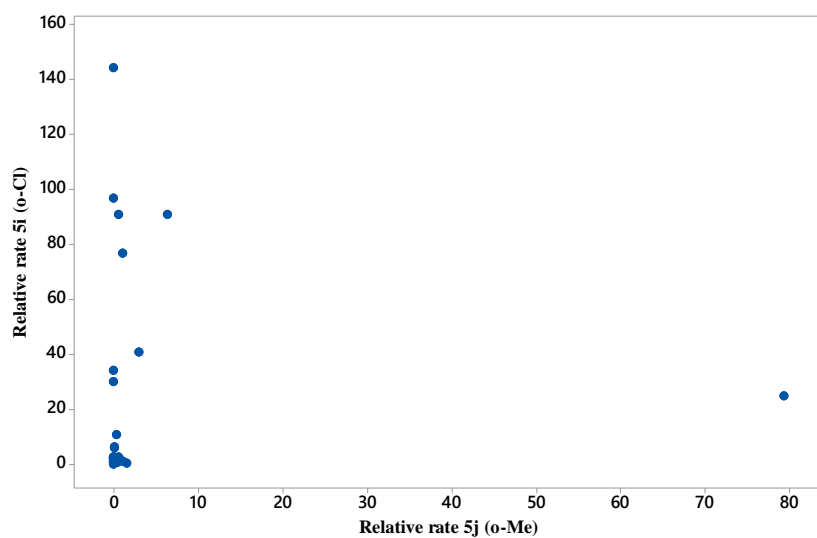


Figure S15. Relative rate for formation of **5i** (*o*-Cl) as a function of relative rate of **5j** (*o*-Me).

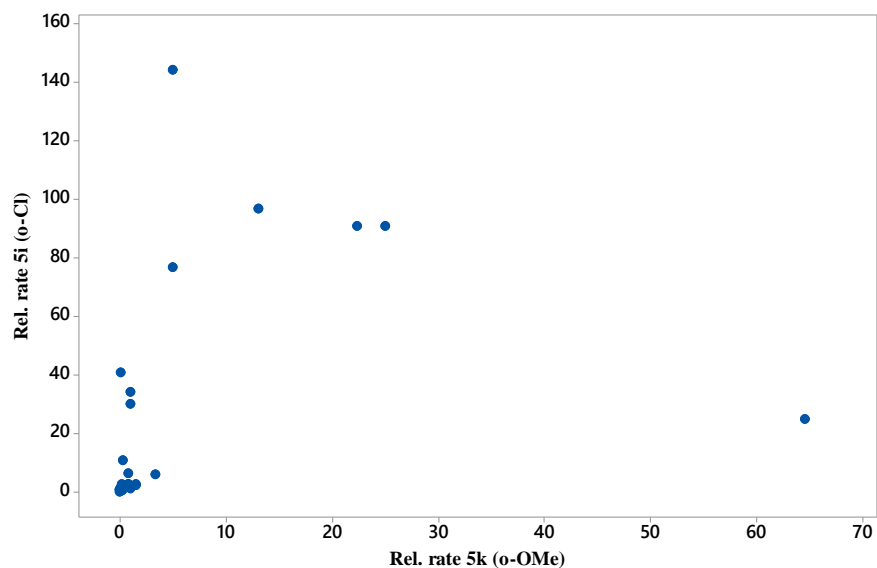


Figure S16. Relative rate for formation of **5i** (*o*-Cl) as a function of relative rate of **5k** (*o*-OMe).

Table S16. Relative rates of selected enzymes based on values reported in Table S13. Values reported to > 1000 was set to 1001 and values < 1 was set to 0.99. The data is sorted by the relative rate displayed by **5l**.

Enzyme preparation	5a (H)	5l (<i>m</i> -Cl)	5m (<i>m</i> -Me)	5n (3,5-diCF ₃)
KRED106	1.0	58.6	24.2	1.0
KRED103	1.0	55.6	20.2	1.0
KRED126	1.0	42.0	15.0	21.0
KRED104	1.0	36.4	14.1	1.0
KRED110	1.0	36.4	14.1	1.0
KRED127	1.0	36.0	14.0	2.0
KRED109	1.0	26.3	10.1	1.0
CR <i>C. glabrata</i> (CgKR2)	1.0	26.0	10.0	ND
KRED102	1.0	21.0	7.5	1.0
PAR <i>Corynebacterium st. (ST-10)</i>	1.0	19.3	ND	ND
ADH <i>Leifsonia sp.</i>	1.0	11.7	ND	ND
KRED108	1.0	7.2	3.5	0.0
KRED114	1.0	7.0	2.1	6.0
KRED125	1.0	6.7	1.8	0.3
KRED116	1.0	6.7	1.2	0.2
KRED113	1.0	5.8	4.2	1.0
KRED117	1.0	5.2	0.9	0.1
KRED105	1.0	5.2	1.7	0.1
ADH <i>S. cerevisiae</i> (YMRC226c)	1.0	5.0	4.5	ND
KRED120	1.0	3.7	2.5	0.1

Enzyme preparation	5a (H)	5l (m-Cl)	5m (m-Me)	5n (3,5-diCF ₃)
KRED124	1.0	3.6	0.6	0.1
KR <i>S stipsos</i> CBS 6045	1.0	3.3	1.5	ND
ADH <i>P. furiosus</i>	1.0	2.9	1.5	1.3
CR <i>C. parapsilosis</i> (CPAR4)	1.0	2.8	ND	ND
KRED 101	1.0	2.6	2.2	0.4
KRED121	1.0	2.6	0.2	1.9
KRED123	1.0	2.5	0.8	2.3
CR <i>C. glabrata</i> (CgKR1)	1.0	2.2	1.2	ND
CR <i>C. parapsilosis</i> (CPAR5)	1.0	2.1	ND	ND
CR <i>C. parapsilosis</i> (CPAR6)	1.0	2.0	ND	ND
KRED128	1.0	2.0	0.4	0.2
KRED 111	1.0	2.0	0.7	1.6
ADH <i>K. caosulate</i>	1.0	1.9	2.2	ND
CR <i>C. parapsilosis</i> (CPAR2)	1.0	1.8	ND	ND
KRED115	1.0	1.8	0.5	1.6
KRED107	1.0	1.2	0.4	0.1
CR <i>K. termotolerans</i>	1.0	1.0	1.0	1.5
CR <i>C. parapsilosis</i> (CPAR1)	1.0	0.8	ND	ND
CR <i>C. parapsilosis</i> -F285A/W286A	1.0	0.4	0.5	ND
CR <i>C. parapsilosis</i> -F285A	1.0	0.4	0.2	ND
CR <i>C. parapsilosis</i> -W286A	1.0	0.2	0.2	ND
CR <i>C. parapsilosis</i> -WT	1.0	0.1	0.2	ND
ADH <i>B. gladioli</i> (BgADH1)	1.0	ND	ND	0.9
ADH <i>B. gladioli</i> (BgADH2)	1.0	ND	ND	1.0
ADH <i>B. gladioli</i> (BgADH5)	1.0	ND	ND	0.9
ADH <i>Chryseobacterium</i> sp CA49	1.0	ND	ND	0.7

Table S17. Statistic of conversion rates of 5l-n relative to that of 5a.

Parameter	5l (m-Cl)	5m (m-Me)	5n (3,5-diCF ₃)
Examples compared	42	35	29
Average relative rates as compared to 5a	11.0	4.7	1.8
# lower rate than 5a	5 (12 %)	12 (34.3 %)	12 (41.4 %)

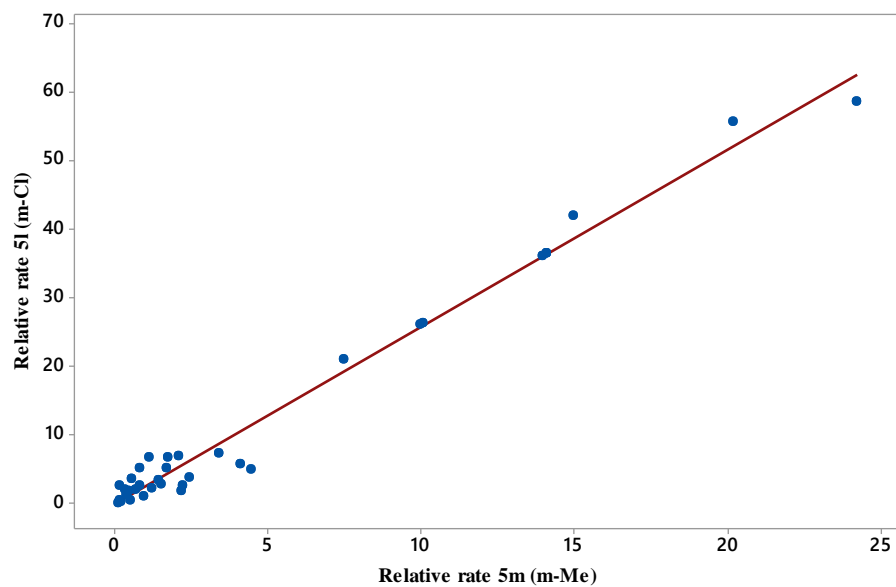


Figure S17. Correlation between relative rates of **5l** and **5m**. Linear regression: Rel. rate **5l**= $-0.23 + 2.58 \times \text{Rel. rate } 5m$, $R^2 = 98.0$, $n = 35$.

5.3 Compounds 5a-8a

Table S18. Rates/conversions reported for compounds **5a-8a**.

Enzyme preparation	Unit	5a (H)	6a (CH ₂ Cl)	7a (Et)	8a (CF ₃)
CR <i>C. magnolia</i>	μmol/min×mg	0.065	0.82	ND	ND
KRED 101	μmol/min×mg		1.15	ND	ND
KRED107	μmol/min×mg		0.03	ND	ND
KRED 111	μmol/min×mg		0.48	ND	ND
KRED112	μmol/min×mg		1.02	ND	ND
KRED113	μmol/min×mg		1.40	ND	ND
KRED114	μmol/min×mg		0.39	ND	ND
KRED115	μmol/min×mg		1.10	ND	ND
KRED118	μmol/min×mg		0.33	ND	ND
KRED121	μmol/min×mg		0.10	ND	ND
KRED123	μmol/min×mg		0.10	ND	ND
KRED130	μmol/min×mg		0.15	ND	ND
KRED131	μmol/min×mg		0.02	ND	ND
ADH <i>P. furiosus</i>	μmol/min×mg	0.013	0.17	ND	ND
CR <i>S. salmonicolor</i> -WT	μmol/min×mg	0.028	0.370	ND	ND
CR <i>K. thermotolerans</i>	μmol/min×mg	0.2	1.90	0.5	14.0
ADH <i>S. cerevisiae</i> (YMRC226c)	μmol/min×mg	0.020	0.075	ND	ND
PAR <i>Corynebacterium st.</i> (ST-10)	μmol/min×mg	0.35	0.08	0.02	ND
ADH <i>Leifsonia sp.</i>	μmol/min×mg	0.06	0.29	ND	1
CR <i>S. coelicolor</i>	Rel. activity	1	8.00	ND	43
CR <i>P. guilliermondii</i> NRRL Y-324	μmol/min×mg	0.23	2.20	ND	4.6
CR <i>C. glabrata</i> (CgKR1)	Conv. (%)	46	88.00	5	ND
CR <i>C. glabrata</i> (CgKR2)	Conv. (%)	2	93.00	2	ND
CR <i>C. glabrata</i> (CgKR1)	μmol/min×mg	0.123	0.20	ND	0.081
ADH <i>K. capsulate</i>	μmol/min×mg	0.410	0.38	ND	ND
CR <i>P. pastoris</i>	μmol/min×mg	0.073	0.05	ND	ND
KR <i>S. stipos</i> CBS 6045	μmol/min×mg	4.95	71.50	ND	124
ADH <i>Chryseobacterium sp. CA49</i>	μmol/min×mg	1.41	1.52	0.109	1.56
ADH <i>L. brevis</i>	k _{cat} /K _M , M ⁻¹ *s ⁻¹	16000	377280	4640	3360
CR BYueD <i>Bacillus sp.</i> ECU0013	μmol/min×mg	0.023	0.01	0.014	1
ADH <i>T. Brockii</i> -WT	Conv. (%)	12	ND	36	ND
ADH <i>T. Brockii</i> -W110A	Conv. (%)	25	ND	16	ND
ADH <i>T. Brockii</i> -W110M	Conv. (%)	98	ND	82	ND
ADH <i>T. Brockii</i> -W110E	Conv. (%)	97	ND	65	ND

Enzyme preparation	Unit	5a (H)	6a (CH ₂ Cl)	7a (Et)	8a (CF ₃)
ADH <i>T. Brockii</i> -I86L/L294N	Conv. (%)	90	ND	86	ND
ADH <i>T. Brockii</i> -A85V/I86N/C295N	Conv. (%)	5	ND	5	ND
ADH <i>T. Brockii</i> -I86N/L294N/C295V	Conv. (%)	5	ND	5	ND
ADH <i>T. Brockii</i> -A85V/I86N/L294V/C295N	Conv. (%)	5	ND	5	ND
ADH <i>T. Brockii</i> -I86V/L294N	Conv. (%)	5	ND	7	ND
ADH <i>T. Brockii</i> -I86N/L294V/C295N	Conv. (%)	96	ND	97	ND
ADH <i>T. Brockii</i> -I86N/C295N	Conv. (%)	97	ND	77	ND
ADH <i>T. Brockii</i> -W110S	Conv. (%)	26	ND	20	ND
ADH <i>T. Brockii</i> -W110L	Conv. (%)	99	ND	98	ND
ADH <i>T. Brockii</i> -I86A	Conv. (%)	98	ND	98	ND
ADH <i>T. Brockii</i> -I86V/W110L/L294Q	Conv. (%)	71	ND	97	ND
ADH <i>T. Brockii</i> -I86Q	Conv. (%)	97	ND	97	ND
ADH <i>T. Brockii</i> -I86N	Conv. (%)	98	ND	99	ND
ADH <i>T. Brockii</i> -A85V/I86Q	Conv. (%)	6	ND	8	ND
ADH <i>T. Brockii</i> -I86V/W110V	Conv. (%)	95	ND	98	ND
ADH <i>T. Brockii</i> -A85V/I86L/W110Q/L294Q	Conv. (%)	5	ND	59	ND
ADH <i>T. Brockii</i> -I86V/L294Q	Conv. (%)	11	ND	24	ND
ADH <i>T. Brockii</i> -I86L/W110Q/L294Q	Conv. (%)	5	ND	10	ND
ADH-R <i>L. kefir</i> (DSM 20587)	μmol/min×mg	558	ND	179	ND
ADH <i>Pseudomonas sp.</i> ATCC 49794	μmol/min×mg	2.1	ND	ND	14.7
ADH <i>T. thermophilus</i> (ADH1)	$\frac{K_{cat}}{K_M}, \text{mM}^{-1}\text{s}^{-1}$	NR	ND	ND	2.3
ADH <i>C. maris</i>	μmol/min×mg	40.4	ND	24.8	NR
CR <i>A. baylyi</i> ATC 3305	Conv. (%)	10.6	ND	43.8	ND
CR <i>L. brevis</i> (LbCR)	μmol/min×mg	1.14	ND	28.8	ND
ADH evo-1.1.200	Conv (%), 14 days	41.0	42.0	ND	ND
Reductase (FabG) <i>Bacillus sp.</i>	μmol/min×mg	0.006	0.28	0.021	ND
CR <i>Y. lipolytica</i> ACA-DC 50109	μmol/min×mg	0.159	2.46	0.187	7.8
AKR Ytbe, <i>Bacillus sp.</i> ECU0013	Rel. activity	9	100	0	140

Table S19. Relative rates/conversion based on values reported in Table S18.

Enzyme preparation	5a (H)	6a (CH ₂ Cl)	7a (Et)	8a (CF ₃)
CR <i>C. magnolia</i>	1.0	12.6	ND	ND
ADH <i>P. furiosus</i>	1.0	13.3	ND	ND
CR <i>S. salmonicolor</i> -WT	1.0	13.2	ND	ND
CR <i>K. thermotolerans</i>	1.0	9.5	2.5	70.0
ADH <i>S. cerevisiae</i> (YMRC226c)	1.0	3.8	ND	ND
PAR <i>Corynebacterium st.</i> (ST-10)	1.0	0.2	0.1	ND

Enzyme preparation	5a (H)	6a (CH ₂ Cl)	7a (Et)	8a (CF ₃)
ADH <i>Leifsonia</i> sp.	1.0	4.8	0.5	16.7
CR <i>S. coelicolor</i>	1.0	8.0	ND	43.0
CR <i>P. guilliermondii</i> NRRL Y-324	1.0	9.6	ND	20.0
CR <i>C. glabrata</i> (CgKR1)	1.0	1.9	0.1	ND
CR <i>C. glabrata</i> (CgKR2)	1.0	46.5	1.0	ND
ADH <i>K. capsulate</i>	1.0	0.9	ND	ND
KR <i>S. stipos</i> CBS 6045	1.0	14.4	ND	25.1
ADH <i>Chryseobacterium</i> sp. CA49	1.0	1.1	0.1	1.1
ADH <i>L. brevis</i>	1.0	23.6	0.3	0.2
CR <i>Bacillus</i> sp (ECU0013)	1.0	0.6	0.6	43.5
ADH <i>T. brockii</i> -WT	1.0	ND	3.0	ND
ADH <i>T. brockii</i> -W110A	1.0	ND	0.6	ND
ADH <i>T. brockii</i> -W110M	1.0	ND	0.8	ND
ADH <i>T. brockii</i> -W110E	1.0	ND	0.7	ND
ADH <i>T. brockii</i> -I86L/L294N	1.0	ND	1.0	ND
ADH <i>T. brockii</i> -A85V/I86N/C295N	1.0	ND	1.0	ND
ADH <i>T. brockii</i> -I86N/L294N/C295V	1.0	ND	1.0	ND
ADH <i>T. brockii</i> -A85V/I86N/L294V/C295N	1.0	ND	1.0	ND
ADH <i>T. brockii</i> -I86V/L294N	1.0	ND	1.4	ND
ADH <i>T. brockii</i> -I86N/L294V/C295N	1.0	ND	1.0	ND
ADH <i>T. brockii</i> -I86N/C295N	1.0	ND	0.8	ND
ADH <i>T. brockii</i> -W110S	1.0	ND	0.8	ND
ADH <i>T. brockii</i> -W110L	1.0	ND	1.0	ND
ADH <i>T. brockii</i> -I86A	1.0	ND	1.0	ND
ADH <i>T. brockii</i> -I86V/W110L/L294Q	1.0	ND	1.4	ND
ADH <i>T. brockii</i> -I86Q	1.0	ND	1.0	ND
ADH <i>T. brockii</i> -I86N	1.0	ND	1.0	ND
ADH <i>T. brockii</i> -A85V/I86Q	1.0	ND	1.3	ND
ADH <i>T. brockii</i> -I86V/W110V	1.0	ND	1.0	ND
ADH <i>T. brockii</i> -A85V/I86L/W110Q/L294Q	1.0	ND	11.8	ND
ADH <i>T. brockii</i> -I86V/L294Q	1.0	ND	2.2	ND
ADH <i>T. brockii</i> -I86L/W110Q/L294Q	1.0	ND	2.0	ND
ADH-R <i>L. kefir</i> (DSM 20587)	1.0	ND	0.3	ND
ADH <i>Pseudomonas</i> sp ATCC 49794	1.0	ND		1470
ADH <i>C. maris</i>	1.0	ND	0.6	ND
Diketoreductase <i>A. baylyi</i> ATC 3305	1.0	ND	4.1	ND
CR LbCR (from <i>L. brevis</i>)	1.0	ND	25.3	ND

Table S20. Statistic of conversion rates of **6a-8a** relative to **5a**.

Parameter	6a (CH ₂ Cl)	7a (Et)	8a (CF ₃)
Examples compared	16	34	9
Average relative rates as compared to 5a	10.3	2.1	>100
# lower rate than 5a	3 (18.8 %)	13 (38.2 %)	1 (11.1 %)

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