

## Supplementary Information

### New Anti-Prelog Stereospecific Whole-Cell Biocatalyst for Asymmetric Reduction of Prochiral Ketones

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**Figure S1.** 16S rDNA sequence of *B. cereus* TQ-2

**Figure S2.** The gene sequence of *gyrB* gene in *B. cereus* TQ-2

**Figure S3.** MALDI-TOF mass spectrum of *B. cereus* TQ-2 proteins for microbial identification

**Figure S4.** Consumption of substrate in reaction with longer reaction time.

**Table S1.** The blast result of *B. cereus* TQ-2 16S rDNA sequence

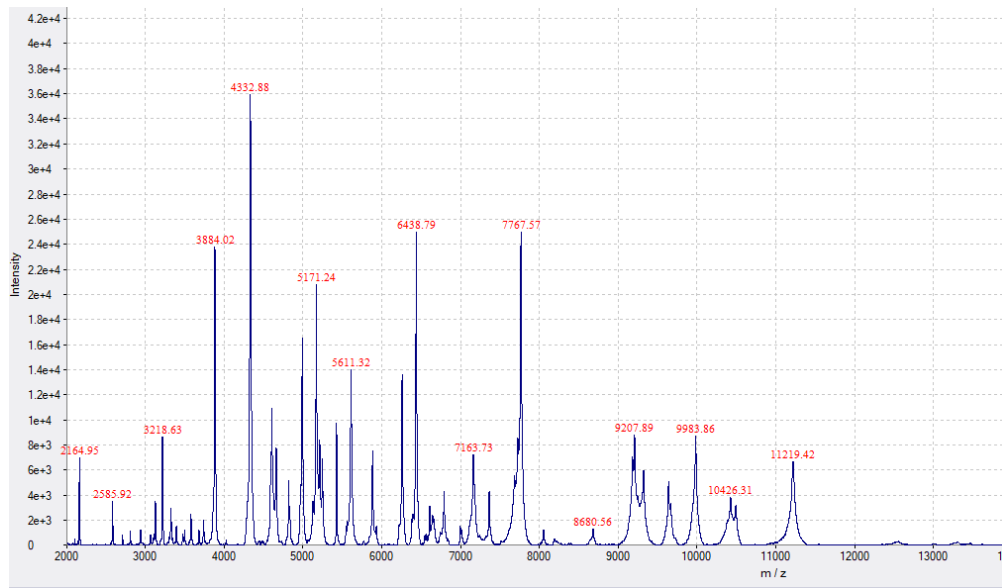
**Table S2.** The Blast result of *gyrB* gene from *B. cereus* TQ-2

TGCAAGTCGAGCGAATGGATTAAGAGCTTGCTCTTATGAAGTTAGCGGCGGACGGGTGAGTAACACG  
TGGGTAACCTGCCATAAGACTGGGATAACTCCGGGAAACCGGGGCTAATACCGGATAACATTTTGA  
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GAACAAGTGCTAGTTGAATAAGCTGGCACCTTGACGGTACCTAACCAGAAAAGCCACGGCTAACTACG  
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ACTTGAGTGCAGAAGAGGAAAAGTGGAATTCATGTGTAGCGGTGAAATGCGTAGAGATATGGAGGA  
ACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAAGTACACTGAGGCGCGAAAGCGTGGGGAGCAAA  
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TTTAGTGCTGAAGTTAACGCATTAAGCACTCCGCCTGGGGAGTACGGCCGCAAGGCTGAAACTCAAA  
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ACCAGGTCTTGACATCCTCTGAAAACCCTAGAGATAGGGCTTCTCCTTCGGGAGCAGAGTGACAGGT  
GGTGCATGGTTGTCGTGAGCTCGTGTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCAACCCCTT  
GATCTTAGTTGCCATCATTAAGTTGGGCACTCTAAGGTGACTGCCGGTGACAAACCGGAGGAAGGTG  
GGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACACGTGCTACAATGGACGGTACAA  
AGAGCTGCAAGACCGCGAGGTGGAGCTAATCTCATAAAACCGTTCTCAGTTCGGATTGTAGGCTGCA  
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TGGAGCCAGCCGCCTAAGGTGACA

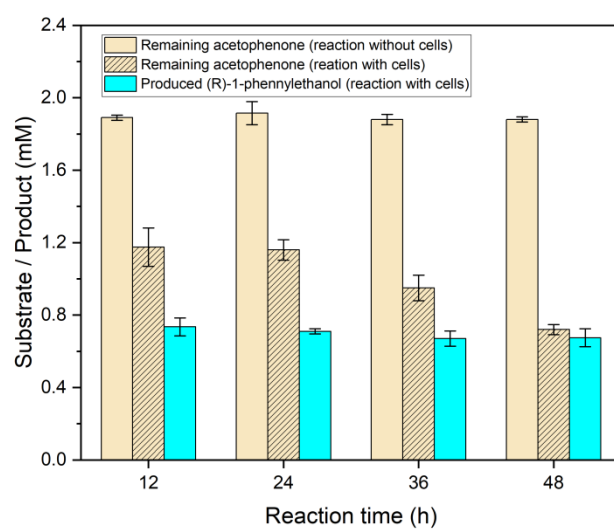
**Figure S1.** 16S rDNA sequence of *B. cereus* TQ-2

TAATTGGTGAACCACGATCAAACAGGAACAATAACTCGCTTTAAGCCGGATCCAGAGA  
TTTTTAAAGAGACGACAGAATATGAATTTGATACGTTAGCGACTCGTATGCGTGAATTA  
GCATTTTTAAATCGTAATATTAAATTAACAATTGAAGATAAGCGTGAACATAAGCAAA  
AGAAAGAATTCCATTATGAAGGTGGAATTAAATCATATGTTGAGCTATTTAAATCGCTC  
AAAATAACCGAATTCATGAAGAGCCTGTGTATGTAGAAGGGTCAAAAGATGGTATTC  
AAGTTGAGGTTTCCTTGCAGTATAACGAAGGATATACAAATAATTTACTCATTTACG  
AATAACATCATACGTATGAA

**Figure S2.** The gene sequence of *gyrB* gene in *B. cereus* TQ-2



**Figure S3.** MALDI-TOF mass spectrum of *B. cereus* TQ-2 strain proteins for microbial identification



**Figure S4.** Consumption of substrate in reaction with longer reaction time. Reactions without whole-cell biocatalyst were performed as control for comparison.

**Table S1.** The blast result of *B. cereus* TQ-2 16S rDNA sequence

Rank	Name	Strain	Accession	Pairwise Similarity (%)	Mismatch/Total nt
1	<i>Bacillus cereus</i>	ATCC 14579	AE016877	99.86014	2/1430
2	<i>Bacillus wiedmannii</i>	FSL W8-0169	LOBC01000053	99.79021	3/1430
3	<i>Bacillus paramycoides</i>	NH24A2	MAOI01000012	99.79021	3/1430
4	<i>Bacillus paranthracis</i>	Mn5	MACE01000012	99.79021	3/1430
5	<i>Bacillus albus</i>	N35-10-2	MAOE01000087	99.79021	3/1430
6	<i>Bacillus luti</i>	TD41	MACI01000041	99.79021	3/1430
7	<i>Bacillus nitratreducens</i>	4049	KJ812430	99.79021	3/1430
8	<i>Bacillus proteolyticus</i>	TD42	MACH01000033	99.72028	4/1430
9	<i>Bacillus tropicus</i>	N24	MACG01000025	99.72028	4/1430
10	<i>Bacillus anthracis</i>	Ames	AE016879	99.72028	4/1430
11	<i>Bacillus pacificus</i>	EB422	KJ812450	99.65035	5/1430
12	<i>Bacillus toyonensis</i>	BCT-7112	CP006863	99.58042	6/1430
13	<i>Bacillus mobilis</i>	0711P9-1	MACF01000036	99.58042	6/1430
14	<i>Bacillus pseudomycoides</i>	DSM 12442	ACMX01000133	99.44056	8/1430
15	<i>Bacillus mycoides</i>	DSM 2048	ACMU01000002	99.37063	9/1430
16	<i>Bacillus cytotoxicus</i>	NVH 391-98	CP000764	97.83217	31/1430
17	<i>Bacillus oryzaecorticis</i>	R1	KF548480	96.28623	41/1104
18	<i>Bacillus tianshenii</i>	YIM M13235	KF811034	95.51507	64/1427
19	<i>Bacillus marisflavi</i>	JCM 11544	LGUE01000011	95.44818	65/1428
20	<i>Bacillus halmapalus</i>	DSM 8723	KV917375	95.37491	66/1427

**Table S2.** The Blast result of *gyrB* gene from *B. cereus* TQ-2

Accession	Description	Max Score	Total Score	Query Cover (%)	E value	Per. Ident. (%)
AF136388.1	<i>Bacillus cereus</i> strain H2 gyrase B subunit ( <i>gyrB</i> ) gene, partial cds	529	529	99	4.00E-146	92.72
CP015589.1	<i>Bacillus cereus</i> strain AR156, complete genome	523	523	99	2.00E-144	92.45
CP045777.1	<i>Bacillus paranthracis</i> strain CFSAN068816 chromosome, complete genome	518	518	99	9.00E-143	92.18
CP026375.1	<i>Bacillus cereus</i> ATCC 10987 chromosome	518	518	99	9.00E-143	92.18
CP026376.1	<i>Bacillus cereus</i> strain G9241 chromosome	518	518	99	9.00E-143	92.18
CP023726.1	<i>Bacillus cereus</i> strain BHU2 chromosome	518	518	99	9.00E-143	92.18
CP023179.1	<i>Bacillus cereus</i> strain CC-1 chromosome, complete genome	518	518	99	9.00E-143	92.18
CP016316.1	<i>Bacillus cereus</i> strain M3, complete sequence	518	518	99	9.00E-143	92.18
CP020937.1	<i>Bacillus cereus</i> strain BC-AK genomic sequence	518	518	99	9.00E-143	92.18
CP009590.1	<i>Bacillus cereus</i> G9241, complete genome	518	518	99	9.00E-143	92.18
CP009369.1	<i>Bacillus cereus</i> strain FM1, complete genome	518	518	99	9.00E-143	92.18