Efficient conversion of hemicellulose into high-value product and electric power by enzyme-engineered bacterial consortia

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Supplementary Table 1. Strains and plasmids used in this study.

name	Relevant genotype	Source
Strains		
E. coli DH5α	F^- λ^- *recA1* Δ (*lacZYA-argF*) *U169 hsdR17 thi-1 gyrA96 supE44 endA1 relA1* Φ80*lacZ*ΔM15	Invitrogen
E. coli BL21 (DE3)	F^- *ompT gal dcm lon hsdSB* (rB^- mB^-) λ(DE3)	Invitrogen
E. coli BL21 (DE3) Δ*xylAB*	F^- *ompT gal dcm lon hsdSB* (rB^- mB^-) λ(DE3) Δ *xylAB*	This study
TtGH8	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-01	This study
SXA	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-02	This study
TtGH8-SXA	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-03	This study
E. coli-TtGH8	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-04	This study
E. coli-SXA	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-05	This study
E. coli-TtGH8-SXA	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-06	This study
XDH	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-07	This study
XylC	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-08	This study
XylD	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-09	This study
XylX	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-10	This study
KGSADH	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-11	This study
XylDK	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-12	This study
E. coli-XDH	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-13	This study
E. coli-XylC	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-14	This study
E. coli-XylD	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-15	This study
E. coli-XylX	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-16	This study
E. coli-KGSADH	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-17	This study
E. coli-XylDX	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-18	This study
E. coli-XylDK	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-19	This study
E. coli-XylDXK	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-20	This study
E. coli-Lac	*E. coli* BL21 (DE3) Δ*xylAB* /pYJ-21	This study
Plasmids		
pET-28a (+)	lacI; expression vector; T7 promoter; Km^r	Novagen
pRE112	suicide vector; Cm^r	Novagen
pYJ-00	pET-28a carrying *InaPb* from *Pseudomonas borealis*; Km^r	This study
pYJ-01	pET-28a carrying *TtGH8* from *Teredinibacter turnerae*; Km^r	This study
pYJ-02	pET-28a carrying *SXA* from *Selenominas ruminantium*; Km^r	This study
pYJ-03	pYJ-01 carrying *SXA* from *Selenominas ruminantium*; Km^r	This study
pYJ-04	pYJ-00 carrying *TtGH8* from *Teredinibacter turnerae*; Km^r	This study
pYJ-05	pYJ-00 carrying *SXA* from *Selenominas*	This study

	ruminantium; Km^r	
pYJ-06	pYJ-04 carrying *SXA* from *Selenominas ruminantium*; Km^r	This study
pYJ-07	pET-28a carrying *XDH* from *Caulobacter crescentus*; Km^r	This study
pYJ-08	pET-28a carrying *XylC* from *Caulobacter crescentus*; Km^r	This study
pYJ-09	pET-28a carrying *XylD* from *Caulobacter crescentus*; Km^r	This study
pYJ-10	pET-28a carrying *XylX* from *Caulobacter crescentus*; Km^r	This study
pYJ-11	pET-28a carrying *KGSADH* from *Caulobacter crescentus*; Km^r	This study
pYJ-12	pYJ-09 carrying *KGSADH* from *Caulobacter crescentus*; Km^r	This study
pYJ-13	pYJ-00 carrying *XDH* from *Caulobacter crescentus*; Km^r	This study
pYJ-14	pYJ-00 carrying *XylC* from *Caulobacter crescentus*; Km^r	This study
pYJ-15	pYJ-00 carrying *XylD* from *Caulobacter crescentus*; Km^r	This study
pYJ-16	pYJ-00 carrying *XylX* from *Caulobacter crescentus*; Km^r	This study
pYJ-17	pYJ-00 carrying *KGSADH* from *Caulobacter crescentus*; Km^r	This study
pYJ-18	pYJ-15 carrying *XylX* from *Caulobacter crescentus*; Km^r	This study
pYJ-19	pYJ-15 carrying *KGSADH* from *Caulobacter crescentus*; Km^r	This study
pYJ-20	pYJ-18 carrying *KGSADH* from *Caulobacter crescentus*; Km^r	This study
pYJ-21	pYJ-00 carrying *laccase* from *Bacillus subtilis*; Km^r	This study
pRE112-Δ*xylAB*	pRE112-Δ*xylAB* carrying upstream and downstream fragments of the *xylAB* from *E. coli* BL21 (DE3); Cm^r	This study

Supplementary Table 2. PCR primers used in this study.

Primer Name	Sequence (5'→3')
INP-F	CATGCCATGGGCATGAACGATGACAAAGTTTTGGT
INP-R	GGAATTCCATATGCACCGCTGTCTCCAGCGTT
pET-28a-F (TtGH8)	ATTCCGGATGGCGAACATCATCATCATCACCACTAAAGC AGCCATCATCATCATC
pET-28a-R (TtGH8)	CCCCGGCGGCGGGACCCATGCCCATGGTATATCTCCTTC T
TtGH8-1-F	GAAGGAGATATACCATGGGCATGGGTCCCGCCGCCGGG GC
TtGH8-1-R	GATGATGATGATGGCTGCTTTAGTGGTGATGATGATGAT GTTCGCCATCCGGAAT
pET-28a-F (SXA)	ACAAGGAGTTGGATCATCACCATCATCATCATTAAAGCA GCCATCATCATCATCA
pET-28a-R (SXA)	ACGGGATTCTGGATATTCATGCCCATGGTATATCTCCTTC
SXA-1-F	GAAGGAGATATACCATGGGCATGAATATCCAGAATCCCG T
SXA-1-R	TGATGATGATGATGGCTGCTTTAATGATGATGATGGTGAT GATCCAACTCCTTGT
pET-28a-TtGH8-F	TACAAGGAGTTGGATCATCACCATCATCATCATTAAAGC AGCCATCATCATCATCA
pET-28a-TtGH8-R	ACGGGATTCTGGATATTCATGGATCCTTCGCCATCCGGA ATCCAGG
SXA-2-F	CCTGGATTCCGGATGGCGAAGGATCCATGAATATCCAGA ATCCCGT
SXA-2-R	TGATGATGATGATGGCTGCTTTAATGATGATGATGGTGAT GATCCAACTCCTTGTA
pET-28a-INP-F (TtGH8)	TGGATTCCGGATGGCGAACATCATCATCATCACCACTAA GGATCCGAATTCGAGCTCCG
pET-28a-INP-R (TtGH8)	GCCCCGGCGGCGGGACCCATCATATGCACCGCTGTCTCC AGCGTTT
TtGH8-2-F	AAACGCTGGAGACAGCGGTGCATATGATGGGTCCCGCC GCCGGGGC
TtGH8-2-R	CGGAGCTCGAATTCGGATCCTTAGTGGTGATGATGATGA TGTTCGCCATCCGGAATCCA
pET-28a-INP-F (SXA)	TACAAGGAGTTGGATCATCACCATCATCATCATTAAGCT AGCATGACTGGTGGACA
pET-28a-INP-R (SXA)	ACGGGATTCTGGATATTCATCATATGCACCGCTGTCTCCA GCGTTT
SXA-3-F	AAACGCTGGAGACAGCGGTGCATATGATGAATATCCAG AATCCCGT
SXA-3-R	TGTCCACCAGTCATGCTAGCTTAATGATGATGATGGTGA TGATCCAACTCCTTGTA

pET-28a-INP-TtGH8-F	TCATCACCATCATCATCATTAAGAATTCGAGCTCCGTCGACA
pET-28a-INP-TtGH8-R	ACGGGATTCTGGATATTCATGGATCCTTCGCCATCCGGAATCCAGG
SXA-4-F	CCTGGATTCCGGATGGCGAAGGATCCATGAATATCCAGAATCCCGT
SXA-4-R	TGTCGACGGAGCTCGAATTCTTAATGATGATGATGGTGAT
pET-28a-F (XDH)	ACCACCACCACCACCACTAAAGCAGCCATCATCATCATCATCACAGCAGCGG
pET-28a-R (XDH)	GGATAGATGGCTGAGGACATGCCCATGGTATATCTCCTTC
XDH-1-F	GAAGGAGATATACCATGGGCATGTCCTCAGCCATCTATCC
XDH-1-R	TGATGATGATGATGGCTGCTTTAGTGGTGGTGGTGGTGGTGACGCCAGCCG
pET-28a-F (XylC)	ACCACCACCACCACCACTAAAGCAGCCATCATCATCATCATCACAGCAGCGG
pET-28a-R (XylC)	CAAGTGACTTGAGCGGTCATGCCCATGGTATATCTCCTTC
XylC-1-F	GAAGGAGATATACCATGGGCATGACCGCTCAAGTCACTTG
XylC-1-R	TGATGATGATGATGGCTGCTTTAGTGGTGGTGGTGGTGGTGGACAAGGCGG
pET-28a-F(XylD)	AATTACCTCGTCATAATCATCACCACCACCACCACCACTAAAGCAGCCATCATCATCAT
pET-28a-F(XylD)	TTACTTAATGCACTACGCATGCCCATGGTATATCTCCTTC
XylD-1-F	GAAGGAGATATACCATGGGCATGCGTAGTGCATTAAGTAA
XylD-1-R	ATGATGATGATGGCTGCTTTAGTGGTGGTGGTGGTGGTGATGATTATGACGAGGTAATT
pET-28a-F(XylX)	TTGCGGGACGTGGGCTTCTGCACCACCACCACCACCACCACTAAAGCAGCCATCATCATCAT
pET-28a-R(XylX)	AGAAACTCGCTTACACCCACGCCCATGGTATATCTCCTTC
XylX-1-F	GAAGGAGATATACCATGGGCGTGGGTGTAAGCGAGTTTCT
XylX-1-R	ATGATGATGATGGCTGCTTTAGTGGTGGTGGTGGTGGTGCAGAAGCCCACGTCCCGCAA
pET-28a-F(KGSADH)	AAACCAGTTATAGTTGGAGTCACCACCACCACCACCACTAAAGCAGCCATCATCATCAT
pET-28a-R(KGSADH)	TGACGTAATGTATCTGTCATGCCCATGGTATATCTCCTTC
KGSADH-1-F	GAAGGAGATATACCATGGGCATGACAGATACATTACGTCA

KGSADH-1-R	ATGATGATGATGGCTGCTTTAGTGGTGGTGGTGGTGGTG ACTCCAACTATAACTGGTTT
pET-28a-XylD-F	AGTTATAGTTGGAGTCACCACCACCACCACCACTAAAG CAGCCATCATCATCATCATCA
pET-28a-XylD-R	TGACGTAATGTATCTGTCATAGATCTATGATTATGACGAG GTAATT
KGSADH-2-F	AATTACCTCGTCATAATCATAGATCTATGACAGATACATT ACGTCA
KGSADH-2-R	TGATGATGATGATGATGGCTGCTTTAGTGGTGGTGGTGG TGGTGACTCCAACTATAACT
pET-28a-INP-F(XDH)	ATCGACGCCGGCTGGCGTCACCACCACCACCACCACTA AGCTAGCATGACTGGTGGACA
pET-28a-INP-R(XDH)	GGATAGATGGCTGAGGACATCATATGCACCGCTGTCTCC A
XDH-2-F	TGGAGACAGCGGTGCATATGATGTCCTCAGCCATCTATC C
XDH-2-R	TGTCCACCAGTCATGCTAGCTTAGTGGTGGTGGTGGTGG TGACGCCAGCCGGCGTCGAT
pET-28a-INP-F(XylC)	CATGAGGTCCGCCTTGTCCACCACCACCACCACCACTA AGCTAGCATGACTGGTGGACA
pET-28a-INP-R(XylC)	CAAGTGACTTGAGCGGTCATCATATGCACCGCTGTCTCC AGCGTTT
XylC-2-F	AAACGCTGGAGACAGCGGTGCATATGATGACCGCTCAA GTCACTTG
XylC-2-R	TGTCCACCAGTCATGCTAGCTTAGTGGTGGTGGTGGTGG TGGACAAGGCGGACCTCATG
pET-28a-INP-F(XylD)	CCTCGTCATAATCATCACCACCACCACCACCACTAAGCT AGCATGACTGGTGGACA
pET-28a-INP-R(XylD)	TTACTTAATGCACTACGCATCATATGCACCGCTGTCTCCA GCGTTT
XylD-2-F	AAACGCTGGAGACAGCGGTGCATATGATGCGTAGTGCA TTAAGTAA
XylD-2-R	TGTCCACCAGTCATGCTAGCTTAGTGGTGGTGGTGGTGG TGATGATTATGACGAGG
pET-28a-INP-F(XylX)	GGACGTGGGCTTCTGCACCACCACCACCACCACTAAGC TAGCATGACTGGTGGACA
pET-28a-INP-R(XylX)	AGAAACTCGCTTACACCCACCATATGCACCGCTGTCTCC AGCGTTT
XylX-2-F	AAACGCTGGAGACAGCGGTGCATATGGTGGGTGTAAGC GAGTTTCT
XylX-2-R	TGTCCACCAGTCATGCTAGCTTAGTGGTGGTGGTGGTGG TGCAGAAGCCCACGTCC
pET-28a-INP-F(KGSADH)	AGTTATAGTTGGAGTCACCACCACCACCACCACTAAGCT AGCATGACTGGTGGACA

pET-28a-INP-R(KGSADH)	TGACGTAATGTATCTGTCATCATATGCACCGCTGTCTCCAGCGTTT
KGSADH-2-F	AAACGCTGGAGACAGCGGTGCATATGATGACAGATACATTACGTCA
KGSADH-2-R	TGTCCACCAGTCATGCTAGCTTAGTGGTGGTGGTGGTGGTGACTCCAACTATAACT
pET-28a-INP-XylD-F(XylX)	GGACGTGGGCTTCTGCACCACCACCACCACCACTAAGCTAGCATGACTGGTGGACA
pET-28a-INP-XylD-R(XylX)	AGAAACTCGCTTACACCCACGGATCCATGATTATGACGAGGTAATT
XylX-3-F	AATTACCTCGTCATAATCATGGATCCGTGGGTGTAAGCGAGTTTCT
XylX-3-R	TGTCCACCAGTCATGCTAGCTTAGTGGTGGTGGTGGTGGTGCAGAAGCCCACGTCC
pET-28a-INP-XylD-F(KGSADH)	AGTTATAGTTGGAGTCACCACCACCACCACCACTAAGCTAGCATGACTGGTGGACA
pET-28a-INP-XylD-R(KGSADH)	TGACGTAATGTATCTGTCATAGATCTATGATTATGACGAGGTAATT
KGSADH-3-F	AATTACCTCGTCATAATCATAGATCTATGACAGATACATTACGTCA
KGSADH-3-R	TGTCCACCAGTCATGCTAGCTTAGTGGTGGTGGTGGTGGTGACTCCAACTATAACT
pET-28a-INP-XylD-KGSADH-F	TTGCGGGACGTGGGCTTCTGAGATCTATGACAGATACATTACGTCA
pET-28a-INP-XylD-KGSADH-R	AGAAACTCGCTTACACCCACAGATCTATGATTATGACGAGGTAATT
XylX-4-F	AATTACCTCGTCATAATCATAGATCTGTGGGTGTAAGCGAGTTTCT
XylX-4-R	TGACGTAATGTATCTGTCATAGATCTCAGAAGCCCACGTCCCGCAA
XylAB-Up-F	TCGATATCGCATGCGGTACCCGCTGAGTAATAATGTCGCATTCCA
XylAB-Up-R	GATTATGGAGTTCAATACGTTATCCCCTGCCTGACC
XylAB-Down-F	GGGATAACGTATTGAACTCCATAATCAGGTAATGCCG
XylAB-Down-R	CCAAGCTTCTTCTAGAGGTACCGAACAGCTTGGCGTTGTTATCTACC
XylAB-1-F	ACGATCTCCATATCTACCAGC
XylAB-1-R	CGCGGCATTACCTGATTATG

Supplementary Table 3. The estimated number of enzyme molecule on surface of per cell based on activities of purified INP-fused enzymes and bacterial strains. $n = 3$ biologically independent experiments. Data are presented as mean ± SD. Source data are provided as a Source Data file.

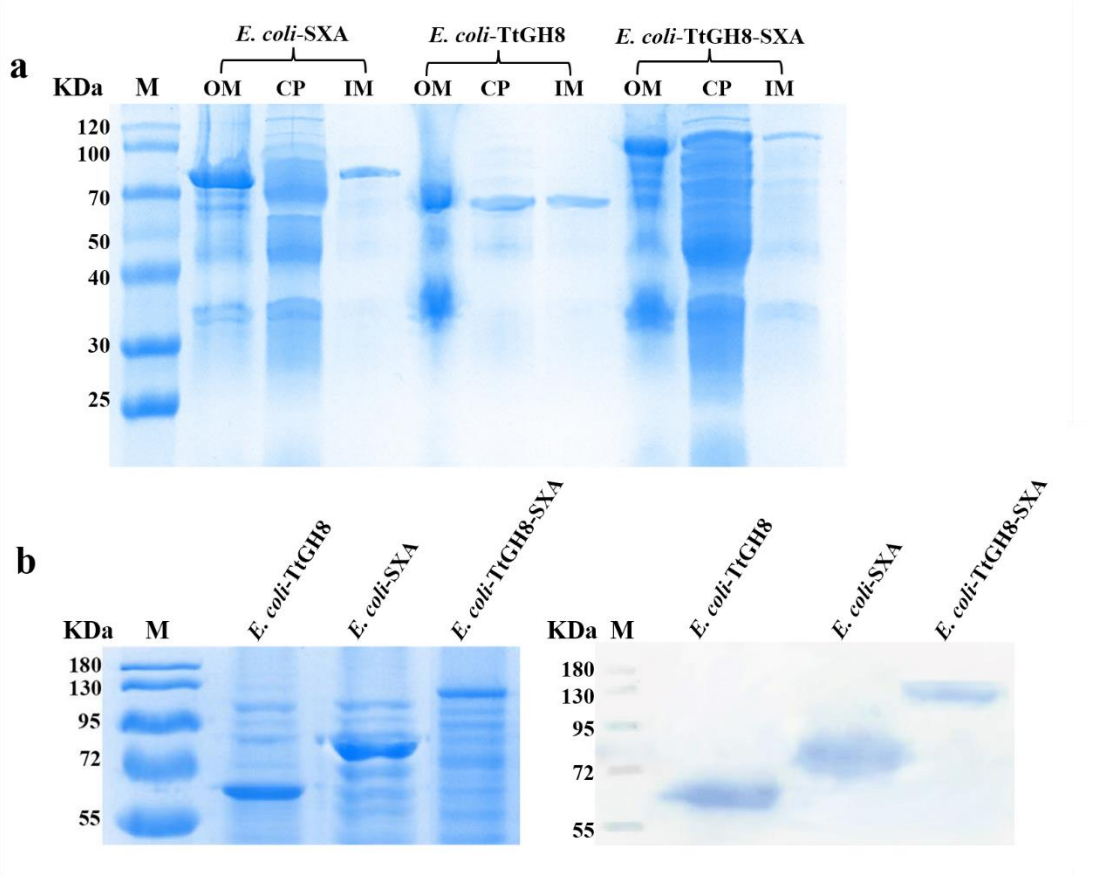
Strains	Whole-cell activity (U/OD_{600})	Purified enzyme activity (U/mg)
E. coli-TtGH8	0.070 ± 0.003	40.80 ± 0.32
E. coli-SXA	14.65 ± 0.22	6250.00 ± 18.60
E. coli-TtGH8-SXA	1.19 ± 0.02	589.71 ± 1.26
E. coli-XDH	1.25 ± 0.04	1195.00 ± 8.60
E. coli-XylC	0.17 ± 0.008	146.93 ± 2.16
E. coli-XylD	0.16 ± 0.005	77.00 ± 3.00
E. coli-KGSADH	0.084 ± 0.003	54.00 ± 6.00
E. coli-XylX	0.044 ± 0.003	35.65 ± 0.25
E. coli-XylDK[a]	0.14 ± 0.005	40.84 ± 0.57

[a] The activity of fusion protein INP-XylD-KGSADH was expressed by the activity of INP-KGSADH.

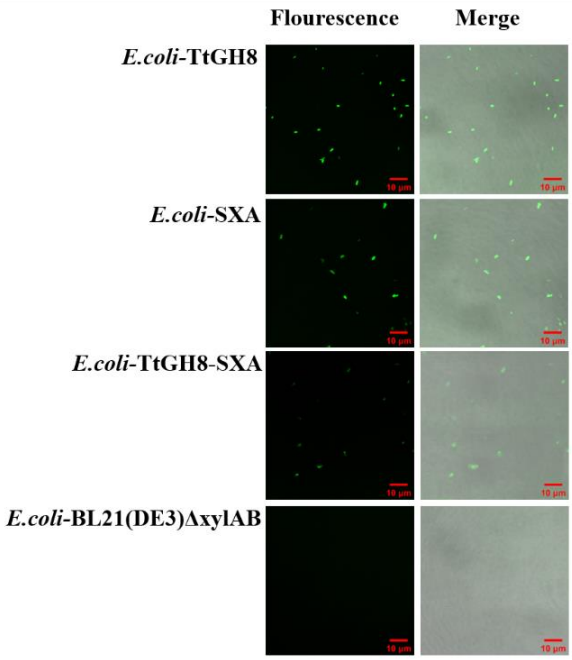
The amounts of enzymes that generate 1 μmol product per min is defined as 1 U.

Supplementary Table 4. Kinetic parameters of enzymes displayed on the surface of bacterial strains. Source data are provided as a Source Data file.

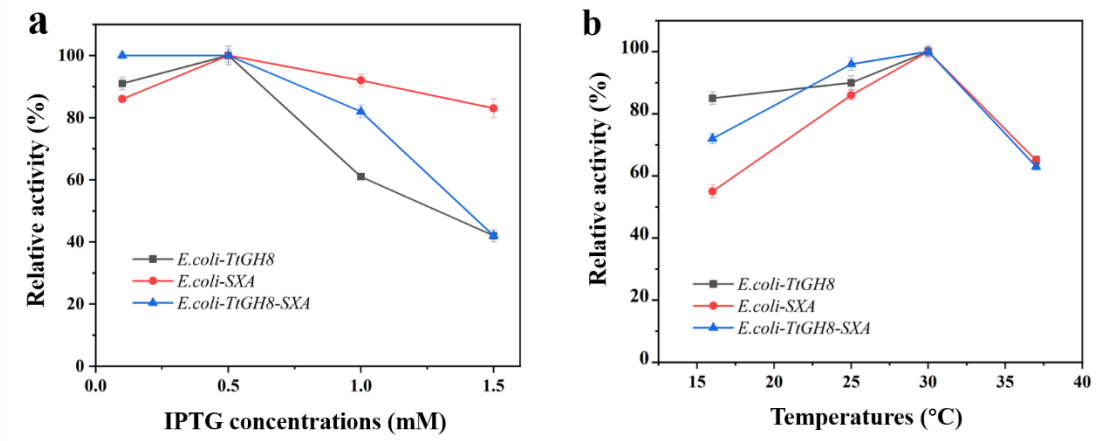
Strain	Substrate	K_m (mM)	K_{cat} (s^{-1})	K_{cat}/K_m ($mM^{-1}·s^{-1}$)
E. coli-XDH	D-xylose	4.99 ± 0.19	11.34 ± 1.21	2.27
E. coli-XylC	D-xylono-lactone	4.79 ± 0.48	8.18 ± 0.30	1.71
E. coli-XylX	2-keto-3-deoxy-d-xylonate	1.72 ± 0.09	0.07 ± 0.006	0.04
E. coli-XylDK	D-xylonic acid	0.16 ± 0.01	3.89 ± 0.10	24.31



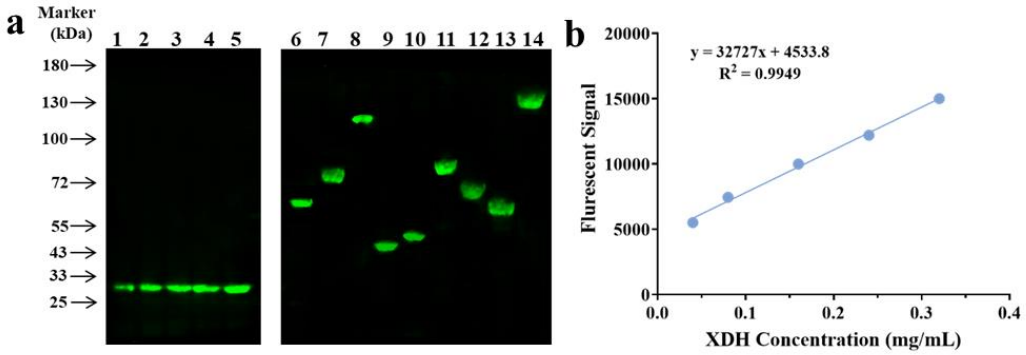
Supplementary Fig. 1. Analysis of up-stream involved proteins expressions and positions by protein electrophoresis. a SDS-PAGE analysis of different fractions of engineered strains *E. coli*-TtGH8, *E. coli*-SXA and *E. coli*-TtGH8-SXA. OM, outer membrane fraction; CP, cytoplasmic fraction; IM, inner membrane fraction. **b** SDS-PAGE (Left) and Western-Blot analysis (Right) of outer membrane fractions of engineered strains *E. coli*-TtGH8, *E. coli*-SXA and *E. coli*-TtGH8-SXA. The experiment was repeated three times independently with similar results. Source data are provided as a Source Data file.



Supplementary Fig. 2. Confirmation of different cell surface-displayed enzymes by confocal imaging. The experiment was repeated three times independently with similar results. Source data are provided as a Source Data file.



Supplementary Fig. 3. Relative activities of whole-cell catalysts involving in the up-stream pathway under different inducer concentrations (a) and expressed temperatures (b). The whole-cell catalysts were *E. coli*-TtGH8 (black line), *E. coli*-SXA (red line) and *E. coli*-TtGH8-SXA (blue line). n = 3 biologically independent experiments. Data are presented as mean ± SD. Source data are provided as a Source Data file.

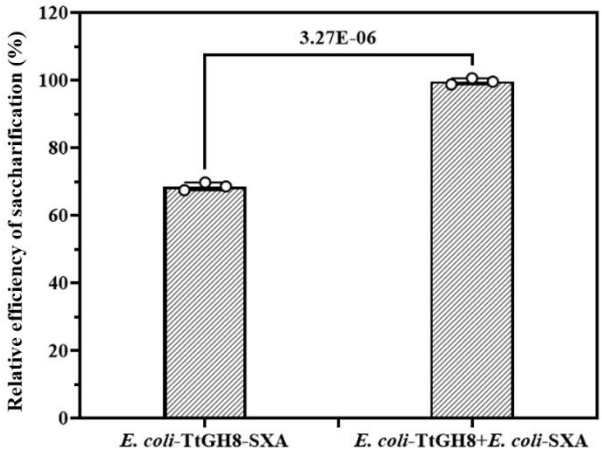


c

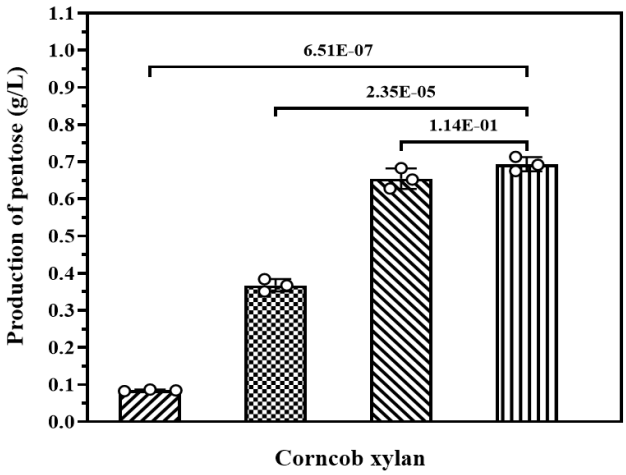
Strains	Flurescent signal	Protein content (g)	Enzyme Mw (Da)	OD_{600}	Cell number	Estimated displayed enzyme number[a]
E. coli-TtGH8	12900	5.11×10^{-6}	64030	58.80	1.88×10^{9}	25560
E. coli-SXA	11900	4.50×10^{-6}	79970	41.85	1.34×10^{9}	25300
E. coli-TtGH8-SXA	12200	4.68×10^{-6}	126000	38.50	1.23×10^{9}	18020
E. coli-XDH	9060	2.77×10^{-6}	45470	51.20	1.64×10^{9}	22590
E. coli-XylC	9070	2.77×10^{-6}	50410	49.36	1.58×10^{9}	21130
E. coli-XylD	10800	3.83×10^{-6}	83460	38.60	1.24×10^{9}	22490
E. coli-KGSADH	10100	3.40×10^{-6}	69410	42.30	1.35×10^{9}	21920
E. coli-XylX	10100	3.40×10^{-6}	59230	41.80	1.34×10^{9}	25950
E. coli-XylDK	14900	6.33×10^{-6}	134870	39.76	1.27×10^{9}	22200

Supplementary Fig. 4. Quantitative Western blot analysis of outer membrane proteins of recombinant strains. a Fluorescent signals generated for each proteins. Lane 1, XDH purified protein (0.04 mg/mL); Lane 2, XDH purified protein (0.08 mg/mL); Lane 3, XDH purified protein (0.16 mg/mL); Lane 4, XDH purified protein (0.24 mg/mL); Lane 5, XDH purified protein (0.32 mg/mL); Lane 6, *E. coli*-TtGH8 outer membrane protein; Lane 7, *E. coli*-SXA outer membrane protein; Lane 8, *E. coli*-TtGH8-SXA outer membrane protein; Lane 9, *E. coli*-TtGH8-SXA outer membrane protein; Lane 10, *E. coli*-XDH outer membrane protein; Lane 11, *E. coli*-XylC outer membrane protein; Lane 12, *E. coli*-XylD outer membrane protein; Lane 13, *E. coli*-KGSADH outer membrane protein; Lane 14, *E. coli*-XylX outer membrane protein; Lane 14, *E. coli*-XylDK outer membrane protein. **b** A standard curve of signal versus known concentrations of purified XDH. c Summary table of data generated from nine samples. Source data are provided as a Source Data file.

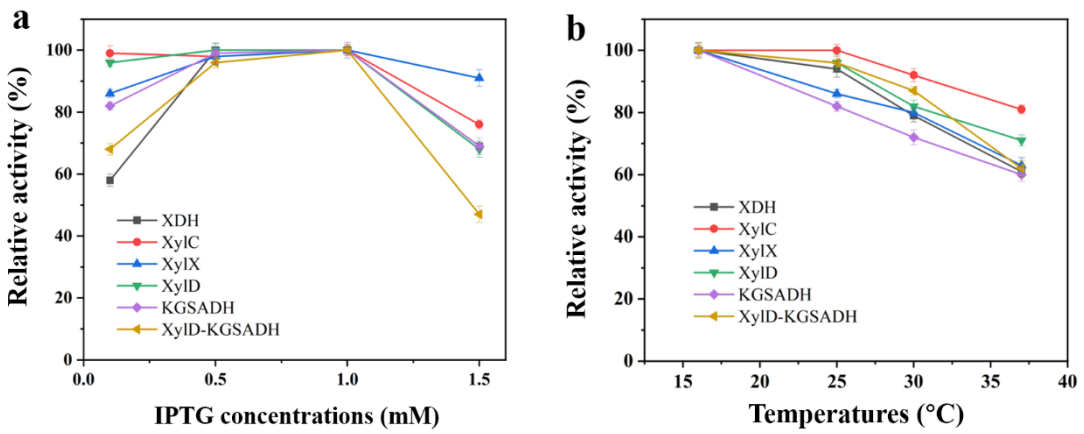
[a] Displayed enzyme number=Protein content/Enzyme Mw/Cell number × N_A. N_A: Avogadro's constant (6.02×10^{23} mol^{-1}).



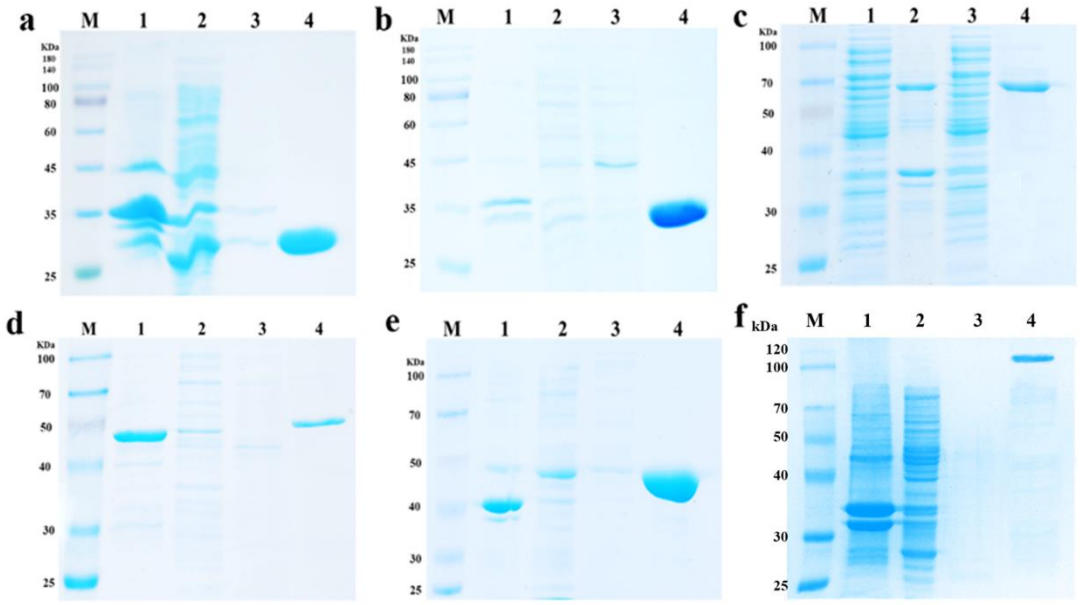
Supplementary Fig. 5. Relative saccharification efficiency towards corncob xylan using enzyme-displaying strains as catalysts. n = 3 biologically independent experiments. Data are presented as mean ± SD. The statistical significance is determined by a two-sided t test, and ***, **, * indicate P<0.001, 0.01, and 0.05, respectively. Source data are provided as a Source Data file.



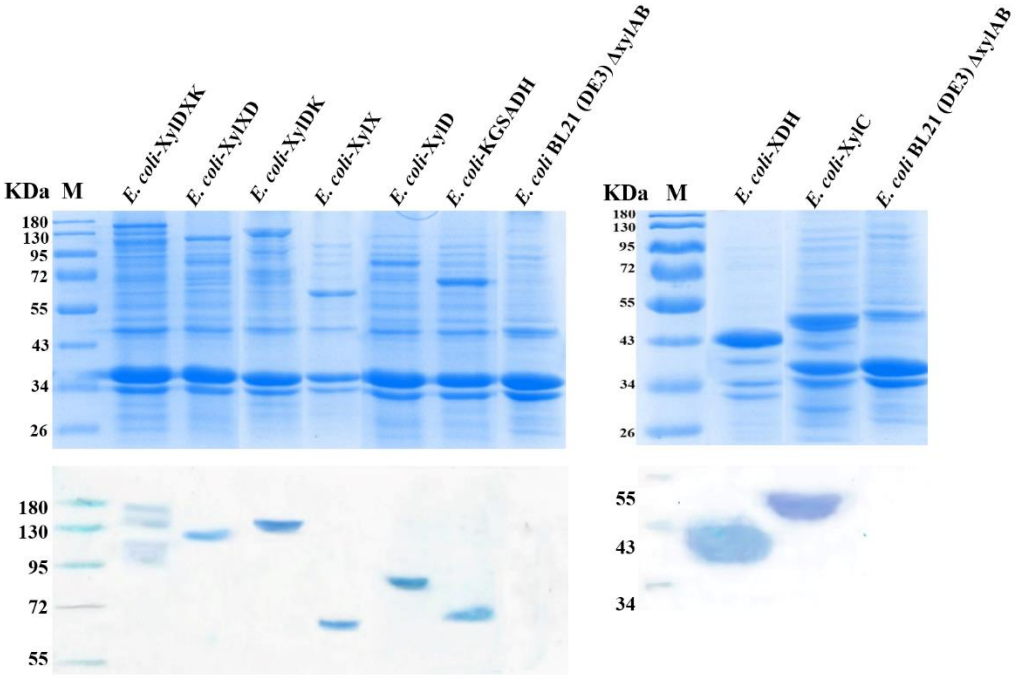
Supplementary Fig. 6. Production of pentose towards from corncob xylan catalyzed by bacterial consortia containing *E. coli*-TtGH8 and *E. coli*-SXA with the cell density ratio of 3:7. The concentrations of corncob xylan were 0.1 g/L (▨), 0.5 g/L (▩), 1 g/L (▧) and 2 g/L (▥). n = 3 biologically independent experiments. Data are presented as mean ± SD. The statistical significance is determined by a two-sided t test, and ***, **, * indicate P<0.001, 0.01, and 0.05, respectively. Source data are provided as a Source Data file.



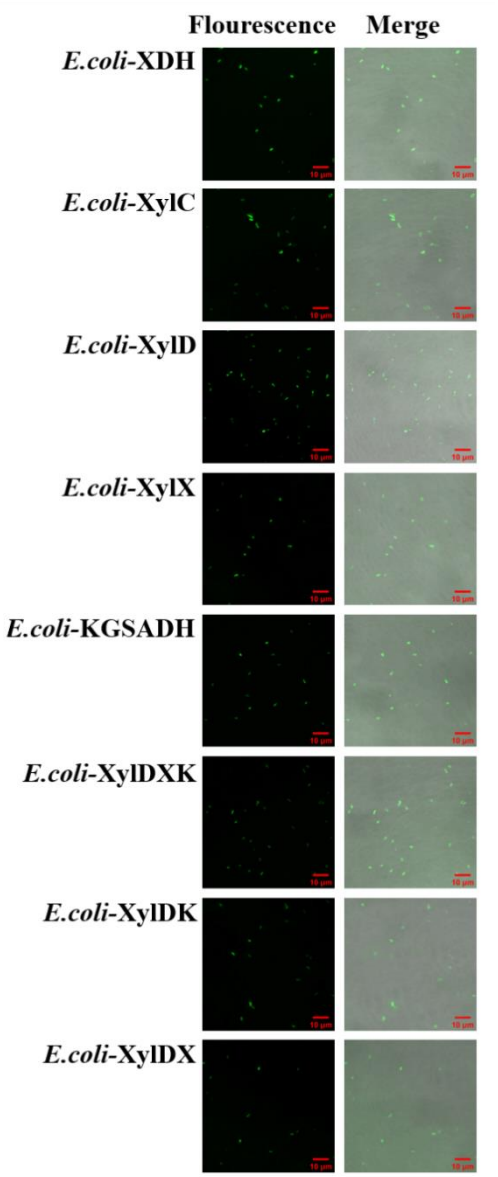
Supplementary Fig. 7. Relative activities of intracellular enzymes under different inducer concentrations (a) and expressed temperatures (b). The enzymes were XDH (black line), XylC (red line), XylX (blue line), XylD (green line), KGSADH (purple line) and XylDK (yellow line). *n* = 3 biologically independent experiments. Data are presented as mean ± SD. Source data are provided as a Source Data file.



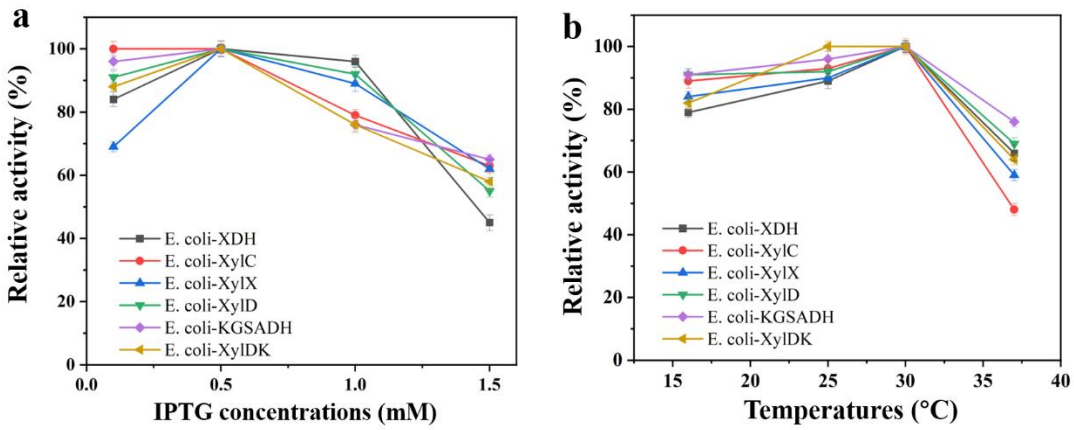
Supplementary Fig. 8. SDS-PAGE analysis of purification of XDH (a), XylC (b), XylD (c), KGSADH (d), XylX (e) and XylD-KGSADH protein (f). Lane 1, precipitation fractions; Lane 2, flow fractions; Lane 3, 50 mM imidazole elution; Lane 4, 200 mM imidazole elution. The experiment was repeated three times independently with similar results. Source data are provided as a Source Data file.



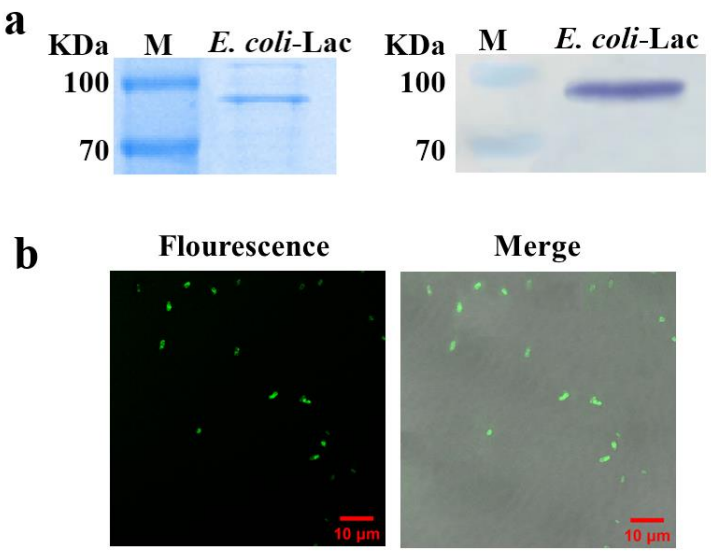
Supplementary Fig. 9. SDS-PAGE (upper) and Western-Blot analysis (down) of outer membrane fractions of engineered strains *E. coli*-XDH, *E. coli*-XylC, *E. coli*-XylD, *E. coli*-XylX, *E. coli*-KGSADH, *E. coli*-XylDK, *E. coli*-XylXD, *E. coli*-XylDXK. The experiment was repeated three times independently with similar results. Source data are provided as a Source Data file.



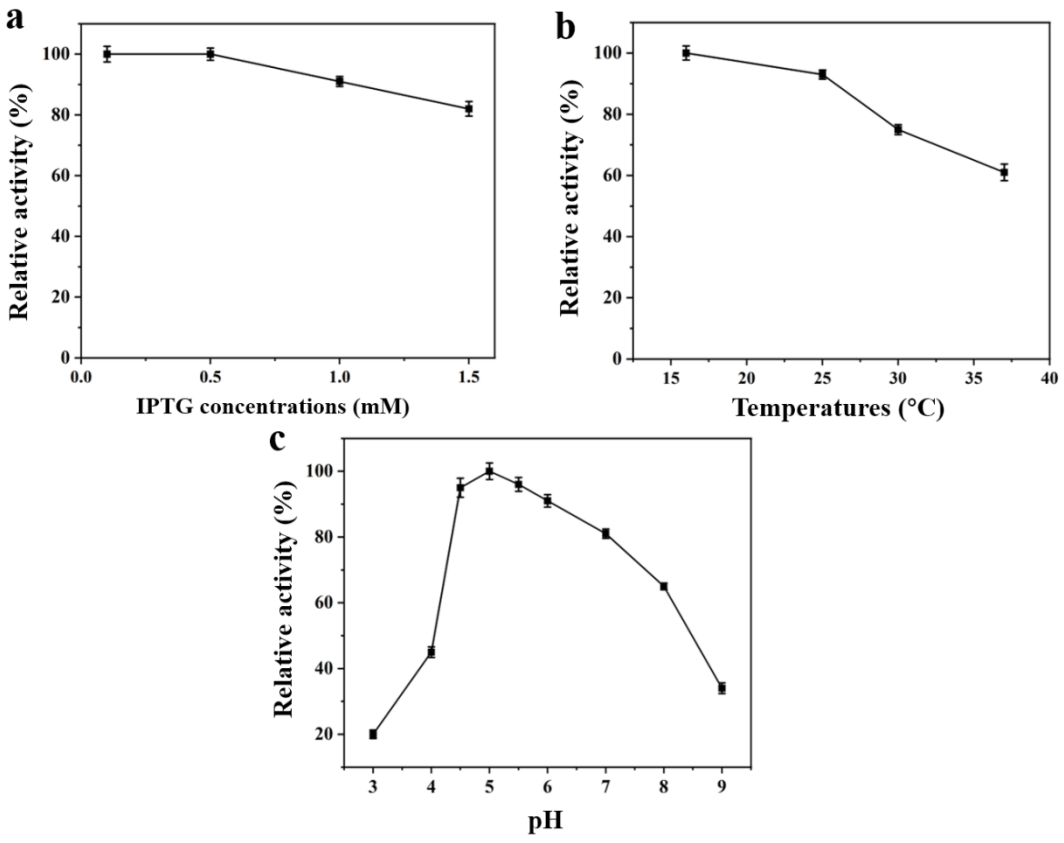
Supplementary Fig. 10. Confirmation of cell surface-displayed enzymes by confocal imaging. The experiment was repeated three times independently with similar results. Source data are provided as a Source Data file.



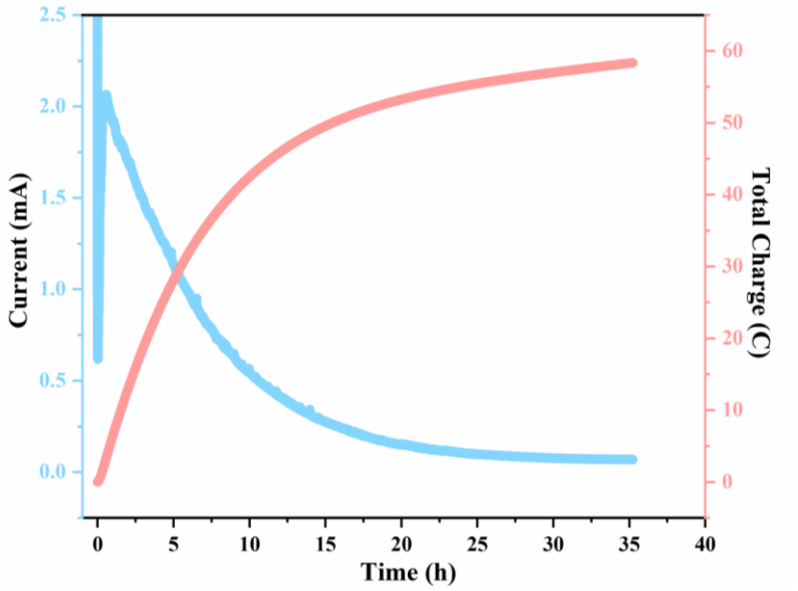
Supplementary Fig. 11. Relative activities of whole-cell catalysts involving in the down-stream pathway under different inducer concentrations (a) and expressed temperatures (b). The whole-cell catalysts were *E. coli*-XDH (black line), *E. coli*-XylC (red line), *E. coli*-XylX (blue line), *E. coli*-XylD (green line), *E. coli*-KGSADH (purple line) and *E. coli*-XylDK (yellow line). n = 3 biologically independent experiments. Data are presented as mean ± SD. Source data are provided as a Source Data file.



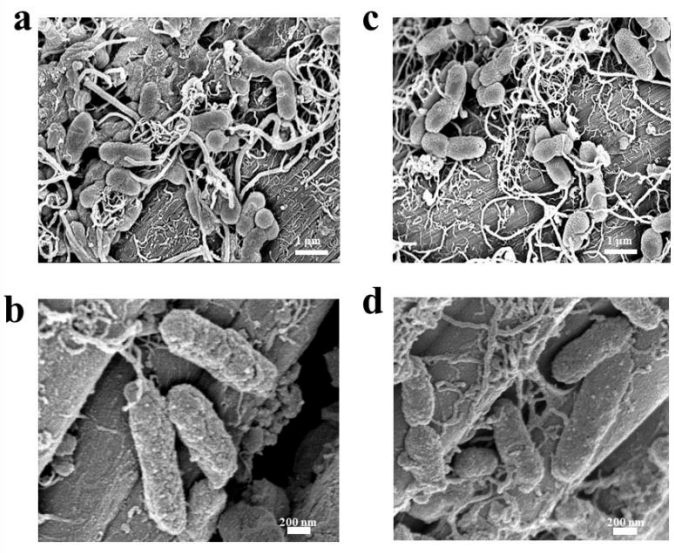
Supplementary Fig. 12. Confirmation of cell surface-displayed enzymes. a SDS-PAGE (Left) and Western-Blot (Right) analysis of outer membrane fractions of engineered strains *E. coli*-Lac. **b** Confocal imaging of engineered strains *E. coli*-Lac. The experiment was repeated three times independently with similar results. Source data are provided as a Source Data file.



Supplementary Fig. 13. Optimization of enzyme activity of whole cell catalyst of *E. coli*-Lac. a Effect of inducer concentration on enzyme activity of whole cell catalyst of *E. coli*-Lac. **b** Effect of expressed temperature on enzyme activity of whole cell catalyst of *E. coli*-Lac. **c** Effect of buffer pH on enzyme activity of whole-cell catalysts of Lac-*E. coli*. $n = 3$ biologically independent experiments. Data are presented as mean ± SD. Source data are provided as a Source Data file.



Supplementary Fig. 14. Profiles of the current produced (blue line) and the total charge (pink line) generated. Source data are provided as a Source Data file.



Supplementary Fig. 15. SEM images of CC/MWCNTs/*E. coli* consortia electrodes before use (a, b) and after 6 days' operation (c, d). The experiment was repeated three times independently with similar results. Source data are provided as a Source Data file.