Supporting Information

A green-by-design system for efficient bio-oxidation of an

unnatural hexapyranose into chiral lactone for building statin side-

chains

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LeADH_NADP_01.ps





Figure S1. Ramachandran plot and errat result of *Le*ADH homology structure.



Figure. S2 Spectra of size-exclusion chromatography on superdex 75, elution volume of *Le*ADH is 66.0 mL. Y = -12.955 ln(X) + 111.8 (Y: elution volume; X: molecular weight), the molecular weight determined to be 33 kDa.



Figure S3. Multiple sequence alignment of *Le*ADH with proteins from different sources. Conserved residues are shaded in red background. The catalytic residues are shown in blue stars. The schematic diagram of secondary structure of *Le*ADH is shown on the top of sequence. The α -helices, 3_{10} -helices and π -helices are displayed as medium, small and large squiggles respectively. β -strands are rendered as arrows, strict β -turns as TT letters and strict α -turns as TTT.



Figure S4. characterization of *Le*ADH. The optimum temperature of *Le*ADH was determined at different temperatures in the range of 20-50°C under standard conditions. The maximum activity was observed at around 35°C. The thermal stability of *Le*ADH was also examined by incubating the purified enzymes (0.1 mg/mL) at different temperatures for 15 min, and the residual activity was assayed. The results showed that T¹₅₀ of *Le*ADH and *Le*ADH_{V3} was 39.6°C and 40.1°C, respectively. The enzyme activity was determined under standard assay condition at various pH (7.0-11.0), the *Le*ADH displayed the highest activity at pH 9.0.



Figure S5. Stability of CTeHP and CTeHL in aqueous medium at various pH. 10 g L⁻¹ of CTeHP and CTeHL were incubated at 30 °C and sampled after 60 and 120 minutes. Data are relative values to the initial GC-FID area of the CTeHP and CTeHL peaks.

Table S1.Primers used in this work.

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LeADH_for	ACG <u>GAATTC</u> ATGTCACAAACTGTCTTT (<i>EcoR</i> I)
LeADH_rev	CCC <u>AAGCTT</u> TTACTTGGCTTCCACAA (<i>Hind</i> III)
85&87_for	CTTCACACAGCATCACCC <u>NDT</u> GTT <u>NDT</u> AAGACCACAGATGTTGAA
85&87_rev	TTCAACATCTGTGGTCTT <u>AHN</u> AAC <u>AHN</u> GGGTGATGCTGTGTGAAG
127&128_for	ACGTTGTGGTTACTTCTTCT <u>NDTNDT</u> ACAATGTTTAATTCCGTAGC
127&128_rev	GCTACGGAATTAAACATTGT <u>AHNAHN</u> AGAAGAAGTAACCACAACGT
129&131_for	TGGTTACTTCTTCTGTTGTC <u>NDT</u> ATG <u>NDT</u> AATTCCGTAGCTGCACCCG
129&131_rev	CGGGTGCAGCTACGGAATT <u>AHN</u> CAT <u>AHN</u> GACAACAGAAGAAGTAACCA
161&162_for	ACACATTGAAGAATCCT <u>NDTNDT</u> TACGGATACCCAGCATC
161&162_rev	GATGCTGGGTATCCGTA <u>AHNAHN</u> AGGATTCTTCAATGTGT
195&196_for	CTCAGTTGCCACAATCCATCCA <u>NDTNDT</u> GTTTTCGGTCCCCAAG
195&196_rev	CTTGGGGACCGAAAAC <u>AHNAHN</u> TGGATGGATTGTGGCAACTGAG
213&217_for	$ggacaaaagtcagttgaac \underline{NDT} tcaagtgag \underline{NDT} ataaacaagattttgaagctg$
213&217_rev	$cagetteaaaatettgtttat\underline{AHN}eteaettga\underline{AHN}gtteaaetgaettttgtee$
235&236_for	ACAAACTTCCAGCAGGTGCT <u>NDTNDT</u> TTTACTGACGTGAGAGAC
235&236_rev	GTCTCTCACGTCAGTAAA <u>AHNAHN</u> AGCACCTGCTGGAAGTTTGT
V3_for	TTCCATATGATGTCACAAACTGTCTTTGTC (Nde I)
V3_rev	TATCTCGAGTTACTTGGCTTCCACAATTTG (Xho I)
SmNOX_for	CCGGAATTCGATGTCGAAAATTGTTATCG (EcoR I)
SmNOX_rev	CACGTCGACTTATTTCGCTTTCAGAGC (Sal I)
V3_for	CCGGAATTCGATGTCACAAACTGTCTTTGTC (EcoR I)

V3_rev CACGTCGACTTACTTGGCTTCCACAATTTG (Sal I)

*Sm*NOX_for TTCCATATGATGTCGAAAATTGTTATCG (*Nde* I)

*Sm*NOX_rev TATCTCGAGTTATTTCGCTTTCAGAGC (*Xho* I)

Metal ion (1 mM)	Relative activity (%)
Zn^{2+}	93.8 ± 3.1
Ni ²⁺	97.9 ± 3.1
Mg^{2+}	94.8 ± 2.1
Cu^{2+}	89.0 ± 5.8
Fe ²⁺	108.2 ± 0.3
Co ²⁺	98.6 ± 3.1
Mn^{2+}	100.3 ± 2.7
Al^{3+}	98.3 ± 1.4
Ca^{2+}	102.1 ± 0.3
Fe ³⁺	101.4 ± 0.3
EDTA	98.6 ± 1.0

 Table S2
 Effect of metal ions and EDTA on LeADH activity.

*Le*ADH was pre-incubated with various metal ions or EDTA for 30 min at 25°C and the residual activity was determined using the standard assay. Residual activity was expressed as a percentage of the activity obtained without addition any metal ions or EDTA.



Figure. S6 Schematic presentation of the plasmid containing *adh* and *nox* genes and analysis of expression level by SDS-PAGE. (A) Structure of the coexpression plasmid pETDuet-*adh-nox*. (B) SDS-PAGE analysis of the pETDuet-*adh-nox* expression. Lane 1, protein marker; Lane 2, soluble fraction of cell-free extract from *E. coli* with pETDuet-*adh-nox*; Lane 3, precipitate fraction. (C) Structure of the coexpression plasmid pETDuet-*nox-adh*. (B) SDS-PAGE analysis of the pETDuet-*nox-adh*. (B) SDS-PAGE analysis of the pETDuet-*nox-adh*. (B) SDS-PAGE analysis of the pETDuet-*nox-adh* expression. Lane 1, protein marker; Lane 2, soluble fraction of cell-free extract from *E. coli* with pETDuet-*nox-adh*. (B) SDS-PAGE analysis of the pETDuet-*nox-adh* expression. Lane 1, protein marker; Lane 2, soluble fraction of cell-free extract from *E. coli* with pETDuet-*nox-adh*. (B) SDS-PAGE analysis of the pETDuet-*nox-adh* expression. Lane 1, protein marker; Lane 2, soluble fraction of cell-free extract from *E. coli* with pETDuet-*nox-adh*. (B) SDS-PAGE analysis of the pETDuet-*nox-adh* expression. Lane 1, protein marker; Lane 2, soluble fraction of cell-free extract from *E. coli* with pETDuet-*nox-adh*; Lane 3, precipitate fraction.