

Supporting information

Novel Transaminase and Laccase from *Streptomyces* spp. Using Combined Identification Approaches

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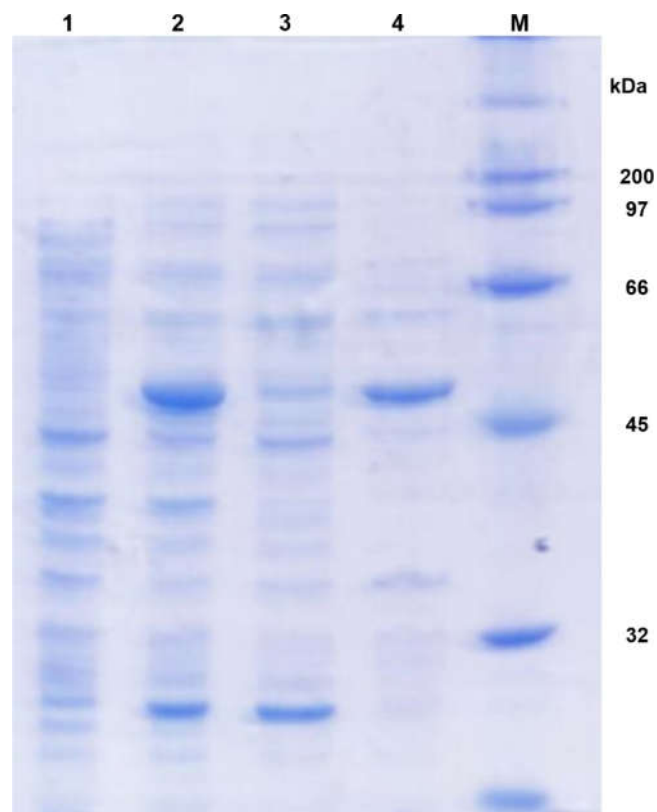


Figure S1. SDS-PAGE *E. coli* Rosetta expressing aminotransferase from pEtite_BV333 TA. 1) before the induction 2) after the induction with IPTG 3) cell lysate 4) purified enzyme M) Marker – SDS-PAGE Standard Broad Range (Bio-Rad, USA).

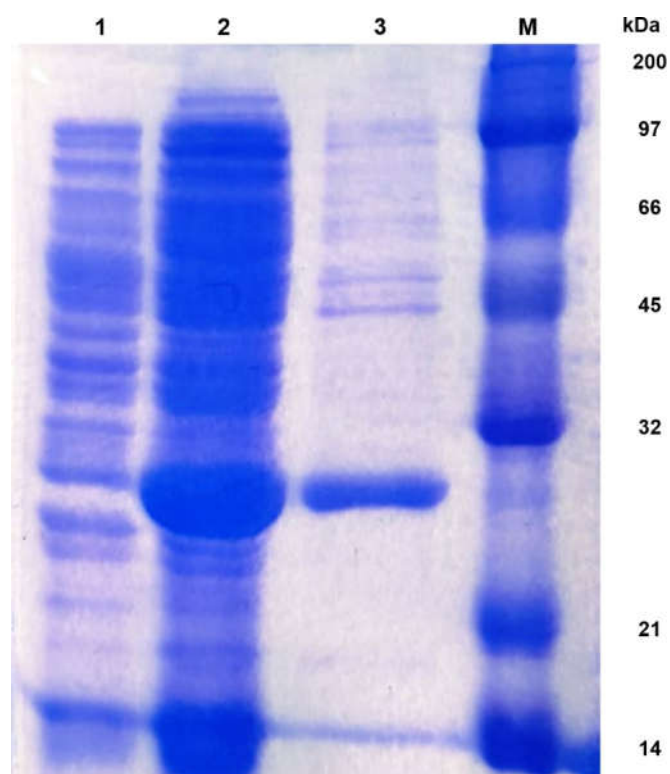


Figure S2. SDS-PAGE gel of purified laccase Sbv286-LAC. 1) before the induction 2) after the induction with IPTG 3) purified enzyme M) Marker – SDS-PAGE Standard Broad Range (Bio-Rad, USA).

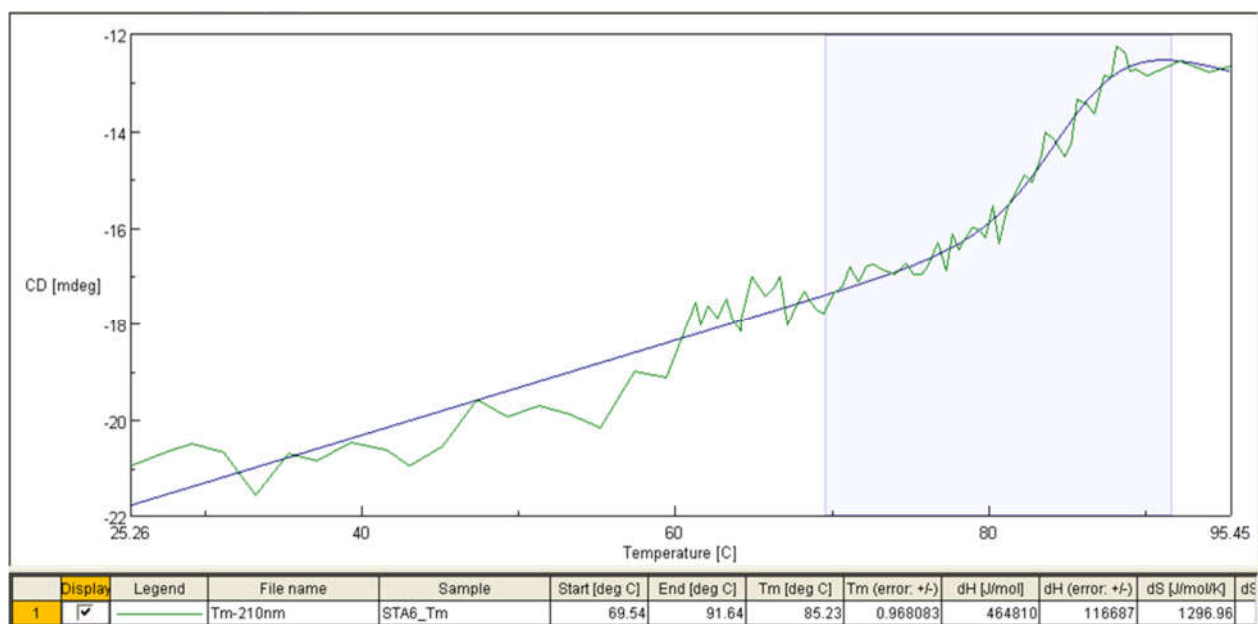


Figure S3. Sbv333-TA melting temperature curve obtained by circular dichroism spectroscopic analysis at 210 nm

Table S1. Bioinformatics tools used to perform phylogenetic classification.

Tool	Reference
TYGS: Type (Strain) Genome Server (TYGS)	Meier-Kolthoff JP, Göker M. TYGS is an automated high-throughput platform for state-of-the-art genome-based taxonomy. <i>Nat. Commun.</i> 2019;10: 2182. DOI: 10.1038/s41467-019-10210-3
RNAmmer	Lagesen K, Hallin P. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. <i>Nucleic Acids Res. Oxford Univ Press;</i> 2007;35: 3100–3108. DOI: 10.1093/nar/gkm160
BLAST	Camacho C, Coulouris G, Avagyan V, Ma N, Papadopoulos J, Bealer K, et al. BLAST+: architecture and applications. <i>BMC Bioinformatics.</i> 2009;10: 421. DOI: 10.1186/1471-2105-10-421
Genome BLAST Distance Phylogeny (GBDP)	Meier-Kolthoff JP, Auch AF, Klenk H-P, Göker M. Genome sequence-based species delimitation with confidence intervals and improved distance functions. <i>BMC Bioinformatics.</i> 2013;14: 60. DOI: 10.1186/1471-2105-14-60
FASTME 2.1.4	Lefort V, Desper R, Gascuel O. FastME 2.0: A comprehensive, accurate, and fast distance-based phylogeny inference program. <i>Mol Biol Evol.</i> 2015;32: 2798–2800. DOI: 10.1093/molbev/msv150
PhyD3	Kreft L, Botzki A, Coppens F, Vandepoele K, Van Bel M. PhyD3: A phylogenetic tree viewer with extended phyloXML support for functional genomics data visualization. <i>Bioinformatics.</i> 2017;33: 2946–2947. DOI: 10.1093/bioinformatics/btx324

Table S2. GenBank accession number of query sequences used in the bioinformatics search for novel ATA. Entry 1-10: (*S*)-selective ATA, Entry 11-18: (*R*)-selective ATA.

Entry	GenBank accession number	Organism
1	WP_011135573	<i>Chromobacterium violaceum</i> ATCC 12472
2	AEA39183.1	<i>Vibrio fluvialis</i> JS17
3	AAK25105.1	<i>Caulobacter vibrioides</i> CB15
4	ABL72050.1	<i>Paracoccus denitrificans</i> PD1222
5	WP_014457322	<i>Acetobacter pasteurianus</i> IFO 3283-01
6	WP_011982390	<i>Ochrobactrum anthropi</i> ATCC 49188
7	WP_003083801.1	<i>Pseudomonas aeruginosa</i> PAO2
8	AAP92672.1	<i>Achromobacter denitrificans</i> Y2k-2
9	KX505387	Uncultured organism
10	KX505388	Uncultured organism
11	KX505389	Uncultured organism
12	BAK39753.1	<i>Arthrobacter</i> sp. KNK168
13	XP_001209325	<i>Aspergillus terreus</i> NIH2624
14	XP_748821.1	<i>Aspergillus fumigatus</i> Af293
15	XP_001261640	<i>Neosartorya fischeri</i> NRRL 181
16	WP_011781668.1	<i>Mycobacterium vanbaalenii</i> PYR-1
17	WP_011647499.1	<i>Hyphomonas neptunium</i> ATCC 15444
18	CAD31279.1	<i>Mesorhizobium loti</i> R7A

Table S3. GenBank accession number of query sequences used in the bioinformatics search for novel Laccases

Entry	GenBank accession number	Organism
1	ABH10611.1	<i>Streptomyces ipomoeae</i>
2	A0A656R8L8	<i>Streptomyces griseorubens</i>
3	3CG8	<i>Streptomyces coelicolor</i>
4	WP_004980371.1	<i>Streptomyces viridosporus</i>
5	WP_128437084.1	<i>Streptomyces cyaneus</i>
6	WP_007386096.1	<i>Streptomyces svaceus</i> ATCC 29083
7	WP_069169798.1	<i>Streptomyces griseus</i>
8	AGE62493.1	<i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168
9	ZP_03054403.1	<i>Bacillus subtilis</i> XF-1
10	AGE62493.1	<i>Bacillus pumilus</i> ATCC 7061
11	BAC00361.1	<i>Corynebacterium glutamicum</i> ATCC 13032
12	AAS81712.1	<i>Thermus thermophilus</i> HB27
13	5B7E_A	<i>E. coli</i> K12

Table S4. Bacterial strains and plasmids used in this study

Bacterial strain/plasmid	Reference
<i>Streptomyces</i> sp. BV129	Spasic et al 2018b
<i>Streptomyces</i> sp. BV286	Spasic et al 2018b
<i>Streptomyces</i> sp. BV333	Spasic et al 2018b
<i>E. coli</i> HI-Control 10G™	Lucigen, Middleton, USA
<i>E. coli</i> BL21(DE3)	Lucigen, Middleton, USA
<i>E. coli</i> Rosetta (DE3)	Merck, Darmstadt, Germany
<i>E. coli</i> Rosetta (DE3)- Sbv333-TA	This study
<i>E. coli</i> Rosetta (DE3)- Sbv286-LAC	This study
<i>E.coli</i> BL21(DE3)-GroEs, GroEL-pETite-Sbv333-TA	This study
pETite (expression vector)	Lucigen, Middleton, USA
pETite-Sbv333-TA	This study
pETite-Sbv286-LAC	This study
pGro7	Takara Bio Inc., Kyoto, Japan

Table S5. Sequencing statistics

Sample ID	Streptomyces sp. BV129	Streptomyces sp. BV286	Streptomyces sp. BV333
Yield (Mbases)	1,197	1,237	1,184
Nr. of reads	7,982,434	8,246,470	7,890,548
Yield after trimming (Mbases)	1,081	1,113	1,065
Nr. of trimmed reads	7,577,220	7,778,364	7,418,590
% of >= Q30 Bases (PF)	92.47	91.93	91.87
Mean Quality Score (PF)	36.93	36.77	36.75

Table S6. Oligonucleotide primers used in this study

Primer name	Sequence
pETite_BV333STA FP	GAA GGA GAT ATA CAT ATG GGG AAC CCG ATA GCC GTG AGC
pETite_BV333STA RP	GTG ATG GTG GTG ATG ATG GAG CTT CGT CCA AGC CTC CGT
pETite_BV286LAC FP	GAA GGA GAT ATA CAT ATG AGC ACC ACG GAC GGC ATG GAC
pETite_BV286LAC RP	GTG ATG GTG GTG ATG ATG GTG CTC GTG CGG CTC GTA CCC
T7 promoter	TAA TAC GAC TCA CTA TAG GG
pETite reverse	CTC AAG ACC CGT TTA GAG GC