Laccase-based biocatalytic systems application in sustainable degradation of pharmaceutically active contaminants

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Abstract

The outflow of pharmaceutically active chemicals (PhACs) exerts a negative impact on biological systems even at extremely low concentrations. For instance, enormous threats to human and aquatic species have resulted from the widespread use of antibiotics in ecosystems, which stimulate the emergence and formation of antibiotic-resistant bacterial species and associated genes. Additionally, it is challenging to eliminate these PhACs by employing conventional physicochemical water treatment techniques. Enzymatic approaches, including laccase, have been identified as a promising alternative to eliminate a broad array of PhACs from water matrices. However, their application in environmental bioremediation is hindered by several factors, including the enzyme's stability and its location in the aqueous environment. Such obstacles may be surmounted by employing laccase immobilization, which enables enhanced stability (including inactivation caused by the substrate), and thus improved catalysis. This review emphasizes the potential hazards of PhACs to aquatic organisms within the detection concentration range of ngL^{-1} to μgL^{-1}, as well as the deployment of laccase-based multifunctional biocatalytic systems for the environmentally friendly mitigation of anticancer drugs, analgesics/NSAIDs, antibiotics, antiepileptic agents, and beta blockers as micropollutants. This approach could reduce the underlying toxicological consequences. In addition, current developments, potential applications, and viewpoints have focused on computer-assisted investigations of laccase-PhACs binding at enzyme cavities and degradability prediction.

Keywords: Laccase; Pharmaceutical compounds; Biocatalysis; Enzyme immobilization; Environmental bioremediation; Ecological hazards; Toxicity

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Data generated from the work is listed below in the numerical and graphical format. More extensive explanations can be found in the source paper.

Table 7. Comparison of the physicochemical features of laccases from various sources.

Laccase origin species	PDB	Amino-acids	Molecular formula	Molecular weight (Da)	Negatively charged residues (Asp + Glu)	Positively charged residues (Arg + Lys)	Theoretical pI	The instability index (II)	Aliphatic index	Grand average of hydropathicity (GRAVY)
Trametes versicolor	1KYA	499	$C_{2399}H_{3600}N_{638}O_{729}S_9$	53331.35	45	20	4.69	26.88	81.34	-0.028
Streptomyces carpinensis	8AIP	293	$C_{1407}H_{2148}N_{412}O_{427}S_{16}$	32180.00	37	37	5.95	41.39	63.45	-0.495
Streptomyces viridosporus	3TBB	313	$C_{1498}H_{2280}N_{444}O_{456}S_{11}$	34157.94	41	31	6.16	34.54	60.73	-0.657
Thermus thermophilus HB27	6Q29	439	$C_{2210}H_{3489}N_{613}O_{602}S_{14}$	48727.60	48	47	7.09	41.29	96.83	-0.146
Coriolopsis trogii	2HRH	496	$C_{2382}H_{3604}N_{636}O_{729}S_9$	53103.18	48	23	4.83	36.55	82.80	-0.082
Cerrena caperata	4JHU	496	$C_{2387}H_{3609}N_{643}O_{729}S_{11}$	53330.44	47	23	4.87	35.38	80.83	-0.127
Streptomyces griseoflavus	7PEN	322	$C_{1511}H_{2319}N_{451}O_{462}S_{13}$	34611.56	37	27	6.06	33.75	66.96	-0.433

Melanocarpus albomyces	3FU7	559	$C_{2764}H_{4153}N_{759}O_{831}S_{15}$	61791.87	62	34	4.91	32.71	78.59	-0.325
Trametes maxima	2H5U	499	$C_{2384}H_{3571}N_{653}O_{734}S_{7}$	53347.93	38	21	5.26	30.41	73.51	-0.207
Coriolopsis gallica	4A2E	496	$C_{2371}H_{3579}N_{631}O_{722}S_{9}$	52763.83	45	21	4.84	31.42	83.25	-0.023

Physicochemical properties have been predicted using the ProtParam – Expasy tool by utilizing amino acid sequences from corresponding PDB IDs.