Table S1. Comparison of selected laccases from different taxa.

Origin and protein name	**Cellular localization**	**Gene (number)**	**Aa length**	**MW (kDa)**	**pI**	**pH optimum**	**Temp. optimum (°C)**	**Glycosylation**	**Redox potential (mV vs. NHE)**	**References**
BACTERIA **Firmicutes**										
Bacillus subtilis, CotA	spore wall		511	65	7.7	7 (SGZ), ≤3 (ABTS)	75		455	[1-3]
Bacillus subtilis WD23	spore wall					6.8 (SGZ)	60			[4]
Bacillus subtilis MTCC 2414	extracellular			52-55		9 (guaiacol)	70			[5]
Bacillus subtilis SF	spore wall									[6]
Bacillus halodurans C-125 (recombinant)	intracellular		500	56		7.5–8.0 (SGZ)	45			[7]
Bacillus sphaericus	spore wall					6 (SGZ, DMP)	60			[8]
Bacillus licheniformis (recombinant)	intracellular			65	7.0	7 (SGZ, DMP), 4.2 (ABTS)				[9]
Bacillus pumilus, Cot A (recombinant)	intracellular	1	510	58		6.5 (SGZ), 4 (ABTS), 7 (DMP)	70			[10]
Bacillus tequilensis SN4, SN4LAC	extracellular			32		6.5 (SGZ), 5.5 (ABTS), 8 (DMP), 8 (guaiacol)	85			[11]
Paenibacillus glucanolyticus SLM1, CuOx (recombinant)		1	541	90		7 (ABTS)	40			[12]
BACTERIA **Proteobacteria** **α-proteobacteria**										

Sinorhizobium meliloti CE52G	intracellular/periplasmic			95		6 (SGZ), 5 (ABTS)				[13]
Sinorhizobium meliloti L3.8	periplasmic	1	649	70	4.77	2.2 (ABTS), 3.5 (caffeic acid), 5.0 (DMP), 5.5 (SGZ), and 6.0 (ferulic acid)	80	3.2%		[14]
Azospirillum lipoferum	intracellular			48.9 - 179.3		6 (SGZ)	30			[15,16]
BACTERIA **Actinobacteria** **Actinobacteria**										
Streptomyces lavendulae REN-7, STSL	mycelia-intracellular/intracellular			73		4.5 (catechol)	50			[17]
Streptomyces psammoticus	intracellular			43	7.9	8.5 (ABTS)	45	10%		[18]
Streptomyces coelicolor, SLAC	extracellular			69±8	6.2 - 8.2,	9.4 (DMP)			430	[19,20]
Streptomyces coelicolor (recombinant)	extracellular			32		9 (DMP), 4 (ABTS)	60			[21]
Streptomyces griseus, EpoA (recombinant)	cytoplasmic		348	114	5.3 - 5.6	6.5 (N,N-dimethyl-p-phenylenediamine sulfate)	40			[22]
Streptomyces ipomea, SilA	extracellular/cytoplasmic			77	6.18	7.5-8.0 (SGZ), 5 (ABTS), 8 (DMP)	60			[23]
Streptomyces cyaneus CECT3335	extracellular			75	5.6	4.5	70			[24]
Streptomyces sviceus, Ssl1 (recombinant)	intracellular	2		98.3		8 (SGZ), 9 (guaiacol,			375 ± 8	[25,26]

						DMP), 4 (ABTS),				
Corynebacterium glutamicum, CgL1 (recombinant)	intracellular	1	493	59			60			[27]
BACTERIA **Proteobacteria** **γ-proteobacteria**										
Marinomonas mediterranea MMB-1, PpoA (recombinant)	intracellular		675	54.3						[28,29]
γ-proteobacterium JB	intracellular			120		6 (SGZ)	55			[30]
Stenotrophomonas maltophilia AAP56	intracellular	1				7 (SGZ)	40			[31]
Escherichia coli W3110, CueO	periplasmic	1		53.4		6.5 (DMP)	55		440, 500	[32-34]
Escherichia coli, PcoA										[35]
Pseudomonas syringae, CopA			577	64						[33,36]
Pseudomonas putida GB-1, CumA		1								[37]
Pseudomonas putida F6	cytoplasmic			59		7 (SGZ)	30			[38]
Xanthomonas campestris, CopA		1	592	67						[36,39]
BACTERIA **Aquificae**										
Aquifex aeolicus, McoA (recombinant)	intracellular (periplasmic-predicted)	1		57.8 (59.5 predicted)	4.2	7 (SGZ), 4 (ABTS)	75			[40]
BACTERIA **Deinococcus-Thermus**										
Thermus thermophilus HB27	intracellular		462	53	7.18	5.5 (SGZ), 4.5 (ABTS)	92			[41]

BACTERIA **Cyanobacteria**										
Arthrospira maxima SAE-25780	extracellular									[42]
Phormidium valderianum BDU 30501	intracellular									[43]
Oscillatoria boryana BDU92181	intracellular									[43]
Spirullina C11	intracellular									[44]
ARCHAEA **Euryarchaeota**										
Haloferax volcanii, LccA (recombinant)	extracellular	1		75-80	acidic	6 (ABTS), 8.4 (SGZ)	45-50	6.9%		[45]
Pyrobaculum aerophilum, McoP (recombinant)	intracellular	1	477	49.6 (52.9 predicted)		7 (SGZ), 3 (ABTS)	85		398	[46]
PLANTS **Algae**										
Tetracystis aeria	extracellular			220		2.5 (ABTS) 7.0 (SGZ) 6.5 (2,6-DMP)		A≥53% B≥27%		[47]
PLANTS **Higher plants**										
Acer pseudoplatanus	extracellular			97±5		6.6 (4-methylcatechol)		45%		[48]
	suspension cultures			115±15	5.2	5.2		40%		[49]

		3			4.5					[50]
Arabidopsis thaliana		17 Lcs *AtLac1-17* organ-specific *TT10*	553-586	64	7.0-9.6					[51,52]
Liriodendron tulipifera	xylem tissues	4	570-586	60.6-61.2	9.3-9.5					[53]
Pinus taeda	xylem			90	9	5.9		22%		[54]
	xylem	8	536-556	59.2-61.7	7.66-9.62					[55]
Populus canadensis	xylem									[50]
Populus euramericana		2		90 110	9.2	-		High manose type *N*-glycan		[50]
Populus trichocarpa	xylem	6								[56]
Prunus persica	fruit			73.5		6		25%		[57,58]
Rhus succedanea						6.4 (hydroquinone) 6.6 (catechol) 6.6 (L-ascorbate)				[59]
Rhus vernicifera				103-120	8.2-9.1			45-55		[60]
						7.5 (hydroquinone) 7.6 (catechol) 7.6 (L-ascorbate)				[59]
									T1: 394-434 T2: ~365 T3: 434-483	[61]

				110		7	25		415	[62]
Schinus molle				96-110		6.2				[63]
FUNGI **Basidiomycota**										
Abortiporus biennis strain J2	extracellular	9		66		5	40			[64]
Agaricus blazei	extracellular			66	4.0	5.5	20			[65]
Armillaria mellea	extracellular	16		59	4.1	3.5				[66]
Athelia rolfsii (= *Sclerotium rolfsii*), SRL	extracellular			55 -86	5.2	2.4 -4.5	62			[67]
Auricularia auricular-judae, Lcc	extracellular		575-801							[68]
Cerrena unicolor, Lac	extracellular	8	510-516	45-62	4.27-5.11	5.5	45-62	1.65-3.51		[69]
Gelatoporia subvermispora (= *Ceriporiopsis subvermispora)*		8	518-525	71-79	3.4-4.82	3-6		10-15		[70-72]
Coprinus cinereus, CcLCC5		13	387-728	56.8		3	55			[73]
Coprinus friesii	extracellular			60	3.5	5-8				[74]
Cryptococcus neoformans	cell wall associated	4	594-641	75						[75]
Cyathus bulleri, lac	extracellular		473-584	5.0		3.5-5.5	30	16		[76]
Daedalea quercina	extracellular	4		69-71	3	2-7	60-70			[77]

Dichomitus squalens	extracellular	12	507-634	65-66	3.5-3.6	3		8-10.5		[78]
Flammulina velutipes, Flac	extracellular		496-670	28-45		5-6.5	30			[78]
Fomes fomentarius	extracellular	5				3.8-4.8	38-52			[79]
Fomitopsis pinicola	extracellular	6	539-604	92	3.8	3	80			[80]
Ganoderma lucidum, lac	extracellular		519-620	43-66		4.5-5.0	30-50			[81,82]
Gymnopus quercophilus (= *Marasmius quercophilus*)			517	60-65		2.6-6.2	80			[83]
Heterobasidion annosum		22	513-560			4.5-5.3				[84]
Irpex lacteus	mycelium	1				3-7				[85]
Lentinula edodes, Lcc	extracellular	4	445-631	72.2	3	4	40	23.8		[86]
Lentinula edodes (= *Lentinus edodes*), Lcc	intracellular	4	445-631	58-74	3.42	3-4.2	40-50	7.5-8.6		[87,88]
Lentinus sajor-caju (= *Pleurotus sajor-caju*)	extracellular		465-532	55-61	4.7-5.61	5	40			[89,90]
Lentinus tigrinus (= *Panus tigrinus*)	extracellular	7	394-568	63-69.1	3.15	3.75	55	6.9		[91,92]
Macrocybe gigantea = *Tricholoma gigantea*			391	43		4	70			[93]
Merulius tremellosus (= *Phlebia tremellosa*)			520	67	3.25					[94]
Panaeolus papilionaceus *Panaeolus sphinctrinus*		2		60	<3.6 <3.55	3-7 3-8				[74]

Perenniporia tephropora	extracellular			63	3.3	4-5				[95]
Phanerodontia chrysosporium (= *Phanerochaete chrysosporium*)	extracellular	5	444-624	66 46,5						[96]
Phlebia radiata	extracellular	5	520-548	60		5	70			[97]
Pleurotus eryngii	extracellular	10	523-533	61-65	4.1-4.2	3.5-4	55-65	1-7		[98]
Pleurotus floridanus (= *Pleurotus florida*)	extracellular		529-533	77-82	4.1	5	50			[99]
Pleurotus ostreatus, POXA	extracellular	13	514-533	40-67	4.1 4.3	3.6-8	25-50	10		[100-102]
Pleurotus pulmonarius,	extracellular		521-533	46		4-8	50	44		[103]
Pleurotus cornucopiae	fruit body			66		4	40			[104]
Pycnoporus sp.	extracellular					4-4.5	70			[105]
Pycnoporus cinnabarinus	extracellular	5	468-643	70-81	3.5-3.7	4-4.5	65	9		[106,107]
Pycnoporus coccineus	extracellular	6	511-518	61.8		4.5-5	65	10	723	[108]
Pycnoporus sanguineus	extracellular	5	518-570	59.5-68		2-5	65-71	7-9	729, 746	[108,109]
Rigidoporus lignosus, POX			515-521	51-60	3.1-3.7	6-7			700-730	[110]
Rhizoctonia solani,		17	416-623	50-100		6-7				[111]
Schizophyllum commune	extracellular and intracellular	2	518-583	62-64		5.4-6				[112]
Trametes troggi POXL	extracellular			53-70	3.3-4.5	2.5-3.5		12	760-790	[110,113,114]

Trametes hirsuta	extracellular		515-525	52-62		3-4.5	50-60			[115,116]
Trametes pubescens, LAP	extracellular	6	508-526	65-68	2.6	3-4.5	50	18		[117,118]
Trametes polyzona	extracellular	3	520	71		2-5				[119]
Trametes versicolor	extracellular	8	520-527	97-100	3.5-5.8	3-5.5	50			[120,121]
Trametes orientalis	extracellular			44		4	80			[122]
Trametes villosa	extracellular		473-520	63	3.5-6.5	5-5.5				[123]
Volvariella volvacea,		11	519	58	3.7	3-5.6	50			[124]
FUNGI **Ascomycota**										
Alternaria alternata		7	598-616	45		3.5-4.5	35-65			[125,126]
Aspergillus nidulans	conidia	4	594-609	36-80				12		[127,128]
Aspergillus flavus (= *Aspergillus oryzae*)	extracellular	6	556-620	60		3	50			[129]
Aspergillus ochraceus	intracellular			68		4	60			[130]
Aureobasidium pullulans		10	570-628	60-70		4.5	45-60			[131,132]
Botrytis cinerea	extracellular	11	561-581	35,5-38				70-80		[133]
Chaetomium thermophilum	extracellular			77-98	5.1	5-65	50-60			[134,135]
Cryphonectria parasitica	extracellular	15	567-591	77		2.5		24		[136]

Fusarium solani	extracellular	4	583-651	72		3	70	12		[137]
Gaeumannomyces graminis	extracellular	8	578-607	190	5.6	4,5				[138]
Melanocarpus albomyces			623	80	4	5-7	60-70			[139]
Neurospora crassa	extracellular	7	598-739	64-64.8				11		[140,141]
Ophiostoma novo-ulmi		3		70-79	5.1					[142]
Podospora anserina	mycelium	3	621	39-97.5		5.5- 7.5		23		[143,144]
Pyricularia grisea (= *Magnaporthe grisea*)	extracellular	9		70		6	30			[145]
Trichoderma atroviride	extracellular	1-6				4.5				[146]
Trichoderma reesei	extracellular	4	589-623			4.5	25			[147]
Trichoderma harzianum	extracellular	1-4	653-720	79		4.5	35		692	[148]
Xylaria polymorpha	extracellular			67	3.1	2.5-5	55-60	7.5		[149]
ANIMALS **Sponges**										
Suberites domuncula, LACC-1_SUBDO		1	785	87	4.8					[150]
ANIMALS **Insects**										
Anophales gambiae, AgLac1		1	1009	110	5.52					[151]
Apis mellifera, Amlac2			731	81.5	6.05					[152]
Bemisia tabaci, LAC1	*salivary glands*		911	103		5 (ABTS)				[153]
Bombyx mori		2	763 740	70 84						[154]

Drosophila melanogaster	3rd instar larva (wandering) cuticle-bound suspension	1				6.5 (4-MC)				[155]
Manduca sexta						6.0				[156]
		2	801 760	88 81	5.15 6.36					[151]
	pupal cuticle purified recombinant	1		84		5 (NADA) 5.5 (NBAD)				[157]
Monochamus alternatus, MaLac2		1	741	81	6.12					[158]
Nephotettix cincticeps, NcLac	salivary glands (Sg) midgut (Mg) Malpighian tubules (Mt) integument incl. cuticle and epidermis (Ep)	1	701-792	77-86	5.52-6.04					[159]
Tribolium castaneum, TcLac2A, TcLac2B		1		77		For TcLac2A 5.5 (Dopamine) 5.5 (NADA) 5.5 (NBAD) 7 (Dopa) 4.5 (ABTS) For TcLac2B 6.0 (Dopamine) 5.5 (NADA) 5.5 (NBAD) 6.5 (Dopa) 4.5 (ABTS)			300 (Dopamine) 260 (NADA) 240 (NBAD) 670 (Dopa)	[160]

SUBSTRATES:

ABTS: 2,2´-azino-bis(3-ethylbenzothiazoline-6-sulphonic acid)

SGZ (syringaldazine): 4-hydroxy-3,5-dimethoxybenzaldehyde azine
2,6-DMP: 2,6-dimethoxyphenol
ACS: 3´,5´-dimethoxy-4´-hydroxyacetophenone (acetosyringone)
NADA: *N*-acetyldopamine
NBAD: *N*-β-alanyldopamine
4-MC: 4-methylcatechol

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