

Unconserved 0 1 2 3 4 5 6 7 8 9 10 Conserved

	10	20	30	40	50
Lpla-J16	-----M	AKKVYTDYFF	DEPAYNTHDG	GYIPL--VTP	KVEPQP-LAI
Ppen-4816	-----	MKNYTDYFF	DEPAFDLHDG	GYVPL--EVS	DAPEKP-LNV
Lpar-4314	-----	MKTYTDYFF	DEPAFDLHDG	GYVPL--EVS	DAPEKP-LNV
Llac-5298	MLKFLSEGEI	TMKNYTDYFF	DEPAFDLHDG	GYVPL--EVS	DAPEKP-LNV
Ppar-3909	-----M	AKQVYNDYFF	DEPAWNTHDG	GYVPL--EEP	TTPOQK-LHV
Paci-5930	-----	MITKYLY	DENAYDYHDG	GYRPF--KKA	PGEEHP-LNV
Ecol-6898	-----M	QRDFLKY--	SVALGV--A	SALPLWSRAV	FAADRPTLPI
Bsub-6077	-----M	TLEKFAD--	--A--	-----	-----LPI
Consistency	0000000002	1353767744	564*443556	6547600433	2444460*49

	60	70	80	90	100
Lpla-J16	PPLLKPDQRQT	DTDDYYTVTA	QESETQFLPG	-KKTKTWGYN	AGFLGQTIVF
Ppen-4816	PPLLKPDKET	ATDVYYTVTA	EAGETQLLPG	-AKTKTWGYN	TSLLGQTIVY
Lpar-4314	PPLLKPDKET	ATDVYYTVTA	EAGETQLLPG	-AKTKTWGYN	TSLLGQTIVY
Llac-5298	PPLLKPDKET	ATDVYYTVTA	EAGEMQLLPG	-ATTKTWGYN	TSLLGQTIVY
Ppar-3909	PAVLQPDKET	DTDMYYTVTA	EEGETQLLPG	-PKTKTWGYN	GSLLGKTIIF
Paci-5930	PAFLKPDRIE	GNEIYYTVTA	QAGETKILPG	-KPTHWTWGYN	GSILGPAIQF
Ecol-6898	PDLLTTNAR-	-NRIQLTIGA	--GQSTF-GG	-KTATTWGYN	GNLLGPAVKL
Bsub-6077	PDTLKPVQQQT	TEKTYEVTM	EECAHQHLHRD	LPPTRLWGYN	GLFPGPPTIEV
Consistency	*46*786656	3665888988	6467577568	045868****	5577*57956

	110	120	130	140	150
Lpla-J16	RNGKQTHIDL	ENKL-----	-----	-----PEL-T	TFHWHGLNVP
Ppen-4816	RRGQHTHVTL	KNTL-----	-----	-----PEL-T	TFHWHGANVS
Lpar-4314	RRGQHTHVTL	KNTL-----	-----	-----PEL-T	TFHWHGANVS
Llac-5298	RRGQHTHVTL	KNTL-----	-----	-----PEL-T	TFHWHGANVS
Ppar-3909	KRGKTIHITL	KNDL-----	-----	-----HEL-T	TFHWHGLNVP
Paci-5930	ETGKTYHVTL	KNEL-----	-----	-----DEV-T	TFHWHGLNIV
Ecol-6898	QRGKAVTVDI	YNQL-----	-----	-----AEE-T	TLHWHGLEVP
Bsub-6077	KRNENVYVKW	MNNLNPSEHFL	PIDHTIHHSD	SQHEEPKVKT	VVHLHG-GVT
Consistency	6787456957	5*4*000000	0000000000	000005*60*	87*7**4794

	160	170	180	190	200
Lpla-J16	GPITDGGCHA	-----PVY	P-GETNHIDF	KVHQPAATTW	LHAHPCPSTA
Ppen-4816	GPYVDGGCHA	-----PVY	P-GESKHIDF	TLEQPATTLW	LHAHPCPSTA
Lpar-4314	GPYVDGGCHA	-----PVY	P-GESKHIDF	TLDQPATTLW	LHAHPCPSTA
Llac-5298	GPYVDGGCHA	-----PVY	P-GESKHIDF	TLEQPATTLW	LHAHPCPSTA
Ppar-3909	GPYIDGGCHA	-----PVY	P-GESSDIEF	VCNQPAATLW	LHAHPCPSTA
Paci-5930	GPYEDGGPHA	-----PVY	PHGERK-ITF	TVDQPAANIW	LHPHPCPETA
Ecol-6898	GE-VDGGPQG	-----II	PPGGKRTVTL	NVDQPAATCW	FHPHQHGKTG
Bsub-6077	PDDSDGYPEA	WFSKDFEQTG	PYFKREVYHY	PNQQRGAILW	YHDHAMALTR
Consistency	7645**7578	0000000686	*077563857	455*88776*	7*5*6666*7

	210	220	230	240	250
Lpla-J16	TQVWKGLATM	VIIKDDVEDQ	LPPLPRNYGVD	DIPVLVLQDRE	FHDDNQFDYR
Ppen-4816	EQVWHGLAAM	VIVKDDHEAS	LPPLPRNYGVD	DIPVILQDRR	FHENNQWDYR
Lpar-4314	EQVWHGLAAM	VIVKDDHEAS	LPPLPRNYGVD	DIPVILQDRR	FHENNQWDYR
Llac-5298	EQVWHGLAAM	VIVKDDHEPS	LPPLPRNYGVD	DIPVILQDRR	FHENNQWDYR
Ppar-3909	QQVWHGLATP	VVVQDDVESK	LPPLPRNYGVD	DFPLVLQDRN	FHEDNQWDYK
Paci-5930	RQVWNGLAAP	VIIITDGHEQS	LKLP RRWGVN	DFPVVLQDRS	YH-DNQLDYK
Ecol-6898	RQVAMGLAGL	VVIEDDEILK	LMLPKQWGID	DVPVIVQDKK	FNADGQIDYQ
Bsub-6077	LNYYAGLVGA	YIIHDPKEKR	LKLP S--GEY	DVPLLITDRT	INEDGSLFYP
Consistency	48*64**855	8995*64736	*5**755*76	*7*7888*95	77577847*6

	260	270	280	290	300
Lpla-J16	ADYD-----	PDGV-Q--	GHTALVNGTV	NPYFDVTTQR	VRLRILDGSN
Ppen-4816	ADYD-----	PDGV-A--	GPTAMINGTI	NPYFDVTTQK	VRLRFLNGAN
Lpar-4314	ADYD-----	PDGV-A--	GPTAMINGTI	NPYFDVTTQK	VRLRFLDGAN
Llac-5298	ADYD-----	PDGV-A--	GPTAMINGTI	NPYFDVTTQK	VRLRFLDGAN
Ppar-3909	ADYD-----	PDGV-Q--	GKTPMINGTI	NPYIDVTTQR	IRLRVLDGAN
Paci-5930	ADYD-----	VDGT-L--	GDYALVNGTV	NPVVNVTKPI	IRLRFLNGSN
Ecol-6898	LNVM-----	TAAV-GWF	GD TLLTNGAI	YPQHAAPRGW	LRLRL LNGCN
Bsub-6077	SGPENPSPSL	PKPSIVPAFC	GD TILVNGKV	WPYLEVEPRK	YRFRVINASN
Consistency	7767000000	0067680500	*48587**79	5*65686554	7*8*69786*

	310	320	330	340	350
Lpla-J16	RREWRLHFND	DLEFAQVASD	GGILPAPVYM	TKVMMTCAER	DEIVVDFGQY
Ppen-4816	RREWRLHFAD	DLPFTQIGGD	GSLLPEPVKF	THLMLTCAER	AEVIVDFGQY
Lpar-4314	RREWRLHFSD	DLPFTQIGGD	GSLLPEPVKF	THLMLTCAER	AEVIVDFGQY
Llac-5298	RREWRLHFSD	DLPFTQIGGD	GSLLPEPVKF	THLMLTCAER	AEVIVDFGQY
Ppar-3909	RREFRLHFND	DLEFAQVASD	GGIMPEPVYF	TKVMLTCAER	DEFIVDFGKY
Paci-5930	RREWRLHFAD	YHPFTQIGSD	GGLLPEAVEM	DRIMLTCAER	ADVLVNFSYD
Ecol-6898	ARSLNFATSD	NRPLYVVIASD	GGLLPEPVKV	SELPVLMGER	FEVLVEVNDN
Bsub-6077	TRTYNLSLDN	GGEFIQIGSD	GGLLPRSVKL	NSFSLAPAER	YDIIIDFTAY
Consistency	6*75786658	546858977*	*789*76*55	64768768**	4878978657

	360	370	380	390	400
Lpla-J16	QPGDEVTLMT	D-----	DTPLCRFR	I-KSFVPDDT	-KLPEHLVDI
Ppen-4816	HEGDEVTLYT	D-----	DVPLLKFR	I-HAFKPDQT	-TLPDKLFDV
Lpar-4314	HEGDEVTLYT	D-----	DVPLLKFR	I-HAFKPDQT	-TLPDKLFDV
Llac-5298	HEGDEVTLYT	D-----	DVPLLKFR	I-HAFKPDQT	-TLPDKLFDV
Ppar-3909	HDGDEVALMS	D-----	DVPLVHFR	I-HQFAKDET	-KLPDHLVDQ
Paci-5930	QPGQEVILQT	D-----	DFNLIKFK	I-GDIKKENM	-LLPSPLAEI
Ecol-6898	KPFDLVTLPV	SQ--MGMAIA	PFDKPHSVMR	I-QPIAISAS	GALPDTLSSL
Bsub-6077	-EGQSIILAN	SEGCGGDANP	ETDANIMQFR	VTKPLAQKDE	SRKPKYLASY
Consistency	4577696*36	7000000000	00*4675589	9044654656	048*63*465

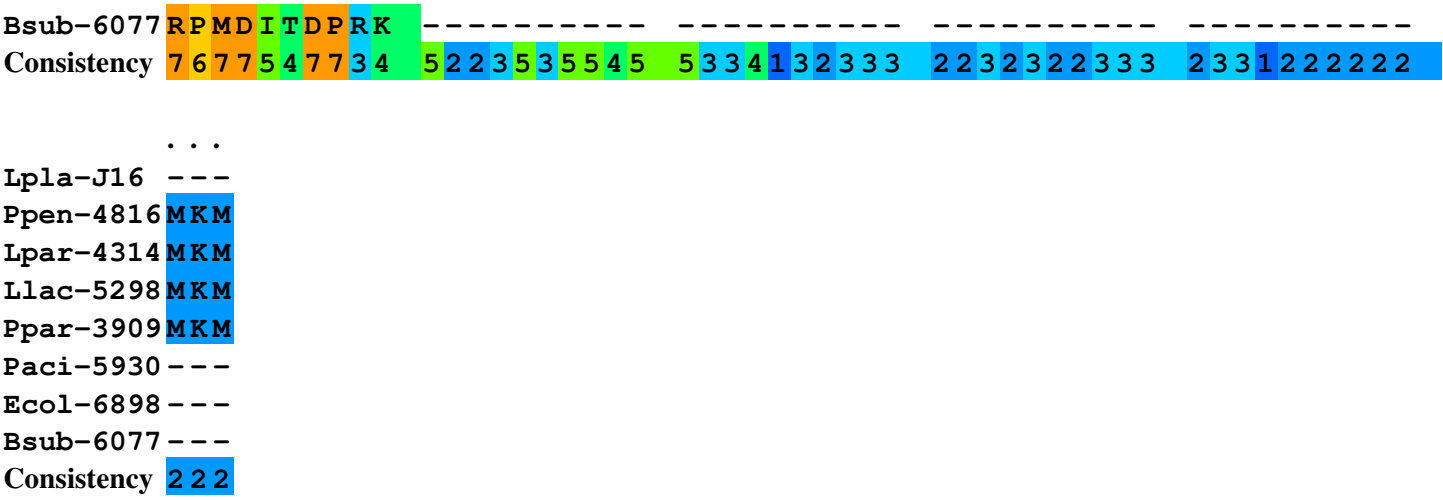
	410	420	430	440	450
Lpla-J16	PDETPTDLP	VRTIT	---MDGM---	DD---	EVA-LD---
Ppen-4816	KAPVVDPALP	VRHV	---MQGM---	DE---	GVA-ID---
Lpar-4314	KAPVVDPALP	VRHV	---MQGM---	DE---	GVA-ID---
Llac-5298	KAPVVDPALP	VRHV	---MHGM---	DE---	GVA-ID---
Ppar-3909	PNLTVTPGTK	TRHV	---MSGM---	DE---	EVA-ID---
Paci-5930	PALSVDENTP	VFKTV	---MSGM---	DD---	QVR-LD---
Ecol-6898	PALPSLDGLT	VRKLQLSMDP	MLDMMGMQML	MEKYGDQ---	AMAGMDHSQM
Bsub-6077	PSVQNERIQN	IRTLK	---LAGTQ---	DEYGR	PVLLLN---
Consistency	6634445455	8747500000	00094*8000	00000*7000	4870880000

	460	470	480	490	500
Lpla-J16	-----	GKKFDM	-----SR	IDARQKV---	GDVAIWEI
Ppen-4816	-----	GKKFAM	-----QR	IDATQPI---	GKAQYWDV
Lpar-4314	-----	GKKFAM	-----QR	IDATQPI---	GKAQYWDV
Llac-5298	-----	GKKFAM	-----QR	IDATQPI---	GKAQYWDV
Ppar-3909	-----	GKKFNM	-----QR	IDARQKV---	GDVVLWDV
Paci-5930	-----	GKLFD	-----QR	IDTRQQV---	DQTQIWEV
Ecol-6898	MGHMGHGMN	HMNHGKKFDF	HHANKINGQA	FDMNKPMPFAA	AKGQYERWVI
Bsub-6077	-----	NKRWH-	-----DP	VTEAPKA---	GTTEIWSI
Consistency	0000000000	0000887846	0000000076	8855757000	0085554*59

	510	520	530	540	550
Lpla-J16	RNTNSTENG	MVHPFHVHGTQ	FRVLAR---	NDG-	-----PVY
Ppen-4816	TNSND-APGM	MVHPFHVHGTQ	FLVLSR---	NGH-	-----APY
Lpar-4314	TNSND-APGM	MVHPFHVHGTQ	FLVLSR---	NGH-	-----APY
Llac-5298	TNSND-APGM	MVHPFHVHGTQ	FLVLSR---	NGH-	-----APY
Ppar-3909	TNTNDMVGGM	IHPFHIHGTQ	FLVLSR---	NGH-	-----APY
Paci-5930	SNTNDMEGGM	IHPFHIHGCQ	FQLIDR---	NGH-	-----AVN
Ecol-6898	SGVGDM--M	LHPFHIHGTQ	FRILSE---	NGK-	-----PPA
Bsub-6077	VNPTQ--G-	THPIHLHLVS	FRVLDRRPFD	IARYQERGEL	SYTGPAVPPP
Consistency	5857712277	7*8*8*778	*588680000	0000008850	0000000664

	560	570	580	590	600
Lpla-J16	PNEHGLKDTV	GVNPGETVRI	KVKF-ELTG-	---VYMYHCH	IIEHEDGMM
Ppen-4816	PNEHGFKDTI	GVNPGETVRL	LVRF-DLPG-	---VYMYHCH	IIEHEDGMM
Lpar-4314	PNEHGFKDTV	GVNPGETVRL	LVRF-DLPG-	---VYMYHCH	IIEHEDGMM
Llac-5298	PNEHGFKDTV	GVNPGETVRL	LVRF-DLPG-	---VYMYHCH	IIEHEDGMM
Ppar-3909	PNEYGWKDTV	SVNPDEHVQI	KVRF-EYTG-	---VYMYHCH	IIEHEDGMM
Paci-5930	PNEHGWKDTI	GVNPNETVRI	RVKF-TKLG-	---IFMYHCH	IIEHEDTMM
Ecol-6898	THRAGWKDTV	KVE-GNVSEV	LVKF-NHDAP	KEHAYMAHCH	LIEHEDTMM
Bsub-6077	PSEKGWKDTI	QAHAGEVLR	AVTFGPYSG-	---RYVWHCH	IIEHEDYDMM
Consistency	8785*5**9	5876786778	4*6*054380	0006986***	98****48**

	610	620	630	640	650
Lpla-J16	AQIESYDPQH	P-QTYHLM	DTLRNAFAKE	QGIKPEDVWM	PGM-----
Ppen-4816	AQIETFDPAK	PKQEYKLMD	DTLMALAKE	RGVKPSEIWM	GGMQSYEKMG
Lpar-4314	AQIETFDPAK	PKQEYKLMD	DTLMALAKE	RGVKPSEIWM	GGMQSYEKMG
Llac-5298	AQIETFDPAK	PKQEYKLMD	DTLMALAKE	RGVKPSEIWM	GGMQSYEKMG
Ppar-3909	AQIESYDPDH	PK-TYKLMD	DTLMHAFAKE	NNIEPKDLWL	GGMGSYEKMG
Paci-5930	AQIEIFDPAH	P-IEYHLM	PHKM-----	-----	-----
Ecol-6898	LGFTV-----	-----	-----	-----	-----



**Figure S1:** Multiple sequence alignment and conservation scoring of the *P. parvulus* 3909, *L. paracasei* 4314, and *L. lactis* 5298 laccases using Praline software [41]. The scoring scheme works from 0 for the least conserved alignment position, up to 10 for the most conserved alignment position, and the identical conserved residues are indicated by asterisks (colour scale indicated on top). Dashes indicate gaps to maximize alignment. Encased inside boxes are the motifs that form the four copper ligands and are highly conserved in laccases (conserved sequence of these motifs are HXHG, HXH, HXXHHX and HCHXXHXXXXXM/L/F [11])