

A novel starch binding laccase from the wheat pathogen *Zymoseptoria tritici* highlights the functional diversity of ascomycete laccases

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Table S1 List of *Zymoseptoria tritici* (ZtrLac1A) and 6 other homologues with bimodular organizations

	Locus number	Length	Identity (Catalytic domain)	CBM	Linker length
<i>Zymoseptoria tritici</i> , ZtrLac1A	XP003852363	723	100%	110	12
<i>Zymoseptoria brevis</i> , ZbrLac1A	KJX94131	723	99%	110	12
<i>Sphaerulina musiva</i> , SmuLac1A	XP_016758816	742	69%	108	32
<i>Pseudocercospora musae</i> , PmuLac1A	KXT09849	746	68%	107	32
<i>Mycosphaerella eumusae</i> , MeuLac1A	KXS98121	719	69%	107	17
<i>Pseudocercospora fijiensis</i> , PfiLac1A	XP_007930185	587	68%	--	--
<i>Dothistroma septosporum</i> , DseLac1A	EME38505	729	68%	107	12
<i>Daldinia eschscholtzii</i> , DesLac1A	AEX97872	418	60%	--	--
<i>Baudoinia panamericana</i> , BpaLac1A	XP_007679364	703	62%	108	17

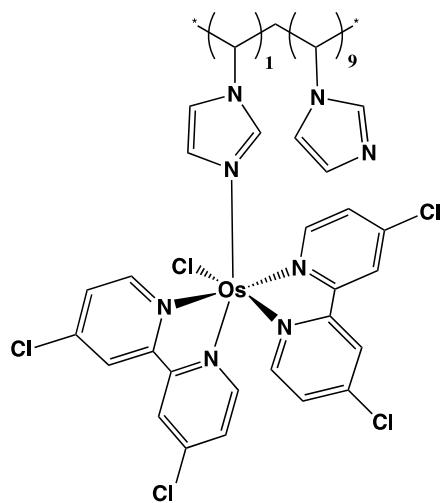


Fig. S1 Chemical structure of the osmium polymer $[\text{Os}(4,4'\text{-dichloro-2,2'-bipyridine})_2(\text{polyvinylimidazole})_{10}\text{Cl}]\cdot\text{Cl}$ with formal potentials $E^\circ = 0.549 \text{ V vs. SHE}$

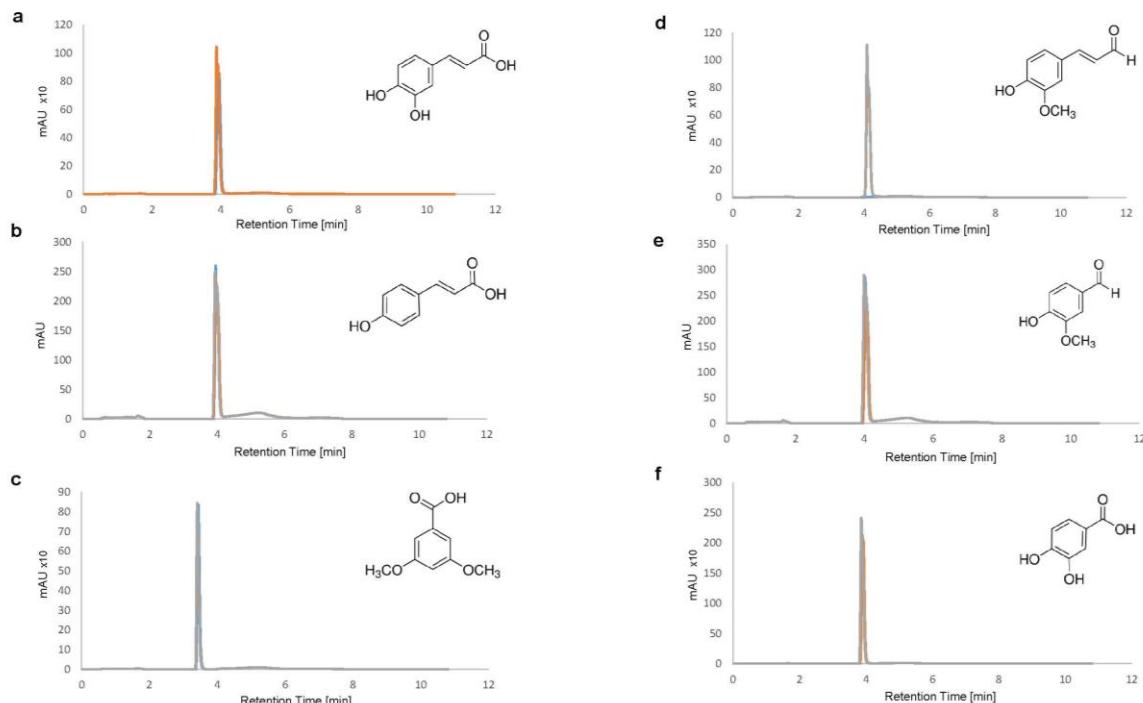
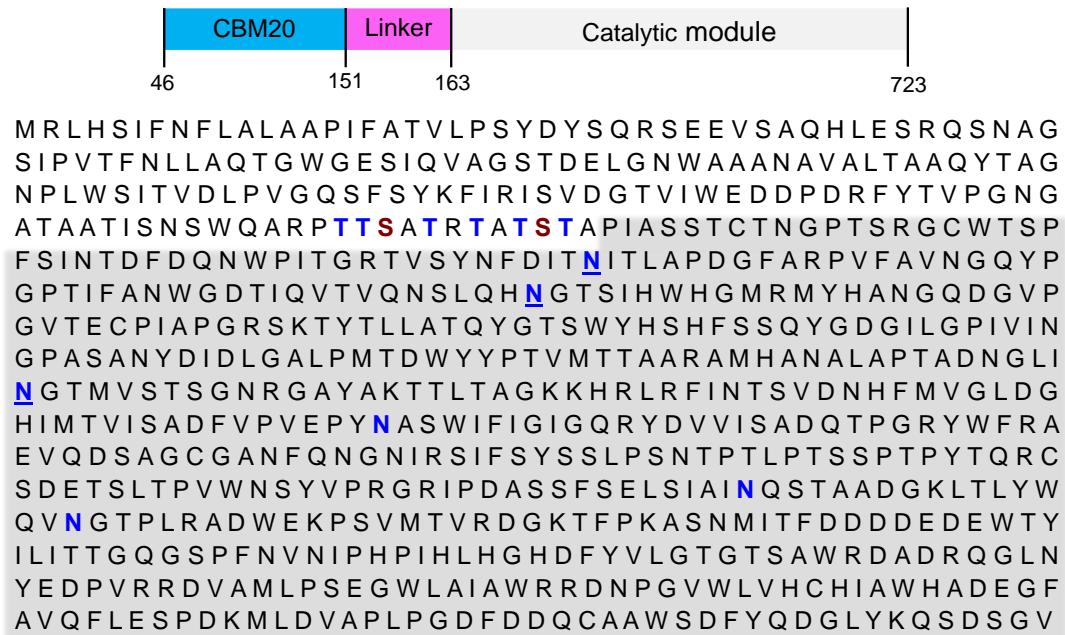


Fig. S2 HPLC ultimate profiles of different aromatic substrates assayed for *ZtrLac1A* activity screening. The substrates are: (a) caffeic acid, (b) *p*-coumaric acid, (c) 3,5 dimethoxybenzoic acid, (d) coniferyl aldehyde, (e) vanillin and (f) 3,4 dihydroxybenzoic acid. All reactions were conducted in 0.5 ml for 45 and 90 min depicted in orange and blue respectively and controls are shown in grey. The reaction mixtures were analyzed by high performance liquid chromatography (HPLC3000), using reversed phase column C-18 (Kinetex LC column 100 mm x 4.6 mm, particle size 2.6 μm). The elution was performed using a gradient of solvent A: water/TFA (100:0.01; v/v), solvent B: acetonitrile/TFA (100:0.01; v/v) and detection was conducted at 285 and 322 nm. The

steps of gradient were linear from 0-4% of B for 5 min, 4-30% of B for 2 min and 30-100% of B for 2 min eluted at flowrate of 1.0 ml/min at room temperature

a



b

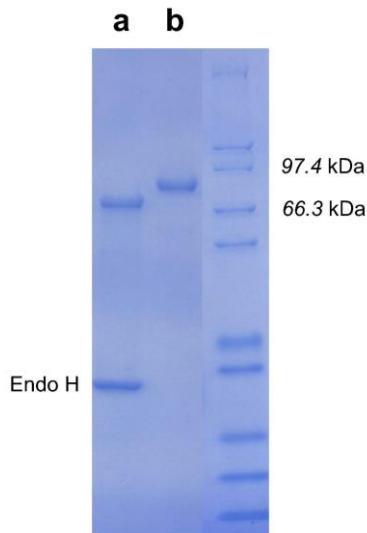


Fig. S3 (a) Laccase catalytic module, carbohydrate binding module and linker are colored in grey, blue and pink, respectively. Asparagine residues predicted to be *N*-glycosylated are colored in blue and those with more than 0.6 potential indicated with underline. (b) Purified *ZtrLac1A* analyzed using SDS-PAGE after EndoH treatment A and before EndoH treatment B. The Mark 12 protein standard (Invitrogen) is in right lane

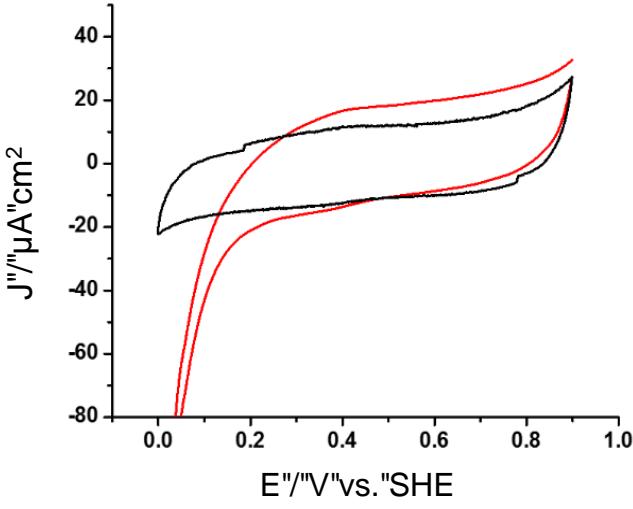


Fig. S4 Voltammograms recorded with naked graphite low-density electrode in N_2 (black line) and in the presence of O_2 (red line); Conditions: 0.1 M acetate buffer pH 4 in 0.1 M $NaClO_4$; scan rate 10 mVs⁻¹

a

Loop A

ZtrLac1A	351	--IP--D-A-SSFSELS--IAIN--	QSTAADKG--LT--LY	ABS19940_1	351	--N-WNN-LETATVG--	KNTA--GL--FK		
CCD50266_1	347	--P--L-S-GNVQLN--VAIN--	IGVDASGP-----I--VT	CEF67058_1	351	--N-WSD-LETATVG--	KNTA--GL--FK		
APA14269_1	347	--P--L-S-GNVDTLN--VAID--	IGVTTSGP-----I--VT	AFG30950_1	345	--S-ST5-TEAATVA--	FNDD--SL--FR		
ALR81978_1	346	--P--L-E-AHVIDL--VAIN--	IGVNNTSGP-----I--VT	XPO03712139_1	353	--T-WAD-TETASVA--	FNEE--NL--FR		
AGZ90172_1	355	--V--V-G-EAKDHKM--EVNS--	FSDPAKDN-----L--FR	AE064417_1	348	--TAAWTE-DEPVITG--	AAPTNA--NY--LW		
CCT61140_1	344	--T--P-K-ELVAGFD--AEY--	TDVTHSNG-----V--VQ	APA07387_1	350	--S-KSA-DEAVTIA--	QNSN--KL--FK		
AHZ58328_1	342	--G--FAT-STQEDIS--VSAP--	TQVVVQGD-----NV--FR	AQA29307_1	349	--Q--NQD-TKNTVITG--	L-APGT--NV--FK		
AHZ58333_1	342	--G--F-S-AGETDIS--VSGP--	SERVTVQGE-----NV--FR	EAQ71537_1	355	--T-WTH-FDLASWN--	RTSD--NL--LR		
AHZ58327_1	342	--G--F-P-GNQSTIP--VSAP--	QRVSIDGD-----MV--FR	CAK48347_1	351	--G--YKS-HNEANVI--	MNSA--GL--YK		
AHZ58330_1	349	--Q-LSS-SDQSVPMMNVSPG--	VSDVNDLGD-----TV--TR	CCT64283_1	352	--D-MEV-IQNANRS--	WNSD--GI--IK		
Mallac1A	348	--S-FVK-RFDNTLP--VALD--	L-TGT-----PL--FV	CEF85471_1	352	--D-HOF-EQNANRTR--	WNED--GI--IK		
AE058496_1	344	--G-FVK-RFDNTLD--VTLD--	T-TGT-----PL--FV	AH265139_1	352	--D-MEV-VENANRS--	EVAE--NA--LL		
ADA41449_1	348	--G-FAK-RADNTLD--VTLD--	T-TGT-----PL--FV	CAA48951_1	344	--F-AXS-TTEEVAI--	EQIA--GR--VD		
AE03715087_1	344	--G-FAK-KPENTLD--VTLD--	T-TGT-----PL--FV	AAY9673_1	351	--A-DVT-DNRAVAV--	FGDV--P L--YL		
TarLac1A	347	--N-FVK-RFSNTLG--VTLD--	I-GGT-----PL--FV	CAK40046_1	353	--GAQMAE-SDVDFTP--	PL-ANGE--LA--LR		
CAA70061_1	348	--G-FTP-RFNNTLP--VSLT--	L-GGT-----PL--FV	ACR16059_1	346	--A-LTR-NFDANL--	PS-QGDN--YA--VR		
CAP61995_1	348	--G-FTP-RFNNTLP--VSLT--	L-GGT-----PL--FV	CAP65571_1	350	--A-LTQ-NFNAVTL--	360	--V-NQI-GPHDYL--IG-EQQK1PTFWEKDP--	R V--HL
EAA27703_1	348	--S-IAL-NTGNTP--ITLD--	G-FV	AG059042_1	327	--A-NPL-AAEDYFR--VGLGNTW--DATNSTG--SV--FL	356	--H-NDY-YIKNSFK--VHL--VGPNEFKDS--MM--HK	
AAA33105_1	350	--G-FVA-ASDNTLD--VQLS--	T-TTR-----K--FV	CCT66683_1	363	--A-NVN-YQNEFSK--VHL--VGPDDTAESS--TL--HK			
XPO03711640_1	348	--V-FRA-SSDNTLN--TAVT--	TKNW-EGV--QR--VY	CEF71993_1	361	--T-PDQ-LKRKTFP--FDVL--KQDNFTMPPE--	GWTGDTPTW		
CDE29442_1	357	--S-FT--TGNTNL--TRLQ--	ISTT-GGI-----SR--VY	CAK46289_1	375	--K-LDERDRSKUL--LGIE--KVDRPHAGD--RF--SW			
EAA27863_1	358	--D-FSD-TKVDTLS--VTLD--	VKEVNKG-----SK--VL	CCT71494_1	376	--E-LN--NRSQCLT--IGLE--VUNRPAVN--NF--TW			
BAB32575_1	348	--E-FTP-NK-NILD--VSLE--	QEPI-HGE-----KI--YR	AH265141_1	374	--K-IN--YTKSQFD--IGLS--KAHRPELM--NF--TW			
AFK76451_1	350	--E-FTP-HK-NILD--VNLT--	TEPV-YQ-----FV	CCT72796_1	374	--K-IN--YTKSQFD--IGLA--KAHRPELM--NF--TW			
XPO03715087_1	356	--Q-FAA-QF-KELP--VDLT--	QVLT-TRG-----TV--FH	ABS19939_1	375	--E-LD--YEKAOFD--IGLK--KXKDRPEKGD--GF--QW			
CDE31732_1	371	--E-FAG-SAVGTLP--VTLE--	FPNH-GRG-----QV--FE	SCH65047_1	383	LNFT--ATK-QTNASHS--LGPP--WY--KH			
ABY89704_1	345	--T-FAA-QA-KSLP--VAFG--	EPAVQNN-----L--VL	AEO64912_1	400	--P-LNN-LTLSFTF--PSHQ--TDDVPY--G--NY--TH			
AHN82367_1	352	--T-FAA-QS-KSMS--VALG--	EPAVQNN-----T--VL	EAA29734_1	383	--P-LNP-LTLSFTY--NARQ--TWDQTLGSG--NY--SH			
BacLac1A	351	--S-LVDEQVS--SAFT--NY--FT	SAFT-----NY--FT	CAE64870_1	375	--S-YVK-TMELQV-----RNAS--G I--VQ			
AAK77953_1	352	--S-LVDEQVS--SAFT--NY--FT	SAFT-----NY--FT	AHC30245_1	372	--D-KTI-ELDISSF--KNAS--NV--TL			
ABM21605_1	351	--S-LVDEQVS--FSA-----NY--FT	FSA-----NY--FT	CCT64574_1	372	--D-KTI-ELDISSF--KNAS--NV--TL			
ABM21603_1	351	--A-LMDEKLN--WILG-----NV--IT	WILG-----NV--IT	ABS19938_1	372	--D-KTI-ELDIASF--KNAS--NI--TL			
ABM21604_1	351	--A-LMDEKLD--WVRG-----NI--LT	WVRG-----NI--LT	CEF84713_1	372	--D-LTL-DLDIELF--KNAS--NV--TL			
APA07533_1	351	--A-LMDEKLD--WVRG-----NI--LT	WVRG-----NI--LT	AGT80114_1	372	--D-LTL-DLDIELF--KNAS--NV--TL			
CAM12502_1	353	--T-ASS-VAEQTLS--FAPG--SA--FT	FAPG-----SA--FT	AHD26939_1	372	--D-LTL-DLDVELH--VNAS--NV--TL			
AGZ62514_1	351	--VTT-TASESLN--FKPD-----SY--FK	FKPD-----SY--FK	ANH22780_1	372	--D-LEY-TLEVKKF--QNAS--NV--NL			
AAK77952_1	340	--S-IMKTTLT--TGGG-----Q	IMKTTLT--TGGG-----Q	ACS45199_1	372	--A-VTH-DIELKVS--KNAT--GH--TL			
EAA30359_2	354	--QR-SFDTYLN--ISTT-----NY--VH	SFDTYLN--ISTT-----NY--VH	EAA34842_1	350	--A-VTK-EMKIEAY--RNAS--D V--FL			
XPO03718807_1	357	--SG-MITQTGL--FSATGDDLGHNW-----FQ	FSATGDDLGHNW-----FQ	CAP67656_1	375	--T-YTQ-TMELIELF--TNAS--NV--TL			
CAP64719_1	361	--FN-TTLENLG--TRPQGVD-GAEW-----FQ	TRPQGVD-GAEW-----FQ	AE054598_1	375	--T-LTH-TMDIELF--TNAS--NV--TL			
EAA61461_1	350	--AG-QENLNWG--WYD-----LPELY--FH	WYD-----LPELY--FH	AE065600_1	375	--A-ITQ-TMDIELF--KNAS--NV--TL			
EAA62557_1	358	--D-YQN-NALASUS--FNED-----HF--FR	FNED-----HF--FR	APA07098_1	378	--STK-NLDINFY--VNET--GT--LL			
CAP98129_1	350	--E-WNN-LTDVTLR--RNNA-----NL--FR	RNNA-----NL--FR	XPO03720855_1	377	--T-TIQ-EFVAE1F--TNSS--G V--SL			
BAE54583_1	354	--NPLYNE-SEPVLG--KNSQ-----SL--YR	KNSQ-----SL--YR	APA14467_1	383	--P-TTQ-HIDIAFG--PNST--GN--YQ			
CCT67757_1	351	--N-WND-LETATVG--KNTA-----GL--FK	KNTA-----GL--FK	AG059052_1	333	--A-TTQ-IINVTLA--QNET--GQ--YL			

b

Loop B

A2zLac1A	429	QGS---P FNV-N- I P I H L H G H D F Y V L - -GT-GTS-A-
CCD50266_1	426	NGN---P F V S I - N V P I H M L H G H D F L L - -GT-GVG-T-
PA14269_1	426	AGQ---P F V S I - N V P I H M L H G H D F Y V L - -GT-GVG-N-
ALR81978_1	425	NGQ---P F V S I - N V P I H M L H G H D F Y V L - -GT-GVG-V-
GAC97012_1	430	---Q I-A- L P I H P I H L H G H D Y V V Y - -GT-GTG-T-
CCT61140_1	419	---T A P -T-Q P H P I H L H G H D F Y V L - -DS-QAN-A-
AH258328_1	420	---G- I A P I H P I H L H G H D F N V I - -SS-GSC-T-
AH258333_1	419	---G- V A P I H P I H L H G H D F N V I - -ST-GLG-T-
AH258327_1	419	---P- V A P I H P I H L H G H D F N V I - -SS-GTG-N-
AH258330_1	427	---I- A N P I H P I H L H G H D F N V I Y Q S G V - -NAG-P-
MalLac1A	422	---E G F F S- L P I P M H L H G H D F L V L - -GR-SPD-VPA--ASQPF-
OEO58496_1	418	GAFF-T- L P I P M H L H G H D F Y V L - -GR-SPD-ESP--AASNEF-
ADA41449_1	422	GAFF-T- L P I P M H L H G H D F Y V L - -GR-SPD-ESP--AASNEF-
OEO68473_1	418	EAVI-S- L P I P M H L H G H D F L V L - -GK-SPV-SPV--GAQVW-
TarLac1A	421	---T N P I V S- L P I P M H L H G H D F L V L - -GR-SPD-ELP--ASQPF-
AA70061_1	422	TGFP-S- L P I P M H L H G H D F L V V - -GR-SPD-QPAG--VPOTTF-
CAP61995_1	422	TGFP-S- L P I P M H L H G H D F L V V - -GR-SPD-QPAG--VPOTTF-
EAA27703_1	417	DGAF-S- L P I P M H L H G H D F L I I - -GR-SPD-VTA--ISQTF-
AAA33105_1	421	TAIGNA- L P I P M H L H G H D F V V I - -GR-SRN-VSP--TAQTF-
XP003711640_1	423	---F P -P- A P I H P I H L H G H D F Y V L - -GR-SAN-MP--
CDP29442_1	433	---S- I P V H R H L H G H D I I I L - -GA-SPA-LAAPINPTNRL-
EAA27863_1	436	---FS- P I P M H L H G H D F L L - -GR-SRF-PANPLVDPGQE-
BAB23257_1	424	---A- L P I P M H L H G H D F L L - -GI-GDG-KF-
AFK76451_1	426	---L- L P I P M H L H G H E N S L L - -GI-GDG-SF-
XPO03715087_1	432	---A- G L P I P M H L H G H D L L L L - -GT-GES-CT-
CDP31732_1	448	---A- L P I P M H L H G H D F L T L - -GI-GSG-TF-
AYA89704_1	422	NAP-P- I A P I H P I H L H G H D S Y I L - -GO-GTQ-G-
AHN82367_1	429	GAP-P- I A P I H P I H L H G H D S Y I L - -GO-GVG-Q-
BacLac1A	421	GF-G- I W P I H P I H L H G H D F V V V - -AQ-EID-V-
AAR77953_1	422	---GF-G- I W P I H P I H L H G H D F Y V V - -AQ-EID-V-
ABM21605_1	421	---GF-G- I W P I H P I H L H G H D F Y V V - -AQ-EAT-V-
ABM21603_1	421	---TA-G- T W P I H P I H L H G H D F Y V V - -GO-EQA-V-
ABM21604_1	422	---HS-G- T W P I H P I H L H G H D F Y V V - -GO-EAA-V-
APA07533_1	422	---HS-G- T W P I H P I H L H G H D F Y V V - -GO-EAA-V-
CAM12502_1	426	---GI-G- L P I P M H L H G H D F W V I - -GO-STG-T-
AGZ26251_1	421	GF-G- L P I P M H L H G H D F W V V - -AO-DVG-T-
AAK77952_1	407	---GP-N- H P I H L H G H D F W T L - -SO-STG-A-
ABA30359_2	425	---NL-G- L E P I P M H L H G H D F W I L - -DO-STG-T-
XP003718807_1	437	LGI-R- I D P I P M H L H G H D F W I L - -SO-DTT-P-
CAP64719_1	438	---Q-I-G- A A P I H P I H L H G H D F W V L - -AAVPG-A-T-
EEA16416_1	421	---LV-N- A Y P F P I H P I H L H G H D F F I L - -AQ-GRG-L-
EEA62557_1	426	---T-I-P- V S P I P M H L H G H D F F I L - -AQ-GTN-P-
CAP98129_1	420	---SF-P- I S P I P M H L H G H D F F I L - -AQ-GSN-P-
BAE54583_1	424	---TL-S- V P P I P M H L H G H D F V V L - -SO-SGS-T-
CCT67757_1	419	---TL-P- V P P I P M H L H G H D F F I L - -AO-GTG-T-

ABS19940_1	419	--AL-P--V	HPIHLHGHDFFIL--	AQ-GTG-T
CEF76058_1	419	--SL-A--V	HPIHLHGHDFSIL--	AQ-GTG-T
AFG30950_1	413	--TF-A--V	HPIHLHGHDFFVL--	AQ-GSG-T
XPO03712139_1	422	--TL-P--V	HPIHLHGHDFFQL--	AQ-GIG-E
ABE64417_1	420	--AL-G--V	HPIHLHGHDFFVL--	AQ-GTG-T
APF07387_1	418	--RI-P--V	HPIHLHGHDIFYL--	SQ-QSS-P
ABA29307_1	418	--AN-T--P	HPIHLHGHDPPVY--	AS-GGS-S
EAO71537_1	423	--NA-S--A	HPIHLHGDFPYLL--	AQ-GSG-R
CAK48347_1	419	--EI-N--V	HPIHLHGDPFIL--	AQ-GKG-S
CCT64283_1	419	--EQ-D--I	IHPHPIHLHGDFQIL--	AQ-GPG-P
CEP85471_1	419	--EL-D--I	IHPHPIHLHGDFYHIL--	AQ-GVG-P
AHZ65139_1	419	--NL-D--I	IHPHPIHLHGDPFQL--	AQ-GSG-P
CAK44895_1	412	--PF-A--QD	HPIHLHGHDFFWL--	AS-GYG-D
AAA99671_1	419	--TM-G--V	HPIHMPIHLGHDFWL--	GA-CTG-T
CAK40446_1	425	--DL-P--V	HPIHLHGHDFFYL--	AQ-GFG-Q
ACR16059_1	417	--LL-P--L	IAPHPIHLHGHDPPYLL--	TR-GRG-R
CAP65571_1	424	--LA-L--P	IAPHPIHLHGHDTPYLL--	AR-GTG-P
BAA08486_1	449	--TPRNILT-P--SV	HPIHLHGHDPAIIL--	AQ-GKG-P
AGO59042_1	417	DQYQEIRVEP--SV	HPIHLHGHDPLIL--	AQ-GLG-K
CCT66683_1	456	KVY--KTQA-P--V	VAHPIIHLHGHDPPVY--	DG-GTE-E
CEF71993_1	461	KIV--KTQA-P--V	VAHPIIHLHGDFVLL--	AS-GDK-E
CAK46289_1	459	--PGESII-P--AA	HPIHMPIHLGHDFPAL--	KQ-SVD-S
CCT71494_1	461	--NKTFR-S--A	IAPHPIHLGHDFPAL--	AQ-GTN-S
AHZ26514_1	460	--K1K1FA-P--VA	HPIHMPIHLGHDFPAL--	AQ-GSD-S
CCT72796_1	460	--PNRAFA-P--VA	HPIHMPIHLGHDFPAL--	AQ-GTN-F
ABS19939_1	460	--PNRAFA-P--VA	HPIHMPIHLGHDFPAL--	AQ-GTN-F
SCB65047_1	461	--PDVRFA-P--VA	HPIHMPIHLGHDFPAL--	AQ-GTN-F
ABE64812_1	454	--LL-P--SN	HPIHLHGSDFVAL--	AQ-ETV-P
AAA29734_1	500	--LDPPVI-P--LLA	HPIHMPIHLGHSDFVAL--	AQ-SEQ-P
CAP64870_1	484	--LGSQLV--PNRGA	HPIWMHGTDVVIL--	GQ-SNE-R
AHC30245_1	444	--P--AA	HPIHMPIHLGNFMVY--	AE-DGLT
CCT64574_1	441	--P--VA	HPIHMPIHLGNFMVY--	HE-GPG-S
ABA19938_1	441	--P--VA	HPIHMPIHLGNFMVY--	HE-GPG-S
CEF84713_1	441	--P--VA	HPIHMPIHLGNFMVY--	HE-GLG-D
AGT80114_1	441	--P--V	VSHPIHMPIHLGNFMVY--	HE-GPG-T
AHD26939_1	441	--P--VA	HPIHMPIHLGNFMVY--	HE-GPG-T
ANH22780_1	441	--P--V	HPIHMPIHLGNFMVY--	HE-GPG-T
ACS45199_1	441	--P--AS	HPIHMPIHLGNFMVY--	HE-GAG-A
EAA34842_1	419	--P--GP	HPIHMPIHLGNYNFVY--	SQ-GPG-D
CAP67656_1	444	--A--GP	HPIHMPIHLGNNPVY--	HE-GPG-D
ABE054598_1	444	--P--SA	HPIHMPIHLGNVY--	HE-GPG-E
ABE065600_1	444	--P--GP	HPIHMPIHLGNHFVY--	HE-GPG-E
APF07098_1	447	--P--AS	HPIHMPIHLGNMQL--	HE-GPG-N
XPO03720855_1	446	--P--GA	HPIHMPIHLGANVVP--	AE-GSG-A
APF14467_1	454	--P--V	VPHPIHMPIHLGHNFVY--	NQ-GVG-T
AGO59052_1	404	--I--RT	IHPHPIHLGHNFVY--	AV-GLG-E

C

Loop C

strLac1A	378	--WQV-	NGTPLRADWKEFPS	/MTVRDG-K-T--FP-
CCD50266_1	372	--WGI-	NESEAIDVNKKFI	/QYVLQDNNG-S--WP-
APA14269_1	372	--WGI-	NEITALDVKDKF	/IQLYVLQDNNG-S--WP-
ALR81978_1	371	--WGI-	NLTADVNNDKF	/LEYVLEGNN-S--WP-
AGZ90172_1	380	--WLI-	DFTPHIVNNNKF	/LETWLGGST-N--FG-
CCT61140_1	368	--WLI-	SHAMVMAIDLDHET	/LQSVMDCGN-T--FP-
AHZ58228_1	369	--WLV-	SHAMVMDWDNSYTF	/LQVADVNNDN-T--FA-
AHZ58333_1	368	--WLV-	NGAMMNIIDFNYTF	/QLQADGNS-T--WN-
AHZ58327_1	368	--WFI-	NGAMMNIIDFNYTF	/LQVADVNNDN-T--FA-
AHZ58330_1	379	--WRI-	HEAS1IDVDWTYTF	/QLQKLQDHNR-S--FP-
Mallac1A	371	--WKV-	NESSDINVNDDGKF	/IDYLTGNT-S--FP-YP-
AE058496_1	367	--WKV-	NESSA1IDWGKFI	/DVYLTQNT-S--FP-
ADA41449_1	371	--WKV-	NESSA1IDNGRAV	/DVYLTQNT-S--FP-
AE068473_1	367	--WKV-	NESSA1IDNWNNF	/DVYDVMKGNL-S--FP-
TarLac1A	370	--WKV-	NGSAINVNDDGKF	/IDYLMGSNN-S--FP-YP-
CAA00761_1	371	--WKV-	NGSAINVNDDGKF	/IDYVIAQNT-S--FP-YP-
CAP61995_1	371	--WKV-	NGSSINVNDDKFI	/DVYVIAQNT-S--FP-YP-
EAA27703_1	366	--WRV-	NGTAINVNWNKF	/LEYVLTQNT-N--YS-
AAA33105_1	370	--WTI-	NGSTLDVNDDHF	/IQLQVINKST-A--WP-
XPO03711640_1	374	--WTV-	NNVDMNITWNDEFT	/LELYVAKRGN-N--IP-
CDF29442_1	381	--WTV-	NNPTMMTNWNDEFT	/LELYVAKRN-N--IP-
EAA28763_1	385	--WSV-	DESA1IDWDKRF	/LEYVVEGNF-T--FP-
BAB32575_1	373	--WRV-	NESSMDVNQWDKF	/IQLQYAEQND-S--FP-
AFK76451_1	375	--WTV-	NEHSMDIENWDKF	/TLYVAAEKNY-T--FP-
XPO03715087_1	381	--WLV-	NGSA1IDVNEKF	/IQLQYAEKNT-S--FP-
CDE31732_1	397	--WRV-	KUTPINNEHDHF	/LEYVLENNNS-S--FP-
AYB89704_1	369	--WTI-	NETQSVUPDGNTE	/PKYVAAENN-N--FP-
AHN82367_1	376	--WTV-	NESSQIVUPDGNTE	/PKYVAAEQN-S--FP-
BacLac1A	367	--WTI-	NESSLLLDWNSPF	/TLK1FNNET-I--FP-
AAK77953_1	368	--WTI-	NESSLLLDWNSPF	/TLK1FNNET-I--FP-
ABM21605_1	367	--WTI-	NESSLVLDWNSPF	/TLK1FNNES-I--FP-
ABM21603_1	367	--WTI-	NESSLVLDWTNF	/TLQVFRNES-I--FP-
ABM21604_1	367	--WTI-	NESSLVLDWTNF	/TLQVFRNES-L--FP-
APA07533_1	367	--WTI-	NESSLVLDWTNF	/TLQVFRNES-L--FP-
CAM12502_1	372	--WTI-	NESSLLLDNDFNT	/FLMIANGES-P--FP-
AGZ62514_1	369	--WTL-	NESSLLLDNDFNT	/FLMIANGES-P--FP-
AAK77952_1	353	--WLF-	NESSLLLDNDFNT	/TLRVNGSS-V--FP-
EAA30359_2	371	--WTI-	NESSLLLDNDFNT	/TLTVLNSGN-I--WP-
XPO03718807_1	380	--WTL-	NESSLVLDWNNSP	/TLQVNGES-L--FP-
CAP64719_1	383	--WTL-	NESSLVLDWSKEV	/LQKVDFDRP-I--FP-
EAA61461_1	370	--WTL-	NEFKALTIDWGT	/TLK1LYNNES-V--FP-
EAA62557_1	377	--WFL-	NESTMVQWYWEFT	/LQLQLNGDD-S--FE-
EAA98129_1	369	--WYL-	NESTMVQWLEWEFT	/LQLQFNNEEN-TP--FP-
BAE54583_1	375	--WKL-	NESTMVHWNDFP	/LQLQYRHTH-S--FP-
CCT67757_1	370	--WML-	NESTMVHDWANT	/LAQVLDNTD-D--FP-

ABS19940_1	370	--WML--	NTSMLWDWANPTLAQVLNDTT-D-FE-
CEF76058_1	370	--WGL--	NTSMLMDWANPTLAQLMNGT-E-FE-
AFG30950_1	364	--WYL--	NTSTMVWEESDPTLSCILNGNT-S-YE-
XPO03712139_1	372	--WYL--	NTTMVWDKNPVTQKVASGNT-S-VF-E
AE064417_1	371	--WVY--	NGSTLDMWSNPQLQVYDNT-A-FN-
APA70387_1	369	--WYL--	NISTFLTEWEDPTLNLVQEKT-T-FS-
AQA29307_1	369	--WYL--	NNVFFSEWEDPTLQVWGNHD-Y-VD-
EAQ71537_1	374	--WYL--	NTCSMSWDNSPNTLAQIHDNAT-E-YK-
CAK48347_1	370	--WYM--	GTFTKAEWDNSPNTLQIANGNT-S-WT-
CCT64283_1	371	--WAL--	NTSTMIAEWGEPSSLKL-NNSA-S-FT-
CEF85471_1	371	--WSL--	NTSTMIAEWDFPSLKL-GHNIV-S-FT-
AH265139_1	371	--WTL--	NTSTMVAEWDFPSLIRKL-RTN-T-FA-
CAK44895_1	363	--WTM--	NTCSFTHEWDPYTMIVANHY-N-T-WA-
AAV99671_1	370	--WAM--	GNTTFINEGXWPSTQCQVYDGN-T-WG-
CAK40046_1	374	--WTM--	GNALNISWSDKPTLQTFEDPD-KM--DWK-
ARL16059_1	367	--WEI--	NSNNSPLTPEPSLKLGDANS-SA-M-
CAP65571_1	371	--WRV--	GGSEFYRPPKPNPVKVQVIDTAEVN-LT-
BAA08486_1	390	--WTI--	KNTAVYIWQDWTPSPSLQKLADHDEE-FP-
AG059042_1	358	--WFL--	CQKLPLVNWSEPSPKKLTIDETAD-FP-
CET66683_1	385	--WVL--	ANSSFLYDWAEPSSLVXIAKSEGWNQNP-C-
CEF71993_1	392	--WVL--	RDSFSYLDWAEPSSLVXKAVAYEWDWKHKWP-
CAK46289_1	395	SAWEV-	NGAPAWNVQYDNLTHLNDNNHT-WH-
CCT71494_1	405	--WAF--	GEFRWLWLDENSPNTLTLERKE-RD-P-
AH265141_1	404	--WSF--	CDNFNLWDENSPNTLTLERKE-RD-P-
CCT72796_1	402	--WAF--	CDNFNLWDENSPNTLNLKN-TT-WN-
ABS19939_1	402	--WAF--	CDNFNLWLNFSNPNTLNLKN-TT-WN-
SCB65047_1	403	--WAF--	CDNFNLWLNFSNPNTLNLNN-DT-WD-
AE064812_1	405	--WTL--	QCKMFWLWDNSPNTLTLERKE-RD-P-
AEE29734_1	427	--WLLRDLPLVEKGGSVHFNLNFNSTPSSL	LDFNTNIQG---G-
CAP64870_1	413	--WLLRDLPNTEHOIGKSMSPFWLSDNSPNTLNLGAAAG---N-	-
ACB103245_1	394	--WTL--	DGEDPRDFNSPNTLQLQTKNNNL-T-YA-
CCT46574_1	391	--WTL--	CGVAARTNINYSNPNTLSSLKLGHN-T-FE-
ABS19938_1	391	--WTL--	CGVAARTNINYSNPNTLSSLKLGHN-T-FE-
CEF84713_1	391	--WSL--	CGVAARTNINYSNPNTLSSLKLGHN-T-FD-
AGT80114_1	391	--WKF--	GGVDFRANYNPNTLSSLKLGHN-S-FE-
AHD26939_1	391	--WRF--	GGVDFRANYNPNTLSSLKLGHN-S-FE-
ANH22780_1	391	--WSE--	GTDDFRGDVNPNTLSSLALGHN-T-FD-
ACS5191_1	391	--WTL--	DGEFRGRNPNSPNTLSSLNLGNL-T-FO-
EAA34842_1	369	--FLP--	DGV SARV DYN PVA DM VKG MN-S-T-FP-
CAP67656_1	394	--WKF--	NGVSMRTDHYNEPVLVANEGN-F-YE-
AE054598_1	394	--WKF--	NGVSMRDHYNPSPVLLANQNG-F-T-YE-
AE065600_1	394	--WKF--	NGVSMRTDHYNPSPVLLANQNG-F-T-YE-
APA70798_1	397	--WEL--	GTSFRANYYNPSPVLLADQGKFN--Y-Y-
XPO03720855_1	394	--FKF--	GTV SARVN DM PVA PLLANQNG-S-T-FP-
APA14467_1	402	--WTM--	INSS FRANYYNPSPVLLANQNG-S-T-YE-
AG059052_1	352	--FYM--	INSS FRANYYNPSPVLLANQNG-S-T-YE-

d**Cu1 site**

ZtrLac1A	498	LHVCHIAWHSSEGFAQFLE-SPDKM--L---D--V-----APLPG---FDFFDQCAA	ABS19940_1	481	LCHCHIGWHTSEGFAQFLE-RSSEI--A---NIS-----TSS---Y VSDVCDGW
CCD50266_1	496	LHVCHIAWHSSEGFAQFLE-SQNQI-N---A-V-----NPISP---S LTNTCNKW	CEP76058_1	481	LCHCHIGWHTSEGFAQFLE-RASEI--P---DIT-----TSS---Y VSDVCDSW
APA14269_1	495	LHVCHIAWHSSEGGLQFILE-TKEKI-N---S-V-----NPISP---A LTETCNNN	AFC30950_1	476	LMBCHIGWHTSEGFAQFLE-RYDEI--A---ATI-----DST---R LEDNCASW
ALR81978_1	493	LHVCHIAWHSSEGGLQFILE-RMSII-K---G-S-----LGDTG---T LTNPCNKW	XO03711640_1	479	LMBCHIGWHTSEGFAQFLE-RYDEI--A---ATI-----DST---R LEDNCASW
AG290172_1	484	LHVCHIAWHSSEGGLQFILE-QKSEI-P---D---T-----LGSLQ---GMGDCGRCW	AEO64417_1	483	LMBCHIGWHTSEGFAQFLE-MOVS---ALL-----DFO---L ESDNCASW
CCT61140_1	481	VNHCHIAWHSSEGGLQFILE-QKSEI-P---D---T-----VTLD---AEWDT CSTW	APR07387_1	483	LMBCHIGWHTSEGFAQFLE-QSEA---P---GIL-----DPW---S LGTCDDW
AH258328_1	480	VNHCHIAWHSSEGGLQFILE-QKSEI-P---D---T-----VTLD---AEWDT CSTW	AQA29307_1	480	LMBCHIGWHTSEGFAQFLE-RVDEI--P---GLF-----DED---K LRSCASW
AH258333_1	480	VNHCHIAWHSSEGGLQFILE-QKSEI-P---D---T-----VTLD---AEWDT CSTW	EAO71537_1	487	LMBCHIGWHTSEGFAQFLE-MOFVW-BKRDLLRN---PMI-----DYA---S LNGTCAAN
AH258334_1	491	LLHVCHIAWHSSEGGLQFILE-QKQDI-P---D---T-----TULG---AWEKT CTNW	CAK48347_1	481	LMBCHIGWHTSEGFAQFLE-SISQL---E---PMI-----DAS---A LEKNCASW
MalLac1A	498	LHVCHIAWHSSEGGLQFILE-QKSEI-P---D---T-----TULG---AWEKT CTNW	CEP76428_1	481	LMBCHIGWHTSEGFAQFLE-QOFIV-REDEI--P---SLV-----SDQEYKD IEEGCKAW
AE058496_1	494	LHVCHIAWHSSEGGLQFILE-RADDE---P---GAVG-----SEPD-----A	CEP76451_1	481	LMBCHIGWHTSEGFAQFLE-REDEI--P---DLV-----SDQEYKD MEKGCKAW
ADA41449_1	498	LHVCHIAWHSSEGGLQFILE-RADDE---P---GAVG-----SEPD-----A	AHC26139_1	481	LMBCHIGWHTSEGFAQFLE-REDEI--P---ALT-----SEQQAKD INQQCKAW
AE068473_1	494	LHVCHIAWHSSEGGLQFILE-RADDE---P---GAVG-----SEPD-----A	CAK44895_1	476	LMBCHIAWHTSEGFAVQLE---RAPEI--A---Y-----DYE---K LNNDTCASW
TarLac1A	498	LHVCHIAWHSSEGGLQFILE-RASDL---P---GAVS-----SEPD-----A	AEO96471_1	482	LMBCHIAWHTSEGFAVQLE---RASEI--P---DLI-----DAD---L MNSTCCAW
CAA70061_1	499	LHVCHIAWHSSEGGLQFILE-RASDL---P---GAVS-----SEPD-----A	AFC40046_1	495	LMBCHIGWHTSEGFAQFQVTE---RESEI--P---TFE-----L LENTCDAW
CAP61995_1	499	LHVCHIAWHSSEGGLQFILE-RENDL---P---NGFS-----QADKN---QHNNN CNAW	ACO40046_1	495	LMBCHIGWHTSEGFAQFQVTE---RESEI--P---TFE-----L LENTCDAW
EAA27703_1	493	LHVCHIAWHSSEGGLQFILE-RENDL---P---NGFS-----QADKN---QHNNN CNAW	CAP65571_1	487	LMBCHIGWHTSEGFAQFQVTE---RESEI--P---TFE-----L LENTCDAW
CDP31732_1	512	LHVCHIAWHSSEGGLQFILE-RQDM---P---NSIS-----PADKK---AFNDN CGDW	BAO08486_1	513	LMBCHIGWHTSEGFAQFQVTE---RESEI--P---TFE-----L LENTCDAW
AAA33105_1	497	LHVCHIAWHSAGLQTFILE-QFASV---AGLN-----TNDVN---Q LNSCKSW	AGOS9042_1	487	LMBCHIGWHTSEGFAQFQVTE---RESEI--P---TFE-----L LENTCDAW
XP003711640_1	493	LHVCHIAWHSAGLQTFILE-QFASV---AGLN-----TNDVN---Q LNSCKSW	CTC76683_1	524	LMBCHIAWHTSEGGLQFILE-SPRVI---G-----PMXK-----SGLLE---TYSET CANN
CDP29442_1	503	LHVCHIAWHSAGLQTFILE-QFASV---AGLN-----TNDVN---Q LNSCKSW	CFE17993_1	529	LMBCHIAWHTSEGGLQFILE-SPRVI---G-----SGLIP---HYSEQ CNNN
EAA27863_1	512	VFHCHIAWPHSEGGLQFILE-RVDRJ---N---DGA1---PNLMP---D LGEKCRDW	CAK46289_1	537	LMBCHIAWHTSEGGLQFILE-OKOKV---Q-----ELLKKDINPDOTARA---Q IDDGCKAW
BAB32575_1	502	VFHCHIAWPHSEGGLQFILE-RVDRJ---N---DGA1---PNLMP---D LGEKCRDW	COT71494_1	531	LMBCHIAWHTSEGGLQFILE-QLME---REDEI--R---RMTS-----EKLKQ---V NDGCKKW
AFK76451_1	498	VFHCHIAWPHSEGGLQFILE-RVDRJ---N---DGA1---PNLMP---D LGEKCRDW	AHC26151_1	528	LMBCHIAWHTSEGGLQFILE-QLME---REDEI--K---KLMT-----ERLRE---TTVR CRNW
XP003715087_1	502	VFHCHIAWPHSEGGLQFILE-RVDRJ---N---DGA1---PNLMP---D LGEKCRDW	CTC72796_1	529	LMBCHIAWHTSEGGLQFILE-QQLL---N-----RILDQY---PEKMKE---V NVRVCNN
CDP31732_1	512	VFHCHIAWPHSEGGLQFILE-RVDRJ---N---DGA1---PNLMP---D LGEKCRDW	ABS19939_1	529	LMBCHIAWHTSEGGLQFILE-QQLL---N-----RILDQY---PEKMKE---V CANN
ABY8704_1	488	VFHCHIAWPHSEGGLQFILE-RVDRJ---N---DGA1---PNLMP---D LGEKCRDW	CDP51240_1	501	LMBCHIAWHTSEGGLQFILE-QQLL---N-----RILDQY---PEKMKE---V CANN
AHNH2367_1	495	VFHCHIAWPHSEGGLQFILE-RVDRJ---N---DGA1---PNLMP---D LGEKCRDW	CEP76450_1	519	LMBCHIAWHTSEGGLQFILE-QQLL---N-----RILDQY---PEKMKE---V CANN
BacLac1A	488	VFHCHIAWPHSEGGLQFILE-RVDRJ---N---DGA1---PNLMP---D LGEKCRDW	CEP76451_1	519	LMBCHIAWHTSEGGLQFILE-QQLL---N-----RILDQY---PEKMKE---V CANN
AAK77953_1	487	VFHCHIAWHSSEGGLQFILE-QSSII-A---VHM-----TDTA-----IFEDT CANN	CAK47934_1	570	LMBCHIAWHTSEGGLQFILE-QQLL---N-----RILDQY---PEKMKE---V CANN
ABM21605_1	486	VFHCHIAWHSSEGGLQFILE-QSSII-A---VHM-----TDTA-----IFEDT CANN	CAK46289_1	556	LMBCHIAWHTSEGGLQFILE-QQLL---N-----RILDQY---PEKMKE---V CANN
ABM21604_1	486	VFHCHIAWHSSEGGLQFILE-QSSII-A---VHM-----TDTA-----IFEDT CANN	CTC76457_1	501	LMBCHIAWHTSEGGLQFILE-QQLL---N-----RILDQY---PEKMKE---V CANN
APA07533_1	487	VFHCHIAWHSSEGGLQFILE-QSSII-A---VHM-----TDTA-----IFEDT CANN	ABM21993_1	501	LMBCHIAWHTSEGGLQFILE-QQLL---N-----RILDQY---PEKMKE---V CANN
CAM12502_1	489	VFHCHIAWHSSEGGLQFILE-QSSII-A---VHM-----TDTA-----IFEDT CANN	CEP84713_1	501	LMBCHIAWHTSEGGLQFILE-QQLL---N-----RILDQY---PEKMKE---V CANN
AGZ62514_1	484	VFHCHIAWHSSEGGLQFILE-QSSII-A---VHM-----TDTA-----IFEDT CANN	AGT80114_1	501	LMBCHIAWHTSEGGLQFILE-QQLL---N-----RILDQY---PEKMKE---V CANN
AAK77952_1	467	VFHCHIAWHSSEGGLQFILE-QSESS---L---PTIG-----TADVS---T FQNT	AHC26139_1	498	LMBCHIAWHTSEGGLQFILE-QQLL---N-----RILDQY---PEKMKE---V CANN
EAA30359_2	490	VFHCHIAWHSSEGGLQFILE-QSESS---L---PTIG-----TADVS---T DSDRT	AC45119_1	502	LMBCHIAWHTSEGGLQFILE-QQLL---N-----RILDQY---PEKMKE---V CANN
XP003718807_1	500	VFHCHIAWHSSEGGLQFILE-QSESS---L---PTIG-----TADVS---T DSDRT	CEP76450_1	479	LMBCHIAWHTSEGGLQFILE-QQLL---N-----RILDQY---PEKMKE---V CANN
CAP64719_1	502	VFHCHIAWHSSEGGLQFILE-QSESS---L---PTIG-----TADVS---T DSDRT	CEP76451_1	501	LMBCHIAWHTSEGGLQFILE-QQLL---N-----RILDQY---PEKMKE---V CANN
EAA61461_1	493	VFHCHIAWHSSEGGLQFILE-QSESS---L---PTIG-----TADVS---T DSDRT	CEP76452_1	502	LMBCHIAWHTSEGGLQFILE-QQLL---N-----RILDQY---PEKMKE---V CANN
EAA62557_1	486	VFHCHIAWPHSEGFAQFLE-RVDEI---R---ENV-----D RDR---FVNNACTW	CEP76453_1	502	LMBCHIAWHTSEGGLQFILE-QQLL---N-----RILDQY---PEKMKE---V CANN
CAP98129_1	480	VFHCHIAWPHSEGFAQFLE-RVDEI---R---ENV-----D RDR---FVNNACTW	APR07098_1	507	LMBCHIAWHTSEGGLQFILE-QQLL---N-----RILDQY---PEKMKE---V CANN
BAE54583_1	485	VFHCHIAWPHSEGFAQFLE-RVDEI---R---ENV-----D RDR---FVNNACTW	XP003720855_1	506	LMBCHIAWHTSEGGLQFILE-QQLL---N-----RILDQY---PEKMKE---V CANN
CCT67757_1	481	VFHCHIAWPHSEGFAQFLE-RVDEI---R---ENV-----D RDR---FVNNACTW	APB14467_1	514	LMBCHIAWHTSEGGLQFILE-QQLL---N-----RILDQY---PEKMKE---V CANN

e**C-terminus**

ZtrLac1A	546	G-----LY---KQS-----DSGV	ABS19940_1	529	-----LI---E QE-----DSGV
CCD50266_1	545	A-----PY---IKT-----DSGV	CEP76058_1	529	-----SI---E QE-----DSGV
APA14269_1	545	A-----PY---FKT-----DSGV	AFC30950_1	524	-----SI---E QE-----DSGV
ALR81978_1	544	A-----PY---IK E-----DSGV	XO03711640_1	533	-----KV---A QE-----DSGI
AG290172_1	544	A-----PY---IK E-----DSGV	AEO64417_1	531	-----GL---K QE-----DSGI
CCT61140_1	533	Y-PNG---IL---IHG-----DSGV	APR07387_1	527	-----PY---H QE-----DSGI
AH258328_1	533	L-----Y-GKRT-----DSGV	AQA29307_1	528	-----NL---E QE-----DSGV
AH258333_1	529	L-----FW-GKRT-----DSGV	EAQ71537_1	537	-----GI---VIA-----DSGV
AH258327_1	530	L-----AY-GKRT-----DSGV	CAK48347_1	529	-----RI---E ED-----DSGI
AH258330_1	540	I-----Y-GPK-----DSGI	CTC76428_1	532	-----KM---E QD-----DSGI
MalLac1A	549	I-----Y-GPK-----DSGI	CEP85471_1	532	-----EM---E QD-----DSGI
AE058496_1	545	I-----Y-GPK-----DSGI	AHC26139_1	532	-----EM---E QD-----DSGI
ADA41449_1	549	I-----Y-GPK-----DSGI	CEP76451_1	522	-----DV---V QE-----DSGV
AE068473_1	549	I-----PP---HKV-----DSGV	CEP76452_1	530	-----AL---V QD-----DSGI
TarLac1A	553	I-----PP---PKI-----DSGV	ACR16059_1	532	-----ETP---D QE-----DSGI
CAA70061_1	550	I-----PP---PKI-----DSGV	CAP65571_1	537	-----ETTD-----DSGI
CAP61995_1	550	I-----PP---PKI-----DSGV	BAA08486_1	567	-----DIPN---DR---P QD-----DSGI
EAA227703_1	544	I-----PP---PKI-----DSGV	AGO59042_1	539	-----NIPH-----NA---T QE-----DSGV
AAA33105_1	548	D-----IP---K QD-----DSGV	CCT66683_1	576	-----NKHN-----NA---T QE-----DSGI
XP003711640_1	541	D-----IP---K QD-----DSGV	CEP71993_1	581	-----NKNK-----NA---T QE-----DSGI
CDP29442_1	551	A-----PP---L QD-----DSGV	CAK46289_1	594	-----ENRWNPD---AR---F QD-----DSGV
ABA27863_1	563	P-----EFPRMKV-----DSGV	CTC71494_1	582	-----NNHWNPV---G1---F QD-----DSGV
BAB32575_1	546	F-----PY---PKV-----DSGV	AHC26151_1	579	-----SNHWNNS---GP---F QD-----DSGV
AAK77951_1	550	F-----PY---PKV-----DSGV	CTC72796_1	582	-----TNLNNAH---I---F QD-----DSGI
AAK77952_1	544	A-----PY---PKL-----DSGV	ABS19939_1	564	-----TNLNNAH---I---F QD-----DSGI
CDP31732_1	559	A-----PY---PKL-----DSGV	SCB65047_1	581	-----TNLNNAH---I---F QD-----DSGI
ABY8704_1	536	T-----DVI---P QD-----DSGV	EAA33200_1	615	-----TNLNNAH---I---F QD-----DSGI
AHN82367_1	543	K-----AY---P QD-----DSGV	CDF31240_1	622	-----TNLNNAH---I---F QD-----DSGV
BacLac1A	535	I-----LF---AE D-----DSGV	AE064812_1	570	-----TV---V QE-----DSGI
AAK77953_1	536	LF---AE D-----DSGV	EAA29739_1	623	-----V-----DV---KK E-----ESGV
ABM21605_1	535	LF---AE D-----DSGV	CAP64870_1	553	-----IP---DVI-----DSQG
ABM21603_1	535	LF---AE D-----DSGV	CCT64574_1	549	-----IP---A QI-----DSGL
ABM21604_1	536	LF---AE D-----DSGV	CEP84713_1	549	-----IP---A QI-----DSGL
APA07533_1	534	LF---AE D-----DSGV	AGT80114_1	549	-----IP---A QI-----DSGL
CAM12502_1	538	KW---A QE-----DSGV	AHD26251_1	549	-----IP---A QI-----DSGL
AGZ62514_1	533	VV---K QD-----DSGV	ANB22780_1	556	-----IP---D QI-----DSGL
AAK77952_1	518	PP---P QD-----DSGV	ACS5199_1	550	-----IP---D QI-----DSGL
EAA30359_2	541	AP---P QE-----DSGV	EAA34842_1	531	-----UV---D QI-----DSGT
XP003718807_1	549	PP---H QD-----DSGV	CAP67665_1	550	-----UV---D QI-----DSGT
CAP64719_1	553	PP---H QD-----DSGV	AE054598_1	550	-----VV---D QI-----DSGT
EAA61461_1	533	VY---H QD-----DSGV	AE065600_1	550	-----VV---D DEI-----DSGV
EAA62557_1	534	GV---E QY-----DSGV	APR07098_1	556	-----VV---D DEI-----DSGV
CAP98129_1	528	DI---D QE-----DSGV	XP003720855_1	554	-----IP---D QI-----DSGV
BAE54583_1	534	FA---IE D-----DSGV	APB14467_1	551	-----Y-----DSGV
CCT67757_1	529	SI---E QE-----DSGV	AGO59052_1	511	-----IV---N QI-----DSGL

Fig. S5 Sequence alignment of ZtrLac1A (catalytic module) along representative members of AA1 subfamily 3 deposited in CAZy database. All three loops A, B, C, Cu1 site ligands as well as the C-terminus regions are depicted in boxes. Fully conserved residues are in red letters, semi-conserved in blue and non-conserved in black. Accession numbers are shown except ZtrLac1A, MalLac1A, TarLac1A and BacLac1A

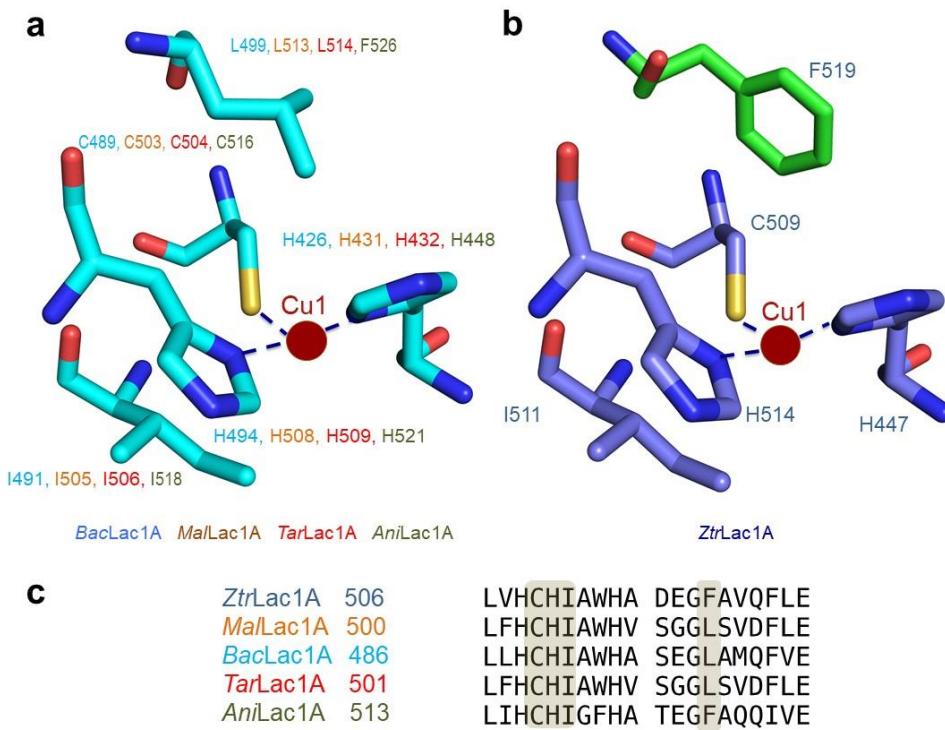


Fig. S6 Architecture of Cu1 copper site in *BacLac1A*, *MalLac1A*, *TarLac1A* and *AniLac1A* (a) and *ZtrLac1A* (b). The Cu1 copper ions are depicted as brown spheres and their coordination bonds are shown in black dashed lines. The structure of *BacLac1A* PDB entry 3SQR was used [41]. (c) Structural sequence alignment of *ZtrLac1A* with *MalLac1A*, *TarLac1A*, *BacLac1A* and *AniLac1A*

References

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