



Supplementary

Evaluation and Proteomic Analysis of Lead Adsorption by Lactic Acid Bacteria

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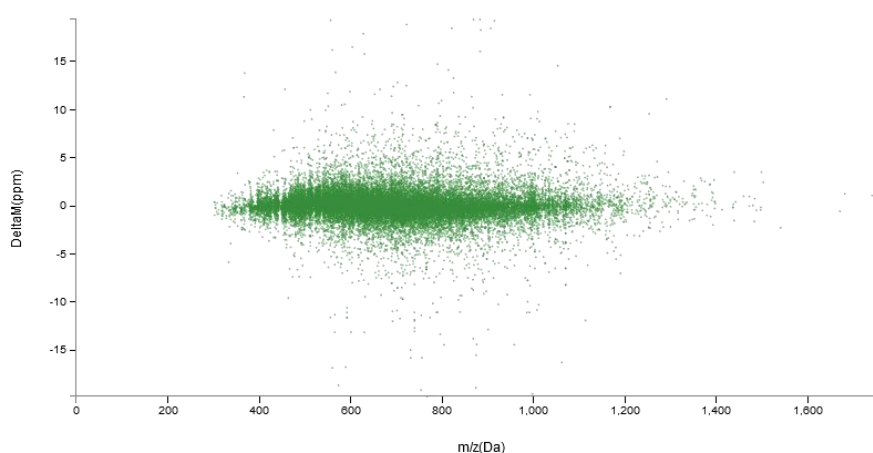


Figure 1. The distribution of peptide matching error. The figure shows the error distribution between the true value and the theoretical value of the relative molecular weight of all matched peptides.

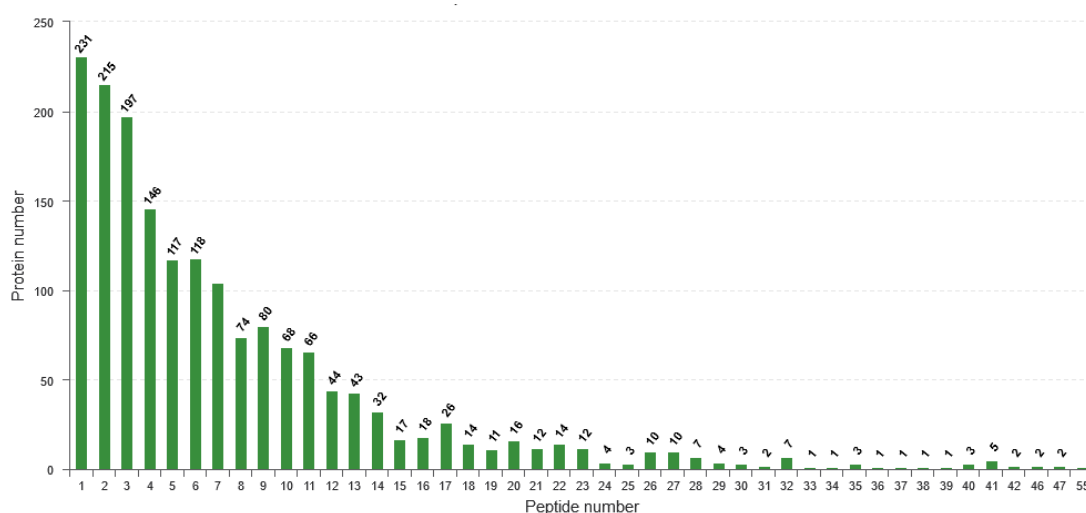


Figure 2. Peptide number distribution. The figure shows the distribution of the number of peptides in the identified protein. The abscissa representing the number of peptides covering the protein and the ordinate representing the number of proteins.

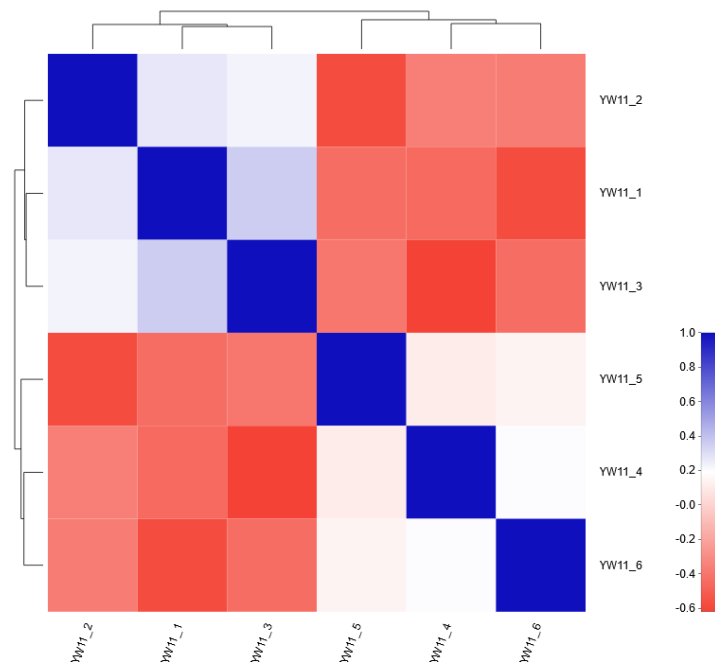


Figure 3. Correlation between samples of YW11. YW11-1,2,3: YW11 in lead - free medium; YW11-4,5,6: YW11 in medium containing lead ions (100mg/L).

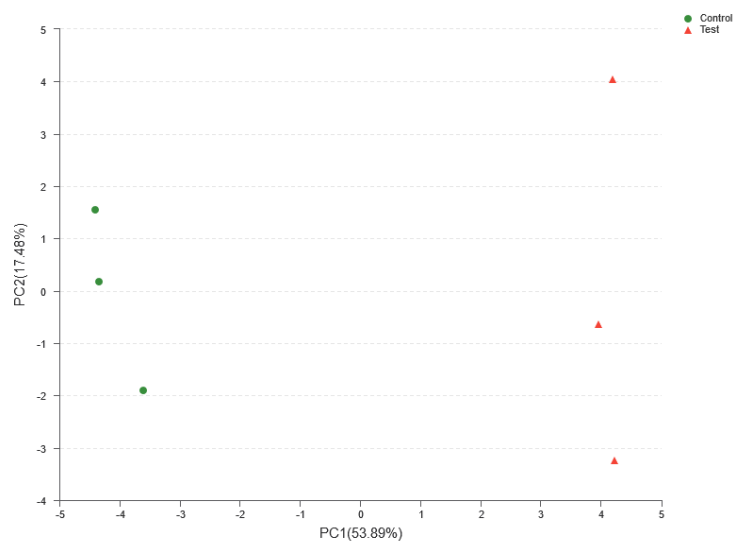


Figure 4. PCA analysis of YW11 proteins. Control: YW11 in lead - free medium; Test: YW11 in medium containing lead ions (100mg/L).

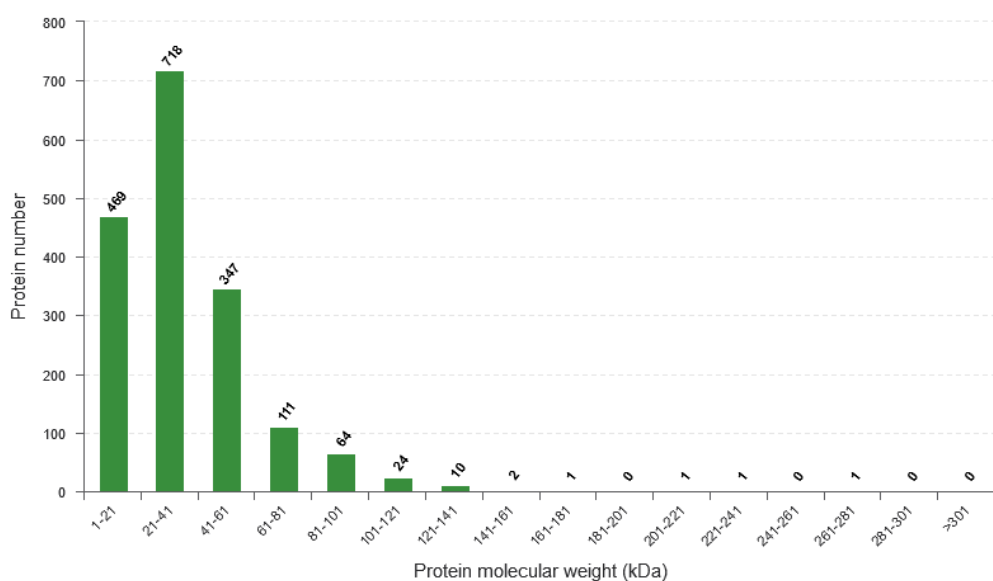


Figure 5. Peptide molecular weight distribution. The figure shows the molecular weight distribution of identified proteins. The abscissa is the distribution range of molecular weight of proteins, and the ordinate is the number of proteins with corresponding molecular weight.

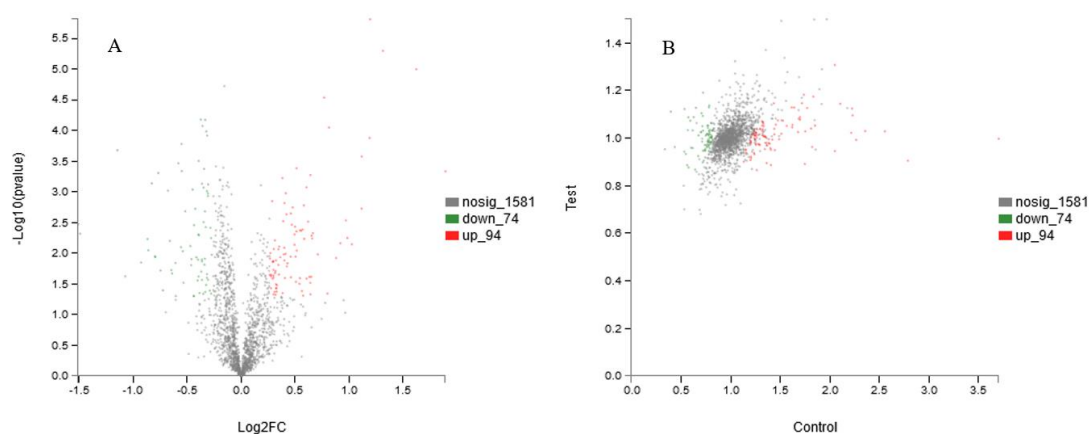


Figure 6. Significant analysis of differentially expressed proteins. (A)Volcano analysis of samples treated with lead ions vs the control.; (B) Scatter analysis of samples treated with lead ions vs the control.

Table S1. Information of identified protein

Accession	Control	Test	pvalue	fc	regulate	significant	description
AA0A01XB59	0.959	0.6157	0.01215	0.642	down	yes	D-aminocyl-L- <i>RNA</i> deacylase OS= <i>Lactobacillus plantarum</i> subsp. <i>argenteorotensis</i> DSM 16365 OX=1423831 GN=did PE=3 SV=1
DVY98	1.029	1.753	2.90E-05	1.704	up	yes	Phosphate binding protein OS= <i>Lactobacillus plantarum</i> subsp. <i>plantarum</i> ATCC 14917 = JCM 1149 = CGMCC 1.2437 OX=525338 GN=psds PE=4 SV=1
AA0A15IG577	1.056	1.623	0.003042	1.537	up	yes	HemH ABC transporter ATP-binding protein OS= <i>Lactobacillus plantarum</i> OX=1590 GN=AYO51_05730 PE=4 SV=1
AA0A253U4Y4	0.95	1.445	0.0008392	1.521	up	yes	Exodeoxyribonuclease 7 small subunit OS= <i>Lactobacillus plantarum</i> subsp. <i>plantarum</i> OX=337330 GN=xseb PE=3 SV=1
AA0A199QFG9	1.086	2.23	0.007091	2.035	up	yes	Transcriptional repressor NrdR OS= <i>Lactobacillus plantarum</i> OX=1590 GN=mrkR PE=3 SV=1
AA0A199QM58	1.023	2.216	0.001862	2.166	up	yes	Peptidoglycan-binding protein OS= <i>Lactobacillus plantarum</i> OX=1590 GN=A0U96_08550 PE=4 SV=1
AA0A267QXX4	0.946	2.051	0.0002637	2.168	up	yes	Peptidoglycan-binding protein OS= <i>Lactobacillus plantarum</i> OX=1590 GN=A8704_14660 PE=4 SV=1
AA0A199QI49	1.175	1.834	0.04642	1.561	up	yes	Adhesin OS= <i>Lactobacillus plantarum</i> OX=1590 GN=A0U96_06145 PE=4 SV=1
AA0A369UCN7	1.053	1.851	8.92E-05	1.758	up	yes	LPTG cell wall anchor domain-containing protein OS= <i>Lactobacillus plantarum</i> OX=1590 GN=DVK84_07570 PE=4 SV=1
AA0A162CPC0	1.026	1.679	0.01033	1.636	up	yes	MORN motif family protein OS= <i>Lactobacillus plantarum</i> OX=1590 GN=Nizo2802_2963 PE=4 SV=1
AA0A0L7Y2V1	0.9057	2.788	9.98E-06	3.078	up	yes	FMN-binding protein OS= <i>Lactobacillus plantarum</i> OX=1590 GN=A8704_12230 PE=4 SV=1
AA0A385PQP5	1.145	2.105	0.01188	1.838	up	yes	DnaD domain protein OS= <i>Lactobacillus plantarum</i> OX=1590 GN=CF198_11100 PE=4 SV=1
AA0A1W6NPV7	1.127	1.771	0.005153	1.571	up	yes	FMN-binding protein OS= <i>Lactobacillus plantarum</i> OX=1590 GN=BI232_04340 PE=4 SV=1
DVY968	0.9437	0.5317	0.0007232	0.563	down	yes	GroES-like protein OS= <i>Lactobacillus plantarum</i> subsp. <i>plantarum</i> ATCC 14917 = JCM 1149 = CGMCC 1.2437 OX=525338 GN=adh PE=3 SV=1
AA0A0M0CIV7	0.877	0.5753	0.01433	0.656	down	yes	Ferrochelatase OS= <i>Lactobacillus plantarum</i> OX=1590 GN=hemH PE=3 SV=1
AA0A0M0CJD8	0.8867	0.561	0.006253	0.633	down	yes	Macro domain ADP-ribose binding module OS= <i>Lactobacillus plantarum</i> OX=1590 GN=AYO51_13380 PE=4 SV=1
AA0A0R1UMI2	0.9633	0.4353	0.0002086	0.452	down	yes	dCMP deaminase OS= <i>Lactobacillus plantarum</i> subsp. <i>argenteorotensis</i> DSM 16365 OX=1423831 GN=FDI0_GI000592 PE=4 SV=1
AA0A1E3KN19	0.954	0.3353	0.003346	0.351	down	yes	Putative ribonuclease T1552 DNase-invertase bin3 OS= <i>Lactobacillus plantarum</i> OX=1590 GN=LP1SA22_03294 PE=4 SV=1
AA0A01V313	0.9337	0.5483	0.0004908	0.587	down	yes	Anaerobic ribonucleoside-triphosphate reductase large subunit OS= <i>Lactobacillus plantarum</i> subsp. <i>argenteorotensis</i> DSM 16365 OX=1423831 GN=FDI0_GI001348 PE=4 SV=1
AA0A0C9FAG5	0.993	2.265	0.0001318	2.261	up	yes	Extracellular protein OS= <i>Lactobacillus plantarum</i> OX=1590 GN=AVR82_06000 PE=4 SV=1
AA0A165XVF0	1.046	1.62	0.02415	1.549	up	yes	Cell shape-determining protein MreC OS= <i>Lactobacillus plantarum</i> OX=1590 GN=Nizo1839_1013 PE=3 SV=1
AA0A102ZHI6	0.8923	1.748	0.002902	1.959	up	yes	LysM domain-containing protein OS= <i>Lactobacillus plantarum</i> OX=1590 GN=CUR48_01040 PE=4 SV=1
AA0A165P076	0.8873	1.406	0.004675	1.585	up	yes	Extracellular protein OS= <i>Lactobacillus plantarum</i> OX=1590 GN=AVR82_00090 PE=4 SV=1
AA0A150RZ68	0.9633	1.822	0.00683	1.891	up	yes	Glycosyl hydrolase family 8 OS= <i>Lactobacillus plantarum</i> OX=1590 GN=AVR82_00090 PE=4 SV=1
TSJ198	1.034	0.567	0.005348	0.548	down	yes	Formate acetyltransferase OS= <i>Lactobacillus plantarum</i> EGD-AQ4 OX=1382301 GN=N692_15475 PE=4 SV=1
AA0A253U2L6	1.094	0.7187	0.04949	0.657	down	yes	50S ribosomal protein L15 OS= <i>Lactobacillus plantarum</i> subsp. <i>plantarum</i> OX=337330 GN=tpd PE=3 SV=1
AA0A1A0DF73	1.105	0.7057	0.01869	0.639	down	yes	50S ribosomal protein L33 OS= <i>Lactobacillus plantarum</i> OX=1590 GN=tpmg PE=3 SV=1
AA0A199QKR6	1.128	0.65	0.01155	0.576	down	yes	30S ribosomal protein S9 OS= <i>Lactobacillus plantarum</i> OX=1590 GN=tpsl PE=3 SV=1
TSK018	1.089	0.626	0.01114	0.575	down	yes	50S ribosomal protein L21 OS= <i>Lactobacillus plantarum</i> EGD-AQ4 OX=1382301 GN=ptlu PE=3 SV=1
DVY815	1.074	0.5917	0.000809	0.551	down	yes	50S ribosomal protein L35 OS= <i>Lactobacillus plantarum</i> subsp. <i>plantarum</i> ATCC 14917 = JCM 1149 = CGMCC 1.2437 OX=525338 GN=pmil PE=3 SV=1
Q88XX4	1.088	0.572	0.01408	0.526	down	yes	50S ribosomal protein L23 OS= <i>Lactobacillus plantarum</i> (strain ATCC BAA-793 / NCIMB 8826 / WCF51) OX=220668 GN=plw PE=3 SV=1
UZWNY2	1.123	0.5337	0.02365	0.475	down	yes	30S ribosomal protein S21 OS= <i>Lactobacillus plantarum</i> AY01 OX=1358413 GN=tpslu PE=3 SV=1
AA0A0C9FAQ2	1.033	0.6157	0.01903	0.596	down	yes	Cys-RNAP(Pro) Cys-RNAP(Cys) deacylase OS= <i>Lactobacillus plantarum</i> OX=1590 GN=ymak PE=3 SV=1
AA0A0R2GAL1	1.012	0.6763	0.0003416	0.668	down	yes	Ribosomal RNA small subunit methyltransferase G OS= <i>Lactobacillus plantarum</i> OX=1590 GN=smg PE=3 SV=1
AA0A162GHW5	0.9977	3.705	0.0004604	3.714	up	yes	Undecarboxylated protein OS= <i>Lactobacillus plantarum</i> OX=1590 GN=lp19_2585 PE=4 SV=1
AA0A0C9F7Y4	1.03	2.357	1.54E-06	2.288	up	yes	Undecarboxylated protein OS= <i>Lactobacillus plantarum</i> (strain ATCC BAA-793 / NCIMB 8826 / WCF51) OX=220668 GN=lp_0444 PE=4 SV=1
P9U29	1.308	2.05	0.0241	1.567	up	yes	Undecarboxylated protein OS= <i>Lactobacillus plantarum</i> (strain ATCC BAA-793 / NCIMB 8826 / WCF51) OX=220668 GN=lp_0444 PE=4 SV=1
AA0A150RQZ5	1.041	1.811	0.04515	1.740	up	yes	Undecarboxylated protein OS= <i>Lactobacillus plantarum</i> OX=1590 GN=AVR82_00885 PE=4 SV=1
AA0A165N2U5	1.089	1.699	0.0005295	1.560	up	yes	Undecarboxylated protein OS= <i>Lactobacillus plantarum</i> OX=1590 GN=Nizo2802_1443 PE=3 SV=1
AA0A0M4ACU4	1.078	1.7	0.005721	1.577	up	yes	Undecarboxylated protein OS= <i>Lactobacillus plantarum</i> OX=1590 GN=AVR82_13000 PE=4 SV=1
M4LXN1	1.082	1.687	0.03018	1.559	up	yes	Undecarboxylated protein OS= <i>Lactobacillus plantarum</i> ZJ316 OX=1284663 GN=j316_3034 PE=4 SV=1
AA0A386RBN5	0.8957	1.363	0.02574	1.522	up	yes	Undecarboxylated protein OS= <i>Lactobacillus plantarum</i> OX=1590 GN=CO218_15800 PE=4 SV=1
AA0A387DFR9	1.192	0.7213	0.04001	0.605	down	yes	Undecarboxylated protein OS= <i>Lactobacillus plantarum</i> OX=1590 GN=CH162_00270 PE=4 SV=1
AA0A0C9CNI2	1.112	0.395	0.004783	0.355	down	yes	Undecarboxylated protein OS= <i>Lactobacillus plantarum</i> OX=1590 GN=WP50_25770 PE=4 SV=1