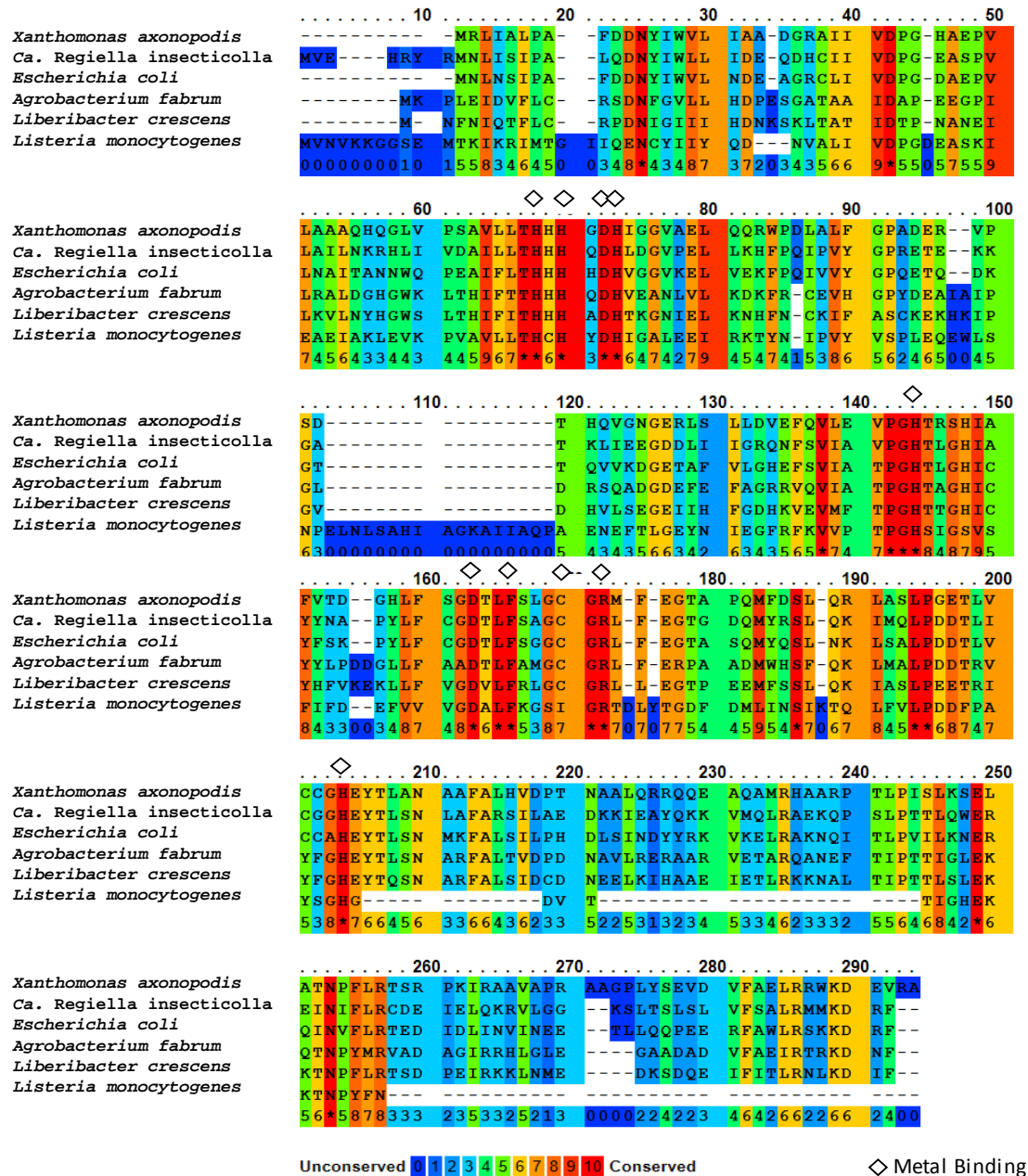


**Supplemental Fig. S1:** Glyoxalase I (GloA) sequence alignments were performed using the Centre for Integrative Bioinformatics PRALINE web tools (<http://www.ibi.vu.nl/programs/pralinewww/>). Default parameters were used for this analysis. The full-length reference sequences for GloA proteins used for sequence alignment were obtained from NCBI database: *Xanthomonas axonopodis* (AEO43772.1), *Agrobacterium fabrum* (NP\_354787.2), *Ca. Regiella insecticola* (WP\_043914972.1), *Liberibacter crescens* (AGA64439.1), *Listeria monocytogenes* (KRJ91490.1), and *Escherichia coli* (AEE56703.1).



**Supplemental Fig. S2:** Glyoxalase II (GloB) sequence alignments were performed using the Centre for Integrative Bioinformatics PRALINE web tools (<http://www.ibi.vu.nl/programs/pralinewww/>). Default parameters were used for this analysis. The full-length reference sequences for GloB proteins used for sequence alignment were obtained from NCBI database: *Xanthomonas axonopodis* (KPL48337.1), *Agrobacterium fabrum* (NP\_356997.2), *Ca. Regiella insecticola* (EFL92625.1), *Liberibacter crescens* (AMC13092.1), *Listeria monocytogenes* (KSZ47095.1), and *Escherichia coli* (EGT71262.1).