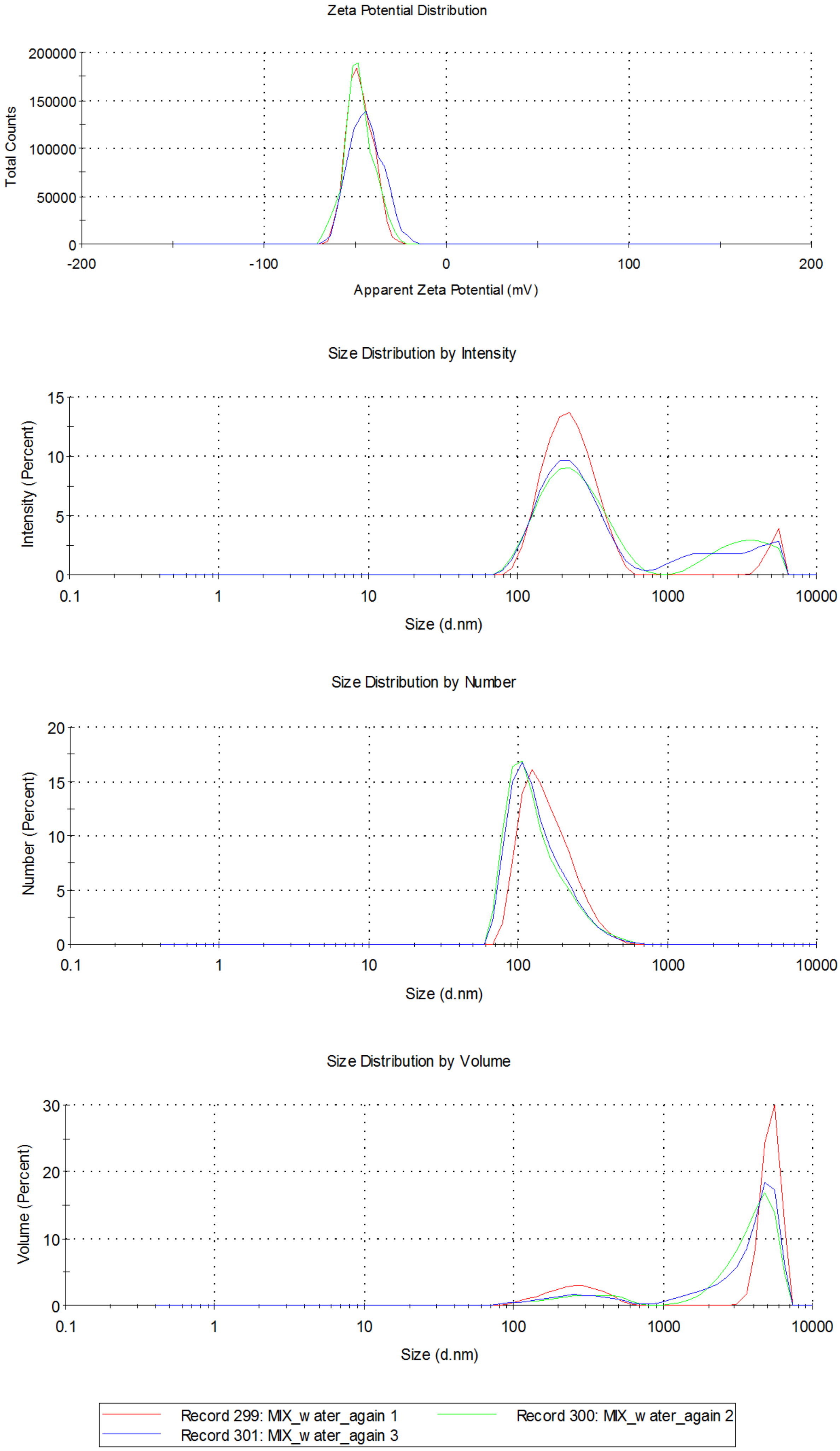
Supplementary materials:

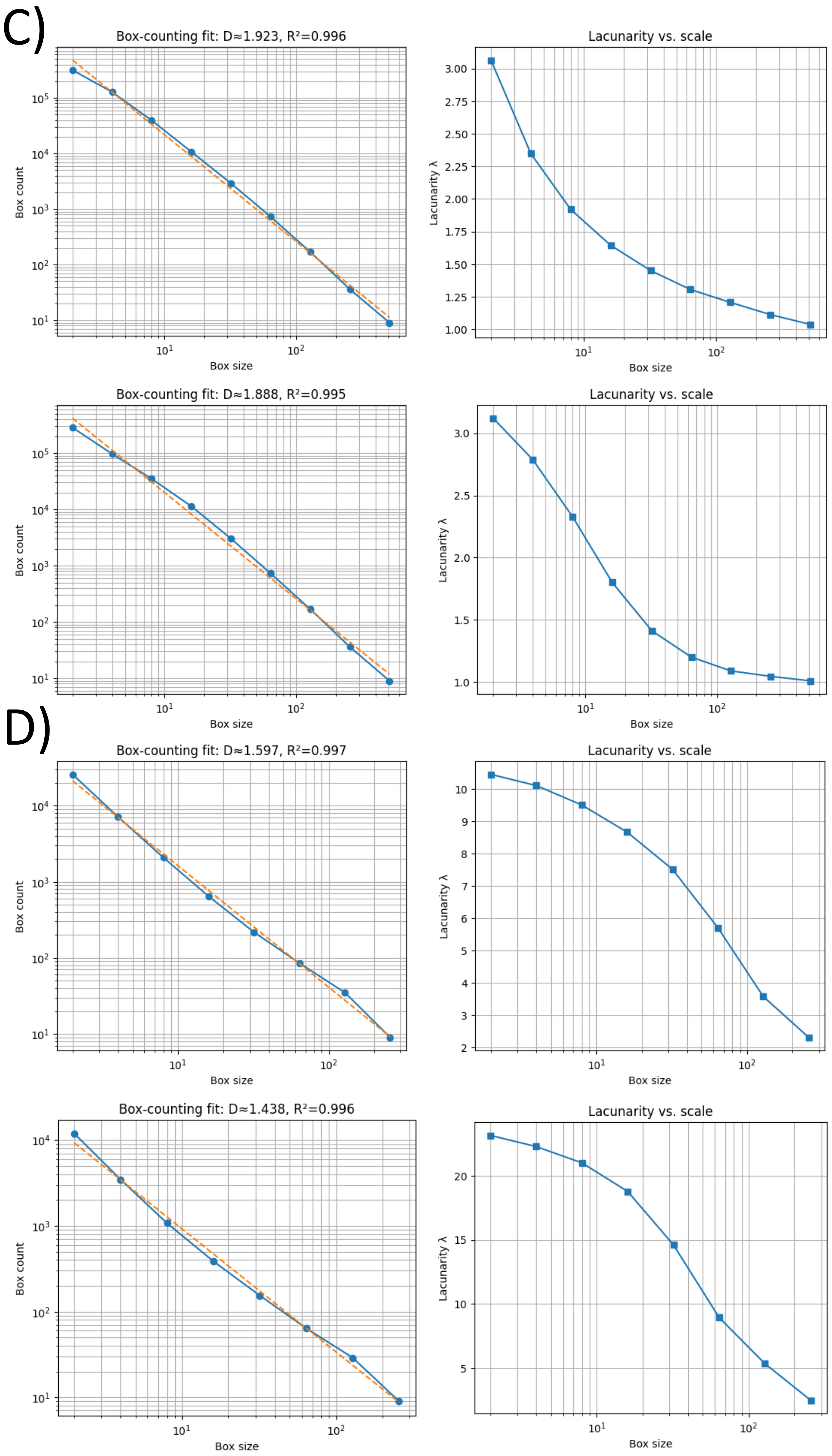
Not so dangerous? PET enviromental-like microplastics and nanoplastics (PET-elMNPs) effect on *Escherichia coli* and environmental bacteria

Ondrej Pencik[1,*], Martin Cerny[2], Jana Tomekova[3], Milada Vodova[3], Hoang-Anh Cao[4], Jiri Kucerik[5], Vendula Hrabalová[6], Katarína Molnárová[3], Jakub Treml[1], Martina Kolackova[3], Jaromir Bacovsky[6]

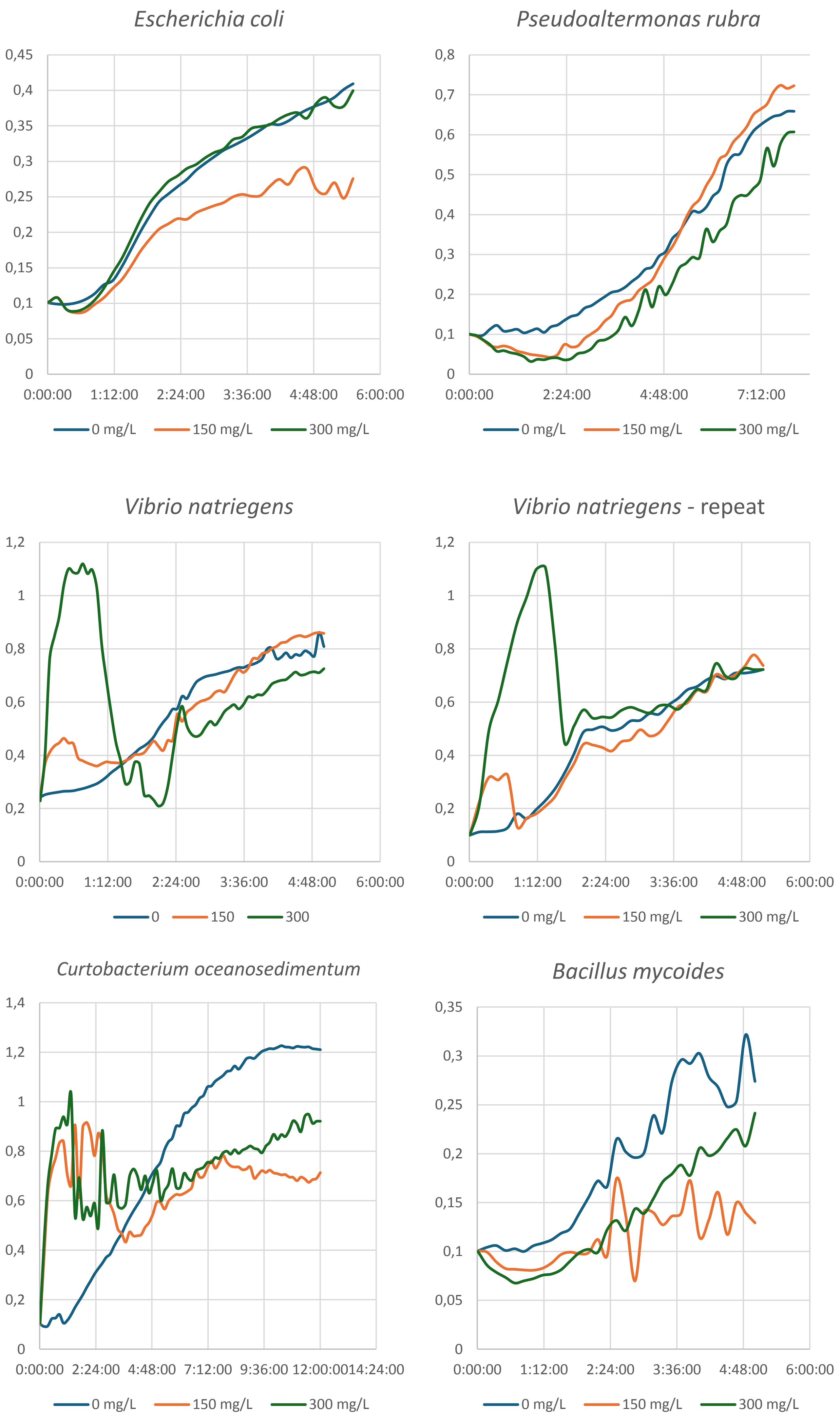
[1]Department of Molecular Pharmacy, Faculty of Pharmacy, Masaryk University, Palackého třída 1946/1, 61200, Brno, Czech Republic
[2]Department of Molecular Biology and Radiobiology, Faculty of AgriSciences, Mendel University in Brno, Zemědělská 1/1665, 613 00 Brno, Czech Republic[3]Department of Chemistry and Biochemistry, Mendel University in Brno, Zemědělská 1665/1, 613 00, Brno, Czech Republic.
[4]Brno University of Technology, Central European Institute of Technology, Brno, Czech Republic
[5]Department of Agrochemistry, Soil Science, Microbiology and Plant Nutrition, Mendel University in Brno, Zemědělská 1665/1, 613 00, Brno, Czech Republic.
[6]Delong Instruments a.s., Palackého třída 3019/153b, 612 00, Brno, Czech Republic



S1: *Zeta-potential and DLS results (Intensity, Number, Volume size distribution). Settings: refractive index 1.575, adsorption coefficient 0.160, temperature 25 °C, equilibration time 120 s, measurement angle of 173° backscatter*

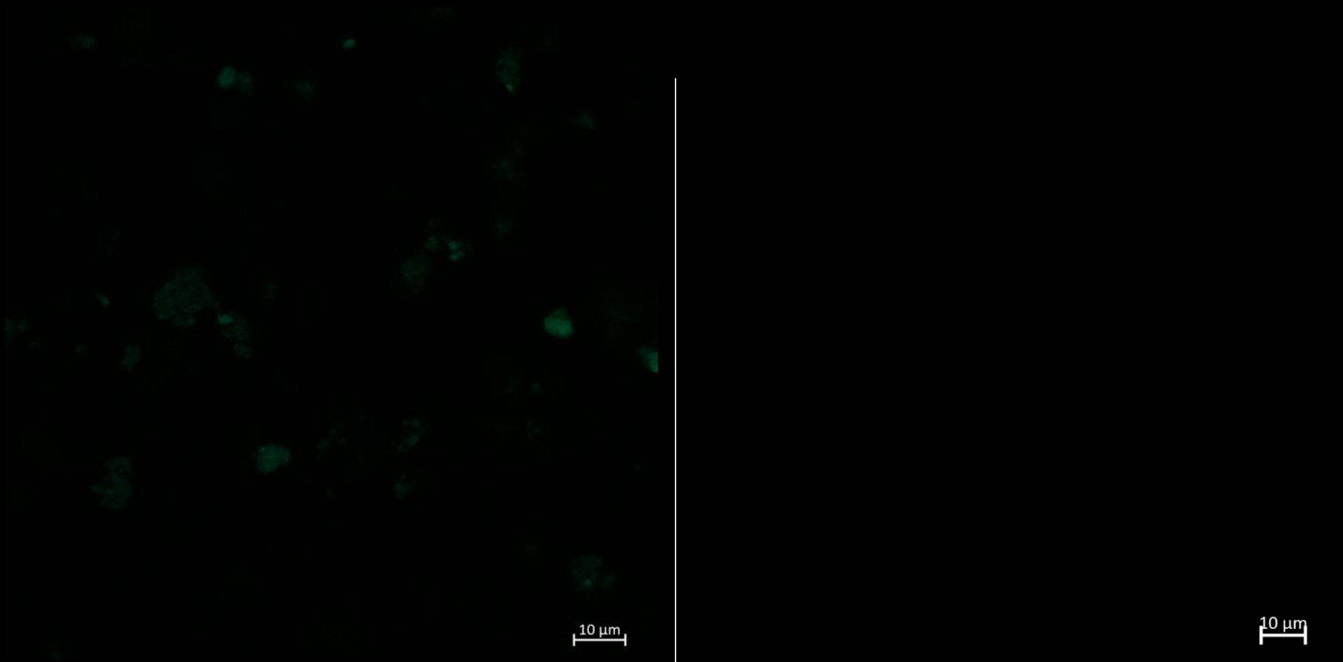


S2: *C) SEM images fractal dimension and lacunarity, D) TEM images fractal dimension and lacunarity calculations*

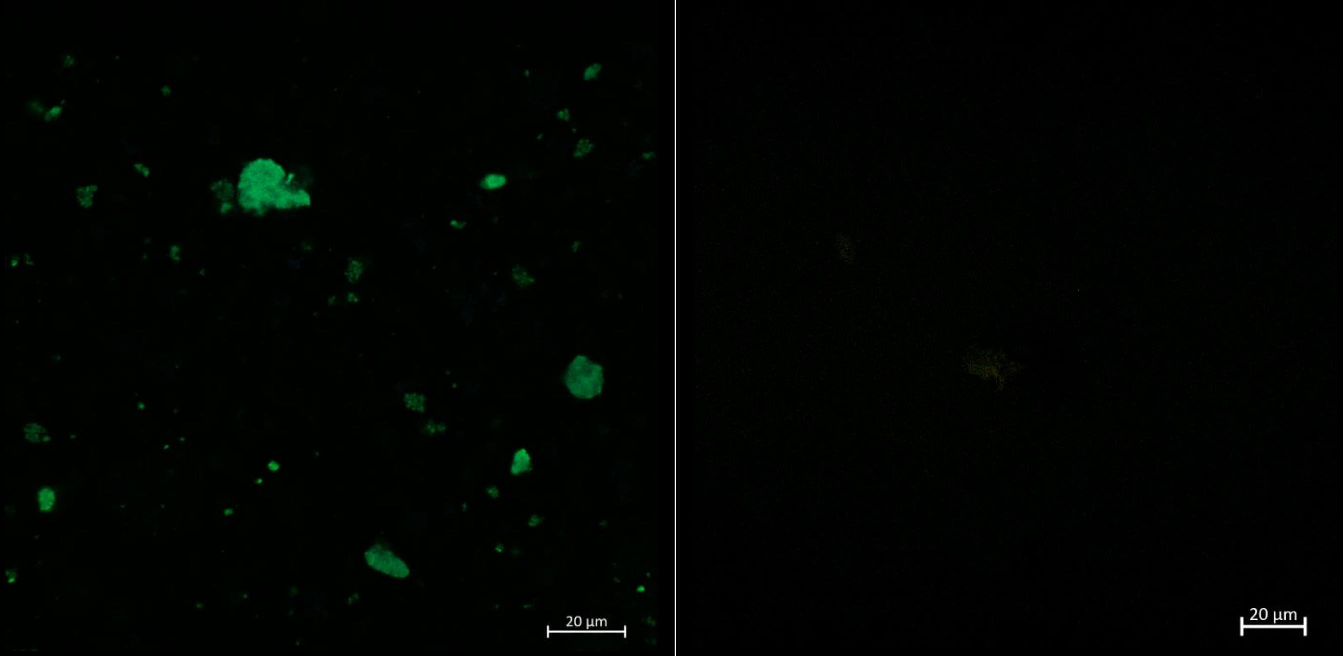


S3: *Growth patterns from proteome/confocal samples. Settings are following: 30 °C (E. coli 37 °C), shaking duration 30 s, shaking amplitude 4 mm, wavelength 600 nm, interval 10 minutes, number of replicates: 4*

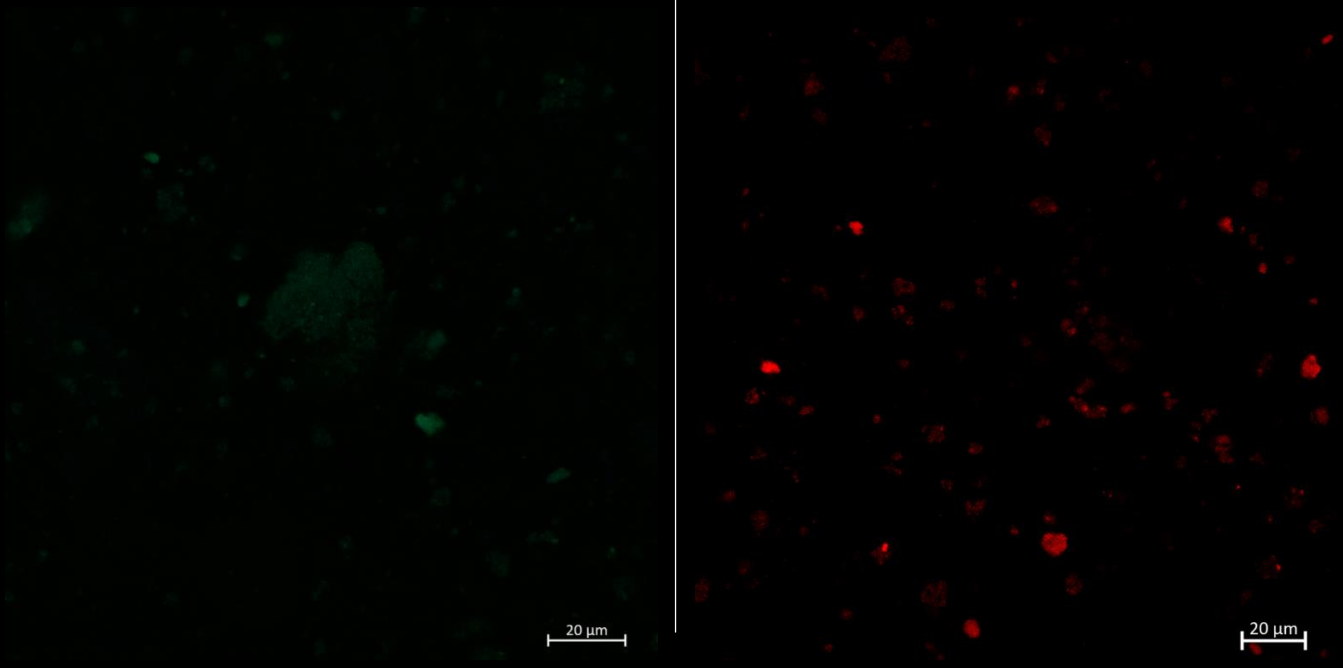
A) (-) Hoechst + CellROX: control **B) (-) PI + FDA: control**



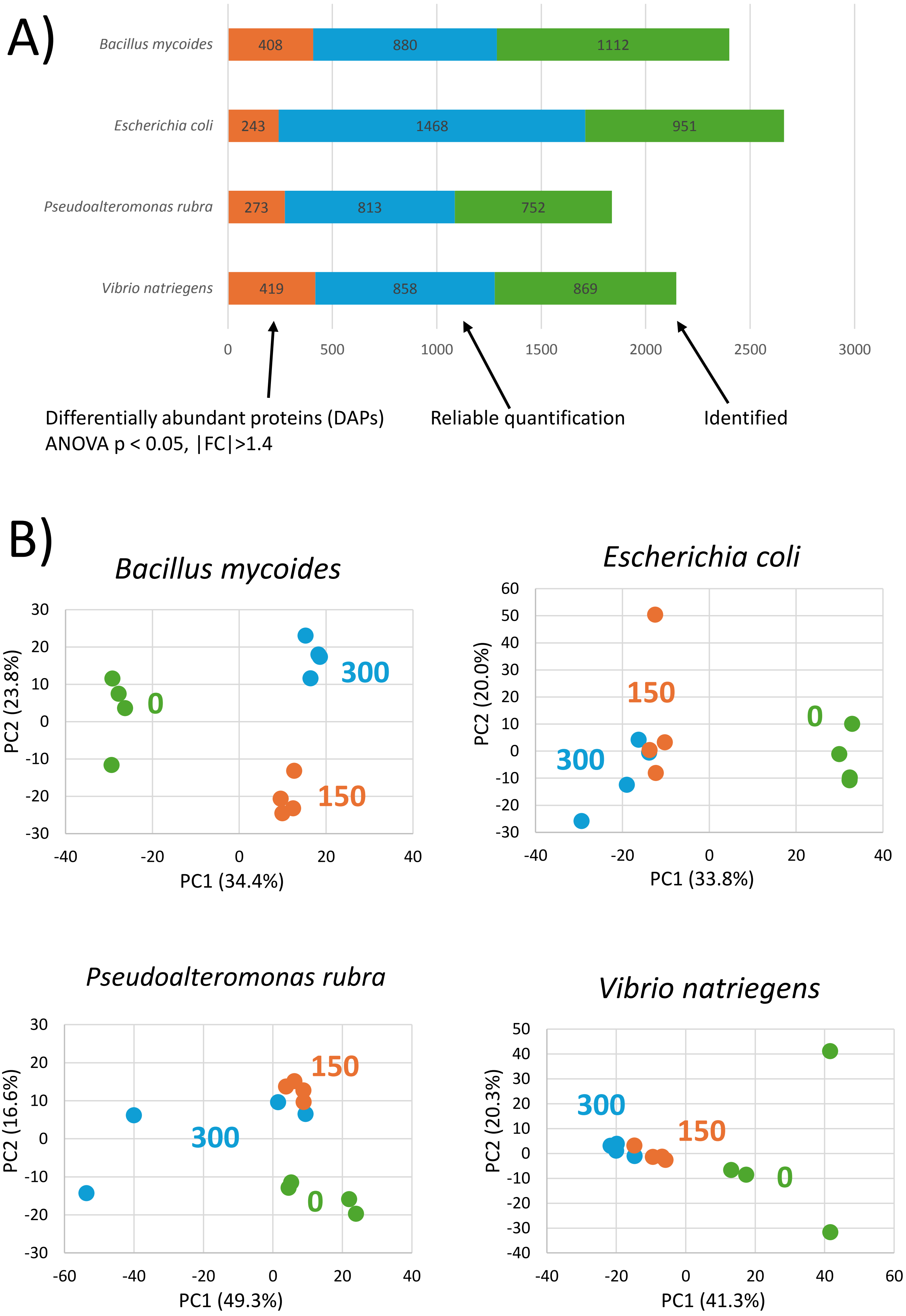
(+) CellROX (+) FDA



(+) Hoechst (+) PI



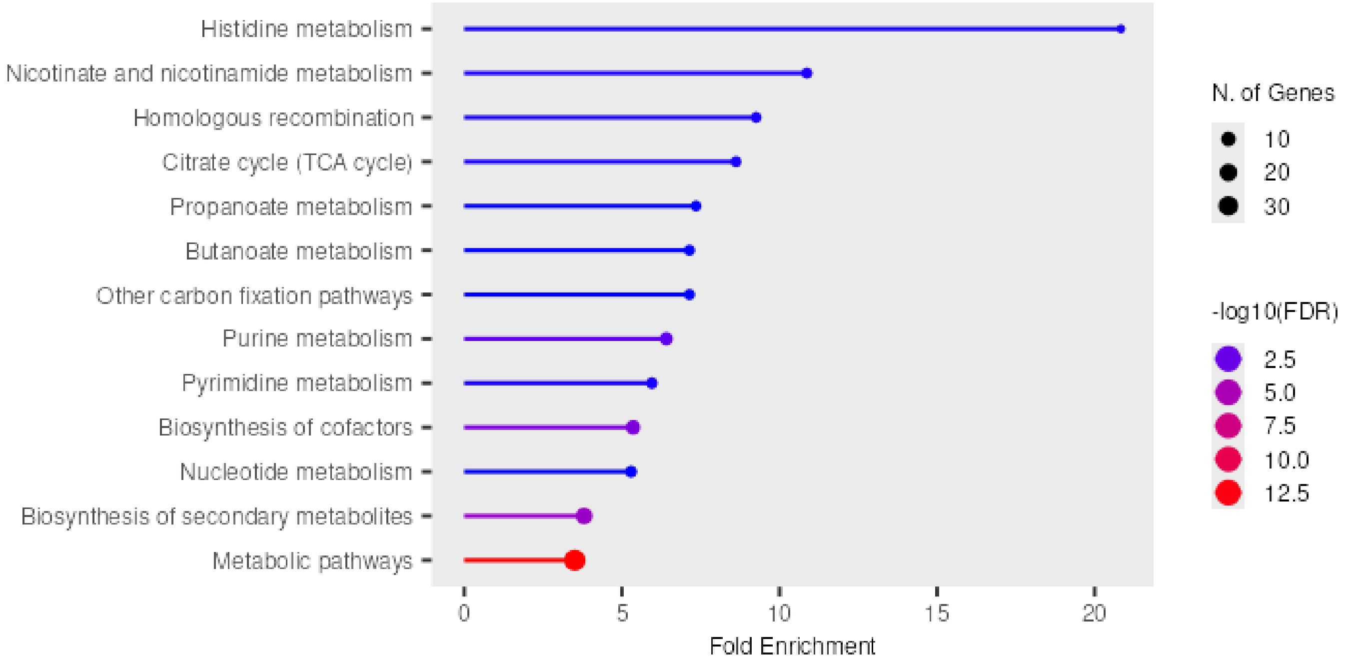
S4: *Negative control for MNPs measurements: A) (up-down line) H + ROX: control (no staining), CellROX staining, Hoechst staining, B) (up-down line) FDA + PI: control (no staining), FDA staining, PI staining*



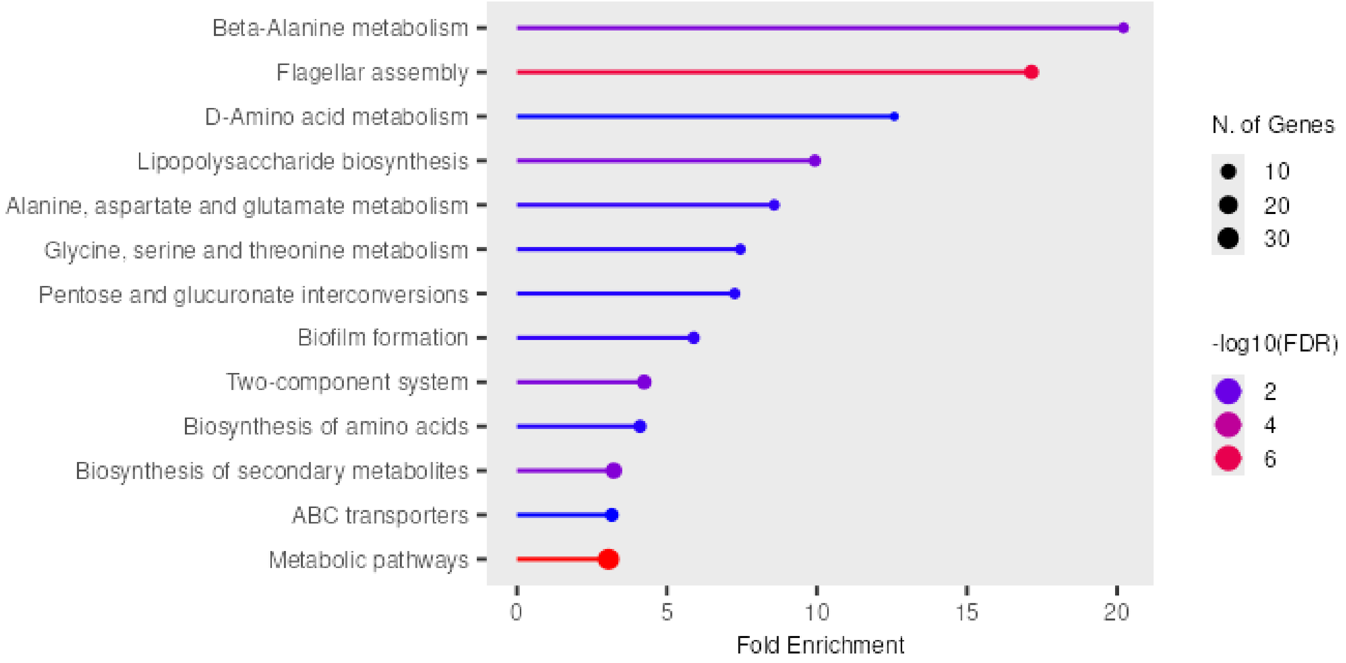
S5: *Proteomic parameters: A) Protein count overview – DAPs, reliable quantified proteins, identified but non-quantified proteins. B) Principal component analysis (PCA) of bacteria.*

Escherichia coli

A) DOWN



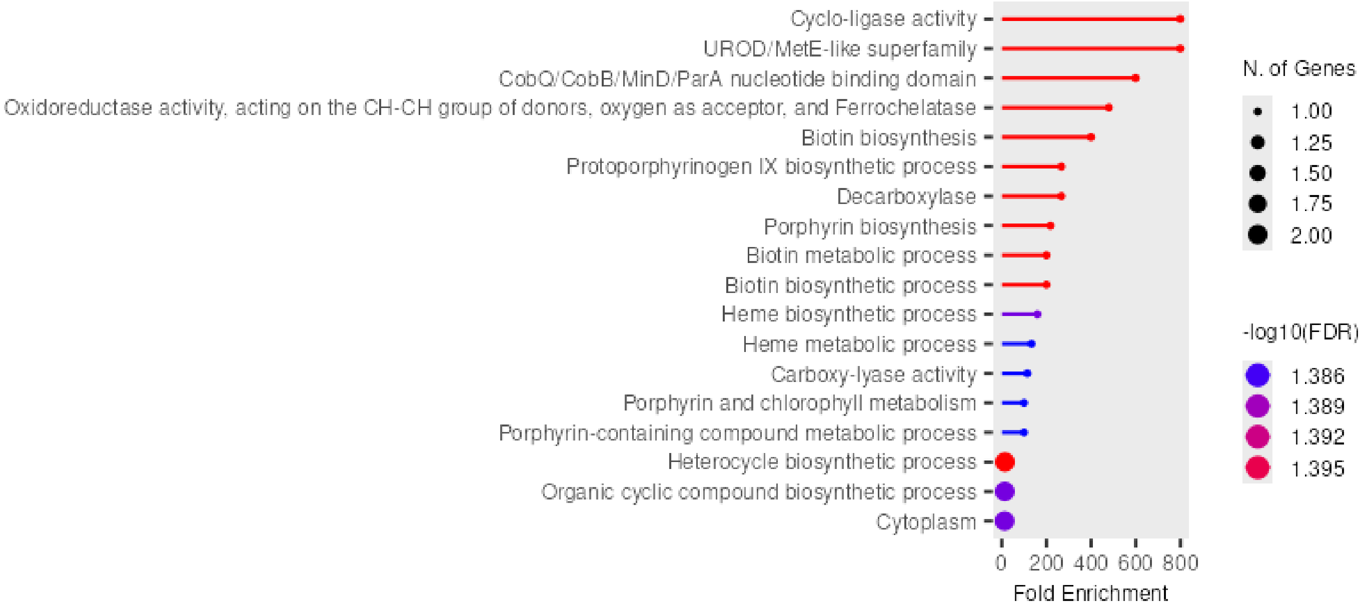
B) UP



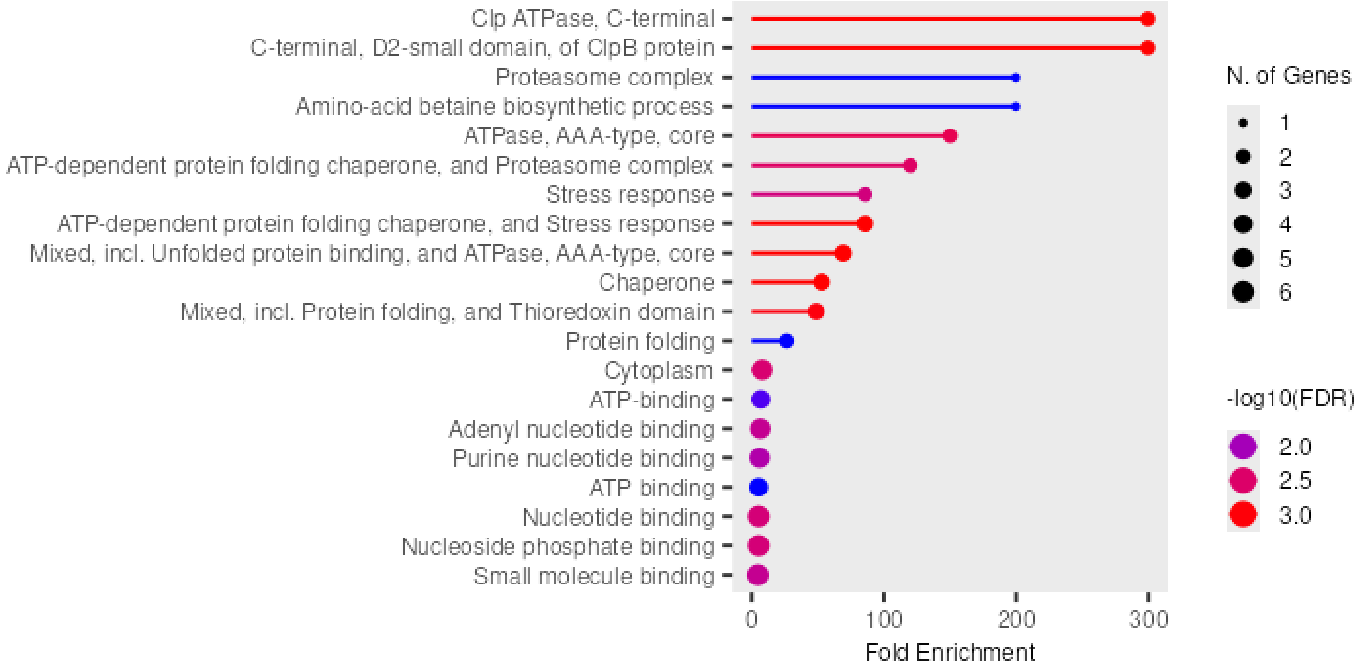
***S6:** ShinyGO gene onthology and enrichment for Escherichia coli K12: a) statistically significant different decreased protein abundance data set (DOWN) derived pathways, b) statistically significant different increased protein abundace data set (UP) derived pathways*

Vibrio natriegens

A) **DOWN**



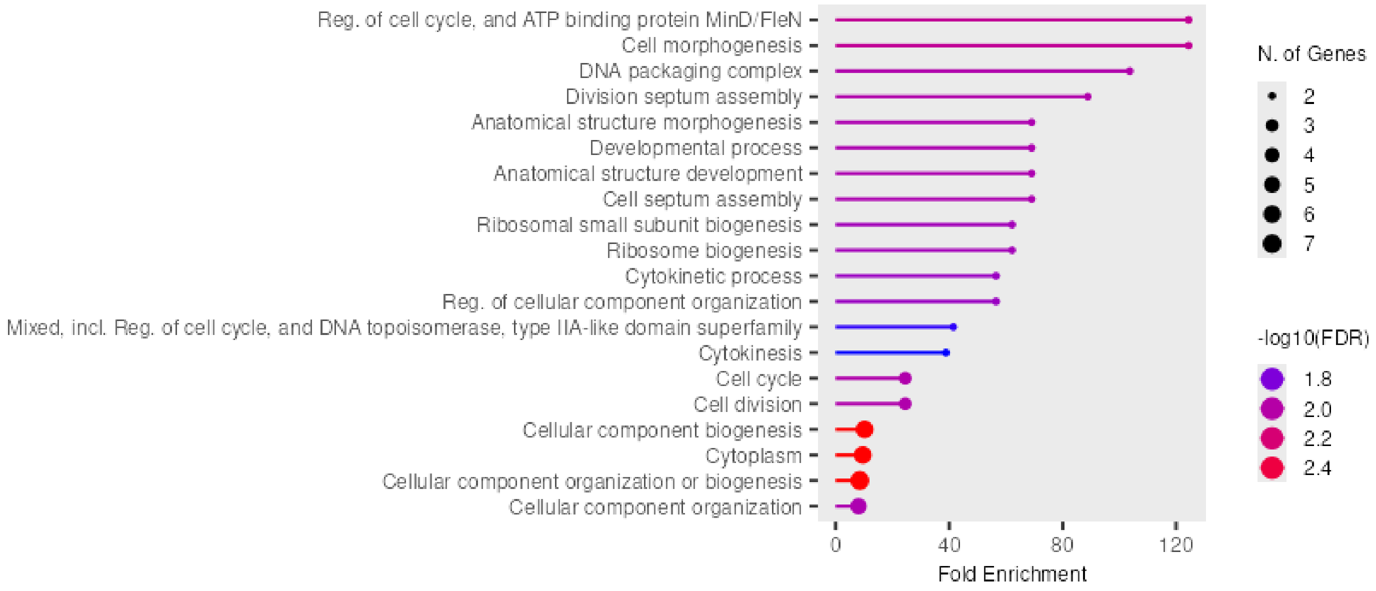
B) **UP**



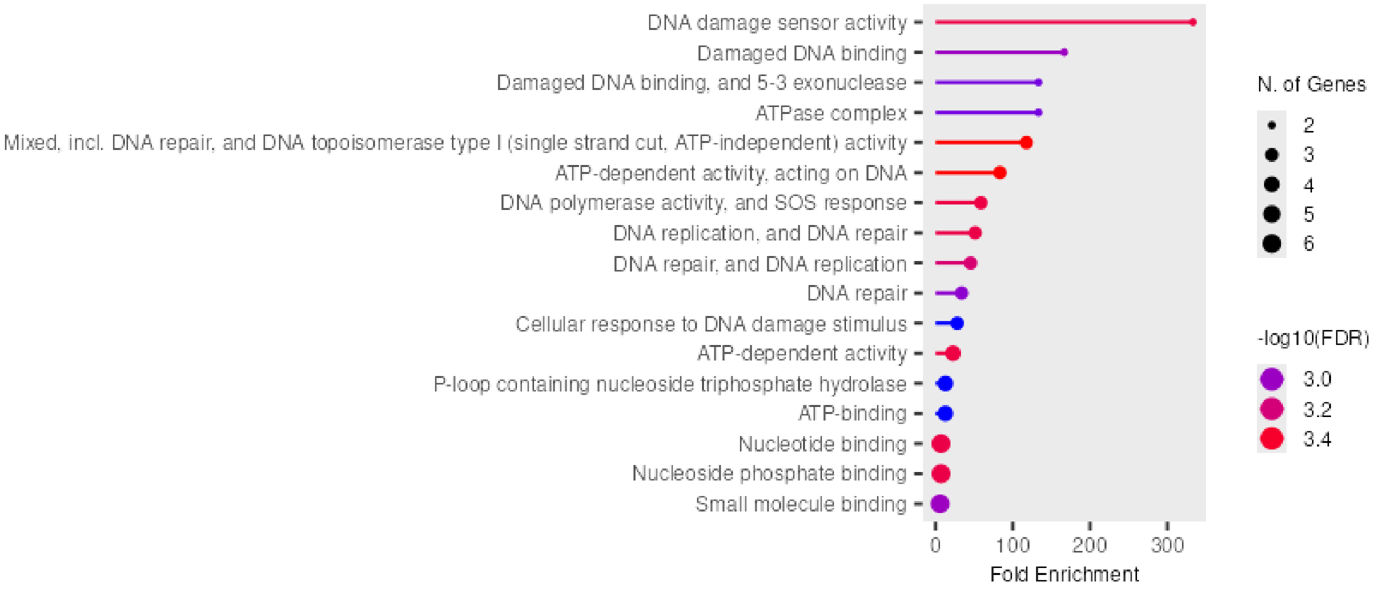
***S7:** ShinyGO gene onthology and enrichment for Vibrio natriegens: a) statistically significant different decreased protein abundance data set (DOWN) derived pathways, b) statistically significant different increased protein abundace data set (UP) derived pathways*

Pseudoalteromonas rubra

A) **DOWN**



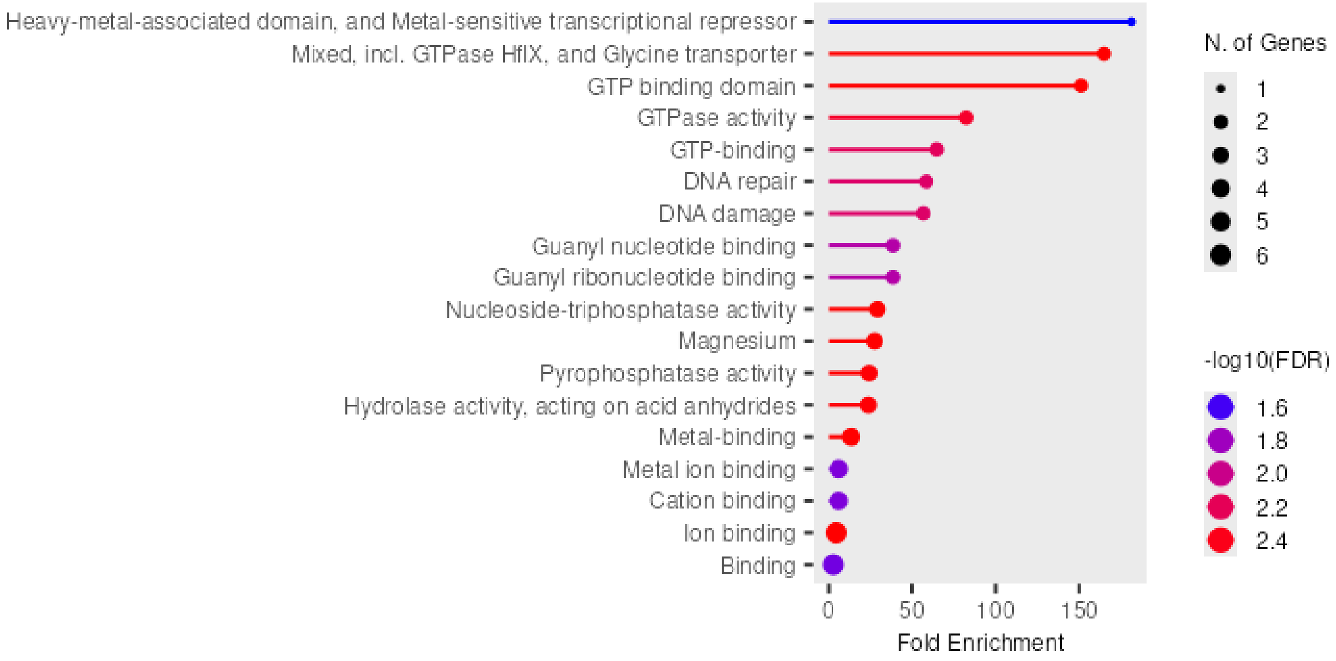
B) **UP**



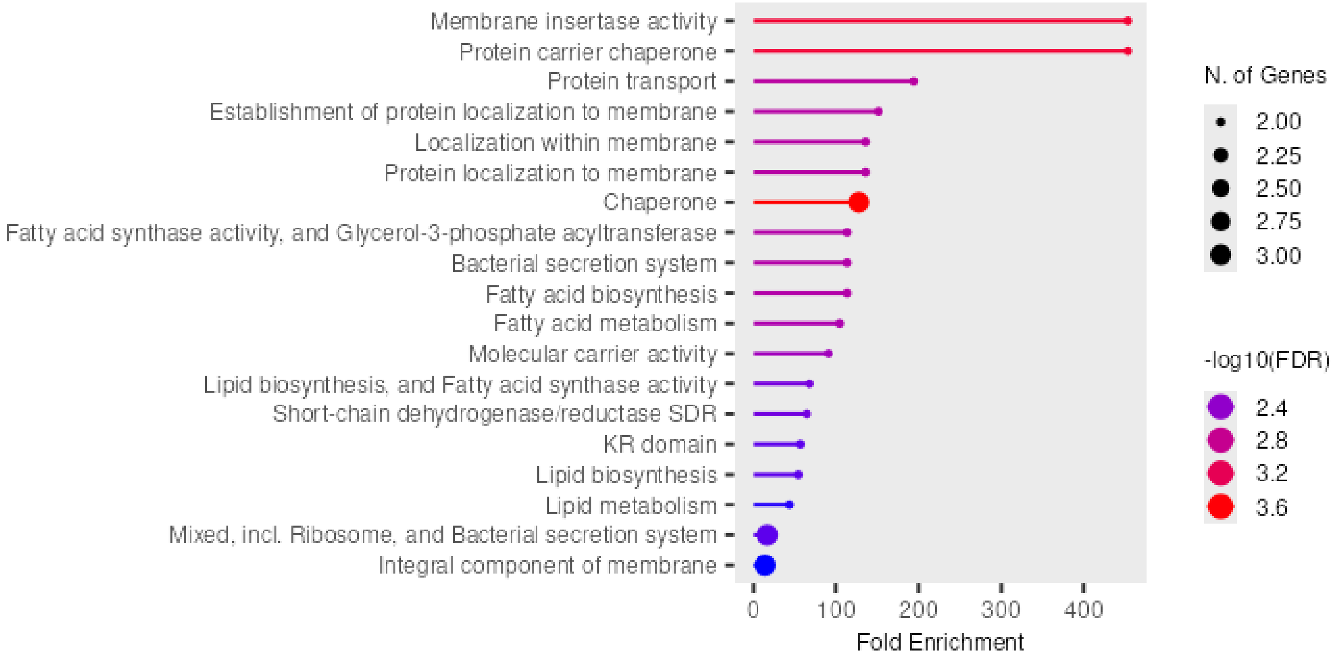
***S8:** ShinyGO gene onthology and enrichment for Pseudoalteromonas rubra: a) statistically significant different decreased protein abundance data set (DOWN) derived pathways, b) statistically significant different increased protein abundace data set (UP) derived pathways*

Bacillus mycoides

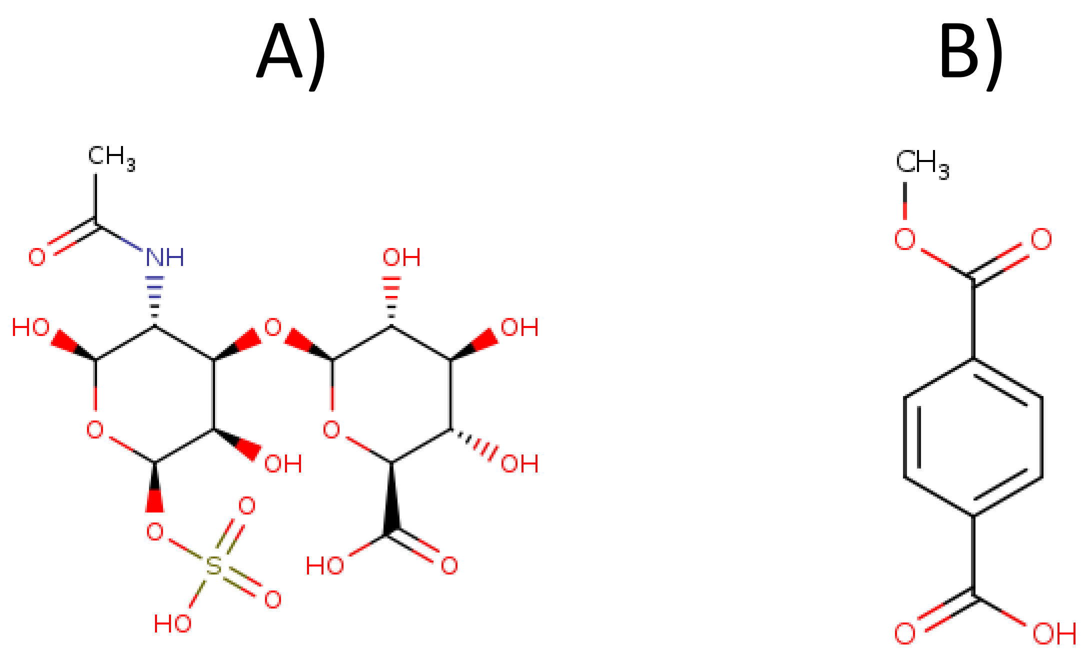
A) DOWN

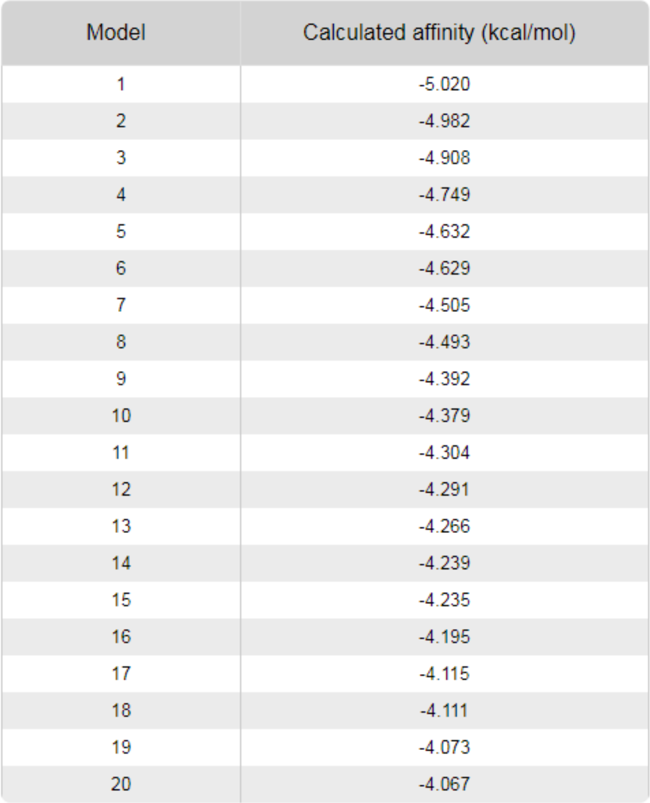


B) UP

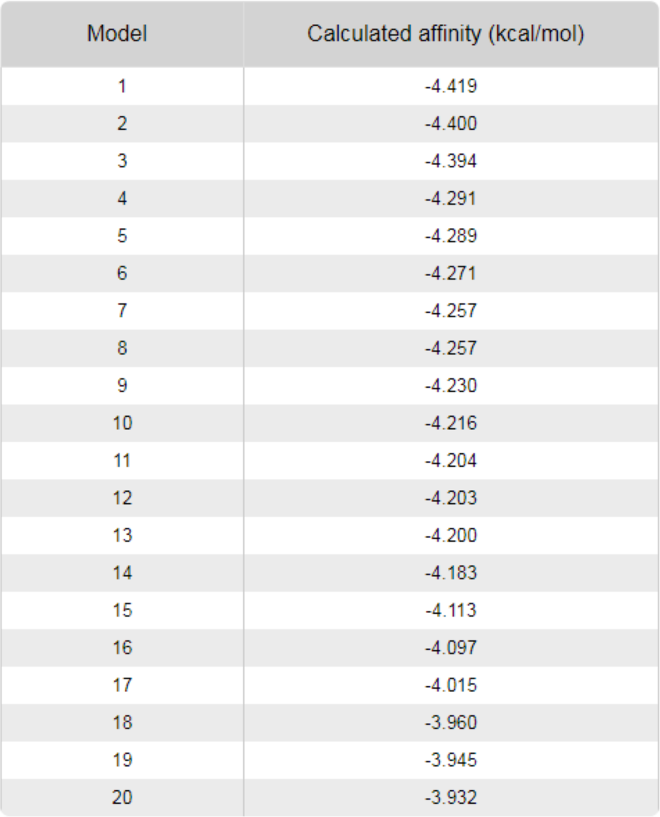


***S9:** ShinyGO gene onthology and enrichment for Bacillus mycoides: a) decreased statistically significant different protein abundance data set (DOWN) derived pathways, b) statistically significant different increased protein abundace data set (UP) derived pathways*





Model	Calculated affinity (kcal/mol)
1	-5.020
2	-4.982
3	-4.908
4	-4.749
5	-4.632
6	-4.629
7	-4.505
8	-4.493
9	-4.392
10	-4.379
11	-4.304
12	-4.291
13	-4.266
14	-4.239
15	-4.235
16	-4.195
17	-4.115
18	-4.111
19	-4.073
20	-4.067



Model	Calculated affinity (kcal/mol)
1	-4.419
2	-4.400
3	-4.394
4	-4.291
5	-4.289
6	-4.271
7	-4.257
8	-4.257
9	-4.230
10	-4.216
11	-4.204
12	-4.203
13	-4.200
14	-4.183
15	-4.113
16	-4.097
17	-4.015
18	-3.960
19	-3.945
20	-3.932

S10: *AutoDock Vina binding affinities for chondroitin AC-lyase: A) Native chondroitin-sulfate monomer substrate binding affinity energy. B) MHET (monohydroxy-ethylene-terephtalate) substrate binding affinity energy.*