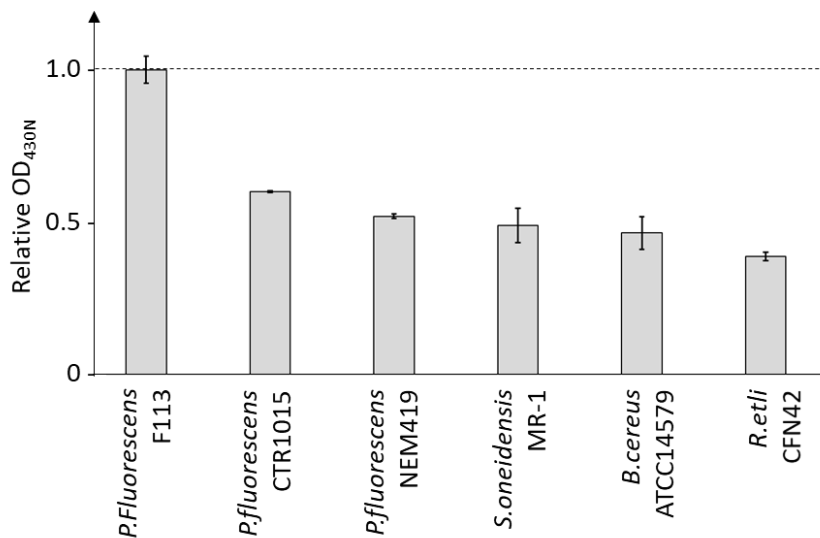


Supplementary Figure 1. Analysis of the pyomelanin production capacity of the studied bacterial strains. A) Absorption spectra of cell-free supernatant from the strain *P. fluorescens* NEM419, obtained by centrifugation from 0, 2, 3 and 6 days of culture. Absorption spectra were recorded in the range of 300–600 nm in a UV–Vis spectrophotometer using sterile culture medium as blank. B) Optical density recorded at 400 nm of cell-free supernatant of the six bacterial strains of the study, obtained after 6 to 10 days of culture. *E. coli* BL21 and *E. coli* BL21 hppd were used as negative and positive control respectively. Error bars are calculated from the standard deviation for each series.



Supplementary Figure 2. Comparison of OD_{430N} of five bacterial strains (*P. fluorescens* CTR1015 and NEM419, *S. oneidensis* MR-1, *B. cereus* ATCC14579 and *R. etli* CFN42) with the one of *P. fluorescens* F113. Each value is obtained by subtracting the mean OD_{430nm} obtained in positive controls (i.e. OD_{430PC}) from the mean OD₄₃₀ obtained in negative controls (i.e. OD_{430NC}). The obtained difference is compared to the one of *P. fluorescens* F113 which has an arbitrary value of 1

and is depicted on this figure as “relative OD_{430N}”. Error bars are calculated from the standard deviation for each series.

B.cereus MKQKSMIDLAAQMEDFFPVRDVDHLE---FVVGNAKQS--SYLLARAFGFKIVAYSGLT 55
S.oneidensis -----MASELNP-LGLLGIEFTEFASSDTDF---MHKVFI DFGFSLK----- 39
R.etli MGPFPHDAPSEITADNP-AGTDGFEFVEFAHPEPEK---LSELFTRMGYVA----- 50
P.kilonensis -----MADLYENP-MGLMGFEFIEFASPTPNT---LEPIFEIMGFTKVA----- 40
L.pneumophila -----MQNNNP-CGLDGF AFLE FSGPDRNK---LHQQFSEMGFQAVA----- 38
P.aeruginosa -----MNAVAKIEQHNP-IGTDGFEFVEFTAPDAKGI EQLRQLFNMMGFTE TA----- 47
A.salmonicida ---MTTSSSSRSH TINP-LGSDGFEFVEYTAAPDAKGI AALKALFVSLGFAEVA----- 50
V.parahaemolyticus -----MVDTYNP-LGTDGFEFVEYTAADSKGI EQLKALFISLGF AE IA----- 42
V.anguillarum -----MTSTFNP-LGTDGFEFVEYTAADPAGIAQLKELFTSLGFAEIA----- 42

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B.cereus GNREKVS YVLVQKNMRFVVS GALSS ENRIAE FVKTHGDGVKDVALLVDDVDKAYSEAVKR 115
S.oneidensis KAKNKDILYKQNDINFLLNKQ--REGFS AKFAKSHGPAICSMGWRVEDASFHRVAVER 97
R.etli RHKTKDITTIWRQGDINIVLNAE--PGSHAARFVAKHGFCAPSMAWRVVDARHAFNHAVSK 108
P.kilonensis THR SKNVHL YRQGA INLILNNE--PHSVASYFAAEHGP SVCGMAFRVKDSQQAYKRALEL 98
L.pneumophila HHKNQDITL FKQGEIQFIVNAA--SHCQAEAHASTHGFGACAMGFKVKDAKAAFQHAI AH 96
P.aeruginosa KHR SKEVFL FQNDINI VLNGS--PTGHVHEFALKHGFSACAMAFRVKNASQAAAYAESQ 105
A.salmonicida KHKHKQCWL YRQGDIN FV VNAE--PHSQAEQFASLHGFSVCGMAFRVADAGKAQFYAITK 108
V.parahaemolyticus KHR SKEAWL YRQGDISFIVNAI--PHSQAEFAKVHGP SVCGMAFRVHDATVALEHAIQN 100
V.anguillarum KHR SKEAWL YRQGDIN FIVNSQ--PHSQAAAFKVHGP SVCGMAFRVHDASVAMQHVQAN 100

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B.cereus GAVAIAPPQELTDEDGLKKA VIGTYGDIHTLVERKNYKGA F-MPGFQKV-----EFNI 169
S.oneidensis GAKAADD-----AKDLPYPAIYIGDLSLIYFIDT FGANNNIYATDFEDLSEPV----- 146
R.etli GAVPYEGN-----DKVLDVPAIVGIGSSLLYFVETYGAKGSAYEAEFDWLGEPN----P 158
P.kilonensis GAQPIHIETG--PMELNLPAIKGIGGAPLYLIDRFEGESSIYDIDFVVFLEGVD----R 150
L.pneumophila GGIAFQDA-P---HANHGLPAIQIGGSIYFVDEEHQ-----PFSHEWNITSP E 142
P.aeruginosa GAKLVGSHAN---FGE LNI P SLEIGGSSLLYLVDRYGD-RS IYDVFDFEIGRS-----A 156
A.salmonicida GAKPFVGKIG---LME LNI PAI YGIGESTLSFVDRYGDKGS IYDVFDFVFPDWQTR--M 162
V.parahaemolyticus GGTEYKTEIG---PMELSPAIYIGIGESLLYFVDRY GK-QS IYDVFDFRYDDADDR--L 153
V.anguillarum GGREYKTIQIG---PMELSPAIYIGIGDLSLLYFVDRYGS-QS IYDVFDFKYADANQR--M 153

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B.cereus PFEESGLI A V D H V M N V E--KMEEWVS YENVMGFKQMIHFD DDDI STEYSALMSKVMTN 227
S.oneidensis ITQEKGFIEVDHLINNVYKGTMEHWANFYKNI FGFTEVRYFD---ISGVOTALVSYALRS 203
R.etli KPLGIGFYLLDHLTHNVFRGNM DKWDFYRNLNFNKQIHF FD---IDGRI TGLVSR AITS 215
P.kilonensis NPFVAGLKI IDHLTHNVYRGRMAYWAGFYEKLFNFREIRYFD---IKGEYTGITSKAMTA 207
L.pneumophila PVVGNGLTAIDHLTHNVYRGNM DKWASFYASIFNFQEI RFFN---IKGKMTGLVSRALGS 199
P.aeruginosa NDNSVGLTYIDHLTHNVKRGQMDVWSGFYERIANFREIRYFD---IEGKLTGLVSRAMTA 213
A.salmonicida AEVDAGLYEIDHLTHNVQRGNM D VWSNFYERIGNFREIRYFD---IEGKLTGLVSRAMTA 219
V.parahaemolyticus AKSDVGLYEIDHLTHNVKQGNM D VWSGFYERIGNFREIRYFD---IEGKLTGLVSRAMTA 210
V.anguillarum TDANVGLFEIDHLTHNVKQGNM D IWSGFYERIGNFREIRYFD---IEGKLTGLVSRAMTA 210

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B.cereus -GSRIKFPINEPADGKRKSIQI EYLFYNGAGVCHLALLTSDIVKTVEALRANGVEFLDT 286
S.oneidensis PDGSFCIPINEGK-GNDKNQID EYLKE YNGPGVCHLAFRSRDIVKSLDAMEGSSIQCLDI 262
R.etli PCGKIRIPINES--KDDTSQIEEYFLKKYRGEIGCHLAVGTEDIYEATDRLADNGLRMPG 273
P.kilonensis PDGMIRIPINES--SKGAGSQIEEFLMKNQIEEYVAFLLD L IKTWHLKIGMRMTA 266
L.pneumophila PCGKIRIPINES--KDDL SQIEEFLHEYHGEIGCHLALNTNDIYKTVNGLRQGVKFLDV 257
P.aeruginosa PCGKIRIPINES--ADDSQIEE F IREYHGEIGCHLALTTDDIYATVRKLRDNGVKFMST 271
A.salmonicida PCGKIRIPINES--SDDKSQIEEYLRQYKGEIGCHLALASSDIYQTIRTLRGRGTGMFPT 277
V.parahaemolyticus PCGKIRIPINES--SDDKSQIEE F IREYNGEIGCHLALTTDDIYQTVQLTRDRGMFPT 268
V.anguillarum PCGKIRIPINES--SDDKSQIEE F IREYNGEIGCHLALSTDDIYQTVRTLREGRGMFPT 268

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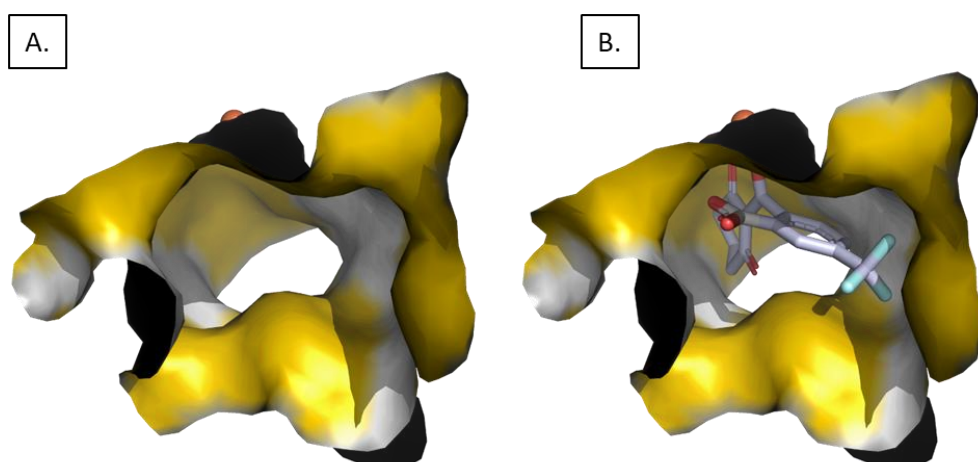
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S.oneidensis -IPEYYDTIFDKVPQVTENDRIKKHQIVDGD-----ESGYLLQIFTKNLFG--PIEF 313
R.etli PPETYDMSYERVGHGDEPIDRMKKGILIDGEGVNVGMTKILLQIFSKTVIG--PIEF 331
P.kilonensis PPDTYYEMLEGRLPNHGEPVDELQSRGILLDGAS--EQGDKRLLQLIFSETLMG--PVFF 322
L.pneumophila -PDTYYEMINDRLPWHKPELNLQHLAEKILIDGEA--DP-KDGLLLQIFYENIFG--PVFF 311
P.aeruginosa -PDTYYEKVDTRVAGHDEPLERLRELNLIDGAE--PG-DDGILLQIFSDTVIG--PIEF 324
A.salmonicida -PDTYYEKVNSRVEGHQEDLASLKDQLIDIGS--PT-KDGILLQIFSDTVIG--PVFF 330
V.parahaemolyticus -PDTYYEKVDERVEGHTEDVSKLRDLQILIDGAE--PT-KDGILLQIFSDTVIG--PVFF 321
V.anguillarum -PDTYYEKVSDRVEGHQEDVDQLKALRLIDGAE--PM-KDGILLQIFSDTVIG--PVFF 321

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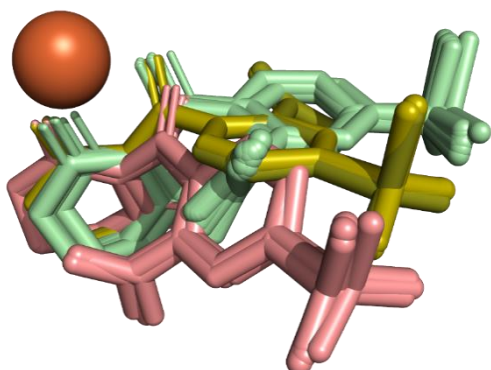
B.cereus EIIQRKGSRGFEGNFKALFESIEREQERRGNL----- 372
S.oneidensis EIIQRKNNLGFEGNFKALFQSIERDQMRGVL----- 346
R.etli EFIQRKGDEGFEGNFKALFESIEADQIKRGGVIGTAAE-- 369
P.kilonensis EFIQRKGGDGFEGNFKALFESIERDQVRRGVLATE---- 358
L.pneumophila EIIQRKGNQGFEGNFKALFEAIERDQVRRGTLKELS--- 348
P.aeruginosa EIIQRKGNQGFEGNFKALFESIEEDQIRRGVI----- 357
A.salmonicida EIIQRKGNEGFEGNFKALFESIEELDQIRRGVHLHGEPDA 370
V.parahaemolyticus EIIQRKGNEGFEGNFKALFESIEEDQIRRGVLSDA---- 357
V.anguillarum EIIQRKGNEGFEGNFKALFESIEEDQIRRGVLSDA---- 357

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Supplementary Figure 3. HPPD protein alignments. *B. cereus* ATCC14579, *S. oneidensis* MR-1, *R. etli* CFN42, *P. fluorescens* F113, *L. pneumophila*, *P. aeruginosa*, *A. salmonicida*, *V. parahaemolyticus* and *V. anguillarum* and protein sequences were retrieved from Genbank (<https://www.ncbi.nlm.nih.gov/genbank/>) and aligned with ClustalW [37]. The amino acids corresponding to the active site of the enzyme are framed in pink. Those involved in the substrate-binding domain are framed in green. Highly conserved amino-acids are framed in violet. “*” indicates perfect alignment. “:” indicates a site belonging to group exhibiting strong similarity. “.” indicates a site belonging to a group exhibiting weak similarity.



Supplementary Figure 4. Lipophilic properties of the substrate HPP binding domain (yellow) of HPPD from *Streptomyces avermitilis*. A) Open substrate binding domain and B) binding domain occupied by NTBC, an HPPD inhibitor. Lipophilic domain was coloured using the YRB script [72].



Supplementary Figure 5. Example of docking results obtained with mesotrione coordinated on the metal dication on homology model of *P. fluorescens* F113. In green, the 18 poses in an

orientation most similar to that observed with inhibitors co-crystalized with HPPD; In gold, the 3 poses in the less favourable orientation; In pink, the 4 in the least desirable orientation.

Supplementary Table 6. Binding energies and number of poses in optimal orientations for sulcotrione, mesotrione and tembotrione in the homology models.

	Sulcotrione		Mesotrione		Tembotrione	
	Binding energy (kcal/mol)	Poses #	Binding energy (kcal/mol)	Poses #	Binding energy (kcal/mol)	Poses #
<i>P. fluorescens</i> F113	-2.2±0.2	20	-1.4±0.2	20	-2.5±0.2	23
<i>S. oneidensis</i> MR-1	-3.3±0.1	24	-2.5±0.2	25	-3.3±0.2	13
<i>B. cereus</i> ATCC14579	-3.0±0.2	23	-2.4±0.2	25	-3.2±0.1	15