

STÉPHANE VUILLEUMIER PUBLICATIONS

As of November 2022, 145 peer-reviewed publications (18 as first author, 29 as corresponding author): 123 journal articles (11 review articles), 1 edited book, 14 book chapters, and 7 peer-reviewed congress proceedings and reports. *h-index*=35, 4477 total citations and 37 citations per publication on average in Web of Science Core Collection.

Peer-reviewed journal articles

145. Husser C, **Vuilleumier S**, Ryckelynck M (2022). FluorMango, an RNA-based fluorogenic biosensor for the direct and specific detection of fluoride. *Small* **2022**, art. 2205232. <https://doi.org/10.1002/smll.202205232>
144. Chaignaud P, Gruffaz C, Borreca A, Fouteau S, Kuhn L, Masbou J, Rouy Z, Hamman P, Imfeld G, Roche D, **Vuilleumier S** (2022). A methylotrophic bacterium growing with the antidiabetic drug metformin as its sole carbon, nitrogen and energy source. *Microorganisms* **10**, art. 2302. <https://doi.org/10.3390/microorganisms10112302>
143. Jarrige D, Haridas S, Bleykasten C, Joly M, Nadalig T, Sancelme M, **Vuilleumier S**, Grigoriev I, Amat. o P, Bringel F (2022). High quality genome of the basidiomycete yeast *Dioszegia hungarica* PDD-24b-2 isolated from cloud water. *G3 Genes|Genomes|Genetics* **12**, art. 403771. <https://doi.org/10.1093/g3journal/jkac282>
142. Jarrige D, Nadalig T, Joly M, Sancelme M, **Vuilleumier S**, Amato P, Bringel F (2022). Complete genome of *Sphingomonas aerolata* PDD-32b-11, isolated from cloud water at the summit of puy de Dôme, France. *Microbiol Res Announc* **11**, art. e00684-00622. <https://doi.org/10.1128/mra.00684-22>
141. Maucourt B, Roche D, Chaignaud P, **Vuilleumier S**, Bringel F (2022) Genome-wide transcription start sites mapping in *Methylobacterium* grown with dichloromethane and methanol. *Microorganisms* **10**, art. 1301. <https://doi.org/10.3390/microorganisms10071301>
140. Geersens E, **Vuilleumier S**, Ryckelynck M (2022) Growth-associated droplet shrinkage for bacterial quantification, growth monitoring and separation by ultrahigh-throughput microfluidics. *ACS Omega* **7**, 12039–12047. <https://pubs.acs.org/doi/10.1021/acsomega.2c00248>
139. Renaudie M, Dumas C, **Vuilleumier S**, Ernst B (2022) New way of valorization of raw coffee silverskin: biohydrogen and acetate production by dark fermentation without exogenous inoculum. *Biores. Technol. Rep.* **17**, art. 100918. <https://doi.org/10.1016/j.biteb.2021.100918>.
138. Prieto M, Weill S, Belfort B, Muller EEL, Masbou J, Lehmann F, **Vuilleumier S**, Imfeld G (2021) Water table fluctuations affect dichloromethane biodegradation in lab-scale aquifers contaminated with organohalides. *Water Res.* **203**, art. 117530. <https://doi.org/10.1016/j.watres.2021.117530>
137. Kröber E, Wende S, Kanukollu S, Buchen-Tschiskale C, Besaury L, Keppler F, **Vuilleumier S**, Kolb S, Bringel F (2021) ¹³C-chloromethane incubations provide evidence for novel bacterial chloromethane degraders in a living tree fern. *Environ. Microbiol.* **23**, 4450-4465. <https://doi.org/10.1111/1462-2920.15638>
136. Renaudie M, Clion V, Dumas C, **Vuilleumier S**, Ernst B (2021) Intensification and optimization of continuous hydrogen production by dark fermentation in a new design liquid/gas hollow fiber membrane bioreactor. *Chem. Eng. J.* **416**, art. 129068.
135. Hellal J, Joulian C, Urien C, Ferreira S, Denonfoux J, Hermon L, **Vuilleumier S**, Imfeld G (2021) Chlorinated ethene biodegradation and associated bacterial taxa in multi-polluted groundwater: insights from biomolecular markers and stable isotope analysis. *Sci. Total Environ.* art. 142950.
134. François E, Dumas C, Gougeon R, Hervé A, **Vuilleumier S**, Ernst B (2021) Unexpected high production of biohydrogen from the endogenous fermentation of grape must deposits. *Bioresour. Technol.* **320**, art. 124334.
133. Renaudie M, Dumas C, **Vuilleumier S**, Ernst B (2021) Biohydrogen production in a continuous liquid/gas hollow fiber membrane bioreactor: efficient retention of hydrogen producing bacteria via granule and biofilm formation. *Bioresour. Technol.* **319**, art. 124203.
132. Hayoun K, Geersens E, Laczny C, Halder R, Lázaro Sánchez C, Manna A, Bringel F, Ryckelynck M, Wilmes P, Muller EEL, Alpha-Bazin B, Armengaud J, **Vuilleumier S** (2020) Dichloromethane degradation pathway from unsequenced *Hyphomicrobium* sp. MC8b rapidly explored by pan-proteomics. *Microorganisms* **8**, art. 1876. <https://doi.org/10.3390/microorganisms8121876>
131. Maucourt B, **Vuilleumier S**, Bringel F (2020) Transcriptional regulation of organohalide pollutant utilisation in bacteria. *FEMS Microbiol. Rev.* **44**, 189-207.

130. Torabi E, Wiegert C, Guyot B, **Vuilleumier S**, Imfeld G (2020) Dissipation of butachlor and S-metolachlor in agricultural soils and responses of bacterial communities: insights from compound-specific isotope and biomolecular analyses. *J. Environ. Sci.* **92**, 163-175.
129. Keppler F, Barnes J, Horst A, Bahlmann E, Luo J, Nadalig T, Greule M, Hartmann SC, **Vuilleumier S** (2020) Chlorine isotope fractionation of the major chloromethane degradation processes in the environment. *Environ Sci. Technol.* **54**, 1634-1645. <https://doi.org/10.1021/acs.est.9b06139>
126. Boachon B, Burdloff Y, Ruan J-X, Rojo R, Bruno V, Robert J, Bringel F, Lesot A, Henry L, Bassard JE, Matthieu S, Lionel A, Kaplan I, Dudareva N, **Vuilleumier S**, Laurence M, André F, Navrot N, Chen X-Y, Werck D (2019) A promiscuous CYP706A3 reduces terpene volatile emission from *Arabidopsis* flowers, with impacts on florivores and floral microbiome. *Plant Cell* **31**, 2947-2972
125. Chevallier M, Della-Negra O, Chaussonnerie S, Barbance A, Muselet D, Lagarde F, Darii E, Ugarte E, Lescop E, Fonknechten N, Weissenbach J, Woignier T, Gallard J-F, **Vuilleumier S**, Imfeld G, Le Paslier D, Saaidi P-L (2019). Natural chlordecone degradation revealed by numerous transformation products characterized in key French West Indies environmental compartments. *Environ. Sci. Technol.* **53**, 6133-6143.
124. Elahi A, Ajaz M, Rehman A, **Vuilleumier S**, Khan Z, Hussain SZ (2019). Isolation, characterization, and multiple heavy metal-resistant and hexavalent chromium-reducing *Microbacterium testaceum* B-HS2 from tannery effluent. *J King Saud University - Science* **31**, 1437-1444.
123. Loyaux-Lawniczak S, **Vuilleumier S**, Geoffroy V (2019). Efficient reduction of iron oxides by *Paenibacillus* spp. strains isolated from tropical soils. *Geomicrobiol. J.* **36**, 422-432.
122. Hermon L, Hellal J, Denonfoux J, **Vuilleumier S**, Imfeld G, Ferreira S, Jouliau C (2019). Functional genes and bacterial communities during organohalide respiration of chloroethenes in microcosms of multi-contaminated groundwater. *Front. Microbiol.* **10**, art. 89.
120. Torgonskaya MT, Zyakun AM, Trotsenko YA, Laurinavichius KS, Kümmel S, **Vuilleumier S**, Richnow HH (2019). Individual stages of bacterial dichloromethane degradation mapped by stable carbon and chlorine isotope abundance ratios. *J. Environ. Sci.* **78**, 147-160.
119. Imfeld G, Besaury L, Maucourt B, Donadello S, Baran N, **Vuilleumier S** (2018). Toward integrative bacterial monitoring of metolachlor toxicity in groundwater. *Front. Microbiol.* **9**, art. 2053.
118. Chaignaud P, Morawe M, Besaury L, Kröber E, **Vuilleumier S**, Bringel F, Kolb S (2018). Methanol consumption drives the bacterial chloromethane sink in a forest soil. *ISME J.* **12**, 2681-2693.
117. Hermon L, Denonfoux J, Hellal J, Jouliau C, Ferreira S, **Vuilleumier S**, Imfeld G (2018). Dichloromethane biodegradation in multi-contaminated groundwater: insights from biomolecular and compound-specific isotope analyses. *Water Res.* **142**, 217-226.
116. Jaeger N, Besaury L, Röhling AN, Koch F, Delort A-M, Gasc C, Greule M, Kolb S, Nadalig T, Peyret P, **Vuilleumier S**, Amato P, Bringel F, Keppler F (2018). Chloromethane formation and degradation in the fern phyllosphere. *Sci. Total Environ.* **634**, 1278-1287. <https://doi.org/10.1016/j.scitotenv.2018.03.316>
115. Bibi-Triki S, Husson G, Maucourt B, **Vuilleumier S**, Carapito C, Bringel F (2018). N-terminome and proteogenomic analysis of the *Methylobacterium extorquens* DM4 reference strain for dichloromethane utilization. *J. Proteomics* **179**, 131-139.
114. Jaeger N, Besaury L, Kröber E, Delort A-M, Greule M, Nadalig T, **Vuilleumier S**, Amato P, Kolb S, Bringel F, Keppler F, Lenhart K (2018). New insights into chloromethane degradation in soils – a combined microbial and two-dimensional isotope approach. *J. Environ. Qual.* **47**, 254-262.
113. Farhan UI Haque M, Besaury L, Nadalig T, Bringel F, Mutterer J, Schaller H, **Vuilleumier S** (2017). Correlated production and consumption of chloromethane in the *Arabidopsis thaliana* phyllosphere. *Sci. Rep.* **7**, art. 17589.
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111. Bringel F, **Vuilleumier S** (2017). Metabolic regulation: A master role for ribulose-1,5-bisphosphate in one-carbon assimilation *Curr. Biol.* **27**, R1127-R1129.
110. Chaignaud P, Maucourt B, Weiman M, Alberti A, Kolb S, Cruveiller S, **Vuilleumier S**, Bringel F (2017). Genomic and transcriptomic analysis of growth-supporting dehalogenation of chlorinated methanes in *Methylobacterium*. *Front. Microbiol.* **8**, art. 1600.
109. Bringel F, Postema CP, Mangenot S, Bibi-Triki S, Chaignaud P, Farhan UI Haque M, Gruffaz C, Hermon L, Louhichi Y, Maucourt B, Muller EEM, Nadalig T, Lajus A, Rouy Z, Médigue C, Barbe V, Janssen DB, **Vuilleumier S** (2017). Genome sequence of the dichloromethane-degrading bacterium *Hyphomicrobium* sp. strain GJ21. *Genome Announc.* **5**, art. 00622-17.

107. Frindte K, Kalyuzhnaya M, Bringel F, Dunfield P, Jetten M, Khmelenina V, Klotz M, Murrell C, Op den Camp H, Sakai Y, Semrau J, Shapiro N, DiSpirito A, Stein S, Svenning M, Trotsenko Y, **Vuilleumier S**, Woyke T, Knief C (2017). Draft genome sequences of two gammaproteobacterial methanotrophs isolated from rice ecosystems. *Genome Announc.* **5**, art. 00526-17.
106. Bradley AS, Swanson PK, Muller EEL, Bringel F, Carroll SM, Pearson A, **Vuilleumier S**, Marx CJ (2017). Hopanoid-free *Methylobacterium extorquens* DM4 overproduces carotenoids and has widespread growth impairment. *PLoS ONE* **12**, art. e0173323.
105. Michener JK, **Vuilleumier S**, Bringel F, Marx CJ (2016). Transfer of a catabolic pathway for chloromethane in *Methylobacterium* strains highlights different limitations for growth with chloromethane or with dichloromethane. *Front. Microbiol.* **7**, art. 1116.
104. DiSpirito AA, Semrau JD, Murrell JC, Gallagher WH, Dennison C, **Vuilleumier S** (2016). Methanobactin and the link between copper and bacterial methane oxidation. *Microbiol. Molec. Biol. Rev.* **80**, 387-409.
103. Flynn JD, Hirayama H, Sakai Y, Dunfield PF, Klotz MG, Knief C, Op den Camp HJ, Jetten MJM, Khmelenina VN, Trotsenko YA, Murrell JC, Semrau JD, Svenning MM, Stein LY, Kyrpides N, Shapiro N, Woyke T, Bringel F, **Vuilleumier S**, DiSpirito AA, Kalyuzhnaya MG (2016). Draft genomes of gammaproteobacterial methanotrophs isolated from marine ecosystems. *Genome Announc.* **4**, art. 01629-15.
101. Al Dine EJ, Mokbel H, Elmoll A, Massemin S, **Vuilleumier S**, Toufaily J, Hanieh T, Millet M (2015). Concomitant evaluation of atmospheric levels of polychlorinated biphenyls, organochlorine pesticides, and polycyclic aromatic hydrocarbons in Strasbourg (France) using pine needle passive samplers. *Environ. Sci. Pollut. Res.* **22**, 17850-17859.
100. Penny C, Gruffaz C, Nadalig T, Cauchie H-M, **Vuilleumier S**, Bringel (2015). Tetrachloromethane-degrading bacterial enrichment cultures and isolates from a contaminated aquifer. *Microorganisms* **3**, 327-343.
99. Sharp CE, Smirnova AV, Kalyuzhnaya MG, Bringel F, Hirayama H, Jetten MS, Khmelenina VN, Klotz MG, Knief C, Kyrpides N, Op den Camp HJ, Reshetnikov AS, Sakai Y, Shapiro N, Trotsenko YA, **Vuilleumier S**, Woyke T, Dunfield PF (2015). Draft genome sequence of the moderately halophilic methanotroph, *Methylohalobius crimeensis* strain 10Ki. *Genome Announc.* **3**, art. 00644-15.
98. Hamilton R, Kits J, Ramonovskaya V, Rozova ON, Yurimoto H, Iguchi H, Khmelenina VN, Sakai Y, Dunfield PF, Klotz MG, Knief C, Op den Camp HJM, Jetten MSM, Bringel F, **Vuilleumier S**, Svenning MM, Shapiro N, Woyke T, Trotsenko YA, Stein LY, Kalyuzhnaya MG (2015). Draft genomes of gammaproteobacterial methanotrophs isolated from terrestrial ecosystems. *Genome Announc.* **3**, art. 00515-15.
97. Elsayed OF, Maillard E, **Vuilleumier S**, Millet M, Imfeld G (2015). Degradation of chloroacetanilide herbicides and bacterial community composition in lab-scale wetlands. *Sci. Tot. Environ.* **520**, 222-231.
96. Michener JK, Camargo Neves AA, **Vuilleumier S**, Bringel F, Marx CJ (2014). Effective use of a horizontally-transferred pathway for dichloromethane catabolism requires post-transfer refinement. *eLife* **3**, art. 04279.
95. Nadalig T, Greule M, Bringel F, Keppler F, **Vuilleumier S** (2014). Probing the diversity of chloromethane-degrading bacteria by comparative genomics and isotopic fractionation. *Front. Microbiol.* **5**, art. 523.
94. Elsayed O, Maillard E, **Vuilleumier S**, Imfeld G (2014). Bacterial communities in batch and continuous-flow wetlands treating the herbicide S-metolachlor. *Sci. Tot. Environ.* **499**, 327-335.
93. Ghiglione JF, Martin-Laurent F, Stachowski-Haberkorn S, Pesce S, **Vuilleumier S** (2014). The coming of age of microbial ecotoxicology: report on the first two meetings in France. *Environ. Sci. Pollut. Res.* **21**, 14241-14245.
92. Michener JK, **Vuilleumier S**, Bringel F, Marx CJ (2014). Phylogeny poorly predicts the utility of a challenging horizontally-transferred gene in *Methylobacterium* strains. *J. Bacteriol.* **196**, 2101-2107.
91. Vorobev A, Jagadevan S, Jain S, Anantharaman K, Dick G, **Vuilleumier S**, Semrau JD (2014). How do facultative methanotrophs utilize multi-carbon compounds for growth? Genomic and transcriptomic analysis of *Methylocystis* strain SB2 grown on methane and on ethanol. *Appl. Environ. Microbiol.* **80**, 3044-3052.
90. Elsayed O, Maillard E, **Vuilleumier S**, Nijenhuis I, Richnow HH, Imfeld G (2014). Using compound specific isotope analysis to assess the degradation of chloroacetanilide herbicides in lab-scale wetlands. *Chemosphere* **99**, 89-95.
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88. Nadalig T, Greule M, Bringel F, **Vuilleumier S**, Keppler F (2013). Hydrogen and carbon isotope fractionation during degradation of chloromethane by methylotrophic bacteria. *MicrobiologyOpen* **2**, 893-900.
87. Semrau JD, Jagadevan S, DiSpirito AA, Khalifa A, Scanlan J, Bergman BH, Freemeier BC, Baral BS, Bandow NL, Vorobev A, Haft DH, **Vuilleumier S**, Murrell JC (2013). Methanobactin and MmoD work in concert to act as the "copper-switch" in methanotrophs. *Environ. Microbiol.* **15**, 3077-3086.
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84. Kits K, Kalyuzhnaya M, Klotz M, Jetten M, Op den Camp H, **Vuilleumier S**, Bringel F, DiSpirito A, Murrell C, Bruce D, Cheng J-F, Copeland A, Goodwin L, Hauser L, Lajus A, Land M, Lapidus A, Lucas S, Médigue C, Pitluck S, Woyke T, Zeytun A, Stein L (2013). Genome sequence of the obligate Gammaproteobacterial methanotroph *Methylobacterium album* strain BG8. *Genome Announc.* **1**, art. 00170-13.
83. Roselli S, Nadalig T, **Vuilleumier S**, Bringel F (2013). Plasmid pCMU01 features chloromethane utilization genes and gene redundancy for vitamin B12- and tetrahydrofolate-dependent chloromethane metabolism in *Methylobacterium extorquens* CM4: a proteomic and bioinformatics study. *PLoS ONE* **8**, art. e56598.
82. Marx CJ, Bringel F, Chistoserdova L, Moulin L, Farhan UI Haque M, Fleischman DE, Gruffaz C, Jourand P, Knief C, Lee M-C, Muller EEL, Nadalig T, Peyraud R, Roselli S, Russ L, Goodwin LA, Ivanova N, Kyrpides N, Lajus A, Land ML, Médigue C, Mikhailova N, Nolan M, Woyke T, Stolyar S, Vorholt JA, **Vuilleumier S** (2012). Complete genome sequences of six strains of the genus *Methylobacterium*. *J. Bacteriol.* **194**, 4746-4748.
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