

## STÉPHANE VUILLEUMIER PUBLICATIONS

As of February 2025, 152 peer-reviewed publications (21 as first author, 31 as corresponding author): 129 journal articles (12 review articles), 1 edited book, 14 book chapters, and 7 peer-reviewed congress proceedings and reports. *h-index*=38, 5189 total citations and 39 citations per publication on average (Web of Science Core Collection).

### Peer-reviewed journal articles

152. Badel C, Bocconetti E, Khodr R, Husser C, Ryckelynck M, **Vuilleumier S** (2025) Complete genome sequence of fluoroacetate-degrading *Caballeronia* sp. S22 strain (DSM 8341) as a reference resource for investigations of microbial defluorination. *Microbiol Resource Announc* **14**, art. e00812-24. <https://doi.org/10.1128/mra.00812-24>
151. **Vuilleumier S**, Barthelmebs L, Corcoll N, Hery M, Karpouzas D, Wick LY (2024) Editorial: thematic issue on microbial ecotoxicology. *FEMS Microbiol Ecol* **100**, art. fia097. <https://doi.org/10.1093/femsec/fia097>
150. Borreca A, **Vuilleumier S**, Imfeld G (2024) Combined effects of micropollutants and their degradation on prokaryotic communities at the sediment-water interface. *Sci Rep* **14**, art. 16840. <https://doi.org/10.1038/s41598-024-67308-y>
149. Renaudie M, Dumas C, **Vuilleumier S**, Ernst B (2024). Spontaneous dark fermentation in a pre-seeded liquid-gas membrane bioreactor: Impact of wine and coffee biowaste microflora on continuous biohydrogen production. *J Cleaner Prod* **437**, art. 140759. <https://doi.org/10.1016/j.jclepro.2024.140759>
148. Hellal J, Barthelmebs L, Bérard A, Cébron A, Cheloni G, Colas S, Cravo-Laureau C, De Clerck C, Gallois N, Hery M, Martin-Laurent F, Martins J, Morin S, Palacios C, Pesce S, Richaume A, **Vuilleumier S** (2023). Unlocking secrets of microbial ecotoxicology: recent achievements and future challenges. *FEMS Microbiol Ecol* **99**, fiad102. <https://doi.org/10.1093/femsec/fiad102>
147. Prieto-Espinoza M, Di Chiara Roupert R, Muller EEL, **Vuilleumier S**, Imfeld G, Weill S (2023). Combining multi-phase flow and pathway-specific reactive transport modeling to investigate the impact of water table fluctuations on dichloromethane biodegradation. *Adv Water Res* **180**, art. 104519. <https://doi.org/10.1016/j.advwatres.2023.104519>
146. Wasmund K, Trueba-Santiso A, Vicent T, Adrian L, **Vuilleumier S**, Marco-Urrea S (2023). Proteogenomics of the novel *Dehalobacterium formicoaceticum* strain EZ94 highlights a key role of methyltransferases during anaerobic dichloromethane degradation. *Environ Sci Pollut Res* **30**, 80602-80612. <https://doi.org/10.1007/s11356-023-28144-1>
145. Husser C, **Vuilleumier S**, Ryckelynck M (2023). FluorMango, an RNA-based fluorogenic biosensor for the direct and specific detection of fluoride. *Small* **19**, 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, Amato 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) <sup>13</sup>C-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. <https://doi.org/10.1016/j.cej.2021.129068>
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. <https://doi.org/10.1016/j.scitotenv.2020.142950>
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. <https://doi.org/10.1016/j.biortech.2020.124334>
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. <https://doi.org/10.1016/j.biortech.2020.124203>
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. <https://doi.org/10.1093/femsre/fuaa002>
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. <https://doi.org/10.1016/j.jes.2020.02.009>
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.
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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, Joulian 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. <https://doi.org/10.1016/j.jes.2018.09.008>
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, Joulian 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.
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112. Mauffrey F, Baccara P-Y, Gruffaz C, **Vuilleumier S**, Imfeld G (2017). Bacterial community structures and herbicide-degrading genes in a stormwater wetland collecting herbicide runoff. *Water Air Soil Pollut.* **28**, art. 452.
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.
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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.
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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.
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86. Farhan UI Haque M, Nadalig T, Bringel F, Schaller H, **Vuilleumier S** (2013). Fluorescence-based bacterial bioreporter for specific detection of methyl halide emissions in the environment. *Appl. Environ. Microbiol.* **79**, 6561-6567.
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