

STÉPHANE VUILLEUMIER PUBLICATIONS

As of 6 January 2022, 139 peer-reviewed publications (18 as first author, 28 as corresponding author): 116 journal articles (11 review articles), 1 edited book, 14 book chapters, and 7 congress proceedings and reports. *h-index*=35, 4255 total citations and 35 citations per publication on average in Web of Science Core Collection.

Peer-reviewed journal articles

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.
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, Jouliau 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, Lazaro Sanchez 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.
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, 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.
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.
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.
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, Caroll 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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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.
89. Kalyuzhnaya MG, Yang S, Rozova ON, Smalley NE, Clubb J, Lamb A, Nagana Gowda GA, Raftery D, Fu Y, Bringel F, **Vuilleumier S**, Trotsenko YA, Beck D, Khmelenina VN, Lidstrom ME (2013). Highly efficient methane biocatalysis revealed in a methanotrophic bacterium. *Nature Commun.* **4**, art. 2785.
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.
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.
85. Khmelenina VN, Beck D, Munk C, Davenport K, Daligault H, Erkkila T, Goodwin L, Gu W, Lo C-C, Scholz M, Teshima H, Xu Y, Chain P, Bringel F, **Vuilleumier S**, DiSpirito A, Dunfield P, Jetten MSM, Klotz MG, Knief C, Murrell JC, Op den Camp HJM, Sakai Y, Semrau S, Svenning M, Stein LY, Trotsenko YA, Kalyuzhnaya MG (2013). Draft genome sequence of *Methylochromobium buryatense* 5G, a haloalkaline-tolerant methanotrophic bacterium. *Genome Announc.* **1**, art. 00053-13.
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 *Methylochromobium album* strain BG8. *Genome Announc.* **1**, art. 00170-13.

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78. Boden R, Cunliffe M, Scanlan J, Moussard H, Kitz K, Klotz MG, Jetten MSM, **Vuilleumier S**, Han J, Peters L, Mikhailova N, Teshima N, Tapia R, Kyrpides N, Ivanova N, Pagani I, Cheng J-F, Goodwin L, Han C, Hauser L, Land M, Lapidus A, Lucas S, Pitluck S, Woyke T, Stein LY, Murrell JC (2011). Complete genome sequence of the aerobic marine methanotroph *Methylohalobium methanicum* MC09. *J. Bacteriol.* **193**, 7001-7002.
77. Svenning MM, Hestnes AG, Wartainen I, Stein LY, Klotz MG, Kalyuzhnaya MG, Spang A, Bringel F, **Vuilleumier S**, Lajus A, Médigue C, Bruce DC, Cheng JF, Goodwin L, Ivanova N, Han J, Han CS, Hauser L, Held B, Land ML, Lapidus A, Lucas S, Nolan M, Pitluck S, Woyke T (2011). Genome sequence of the Arctic methanotroph *Methylobacter tundripaludum* SV96. *J. Bacteriol.* **193**, 6418-6419.
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75. Kittichotirat W, Good N, Hall R, Bringel F, Lajus A, Médigue C, Smalley N, Beck D, Bumgarner R, **Vuilleumier S**, Kalyuzhnaya MG (2011). Genome sequence of *Methyloversatilis universalis* FAM5^T, a methylotrophic representative of the order *Rhodocyclales*. *J. Bacteriol.* **193**, 4541-4542.
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73. Muller E, Hourcade E, Louhichi Y, Hammann P, **Vuilleumier S**, Bringel F (2011). Functional genomics of dichloromethane utilisation in *Methylobacterium extorquens* DM4. *Environ. Microbiol.* **13**, 2518-2535.
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