

STÉPHANE VUILLEUMIER PUBLICATIONS

As of December 2024, 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*=37, 5099 total citations and 38 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** (in press) Complete genome sequence of fluoroacetate-degrading *Caballeronia* sp. S22 strain (DSM 8341) as a reference resource for investigations of microbial defluorination. *Microbiol Resource Announc* MRA00812-24R1.
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 Giulia, Colas S, Cravo-Laureau C, De Clerck C, Gallois N, Hery M, Martin-Laurent F, Martins J, Morin S, Palacios C, Pesce S, Richaume-Jolion Agnès, **Vuilleumier S** (2023). Combining multi-phase flow and pathway-specific reactive transport modeling to investigate the impact of water table fluctuations on dichloromethane biodegradation. *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/sml.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) 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. <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.
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. <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.
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, 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. <https://doi.org/10.3390/microorganisms3030327>
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, Ramonovskay 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, Bindow 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 *Methylococcoides burtonensis* 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 *Methylococcoides burtonensis* 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.

81. Khadem FA, Wieczorek AS, Pol A, **Vuilleumier S**, Harhangi HR, Dunfield PF, Kalyuzhnaya MG, Murrell JC, Francois K-J, Stunnenberg HG, Stein LY, DiSpirito AA, Semrau JD, Lajus A, Médigue C, Klotz MG, Jetten MSM, Op den Camp HJM (2012). Draft genome sequence of the volcano-inhabiting thermoacidophilic methanotroph *Methylacidiphilum fumarolicum* strain SolV. *J. Bacteriol.* **194**, 3729-3730.
80. Imfeld G, **Vuilleumier S** (2012). Measuring the effects of pesticides on bacterial communities in soil: a critical review. *Eur. J. Soil Biol.* **49**, 22-30. <https://doi.org/10.1016/j.ejsobi.2011.11.010>
79. **Vuilleumier S**, Khmelenina VN, Bringel F, Reshetnikov AS, Lajus A, Mangenot S, Rouy Z, Op den Camp HJM, Jetten MSM, DiSpirito AA, Dunfield P, Klotz MG, Semrau JD, Stein LY, Barbe V, Médigue C, Trotsenko YA, Kalyuzhnaya MG (2012). Genome sequence of the haloalkaliphilic methanotrophic bacterium *Methylomicrobium alcaliphilum* 20Z. *J. Bacteriol.* **194**, 551-552.
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 *Methylomonas methanica* MC09. *J. Bacteriol.* **193**, 7001-7002.
77. Svenning MM, Hestnes AG, Warttinen 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.
76. **Vuilleumier S**, Nadalig T, Farhan UI Haque M, Magdelenat G, Lajus A, Roselli S, Muller EEL, Gruffaz C, Barbe V, Médigue C, Bringel F (2011). Complete genome sequence of the chloromethane-degrading strain *Hyphomicrobium* sp. strain MC1. *J. Bacteriol.* **193**, 5035-5036.
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.
74. Semrau JD, DiSpirito AA, **Vuilleumier S** (2011). Facultative methanotrophy: False leads, true results, and suggestions for future research. *FEMS Microbiol. Lett.* **323**, 1-12.
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. <https://doi.org/10.1111/j.1462-2920.2011.02524.x>
72. Nadalig T, Farhan UI Haque M, Roselli S, Schaller H, Bringel F, **Vuilleumier S** (2011). Detection and isolation of chloromethane-degrading bacteria from the *Arabidopsis thaliana* phyllosphere, and characterization of chloromethane utilisation genes. *FEMS Microbiol Ecol.* **77**, 438-448.
71. Bois P, Huguenot D, Norini MP, Farhan UI Haque M, **Vuilleumier S**, Lebeau T (2011). Herbicide degradation and copper complexation by bacterial mixed cultures from a vineyard stormwater basin. *J. Soils Sediments* **11**, 860-873.
70. Muller E, Bringel F, **Vuilleumier S** (2011). Dichloromethane-degrading bacteria in the genomic age. *Res. Microbiol.* **162**, 869-876.
69. Torgonskaya ML, Doronina NV, Hourcade E, Trotsenko YA, **Vuilleumier S** (2011). Chloride-specific adaptive response in aerobic methylotrophic dichloromethane-utilising bacteria. *J. Basic Microbiol.* **51**, 296-303.
68. Stein LY, Bringel F, DiSpirito AA, Han S, Jetten MSM, Kalyuzhnaya MG, Kits KD, Klotz MG, Op den Camp HJM, Semrau JD, **Vuilleumier S**, Bruce F, Cheng JF, Copeland A, Davenport KW, Goodwin L, Han S, Hauser L, Lajus A, Land ML, Lapidus A, Lucas S, Médigue C, Pitluck S, Woyke T (2011). Genome sequence of the methanotrophic Alphaproteobacterium, *Methylocystis* sp. Rockwell (ATCC 49242). *J. Bacteriol.* **193**, 2668-2669.
66. Rozova ON, Khmelenina VN, **Vuilleumier S**, Trotsenko YA (2010). Characterization of recombinant pyrophosphate-dependent 6-phosphofructokinase from halotolerant methanotroph *Methylomicrobium alcaliphilum* 20Z. *Res. Microbiol.* **161**, 861-868.
65. Stein LY, Semrau JD, DiSpirito AA, Crombie A, Murrell JC, **Vuilleumier S**, Kalyuzhnaya MG, Op den Camp HJM, Bringel F, Bruce F, Cheng JF, Copeland A, Goodwin L, Han S, Hauser L, Jetten MSM, Lajus A, Land ML, Lapidus A, Lucas S, Médigue C, Pitluck S, Woyke T, Yoon S, Zeytun A, Klotz MG (2010). Genome sequence of the obligate methanotroph, *Methylosinus trichosporium* strain OB3b. *J. Bacteriol.* **192**, 6497-6498.
64. Krentz BD, Mulheron HJ, Semrau JD, DiSpirito AA, Bandow NL, Haft DH, **Vuilleumier S**, Murrell JC, McEllistrem MT, Hartsel SC, Gallagher WH (2010). A comparison of methanobactins from *Methylosinus*

trichosporium OB3b and *Methylocystis* strain SB2 predicts methanobactins are synthesized from diverse ribosomally produced peptide precursors modified to create a common core for binding and reducing copper ions. *Biochemistry* **49**, 10117-10130.

63. Todorova TT, Kujumdzieva AV, **Vuilleumier S** (2010). Non-enzymatic roles for the *URE2* glutathione S-transferase in the response of *Saccharomyces cerevisiae* to arsenic. *Arch. Microbiol.* **192**, 909-918.
62. Penny C, **Vuilleumier S**, Bringel F (2010). Microbial degradation of tetrachloromethane: mechanisms and perspectives for bioremediation. *FEMS Microbiol Ecol.* **74**, 257-275.
61. Penny C, Nadalig T, Alioua M, Gruffaz C, **Vuilleumier S**, Bringel F (2010). Coupling of denaturing high performance liquid chromatography and terminal restriction fragment length polymorphism with precise fragment sizing for microbial community profiling and characterization. *Appl. Environ. Microbiol.* **76**, 648-651.
60. Todorova TT, Petrova V, **Vuilleumier S**, Kujumdzieva A (2009). Response to different oxidants of *Saccharomyces cerevisiae* $\Delta ure2$ mutant. *Arch. Microbiol.* **191**, 837-845.
59. **Vuilleumier S**, Chistoserdova L, Lee MC, Bringel F, Lajus A, Zhou Y, Gourion B, Barbe V, Chang J, Cruveiller S, Dossat C, Gillett W, Gruffaz C, Haugen E, Hourcade E, Levy R, Mangenot S, Muller E, Nadalig T, Pagni M, Penny C, Peyraud R, Robinson DG, Roche D, Rouy Z, Saenampechek C, Salvagnol G, Vallenet D, Wu Z, Marx CJ, Vorholt JA, Olson MV, Kaul R, Weissenbach J, Médigue C, Lidstrom ME (2009). *Methylobacterium* genome sequences: a reference blueprint to investigate microbial metabolism of C1 compounds from natural and industrial sources. *PLoS ONE* **4**, art. e5584.
58. Firsova J, Doronina N, Lang E, Spröer C, **Vuilleumier S**, Trotsenko YA (2009). *Ancylobacter dichloromethanicus* sp. nov. - a new aerobic facultatively methylotrophic bacterium utilizing dichloromethane. *Syst. Appl. Microbiol.* **32**, 227-232.
55. Bringel F, **Vuilleumier S**, Ploetze F (2008). Low carbamoyl phosphate pools may drive *Lactobacillus plantarum* CO₂-dependent growth phenotype. *J. Molec. Microbiol. Biotechnol.* **14**, 22-30.
54. Tralau T, **Vuilleumier S**, Thibault C, Campbell BJ, Hart A, Kertesz MA (2007). Transcriptomic analysis of the sulfate starvation response of *Pseudomonas aeruginosa*. *J. Bacteriol.* **189**, 6743-6750.
53. Todorova T, **Vuilleumier S**, Kujumdzieva A (2007). Role of glutathione S-transferases and glutathione in arsenic and peroxide resistance in *Saccharomyces cerevisiae*: a reverse genetic analysis approach. *Biotech. Biotech. Eq.* **21**, 348-352.
52. Schröder P, Navarro-Aviñó J, Azaizeh A, Goldhirsh AG, DiGregorio S, Komives T, Langergraber G, Lenz A, Maestri E, Memon AR, Ranalli A, Sebastiani L, Smrcek S, Vanek T, **Vuilleumier S**, Wissing F (2007). Using phytoremediation technologies to upgrade waste water treatment in Europe. *Environ. Sci. Pollution Rep.* **14**, 490-497.
51. Hauser F, Lindemann A, **Vuilleumier S**, Patrignani A, Schlapbach R, Fischer HM, Hennecke H (2006). Design and validation of a partial-genome microarray for transcriptional profiling of the *Bradyrhizobium japonicum* symbiotic gene region. *Molec. Genet. Genom.* **275**, 55-67.
50. Stourman NV, Rose JH, **Vuilleumier S**, Armstrong RN (2003). Catalytic mechanism of dichloromethane dehalogenase from *Methylophilus* sp. strain DM11. *Biochemistry* **42**, 11048-11056.
49. Studer A, McAnulla C, Büchele R, Leisinger T, **Vuilleumier S** (2002). Chloromethane induced genes define a third C1 utilization pathway in *Methylobacterium chloromethanicum* CM4. *J. Bacteriol.* **184**, 3476-3482.
48. Kayser MF, Ucurum Z, **Vuilleumier S** (2002). Dichloromethane metabolism and C1 utilization genes in *Methylobacterium* strains. *Microbiology* **148**, 1915-1922.
47. **Vuilleumier S**, Pagni M (2002). Bacterial glutathione S-transferases: new lessons from bacterial genomes. *Applied Microbiol. Biotechnol.* **58**, 138-146.
45. Wheeler JB, Stourman NV, Thier R, Dommermuth A, **Vuilleumier S**, Rose JA, Armstrong RN, Guengerich FP (2001). Conjugation of haloalkanes by bacterial and mammalian glutathione transferases: mono- and dihalomethanes. *Chem. Res. Toxicol.* **14**, 1118-1127.
44. Kayser MF, **Vuilleumier S** (2001). Dehalogenation of dichloromethane by dichloromethane dehalogenase/glutathione S-transferase leads to formation of DNA adducts. *J. Bacteriol.* **183**, 5209-5212.
43. Gisi D, Maillard J, Flanagan JU, Rossjohn J, Chelvanayagam G, Board PG, Parker MW, Leisinger T, **Vuilleumier S** (2001). Dichloromethane mediated *in vivo* selection and functional characterization of rat glutathione S-transferase theta 1-1 variants. *Eur. J. Biochem.* **268**, 4001-4010.
42. Studer A, Stupperich E, **Vuilleumier S**, Leisinger T (2001). Chloromethane:tetrahydrofolate methyl transfer by two proteins from *Methylobacterium chloromethanicum* strain CM4. *Eur. J. Biochem.* **268**, 2931-2938.

41. **Vuilleumier S**, Ivoš N, Dean M, Leisinger T (2001). Sequence variation in dichloromethane dehalogenases/glutathione S-transferases. *Microbiology* **147**, 611-619.
40. **Vuilleumier S**, Ucurum Z, Oelhafen S, Armengaud J, Wittich RM, Timmis KN (2001). The glutathione S-transferase OrfE3 of the dioxin-degrading bacterium *Sphingomonas* sp. RW1 displays maleylpyruvate isomerase activity. *Chemico-Biological Interactions* **133**, 265-267.
38. McAnulla C, Woodall CA, McDonald IR, Studer A, **Vuilleumier S**, Leisinger T, Murrell JC (2001). Chloromethane utilization gene cluster from *Hyphomicrobium chloromethanicum* strain CM2 and development of functional gene probes to detect halomethane degrading bacteria. *Appl. Environ. Microbiol.* **67**, 307-316.
37. Evans G, Ferguson GP, Booth IR, **Vuilleumier S** (2000). Growth inhibition of *Escherichia coli* by dichloromethane in cells expressing dichloromethane dehalogenase/glutathione S-transferase. *Microbiology* **146**, 2967-2975.
36. Kayser MF, Stumpp MT, **Vuilleumier S** (2000). DNA polymerase I is essential for growth of *Methylobacterium dichloromethanicum* DM4 with dichloromethane. *J. Bacteriol.* **182**, 5433-5439.
34. Studer A, **Vuilleumier S**, Leisinger T (1999). Properties of the methylcobalamin:H₄folate methyltransferase involved in chloromethane utilization by *Methylobacterium* sp. strain CM4. *Eur. J. Biochem.* **264**, 242-249.
33. Gisi D, Leisinger T, **Vuilleumier S** (1999). Enzyme-mediated dichloromethane toxicity and mutagenicity of bacterial and mammalian dichloromethane-active glutathione S-transferases. *Arch. Toxicol.* **73**, 71-79.
32. Vannelli T, Messmer M, Studer A, **Vuilleumier S**, Leisinger T (1999). A corrinoid-dependent catabolic pathway for growth of a *Methylobacterium* strain with chloromethane. *Proc. Natl. Acad. Sci. USA* **96**, 4615-4620.
31. Cai B, **Vuilleumier S**, Wackett LP (1998). Site-directed mutagenesis of the dichloromethane dehalogenase gene from *Methylophilus* sp. strain DM11 [in Chinese]. *Wei Sheng Wu Xue Bao* **38**, 163-167.
30. Cai B, **Vuilleumier S**, Wackett LP (1998). Purification and characterization of the mutant enzyme W117Y of the dichloromethane dehalogenase from *Methylophilus* sp. strain DM11. *Ann. NY Acad. Sci.* **864**, 210-213.
29. Gisi D, Traber H, Willi L, Leisinger T, **Vuilleumier S** (1998). Effects of bacterial host and dichloromethane dehalogenase on the competitiveness of methylotrophic bacteria growing with dichloromethane. *Appl. Environ. Chem.* **64**, 1194-1202.
27. **Vuilleumier S**, Sorribas H, Leisinger T (1997). Identification of a novel determinant of glutathione affinity in dichloromethane dehalogenases / glutathione S-transferases. *Biochem. Biophys. Res. Commun.* **238**, 452-456.
26. Schmid-Appert M, Zoller K, Traber H, **Vuilleumier S**, Leisinger T (1997). Association of newly discovered IS elements with the dichloromethane utilization genes of methylotrophic bacteria. *Microbiology* **143**, 2557-2567.
25. **Vuilleumier S** (1997). Bacterial glutathione-S-transferases: what are they good for? *J. Bacteriol.* **179**, 1431-1441.
24. **Vuilleumier S**, Leisinger T (1996). Protein engineering studies on dichloromethane dehalogenase/glutathione S-transferase from *Methylophilus* sp. strain DM11: Ser12 but not Tyr6 is required for enzymatic activity. *Eur. J. Biochem.* **239**, 410-417.
23. Tissot AC, **Vuilleumier S**, Fersht AR (1996). Importance of two buried salt bridges in the stability and folding pathway of barnase. *Biochemistry* **35**, 6786-6794.
20. Arcus VL, **Vuilleumier S**, Freund SV, Bycroft M, Fersht AR (1995). A comparison of the pH-, urea-, and temperature-denatured states of barnase by heteronuclear NMR: implications for the initiation of protein folding. *J. Mol. Biol.* **254**, 305-321.
19. Leisinger T, Bader R, Hermann R, Schmid-Appert M, **Vuilleumier S** (1994). Microbes, enzymes and genes involved in dichloromethane utilization. *Biodegradation* **5**, 237-248.
18. Arcus VL, **Vuilleumier S**, Freund SV, Bycroft M, Fersht AR (1994). Towards solving the folding pathway of barnase: the complete backbone 13C, 15N and 1H NMR assignments of its pH denatured state. *Proc. Natl. Acad. Sci. USA* **91**, 9412-9416.
16. Oliveberg M, **Vuilleumier S**, Fersht AR (1994). Thermodynamic study of the acid denaturation of barnase and its dependence on ionic strength: evidence for residual electrostatic interactions in the acid/thermally denatured state. *Biochemistry*, **33**, 8826-8832.

15. **Vuilleumier S**, Fersht AR (1994). Insertion in barnase of a loop sequence from ribonuclease T1: exploring sequence and structure alignments by protein engineering. *Eur. J. Biochem.* **221**, 1003-1012.
14. **Vuilleumier S**, Sancho J, Loewenthal R, Fersht AR (1993). Circular dichroism studies of barnase and its mutants: characterization of the contribution of aromatic side chains. *Biochemistry*, **32**, 10303-10313.
13. **Vuilleumier S**, Mutter M (1993). Synthetic peptide and template-assembled synthetic protein models of the hen egg white lysozyme 87-97 helix: importance of a protein-like framework for conformational stability in a short peptide sequence. *Biopolymers* **33**, 389-400.
8. Ernest I, **Vuilleumier S**, Fritz H, Mutter M (1990). Synthesis of a 4-helix bundle-like template-assembled protein (TASP) by condensation of a protected peptide on a conformationally constrained cyclic carrier. *Tetrahedron Lett.* **31**, 4015-4018.
6. Mutter M, **Vuilleumier S** (1989). A chemical approach to protein design - Template-assembled synthetic proteins (TASP). *Angew. Chem. Int. Ed. Engl.* **28**, 535-554. [Ein chemischer Weg zu neuen Proteinen - Templat-assoziierte synthetische Proteine (TASP). *Angew. Chem.* **101**, 551-571.]
4. Mutter M, Altmann E, Altmann KH, Hersperger R, Koziej P, Nebel K, Tuchscherer G, **Vuilleumier S**, Gremlich HU, Müller K (1988). The construction of new proteins. Part III. Artificial folding units by assembly of amphiphilic secondary structures on a template. *Helv. Chim. Acta* **71**, 835-847.
3. Mutter M, Altmann KH, Tuchscherer G, **Vuilleumier S** (1988). Strategies for the de novo design of proteins. *Tetrahedron* **44**, 771-785.
1. Mutter M, Altmann KH, Müller K, **Vuilleumier S**, Vorherr T (1986). Approaches to synthetic vaccines. Design of epitope-containing amphiphilic peptides matching the antigenic structure in the native protein. *Helv. Chim. Acta* **69**, 985-995.

Peer-reviewed book

127. Hamman P, **Vuilleumier S** (eds) (2019) Sustainability Research in the Upper Rhine Region - Concepts and Case Studies, 345 pp., ISBN 978-2-86820-549-0, Presses Universitaires de Strasbourg, Strasbourg.

Peer-reviewed book chapters

128. Hamman P, **Vuilleumier S** (2019) Introduction. In Sustainability Research in the Upper Rhine Region - Concepts and Case Studies (Hamman P and **Vuilleumier S**, eds), pp. 11-23, Presses Universitaires de Strasbourg, Strasbourg.
121. Bringel F, Besaury L, Amato P, Kröber E, Kolb S, Keppler F, **Vuilleumier S**, Nadalig T (2019). Methylophs and methyloph populations for chloromethane degradation. In Methylophs and Methyloph Communities (Chistoserdova L, ed), *Curr. Issues Molec. Biol.* **33**, 149-172. <https://doi.org/10.21775/cimb.033.149>
108. **Vuilleumier S**, Farhan Ul Haque M, Gruffaz C, Besaury L (2017) Microbiological energy valorisation of grape marc. In Innovations for sustainable biomass utilisation in the Upper Rhine region (Schumacher K, Fichtner W, Schultmann F (eds.), *Produktion und Energie* **18**, pp. 95-103, KIT Scientific Publishing, Karlsruhe.
67. Imfeld G, Bringel F, **Vuilleumier S** (2011). Bacterial tolerance in contaminated soils: potential of the PICT approach in microbial ecology. In: *Tolerance to Environmental Contaminants* (Amiard-Triquet C, Rainbow PS, Roméo M, eds.), CRC Press, Boca Raton, Chapter 14, 335-364.
46. **Vuilleumier S** (2002). Coping with a halogenated one-carbon diet: aerobic dichloromethane-mineralising bacteria. In Hofman M and Anne J (Series eds.) Focus on Biotechnology Series, Vol. 3A, pp. 105-131, Agathos S and Reineke W (eds.), Biotechnology for the environment, Kluwer Academic Publishers BV, Dordrecht, The Netherlands.
39. **Vuilleumier S** (2001). Bacterial glutathione S-transferases and the detoxification of xenobiotics: dehalogenation through glutathione conjugation and beyond. In: *Pesticide Biotransformations in plants and microorganisms* (Hall JC, Hoagland RE, and Zablutowicz RW, eds.), American Chemical Society Symposia Vol. 777, Oxford University Press, Oxford, pp. 240-252.
35. **Vuilleumier S**, Gisi D, Stumpp MT, Leisinger T (2000). Bacterial dichloromethane dehalogenases: a particular brand of glutathione S-transferases. *Clin. Chem. Enzymol. Comm.* **8**, 367-378.
28. Leisinger T, Gisi D, Mägli A, Sorribas H, Vannelli T, **Vuilleumier S** (1997). Bacterial dehalogenation of chlorinated methanes. In: Mechanisms of biohalogenation and dehalogenation (Janssen DB, Soda K and Wever R, eds.), Proceedings of the colloquium, Amsterdam, 16-18 September 1996, pp. 185-194, NorthHolland, Amsterdam.

22. **Vuilleumier S** (1996). Les éprouvettes sont-elles recyclables ? In : *Natures en tête* (GHK, eds.), pp. 239-251. Musée d'Ethnographie, Neuchâtel.
17. **Vuilleumier S** (1994). Du gène à la vache à lait et de la vache à l'homme. In: *Marx 2000* (J. Hainard and R. Kaehr, eds.), pp. 145-150. Musée d'Ethnographie, Neuchâtel.
11. Fersht AR, Matouschek A, Sancho J, Serrano L, **Vuilleumier S** (1992). Pathway of protein folding. In: *Structure and activity of enzymes, Faraday Discussions* **93**, pp. 183-193, Royal Society of Chemistry, London.
8. **Vuilleumier S**, Mutter M (1992). Antigen mimicry with synthetic peptides. In: *Structure of antigens* (van Regenmortel MHV, ed.), Volume 1, Chapter 3, pp. 43-54, CRC Press, Boca Raton.
7. Mutter M, Altmann KH, Tuchscherer G, **Vuilleumier S** (1989). Template assembled synthetic proteins. In *Chemistry of Peptides and Proteins* Vol. 4 (König WA and Voelter W., eds.), Attempto Verlag, Tübingen, pp. 213-222.
5. **Vuilleumier S**, Mutter M (1989). Towards the construction of new proteins. In: *Advances in Protein Design, Int. Workshop 1988* (Blöcker H, Collins J, Schmid RD, Schomburg D, eds.), GBF Monograph 12, pp. 93102, VCH-Verlag, Weinheim.

Proceedings and other publications

(Publications without peer review are not numbered)

- Pitrou P, Jullien L, *collectif La Vie à l'œuvre* (2021). L'intelligence collective à l'œuvre / Collective intelligence in the making (bilingue français/anglais). In *Stream 05 – Les nouvelles intelligences* (Chiambaretta P; ed.), pp. 467-488, PCA-Stream editions, Paris, ISBN 978-2-9575780-0-9.
- Collectif la vie à l'œuvre* : Pitrou P, Jullien L, Becker J, Desprat N, d'Onofrio S, de Castro T, Danzinger E, Dittmar P-O, Ferrand E, Giraud L, Guyot F, Iribarren L, Jeancolas C, Kamili L, Letouzey E, Mercier D, Nghe P, Peysson D, Praet I, Provost F, Sautchuk C, Triller A, Villard C, **Vuilleumier S**.
102. Faure D, Bonin P, Duran R, *the Microbial Ecology EC2CO Consortium* (52 other authors in alphabetical order; last: **Vuilleumier S**) (2015) Environmental microbiology as a mosaic of explored ecosystems and issues. *Environ Sci Pollut Res* **22**, 13577-13598.
- Martin-Laurent F, Merlin C, **Vuilleumier S**, Imfeld G, Vogel TM, Cecillon S, Achouak W, Benoit P, Mamy L, Mougin C, Patureau D, Chovelon J-M, Pesce S, Ugarte E, Le Paslier D (2014). Biodechlorid search for evidence for microbial degradation of chlordecone in French West Indies contaminated soils. Intersoil Conference, March 2014.
- Martin-Laurent F, Achouak W, Benoit P, Chovelon J-M, Devers M, Heraud C, Imfeld G, Latrille E, Le Paslier D, Li Z, Mamy L, Merlin C, Mougin C, Nelieu S, Patureau D, Pesce S, Rossard V, Servien R, Steinberg C, **Vuilleumier S**, Vogel TM (2013). Recherche de la signature biologique de la dégradation de la chlordécone dans les sols des antilles (Biodechlorid). AAP INRA Demichlorid, Plan National d'Action Chlordécone, Rapport final, 179 p. <hal-03266671>
- Bringel F, Penny C, Achilles J, Gruffaz C, Nadalig T, **Vuilleumier S** (2010). Halogen1cs- Etude du fonctionnement d'un écosystème contaminé par des composés toxiques halogénés en C1. *Actes du colloque de restitution du programme EC2CO 2010*, Toulouse, 23-25 November 2010.
- Vuilleumier S** (2010) Potential uses of genomic investigations for natural remediation of chlorinated pollutants. *Actes du colloque Intersol 2010*, Paris, 17 March 2010.
- Vuilleumier S**, Penny C, Nadalig T, Roselli S, Muller E, Gruffaz C, Louhichi Y, Achilles J, Bringel F (2009). Dégradation microbienne des méthanes chlorés : voies métaboliques, génomique, suivi de populations sur site contaminé, et perspectives pour la dépollution. *Deuxièmes rencontres nationales de la Recherche sur les sites et sols pollués*. Paris (France), 20-21 October 2009.
57. David M, Bringel F, Pagni M, Gilmartin N, Boubakri H, Nadalig T, Simonet P, Vogel T, **Vuilleumier S** (2008). Diversité et évolution des déshalogénases bactériennes : détection bioinformatique et perspectives de recherche. *Les Actes du BRG* **7**, 83-94.
 56. **Vuilleumier S** (2008) Réseau Alsace de Laboratoires en Ingénierie et Sciences de l'Environnement (REALISE). In *Sciences en société au XXIe siècle* (Alix JP, Ancori B, Petit P, eds.), pp. 208-214, CNRS Editions, Paris.
- Vuilleumier S** (1999) Bacterial GST and their role in the detoxification of pesticides and other xenobiotics. *Abstracts of papers of the American Chemical Society* **218**, U117.
21. Leisinger T, Mägli A, Schmid-Appert M, Zoller K, **Vuilleumier S** (1996). Evolution of dichloromethane utilization. In: *Microbial growth on C1 compounds* (Lidstrom ME and Tabita FR, eds.), Proceedings of the 8th International C1 Symposium, pp. 261-268, Kluwer Academic Publishers, Dordrecht.

- Arcus VL, Vuilleumier S, Freund SMV, Bycroft M, Fersht AR (1995). Toward solving the folding pathway of barnase – the backbone C-13, N-14 and 1-HNMR assignments of its pH denatured and urea-denatured states. *J Cell Biochem Suppl.* **21B**, 42.
12. Mutter M, Carey RI, Dörner B, Ernest I, Flögel R, Giezendanner U, Rivier JE, Servis C, Sigel C, Steiner V, Tuchscherer G, **Vuilleumier S**, Wyss D (1992). The TASP-Concept: from template-assembled synthetic proteins to protein surface mimetics. In: *Peptides Chemistry and Biology* (Smith JA and Rivier JE, eds.), Proceedings of the Twelfth American Peptide Symposium, pp. 326-328, ESCOM, Leiden.
9. Mutter M, Altmann KH, Carey RI, Ernest I, Floegel R, Wyss D, **Vuilleumier S**, Rivier JE, Tuchscherer G (1991). Novel approaches to template assembled synthetic proteins (TASP). *Peptides 1990*, Proceedings of the 21st European Peptide Symposium, pp. 249-250.
2. Mutter M, Altmann KH, Vorherr T, **Vuilleumier S** (1987). The construction of new proteins. design, synthesis and conformational properties of polypeptides with ' $\beta\alpha\beta$ '-topology. In: *Peptides 1986* (Theodoropoulos D, ed.), pp. 307-310, De Gruyter, Berlin.

Patents

- Ernst B, Gougeon R, François-Lopez E, Dumas C, **Vuilleumier S**, Alexandre H. Process of production of hydrogen by dark fermentation from biomasses from the wine industry, without addition of microbial consortium? European Patent (25 May 2019, No 3186359).
- Ernst B, Gougeon R, François-Lopez E, Dumas C, **Vuilleumier S**, Alexandre H. Procédé de production d'hydrogène par fermentation obscure à partir de biomasses issues de la filière vitivinicole, sans apport de consortium microbien. French patent (15 October 2014, N°14 59895).

Thesis manuscripts

- Vuilleumier S** (2000). Dichloromethane dehalogenases and beyond: bacterial glutathione S-transferases and associated metabolism. Habilitationsschrift, ETH Zurich.
- Vuilleumier S** (1990). Stabilisation of helix conformation in model synthetic peptides: studies on peptide conformation and antigenicity. PhD Thesis, under the direction of Prof. M. Mutter, Institut für Organische Chemie, Universität Basel.
- Vuilleumier S** (1985). Untersuchungen zum Reaktionsmechanismus von Isocitrat Lyase. Diploma thesis, under the direction of Prof. D. Arigoni, Institut für Organische Chemie, ETH Zurich.