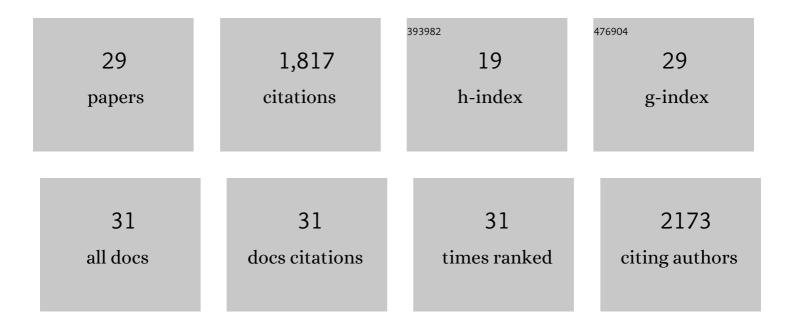
## Virginie Chapon

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Discovery and characterization of UipA, a uranium- and iron-binding PepSY protein involved in uranium tolerance by soil bacteria. ISME Journal, 2022, 16, 705-716.	4.4	13
2	A multiparametric study on the dissolution of synthetic brannerite. Npj Materials Degradation, 2021, 5, .	2.6	5
3	Delineation of cellular stages and identification of key proteins for reduction and biotransformation of Se(IV) by Stenotrophomonas bentonitica BII-R7. Journal of Hazardous Materials, 2021, 418, 126150.	6.5	20
4	Geochemical fingerprints of brannerite (UTi <sub>2</sub> O <sub>6</sub> ): an integrated study. Mineralogical Magazine, 2020, 84, 313-334.	0.6	8
5	Sequestration of Radionuclides Radium-226 and Strontium-90 by Cyanobacteria Forming Intracellular Calcium Carbonates. Environmental Science & Technology, 2019, 53, 12639-12647.	4.6	33
6	Direct synthesis of pure brannerite UTi2O6. Journal of Nuclear Materials, 2019, 515, 401-406.	1.3	12
7	Complete Genome Sequences of Four <i>Microbacterium</i> Strains Isolated from Metal- and Radionuclide-Rich Soils. Microbiology Resource Announcements, 2019, 8, .	0.3	3
8	Proteogenomic insights into uranium tolerance of a Chernobyl's Microbacterium bacterial isolate. Journal of Proteomics, 2018, 177, 148-157.	1.2	43
9	Proteomics data for characterizing Microbacterium oleivorans A9, an uranium-tolerant actinobacterium isolated near the Chernobyl nuclear power plant. Data in Brief, 2018, 21, 1125-1129.	0.5	3
10	Draft Genome Sequence of Microbacterium oleivorans Strain A9, a Bacterium Isolated from Chernobyl Radionuclide-Contaminated Soil. Genome Announcements, 2017, 5, .	0.8	6
11	Soil prokaryotic communities in Chernobyl waste disposal trench T22 are modulated by organic matter and radionuclide contamination. FEMS Microbiology Ecology, 2017, 93, .	1.3	20
12	Sponging up metals: Bacteria associated with the marine sponge Spongia officinalis. Marine Environmental Research, 2015, 104, 20-30.	1.1	56
13	Use of combined microscopic and spectroscopic techniques to reveal interactions between uranium and Microbacterium sp. A9, a strain isolated from the Chernobyl exclusion zone. Journal of Hazardous Materials, 2015, 285, 285-293.	6.5	42
14	Escherichia coli Response to Uranyl Exposure at Low pH and Associated Protein Regulations. PLoS ONE, 2014, 9, e89863.	1.1	20
15	Exploration of <i>Deinococcusâ€Thermus</i> molecular diversity by novel groupâ€specific <scp>PCR</scp> primers. MicrobiologyOpen, 2013, 2, 862-872.	1.2	57
16	Microbacterium lemovicicum sp. nov., a bacterium isolated from a natural uranium-rich soil. International Journal of Systematic and Evolutionary Microbiology, 2013, 63, 2600-2606.	0.8	25
17	Microbial diversity in contaminated soils along the T22 trench of the Chernobyl experimental platform. Applied Geochemistry, 2012, 27, 1375-1383.	1.4	38
18	Uranium Interaction with Two Multi-Resistant Environmental Bacteria: Cupriavidus metallidurans CH34 and Rhodopseudomonas palustris. PLoS ONE, 2012, 7, e51783.	1.1	31

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19	Influence of Uranium on Bacterial Communities: A Comparison of Natural Uranium-Rich Soils with Controls. PLoS ONE, 2011, 6, e25771.	1.1	75
20	Microbial diversity on the Tatahouine meteorite. Meteoritics and Planetary Science, 2006, 41, 1249-1265.	0.7	35
21	The desert of Tataouine: an extreme environment that hosts a wide diversity of microorganisms and radiotolerant bacteria. Environmental Microbiology, 2006, 8, 514-525.	1.8	192
22	Deinococcus deserti sp. nov., a gamma-radiation-tolerant bacterium isolated from the Sahara Desert. International Journal of Systematic and Evolutionary Microbiology, 2005, 55, 2441-2446.	0.8	154
23	Molecular hydrogen from water radiolysis as an energy source for bacterial growth in a basin containing irradiating waste. FEMS Microbiology Letters, 2004, 240, 155-162.	0.7	30
24	Type II protein secretion in gram-negative pathogenic bacteria: the study of the structure/secretion relationships of the cellulase cel5 (formerly EGZ) from Erwinia chrysanthemi 1 1Edited by I. B. Holland. Journal of Molecular Biology, 2001, 310, 1055-1066.	2.0	55
25	Alteration of a single tryptophan residue of the cellulose-binding domain blocks secretion of the Erwinia chrysanthemiCel5 cellulase (ex-EGZ) via the type II system. Journal of Molecular Biology, 2000, 303, 117-123.	2.0	23
26	RpoS-dependent stress tolerance in Pseudomonas aeruginosa. Microbiology (United Kingdom), 1999, 145, 835-844.	0.7	129
27	Assembly of XcpR in the Cytoplasmic Membrane Is Required for Extracellular Protein Secretion in <i>Pseudomonas aeruginosa</i> . Journal of Bacteriology, 1999, 181, 382-388.	1.0	53
28	Regulation of the xcp secretion pathway by multiple quorumâ€sensing modulons in Pseudomonas aeruginosa. Molecular Microbiology, 1997, 24, 1169-1178.	1.2	144
29	Multiple N-acyl-L-homoserine lactone signal molecules regulate production of virulence determinants and secondary metabolites in Pseudomonas aeruginosa Proceedings of the National Academy of Sciences of the United States of America. 1995. 92. 9427-9431.	3.3	492