

# Eveline Peeters

## List of Publications by Year in descending order

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Version: 2024-02-01

45  
papers

1,329  
citations

377584

21  
h-index

425179

34  
g-index

45  
all docs

45  
docs citations

45  
times ranked

936  
citing authors

#	ARTICLE	IF	CITATIONS
1	Engineering transcriptional regulation in Escherichia coli using an archaeal TetR-family transcription factor. <i>Gene</i> , 2022, 809, 146010.	1.0	0
2	DNA-Binding Properties of a Novel Crenarchaeal Chromatin-Organizing Protein in <i>Sulfolobus acidocaldarius</i> . <i>Biomolecules</i> , 2022, 12, 524.	1.8	1
3	Functional Grading of Mycelium Materials with Inorganic Particles: The Effect of Nanoclay on the Biological, Chemical and Mechanical Properties. <i>Biomimetics</i> , 2022, 7, 57.	1.5	12
4	Large-scale robotic extrusion-based additive manufacturing with living mycelium materials. <i>Sustainable Futures</i> , 2022, 4, 100085.	1.5	11
5	The biology of thermoacidophilic archaea from the order <i>Sulfolobales</i> . <i>FEMS Microbiology Reviews</i> , 2021, 45, .	3.9	24
6	Comprehensive genomic analysis reveals virulence factors and antibiotic resistance genes in <i>Pantoea agglomerans</i> KM1, a potential opportunistic pathogen. <i>PLoS ONE</i> , 2021, 16, e0239792.	1.1	21
7	Growing living and multifunctional mycelium composites for large-scale formwork applications using robotic abrasive wire-cutting. <i>Construction and Building Materials</i> , 2021, 283, 122732.	3.2	45
8	Comparative genomics of DNA-binding transcription factors in archaeal and bacterial organisms. <i>PLoS ONE</i> , 2021, 16, e0254025.	1.1	0
9	A review on the potential of filamentous fungi for microbial self-healing of concrete. <i>Fungal Biology and Biotechnology</i> , 2021, 8, 16.	2.5	23
10	Mechanical characteristics of bacterial cellulose-reinforced mycelium composite materials. <i>Fungal Biology and Biotechnology</i> , 2021, 8, 18.	2.5	27
11	Current state and future prospects of pure mycelium materials. <i>Fungal Biology and Biotechnology</i> , 2021, 8, 20.	2.5	55
12	Phosphorylation of the acyl-CoA binding pocket of the FadR transcription regulator in <i>Sulfolobus acidocaldarius</i> . <i>Biochimie</i> , 2020, 175, 120-124.	1.3	9
13	Defining heat shock response for the thermoacidophilic model crenarchaeon <i>Sulfolobus acidocaldarius</i> . <i>Extremophiles</i> , 2020, 24, 681-692.	0.9	11
14	A comprehensive framework for the production of mycelium-based lignocellulosic composites. <i>Science of the Total Environment</i> , 2020, 725, 138431.	3.9	116
15	Mechanical, physical and chemical characterisation of mycelium-based composites with different types of lignocellulosic substrates. <i>PLoS ONE</i> , 2019, 14, e0213954.	1.1	119
16	Competitive Repression of the artPIQM Operon for Arginine and Ornithine Transport by Arginine Repressor and Leucine-Responsive Regulatory Protein in <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1563.	1.5	9
17	Editorial overview: Tissue, cell and pathway engineering. <i>Current Opinion in Biotechnology</i> , 2019, 59, iii-v.	3.3	0
18	YtrASa, a GntR-Family Transcription Factor, Represses Two Genetic Loci Encoding Membrane Proteins in <i>Sulfolobus acidocaldarius</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2084.	1.5	9

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19	Transcription Regulators in Archaea: Homologies and Differences with Bacterial Regulators. <i>Journal of Molecular Biology</i> , 2019, 431, 4132-4146.	2.0	43
20	Non-monotonic auto-regulation in single gene circuits. <i>PLoS ONE</i> , 2019, 14, e0216089.	1.1	1
21	A TetR-family transcription factor regulates fatty acid metabolism in the archaeal model organism <i>Sulfolobus acidocaldarius</i> . <i>Nature Communications</i> , 2019, 10, 1542.	5.8	43
22	Structure of the Prx6-subfamily 1-Cys peroxiredoxin from <i>Sulfolobus islandicus</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 428-434.	0.4	6
23	Heat shock response in archaea. <i>Emerging Topics in Life Sciences</i> , 2018, 2, 581-593.	1.1	13
24	Wing phosphorylation is a major functional determinant of the Lrs14-type biofilm and motility regulator AbfR1 in <i>Sulfolobus acidocaldarius</i> . <i>Molecular Microbiology</i> , 2017, 105, 777-793.	1.2	32
25	DNA-Interacting Characteristics of the Archaeal Rudiviral Protein SIRV2_Gp1. <i>Viruses</i> , 2017, 9, 190.	1.5	10
26	Transcription Factor-Mediated Gene Regulation in Archaea. <i>Nucleic Acids and Molecular Biology</i> , 2017, , 27-69.	0.2	7
27	The genome-scale DNA-binding profile of BarR, a $\beta$ -alanine responsive transcription factor in the archaeon <i>Sulfolobus acidocaldarius</i> . <i>BMC Genomics</i> , 2016, 17, 569.	1.2	18
28	The interplay between nucleoid organization and transcription in archaeal genomes. <i>Nature Reviews Microbiology</i> , 2015, 13, 333-341.	13.6	96
29	The $\epsilon$ -Densitometric Image Analysis Software™ and Its Application to Determine Stepwise Equilibrium Constants from Electrophoretic Mobility Shift Assays. <i>PLoS ONE</i> , 2014, 9, e85146.	1.1	9
30	<i>BarR</i> , an <i>Lrp</i> -type transcription factor in <i>Sulfolobus acidocaldarius</i> , regulates an aminotransferase gene in a $\beta$ -alanine responsive manner. <i>Molecular Microbiology</i> , 2014, 92, 625-639.	1.2	20
31	The one-component system <i>ArnR</i> : a membrane-bound activator of the crenarchaeal archaeum. <i>Molecular Microbiology</i> , 2013, 88, 125-139.	1.2	53
32	The genome-wide binding profile of the <i>Sulfolobus solfataricus</i> transcription factor Ss-LrpB shows binding events beyond direct transcription regulation. <i>BMC Genomics</i> , 2013, 14, 828.	1.2	21
33	A thermodynamic model of the cooperative interaction between the archaeal transcription factor Ss-LrpB and its tripartite operator DNA. <i>Gene</i> , 2013, 524, 330-340.	1.0	15
34	<i>Cis</i> -regulatory logic in archaeal transcription. <i>Biochemical Society Transactions</i> , 2013, 41, 326-331.	1.6	49
35	Lrs14 transcriptional regulators influence biofilm formation and cell motility of Crenarchaea. <i>ISME Journal</i> , 2013, 7, 1886-1898.	4.4	63
36	Expanded target and cofactor repertoire for the transcriptional activator LysM from <i>Sulfolobus</i> . <i>Nucleic Acids Research</i> , 2013, 41, 2932-2949.	6.5	21

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37	Nanobody <sup>®</sup> -based chromatin immunoprecipitation/micro-array analysis for genome-wide identification of transcription factor DNA binding sites. <i>Nucleic Acids Research</i> , 2013, 41, e59-e59.	6.5	25
38	SsLrp from <i>Sulfolobus acidocaldarius</i> is a versatile, glutamine-responsive, and architectural transcriptional regulator. <i>MicrobiologyOpen</i> , 2013, 2, 75-93.	1.2	26
39	The Lrp Family of Transcription Regulators in Archaea. <i>Archaea</i> , 2010, 2010, 1-10.	2.3	83
40	SsLrpB, a transcriptional regulator from <i>Sulfolobus solfataricus</i> , regulates a gene cluster with a pyruvate ferredoxin oxidoreductase-encoding operon and permease genes. <i>Molecular Microbiology</i> , 2009, 71, 972-988.	1.2	44
41	Competitive activation of the <i>Escherichia coli argO</i> gene coding for an arginine exporter by the transcriptional regulators Lrp and ArgP. <i>Molecular Microbiology</i> , 2009, 74, 1513-1526.	1.2	21
42	Analysis of the DNA-binding sequence specificity of the archaeal transcriptional regulator Ss-LrpB from <i>Sulfolobus solfataricus</i> by systematic mutagenesis and high resolution contact probing. <i>Nucleic Acids Research</i> , 2006, 35, 623-633.	6.5	24
43	Ss-LrpB from <i>Sulfolobus solfataricus</i> Condenses about 100 Base Pairs of Its Own Operator DNA into Globular Nucleoprotein Complexes. <i>Journal of Biological Chemistry</i> , 2006, 281, 11721-11728.	1.6	22
44	Ss-LrpB, a novel Lrp-like regulator of <i>Sulfolobus solfataricus</i> P2, binds cooperatively to three conserved targets in its own control region. <i>Molecular Microbiology</i> , 2004, 54, 321-336.	1.2	61
45	Mycelium Composites and their Biodegradability: An Exploration on the Disintegration of Mycelium-Based Materials in Soil. , 0, , .		11