



## Curriculum vitae



## Personal Information

<b>FIRST NAME / SURNAME</b>	<b>Marnix Medema</b>
<b>ADDRESS (PRIVATE)</b>	Soetendaalseweg 16A, 6721XB Bennekom, NL
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<b>NATIONALITY</b>	Dutch
<b>DATE OF BIRTH</b>	24.01.1986
<b>GENDER</b>	Male

## Work Experience &amp; Education

<b>DATES</b>	March 2015 - present
<b>EMPLOYER</b>	Wageningen University, Wageningen, The Netherlands
<b>POSITION</b>	Assistant Professor
<b>DATES</b>	August 2013 - February 2015
<b>EMPLOYER</b>	MPI for Marine Microbiology, Bremen, Germany
<b>POSITION</b>	Postdoctoral Researcher
<b>DATES</b>	September 2010 - March 2011
<b>EMPLOYER</b>	University of California, San Francisco, USA
<b>POSITION</b>	Visiting Research Scholar
<b>DATES</b>	September 2009 - August 2013
<b>EMPLOYER</b>	University of Groningen, The Netherlands
<b>POSITION</b>	PhD Student
<b>DATE / DISTINCTION</b>	27.09.2013, <i>cum laude</i> **
<b>DATES</b>	September 2006 - August 2008
<b>QUALIFICATION AWARDED</b>	Master of Science Biomolecular Science, <i>cum laude</i> **
<b>INSTITUTION</b>	University of Groningen, The Netherlands
<b>DATES</b>	September 2003 - August 2006
<b>QUALIFICATION AWARDED</b>	Bachelor of Science Biology, <i>cum laude</i> **
<b>INSTITUTION</b>	Radboud University Nijmegen, The Netherlands

\*\* In the Netherlands, only two classes of honors are used: eervolle vermelding ("honorable mention") and cum laude, typically only to mark exceptional achievement. [...] Generally, less than 20% receive the "honorable mention" distinction, and "cum laude" is even harder to attain (less than 1%-5% depending on the university and study program).  
Source: [http://en.wikipedia.org/wiki/Latin\\_honors](http://en.wikipedia.org/wiki/Latin_honors)



Dr. Marnix Medema

## Citation Analysis

Below is a table of my citation statistics from Google Scholar and Web of Science, as measured on October 31st, 2018:

	Google Scholar	Web of Science
Total publications	63	55
Total citations	5652	3546
H-index	28	22
Citations in 2015	736	450
Citations in 2016	1050	705
Citations in 2017	1277	861

Out of the 55 publications indexed in WoS, 10 were marked as 'Highly Cited Papers', meaning that they received enough citations as of October 2018 to place them in the top 1% of their academic fields based on a highly cited threshold for the field and publication year.

## List of Publications – key publications are marked

1. Navarro-Muñoz JC\*, Selem-Mojica N\*, Mullowney M\*, Kautsar S, Tryon H, Parkinson E, De Los Santos ELC, Yeong M, Cruz-Morales P, Abubucker S, Roeters A, Lokhorst W, Fernandez-Guerra A, Dias Cappellini LT, Thomson R, Metcalf WW, Kelleher NL, Barona Gomez F#, Medema MH# (2018) A computational framework for rapid exploration and prioritization of biosynthetic diversity from large-scale genomic data. *BioRxiv*, doi:10.1101/445270. **#key publication**
2. Carrión VJ, Cordovez V, Tyc O, Etalo DW, de Bruijn I, de Jager VCL, Medema MH, Eberl L, Raaijmakers JM. Involvement of Burkholderiaceae and sulfurous volatiles in disease-suppressive soils. *The ISME Journal*, 12(9):2307-2321.
3. Bahram M, Hildebrand F, Forslund SK, Anderson JL, Soudzilovskaia NA, Bodegom PM, Bengtsson-Palme J, Anslan S, Coelho LP, Harend H, Huerta-Cepas J, Medema MH, Maltz MR, Mundra S, Olsson PA, Pent M, Pölme S, Sunagawa S, Ryberg M, Tedersoo L, Bork P. Structure and function of the global topsoil microbiome. *Nature*, 560(7717):233-237.
4. Epstein SC, Charkoudian LK, Medema MH (2018) A standardized workflow for submitting data to the Minimum Information about a Biosynthetic Gene cluster (MIBiG) repository: prospects for research-based educational experiences. *Standards in Genomic Sciences*, 13:16.
5. Hoogendoorn K, Barra L, Waalwijk C, Dickschat JS, van der Lee TAJ, Medema MH (2018) Evolution and diversity of biosynthetic gene clusters in *Fusarium*. *Frontiers in Microbiology*, 9:1158.
6. Sosio M, Gaspari E, Iorio M, Pessina S, Medema MH, Bernasconi A, Simone M, Maffioli SI, Ebricht RH, Donadio S (2018) Analysis of the pseudouridimycin biosynthetic pathway provides insights into the formation of C-nucleoside antibiotics. *Cell Chemical Biology*, 25(5):540-549.

7. Harvey CJB, Tang M, Schlecht U, Horecka J, Fischer CR, Lin HC, Li J, Naughton B, Cherry J, Miranda M, Li YF, Chu AM, Hennessy JR, Vandova GA, Inglis D, Aiyar RS, Steinmetz LM, Davis RW, Medema MH, Sattely E, Khosla C, St Onge RP, Tang Y, Hillenmeyer ME. HEx: A heterologous expression platform for the discovery of fungal natural products. *Science Advances*, 4(4):eaar5459.
8. Casini A, Chang FY, Eluere R, King AM, Young EM, Dudley QM, Karim A, Pratt K, Bristol C, Forget A, Ghodasara A, Warden-Rothman R, Gan R, Cristofaro A, Borujeni AE, Ryu MH, Li J, Kwon YC, Wang H, Tatsis E, Rodriguez-Lopez C, O'Connor S, Medema MH, Fischbach MA, Jewett MC, Voigt C, Gordon DB (2018) A pressure test to make 10 molecules in 90 days: external evaluation of methods to engineer biology. *Journal of the American Chemical Society*, 140(12):4302-4316.
9. Brotherton CA, Medema MH, Greenberg EP (2018) *luxR* homolog-linked biosynthetic gene clusters in Proteobacteria. *mSystems*, e00208-17.
10. Medema MH (2018) Computational genomics of specialized metabolism: from natural product discovery to microbiome ecology. *mSystems*, e00182-17. **#key publication**
11. Loureiro C, Medema MH, van der Oost J, Sipkema D (2017) Exploration and exploitation of the environment for novel specialized metabolites. *Current Opinion in Biotechnology*, 50:206-213.
12. Oyserman BO, Medema MH, Raaijmakers JR (2018) Road MAPs to engineer host microbiomes. *Current Opinion in Microbiology*, 43: 46-54.
13. Blin K, Uk HU, Medema MH, Weber T (2017) Recent development of antiSMASH and other computational approaches to mine secondary metabolite biosynthetic gene clusters. *Briefings in Bioinformatics*, accepted.
14. Kautsar SA, Suarez Duran HG, Medema MH (2017) Genomic identification and analysis of specialized metabolite biosynthetic gene clusters in plants using PlantSMASH. *Methods in Molecular Biology*, 1795:173-188.
15. Haas K, Heemstra J, Medema MH, Charkoudian L (2017) Collaborating with undergraduates to contribute to biochemistry community resources. *Biochemistry*, doi:10.1021/acs.biochem.7b00872.
16. Cheng X, Etalo DW, van de Mortel JE, Dekkers E, Nguyen L, Medema MH, Raaijmakers JM. (2017) Genome-wide analysis of bacterial determinants of plant growth promotion and induced systemic resistance by *Pseudomonas fluorescens*. *Environmental Microbiology*, doi: 10.1111/1462-2920.13927.
17. Cenicerros A, Dijkhuizen L\*, Petrusma M, Medema MH\* (2017) Genome-based exploration of the specialized metabolic capacities of the genus *Rhodococcus*. *BMC Genomics* 18(1): 593.
18. Huang AC, Kautsar SA, Hong YJ, Medema MH, Bond AD, Tantillo DJ, Osbourn A. (2017) Unearthing a sesterterpene biosynthetic repertoire in the Brassicaceae through genome mining reveals convergent evolution. *Proc Natl Acad Sci U S A*. 114(29):E6005-E6014.
19. Chevrette MG, Aicheler F, Kohlbacher O, Currie CR, Medema MH (2017) SANDPUMA: ensemble predictions of nonribosomal peptide chemistry reveals biosynthetic diversity across Actinobacteria. *Bioinformatics* 33(20): 3202-3210. **#key publication**
20. Gaiser RA, Medema MH, Kleerebezem M, van Baarlen P, Wells JM (2017) Draft genome sequence of a porcine commensal *Rothia nasimurium* encoding an NRPS producing the ionophore antibiotic valinomycin. *Genome Announcements* 5(22): e00453-17.

21. Blin K, Wolf T, Chevrette MG, Lu X, Schwalen CJ, Kautsar SA, Suarez Duran HG, de Los Santos ELC, Kim HU, Nave M, Dickschat JS, Mitchell DA, Shelest E, Breitling R, Takano E, Lee SY, Weber T\*, [Medema MH\\*](#) (2017) antiSMASH 4.0-improvements in chemistry prediction and gene cluster boundary identification. *Nucleic Acids Research* W1: W36-W41.
22. Kautsar SA, Duran HGS, Blin K, Osbourn A, [Medema MH](#) (2017) PlantiSMASH: automated identification, annotation and expression analysis of plant biosynthetic gene clusters. *Nucleic Acids Research* 45: W55-W63. **[#key publication](#)**
23. Tracanna V, De Jong A, [Medema MH\\*](#), Kuipers OP\* (2016) Mining prokaryotes for antimicrobial compounds: from diversity to function. *FEMS Microbiology Reviews* 41(3): 417-429.
24. Wu C, [Medema MH](#), Läkamp RM, Zhang L, Dorrestein PC, Choi YH, van Wezel GP (2016) Leucanicidin and endophenazines result from post-PKS methyl-rhamnosylation by the same tailoring enzymes in *Kitasatospora* sp. MBT66. *ACS Chemical Biology* 11: 478-490.
25. van der Lee TAJ, [Medema MH](#) (2016) Computational strategies for genome-based natural product discovery and engineering in fungi. *Fungal Genetics & Biology* 89: 29-36.
26. Li YF, Tsai KJS, Harvey CJB, Ary BE, Berlew EE, Boehman BL, Findley DM, Friant AG, Gardner CA, Gould MP, Ha JH, Lilley BK, McKinsty EL, Nawal S, Parry RC, Rothschild KW, Silbert SD, Tentilucci MD, Thurston AM, Wai RB, Yoon Y, [Medema MH](#), Hillenmeyer ME, Charkoudian LK (2016) Comprehensive curation and analysis of fungal biosynthetic gene clusters of published natural products. *Fungal Genetics & Biology* 89: 18-28.
27. Zhao H\*, [Medema MH\\*](#) (2016) Standardization for natural product synthetic biology. *Natural Product Reports* 33: 920-924.
28. [Medema MH\\*](#), Osbourn A\* (2016) Computational genomic identification and functional reconstitution of plant natural product biosynthetic pathways. *Natural Product Reports* 33: 951-962.
29. [Medema MH\\*](#), Zhao H\* (2016) Editorial: synthetic biology and bioinformatics. *Natural Product Reports* 33: 913-914.
30. Blin K, [Medema MH](#), Kottmann R, Lee SY, Weber T (2016) The antiSMASH database, a comprehensive database of microbial secondary metabolite biosynthetic gene clusters. *Nucleic Acids Research* 45 (D1): D555-D559.
31. Nguyen DD, Melnik AV, Koyama N, Lu X, Schorn M, Fang J, Aguinaldo K, Lincecum TL Jr, Ghequire MG, Carrion VJ, Cheng TL, Duggan BM, Malone JG, Mauchline TH, Sanchez LM, Kilpatrick AM, Raaijmakers JM, Mot R, Moore BS, [Medema MH#](#), Dorrestein PC# (2016) Indexing the *Pseudomonas* specialized metabolome enabled the discovery of poaeamide B and the bananamides. *Nature Microbiology* 2: 16197. **[#key publication](#)**
32. Salo OV, Ries M, [Medema MH](#), Lankhorst PP, Vreeken RJ, Bovenberg RA, Driessen AJ (2015) Genomic mutational analysis of the impact of the classical strain improvement program on  $\beta$ -lactam producing *Penicillium chrysogenum*. *BMC Genomics* 16: 937.
33. [Medema MH\\*](#) & Fischbach MA\* (2015) Computational approaches to natural product discovery. *Nature Chemical Biology* 11: 639-648. **[#key publication](#)**
34. [MH Medema](#),  $\pm 100$  co-authors, FO Glöckner (2015) Minimum Information about a Biosynthetic Gene cluster. *Nature Chemical Biology* 11: 625-631. **[#key publication](#)**

35. Weber T, Blin K, Duddela S, Krug D, Kim HU, Bruccoleri R, Lee SY, Fischbach MA, Müller R, Breitling R, Takano E, [Medema MH](#) (2015) antiSMASH 3.0 - A comprehensive resource for the genome mining of biosynthetic gene clusters. *Nucleic Acids Research* 43: W237-W243.
36. Diez V, Loznik M, Taylor S, Winn M, Rattray JW, Podmore H, Micklefield J, Goodacre R, [Medema MH](#), Müller U, Bovenberg RAL, Janssen DB, Takano E (2015) Functional exchangeability of oxidase and dehydrogenase reactions in the biosynthesis of hydroxyphenylglycine, a non-ribosomal peptide building block. *ACS Synthetic Biology* 4: 796-807.
37. Cimermancic P\*, [Medema MH\\*](#), Claesen J\*, Kurita K, Wieland Brown LC, Mavrommatis K, Pati A, Godfrey PA, Koehrsen M, Clardy J, Birren BW, Breitling R, Takano E, Sali A, Lington RG, Fischbach MA (2014) Insights into secondary metabolism from a global analysis of bacterial biosynthetic gene clusters. *Cell* 158: 412-21. **#key publication**
38. [Medema MH\\*](#), Cimermancic P\*, Sali A, Takano E, Fischbach MA (2014) A systematic computational analysis of biosynthetic gene cluster evolution: Lessons for engineering biosynthesis. *PLoS Computational Biology* 10(12): e1004016.
39. [Medema MH](#), Paalvast T, Nguyen DD, Melnik A, Dorrestein PC, Takano E, Breitling R (2014) Pep2Path: Automated mass spectrometry-guided genome mining of peptidic natural products. *PLoS Computational Biology* 10(9): e1003822.
40. Blin K\*, [Medema MH\\*](#), Kazempour D, Fischbach MA, Breitling R, Takano E, Weber T (2013) antiSMASH 2.0 - a versatile platform for genome mining of secondary metabolite producers. *Nucleic Acids Research* 41: W204-W212.
41. L Schriml et al. (47 authors) (2013) The 15th Genomic Standards Consortium meeting. *Standards in Genomic Sciences* 8: 124-164.
42. Nguyen DD, Wu CH, Moree WJ, Lamsa A, [Medema MH](#), Zhao X, Gavilan RG, Aparicio M, Atencio L, Jackson C, Ballesteros J, Sanchez J, Watrous JD, Phelan VV, van de Wiel C, Kersten RD, Mehnaz S, de Mot R, Shank EA, Charusanti P, Nagarajan H, Duggan BM, Moore BS, Bandeira N, Palsson BØ, Pogliano K, Gutiérrez M, Dorrestein PC (2013) MS/MS networking guided analysis of molecule and gene cluster families. *Proceedings of the National Academy of Sciences USA* 110: E2611-E2620.
43. Frasch H, [Medema MH](#), Takano E, Breitling R (2013) Design-based re-engineering of biosynthetic gene clusters: plug-and-play in practice. *Current Opinion in Biotechnology* 24:1144-1150.
44. [Medema MH](#), Takano E, Breitling R (2013) Detecting sequence homology at the gene cluster level with MultiGeneBlast. *Molecular Biology and Evolution* 30: 1218-1223.
45. Tobias NJ, Doig KD, [Medema MH](#), Chen H, Haring V, Moore R, Seemann T, Stinear TP (2013) Complete genome sequence of the frog pathogen *Mycobacterium ulcerans* ecovar Liflandii. *Journal of Bacteriology* 195: 556-564.
46. Zakrzewski P\*, [Medema MH\\*](#), Gevorgyan A, Kierzek AM, Takano E, Breitling R (2012) MultiMetEval: comparative and multi-objective analysis of genome-scale metabolic models. *PLoS ONE* 7: e51511.
47. Fedorova ND, Moktali V, [Medema MH](#) (2012) Bioinformatics approaches and software for detection of secondary metabolic gene clusters. *Methods in Molecular Biology* 944: 23-45.
48. Nguyen QT, Merlo EM, [Medema MH](#), Jankevics A, Breitling R, Takano E (2012) Metabolomics methods for the synthetic biology of secondary metabolism. *FEBS Letters* 586:2177-2183.

49. [Medema MH](#), van Raaphorst R, Takano E, Breitling R (2012) Computational tools for the synthetic design of biochemical pathways. *Nature Reviews Microbiology* 10: 191-202. **#key publication**
50. [Medema MH\\*](#), Alam MT\*, Breitling R, Takano E (2011) The future of industrial antibiotic production: from random mutagenesis to synthetic biology. *Bioengineered Bugs* 2(4): 230-233.
51. Alam MT, [Medema MH](#), Takano E, Breitling R (2011) Comparative genome-scale metabolic modeling of actinomycetes: the topology of essential core metabolism. *FEBS Letters* 585(14): 2389-2394.
52. [Medema MH](#), Blin K, Cimermancic P, de Jager V, Zakrzewski P, Fischbach MA, Weber T, Takano E, Breitling R (2011) antiSMASH: rapid identification, annotation and analysis of secondary metabolite biosynthesis gene clusters in bacterial and fungal genome sequences. *Nucleic Acids Research* 39: W339-W346. **#key publication**
53. Röttig M, [Medema MH](#), Blin K, Rausch C, Weber T, Kohlbacher O (2011) NRPSPredictor2 - a web server for predicting NRPS adenylation domain specificity. *Nucleic Acids Research* 39: W362-W367.
54. [Medema MH](#), Breitling R, Takano E (2011) Synthetic biology in *Streptomyces* bacteria. *Methods in Enzymology* 497: 485-502.
55. [Medema MH\\*](#), Alam MT\*, Heijne WH, van den Berg MA, Müller U, Trefzer A, Bovenberg RA, Breitling R, Takano E (2011) Genome-wide gene expression changes in an industrial clavulanic acid overproduction strain of *Streptomyces clavuligerus*. *Microbial Biotechnology* 4(2): 300-305.
56. [Medema MH](#), Breitling R, Bovenberg RA, Takano E (2011) Exploiting plug-and-play synthetic biology for drug discovery and production on microorganisms. *Nature Reviews Microbiology* 9(2): 131-137. **#key publication**
57. [Medema MH](#), Trefzer A, Kovalchuk A, van den Berg M, Müller U, Heijne W, Wu L, Alam MT, Ronning CM, Nierman WC, Bovenberg RA, Breitling R, and Takano E (2010) The sequence of a 1.8-Mb bacterial linear plasmid reveals a rich evolutionary reservoir of secondary metabolic pathways. *Genome Biology and Evolution* 2: 212-224.
58. [Medema MH\\*](#), Zhou M\*, van Hijum SAFT, Wessels HJTC, Gloerich J, Siezen RJ, Strous M (2010) A predicted physicochemically distinct sub-proteome associated with the intracellular organelle of the anammox bacterium *Kuenenia stuttgartiensis*. *BMC Genomics* 11: 299.
59. Van Hijum SAFT\*, [Medema MH\\*](#), Kuipers OP (2009) Mechanisms and evolution of control logic in prokaryotic transcriptional regulation. *Microbiology and Molecular Biology Reviews* 73(3): 481-509.
60. Ettwig KF, Shima S, van de Pas-Schoonen KT, Kahnt J, [Medema MH](#), op den Camp HJM, Jetten MSM, Strous M (2009) Denitrifying bacteria oxidize methane in the absence of archaea. *Environmental Microbiology* 75(11): 3656-3662.

\* Contributed equally      # Co-corresponding author

## Media Coverage

In September 2016, I was featured by New Scientist as one of the 25 candidates in The Netherlands and Belgium for the prize 'Wetenschapstalent 2016' (Scientific Talent 2016). Also, my research was featured in 'NRC Handelsblad' ('Laten we het eens over wetenschap hebben', 11 oktober 2016) and 'Elsevier Magazine' ('Deze vijf talenten zijn begaafde speurders', 18 november 2016).

Links:

- <https://newscientist.nl/blogs/new-scientist-wetenschapstalent-2016-kandidaten/>
- <https://www.nrc.nl/nieuws/2016/10/11/laten-we-het-eens-over-wetenschap-hebben-4718412-a1526012>
- <http://www.elsevierweekblad.nl/kennis/achtergrond/2016/11/deze-vijf-talenten-zijn-begaafde-speurders-2920931W/>

## Acquisition: awarded project proposals

Since starting at Wageningen University in March 2015, I have acquired the following research funding:

Funding agency	Role	Total kE budget	kE for my group
NWO Veni	Main applicant	250	250
NWO Groen	Coordinator	808	220
EPS TT Strategic Funds call	Main applicant	259	259
ZonMW	Hotel manager	30	30
ZonMW	Hotel manager	30	30
NIH Genomes to Natural Products	Main applicant	100	100
NIH Genomes to Natural Products	Main applicant	40	40
Top Sector Horticulture	Main applicant	50	50
DARPA, via UCSF/Stanford	PI	276	276
ERA-NET CoBioTech	Co-applicant	1508	171
NWO-TTW NACTAR	Coordinator	760	254
NWO ASDI eScience Centre	Co-applicant	249	249
<b>Total</b>			<b>1929</b>

## List of invited and keynote lectures

\*including planned lectures for coming months

Date	Venue	Type
March 2018	John Innes Centre Friday Seminar, Norwich, UK	Invited seminar
March 2018	MiCom 2018, 7th International Conference on Microbial Communication, Jena, Germany	Keynote lecture
February 2018	2nd Plant Microbiome Symposium, Amsterdam, The Netherlands	Keynote lecture
November 2017	ETH Zürich, Institute of Microbiology Seminar Series, Zürich, Switzerland	Invited seminar
September 2017	Italian Society of General Microbiology and Biotechnology, Annual Meeting, Palermo, Italy	Keynote lecture
August 2017	Novartis Institute for Biomedical Research, Boston, USA	Invited lecture
August 2017	Genomes to Natural Products Annual Meeting, New York, USA	Invited lecture
July 2017	University of Washington, Seattle, Department of Microbiology	Invited seminar
July 2017	American Society of Pharmacognosy 2017, Portland, USA	Invited lecture
June 2017	University Medical Centre Groningen, Department of Genetics	Invited seminar
May 2017	Decoding and Recoding Biological Systems Symposium, Norwich Research Park, Norwich, UK	Invited lecture
January 2017	STW Back2Roots programme meeting, Wageningen, The Netherlands	Keynote lecture
December 2016	SINTEF, Trondheim, Norway	Invited seminar
October 2016	Baseclear BV, Leiden, The Netherlands	Invited seminar
October 2016	Genetics of Industrial Microorganisms 2016, Wuhan, China	Invited lecture
September 2016	University of Illinois, Urbana-Champaign, Biochemistry Seminar, Urbana-Champaign, USA	Invited seminar
September 2016	NIH Genomes to Natural Products Annual Meeting, Stanford, USA	Two invited lectures
September 2016	GARNet 2016: Innovation in the Plant Sciences, Cardiff, UK	Invited lecture
August 2016	NPRONET meeting 'Genomics-Driven Approaches to Bioactive Natural Product Discovery', Syngenta - Jealott's Hill, UK	Keynote lecture
June 2016	Utrecht Bioinformatic Seminar Series, Utrecht, The Netherlands	Invited seminar
March 2016	Helmholtz Institute for Pharmaceutical Sciences, Saarbrücken, Germany	Invited seminar
February 2016	1st Plant Microbiome Symposium, EMBRAPA, Jaguariuna, Brazil	Keynote lecture
January 2016	Computational Methods for Natural Products Discovery Conference, NIH Technology Center for Computational Mass Spectrometry (CCMS) at UCSD, San Diego, USA	Keynote lecture
October 2015	Fraunhofer-Sanofi Excellence Centre for Natural Products Research, Frankfurt, Germany	Invited lecture



Date	Venue	Type
September 2015	European Bioinformatics Institute Metagenomics Course - Hinxton, UK	Keynote lecture
August 2015	Princeton University, Department of Molecular Biology - Princeton, USA	Invited seminar
August 2015	Annual Meeting of the Society for Industrial Microbiology & Biotechnology - Philadelphia, USA	Invited lecture
July 2015	Novartis - Basel, Switzerland	Invited lecture
July 2015	High-Value Chemicals from Plants Workshop - Norwich, UK	Invited lecture
July 2015	Annual Conference of the International Society for Computational Biology (ISMB) - Dublin, Ireland	Selected talk, Highlights Track
May 2015	DOE Joint Genome Institute Genomes to Secondary Metabolites Workshop - Walnut Creek, USA	Invited lecture
May 2015	17th Genomic Standards Consortium Meeting - Walnut Creek, USA	Invited lecture
May 2015	Novozymes - Copenhagen, Denmark	Invited seminar
March 2015	Marine Micr'Omics for Biotech Applications Industry Expert Workshop - Madrid, Spain	Invited lecture

## List of reviews performed

In the past three years, I have performed peer reviews for several scientific journals:

- Nature Chemical Biology
- Nature Microbiology
- Nature Communications
- Cell Chemical Biology
- ACS Chemical Biology
- The ISME Journal
- New Phytologist
- Natural Product Reports
- Nucleic Acids Research
- BMC Genomics
- Analytical Chemistry
- Journal of Antibiotics
- Microbiology
- Biotechnology Journal
- Marine Genomics
- Scientific Reports
- PeerJ
- Biotechnology Advances

Also, I have performed reviews for the following grant agencies:

- ERANET (reviewing committee)
- ERC Starting Grant
- ERC Consolidator Grant
- ERC Advanced Grant
- BBSRC (UK)
- Czech Health Research Council

## Conference organisations and session chairing

In May 2015, I co-organised an international workshop on Genomes to Secondary Metabolites, held at the DOE Joint Genome Institute (JGI). I co-chaired this meeting with Dr. Amrita Pati from the JGI. Besides this, I have also co-chaired a session on 'Genome Mining and Synthetic Biology' at the International Symposium on the Biology of Actinomycetes (ISBA) in Jeju, Korea, in 2017, together with Prof. Huimin Zhao (University of Illinois, Urbana-Champaign), and will chair a session on 'Bioinformatic tools and Big Data approaches' at the 14th International Symposium on the Genetics of Industrial Microorganisms in Pisa, Italy, together with Alessio Mengoni.

## Editorial work

In 2016, I was editor of a special issue of *Natural Product Reports* (IF: 11.014) on Synthetic Biology and Bioinformatics, together with Prof. Dr. Huimin Zhao (University of Illinois, Urbana-Champaign).

In 2018, I became a member of the editorial board of *Natural Product Reports*.

Currently, I am an editor of a special issue on 'Big Data Approaches for Industrial Microorganisms' for *FEMS Microbiology Letters*, together with Dr. Stefano Donadio (NAICON, Italy).

## Awards

During my career, I have thus far received the following honours and awards:

- NBIC Young Investigator Award 2014. *Netherlands Bioinformatics Centre / BioSB Graduate School*.
- Audience Award and Second Prize, Van Swinderen Prize, Dutch Royal Natural Sciences Society Groningen. December 2014.
- Featured candidate for 'Scientific Talent 2016' by *New Scientist*.

## Scientific Advisory Boards and Consultancy

I am a member of the scientific advisory boards of Hexagon Bio (Menlo Park, CA; <http://www.hexagonbio.com>) and the NWO-TTW Perspective Programme 'Back to the Roots'. I have acted as a scientific consultant to NGM Biopharmaceuticals, Third Rock Ventures and Flagship VentureLabs.