



Curriculum vitae



Personal Information

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|-----------------------------|---|
| FIRST NAME / SURNAME | Marnix Medema |
| ADDRESS (PRIVATE) | Soetendaalseweg 16A, 6721XB Bennekom, NL |
| ADDRESS (WORK) | Droevendaalsesteeg 1, 6708PB Wageningen, NL |
| TEL | +31317484706 / +31654758321 (cell) |
| EMAIL | marnix.medema@wur.nl |
| WEB | http://www.marnixmedema.nl |
| NATIONALITY | Dutch |
| DATE OF BIRTH | 24.01.1986 |
| GENDER | Male |

Work Experience

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|------------------------|--|
| DATES | March 2015 - present |
| EMPLOYER | Wageningen University |
| ADDRESS | Wageningen, The Netherlands |
| POSITION | Assistant Professor |
| DATES | August 2013 - February 2015 |
| EMPLOYER | Max Planck Institute for Marine Microbiology |
| ADDRESS | Bremen, Germany |
| POSITION | Postdoctoral Researcher |
| DATES | September 2010 - March 2011 |
| EMPLOYER | University of California, San Francisco |
| ADDRESS | San Francisco, USA |
| POSITION | Visiting Research Scholar |
| DATES | September 2009 - August 2013 |
| EMPLOYER | University of Groningen |
| ADDRESS | Groningen, The Netherlands |
| POSITION | PhD Student |
| GRADUATION DATE | 27.09.2013 |
| DISTINCTION | <i>cum laude</i> ** |

Education and Training

DATES September 2006 - August 2008
QUALIFICATION AWARDED Master of Science
PRINCIPAL STUDIES Biomolecular Science (Top Master Programme)
INSTITUTION University of Groningen, The Netherlands
DISTINCTION *cum laude* **

DATES September 2003 - August 2006
QUALIFICATION AWARDED Bachelor of Science
PRINCIPAL STUDIES Biology
INSTITUTION Radboud University Nijmegen, The Netherlands
EXTRA CURRICULUM Honours Programme
DISTINCTION *cum laude* **

Grants Acquired

NAME NWO Rubicon grant for 2-year postdoc at MPI Bremen
DATE RECEIVED April 2013
DETAILS Ranked 1st out of 48 applications in Life Sciences

NAME Humboldt Postdoctoral Fellowship
DATE RECEIVED June 2013
DETAILS Declined because of incompatibility with Rubicon

NAME Several Travel Grants
DATE RECEIVED 2010-2014
DETAILS Boehringer Ingelheim Fonds Travel Grant, FEMS Meeting Attendance Grant, SSBN Travel Grant, EMBO Travel Grant, RSC Travel Grant, SGM Travel Grant

Awards

NAME NBIC Young Investigator Award 2014
DATE April 2014

NAME Audience Award & Second Prize, van Swinderen Prize, Dutch Royal Natural Sciences Society
DATE December 2014

Conference Presentations

- JANUARY 2015** DECHEMA Symposium "Synthetic Pathways and Synthetic Enzyme Cascades", Frankfurt, Germany (invited talk)
- DECEMBER 2014** Netherlands Metagenomics Platform Meeting, Nijmegen, the Netherlands (invited talk)
- SEPTEMBER 2014** ESF-EMBO Meeting "Synthetic Biology of antibiotics II" Sant Feliu de Guixols, Spain (selected talk)
- APRIL 2014** Netherlands Bioinformatics (NBIC) Conference Lunteren, The Netherlands (award lecture)
- MARCH 2014** Gordon Research Seminar on Marine Natural Products Ventura, USA (selected talk)
- MARCH 2014** 16th Genomic Standards Consortium Meeting Oxford, UK (selected talk)
- OCTOBER 2013** BASF Bio-symposium Asselheim, Germany (invited talk)
- OCTOBER 2013** Workshop MicroB3-MetaExplore Groningen, The Netherlands (invited talk)
- APRIL 2013** 15th Genomic Standards Consortium Meeting Bethesda, USA (selected talk)
- APRIL 2013** Netherlands Bioinformatics (NBIC) Conference Lunteren, The Netherlands (selected talk)
- MARCH 2013** Annual German Microbiology (VAAM) Meeting Bremen, Germany (selected talk)
- NOVEMBER 2012** Leiden University Leiden, The Netherlands (invited talk)
- OCTOBER 2012** NBIC HotTopics Meeting Synthetic Biology Utrecht, The Netherlands (invited talk)
- SEPTEMBER 2012** International VAAM Workshop Braunschweig, Germany (selected talk)
- SEPTEMBER 2012** RSC Conference "Directing Biosynthesis III" Nottingham, UK (selected talk)
- APRIL 2012** Young Microbiologists Symposium, JIC Norwich, UK (selected talk)
- MARCH 2012** Netherlands Bioinformatics (NBIC) Conference Lunteren, The Netherlands (selected talk)
- DECEMBER 2011** 16th Actinomycete Microbiology (ISBA) Meeting Puerto Vallarta, Mexico (invited talk)
- OCTOBER 2011** ESF-EMBO Meeting "Synthetic Biology of antibiotics" Sant Feliu de Guixols, Spain (selected talk)
- SEPTEMBER 2011** International VAAM Workshop Bonn, Germany (selected talk)
- JUNE 2011** "From Natural Products to Chemical Biology IV" (RSC) Bristol, UK (selected talk)

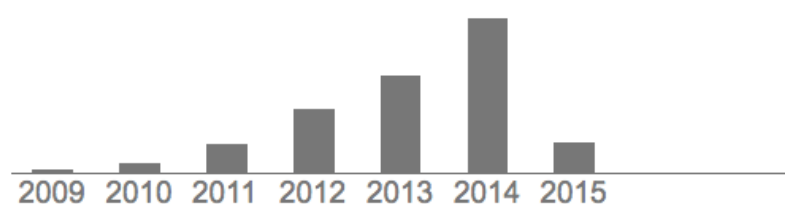


List of Publications

as of March 10th, 2015

Overview

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|---------------------------|------|
| Number of publications | 25 |
| Total Number of citations | 1350 |
| h-index | 16 |
| i10-index | 19 |



* Source: Google Scholar. <http://scholar.google.nl/citations?user=BByKtkUAAAAJ>

Key Publications

INSIGHTS INTO SECONDARY METABOLISM FROM A GLOBAL ANALYSIS OF BACTERIAL BIOSYNTHETIC GENE CLUSTERS

P Cimermancic*, [MH Medema](#)*, J Claesen*, K Kurita, LC Wieland Brown, K Mavrommatis, A Pati, PA Godfrey, M Koehrsen, J Clardy, BW Birren, R Breitling, E Takano, A Sali, RG Lington, MA Fischbach
Cell, 158: 412-21 (2014)

ANTISMASH: RAPID IDENTIFICATION, ANNOTATION AND ANALYSIS OF SECONDARY METABOLITE BIOSYNTHESIS GENE CLUSTERS IN BACTERIAL AND FUNGAL GENOME SEQUENCES

[MH Medema](#), K Blin, P Cimermancic, V de Jager, P Zakrzewski, MA Fischbach, T Weber, E Takano, R Breitling
Nucleic Acids Research 39: W339-W346 (2011). Cited 288 times.

EXPLOITING PLUG-AND-PLAY SYNTHETIC BIOLOGY FOR DRUG DISCOVERY AND PRODUCTION IN MICROORGANISMS

[MH Medema](#), R Breitling, RA Bovenberg, E Takano
Nature Reviews Microbiology 9(2): 131-137 (2011). Cited 76 times.

THE MINIMUM INFORMATION ABOUT A BIOSYNTHETIC GENE CLUSTER (MIBIG) SPECIFICATION

[MH Medema](#), ±100 co-authors, FO Glöckner
Nature Chemical Biology, in revision (2014).

COMPUTATIONAL TOOLS FOR THE SYNTHETIC DESIGN OF BIOCHEMICAL PATHWAYS

[MH Medema](#), R van Raaphorst, E Takano, R Breitling
Nature Reviews Microbiology 10: 191-202 (2012). Cited 76 times.

* Contributed equally



All Publications

1. Medema MH & Fischbach MA (2015) Computational approaches to natural product discovery. *Nature Chemical Biology*, in revision.
2. MH Medema, ±100 co-authors, FO Glöckner (2015) The Minimum Information about a Biosynthetic Gene cluster (MIBiG) specification. *Nature Chemical Biology*, in revision.
3. 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*, submitted.
4. 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*, DOI: 10.1021/sb500368w.
5. 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.
6. 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.
7. 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.
8. 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.
9. L Schriml et al. (47 authors) (2013) The 15th Genomic Standards Consortium meeting. *Standards in Genomic Sciences* 8: 124-164.
10. 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, Pálsson 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.
11. Frasc 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.
12. Medema MH, Takano E, Breitling R (2013) Detecting sequence homology at the gene cluster level with MultiGeneBlast. *Molecular Biology and Evolution* 30: 1218-1223.
13. 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.



List of Publications - *continued*

14. 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.
15. 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.
16. 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.
17. 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.
18. 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.
19. 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.
20. 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.
21. 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.
22. Medema MH, Breitling R, Takano E (2011) Synthetic biology in *Streptomyces* bacteria. *Methods in Enzymology* 497: 485-502.
23. 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.
24. 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.
25. 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.
26. 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.
27. 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.

- 28.** 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