

Michelle M. Meyer

Boston College Dept. of Biology
Higgins 444A
140 Commonwealth Ave
Chestnut Hill, MA 02467

phone: 617-552-0735
e-mail: m.meyer@bc.edu
<http://bioinformatics.bc.edu/meyerlab>

Education

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| California Institute of Technology, Pasadena, CA PhD in Biochemistry and Molecular Biophysics | 2006 |
| Rice University, Houston, TX BS Chemistry, BA Biochemistry, <i>cum laude</i> | 2001 |

Academic/Research Positions

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| Boston College, Chestnut Hill, MA Associate Professor, Department of Biology | 2016-present |
| Boston College, Chestnut Hill, MA Assistant Professor, Department of Biology | 2010-2016 |
| Yale University, New Haven, CT NRSA Postdoctoral Fellow with Professor Ronald R. Breaker | 2006-2010 |
| California Institute of Technology, Pasadena, CA HHMI Predoctoral Fellow with Professor Frances H. Arnold | 2001-2006 |
| Rice University, Houston, TX Undergraduate Research Assistant with Professor Seiichi P. T. Matsuda | 1998-2001 |

Awards and Honors

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| Alfred P. Sloan Foundation Research Fellowship | 2012-2014 |
| NIH National Research Service Award Postdoctoral Fellowship | 2007-2010 |
| Caltech Graduate Dean's Award for Outstanding Community Service | 2006 |
| Kavli Nanoscience Institute Graduate Travel Stipend | 2005 |
| Howard Hughes Medical Foundation Predoctoral Fellowship | 2001-2006 |
| National Science Foundation Doctoral Fellowship (declined) | 2001 |
| Hertz Foundation Graduate Research Grant | 2001 |
| American Society of Pharmacognosy Undergraduate Research Grant | 1999 |

Professional Memberships

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| American Chemical Society | 2001-current |
| RNA Society | 2008-current |
| International Society of Computational Biology | 2010-current |
| American Society for Microbiology | 2010-current |
| American Association for the Advancement of Science | 2010-current |
| Society for Molecular Biology and Evolution | 2012-current |

Peer Reviewed Publications

At Boston College

- Pei S, Slinger BL, Meyer MM: Recognizing RNA structural motifs in HTS-SELEX data. *BMC Bioinformatics* 2017 **18**:298.
- Slinger BL and Meyer MM: Regulators RNAs are readily derived from *in vitro* selected aptamers to ribosomal protein S15. *Nucleic Acids Research* 2016 **44**: 9331-9341.
- Slinger BL, Newman H**, Lee Y**, Pei S, Meyer MM: Co-evolution of bacterial ribosomal protein S15 with diverse mRNA regulatory structures *PLOS Genetics* 2015.**11**: e1005720.
- Babina AM, Soo MW**, Fu Y, Meyer MM: An S6:S18 complex regulates translation of *rpsF RNA* 2015 **21** (12): 2039-2046.
- Pei S, Anthony J, Meyer MM: The structural ensemble neutrality as a feature for structured RNA classification. *BMC Genomics* 2015, **16**:77.
- Lorenz, DR, Meyer LF, Grady PJ, Meyer MM, Cam HP: Heterochromatin assembly and transcriptome repression by Set1 in coordination with a class II histone deacetylase. *Elife* 2014, 10.7554/eLife.04506.
- Dotu I, Garcia-Martin JA, Slinger BL, Mechery V, Meyer MM, Clote P: Complete RNA inverse folding: computational design of functional hammerhead ribozymes. *Nucleic Acids Research* 2014, **42**:11752-11762.
- Slinger BL, Deiorio-Hagger K, Anthony J, Gilligan M**, Meyer MM: Discovery and validation of novel and distinct RNA regulators for ribosomal protein S15. *BMC Genomics* 2014, **15**:657.
- Fu Y, Deiorio-Hagger K, Soo MW**, Meyer MM: A broadly distributed motif in the 5'-UTR of *rpsF* interacts with an S6:S18 complex. *RNA* 2014 **20**:168-176.
- Deiorio-Hagggar K, Anthony J, Meyer MM: RNA Structures Regulating Ribosomal Protein Biosynthesis in Bacilli. *RNA Biology* 2013 **10**:1180-1184.
- Fu Y, Deiorio-Hagggar K, Anthony J, Meyer MM: Most RNAs regulating ribosomal protein biosynthesis in *E. coli* are narrowly distributed to Gammaproteobacteria. *Nucleic Acids Research* 2013 **41**:3491-3503.
- Miller C, Anthony J, Meyer MM, Marth G: Scribl: An HTML5 Canvas-based graphic library for visualizing genomic data over the web. *Bioinformatics* 2013, **29**:381-383
- Zarringhalam K, Meyer MM, Dotu I, Chuang J, Clote P: Integrating chemical footprinting data into RNA secondary structure prediction. *PLOS ONE* 2012, **7(10)**: e45160.

** undergraduate student author

Undergraduate, Graduate, and Postdoctoral Research:

- Meyer MM, Hammond MC, Salinas Y, Roth A, Sudarsan N, Breaker RR: Aspects of ligand identification of challenging riboswitch candidates. *RNA Biology* 2011, **8**:5-10.
- Weinberg Z, Perreault P, Meyer MM, Breaker RR: Exceptional Structured Non-coding RNAs Revealed by Bacterial Metagenome Analysis. *Nature* 2009, **462**:656-659.
- Poiata E, Meyer MM, Ames TD, Breaker RR: A variant riboswitch aptamer class of *S*-adenosylmethionine common in marine bacteria. *RNA* 2009, **15**:2046-2056.
- Meyer MM, Ames TD, Smith DP, Weinberg Z, Schwalbach MS, Giovannoni SJ, Breaker RR: Identification of candidate structured RNAs in the marine organism '*Candidatus Pelagibacter ubique*'. *BMC Genomics* 2009, **10**:268.
- Tripp HJ, Schwalbach MS, Meyer MM, Kitner JB, Breaker RR, Giovannoni SJ: '*Candidatus Pelagibacter ubique*' is a functional glycine-serine auxotroph with a glycine riboswitch preceding malate synthase. *Environmental Microbiology* 2009, **11**:230-238.
- Meyer MM, Roth A, Chervin S, Garcia GA, Breaker RR: Confirmation of a second natural preQ₁-binding aptamer. *RNA* 2008 **14**:685-695.

- Meyer MM, Hochrein L, Arnold FH: Structure-Guided Recombination of Distantly Related beta-lactamases. *Prot. Eng. Des. Sel.* 2006, **19**:563-570.
- Drummond DA, Silberg JJ, Meyer MM, Wilke CO, Arnold FH: On the conservative nature of intragenic recombination. *Proc. Natl. Acad. Sci.* 2005, **102**:5380-5385.
- Meyer MM, Silberg JJ, Voigt CA, Endelman JB, Mayo SL, Wang ZG, Arnold FH: Library analysis of SCHEMA-guided protein recombination. *Protein Sci.* 2003, **12**:1686-1693.
- Segura MJR, Lodeiro S, Meyer MM, Patel AJ, Matsuda SPT: Directed evolution experiments reveal mutations at cycloartenol synthase residue His477 that dramatically alter catalysis. *Org. Lett.* 2002, **4**:4459-4462.
- Meyer MM, Xu R, Matsuda SPT: Directed evolution to generate cycloartenol synthase mutants that produce lanosterol. *Org. Lett.* 2002, **4**:1395-1398.
- Meyer MM, Segura MJR, Wilson WK, Matsuda SPT: Oxidosqualene cyclase residues that promote formation of cycloartenol, lanosterol, and parkeol. *Angew. Chem.* 2000, **39**:4090-4092.
- Segura MJR, Meyer MM, Matsuda SPT: *Arabidopsis thaliana* LUP1 converts oxidosqualene to multiple triterpene alcohols and a triterpene diol *Org. Lett.* 2000, **2**:2257-2259.
- Matsuda SPT, Darr LB, Hart EA, Herrera JBR, McCann KE, Meyer MM, Pang J, Schepmann HR, Wilson WK: Steric bulk at cycloartenol synthase position 481 influences cyclization and deprotonation. *Org. Lett.* 2000, **2**:2261-2263.
- Godzina SM, Lovato MA, Meyer MM, Foster KA, Wilson WK, Gu W, de Hostos EL, Matsuda SPT: Cloning and characterization of the *Dictyostelium discoideum* cycloartenol synthase cDNA. *Lipids* 2000, **36**:249-255.

Patents

- Riboswitches and methods and compositions for use of and with riboswitches. Inventors: RR Breaker, Z Weinberg, N Sudarsan, X Wang, MM Meyer, A Roth, EE Regulski. US 2010/0286082, EP 2164996 (2010/3/24)

Reviews/Book Chapters

- Meyer MM: The role of mRNA structure in bacterial translational regulation. *WIREs RNA* 2016 doi: 10.1002/wrna.1370.
- Saab-Rincon G, Li Y, Meyer MM, Carbone M, Landwehr M, Arnold FA: “Protein Engineering by Structure-Guided SCHEMA Recombination” In *Protein Engineering Handbook* 2009 Eds. Lutz S & Bornscheuer UT, pp. 481-492.
- Meyer, MM Hiraga K, Arnold FH: “Site-directed Recombination” In *Current Protocols in Protein Science* 2006 Eds. Coligan JE, Dunn BM, Speicher DW, Wingfield PT, pp. 26.2.1-26.2.17.
- Bloom JD, Meyer MM, Meinhold P, Otey CR, MacMillan D, Arnold FH: Evolving strategies for enzyme engineering. *Current Opinion. Struc. Biol.* 2005, **15**:447-452.

Current External Funding

NIH: R01GM115931 (multi-PI with T. van Opijnen, Meyer is contact PI) 9/2015-8/2019
Evolutionary forces that maintain structured RNA regulators in commensal and pathogenic bacteria
Total: \$1,236,350 Direct: \$790,000

NIH: R21DE025051-01-A1 (PI) 12/2015-11/2017
Investigating RNA Regulators of Metabolism in the Oral Microbiome
Total: \$390,000 Direct: \$250,000

NSF: 1715440 MCB Investigator Initiated Research (PI) 7/2017-6/2020
The role of protein specificity in the evolution of RNA regulators
Total: \$670,000 Direct: \$446,000

Completed External Funding

NSF: MCB:1411970 Investigator Initiated Research (PI) 7/2014-6/2017
RNA Structures Regulating Ribosomal Protein Biosynthesis in Gram-Positive Bacteria
Total: \$500,000 Direct: \$320,000

NSF DBI:1262439 (Key Personnel) 8/2013-7/2016
ABI Innovation: Engineering molecular scissors by computational design with experimental validation
Total: \$700,000 Direct: \$447,000
(PI: P. Clote; I. Dotu)

Alfred P. Sloan Foundation Fellowship (PI) 9/2012-8/2014
Total: \$50,000 Direct: \$50,000

PhRMA Foundation: Informatics Starter Grant 1/2012-12/2012
Tools for Non-Coding RNA Discovery in the Human Microbiome
Total: \$60,000 Direct: \$55,000

NIH Ruth L. Kirschstein NRSA Fellowship 8/2007-7/2010
Characterization of natural mRNA genetic switches that bind metabolites
Total: \$148,202 Direct: \$148,202

Completed Internal Funding:

Boston College: Research Incentive Grant 6/2014-5/2015
Total: \$15,000

Mentored Awards:

American Society for Microbiology Undergraduate Research Fellowship (to Nicholas Lea, 2015)
American Society for Microbiology Undergraduate Research Fellowship (to Mark Soo, 2013)

Teaching

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| Bi8360 | Current Methods in Microbiology (3 credit hour graduate class, 5 students) | Spring 2017 |
| Bi5520 | Synthetic Biology (2 credit hour, undergraduate class, 12 students) | Fall 2016 |
| Bi5520 | Synthetic Biology (2 credit hour, undergraduate class, 11 students) | Spring 2016 |
| Bi4170 | Microbial Genetics (3 credit hour undergraduate class, 45 students) | Spring 2016 |
| Bi6180 | Scientific Proposal Writing (3 credit hour graduate class, 10 students) | Spring 2015 |
| Bi4170 | Microbial Genetics (3 credit hour undergraduate class, 12 students) | Spring 2015 |
| Bi6180 | Scientific Proposal Writing (3 credit hour graduate class, 3 students) | Spring 2014 |
| Bi4170 | Microbial Genetics (3 credit hour undergraduate class, 32 students) | Spring 2014 |
| Bi6180 | Scientific Proposal Writing (3 credit hour graduate class, 6 students) | Spring 2013 |
| Bi4170 | Microbial Genetics (3 credit hour undergraduate class, 33 students) | Spring 2013 |
| Bi4170 | Microbial Genetics (3 credit hour undergraduate class, 27 students) | Spring 2012 |
| Bi8020 | Synthetic Biology graduate seminar (3 credit hour seminar, 15 students) | Spring 2011 |

Professional Service

Scientific Advisory Board:

European Bioinformatics Institute: Rfam and RNA Central Databases

Associate Editor:

Genome Biology and Evolution (2015-2018)

Journal Reviewing:

Bioinformatics, PLoS ONE, PLoS Genetics, PLoS Computational Biology, ACS Synthetic Biology, RNA Biology, RNA, Nucleic Acids Research, Genome Biology, BMC Evolutionary Biology, BMC Bioinformatics, BMC Genomics, Journal of Molecular Evolution, The Protein Journal, Biophysical Journal,

Grant Reviewing:

NSF MCB review panel (2015, 2016)

NSF *ad hoc* reviewer BIO:CAREER (2014, 2016, 2017)

NIH-NIAID stage 1 reviewer for CETR (Centers for Excellence in Translational Research, U19) (2013)

German-Israeli Foundation for Scientific Research and Development, (2012)