

Curriculum Vitae: AMANDA BIRMINGHAM

EDUCATION

1997 B.A., Amherst College, Amherst, MA
Summa Cum Laude triple major in Physics, Astronomy, and English
Thesis with High Distinction: On the Star Formation History of the Rho Ophiuchus
Molecular Cloud Complex

Additional Coursework:

2006 Colorado State University, Fort Collins, CO (Statistics)
Statistics for Engineers and Scientists (grade: A+)

2003 University of Colorado, Boulder, CO (Computer Science)
Graduate courses: Readings in Cognitive Science, User Interface Design (grades: A)

EMPLOYMENT

2015 – Present: Center for Computational Biology and Bioinformatics, University of California, San Diego, CA

- Computational Biologist
 - Instituted cloud-based, best-of-breed analysis pipeline for microbiome data
 - Provided fee-for-service RNA-Seq analyses to basic researchers and clinicians
 - Developed novel software supporting end-user analysis of whole-genome mutation data
 - Contributed to [qiita](#) open-source microbiome resource

2004 – 2014: Dharmacon, part of GE Healthcare (previously Thermo Fisher Scientific), Lafayette, CO

- Highlights
 - Built bioinformatics team serving three corporate sites on two continents
 - Completed 100% of team goals for last 3 years, 94% in last 10
 - Successfully managed group through four corporate mergers, sales, and acquisitions
 - Presented talks at >20 conferences and seminar series in North America, Europe, and Asia
 - Nominated twice for company's highest award, the worldwide Customer Allegiance Star
- Bioinformatics Manager 2 (2011 – 2014)
 - Managed >\$350,000 annual personnel budget, including setting salaries, raises, and bonuses
 - Headed 5-person team awarded 1-year, one million dollar internal Intensifying Innovation grant
 - Spearheaded collaboration between RNAi Global and National Center for Biotechnology Information to expand [BioAssay](#) database to include public RNAi data storage
 - Acted as sole industry representative to international [RNA Ontology Consortium](#)
 - Instituted quarterly reannotation of ~1.5 million products to meet longstanding customer need
 - Developed C# software to design new [Lincode](#) product line targeting non-coding RNAs
- Bioinformatics Manager (2006 – 2011)
 - Built team from one member to six full-time employees, including hiring and termination
 - Trained, supervised, evaluated and, as necessary, disciplined local and remote team members
 - Authored first-in-class open-source [NoiseMaker](#) software for screening simulations
 - Co-authored international data specifications as part of [MIARE](#) and [MIACA](#) standards teams
 - Led Informatics Working Group of 60+-institute [RNAi Global Initiative](#)
 - First-authored seminal RNAi high-throughput [data analysis guidelines](#) cited >200 times
 - Worked directly with largest customers to provide expert analysis services and support

- Developed classifier algorithms for [ON-TARGETplus](#) and [SMARTvector](#) product line design
- Instituted unit-testing, source branching, and peer code reviews to ensure software quality
- Bioinformatics Software Developer (2004 - 2006)
 - First-authored ground-breaking [computational biology research](#) cited >600 times
 - Developed core product design software using C#, VB.NET and ASP.NET in Visual Studio
 - Parallelized product design code and infrastructure, increasing performance by 400%
 - Performed extensive capture and curation of public data from NCBI, EMBL, and miRBase

2002 – 2004: Molecular, Cellular, and Developmental Biology Dept., University of Colorado, Boulder, CO (Principal Investigator: Michael Yarus)

- Professional Research Assistant
 - Co-developed [BayesFold](#), a Bayesian-statistics-based RNA structure prediction package
 - Contributed to [PyCogent](#) open-source software library for genomic biology
 - Wrote first-in-class software to automatically design primers for SELEX

1999 – 2001: Elity Systems, Inc., Somerset, NJ

- Highlights
 - Helped build real-time-marketing start-up successfully sold to Fidelity Investments
 - Received first annual Elity Value Award
- GUI Team Leader (2000 – 2001)
 - Headed User Interface team, directing six junior and senior developers
 - Hired, trained, and evaluated employees, and set performance improvement plans as needed
 - Planned projects end-to-end, including requirements gathering, scoping, and resource allocation
 - Worked with customers for requirements gathering, product installs, training, and tech support
- Senior Software Developer (2000)
 - Created web-based GUIs for advertising software product with HTML, ASP, VB, and XSLT
 - Designed and implemented schema of multiple sections of product's database in SQL Server
 - Wrote both internal and end-user product documentation
- Software Developer (1999 - 2000)
 - Created reporting programs in VBA, VB 6.0, ASP, and Perl

1998 – 1999: Astronomy Dept., University of Massachusetts, Amherst, MA (Principal Investigator: Stephen Strom)

- Research Assistant
 - Carried out data analyses in C and Perl to investigate modes of stellar formation

INTERNSHIPS

1997 Arecibo Observatory (Arecibo, PR)
 1995 Cornell University, Dept. of Astronomy (Ithaca, NY)
 1994 Amherst College, Dept. of Physics (Amherst, MA)
 1993 NASA Lewis Research Center, Electrophysics Branch (Cleveland, OH)

HONORS AND AWARDS

2013 Customer Allegiance Star Award nominee Q2
 2008 Customer Allegiance Star Award nominee Q1
 2005 IEEE Computational Systems Bioinformatics Conference Best Poster Award recipient
 2000 1st Annual Elity Value Award recipient
 1997 Phi Beta Kappa member
 1994 Hughes Fellow, Amherst College, Amherst, MA

- 1994 Amherst College Porter Prize in Astronomy recipient
 1993 Valedictorian, Olmsted Falls High School, Olmsted Falls, OH
 1993 National Merit Finalist
 1993 State of Ohio Robert Byrd Scholarship recipient

PUBLICATIONS

Peer-reviewed

1. McDonald, D., **Birmingham, A.**, & Knight, R. (In press) Context and the human microbiome. *Microbiome*.
2. Anderson, E.M., Haupt, A., Schiel, J.A., Chou, E., Machado, H.B., Strezoska, Ž., Lenger, S., McClelland, S., **Birmingham, A.**, Vermeulen, A., & Smith, A.V. (2015) Systematic analysis of CRISPR-Cas9 mismatch tolerance reveals low levels of off-target activity. *J Biotechnol.* 17(211), 56-65.
3. Barrangou, R. *, **Birmingham, A.***, Wiemann, S., Beijersbergen, R., Hornung, V., & Smith, A. (2015) Advances in CRISPR-Cas9 genome engineering: lessons learned from RNA interference. *Nucleic Acids Research*, 43(7), 3407-19. **[*Co-first authors]**
4. Stombaugh, J., Licon, A., Strezoska, Ž., Stahl, J., Anderson, S.B., Banos, M., Smith, A., **Birmingham, A.**, & Vermeulen, A. (2015) The Power Decoder simulator for the evaluation of pooled shRNA screen performance. *J Biomol Screen.* 20(8), 965-75.
5. **Birmingham, A.***, Kaufmann, A. *, & Kozak, K. * (2014). RNAi and off-target effects. *Frontiers in RNAi, Vol. 1*, 3-20. **[*Co-first authors]**
6. Schmidt, E.E., Banos, M.S., Smith, J.A., **Birmingham, A.**, Boutros, M., & Shamu, C.E. Public repositories for RNAi screening data. (2014) *Frontiers in RNAi, Vol. 1*, 40-57.
7. Rocca-Serra, P., Bellaousov, S., **Birmingham, A.**, Chen, C., Cordero, P., Das, R., Davis-Neulander, L., Duncan, C. D., Halvorsen, M., Knight, R., Leontis, N. B., Mathews, D. H., Ritz, J., Stombaugh, J., Weeks, K. M., Zirbel, C. L., & Laederach, A. (2011). Sharing and archiving nucleic acid structure mapping data. *RNA*, 17(7), 1204-1212.
8. **Birmingham, A.**, Clemente, J. C., Desai, N., Gilbert, J., Gonzalez, A., Kyripides, N., Meyer, F., Nawrocki, E., Sterk, P., Stombaugh, J., Weinberg, Z., Wendel, D., Leontis, N. B., Zirbel, C., Knight, R., & Laederach, A. (2011). Meeting report of the RNA Ontology Consortium January 8-9, 2011. *Standards in Genomic Sciences*, 4(2), 252.
9. Kwan, P., & **Birmingham, A.** (2010). NoiseMaker: Simulated Screens for Statistical Assessment. *Bioinformatics*, 26(19), 2484-2485.
10. **Birmingham, A.**, Selfors, L. M., Forster, T., Wrobel, D., Kennedy, C. J., Shanks, E., Santoyo-Lopez, J., Dunican, D. J., Long, A., Kelleher, D., Smith, Q., Beijersbergen, R. L., Ghazal, P., & Shamu, C. E. (2009). Statistical methods for analysis of high-throughput RNA interference screens. *Nature Methods*, 6(8), 569-575.
11. Brown, J. W., **Birmingham, A.**, Griffiths, P. E., Jossinet, F., Kachouri-Lafond, R., Knight, R., Lang, B. F., Leontis, N., Steger, G., Stombaugh, J., & Westhof, E. (2009). The RNA structure alignment ontology. *RNA*, 15(9), 1623-1631.
12. Anderson, E. M., **Birmingham, A.**, Baskerville, S., Reynolds, A., Maksimova, E., Leake, D., Fedorov, Y., Karpilow, J., & Khvorova, A. (2008). Experimental validation of the importance of seed complement frequency to siRNA specificity. *RNA*, 14(5), 853-861.
13. Peirce, J. L., Broman, K. W., Lu, L., Chesler, E. J., Zhou, G., Airey, D. C., **Birmingham, A. E.**, & Williams, R. W. (2008). Genome Reshuffling for Advanced Intercross Permutation (GRAIP): simulation and permutation for advanced intercross population analysis. *PLoS One*, 3(4), e1977.
14. **Birmingham, A.**, Anderson, E., Sullivan, K., Reynolds, A., Boese, Q., Leake, D., Karpilow, J., & Khvorova, A. (2007). A protocol for designing siRNAs with high functionality and specificity. *Nature Protocols*, 2(9), 2068-2078.
15. Knight, R., Maxwell, P., **Birmingham, A.**, Carnes, J., Caporaso, J. G., Easton, B. C., Eaton, M., Hamady, M., Lindsay, H., Liu, Z., Lozupone, C., McDonald, D., Robeson, M., Sammut, R., Smit,

- S., Wakefield, M. J., Widmann, J., Wikman, S., Wilson, S., Ying, H., & Huttley, G. A. (2007). PyCogent: a toolkit for making sense from sequence. *Genome Biology*, 8(8), R171.
16. Fedorov, Y., Anderson, E., **Birmingham, A.**, Reynolds, A., Karpilow, J., Robinson, K., Leake, D., Marshall, W.S., & Khvorova, A. (2006). Off-target effects by siRNA can induce toxic phenotype. *RNA*, 12(7), 1188-1196.
 17. **Birmingham, A.**, Anderson, E. M., Reynolds, A., Ilesley-Tyree, D., Leake, D., Fedorov, Y., Baskerville, S., Maksimova, E., Robinson, K., Karpilow, J., Marshall, W. S., & Khvorova, A. (2006). 3' UTR seed matches, but not overall identity, are associated with RNAi off-targets. *Nature Methods*, 3(3), 199-204.
 18. **Birmingham, A.**, Anderson, E. M., Marshall, W. S., & Khvorova, A. (2005). Maximum sequence alignment fails to predict off-targeted gene regulation by RNAi. In *Computational Systems Bioinformatics Conference, 2005. Workshops and Poster Abstracts. IEEE* (pp. 233-234). IEEE.
 19. Knight, R., **Birmingham, A.**, & Yarus, M. (2004). BayesFold: rational 2° folds that combine thermodynamic, covariation, and chemical data for aligned RNA sequences. *RNA*, 10(9), 1323-1336.
 20. Rebull, L. M., Makidon, R. B., Strom, S. E., Hillenbrand, L. A., **Birmingham, A.**, Patten, B. M., Jones, B. F., Yagi, H., & Adams, Mark T. (2002). Circumstellar Disk Candidates Identified in NGC 2264. *The Astronomical Journal*, 123(3), 1528-1547.
 21. Rebull, L. M., Makidon, R. B., Strom, S. E., Hillenbrand, L. A., **Birmingham, A.**, Patten, B. M., Jones, B. F., Yagi, H., & Adams, MT. (2001). Circumstellar Disk Candidates Identified in NGC 2264. *Bulletin of the American Astronomical Society*, 33(4), 1435.

Non-peer-reviewed

1. Gross, M.M., Anderson, E.M., Sullivan, K., Robertson, B., Birmingham, A., Leake, D., & Vermeulen, A. (2015) Reciprocal microRNA modulation identifies gene targets in a biological context. Dharmacon (part of GE Healthcare) applications note.
2. de Zwart, I., Lozupone, C., Knight, R., Birmingham, A., Illangasekare, M., Jadhav, V., Legiewicz, M., Majerfeld, I., Widmann, J., & Yarus, M. (2005). Artificial Selection: Finding Function amongst Randomized Sequences. *Handbook of RNA Biochemistry*, 783-806.
3. Birmingham, A. (2002). Of Astronomical Proportions, *Science*, 298(5594), 859. [Product review].
4. Birmingham, A. (1997). On the Star Formation History of the Rho Ophiuchus Molecular Cloud Complex. [Undergraduate thesis, Amherst College, Amherst, MA].

PATENTS AND APPLICATIONS

Granted patents

1. US Patent 8,841,267. Kelley, M., **Birmingham, A.**, Karpilow, J., Khvorova, A., & Sullivan, K. "Micro-RNA scaffolds, non-naturally occurring micro-RNAs, and methods for optimizing non-naturally occurring micro-RNAs".
2. European Patent EP2155911. Kelley, M., **Birmingham, A.**, Karpilow, J., Khvorova, A., & Sullivan, K. "Micro-RNA scaffolds, non-naturally occurring micro-RNAs, and methods for optimizing non-naturally occurring micro-RNAs".
3. European Patent EP2160477. Kelley, M., **Birmingham, A.**, Karpilow, J., Khvorova, A., & Sullivan, K. "Micro-RNA scaffolds and non-naturally occurring micro-RNAs".
4. Chinese Patent 2,687,336. Kelley, M., **Birmingham, A.**, Karpilow, J., Khvorova, A., & Sullivan, K. "Micro-RNA scaffolds and non-naturally occurring micro-RNAs".

Applications

1. US Patent Application 11/724,346. **Birmingham, A.**, Anderson, E., Reynolds, A., Leake, D., Baskerville, S., Fedorov, Y., Karpilow, J., Marshall, W., & Khvorova, A. "Methods, libraries and computer program products for gene silencing with reduced off-target effects".
2. US Patent Application 11/825,461. **Birmingham, A.**, Anderson, E., Reynolds, A., Leake, D., Baskerville, S., Fedorov, Y., Karpilow, J., Marshall, W., & Khvorova, A. "Methods, libraries and computer program products for determining whether siRNA induced phenotypes are due to off-target effects".
3. US Patent 8,841,267. Kelley, M., **Birmingham, A.**, Karpilow, J., Khvorova, A., & Sullivan, K. "Micro-RNA scaffolds, non-naturally occurring micro-RNAs, and methods for optimizing non-naturally occurring micro-RNAs".
4. World Intellectual Property Organization Patent Application PCT/US2008/064,458. Kelley, M., **Birmingham, A.**, Karpilow, J., Khvorova, A., & Sullivan, K. "Micro-RNA scaffolds, non-naturally occurring micro-RNAs, and methods for optimizing non-naturally occurring micro-RNAs".
5. US Patent Application 14/454,436. Kelley, M., **Birmingham, A.**, Karpilow, J., Khvorova, A., & Sullivan, K. "Micro-RNA scaffolds and non-naturally occurring micro-RNAs".
6. World Intellectual Property Organization Patent Application PCT/US2008/064,462. Kelley, M., **Birmingham, A.**, Karpilow, J., Khvorova, A., & Sullivan, K. "Micro-RNA scaffolds and non-naturally occurring micro-RNAs".

PRESENTATIONS AT PROFESSIONAL MEETINGS

Talks

- 2015 "Starting Small: An Introduction to Microbiome 16S Data Analysis". Host-Microbiome Symbiosis: Old Friends and Foes (European Campus of Excellence European Summer School).
- 2014 "Targeting and Off-targeting of Long Noncoding RNAs by siRNAs". RNAi Global Initiative, 16th Meeting.
- 2014 "Riding the Data Wave: Analysis of High-Throughput RNAi Screens". RNAi Global Initiative, 16th Meeting.
- 2014 "Targeting and Off-targeting of Long Noncoding RNAs by siRNAs". Long Noncoding RNAs: Marching Toward Mechanism (Keystone Symposium).
- 2013 "Methods for Analysis of High-Throughput RNAi Screens". RNA, MicroRNAs & Single Cell Biology, 10th Meeting.
- 2013 "Riding the Data Wave: Analysis of High-Throughput RNAi Screens". RNAi Global Initiative, 15th Meeting.
- 2012 "High-Throughput Screening Data Analysis Workflow". RNAi Global Initiative, 14th Meeting.
- 2011 "Seed Enrichment in High-Throughput Screening Hits Demonstrates That miRNA-like Off-Targets Are Assay-Specific". RNA Society, 15th Annual Meeting.
- 2011 "Better Than the Real Thing: In Silico Screens for Statistical Selection". RNAi Global Initiative, 12th Meeting.
- 2011 Invited Talk: "Better Than the Real Thing: In Silico Screens for Statistical Selection". The IAENG International Conference on Bioinformatics 2011, part of The International MultiConference of Engineers and Computer Scientists 2011, 6th Annual Meeting.
- 2010 "The Hit List Mystery: Why We Need Public Data Deposition". RNAi Global Initiative, 11th Meeting.
- 2010 Invited Talk: "Computational Assessment of Screening Statistics for RNAi". Biomolecular Screening: Advanced Applications Across Academia, Government, and Industry (SBS Symposium).
- 2010 "Computational Assessment of Screening Statistics". Intelligent Systems in Molecular Biology

- (ISMB) 2010, 18th Annual Meeting.
- 2010 "Pathway Analysis Guidelines Project". RNAi Global Initiative, 10th Meeting.
- 2009 "Searching Seed-Space: Automated Seed Cluster Identification in Screen Results". RNAi Global Initiative, 9th Meeting.
- 2009 "Tomorrow, the World!: Toward World-wide Data Sharing Through NCBI". RNAi Global Initiative, 8th Meeting.
- 2008 "Rise of the Machines: Machine Learning for High Content Data Analysis". RNAi Global Initiative, 7th Meeting.
- 2008 "Standardizing RNAi". RNA Ontology Consortium, 4th Annual Meeting.
- 2008 "Preparing for Pathway Analysis: A Case Study". RNAi Global Initiative, 5th Meeting.
- 2007 "Computational Challenges in RNAi Gene Silencing". World Congress in Computer Science, Computer Engineering, and Applied Computing (WORLDCOMP) 2007.
- 2007 "NoiseMaker: Computational Assessment of Screening Statistics". RNAi Global Initiative, 4th Meeting.
- 2006 "New Sequence Offering: Making the Most of the Collection". RNAi Global Initiative, 3rd Meeting.
- 2006 "Analysis of a 10-Lab RNAi Pilot Screen: the Case for Standardization". RNAi Global Initiative, 2nd Meeting.
- 2004 "Maximum Sequence Alignment Fails To Predict Off-targeted Gene Regulation By RNAi". Rocky Mountain Regional Bioinformatics Conference, 2nd Annual Meeting.

Posters

- 2014 Haupt, A., Anderson, A., Strezoska, Ž., Machado, H., McClelland, S., Mayer, M., Rocker, A., Vermeulen, A., **Birmingham, A.**, Kelley, M., & Smith, A. "Cas9 driven by an optimal promoter improves gene editing in eukaryotic cell lines when paired with synthetic crRNA and tracrRNA". Discovery On-Target, 12th Annual Meeting.
- 2014 Mayer, M., McClelland, S., Anderson, S., van Brabant Smith, A., Vermeulen, A., & **Birmingham, A.** "Targeting and Off-targeting of Long Non-coding RNAs by siRNAs". Long Noncoding RNAs: Marching Toward Mechanism (Keystone Symposium).
- 2014 Licon, A., Strezoska, Z., Stombaugh, J., Banos, M., Stahl, J., Anderson, S.B., Leake, D., van Brabant Smith, A., **Birmingham, A.**, & Vermeulen, A. "Power Decoder—A Simulator for the Evaluation of Pooled shRNA Screen Performance". RNA Silencing (Keystone Symposium).
- 2012 Rocca-Serra, P., Bellaousov, S., **Birmingham, A.**, Chen, C., Cordero, P., Das, R., Davis-Neulander, L., Duncan, C., Halvorsen, M., Knight, R., Leontis, N., Mathews, D., Ritz, J., Stombaugh, J., Weeks, K., Zirbel, C., & Laederach, A. "Sharing and Archiving Nucleic Acid Structure Mapping Data". RNA Society, 17th Annual Meeting.
- 2010 **Birmingham, A.**, Strezoska, Z., Maksimova, E., Quinn, J., Kwan, P., Smith, A., Vermeulen, A., Howell, M., & Leake, D. "Seed Enrichment in Screening Hits Demonstrates the miRNA-like Off-Targets are Assay-Specific". Mechanism and Biology of Silencing (Keystone Symposium).
- 2010 Laederach, A., Bellaousov, S., **Birmingham, A.**, Davis-Neulander, L., Leontis, N., Mathews, D., Rocca-Serra, P., Stombaugh, J., Weeks, K., Zirbel, C., & Knight, R. "Standardization and Classification of Single Nucleotide Resolution Nucleic Acid Structure Mapping (SNRNASM) Experiments". RNA Society, 15th Annual Meeting.
- 2010 van Brabant Smith, A., Maksimova, E., Brenton, M., Deiparine, M., Edwards, R., Kwan, P., **Birmingham, A.**, & Leake, D. "Strategies for Improving RNAi Screening Success: Using a Ubiquitin-EGFP Assay to Identify Druggable Genes Required for Proteasome Function". Society for Biomolecular Screening, 16th Annual Meeting.
- 2009 van Brabant Smith, A., Deiparine, M., Maksimova, E., Brenton, M., **Birmingham, A.**, Kwan, P., & Leake, D. "Genome-Wide RNAi Screening as a Strategy for Target Identification and Validation". Society for Biomolecular Screening, 15th Annual Meeting.

- 2008 Anderson, E.M.*, **Birmingham, A.***, Mayer, M., Maksimova, E., Reynolds, A., Khvorova, A., & Leake, D. "Context-Based miRNA Targeting Models Applied to siRNA Off-Targeting". RNA Society, 13th Annual Meeting. [***Co-first authors**]
- 2008 Anderson, E.M.*, **Birmingham, A.***, Mayer, M., Maksimova, E., Reynolds, A., Khvorova, A., & Leake, D. "Context-Based miRNA Targeting Models Applied to siRNA Off-Targeting". RNAi, MicroRNA, and Non-Coding RNA (Keystone Symposium). [***Co-first authors**]
- 2007 Sullivan, K., Hamady, M., Knight, R., Marshall, W. S., Khvorova, A., & **Birmingham, A.** "Fast-FIND Sequence Similarity Search: An Improved Approach for siRNA Design". MicroRNAs and siRNAs: Biological Functions and Mechanisms (Keystone Symposium).
- 2007 Wiemann, S., Argo, S., Mehrle, A., Hahne, F., Hermjakob, H., Apweiler, R., Arlt, S., Bielke, W., **Birmingham, A.**, Boese, Q., Bork, P., Buchholz, F., Cai, X., Camon, C., Carninci, P., Chanda, S., Chen, Z., Cusick, M., Echeverri, C., Eils, J., Eils, R., Frank, R., Fraser, A., Girod, A., Haedrich, B., Hannus, M., Harris, M., Hayashizaki, Y., Hide, W., Hofmann, O., Huber, P., Hyman, A., Kallioniemi, O., Khvorova, A., Koski, L., Kraybill, B., LaBaer, J., Landegren, U., Lawerenz, C., Lehrach, H., Liu, F., Majety, M., Mathey-Prevot, B., Mills, G., Nomura, N., The OBI working group, Perrimon, N., Pizarro, A., Poustka, A., Quackenbush, J., Rosenfelder, H., Sahin, O., Salehi-Ashtiani, K., Sasse, F., Saueremann, M., Schimmer, A., Schmidt, C., Selfors, L., Shamu, C., Sönnichsen, B., Taylor, C., Temple, G., Vidal, M., & Wrobel, D. "The MIACA minimum information guideline for cellular assays and systems biology". HUGO's 12th Human Genome Meeting.
- 2007 Anderson, E.M., **Birmingham, A.**, Baskerville, S., Reynolds, A., Maksimova, E., Leake, D., Fedorov, Y., Karpilow, J., Marshall, W. S., & Khvorova, A. "Low Genome-Wide 3' UTR Seed Complement Frequency is Predictive of siRNA Specificity". MicroRNAs and siRNAs: Biological Functions and Mechanisms (Keystone Symposium).
- 2005 Reynolds, A., Fedorov, Y., Anderson, E., Vermeulen, A., **Birmingham, A.**, Eklund, T., Robinson, K., Leake, D., Karpilow, J., Marshall, W., & Khvorova, A. "Key Considerations for Performing RNAi in Neuronal Tissues". Society for Neuroscience, 35th Annual Meeting.
- 2005 **Birmingham, A.**, Anderson, E. M., Marshall, W. S., & Khvorova, A. "Maximum Sequence Alignment Fails to Predict Off-targeted Gene Regulation by RNAi". IEEE Computational Systems Bioinformatics Conference, 4th Annual Meeting.
- 2003 **Birmingham, A.**, Knight, R., & Yarus, M. "BayesFold: Combining Thermodynamic, Sequence, and Chemical Data to Predict Secondary Structures for RNA Alignments". RNA Society, 8th Annual Meeting.
- 2001 Rebull, L. M., Makidon, R. B., Strom, S. E., Hillenbrand, L. A., **Birmingham, A.**, Patten, B. M., Jones, B. F., Yagi, H., & Adams, M. T. "Circumstellar Disk Candidates Identified in NGC 2264". American Astronomical Society, 199th AAS Meeting.
- 1998 **Birmingham, A.**, Eder, J., and Salter, C. "The Relation between Gas Density and Star Formation in S0 Galaxies". American Astronomical Society, 191st AAS Meeting.

RESEARCH SEMINARS

- 2015 San Diego Bioinformatics Users Series, San Diego, CA
- 2014 University of Colorado at Boulder Bioinformatics Supergroup, Boulder, CO
- 2010 Weizmann Institute of Science, Rehovot, Israel
- 2010 International Centre for Genetic Engineering and Biotechnology, Trieste, Italy
- 2008 Institute of Organic Chemistry and Biochemistry, Academy of Sciences of the Czech Republic, Prague, Czech Republic
- 2006 University of Colorado at Denver Center for Computational Biology, Denver, CO
- 2005 Bay Area RNA Club, San Francisco, CA

PEER REVIEW

Refereed papers submitted to the journals

- Nature Methods
- Bioinformatics
- Nucleic Acids Research
- Journal of Biomolecular Screening
- BMC Bioinformatics
- BMC Genomics
- FEBS Letters
- Biotechnology Journal
- Expert Opinion on Drug Discovery

COMPUTER SKILLS

Current experience with:

C#	Python	SQL	R	Bioconductor	Weka	Git
QIIME	HTML	CSS	Office	Linux	Macintosh	Windows

Previous experience with:

VB.NET/6.0	ASP.NET	Java	JavaScript	Perl	C/C++	FORTRAN
Photoshop	Illustrator	SVG	XSL/XSLT	XML	UML	Visio

COMMUNITY LEADERSHIP

- Served three terms as Trustee and then Secretary for Boulder Valley UU Fellowship
- Volunteered as community leader for Boulder Valley Community Action Network
- Participated in PICO Network nationwide leadership training for community organizers

ADDITIONAL INFORMATION

LinkedIn: <http://www.linkedin.com/in/amandabirmingham>

Google Scholar: <http://scholar.google.com/citations?user=R69sgsEAAAJ>