

# Craig B. Lowe

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Dept. of Molecular Genetics and Microbiology  
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## Position

2018- Assistant Professor, Molecular Genetics and Microbiology, Duke University

## Education

2010-2018 Postdoctoral fellow, Stanford University, *David Kingsley laboratory*

2004-2010 PhD in Bioinformatics, UC Santa Cruz, *David Haussler laboratory*

2000-2004 BS in Computer Science, Cornell University, *with honors and latin honors*

## Research Interests

Genetic basis of phenotypic variation in vertebrates ; copy number variation ; human evolution ; human disease ; mobile genetic elements ; genome engineering ; reconstructing ancestral genotypes

## Research Experience

2010–2018 Developmental Genetics, Stanford University, *David Kingsley laboratory*

- Discovered novel copy number variants in a calcium channel that strongly correlate with the risk of developing schizophrenia and bipolar disorder
- Identified thousands of adaptive copy number variants associated with stickleback fish repeatedly colonizing freshwater habitats and performed transgenic assays to understand functional consequences

2004–2010 Bioinformatics, UC Santa Cruz, *David Haussler laboratory*

- Inferred the history of conserved noncoding elements in humans and discovered three macroevolutionary periods of vertebrate evolution
- Implicated >11% of human conserved noncoding DNA as originating from mobile element insertions
- Functionally characterized multiple mobile element insertions that regulate nearby genes using cell culture and transgenic animals
- Demonstrated that the ability to infer the genetic changes on the human lineage is dependent on maintaining biodiversity
- Identified genomic regions that rapidly evolved in dinosaurs

2002–2004 Computer Science, Cornell University, *Ron Elber laboratory*

- Accelerated protein similarity searches by creating a small set of proteins that span structural space

## Teaching Experience

2011-2018 Mentored 5 undergraduate and graduate students

- 4 women ; 1 underrepresented minority
- 4 rotation students (3 joined lab) ; 1 undergraduate/masters student
- 4 in Genetics dept. ; 1 in Computer Science dept.

2011 Two Week Stickleback Molecular Genetics Course, Stanford University

- Co-taught Transgenics and Field Collection sections of the course

2008 Teaching Assistant, Dept. of Biology, UC Santa Cruz

- Biology 105: Genetics

## Honors and Awards

2011	Stephen J. O'Brien Award from the American Genetic Association (for <i>Endangered Species Hold Clues to Human Evolution</i> )
2006,2009	Outstanding Presentation, UCSC Grad. Research Symp.
2007	Outstanding Presentation, UCSC Grad. Research Symp. (honorable mention)
2005	NSF Graduate Research Fellowship (honorable mention)
2004	Graduation with Honors and Latin Honors
2000-2004	Dean's List 6 semesters
2002	Degenfelder Family Scholarship

## Reviewer

Science ; New England Journal of Medicine ; PNAS ; Philosophical Transactions B ; Genome Research ;  
Genome Biology and Evolution ; BMC Genomics ; Genomics ; PLoS Computational Biology

## Invited Talks

2018	<i>Fishing for the genetic basis of vertebrate phenotypes</i> Bio-Pop Seminar Series, UNC Chapel Hill, Chapel Hill, NC
2011	<i>Three Periods of Regulatory Innovation during Vertebrate Evolution</i> Centers of Excellence in Genomic Science Meeting, Boston, MA
2011	<i>Three Periods of Regulatory Innovation during Vertebrate Evolution</i> Genome 10K Meeting, Santa Cruz, CA
2009	<i>Mobile Elements Perturb Human Developmental Regulatory Networks</i> University of Muenster, Muenster, Germany
2007	<i>The Origins of Functional Elements in the Human Genome</i> Stanford University, Stanford, CA
2004	<i>Protein Structure Prediction</i> Presentation to GE Chairman and CEO, Jeffrey Immelt, Ithaca, NY

## Publications

J. Song\*, **C. B. Lowe\***, D. M. Kingsley.

Characterization of a human-specific tandem repeat associated with bipolar disorder and schizophrenia.

*Am J Hum Genet.* 2018 Sep 6;103(3):421-430. bioRxiv 311795.

**C. B. Lowe\***, N. Sanchez-Luege\*, T. R. Howes, S. D. Brady, R. R. Richardson, F. C. Jones, M. A. Bell, D. M. Kingsley.

Detecting differential copy number variation between groups of samples.

*Genome Res.* 2018 Feb;28(2):256-265.

**C. B. Lowe**, J. A. Clarke, A. J. Baker, D. Haussler, S. V. Edwards.

Feather development genes and associated regulatory innovation predate the origin of Dinosauria.

*Mol Biol Evol.* 2015 Jan;32(1):23-8.

**C. B. Lowe** and D. Haussler.

29 mammalian genomes reveal novel exaptations of mobile elements for likely regulatory functions in the human genome.

*PLoS ONE*, 7(8):e43128, 2012.

29 mammals sequencing and analysis consortium. **(co-2nd author)**

A high-resolution map of human evolutionary constraint using 29 mammals.

*Nature*, 478(7370):476–482, Oct 2011.

Anolis genome sequencing consortium. **(8th author)**

The genome of the green anole lizard and a comparative analysis with birds and mammals.

*Nature*, 477(7366):587–591, Sep 2011.

**C. B. Lowe**, M. Kellis, A. Siepel, B. J. Raney, M. Clamp, S. R. Salama, D. M. Kingsley, K. Lindblad-Toh, and D. Haussler.

Three periods of regulatory innovation during vertebrate evolution.

*Science*, 333:1019–1024, Aug 2011.

C. Y. McLean, D. Bristor, M. Hiller, S. L. Clarke, B. T. Schaar, **C. B. Lowe**, A. M. Wenger, and G. Bejerano.

GREAT improves functional interpretation of cis-regulatory regions.

*Nat. Biotechnol.*, 28:495–501, May 2010.

**C. B. Lowe**, G. Bejerano, S. R. Salama, and D. Haussler.

Endangered species hold clues to human evolution.

*J. Hered.*, 101:437–447, 2010.

J. Zhu, J. Z. Sanborn, M. Diekhans, **C. B. Lowe**, T. H. Pringle, and D. Haussler.

Comparative genomics search for losses of long-established genes on the human lineage.

*PLoS Comput. Biol.*, 3:e247, Dec 2007.

T. Wang, J. Zeng, **C. B. Lowe**, R. G. Sellers, S. R. Salama, M. Yang, S. M. Burgess, R. K. Brachmann, and D. Haussler.

Species-specific endogenous retroviruses shape the transcriptional network of the human tumor suppressor protein p53.

*Proc. Natl. Acad. Sci. U.S.A.*, 104:18613–18618, Nov 2007.

**C. B. Lowe**, G. Bejerano, and D. Haussler.

Thousands of human mobile element fragments undergo strong purifying selection near developmental genes.

*Proc. Natl. Acad. Sci. U.S.A.*, 104:8005–8010, May 2007.

G. Bejerano, **C. B. Lowe**, N. Ahituv, B. King, A. Siepel, S. R. Salama, E. M. Rubin, W. J. Kent, and D. Haussler.

A distal enhancer and an ultraconserved exon are derived from a novel retroposon.

*Nature*, 441:87–90, May 2006.