

# Shaun Hunter

---

shaun.hunter.phd@gmail.com

## SUMMARY

Molecular biology Ph.D. with 10 years of research experience looking for a research position in a dynamic, goal-oriented environment. Studied microRNA regulation during development and cellular differentiation using both molecular and bioinformatic approaches. Work productively in a team, as well as independently.

## EDUCATION

**Washington University in St. Louis**, 2002, BA in Biology *summa cum laude*

- Minor in Computer Science

**University of California, San Diego (UCSD)**, 2009, Ph.D. in Biology.

## LEADERSHIP EXPERIENCE

- Lead a small team in the last year of my graduate project in the implementation and analysis of a reporter expression assay on dozens of transgenic lines at multiple developmental stages. Created schedules and coordinated activities of my group to efficiently manage a large-scale project to a timely conclusion, as well as establish the foundation for the continuation of the project in a new direction by the rest of the team.
- Trained, in theory and in practice, team members and other lab members with a wide range of experience from undergraduates to post docs on molecular biology, genetics and bioinformatic techniques, such as RNA interference, PCR, plasmid cloning, sequence analysis, RNA extraction, and Northern blot analysis.

## RESEARCH EXPERIENCE

**University of California at San Diego, Department of Pediatrics**

- **Postdoctoral Scholar**, Oct. 2010 - Present.  
Characterized the microRNA and target profiles in differentiating human embryonic stem cells (hESCs) using next generation sequencing (NGS) technologies. Designed expression vectors to overexpress microRNAs in established cell lines as well as in hESCs. Assayed microRNA, target mRNA and biomarker gene expression using several methods including qPCR, Northern, and NGS Digital Gene Expression.

**University of California at San Diego, Division of Biological Sciences**

- **Graduate Research Assistant**, Sep. 2002- Oct. 2009.  
Designed and implemented an analytical scheme to globally analyze the regulatory network of the conserved microRNA, and tumor suppressor, let-7, moving from higher-throughput to lower-throughput methods. Used microarray analysis to find ~2500 genes up-regulated in let-7 mutants. Used bioinformatic criteria followed by phenotypic assays to prioritize and test regulatory candidates by RNA interference for biologically significant interactions. Discovered regulatory interactions with several known developmental and cellular regulatory genes. Designed, refined and implemented a reporter gene expression assay to validate high priority candidates as direct targets. Led a small team in analyzing ~50 strains with this assay.

Shaun Hunter

Other projects and experience:

- As part of team efforts, characterized the primary transcript of *let-7*, showing some of the earliest evidence of RNA Pol II transcription of microRNAs, and demonstrated that microRNAs (*lin-4* and *let-7*) can negatively regulate targets by directing target mRNA degradation contrary to the established model.
- Initiated a project combining Immuno-precipitation and Solexa sequencing to find all of the microRNA target binding sites in *C. elegans*.
- Designed and cloned plasmids for a variety of purposes including vector improvement, increasing transformation efficiency, rescue analysis and reporter gene assays
- Wrote and modified PERL scripts for various genomic analyses, including PCR primer mispriming analysis, BLAST parsing, and simple sequence repeat analysis.

### **Washington University School of Medicine in St. Louis, Department of Genetics**

- **Undergraduate Research Assistant**, August 1998- May 2002
- **Laboratory Technician** May. 2002- Aug. 2002.

Organized an ongoing positional cloning project in zebrafish. Created the biggest physical contig of the zebrafish genome at the time. Contributed this data as well as an assembly of whole genome shotgun traces to the beginning zebrafish genome sequencing project. Used both plate sequencing and later capillary sequencing machines to generate new markers for further genetic and physical mapping.

### **SKILLS & TECHNIQUES**

#### **Molecular Biology:**

- | DNA  | RNA  | Protein   |
|--|--|---|
| <ul style="list-style-type: none"><li>• Sequencing</li><li>• Southern</li><li>• Genetic mapping</li><li>• PCR, primer design and cloning</li></ul> | <ul style="list-style-type: none"><li>• RNA and DNA isolation</li><li>• qPCR</li><li>• Microarray analysis</li><li>• RACE</li><li>• cDNA synthesis and cloning</li><li>• Northern (agarose and PAGE)</li></ul> | <ul style="list-style-type: none"><li>• Immunohistochemistry</li><li>• Western blot</li><li>• Immunoprecipitation</li></ul> |

#### **Cell Biology**

- Growth and maintenance of hESC (e.g. CyThera49) and established cell lines (e.g. HEK293)
- Transfection (Lipofectamine, Neon)
- Differentiation of hESCs

#### **Bioinformatics:**

- Programming in PERL, Java and C++
- Contig assembly
- Sequence alignments (BLAST, CLUSTALW)

#### **Software Experience:**

- |   |   |   |
|---|---|---|
| <ul style="list-style-type: none"><li>• Sequencher, DNA Star, and VectorNTI</li></ul> | <ul style="list-style-type: none"><li>• MS Office suite</li></ul> | <ul style="list-style-type: none"><li>• Adobe Photoshop and Illustrator</li></ul> |
|---|---|---|

Shaun Hunter

- Windows
- Mac OsX
- Unix/Linux

### **PUBLICATIONS**

**Hunter S**, Melnik-Martinez K, Yeo G, Pasquinelli AE. 2010. Functional genomic analysis of the *let-7* regulatory network reveals targets with roles in growth and development. In preparation.

Bagga S, Bracht J, **Hunter S**, Massirer K, Holtz J, Eachus R, Pasquinelli AE. 2005. Regulation by *let-7* and *lin-4* miRNAs results in target mRNA degradation. *Cell*. 122(4):553-63.

Pasquinelli AE, **Hunter S**, Bracht J. MicroRNAs: a developing story. 2005. *Current Opinions in Genetics and Development*.15(2):200-5.

Bracht J<sup>1</sup>, **Hunter S**<sup>1</sup>, Eachus R, Weeks P, Pasquinelli AE. 2004. Trans-splicing and polyadenylation of *let-7* microRNA primary transcripts. *RNA*. 10(10):1586-94.

<sup>1</sup>Authors contributed equally

### **SELECTED MEETING PRESENTATIONS**

**Hunter S**, Holtz J, Yeo G, Pasquinelli AE. 2007. Global analysis of the *let-7* regulatory pathway in *C. elegans*. Poster- International Worm Meeting, Los Angeles, California.

**Hunter S**, Bagga S, Bracht J, Massirer K, Holtz J, Eachus R, Pasquinelli AE. 2005. MicroRNAs Direct Target mRNA Cleavage in *C. elegans*. Platform- International Meeting of the RNA Society. Banff, Alberta, Canada.

**Hunter S** and Pasquinelli AE. 2005. Reporter based investigation of miRNA function. Poster- International Worm Meeting, Los Angeles, California.

### **HONORS & AWARDS**

**NIH Cell and Molecular Genetics** Trainee, 2002-2005

**NIH Endocrinology** Trainee 2005-2007

References available upon request.