

# JUSTIN THOMAS REESE

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## SUMMARY

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I am a biologist with experience in all aspects of research and teaching. I am a native English speaker with excellent communication skills. I am seeking a position that will allow me to apply these skills and contribute meaningfully to cross-cultural projects involving Thai and foreign nationals.

## EXPERIENCE

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**2014 - 2015**

**Khon Kaen University**

*Research Professor*

- Developed computational biology projects to aid in treatment of cholangiocarcinoma and nasopharyngeal carcinoma in coordination with Khon Kaen University faculty
- Advised Khon Kaen University faculty and students dealing with computational biology data related to existing projects
- Assisted faculty and students in preparation of scientific manuscripts and presentations

**2010 – 2015**

**Genformatic, LLC**

*Chief Operating Officer*

- Managed bioinformatics team that performed genome variant detection and bespoke bioinformatics analyses for Genformatic, LLC, generating revenue and producing several peer-reviewed research papers
- Led development of several bioinformatic products, including novel software for improving genome variant detection, custom SNP and indel calling pipeline and genome variant annotation pipeline
- Assisted in business development

**2012 – 2013**

**University of Missouri**

*Assistant Research Professor*

- Lead developer of bovinegenome.org and hymenopteragenome.org, web portals to display information pertaining to the *Bos taurus* and hymenopteran genomes (e.g. *Apis mellifera*, *Nasonia vitripennis*) genomes, respectively
- Developed novel software and designed/maintained IT infrastructure for the annotation of genes in three genomes: *Apis mellifera*, *Nasonia vitripennis*, *Bos taurus*
- Developed scientific software for research and analysis of several newly sequenced genomes, including *Apis mellifera*, *Bos taurus*, *Strongylocentrotus purpuratus*, *Nasonia vitripennis*, *Tribolium castaneum*, *Atta cephalotes*, *Pogomyrmex barbatus*, *Linepithema humile* and *Pediculus humanus*.
- Lectured on bioinformatics and scientific programming

**2006 – 2012**

**Georgetown University**

*Affiliate Research Professor*

- Lead developer of bovinegenome.org and hymenopteragenome.org, web portals to display information pertaining to the *Bos taurus* and hymenopteran genomes (e.g. *Apis mellifera*, *Nasonia vitripennis*) genomes, respectively
- Developed novel software and designed/maintained IT infrastructure for the annotation of genes in three genomes: *Apis mellifera*, *Nasonia vitripennis*, *Bos taurus*
- Developed scientific software for research and analysis of several newly sequenced genomes, including *Apis mellifera*, *Bos taurus*, *Strongylocentrotus purpuratus*, *Nasonia vitripennis*, *Tribolium castaneum*, *Atta cephalotes*, *Pogomyrmex barbatus*, *Linepithema humile* and *Pediculus humanus*.
- Lectured on bioinformatics and scientific programming

**2004 – 2006**

**Texas A&M University**

*Research Associate*

- Lead developer of hymenopteragenome.org, web portals to display information pertaining to hymenopteran genomes (e.g. *Apis mellifera*, *Nasonia vitripennis*) genomes, respectively
- Training of graduate students and postdoctoral staff as required

**2004 – 2005**

**First Global Community College, Nong Khai, Thailand**

*Lecturer/Director of Science (Part-time Volunteer)*

- Set up and administered a science and IT program consisting of six teachers
- Taught science and computer classes

**1998 – 2004**

**University of Virginia (Laboratory of William Pearson)**

*Graduate student*

- Investigated the evolution of repeated sequences in protein and DNA
- Developed a mathematical model to explain the evolution of proteins in bacterial genomes
- Developed formula for optimal gap penalties for sequence alignment and database searching, improving sensitivity and selectivity of sequence analysis tools (FASTA, BLAST)
- Acquired a broad range of computer skills, including proficiency in several computer languages

EDUCATION

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<b>Ph.D.</b>	<b>University of Virginia</b>	<b>May 2004</b>
Expertise: Computational biology and bioinformatics		
<b>M.S.</b>	<b>University of Georgia</b>	<b>August 1997</b>
Expertise: Immunology		
<b>B.S.</b>	<b>Clemson University</b>	<b>December 1994</b>
Major: Biochemistry ( <i>cum laude</i> )		

SKILLS

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- Excellent communication skills
- Experienced in manuscript preparation, editing and review
- Experienced in undergraduate and graduate teaching and training
- Proficient in several programming languages (PERL, Ruby, C, Java, R, S-Plus, shell scripting)

## LANGUAGES

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- English: native speaker, excellent speaking and writing skills
- Thai: fluent in spoken Thai, intermediate reading and writing skills
- Lao: elementary knowledge of spoken and written Lao
- Spanish: elementary knowledge of spoken and written Spanish

## PUBLICATIONS

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Cantarel, B., Weaver, D., McNeill, N., Zhang, Jianhua, Z., Mackey, A., **Reese, J.** (2014). BAYSIC: a Bayesian method for combining sets of genome variants with improved specificity and sensitivity. *BMC Genomics*, 15(1), 104.

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Elsik, C., Worley, K., Bennett, A., Beyre, M., Camara, F., Childers, C., de Graff, Debyser, G., Deng, J., Devreese, B., Elhaik, E., Evans, J., Foster, L., Graur, D., Guigo, R., Hoff, K., Holder, M., Hudson, M., Hunt, G., Jiang, H., Joshi, V., Khetani, R., Kosarev, P., Kovar, C., Ma, J., Maleszkza, R., Moritz, R., Muñoz-Torres, M., Murphy, T., Muzny, M., Newsham, F., **Reese, J.**, Robertson, M., Robinson, G., Rueppel, O., Solovyev, V., Stanke, M., Stolle, E., Tsuruda, J., Van Vaerenbergh, M., Waterhouse, R., Weaver, D., Whitfield, C., Wu, Y., Zdobnov, E., Lan, Z., Zhu, D. and Gibbs, R. (2014). Finding the missing honey bee genes: lessons learned from a genome upgrade. *BMC Genomics*, 15(1), 86.

**Reese, J.**, Christenson, M., Leng, N., Saha, S., Cantarel, B., Lindeberg, M., Tamborindeguy, C., MacCarthy, J., Weaver, D., Trease, A., Ready, S., Davis, V., McCormick, C., Haudenschild, C., Han, S., Johnson, S., Shelby, K., Huang, H., Bextine, B., Shatters, R., Hall, D., Davis, P. and Hunter, W. (2013). Characterization of the Asian Citrus Psyllid Transcriptome. *J Genomics*, 2:54-58.

Lee, E., Helt, G., **Reese, J.**, Muñoz-Torres, M., Childers, C., Buels, R., Stein, L., Holmes, I., Elsik, C. and Lewis, S. (2013). Web Apollo: A Web-based Genomic Annotation Editing Platform. *Genome Biology*, 14, R93.

Simola, D. F., Wissler, L., Donahue, G., Waterhouse, R. M., Helmkampf, M., Roux, J., Nygaard, S., Glastad, K., Hagen, D., Viljakainen, L., **Reese, J.**, Hunt, B., Graur, D., Elhaik, E., Kriventseva, E., Wen, J., Parker, B., Cash, E., Privman, E., Childers, C., Muñoz-Torres, M., Boomsma, J., Bornberg-Bauer, E., Currie, C., Elsik, C., Suen, G., Goodisman, M., Keller, L., Liebig, J., Rawls, A., Reinberg, D., Smith, C. D., Smith, C. R., Tsutsui, N., Wurm, Y., Zdobnov, E., Berger, S. and Gadau, J. (2013). Social insect genomes exhibit dramatic evolution in gene composition and regulation while preserving regulatory features linked to sociality. *Genome research*, 23(8), 1235-1247.

Saha, S., Hunter, W. B., **Reese, J.**, Morgan, J. K., Marutani-Hert, M., Huang, H., and Lindeberg, M. (2012). Survey of endosymbionts in the *Diaphorina citri* metagenome and assembly of a *Wolbachia* wDi draft genome. *PLoS One*, 7(11), e50067.

Smith, C.D., Abouheif, E., Benton, R., Croset, V., Currie, C.R., Elhaik, E., Elsik, C.G., Fave, M-J, Fernandes, V., Gadau, J., Gibson, J.D., Graur, D., Hagen, D.E., Helmkampf, M., Holt, C., Hu, H., Johnson, B.R., Johnson, R.M., Abderrahman, K., Kim, J.K., Mathis, K.A., Munoz-Torres, M.C., Murphy, M.C., Nakamura, R., Nigam, S., Overson, R., Placek, J., Rajakumar, R., **Reese, J.T.**, Robertson, H.M., Smith, C.R., Suen, G., Tao, S., Torres, C.W., van Wilgenburg, E., Viljakainen, L., Vinniegra, A-S. I., Walden, K.K.O., Yandell, M.D., Zimin, A. & N.D. Tsutsui (2011). The Genome of the Globally Widespread and Invasive Argentine Ant (*Linepithema humile*). *Proceedings of the National Academy of Sciences USA*. 108:5667-5672.

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Benton, R., Cash, E., Croset, V., Currie, C.R., Elhaik, E., Elsik, C.G., Fave, M.-J., Ferandes, V., Gibson, J.D., Graur, D., Gronenber, W., Grubbs, K.J., Hagen, D., Vinniegra, A.-S.I., Johnson, B.R., Johnson, R., Khila, A., Kim, J.W., Mathis, K.A., Munoz-Torres, M.C., Murphy, M.C., Mustard, J.A., Nakamura, R., Neihuis, O., Nigham, S., Overson, R., Placek, J., Rajakumar, R., **Reese, J.**, Suen, G., Shu, T., Torres, C.W., Tsutsui, N.D., Viljakainen, L., Wolschin, F. & J. Gadau (2011). A Draft Genome of the Red Harvester Ant, *Pogonomyrmex barbatus*: a Model for Reproductive Division of Labor and Social Complexity. *Proceedings of the National Academy of Sciences USA*.

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Munoz-Torres, M.,\* **Reese, J.**,\* Childers, C.,\* Bennett, A., Sundaram, J., Childs, K., Anzola, J., Milshina, N. and Elsik, C. (2010) Hymenoptera Genome Database: integrated community resources for insect species of the order Hymenoptera. *Nucleic Acids Res.* 39:D658-662.

**Reese, J.**,\* Childers, C.,\* Sundaram, J.,\* Dickens, M., Childs, K., Vile, D. and Elsik, C. (2010) Bovine Genome Database: supporting community annotation and analysis of the *Bos taurus* genome. *BMC Genomics.* 11:645.

**Reese, J.**, as member of The *Nasonia* Genome Working Group (2010) Functional and Evolutionary Insights from the Genomes of Three Parasitoid *Nasonia* Species. *Science.* 327:343 – 348.

**Reese, J.**, as member of Tribolium Genome Sequencing Consortium (2008) The genome of the model beetle and pest *Tribolium castaneum*. *Nature.* 2008 452:949-55

Weaver, D., Anzola, J., Evans, J., Reid, J., **Reese, J.**, Childs, K., Zdobnov, E., Samanta, M., Miller, J. and Elsik, C. (2007) Computational and transcriptional evidence for microRNAs in the honey bee genome. *Genome Biology.* 8:R97.

Robertson, H., **Reese, J.**, Milshina, N., Agarwala, R., Solignac, M., Walden, K., and Elsik, E. (2007) Manual superscaffolding of honey bee (*Apis mellifera*) chromosomes 12-16: implications for the draft genome assembly version 4, gene annotation, and chromosome structure. *Insect Molecular Biology.* 16:401-410.

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**Reese, J.** as member of the Honeybee Genome Sequencing Consortium (2006) Insights into social insects from the genome of the honeybee *Apis mellifera*. *Nature.* 443:931-949.

Miyake, T., **Reese, J.**, Loch, C., Auble D. and Li, R. (2004) Genome-wide Analysis of ARS Binding Factor 1 (Abf1p)-Mediated Transcriptional Regulation in *Saccharomyces cerevisiae*. *J. Biol. Chem.* 2004 Jun 2

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cells Marks CD4+CD8+ Subset Undergoing Selection in the Thymus. *Dev. Immunol.* 8(2):107-21.