

AndrewChatr-aryamontri, Ph.D.  
Research Scientist, University of Montreal, Canada

My main scientific interest focuses on the study of biological networks and embraces several different aspects, from data curation and analysis to data integration, data sharing and text-mining. I have several years of experience in managing biological databases. I am currently member of the BioGRID database and previously, I was the manager of the MINT (Molecular INTeraction) database. I am also a member of the HUPO-PSI molecular interaction workgroup, for the standardization of the representation of molecular interactions.

I believe that biocuration plays a pivotal role for the advance of science not only by providing the scientific community with high-quality datasets but also by fostering the cross-talk between different and distant communities.

In fact biological databases and curators communicate now with researchers from many different fields on a daily basis, including text-miners, ontologists, pure computational biologists and, of course, wet-lab biologists.

I therefore believe that this is an exiting time for the Biocuration Society. The Society that has the opportunity to contribute to guide and educate the biomedical field in the best practices of data annotation, standardization, biological concepts definitions and data interpretation in addition to supporting advances in these related fields.

By joining the ISB Executive Committee I would like to use my enthusiasm and experience to support the growth of the Society.

Conflict of interest: none declared.

## Education

2000 B.S. (Hons) Biological Sciences, University of Rome “La Sapienza”, Italy.  
2001-2004 Ph.D. Molecular Sciences, University of Rome “Tor Vergata”, Italy.

## Positions

2000-2001 Research Fellow, Dept. Molecular Biology, University of Rome, “Tor Vergata”, Italy  
2004-2009 Postdoctoral Fellow, Dept. of Genetics, University of Rome “Tor Vergata”, Italy  
2009 to 2011 Research Scientist, University of Edinburgh, UK  
2011 to present Research Scientist, University of Montreal, Canada

## Membership in Professional Societies and Appointments in Scientific Committees and Advisory Boards

2005 to present Member of PSI-MI (Proteomics Standards Initiative – Molecular Interactions) controlled-vocabulary and ontology editorial group  
2009 to present Member of the BioCreative User Advisory Group (2009-to present)  
2014-2015 Organizer of the Collaborative Biocurator Assistant Task (BioC) – BioCreative V  
2009 to present Member of the Biocuration Society

## Journal Reviewer

BMC Bioinformatics, Bioinformatics, FEBS Letters, Proteomics, Trends in Biochemical Sciences, DATABASE, Journal of Proteomics, Nucleic Acids Research, Nature Methods.

## Teaching

2003-2004 Instructor, Molecular Biology Course University of Rome “Tor Vergata”, Italy  
2004-2005 Instructor, Bioinformatics, University of Rome “Tor Vergata”, Italy  
2009 Teaching Assistant, Genetics, University of Rome “Tor Vergata”, Italy  
2009 EMBO Practical course on Networks in Biology, Bologna, Italy  
2011 Bioinformatics, PhD Programme, Spring Course University of Edinburgh, UK

## Selected Publications

(+ Co-first authorship)

1. **Chatr-Aryamontri A**, Breitkreutz BJ, Oughtred R, Boucher L, Heinicke S, Chen D, Stark C, Breitkreutz A, Kolas N, O'Donnell L, Reguly T, Nixon J, Ramage L, Winter A, Sellam A, Chang C, Hirschman J, Theesfeld C, Rust J, Livstone MS, Dolinski K, Tyers M. *The BioGRID interaction database: 2015 update*. Nucleic Acids Res. 2015 Jan;43(Database issue):D470-8
2. Dolinski K, **Chatr-Aryamontri A**, Tyers M. *Systematic curation of protein and genetic interaction data for computable biology*. BMC Biol. 2013 Apr 15;11:43
3. Arighi CN, Carterette B, Cohen KB, Krallinger M, Wilbur WJ, Fey P, Dodson R, Cooper L, Van Slyke CE, Dahdul W, Mabee P, Li D, Harris B, Gillespie M, Jimenez S, Roberts P, Matthews L, Becker K, Drabkin H, Bello S, Licata L, **Chatr-aryamontri A**, Schaeffer ML, Park JJ, Haendel M, Van Auken K, Li Y, Chan J, Muller HM, Cui H, Balhoff JP, Wu JC, Lu Z, Wei CH, Tudor CO, Raja K, Subramani S, Natarajan J, Cejuela JM, Dubey P, and Wu C. *An Overview of the BioCreative 2012 Workshop Track III: Interactive Text Mining Task*. Database. 2013 Jan 17;2013:bas056
4. Hirschman L, Burns GA, Krallinger M, Arighi C, Cohen KB, Valencia A, Wu CH, **Chatr-aryamontri A**, Dowell KG, Huala E, Lourenço A, Nash R, Veuthey AL, Wieggers T and Winter AG. *Text Mining for the Biocuration Workflow*. Database. 2012 Apr 18;2012:bas020
5. Krallinger M, Leitner F, Vazquez M, Salgado D, Marcelle C, Tyers M, Valencia A, **Chatr-aryamontri A**
6. How to link ontologies and protein-protein interactions to literature: text-mining approaches and the BioCreative experience. Database (Oxford). 2012 Mar 21;2012:bas017
7. Kiel C, Vogt A, Campagna A, **Chatr-aryamontri A**, Swiatek-de Lange M, Beer M, Bolz S, Mack AF, Kinkl N, Cesareni G, Serrano L & Ueffing M. *Structural and functional protein network analyses predict novel signaling functions for rhodopsin*. Mol Syst Biol. 2011 Nov 22;7:551
8. \*Leitner F, \***Chatr-aryamontri A**, Mardis S, Ceol A, Krallinger M, Licata L, Hirschman L, Cesareni G and Valencia A. *The FEBS Letters/BioCreative II.5 Experiment: Making Biological Information Accessible*. Nature Biotechnology 2010, 28, 897–899.
9. \***Chatr-aryamontri A**, \*Kerrien S, \*Khadake, J, Orchard S, Ceol A, Licata L, Castagnoli L, Costa S, Derow C, Huntley R, Aranda B, Leroy C, Thorneycroft D, Apweiler R, Cesareni G and Hermjakob H
10. *MINT and IntAct contribute to the Second BioCreative Challenge: serving the text-mining community with high quality molecular interaction data*. Genome Biology 2008, 9(Suppl 2):S5
11. Ceol A, **Chatr-Aryamontri A**, Licata L, Cesareni G. *Linking entries in protein interaction databases to structured text: The FEBS Letters experiment*. FEBS Lett. 2008 Mar 6
12. Kerrien S, Orchard S, Montecchi-Palazzi L, Aranda B, Quinn AF, Vinod N, Bader GD, Xenarios I, Wojcik J, Sherman D, Tyers M, Salama JJ, Moore S, Ceol A, **Chatr-aryamontri A**, Oesterheld M, Stümpflen V, Salwinski L, Nerothin J, Cerami E, Cusick ME, Vidal M, Gilson M, Armstrong J, Woollard P, Hogue C, Eisenberg D, Cesareni G, Apweiler R, Hermjakob H *Broadening the horizon - level 2.5 of the HUPO-PSI format for molecular interactions*. BMC Biol. 2007;5:44.

**Cecilia Arighi, PhD**

Associate Professor (Research), Center for Bioinformatics and Computational Biology, University of Delaware

Principal Investigator, BioCreative Conference Grant, 2014-present

Co-Investigator, Protein Ontology Consortium, 2007-present

Co-Investigator, NSF ABI (Advances in Biological Informatics) Development grant, 2011-present

Lead Curator, UniProt Consortium at Protein Information Resource; PIR Executive Committee, 2010-present

Editorial Board, Database: The Journal of Biological Databases and Curation, 2014-present

Steering Committee, BioCreative Challenge Evaluations and Workshops, 2010-present

Editor, BioCreative Conference Proceedings (4) and BioCreative Database Virtual Issues (4), 2010-present

Member, International Society for Biocuration (ISB), since its inception

Workshop Organizer (3<sup>rd</sup>, 5<sup>th</sup>-7<sup>th</sup>) and Session Co-Chair (5<sup>th</sup> and 8<sup>th</sup>), ISB International Conference

I have been working in the biocuration field since 2005 when I joined the Protein Information Resource (PIR) as a senior scientist. The focus of my research has closely aligned with the stated ISB primary goals, namely the “accurate and comprehensive representation of biological knowledge, as well as easy access to this data for working scientists and a basis for computational analysis”, via active participation in several international consortium projects that aim at reaching these goals, including UniProt, Protein Ontology and BioCreative. I have extensive experience in organizing conferences (Co-organized BioCreative since 2010, and Protein Ontology Annual Meetings 2007-2010). I have also been involved in multiple scientific program committees, including the ISB, plus experience in writing successful proposals for conference funding. I have cast a wide network of collaborators that expands beyond the biocuration field, and includes text mining, pharma, research, and publishing houses, where I have been strongly advocating for biocuration. To foster connections with user communities to ensure that databases and accompanying tools meet specific user needs, I have been working on bringing together the text mining and biocuration communities via the BioCreative interactive task. For this activity, biocurators participate to test text mining systems that are relevant to their curation task, so they are exposed to state-of-the-art tools, interact with their developers, provide direct feedback and potentially can become future adopters. One of my highest interests involves training the next generation of biocurators, and promoting community curation. I have included biocuration activities as part of the curriculum in graduate level bioinformatics courses and organizing multiple workshops which included community annotation (skate genome annotation project, and PRO workshops).

I would also like to highlight my commitment and enthusiasm towards the society throughout these years. I have attended and actively participated in six of the eight ISB meetings so far: presenting posters, giving oral presentations in mains sessions, co-chairing sessions, organizing workshops, participating in working groups (current part of the “money for biocuration” working group), and as part of the scientific committee.

I would like to see the ISB grow, to continue to educate the research community and the funding agencies so biocuration can be appreciated and sustainable. I enthusiastically support the ISB mission and I would do my best to significantly contribute to the ISB Executive Committee if elected.

**What can I bring to ISB?**

- Bridging biocuration and text mining communities
- Extensive experience in conference organization and on scientific program committees
- Experience in conference grant
- Engagement, outreach to and collaboration with the user community
- Network of collaborators encompassing biocuration, text mining, pharma, research and publishing

- My enthusiasm, hard work and smile!

**Publications** in Google Scholar: <https://scholar.google.com/citations?hl=en&btnA=1&user=NUIAfUwAAAAJ>  
(>45 peer-reviewed publications)



Cecilia Arighi (ORCID: 0000-0002-0803-4817)

ResearchGate: [https://www.researchgate.net/profile/Cecilia\\_Arighi2](https://www.researchgate.net/profile/Cecilia_Arighi2)

**Conflict of interest:**

<b>Journal/organization</b>	<b>Role</b>
Protein Information Resource (PIR) Database	Member of Executive Committee Member of Editorial Board
Pistoia Alliance	Member
International Society for Computational Biology (ISCB)	Society Member
ISCB Student council group US Northeast region	Advisor
BioCreative User Advisory Group	Co-Chair



Cecilia Arighi (ORCID: 0000-0002-0803-4817)

## **Christopher I Hunter, PhD.**

Lead Biocurator, GigaDB, GigaScience Journal, BGI-Hong Kong

ORCID: [0000-0002-1335-0881](https://orcid.org/0000-0002-1335-0881)

### **Statement of Intent for Election to the ISB Executive Committee, 2015.**

#### **I. Biographical Sketch:**

Like many people in biocuration I sort of fell into the role. For me it was a natural fit, even during my PhD and early research career I found myself cataloguing and classifying things in order to make better sense of them. So when the opportunity arose to join the European Nucleotide Archive at EBI as a curator it was an easy decision to take it. During my time with ENA and later, still in the EBI with the Metagenomics resource team, I was involved not only in helping many scientists structure their data appropriately, but also in the design and user testing of submission tools and wizards to allow greater autonomy to the users. My commitment to the promotion of well structured and annotated resources has since continued in my role at GigaDB, where I curate a much wider variety of biological data. All the annotation is stored in a purpose built database where relationships between objects can be represented explicitly. As far as possible attribute names are selected from community agreed standards and where possible terms are selected from ontologies. Both standards and ontologies are keys to good curation and given the broad scope of data that I work with I have had to become aware of a wide variety of communities that are working to create and improve these tools for curators and researchers. I have been directly involved in the creation of the GSC MIxS set of standards, and actively contribute to their ongoing development, as well working with the ISA team to help increase the utility and uptake of those tools. To read more about me please visit my LinkedIn page (<https://hk.linkedin.com/in/chr1shunter>)

#### **II Motivation to join EC and Intended Contributions:**

I am already committed to all of the goals of the society as they align very closely with those of my current position. I am active in the promotion of all biocuration activities and firmly believe that the key to pushing research forward is the curation of all data at point of creation, which requires the education and training of all young researchers in the basics of curation. To accomplish this we need to promote funding for activities and resources to allow us to most effectively share curation tools and the expertise of those already committed to the field.

I am also a member of the newly formed China Biocuration Society, this together with being based in Hong Kong, means I am ideally placed to help push the ISBs activities further in Asia where the field is still very new. Having regularly worked with researchers at BGI and CNGB, as well as others from all over Asia (e.g. Japan, Singapore, Malaysia, Philippines etc.) I am aware of the challenges facing curation in this area and I'm prepared to spearhead the push for better curation here.

### **III. Statement on Conflict of Interests:**

Dear Members of the ISB 2015 Nomination Committee,

I am writing this letter to state that, to the best of my knowledge, I have no affiliation or relationship that prevents me from performing duties as a member of the Executive Committee of the International Society for Biocuration, should I be elected. However, as the governance guideline state, I must make you aware that I am employed by the journal GigaScience, as the lead biocurator to the database (GigaDB) where we host all the data used in the journal articles. I have no direct control over the editorial processes for manuscript selection.

I am a member of the following relevant communities, none of which would provide a conflict of interest: International Society for Biocuration (ISB), China Biocuration Society, International Society for Computational Biology (ISCB), Genomics Standards Consortium (GSC).

I understand that I must contact both the ISB and the Nomination Committee if a conflict exists or arises during my service.

Sincerely,

Christopher I Hunter, PhD.

GigaScience Database, BGI-Hong Kong, 16 Dai Fu Street, Tai Po Industrial Estate, Tai Po, Hong Kong

LinkedIN: <https://hk.linkedin.com/in/chr1shunter>

## Harold J Drabkin, Ph.D.

Senior Scientific Curator, Mouse Genome Informatics, The Jackson Laboratory, 600 Main Street, Bar Harbor, ME, PHONE: 207-288-6650, FAX: (207-288-6131), EMAIL: harold.drabkin@jax.org

### *Training*

- University of Hartford, West Hartford, CT. BS. Biology, BA Chemistry, 1972
- Wesleyan University, Middletown, CT, Ph.D., Biology, 1977
- Postdoctoral Fellow, Dept. of Biochemistry, Roche Institute of Molecular Biology, Nutley NJ, 1977-1980
- Postdoctoral Fellow (1980-1982) and Associate (1982-1992), Dept. of Biology, MIT, Cambridge, MA

### *Professional Appointments*

- Research Scientist, Dept. of Biology, MIT, 1992-2000
- Lecturer, Dept. of Biology, MIT 1997-2000
- Instructor, Dept. of Biology, Northeastern University, Boston, MA 1998
- Distance Learning Faculty, Charter Oak State College, CT, 2000-present
- Instructor in Biochemistry, College of the Atlantic, ME 2008.
- Senior Scientific Curator, Jackson Laboratory, 2000-present

### *Selected publications most closely related to current project*

- **Drabkin HJ**, Christie KR, Dolan ME, Hill DP, Ni L, Sitnikov D, Blake JA. Application of comparative biology in GO functional annotation: the mouse model. *Mamm Genome*. 2015 Jul 4. [Epub ahead of print] PubMed PMID: 26141960
- Gene Ontology Consortium. Gene Ontology Consortium: going forward. *Nucleic Acids Res*. 2015 Jan;43(Database issue):D1049-56. doi: 10.1093/nar/gku1179. Epub 2014 Nov 26. PubMed PMID: 25428369; PubMed Central PMCID: PMC4383973.
- Wick HC, **Drabkin H**, Ngu H, Sackman M, Fournier C, Haggett J, Blake JA, Bianchi DW et al. DFLAT: functional annotation for human development. *BMC Bioinformatics* 2014, 15:45 (7 February 2014)
- Natale DA, Arighi CN, Blake JA, Bult CJ, Christie KR, Cowart J, D'Eustachio P, Diehl AD, **Drabkin HJ**, Helfer O, Huang H, Masci AM, Ren J, Roberts NV, Ross K, Ruttenberg A, Shamovsky V, Smith B, Yerramalla MS, Zhang J, Aljanahi A, Celen I, Gan C, Lv M, Schuster-Lezell E, Wu CH. Protein Ontology: a controlled structured network of protein entities. *Nucleic Acids Res*. 2013 Nov 21. [Epub ahead of print] PubMed PMID: 24270789.
- Roncaglia P, Martone ME, Hill DP, Berardini TZ, Foulger RE, Imam FT, **Drabkin H**, Mungall CJ, Lomax J. The Gene Ontology (GO) Cellular Component Ontology: integration with SAO (Subcellular Anatomy Ontology) and other recent developments. *J Biomed Semantics*. 2013 Oct 7;4(1):20. doi: 10.1186/2041-1480-4-20. PubMed PMID: 24093723.

### *Statement of Intent:*

As funding for Biomedical Research tightens further, it is of the utmost importance to educate and lobby both the public and the scientific community on the critical role that scientific database curation plays in providing resources that summarize and integrate current biological knowledge from various fields, and serve as a platform to rationally approach the ever increasing volume of data being generated. As an instructor in genetics for non-science majors, I introduce my students to biological databases to demonstrate their importance. As a board member, I would do my best to use my current and past experience to bolster awareness and support for scientific curation.

***Conflict of Interest Statement***

I, Harold J Drabkin, a member of the ISB declare that

I am currently employed by the Jackson Laboratory in Bar Harbor, ME, for the Mouse Genome Database as a scientific curator, and by the Charter Oak State College in New Britain CT, as distant learning faculty. To the best of my knowledge, I do not have any relationship with any organization/person that is transacting, has transacted or may transact business with the ISB and to the best of my knowledge, have no relationships with organizations/persons that may give rise to a conflict of interestj

I understand that if a conflict of interest does arise after this disclosure, I will report it to one of the Board officers immediately.

Harold J Drabkin

Date Aug 27, 2015

A handwritten signature in black ink on a light gray rectangular background. The signature reads "Harold J Drabkin" in a cursive script.

## **Marc E. Gillespie - Statement of Intent**

### **Intended Contributions/Reason for Running**

My excitement and curiosity are most strongly driven by the biocuration projects that I work on. The creation of the ISB is a boon for us who are lucky enough to know about it; there are still many who do not. In preparing for the 2014 Biocuration meeting I met numerous people who would benefit from the ISB, but had heard nothing of it. My goal is the expansion of the ISB, while still maintaining the robust sense of spirit and dynamism that we have now. I look forward to the opportunity to serve the society.

### **Bio-sketch:**

I received my doctorate in Oncological Sciences from the University of Utah in 1998 and am now a Professor in the Department of Pharmaceutical Sciences at St. John's University College of Pharmacy and Health Sciences in New York City. I received a BA in Zoology from the University of Vermont, worked as a lab technician at Cold Spring Harbor Laboratory and New York University Medical Center. My post doctoral fellowship was done at Memorial Sloan Kettering's Sloan Kettering Institute in NYC, working in x-ray crystallography.

I am trained as a molecular biologist with specialties in protein biochemistry, bioinformatics, biocuration, proteomics, and toxicology. My work in biocuration began when I joined the Reactome Team in 2003, guiding curation on Reactome modules, a pathway database of cellular level processes from "simple" events (biochemical reactions), to "complex" biological process (cell cycle). Much as I learned and grew in bioinformatics, I have been honored to grow into biocuration with the Reactome Project. I was a co-chair for the 2014 Biocuration meeting in Toronto, where I had the distinct pleasure of working more directly with the ISB.

I lead a research group focused on bioinformatics and biomarker discovery at St. John's University. Current projects range from the identification of chronic low-level lead exposure and manganese toxicity biomarkers to the mechanics of inflammatory inhibitor release. I served the University as a interim director of the Institute for Biotechnology, currently Chair the Institutional Biosafety Committee, lead institutional accreditation efforts and assessment.

I have taught courses in pharmacogenomics, public health, human anatomy & physiology, toxicogenomics, and molecular biology and have experience from academia and industry to public health policy. I have been learning, conducting, developing tools for, and teaching science for more than thirty years and am active at all levels of science.

## ISB Election Conflict of Interest Statement

### Declaration of Interest

<b>Person or organization</b>	<b>Nature of relationship and/or nature of conflict of interest</b>
Professor – St. John’s University	None
Biocurator – Reactome.org	None
Review Board - Research & Practice In Assessment	None
Adjunct Professor - New York University School Of Medicine	None
Chair – Committee on Outcomes And Assessment – St. John’s University	None
Chair – Institutional BioSafety Committee – St. John’s University	None
Review Board - Research & Practice In Assessment	None
Chief Editor – Vincention Social Action & Service Journal - – St. John’s University	None
Vice President Elect, Molecular and Systems Biology Specialty Section – Society of Toxicology	None

Name: Marc E. Gillespie

Date: 8 September 2015

Sept. 1<sup>st</sup>, 2015  
Melissa Haendel  
Letter of Intent to run for ISB executive committee

To the ISB Nominating committee:

I am running for a position on the ISB executive committee because I believe that biocurators are a critical part of the scholarly communication cycle and because I think I can help promote their inclusion and attribution throughout the research landscape.

Biocurators are a new breed of scientist, they are trained in biology as well as in information science. This makes them highly skilled to support the process of science - all the way from conception to extraction of knowledge from the literature. Unfortunately, the lion's share of a biocurators' time is spent on the latter, often chasing down authors for information that they did not know they needed to include in their publication. Their work to make the fuzzy details of science exact so as to make the data operational has been largely unrecognized.

I work in a biomedical library. I see that libraries everywhere are now trying to understand how can they better support their local research communities with respect to data management and the publication of data. For the most part, libraries do not yet have these skills and are unaware of the Biocuration Society and yet, this is exactly the community that is most aligned with the needs of biologically focused-libraries and their research communities. If only more biocurators were situated in libraries, and consulted on grants and projects whereby they could help design data management and publication plans *a priori*. This is really akin to the statistician being consulted after the data has been collected - it is often too late to perform sophisticated and/or sufficient analysis. Biocurators simply need to be part of the research planning process. Similarly, during the publication process, it is often possible to check a box saying that the work needs to be reviewed by a statistician. It seems to me that given that the content of the paper, data reuse, and scientific reproducibility all depend on how specific the elements of the science are conveyed, that a biocurator should be part of the review process as well.

I think that the ISB should continue efforts to coordinate with journals and funding agencies to include biocurators on editorial boards and review panels for publications and grant submissions. Further, biocurators need better attribution for their silent work - open reviews, authorship, and use of provenance models for their stewardship of the data are all important. Finally, biocurators need a career development just like any scientist. Putting into place computational training for those more biologically focused, and biological training for those more technical, all help grease the wheels of data processing and publication. Attribution for such contributions is no different than attribution in a publication - helping biocurators record their scholarly work, develop their reputations, and find their career paths in this emerging field.

I have responded to a number of NIH Requests for Information, where I regularly point out how biocuration, inclusion of biocurators, and/or development of biocuration skills are all lacking in program announcements and requests for proposals. The recent NIH supplement available for “informationists” to be added to one’s existing grant is a step in the right direction, but we need this idea to become commonplace in researcher’s and funder’s minds. I also am a member of the US NIH Big-Data-to-Knowledge (BD2K) program. Recently, I co-chaired a BD2K workshop at NIH to identify barriers in the development of data standards – financially, technically, and socially – much of which is performed by biocurators. Finally, biocurators can also be teachers – we can actually help researchers learn data curation skills that can help support the whole scholarly communication cycle as well as attribution of biocurators. Libraries can be a key partner to execute this plan, but are not the only vehicle.

As a current member of the ISB executive committee, I would continue to aim to further partnership with libraries, publishers, data repositories and inclusion of biocurators in the whole scholarly communication cycle.

**Declaration of Interest**

<b>Person or organization</b>	<b>Nature of relationship and/or nature of conflict of interest</b>
Journal: Journal of Biomedical Semantics	Editorial Board member, guest editor
Person: Suzanna Lewis	Co-author and co-investigator
Person: Marc Robinson-Rechavi	Co-author
Activity: Reproducibility Initiative	Board member
Activity: OBO Foundry	Coordinating member
Activity: Phenoscape	Project member
Activity: Resource Identification Initiative	Co-Director
Activity: Monarch Initiative	PI
Person: Monte Westerfield	Previous employer and co-author
Person: Chris Shaffer	Current employer
Journal: Database	Editorial board member

**Biography:**

Dr. Haendel has a BA from Reed College in Chemistry and a Ph.D. in Neuroscience from the University of Wisconsin, Madison. She was trained in molecular and developmental biology, using chick, mouse, and zebrafish model systems. She is currently the basic

research PI of the Monarch Initiative, with the aim of providing integrated access to human and model systems genotype-phenotype data for the purposes of disease hypothesis exploration. Dr. Haendel led zebrafish genome nomenclature and ontology interoperability efforts for the Zebrafish Model Organism Database (ZFIN). More recently, she has been leading efforts to assess reproducibility relating to specification of model systems in the literature. She also participates in development of eagle-i and VIVO, designed to collect and disseminate information about biomedical resources and enable research profiling, and to promote collaboration across translational boundaries. Her research interests are in using ontologies to promote synthetic science through connections within biomedical data, to utilize information science during the course of research and its publication, to promote team science, and to enable scientific reproducibility. She has been a strong proponent of attribution for all types of contribution to the research landscape, including biocuration.

Intent:

I have been a Biocurator for 14 years now (with the Saccharomyces Genome Database and the Gene Ontology Consortium) and I would like to join the Executive committee to support all the great work they have been doing. Joining the Executive committee will help me support and promote the interests of biocurators. In particular, I would like to reach out to curators to understand their training needs for career development.

Biographical Sketch:

I received my PhD in Biophysics from SUNY Buffalo in 1997. Following, I was a post-doctoral scholar in the Biochemistry Department at Stanford University. After a brief stint at a start up company, I moved to Mike Cherry's group to be a Biocurator and I have been there since.

Conflict of Interest:

None!

Thanks,

Rama

## Nomination for membership of the ISB Executive Committee

Sandra Orchard  
EMBL-EBI

orchard@ebi.ac.uk

I have worked in Biocuration for over 13 years and look to serve on the Executive Committee to help promote and develop Biocuration as a career that is recognised and appreciated beyond our own community. I would look to find ways to strengthen the opportunities for training for biocurators, both at an early stage in their careers to help them do their job, but also as their role develops to gain qualifications which are externally recognised and give credit to the many aspects of the work of a curator. I also feel we need to find ways of more pro-actively approaching funding agencies, and ensure that the value of curation is recognised when grants are being discussed and awarded. I would be interested in reaching out to industry to support us in this effort – the pharmaceutical, nutraceutical and agrochemical industries all use the results of our work and could supply valuable evidence to its significance and also help by publicly stating how important the curation of scientific data is to the work of the entire research community.

I have worked at the EMBL-EBI (European Bioinformatics Institute) first as a Curator for UniProt, InterPro and Gene Ontology) and then for the IntAct Molecular interaction database. Prior to this, I worked as an enzymologist in the pharmaceutical industry, for Roche Products Ltd. I was project leader for IntAct for a number of years and more recently become the Molecular Interaction Team leader. I was a member of the local organizing committee for the 2013 Biocuration meeting held in Cambridge, UK, where I was responsible for the finances, and have recently been asked to act as the non-executive Financial Officer of the ISB.

I am an Executive Editor of the Journal of Proteomics & Bioinformatics and the Map Kinase Journal and have no known conflict of interest to declare.

Stacia R. Engel, Ph.D.  
Stanford University

Senior Biocuration Scientist, *Saccharomyces* Genome Database (2002 – present)  
Curation Group Leader, *Saccharomyces* Genome Database (2014 – present)

## I. Biographical Sketch

I have been working as a Biocurator since February 2002, when I joined the *Saccharomyces* Genome Database (SGD). Prior to that, as a geneticist studying both natural and cultivated yeasts, fungi, and bacteria in industrial settings for 6 years, I came to rely upon and greatly relish the treasure trove of information gathered, curated, and served up by SGD. It was an invaluable resource that greatly enhanced my own research, and I became convinced that biocuration and the free dissemination of knowledge were among the most noble of scientific endeavors that one could pursue.

The early part of my career involved the investigation of genome evolution in different vertebrate systems. This also involved the development of genetic techniques and markers with broad taxonomic applicability for the study of population structure, making use of differences in DNA variability both within a single genome, and between similar genomes within higher taxa. I demonstrated that conserved and variable regions are interspersed, and can be exploited as necessary to study population genetics and structure. Further, I provided evidence that sequence evolution in conjunction with the fossil record (specimens and the geographic strata in which they are found) can be used to calculate molecular clocks, which can then be used to estimate divergence times, speciation events, and continental bioinvasions.

Having established the utility and exploitation of DNA variability to identify and distinguish organisms at different taxonomic levels within vertebrates, I shifted my focus to microbial systems. The next phase of my career was spent studying the biology and behavior of various filamentous fungi, yeast, and bacteria in their natural habitats within industrial settings. I combined these sets of knowledge to develop ways to differentiate closely related organisms in the three microbial systems (filamentous fungi, yeast, and bacteria). I further developed these genetic methods into quick, infallible diagnostic tests for research into fermentation population dynamics and quality assurance in production environments.

Complete List of Published Work in MyBibliography:  
<http://www.ncbi.nlm.nih.gov/myncbi/browse/collection/40700673/>

## II. Motivation and Intended Contributions

The current phase of my career is focused on the use and creation of annotation systems to represent genomic data and scientific results from the literature. Scientific experimentation is the foundation for our understanding of the world around us. Biocuration collects, organizes, and preserves these experimental results in perpetuity, and contributes to the building of accumulated

scientific knowledge. My work involves the identification, validation, and integration of published scientific information into encyclopedic databases. I have also been actively maintaining the sequence and expanding the annotation of the *Saccharomyces cerevisiae* reference genome, and in recent years, have been promoting its expansion to a highly curated 12-genome reference panel.

As a member of the ISB Executive Committee, I will work to educate scientists about annotation activities and standards maintained by biocurators, and will proselytize about the fundamental value of biocuration to the advancement of science. I will promote biocuration as a profession, work to increase its visibility, and advocate for the recognition of biocurators and the outstanding work we do. Increased value and prominence can aid in the current mission of increasing funding support.

### III. Conflicts of Interest

I have no current affiliations or relationships that would prevent me from serving on the ISB Executive Committee.

#### Professional Memberships:

2002 – present	Member, Genetics Society of America
2006 – present	Member, International Society of Biocuration
2015 – present	Member, American Society of Human Genetics

Dear nominating committee,

I am registering my intent to run for a position on the Executive Committee.

My motivation to join the EC is driven by my belief that biocurators are the primary guardians of our research heritage. Every bit of knowledge gained is predicated on hypotheses drawn from existing knowledge. And when knowledge is lost, the rate at which we can gain a better understanding of the world we are a part of is slowed.

I have had the pleasure of facilitating biocurators since the profession was born in early nineties (coincident with the early Internet). I would like to contribute to the EC a computational perspective, how to best enable this crucial work through improvement in their work environment. The Web is a wonderful soapbox for publishing data of all kinds. Labs of all sizes are distributing their results and conclusions to the entire world. As laboratory instruments continue to improve, the sheer volume of this information is going to continue to increase super-linearly. Providing access to it is straightforward from a technical standpoint, but if you are a consumer, trying to locate particular data, then trolling the Web is not much better than rolling dice. Zipf's law applies, and the things you are most interested in can only be found in a tiny minority of the items available on the Web. Biocuration vastly improves the odds to put it mildly.

As far as my background, my research focuses on developing methods for improved integration and analysis of biological data assets. I began working in this area when I directed the Berkeley *Drosophila* Genome Project (BDGP) Informatics group, ultimately culminating in the successful publication of the annotated *Drosophila* genome in March 2000. More recently I collaborated with Drs. Lincoln Stein and Gos Micklem on the Data Coordinating Center for modENCODE, collecting both raw data and meta-data (ontologically described) from almost 40 different international laboratories. Over these years, I have brought people from a wide range of different backgrounds together: software developers, biological curators, students (undergraduate and graduate), and post-doctoral researchers to work efficiently and productively. My work has centered upon developing curational tools, covering a wide spectrum of science: from genomic feature annotation using tools such as Apollo and JBrowse (a genomics feature editor now used by numerous small genome projects and educators), to data management (e.g. the Chado database used by hundreds of small genome projects), to the most advanced use of ontologies as a formal semantic framework for organizing data. Most relevant here is the development and use of ontologies as semantic frameworks for data integration. I am one of the original founders of the Gene Ontology Consortium on which I am currently a PI. In addition my group continues to oversee the logical design and development of the other elemental key ontologies such as: Cell Types, Qualities, Sequence, and UBERON (a cross-species anatomical ontology that enables cross-species comparisons in a systematic manner. I am keenly interested in practical, real-world applications to solve biology's data management challenges. As part of the MONARCH initiative to link diseases to animal model organism resources (funded by the NIH office of the director) we are exploring the practicalities of reasoning over representations of phenotypes. In addition one of my roles in the Gene Ontology Consortium is the development of the Phylogenetic Annotation Inferencing Tool (PAINT) tool, which provides us with the ability to gain additional insights based on evolutionary relationships.

Best regards, Suzi

p.s. Matriculated from the University of Michigan, both undergraduate (Microbiology) and graduate (Systems Engineering)

**Zhang Zhang, PhD**

Principal Investigator

Professor in the "100-Talent Program" of Chinese Academy of Sciences

Beijing Institute of Genomics, Chinese Academy of Sciences

No. 1 Beichen West Road, Chaoyang District

Beijing 100101, China

Lab website: <http://cbb.big.ac.cn>**Statement of Intent for the Election of the ISB Executive Committee 2015**

Dear Members of the ISB 2015 Nomination Committee,

I am very enthusiastic to stand for election to the ISB Executive Committee. The following is the required information, including motivations & intended contributions, biographical sketch, and statement on conflict of interests.

**I. Motivations & Intended Contributions**

China is now a powerhouse in generating biological data, but there is very few project that aims to make the *big* data comprehensively organized and publicly accessible to the scientific community worldwide. As biocuration becomes increasingly critical in translating big data into big discovery, China has a huge amount of biological data available, which have yet to be fully curated; therefore, my motivations to stand for the election to the ISB Executive Committee include (1) to raise general awareness in China of the significant role of biocuration, (2) to promote biomedical data exchange between China and other countries to benefit the wider world of biomedical sciences, and (3) to enhance the significance of biocuration in transforming big data into big discovery. Accordingly, my intended contributions include encouraging and recruiting qualified scientists in China to the biocuration field, fostering and building collaborations with databases and users in China to achieve big data exchange and sharing at the global scale more broadly than ever, and ultimately advancing the goals of ISB.

**II. Biographical Sketch**

I am currently a Professor of Beijing Genomics Institute (BIG), Chinese Academy of Sciences (CAS). I obtained my PhD degree in Bioinformatics from Institute of Computing Technology, CAS in 2007. Prior to joining BIG, I worked as Postdoctoral Associate at Yale University from 2007-2009 and then as Research Scientist at King Abdullah University of Science and Technology from 2009-2011. In September 2011, I was selected in the "100-Talent Program" of CAS. My research interests lie primarily in big data integration and computational molecular evolution.

Over the past few years, I have led multiple projects that dedicate to build biological databases by integrating various omics data and promoting curatorial activities among researchers from a wide range of fields with different levels of experience in China. Particularly, my group constructed two wiki-based databases, RiceWiki and LncRNAWiki, aiming to harness collective intelligence in community curation of rice genes and human long non-coding RNAs, respectively. In addition, we also developed *AuthorReward* (an extension to MediaWiki, that is able to quantify users' contribution and give explicit authorship) and proposed to provide a standard practice to reward community curation in wiki-based databases. Considering the huge population in China, community curation bears the potential to deal with big data curation and accordingly enhance the significance of biocuration in the advancement of scientific knowledge. Currently, my group is working on IC4R (Information Commons for Rice),

integrating various omics data of rice from multiple committed projects via web application programming interfaces.

The International Biocuration Conference (IBC) is an important event for biocurators and database developers to disseminate experiences and foster collaborations. The 8th IBC held in April 2015 was hosted for the first time by China. As one of organizing committee chairs, I was extensively involved in the conference organization, which has been led to its success, as testified by more than 270 participants from academia and industry gathered in Beijing. I also promoted dissemination of ISB as well as biocuration by participating in the Chinese translation of biocuration and the establishment of a sub-society for “*Big Biological Data and Biocuration*” officially affiliated under *Genetics Society of China* (one of most influential biological-related societies in China) in April 2015 during the 8th IBC.

Professional activities relevant to biocuration:

1. PI. Information Commons for Rice, <http://ic4r.org>
2. PI. Database Commons: a catalogue of biological databases, <http://databasecommons.org>
3. PI. RiceWiki: a wiki-based database for community curation of rice genes, an IC4R committed project, <http://ricewiki.big.ac.cn>
4. PI. LncRNAWiki: harnessing collective intelligence for community curation of human long non-coding RNAs, <http://lncrna.big.ac.cn>
5. PI. MethBank: a DNA methylome programming database, <http://dnamethylome.org>

### III. Statement on Conflict of Interests

Here I am writing to state that, to my best knowledge, I have no affiliation or relationship that prevents me from performing duties as a member of the Executive Committee of the International Society for Biocuration, should I be elected.

Memberships and service to the scientific community:

1. Membership: *International Society for Biocuration (ISB)*, *Genetics Society of China*
2. Reviewer: *Bioinformatics*, *BMC Bioinformatics*, *BMC Evolutionary Biology*, *BMC Genomics*, *BMC Plant Biology*, *BMC Systems Biology*, *Briefings in Bioinformatics*, *Chinese Bulletin of Life Sciences*, *Current Bioinformatics*, *Database*, *Evolutionary Bioinformatics*, *Gene*, *Genome Biology*, *Genomics Proteomics & Bioinformatics*, *In Silico Biology*, *Integrative Zoology*, *Journal of Bioinformatics and Computational Biology*, *Journal of Molecular Evolution*, *Molecular Biology and Evolution*, *PLoS ONE*, *PLoS Pathogens*, *RNA*
3. Editorial position: *Biology Direct (Editorial Board Member; 2013—)*, *PLoS ONE (Academic Editor; 2012—)*, *Genomics, Proteomics & Bioinformatics (Associate Editor-in-Chief; 2012—)*, *Frontiers in Statistical Genetics and Methodology (Review Editor; 2011—)*

I understand that I must contact both the ISB and the Nomination Committee if a conflict exists or arises during my service.

Thank you very much for your time and consideration. Look forward to hearing from you soon!

Sincerely,

Zhang Zhang, PhD