



Department of the Interior  
U.S. Fish and Wildlife Service

OMB No. 1018-0093  
Expires 05/31/2017

**Federal Fish and Wildlife Permit Application Form**

Return to: U.S. Fish and Wildlife Service  
Division of Management Authority (DMA)  
Branch of Permits, MS: IA  
5275 Leesburg Pike  
Falls Church, VA 22041-3803  
1-800-358-2104 or 703-358-2104

Type of Activity:  
**CERTIFICATE OF SCIENTIFIC EXCHANGE - COSE (CITES)**  
☒ New Application  
Requesting Re-issuance/Amendment of Permit# \_\_\_\_\_

RCVD JUN 09 2017

LB

Complete Sections A or B, and C, D, and E of this application. U.S. address may be required in Section C, see instructions for details.  
See attached instruction pages for information on how to make your application complete and help avoid unnecessary delays.

A. Complete if applying as an individual			
1.a. Last name Fedrigo	1.b. First name Olivier	1.c. Middle name or initial [REDACTED]	1.d. Suffix
2. Date of birth (mm/dd/yyyy) [REDACTED]	3. Social Security No. [REDACTED]	4. Occupation Director, Vert. Gen. Lab	5. Affiliation/ Doing business as (see instructions) The Rockefeller University
6.a. Telephone number [REDACTED]	6.d. E-mail address ofedrigo@rockefeller.edu		

B. Complete if applying on behalf of a business, corporation, public agency, Tribe or institution			
1.a. Name of business, agency, Tribe, or institution		1.b. Doing business as (dba)	
2. Tax identification no.		3. Description of business, agency, Tribe, or institution	
4.a. Principal officer Last name	4.b. Principal officer First name	4.c. Principal officer Middle name/ initial	4.d. Suffix
5. Principal officer title		6. Primary contact name	
7.a. Business telephone number	7.b. Alternate telephone number	7.c. Business fax number	7.d. Business e-mail address

C. All applicants complete address information					
1.a. Physical address (Street address; Apartment #, Suite #, or Room #; no P.O. Boxes) The Rockefeller University, 1230 York Ave					
1.b. City New York	1.c. State NY	1.d. Zip code/Postal code: 10065	1.e. County/Province New York	1.f. Country USA	
2.a. Mailing Address (include if different than physical address; include name of contact person if applicable) The Rockefeller University, 1230 York Ave, Box 366					
2.b. City New York	2.c. State NY	2.d. Zip code/Postal code: 10065	2.e. County/Province New York	2.f. Country USA	

D. All applicants MUST complete	
1.	Attach check or money order payable to the U.S. FISH AND WILDLIFE SERVICE in the amount of \$100, nonrefundable processing fee. Federal, Tribal, State, and local government agencies, and those acting on behalf of such agencies, are exempt from the processing fee – attach documentation of fee exempt status as outlined in instructions. (50 CFR 13.11(d))
2.	Do you currently have or have you ever had any Federal Fish and Wildlife permits? Yes <input type="checkbox"/> If yes, list the number of the most current permit you have held or that you are applying to renew/re-issue: _____ No <input checked="" type="checkbox"/>
3.	Certification: I hereby certify that I have read and am familiar with the regulations contained in Title 50, Part 13 of the Code of Federal Regulations and the other applicable parts in subchapter B of Chapter I of Title 50, and I certify that the information submitted in this application for a permit is complete and accurate to the best of my knowledge and belief. I understand that any false statement herein may subject me to the criminal penalties of 18 U.S.C. 1001.  Signature (in blue ink) of applicant/person responsible for permit (No photocopied or stamped signatures) _____ Date of signature (mm/dd/yyyy) 06/06/2017

## E. CERTIFICATE OF SCIENTIFIC EXCHANGE (COSE) (CITES)

**Note 1.** A Certificate of Scientific Exchange (COSE) only authorizes the non-commercial loan, donation or exchange between scientists or scientific institutions registered by a Management Authority of their country, of preserved, dried or embedded specimens, herbarium specimens and live plant material which carries a label issued or approved by a Management Authority. The CITES web site has a list of all registered institutions at [http://www.cites.org/common/reg/e\\_si.html](http://www.cites.org/common/reg/e_si.html). If specimens are protected by other U.S. laws and/or treaties, such as the Endangered Species Act, Marine Mammal Protection Act, Migratory Bird Treaty Act, or Bald and Golden Eagle Protection Act, you are required to obtain additional authorizations prior to any export or re-import of those specimens.

**Note 2.** A COSE cannot be used with specimens collected by field researchers unless such specimens are first accessioned into the collection of a registered facility in the state of origin. For the import or export of specimens that are not part of your museum collection, have not yet been collected, or accessioned into your collect, you will probably need to submit form 3-200-37. If you have questions, please contact the Division of Management Authority at the telephone number on page one.

**For re-issuance, include the original certificate and the annual report (see Form 3-200-39a).** The report is a summary of all imports and exports conducted under the COSE for the past year; including information that appears on the COSE container label such as scientific name and common name, date sent, description of specimen, acquisition number, receiving institution, country, and COSE number.

**ENTER an "X" in the box that applies.**

1. Is the institution or collection an accredited scientific institution/collection? If yes, indicate the name of the accrediting organization. If additional relevant information about the institution is available on the web, please provide the URL address. If no, provide additional information related to the institution's standards for record-keeping for and accessibility to the collection.

☒ YES      ☐ NO

2. Are the collections and associated data permanently housed and professionally curated? If yes, how long have the collections been permanently housed and professionally curated. Provide the physical address for the collection and the name and contact information for the curator.

☒ YES      ☐ NO

3. Are all accessions properly recorded in a permanent catalogue?

☒ YES      ☐ NO

4. As appropriate, ENTER approximate number of accessioned specimens:

<u>      </u> Mammals	<u>  ✓  </u> Birds (2922 specimens)
<u>      </u> Insects/Arachnids	<u>      </u> Other Invertebrates
<u>      </u> Reptiles/Amphibians	<u>      </u> Vascular Plants
<u>      </u> Fish	<u>      </u> Other (specify: _____)

5. Do you maintain any specimens protected under the Marine Mammal Protection Act?

       YES        ✓   NO

- a. If "yes," do you intend to import or export these specimens? \_\_\_\_\_
- b. If "yes", provide a copy of your MMPA authorization for this activity.

6. Do you maintain or intend to obtain any specimens protected under the Endangered Species Act?

  ✓   YES             NO

- a. If "yes", do you intend to import or export these specimens? import, ESA in progress
- b. If "yes", provide a copy of your ESA authorization for this activity.

7. Do you maintain or intend to obtain any specimens protected under the Migratory Bird Treaty Act?

  ✓   YES             NO

- a. If "yes", do you intend to import or export these specimens? import, MBTA in progress
- b. If "yes", provide a copy of your MBTA authorization for this activity.

8. Do you maintain any specimens protected under the Bald and Golden Eagle Protection Act?

  ✓   YES             NO

- a. If "yes", do you intend to import or export these specimens? import, MBTA in progress
- b. If "yes", provide a copy of your MBTA authorization for this activity.

9. Are specimens accessible to qualified users from outside your institution?

       YES        ✓   NO

ENTER approximate number:	In the United States	Outside the United States
Loans last year:	_____	_____
Exchanges last year:	_____	_____
Donations last year:	_____	_____

10. Are permanent records maintained on specimens that are loaned or transferred?  
☐ YES ☒ NO
11. Are specimens acquired primarily for the purpose of research, the results of which are to be reported in scientific publications?  
☒ YES ☐ NO
12. Are specimens prepared and the collections arranged in a manner that ensures their availability?  
☒ YES ☐ NO
13. Are data on specimen labels, permanent catalogues, and other records as accurate as possible?  
☒ YES ☐ NO
14. To the best of your knowledge, were the specimens in your collection acquired legally under the relevant laws of the country where they were obtained and the United States (e.g., import permits, collection permits, take permits, land owner permission)?  
☒ YES ☐ NO
15. Are all specimens of species included in Appendix I of CITES permanently and centrally housed under direct control of the scientific institution as indicated in CITES Resolution Conference 11.15 ([www.cites.org](http://www.cites.org))?  
☐ YES ☒ NO
16. Are Appendix I specimens intended for exchange managed in such a manner to preclude their use solely as decorations or trophies, or for other purposes incompatible with the principles of CITES?  
☐ YES ☒ NO
17. All international shipment(s) must be through a designated port. A list of designated ports (where an inspector is posted) is available from <http://www.fws.gov/le/designated-ports.html>. If you wish to use a port not listed, please contact the Office of Law Enforcement for a Designated Port Exemption Permit (form 3-200-2).
18. Name and address where you wish permit mailed, if different from page 1 (All permits will be mailed via the U.S. Postal Service, unless you identify an alternative means below):
19. If you wish the permit to be delivered by means other than USPS regular mail, provide an air bill, pre-paid envelope, or billing information. If you do not have a pre-paid envelope or air bill and wish to pay for a courier service with your credit card, please check the box below. Please DO NOT include credit card number or other information; you will be contacted for this information.

☒ If a certificate is issued, please send it via a courier service to the address on page 1 or question 19. I understand that you will contact me for my credit card information once the application has been processed.



20. Who should we contact if we have questions about the application? (Include name, phone number, and email):

Olivier Fedrigo, [REDACTED], ofedrigo@rockefeller.edu  
Jacquelyn Mountcastle, [REDACTED], jmountcast@rockefeller.edu

21. **Disqualification Factor.** A conviction, or entry of a plea of guilty or nolo contendere, for a felony violation of the Lacey Act, the Migratory Bird Treaty Act, or the Bald and Golden Eagle Protection Act disqualifies any such person from receiving or exercising the privileges of a permit, unless such disqualification has been expressly waived by the Service Director in response to a written petition. (50 CFR 13.21(c)) Have you or any of the owners of the business, if applying as a business, been convicted, or entered a plea of guilty or nolo contendere, forfeited collateral, or are currently under charges for any violations of the laws mentioned above?

     Yes    ☒ No    If you answered "Yes" provide: a) the individual's name, b) date of charge, c) charge(s),  
d) location of incident, e) court, and f) action taken for each violation.

THIS CHECK INCLUDES VARIOUS SECURITY FEATURES INCLUDING COLORED BACKGROUND & PRINTED WATER



THE ROCKEFELLER UNIVERSITY  
1230 YORK AVENUE  
NEW YORK, NY 10065-6399

JP Morgan Chase Bank, N.A.  
Syracuse, NY 13208

50-837  
213

No

Date	Number	Amount
Jun 7, 2017	399290	100.00

PAY

One Hundred Dollars And Zero Cents\*\*\*\*\*

VOID AFTER 90 DAYS

To the Order of:

U.S. FISH AND WILDLIFE SERVICE  
P.O. BOX 779  
HADLEY, MA 01035-0779  
United States

James Happle





Dziwulski, Kara &lt;kara\_dziwulski@fws.gov&gt;

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**CITES COSE PRT# 39804C**

1 message

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**Dziwulski, Kara** <kara\_dziwulski@fws.gov>  
To: ofedrigo@rockefeller.edu

Mon, Jul 10, 2017 at 3:39 PM

Mr. Fedrigo,

My name is Kara and I am a biologist with the USFWS Management Authority. I received your application for a Certificate of Scientific Exchange (COSE) but noticed you applied on behalf of yourself not on behalf of The Rockefeller University (a business).

Because we do not issue COSE's to individuals we will need you to re-complete the first page of the application as a business and send a copy back to me. The principal officer has to be someone tied to the university that has the authority to sign government documents on the university's behalf (perhaps a department head). If this is not you, please feel free to list yourself as the primary contact name for the application.

Once I get this corrected information from you I can continue with the issuance of your permit.

Thanks,

Kara

***If we do not receive the information requested above within 45 days from the date of this email, your incomplete application will be placed in our inactive files and we will not complete your request for a permit.***

--

Kara Dziwulski  
Permits Biologist  
Division of Management Authority  
U.S. Fish and Wildlife Service  
Office of International Affairs  
5275 Leesburg Pike, MS:IA  
Falls Church, VA 22041-3803  
703-358-1797



Department of the Interior  
U.S. Fish and Wildlife Service

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**Type of Activity:**  
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☒ New Application  
Requesting Re-issuance/Amendment of Permit# \_\_\_\_\_

Complete Sections A or B, and C, D, and E of this application. U.S. address may be required in Section C, see instructions for details.  
See attached instruction pages for information on how to make your application complete and help avoid unnecessary delays.

A. Complete if applying as an individual			
1.a. Last name	1.b. First name	1.c. Middle name or initial	1.d. Suffix
2. Date of birth (mm/dd/yyyy)	3. Social Security No.	4. Occupation	5. Affiliation/ Doing business as (see instructions)
6.a. Telephone number	6.b. Alternate telephone number	6.c. Fax number	6.d. E-mail address

B. Complete if applying on behalf of a business, corporation, public agency, Tribe or institution			
1.a. Name of business, agency, Tribe, or institution <b>The Rockefeller University</b>		1.b. Doing business as (dba) <b>N/A</b>	
2. Tax identification no. <b>119464</b>		3. Description of business, agency, Tribe, or institution <b>University</b>	
4.a. Principal officer Last name <b>Jarvis</b>	4.b. Principal officer First name <b>Erich</b>	4.c. Principal officer Middle name/ initial [REDACTED]	4.d. Suffix
5. Principal officer title <b>Professor, head of laboratory</b>		6. Primary contact name <b>olivier Fedrigo</b>	
7.a. Business telephone number <b>212-327-8806</b>	7.b. Alternate telephone number [REDACTED]	7.c. Business fax number <b>212-327-8106</b>	7.d. Business e-mail address <b>ejarvis@Rockefeller.edu</b>

C. All applicants complete address information					
1.a. Physical address (Street address; Apartment #, Suite #, or Room #, no P.O. Boxes) <b>The Rockefeller University, 1230 York Avenue</b>					
1.b. City <b>NEW YORK</b>	1.c. State <b>NY</b>	1.d. Zip code/Postal code: <b>10065</b>	1.e. County/Province <b>NEW YORK</b>	1.f. Country <b>USA</b>	
2.a. Mailing Address (include if different than physical address; include name of contact person if applicable) <b>The Rockefeller University, 1230 York Avenue, Box 366</b>					
2.b. City <b>NEW YORK</b>	2.c. State <b>NY</b>	2.d. Zip code/Postal code: <b>10065</b>	2.e. County/Province <b>NEW YORK</b>	2.f. Country <b>USA</b>	

D. All applicants MUST complete	
1. Attach check or money order payable to the U.S. FISH AND WILDLIFE SERVICE in the amount of \$100, nonrefundable processing fee. Federal, Tribal, State, and local government agencies, and those acting on behalf of such agencies, are exempt from the processing fee – attach documentation of fee exempt status as outlined in instructions. (50 CFR 13.11(d))	
2. Do you currently have or have you ever had any Federal Fish and Wildlife permits? Yes <input type="checkbox"/> If yes, list the number of the most current permit you have held or that you are applying to renew/re-issue: _____ No <input checked="" type="checkbox"/>	
3. Certification: I hereby certify that I have read and am familiar with the regulations contained in Title 50, Part 13 of the Code of Federal Regulations and the other applicable parts in subchapter B of Chapter I of Title 50, and I certify that the information submitted in this application for a permit is complete and accurate to the best of my knowledge and understanding that any false statement herein may subject me to the criminal penalties of 18 U.S.C. 1001. <b>[Signature]</b> Signature (in blue ink) of applicant/person responsible for permit (No photocopied or stamped signatures) <b>07-12-17</b> Date of signature (mm/dd/yyyy)	



## E. CERTIFICATE OF SCIENTIFIC EXCHANGE (COSE) (CITES)

**Note 1.** A Certificate of Scientific Exchange (COSE) only authorizes the non-commercial loan, donation or exchange between scientists or scientific institutions registered by a Management Authority of their country, of preserved, dried or embedded specimens, herbarium specimens and live plant material which carries a label issued or approved by a Management Authority. The CITES web site has a list of all registered institutions at [http://www.cites.org/common/reg/e\\_si.html](http://www.cites.org/common/reg/e_si.html). If specimens are protected by other U.S. laws and/or treaties, such as the Endangered Species Act, Marine Mammal Protection Act, Migratory Bird Treaty Act, or Bald and Golden Eagle Protection Act, you are required to obtain additional authorizations prior to any export or re-import of those specimens.

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**For re-issuance, include the original certificate and the annual report (see Form 3-200-39a).** The report is a summary of all imports and exports conducted under the COSE for the past year; including information that appears on the COSE container label such as scientific name and common name, date sent, description of specimen, acquisition number, receiving institution, country, and COSE number.

**ENTER an "X" in the box that applies.**

1. Is the institution or collection an accredited scientific institution/collection? If yes, indicate the name of the accrediting organization. If additional relevant information about the institution is available on the web, please provide the URL address. If no, provide additional information related to the institution's standards for record-keeping for and accessibility to the collection.  
☒ YES      ☐ NO
  
2. Are the collections and associated data permanently housed and professionally curated? If yes, how long have the collections been permanently housed and professionally curated. Provide the physical address for the collection and the name and contact information for the curator.  
☒ YES      ☐ NO
  
3. Are all accessions properly recorded in a permanent catalogue?  
☒ YES      ☐ NO

4. As appropriate, ENTER approximate number of accessioned specimens:
- |  |   |
|--|---|
| <input type="text"/> Mammals             | <input checked="" type="checkbox"/> Birds   |
| <input type="text"/> Insects/Arachnids   | <input type="text"/> Other Invertebrates    |
| <input type="text"/> Reptiles/Amphibians | <input type="text"/> Vascular Plants        |
| <input type="text"/> Fish                | <input type="text"/> Other (specify: _____) |

5. Do you maintain any specimens protected under the Marine Mammal Protection Act?

YES ☒ NO

- a. If "yes," do you intend to import or export these specimens? \_\_\_\_\_
- b. If "yes", provide a copy of your MMPA authorization for this activity.

6. Do you maintain or intend to obtain any specimens protected under the Endangered Species Act?

☒ YES  NO

- a. If "yes", do you intend to import or export these specimens? \_\_\_\_\_
- b. If "yes", provide a copy of your ESA authorization for this activity.

7. Do you maintain or intend to obtain any specimens protected under the Migratory Bird Treaty Act?

☒ YES  NO

- a. If "yes", do you intend to import or export these specimens? \_\_\_\_\_
- b. If "yes", provide a copy of your MBTA authorization for this activity.

8. Do you maintain any specimens protected under the Bald and Golden Eagle Protection Act?

☒ YES  NO

- a. If "yes", do you intend to import or export these specimens? \_\_\_\_\_
- b. If "yes", provide a copy of your MBTA authorization for this activity.

9. Are specimens accessible to qualified users from outside your institution?

YES ☒ NO

ENTER approximate number:	In the United States	Outside the United States
Loans last year:	_____	_____
Exchanges last year:	_____	_____
Donations last year:	_____	_____



10. Are permanent records maintained on specimens that are loaned or transferred?  
☐ YES ☒ NO
11. Are specimens acquired primarily for the purpose of research, the results of which are to be reported in scientific publications?  
☒ YES ☐ NO
12. Are specimens prepared and the collections arranged in a manner that ensures their availability?  
☒ YES ☐ NO
13. Are data on specimen labels, permanent catalogues, and other records as accurate as possible?  
☒ YES ☐ NO
14. To the best of your knowledge, were the specimens in your collection acquired legally under the relevant laws of the country where they were obtained and the United States (e.g., import permits, collection permits, take permits, land owner permission)?  
☒ YES ☐ NO
15. Are all specimens of species included in Appendix I of CITES permanently and centrally housed under direct control of the scientific institution as indicated in CITES Resolution Conference 11.15 ([www.cites.org](http://www.cites.org))?  
☐ YES ☒ NO
16. Are Appendix I specimens intended for exchange managed in such a manner to preclude their use solely as decorations or trophies, or for other purposes incompatible with the principles of CITES?  
☐ YES ☒ NO
17. All international shipment(s) must be through a designated port. A list of designated ports (where an inspector is posted) is available from <http://www.fws.gov/le/designated-ports.html>. If you wish to use a port not listed, please contact the Office of Law Enforcement for a Designated Port Exemption Permit (form 3-200-2).
18. Name and address where you wish permit mailed, **if** different from page 1 (All permits will be mailed via the U.S. Postal Service, unless you identify an alternative means below):
19. If you wish the permit to be delivered by means other than USPS regular mail, provide an air bill, pre-paid envelope, or billing information. If you do not have a pre-paid envelope or air bill and wish to pay for a courier service with your credit card, please check the box below. Please **DO NOT** include credit card number or other information; you will be contacted for this information.

☒ If a certificate is issued, please send it via a courier service to the address on page 1 or question 19. I understand that you will contact me for my credit card information once the application has been processed.



20. Who should we contact if we have questions about the application? (Include name, phone number, and email):  
Olivier Fedrigo, [REDACTED] ofedrigo@rockefeller.edu  
Jacquelyn Mountcastle, [REDACTED] jmountcast@rockefeller.edu

21. **Disqualification Factor.** A conviction, or entry of a plea of guilty or nolo contendere, for a felony violation of the Lacey Act, the Migratory Bird Treaty Act, or the Bald and Golden Eagle Protection Act disqualifies any such person from receiving or exercising the privileges of a permit, unless such disqualification has been expressly waived by the Service Director in response to a written petition. (50 CFR 13.21(c)) Have you or any of the owners of the business, if applying as a business, been convicted, or entered a plea of guilty or nolo contendere, forfeited collateral, or are currently under charges for any violations of the laws mentioned above?

☐ Yes ☒ No If you answered "Yes" provide: a) the individual's name, b) date of charge, c) charge(s), d) location of incident, e) court, and f) action taken for each violation.



Dziwulski, Kara &lt;kara\_dziwulski@fws.gov&gt;

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**CITES COSE PRT# 39804C**

8 messages

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**Dziwulski, Kara** <kara\_dziwulski@fws.gov>  
To: ofedrigo@rockefeller.edu

Mon, Jul 10, 2017 at 3:39 PM

Mr. Fedrigo,

My name is Kara and I am a biologist with the USFWS Management Authority. I received your application for a Certificate of Scientific Exchange (COSE) but noticed you applied on behalf of yourself not on behalf of The Rockefeller University (a business).

Because we do not issue COSE's to individuals we will need you to re-complete the first page of the application as a business and send a copy back to me. The principal officer has to be someone tied to the university that has the authority to sign government documents on the university's behalf (perhaps a department head). If this is not you, please feel free to list yourself as the primary contact name for the application.

Once I get this corrected information from you I can continue with the issuance of your permit.

Thanks,

Kara

***If we do not receive the information requested above within 45 days from the date of this email, your incomplete application will be placed in our inactive files and we will not complete your request for a permit.***

--

Kara Dziwulski  
Permits Biologist  
Division of Management Authority  
U.S. Fish and Wildlife Service  
Office of International Affairs  
5275 Leesburg Pike, MS:IA  
Falls Church, VA 22041-3803  
703-358-1797

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**Olivier Fedrigo** <ofedrigo@mail.rockefeller.edu>

Mon, Jul 10, 2017 at 4:37 PM

To: "Dziwulski, Kara" &lt;kara\_dziwulski@fws.gov&gt;

Cc: Jacquelyn Mountcastle &lt;jmountcast@mail.rockefeller.edu&gt;, Gaitree McNab &lt;gmcnab@mail.rockefeller.edu&gt;, Amy Wilkerson &lt;wilkeram@mail.rockefeller.edu&gt;

Good afternoon Kara,

Thank you very much for the updates.

I have cc'ed to this email Ms. Gaitree McNab (Biosafety officer) and Ms. Amy Wilkerson (Associate Vice President for Research Support) from Rockefeller University. They may have insight on how to move forward with the application.

We will get back to you shortly.

Thanks again.

Olivier

Olivier Fedrigo, Ph.D.  
Director, Vertebrate Genome Laboratory  
The Rockefeller University  
1230 York Avenue  
New York, NY 10065

Tel: (212) 327-8216 | Fax: (212) 327-8276  
Email: [ofedrigo@rockefeller.edu](mailto:ofedrigo@rockefeller.edu)  
Twitter: @ofedrigo  
Meeting scheduling: <https://vertebrategenomelaboratory.youcanbook.me>  
[Quoted text hidden]

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**Gaitree McNab** <[gmcnab@mail.rockefeller.edu](mailto:gmcnab@mail.rockefeller.edu)>

Mon, Jul 10, 2017 at 8:23 PM

To: Olivier Fedrigo <[ofedrigo@mail.rockefeller.edu](mailto:ofedrigo@mail.rockefeller.edu)>

Cc: "Dziwulski, Kara" <[kara\\_dziwulski@fws.gov](mailto:kara_dziwulski@fws.gov)>, Jacquelyn Mountcastle <[jmountcast@mail.rockefeller.edu](mailto:jmountcast@mail.rockefeller.edu)>, Amy Wilkerson <[wilkera@mail.rockefeller.edu](mailto:wilkera@mail.rockefeller.edu)>

Dear Olivier,

What I meant when I said you will need to apply to CITES as an individual for the permit was that you will be the holder of the permit as an employee of The University. The University cannot be issued a broad permit by CITES but to an individual doing specific experiments. It is similar to The USDA permitting process where you will be the holder of a permit because you are conducting experiments with the bird samples you will be permitted by the USDA to receive here at The University.

Thank you.

Gaitree

Sent from my iPad

[Quoted text hidden]

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**Dziwulski, Kara** <[kara\\_dziwulski@fws.gov](mailto:kara_dziwulski@fws.gov)>

Tue, Jul 11, 2017 at 8:33 AM

To: "Barry, Anna" <[anna\\_barry@fws.gov](mailto:anna_barry@fws.gov)>

Hey Anna,

Can you provide me some guidance on this? Are we technically able to supply a COSE to an individual since it is stated that way in the application?

Thanks,

Kara

[Quoted text hidden]

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**Gaitree McNab** <[gmcnab@mail.rockefeller.edu](mailto:gmcnab@mail.rockefeller.edu)>

Wed, Jul 12, 2017 at 8:53 AM

To: "Dziwulski, Kara" <[kara\\_dziwulski@fws.gov](mailto:kara_dziwulski@fws.gov)>

Cc: Jacquelyn Mountcastle <[jmountcast@mail.rockefeller.edu](mailto:jmountcast@mail.rockefeller.edu)>, Olivier Fedrigo <[ofedrigo@mail.rockefeller.edu](mailto:ofedrigo@mail.rockefeller.edu)>

Dear Ms. Dziwulski,

I'm following up on the voice mail I left you yesterday asking for help to fill out the application. I'm assisting Dr. Olivier Fedrigo in applying for the permit as an employee of the Rockefeller University, as you suggested below but still have some questions.

I think it will be best if we review the application over the phone instead of back and forth emails. Please give me a call at your earliest convenience.

Thank you.

Sincerely,

*Gaitree McNab*

*Biosafety Officer*

*Laboratory Safety & Environmental Health*

*The Rockefeller University*

*1230 York Avenue*

*New York, NY 10065*



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**From:** Olivier Fedrigo  
**Sent:** Monday, July 10, 2017 4:38 PM  
**To:** Dziwulski, Kara  
**Cc:** Jacquelyn Mountcastle; Gaitree McNab; Amy Wilkerson  
**Subject:** Re: CITES COSE PRT# 39804C

Good afternoon Kara,

[Quoted text hidden]

---

**Olivier Fedrigo** <ofedrigo@mail.rockefeller.edu> Wed, Jul 12, 2017 at 3:14 PM  
To: "Dziwulski, Kara" <kara\_dziwulski@fws.gov>  
Cc: Gaitree McNab <gmcnab@mail.rockefeller.edu>, Jacquelyn Mountcastle <jmountcast@mail.rockefeller.edu>, Erich Jarvis <ejarvis@mail.rockefeller.edu>

Good morning Kara,

Thank you for working details with Gaitree.

Here attached is the updated application.

Please met know if you have any questions.

What would be the ETA to get this approved?

Thank you very much,

Olivier

---

**2 attachments**



**COSE\_application2.pdf**  
1843K



**ATT00001.htm**  
8K

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**Olivier Fedrigo** <ofedrigo@mail.rockefeller.edu> Mon, Jul 17, 2017 at 10:24 AM  
To: "Dziwulski, Kara" <kara\_dziwulski@fws.gov>  
Cc: Gaitree McNab <gmcnab@mail.rockefeller.edu>, Jacquelyn Mountcastle <jmountcast@mail.rockefeller.edu>, Erich Jarvis <ejarvis@mail.rockefeller.edu>

Good morning Kara,

I am just checking that you have received the amended application.  
Let me know.

Thank you very much,

Olivier

Olivier Fedrigo, Ph.D.  
Director, Vertebrate Genome Laboratory  
The Rockefeller University  
1230 York Avenue  
New York, NY 10065

Tel: (212) 327-8216 | Fax: (212) 327-8276  
Email: [ofedrigo@rockefeller.edu](mailto:ofedrigo@rockefeller.edu)  
Twitter: [@ofedrigo](https://twitter.com/ofedrigo)  
Meeting scheduling: <https://vertebrategenomelaboratory.youcanbook.me>

[Quoted text hidden]

[Quoted text hidden]

<COSE\_application2.pdf>

Olivier Fedrigo, Ph.D.  
Director, Vertebrate Genome Laboratory  
The Rockefeller University  
1230 York Avenue  
New York, NY 10065

Tel: (212) 327-8216 | Fax: (212) 327-8276  
Email: [ofedrigo@rockefeller.edu](mailto:ofedrigo@rockefeller.edu)  
Twitter: [@ofedrigo](https://twitter.com/ofedrigo)  
Meeting scheduling: <https://vertebrategenomelaboratory.youcanbook.me>

On Jul 10, 2017, at 3:39 PM, Dziwulski, Kara <[kara\\_dziwulski@fws.gov](mailto:kara_dziwulski@fws.gov)> wrote:

[Quoted text hidden]

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**Dziwulski, Kara** <[kara\\_dziwulski@fws.gov](mailto:kara_dziwulski@fws.gov)>

Mon, Jul 17, 2017 at 10:28 AM

To: Olivier Fedrigo <[ofedrigo@mail.rockefeller.edu](mailto:ofedrigo@mail.rockefeller.edu)>

Cc: Gaitree McNab <[gmcnab@mail.rockefeller.edu](mailto:gmcnab@mail.rockefeller.edu)>, Jacquelyn Mountcastle <[jmountcast@mail.rockefeller.edu](mailto:jmountcast@mail.rockefeller.edu)>, Erich Jarvis <[ejarvis@mail.rockefeller.edu](mailto:ejarvis@mail.rockefeller.edu)>

I did receive it!

Thanks,

Kara

[Quoted text hidden]





Department of the Interior  
U.S. Fish and Wildlife Service

OMB No. 1018-0093  
Expires 05/31/2017

**Federal Fish and Wildlife Permit Application Form**

**Return to:** U.S. Fish and Wildlife Service  
Division of Management Authority (DMA)  
Branch of Permits, MS: IA  
5275 Leesburg Pike  
Falls Church, VA 22041-3803  
1-800-358-2104 or 703-358-2104

**Type of Activity:**

**CERTIFICATE OF SCIENTIFIC EXCHANGE - COSE (CITES)**

☒ **New Application**

**Requesting Re-issuance/Amendment of Permit#** \_\_\_\_\_

RCVD JUN 09 2017

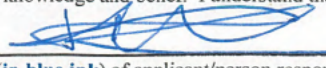
LB

Complete Sections A or B, and C, D, and E of this application. U.S. address may be required in Section C, see instructions for details.  
See attached instruction pages for information on how to make your application complete and help avoid unnecessary delays.

<b>A. Complete if applying as an individual</b>			
1.a. Last name Fedrigo	1.b. First name Olivier	1.c. Middle name or initial [REDACTED]	1.d. Suffix
2. Date of birth (mm/dd/yyyy) [REDACTED]	3. Social Security No. [REDACTED]	4. Occupation Director, Vert. Gen. Lab	5. Affiliation/ Doing business as (see instructions) The Rockefeller University
6.a. Telephone number [REDACTED]	6.b. Alternate telephone number [REDACTED]	6.c. Fax number [REDACTED]	6.d. E-mail address ofedrigo@rockefeller.edu

<b>B. Complete if applying on behalf of a business, corporation, public agency, Tribe or institution</b>			
1.a. Name of business, agency, Tribe, or institution		1.b. Doing business as (dba)	
2. Tax identification no.		3. Description of business, agency, Tribe, or institution	
4.a. Principal officer Last name	4.b. Principal officer First name	4.c. Principal officer Middle name/ initial	4.d. Suffix
5. Principal officer title		6. Primary contact name	
7.a. Business telephone number	7.b. Alternate telephone number	7.c. Business fax number	7.d. Business e-mail address

<b>C. All applicants complete address information</b>					
1.a. Physical address (Street address; Apartment #, Suite #, or Room #; no P.O. Boxes) The Rockefeller University, 1230 York Ave					
1.b. City New York	1.c. State NY	1.d. Zip code/Postal code: 10065	1.e. County/Province New York	1.f. Country USA	
2.a. Mailing Address (include if different than physical address; include name of contact person if applicable) The Rockefeller University, 1230 York Ave, Box 366					
2.b. City New York	2.c. State NY	2.d. Zip code/Postal code: 10065	2.e. County/Province New York	2.f. Country USA	

<b>D. All applicants MUST complete</b>	
1.	Attach check or money order payable to the U.S. FISH AND WILDLIFE SERVICE in the amount of \$100, nonrefundable processing fee. Federal, Tribal, State, and local government agencies, and those acting on behalf of such agencies, are exempt from the processing fee – <i>attach documentation of fee exempt status as outlined in instructions.</i> (50 CFR 13.11(d))
2.	Do you currently have or have you ever had any Federal Fish and Wildlife permits? Yes <input type="checkbox"/> If yes, list the number of the most current permit you have held or that you are applying to renew/re-issue: _____ No <input checked="" type="checkbox"/>
3.	Certification: I hereby certify that I have read and am familiar with the regulations contained in <i>Title 50, Part 13 of the Code of Federal Regulations</i> and the other applicable parts in subchapter B of Chapter I of Title 50, and I certify that the information submitted in this application for a permit is complete and accurate to the best of my knowledge and belief. I understand that any false statement herein may subject me to the criminal penalties of 18 U.S.C. 1001.   Signature (in blue ink) of applicant/person responsible for permit (No photocopied or stamped signatures)      0606/2017 Date of signature (mm/dd/yyyy)



## E. CERTIFICATE OF SCIENTIFIC EXCHANGE (COSE) (CITES)

**Note 1.** A Certificate of Scientific Exchange (COSE) only authorizes the non-commercial loan, donation or exchange between scientists or scientific institutions registered by a Management Authority of their country, of preserved, dried or embedded specimens, herbarium specimens and live plant material which carries a label issued or approved by a Management Authority. The CITES web site has a list of all registered institutions at [http://www.cites.org/common/reg/e\\_si.html](http://www.cites.org/common/reg/e_si.html). If specimens are protected by other U.S. laws and/or treaties, such as the Endangered Species Act, Marine Mammal Protection Act, Migratory Bird Treaty Act, or Bald and Golden Eagle Protection Act, you are required to obtain additional authorizations prior to any export or re-import of those specimens.

**Note 2.** A COSE cannot be used with specimens collected by field researchers unless such specimens are first accessioned into the collection of a registered facility in the state of origin. For the import or export of specimens that are not part of your museum collection, have not yet been collected, or accessioned into your collect, you will probably need to submit form 3-200-37. If you have questions, please contact the Division of Management Authority at the telephone number on page one.

**For re-issuance, include the original certificate and the annual report (see Form 3-200-39a).** The report is a summary of all imports and exports conducted under the COSE for the past year; including information that appears on the COSE container label such as scientific name and common name, date sent, description of specimen, acquisition number, receiving institution, country, and COSE number.

**ENTER an "X" in the box that applies.**

1. Is the institution or collection an accredited scientific institution/collection? If yes, indicate the name of the accrediting organization. If additional relevant information about the institution is available on the web, please provide the URL address. If no, provide additional information related to the institution's standards for record-keeping for and accessibility to the collection.  
☒ YES      ☐ NO
  
2. Are the collections and associated data permanently housed and professionally curated? If yes, how long have the collections been permanently housed and professionally curated. Provide the physical address for the collection and the name and contact information for the curator.  
☒ YES      ☐ NO
  
3. Are all accessions properly recorded in a permanent catalogue?  
☒ YES      ☐ NO



4. As appropriate, ENTER approximate number of accessioned specimens:

<input type="checkbox"/> Mammals	<input checked="" type="checkbox"/> Birds (2922 specimens)
<input type="checkbox"/> Insects/Arachnids	<input type="checkbox"/> Other Invertebrates
<input type="checkbox"/> Reptiles/Amphibians	<input type="checkbox"/> Vascular Plants
<input type="checkbox"/> Fish	<input type="checkbox"/> Other (specify: _____)

5. Do you maintain any specimens protected under the Marine Mammal Protection Act?

☐ YES ☒ NO

a. If "yes," do you intend to import or export these specimens? \_\_\_\_\_

b. If "yes", provide a copy of your MMPA authorization for this activity.

6. Do you maintain or intend to obtain any specimens protected under the Endangered Species Act?

☒ YES ☐ NO

a. If "yes", do you intend to import or export these specimens? import, ESA in progress

b. If "yes", provide a copy of your ESA authorization for this activity.

7. Do you maintain or intend to obtain any specimens protected under the Migratory Bird Treaty Act?

☒ YES ☐ NO

a. If "yes", do you intend to import or export these specimens? import, MBTA in progress

b. If "yes", provide a copy of your MBTA authorization for this activity.

8. Do you maintain any specimens protected under the Bald and Golden Eagle Protection Act?

☒ YES ☐ NO

a. If "yes", do you intend to import or export these specimens? import, MBTA in progress

b. If "yes", provide a copy of your MBTA authorization for this activity.

9. Are specimens accessible to qualified users from outside your institution?

☐ YES ☒ NO

ENTER approximate number:	In the United States	Outside the United States
Loans last year:	_____	_____
Exchanges last year:	_____	_____
Donations last year:	_____	_____

10. Are permanent records maintained on specimens that are loaned or transferred?  
☐ YES ☒ NO
11. Are specimens acquired primarily for the purpose of research, the results of which are to be reported in scientific publications?  
☒ YES ☐ NO
12. Are specimens prepared and the collections arranged in a manner that ensures their availability?  
☒ YES ☐ NO
13. Are data on specimen labels, permanent catalogues, and other records as accurate as possible?  
☒ YES ☐ NO
14. To the best of your knowledge, were the specimens in your collection acquired legally under the relevant laws of the country where they were obtained and the United States (e.g., import permits, collection permits, take permits, land owner permission)?  
☒ YES ☐ NO
15. Are all specimens of species included in Appendix I of CITES permanently and centrally housed under direct control of the scientific institution as indicated in CITES Resolution Conference 11.15 ([www.cites.org](http://www.cites.org))?  
☐ YES ☒ NO
16. Are Appendix I specimens intended for exchange managed in such a manner to preclude their use solely as decorations or trophies, or for other purposes incompatible with the principles of CITES?  
☐ YES ☒ NO
17. All international shipment(s) must be through a designated port. A list of designated ports (where an inspector is posted) is available from <http://www.fws.gov/le/designated-ports.html>. If you wish to use a port not listed, please contact the Office of Law Enforcement for a Designated Port Exemption Permit (form 3-200-2).
18. Name and address where you wish permit mailed, **if** different from page 1 (All permits will be mailed via the U.S. Postal Service, unless you identify an alternative means below):
19. If you wish the permit to be delivered by means other than USPS regular mail, provide an air bill, pre-paid envelope, or billing information. If you do not have a pre-paid envelope or air bill and wish to pay for a courier service with your credit card, please check the box below. Please **DO NOT** include credit card number or other information; you will be contacted for this information.

☒ If a certificate is issued, please send it via a courier service to the address on page 1 or question 19. I understand that you will contact me for my credit card information once the application has been processed.



20. Who should we contact if we have questions about the application? (Include name, phone number, and email):

Olivier Fedrigo [REDACTED] ofedrigo@rockefeller.edu

Jacquelyn Mountcastle, [REDACTED] jmountcast@rockefeller.edu

21. **Disqualification Factor.** A conviction, or entry of a plea of guilty or nolo contendere, for a felony violation of the Lacey Act, the Migratory Bird Treaty Act, or the Bald and Golden Eagle Protection Act disqualifies any such person from receiving or exercising the privileges of a permit, unless such disqualification has been expressly waived by the Service Director in response to a written petition. (50 CFR 13.21(c)) Have you or any of the owners of the business, if applying as a business, been convicted, or entered a plea of guilty or nolo contendere, forfeited collateral, or are currently under charges for any violations of the laws mentioned above?

☐ Yes ☒ No If you answered "Yes" provide: a) the individual's name, b) date of charge, c) charge(s), d) location of incident, e) court, and f) action taken for each violation.

THIS CHECK INCLUDES VARIOUS SECURITY FEATURES INCLUDING COLORED BACKGROUND & PRINTED WATERMARK



THE ROCKEFELLER UNIVERSITY  
1230 YORK AVENUE  
NEW YORK, NY • 10065-6399

JP Morgan Chase Bank, N.A.

50-937  
213

No. [REDACTED]

Syracuse, NY 13206

Date	Number	Amount
Jun 7, 2017	399290	100.00

VOID AFTER 90 DAYS

PAY

One Hundred Dollars And Zero Cents\*\*\*\*\*

To the Order of:

U.S. FISH AND WILDLIFE SERVICE  
P.O. BOX 779  
HADLEY, MA 01035-0779  
United States

*James H. Apple*





Department of the Interior  
U.S. Fish and Wildlife Service

OMB No. 1018-0093  
Expires 05/31/2017

**Federal Fish and Wildlife Permit Application Form**

Return to: U.S. Fish and Wildlife Service  
Division of Management Authority (DMA)  
Branch of Permits, MS: IA  
5275 Leesburg Pike  
Falls Church, VA 22041-3803  
1-800-358-2104 or 703-358-2104

Type of Activity:  
**CERTIFICATE OF SCIENTIFIC EXCHANGE - COSE (CITES)**  
☒ New Application  
Requesting Re-issuance/Amendment of Permit# \_\_\_\_\_

Complete Sections A or B, and C, D, and E of this application. U.S. address may be required in Section C, see instructions for details.  
See attached instruction pages for information on how to make your application complete and help avoid unnecessary delays.

A. Complete if applying as an individual			
1.a. Last name	1.b. First name	1.c. Middle name or initial	1.d. Suffix
2. Date of birth (mm/dd/yyyy)	3. Social Security No.	4. Occupation	5. Affiliation/ Doing business as (see instructions)
6.a. Telephone number	6.b. Alternate telephone number	6.c. Fax number	6.d. E-mail address

B. Complete if applying on behalf of a business, corporation, public agency, Tribe or institution			
1.a. Name of business, agency, Tribe, or institution <b>The Rockefeller University</b>		1.b. Doing business as (dba) <b>N/A</b>	
2. Tax identification no. <b>119464</b>		3. Description of business, agency, Tribe, or institution <b>University</b>	
4.a. Principal officer Last name <b>Jarvis</b>	4.b. Principal officer First name <b>Erich</b>	4.c. Principal officer Middle name/ initial <b>[REDACTED]</b>	4.d. Suffix
5. Principal officer title <b>Professor, head of Laboratory</b>		6. Primary contact name <b>olivier Fedrigo</b>	
7.a. Business telephone number <b>212-327-8806</b>	7.b. Alternate telephone number <b>[REDACTED]</b>	7.c. Business fax number <b>212-327-8106</b>	7.d. Business e-mail address <b>ejarvis@Rockefeller.edu</b>

C. All applicants complete address information					
1.a. Physical address (Street address, Apartment #, Suite #, or Room #; no P.O. Boxes) <b>The Rockefeller University, 1230 York Avenue</b>					
1.b. City <b>NEW YORK</b>	1.c. State <b>NY</b>	1.d. Zip code/Postal code: <b>10065</b>	1.e. County/Province <b>NEW YORK</b>	1.f. Country <b>USA</b>	
2.a. Mailing Address (include if different than physical address; include name of contact person if applicable) <b>The Rockefeller University, 1230 York Avenue, Box 366</b>					
2.b. City <b>NEW YORK</b>	2.c. State <b>NY</b>	2.d. Zip code/Postal code: <b>10065</b>	2.e. County/Province <b>NEW YORK</b>	2.f. Country <b>USA</b>	

D. All applicants MUST complete	
1. Attach check or money order payable to the U.S. FISH AND WILDLIFE SERVICE in the amount of \$100, nonrefundable processing fee. Federal, Tribal, State, and local government agencies, and those acting on behalf of such agencies, are exempt from the processing fee – attach documentation of fee exempt status as outlined in instructions. (50 CFR 13.11(d))	
2. Do you currently have or have you ever had any Federal Fish and Wildlife permits? Yes <input type="checkbox"/> If yes, list the number of the most current permit you have held or that you are applying to renew/re-issue: _____ No <input checked="" type="checkbox"/>	
3. Certification: I hereby certify that I have read and am familiar with the regulations contained in Title 50, Part 13 of the Code of Federal Regulations and the other applicable parts in subchapter B of Chapter I of Title 50, and I certify that the information submitted in this application for a permit is complete and accurate to the best of my knowledge and understanding that any false statement herein may subject me to the criminal penalties of 18 U.S.C. 1001. <b>[Signature]</b> Signature (in blue ink) of applicant/person responsible for permit (No photocopied or stamped signatures) <b>07-12-17</b> Date of signature (mm/dd/yyyy)	



## E. CERTIFICATE OF SCIENTIFIC EXCHANGE (COSE) (CITES)

**Note 1.** A Certificate of Scientific Exchange (COSE) only authorizes the non-commercial loan, donation or exchange between scientists or scientific institutions registered by a Management Authority of their country, of preserved, dried or embedded specimens, herbarium specimens and live plant material which carries a label issued or approved by a Management Authority. The CITES web site has a list of all registered institutions at [http://www.cites.org/common/reg/e\\_si.html](http://www.cites.org/common/reg/e_si.html). If specimens are protected by other U.S. laws and/or treaties, such as the Endangered Species Act, Marine Mammal Protection Act, Migratory Bird Treaty Act, or Bald and Golden Eagle Protection Act, you are required to obtain additional authorizations prior to any export or re-import of those specimens.

**Note 2.** A COSE cannot be used with specimens collected by field researchers unless such specimens are first accessioned into the collection of a registered facility in the state of origin. For the import or export of specimens that are not part of your museum collection, have not yet been collected, or accessioned into your collect, you will probably need to submit form 3-200-37. If you have questions, please contact the Division of Management Authority at the telephone number on page one.

**For re-issuance, include the original certificate and the annual report (see Form 3-200-39a).** The report is a summary of all imports and exports conducted under the COSE for the past year; including information that appears on the COSE container label such as scientific name and common name, date sent, description of specimen, acquisition number, receiving institution, country, and COSE number.

**ENTER an "X" in the box that applies.**

1. Is the institution or collection an accredited scientific institution/collection? If yes, indicate the name of the accrediting organization. If additional relevant information about the institution is available on the web, please provide the URL address. If no, provide additional information related to the institution's standards for record-keeping for and accessibility to the collection.

☒ YES ☐ NO

2. Are the collections and associated data permanently housed and professionally curated? If yes, how long have the collections been permanently housed and professionally curated. Provide the physical address for the collection and the name and contact information for the curator.

☒ YES ☐ NO

3. Are all accessions properly recorded in a permanent catalogue?

☒ YES ☐ NO

4. As appropriate, ENTER approximate number of accessioned specimens:

Mammals

✓ Birds

Insects/Arachnids

### Other Invertebrates

Reptiles/Amphibians

## Vascular Plants

Fish

\_\_\_\_\_ Other (specify: \_\_\_\_\_)

5. Do you maintain any specimens protected under the Marine Mammal Protection Act?

\_\_\_\_\_ YES      ✓ NO

a. If "yes," do you intend to import or export these specimens? \_\_\_\_\_

b. If “yes”, provide a copy of your MMPA authorization for this activity.

6. Do you maintain or intend to obtain any specimens protected under the Endangered Species Act?

✓ YES        NO

a. If "yes", do you intend to import or export these specimens? \_\_\_\_\_

b. If "yes", provide a copy of your ESA authorization for this activity.

7. Do you maintain or intend to obtain any specimens protected under the Migratory Bird Treaty Act?

☒ YES ☐ NO

a. If "yes", do you intend to import or export these specimens? \_\_\_\_\_

b. If "yes", provide a copy of your MBTA authorization for this activity.

8. Do you maintain any specimens protected under the Bald and Golden Eagle Protection Act?

✓ YES             NO

a. If "yes", do you intend to import or export these specimens? \_\_\_\_\_

b. If "yes", provide a copy of your MBTA authorization for this activity.

9. Are specimens accessible to qualified users from outside your institution?

YES ☒ NO

ENTER approximate number:

## In the United States

### Outside the United States

Loans last year:

---

Exchanges last year:

\_\_\_\_\_

---

Donations last year:

---

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10. Are permanent records maintained on specimens that are loaned or transferred?  
☐ YES ☒ NO
11. Are specimens acquired primarily for the purpose of research, the results of which are to be reported in scientific publications?  
☒ YES ☐ NO
12. Are specimens prepared and the collections arranged in a manner that ensures their availability?  
☒ YES ☐ NO
13. Are data on specimen labels, permanent catalogues, and other records as accurate as possible?  
☒ YES ☐ NO
14. To the best of your knowledge, were the specimens in your collection acquired legally under the relevant laws of the country where they were obtained and the United States (e.g., import permits, collection permits, take permits, land owner permission)?  
☒ YES ☐ NO
15. Are all specimens of species included in Appendix I of CITES permanently and centrally housed under direct control of the scientific institution as indicated in CITES Resolution Conference 11.15 ([www.cites.org](http://www.cites.org))?  
☐ YES ☒ NO
16. Are Appendix I specimens intended for exchange managed in such a manner to preclude their use solely as decorations or trophies, or for other purposes incompatible with the principles of CITES?  
☐ YES ☒ NO
17. All international shipment(s) must be through a designated port. A list of designated ports (where an inspector is posted) is available from <http://www.fws.gov/le/designated-ports.html>. If you wish to use a port not listed, please contact the Office of Law Enforcement for a Designated Port Exemption Permit (form 3-200-2).
18. Name and address where you wish permit mailed, if different from page 1 (All permits will be mailed via the U.S. Postal Service, unless you identify an alternative means below):
19. If you wish the permit to be delivered by means other than USPS regular mail, provide an air bill, pre-paid envelope, or billing information. If you do not have a pre-paid envelope or air bill and wish to pay for a courier service with your credit card, please check the box below. Please DO NOT include credit card number or other information; you will be contacted for this information.

☒ If a certificate is issued, please send it via a courier service to the address on page 1 or question 19. I understand that you will contact me for my credit card information once the application has been processed.

20. Who should we contact if we have questions about the application? (Include name, phone number, and email):

Olivier Fedrigo, [REDACTED] ofedrigo@rockefeller.edu

Jacquelyn Mountcastle, [REDACTED] jmountcast@rockefeller.edu

21. **Disqualification Factor.** A conviction, or entry of a plea of guilty or nolo contendere, for a felony violation of the Lacey Act, the Migratory Bird Treaty Act, or the Bald and Golden Eagle Protection Act disqualifies any such person from receiving or exercising the privileges of a permit, unless such disqualification has been expressly waived by the Service Director in response to a written petition. (50 CFR 13.21(c)) Have you or any of the owners of the business, if applying as a business, been convicted, or entered a plea of guilty or nolo contendere, forfeited collateral, or are currently under charges for any violations of the laws mentioned above?

☐ Yes ☒ No If you answered "Yes" provide: a) the individual's name, b) date of charge, c) charge(s), d) location of incident, e) court, and f) action taken for each violation.

CONVERSATION RECORD			
NAME: Dr. Olivier [REDACTED] Fedrigo			PRT# 43635C
TIME: afternoon	DATE: 3/28/18	PHONE No:	
SUBJECT: Questions About Permit Needed Subspecies info			
<p>Had Web Ex Conference with Dr. Fedrigo and his team about if a COSE application is appropriate for what he is looking to do.</p> <ul style="list-style-type: none"> <li>• Jackie will be helping him get his permit together</li> <li>• Goal: It is run by the genome 10,000 – Vertebrate Genome Project. Want to sequence the genomes of all 66,000 species. Collaborating with other people world wide.</li> <li>• Main project worldwide for vertebrate genomes (66,000)</li> <li>• A lot of them are endangered and threatened species.</li> <li>• Worked with CITES to get permits for Kukapo parrot in New Zeland previously</li> <li>• 8,000 endangered vertebrate species</li> <li>• Some samples are from the field and some people have other permits</li> <li>• There is apparently some other researcher, Bob Murphy, who studies turtles, that says he is CITES exempt. With University of Toronto in Canada.</li> <li>• Jason Howard with Duke University – kukapoo species</li> <li>• Primary goal of this project is to get fresh and frozen tissue both from researchers and museums. Sometimes toe pads.</li> <li>• Looking to import mostly. Sometimes they might export to the UK.</li> <li>• They are looking to also bring in Marine Mammal samples.</li> <li>• McArthur Foundation grant -100 million dollars – wanting all endangered species to be genetically sequenced (plan to submit this elsewhere)</li> <li>• Will need to have allowance for all endangered and threatened species</li> <li>• Working with The Frozen Arc – San Diego Zoo.</li> <li>• Phase I – ordinal species – 260 Species (some are endangered) <ul style="list-style-type: none"> <li>○ Want to have them done by mid- 2018. Endangered.</li> <li>○ Have a list of target species for 2018</li> </ul> </li> <li>• 2014 – genomes – in Ashboro, NC. Sequenced in China. Protection for bald eagle.</li> <li>• <b>COSE- Need to double-check about the ability to share frozen tissue or blood samples.</b></li> <li>• <b>Told them the restrictions under a COSE: (1) both institutions must have COSE, (2) only CITES listed species, (3) Must be accessioned under a COSE, can't use all specimen up, (4) No live animals, (5) not for commercial purpose</b></li> </ul>			
Signature: Kara E. Dziwulski		Date: 3/28/18	

1/19/2018

DEPARTMENT OF THE INTERIOR Mail - CITES COSE PRT# 39804C

The Rockefeller University  
1230 York Avenue  
New York, NY 10065

Tel: [REDACTED] Fax: (212) 327-8276  
Email: [ofedrigo@rockefeller.edu](mailto:ofedrigo@rockefeller.edu)  
Twitter: @ofedrigo  
Meeting scheduling: <https://vertebrategenomelaboratory.youcanbook.me>

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[Quoted text hidden]

<COSE\_application2.pdf>

Olivier Fedrigo, Ph.D.  
Director, Vertebrate Genome Laboratory  
The Rockefeller University  
1230 York Avenue  
New York, NY 10065

Tel: [REDACTED] | Fax: (212) 327-8276  
Email: [ofedrigo@rockefeller.edu](mailto:ofedrigo@rockefeller.edu)  
Twitter: @ofedrigo  
Meeting scheduling: <https://vertebrategenomelaboratory.youcanbook.me>

On Jul 10, 2017, at 3:39 PM, Dziwulski, Kara <[kara\\_dziwulski@fws.gov](mailto:kara_dziwulski@fws.gov)> wrote:

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**Dziwulski, Kara** <[kara\\_dziwulski@fws.gov](mailto:kara_dziwulski@fws.gov)>

Mon, Jul 17, 2017 at 10:28 AM

To: Olivier Fedrigo <[ofedrigo@mail.rockefeller.edu](mailto:ofedrigo@mail.rockefeller.edu)>

Cc: Gaitree McNab <[gmcnab@mail.rockefeller.edu](mailto:gmcnab@mail.rockefeller.edu)>, Jacquelyn Mountcastle <[jmountcast@mail.rockefeller.edu](mailto:jmountcast@mail.rockefeller.edu)>, Erich Jarvis <[ejarvis@mail.rockefeller.edu](mailto:ejarvis@mail.rockefeller.edu)>

I did receive it!

Thanks,

Kara

[Quoted text hidden]

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**Olivier Fedrigo** <[ofedrigo@mail.rockefeller.edu](mailto:ofedrigo@mail.rockefeller.edu)>

Mon, Aug 7, 2017 at 2:41 PM

To: "Dziwulski, Kara" <[kara\\_dziwulski@fws.gov](mailto:kara_dziwulski@fws.gov)>

Cc: Erich Jarvis <[ejarvis@mail.rockefeller.edu](mailto:ejarvis@mail.rockefeller.edu)>

Good afternoon Kara,

I was wondering if you had any questions regarding our application and what would be the potential timeline to get it approved.

Thank you,

Olivier

Olivier Fedrigo, Ph.D.  
Director, Vertebrate Genome Laboratory  
The Rockefeller University  
1230 York Avenue  
New York, NY 10065

Tel: [REDACTED] | Fax: (212) 327-8276  
Email: [ofedrigo@rockefeller.edu](mailto:ofedrigo@rockefeller.edu)  
Twitter: @ofedrigo  
Meeting scheduling: <https://vertebrategenomelaboratory.youcanbook.me>

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**Dziwulski, Kara** <[kara\\_dziwulski@fws.gov](mailto:kara_dziwulski@fws.gov)>

Mon, Aug 7, 2017 at 2:48 PM

To: Olivier Fedrigo <[ofedrigo@mail.rockefeller.edu](mailto:ofedrigo@mail.rockefeller.edu)>

Oliver,

I do not have any questions but your permit is currently down with the CITES Scientific Authority for a non-detriment finding. They have 45 days to complete this finding and it was given on July 11th.

Therefore, they have until August 25th to complete their finding. After that I can issue the permit.

If you want to check in with me again at the end of the month that would be great.

Thanks,

Kara

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**Olivier Fedrigo** <[ofedrigo@mail.rockefeller.edu](mailto:ofedrigo@mail.rockefeller.edu)>

Thu, Aug 24, 2017 at 2:09 AM

To: "Dziwulski, Kara" <[kara\\_dziwulski@fws.gov](mailto:kara_dziwulski@fws.gov)>

Cc: Erich Jarvis <[ejarvis@mail.rockefeller.edu](mailto:ejarvis@mail.rockefeller.edu)>

Good morning Kara,

I hope you had a good summer.

I was wondering if you have heard from the CITES Scientific Authority.

Thank you very much,

1/19/2018

DEPARTMENT OF THE INTERIOR Mail - CITES COSE PRT# 39804C

Olivier

[Quoted text hidden]

**Dziwulski, Kara** <kara\_dziwulski@fws.gov>  
To: Olivier Fedrigo <ofedrigo@mail.rockefeller.edu>  
Cc: Erich Jarvis <ejarvis@mail.rockefeller.edu>

Thu, Aug 24, 2017 at 3:41 PM

Oliver,

Thank you for your email, I hope you are having a good summer too.

I sent an email down to the CITES Scientific Authority today regarding the status of your finding. They are still working on it, but it is on their radar to complete soon.

Thanks for your patience,

Kara

[Quoted text hidden]

**Erich Jarvis** <ejarvis@mail.rockefeller.edu>  
To: "Dziwulski, Kara" <kara\_dziwulski@fws.gov>  
Cc: Olivier Fedrigo <ofedrigo@mail.rockefeller.edu>

Sun, Aug 27, 2017 at 3:10 PM

Dear Kara,

Thank for the update. I really appreciate it. I wanted to introduce myself further, as the principle investigator on the application.

As you might be aware from our application and your communications with Olivier, I am chair of an international consortium called the Genome 10K (G10K), whose mission it is to sequence the genomes of all 66,000 vertebrate species on the planet, and deposit the data in a Genome Ark database for scientist and the public, nationally and internationally. One of our main milestone goals is to sequence species representing all ~10,000 genera, and hence G10K. We have an international meeting next week Aug 22-25th in the Norwich, UK. <http://www.earlham.ac.uk/genome-10k-and-genome-science-conference#Day3-3>.

At the meeting on Thurs Aug 24th, Olivier and I are to report an update to the council members in a workshop presentation on our efforts to secure a blanket CITES permit. I was wondering if it were possible there would be any answer to our request this coming week, such that we could report on our ability to obtain samples of endangered species?


More importantly, here are some species that are expected to go extinct within the coming year, and we need the permits to obtain those tissue to preserve their genomes digitally before they go extinct, and possibly help prevent them from going extinct. So, any urgency you could put into our application would be greatly appreciated. We are trying to reduce barriers as much as possible to make this project possible, which will be beneficial to everyone in the planet and our environment.

We look forward to hearing from you at your earliest convenience.

Best

Erich

[Quoted text hidden]

Erich  Jarvis, Ph.D.  
Investigator, Howard Hughes Medical Institute  
Professor, The Rockefeller University, Box 54  
[1230 York Avenue, New York, New York 10065](http://www.jarvislab.net/)

<http://www.jarvislab.net/>  
<http://www.jarvislab.net/Publications.html>

**Erich Jarvis** <ejarvis@mail.rockefeller.edu>  
To: "Dziwulski, Kara" <kara\_dziwulski@fws.gov>  
Cc: Olivier Fedrigo <ofedrigo@mail.rockefeller.edu>

Sun, Aug 27, 2017 at 3:13 PM

Dear Kara,

I am correcting the dates below. Our meeting next week is Aug 29th to Sep 1st. We are presenting our update on permits this coming Thurs Aug 31st.

Best

Erich

[Quoted text hidden]

**Dziwulski, Kara** <kara\_dziwulski@fws.gov>  
To: Erich Jarvis <ejarvis@mail.rockefeller.edu>  
Cc: Olivier Fedrigo <ofedrigo@mail.rockefeller.edu>

Mon, Aug 28, 2017 at 11:26 AM

Dr. Jarvis,

I am worried you might not fully understand your authorization under a CITES COSE. The permit that you and Oliver are applying for is a CITES Certificate of Scientific Exchange. This will allow you to share CITES listed specimens between other COSE certified institutions under CITES (if an institution does not have a CITES COSE you can not exchange with them). Under a COSE you can share specimens that are part of your collection, but the specimens can not be "used up" during the exchange (aka. there needs to be remaining components of the specimen that get returned to the holding institution after being borrowed).

Keep in mind that this permit only covers you for animals that are listed ONLY under CITES. If a species is also protected under the ESA, Bald and Golden Eagle Protection Act, Migratory Bird Treaty Act, or Wild Bird Conservation Act you will need to get subsequent permits to cover you for those aspects.

Also, considering your application shows you only have bird specimens in your possession, your COSE only allows you for animal museum specimens

Therefore, should only be considered a blanket permit for specimens in your collection that are ONLY CITES listed. Also, any tissues that get shared under your COSE, can not get used up completely during the exchange.

Thanks,

Kara

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**Erich Jarvis** <ejarvis@mail.rockefeller.edu>  
To: "Dziwulski, Kara" <kara\_dziwulski@fws.gov>  
Cc: Olivier Fedrigo <ofedrigo@mail.rockefeller.edu>

Mon, Aug 28, 2017 at 11:54 AM



1/19/2018

DEPARTMENT OF THE INTERIOR Mail - CITES COSE PRT# 39804C

Dear Kara,

Thank you for the clarification. I will discuss these further with Olivier, keep a look out for any updates you have, and contact you if we have further questions. I look forward to the application being approved.

Best

Erich  
[Quoted text hidden]

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**Olivier Fedrigo** <ofedrigo@mail.rockefeller.edu>  
To: "Dziwulski, Kara" <kara\_dziwulski@fws.gov>  
Cc: Erich Jarvis <ejarvis@mail.rockefeller.edu>

Mon, Sep 11, 2017 at 12:59 PM

Good afternoon Kara,

I hope you are doing well. Do you have any news from the CITES Scientific Authority?  
Please do not hesitate to let us know if they have any questions or need more information regarding our project and the use of the samples.

Thank you very much,

Olivier

Olivier Fedrigo, Ph.D.  
Director, Vertebrate Genome Laboratory  
The Rockefeller University  
1230 York Avenue  
New York, NY 10065

Tel: (212) 327-8216 | Fax: (212) 327-8276  
Email: [ofedrigo@rockefeller.edu](mailto:ofedrigo@rockefeller.edu)  
Twitter: @ofedrigo  
Meeting scheduling: <https://vertebrategenomelaboratory.youcanbook.me>

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**Dziwulski, Kara** <kara\_dziwulski@fws.gov>  
To: Olivier Fedrigo <ofedrigo@mail.rockefeller.edu>  
Cc: Erich Jarvis <ejarvis@mail.rockefeller.edu>

Mon, Sep 18, 2017 at 2:52 PM

Olivier,

Sorry, for the delayed response back to your email. I was out of the office last week.

In my absence I received the following questions from the Scientific Authority which they would like you to answer in order to complete their non-detriment finding:

1. How/By which organization is the bird collection at The Rockefeller University accredited? Is there a URL that references the collection? Is there additional information available about record-keeping and accessibility?
2. Where is the bird collection housed and curated (physical address)? Contact information for the curator?
3. Since this is a new application, we understand that no previous exchanges have taken place. If this application is approved, how would Rockefeller University bird specimens be made accessible to qualified users from outside the university? Some institutions require the submission of a detailed written request that is subject to an internal peer review committee. Other institutions are less formal. Process at Rockefeller University?
4. Since this application would apply only to accessioned specimens loaned or transferred between institutions, we assume that these loans or transfers would be tracked and permanent records maintained. Would that not be the case at Rockefeller University?
5. CITES Resolution Conf. 11.15 (Rev. CoP12) on *Non-commercial loan, donation or exchange of museum and herbarium specimens* describes the conditions for these loans or transfers. Isn't the bird collection, including CITES Appendix I specimens, permanently and centrally housed and directly under the control of Rockefeller University? If approved, wouldn't the specimens of the bird collection covered under this application be managed in compliance with Resolution Conf. 11.15 (Rev. CoP12)?
6. In accordance with the principles of CITES, Appendix I specimens intended for exchange may not be loaned or transferred for use solely as decorations or trophies. We assume that the use of these specimens is scientific exchange. Would that not be the case at Rockefeller University?

Thanks,

Kara  
[Quoted text hidden]

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**Erich Jarvis** <ejarvis@mail.rockefeller.edu>  
To: "Dziwulski, Kara" <kara\_dziwulski@fws.gov>  
Cc: Olivier Fedrigo <ofedrigo@mail.rockefeller.edu>, Sadye Paez <spaez@mail.rockefeller.edu>, Jackie Mountcastle [REDACTED]

Tue, Sep 19, 2017 at 10:48 PM

Dear Kara,

Thank you for moving our application along.

I can see by the line of questioning that we might have not been clear enough in our application on the purpose of the permit request. I think it is going to be easier to discuss this by phone or webex meeting, including with the Scientific Authority if possible. All the questions are about birds, but we are applying for vertebrate species broadly. The questions appear to possibly pertain to curators of museum tissue collections, whereas although we have built up a tissue collection, these have come to us from museums and other sources, as our main mission is to generate high quality genome assemblies for all vertebrate species as part of the international Vertebrate Genomes Project (VGP), managed by the Genome10K consortium.

There are a number of people in our consortium that already have CITES permits, and several that are CITES exempt. What we are trying to do is to get permission to send samples of all endangered species to the Vertebrate Genome Lab at Rockefeller, which is sequencing most of the genomes for the VGP.

The form does not have an area to write such a description as far as I could, which I think might be adding to the lack of clarity on our part. What I would like to request is that we have a conference call with you and other members of our consortium that have CITES permits or are CITES exempt to figure out what the best way to go about this, and also to be able to get more clarity on the questions the Scientific Authority asked (specifically about birds).

To help further understand our mission, especially for endangered species, is the following public video we created for an application of \$100M to the MacArthur Foundation to sequence all endangered species. We did not obtain those funds, but we have since obtained other funds from other sources to now start doing some of the most critical endangered species that may go extinct within the next 5 years.

<https://www.youtube.com/watch?v=EwNR66FXwVk>

Sadye Paez in our lab can help set up the time.

Best

Erich

Kara

[Quoted text hidden]

Erich Jarvis &lt;ejarvis@mail.rockefeller.edu&gt;

To: "Dziwulski, Kara" &lt;kara\_dziwulski@fws.gov&gt;

Cc: Sadye Paez &lt;spaez@mail.rockefeller.edu&gt;, Olivier Fedrigo &lt;ofedrigo@mail.rockefeller.edu&gt;, Jackie Mountcastle &lt;[REDACTED]&gt;

Thu, Oct 5, 2017 at 12:06 PM

Hi Kara,

Checking if you are having trouble calling in?

You can call in on your computer at:

<https://hhmi.webex.com/hhmi/j.php?MTID=m6caa325177220c0d94e060342f252dc5>

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Dziwulski, Kara &lt;kara\_dziwulski@fws.gov&gt;

To: Erich Jarvis &lt;ejarvis@mail.rockefeller.edu&gt;

Cc: Sadye Paez &lt;spaez@mail.rockefeller.edu&gt;, Olivier Fedrigo &lt;ofedrigo@mail.rockefeller.edu&gt;, Jackie Mountcastle &lt;[REDACTED]&gt;

Wed, Oct 18, 2017 at 4:53 PM

Dr. Jarvis et al.,

I had a meeting with my supervisor, Mary Coligano, and the head of the Branch of Permits, Tim Van Norman, today and we discussed what the next steps for you guys regarding the type of permit you are requesting from our office.

First, since it is apparent a COSE is not sufficient for the activities you are requesting authorization for, you will need to complete a 3-200-37 form and email it to me. This will replace your application for a COSE.

<https://www.fws.gov/international/pdf/permit-application-form-3-200-37-export-import-interstate-and-foreign-commerce-take-of-animals.pdf>

In this application please make sure you include:

- A project proposal outlining the goal of the project, and what actions you are seeking authorization for.
- A species list of what species you are targeting for import over the next 5 years
- CV's of the researchers on your team and their experience as it relates to the goals of your research activities
- Describe as much as possible the following:
  - What kind of samples you will import (e.g. frozen tissue)
  - The size of the samples (e.g. 2 cm cubes of frozen tissue)
  - How many samples you expect total (e.g. importing at least 66,000 tissue samples total)
  - How many samples will be collected per species (e.g. estimate 10 tissue samples from clouded leopards)
  - If you are going to have any restrictions on how many samples you will allow to be collected per animal (e.g. ensure no more than 2 tissue samples will be taken per animal).
- How will this research benefit these species in the wild?
- Where will the samples be housed?
- Is it the researcher or the university who will have ultimate ownership of the samples? (should apply as whichever has the ownership)
- Who are your collaborators you will be receiving samples from? Will they have valid collection permits in the countries the samples are collected? What will be their experience collecting such samples?
- Will you be collecting any samples yourselves?

**\*\*Please be aware that you will need to work with other countries for CITES Export Permits. If you are working with individuals who have CITES Export Permits/CITES Import Permits please note that it does not mean they will have authorization under their permit to send samples to you directly. They will need a separate permit to do that. That being said, if the exchange of the samples occurs in the U.S. after they have been legally exported/imported to the individual, there would be no permit required from our office for such an exchange (as long as no money is exchanged, and none of the samples are of marine mammals).**

**\*\*Please be aware that you will need to work with other USFWS offices to gain authorization under the Bald and Golden Eagle Act and Migratory Bird Treaty Acts.**

***\*\*Please note that authorization for marine mammals requires you to submit an entirely separate application to our office (attached below). If you are still looking to import any samples of animals under the MMPA, please submit the application to our office so it can be processed as an entirely new application -- separate from this one.***

Our next step is to speak with the CITES Division of Scientific Authority to see if there are any additional information requirements they would like from you up-front before we schedule a conference call involving you, DMA, and DSA all together. We will be in touch soon if they have any other specific requests at the moment.


If you have any questions please feel free to give me a call: 703-358-1797.

Thanks,

Kara

***If we do not receive the information requested above within 45 days from the date of this email, your incomplete application will be placed in our inactive files and we will not complete your request for a permit.***

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 3-200-43 rev 8-25-17.doc  
239K

Erich Jarvis &lt;ejarvis@mail.rockefeller.edu&gt;

To: "Dziwulski, Kara" &lt;kara\_dziwulski@fws.gov&gt;

Cc: Sadye Paez &lt;spaez@mail.rockefeller.edu&gt;, Olivier Fedrigo &lt;ofedrigo@mail.rockefeller.edu&gt;, Jackie Mountcastle &lt;[REDACTED]&gt;

Wed, Oct 18, 2017 at 5:15 PM

Hi Kara,

Thank you for getting back to us. As our goal is to sequence the genomes of all 66,000 vertebrate species, our list will be those species plus a few invertebrate outgroups. However, if the species is not endangered should we include it in the list? Currently, there are about 8000 of the 66000 vertebrate species that IUCN has on their endangered list. Each year species are added, some taken off. Would it be safer to include all 66000 species, or should we only include that classified as endangered as of now.

For people's CVs, this is an international project. Do you want CVs of our non-US collaborators that are in the co-leadership positions of the project?



Best

Erich

[Quoted text hidden]

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&lt;3-200-43 rev 8-25-17.doc&gt;

Erich D. Jarvis, Ph.D.

Inves igator, Howard Hughes Medical Institute  
Professor, The Rockefeller University, Box 54  
1230 York Avenue, New York, New York 10065

<http://www.jarvislab.net/><http://www.jarvislab.net/Publications.html>

**Dziwulski, Kara** <kara\_dziwulski@fws.gov>  
To: "Cogliano, Mary" <mary\_cogliano@fws.gov>

Wed, Oct 18, 2017 at 7:55 PM

Hey Mary,

Can you provide me some guidance on what I should instruct Erich to provide me with? I am debating the best way for him to give us this information? Obviously a list of 66,000 species might be a bit much? Maybe genus listed?

Help?!?

Thanks,

Kara

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**Dziwulski, Kara** <kara\_dziwulski@fws.gov>  
To: Erich Jarvis <ejarvis@mail.rockefeller.edu>

Mon, Oct 30, 2017 at 4:25 PM

Erich,

Your questions were discussed between DMA and DSA last week and it was decided that we do not need you to provide us an en ire list of all the vertebrate species you will be targe ing. We do however, want a list of all Endangered Species Act threatened or endangered, or CITES appendix I listed invertebrates, you might be wanting au horization for.

Please keep in mind that we do not work off the IUCN criteria for what is threatened or endangered. We only regulate species who are listed under the Endangered Species Act as threatened or endangered.

In addi ion to the questions I sent you previously, please be sure to provide us in your new application a full research proposal hat clearly outlines what you are going to be doing with the samples you import, and how this research will benefit hese species in the wild.

Is there going to be phased approach to what species you plan on targeting first for import?

Also, are you going to be importing samples taken from only wild animals or will you also be importing samples from captive and/or cap ive-bred animals?

Thanks,

Kara

[Quoted text hidden]

**Dziwulski, Kara** <kara\_dziwulski@fws.gov>  
To: Erich Jarvis <ejarvis@mail.rockefeller.edu>

Thu, Dec 14, 2017 at 3:22 PM

Cc: Sadye Paez <spaez@mail.rockefeller.edu>, Olivier Fedrigo <ofedrigo@mail.rockefeller.edu>, Jackie Mountcastle [REDACTED]

Erich,

This is a reminder that I needed addi ional informa ion from you in order to move forward with your applica ion. Technically, if we do not receive requested information within 45 calendar days it is our office policy to abandon your application.

Given potential holiday-related delays, I will **extend your information submission window until January 4th**. On that date, if we s ill have not received additional information from you, your permit application will officially be abandoned.

Thank you,

Kara

[Quoted text hidden]

**Erich Jarvis** <ejarvis@mail.rockefeller.edu>  
To: "Dziwulski, Kara" <kara\_dziwulski@fws.gov>

Fri, Dec 15, 2017 at 5:02 PM

Cc: Sadye Paez <spaez@mail.rockefeller.edu>, Olivier Fedrigo <ofedrigo@mail.rockefeller.edu>, Jackie Mountcastle [REDACTED]

Dear Kara,

Thanks for he reminder and the extension. Yes, we will work to get his in on Jan 4th.

Best

Erich

[Quoted text hidden]

**Erich Jarvis** <ejarvis@mail.rockefeller.edu>  
To: "Dziwulski, Kara" <kara\_dziwulski@fws.gov>

Cc: Sadye Paez <spaez@mail.rockefeller.edu>, Olivier Fedrigo <ofedrigo@mail.rockefeller.edu>, Jackie Mountcastle [REDACTED]

Dear Kara,

We have been working on the application over the holiday, but it would be helpful if I had a few more days. I need to finish up items and still need to get revisions from G10K members. With it Monday, Jan 8th?

I do also have some questions I need feedback on.

**1. Applying as an individual vs institution:** If applying as an individual, is it possible to have 2 or more individuals from the same institution (such as Olivier and myself) be the applicants? I US be the applicants? If applying as an institution, is it possible that the G10K organization apply as an institution, with myself as the Chair? We are not a 501c nonprofit group, but we are an

**2. Final long-term storage of samples:** Related to the above, for long-term storage of remaining samples not used for the initial genome sequencing and that do not need to be returned to the possibly sending them the tissue to be held at the Smithsonian's National Museum of Natural History's frozen Biorepository in Washington DC. This will ensure that the samples that become possible future upgrades and discovery. So in a typical transaction in the project, tissue of an endangered species will be received at the Rockefeller University genome laboratory in NY, we pass steps in the pipeline, and when the genome is complete and publicly available, we wish then to have the remaining unused tissue sent to the Smithsonian long-term frozen collection. If this is

**3. Species to be included in the permit:** Although our long-term goal is to sequence the genomes of at least one individual from all ~66,000 vertebrate species, it is not clear to me which of for? You mentioned in an email response that the US Endangered Species Act list is different than the IUCN red list. So, we will mention plan to include 66,000 species, including the 8000 on But the permit should be specific for the US Fish and Wildlife list? For that list, it is hard to get a single number of species online. <https://www.fws.gov/endangered/>. Do you have a complete list

**4. Vertebrates vs others:** Although we are applying for vertebrate species, some of the leadership of the G10K group (with myself on the committee) are following in the G10K's footsteps to planet (called the Earth Biogenomes Project). This group will eventually request a similar kind of permit for non-vertebrate eukaryotic species. I wonder if you think it would be worth it and possible request?

Looking forward to hear from you

Best

Erich

On Dec 14, 2017, at 3:22 PM, Dziwulski, Kara <[kara\\_dziwulski@fws.gov](mailto:kara_dziwulski@fws.gov)> wrote:

Erich,

This is a reminder that I needed additional information from you in order to move forward with your application. Technically, if we do not receive requested information within 45 calendar

Given potential holiday-related delays, I will **extend your information submission window until January 4th**. On that date, if we still have not received additional information from you

Thank you,

Kara

On Mon, Oct 30, 2017 at 4:25 PM, Dziwulski, Kara <[kara\\_dziwulski@fws.gov](mailto:kara_dziwulski@fws.gov)> wrote:

Erich,

Your questions were discussed between DMA and DSA last week and it was decided that we do not need you to provide us an entire list of all the vertebrate species you will be targeting threatened or endangered, or CITES appendix I listed invertebrates, you might be wanting authorization for.

Please keep in mind that we do not work off the IUCN criteria for what is threatened or endangered. We only regulate species who are listed under the Endangered Species Act as

In addition to the questions I sent you previously, please be sure to provide us in your new application a full research proposal that clearly outlines what you are going to be doing with species in the wild.

Is there going to be a phased approach to what species you plan on targeting first for import?

Also, are you going to be importing samples taken from only wild animals or will you also be importing samples from captive and/or captive-bred animals?

Thanks,

Kara

On Wed, Oct 18, 2017 at 5:15 PM, Erich Jarvis <[ejarvis@mail.rockefeller.edu](mailto:ejarvis@mail.rockefeller.edu)> wrote:

Hi Kara,

Thank you for getting back to us. As our goal is to sequence the genomes of all 66,000 vertebrate species, our list will be those species plus a few invertebrate outgroups. However Currently, there are about 8000 of the 66000 vertebrate species that IUCN has on their endangered list. Each year species are added, some taken off. Would it be safer to include endangered as of now.

For people's CVs, this is an international project. Do you want CVs of our non-US collaborators that are in the co-leadership positions of the project?

Best

Erich

On Oct 18, 2017, at 4:53 PM, Dziwulski, Kara <[kara\\_dziwulski@fws.gov](mailto:kara_dziwulski@fws.gov)> wrote:

Dr. Jarvis et al.,

I had a meeting with my supervisor, Mary Coligano, and the head of the Branch of Permits, Tim Van Norman, today and we discussed what the next steps for you guys regarding

First, since it is apparent a COSE is not sufficient for the activities you are requesting authorization for, you will need to complete a 3-200-37 form and email it to me. This will

<https://www.fws.gov/international/pdf/permit-application-form-3-200-37-export-import-interstate-and-foreign-commerce-take-of-animals.pdf>

In this application please make sure you include:

- A project proposal outlining the goal of the project, and what actions you are seeking authorization for.
- A species list of what species you are targeting for import over the next 5 years
- CV's of the researchers on your team and their experience as it relates to the goals of your research activities
- Describe as much as possible the following:
  - What kind of samples you will import (e.g. frozen tissue)
  - The size of the samples (e.g. 2 cm cubes of frozen tissue)
  - How many samples you expect total (e.g. importing at least 66,000 tissue samples total)

## A Digital Genome Ark Library

Modified from G10K 2016 MacArthur 100&change and 2017 HHMI VGP proposals

Last update Jan 9<sup>th</sup>, 2017 (Sent to US Fish and Wildlife)

Our planet is experiencing its 6<sup>th</sup> mass extinction event, and human activities are in part responsible. Imagine losing the 1 in 8 endangered vertebrate species to extinction on the US Fish and Wildlife and IUCN Red List<sup>1</sup>. Now add hundreds more each year. Species loss is damaging the food chain, ecosystems, climate, and human societies. A major challenge for saving species has been no cost-effective and sufficient technology to generate high-quality genomes. Our team, the [Genome 10K Consortium](#), have devised a revolutionary solution at a fraction of the cost. We will implement this solution in our [Vertebrate Genomes Project](#) (VGP) to create an open-access **Digital Genome Ark Library**. This library will catalog at least one high-quality, near-gapless, chromosome-level, phased, and annotated reference genome assembly of all approximately 66,000 vertebrate species, and to utilize those genomes to address fundamental questions in biology, disease, and conservation. We will conduct the VGP in taxonomic phases, from orders (Phase 1), families (Phase 2), and genera (Phase 3), to eventually all species (Phase 4; **Fig. 1**), focusing high priority on endangered species at each phase. We will use the Library to identify species most genetically at risk to extinction, help implement interventions, and become a model to preserve all life<sup>2</sup>.

**Our Team:** The G10K consortium is a multidisciplinary group of tissue curators, biologists, conservationists, computer scientists, outreach educators and more, whose purpose is to use genomic analysis to understand complex life and become better stewards of the planet. They include world leaders in endangered species selection (IUCN), sample collection (The Frozen Ark and museums), specimen transport of endangered species samples, genome assembly (genome centers), bioinformatics, and conservation genomics. With over 150 persons at over 50 institutions in nearly all continents, we have four levels of organization: 1) Team Leaders/Members with distinct roles who conduct the project on a daily basis; 2) Collaborators who contribute at all levels; 3) Industry partners who help us enhance our solution and provide services; and 4) Distinguished Advisors who help guide the project. We have weekly international conference calls, utilize online communication and project management tools, and hold annual meetings, rotating location internationally, to achieve milestones and plan future directions. We have an open-door policy for anyone that wishes to participate.

Our team leaders have successfully conducted previous large-scale international genome projects, bringing together persons with multidisciplinary expertise, and include leaders from the past Human Genome Project<sup>3</sup>, Cancer Genome Atlas Project<sup>4,5</sup>, Autism Speaks Genome Project<sup>6,7</sup>, and the Avian Phylogenomics Project<sup>8,9</sup>. This last project, led by [G10K Council](#) members Drs. Jarvis, Zhang, and Gilbert with 200+ researchers from 80 institutions in 20 countries, was transformative because we sequenced genomes of birds in all 40+ orders, including 7 endangered species with DNA isolated from frozen tissue samples<sup>10</sup>. We published 50+ peer-reviewed papers in 2 years (including 8 featured in *Science* magazine)<sup>9-12</sup> that reported paradigm-shifting discoveries encompassing diverse topics like the bird tree of life<sup>13</sup>, genome evolution<sup>14</sup>, new algorithms<sup>15,16</sup>, genetic susceptibility to extinction-inducing stressors (e.g. pathogens, toxins, and climate change)<sup>10</sup>, and genetics of complex traits (e.g. vocal learning and spoken-language)<sup>17,18</sup>. Thus, our team is uniquely positioned to execute this project.

**The Problem:** Earth is in the midst of its 6<sup>th</sup> mass extinction event, the worst since the die-off of dinosaurs 66 million years ago<sup>19,20</sup>. However, this one is caused by human activities, including habitat destruction, pollution, climate change, and more. Currently the US Endangered Species Act estimates that 442 species of vertebrates are endangered in the USA alone, and IUCN Red List estimates that 8,374 worldwide (12.69%) are vulnerable, endangered, or critically endangered, with the rate increasing every year<sup>1</sup>. We are in a race against time to save their genetic information before they are lost forever. Because population size is not always indicative of genetic diversity, without the genome it is difficult to identify which species face imminent extinction and need conservation focus now. Scientists (including team members) are working on gene-editing technology to save or even resurrect extinct species<sup>21-24</sup>, but their methods also require high-resolution genomes. Current genome sequencing methods miss critical genome regions. Parts of genes are missing, some are incorrectly assembled, while others are completely missing from the assemblies despite pieces being found in the raw sequence reads<sup>25</sup>. Due to these fragmented, error-prone assemblies, researchers have had to clone, re-sequence, and correct individual genes. In some cases, the gene structures are too complex, too long, or too closely related. Thus, these 1<sup>st</sup> and 2<sup>nd</sup> generation sequencing approaches cause scientists to spend extraordinary amounts of collective time, effort, and money to fix gene sequences and structure. In many other instances, investigators do not even know that they are working with incorrect gene sequences and structures, impacting many scientific findings and scientific progress. In the meantime, conservation groups like zoos<sup>26</sup>, museums<sup>27</sup>, and companies (including team members) have begun creating “frozen arks”<sup>28</sup> to preserve tissue samples, but these samples can degrade over time and the freezers can break and thaw out. The VGP leadership has worked feverishly to develop the needed cost-effective technology and infrastructure, and we now have a solution to create a high-resolution, complete, chromosomal-level digital Genome Ark Library.

**Our Solution:** We of the G10K consortium spent the past three years from 2015-2017 working with the major sequencing and assembly companies (e.g. [Illumina](#), [Pacific Biosciences](#), [Oxford Nanopore](#), [Bionano Genomics](#), [10X Genomics](#), [NRGene](#), [Dovetail Genomics](#), [Phase Genomics](#), [Arima Genomics](#)), major sequencing centers ([BGI](#), [Broad Institute](#), [Sanger Institute](#), [Washington University Genome Center](#)), major public genome archive and annotation centers ([NCBI](#), [Ensembl](#), [UCSC](#)), and experts in academia and government (NIH, NSF) to test, improve, and generate new approaches for producing the highest quality, error-free, 3<sup>rd</sup> generation reference genome assemblies achievable, for the least cost possible. Our current pipeline that generates the high-quality chromosomal-level vertebrate genome assemblies consist of a combination of four new technologies with increasing genome-scale organization: 1) Generate long-read DNA sequences and stitch them together into long continuous DNA molecules, called contigs (*Pacific Biosciences*); 2) Stitch contigs into long-range scaffolds, which contain some gaps (*Bionano Genomics*, *10X Genomics*); 3) Use natural ultra-long-range chromosome interactions to assemble scaffolds into chromosomes (*Arima Genomics*); and 4) Fill in gaps with unassembled long-reads (*Pacbio Jelly algorithm*). At each stage, we maintain maternal and paternal chromosome phasing. In our new assemblies, we find duplications are now correctly assembled, 100s-1000s of nucleotide errors within difficult to sequence regions are correctly called, missing or incorrect protein coding sequences are correctly annotated, 10,000s of gaps are filled, particularly in GC-rich gene regulatory regions, and haplotype differences are correctly phased<sup>29</sup>.

To date, of the over 335 vertebrate genomes in the public NCBI database, only 9 meet our metric ([G10K online table](#), green shading). Of these 9, 7 were done by members of our



G10K group using the above approaches. The other 2 are human and mouse, and were only brought to this quality level after billions (human) and millions (mouse) of dollars were spent for continuous correction of these assemblies. However, none of these 9 genomes have been phased, and thus have errors related to haplotype collapsing. Our approach, with negotiated discounts specific for G10K (see budget), allow us to conduct the VGP for all ~66,000 vertebrate species at a fraction of the cost used to generate and fix the human and mouse genomes alone. Reagent cost negotiations allowed us to reach our target ~\$10,000–40,000/species depending on genome size. Therefore, we plan to use the current pipeline that we have developed to conduct Phase 1 of the VGP, [260 species](#) representing all vertebrate orders that evolved before and soon after the last mass extinction event 66 million years ago, including endangered species.

We will sequence the heterogametic sex to obtain genetic information of both sex chromosomes. Because we reduced the amount of starting tissue to several hundred micrograms, we obtain enough DNA from smaller samples and do not harm animals during sample collection for blood collection of endangered species. As we proceed to maximize phylogenetic breadth and complete a vertebrate family tree at each phylogenetic level (orders, family, genus, and then all species), we will prioritize the most critically endangered species first.

**Evidence of Effectiveness:** We have validated our novel genome assembly solution on 7 species representing vertebrate diversity: a hummingbird, a songbird, an endangered parrot (Kākāpō), sea bass, goat, endangered gorilla, and human<sup>30-32</sup> (plus several studies in preparation). We discovered new genomic regions, including areas that control gene regulation, gene function, and immunity (MHC genes). Our whole genome data on the nearly extinct Kākāpō parrot with only ~150 individuals left on the planet is now being used to help manage breeding and rescue of that species<sup>33</sup>. In other related projects, VGP members have shown the power of conservation genomics in informing rescue efforts of endangered species. Man-made toxins, such as pesticides, are partially responsible for the decline of the bald eagle in the Americas and crested ibis in Asia, of which the latter had only two breeding pairs alive on Earth by 1985. When we compared the genomes of these two bird species to other avians that are not threatened, we found in the threatened species genetic susceptibilities in immune and metabolic pathway genes to climate change-induced diseases and human environmental toxins, respectively<sup>10</sup>. These genomic results as well as related discoveries on the endangered California condor<sup>34</sup>, where once only 5 animals were left on the planet, are now being used in a pioneering fashion to manage the recovering breeding colonies and develop a carrier test for the genetic susceptibilities to toxins and disease. Thus, our results are already directly informing conservation efforts.

**Helping Endangered Species in the Wild:** With an open-access digital Genome Ark Library of chromosomal-level genomes of all endangered vertebrate species, we will perform genetic diversity tests to identify species most critical of becoming extinct within 10 years. This is possible from even analyzing the genome of one animal because diversity is determined by differences between paternal and maternal chromosomes. Nearly all of each species' history is in the genome of each individual of that species. We will identify genes that make some species more sensitive to man-made toxins. Our results will help other conservation groups on where to focus efforts where needed most. This includes using the genomes as references for captive breeding program of endangered species.

**Expected Publications from the VGP Phase 1.** Based on the past Avian Phylogenomics Project<sup>9,11</sup>, analyses of the ordinal-level reference genomes from the VGP are expected to generate well over 50 publications on a vast range of topics in proposed special issues of *Nature* or *Science* and other journals for which we have already received Editor solicitations. We will use Phase 1 genomes to generate the first ordinal-level genome-scale tree across vertebrates, which should help resolve many controversies in species' relationships specifically and phylogenomics generally<sup>13</sup>. Because we used a 50 MYA divergence time for species selection, the tree will allow us to determine whether all vertebrate lineages were impacted during the 5th mass extinction event 66 MYA in the same or different ways, what types of lineages survived, and whether there are differences in post mass-extinction diversification for species that live in water, land, and/or air<sup>13</sup>. Crucially, it will enable us to make predictions about species undergoing our now human-induced 6<sup>th</sup> mass extinction and how we can intervene through conservation efforts.

The ordinal-level reference VGP will lead to a new era of comparative genomic studies, allowing us to gain unprecedented insight into the genomics of specialized and convergent traits among vertebrate lineages. We will perform comparative genomic studies on vocal learning, a rare trait necessary for spoken language, sex determination, parental care, immunity, among others. The rare vocal-learning species selected, including humans and song-learning birds, will allow us to identify the GC-rich regulatory regions predicted to drive specialized expression of genes within brain vocal nuclei, genes which when mutated are associated with speech and speech-related autistic disorders<sup>35,36</sup>. With the brain transcriptomes and single-cell RNA sequencing of neurons across different vertebrate lineages, we will try to resolve longstanding questions regarding brain cell-type homologies across vertebrates<sup>37-39</sup>.

In collaboration with Ensembl, NCBI, and UCSC annotation groups, will use the more complete, more error-free VGP genomes to clean up gene homology across species, including humans, and devise a more universal gene nomenclature based on synteny and gene/genome evolution<sup>40-42</sup>. We will infer the evolutionary origin of all bases in the human genome, for at least the 50 MYA divergence time, and determine which are conserved across vertebrates. This will allow researchers to significantly narrow down the range of searchable mutations among the rare variants in the human population that are candidate genetic causes for a wide range of diseases<sup>43</sup>.

We will also use the genomic data to develop new bioinformatic algorithms for genome assemblies, alignments, annotations, ancestral sequence and chromosome reconstructions, species trees, comparative genomics, and disease associations. This includes developing algorithms that can generate error-free genome assemblies for different animal lineages, which have different assembly needs due to differences in reduced or greatly expanded genomes ranging in sizes from 0.5 to 50 Gb. The larger genomes often have greater amounts of partial or whole genome duplications, making genome assembly more challenging.

**Timeline and Milestones.** It currently takes 2-3 months/species for the entire pipeline. However, our timeline is in part most limited by available funding and time to obtain permit approvals. We have raised funding for over 70 of the 260 Phase 1 species, including endangered species. We expect to generate about 12 genomes per week, or 2 years to complete phase 1. To complete all phases for all 66,000 species within 10 years, we will need to increase production to 115 species per week. For this reason, there is a need to not only scale-up genome sequencing, but the ability to rapidly obtain tissue samples. Our goal that full funding is in place, to have the completion of all endangered species within 6 years.

**Risk Assessment:** We envision three principal risks:

1. The most significant risk is time, including securing funding and permits for this essential project as we race with the extinction clock.
2. We found that ~30% of previously frozen samples in museum collections (~2000 tested) fail quality standards, containing degraded DNA. This risk will be mitigated by processing the most critically endangered species first, ensuring that replacement samples are obtained before possible extinction and appropriate protocols are used for preservation.
3. Our sequencing rate is highly dependent on capacity and computational power. To mitigate this risk, eight Genome Centers around the world promised to allocate acquired long-read sequencers and computational resources to achieve this project. Our partnership AWS has will help make the compute possible, with free data storage.

These commitments from around the world, spanning the USA, Columbia, Russia, Australia, and other countries in Europe, Asia, and Africa are testament to how leading international organizations regard the reference VGP for urgently executing our solution.

**Evaluation:** Our main measure to evaluate whether our project is successful will be the scaling of our operations to the point that we successfully generate high-quality chromosome-level reference assemblies of ~6000 new species/year, which in of itself will be unprecedented. Our secondary measure will be on whether the digital Genome Ark library begins to help save species from extinction, save ecosystems, and impacts science, human society and survival. For monitoring the progress of both outcomes, we have built a project management team experienced with capacity building, coordinating international efforts, and collecting data. Where obstacles are noted, we will be agile to change through our weekly conference calls. For evaluation, we will perform analysts to assess whether any animals have been saved from extinction through our efforts and societal impact of our organization, through publications, website interactions, conferences, media coverage, and education/outreach programs. We will continuously assess, develop, and utilize advancements in technology to improve genome assemblies and the impact of the Genome Ark on science and conservation.

**Previous Performance of Team:** VGPs previous performance is in the successes of the G10K and B10K consortiums. Since its inception in 2009 <sup>44</sup>, the G10K consortium holds annual meetings, supported by over 20 foundations and companies, where leaders in genomics, conservation, and more, update the field and make future plans. We formed and held the well-known Assemblathon and Alignathon genome competitions to improve assembly and DNA alignments. Our Assemblathon 2 publication<sup>45</sup> has been designated by Thomson Scientific as among the top 1% cited papers in its field of multidisciplinary science, and served as a basis for improvements in algorithms that contributed to our solution. We formed a frozen biospecimen database of over 16,000 vertebrate species from around the world, ready to be sequenced. We formed a leadership structure, consisting of a [G10K Council](#) with a wide range of expertise, taxon chairs for each major vertebrate class, and a grant-writing team. Discoveries from the Avian Phylogenomics Project, predecessor of the B10K consortium, was designated “The most important work on birds this century”<sup>46</sup>, a “Quantum Leap in Avian Biology”<sup>47</sup>, and the top science stories of 2014<sup>12,48</sup>. With these previous successes, we are uniquely positioned to conduct our reference VGP.

**Organizational Capacity:** The VGP team leadership, members, collaborators, industry partners, and advisors have been carefully chosen to ensure the complete range of required expertise and international distribution, and as well as being at the forefronts of their respective fields. We possess the ability to scale-up our efforts based on our past experiences. For example, for the Avian Phylogenomic Project, within two years, we were able to scale from only a few genomes/year to 48 genomes in 2 years, by improving sequencing capacity and algorithms for genome assembly, annotation, and data analyses<sup>13,14</sup>. With the expanded infrastructure, personnel, equipment, and computational resources acquired since then, we will reach our target 260 ordinal reference genomes, and begin impacting saving species. The strategic partnerships we formed to ensure that we have the necessary support to execute every stage of the project. Given our open-door policy of collaboration, we expect others that wish to participate to continually be added as partners, expanding and enhancing this global project.

**Budget.** To make this project affordable, we negotiated competitive discounts with nearly all of the sequencing and compute companies we worked with on testing and developing protocols for the VGP, ranging from 10%-80% off the list price, averaging a ~45% reduction in total cost per species for our current VGP pipeline (**Fig. 2**). As an example, a 1Gb bird genome using our pipeline would normally cost about \$26,500 whereas our negotiated cost is \$15,000 (**Table 1** in budget). A 3.5Gb mammal genome would normally cost \$75,500, whereas our negotiated discounted cost is \$43,500 (**Table 1**). Our discounted pipeline includes for each species: sample processing; high-molecular weight DNA preparation; genome libraries; PacBio long-read sequencing; Bionano optical maps; 10X Genomics linked-reads; Arima Genomics HiC libraries and sequencing; DNANexus assembly compute; AWS free data storage; alignments and annotation by NCBI, Ensemble, and UCSC; and labor to generate the data. By contrast, the current lesser-quality Sanger-based and cytogenetically mapped zebra finch reference genome cost over \$8,000,000 for one species, and the human genome cost over \$2.8 billion. The discounts were given to G10K because of expected VGP volume, public recognition working with the G10K-VGP, and the positive scientific mission of the VGP. To receive these discounts, all sequencing will have to be performed in large volume, starting with the 260 ordinal-level species. Costs will be lower where there are existing data (e.g. PacBio reads).

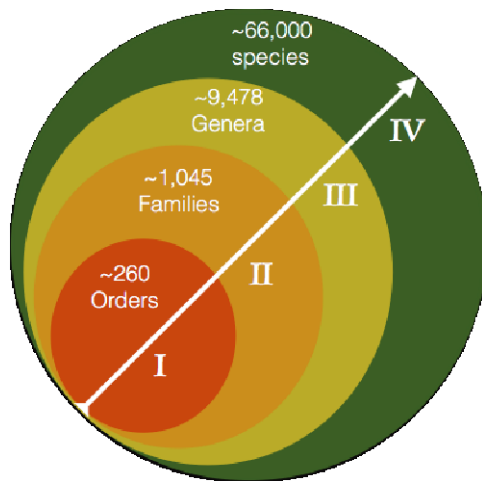
The estimated total costs for the ~260 Phase 1 species (minus 5 of 6 large salamander genomes > 10Gb) is \$7.1M and for IsoSeq RNA annotation is \$0.39M (**Table 2**). With 6 ordinal species currently nearing completion, the necessary PacBio reads available for 9 other species, and the raising of \$2.1M by the G10K leadership through grassroots funding from the laboratory budgets of over 28 individual investigators, we are raising an additional \$4.8M to complete VGP Phase 1 (**Table 2**). These funds will help complete arguably the largest, highest-quality, most diverse, and most comprehensive vertebrate genomes project to date. It will be an investment that builds the momentum needed for the G10K to raise the funds from other agencies for Phases 2, 3, and 4. Importantly this investment will save the scientific community the extraordinary amounts of collective time, effort, and money to correct poor-quality genomes for their research projects and prevent untold amounts of errors in scientific publications.

In terms of personal and equipment, we already have the needs to support about 12 genomes per week. These personnel include a project management coordinator, genome sequencing coordinator, technicians, bioinformaticians, database and website specialists, and an outreach coordinator, among other staff. To get to 115 genomes per week, we will have to scale up personal, equipment, and budget 10-fold, which we working on doing.

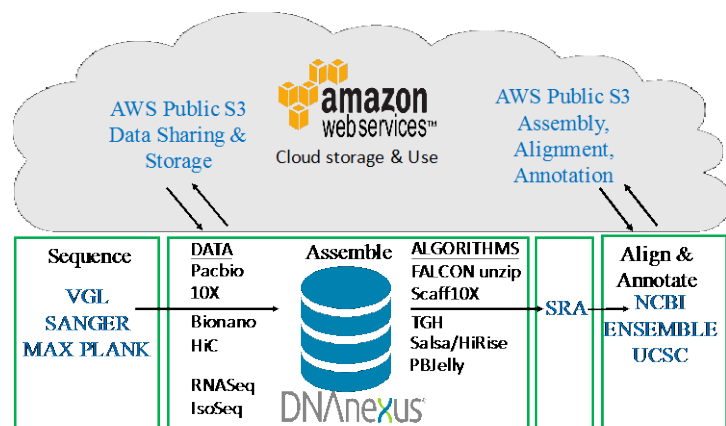


**Sustainability:** For sustainability, because the Genome Ark Library will be linked with open-access government-supported databases, the Library is expected to have a long lifetime. Because we save tissue, cells, or DNA of representative individuals of all species sequenced, we will be able to go back to the original samples and incorporate any improvements in technology that may occur over time. We will also create a structure whereby any individual or agency can contribute funds to preserve the genetic data of a species or set of species. Currently dozens of scientists are doing so for their preferred species of interests, and we expect that number to increase to the hundreds and eventually thousands of scientists. This will be one mechanism of how the VGP will eventually populate the Genome Ark Library with all 66,000 vertebrate species. Long-term, we expect our approach and Library to eventually become a Genome Ark repository for all of life. The data generated may help to slow if not help reverse the 6<sup>th</sup> mass extinction for all life. Thus, our project's potential impact extends beyond vertebrates.

**Broader Impacts:** We believe that knowledge gained from the reference VGP and the Genome Ark will help humankind become better stewards of the planet and our own species' survival. We expect to learn about genetic susceptibilities and resistances in different species, including humans, to human-made toxins and pathogens. We will advance our understanding of conservation and biodiversity, the interrelatedness of all vertebrate species, the genetics of complex trait differences between species, and health and disease. Instead of having only frozen tissues that could be accidentally destroyed, we will have a digital genome library that can be exponentially amplified for years to come. Eventually, the genomes could be used not only to help recover endangered species, but resurrect species that have gone extinct. Based on the thousands of media outlets that have highlighted G10K, we believe that our VGP project will raise the public consciousness of science and our interrelatedness with non-human species.



**Fig. 1. VGP Phases.** The 4 Phases are based on systematic classifications. The 260 orders for Phase 1 are discussed in the main text. Once each phase is completed, they are subtracted from the total. With 260 orders completed, 785 (1045-260) families will need to be completed for Phase 2.



**Fig. 2. VGP pipeline.** Shown are steps from sample processing, sequence data generation, application with assembly algorithms, and annotation, to uploading to public databases. This represents a 4-way partnership between the sequence data generators and assemblers, DNANexus, AWS, and annotation centers.

## Budget values

Table 1.

Genome size (Gb)	TOTAL - Full price	TOTAL - G10K-VGP discount
0.5	\$16,500.00	\$9,500.00
1	\$26,500.00	\$15,000.00
1.5	\$36,000.00	\$21,000.00
2	\$46,000.00	\$26,500.00
2.5	\$55,500.00	\$32,000.00
3	\$65,500.00	\$38,000.00
3.5	\$75,500.00	\$43,500.00
4	\$87,500.00	\$50,500.00
4.5	\$97,000.00	\$56,500.00
5	\$107,500.00	\$62,500.00
5.5	\$117,500.00	\$68,000.00
6	\$127,000.00	\$74,000.00

### RNA Annotation Cost (brain & gonads)

IsoSeq	\$2,000.00	\$1,500.00
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Table 2.

Vertebrate classes	# Order species	Gb total	Gb/species	Expected \$
Mammals	58	200.99	3.5	\$2,375,578
Birds	52	68.91	1.3	\$816,480
Alligators	3	7.30	2.4	\$89,223
Turtles	14	34.16	2.4	\$405,812
Sakes & Lizards	15	34.47	2.3	\$390,000
Frogs	20	67.33	3.4	\$797,829
Salamanders	6	234.00	39.0	\$2,765,234
Caecilians	4	13.00	3.3	\$156,507
Fish	72	81.96	1.1	\$970,524
Sharks	13	75.21	5.8	\$890,728
Lung/Hagfish	3	9.63	3.2	\$116,727
Invertebrates	4	3.32	0.8	\$42,242
Total (- salamanders)	258	596.28	29.54	\$7,051,650
Total annotation				\$387,000
Funds spent or obtained				(\$2,100,000)
Projected additional discounts with increased volume				(\$500,000)
Total required				\$4,838,650

**Table 2. G10K-negotiated discounted pricing for the reference VGP genomes.** Full price is the list price cost. Discounted price reflects negotiated pricing by the G10K for the VGP. This represents ~45% total reduction in cost. Cost is calculated based on genome size of species in increments of 0.5Gb. The bigger the genome size, the more sequencing needed to obtain the needed coverage, and therefore the more sequencing reagents, sequencing time, and labor time needed. Package includes: 60X PacBio long-reads; >80X Bionano optical maps; 68X of 10X-Genomics linked reads; 68X of Arima HiC; DNANexus assembly compute; Data storage on AWS (free for VGP); Annotation by Ensemble/NCBI/UCSC; Shipping within project; Tissue DNA preparation; Library constructions; Miscellaneous reagents; and Labor.

**Table 3: Estimated cost for the ordinal reference VGP.** Costs are estimated on 262 ordinal-level vertebrate and 4 invertebrate outgroup species in the following VGP list: [https://docs.google.com/spreadsheets/d/1Jwiv6Kwc6VIn1UMMhnG6kvFCxiwGdC5b7p\\_HtbDOMOs/edit?usp=sharing](https://docs.google.com/spreadsheets/d/1Jwiv6Kwc6VIn1UMMhnG6kvFCxiwGdC5b7p_HtbDOMOs/edit?usp=sharing). Costs include G10K-negotiated discounted pricing from Pacific Biosciences, Bionano Genomics, 10X Genomics, Arima Genomics, and DNANexus. #Order species: Number of species within the vertebrate class to be sequenced. Gb total: Total amount of Gb to be sequenced for the number of species selected. Gb/species: Average Gb per species to be sequenced within each vertebrate class. Expected \$: Estimated cost for each class based on average Gb/species, annotation, alignments, funds already obtained, projected agreed on discounts as reagent volume increases, and total required to complete the VGP.

## References:

- 1 [US Fish and Wildlife List](#) and [IUCN Red List](#) 2018.
- 2 Jarvis, E. D. Perspectives from the Avian Phylogenomics Project: Questions that Can Be Answered with Sequencing All Genomes of a Vertebrate Class. *Annu Rev Anim Biosci*, Vol 4 **4**, 45-59, doi:10.1146/annurev-animal-021815-111216 (2016).
- 3 Lander, E. S. *et al.* Initial sequencing and analysis of the human genome. *Nature* **409**, 860-921 (2001).
- 4 Weinstein, J. N. *et al.* The cancer genome atlas pan-cancer analysis project. *Nat Genet* **45**, 1113-1120, doi:10.1038/ng.2764 (2013).
- 5 Cancer Genome Atlas Website: <http://cancergenome.nih.gov>.
- 6 Szatmari, P. *et al.* Mapping autism risk loci using genetic linkage and chromosomal rearrangements. *Nat Genet* **39**, 319-328, doi:10.1038/ng1985 (2007).
- 7 Autism Speaks Genome Project Website: <https://www.autismspeaks.org/science/initiatives/autism-genome-project>.
- 8 Zhang, G., Jarvis, E. D. & Gilbert, M. T. P. A flock of genomes. *Science* **346**, 1308-1309 (2014).
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Dziwulski, Kara &lt;kara\_dziwulski@fws.gov&gt;

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**US Fish and Wildlife Application Jarvis, Fedrigo**

2 messages

**Erich Jarvis** <ejarvis@mail.rockefeller.edu>

Tue, Jan 9, 2018 at 6:49 PM

To: "Dziwulski, Kara" &lt;kara\_dziwulski@fws.gov&gt;

Cc: Olivier Fedrigo <ofedrigo@mail.rockefeller.edu>, Sadye Paez <spaez@mail.rockefeller.edu>, Jackie Mountcastle  
[REDACTED]

Dear Kara,

We have finally finished a draft of the special application for the G10K reference Vertebrate Genomes Project. Attached are:

1. Permit application for Jarvis, G10K Chair
2. Permit application for Fedrigo, VGP Sequencing Director, in case you allow the application to be in two names.
3. Applications explanation on questions E-H, and additional questions you asked by email on Oct 18, 2017
4. Our VGP proposal with items relevant to our application.

Let me know if there is anything else needed, and other revisions. We will separately now fill out the marine mammal application you sent.

Best

Erich

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**8 attachments****permit-application-form-3-200-37-export-import-interstate-and-foreign-commerce-take-of-animals G10K v1 Jarvis.pdf**  
150K**ATT00001.htm**  
1K**permit-application-form-3-200-37-export-import-interstate-and-foreign-commerce-take-of-animals G10K v1 Fedrigo.pdf**  
307K**ATT00002.htm**  
1K**VGP US Fish & Wildlife application explanation v2.docx**  
32K**ATT00003.htm**  
1K**VGP Proposal USFWL v2.doc**  
542K**ATT00004.htm**  
2K**Dziwulski, Kara** <kara\_dziwulski@fws.gov>

Fri, Jan 19, 2018 at 11:43 AM

To: Erich Jarvis &lt;ejarvis@mail.rockefeller.edu&gt;

Cc: Olivier Fedrigo <ofedrigo@mail.rockefeller.edu>, Sadye Paez <spaez@mail.rockefeller.edu>, Jackie Mountcastle  
[REDACTED]

Erich,

I am sorry for the delay in getting back to you! I still have your questions on my radar, things have just been hectic in our office and it has been hard for me to pin down the individuals I need to consult in order to answer your questions appropriately. .

Thank you for the application. I am not still not 100% sure the application can be put in 2 names, I plan on discussing this (and your other questions) with my supervisor by end of next week. In addition, I will review the new application materials you submitted, share it with the CITES Scientific Authority, and get back to you if there is any additional information we would like.

Thanks,

Kara

[Quoted text hidden]

--

Kara Dziwulski  
Permits Biologist  
Division of Management Authority  
U.S. Fish and Wildlife Service  
Office of International Affairs  
5275 Leesburg Pike, MS:IA  
Falls Church, VA 22041-3803  
703-358-1797

## **Attachment of answers E-H and additional questions (G10K Jarvis, Fedrigo application)**

The answers below are in response to questions asked in the formal USFWL application and additional questions sent by Kara Dziwulski, Permits Biologist, Division of Management Authority in Falls Church, sent in an email of Oct 18, 2017. These additional questions reflect that this is a specialized application for a large-scale, international, genomes project.

### **Goal of the project and actions we are seeking authorization for**

The reference [Vertebrate Genomes Project](#) (VGP) is an international, multidisciplinary project led by the vertebrate [Genome 10K](#) (G10K) consortium, with participants from all continents. The goal of the reference VGP is to create a digital open-access Genome Ark library cataloging at least one high-quality, near-gapless, chromosome-level, phased, and annotated reference genome assembly of all approximately 66,000 vertebrate species, and to utilize those genomes to address fundamental questions in biology, disease, and conservation. High-quality error-free genome assemblies and annotations with the latest technologies are necessary, as current 1<sup>st</sup> and 2<sup>nd</sup> generation genome sequencing approaches generate numerous errors that cause a variety of problems in downstream analyses. Towards this goal, the G10K consortium has developed a sequencing, assembly, and annotation pipeline that yields the highest-quality genomes to date, and at an affordable negotiated cost. We have built an international infrastructure that includes all required stages for the project, from fund raising, sample collection and processing, genome sequencing and annotation, high level compute, and public data releases in our digital Genome Ark (via DNANexus and Amazon Web Services), the [National Center for Biotechnology Information](#) (NCBI) and [UCSC genome browser](#) in the U.S., and [Ensembl](#) in the U.K. Relevant to this application, we formed a VGP-conservation group that oversees the coalescing of research groups and analyses of data for saving species from extinction and helping them in wild. We are conducting the VGP in phases according to phylogenetic scale, with Phase 1 being approximately [260 species](#) representing all vertebrate orders that evolved before and soon after the last mass extinction event 66 million years ago. While doing this in phases, we will focus our highest priority on those species currently on the US Endangered Species Act, IUCN red, and CITES list of most endangered (Appendix I). This project is being used a model for the developing [Earth Biogenome Project](#) to eventually sequence the genomes of all life on Earth.

To help make this project possible, here we seek a US Fish and Wildlife permit in the broadest terms possible for the import and export of tissue samples of all designated endangered and protected vertebrate species that requires import and/or export permits (**Table 1**). The central receiving repository of the samples will be the [Vertebrate Genome Laboratory](#) (VGL) at the Rockefeller University. Most of the sequencing will be done at this laboratory, but some reactions require sending parts of samples to other laboratories within and outside of the US, and thus the need for export. For long-term storage of remaining samples not used for the initial genome sequencing and that do not need to be returned to the original source, we wish to send them to the Smithsonian's [National Museum of Natural History's frozen Biorepository](#). This will ensure that the samples that become the world's first high-quality reference genomes has a long-life for possible future upgrades and discovery.



	<a href="#">US Fish &amp; Wild</a>	<a href="#">CITES Appendix I</a>
Mammals	All 95	All 318
Birds	All 102	All 155
Reptiles	All 45	All 87
Amphibians	All 36	All 24
Fish	All 164	All 16

**Table 1:** List of protected species seeking permission for (as of Jan 2018)

### **Research team and their experience as it relates to the goals of our research activities**

The VGP is managed by the [G10K leadership](#). This includes the Chair, Erich Jarvis Ph.D., at the Rockefeller University and co-director of the VGL, a 14-member Council consisting of leaders in the genomics, conservation, and other specialties, and 16 G10K-VGP sub-committees that run the everyday operations, from permits, sample procurement (lead by taxon specific experts), genome assemblies, alignments, annotations, and outreach. The Council members include the leaderships of other vertebrate group initiatives, including the [B10K](#) for all bird genomes and [Bat1K](#) for all bat genomes. Some committees meet online once per week, and all committees report to the core VGP committee in a once-per-month conference call open to all 250+ G10K members, where high-level decisions take place. The G10K members meet in person at least once per year at an international conference that they organize, at different locations each year. The G10K formed a set of [ByLaws](#) that governs its organization and membership. This includes an open-door policy of accepting participants into the G10K and its VGP project. Staff at the VGL at Rockefeller help coordinate transfer of funds, samples, and data among participants.

### **E. EXPORT/RE-EXPORT/IMPORT/INTERSTATE AND FOREIGN COMMERCE/TAKE OF NON-NATIVE ANIMALS**

Question 2 in : We seek a permit to import (receive) or export tissue or blood samples for the reference VGP all 442 endangered vertebrate species in the US (US Fish and Wild life list) and 5,728 vertebrate species and subspecies protected by CITES (Appendices I, II, and III) including additional species that will be designated endangered while the permit is active. The samples will be fresh frozen tissue or blood. We require up to 500 mg of tissue or ~1mL of nucleated blood (~3–5mL for enucleated species) with current protocols for generating assembled genomes. One sample per animal is sufficient for generating the assembled genome, but one or more are necessary for RNA transcriptome annotation of the genome. For RNA annotation, we need no more than 20 mg of tissue, preferably brain or gonads for the greatest transcriptome diversity. When it is not possible to obtain such additional tissues due to saving the remaining animals from extinction, we can take blood or a skin biopsy for transcriptome annotation that does not require euthanization. In total, this adds up to a minimum of 1 sample per animal and up to a preferred 4 samples per animal when possible. We seek imports mostly for the heterogametic sex, so that both sex chromosomes can be sequenced.

Question 3: The current location of many tissue and blood specimens that we will use are in many museum and university collections within and outside of the US, that are partnering or will partner with G10K and wish to send samples to the VGL to be processed as a reference genome for given species. Examples institutions include the Smithsonian Museum Biorepository, Louisiana

Museum of Natural History, the San Diego Frozen Zoo, The Natural History Museum of Denmark, The Chinese National GeneBank, to name a few. In addition, when samples are not either sufficient quality, amount, or type of tissue, or have not yet been collected, we expect to receive samples collected from zoo or wild animals. In these cases, these will be collaborators contributing to the reference VGP. In most cases, for endangered species, we expect these samples to have been obtained from natural deaths, sick animals, or a need to get a genome to save the species from extinction. In some cases, this will only be blood samples to prevent euthanization.

We will only accept samples from institutions or persons with valid collection permits in the countries the samples are collected from. We will require that they send a copy of their permit before receiving the samples. Also, we will only work with persons who have experience in collecting samples, including museum curators, animal care takers, and scientist studying specific species. In cases where we believe someone does not have sufficient experience and collecting and preserving samples in the manner required, we will train them first before collection.

In some cases, members of our Rockefeller VGL will collect the samples ourselves. Dr. Jarvis of the VGL has 27 years of experience in collecting and preserving tissue samples for genomics and other needs. He has experience in handling laboratory and wild avian, mammalian, reptilian, and other vertebrate species, having published both laboratory and wild caught animal studies. He will oversee the collection of samples by VGL personnel, and consult with other experts of the G10K consortium when needed.

Question 4: We will receive most samples (whether from origins within or outside the US) at the VGL of the Rockefeller University in New York. The main contact persons and address for receipt is:

Olivier Fedrigo, Ph.D., Director of the Vertebrate Genome Lab  
Erich D. Jarvis, Ph.D., Co-director of the Vertebrate Genome Lab  
The Rockefeller University  
Box 54  
1230 York Avenue  
New York, New York, 10065 USA

For some reactions, we will need to ship parts of samples to other locations within and outside of the US. This currently includes [Arima Genomics](#) in San Diego (Siddarth Selvaraj, PhD, contact) for HiC reactions, the [Frozen Zoo](#) in San Diego (Oliver Ryder, PhD, contact) for cell culture propagation, [Institute for Genome Biology at UC Davis](#) (Harris Lewin, PhD, contact) for genome sequencing all within the US; and The [Sanger Institute in Hinxton](#), Cambridge UK (Richard Durbin, PhD, contact) for genome sequencing, and [The Max Plank Institute in Dresden Germany](#) (Gene Myers, PhD, contact) for genome sequencing.

Once each animals' genome is completed, we will use one of three options for long-term frozen housing of the unused remainder of the samples received, in the following order of priority:

1. Storage at the [Smithsonian Biorepository](#) in Maryland, USA
2. Storage at the VGL at the Rockefeller University in New York, USA
3. Return the remainder back to the original owner if requested.

The person currently responsible for overseeing receipt of samples from the VGL for long-term storage at the Smithsonian is [Jonathan Codington](#), PhD, Director of the Smithsonian, Global Genome Initiative. Ultimate ownership of samples will be either the original providers or released to the VGL or Smithsonian, which will be determined on a case-by-case basis.

## **F. SOURCE OF SPECIMEN**

The sources of the specimens are described in Question 3 above. In addition, we note here that for samples freshly obtained from both captive bred animals and wild animals, we will collect the meta-data on those individual animals. These meta-data are required for our VGP, and by the public NCBI and Ensembl genome annotation centers. Such meta-data will include:

Question 5: Captive bred animals.

- i. Scientific name (genus, species, and, if applicable, subspecies) and common name
- ii. Name and address of the facility where each animal was bred and born
- iii. Birth/hatch date (mm/dd/yyyy), sex, and identification information if available
- v. Location (name of facility, address, city, State/province, postal code) of parental stock
- vi. Copies of documentation demonstrating the history of transactions (e.g., chain of ownership of the animal) and a signed and dated statement from the breeder as such

Question 6: Wild animals.

- i. Scientific name (genus, species, and, if applicable, subspecies) and common name
- ii.. Specific location of where, when, and by whom (name and address) the specimen was removed from the wild
- iii. Purpose of removal and length or approximate length of time held in captivity
- iv. Copies of foreign or domestic collecting permits, license, contract or agreement
- v. Documentation showing that the specimen(s) was legally obtained by the applicant
- vi. Copies of any applicable State, Tribal, Federal, or Foreign government permits or licenses that authorized the removal of this animal from the wild.

## **G. JUSTIFICATION FOR REQUESTED ACTIVITY.**

Question 7: Justification for the project is in the attached proposal titled “A Digital Genome Ark Library”. Here we argue the need for high-quality, error-free genomes to help save the genetic information and the species for intervention for preventing extinction. Also attached are CVs of the G10K Council members and relevant committee chairs for this project.

Question 8: Statement on how the activities will enhance and benefit the species in the wild. This is described in the attached proposal. In brief, paraphrasing from that proposal, with an open-access digital Genome Ark Library of chromosomal-level genomes of all endangered vertebrate species, we will perform genetic diversity tests to help focus conservation efforts on those species that need it the most. We will identify genes that make some species more sensitive to man-made toxins, and which can then be targeted for genome editing or environmental policies. The genomes will also be used as references for captive breeding program of endangered species, helping to maintain genetic diversity in the population to prevent extinction.

Question 9: Permission is not being sought to maintain live endangered animals in captivity specifically by the VGP leadership for this permit. Any such activities, should they occur, we be done under separate permits.

#### **H. IMPORTS, EXPORTS, OR RE-EXPORTS.**

Questions 10–15: Samples will not be used for commercial purposes. The main purpose of this project is scientific, including for species conservation. We will obtain the necessary additional permits needed, such as those needed for marine mammals. For re-export of remaining unused samples to the original owner, we will provide the original important documents with the re-export. All international imports and exports will be made through designated [US Fish and Wildlife ports](#).





Department of the Interior  
U.S. Fish and Wildlife Service

OMB No 1018-0093  
Expires 05/31/2017

## Federal Fish and Wildlife Permit Application Form

**Return to:** U.S. Fish and Wildlife Service  
Division of Management Authority (DMA)  
Branch of Permits, MS: IA  
5275 Leesburg Pike  
Falls Church, VA 22041-3803  
1-800-358-2104 or 703-358-2104

**Type of Activity:**  
**EXPORT/RE-EXPORT/IMPORT/INTERSTATE AND  
FOREIGN COMMERCE/TAKE OF ANIMALS  
(LIVE/ SAMPLES/PARTS/PRODUCTS) (ESA and/or CITES)**  
**(circle/highlight proposed activity)**

☒ **New Application**  
☐ **Requesting Re-issuance/Amendment of Permit#:** \_\_\_\_\_

Complete Sections A or B, and C through H of this application. U.S. address may be required in Section C, see instructions for details.  
See attached instruction pages for information on how to make your application complete and help avoid unnecessary delays.

<b>A. Complete if applying as an individual</b>			
1.a. Last name Fedrigo		1.b. First name Olivier	1.c. Middle name or initial [REDACTED]
2. Date of birth (mm/dd/yyyy) [REDACTED]		3. Social Security No. [REDACTED]	1.d. Suffix Dr.
4. Occupation Scientist		5. Affiliation/ Doing business as (see instructions) Rockefeller University	
6.a. Telephone number [REDACTED]	6.b. Alternate telephone number [REDACTED]	6.c. Fax number [REDACTED]	6.d. E-mail address ofedrigo@rockefeller.edu

<b>B. Complete if applying on behalf of a business, corporation, public agency, Tribe, or institution</b>			
1.a. Name of business, agency, Tribe, or institution		1.b. Doing business as (dba)	
2. Tax identification no.		3. Description of business, agency, Tribe, or institution	
4.a. Principal officer Last name	4.b. Principal officer First name	4.c. Principal officer Middle name/ initial	4.d. Suffix
5. Principal officer title		6. Primary contact name	
7.a. Business telephone number	7.b. Alternate telephone number	7.c. Business fax number	7.d. Business e-mail address

<b>C. All applicants complete address information</b>				
1.a. Physical address (Street address; Apartment #, Suite #, or Room #; no P.O. Boxes) The Rockefeller University, 1230 York Avenue, Box 366				
1.b. City New York	1.c. State New York	1.d. Zip code/Postal code: 10065	1.e. County/Province New York	1.f. Country USA
2.a. Mailing Address (include if different than physical address; include name of contact person if applicable)				
2.b. City	2.c. State	2.d. Zip code/Postal code:	2.e. County/Province	2.f. Country

<b>D. All applicants MUST complete</b>	
1.	Attach check or money order payable to the U.S. FISH AND WILDLIFE SERVICE in the amount of \$100 nonrefundable processing fee. Federal, Tribal, State, and local government agencies, and those acting on behalf of such agencies, are exempt from the processing fee – <i>attach documentation of fee exempt status as outlined in instructions.</i> (50 CFR 13.11(d))
2.	Do you currently have or have you ever had any Federal Fish and Wildlife permits? Yes <input type="checkbox"/> If yes, list the number of the most current permit you have held or that you are applying to renew/re-issue: _____ No <input type="checkbox"/>
3.	Certification: I hereby certify that I have read and am familiar with the regulations contained in <b>Title 50, Part 13 of the Code of Federal Regulations</b> and the other <b>applicable parts in subchapter B of Chapter I of Title 50</b> , and I certify that the information submitted in this application for a permit is complete and accurate to the best of my knowledge and belief. I understand that any false statement herein may subject me to the criminal penalties of 18 U.S.C. 1001.
Signature (in blue ink) of applicant/person responsible for permit (No photocopied or stamped signatures) _____ Date of signature (mm/dd/yyyy) _____	

**E. EXPORT/RE-EXPORT/IMPORT/INTERSTATE AND FOREIGN COMMERCE/TAKE OF NON-NATIVE ANIMALS (Live/samples/parts/products) (CITES and/or ESA)**

*Allow at least 90 days for the application to be processed. Applications for endangered species permits must be published in the Federal Register for a 30-day public comment period.*

Complete all questions on the application. Mark questions that are not applicable with "N/A". If needed, use a separate sheet of paper. On all attachments or separate sheets you submit, indicate the application question number you are addressing. If you are applying for multiple specimens, be sure to indicate which specimen you are addressing in each response.

1. What activity are you requesting authorization to carry out (Indicate appropriate activities):

EXPORT ☒

INTERSTATE COMMERCE ☐

IMPORT ☒

FOREIGN COMMERCE ☐

\*Interstate Commerce permits authorize the sale of endangered and threatened species across State lines, but only for that will contribute to enhancing the propagation or survival of that species. Captive-breeding alone will not generally meet this requirement. Scientific research must be related to the species to be permitted. Interstate commerce activities with wildlife require the buyer to obtain a permit prior to the sale.

2. For EACH animal/specimen involved in the proposed activity provide:

Scientific name (genus, species, and, if applicable, subspecies)	Common Name	Birth/Hatch Date (mm/dd/yyyy) Or Approximate date	Quantity	Gender, if known	Permanent markings (e.g., tattoo, ID #, microchip #, scars), if alive	Type of Sample or product (e.g., blood, tissue, DNA)
EXAMPLE: <i>Macaca fascicularis</i>	Crab-eating macaque					
See attached on "Specimens"						

3. The current location of the specimen(s) (address and country):

Name:

Business Name:

Address:

Address:

City:

State/Province:

Country, Postal Code:

4. Recipient/Sender:
- If export, provide name and address of the recipient in the foreign country.
  - If import, provide name and address of the exporter in the foreign country.
  - If interstate or foreign commerce, provide name and address of recipient.

Name:

Business Name:

Address:

Address:

City:

State/Province:

Country, Postal Code:

**F. SOURCE OF SPECIMEN (answer question 5 or 6 for each animal/specimen involved, as appropriate).**

5. For each animal or animal from which specimen are obtained born in captivity:
- a. If you are the **breeder** of the specimen(s), please provide a signed and dated statement that includes the following:
    - i. Scientific name (genus, species, and, if applicable, subspecies) and common name;
    - ii. That the animal was bred and born at your facility;
    - iii. Birth/hatch date (mm/dd/yyyy), and, if applicable, identification information (as described in question 2b above);
    - iv. Name and address of your facility where each animal was bred and born; and
    - v. Location (Name of facility, address, city, State/province, postal code) of parental stock.
  - b. If you are **NOT the breeder** of the specimen(s), provide copies of documentation showing that you acquired the animal from the breeder or documentation demonstrating the history of transactions (e.g., chain of ownership of the animal) and a signed and dated statement from the breeder or breeder's record that clearly includes the following:
    - i. Scientific name (genus, species, and, if applicable, subspecies) and common name;
    - ii. That each animal was bred and born/hatched at his/her facility;
    - iii. Birth/hatch date (mm/dd/yyyy), and, if applicable, identification information (as described in question 2b above);
    - iv. Name and address of the breeder's facility; and
    - v. Location (name of facility, address, city, State/province, postal code) of parental stock.

6. For each animal/specimen **taken from the wild**, provide the following:
  - a. Scientific name (genus, species, and, if applicable, subspecies) and common name;
  - b. Specific location of where, when, and by whom (name and address) the specimen was removed from the wild;
  - c. Purpose of removal and length or approximate length of time held in captivity;
  - d. Describe your efforts to use captive specimens (e.g., captive-born, captive-held), or parts thereof, in lieu of taking animals from the wild.
  - e. Copies of your foreign or domestic collecting permit, license, contract or agreement;
  - f. Documentation showing that the specimen(s) was legally obtained by the applicant; and
  - g. Copies of any applicable State, Tribal, Federal, or Foreign government permits or licenses that authorized the removal of this animal from the wild.

#### **G. JUSTIFICATION FOR REQUESTED ACTIVITY.**

7. Provide a full statement justifying the proposed activity, particularly the following:
  - a. Describe the purpose of your proposed activity. For example, if the purpose is scientific research, attach a copy of your research proposal outlining the purpose, objectives, methods (e.g., specific information on survey/collection methods, sampling regime, equipment to be used), and whether similar work has already been done or is currently being done. If the purpose is conservation education, provide copies of educational materials (e.g., handouts, text of signage or public presentations), and include the purpose and objectives of the proposed activity. If the purpose is for propagation for conservation purposes, provide a description of how the species will be propagated, disposition of progeny, and cooperative agreements that are/will be established for re-introduction.
  - b. Description of the technical expertise of each person (please include CV or resume), as it relates to the proposed activities. If the proposed activity involves the import of live animals, include the experience of each animal caretaker working with the species.
  - c. Copies of contracts, agreements or other documents that identify persons involved and dates of activities for which authorization is being requested.
8. Provide a statement on how the activities will **enhance or benefit the wild population** (e.g., in-situ and ex-situ projects).
9. If live specimens are to be held in captivity as part of the proposed activity:
  - a. Provide a detailed description (e.g., size, construction materials, protection from the elements) and photographs or diagrams (no blueprints, please) clearly depicting the existing facilities **where the wildlife will be maintained**. If the specimens will be housed at multiple facilities, either immediately or within the next year, provide a full description of each facility. If you are unsure of which facilities may be receiving specimens (e.g., SSP has not made final decision), please indicate likely candidates and the mechanism that will be used to determine recipient facilities.
  - b. A statement of the specific technical experience of CV or resume available to the recipient(s) for maintaining and propagating live specimens of the same or similar species.
  - c. The number of years each species has been maintained at the facility;
  - d. The number of births by year for each species for the last 5 years; and
  - e. Mortalities at the facility with these or similar species in the last 5 years, causes of such mortalities, and steps taken to avoid or decrease such mortalities.



## H. IMPORTS, EXPORTS, OR RE-EXPORTS.

10. For shipment of LIVE specimens, the transport conditions for animals must comply with the CITES Guidelines for Transport of Live Animals or, in the case of air transport, with the International Air Transport Association (IATA) live animal regulations (contact airline for information). As such, describe:
  - i. The type, size, and construction of any shipping container; and
  - ii. The arrangements for watering or otherwise caring for the wildlife during transport.
11. **For import of LIVE CITES Appendix-I marine mammal specimens**, provide a copy of your FWS or NOAA Fisheries permit or authorization.
12. For import of CITES **Appendix-I listed species**, provide information to show the import is not for primarily commercial purposes as outlined in Resolution Conf. 5.10 ([www.cites.org](http://www.cites.org)).
13. For export of CITES **Appendix-I species**, provide a copy of the CITES import permit, or evidence one will be issued by the Management Authority of the country to which you plan to export the specimen(s). In accordance with Article III of the CITES treaty, it is required that import permits are issued before the corresponding export permit.
14. If the specimen is being **re-exported** (e.g., exporting a specimen that was previously imported into the United States), provide:
  - a. A copy of the canceled CITES export or re-export document issued by the appropriate CITES office in the country from which the wildlife was imported (if applicable); and
  - b. A cleared copy of Form 3-177, wildlife Declaration for Import (hard copy or electronic release); **or**
  - c. If you did not make the original import, provide a copy of the importer's documents outlined above and the invoice or other documentation that shows you acquired the wildlife from the original importer or history of transactions which demonstrate chain of ownership.
15. All international shipment(s) must be through a designated port. A list of designated ports (where an inspector is posted) is available from <http://www.fws.gov/le/designated-ports.html>. If you wish to use a port not listed, please contact the Office of Law Enforcement for a Designated Port Exemption Permit (form 3-200-2).
16. Name and address where you wish permit mailed, **if** different from page 1 (All permits will be mailed via the U.S. Postal Service, unless you identify an alternative means below):
17. If you wish the permit to be delivered by means other than USPS regular mail, provide an air bill, pre-paid envelope, or billing information. If you do not have a pre-paid envelope or air bill and wish to pay for a courier service with your credit card, please check the box below. Please **DO NOT** include credit card number or other information; you will be contacted for this information.  
☒ If a permit is issued, please send it via a courier service to the address on page 1 or question 11. I understand that you will contact me for my credit card information once the application has been processed.

18. Who should we contact if we have questions about the application? (Include name, phone number, and email):

[REDACTED]

19. **Disqualification Factor.** A conviction, or entry of a plea of guilty or nolo contendere, for a felony violation of the Lacey Act, the Migratory Bird Treaty Act, or the Bald and Golden Eagle Protection Act disqualifies any such person from receiving or exercising the privileges of a permit, unless such disqualification has been expressly waived by the Service Director in response to a written petition. (50 CFR 13.21(c)) Have you or any of the owners of the business, if applying as a business, been convicted, or entered a plea of guilty or nolo contendere, forfeited collateral, or are currently under charges for any violations of the laws mentioned above?

☐ Yes ☒ No If you answered "Yes" provide: a) the individual's name, b) date of charge, c) charge(s), d) location of incident, e) court, and f) action taken for each violation.



Department of the Interior  
U.S. Fish and Wildlife Service

OMB No 1018-0093  
Expires 05/31/2017

## Federal Fish and Wildlife Permit Application Form

**Return to:** U.S. Fish and Wildlife Service  
Division of Management Authority (DMA)  
Branch of Permits, MS: IA  
5275 Leesburg Pike  
Falls Church, VA 22041-3803  
1-800-358-2104 or 703-358-2104

**Type of Activity:**  
**EXPORT/RE-EXPORT/IMPORT/INTERSTATE AND  
FOREIGN COMMERCE/TAKE OF ANIMALS  
(LIVE/ SAMPLES/PARTS/PRODUCTS) (ESA and/or CITES)**  
**(circle/highlight proposed activity)**

☒ **New Application**  
☐ **Requesting Re-issuance/Amendment of Permit#:** \_\_\_\_\_

Complete Sections A or B, and C through H of this application. U.S. address may be required in Section C, see instructions for details.  
**See attached instruction pages for information on how to make your application complete and help avoid unnecessary delays.**

<b>A. Complete if applying as an individual</b>			
1.a. Last name Fedrigo	1.b. First name Olivier	1.c. Middle name or initial [REDACTED]	1.d. Suffix Dr.
2. Date of birth (mm/dd/yyyy) [REDACTED]	3. Social Security No. [REDACTED]	4. Occupation Scientist	5. Affiliation/ Doing business as (see instructions) Rockefeller University
6.a. Telephone number [REDACTED]	6.b. Alternate telephone number [REDACTED]	6.c. Fax number [REDACTED]	6.d. E-mail address ofedrigo@rockefeller.edu

<b>B. Complete if applying on behalf of a business, corporation, public agency, Tribe, or institution</b>			
1.a. Name of business, agency, Tribe, or institution		1.b. Doing business as (dba)	
2. Tax identification no.		3. Description of business, agency, Tribe, or institution	
4.a. Principal officer Last name	4.b. Principal officer First name	4.c. Principal officer Middle name/ initial	4.d. Suffix
5. Principal officer title		6. Primary contact name	
7.a. Business telephone number	7.b. Alternate telephone number	7.c. Business fax number	7.d. Business e-mail address

<b>C. All applicants complete address information</b>				
1.a. Physical address (Street address; Apartment #, Suite #, or Room #; no P.O. Boxes) The Rockefeller University, 1230 York Avenue, Box 366				
1.b. City New York	1.c. State New York	1.d. Zip code/Postal code: 10065	1.e. County/Province New York	1.f. Country USA
2.a. Mailing Address (include if different than physical address; include name of contact person if applicable)				
2.b. City	2.c. State	2.d. Zip code/Postal code:	2.e. County/Province	2.f. Country

<b>D. All applicants MUST complete</b>	
1.	Attach check or money order payable to the U.S. FISH AND WILDLIFE SERVICE in the amount of \$100 nonrefundable processing fee. Federal, Tribal, State, and local government agencies, and those acting on behalf of such agencies, are exempt from the processing fee – <i>attach documentation of fee exempt status as outlined in instructions.</i> (50 CFR 13.11(d))
2.	Do you currently have or have you ever had any Federal Fish and Wildlife permits? Yes <input type="checkbox"/> If yes, list the number of the most current permit you have held or that you are applying to renew/re-issue: _____ No <input type="checkbox"/>
3.	Certification: I hereby certify that I have read and am familiar with the regulations contained in <b>Title 50, Part 13 of the Code of Federal Regulations</b> and the other <b>applicable parts in subchapter B of Chapter I of Title 50</b> , and I certify that the information submitted in this application for a permit is complete and accurate to the best of my knowledge and belief. I understand that any false statement herein may subject me to the criminal penalties of 18 U.S.C. 1001.
Signature (in blue ink) of applicant/person responsible for permit (No photocopied or stamped signatures) _____ Date of signature (mm/dd/yyyy) _____	

**E. EXPORT/RE-EXPORT/IMPORT/INTERSTATE AND FOREIGN COMMERCE/TAKE OF NON-NATIVE ANIMALS (Live/samples/parts/products) (CITES and/or ESA)**

*Allow at least 90 days for the application to be processed. Applications for endangered species permits must be published in the Federal Register for a 30-day public comment period.*

Complete all questions on the application. Mark questions that are not applicable with "N/A". If needed, use a separate sheet of paper. On all attachments or separate sheets you submit, indicate the application question number you are addressing. If you are applying for multiple specimens, be sure to indicate which specimen you are addressing in each response.

1. What activity are you requesting authorization to carry out (Indicate appropriate activities):

EXPORT ☒

INTERSTATE COMMERCE ☐

IMPORT ☒

FOREIGN COMMERCE ☐

\*Interstate Commerce permits authorize the sale of endangered and threatened species across State lines, but only for that will contribute to enhancing the propagation or survival of that species. Captive-breeding alone will not generally meet this requirement. Scientific research must be related to the species to be permitted. Interstate commerce activities with wildlife require the buyer to obtain a permit prior to the sale.

2. For EACH animal/specimen involved in the proposed activity provide:

Scientific name (genus, species, and, if applicable, subspecies)	Common Name	Birth/Hatch Date (mm/dd/yyyy) Or Approximate date	Quantity	Gender, if known	Permanent markings (e.g., tattoo, ID #, microchip #, scars), if alive	Type of Sample or product (e.g., blood, tissue, DNA)
EXAMPLE: <i>Macaca fascicularis</i>	Crab-eating macaque					
See attached on "Specimens"						

3. The current location of the specimen(s) (address and country):

Name:

Business Name:

Address:

Address:

City:

State/Province:

Country, Postal Code:



4. Recipient/Sender:
- If export, provide name and address of the recipient in the foreign country.
  - If import, provide name and address of the exporter in the foreign country.
  - If interstate or foreign commerce, provide name and address of recipient.

Name:

Business Name:

Address:

Address:

City:

State/Province:

Country, Postal Code:

**F. SOURCE OF SPECIMEN (answer question 5 or 6 for each animal/specimen involved, as appropriate).**

5. For each animal or animal from which specimen are obtained born in captivity:
- a. If you are the **breeder** of the specimen(s), please provide a signed and dated statement that includes the following:
    - i. Scientific name (genus, species, and, if applicable, subspecies) and common name;
    - ii. That the animal was bred and born at your facility;
    - iii. Birth/hatch date (mm/dd/yyyy), and, if applicable, identification information (as described in question 2b above);
    - iv. Name and address of your facility where each animal was bred and born; and
    - v. Location (Name of facility, address, city, State/province, postal code) of parental stock.
  - b. If you are **NOT the breeder** of the specimen(s), provide copies of documentation showing that you acquired the animal from the breeder or documentation demonstrating the history of transactions (e.g., chain of ownership of the animal) and a signed and dated statement from the breeder or breeder's record that clearly includes the following:
    - i. Scientific name (genus, species, and, if applicable, subspecies) and common name;
    - ii. That each animal was bred and born/hatched at his/her facility;
    - iii. Birth/hatch date (mm/dd/yyyy), and, if applicable, identification information (as described in question 2b above);
    - iv. Name and address of the breeder's facility; and
    - v. Location (name of facility, address, city, State/province, postal code) of parental stock.

6. For each animal/specimen **taken from the wild**, provide the following:
  - a. Scientific name (genus, species, and, if applicable, subspecies) and common name;
  - b. Specific location of where, when, and by whom (name and address) the specimen was removed from the wild;
  - c. Purpose of removal and length or approximate length of time held in captivity;
  - d. Describe your efforts to use captive specimens (e.g., captive-born, captive-held), or parts thereof, in lieu of taking animals from the wild.
  - e. Copies of your foreign or domestic collecting permit, license, contract or agreement;
  - f. Documentation showing that the specimen(s) was legally obtained by the applicant; and
  - g. Copies of any applicable State, Tribal, Federal, or Foreign government permits or licenses that authorized the removal of this animal from the wild.

#### **G. JUSTIFICATION FOR REQUESTED ACTIVITY.**

7. Provide a full statement justifying the proposed activity, particularly the following:
  - a. Describe the purpose of your proposed activity. For example, if the purpose is scientific research, attach a copy of your research proposal outlining the purpose, objectives, methods (e.g., specific information on survey/collection methods, sampling regime, equipment to be used), and whether similar work has already been done or is currently being done. If the purpose is conservation education, provide copies of educational materials (e.g., handouts, text of signage or public presentations), and include the purpose and objectives of the proposed activity. If the purpose is for propagation for conservation purposes, provide a description of how the species will be propagated, disposition of progeny, and cooperative agreements that are/will be established for re-introduction.
  - b. Description of the technical expertise of each person (please include CV or resume), as it relates to the proposed activities. If the proposed activity involves the import of live animals, include the experience of each animal caretaker working with the species.
  - c. Copies of contracts, agreements or other documents that identify persons involved and dates of activities for which authorization is being requested.
8. Provide a statement on how the activities will **enhance or benefit the wild population** (e.g., in-situ and ex-situ projects).
9. If live specimens are to be held in captivity as part of the proposed activity:
  - a. Provide a detailed description (e.g., size, construction materials, protection from the elements) and photographs or diagrams (no blueprints, please) clearly depicting the existing facilities **where the wildlife will be maintained**. If the specimens will be housed at multiple facilities, either immediately or within the next year, provide a full description of each facility. If you are unsure of which facilities may be receiving specimens (e.g., SSP has not made final decision), please indicate likely candidates and the mechanism that will be used to determine recipient facilities.
  - b. A statement of the specific technical experience of CV or resume available to the recipient(s) for maintaining and propagating live specimens of the same or similar species.
  - c. The number of years each species has been maintained at the facility;
  - d. The number of births by year for each species for the last 5 years; and
  - e. Mortalities at the facility with these or similar species in the last 5 years, causes of such mortalities, and steps taken to avoid or decrease such mortalities.

## H. IMPORTS, EXPORTS, OR RE-EXPORTS.

10. For shipment of LIVE specimens, the transport conditions for animals must comply with the CITES Guidelines for Transport of Live Animals or, in the case of air transport, with the International Air Transport Association (IATA) live animal regulations (contact airline for information). As such, describe:
  - i. The type, size, and construction of any shipping container; and
  - ii. The arrangements for watering or otherwise caring for the wildlife during transport.
11. **For import of LIVE CITES Appendix-I marine mammal specimens**, provide a copy of your FWS or NOAA Fisheries permit or authorization.
12. For import of CITES **Appendix-I listed species**, provide information to show the import is not for primarily commercial purposes as outlined in Resolution Conf. 5.10 ([www.cites.org](http://www.cites.org)).
13. For export of CITES **Appendix-I species**, provide a copy of the CITES import permit, or evidence one will be issued by the Management Authority of the country to which you plan to export the specimen(s). In accordance with Article III of the CITES treaty, it is required that import permits are issued before the corresponding export permit.
14. If the specimen is being **re-exported** (e.g., exporting a specimen that was previously imported into the United States), provide:
  - a. A copy of the canceled CITES export or re-export document issued by the appropriate CITES office in the country from which the wildlife was imported (if applicable); and
  - b. A cleared copy of Form 3-177, wildlife Declaration for Import (hard copy or electronic release); **or**
  - c. If you did not make the original import, provide a copy of the importer's documents outlined above and the invoice or other documentation that shows you acquired the wildlife from the original importer or history of transactions which demonstrate chain of ownership.
15. All international shipment(s) must be through a designated port. A list of designated ports (where an inspector is posted) is available from <http://www.fws.gov/le/designated-ports.html>. If you wish to use a port not listed, please contact the Office of Law Enforcement for a Designated Port Exemption Permit (form 3-200-2).
16. Name and address where you wish permit mailed, **if** different from page 1 (All permits will be mailed via the U.S. Postal Service, unless you identify an alternative means below):
17. If you wish the permit to be delivered by means other than USPS regular mail, provide an air bill, pre-paid envelope, or billing information. If you do not have a pre-paid envelope or air bill and wish to pay for a courier service with your credit card, please check the box below. Please **DO NOT** include credit card number or other information; you will be contacted for this information.  
☒ If a permit is issued, please send it via a courier service to the address on page 1 or question 11. I understand that you will contact me for my credit card information once the application has been processed.

18. Who should we contact if we have questions about the application? (Include name, phone number, and email):

[REDACTED]

19. **Disqualification Factor.** A conviction, or entry of a plea of guilty or nolo contendere, for a felony violation of the Lacey Act, the Migratory Bird Treaty Act, or the Bald and Golden Eagle Protection Act disqualifies any such person from receiving or exercising the privileges of a permit, unless such disqualification has been expressly waived by the Service Director in response to a written petition. (50 CFR 13.21(c)) Have you or any of the owners of the business, if applying as a business, been convicted, or entered a plea of guilty or nolo contendere, forfeited collateral, or are currently under charges for any violations of the laws mentioned above?

☐ Yes ☒ No If you answered "Yes" provide: a) the individual's name, b) date of charge, c) charge(s), d) location of incident, e) court, and f) action taken for each violation.



# **Professor Emma Teeling, B.Sc., M.Sc., Ph.D., MRIA**

School of Biology and Environmental Science, University College

Phone: + ; E-mail: [emma.teeling@ucd.ie](mailto:emma.teeling@ucd.ie); Web: <http://batlab.ucd.ie/>

## **Biography:**

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Prof. Emma Teeling is a world-class international leader in the cross-cutting fields of mammalian phylogenetics and comparative genomics, with particular expertise in bat biology. She established the Laboratory of Molecular Evolution and Mammalian Phylogenetics in 2005 and is the Founding Director of the Centre for Irish Bat Research at University College . She has been awarded a prestigious European Research Council (ERC) Starting grant ( ) and a Science Foundation , President of Young Researcher Award . She successfully leads a prolific, internationally renowned research team of typically 10 people and has secured over €4.5M in research funding. Her record of leadership and research excellence is demonstrated by her publication record of >85 internationally peer-reviewed papers, 5 book chapters, 3 invited subject reviews. A number of these publications have over-turned conventional paradigms in mammalian biology and therefore have been published in high profile journals such as *Nature* (n=1), *Science* (n=4), *Proceedings of the National Academy of Sciences* (n=3), and *Nature Communications* (n=1). Her high standing in the international community is highlighted by a total citation record of 6560; prestigious international keynote lectures; invited high profile collaborations such as Genome 10K (includes 64 scientific leaders assembled to sequence 10,000 vertebrate genomes); and, high profile invited public presentations (e.g. TEDx talk; ~481,149 views; BBC's Science Club with Dara O'Briain).

## **Research:**

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Prof. Teeling's integrative research in the fields of zoology, phylogenetics, genomics and conservation biology uncovers the genetic signatures of survival that enables species to adapt to an ever-changing environment. The two main goals of her research are: (1) study unique model species to better understand the structure and function of the human genome to inform medicine and molecular biology; (2) understand and thereafter conserve, natural populations.

## **Career Profile:**

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- **European Research Council Starting Investigator,**
- **Professor in Evolution and Genetics,**
- **Director of the Centre for Irish Bat Research,**
- **President of Ireland Young Researcher,**
- **Lecturer in Evolution and Genetics ( )** School of Biology and Environmental Science, ).
- **Postdoctoral Research Fellow,** Laboratory of Genomic Diversity, National Cancer Institute,

## **Education:**

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- **Ph.D. in Molecular Phylogenetics,** niversity nd  
University of .
- **M.Sc. in Animal Behavior and Animal Welfare,** University of nd  
Ecological Institute,
- **B.Sc. in Zoology, 1st Class Honors,**

## Scientific Leadership:

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Prof. Teeling recognizes the power of leading and integrating diverse researchers and scientific fields to address the grand challenges in science and society. She has conceived of and leads a new collaboration between a grass-roots conservation society in Brittany, France ([www.bretagne-vivante.org](http://www.bretagne-vivante.org)); bat researchers in Italy, Slovenia, UK, Germany; molecular biologists in Ireland, France, UK, Germany to uncover the molecular basis of exceptional ageing in wild bats, as part of her current ERC starting grant AGELESS. She is the director and co-founder of BAT1K, a consortium of scientists, academics and bat lovers united to conserve and sequence the genome of all 1300 species of bats. She is the founder and director of the Centre for Irish Bat Research ([www.cibr.ie](http://www.cibr.ie)); the co-founder of the White Nose Syndrome European consortium (67 scientists from 29 countries). She has led researchers in Thailand, Myanmar, UK and Ireland to work together to understand how species arise and evolve. Her leadership ability is demonstrated by an excellent track record of research funding, prestigious international keynote lectures (e.g. Royal Society London, 2015); numerous invitations to teach at highly recognized workshops (e.g. Conservation Genetics Workshop, Puerto Rico 2015; Hungry 2016); nominations and elections to international scientific councils (e.g. Royal Irish Academy; Irish Research Council; Council of Society of Molecular Biology and Evolution (MBE); Executive Committee G10K; and, editorial boards (e.g. Assoc. Editor, MBE); awarded Chevalier des Palmes Académiques, 2017 by the French Government.

## Teaching:

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Prof. Teeling is a key member of the first year undergraduate teaching team at [REDACTED] since [REDACTED], teaching classes of >400 students. She has spearheaded the teaching of evolutionary biology, genetics and phylogenetics to undergraduate and MSc students at all levels. She is responsible for revolutionizing the first year teaching program, introducing and driving the use of an online tutorial system, now adopted throughout most biology first year modules. This new teaching method has significantly improved grades and is much appreciated by the students. She has introduced a new tutorial system for 3<sup>rd</sup> year evolutionary biology students, to enhance the comprehension of complex evolutionary theories to classes of >100 students, whom had previously had found these topics intangible and difficult when taught through didactic lecturing alone. Students have ranked Prof. Teeling's teaching ability very highly, reflecting her dedication to inspire and teach students: *"Dr Teeling's enthusiasm for teaching this module ensured that I stayed focused during class in the genetics section of this module. Absolutely loved genetics and will be choosing it as a subject next year!"*

- *Course coordinator and lecturer:*
  - 1<sup>st</sup> Year: Cell Biology and Genetics, Biol10110/Biol10020 (>400 students)
  - 3<sup>rd</sup> Year: Evolution, Zool30030 (>100 students)
  - 4<sup>th</sup> Year: Molecular Phylogenetics and Evolution, Zool40040 (>40 students)
  - M.Sc.: Current Developments in Evolutionary Biology, Biol40070 (>10 students)
- *Course lecturer:*
  - 1<sup>st</sup> Year: Medical Zoology, Zool10010 (>100 students)
  - 1<sup>st</sup> Year: Organismal Diversity, Biol10100 (>250 students)
  - 1<sup>st</sup> Year: Biology Tutorials, Sci10010 (>6 students)
  - 2<sup>nd</sup> Year: Biology Tutorials, Biol20030 (>6 students)
  - 2<sup>nd</sup> Year: Animal and Plant Genetics, Gen20010 (>200 students)
  - 3<sup>rd</sup> Year: Evolutionary Biology Tutorials, Zool30030 (>100 students)
  - M.Sc.: Evolution in the Open, Biol40260 (>10 students)

## **Student Mentoring and Research Supervision:**

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- Currently supervising: 1 Research Scientist; 3 Postdoctoral Research Fellows; 5 Ph.D. students; 1 M.Sc. student.
- Supervised >50 fourth year research dissertations; 7 M.Sc. summer projects.
- Supervised 5 visiting undergraduate students and 9 visiting Ph.D./M.Sc. students (UK, China, Thailand, Italy, Spain, Switzerland, France).
- **6 M.Sc. students graduated:** Keith [REDACTED]; Alisha [REDACTED]; John [REDACTED]; Paul [REDACTED] ([REDACTED] co-supervised; Sara [REDACTED] ([REDACTED] Aisling [REDACTED] ([REDACTED]).
- **9 Ph.D. students graduated:** Una [REDACTED] ([REDACTED] Stephen [REDACTED] ([REDACTED] Graham [REDACTED]); Bruno [REDACTED]; Daniel [REDACTED] Serena [REDACTED] ([REDACTED] Sara [REDACTED]); Sebastien [REDACTED]); Sinead Nic [REDACTED] ([REDACTED] co-supervised.
- **5 Past Postdoctoral Research Fellows:** Dr. Aurore [REDACTED] Dr. Sebastien [REDACTED] Dr. Emma [REDACTED]); Dr. Jennifer [REDACTED]; Dr. Michael [REDACTED]).

## **Notable Invited Talks/Presentations:**

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- **Institute for Translation Medicine and Therapeutics**, Penn, PA, USA, Genomic Basis of Extended Longevity, [REDACTED].
- **Plenary, Genome 10K and Genome Science Conference**, Earlham Institute, UK, Growing Old Yet Staying Young, [REDACTED].
- **Plenary, 14<sup>th</sup> European Bat Research Symposium**, Donostia, The Basque Country, Extraordinary Adaptations in Bats, [REDACTED].
- **Konrad Lorenz Institute of Ethology**, Vienna, Ageing in Bats, [REDACTED].
- **University of Uzhgorod**, Ukraine, Telomeres and Ageing in Bats, [REDACTED].
- **Future Health Summit**, Dublin, Secret of Healthy Ageing, [REDACTED].
- **Plenary, Berlin Bat Meeting**, Berlin, Germany, Are Bats Special, [REDACTED].
- **Plenary, AGBT**, Florida, USA, Genomic Basis of Extended longevity in Bats, [REDACTED].
- **University of Bern**, Switzerland, Evolution of Longevity in Mammals, [REDACTED].
- **Natural History Museum**, London, Halted Ageing in Bats, [REDACTED].
- **Conservation Genetics**, Hungary, Phylogenetics of Bats, [REDACTED].
- **ConGenomics**, Portugal, Conservation Genomics in Bats, [REDACTED].
- **Plenary, BritBats**, London, Evolution of Ageing in Bats, [REDACTED].
- **Royal Society** London, Evolution of Mammals, [REDACTED].
- **Barcelona Biomedical Research Park**, Spain, Ageing in Bats, [REDACTED].
- **Smithsonian Conservation Institute**, Washington DC, Bat Genomics, [REDACTED].
- **Open Public Lecture, Puerto Rico**, Conservation and Bats, [REDACTED].

- **SoapBox Science Dublin**, Promoting women in Science, [REDACTED].
- **“Destination Europe”** Invited Plenary Speaker, San Francisco, Promoting European and Irish Science, [REDACTED].
- **“Science Club live at the Mansion House”** hosted by Dara O’Brian, >700 people, [REDACTED]
- Invited **Expert Guest Appearance on BBC’s “Science Club with Dara O’Brian”**, [REDACTED]
- Invited to give a **TEDx talk for > 2000 people**, Bord Gáis Theatre, [REDACTED]
- **>55 Invited Talks** in e.g. Ireland, UK, USA, China, Germany, Austria, Puerto Rico, Mexico, Spain, Thailand, Poland, Czech Republic and Australia including **>14 Keynote/Plenary Lectures**.
- Research group has given **>140 presentations** in over 18 countries.
- Invited speaker as an ambassador for Irish Science with the **President of Ireland, Prof. Mary McAleese** at the White Head Institute, Massachusetts, USA ([REDACTED])

## Funding:

### > €4.5 Million in lead PI funding (2005-2017)

Period	Funding Agency	Amount €	Title
[REDACTED]	UCD Seed Funding	[REDACTED]	How to fight a deadly virus and win: uncovering the exceptional immunity of bats
[REDACTED]	SBES School-Studentship	[REDACTED]	The molecular basis of exceptional longevity in bats. (Ph.D. Andrea Locatelli).
[REDACTED]	UCD Seed Funding	[REDACTED]	The role of the microbiome in halted ageing?
[REDACTED]	SFI Discover Science	[REDACTED]	Ecology and Evolution In Action: Lessons from Bats
[REDACTED]	UCD-CSC Studentship	[REDACTED]	Bat ‘Wildlife’ transcriptomics uncovers the mechanisms of halted ageing in mammals (Ph.D. Huang Zixia)
[REDACTED]	ERC Starting Grant	[REDACTED]	AGELESS: Comparative genomics / ‘wildlife’ transcriptomics uncovers the mechanisms of halted ageing in mammals
[REDACTED]	UCD Seed Funding	[REDACTED]	Conservation of Rare and Endangered Frogs in India
[REDACTED]	PRTL-PhD Funding	[REDACTED]	The Effect of Wind Farms on Irish bats
[REDACTED]	IRC-Studentship	[REDACTED]	Systematic studies of the Asian horned frogs (Ph.D. Stephen Mahony)
[REDACTED]	IRC–Marie Curie Postdoctoral Fellowship	[REDACTED]	The Role of Sensory Ecology in Species Recognition and its Implications for Speciation (Dr. Sebastien Puechmaille)
[REDACTED]	UCD Seed Funding	[REDACTED]	Multitasking Multi-Gene Families
[REDACTED]	Science Foundation Ireland (STFI)	[REDACTED]	Next Generation Sequencing Investigates the Evolution of Olfaction in Mammals
[REDACTED]	FCT-Studentship	[REDACTED]	A Molecular Investigation into Mammalian Vision (Ph.D. Bruno Fonseca Simoes)
[REDACTED]	National Parks and Wildlife Service	[REDACTED]	Centre for Irish Bat Research
[REDACTED]	IRC-Studentship	[REDACTED]	Molecular Evolution of Hearing in Mammals (M.Sc. John Kirwan)
[REDACTED]	Irish Heritage Council	[REDACTED]	Conservation of the Whiskered Bat ( <i>Myotis mystacinus</i> ) in Ireland
[REDACTED]	IRC- Studentship	[REDACTED]	The Ecology and Phylogeography of the Whiskered Bat in Ireland (Ph.D. Daniel Buckley)
[REDACTED]	Science Foundation Ireland (PIYRA)	[REDACTED]	A Comparative Genomic Investigation into the Molecular Mechanisms and Evolution of Sensory

			Perception in Mammals
██████	IRC- Studentship	██████	Conservation and Phylogeography of the Endangered Lesser Horseshoe Bat (Ph.D. Serena Dool)
██████	IRC- Studentship	██████	Molecular Evolution of Olfactory Receptors in Mammals (Ph.D. Sara Hayden)
██████	UCD Seed Funding	██████	The Evolution of Mammalian Olfaction
██████	Science Foundation Ireland (RFP)	██████	A Molecular Investigation into the Population Dynamics Conservation Status of the World's Smallest Mammal, <i>Craseonycteris thonglongyai</i>

CSC= Chinese Scholarship Council; ERC= European Research Council; FCT= Portuguese Ministry for Science Technology and Higher Education; IRC = Irish Research Council; PIYRA= President of Ireland Young Investigator Award; PI= Principal Investigator; RFP= Research Frontiers Programme; STTF= Short Term Travel Fellowship.

## Roles of Responsibility Within ████████

- Head of the Research and Innovation, School of Biology and Environmental Science, ████████ ████████
- Elected Member of the Governing Authority of ████████ ████████
- Earth Institute, Evolution and Ecology Strand Leader, ████████
- Founder and Leader of the Laboratory of Molecular Evolution and Mammalian Phylogenetics, ████████
- Founder and Director of the Centre for Irish Bat Research, ████████t;
- Earth Institute Executive Member, ████████
- ████████ Animal Research Ethics Committee member, ████████
- Presidential Nomination to ████████ President's Lunch Time Seminar's Committee, ████████
- ████████ Seed Funding Committee member, ████████
- ████████ Research IT Steering Group member, ████████;
- ████████ Science Foresight Committee member- ████████
- ████████ SFI Overhead Investment Plan Advisory Group member, ████████;
- SBES Research and Innovation committee member, ████████;
- SBES Theme Leader of the Evolution and Population Biology Group, ████████
- SBES Seminar Series coordinator, ████████;
- Member and presenter for 'The Campaign for UCD' – ████████
- Leader of the SBES Molecular Biology advisory group, ████████
- Earth Institute Theme Group member - ████████

## Additional Achievements:

- Awarded **Chevalier des Palmes Académiques** by French government (██████)
- Elected Member of the **Royal Irish Academy** (██████).
- Elected Board Member of the **Irish Research Council** ████████.
- Elected **Council Member**: Society of Molecular Biology and Evolution (██████).



- Invited **Associate Editor**: *Molecular Biology and Evolution*, impact factor 10.4, [REDACTED]
- **Member of the Editorial Board**: *Journal of Mammalian Evolution* ([REDACTED] *Acta Chiropterologica* ([REDACTED]); *Organisms Diversity & Evolution* ([REDACTED]).
- **Vice-Chair**: Wild Geese Network of Scientists ([REDACTED]).
- Developed a **Science for Schools** online transition year syllabus for high school students using bats a model to explore difficult concepts in Evolution and Ecology. > 3000 downloads since [REDACTED] < <http://www.ucd.ie/scienceforschools/>>.
- **Key collaborations**:
  - Co-Founder and Director of **BAT1K**- Consortium united to sequence the genome of all 1200 bat species [www.bat1k.com](http://www.bat1k.com).
  - Executive Board Member of **Genome 10K community** ([www.genome10k.org](http://www.genome10k.org))
  - Invited member and active participant in the **NSF funded Mammal Tree of Life Project**
  - Co-Founder and Leader of the **European White Nose Syndrome Consortium**
  - Irish representative with Dublin Zoo of the **Frozen Ark Conservation Initiative**.
- Listed in the **top 100 female Irish scientists**  
<<http://www.siliconrepublic.com/careers/item/36073-wit2014>>.
- Short-listed **Eisenhower Fellow**, Ireland ([REDACTED])
- Invited ‘**Leonardo**’ of the Science Gallery, Dublin (2[REDACTED]).
- **Conference organizer**: Society for Molecular Biology and Evolution meeting (SMBE [REDACTED], Dublin, 2012 (>1500 delegates).
- **Symposium organizer**: SMBE Chicago, USA, 2013; [REDACTED] International Bat Research Conference, Mexico, [REDACTED]; [REDACTED] International Bat Research Conference, Poland, [REDACTED]
- **Organizing committee member**: [REDACTED] European Bat Research Meeting, Ireland, [REDACTED]
- **Regional director** for the Washington D.C. chapter of BioLink Ireland-USA, [REDACTED]
- **External examiner for eight international Ph. D. theses**: France; South Africa; Czech Republic; UK X 2; Switzerland; Ireland X 2.
- **Invited grant reviewer** for the NSF Research in Undergraduate Institutions Awards and Collaborative Projects [REDACTED] National Geographic Society, [REDACTED] NSERC Canada [REDACTED] U.S.-Israel Binational Science Foundation [REDACTED]
- **Public Outreach**:
  - Research was part of television series “**10 Things to Know about Ageing**”, filmed on field work in Brittany, France, [REDACTED] by National Irish Television Network (RTE)
  - Public Evening Lecture- **Skeptic’s Society of Ireland**, Dublin, [REDACTED]
  - Public Evening Lecture- **Institute of Biology**, Dublin, [REDACTED].

- Invited guest, “*Friends of Aoibhinn*”, national radio, 60 minute chat show detailing life as a scientist, [REDACTED].

- “**Science Club live at the Mansion House**” hosted by Dara O’Brian, >700 people, [REDACTED]

-Invited Expert Guest Appearance on BBC’s “**Science Club with Dara O’Brian**”, [REDACTED]

-Invited inaugural **STEM** on stage speaker for Women in Technology and Science, [REDACTED]

<http://www.siliconrepublic.com/innovation/item/31834-wit2013/>

-Invited **TEDx** speaker, BGET theatre ~2300 people, Sept. 2012. ~**426,800 views**  
[http://www.ted.com/talks/emma\\_teeling\\_the\\_secret\\_of\\_the\\_bat\\_genome.html](http://www.ted.com/talks/emma_teeling_the_secret_of_the_bat_genome.html)

-Invited Speaker –Children’s ARK museum, Dublin, [REDACTED]

- **Created Movie on Research for:**

**UCD Faces of Research, 2012**

<http://www.youtube.com/watch?v=Mz8dVfVqSS8&feature=youtu.be>

**UCD Earth Institute, 2009**

[http://www.ucd.ie/expertiseatucd/researchshowcase/earthinstitute/02\\_emma\\_teeling.html](http://www.ucd.ie/expertiseatucd/researchshowcase/earthinstitute/02_emma_teeling.html)

- Invited speaker at local schools numerous times for Science week: e.g. Blackrock College, Rosemont, St. Teresians, Belgrove Junior Boys School, St. Colombas.

-Provided >**50 scientific** interviews for newspaper articles, popular radio / television programmes and scientific magazines (e.g. *RTE News; Science, Nature, New Scientist, Irish Times; Mooney Goes Wild; Ireland AM; News Talk, Spin FM, BBC, RTE1, Moncreiff Show*).

-Research was highlighted for an entire episode in one of Ireland’s leading wildlife T.V. shows- ‘**Living the Wildlife**’

-**Invited by the President of Ireland, Prof. Mary McAleese** to be the Irish Scientific community representative in an intimate radio show, Conversations at the Arás, Dec. 2009.

-Highlighted in the Royal Irish Academy’s publication “*Flashes of Brilliance*” as a leading, upcoming Irish scientist.

-Research was selected as part of a session at the Euroscience Open Forum, Turin (ESOF 2010) entitled “*450 million years of climate change and evolution. What can bats, plants and fish tell us about adaptation, speciation and extinction*”.

- **Invited reviewer** numerous times for “*Science*”, “*Nature*”, “*Nature Communications*”, “*Proceedings of the Royal Society*”, “*Molecular Phylogenetics and Evolution*”, “*Journal of Mammalian Evolution*”, “*Acta Chiropterologica*”, “*Journal of Heredity*”, “*Bioinformatics*”, “*Journal of Mammalogy*”, “*PLoS Biology*”, “*PLOS one*” “*Molecular Ecology*”, “*Zoologica Scripta*”, “*Genetics Research*”, “*Proceedings of the Royal Irish Academy*”, “*BMC Genetics*”, “*PNAS*”

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## Peer Reviewed Publications:

Google scholar: h-index =29; Total = 85 published/in press; citations =6560;

\*papers where I am senior/corresponding/lead

1. \***E. C. Teeling**, S. C. Vernes, L. M. Davalos, D. A. Ray, M. T. P. Gilbert, E. Myers. (2018). Bat Biology, Genomes, and the Bat1K Project: To generate chromosome-level genomes for all living bat species. *Annual Review Animal Biosciences* (In Press).
2. \*N. M. Foley, G. M. Hughes, Z. Huang, M. Clarke, D. Jebb, C. V. Whelan, E. J. Petit, F. Touzalin, O. Farcy, G. Jones, R. D. Ransome, M. J. O’Connell, G. Kerth, H. Rebelo, L. Rodrigues, S. J. Puechmaille & **E. C. Teeling**. Growing old, yet staying young: the role of telomeres in bats’ exceptional longevity. *Science Advances* (In Press).
3. M. Beaulieu, B. Lüdtkeb, F. Touzalin, S. Dool, **E. C. Teeling** & S. J. Puechmaille. Comparing what is ecologically comparable in interspecific ageing studies. *Ageing Research Reviews* (In Revision).
4. \*G. M. Hughes, E. M. Boston, J. A. Finarelli, W. J. Murphy, D. G. Higgins & **E. C. Teeling**. The role of olfactory receptor evolution in mammalian niche specialization. *Molecular Biology and Evolution* (In Revision).
5. \*S. Mahony, R. G. Kamei, S.D. Biju, **Emma C. Teeling**. Uncovering cryptic diversity within the White-lipped horned frogs, Megophrys major species complex (Amphibia: Megophryidae): insights into how SNP heterozygosity affects phylogenetic inference and species delimitation. *Zoo Taxa* (In Review).
6. \*G. M. Hughes, J. Leech, S. J. Puechmaille, J. V. Lopez & **E. C. Teeling**. (2018). Is there a link between aging and microbiome diversity in exceptional mammalian longevity? *PeerJ* 6, e4174.
7. \*Z. Huang & **E. C. Teeling**. (2017). ExUTR: a novel pipeline for large-scale prediction of 3’-UTR sequences from NGS data. *BMC Genomics* 18 (1), 847.
8. \*Joanna Kacprzyk, G. Hughes, E. M. Palsson-McDermott, S. R. Quinn, S. J. Puechmaille, L. A. J. O’Neill & **E. C. Teeling**. (2017). Potent anti-inflammatory response in bat macrophages linked to extended longevity and viral tolerance. *Acta Chiropterologica* 19(2), 219–228.
9. M. Carr, G. Gonzalez, M. Sasaki, S. E. Dool, K. Ito, A. Ishii, B. M. Hang’ombe, A. S. Mweene, **E. C. Teeling**, W. W. Hall, Y. Orba, & H. Sawa. (2017). Identification of the same polyomavirus species in different African horseshoe bat species is indicative of short range host-switching events. *Journal of General Virology* 98 (11), 2771-2785.
10. H. V. Figueiró, G. Li, F. J. Trindade, J. Assis, F. Pais, G. Fernandes, S. H. D. Santos, G. M. Hughes, A. Komissarov, A. Antunes, C. S. Trinca, M. R. Rodrigues, T. Linderoth, K. Bi, L. Silveira, F. C. C. Azevedo, D. Kantek, E. Ramalho, R. A. Brassaloti, P. M. S. Villela, A. L. V. Nunes, R. H. F. Teixeira, R. G. Morato, D. Loska, P. Saragüeta, T. Gabaldón, **E. C. Teeling**, S. J. O’Brien, R. Nielsen, L. L. Coutinho, G. Oliveira, W. J. Murphy & E. Eizirik. (2017). Genome-wide signatures of complex introgression and adaptive evolution in the big cats. *Science Advances* 3 (7), e1700299.
11. \*N. M. Foley, S. M. Goodman, C. V. Whelan, S. J. Puechmaille & **E. C. Teeling**. (2017). Towards navigating the Minotaur’s Labyrinth: Cryptic diversity and taxonomic revision within the speciose genus *Hipposideros* (Hipposideridae). *Acta Chiropterologica* 19(1), 1–18.

12. \*Z. Wang, T. Zhu, N. Fang, J. Zhang, L. Zhang, J. Pang, **E. C. Teeling** & S. Zhang. (2017). Embryonic development supports a single origin of echolocation in bats. *Nature Ecology and Evolution* 1, 0021. doi:10.1038/s41559-016-0021
13. \*S. Mahony, N. M. Foley, S. D. Biju & **E. C. Teeling**. Evolutionary History of the Asian Horned Frogs (Megophryinae): Integrative Approaches to Timetree Dating in the Absence of a Fossil Record. (2017). *Molecular Biology and Evolution* 34 (3), 744-771.
14. \*Z. Huang, D. Jebb & **E. C. Teeling**. (2016). Blood miRNomes and transcriptomes reveal novel longevity mechanisms in the long-lived bat, *Myotis myotis*. *BMC Genomics* 17(1), 906.
15. \*S. E. Dool, S. J. Puechmaille, C. Kelleher, K. McAney & **E. C. Teeling**. (2016). The effects of human-mediated habitat fragmentation on a sedentary woodland-associated species (*Rhinolophus hipposideros*) at its range margin. *Acta Chiropterologica* 18(2): 377–393.
16. \*A. G. Locatelli, D. Jebb & **E. C. Teeling**. (2016). The complete mitochondrial genome of Kuhl's pipistrelle, *Pipistrellus kuhlii* (Chiroptera: Vespertilionidae) *Mitochondrial DNA Part B* 1 (1), 423-424.
17. \*N. M. Foley, M. S. Springer & **E. C. Teeling**. (2016). Mammal Madness: Is the mammal tree of life not yet resolved? *Philosophical Transactions of the Royal Society B* (1699), 20150140.
18. \*D. J. A. Orr, **E. C. Teeling**, S. J. Puechmaille, & J. A. Finarelli. (2016). Patterns of orofacial clefting in the facial morphology of bats: a possible naturally-occurring model of cleft palate. *Journal of Anatomy* doi: 10.1111/joa.12510.
19. J. Kacprzyk, **E. C. Teeling**, C. Kelleher & M. Volleth. (2016). Wing membrane biopsies for bat cytogenetics: finding of 2n=54 in Irish *Rhinolophus hipposideros* (Rhinolophidae, Chiroptera, Mammalia) supports two geographically separated chromosomal variants in Europe. *Cytogenetic and Genomic Research* 148 (4), 279-283.
20. \***E. C. Teeling**, G. M. Jones & S. J. Rossiter. (2016). Phylogeny, Genes, and Hearing- Implications for the Evolution of Hearing and Echolocation in Bats Bioacoustics p.g. 25-54, Eds. B. Fenton and A.N. Pooper. Springer (Reviewed Invited Book Chapter.)
21. \*S. E. Dool, S. J. Puechmaille, N. M. Foley, B. Allegrinie, A. Bastian, G. L. Mutumia, T. G. Malulekea, J. Lizelle Odendaal, **E. C. Teeling** & D. S. Jacobs. (2016). Nuclear introns outperform mitochondrial DNA in phylogenetic reconstruction: lessons from horseshoe bats (Rhinolophidae: Chiroptera). *Molecular Phylogenetics and Evolution* 97, 196-212.
22. \*D. Jebb, N. M. Foley, S. J. Puechmaille, **E. C. Teeling**. (2015). The complete mitochondrial genome of the Greater Mouse-Eared Bat, *Myotis myotis* (Chiroptera: Vespertilionidae). *Mitochondrial DNA* 1-3.
23. \*H. Zixia, A. Gallot, N.T. Lao, S.J. Puechmaille, N. M. Foley, D. Jebb, M. Bekaert, **E. C. Teeling**. (2015) A non-lethal sampling method to obtain, generate and assemble whole-blood transcriptomes from small, wild mammals. *Molecular Ecology Resources* DOI: 10.1111/1755-0998.12447

24. \*N. M. Foley, V. D. Thong, P. Soisook, S. M. Goodman, K. Armstrong, D. Jacobs, S. J. Puechmaille & **E. C. Teeling**. (2015). How and why overcome the impediments to resolution: lessons from rhinolophid and hipposiderid bats. *Molecular Biology and Evolution* 32 (2), 313-333.
25. \*Boston, E.S.M., S. P. Puechmaille, F. Clissmann & **E. C. Teeling**. (2014). Further evidence for cryptic north-western refugia in Europe: mitochondrial phylogeography of the sibling species *Pipistrellus pipistrellus* and *Pipistrellus pygmaeus*. *Acta Chiropterologica* 16 (2), 263-277.
26. \*B. J. McMahon, **E. C. Teeling**, Jacob Höglund. How and why should we implement genomics into conservation? (2014). *Evolutionary Applications* 7 (9), 999-1007.
27. \*S. Hayden & **E. C. Teeling**. (2014). The molecular biology of olfaction in vertebrates *Anatomical Records* 297 (11), 2216-2226.
28. \*S. Hayden, L. Davalos , M. Bekaert , A. Goodbla , W. J. Murphy, **E. C. Teeling**. A Cluster of Olfactory Receptor Genes Linked to Frugivory in Bats. (2014). *Molecular Biology and Evolution* 31 (4), 917-927.
29. \*S. J. Puechmaille, M. Schuchmann, S. Zsebok, I. Borissov, **E. C. Teeling** & B. M. Siemers. (2014). Female mate choice drives the evolution of high frequency in echolocating bats *PloS One* 9 (7), e103452.
30. \*S. J. Puechmaille & **E. C. Teeling**. (2014). Non-invasive genetics can help find rare species: a case study with *Rhinolophus mehelyi* (Rhinolophidae: Chiroptera). *Mammalia* 78 (2), 251-255.
31. \*G. M. Hughes, **E. C. Teeling**, D. G. Higgins. (2014). Loss of olfactory receptor function in hominid evolution. *PloS One* 9(1), e84714.
32. C. C. Morgan, A. M. McCartney, M. T.A. Donoghue, N. B. Loughran, C. Spillane, **E. C. Teeling**, M. J. O'Connell. (2013). Molecular adaptation of telomere associated genes in mammals *BMC Evolutionary Biology* 13(1): 251.
33. \*S. Mahony, **E. C. Teeling**, S.D. Biju. (2013). Three new species of horned frogs, Megophrys (Amphibia: Megophryidae), from northeast India, with a resolution to the identity of *Megophrys boettgeri* populations reported from the region. *Zootaxa* 3722: 143-169.
34. M.S. Springer, R.W. Meredith, **E. C. Teeling**, W.J. Murphy. (2013). Technical Comment on “The Placental Mammal Ancestor and the Post–K-Pg Radiation of Placentals” *Science* 341: 613-613.
35. \***E. C. Teeling** & S. B. Hedges. (2013). Making the impossible possible: rooting the tree of placental mammals. *Molecular Biology and Evolution* 30(9): 1999-2000.
36. \*G. Jones, **E. C. Teeling**, S. J. Rossiter. (2013). From the ultrasonic to the infrared: molecular evolution and the sensory biology of bats. *Frontiers in Integrative Physiology* 4: 117.



37. \*S. E. Dool, S. J. Puechmaille, C. Dietz, J. Juste, C. Ibáñez, P. Hulva, S. G. Roué, E. J. Petit, G. Jones, S. J. Rossiter, **E. C. Teeling**. (2013) Phylogeography and postglacial recolonisation of Europe by *Rhinolophus hipposideros*: evidence from multiple genetic markers. *Molecular Ecology* 22 (15): 4055-4070.
38. \*D. D. Scott, S. Fitzpatrick, D. A. Bailie, E. S. M. Boston, M. G. Lundy, D. J. Buckley, **E. C. Teeling**, W. I. Montgomery, P. A. Prodöhl. (2013). Isolation and characterization of eight polymorphic microsatellite loci for Natterer's bat, *Myotis nattereri* (Vespertilionidae, Chiroptera). *Conservation Genetic Resources* DOI: 10.1007/s12686-013-9871-2.
39. \*G. M. Hughes, L. Gang, W. J. Murphy, D. G. Higgins, **E. C. Teeling**. (2013). Using Illumina Next Generation Sequencing Technologies to Sequence Multigene Families in *de novo* Species. *Molecular Ecology Resources* 13(3): 510-521.
40. \*J. Kirwan, M. Bekaert, J. M. Commins, K. T. J. Davies, S. J. Rossiter, **E. C. Teeling**. (2013). A Phylomedicine Approach to Understanding the Evolution of Auditory Sensory Perception and Disease in Mammals. *Evolutionary Applications* 6(3): 412-422.
41. M. G. Lundy, A. Harrison, D. J. Buckley, E. S. Boston, D. D. Scott, **E. C. Teeling**, W. I. Montgomery, J. D.R Houghton. (2013). Prey field switching based on preferential behaviour can induce Levy flights. *Journal of the Royal Society Interface* 10(78): 20120489.
42. \*D. J. Buckley, M. G. Lundy, E. S. M. Boston, D. D. Scott, Y. Gager, P. Prodohl, F. Marnell, W. I. Montgomery, **E. C. Teeling**. (2012). The spatial ecology of the whiskered bat (*Myotis mystacinus*) at the western extreme of its range provides evidence of regional adaptation. *Mammalian Biology - Zeitschrift für Säugetierkunde* 78(3): 198–204.
43. \*S. M. Goodman, S. Puechmaille, N. Friedli-Weyeneth, J. Gerlach, M. Ruedi, C. Schoeman, W.T. Stanley, **E. C. Teeling**. (2012). Phylogeny of the Emballonurini bats (Family Emballonuridae): new genus of Emballonura and species of Coleura. *Journal of Mammalogy* 93(6): 1440-1455.
44. \*E. Boston, S. Puechmaille, D. Buckley, M. Lundy, D. Scott, P. Prodohl, I. W. Montgomery, **E. C. Teeling**. (2012). Empirical assessment of non-invasive population genetics in bats: comparison of DNA quality from faecal and tissue samples. *Acta Chiropterologica* 14(1): 45-52.
45. \*M. G. Lundy, D. J. Buckley, E. S. M. Boston, D. D. Scott, P. A. Prodöhl, F. Marnell, **E. C. Teeling**, W. I. Montgomery. (2012). Behavioural context of multi-scale species distribution models assessed by radio-tracking. *Basic and Applied Ecology* 13(2): 188-195.
46. M. Ruedi, N. Friedli-Weyeneth, **E. C. Teeling**, S. J. Puechmaille, S. M. Goodman. (2012). Biogeography of Old World emballonurine bats (Chiroptera: Emballonuridae) inferred with mitochondrial and nuclear DNA. *Molecular Phylogenetics and Evolution* 64(1): 204-211.
47. \***E. C. Teeling**, S. E. Dool & M. S. Springer. Phylogenies, fossils and functional genes: The evolution of echolocation in bats. (2012). In: *Evolutionary History of Bats: Fossils, Molecules, and Morphology*, eds. G. F. Gunnell and N. B. Simmons. Cambridge: Cambridge University Press pp. 1-21. (Reviewed Invited Book Chapter) .
48. \*S. J. Puechmaille, B. Allegrini, E. M. S. Boston, M. J. Dubourg-Savage, A. Evin, Y. Le Bris, A. Knochel, V. Lecoq, M. Lemaire, D. Rist & **E. C. Teeling**. Genetic analyses reveal

- further cryptic lineages within the *Myotis nattereri* species complex. (2012) *Mammalian Biology - Zeitschrift für Säugetierkunde* 77(3): 224-228.
49. V. D. Thong, S. J. Puechmaille, A. Denzinger, P. J. J. Bates, C. Dietz, G. Csorba, P. Soisook, **E. C. Teeling**, S. Matsumura, N. Furey H.-U. & Schnitzler. Systematics of the *Hipposideros turpis* complex with a description of a new subspecies from Vietnam (2012). *Mammal Review* 42(2): 166-192.
  50. V. D. Thong, S. J. Puechmaille, A. Denzinger, P. J. Bates, C. Dietz, G. Csorba, P. Soisook, **E. C. Teeling**, S. Matsumura, N. Furey & H-U. Schnitzler. (2012). A new species of *Hipposideros* (Chiroptera: Hipposideridae) from Vietnam. *Journal of Mammalogy* 93: 1-11.
  51. \*K. T. J. Davies, J. A. Cotton, J. Kirwan, **E. C. Teeling** & S. J. Rossiter. (2011). Parallel signatures of sequence evolution among hearing genes in echolocating mammals: an emerging model of genetic convergence. *Heredity* 108 (5): 480-489.
  52. M. Ar Gouilh, S. J. Puechmaille, J. P. Gonzalez, **E. C. Teeling**, K. Pattamaporn & J-C. Manuguerra. (2011). SARS-Coronavirus ancestors foot-prints in South-East Asia and bat colonies: the refuge theory. *Infection Genetics and Evolution* 11(7): 1690-1702.
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79. \*M. J. R. Pereira, H. Rebelo, **E. C. Teeling**, S. J. O'Brien, Tin Nwe, I. Mackie, Si Si Hla Bu, Khin Maung Swe, Khin Mie Mie & P. J. J. Bates. (2006). Status of the world's smallest mammal, the bumble-bee bat *Craseonycteris thonglongyai*, in Myanmar. *Oryx* 40: 456-463.
80. W. E. Johnson, E. Eizirik, J. Pecon-Slaterry, W. J. Murphy, A. Antunes, **E. C. Teeling** & S. J. O'Brien. (2006). Explosive Late Miocene Radiation of the Felidae Family. *Science* 311: 73-77.
81. \***E. C. Teeling**, M. S. Springer, O. Madsen, P. J. Bates, S. J. O'Brien & W. J. Murphy. (2005). A Molecular Phylogeny for Bats Illuminates Biogeography and the Fossil Record. *Science* 307: 580-584.
82. A. J. Pearks Wilkerson, **E. C. Teeling**, J. L. Troyer, G. Kahila Bar-Gal, M. Roelke-Parker, Laurie Marker, J. Pecon-Slaterry & S. J. O'Brien. (2004). SARS-Related coronavirus outbreak and host genetic influence: Lessons from cheetahs. *Current Biology* 14: R227-8.
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85. W. J. Murphy, E. Eizirik, S. J. O'Brien, O. Madsen, M. Scally, C. Douady, **E. C. Teeling**, M. J. Stanhope, W. W. de Jong & M. S. Springer. (2001). Resolution of the early placental mammal radiation using Bayesian phylogenetics. *Science* 294: 2348-2351.
86. M. S. Springer, **E. C. Teeling** & M. J. Stanhope. (2001). External nasal cartilages in bats: Evidence for microchiropteran monophyly? *Journal of Mammalian Evolution* 8: 231-236.
87. \*M. S. Springer, **E. C. Teeling**, O. Madsen, M. J. Stanhope & W. W. de Jong. (2001). Integrated fossil and molecular data reconstruct bat echolocation. *Proceedings of the National Academy of Sciences* 98: 6241-6246.
88. \***E. C. Teeling**, M. Scally, D. J. Kao, M. L. Romagnoli, M. S. Springer & M. J. Stanhope. (2000). Molecular evidence regarding the origin of echolocation and flight in bats. *Nature* 403: 188-192.

### **Other Non-Peer Reviewed Publications:**

89. \***E. C. Teeling** (2017). *Myotis mystacinus* in *Atlas of Mammals in Ireland* eds. L. Lysaght & F. Marnell.
  90. \***E. C. Teeling** (2015). "Why do some animals sleep all winter?" Science of Christmas Supplement, *Irish Independent* 14 Dec.
  91. \***E. C. Teeling** & N. Foley (2015). "Why we love batty summer nights?" Science of Summer Supplement, *Irish Independent* 18 June.
  92. \***The White Nose Syndrome Consortium** (2010). The Potential Threat of White Nose Syndrome to European Bats: An Action Plan. *Eurobats Report* April 2010.
  93. \***E. C. Teeling**. (2006). The Age of Genomics. *Irish Wildlife*, 2(8): 6-7.
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# Curriculum Vitae for Richard [REDACTED] DURBIN

Department of Genetics

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WWW: <http://www.sanger.ac.uk/people/directory/durbin-richard> (to be updated to [gen.cam.ac.uk](http://gen.cam.ac.uk))

[REDACTED] [REDACTED] [REDACTED] [REDACTED]

October 2017 – now: **Al Kindi Professor of Mathematical and Computational Genetics, Department of Genetics, University of Cambridge.** Also Associate Faculty member, Wellcome Trust Sanger Institute.

[REDACTED] **Senior Research Fellow**, Churchill College, Cambridge

[REDACTED] **Honorary Professor of Computational Genomics**, Cambridge University Department of Applied Mathematics and Theoretical Physics.

[REDACTED] [REDACTED] **Senior Group Leader at the Wellcome Trust Sanger Institute** (until 12/01 the Sanger Centre). Acting Head of Computational Genomics ([REDACTED]) Joint Head of Human Genetics ([REDACTED]), Deputy Director ([REDACTED]), Head of Informatics ([REDACTED]). From 2007 my main focus has been on studying human genetic variation using new sequencing technologies, including as co-chair of the international 1000 Genomes Project, principal investigator for the UK10K project, and co-PI for the HipSci (Human IPS Cell Initiative) project, alongside theoretical and methodological work in sequence data analysis, statistical and population genetics. Previously I led the informatics support for large scale genome projects, the Acedb and Wormbase groups, the initial development of the Pfam and TreeFam data resources, and carried out research on probabilistic models and statistical methods for sequence analysis.

[REDACTED] Study leave at National Center for Biotechnology Information, NIH, USA.

[REDACTED] Study leave with joint affiliation to the University of Cambridge Computer Laboratory and the MRC Laboratory of Molecular Biology.

[REDACTED] **Staff member at MRC Laboratory of Molecular Biology**

[REDACTED] non-clinical scientific grade II

[REDACTED] non-clinical scientific grade I

I worked on informatics for genome data management and analysis for the *C. elegans* and human sequencing projects, including with Jean Thierry-Mieg on the genome database ACEDB. I also made two short working visits abroad:

[REDACTED] Visitor at the International Computer Science Institute, Berkeley

[REDACTED] Visiting Professor in Theoretical Physics at the University of Montpellier, France.

[REDACTED] **Lucille P Markey Visiting Fellow in the Department of Psychology, Stanford University**, sponsored by Professor David Rumelhart.

I worked on a theoretical framework for linking function and spatial organisation in the cortex, and on neural network theory and machine learning.

**Research Fellow in Biological Information Processing at King's College Research Centre, King's College, Cambridge, England**

I collaborated with Dr Graeme Mitchison in research on optimality of neural mappings, and on learning algorithms. I also helped develop the MRC/BIORAD confocal laser scanning microscope.

**Research Student at the MRC Laboratory of Molecular Biology, Cambridge, England**

PhD thesis approved July 1987 (only received 2003). Supervisor: Dr John White. Thesis title: Studies on the Development and Organisation of the Nervous System of *Caenorhabditis elegans*.

**Fulbright Visiting Scholar in Biophysics at Harvard University**

I took biology courses and worked in the laboratory of Professors SC Harrison and DC Wiley on X-ray crystallography software for the Xentronics area detector.

**Undergraduate in Mathematics at St John's College, Cambridge**

Entrance scholarship Various college prizes

Tripes: 1st Class Part Ia and Part Ib, 2nd Class Part II

BA (Hons) in Mathematics, Cambridge University

**Awards and Activities**

Elected Fellow of the Royal Society Member of the European Molecular Biology Organisation (EMBO) Fellow of the International Society for Computational Biology (ISCB)

Gabor Medal of the Royal Society, International Steven Hoogendijk Award, Rotterdam, Lord Lloyd of Kilgerran Award of The Foundation for Science and Technology, Mullard Medal of the Royal Society, jointly with J White, B Amos and M Fordham for development of a confocal laser scanning microscope (previous work at the MRC LMB). This development also won a Queen's Award for Technology for the MRC in

UK based scientist with the most citations to high impact papers according to Thomson Reuters ScienceWatch (4,335 citations to 16 papers that each rank in the top 1% for citations in their field and year). Member of Thomson Reuters Highly Cited lists Biology & Biochemistry, Computer Science, Molecular Biology & Genetics.

Fellow of the Royal Statistical Society, Member of the Genetics Society, Human Genome Organisation, London Mathematical Society.

Member of editorial board for Neural Computation, Genome Research, GENE-COMBIS, Genome Biology, BMC Bioinformatics from BMC Biology, PLoS Computational Biology, GigaScience from

Member of the Expert Working Group chaired by Kay Davies for the OST Committee on the Human Mapping Project in the UK BBSRC Bioinformatics Steering Group, Bioinformatics Panel, MRC Bioinformatics Advisory Committee from

Science Committee for UK BioBank [REDACTED], Chair of UK BioBank Data Management Subgroup [REDACTED], Member of Royal Society Panel on Pharmacogenetics [REDACTED] Bioinformatics Institute of Singapore External Review panel [REDACTED] Co-chair of the 1000 Genomes Project [REDACTED], Co-director of the Wellcome Trust Mathematical Genomics in Medicine PhD Programme at Cambridge University [REDACTED] (Director from [REDACTED] Co-chair of the Data Working Group of the Global Alliance for Genomics and Health [REDACTED]. Chair of the Population Genomics GeCIP for the UK100K Genomes Project [REDACTED]

Conference (co-)organiser of: European *C. elegans* Meeting ([REDACTED] INYS/CAS meeting Beijing ([REDACTED] International Biometric Society meeting on Statistical Methods for Genome-Wide Association Studies, Hinxton ([REDACTED] Newton Institute workshop on High Dimensional Statistics in Biology ([REDACTED] Cold Spring Harbor/Wellcome Trust Conference on Genome Informatics ([REDACTED], 1000 Genomes Project and Beyond, Cambridge ([REDACTED] Smithsonian Global Biodiversity Genomics Conference ([REDACTED] Scientific Organizing Committee) plus various smaller workshops.

Member of Scientific Advisory Board for *Saccharomyces* Genome Database [REDACTED] ArrayExpress Database [REDACTED], *C. elegans* Knockout Consortium, [REDACTED], WT Aging Research Consortium [REDACTED], Oxford University Department of Statistics [REDACTED] CRG Institute Barcelona ([REDACTED] MPI-CBG Institute Dresden ([REDACTED] Helsinki Institute for Information Technology ([REDACTED] MPI Science of Human History Jena ([REDACTED]

Member of Scientific Advisory Board of Compugen Ltd (Israel) [REDACTED] Solexa Ltd [REDACTED] 2006, Dovetail Genomics LLC (USA) [REDACTED] Member of Technical Computing Advisory Board, Microsoft Inc (USA) [REDACTED] Co-founder of Congenica Ltd, non-executive director [REDACTED], consultant [REDACTED]

[REDACTED] Member of British team of six to the International Mathematical Olympiad. Personal [REDACTED] prize in [REDACTED] (approx 50th). Personal [REDACTED] prize in [REDACTED] (approx 20th).

US Patent 7,351,532. DNA sequence analysis. Inventors: Harold Swerdlow, Colin Barnes, John Todd, Richard Durbin. Assignee: Solexa Ltd (now Illumina Inc).

Google Scholar [REDACTED] 137,306 citations (76,215 since [REDACTED] h-index 113 ([REDACTED]

#### **Grants held since [REDACTED] (reverse order)**

“Whole genome sequence based analysis of genetic variation and genome evolution”, Wellcome Trust Investigator Award, [REDACTED]

“British Autozygosity Population Gene Function Study” Wellcome Trust Strategic Award to D. van Heel, R. Trembath and others, one postdoc position to Sanger for 2 years, [REDACTED] 3 hours per week, 1 calendar month per year)

“Human iPS cell Initiative (HiPSci)” Wellcome Trust/MRC grant, co-PI with Fiona Watt (KCL, London) and others, approx [REDACTED] to Sanger, [REDACTED] (2.7 calendar), renewed until [REDACTED] with additional [REDACTED].

“European Sequencing and Genotyping Infrastructure (ESGI)” with S. Sauer and others, EU Framework 7 network, approx [REDACTED] to Sanger [REDACTED] (0.6 calendar)

"Identifying biomarkers of ageing using whole transcriptome sequencing (EuroBATS)" with T. Spector, M. Dermitzakis and others, EU Framework 7 project, approx [REDACTED] to Sanger [REDACTED] (0.6 calendar)

"10,000 UK genome sequences: accessing the role of rare genetic variants in health and disease", Wellcome Trust Strategic Award, £ [REDACTED] plus \$ [REDACTED] [REDACTED] (3.6 calendar)

"Extending The Value of Nematode Genomic Data with WormBase", MRC, [REDACTED] (MRC contribution under FEC costing) [REDACTED] (0.6 calendar)

"WormBase: a core data resource for *C. elegans* and other nematodes", NIH(NHGRI) grant [REDACTED]  
[REDACTED] 2008-7/2013 (0.6 calendar)

"Genetic and functional genomic research", Microsoft Research collaborative grant, with John Winn (Microsoft Research Cambridge), \$ [REDACTED] to Sanger [REDACTED] (0.6 calendar)

"Perceptual Genetics", Gatsby Foundation grant with J Mollon (Experimental Psychology, Cambridge) and G Mitchison, approx £ [REDACTED] to Sanger [REDACTED] (0.3 calendar)

"BioSapiens: bioinformatics for human health", EU network of excellence coordinated by J Thornton (many participants) approx € [REDACTED] to Sanger [REDACTED]

"MITOCHECK: Functional genomic analysis of mitotic checkpoints", EU grant with J-M Peters, T Hyman, J Ellenberg, K Nasmyth et al., € [REDACTED] total, € [REDACTED] to Sanger, [REDACTED]

"WormBase: a core data resource for *C. elegans* biology", NIH(NHGRI) grant with P. Sternberg, L. Stein, J. Spieth, \$ [REDACTED] total, [REDACTED] 8

"Genome interpretation in *C. elegans*", MRC programme grant with J. Rogers, £ [REDACTED] [REDACTED] [REDACTED].

"Ensembl: current, complete and consistent annotation of large scale genome sequence", Wellcome Trust grant with G. Cameron, T. Hubbard, E. Birney, M. Clamp, £ [REDACTED] [REDACTED]

"WormBase: a core data resource for *C. elegans* biology", NIH(NHGRI) grant with P. Sternberg, L. Stein, J. Spieth, \$ [REDACTED] total, [REDACTED]

"A UK mouse genome sequencing programme", MRC grant with S. Brown et al., £ [REDACTED] total [REDACTED]

"The creation of an integrated resource of protein domains and functional site (Interpro) and its application to accelerate protein functional analysis." EC grant with R. Apweiler et al. € [REDACTED] to Sanger, [REDACTED]

"Mouse genomic sequencing (a pilot study)" Wellcome Trust grant with J. Rogers and D. Bentley, £ [REDACTED] total [REDACTED]

"Genome interpretation in *C. elegans*", MRC programme grant with A. Coulson, J. Sulston, £ [REDACTED] total [REDACTED]



“Pfam Protein Families Database”, Wellcome Trust project grant, [REDACTED] [REDACTED]

“EVRHEST: Transcript map of the human genome by radiation hybrid mapping of EST’s” EC grant with M. James, J. Beckman, € [REDACTED] total, [REDACTED]

**Invited Lectures** [REDACTED] **(reverse order)**

[REDACTED] Keynote at ECCB Satellite on Pangenomes, Den Haag  
[REDACTED] Keynote at Quantitative Genomics one day meeting, London  
[REDACTED] International Conference on Human Genetics, Kyoto  
[REDACTED] Festival of Genomics, London  
[REDACTED] International Genomics Summit, Qingdao, China  
[REDACTED] Plenary lecture, ICG-10, Shenzhen, China  
[REDACTED] Probabilistic Models for Genomics, Cold Spring Harbor, USA  
[REDACTED] Alan Turing Institute workshop on Data Science for Health, Cambridge  
[REDACTED] Keynote lecture, HiTSeq meeting at ISMB/ECMB annual meeting, Dublin, Ireland  
[REDACTED] European School of Information Theory, Zandvoort, Netherlands  
[REDACTED] Global Alliance for Genomics and Health, London  
[REDACTED] Highgate School, London  
[REDACTED] Calico Inc, South San Francisco, USA  
[REDACTED] Genome10K, Santa Cruz, USA  
[REDACTED] The Human Mutation Rate, Leipzig, Germany  
[REDACTED] Shaping cells and organisms, Cologne, Germany  
[REDACTED] Plenary Lecture FEBS-EMBO meeting, Paris, France  
[REDACTED] Biological Sequence Analysis and Probabilistic Models, Oxford  
[REDACTED] 1000 Genomes Project and Beyond, Cambridge  
[REDACTED] Qatar Genome Meeting, Qatar  
[REDACTED] From bioinformatics to therapeutics, Qatar  
[REDACTED] Human Evolution in the Genomic Era EMBO meeting, Leicester  
[REDACTED] Mathematical, Statistical and Computational Aspects of Metagenomics meeting, Newton  
[REDACTED] Institute, Cambridge  
[REDACTED] Plenary at Evolutionary Genetics & Genomics Symposium (EGGS), Cambridge  
[REDACTED] Department of Biology, University of Copenhagen, Denmark  
[REDACTED] Netherhall seminar on the Origin of Human Beings, London  
[REDACTED] Keynote speaker, Computational Biology & Innovation PhD Symposium, Dublin  
[REDACTED] Plenary lecture, NIPS meeting, Lake Tahoe, USA  
[REDACTED] Keynote speaker, Precision Medicine meeting, Cold Spring Harbor, USA  
[REDACTED] Plenary lecture, SMBE meeting, Chicago, USA  
[REDACTED] IRCAN Inaugural Meeting, Nice, France  
[REDACTED] Google Inc, Menlo Park, USA  
[REDACTED] National Consortium for Data Science Leadership meeting, North Carolina USA  
[REDACTED] Genome 10K workshop, Fort Lauderdale, Florida USA  
[REDACTED] Plenary speaker, Genomic Disorders meeting, Cambridge  
[REDACTED] Biological Sequence Analysis meeting, Janelia Farm, Virginia USA  
[REDACTED] ESGI Symposium, Berlin, Germany  
[REDACTED] New Frontiers in Personal Genomics Symposium, Nijmegen, Netherlands  
[REDACTED] CRI Symposium, Cambridge  
[REDACTED] EMBL Students Meeting, Heidelberg, Germany  
[REDACTED] EMBO meeting, Nice, France  
[REDACTED] Department of Computer Science, Helsinki, Finland



Chinese Academy of Sciences Evolution Institute, Kunming, China  
BGI, Shenzhen, China

Plenary lecture, ISMB, Long Beach, California USA  
1000 Genomes Project Community Meeting, Ann Arbor, Michigan USA  
International Congress on Quantitative Genetics, Edinburgh  
Plenary lecture, RECOMB, Barcelona Spain  
Genomic Disorders meeting, Hinxton

Meeting on Coancestry, Ancestry and Population Genomics, IPAM, UCLA, USA  
Invited lecture, UC Santa Cruz, USA  
ICG-VI, Shenzhen, China

Genetics of Common Disease meeting, Hinxton  
Human Genetics Gordon Conference, Rhode Island, USA  
Illumina Technology meeting, Verona, Italy  
Leena Peltonen Symposium, Helsinki, Finland  
Whittle Symposium, Centre for Mathematical Sciences, U Cambridge  
Genome10K meeting, UC Santa Cruz

Department of Computer Science, Helsinki University, Finland  
FIMM, Helsinki, Finland  
University of Hanoi, Vietnam

Plenary Speaker ICG-V, Shenzhen, China  
Genome Informatics meeting, Cold Spring Harbor USA  
British Society for Human Genetics, Warwick  
WTCHG, Oxford  
EMBO Symposium, Heidelberg, Germany  
European Society of Human Genetics, Stockholm, Sweden  
RECOMB Comparative Genomics, Hungary  
Genomics of Common Disease meeting, Hinxton  
Pharmacogenetics meeting, Hinxton  
Invited speaker, MRC HGU, Edinburgh  
Invited speaker, Royal Statistical Society meeting, Edinburgh  
External invited speaker, Microsoft Research Technical Advisory Board meeting,

Cambridge

Plenary invited speaker, Cambridge Computational Biology Institute annual symposium,  
Cambridge

Invited speaker, ESRC Symposium on Personal Genomics, Cambridge  
Invited lecture, Department of Human Genetics, University of Chicago  
Speaker, Biology of Genomes meeting, Cold Spring Harbor  
Invited Dahlem lecture, Max Planck Institut, Berlin  
Invited speaker, European Biobank (PHOEBE) meeting, Brussels  
Invited speaker, Spring Meeting, University of Cologne  
Invited speaker, Genomic Disorders Meeting, Hinxton  
Invited lecture, Centre for Mathematics Sciences, University of Cambridge  
Invited lecture, Dept of Genetics, University of Nottingham  
Two invited lectures, BGI Shenzhen  
Invited lecture, deCODE Genetics, Reykjavik  
Invited lecture, Dept of Biology, University of Manchester  
Invited speaker at WT/CSH conference on Genome Informatics, Hinxton  
Invited speaker at Genomics of Common Disease meeting, Cambridge USA  
Plenary invited speaker at French Bioinformatics Conference (JOBIM), Lille  
Invited speaker at meeting on Malaria Genomics, Hinxton  
Invited lecture at Oxford University Mathematical Genetics Seminar  
Speaker at Cold Spring Harbor Biology of Genomes Meeting

Invited lecture at John Innes Centre, Norwich  
 Invited "Mendel lecture", Mendel Museum, Augustinian Abbey, Brno  
 Invited speaker, Sanger-Cambridge PhD Symposium (SCAMPS)  
 Organiser and speaker at High Dimensional Statistics in Biology, Newton Institute  
 Speaker at Keystone Meeting on Complex Traits  
 Plenary speaker at Advances in Genome Biology and Technology (AGBT), Marco Island  
 Invited speaker, EMBL Students' Symposium, Heidelberg  
 Invited speaker at workshop on Bacterial Genomics, Oxford  
 Invited speaker at International Biometric Society meeting, Hinxton  
 Organiser and speaker at workshop on Sequencing 1000 Human Genomes, Cambridge  
 Invited lecture at CNR Institute, Naples  
 Speaker at Cold Spring Harbor Genome Biology Meeting  
 Invited lecture at Oxford University Biochemistry Department  
 Invited speaker and co-organiser at Young Scientist's forum in Beijing (British Council)  
 Invited lecture at York University Computational Biology programme  
 Invited speaker at International Human Genome meeting, Hangzhou, China  
 Speaker at Cold Spring Harbor Genome Biology Meeting  
 Invited speaker at Course on Computational Biology, Hangzhou, China  
 Invited speaker at Genetics Society of America Conference, San Diego  
 Invited speaker at Asia High Performance Computing Conference, Beijing  
 Speaker at Cold Spring Harbor Genome Informatics Conference  
 Plenary invited speaker at ECCB (European Conference on Computational Biology), Madrid  
 Invited speaker at Genome Sciences Symposium, Seattle  
 Invited speaker at Swedish Informatics Symposium, Lund  
 Invited lecture to Cambridge Centre for Computational Biology  
 Invited speaker at Genome Informatics Meeting, Reston, Virginia  
 Invited speaker at European Science Open Forum workshop on Open Access, Stockholm  
 Invited speaker at European Science Open Forum workshop on Life on a Chip, Stockholm  
 Invited lecture at MRC Human Genetics Unit, Edinburgh  
 Speaker at Young Scientists' forum in Beijing (British Council and Chinese Academy)  
 Invited speaker at Workshop on Mathematical Biology, Newton Institute, Cambridge  
 Speaker at Keystone Symposium on Human Variation  
 Invited lectures at the Hubrecht Laboratory, Utrecht  
 Invited speaker at workshop on UK approaches to Systems Biology  
 Plenary invited speaker at ELSO 2003 (European Life Sciences Organisation), Dresden Germany  
 Invited speaker at "*C. elegans* past, present and future: the not-so-humble worm", Hinxton UK  
 Invited speaker at Gordon Conference on "Bioinformatics: from predictive models to inference", Oxford UK  
 Plenary invited speaker at Royal Statistical Society annual theme conference on "Statistical genetics and bioinformatics", Diepenbeek Belgium  
 Invited speaker at Cambridge University Government Policy Programme seminar on "Communications Technology", Cambridge UK  
 Invited speaker at "Ownership & Control: managing IPR in the universities", London UK  
 Plenary invited speaker at InfoTechPharma London UK  
 Invited speaker at "The UK Biological Grid: Data and Computation", workshop Hinxton UK

■ Invited speaker at Royal Netherlands Academy of Arts and Sciences conference on "State Space and Unobserved Components", Amsterdam Netherlands

■ Invited speaker at "Theory of Computation and the Sciences", Berkeley USA

■ Invited lecture at Washington University (invited by the students in genetics and computational biology), St Louis USA

■ Invited speaker at "Learning" meeting, Snowbird USA

Invited lectures at Bioinformatics training workshop, Les Diablerets Switzerland

Invited lecture at the Computer Laboratory, Cambridge University UK

■ Invited speaker at Royal Statistical Society meeting on "Bioinformatics and Statistical Computing", London UK

■ Invited lecture at the Gatsby Institute, London UK

Invited participant at the UCSC Human Genome Workshop, Santa Cruz USA

■ Plenary speaker at ACL 2001 (Association for Computational Linguistics), Toulouse France

■ Invited lecture at the MRC Laboratory of Molecular Biology, Cambridge UK

Invited speaker at Harvard symposium on Functional Genomics, Cambridge USA

Invited external speaker at Howard Hughes investigators meeting, Washington USA

Invited lecture at Hewlett Packard Research Laboratory, Palo Alto USA

■ Invited speaker at meeting on "Computational Linguistics and Bioinformatics", Philadelphia USA

■ Invited lecture at Department of Biology, California Institute of Technology, Pasadena USA

## Supervision, committees etc.

PhD students (most recent first)

Name of student:	Viva date:	Current Position:
Marcus [REDACTED]	N/A	Current student (MGM programme)
Eric [REDACTED]	N/A	Current student (NIH-OxCam)
Erik [REDACTED]	N/A	Current student (WTSI)
Vagheesh Narasimhan (joint with Chris [REDACTED])	[REDACTED]	Postdoc with David Reich (Harvard)
Milan Malinsky (joint with Eric [REDACTED])	[REDACTED]	Postdoc with Walter Salzburger (Basel)
Zhihao [REDACTED]	[REDACTED]	Genomics PLC, Oxford
Jared [REDACTED]	[REDACTED]	Assistant Professor, OICR Toronto
Weldon [REDACTED]	[REDACTED]	Boston Consulting Group
Leopold [REDACTED]	[REDACTED]	Group Leader, Sanger Institute
Mark [REDACTED]	[REDACTED]	VP JP Morgan Asset Management
Lachlan [REDACTED]	[REDACTED]	Associate Professor, IMB, U Queensland
Ashwin [REDACTED]	[REDACTED]	Assistant Vice President, Citigroup
Kevin [REDACTED]	[REDACTED]	Team Leader, EBI
Irmtraud [REDACTED]	[REDACTED]	Professor, FU Berlin and Max Delbruck Center, Berlin
Ewan [REDACTED]	[REDACTED]	Senior Scientist, Joint Director, EBI
Steven [REDACTED]	[REDACTED]	Professor, Genome Center, Vancouver
Ian [REDACTED]	[REDACTED]	Associate Professor, UC Berkeley
Erik [REDACTED]	[REDACTED]	Professor, Karolinska Institut

Masters students (most recent first)

Name of student:	Viva date:	Current Position:
Kelley [REDACTED]	[REDACTED]	Assistant Professor, University of Washington
Daniel [REDACTED]	[REDACTED]	Postdoc?, Stanford University
Aaron [REDACTED]	[REDACTED]	Associate Professor, School of Public Policy, Georgia Tech

Postdoctoral fellows supervised (most recent first):

Dates:	Name of fellow:	Current Position:
[REDACTED]	Iliana [REDACTED]	Current postdoc
[REDACTED]	Jack [REDACTED]	Current postdoc
[REDACTED]	Rui [REDACTED]	Current postdoc
[REDACTED]	Matthew [REDACTED]	Current postdoc
[REDACTED]	Hannes [REDACTED]	Current postdoc

██████████	Jouni ██████████ (joint with Thomas ██████████)	Research Associate, UC Santa Cruz
██████████	David ██████████	Unknown
██████████	Andreas ██████████	Bioinformatics facility leader, University of Gottingen
██████████	Vladimir ██████████	Postdoc, UC Berkeley
██████████	Stephan ██████████	MPI-Jena Junior Group Leader
██████████	Andrew ██████████	Postdoc, University of Geneva
██████████	Karola ██████████	Project Leader, University of Cambridge Medical School
██████████	Kees ██████████ (joint supervised with Willem ██████████)	Assistant Professor, Radboud University Medical Center, Nijmegen
██████████	Kimmo ██████████	Helsinki University Research Associate
██████████	Quang ██████████	WTCHG Oxford postdoc
██████████	Aylwyn ██████████	Lecturer, Genetics, U Cambridge
██████████	Heng ██████████	Fellow, Broad Institute
██████████	Avril ██████████	Senior Bioinformatician, WTSI
██████████	Jean-Karim ██████████	Bioinformatics Scientist, EMBL
██████████	Jose ██████████	unknown
██████████	Alan ██████████	Associate Professor, U Toronto
██████████	Ian ██████████	Associate Professor, UC Davis
██████████	Marc ██████████	Learning Engineer, U Lausanne
██████████	Niclas ██████████	Team Leader, Astra Zeneca R&D
██████████	Alex ██████████	Senior Group Leader, EBI
██████████	Sean ██████████	Professor, Harvard University

### **University of Cambridge committees**

Departmental Strategy Committee: ██████████

Departmental Graduate Education Committee: ██████████

### **Sanger Institute committees (since ██████████)**

Board of Management: ██████████

Informatics Committee (formerly IGL): 1 ██████████ (chair), ██████████ (chair since ██████████)

Sequencing Committee: ██████████

Athena Swan Self-Assessment Team: ██████████

Cellular Genetics and Phenotyping Committee ██████████

PDF (post-doctoral fellow) Development Committee: ██████████

Faculty search committees: ██████████

Finance and Budget Committee: ██████████ (chair)



**M Thomas ■ Gilbert**  
Professor of Palaeogenomics  
Natural History Museum of Denmark

Natural History Museum of ■  
University of ■  
■  
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■  
■

e-mail: [tgilbert@snm.ku.dk](mailto:tgilbert@snm.ku.dk)

**Education/Employment**

■ First class degree, BA Biological Sciences, ■ College, University of ■  
■ D.Phil, New College/Department of Zoology, University of ■  
■ Research Intern, Estonian Biocentre, University of ■  
■ Post-doctoral Research Associate, Department of Ecology and Evolutionary  
Biology, University of ■  
■ ■-European Fellow, Ancient DNA and Evolution Group,  
■ and Biological Institutes, University of ■  
■ Associate Research Professor, Institute for Biology, University of  
■  
■ Associate Research Professor, Natural History Museum of ■  
University of ■  
■ Associate Professor, Natural History Museum of ■  
■ Professor of Palaeogenomics, Natural History Museum of ■  
■ Head of Section, GeoGenetics, Natural History Museum of ■  
■ Head of Section, Evolutionary Genomics, Natural History Museum of  
■

**Academic Awards**

■ Academic Scholar, Oriel College Oxford  
■ Wellcome Trust Prize PhD Studentship in Bioarchaeology  
■ Marie Curie Intra-European Fellowship  
■ ‘Skou’ Associate Professor Award  
■ ‘Elite Young Scientist’ Award  
■ Honorary Fellow, University of York, UK  
■ Lundbeck Foundation Junior Group Leader Fellowship  
■ *Sapere Aude* DFF-Starting Grant Award  
■ Walter Murdoch Adjunct Professorship, Murdoch University (Australia)  
■ Adjunct Professorship, Curtin University (Australia)  
■ Lundbeck Foundation Young Scientist Award  
■ Science Advisory Board, Copenhagen Zoo  
■ ERC Consolidator Grant

**Recent Grants Awarded**

■ Marie Curie Intra-European Fellowship ■ - ‘FORMAPLEX’ (ca. ■  
Euros)

International Symposium Grant, Fundacion Ramon Areces, Madrid, Spain. (Co-application with Dr Anders Götherström, Uppsala University, to hold a 14-person invited speaker symposium on the 'State of the Art of Ancient DNA' in Madrid, ■■■■■)

Danish National Science Research Council 'Skou' Grant (Tailoring the power of the 454 to ancient DNA studies) (ca. ■■■■■ Euros)

Marie Curie Early Stage Training Network (LeCHE – Lactase Persistence and the Early Cultural History of Europe). Coapplicant, PI of University of Copenhagen section (ca. ■■■■■ Euros)

Danish National Science Foundation PALEO-RNA: Investigating the domestication of maize using new biomolecular approaches. (ca. ■■■■■ Euros)

Danish National Science Foundation Disease Discovery of new infectious agents by metagenomic sequencing. Co-applicant, (ca. ■■■■■ Euros)

Host - Marie Curie Intra-European Fellowship ■■■■■ - 'ROOTS' (ca. ■■■■■ Euros)

Danish Basic Science Foundation. Centre for GeoGenetics. Co-applicant, (ca. ■■■■■ Euros)

Lundbeckfonden ■■■■■ PhD stipend 'Phylogenomic analysis of the origin, and spread, of Influenza A'. (ca. ■■■■■ Euros)

■■■■■ Lundbeckfonden Junior Group Leader Fellowship 'Pathogen Paleogenomics' (ca. ■■■■■ Euros)

Danish Council for Independent Research ■■■■■ Sapere Aude Award 'Biomolecular characterization of the domestication of maize' (ca. ■■■■■ Euros)

Host - Marie Curie Intra-European Fellowship ■■■■■ - 'MaizeKey' (ca. ■■■■■ Euros)

Host - Marie Curie Intra-European Fellowship ■■■■■ - 'KWAFF10' (ca. ■■■■■ Euros)

Coordinator, Marie Curie Early Stage Training Network (EUROTAST) (ca. ■■■■■ Euros, ■■■■■ to Copenhagen)

Host - Marie Curie Intra-European Fellowship ■■■■■ - 'SIMBA' (ca. ■■■■■ Euros)

ARC ■■■■■ – Ancient DNA from cave sediments: a new horizon in the archaeology of Aboriginal Australia. Co-applicant (AUD ■■■■■)

Host - Marie Curie Intra-European Fellowship ■■■■■ - 'BIRDATLAS' (ca. ■■■■■ Euros)

Host - Marie Curie Intra-European Fellowship ■■■■■ - 'AGORA' (ca. ■■■■■ Euros)

ARC ■■■■■ 'Troublesome ticks: development and application of a molecular toolkit to investigate zoonotic tick-borne pathogens in Australia. Co-applicant (AUD ■■■■■)

Host - Danish Council for Independent Research/FNU Mobilex grant ■■■■■ – Deciphering the northward spread of maize: a state-of-the-art computational and molecular analysis (EUR ■■■■■)

Højteknologifonden 'FoodGenomics' grant (ca. ■■■■■ Euros)

Danish Council for Independent Research ■■■■■ 'Wine-ometrics: Countering Wine Fraud Through Microbiome Fingerprinting of Wine. (ca. ■■■■■ Euros)

Copenhagen PI, Marie Curie Early Stage Training Network (MICROWINE) (ca. ■■■■■ Euros, ca. ■■■■■ to Copenhagen)

Innovationsfonden ‘NewPlan’ grant. Co-applicant (ca. [REDACTED] Euros to Copenhagen)  
Host – Carlsberg Postdoctoral Fellowship to Shyam Gopalakrishnan (ca. [REDACTED] Euros)  
Host - Marie Curie Intra-European Fellowship [REDACTED] - ‘WHEREWOLF’ (ca. [REDACTED] Euros)  
Host - Marie Curie Intra-European Fellowship [REDACTED] - ‘BARREN’ (ca. [REDACTED] Euros)  
Host - Marie Curie Intra-European Fellowship [REDACTED] - ‘AFTERTHEICE’ (ca. [REDACTED] Euros)  
Host - Danish Council for Independent Research/FNU Mobilex grant– Do microbiomes drive ecological adaptation in vertebrates? Answers from the metagenomic analysis of ancient DNA from guano deposits (EUR [REDACTED] Copenhagen PI, Marie Curie European Joint Doctorate (ArchSci2020) (ca. 4.1 million Euros, ca. [REDACTED] Euros to Copenhagen)  
ERC Consolidator Grant [REDACTED] -EXTINCTION GENOMICS. [REDACTED] Euros)  
Host - Marie Curie Intra-European Fellowship [REDACTED] - ‘EPICDOMESTIC’ (ca. [REDACTED] Euros)  
Host – Carlsberg Postdoctoral Fellowship to Ostaizka Aizpurua (ca. [REDACTED] Euros)  
Host – Carlsberg Postdoctoral Fellowship to Morten Limborg (ca. [REDACTED] Euros)  
Host – DNRF Niels Bohr Professorship in Palaeoproteomics to Matthew Collins (ca. [REDACTED] Euros)  
Innovationsfonden ‘FoodTranscriptomics’ grant. Co-PI (ca. [REDACTED] Euros to Copenhagen)  
Host - Marie Curie Intra-European Fellowship [REDACTED] - ‘ICESTOP’ (ca. [REDACTED] Euros)  
Aage V. Jensen Foundation ‘DNAMARK’ grant. (ca. [REDACTED] Euros)  
Villum Experiment grant 17417 ‘Was animal domestication driven by gut microbiome humanisation?’ (ca. [REDACTED] Euros)  
Norwegian Seafood Research Fund (FHF) grant [REDACTED] (ca. [REDACTED] Euros)  
Carlsbergfondet Research Infrastructure Grant C17-[REDACTED] (ca. [REDACTED] Euros)

### Symposia Coordinated

- [REDACTED] Ancient DNA – Damage, Retrieval and Repair. University of Oxford
- [REDACTED] International Symposium on Ancient DNA. Fundacion Ramon Areces, Madrid, Spain
- [REDACTED] International Symposia of Biomolecular Archaeology IV, Copenhagen, [REDACTED]

### Academic Contributions

I am an academic editor of *Archaeological and Anthropological Science*; *Evolution, Medicine and Public Health*; *Open Quaternary*; and *Methods in Ecology and Evolution*, and have guest edited an issue of *Viruses*. I also act as an *ad hoc* reviewer to a wide range of journals, including *Science*, *Nature*, *PNAS*, *PLoS Biology*, *Molecular Biology and Evolution*, *Molecular Ecology*, *Journal of Archaeological Sciences*, *Biology Letters*, *Current Biology*, *Nature Reviews Genetics* and *American Journal of Physical Anthropology*. In addition I am the co-coordinator (with Guojie Zhang/BGI and Erich Jarvis/Duke) of the 10,000 Avian Genome Sequencing Consortium (Birds10K), the former coordinator of the Marie Curie Actions FP7 International Training Network ‘EUROTAST’ (a 10 partner/15 fellow Training Network focusing on the Trans-Atlantic Slave Trade), the Danish coordinator of Marie Curie Actions H2020 ArchSci2020 European Joint

Doctorate Network, and the host to DNRF Niels Bohr Professor of Palaeoproteomics, Matthew Collins.

### Teaching

I teach significant components of the UCPH 'Evolutionary Medicine' MSc course, contribute lectures to the UCPH 'Ancient DNA and Evolution', 'Origins' and 'Comparative Anatomy' and 'Genomics' courses, and coordinate the 'East Africa' BSc course.

### Supervision

Research group currently contains 2 Assistant Professors, 10 Postdoctoral researchers, 13 PhD students and 3 MSc students.

### Former Postdocs

Maria Avila-Arcos (■■■■ Ross ■■■■ Paula ■■■■), Enrico ■■■■ Rute da ■■■■), Andrew ■■■■), Mike ■■■■, Peter ■■■■), Temitope ■■■■), Morten ■■■■-■■■■ Ricardo John ■■■■), Rosalia Piñeiro ■■■■), Angela Maria Oliveira ■■■■), Faazah ■■■■), Jose Samaniego ■■■■), Hannes ■■■■), Nathan ■■■■)

### Former PhD Students

Alonzo Alfaro-■■■■ Maria Ávila-■■■■ Luise Ørsted ■■■■-■■■■ Kristine ■■■■), Christian ■■■■), Paula ■■■■-■■■■ Christian ■■■■), Jose Samaniego ■■■■), Sarah ■■■■, Katharina ■■■■), Rasmus Gren ■■■■ Marie-Louise ■■■■), Cai ■■■■), Qiye ■■■■), Inge ■■■■ Sandra Abel ■■■■), Jazmin Ramos ■■■■), Marcela Sandoval ■■■■), Ida Bærholm ■■■■), Mikkel ■■■■ Jessica ■■■■), Inger ■■■■), Marie Lisandra Zepeda ■■■■ ■■■■

### PhD Theses Examined

Céline ■■■■ (University of Paris XI, France, ■■■■ Alison ■■■■ (McMaster University, Canada, ■■■■ Henrik Hjarvard ■■■■ (University of Copenhagen ■■■■ Giada ■■■■ (University of Zurich, ■■■■ Peter ■■■■ (University of Copenhagen, ■■■■ Annemarie ■■■■ (University of KwaZulu-Natal, South Africa, ■■■■ Peter ■■■■ (Royal Holloway, UK, ■■■■ Zixia ■■■■ (UC Dublin, ■■■■ Kristian Kjellerup ■■■■ (University of Copenhagen, Denmark, ■■■■ Stephanie ■■■■ (McMaster University, Canada, ■■■■ Karen ■■■■ (University of Copenhagen, ■■■■ Nuria ■■■■ (University of Santiago de Compostela, Spain, ■■■■ Iñigo ■■■■ (UPF, Spain, ■■■■ Lourdes ■■■■ (UPF, Spain, ■■■■ Federico Sánchez ■■■■ (UPF, Spain, ■■■■ Andaine Seguin-■■■■ (University of Copenhagen, ■■■■ Lee Ping ■■■■ (University of Malaya, Malaysia, ■■■■ Oliver ■■■■ (University of Warwick, UK, ■■■■ Cristina ■■■■ (University Complutense Madrid, ■■■■

### Published/in press Peer Review Papers = 264, Book Chapters =13

First author Peer Review Papers = 30

Senior author Peer Review Papers = 72

Web of Science: H-index = 64, Citations = 12,245

Journals published in include *Science* (28), *Nature* (5), *Nature Genetics* (2), *Nature Plants* (1), *Nature Ecology and Evolution* (1), *Nature Communications* (5), *PNAS* (15)

## Refereed Publications

1. Zepeda Mendoza L, Xiong Z, Escalera-Zamudio M, Runge AK, Thézée J, Streicker D, Frank HK, Loza-Rubio E, Liu S, Ryder OA, Samaniego Castruita JA, Katzourakis A, Pacheco G, Taboada B, Löber U, Pybus OG, Li Y, Rojas-Anaya E, Bohmann K, Carmona Baez A, Arias CF, Liu S, Greenwood AD, Bertelsen MF, White NE, Bunce M, Zhang G, Sicheritz-Pontén T, **Gilbert MTP** (*in press*) Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. **Nature Ecology and Evolution**
2. Barnett R, Sinding MHS, Vieira FG, Zepeda Mendoza ML, Bonnet M, Araldi A, Kienast I, Zambarda A, Yamaguchi N, Henschel P, **Gilbert MTP** (*in press*) No longer locally extinct? Tracing the origins of a lion (*Panthera leo*) living in Gabon. **Conservation Genetics**
3. Limborg MT, Alberdi A, Kodama M, Roggenbuck M, Kristiansen K, **Gilbert MTP** (*in press*) Applied Hologenomics: Feasibility and potentials in aquaculture. **Trends in Biotechnology**
4. Aizpurua O, Budinski I, Gerogiakakis P, Gopalakrishnan S, Ibanez C, Mata V, Rebelo H, Russo D, Szodoray-Paradi F, Zhelyazkova V, Zrnica V, **Gilbert MTP**, Alberdi A (*in press*) Agriculture shapes the trophic niche of a bat preying on multiple pest arthropods across Europe: evidence from DNA metabarcoding. **Molecular Ecology** DOI: 10.1111/mec.14474
5. Díez-del-Molino D, Sánchez-Barreiro F, Barnes I, **Gilbert MTP**, Dalén L (*in press*) Quantifying temporal genomic erosion in endangered species. **Trends in Ecology and Evolution** DOI: 10.1016/j.tree.2017.12.002
6. Liu Y-H, Wang L, Xu T, Guo X, Li Y, Yin T-T, Yang H-C, Hu Y, Adeola AC, Sanke AJ, Otecko NO, Wang M, Ma Y, Charles OS, Sinding MHS, Gopalakrishnan S, Samaniego JA, Hansen AJ, Fernandes C, Gaubert P, Budd J, Dawuda PM, Rueness EK, Jiang L, Zhai W, **Gilbert MTP**, Peng M-S, Qi X, Wang G-D, Zhang Y-P (*in press*) Whole-genome sequencing of African dogs provides insights into adaptations against tropical parasites. **Molecular Biology and Evolution** DOI: 10.1093/molbev/msx258
7. Teeling E, Vernes S, Davalos L, Ray DA, **Gilbert MTP**, Meyers E, and Bat1k Consortium (*in press*) Bat Biology, Genomes, and the Bat1K Project: To Generate Chromosome-Level Genomes for all Living Bat Species. **Annual Review Animal Biosciences** DOI: 10.1146/annurev-animal-022516-022811
8. Carøe C, Gopalakrishnan S, Vinner L, Mak SST, Sinding M-H S, Samaniego Castruita JA, Wales N, Sicheritz-Pontén T, **Gilbert MTP** (*in press*) Single-tube library preparation for degraded DNA. **Methods in Ecology and Evolution** DOI: 10.1111/2041-210X.12871
9. Alberdi A, Aizpurua O, **Gilbert MTP**, Bohmann K (*in press*) Scrutinizing key steps for reliable metabarcoding of environmental samples. **Methods in Ecology and Evolution** DOI: 10.1111/2041-210X.12849
10. Murray GGR, Soares AER, Novak BJ, Schaefer NK, Cahill JA, Baker AJ, Demboski JR, Doll A, da Fonseca RR, Fulton TL, **Gilbert MTP**, Heintzmann PD, Letts B, McIntosh G, O'Connell BL, Peck M, Pipes M-L, Rice ES, Santos KM, Sohrweide AG, Vohr SH, Corbett-Detig RB, Green RE, Shapiro B (2017) Natural selection shaped the rise and fall of passenger pigeon genomic diversity. **Science** **358**:951-954
11. Sandoval-Velasco M, Lundstrøm IKC, Wales N, Ávila-Arcos M, Schroeder H, **Gilbert MTP** (2017) Relative performance of two DNA extraction and library preparation methods on archaeological human teeth samples. **Science and Technology of Archaeological Research** **3**:80-88
12. Fortes-Lima C, Gessain A, Ruiz-Linares A, Bortolini M-C, Migot-Nabias F, Bellis G, Moreno-Meyer JV, Restrepo BN, Rojas W, Avendaño-Tamayo E, Bedoya G, Orlando L,



- Salas A, Helgason A, **Gilbert MTP**, Sikora M, Schroeder H, Dugoujon J-M (2017) Genome-wide ancestry and demographic history of African-descendant Maroon communities from French Guiana and Suriname. **American Journal of Human Genetics** **101:725-736**
13. Paijmans JLA, Barnett R, **Gilbert MTP**, Zepeda-Mendoza ML, Reumer JWF, de Vos J, Zazula G, Nagel D, Baryshnikov GF, Leonard JA, Rohland N, Westbury M, Barlow A, Hofreiter M (2017) Evolutionary history of sabre-toothed cats based on ancient mitogenomics. **Current Biology** **27:1-7**
14. **Gilbert MTP** (2017) Documenting DNA in the dust. **Molecular Ecology** **26:969-971**
15. Salleh FM, Ramos-Madriral J, Peñaloza F, Liu S, Sinding M-HS, Patel RP, Martins R, Lenz D, Fickel J, Roos C, Shamsir MH, Azman MS, Lim BK, Rossiter SJ, Wilting A, **Gilbert MTP** (2017) An expanded mammal mitogenome dataset from Southeast Asia. **Gigascience** **6: 1-8** DOI: 10.1093/gigascience/gix053
16. Mak S, Gopalakrishnan S, Carøe CC, Geng C, Liu S, Sinding M-HS, Kuderna LFK, Zhang W, Fu S, Vieira FG, Germonpré M, Bocherens H, Fedorov S, Petersen B, Sicheritz-Pontén T, Marques-Bonet T, Zhang G, Jiang H, **Gilbert MTP** (2017) Comparative performance of the BGISEQ-500 versus Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. **Gigascience** **6:8** DOI: 10.1093/gigascience/gix049
17. Thomas JE, Carvalho GR, Haile J, Martin MD, Samaniego-Castruita JA, Niemann J, Sinding M-H S, Sandoval-Velasco M, Rawlence NJ, Fuller E, Fields J, Hofreiter M, Steward JR, **Gilbert MTP**, Knapp M (2017) An 'Aukward' tale: A genetic approach to discover the whereabouts of the last great auks. **Genes** **8:164**
18. Gopalakrishnan S, Samaniego Castruita JA, Sinding MH, Kuderna LF, Räikkönen J, Petersen B, Sicheritz-Pontén T, Larson G, Orlando L, Marques-Bonet T, Hansen AJ, Dalén L, **Gilbert MTP** (2017) The wolf reference genome sequence (*Canis lupus lupus*) and its implications for *Canis* spp. population genomics. **BMC Genomics** **18:495**
19. Bush A, Sollman R, Wilting A, Bohmann K, Cole B, Baltzer H, Martius C, Zlinsky A, Calvignac-Spencer S, Cobbold CA, Dawson TP, Emerson BC, Ferrier S, **Gilbert MTP**, Herold M, Jones L, Leendertz FH, Matthews L, Millington JDA, Olson JR, Ovaskainen O, Raffaelli D, Reeve R, Rodel M-O, Rodgers T, Snape S, Visseren-Hamakers I, Vogler AP, White PCL, Wooster MJ, Yu DW (2017) Connecting Earth observation to biodiversity and ecosystem services. **Nature Ecology and Evolution** **1:0176** doi:10.1038/s41559-017-0176
20. Robertson SI, **Gilbert MTP**, Campos PF, Salleh FM, Tridico S, Hills D (2017) Lowe's Otter Civet *Cynogale lowei* does not exist. **Small Carnivore Conservation** **55:42-58**.
21. Conlon BH, Mitchell J, de Beer ZW, Carøe C, **Gilbert MTP**, Eilenberg J, Poulsen M, de Fine Licht HH (2017) Draft genome of the fungus-growing termite pathogenic fungus *Ophiocordyceps bispora* (Ophiocordycipitaceae, Hypocreales, Ascomycota). **Data in Brief** **11:537-542**
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## Curriculum Vitae

### David Haussler

Investigator, Howard Hughes Medical Institute  
Distinguished Professor, Biomolecular Engineering, University of California, Santa Cruz  
Scientific Director, UC Santa Cruz Genomics Institute, University of California, Santa Cruz  
Co-founder, Global Alliance for Genomics and Health  
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## EMPLOYMENT HISTORY

- [REDACTED] Distinguished Professor, Biomolecular Engineering, University of California, Santa Cruz
- [REDACTED] Adjunct Professor, Department of Bioengineering and Therapeutic Sciences, University of California, San Francisco
- [REDACTED] Consulting Professor, Stanford University School of Medicine (Medical Informatics)
- [REDACTED] Investigator, [REDACTED] Medical Institute
- [REDACTED] Visiting Scientist and Co-Director of special scientific program, [REDACTED] Institute for Mathematical Sciences and [REDACTED] Centre, [REDACTED]
- [REDACTED] Professor, Computer Science, University of [REDACTED]
- [REDACTED] Visiting Scientist, [REDACTED] Sciences Research Institute, [REDACTED]
- [REDACTED] Associate Professor, Computer Science, University of [REDACTED]
- [REDACTED] Assistant Professor, Computer Science, University of [REDACTED]
- [REDACTED] Visiting Scientist, Université [REDACTED]
- [REDACTED] Assistant Professor, Mathematics and Computer Science, University of [REDACTED]

## CONSULTING AND COMMITTEES

- [REDACTED] Member, Earth BioGenome Project (EBG) Working Group
- [REDACTED] Consultant and external advisory committee member, ChanZuckerburg Initiative
- [REDACTED] - Member, Secretary of Energy (SEAB) Task Force on Biomedical Sciences
- [REDACTED] - Vice Chair of Steering Committee, Global Alliance for Genomics and Health
- [REDACTED] - Consultant and external advisory committee member, Genomic Data Commons (GDC), Bethesda, MA
- [REDACTED] Consultant and external advisory committee member, Simons Center for Quantitative Biology, Cold Spring Harbor, NY

██████████ Consultant and scientific advisory board member, Canadian Bioinformatics Node, Toronto, Canada

██████████ Chief scientific advisor, Dovetail Genomics, Santa Cruz, CA

██████████ Consultant and scientific advisory board member, New York Genome Center, New York, NY

██████████ Founder and co-chair of Data Working Group, Global Alliance for Genomics and Health

██████████ Consultant and scientific advisory board member, Two Pore Guys, Santa Cruz, CA

██████████ Consultant and scientific advisory board member, Five3 genomics, Santa Cruz, CA

██████████ Consultant and scientific advisory board member, PharmGKB, Stanford, CA

██████████ Advisor, Xconomy San Francisco, San Francisco, CA

██████████ Scientific advisory board member, International Barcode of Life, Toronto, Ontario, Canada

██████████ Consultant and scientific advisory board member, Pacific Biosciences, Menlo Park, CA

██████████ External Advisor, Beckman Institute at Caltech, CA.

██████████ Member, The Cancer Genome Atlas Steering Committee, National Cancer Institute.

██████████ Scientific advisory board member, Eli & Edythe L. Broad Institute Board of Scientific Counselors, Boston, MA

██████████ Consultant and member of scientific advisory board, Affymetrix, Inc., Santa Clara, CA

██████████ Consultant and founding member, scientific advisory board, Neomorphic, Inc., Berkeley, CA

██████████ Consultant, Xerox, Inc., Xerox Park, Palo Alto, CA

██████████ Consultant, Seville Technology, Boulder, CO

██████████ Consultant, Interactive Systems Corp., Santa Monica, CA

## EDUCATION

Ph.D. ██████████ University of ██████████ at ██████████ Computer Science,  
Received Graduate Student Research Award

M.S. ██████████ ██████████ State University at ██████████, Applied Mathematics,  
Received Mathematics Award

B.A. ██████████ ██████████ College, ██████████ Mathematics  
██████████, received Julia Bower Mathematics Award

## HONORS & AWARDS

██████████ Dan David Prize, Tel Aviv University, ██████████ Future - Bioinformatics

██████████ Innovations in Networking Award, Corporation for Education Network Initiatives in California (Cenic)

██████████ Weldon Memorial Prize, University of Oxford

██████████ Curt Stern Award, American Society of Human Genetics

████	Fellow, International Society for Computational Biology
████	Senior Scientist Accomplishment Award, International Society for Computational Biology
████	Member, National Academy of Sciences
████	Fellow, American Academy of Arts and Sciences
████	Dickson Prize in Science, Carnegie Mellon University
████	World Technology Network Award, IT Software Category
████	Classic Paper Award, American Association of Artificial Intelligence, for "Quantifying the inductive bias in concept learning," █████
████	Distinguished Engineering Alumni Award, University of Colorado, Boulder
████	Allen Newell Award, Association for Computing Machinery and the American Association for Artificial Intelligence
████	Distinguished Scientist of the Year Award Clinical Ligand Assay Society
████	Tech Award Laureate, San Jose Tech Museum of Innovation
████	Fellow, American Association for the Advancement of Science
████████	UCSC Faculty Research Lecturer
████	Scientist of the Year Award, Research & Development Magazine
████	Featured Scientist, Incyte Genomics
████	Fellow, California Academy of Sciences
████████	Awarded UC Presidential Chair of Computer Science
████	Fellow, American Association of Artificial Intelligence

## PROFESSIONAL SERVICE

### Memberships

████	Member, IEEE
████	Member, Association for Computing Machinery
████	Member, Society of Immunotherapy of Cancer
████	Fellow, International Society for Computational Biology
████	Member, American Genetic Association
████	Member, American Association for Cancer Research
████	Member, National Academy of Sciences
████	Member, American Academy of Arts & Science
████	Member, International Society for Stem Cell Research



- Member, American Society of Human Genetics
- Member, Institute of Mathematical Statistics
- Fellow, American Association for the Advancement of Science
- Fellow, California Academy of Sciences
- Fellow, American Association of Artificial Intelligence
- Member, Association for Computing Machinery

## Professional Associations

- Co-founder, Global Alliance for Genomics and Health, New York.
- Co-founder, Genome 10K Project.
- Member, Extracellular Action Potential (EAP) Beckman Institute.
- Member, Breast Cancer Dream Team, Stand up to Cancer (SU2C).
- Member, The Cancer Genome Atlas Steering Committee, National Cancer Institute.

## PUBLICATIONS AND SCHOLARLY WORK

### Contribution to Science

Citations to scientific papers: >151,000 citations, h-index 146, i10-index 276, November 9, 2017

### Books and Book Chapters

Harte R A, Diekhans M, Kent WJ, Haussler D. Guide to the UCSC Genome Browser. Cambridge, MA: NPG Education, 2010. <http://www.nature.com/scitable/ebooks/guide-to-the-ucsc-genome-browser-16569863>.

Harte RA, Karolchik D, Kuhn RM, Kent WJ, Haussler D. Databases and Genome Browsers. In Speicher M, Antonarakis S, Motulsky AG. (eds): Vogel and Motulsky's Human Genetics, Principles and Approaches, 4th Edition, Springer, New York, 2009

Siepel A, Haussler D. Phylogenetic hidden Markov models. In Nielsen R (ed): Statistical Methods in Molecular Evolution, Springer, 2004.

Haussler D, Oppen M. Metric entropy and minimax risk in classification. In Mycielski J, Rozenberg G, Salomaa A (eds): Lecture Notes in Computer Science: Studies in Logic and Computer Science, 1997:1261:212-35.

Haussler D, Barron A. How well do Bayes methods work for on-line prediction of +1,-1 values? In Proceedings of the Third NEC Symposium on Computation and Cognition, SIAM, Princeton, NJ, 1992:74-100.

Haussler D, Warmuth M. The probably approximately correct (PAC) and other learning models. In Workshop on Supervised Learning, Santa Fe Institute Press, 1995.

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Haussler D. Generalizing the PAC model. In Mehra P, Wah BW (eds): Artificial Neural Networks: Concepts and Theory, IEEE Society Press, 1992.

Haussler D. Probably approximately correct (PAC) learning and decision-theoretic generalizations. In Smolensky P, Mozer MC, Rumelhart DE (eds): Mathematical Perspectives on Neural Networks, Lawrence Erlbaum Associates, Mahwah, NJ, 1996:651-706.

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Haussler D. Applying Valiant's learning framework to AI concept learning problems. In Michalski R, Kodratoff Y. (eds): Machine Learning: An Artificial Intelligence Approach, Vol. III, Morgan Kaufmann, Los Altos, 1990:641-69.

## Edited Books

Proceedings of the Fifth ACM Workshop on Computational Learning Theory, ACM, 1992.

Proceedings of the Second Workshop on Computational Learning Theory, Morgan Kaufmann, Los Altos, CA, 1989. (with R. Rivest and M. Warmuth).

Proceedings of the First Workshop on Computational Learning Theory, Morgan Kaufmann, Los Altos, CA, 1988 (with L. Pitt).

## Peer-Reviewed Journal Publications

Newton Y, Novak AM, Swatloski T, McColl DC, Chopra S, Graim K, Weinstein AS, Baertsch R, Salama SR, Ellrott K, Chopra M, Goldstein TC, Haussler D, Morozova O, Stuart JM. TumorMap: Exploring the Molecular Similarities of Cancer Samples in an Interactive Portal. *Cancer Res.* 2017 Nov 1;77(21):e111-e114. doi: 10.1158/0008-5472.CAN-17-0580. PMID: 29092953

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## Edited Journals

1996-	Associate Editor, <i>Journal of Computational Biology</i>
2005-2012	Associate Editor, <i>Public Library of Science Computational Genomics</i>
2001-2005	Editorial Board, <i>Drug Discovery Today</i>
1996-2002	Editorial Board, <i>Neural Computing Surveys</i>
1995-2002	Editorial Board, <i>Journal of Neurocomputing</i>
1993-1995	Editorial Board, <i>Journal of Artificial Intelligence Research</i>
1988-1997	Associate Editor, <i>Machine Learning</i>
1988-1997	Guest Editor, <i>Machine Learning</i> , special issue on recent theoretical directions in Machine Learning. Spring, 1988

## Papers in Conference Proceedings

Morozova O, Salama SR, Bjork I, Goldstein TC, Mueller S, Sender LS, Sweet-Cordero A, Hausssler D. Comparative genomic analysis for pediatric cancer patients evaluated in a California Initiative to Advance Precision Medicine Demonstration Project. *American Society of Clinical Oncology*. 2017 May 20. DOI: 10.1200/JCO.2017.35.15\_suppl.TPS10578 *Journal of Clinical Oncology* 35, no. 15\_suppl

Hausssler D, Smuga-Otto M, Paten B, Novak AM, Nikitin S, Zueva M, Miagkov D. A Flow Procedure for the Linearization of Genome Sequence Graphs. *International Conference on Research in Computational Molecular Biology*. Springer, Cham. 2017 May 3. p. 34-49. DOI: 10.1007/978-3-319-56970-3\_3

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Siepel A, Haussler D. Computational identification of evolutionarily conserved exons. Proceedings of the 8th International Conference on Research in Computational Molecular Biology, RECOMB, 2004:177-86.

Jojic V, Jojic N, Meek C, Geiger D, Siepel A, Haussler D, Heckerman D. Efficient approximations for learning phylogenetic HMM models from data. Proceedings of ISMB 2004 and Bioinformatics, 2004.

Siepel A, Haussler D. Computational identification of evolutionarily conserved exons. Proceedings of the 8th Annual International Conference on Research in Computational Molecular Biology, RECOMB, 2004.

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Wang H, Hubbell E, Hu JS, Mei G, Cline M, Lu G, Clark T, Saini-Rose MA, Ares M, Kulp DC, Haussler D. Gene-structure-based splice variant deconvolution using a microarray platform. Proceedings of ISMB and Bioinformatics, 2003:19(Suppl. 1):i315-22.

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Krogh A, Mian IS, Haussler D. Parsing DNA with hidden Markov models. Alternative Readings of the Genetic Code, Parknasilla, County Kerry, Ireland, May 1993.

Haussler D, Krogh A, Brown M, Mian IS, Sjölander K. Protein modeling with hidden Markov models: an analysis of globins. 26th Hawaii Systems Conference, January 1993. [Awarded best paper in AI methods in biotechnology track].

Cesa-Bianchi N, Freund Y, Helmbold D, Haussler D, Schapire R, Warmuth M. How to use expert advice, (extended abstract), 25th ACM Symposium on Theoretical Computer Science (STOC), 1993:382-91.

Haussler D, Krogh A. DNA Alignment and clustering. Neural Networks for Computing, Snowbird, UT, Sandi von Pier (ed), AT&T Bell Laboratories, Crawfords Corner Road, Rm. 4E-422, Holmdel, NJ 07733. April 7, 1992.

Haussler D, Barron A. How well do Bayes methods work for on-line prediction of +1,-1 values? 3rd NEC Symposium on Computation and Cognition, Princeton, NJ, 1992.

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Haussler D, Kearns M, Schapire R. Bounds on the sample complexity of Bayesian learning using information theory and the VC dimension. 4th Workshop on Computational Learning Theory (COLT), Santa Cruz, CA, August 1991:61-74.

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Haussler D, Long P. A generalization of Sauer's lemma. Southeastern Conference on Combinatorics, Graph Theory and Computing, Baton Rouge, LA, February 1991.

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Haussler D. Generalizing the PAC Model: Sample size bounds from metric dimension-based uniform convergence results. 1989 IEEE Symp. on Foundations of Computer Science (FOCS), Research Triangle, NC, October 1989;40 5.

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Haussler D, Littlestone N, Warmuth M. Predicting 0,1-functions on randomly drawn points. 29th IEEE Symposium on Foundations of Computer Science, White Plains, NY, October 1988:100 9.

Haussler D, Kearns M, Littlestone N, Warmuth M. Equivalence for models of polynomial learnability. 1st Workshop on Computational Learning Theory, MIT, Cambridge, MA, August 1988.

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Ehrenfeucht A, Haussler D, Kearns M, Valiant L. A general lower bound on the number of examples needed for learning. First Workshop on Computational Learning Theory, MIT, Cambridge, MA, August 1988.

Haussler D. Learning conjunctive concepts in structural domains. AAA, Seattle, WA, July 1987:466 70.

Haussler D. Bias, Version spaces and Valiant's learning framework. 4th International Workshop on Machine Learning, Irvine, CA, June 1987.

Alon N, Haussler D, Welzl E. Partitioning and geometric embedding of range spaces of finite Vapnik-Chervonenkis dimension. 3rd International Conference on Computational Geometry, Waterloo, Canada, June 1987:331 40.

Blumer A, Ehrenfeucht A, Haussler D. Average sizes of suffix trees and DAWGs. 1st Montreal Conference on Combinatorics and Computer Science, University of Montreal, Canada. May 1987.

Haussler D. Learning internal disjunctive concepts. 20th Asilomar Conference on Signals, Systems and Computers, Pacific Grove, CA. November 1986.

Haussler D. Quantifying the inductive bias in concept learning. AAAI, Philadelphia, PA, August, 1986.

Haussler D, Welzl E. Range spaces and Epsilon-nets. SIAM Workshop on Computational and Discrete Geometry, Santa Cruz, CA, July 1986.

Haussler D. A methodology for assessing the learnability of knowledge structures. 1st Annual Rocky Mountain Conference on Artificial Intelligence, Boulder, CO, June 1986.

Haussler D, Welzl E. Epsilon-nets and simplex range queries. 2nd International Conference on Computational Geometry, Yorktown Heights, NY, June 1986.

Blumer A, Ehrenfeucht A, Haussler D, Warmuth M. Classifying learnable geometric concepts with the Vapnik-Chervonenkis dimension. 18th ACM Symposium on Theoretical Computational Science, Berkeley, CA, May 1986:273-82.

Bucher W, Ehrenfeucht A, Haussler D. On total regulators generated by derivation relations. Proc. 12th International Coll. Aut. Lang. Prog, Nafplion, Greece, July 1985:71-9.

Main MG, Bucher W, Haussler D. Applications of an infinite squarefree co-CFL. Proc. 12th International Coll. Aut. Lang. Prog., Nafplion, Greece, July 1985:404-12.

Blumer A, Blumer J, Ehrenfeucht A, Haussler D, McConnell R. Building the minimal DFA for the set of all subwords of a word on-line in linear time. Proc. 11th International Coll. Aut. Lang. Prog., Antwerp, Belgium, July 1984:109-18.

Blumer A, Blumer J, Ehrenfeucht A, Haussler D, McConnell R. Building a complete inverted file for a set of text files in linear time. Proceedings of the 16th ACM Symposium on Theoretical Computational Science, Washington, D.C., May 1984:349-58.

## Other Publications

Lawler M, Haussler D, Siu LL, Haendel MA, McMurry JA, Knoppers BM, Chanock SJ, Calvo F, The BT, Walia G, Banks I, P Yu PP, Staudt LM, Sawyers CL. Sharing Clinical and Genomic Data on Cancer-The Need for Global Solutions. New England Journal of Medicine. Massachusetts Medical Soc. 2017 May 25. doi/full/10.1056/NEJMp1612254. Vol 376, Iss 21, 2006-2009

Novak AM, Hickey G, Garrison E, Blum S, Connelly A, Dilthey A, Eizenga J, Elmohamed, MA Saleh, Guthrie S, Kahles A, Keenan S, Kelleher J, Kural D, Li H, Lin MF, Miga K, Ouyang N, Rakocvic G, Maciek Smuga-Otto M, Alexander Wait Zaranek AW, Richard Durbin R, Gil McVean G, Haussler D, Paten B. Genome Graphs. Cold Spring Harbor Labs Journals. bioRxiv. 2017 Jan 1. 101378. doi:https://doi.org/10.1101/101378

Hiranuma N, Liu J, Song C, Goldsmith J, Dorschner M, Pritchard C, Burton K, Mahen E, Blau S, Senecal F, Monsky W, Parker S, Schmechel S, Allison S, Gadi VK, Salama SR, Radenbaugh A, Goldman M, Johnsen J, Heimfeld S, Komashko V, LaMadrid-Hermannfeldt M, Duan Z, Benz S, Soon-Shiong P, Haussler D, Zhu J, Ruzzo W, Noble W, Blau CA. Cis-Compound Mutations are Prevalent in Triple Negative Breast Cancer and Can Drive Tumor Progression. Cold Spring Harbor Labs Journals. bioRxiv 2016 January 1. 085316. doi: https://doi.org/10.1101/085316

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Ballinger T, Adam D Ewing AD, Haussler D. Retrotransposon mobilization in cancer genomes. arXiv preprint arXiv: 2015 January 18. 1501.04268v1 [q-bio.GN]

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Zerbino DR, Paten B, Hickey G, Haussler D. An algebraic framework to sample the rearrangement histories of a cancer metagenome with double cut and join, duplication and deletion events. arXiv. 2013 March 22. 1303.5569v2 [q-bio.GN]

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Roskin KM, Diekhans M, Kent, WJ, Haussler D. Score functions for assessing conservation in locally aligned regions of DNA from two species. University of California, Santa Cruz, Santa Cruz, CA Tech Report UCSC-CRL-02-30. Sep, 2002.

Haussler D. The challenge of bioinformatics. R&D Magazine. 2001 Nov;43(11):8S-SC3 (in conjunction with Scientist of the Year Award).

Kent WJ, Haussler D. GigAssembler: an algorithm for the initial assembly of the human genome working draft. UCSC-CRL-00-17, December 27, 2000.

Haussler D, Jaakkola T, Winters-Hilt S. Tradeoffs between generative and discriminative hidden Markov models. Computer Science Department, University of California, Santa Cruz, Santa Cruz, CA. 1998.

## OUTSIDE PROFESSIONAL ACTIVITIES

### Conferences and Meetings, Invited

■  
"The California Kids Cancer Comparison: harnessing the power of big data to benefit single patients in California ... and now, around the world," invited keynote speaker, ■ California Initiative to Advance Precision Medicine conference, California Initiative to Advance Precision Medicine La Jolla, CA. October

"Treehouse Pediatric Cancer Consortium, invited keynote speaker, Annual Stanford Center for Genomics and Personalized Medicine Symposium, Stanford, Palo Alto, CA. April

"Facilitating a culture of responsible and effective sharing of genome data," invited speaker, BioData World Congress, BioData World Series, San Francisco. April

"The Global Alliance for Genomics and Health: Sharing Data for Genomic Medicine," invited speaker. ■ Sage Bionetworks Assembly: Mapping Open Ecosystems, Sage Assembly, Seattle, WA. April

"Sharing data for genomic medicine," invited speaker, Bioinformatics for Big Data, Molecular Medicine Tri-Conference, San Francisco, CA. February

"Data Sharing in the Treehouse Childhood Cancer Initiative: The power of big data to defeat childhood cancer," St. Baldrick's Foundation Board Meeting, St. Baldrick's, Monrovia, CA. February

"The Global Alliance for Genomics and Health: Accessibility of Data for Medicine," PMWC ■ Silicon Valley, Personalized Medicine World Conference, Mountain View, CA. January

"The Global Alliance for Genomics and Health: Accessibility of Data for Medicine," invited speaker and panelist, SU2C Scientific Summit, Stand up 2 Cancer, Santa Monica, CA. January

■  
"A public ledger to share all the world's cancer mutations," invited speaker, Festival of Genomes, San Diego, CA. September.

"Global Sharing of Genomic Information for Precision Medicine," invited speaker, Anschutz Medical Campus, Aurora, CO. August

"The Human Genome," invited speaker, Commonwealth Club of California, San Francisco, CA. ■

"Global Alliance for Genomics and Health: Genome Data Sharing," invited speaker, Center for International Security and Cooperation, Stanford, Palo Alto, CA. May

"Global Sharing of Better and More Genomes." Invited speaker, ■ International Congress of Human Genetics Conference, Kyoto, Japan. April

Global Sharing of Genomic Information for Precision Medicine,” invited keynote speaker, [REDACTED] AMIA Joint Summit: Plenary Session, American Medical Informatics Association, San Francisco, CA. March

“BRCA Challenge,” invited speaker, Inaugural Precision Medicine, Molecular Medicine Tri-Conference, San Francisco, CA. March

“Cancer genomics and data sharing,” invited speaker, [REDACTED] Future of Genomics Medicine, Scripps, La Jolla, CA. March

“Computer Science Meets Genetics in the Genome Era,” invited speaker, Special Beckman Institute Functional Genomics Center Seminar, Caltech, Pasadena, CA. March

“Global sharing of better and more genomes,” invited speaker, Advances in Genome Biology and Technology [REDACTED] Advances in Genome Biology and Technology, Orlando, FL. February

“Global Alliance for Genomics and Health,” invited speaker, Personalized Medicine World Conference (PMWC) [REDACTED] Silicon Valley, Personalize Medicine Worldwide Conference, International, Mountain View, CA. January

[REDACTED]  
“Harnessing Global Genomic Data to Defeat Cancer,” invite speaker, CARIS Scientific Board Meeting, Caris Life Sciences, Scottsdale, AZ. December

“Odyssey Into the Human Genome, invited speaker, Annual Regional Meeting, San Francisco Area Mensa, Santa Cruz, CA. November

“The Data Working Group of the Global Alliance for Genomics and Health,” invited speaker and panelist, Probabilistic Modeling in Genomics, Cold Spring Harbor, NY. October

“Harnessing Global Genomic Data for Discovery,” invited speaker, Future Sequencing Technologies and Applications, Genomics Institute of the Novartis Research Foundation, La Jolla, CA. September

“Big Data,” invited panelist, Aspen Cancer Conference Special Evening, Aspen Cancer Conference, Aspen CO. July

“Antigen Recognition Project,” invited speaker, SU2C - Google[x] Technology and Analysis Satellite Meeting, Stand up 2 Cancer, Boston, MA. July

“Federated BRCA Data Sharing: Lessons and Visions, invited speaker, BRCA Challenge, Global Alliance for Genomics and Health, Paris, France, June.

“Bioinformatics to enable cancer immunotherapy,” invited speaker, Immunology Meeting, Stand up 2 Cancer, Boston, MA. June

“BD2K Centers of Excellence,” invited speaker Big Data in BioMedicine, Stanford University, Palo Alto, CA. May

“Odyssey into the human genome,” invited award winner, [REDACTED] Dan David Prize, University of Tel Aviv, Tel Aviv, Israel. May

“Global Alliance for Genomics and Health,” invited speaker, [REDACTED] TEDx Santa Cruz, April

“Calling both simple and complex mutations in cancer genome,” invited speaker, Identifying Drug Targets with Computational Genomics, [REDACTED] Annual Meeting, American Association for Cancer Research, Philadelphia, PA. April

“Global Alliance for Genomics and Health,” invited speaker, Annual UC system-wide conference, UC Academic Business Officers Group (ABOG), Santa Cruz, CA. April

“Technology and Big Data,” invited speaker, Big Data, Genomics, and Precision Medicine Program, National Human Genome Research Institute, San Jose, CA. April

"Big Data to Knowledge (BD2K) Centers of Excellence", invited speaker, AMIA Translational Bioinformatics Conference, San Francisco, CA. March

"Stable reference structures for human genome analysis," invited featured speaker, Genome and Transcriptome Analysis, Molecular Medicine Tri-Conference. San Francisco, CA. February

"Global exchange of human genetic data for medicine and research," invited keynote speaker, Bioinformatics for Big Data Track, Medicine Tri-Conference. San Francisco, CA. February

"Global Alliance for Genomics and Health," invited speaker, Large Sequence Data Analysis & Clinical Interpretation, Personalized Medicine World Conference [REDACTED] Mountain View, CA January

"Global exchange of human genetic data for medicine and research," invited keynote speaker, Pacific Symposium on Biocomputing [REDACTED] Kona, HI, January

[REDACTED]  
"Global exchange of human genetic data for medicine and research," invited keynote speaker, Cold Spring Harbor Biological Data Sciences, Cold Spring Harbor, NY. November.

"Discovering and representing subclones in cancer tissues from analysis of whole genome sequencing data," invited speaker, Tumor Heterogeneity Symposium, Stanford Cancer Institute, Palo Alto, CA. October

"Peptide Antigen Display and Recognition: a New Fusion of Genomics and Proteomics," invited speaker, Future Opportunities for Genomic Sequencing, NHGRI, Bethesda, MD. July

Participatory Biology Panel, invited panelist, Techonomy Bio conference, Techonomy, San Jose, CA. June

"Large-scale Cancer Genomics," invited speaker, Sadler Memorial Lecture, University of Colorado, Denver, Denver CO. May

"Large-scale Cancer Genomics," invited speaker, [REDACTED] BioFrontiers Symposium on Big Data, University of Colorado, Boulder, Boulder, CO. May

"Large-scale Cancer Genomics," invited speaker, Sequence the City - Metagenomics in the Era of Big Data, IBM: Almaden Institute, San Jose, CA. May

"Large-scale Cancer Genomics," invited speaker, AACR Annual Meeting [REDACTED] American Association for Cancer Research, San Diego, CA. April

"Large-scale Cancer Genomics," invited speaker, Big Data in Biology, Keystone Symposium on Molecular and Cellular Biology, San Francisco, CA. March

"Large-scale Cancer Genomics," invited speaker, Big Data in Biology, Simons Foundation, Biotech Symposium, New York, NY. March

"Large-scale Cancer Genomics," invited speaker, Evening Lectures in Genomics, New York Genome Center, New York, NY. March

"Cancer Genomics," invited speaker, Bioinformatics for Big Data, [REDACTED] Molecular Medicine Tri-conference, Cambridge Healthtech Institute, San Francisco, CA. February

[REDACTED]  
"Cancer Genomics," invited speaker, Global SIP Symposium: Bioinformatics and System Biology, University of Texas, Austin, TX. December.

"Comparative analysis of cortical neuron development in a stem cell model of primate neurogenesis," invited speaker, Howard Hughes Medical Institute Scientific meeting, Howard Hughes Medical Institute, Ashburn, VA. October.

"A global alliance for genomic and clinical data," invited keynote speaker, Beyond the Genome, BioMed Center, San Francisco, CA. October.

"Genome data in the cloud," invited speaker, The 8th Scientific Workshop, International Cancer Genome Consortium, Toronto, Canada. October.

"Large-scale comparative genomics for cancer research," invited speaker, Statistical Data Integration Challenges in Computational Biology: Regulatory Networks and Personalized Medicine, Banff International Research Station for Mathematical Innovation and Discovery (BIRS), Banff, Canada. August.

"Cancer Genomics," invited speaker, Microsoft Research Faculty Summit, Microsoft, Redmond, WA. July.

"Large-scale Comparative Genomics for cancer research," invited speaker, [REDACTED] Human Genome Meeting and 21<sup>st</sup> International Congress of Genetics, Human Genome Organization (HUGO) and International Genetics Federation (IGF), Singapore, Singapore, April.

"Generalizations of the Fourier transform to Gelfand pairs provide a continuous time Markov model for the evolution of genomes via rearrangements and substitutions" invited speaker, Janelia Biological Sequence Analysis Conference, Howard Hughes Medical Institute, Ashburn, VA. March.

"Cancer Genomics," invited speaker, Doc Talk lecture series, American Cancer Society, Santa Cruz, CA. February.

"Large scale Cancer Genomics analysis," invited speaker, Pacific Symposium on Biocomputing [REDACTED] The Future of Genome-Based Medicine, Kona, HI. January.

[REDACTED]  
"Benchmarking study—DNA sequence variance/rearrangement calls: algorithm comparison across centers," invited speaker, The Cancer Genome Atlas Semi-Annual Steering Committee Meeting, The Cancer Genome Atlas, Crystal City, VA. November.

"One million cancer genomes", invited speaker, Techonomy [REDACTED] Techonomy, Tucson, AZ. November.

"The UCSC Cancer Genomics Hub," invited keynote speaker, [REDACTED] Uninex Symposium, Operating Systems Design and Implementation, Hollywood, CA. October.

"Somatic mutations in cancer as assessed by whole genome sequencing," invited speaker, Identification and annotation of SNPs in the context of structure, function, and disease meeting, Special Interest Group (SNP-SIG), Long Beach, CA. July.

"Three periods of regulatory innovation during vertebrate evolution," invited speaker, EMBO: Evolution in the Time of Genomics, Genetic Information Research Institute, Venice, Italy. May.

"Mutation calling," invited speaker, The Cancer Genome Atlas Semi-Annual Steering Committee Meeting, The Cancer Genome Atlas, Houston TX. April.

"UCSC Cancer Genomics Hub," invited speaker, The Cancer Genome Atlas Semi-Annual Steering Committee Meeting, The Cancer Genome Atlas, Houston TX. April.

"Personal cancer genomics," invited keynote speaker, [REDACTED] Sage Bionetworks Commons Congress, Sage Bionetworks Commons Congress, San Francisco, CA. April.

"Cancer genomics," invited speaker, Genome Informatics Alliance [REDACTED] Genome Informatics Alliance, Newberg OR. March.



"Benchmarking mutation calls," invited speaker, [REDACTED] International Cancer Genome Consortium workshop, International Cancer Genome Consortium, Cannes, France. March.

"Aspects of the evolutionary impact of retrotransposons on vertebrate genomes," invited speaker, Genetic Information Genomic Impact, [REDACTED] International Conference on Genomic Impact of Eukaryotic Transposable Element, Pacific Grove. February.

"Personal genomics," invited speaker, Pacific Symposium on Biocomputing, Kona, HI. January.

[REDACTED]

"Genomic analysis for pathway characterization," invited speaker, San Antonio Breast Cancer Symposium, San Antonio, TX. December.

"Large-scale cancer genomics data analysis," invited speaker, Enabling Cancer Research through TCGA, The Cancer Genomics Atlas, Houston, TX. November.

"CGHub: A next generation repository for next generation sequence data," invited speaker, Enabling Cancer Research through TCGA, The Cancer Genomics Atlas, Houston, TX. November.

"Cancer genomics," invited speaker, Howard Hughes Medical Institute, Chevy Chase, MD. November.

"Cancer genomics in the TCGA TARGET and ICGC projects," invited speaker, Translation of the cancer genome meeting, American Association for Cancer Research (AACR) San Francisco, CA. October.

"Cancer genomics," invited speaker, Inaugural Bio-IT Cloud Summit: Cloud Computing Conference, Bio-IT World and Cambridge Healthtech Institute, La Jolla, CA. September.

"Epigenomics of stem and cancer cells: computational challenges," invited speaker, [REDACTED] CIRM Grantee Meetings, California Institute for Regenerative Medicine, San Francisco, CA. September.

"Cancer genomics," keynote speaker, SIGKDD [REDACTED] Association for Computing Machinery, San Diego, CA. August.

"Cancer genomics," invited speaker, Spring Epigenetics, Genentech, Woodside, CA. May.

"The large-scale analysis tool building perspective: The need for access to data sets, standard exchange formats, and bringing computing to the data," invited speaker, The Collection, Storage, Management, and Distribution of Next-Generation Sequence Data, National Institutes of Health, Gaithersburg, MD. April.

"Mutation analysis," invited speaker, The Cancer Genome Atlas (TCGA) Semi-Annual Steering Committee Meeting, The Cancer Genome Atlas. Bethesda, MD. April.

"Cancer genomics in the TCGA project," invited speaker, DARPA CAP3 workshop, National Cancer Institute, Bethesda, MD. April.

"Cancer genomics in the TCGA Project," invited speaker, Conference on Systems Biology: Confronting the Complexity of Cancer, AACR/NCI, La Jolla, CA. February.

"Cancer genomics: the Next Step for SU2C," invited speaker, Stand Up 2 Cancer Dream Team Summit, Miami, FL. January.

"Personal genomics," invited speaker, Pacific Symposium on Biocomputing, Kona, HI. January.

[REDACTED]

"Genomics and the Genome 10K Project," invited speaker, Chance and Necessity in Evolution, International Union of Biological Sciences & Istituto per gli Studi Filosofici of Naples, Ravello, Italy. October.

"Cancer genomics and the TCGA project," invited speaker, Molecular Diagnostics in Cancer Therapeutic Development, American Association for Cancer Research, Denver, CO. September.

"Cancer genomics data analysis," invited speaker, Pfizer, Cancer Genomics Data Analysis, San Diego, CA. August.

"Comparative genomics and the Genome 10K Project," invited speaker, American Genetic Association, Conservation Genomics, Hilo, HI. July.

"\$1000 Genomes," invited speaker, HiTSeq, Intelligent Systems for Molecular Biology, Boston, MA. July.

"\$100 Genomes," invited speaker, Jason Study, The MITRE Corporation, San Diego, CA. June.

"TCGA data analysis pipeline," invited speaker, The Cancer Genome Atlas Steering Committee. Bethesda, MD. April.

"Comparative genomics for vertebrates," invited speaker, National Human Genome Research Institute Informatics and Analysis Planning Meeting, Bethesda, MD. April.

"TCGA Data analysis and dissemination," invited speaker, American Association for Cancer Research Annual Meeting The Cancer Genome Atlas. Washington, DC. April.

"Mapping cancer genomics data to pathways," invited speaker, Cancer Profiling and Pathways Conference, San Francisco, CA. February.

"The supercomputing challenge to decode the evolution and diversity of our genomes," invited speaker, Supercomputing Conference, Portland, OR. November.

"Genomes in the Clouds: UCSC genomics browsers and distributed bio computation," invited speaker, Supercomputing Conference, Portland, OR. November.

"Reconstructing the 500 million year record of evolution in the vertebrate genome," featured lecturer, Annual Meeting of the Fellows of the California Academy of Sciences, San Francisco, CA. October.

"The evolution of non-coding functional elements in our genome," invited speaker, Evolution of the Molecular Landscape, Cold Spring Harbor Symposium, Cold Spring Harbor, NY. May.

"The evolution of non-coding functional elements in our genome," invited speaker, Harvey Mudd College, Pasadena, CA. April.

"Transposon-induced rewriting of vertebrate gene regulation," invited speaker, AAAS Annual Meeting: Our Life and its Life: Origins and Futures, Chicago, IL. February.

"Statistical and algorithmic methods to explore evolution," invited speaker, NIH Darwin Day, Bethesda, MD. February.

"Molecular evolution and disease," invited speaker, HHMI Scientific Meeting: Human Disease, Genetics, Models and Progress Toward Treatments, Chevy Chase, MD. February.

"Evidence that transposons shaped vertebrate gene regulatory networks," invited speaker, International Conference and Workshop Genomic Impact of Eukaryotic Transposable Elements, Asilomar, Monterey, CA. February.

"UCSC cancer genomics browser for TCGA data," invited speaker, TCGA Steering Committee, Washington, D.C. December.

"Non-coding RNA: Red-headed stepchild of the human genome," invited speaker, 58th Annual Meeting of ASHG, Philadelphia, PA. November.

"Human gene predictions," MGC-ESC Meeting, invited speaker, Rockville, MD. September.

"100 million years of evolutionary history of the human genome," invited speaker, ISCB Conference, Toronto, CAN. July.

"100 million years of evolutionary history of the human genome," invited speaker, [REDACTED] Conference on AAAI-08, Chicago, IL. July.

"Computing how we became human," invited speaker, [REDACTED] ACM Symposium on Theory of Computing, Victoria, BC. May.

"A rapidly evolved RNA gene may have played a role in the evolution of the cerebral cortex," invited speaker, European Human Genetics Conference, Barcelona, Spain. May.

"100 million years of evolutionary history of the human genome," plenary speaker, HapMap, Human Evolution and the Future of Life, Copenhagen, Denmark. May.

"Evolutionary genomics of the human genome," Distinguished Lecturer, Computer Science Columbia University, New York, NY. May.

"Computing how we became human," invited speaker, Renaissance Technologies Corporation Symposium, New York, NY. May.

"The personal genome: consequences for society," invited speaker, 7th Annual Genome Sciences Symposium, Seattle, WA. April.

"The infinite sites model of genome evolution," invited speaker, Gordon Conference in Molecular Evolution, Ventura, CA. February.

[REDACTED]

"Reconstructing 100 million years of human evolutionary history," honored speaker, NIH Intramural Sequencing Center's 10th Anniversary Symposium, Bethesda, MD. October.

"Rapidly evolving non-coding regions and brain evolution," honored speaker, [REDACTED] Annual American Society of Human Genetics Meeting, San Diego, CA. August.

"Reconstructing 100 million years of human evolutionary history," invited speaker, Pacific Biosciences, Menlo Park, CA. July.

"Reconstructing 100 million years of human evolutionary history," honored speaker, Vertebrate Comparative Genomics, US National Academy of Sciences and the Australian Academy of Science, Beckman Center of the National Academy of Sciences, Irvine, CA. May.

"The infinite sites model of genome evolution," Biology of Genomes meeting, invited speaker, Cold Springs Harbor Conference, Cold Springs Harbor, NY. May.

[REDACTED]

"Reconstructing 100 million years of human evolutionary history," Johns Hopkins University, Baltimore, MD. November.

"Ultraconserved elements, living fossil transposons, and rapid bursts of change: reconstructing the uneven evolutionary history of the human genome," invited speaker, International Symposium on Genomics, Hangzhou, China. October.

"Reconstructing 100 million years of human evolutionary history," honored speaker, Scientific Forum for Cabrillo Festival of Contemporary Music, world premiere of the Frans Lanting orchestral-photographic performance "Life: A Journey Through Time," Santa Cruz, CA. July.

"Exploring the evolutionary history of the human genome over the last 100 million years," keynote address, ACM SIGMOD International conference on Management of Data, Chicago, IL. June.

"Ultraconserved elements, living fossil transposons, and rapid bursts of change: reconstructing the uneven evolutionary history of the human genome," 23rd International Conference on Machine Learning (ICML), Carnegie Mellon University, Pittsburgh, PA. June.

"Ultraconserved elements, living fossil transposons, distal enhancers, and mysterious RNA genes: reconstructing the detailed evolutionary history of the human genome," Annual Society for Molecular Biology and Evolution Meeting, Genomes, Evolution, and Bioinformatics, Arizona State University, Tempe. May.

"Ultraconserved elements, living fossil transposons, distal enhancers, and mysterious RNA genes: reconstructing the detailed evolutionary history of the human genome," inaugural speech, Broad Distinguished Lecture Series in Computational Biology, Eli & Edythe L. Broad Institute, Cambridge, MA. May.

"Feasibility of reconstructing the 100 million year history of the human genome," Genomes and Biology, Cold Spring Harbor, NY. May.

"Applying comparative genomics to assist in the completion of the Mammalian Gene Collection," Mammalian Gene Collection Annual Meeting, Washington, DC. April.

"The infinite sites model of genome evolution," Workshop on Reconstruction of Ancestral Genomes, Barbados. April.

"Ultraconserved elements, living fossil transposons, and rapid bursts of change: reconstructing the uneven evolutionary history of the human genome," keynote address, 10th Annual Conference on Research in Computational Molecular Biology, Venice, Italy. March.

"Ultraconserved elements, living fossil transposons, and rapid bursts of change: reconstructing the uneven evolutionary history of the human genome," keynote address, Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor, NY. March.

"Ultraconserved elements, living fossil transposons, and rapid bursts of change: reconstructing the uneven evolutionary history of the human genome," Dickson Prize award talk, Carnegie-Mellon University, Pittsburgh, PA. March.

"Ultraconserved elements, living fossil transposons, distal enhancers, and mysterious RNA genes: reconstructing the detailed evolutionary history of the human genome," Integrative Graduate Education and Research Traineeships, University of Arizona, Tucson. January.

 "Health, medicine, and biotechnology," keynote address, World Technology Summit, San Francisco, CA. November.

"Using evolution to explore the human genome," honored speaker, European Bioinformatics Institute, Hinxton, UK. November.

"Using evolution to explore the human genome," Evolutionary Genomics Meeting, The Stazione Zoologica Anton Dohrn, Naples, Italy. October.

"Using evolution to explore the human genome," keynote address, Genome Informatics Conference, Cold Spring Harbor, NY. October.

"Using evolution to explore the human genome," keynote address, IEEE Workshop on Computer Vision Methods for Bioinformatics, San Diego, CA. June.

"Computational reconstruction of an ancestral mammalian chromosome," keynote address, Cold Spring Harbor Conference, Cold Spring Harbor, NY. May.

"Reconstructing an ancestral mammalian chromosome," keynote address, Cold Spring Harbor Conference, Cold Spring Harbor, NY. May.

"Ultraconserved elements in the human genome," European Human Genetics Conference, Prague, Czech Republic. May.

"Impact of human genome research: present and future," Mervyn Young Memorial Lecture, University of Colorado, Boulder, CO. April.

"Using evolution to explore the human genome," Distinguished Engineering Alumni Award Seminar, University of Colorado, Boulder, CO. April.

"Impact of human genome research: present and future," honored speaker, Mervyn Young Memorial Lecture, University of Colorado, Boulder, CO. April.

██████  
"Using evolution to explore the human genome," honored speaker, University of Washington, CSE Distinguished Lecture, Seattle, WA. December.

"Impact of human genome research: present and future," Mervyn Young Memorial Lecture, University of Colorado, Boulder, April.

"Using evolution to explore the human genome," Distinguished Engineering Alumni Award Seminar, University of Colorado, Boulder. April.

"Impact of human genome research: present and future," honored speaker, Mervyn Young Memorial Lecture, University of Colorado, Boulder. April.

"Comparative genomics to identify functional elements in the human genome," Molecular Medicine Tri-Conference, San Francisco, CA. March.

"The power of multiple vertebrate genome sequences," Keystone Symposia, Steamboat Springs, CO. March.

"Reconstructing an ancestral mammalian genome in silico," Gordon Research Conference in Molecular Evolution, Ventura, CA. February.

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"Using comparative genomics to predict functional elements in the human genome," Distinguished Speaker Series, Sloan-Swartz Center for Theoretical Neurobiology Seminar, Colorado State University, Ft. Collins. November.

"Using comparative genomics to predict functional elements in the human genome," ██████ Distinguished Seminar Series, Department of Computer Science, University of British Columbia, Canada. November.

"Using comparative genomics to predict functional elements in the human genome," XIX International Congress of Genetics, Melbourne, Australia. July.

"Identifying functional elements in the human genome by tracing the evolutionary history of the bases: a key challenge for comparative genomics," Intelligent Systems for Molecular Biology, Brisbane, Australia. June.

"Bioinformatics, genome evolution and the challenge of identifying functional elements in the human genome," The Genome of Homo Sapiens. Symposium on Quantitative Biology, Cold Spring Harbor, NY. May.

"Computational genomics on mammals: sequence, function, and evolution," Intra- and Intercellular Communication Science Meeting, Howard Hughes Medical Institute, Washington, DC. April.

"Bioinformatics, genome evolution and the challenge of identifying functional elements in the human genome," Distinguished Science Seminar, Affymetrix, Santa Clara, CA. April.

"Computational analysis of the human and other mammalian genomes," International Conference on Artificial Intelligence and Statistics, Key West, FL. January.

"Computational analysis of the human and other mammalian genomes," Oncogenomics, Phoenix, AZ. January.

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"Computational analysis of the human and mouse genomes," Conference on Signals, Systems, and Computers, Asilomar Conference Center, Pacific Grove, CA. November.

"The working drafts of the human and mouse genomes," Osong International Bio Conference, South Korea. October.

"The working drafts of the human and mouse genomes," IBC's Post-Genomic Bioinformatics Conference, San Francisco, CA. June.

"Assembly and initial analysis of the working draft of the human genome," Clinical Ligand Assay Society, in conjunction with Boston Biomedica/CLAS Distinguished Scientist of the Year Award, ██████ Annual Meeting, Houston, TX. May.

"Initial computational analysis of the public working drafts of the human and mouse genomes, and the long road ahead," Genomes and Biology Conference, Cold Spring Harbor, NY. May.

"Status of the human and mouse working draft genomes, and some early comparisons," Genes and Genomes in Health and Disease, Howard Hughes Medical Institute, Washington, DC. March.

"Status of the human genome working draft: map, assembly and web access," Advances in Genome Biology & Technology, joint meeting with Automation in Mapping & DNA Sequencing, Marco Island, FL. February.

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"Overview of the human genome project and the construction of the working draft," and "Exploring the working draft of the human genome," NATO ASI on Artificial Intelligence and Heuristic Methods for Bioinformatics, San Miniato, Italy. October.

"Assembly and annotation of the public human genome working draft," ██████ International Genome Sequencing and Analysis Conference, San Diego, CA. October.

"Assembly and annotation of the working draft of the human genome," Gordon Research Conference on Human Molecular Genetics, Newport, RI. August.

"The public working draft of the human genome," keynote address, CHI Bioinformatics and Genome Research, San Francisco, CA. June.

"The public working draft of the human genome," ██████ Annual Symposium on the Interface of Computer Science and Statistics, Costa Mesa, CA. May.

"Assembly and initial analysis of a working draft of the human genome," New Frontiers in Structural and Computational Biology, Howard Hughes Medical Institute, Chevy Chase, MD. March.

"A working draft of the human genome," Pacific Symposium on Biocomputing, Mauna Lani, HI. January.

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"Hidden Markov models, Fisher kernels and support vector machines for biosequence analysis," Bioinformatics, Elsinore, Denmark. April.

"Computational prediction of genes and gene function from high-throughput genomics data," Association for the Advancement of Artificial Intelligence, Washington, D.C. February.

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"Computational analysis of high-throughput genomics data using hidden Markov models and support vector machines," keynote speaker, ██████████ Annual Genome Informatics Workshop, Tokyo. December.

"Analysis of microarray gene expression data using support vector machines," In Silico Biology: Sequence, Structure and Function, Atlanta, GA. November.

"Combining discriminative classification methods with hidden Markov models for more effective biosequence analysis," 8th Bioinformatics and Genome Research Conference, San Francisco, CA. June.

"Hidden Markov models and Fisher kernels for biosequence analysis," Learning, ██████████ Annual Workshop, Snowbird, UT. April.

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"A new discriminative methodology for detecting remote protein homologies," ██████████ Annual Computational Structural Biology Research Meeting, Monterey, CA. December.

"Statistical methods in biosequence analysis: discriminative vs. generative models," ██████████ Annual Conference on Computational Genomics, Reston, VA. November.

"Models and methods in biosequence analysis," International Conference on Problems in Biophysics, Moscow. June.

"Hidden Markov models for protein families," Structure-Function Based Genomics Symposium, London, England. April.

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"Statistical genome analysis: hidden Markov methods," Newton Seminar, Isaac Newton Institute, Cambridge, England. October.

"A brief look at some machine learning problems in genomics," keynote lecture, ██████████ International Conference on Computational Learning Theory, Vanderbilt University, Nashville, TN. July.

"Design of the Genie genefinder," Finding Genes: Computational Analysis of DNA Sequences, Cold Spring Harbor, NY. March.

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"VC dimension, covering numbers and worst-case prediction of individual sequences," ICMS Workshop on the Vapnik-Chervonenkis Dimension, Edinburgh, Scotland. September.

"Using hidden Markov models for biosequence analysis," keynote lecture, ██████████ International Conference on Intelligent Systems in Molecular Biology, St. Louis, MO. June.

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"Using hidden Markov models to search biosequence databases," Workshop on Knowledge, Discovery and Database Mining, Montreal, Canada. August.

"Hidden Markov and related statistical models: how they have been applied to biosequence analysis," Workshop on Uncertainty in Artificial Intelligence, Montreal, Canada. August.



"Hidden Markov models in biosequence analysis," Workshop on Biosequence Analysis, Aspen Center for Physics, Aspen, CO. June.

"Prediction, data compression and metric dimension," [REDACTED] ACM Symposium on Computational Geometry, Vancouver, Canada. June.

"Hidden Markov models for proteins," DIMACS Workshop on Sequence Based Methods for Protein Folding, Rutgers, NJ. March.

"Bounds on the mutual information between a parameter and a sequence of conditionally independent observations," Workshop on Theory of Neural Networks, Pohang, Korea. February.

[REDACTED]  
"Hidden Markov models for multiple alignments and database search for proteins," Meeting on Critical Assessment of Techniques for Protein Structure Prediction, Asilomar Conference Center, Pacific Grove, CA. December.

"Using stochastic context-free grammars to fold, align and model homologous RNA sequences," Workshop on the Fusion of Molecular Biology and Knowledge Information Processing, Tokyo, Japan. December.

[REDACTED]  
"Hidden Markov models and beyond," Macromolecules, Genes and Computers: Chapter Three, Waterville, NH. August.

"On-line prediction: models from computational learning theory and statistics," Learning Days in Jerusalem Conference, Jerusalem, Israel. May.

[REDACTED]  
"How to use expert advice," 6th Conference on Neural Information Processing Systems, post-meeting workshop on Bayesian Methods, Vail, CO.

"Hidden Markov models for protein families," 6th Conference on Neural Information Processing Systems, post-meeting workshop on hidden Markov Models, Vail, CO.

"Hidden Markov models for protein families" and "Bayes Methods for Prediction," Workshop on Supervised Learning, Santa Fe, NM.

"How well do Bayes Methods work for on-line prediction of +1,-1 values?" [REDACTED] NEC Symposium on Computation and Cognition, Princeton, NJ.

[REDACTED]  
"How well do Bayes methods work?" 5th Conference on Neural Information Processing Systems, post-meeting workshop on Bayesian methods, Vail, CO.

"Uniting the VC and TLS theories of generalization," Neural Networks for Computing, Snowbird, UT. April.

"Computational learning theory," 3rd Woodward Conference on Modeling Complex Phenomena, San Jose, CA. April.

[REDACTED]  
"Learnability and the metric dimension: decision theoretic generalizations of the PAC learning model," [REDACTED] International Workshop on Algorithmic Theory, Tokyo, Japan. October.

"Probably approximately correct learning," National Conference, Association for the Advancement of Artificial Intelligence, Boston, MA. July.

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"Complexity issues in learning from random examples," Annual Meeting of the Society for Industrial and Applied Mathematics, Mini-symposium on Neural Computing, San Diego, CA. July.

"Bounds on sufficient training set size when learning from random examples," Neural Networks for Computing, Snowbird, UT. April.

"Probably approximately correct learning," Discovery and Learning: Philosophical and Computational Perspectives, Pittsburgh, PA. April.

"Generalization in neural networks: a computational learning theory perspective," Annual Meeting of the American Association for the Advancement of Science, San Francisco, CA. January.

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"Theoretical results in machine learning," ██████████ International Conference on Machine Learning, Ann Arbor, MI. June.

## **Talks and Presentations at Colleges and Universities, Invited speaker**

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"Genome evolution: battling transposons," invited speaker, Fall BME 280, University of California, Santa Cruz, CA. November

"Genomics at UCSC," invited speaker, Bioethics BME 80G, University of California, Santa Cruz, CA. October

"Data Driven Solutions for Silicon Valley: A Conversation with Distinguished Leaders," invited panelist, UCSC/Silicon Valley Regional Data Trust, San Jose, CA. January

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"Can we find the genetic changes that make us human?," invited speaker, Original Thinkers Series, University of California, Santa Cruz, Washington DC. November

"Genomes and cancer," invited speaker, UCSC Faculty Research Seminar, University of California, Santa Cruz, CA. November

"Can we find the genetic changes that make us human?," invited speaker, UCSC BME 280B Seminar Series, University of California, Santa Cruz, CA. November

"Genomes and cancer," invited speaker, The Pebble Beach & Tennis Club, University of California, Santa Cruz, Pebble Beach, CA. November

"Genomes," invited speaker, UCSC Emeriti Association, University of California, Santa Cruz, CA. October

"Cancer Genomics," invited speaker, Bioethics guest lecture, University of California, Santa Cruz, CA. October

"Can we decode cancer?" invited speaker, UCSC Silicon Valley Open House, University of California, Santa Cruz, Santa Clara, CA. September

"California Kids Cancer Comparison project," invited keynote speaker, University of California Computing Services Meeting, University of California, Santa Cruz, CA. July

"Global Alliance for Genomics and Health," invited speaker, 17th Bioengineering Institute of California Symposium, University of California, San Francisco, CA. June

"California Kids Cancer Comparison project," invited speaker, Treehouse Event, University of California, Santa Cruz, Santa Cruz, CA. June

"Odyssey," invited speaker, Silicon Valley Original Thinkers, University of California, Santa Cruz, Palo Alto, CA. May

"Molecular characterization for diagnoses and treatment," invited speaker, Computational Cancer Biology workshop, Simons Institute, UC Berkeley. February

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"Elementary mathematics behind phenomena like the evolution of life," invited speaker, Mathematics Colloquium, University of California Santa Cruz. October.

"Genomics and Cancer," invited speaker, BME280B seminar, University of California Santa Cruz. October.

"Odyssey Into the Human Genome," invited speaker, UCSC - Santa Cruz County Estate Planning Council breakfast, University of California, Santa Cruz. October

"Harnessing Global Genomic Data," invited speaker, UCSC BioEngineering Symposium, University of California, Santa Cruz. June

"Global Alliance for Genomics and Health," invited speaker, UCSC Dean's club dinner, University of California, Santa Cruz, Los Gatos. April

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"Cancer Genomics," invited speaker, BME280B seminar, University of California Santa Cruz. November.

"New hypothesis about the evolution of human brain size," invited speaker, Computational Approaches to Evolution, The Simons Institute for the Theory of Computing, University of California, Berkeley. March

"Creating (and Mapping to) a Universal Reference Genome," invited speaker, Computation-Intensive Probabilistic and Statistical Methods for Large-Scale Population Genomic, The Simons Institute for the Theory of Computing, University of California, Berkeley. February

"Large-scale Cancer Genomics," invited speaker, Cancer Genomics Symposium, Berkeley Training Program: Genomics and Computational Biology, University of California, Berkeley. January.

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"The quest to conquer cancer: Computer geeks to the rescue," invited speaker, ██████████ Century Club members annual lunch, University of California Santa Cruz. November.

"Genome evolution and cancer genomics," invited speaker, BME280B seminar, University of California Santa Cruz. October.

"The quest to conquer cancer: Computer geeks to the rescue!" invited speaker, Local Roots, Global Impact, University of California Santa Cruz. October.

"Cancer Genomics," invited keynote address, Chemical and Systems Biology Department, Stanford, Santa Cruz, CA. September.

"Big data and new models needed to study DNA variation in cancer," invited speaker, Oxford Big Data in Biomedicine Conference, Stanford University, Palo Alto, CA. May.

"Big data and new models needed to study DNA variation in evolution and cancer," invited speaker, Frontiers in Interdisciplinary Biosciences, Stanford University, Palo Alto, CA. May.

"Big data and new models needed to study DNA variation in evolution and cancer," invited speaker, Simons institute: Visions of Computing, Simons institute, UC Berkeley, CA. April.

"Cancer Genomics," invited plenary speaker, [REDACTED] Information Theory and applications Workshop, University of California San Diego, San Diego CA. February.

"Cancer Genomics," invited speaker, Nanobiotechnology Seminar Series, Stanford University, Palo Alto, CA. January.

[REDACTED]  
"Genomics" invited speaker, Bioethics class lecture, University of California Santa Cruz. November.

"The UCSC Cancer Genomics Hub," invited keynote speaker, [REDACTED] Nature/Institute of Genomic Medicine Annual 2012 Symposium, UCSD Institute of Genomic Medicine, University of California, San Diego. November.

"Genomics gets personal," invited keynote speaker, Genomics Gets Personal: Property, Persons, Privacy, University of California Santa Cruz and California Institute for Quantitative Biosciences (QB3), San Francisco, CA. September.

"The UCSC Cancer Genomics Hub," invited speaker, Research Review Day, University of California Santa Cruz. September.

"Cancer Genomics," invited speaker, The [REDACTED] Birthday Symposium for Andrzej Ehrenfeucht, Distinguished Professor of Computer Science, University of Colorado, Boulder. September.

"Cancer Genomics," invited speaker, Simons Institute for the Theory of Computing, University of California, Berkeley. July.

"Analysis of cancer genomics," Machine Learning Summer School, University of California, Santa Cruz. July.

"Cancer genomics," invited speaker, Human Genomics, Upper Division, Stanford University, Palo Alto, CA. May.

"Cancer Genomics," invited keynote speaker, 30 Years of Computational Biology at USC, University of Southern California, Los Angeles, CA. March.

"Cancer Genomics," invited speaker, Santa Cruz Philosophical Society's Dinner and a Lecture series, Santa Cruz Philosophical Society, Santa Cruz. March.

[REDACTED]  
"Cancer Genomics," invited speaker, Caltech General Biology Seminar Series, Pasadena, CA. December.

"The evolution of non-coding functional elements in our genome," invited speaker, Evolutionary Genomics, Institute for Pure and Applied Mathematics (IPAM), University of California, Los Angeles. November.

"Cancer Genomics in the TCGA TARGET and ICGC projects," invited speaker, Sanford Statistics Seminar, Stanford University, Palo Alto, CA. November.

"Cancer Genomics," invited speaker, Wellcome Trust Sanger Institute, Cambridge, UK. October.

"Cancer Genomics," invited speaker and honoree, Weldon Memorial Prize, Oxford University, Oxford, UK. October.

"At the dawn of personalized medicine," invited speaker, Santa Cruz Foundation Forum, University of California, Santa Cruz. October.

"Cancer Genomics in the TCGA, TARGET, and ICGC projects," plenary speaker, Research review Day, University of California, Santa Cruz. October.

"Cancer and evolutionary genomics," invited speaker, Next-generation Sequencing Technology & Algorithms for Primary Data Analysis, Institute for Pure and Applied Mathematics (IPAM), University of California, Los Angeles. October.

"Cancer genomics and the TCGA project," invited speaker, Evolution and Cancer Conference, University of California, San Francisco. June.

"Cancer Genomics," invited speaker, AMP Lab Summer Retreat, University of California, Berkeley, Santa Cruz, CA May.

"Cancer Genomics," plenary speaker, Theory of Computation as a Lens on the Sciences, Computer Science Division, University of California, Berkeley. May.

"Cancer Genomics in the TCGA project," invited speaker, Integrative Cancer Biology Program, Center for Cancer Systems Biology, Stanford University, Palo Alto, CA. April.

██████████  
"Cancer Genomics data analysis," invited speaker, Moore's UCSD Cancer Center, Translational Oncology Symposium, San Diego, CA. August

"Cactus graphs for genome comparisons," invited speaker, CASB-16, University of California, San Diego. May.

"Rearranging genomes," invited speaker, RECOMB be 2010, University of California, San Diego. May.

"The Genome 10K Project: a genetic map of 10,000 species," invited speaker, UCSC Women's Club, University of California, Santa Cruz. March.

██████████  
"Cancer Genomics: the informatics of discovery from billions of measurements," featured speaker, Biomedical Sciences Seminar Series, University of California, San Francisco. October.

"Molecular evolution and cancer genetics," invited speaker, Bioethics class lecture, University of California, Santa Cruz. October.

"Molecular evolution and cancer genetics," invited speaker, Cancer Genetics Program Meeting, University of California, San Francisco. September.

"Molecular evolution and cancer genetics," keynote speaker, 8th Annual International Conference on Computational Systems Bioinformatics, Stanford University, Palo Alto, CA. August.

"100 million years of evolutionary history of the human genome," invited speaker, Jon Postel Distinguished Lecture, University of California, Los Angeles. January.

██████████  
"The Human Genome Project: 100 years of Human Evolution," invited speaker, Bioethics class lecture, University of California, Santa Cruz. October.

"A rapidly evolved RNA gene may have played a role in the evolution of cerebral cortex," invited speaker, Anatomy, Development, and Evolution of the Brain, University of California, Santa Barbara. April.

██████████  
"The Human Genome Project," invited speaker, Bioethics class lecture, University of California, Santa Cruz. October.

"Reconstructing the evolutionary history of the human genome," Frontiers in Biology seminar series, Stanford University, Palo Alto, CA. May.

"A rapidly evolved RNA gene may have played a role in the evolution of the cerebral cortex," honored speaker, UCSD Project for Explaining the Origin of Humans Symposium, La Jolla, CA. March.

■  
"Reconstructing the evolutionary history of the human genome," 3rd University of California, Santa Cruz/QB3 Symposium of Bioinformatics, Santa Cruz, CA. December.

"Reconstructing 100 million years of human evolutionary history," Center for Algorithmic and System Biology Algorithmic Biology Meeting, University of California, San Diego, La Jolla, CA. November.

"Reconstructing 100 million years of human evolutionary history," invited speaker, Beckman Center for Molecular and Genetic Medicine at Stanford, Palo Alto, CA. October.

"Exploring the evolutionary history of the human genome over the last 100 million years," Human Evolution Symposium, University of California, San Francisco, CA. May.

"Ultraconserved elements, living fossil transposons, distal enhancers, and mysterious RNA genes: reconstructing the detailed evolutionary history of the human genome," Institute for Pure and Applied Mathematics, University of California, Los Angeles. January.

"Exploration of the Human Genome," invited speaker, Bioethics class lecture, University of California, Santa Cruz. January.

■  
"Using evolution to explore the human genome," invited speaker, Computational and Genomic Biology Seminar Series, University of California, Berkeley. November.

"Using evolution to explore the human genome," honored speaker, UC System-Wide Bioengineering Symposium, University of California, Santa Cruz. June.

■  
"Using evolution to explore the human genome," National Academy of Science Sackler Colloquium, Stanford University, Palo Alto, CA. October.

"Comparing the human, chimp, mouse and rat genomes: using evolution to predict functional elements in the human genome," Chemistry and Genomics Seminar, Stanford University, Palo Alto, CA. March.

"Comparing the human, chimp, mouse and rat genomes: using evolution to predict functional elements in the human genome," Sali Labs, University of California, San Francisco, CA. January.

■  
"Initial computational analysis of the public working drafts of the human and mouse genomes, and the long road ahead," Workshop on Theory of Computation and the Sciences, Berkeley, CA. May.

■  
"A working draft of the human genome," Biomedical Computation at Stanford, Stanford University, Palo Alto, CA. October.

■  
"Using hidden Markov models for biosequence analysis: recent tests and new methods," Understanding the Genome: Technological and Mathematical Challenges, Mathematical Sciences Research Institute, Berkeley, CA. May.

■  
"Hidden Markov Models for Biosequence Analysis," Workshop on Theoretical and Computational Biology, Lawrence Berkeley National Laboratory, Berkeley, CA. August.

██████████  
"Information theory, VC dimension and the Bayesian approach to machine learning," Workshop on Computational Learning Theory and Natural Learning Systems, Berkeley, CA. September.

## UNIVERSITY SERVICE

### Service to the University

██████████ Chair, review committee, Biomedical Informatics Degree Program, University of ██████████  
██████████ Panel member, Life Sciences Division Review Committee, ██████████ National Laboratory  
██████████ Scientific co-director, ██████████ Institute for Quantitative Biosciences (QB3)  
██████████ Member, ██████████ System-Wide Life Science Informatics Working Group

### Other Service to the Campus

██████████ Director, Cancer Genomics Hub, ██████████  
██████████ Director, Institute for the Biology of Stem Cells, ██████████  
██████████ Director, Training Program in the Systems Biology of Stem Cells, ██████████  
██████████ Director, ██████████ Center for Biomolecular Science and Engineering

## RESEARCH INTERESTS

Bioinformatics, genomics, computational genomic data analysis, molecular evolution and comparative genomics, genomic and clinical data sharing and standards, cancer genomics, neurodevelopment, stem cell research, immunogenomics, information theory, pattern recognition, machine learning, artificial intelligence, information theory, theoretical computer science

## RECENT TEACHING INTERESTS

Computational genomics, comparative genomics, cancer genomics

## COURSES TAUGHT

### Current courses:

Cancer Genomics Seminar

Comparative Genomics Seminar

Computational Genomics

### Previous courses:

Bioinformatics and Genomics Seminar

Bioinformatics

The Nature of Computation: Introduction to Computer Science Introduction to Programming

Abstract Data Types



Discrete Mathematics

Data Structures and Algorithms

Probabilistic Algorithms and Average Case Complexity

Theory of Automata and Formal Languages

Theory of Computation

Artificial Intelligence

Machine Learning

Neural Computation

## CURRICULUM VITAE

Erich [REDACTED] Jarvis

Updated 10/16/2017

Professor, Laboratory of Neurogenetics of Language  
Investigator, Howard Hughes Medical Institute  
The Rockefeller University, Box 54, New York, NY 10065  
Phone [REDACTED]  
ejarvis@rockefeller.edu

### EDUCATION

[REDACTED] High School: [REDACTED] Major, High School of the [REDACTED]  
[REDACTED] Scholarships to [REDACTED] Schools, [REDACTED]  
[REDACTED] Undergraduate: B.A., Double major: Biology & Mathematics. Minor: Chemistry. [REDACTED]  
[REDACTED] College, [REDACTED]  
[REDACTED] Graduate: Ph.D., Molecular Neurobiology & Animal Behavior, The [REDACTED] University,  
[REDACTED]  
[REDACTED] Postdoctoral: Molecular Neurobiology & Animal Behavior, The [REDACTED] University,  
[REDACTED]

### RESEARCH & PROFESSIONAL POSITIONS

[REDACTED] Undergraduate research: Molecular biology of protein synthesis genes in bacteria; studied with Dr. Rivka Rudner, [REDACTED] College, [REDACTED]  
[REDACTED] Graduate research: PhD *A Window into the Molecular Biology of Song Associative Learning and Memory in Songbirds*, with Dr. Fernando Nottebohm, The [REDACTED] University, [REDACTED]  
[REDACTED] Post-Doctoral research: Molecular biology of vocal learning, with Dr. Fernando Nottebohm, The [REDACTED] University, [REDACTED]  
[REDACTED] Research Associate, Adjunct: [REDACTED] College, [REDACTED] Supervised lab of former undergraduate advisor Dr. Rivka Rudner for 6 months while she was on sabbatical.  
[REDACTED] Assistant Professor, Adjunct: The [REDACTED] University, [REDACTED]  
[REDACTED] Assistant Professor, Department of Neurobiology, [REDACTED] University Medical Center ([REDACTED])  
[REDACTED] Assistant Professor, Fellow: Center for Cognitive Neuroscience, [REDACTED] University, [REDACTED]  
[REDACTED] Assistant Professor, Center for Bioinformatics & Computational Biology, [REDACTED] University, [REDACTED]  
[REDACTED] Assistant Professor, Allied Faculty: Psychological & Brain Sciences, [REDACTED] University, [REDACTED]  
[REDACTED] Assistant Professor, Faculty: Development Biology Program, [REDACTED]  
[REDACTED] Investigator, [REDACTED] Medical Institute ([REDACTED] Successful renewal in [REDACTED])  
[REDACTED] Visiting Researcher: [REDACTED] Science Institute, [REDACTED]  
[REDACTED] Full Professor, Tenure: Neurobiology & departments above, [REDACTED] University, [REDACTED]  
[REDACTED] Full Professor, Tenure: The [REDACTED] University, [REDACTED]  
[REDACTED] Director, The [REDACTED] University Field Research Center, [REDACTED]

### TEACHING & RELATED COMMITTEES

[REDACTED] Trained inner-city high school students of under-represented backgrounds to gain laboratory research experience, Science Outreach Program of [REDACTED]  
[REDACTED] Trained high school, undergrad & graduate students in neuroscience research, [REDACTED]  
[REDACTED] Medical student core neuroscience course, [REDACTED]  
[REDACTED] Graduate Student Steering Committee, Department of Neurobiology, [REDACTED]  
[REDACTED] Graduate Student Admissions Committee, Department of Neurobiology, [REDACTED]  
[REDACTED] Cognitive neuroscience graduate course, [REDACTED] University, [REDACTED]  
[REDACTED] Graduate core neuroanatomy course, [REDACTED]  
[REDACTED] Undergraduate neuroscience course, [REDACTED]  
[REDACTED] Graduate neuroethology course, [REDACTED]  
[REDACTED] Graduate neuroscience lecture training course, [REDACTED]  
[REDACTED] Graduate student core neuroscience course, [REDACTED]  
[REDACTED] Director, Graduate Concepts in Neuroscience course: Cellular & Molecular Neurobiology, [REDACTED]

Vocal learning graduate course, Department of Neurobiology,  
Synaptic plasticity graduate course, Department of Neurobiology,

## MEMBERSHIPS, ADVISORY & EDITORIAL BOARDS, CONSULTING, & COMMITTEES

As undergrad, organized first Hunter College MBRS/MARC Science Day Symposium  
As grad, organized first Rockefeller University Space Science Lecture Series  
Member, Society for Neuroscience  
Member, J.B. Johnston Neuroscience Organization  
Organizer, Avian Brain Nomenclature Consortium that changed the 100-year old outdated understanding of the avian and thus vertebrate brain evolution  
Council Member, Duke University President's Council on Black Affairs, NC  
Founding Member, Black Collective at Duke (BCD), Duke University, NC  
Member, Society for Advancement of Chicanos & Native Americans (SACNAS)  
International Society for Neuroethology  
Invited Advisor, NSF Task Group for Enhancing Support for Transformative Research.  
Elected Member, Duke University Medical Center Basic Sciences Faculty Steering Committee  
Committee on Diversity in Neuroscience (C-DIN), The Society for Neuroscience. Renamed Diversity in Neuroscience Subcommittee (DINS) in  
Invited Panelist, NIH Director's Pioneer Award Reviewer  
Invited Panelist, NIH Director's New Innovator Award Reviewer  
Invited Advisor, NIH Fostering Innovation Workshop.  
Advisory Committee to the NIH Director (ACD; Elias Zerhouni): Subcommittee on Peer Review; Reviewed, developed and recommended new mechanisms for funding more innovative and transformative research, and implemented by NIH beginning  
Nominated member, The Dana Alliance for Brain Initiatives  
Director and PI, Neuroscience Scholars Program, The Society for Neuroscience  
Duke Center for Proteomics Board  
NIMH National Advisory Mental Health Council, ad-hoc.  
Genome 10K co-organizer; Co-PI 2; Chair -present  
External Advisory Committee for Science, Hunter College, NY  
ENSEMBL database Science Advisory Board  
Editorial Board, the Journal of Comparative Neurobiology  
Editorial Board, Neuroscience Research  
NSF workshop on Obama Brain Mapping Initiative  
Co-coordinator and co-founder of B10K project to sequence genomes of all bird species.  
Distinguished Editor, Editorial Review Board, NIH Director's New Innovator Award  
Advisory Board, Society for Neuroscience – Neuroscience Scholars Program.  
Duke Basic Sciences Faculty Steering Committee  
Duke Medical School Deans Advisory Council on Underrepresented Minority Faculty  
Editorial Board of Language Sciences, Frontiers in Psychology.

## AWARDS & HONORS

NIH-Minority Biomedical Research Support (MBRS) Traineeship  
First Place Award for Excellence in Biomedical Research, NIH-MBRS Annual Symposium  
NIGMS-Minority Access to Research Careers (MARC) Honors Undergraduate Fellowship  
MARC-NIGMS Pre-Doctoral National Research Service Award  
FORD Foundation Pre-Doctoral Fellowship  
Society for Neuroscience Travel Fellowship for Under-Represented Scientists  
NIMH Dissertation Grant  
NIMH Neuroscience Postdoctoral Training Grant  
Rockefeller University Kluge Postdoctoral Fellowship  
George H. Hitching's Young Investigator Award, NC Triangle Foundation, one person/year  
Esther & Joseph Klingenstein Award in Neuroscience  
Whitehall Foundation Award in Neuroscience, 2nd highest score  
David and Lucille Packard Foundation Award  
Hall of Fame: Hunter College Search for Education, Elevation & Knowledge (SEEK), NY  
Duke University Provost Bioinformatic Award

■ Duke University Provost Computational Biology Award  
 Hall of Fame: Alumni Association of Hunter College  
 Human Frontiers in Science Program Young Investigators Award  
 ■ NSF Alan T. Waterman Award. NSF's highest award for young investigators given annually to one scientist or engineer under the age of 35 who made a significant discovery/impact in science. Awarded for molecular approach and findings to map brain areas involved in behavior.  
 ■ Wall of Fame: Duke University Medical Center  
 The 2003 Distinguished Alumni Award of the City University of New York  
 ■ Intranet Linguists of the Year for ■  
 ■ Dominion Award: Strong Men and Women of Excellence: African American Leaders. Prior awardees include Arthur Ash, Maya Angelou, Oprah Winfrey, and Michael Jordan.  
 ■ American Philosophical Society Award  
 NIH Director's Pioneer Award. Given annually to top ~1.5% of applicants.  
 NOVA Science Now documentary of Dr. Jarvis and his research.  
 National Science Foundation top 10 science stories of ■ avian/vertebrate brain evolution.  
 Discover magazine top 100 science discoveries of ■ avian brain nomenclature listed at #51.  
 Diverse magazine's top 10 emerging scholars of ■  
 Popular Science Magazine's Brilliant 10 of ■ under the age of 45  
 People Magazine's, Sexiest Brain Researcher, ■  
 Mental Floss Magazine's 10 Trail blazing scientist of ■  
 ■ Creator Synectics' top 100 geniuses  
 HHMI Investigator Award  
 ■ Ruth & A Morris Williams Prize. Duke University Medical Center's highest award under the age of 45  
 ■ Duke University's 50 most powerful living men & women, past & current, Duke Towerview magazine  
 ■ History Makers Documentary: African American Leaders in Science. Chicago, IL  
 ■ North Western University "Distinguished Role Model in Science" award. Evanston, IL  
 ■ Futurish magazine's ■ Citizens of the Next Century (<http://www.future-ish.com/2010/12/next-century-citizens.html>)  
 ■ Co-recipient of Summit Award from the American Society for Association Executives (ASAE) for the Society for Neuroscience's Neuroscience Scholars Program, for URM.  
 ■ Science magazine working life article on Jarvis. **Science by any means necessary.** (■ *Science* 347 (6222):686. <http://www.sciencemag.org/content/347/6222/686.short>)  
 ■ Science Careers article on Jarvis. **Following the birdsong of Science.** (■ [http://sciencecareers.sciencemag.org/career\\_magazine/previous\\_issues/articles/2015\\_01\\_19/caredit.a1500015](http://sciencecareers.sciencemag.org/career_magazine/previous_issues/articles/2015_01_19/caredit.a1500015))  
 ■ American Society for Cell Biology's Ernest Everett Just award for impact on diversity in science  
 ■ Langford Award: Duke University's outstanding research for full professor promotion

# **NAMED, HONORARY, & KEYNOTE LECTURES (112 out of >280 invited lectures since ■)**

- ■ Speaker: International Emperor's Award in Biology, Nagoya, Japan
- ■ Plenary Speaker: Research Centers for Minority Institutions (RCMI)-Symposium, Puerto Rico
- ■ Distinguished Speaker: ■ Annual Puerto Rico Neuroscience Conference, Isle Verde, PR
- ■ Plenary Lecturer: Atlantic Symposium on Computational Biology, Genome Systems & Tech, NC
- ■ Baptista Memorial Symposium: International Ornithology Conference, Beijing, China
- ■ Lecture and Discussant: Gordon Research Conference in Neuroethology, Oxford, UK
- ■ Leaders in Scientific Discovery: Conversations with two nobel laureates (Cech & Gilman) and a Waterman awardee (Jarvis). Celebrating 40 years of NIGMS & 30 of MBRS, New Orleans, LA
- ■ Lecturer: The National Academy of Science's US-Japan meeting, Irvine, CA
- ■ Keynote Speaker: Duke University Undergraduate Visitation Week, minority student recruitment.
- ■ Topical Lecturer: AAAS meeting, Denver, CO

- Keynote Speaker: National Science Foundation, African American History Month Series, Washington, DC
- Keynote Speaker: Howard University Graduate School, Washington, DC
- Keynote Speaker: Society for Advancement of Chicanos & Native Americans, Albuquerque, NM
- The ISIS ■ Keynote Inspirational Speaker: University of North Carolina, Chapel Hill, NC
- The ■ Howard Hughes Professor's Lecture: Columbia University, New York, NY
- Keynote Speaker: NC Health Careers Access Program, Greensboro, NC
- The ■ Chancellor's Scholars Lecturer: Fayetteville University, Fayetteville, NC
- Keynote Speaker: Education for Sustainable Development Conference, Yale University, CT
- Keynote Speaker: NIMH intramural annual conference, Gettysburg, VA.
- Keynote Speaker: Society of Neuroethology Congress, Budapest, Hungary.
- Langford Lecture Provost Award: Duke University's outstanding research for tenure promotion.
- Keynote Speaker: RCMI ■ Anniversary Symposium, City College, NY
- Annual Duke Perkins Library Lecturer, Duke University, Durham, NC.
- Keynote Speaker: HBCU-UP National Research Conference, Baltimore, MD
- Keynote Speaker: National Institutes of Aging, Black History Month Lecturer, Bethesda, MD
- NIMH Director's Lecturer, Bethesda, MD
- NIDCD Council Lecturer, Bethesda, MD
- Plenary Lecturer: ■ International Ornithology Congress, Hamburg, Germany
- Distinguished Lecturer: NC Central University, Durham, NC
- The ■ James Holland Memorial Lecturer, Indiana University, Bloomington, IN
- Symposium Speaker: Deciphering Evolution, American Society for Cell Biology, San Diego, CA
- Keynote Speaker: ■ NEURON Conference, Simmons College, Boston, MA
- Keynote Speaker: ■ Beta Kappa Chi Honor Society & National Institute of Science Conference, Greensboro, NC
- The ■ Darwin Day Lecturer: Virginia Commonwealth University, Richmond, VA
- BioX Lecturer: Stanford University, Stanford, CA
- Honored Guest Speaker: Adventures of the Mind youth conference, Morehouse University, GA
- Public Symposium Speaker: Conference on Birdsong, Speech, & Language, Utrecht, Netherlands
- Keynote Speaker: University of Colorado HSC, Annual Neuroscience Retreat, Keystone, CO.
- Keynote Speaker: National Association of Biology Teachers, Atlanta, GA
- Symposium Speaker: International Seminar on Language Evolution, St. Andrews, UK
- The ■ Dodgen Lecturer: Mississippi Academy of Sciences, Olive Branch, MS
- Keynote Speaker: Biology Leadership Conference, Isle of Palms, SC
- Keynote Speaker: South East Nerve Net Conference, Atlanta, GA
- Keynote Speaker: NIGMS Institutional Research & Academic Career Development Awards Conference, UNC Chapel Hill, NC
- The 2008 Martinez-Townsend Endowed Lecturer, MBL, Cold Spring Harbor, MA
- Friday Evening Lecturer, MBL, Cold Spring Harbor, MA
- Presidential Symp Lecturer: Society for Behavioral Neuroendocrinology, Groningen, Netherlands
- FENS Symposium Speaker: Developing and Wiring the Brain, Geneva, Switzerland
- Plenary Lecturer: ■ RCMI Symposium on Health Disparities, Honolulu, Hawaii
- Keynote Lecturer: Annual Neonatal-Perinatal Research Conference, Duke University, NC
- National Academy of Science (NAS) Evolution of Medicine Lecturer, Celebrating Darwin's 200<sup>th</sup> Birthday, Washington, DC
- New Scientist's Magazine Keynote: ■ NYC Minority Graduate Student Network conference, NYU Langone Medical Center, New York, NY
- Keynote Speaker: Neonatal Perinatal Institute Annual Lecture, Duke University, Durham, NC.
- Keynote Speaker: HHMI summer EXROP conference, Chevy Chase, MD
- Keynote Speaker: NC Triangle Area HHMI Alumni Conference, Durham, NC.
- 200<sup>th</sup> Birthday Celebration Lecture. Darwin's Evolution, Swedish Museum of Natural History, Stockholm, Sweden

- Keynote Speaker: AUDUBON North Carolina Statewide Conference, Durham, NC.
  - Keynote Speaker: American Ornithology Union Conference, University of Pennsylvania, PA
  - Barack Distinguished Lecturer: University of Vermont, Burlington, VT
  - Invited symposium lecturer, Darwin and Brain Evolution, Society for Neuroscience, Chicago, IL
  - World Science Festival Speaker: Avian Einstein's, New York University, NY
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- ■ USA Science and Engineering Festival, Meet the Scientist, Washington, DC
  - Scientist Role Model. Science Makers, African Americans in Science, Chicago, IL.
  - Plenary Speaker: Roche 454 Sequencing Corp. North American Users Group Meeting. Providence, RI.
  - Symposium Speaker: Neuroethology Congress, Salamanca, Spain.
  - Plenary Speaker: 11th Science of Aphasia Conference, Potsdam, Germany.
  - Symposium Speaker: NIH symposium, ■ Anniversary of OLAW "Animal Welfare and Scientific Research, Bethesda, MD.
  - The ■ Distinguished Role Model in Life Sciences Lecturer, Northwestern University, Chicago, IL.
- 
- Roche 454 Sponsored Speaker: Plant and Animal Genome Meeting, San Diego, CA
  - University-Wide Keynote Speaker: Morris College Science in Action Week, Sumter, SC.
  - The ■ Karlovitz Memorial Lecturer: Georgia Institute of Technology, Atlanta, GA.
  - The ■ Juanita Greer White Memorial Lecturer: University Nevada, Las Vegas, NV
  - The ■ Schmidt-Nielson Memorial Lecture: Duke University, Durham, NC
  - Keynote Speaker: North Carolina High School Science Festival, Durham, NC
  - Keynote Speaker: Annual Baylor Graduate School of Biomedicine Symposium, Houston, TX
  - Symposium Speaker: ■ Anniversary Scholars in Neuroscience Symposium, Society for Neuroscience, Washington, DC.
- 
- The ■ Isabelle Sprague Lecturer: Mt Holyoke College, South Hadley, MA
  - NIH Director's Wednesday Afternoon Lecture Series, Bethesda, MD
  - Keynote Lecturer: Pacific Rim Brain and Evolution Science Conference, Tokyo, Japan
  - Plenary Lecture: Biennial Symposium on Brain and Mind in the Asia and Pacific, Tokyo, Japan.
  - Keynote Lecturer: Avian Systems Biology Conference, Nagoya, Japan
  - Distinguished Neuroscience Lecturer: University Texas, San Antonio, TX
  - Keynote Lecture: Duke Bouchet Society Black Tie Dinner, Durham, NC
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- The ■ Curtis L. Parker Lecturer: Morehouse School of Medicine, Atlanta, GA
  - Symposium Speaker: AAAS meeting, Language Organ, Boston, MA
  - Keynote Speaker: Graduate Student Symposium, University Maryland Baltimore County, MD
  - Congressional Hearing Lecture: Diversity in Science, Washington, DC
  - Keynote Speaker: SPIRE Summer Research Program, University North Carolina, NC.
  - Symposium speaker: ■ Anniversary of Institute Symposium, Networks in the Nervous System, National Autonomous University of Mexico, Queretaro, Mexico.
- 
- Featured Speaker: USA Science & Engineering Festival Nifty Fifty Event, Woodrow Wilson High School, Washington DC
  - Commencement Speaker: University of Texas San Antonio's Medical Center graduate student graduation, San Antonio, TX
  - Public Lecture: Ensembl Science Public Lecture Day, Wellcome Trust, Hinxton, UK
  - Keynote speaker: Ultrasonic Communication in Rodents Meeting, Tokyo, Japan
  - Distinguished lecturer: ■ International Ornithological Congress, Tokyo, Japan
  - Brain & Behavior Distinguished Lecture Series, Georgia State University, Atlanta, GA
  - New Horizons in Science Speaker: Shaking the bird family tree, ScienceWriters Conference, Columbus, OH.
  - Symposium Lecture: Evolution of Nervous Systems, Society for Neuroscience, Washington, DC
  - Smithsonian Lecture for Opening Ceremony of Institute of Biodiversity Genomics, and Special avian genomes issue in *Science* magazine, Washington, DC

- Plenary Lecture: Advances in Genome Biology & Technology Conference (AGBT), Marco, FL
- Distinguished Fellow SAGE Speaker: SAGE Center for the Study of the Mind, University of California, Santa Barbara, CA
- Keynote Speaker: University of Alabama ■ NEURAL conference, Birmingham, AL
- Symposium Speaker: ■ Annual Cracking the Neural Code Symposium, Stanford, CA
- Sharon Silbiger Lecture Award: Albert Einstein College of Medicine, New York, NY
- Theodosia Hamilton Hadley memorial lecturer award: Western Michigan University, MI
- Ernest Everett Just Lecture Award: American Society For Cell Biology, San Diego, CA
- Donders Lecturer: Max Planck Institute for Psycholinguistics, Nijmegen, The Netherlands

- Plenary Lecturer: Plant & Animal Genome Meeting, San Diego, CA
- Martin Luther King Jr. Lecturer: Virginia Tech, Blacksburg, VA
- Plenary Speaker: Evolution of Language conference, New Orleans, LA
- Deans Award Lecture in Neuroscience, LSU Medical School, New Orleans, LA
- Keynote Speaker: Avian Model Systems conference, Taipei, Taiwan (sponsor Academia Sinica)
- Ed Arbus memorial lecturer: University of Arizona, Tuscon, AZ
- Symposium in my honor: Seoul National University, South Korea.
- Mt Sinai Friedman Lecture Award: Mt Sinai University, New York, NY

- Plenary Lecture: Earth Global Biodiversity Conference, Smithsonian, Washington, DC
- Plenary Lecture: IEEE Aerospace Conference, Big Sky, Montana.
- Keynote: Geneseo State University GREAT Day. Jack & Carol Kramer Endowed Lectureship
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## WEB SITES

Jarvis Lab: <http://www.jarvislab.net/>

Avian Brain Hub: <http://avianbrain.org/>

Songbird Brain Transcriptome Database: <http://songbirdtranscriptome.net>

Comparative avian genome resource: <http://aviangenomes.org/>

Avian phylogenomics: <http://avian.genomics.cn/en/index.html>

B10K bird all 10,000 genomes project: <http://b10k.genomics.cn>

G10K vertebrate 10,000 genomes project: <https://genome10k.soe.ucsc.edu>

## PUBLICATIONS

**Peer-reviewed publications:** pdfs can be found at <http://www.jarvislab.net/Publications.html>.

### *Publications from undergraduate research (7 articles)*

1. LaFauci G, Widom RL, Eisner R, **Jarvis ED**, Rudner R. Mapping of rRNA genes with integrable plasmids in *Bacillus subtilis*. (1986) *J. Bacteriol.* 165:204-214.
2. Widom RL, **Jarvis ED**, LaFauci G, Rudner R. Instability of rRNA operons in *Bacillus subtilis*. (1988). *J. Bacteriol.* 170:605-610.
3. **Jarvis ED**, Widom R, LaFauci G, Setoguchi Y, Richter IR, Rudner R. Chromosomal Organizations of rRNA operons in *Bacillus subtilis*. (1988) *Genetics* 120:625-635.
4. **Jarvis ED**, Cheng S, Rudner R. Genetic structure and DNA sequences at junctions involved in the rearrangements of *Bacillus subtilis* strains carrying the *trpE26* mutation. (1990) *Genetics* 126:785-797.



5. Rivas MV, **Jarvis ED**, Rudner R. The structure of the *trpE*, *trpD* and 5' *trpC* genes of *Bacillus pumilus*. (1990) *Gene* 87:71-78.
6. Rudner R, Severestt A, Buchholz S, Studamire B, White AM, **Jarvis ED**. Two tRNA gene clusters associated with ribosomal RNA operons *rrnD* and *rrnE* in *Bacillus subtilis*. (1993) *J. Bacteriol.* 175:503-509.
7. Rudner R, Studamire B, **Jarvis ED**. Determination of restriction fragment length polymorphisms in bacteria using ribosomal RNA genes. (1994) *Methods in Enzymology* 235:184-196.

***Publications from graduate research (3 articles)***

8. **Jarvis ED**, Mello CV, Nottebohm F. Associative learning and stimulus novelty influence the song-induced expression of an immediate early gene in the canary forebrain. (1995) *Learning & Memory* 2:62-80. *Cited by the journal as one of the top 10 articles of the year.*
9. Chew SJ, Mello CV, Nottebohm F, **Jarvis ED**, Vicario D. Decrements in auditory responses to a repeated conspecific song are long-lasting and require two periods of protein synthesis in the songbird forebrain. (1995) *Proc. Natl. Acad. Sci.* 92:3406-3410.
10. Rivas M, **Jarvis ED**, Morisaki S, Carbonado H, Gottlieb AB, Krueger J. Identification of aberrantly regulated genes in diseased skin using the cDNA differential display technique. (1997) *J. Invest. Derm.* 108:188-194.

***Publications from postdoctoral research (10 articles)***

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***Publications since tenured Full Professor in Feb 2016 (7 articles)***

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4. Rudner R, **Jarvis ED**, Widom RL. Chromosomal organization and spontaneous deletions of rrn operons in *Bacillus subtilis*. (1988) In: Genetics and Biotechnology of Bacilli Vol 2. JA Hoch, AT Ganesan (eds). Academic Press, San Diego. pp. 115-120.

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***Chapter published from my postdoctoral research (1 publication)***

6. Mello CV, **Jarvis ED**. Applying differential display to brain research. (1999) In: Techniques for Behavioral and Neural Sciences. Crusio WE, Gerlai RT (eds). Elsevier Science, Netherlands, Amsterdam. 13:200-211.

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7. Modulation of movement by the basal ganglia. Chapter 17 In: Neuroscience, 2<sup>nd</sup> edition. Hall W, Nicolelis M, **Jarvis ED** (2000). Purves D, Augustine GJ, Fitzpatrick D, Katz LC, McNamara JO, Williams M (eds). Sinauer Associates, MA. pp. 391-407. (3<sup>rd</sup> edition in 2004)
8. Modulation of movement by the cerebellum. Chapter 18 In: Neuroscience, 2<sup>nd</sup> edition. Hall W, **Jarvis ED** (2000). D Purves, GJ Augustine, D. Fitzpatrick, LC Katz, JO McNamara, Williams M (eds). Sinauer Associates, MA. pp. 409-426. (3<sup>rd</sup> edition in 2004)
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***Chapters published since tenured Associate Professor at Duke (14 publications)***

10. **Jarvis ED** Evolution of vocal learning systems in birds and humans. (2006) In: Evolution of Nervous Systems. Kaas J (ed). 2:213-228.
11. Riener A, Perkel DJ, Mello CV, **Jarvis ED**. Songbirds and the revised avian brain nomenclature. (2008) In: The Neuroscience of Birdsong. Ziegler and Marler (eds). Cambridge University Press. pp. 58-62.
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13. **Jarvis ED**. Bird Brain: Evolution. (2009) In: Encyclopedia of Neuroscience. Squire LR (ed). Oxford: Academic Press 2:209-215.
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16. Rivas M, **Jarvis ED**. Behaviorally regulated mRNA and protein expression in the songbird brain. (2009) In: Neuroproteomics. Frontiers in Neuroscience series. Alzate O (ed). pp. 239-262.
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21. Wada K, Chen C-C, **Jarvis ED**. Detecting neural activity-dependent immediate early gene expression in the brain. *Methods in Neuroethological Research*. (2013) 133-149.
22. Wada K, Chen C-C, **Jarvis ED**. Molecular profiling reveals insight into avian brain organization and functional columnar commonalities with mammals. (2016) In: Shaping the design of brain systems: From single cell origins to higher cognitive function. Shigeno S, Murakami Y, Nomura T (eds.). Springer (in press).

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### **EDUCATION**

[REDACTED] Ph.D., Biology, University of [REDACTED]  
Dr. Robert K. Wayne, Thesis advisor

[REDACTED] B.A.\*, Biology, [REDACTED] College, [REDACTED]

### **RESEARCH INTERESTS**

Evolutionary genomics; conservation genomics; biology of genomes; understanding the patterns and processes that cause divergence among genes, genomes, populations and species; molecular evolution; biogeography; ancient DNA.

### **POSITIONS HELD TO DATE**

2016-present George E. Burch Fellow in Theoretic Medicine and Affiliated Theoretic Science,  
Smithsonian Conservation Biology Institute, Washington, D.C.

2013-present Research Scientist, Smithsonian Conservation Biology Institute,  
National Zoological Park, Washington, D.C.

2012-present Senior Fellow, Theodosius Dobzhansky Center for Genome Bioinformatics,  
Saint Petersburg State University, Russian Federation

[REDACTED] Cancer Research Training Award Fellow, Laboratory of Genomic Diversity,  
[REDACTED] National Laboratory for Cancer Research, [REDACTED]

[REDACTED] Postdoctoral Researcher, University of [REDACTED]  
Project titles: 1) "Collaborative Research: A complete species level phylogeny of the Carnivora" and 2) "Collaborative Research: Analysis of a Forty Thousand Year Record of Genetic and Environmental Change in the Arctic."

[REDACTED] Lecturer, University of [REDACTED]

[REDACTED] Graduate Research Assistant, University of [REDACTED]  
(with Dr. Tom Smith)



██████████ Graduate Teaching Assistant and Fellow

██████████ Research Technician, University of ██████████ (with Dr. Robert Wayne)

## PEER-REVIEWED PUBLICATIONS

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- 2017      **50.** Yurchenko A, K Prager, D Greenfield, C Greenfield, M Wang, B vonHoldt, B Van Valkenburgh, RK Wayne, **K-P KOEPFLI**. In preparation. Disjunct and divergent: Climate-driven vicariance in the black-backed jackal (*Canis mesomelas*).
- 49.** Tsuchiya MTN, **K-P KOEPFLI**, G Mourão, E Eizirik. In preparation. Comparative phylogeography reveals contrasting demographic histories in two Neotropical procyonids (*Nasua nasua* and *Procyon cancrivorus*).
- 48.** Ibis O, S Ozcan, **K-P KOEPFLI**, C Tez. In preparation. Genetic analysis of Turkish martens based on mitochondrial cytochrome *b* sequences: Do two species of the genus *Martes* occur in Anatolia?
- 47.** Nigenda-Morales S, ME Gompper, D Valenzuela-Galvan, AR Lay, KM Kapheim, C Hass, S Booth-Binczik, G Booth-Binczik, B Hirsch, K McFadden, RK Wayne, **K-P KOEPFLI**. Submitted. Phylogeographic and diversification patterns of the white-nosed coati (*Nasua narica*): Evidence for south-to-north colonization of North America.
- 46.** Gopalakrishnan S, MHS Sinding, J Ramos-Madrigal, J Niemann, JAS Castruita, FG Vieira, C Carøe, MdM Montero, L Kuderna, A serres, S Han, VM González, YH Liu, GD Wang, T Marques-Bonet, S Mirarab, C Fernandes, P Gaubert, **K-P KOEPFLI**, J Budd, EK Rueness, MPH Jørgensen, B Petersen, T Sicheritz-Ponten, L Bachmann, O Wiig, AJ Hansen, MTP Gilbert. Submitted. Interspecific hybridisation and gene flow shaped the evolution of the genus *Canis*. *Current Biology*.
- 45.** **KOEPFLI K-P**, D Wildt, G Tamazian, P Dobrynin, AA Yurchenko, A Komissarov, K Krashenninnikova, S Kliver, S Kolchanova, C Kim, JH Grau, R Godinho, M Gonçalves, M Carneiro, P Vaz Pinto, N Ferrand, A Antunes, B Kim, KE Lohmueller, J Maldonado, GM Ferrie, L Chemnick, OA Ryder, WE Johnson, P Comizzoli, SJ O'Brien, B Pukazhenthi. Submitted. Draft genome of the sable antelope (*Hippotragus niger*): A resource for monitoring diversity in *ex situ* and *in situ* populations. *GigaScience*.
- 44.** Mitra S, **K-P KOEPFLI**, A Gaur. Submitted. First complete mitogenome from the monotypic genus *Arctictis* confirms its phylogenetic position within Viverridae. *Journal of Heredity*.
- 43.** Grau JH, T Hackl, **K-P KOEPFLI**, M Hofreiter. Submitted. Improving draft genome contiguity with reference-derived *in silico* mate-pair libraries. *GigaScience*.
- 42.** Kukekova A, JL Johnson, X Xiang, S Feng, S Liu, HM Rando, AV Kharlamova, Y

Herbeck, NA Serdyukova, Z Xiong, V Beklemischeva, **K-P KOEPFLI**, RG Gulevich, AV Vladimirova, JP Hekman, PL Perelman, AS Graphodatsky, SJ O'Brien, X Wang, AG Clark, GM Acland, LN Trut, G Zhang. Submitted. Red fox genome assembly identifies genomic regions associated with tame and aggressive behaviors. *Nature Ecology and Evolution*.

**41.** Harper CK, A Ludwig, AB Clarke, KJ Makgopela, A Yurchenko, AJ Guthrie, P Dobrynin, G Tamazian, RH Emslie, M van Heerden, MS Hofmeyr, RB Potter, JS Roets, P Beytell, MY Otiende, L Kariuki, R du Toit, N Anderson, J Okori, A Antonik, **K-P KOEPFLI**, PN Thompson, SJ O'Brien. In press. Robust forensic matching of confiscated horns and tissues to individual poached African rhinoceros. *Current Biology*.

**40.** He K, T Wan, **K-P KOEPFLI**, W Jin, S-Y Liu, X-L Jiang. Submitted. Cryptic phylogeographic history sheds light on the generation of species diversity in sky-island mountains. 2017. *bioRxiv* doi: <https://doi.org/10.1101/199786>

**39.** **KOEPFLI K-P**, JW Dragoo, X Wang. 2017. The evolutionary history and molecular systematics of the Musteloidea. In: Macdonald, DW, C Newman, L Harrington (eds.). *The Biology and Conservation of Musteloids*. Oxford: Oxford University Press.

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**38.** Ceriaco LM, EE Gutiérrez, A Dubois A and 490 signatories. 2016. Photography-based taxonomy is inadequate, unnecessary, and potentially harmful for biological sciences. *Zootaxa* 4196: 435-445.

**37.** Yusoff AI, TK Tan, R Hari, **K-P KOEPFLI**, WY Wee, A Antunes, FT Sitam, JRR Japning, KV Karuppannan, GJ Wong, L Lipovich, WC Warren, SJ O'Brien, SW Choo. 2016. De novo sequencing, assembly and analysis of eight different transcriptomes from the Malayan pangolin. *Scientific Reports* 6: 28199.

**36.** Choo SW, M Rayko, TK Tan, R Hari, A Komissarov, W Yee Wee, A Yurchenko, S Kliver, G Tamazian, A Antunes, RK Wilson, WC Warren, **K-P KOEPFLI**, P Minx, K Krashenninnikova, IC Paterson, P Dobrynin, FT Sitam, JRR Japning, WE Johnson, AM Yusoff, S-J Luo, KV Karuppannan, G Fang, D Zheng, MB Gerstein, L Lipovich, SJ O'Brien, GJ Wong. 2016. Pangolin genomes reveal coevolution of mammalian scales and immunity. *Genome Research* 26: 1312-1322.

**35.** Tamazian G, P Dobrynin, K Krashenninnikova, A Komissarov, **K-P KOEPFLI**, SJ O'Brien. 2016. Chromosomer: a reference-based genome arrangement tool for producing draft chromosome sequences. *GigaScience* 5:38.

**34.** O'Brien SJ, **K-P KOEPFLI**, E Eizirik, W Johnson, C Driscoll, A Antunes, A Schmidt-Küntzel, L Marker, P Dobrynin. 2016. Response to comment by Faurby, Werdelin and Svenning. *Genome Biology* 17: 90.

**33.** Spencer PBS, AA Yurchenko, VA David, R Scott, **K-P KOEPFLI**, C Driscoll, SJ O'Brien, M

Menotti-Raymond. 2016. The population origins and expansion of feral cats in Australia. *Journal of Heredity* 107: 104-114.

- 2015
- 32.** Dobrynin P, S Liu, G Tamazian, Z Xiong, A A Yurchenko, K Krasheninnikova, S Kliver, A Schmidt-Küntzel, **K-P KOEPFLI**, W Johnson, LFK Kuderna, R García-Pérez, M de Manuel, R Godinez, A Komissarov, A Makunin, V Brukhin, W Qiu, Long Zhou, F Li, J Yi, C Driscoll, A Antunes, T Oleksyk, E Eizirik, P Perelman, M Roelke, D Wildt, M Diekhans, T Marques-Bonet, L Marker, J Bhak, J Wang, G Zhang, SJ O'Brien. 2015. Genomic legacy of the African cheetah, *Acinonyx jubatus*. *Genome Biology* 16: 277.
- 31.** **KOEPFLI K-P\***, J Pollinger\*, R Godinho, J Robinson, A Lea, S Hendricks, RM Schweizer, O Thalmann, P Silva, Z Fan, AA Yurchenko, P Dobrynin, A Makunin, JA Cahill, B Shapiro, F Álvares, JC Brito, E Geffen, JA Leonard, KM Helgen, WE Johnson, SJ O'Brien, B Van Valkenburgh, RK Wayne. 2015. Genome-wide evidence reveals that African and Eurasian golden jackals are distinct species. *Current Biology* 25: 2158-2165. \*equally contributed
- 30.** **KOEPFLI K-P**, B Paten, the Genome 10K Community of Scientists, SJ O'Brien. 2015. The Genome 10K Project - A Way Forward. *Annual Review of Animal Biosciences*. 3: 57-111.
- 2014
- 29.** Jarvis ED, S Mirarab, AJ Aberer, B Li, P Houde, C Li, SYW Ho, BC Faircloth, B Nabholz, JT Howard, A Suh, CC Weber, RR da Fonseca, J Li, F Zhang, H Li, L Zhou, N Narula, L Liu, G Ganapathy, B Boussau, MdS Bayzid, V Zavidovych, S Subramanian, T Gabaldón, S Capella-Gutiérrez, J Huerta-Cepas, B Rekepalli, K Munch, M Schierup, B Lindow, WC Warren, D Ray, RE Green, M Bruford, X Zhan, A Dixon, S Li, N Li, Y Huang, EP Derryberry, MF Bertelsen, F Sheldon, RT Brumfield, C Mello, PV Lovell, M Wirthlin, JA Samaniego, AMV Velazquez, AAlfaro-Núñez, PF Campos, T Sicheritz-Ponten, A Pas, T Bailey, P Scofield, M Bunce, D Lambert, Qi Zhou, P Perelman, AC Driskell, G Ruby, B Shapiro, Z Xiong, Y Zeng, S Liu, Z Li, B Liu, K Wu, J Xiao, X Yinqi, Q Zheng, Y Zhang, H Yang, J Wang, L Smeds, FE Rheindt, M Braun, J Fjeldsa, L Orlando, K Barker, KA Jønsson, W Johnson, **K-P KOEPFLI**, S O'Brien, D Haussler, OA Ryder, C Rahbek, E Willerslev, GR Graves, TC Glenn, J McCormack, D Burt, H Ellegren, P Alström, S Edwards, A Stamatakis, DP Mindell, J Cracraft, EL Braun, T Warnow, W Jun, MTP Gilbert, G Zhang. 2014. Whole genome analyses resolve the early branches in the Tree of Life of modern birds. *Science* 346: 1320-1331.
- 28.** Johnson WE and **K-P KOEPFLI**. 2014 The role of genomics in conservation and reproductive sciences. In: Holt, W.V., J.L. Brown, and P. Comizzoli (eds.). *Reproductive Sciences in Animal Conservation: Progress and Prospects*. Series: *Advances in Experimental Medicine and Biology*, vol 753. New York: Springer. Pp 71-96.
- 27.** Tamazian G, S Simonov, P Dobrynin, A Makunin, A Logachev, A Komissarov, A Shevchenko, V Brukhin, N Cherkasov, A Svitin, , **K-P KOEPFLI**, J Pontius,

- CA Driscoll, K Blackstone, C Barr, D Goldman, A Antunes, J Quilez, B Lorente-Galdos, C Alkan, T Marques-Bonet, M Menotti-Raymond, VA David, K Narfström, and SJ O'Brien. 2014. Annotated features of domestic cat-*Felis catus* genome. *GigaScience*. 3: 13.
- 2013
- 26.** O'Brien SJ and **K-P KOEPFLI**. 2013. Evolution: A new cat species emerges. *Current Biology* 23: R1103-R1105.
- 25.** Thalmann O, B Shapiro, P Cui, VJ Schuenemann, S Rankin, D Greenfield, M Germonpré, M Sablin, F López-Giraldez, H Napierala, H-P Uerpmann, D Loponte, A Acosta, L Giemsch, B Worthington, J Buikstra, A Druzhkova, AS Graphodatski, ND Ovodov, N Wahlberg, RM Schweizer, **K-P KOEPFLI**, JA Leonard, M Meyer, J Krause, S Pääbo, RE Green and RK Wayne. 2013. Complete mitochondrial genomes of ancient canines suggest a European origin of domestic dogs. *Science* 342: 871-874.
- 24.** Cho YS, L Hu, H Hou, H Lee, J Xu, S Kwon, S Oh, H-M Kim, S Jho, S Kim, Y-A Shin, B C Kim, H Kim, C Kim, S-J Luo, W Johnson, **K-P KOEPFLI**, A Schmidt-Küntzel, JA Turner, L Marker, C Harper, SM Miller, W Jacobs, LD Bertola, TH Kim, S Lee, Q Zhou, H-J Jung, X Xu, P Gadhvi, P Xu, Y Xiong, Y Luo, S Pan, C Gou, X Chu, J Zhang, S Liu, J He, Y Chen, L Yang, Y Yang, J He, S Liu, J Wang, CH Kim, H Kwak, J-S Kim, S Hwang, J Ko, C-B Kim, S Kim, D Bayarlkhangva, W K Paek, S-J Kim, SJ O'Brien, J Wang, and J Bhak. 2013. The tiger genome and comparative analysis with lion and snow leopard genomes. *Nature Communications* 4: 2433 doi: 10.1038/ncomms3433.
- 23.** Bornholdt R, KM Helgen, **K-P KOEPFLI**, LR de Oliveira, M Lucherini, and E Eizirik. 2013. Taxonomic revision of genus *Galictis* (Carnivora: Mustelidae): species delimitation, morphological diagnosis and refined mapping of geographic distribution. *Zoological Journal of the Linnean Society* 167: 449-472.
- 2012
- 22.** Wong PBY, EO Wiley, WE Johnson, OA Ryder, SJ O'Brien, D Haussler, **K-P KOEPFLI**, ML Houck, P Perelman, G Mastromonaco, AC Bentley, B Venkatesh, Y-P Zhang, RW Murphy, and Genome 10K Community of Scientists. 2012. Tissue sampling methods and standards for vertebrate genomics. *GigaScience*. 1: 8.
- 21.** Trinca, CS, FCW Rosas, B De Thoisy, HF Waldemarin, **K-P KOEPFLI**, JDA Vianna, and E Eizirik. 2012. Phylogeography and demographic history of the Neotropical otter (*Lontra longicaudis*). *Journal of Heredity*. 103: 479-492.
- 2011
- 20.** Lorenzen, E, D Noguès-Bravo, L Orlando, J Weinstock, J Binladen, KA Marske, J Haile, MK Borregaard, A Ugan, N Gilles Yoccoz, E Coissac, G Gussarova, C Brochmann, P Taberlet, MTP Gilbert, R Nielsen, SYW Ho, T Goebel, KE Graf, D Byers, JT Stenderup, M Rasmussen, P Campos, J Leonard, **K-P KOEPFLI**, D Froese, G Zazula, T Stafford, T Higham, K Munch, K Aaris-Sørensen, G Baryshnikov, P Batra, JA Burns, N Conard, SP Davydov, B van Geel, B Gravendee, B Hockett, D Jenkins,

- P Kosintsev, T Kuznetsova, L Xulong, L Martin, D Mol, M Meldgaard, E Stephan, M Sablin, R Sommer, T Sipko, E Scott, A Tikhonov, A Telka, R Willerslev, RK Wayne, A Cooper, M Hofreiter, A Sher, B Shapiro, C Rahbek, and E Willerslev. 2011. Individualistic species responses to climate and humans determine Late Quaternary megafaunal extinction and survival. *Nature* 479: 359-364.
- 19.** Shrestha, B, JM Reed, PT Starks, GE Kaufman, JV Goldstone, ME Roelke, SJ O'Brien, **K-P KOEPFLI**, LG Frank, and MH Court. 2011. Evolution of a major drug metabolizing enzyme defect in the domestic cat and other Felidae: phylogenetic timing and the role of hypercarnivory. *PLoS One* 6(3): e18046.
- 2010 **18.** Eizirik E, WJ Murphy, **K-P KOEPFLI**, WE Johnson, J Dragoo, RK Wayne, SJ O'Brien. 2010. Pattern and timing of diversification of the mammalian order Carnivora inferred from multiple nuclear gene sequences. *Molecular Phylogenetics and Evolution* 56: 49-63.
- 2009 **17.** Slater, GJ, O Thalmann, JA Leonard, RM Schweizer, **K-P KOEPFLI**, JP Pollinger, NJ Rawlence, JJ Austin, A Cooper, and RK Wayne. 2009. Solving a Darwinian Mystery: Evolutionary History of the Falkland Island Wolf. *Current Biology* 19: R937-R938.
- 16.** Helgen, KM, R Kays, LE Helgen, MTN Tsuchiya-Jerep, CM Pinto, **K-P KOEPFLI**, E Eizirik, and JE Maldonado. 2009. Taxonomic boundaries and geographic distributions revealed by an integrative systematic overview of the mountain coatis, *Nasua* (Carnivora: Procyonidae). *Small Carnivore Conservation* 41: 65-74.
- 2008 **15.** **KOEPFLI, K-P**, K Deere, GJ Slater, C Begg, K Begg, L Grassman, M Lucherini, G Veron, and RK Wayne. 2008. Multigene phylogeny of the Mustelidae: resolving relationships, tempo and biogeographic history of a mammalian adaptive radiation. *BMC Biology* 6: 10.
- 14.** **KOEPFLI, K-P**, B Kanchanasaka, H Sasaki, H Jacques, KDY Louie, T Hoai, N X Dang, E Geffen, A Gutleb, S-y Han, TM Heggberget, L LaFontaine, H Lee, R Melisch, J Ruiz-Olmo, M Santos-Reis, VE Sidorovich, M Stubbe, and RK Wayne. 2008. Establishing the foundation for an applied molecular taxonomy of otters in Southeast Asia. *Conservation Genetics* 9: 1589-1604.
- 2007 **13.** Brown, DM, RA Brenneman, **K-P KOEPFLI**, JP Pollinger, B Milá, NJ Georgiadis, EE Louis, Jr, GF Grether, DK Jacobs, and RK Wayne. 2007. Extensive population genetic structure in the giraffe. *BMC Biology* 5: 57.
- 12.** **KOEPFLI, K-P**, ME Gompper, E Eizirik, CC Ho, L Linden, JE Maldonado, and RK Wayne. 2007. Phylogeny of the Procyonidae (Mammalia: Carnivora): Molecules, morphology and the Great American Interchange. *Molecular Phylogenetics and Evolution* 43: 1076-1095.

- 2006 **11. KOEPFLI, K-P**, S Jenks, E Eizirik, T Zahirpour, B Van Valkenburgh, RK Wayne. 2006. Molecular Systematics of the Hyaenidae: Relationships of a relictual lineage resolved by a molecular supermatrix. *Molecular Phylogenetics and Evolution* 38: 603-620.
- 2005 **10.** Lindblad-Toh, K, CM Wade, TS Mikkelsen, EK Karlsson, DB Jaffe, M Kamal, M Clamp, JL Chang, EJ Kulbokas, III, MC Zody, E Mauceli, X Xie, M Breen, RK Wayne, EA Ostrander, CP Ponting, F Galibert, DR Smith, PJ deJong, E Kirkness, P Alvarez, T Biagi, W Brockman, J Butler, C-W Chin, A Cook, J Cuff, MJ Daly, D DeCaprio, S Gnerre, M Grabherr, M Kellis, M Kleber, C. Bardeleben, L Goodstadt, A Heger, C Hitte, L Kim, **K-P KOEPFLI**, HG Parker, JP Pollinger, SMJ Searle, NB Sutter, R Thomas, C Webber, Broad Sequencing Platform members and ES Lander. 2005. Genome sequence, comparative analysis and haplotype structure of the domestic dog. *Nature* 438:803-819.
- 2003 **9. KOEPFLI, K-P** and RK Wayne. 2003. Type-1 STS markers are more informative than cytochrome *b* in phylogenetic reconstruction of the Mustelidae (Mammalia: Carnivora). *Systematic Biology* 52: 571-593.
- 8.** Amrine-Madsen, H, **K-P KOEPFLI**, RK Wayne and MS Springer. 2003. A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships. *Molecular Phylogenetics and Evolution* 28: 225-240.
- 2000 **7.** Dallas, JF, DN Carss, F Marshall, **K-P KOEPFLI**, H Kruuk, SB Piertney, and PJ Bacon. 2000. Sex identification of the Eurasian otter *Lutra lutra* by PCR typing of spraints. *Conservation Genetics* 1: 181-183.
- 1998 **6. KOEPFLI, K-P** and RK Wayne. 1998. Phylogenetic relationships of otters (Carnivora: Mustelidae) based on mitochondrial cytochrome *b* sequences. *Journal of Zoology (London)* 246: 401-416.
- 1997 **5.** Wayne, RK, E Geffen, DJ Girman, **K-P KOEPFLI**, LM Lau, and CR Marshall. 1997. Molecular systematics of the Canidae. *Systematic Biology* 46: 622-653.
- 1996 **4.** Wayne, RK and **K-P KOEPFLI**. 1996. Demographic and historical effects on genetic variation of Carnivores. In: Gittleman, J. (ed.). *Carnivore Behavior, Ecology, and Evolution, Vol. II*. Ithaca: Cornell University Press. Pp. 453-484.
- 3.** Anderson, CG, J Gittleman, **K-P KOEPFLI**, and RK Wayne. 1996. Sea otter systematics and conservation: which are critical subspecies? *Endangered Species Update* 12: 6-10.
- 1993 **2.** Mercure, A, K Ralls, **K-P KOEPFLI**, and RK Wayne. 1993. Genetic subdivisions among small canids: mitochondrial DNA differentiation of swift, kit, and arctic foxes. *Evolution* 47: 1313-1328.

1. Van Valkenburgh, B and **K-P KOEPFLI**. 1993. Cranial and dental adaptations to predation in canids. In: Dunstone, N. and M.L. Gorman (eds.). *Mammals as Predators. Symposium of the Zoological Society of London* 65, pp. 15-37.

## GRANTS AND AWARDS

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█ The George E. Burch Fellowship in Theoretic Medicine and Affiliated Theoretic Medicine (\$█)

█ Friends of the National Zoo (FONZ) Conservation Grant, PI (\$█)

█ National Science Foundation, "Selection in Bottlenecked Populations," co-PI (\$█)

█ Smithsonian Institution Competitive Pell Grants Program in Science, "Application of Genomics to Investigate Genetic Recovery in the Endangered Black-footed ferret." co-PI (\$█)

█ Cancer Research Training Award Fellow, National Cancer Institute (\$█)

█ National Science Foundation, "Collaborative Research: A complete species level phylogeny of the Carnivora," co-investigator (\$█)

█ University of California, Los Angeles – Outstanding Lecturer Award

█ University of California, Los Angeles - Dissertation Year Fellowship Award (\$█)

█ University of California, Los Angeles - A.M. Schechtman Award for Outstanding Teaching Assistant

█ University of California, Los Angeles - Quarter Fellowship (\$█)

█ University of California, Los Angeles - Research Grant (\$█)

█ University of California, Los Angeles - Quarter Fellowship (\$█)

█ University of California, Los Angeles - Research Grant (\$█)

█ University of California, Los Angeles - Quarter Fellowship (\$█)

█ Zoological Society of San Diego - Research Grant (\$█)

█ Genetic Resources Conservation Program, University of California - Research Grant (with Dr. Robert Wayne, \$█)

## TEACHING EXPERIENCE

---

█ **Lecturer, Molecular Biology and Evolution**, University of █

█ **Seminar Instructor**, "Why do men have nipples? And other explorations into the evolution of the human animal." University of █

█ **Lecturer, Vertebrate Morphology**, University of █

█ **Graduate Teaching Fellow, Origin and Evolution of the Cosmos and Life**, General Education Cluster Course, University of █

█ **Graduate Teaching Assistant and Fellow**, courses taught including: Conservation Biology, Evolution, Vertebrate Biology, Vertebrate Morphology, Principles of Modern Biology, and Organismic and Environmental Biology Laboratory, University of █



## **STUDENT RESEARCH MENTORING**

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### **Smithsonian Conservation Biology Institute**

Mirian [REDACTED] Ph.D. student, George Mason University  
Jennifer [REDACTED] Ph.D. student, Cornell University  
Audra [REDACTED] Master's student, University of Michigan

### **Theodosius Dobzhansky Center for Genome Bioinformatics, St. Petersburg State University, Russia**

Andrey [REDACTED] postdoctoral researcher  
Pavel [REDACTED] Ph.D. student  
Alexei [REDACTED] Ph.D. student  
Ksenia [REDACTED] Ph.D. student  
Gaik [REDACTED] Ph.D. student

### **Frederick National Laboratory for Cancer Research**

Joanna [REDACTED] Post-baccalaureate research technician  
Jessica [REDACTED] Student Internship Program, Thomas Johnson High School  
Ms. Hannah [REDACTED] Student Internship Program, Thomas Johnson High School

### **University of California, Los Angeles**

Osman [REDACTED] Visiting Ph.D. student, Erciyes University, Turkey  
Anna [REDACTED] Independent Research Project student  
Margaret [REDACTED] Independent Research Project student  
Lynette [REDACTED] Independent Research Project student  
Tylor [REDACTED] Independent Research Project student  
Emma [REDACTED] Independent Research Project student  
Alice [REDACTED] Independent Research Project student  
Toan Vong [REDACTED] Master's student  
Karen M. [REDACTED] Ph.D. student  
Maria Paz Lourdes [REDACTED] Independent Research Project student  
Cheuk Chung [REDACTED] Student Research Project and Independent Research Project student  
Leif [REDACTED] Independent Research Project student  
Tannaz [REDACTED] Independent Research Project student  
Michelle [REDACTED] Independent Research Project student  
Kate [REDACTED] Independent Research Project student  
Ruth [REDACTED] Independent Research Project student  
Lisa [REDACTED] Visiting Master's student, Moss Landing Marine Laboratories  
Robert [REDACTED] Independent Research Project student

## **INVITED SEMINARS/SPEAKER**

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[REDACTED] Universidad De Los Andes, Department of Biological Sciences, Bogotá, Colombia  
[REDACTED] **Plenary speaker**, [REDACTED] Internal Conference on Behavior, Physiology and Genetics of Wildlife, Leibniz Institute for Zoo and Wildlife Research, Berlin, Germany  
[REDACTED] Conservation Immersion Seminar – Genomics; Smithsonian Conservation Biology Institute, Washington, D.C.

American University, Department of Biology, Washington, D.C.  
 UCLA/La Kretz Conservation Genomics Workshop, Calabasas, California  
 California State University, Los Angeles, California  
 CIBIO-InBio, Research Center in Biodiversity and Genetic Resources,  
 University of Porto, Portugal  
 Hungarian Museum of Natural History, Budapest, Hungary  
 Dickinson College, Department of Biology, Carlisle, Pennsylvania  
 CIBIO-InBio, Research Center in Biodiversity and Genetic Resources,  
 University of Porto, Portugal  
 Establishing a National and Global Network Framework to Support Predictive  
 Biodiversity Genomics: The Earth BioGenome Project, Washington, D.C.  
 Princeton University, Princeton, New Jersey  
**Keynote speaker**, Smithsonian Conservation Biology Institute Student Research  
 Symposium, Washington, D.C.  
 Vertebrate Zoology, National Museum of Natural History, Smithsonian Institution,  
 Washington, D.C.  
**Plenary speaker**, XII IUCN OSG International Otter Congress, Universidade Federal do  
 Rio de Janeiro, Brazil  
 Smithsonian Conservation Biology Institute, Washington, D.C.  
**Plenary speaker**, Wild Musteloid Conference, Oxford University, United Kingdom  
 Monell Chemical Senses Center, Philadelphia, Pennsylvania  
 Theodosius Dobzhansky Center for Genome Bioinformatics, Saint Petersburg State  
 University, Russian Federation  
 Vertebrate Zoology, National Museum of Natural History, Smithsonian Institution  
 Pontifícia Universidade do Rio Grande do Sul, Brazil  
 California State University, Los Angeles, California

## INVITED INSTRUCTOR

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Recent Advances in Conservation Genetics Course, Tihany, Hungary  
 Conservation Breeding Centers for Sustainability, Front Royal, VA, USA  
 Recent Advances in Conservation Genetics Course, Rincon, Puerto Rico  
 Recent Advances in Conservation Genetics Course, Southern African Wildlife College,  
 Hoedspruit, South Africa  
 Recent Advances in Conservation Genetics Course, Gamboa, Panama  
 Recent Advances in Conservation Genetics Course, Aquidauana, Brazil  
 Recent Advances in Conservation Genetics Course, White Oak Conservation  
 Center, FL, USA

## INVITED WORKSHOPS

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- Programming for Bioinformatics, Institute for Genome Sciences, University of Maryland School of Medicine, Baltimore, Maryland
- Workshop on Sequence Alignment and Tree Estimation, National Museum of Natural History, Washington, D.C.
- Genomics Training Workshop, Institute for Genome Sciences, University of Maryland School of Medicine, Baltimore, Maryland
- Workshop on Molecular Evolution, Marine Biological Laboratory, Woods Hole, Massachusetts

## CONTRIBUTED PRESENTATIONS

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- **Koepfli, K.-P.** Conservation Centers for Species Survival (C2S2) Annual Meeting, Fossil Rim Wildlife Center, Glen Rose, Texas
- **Koepfli, K.-P.** XIII International Otter Congress, Singapore Zoo, Singapore
- **Koepfli, K.-P.** Conservation Centers for Species Survival (C2S2) Annual Meeting, San Diego Zoo Global, San Diego, California
- **Koepfli, K.-P.** Conservation Centers for Species Survival (C2S2) Annual Meeting, Henry Doorly Zoo, Omaha, Nebraska
- **Koepfli, K.-P.** ■ Genome 10K Conference, Santa Cruz, California
- **Koepfli, K.-P.** Conservation Centers for Species Survival (C2S2) Annual Meeting, White Oak Conservation Center, Florida
- **Koepfli, K.-P.** ■ Genome 10K Community of Scientists Workshop and Conference, Fort Lauderdale/Hollywood, Florida “The Genome 10K Project: Looking Ahead.”
- **Koepfli, K.-P.** 2nd International Conference on the Progress of 1000 Plant and Animal Reference Genomes Project, Shenzhen, China. “Carnivoran Genomics: What we’ve learned so far and where we’re going next.”
- Friscia, A and **Koepfli, K.-P.** “Mustelidae: A model family in a model order.” ■ Annual Meeting, Society of Vertebrate Paleontology, Austin, Texas.
- **Koepfli, K.-P.,** B. Kanchanasaka, H. Sasaki, S. Han, and H. Jacques. “Taxonomic validity of the hairy-nosed otter (*Lutra sumatrana*) and phylogenetic relationships among the otters of Southeast Asia.” Ninth International Otter Colloquium, Frostburg, Maryland, USA.
- **Koepfli, K.-P.,** T. Zahirpour, S. Jenks, and R. K. Wayne. “Molecular Systematics

of a Relictual Lineage: The Hyaenidae (Mammalia: Carnivora).” Society of Integrative and Comparative Biology Annual Meeting, New Orleans, Louisiana.

██████ Koepfli, K.-P. and R. K. Wayne. “Conservation implications of a new phylogenetic hypothesis for the Mustelidae based on nuclear and mitochondrial DNA sequences.” Defenders of Wildlife Carnivores ██████ Conference, Monterey, California.

██████ Koepfli, K.-P. and R. K. Wayne. “Genomic tools for molecular systematics: a molecular phylogeny of the Mustelidae (Mammalia: Carnivora) inferred from multiple sequence-tagged sites.” ██████ Annual Meeting of The American Society of Mammalogists, Lake Charles, Louisiana.

██████ Koepfli, K.-P. and R. K. Wayne. “Genomic tools for molecular systematics: a molecular phylogeny of the Mustelidae (Mammalia: Carnivora) inferred from multiple sequence-tagged sites.” Society of Integrative and Comparative Biology Annual Meeting, Anaheim, California.

██████ Koepfli, K.-P. and R. K. Wayne. “Phylogenetic relationships of otters (Carnivora: Mustelidae) based on mitochondrial cytochrome *b* sequences.” Seventh International Otter Colloquium, Trebon, Czech Republic.

██████ Koepfli, K.-P. and R. K. Wayne. “Molecular phylogenetics of otters (Carnivora: Mustelidae) based on mitochondrial cytochrome *b* sequences.” Seventh International Theriological Congress, Acapulco, Mexico. [poster]

██████ Koepfli, K.-P. and R. K. Wayne. “Conservation genetics of the sea otter and the Eurasian otter.” Sixth International Otter Colloquium, Pietermaritzburg, Republic of South Africa.

## SYNERGISTIC ACTIVITIES

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██████ Scientific Organizing Committee, BioGenomics2017: Global Biodiversity Genomics Conference, Washington, D.C.

██████████ Co-organizer, Recent Advances in Conservation Genetics Course, Tihany, Hungary

██████████ Co-organizer, 2015 Genome 10K Conference, Santa Cruz, California

██████████ Co-organizer, Recent Advances in Conservation Genetics Course, Rincon, Puerto Rico

██████████ Review Editor, Phylogenetics, Phylogenomics, and Systematics section, *Frontiers in Ecology and Evolution*

██████ Co-organizer, Recent Advances in Conservation Genetics Course, Southern African Wildlife College, Hoedspruit, South Africa

██████ Co-organizer, 3<sup>rd</sup> Genome 10K Community of Scientists Workshop and Conference, Fort Lauderdale/Hollywood, Florida

██████ Assistant Editor for *Molecular Genetic Approaches in Conservation*, T.B. Smith and R.K. Wayne (Eds.), 1996, Oxford University Press.

## SERVICE AS PEER REVIEWER

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National Science Foundation, *Acta Theriologica*, *Animal Conservation*, *Annual Review of Animal Biosciences*, *Behavioral Ecology and Sociobiology*, *Belgian Journal of Zoology*, *Biological Conservation*, *BMC Biology*, *BMC Evolutionary Biology*, *BMC Genomics*, *Canadian Journal of Zoology*, *Check List*, *Conservation Biology*, *Conservation Genetics*, *Conservation Letters*, *Current Biology*, *Evolutionary Biology*, *Folia Zoologica*, *Frontiers in Ecology and Evolution*, *Genome Biology and Evolution*, *GigaScience*, *Journal of Heredity*, *Journal of Mammalogy*, *Journal of Molecular Evolution*, *Mammal Research*, *Molecular Ecology*, *Molecular Ecology Resources*, *Molecular Phylogenetics and Evolution*, *Molecular Biology and Evolution*, *Molecular and Cellular Probes*, *Nature*, *Open Journal of Genetics*, *PeerJ*, *PLoS One*, *Scientific Reports*, *Zoologica Scripta*, *Zoological Journal of the Linnean Society*, *ZooKeys*

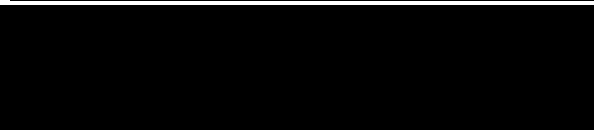
## **PROFESSIONAL MEMBERSHIPS**

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Secretary, Genome 10K Project  
Member, IUCN Species Survival Commission  
Member, IUCN Otter Specialist Group  
Member, IUCN Small Carnivore Specialist Group  
Member, Conservation Centers for Species Survival (C2S2)  
Professional Associate, Association of Zoos & Aquariums  
American Genetic Association  
American Society of Mammalogists  
Society for Molecular Biology and Evolution  
The International Biogeography Society

## **LANGUAGES**

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## Harris ■ Lewin

Distinguished Professor of Evolution and Ecology, College of Biological Sciences  
Distinguished Professor of Population Health and Reproduction, School of Veterinary Medicine  
Robert and Rosabel Osborne Endowed Chair  
4321 Genome and Biomedical Sciences Facility  
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### PROFESSIONAL PREPARATION:

■ University, ■	B.S. ■	Animal Science
■ University, ■	M.S. ■	Animal Breeding & Genetics
University of ■	Ph.D. ■	Immunology

### APPOINTMENTS AND POSITIONS:

Distinguished Professor, Department of Evolution and Ecology; Robert and Rosabel Osborne Endowed Chair, University of ■  
Vice Chancellor for Research, University of ■  
Professor Emeritus, University of ■  
Founding Director, Institute for Genomic Biology, University of ■  
Professor, Center for Advanced Study, University of ■  
Research Professor, Microelectronics Laboratory, University of ■  
Gutgsell Endowed Chair, University of ■  
Professor, Dept. of Animal Sciences, University of ■  
Center for Advanced Study Resident Associate, University of ■  
Founding Director, W. M. Keck Center for Comparative and Functional Genomics, University of ■ at ■  
Director, University of ■ Biotechnology Center, ■  
Senior Scientist, National Center for Supercomputing Applications, University of ■  
Associate Professor, Dept. of Animal Sciences, University of ■  
Visiting Associate Professor, Section of Molecular Biology, University of ■  
Visiting Scientist, Dept. Animal Genetics, National Veterinary Institute, ■  
Assistant Professor, Dept. of Animal Sciences, University of ■

### FIVE RELATED PUBLICATIONS: (selected from a total of 195 peer reviewed articles, 21 book chapters and 5 patents and copyrights)

Bryan, C. J., H. A. Lewin, K.-L. Ma, D. M. Larkin, G. I. Guterman, J. Kim. 2017. Synteny Explorer: an interactive visualization application for teaching genomic evolution. *IEEE Trans Vis Comput Graph*. 23:711-720.  
Kim, J., M. Farre, L. Auvil, B. Capitanu, D. M. Larkin, J. Ma, H. A. Lewin. 2017. Reconstruction and evolutionary history of eutherian chromosomes. *Proc. Natl Acad. Sci. (USA)* **114**:E5379-E5388.  
Kim, J., D. M. Larkin, Q. Cai, Asan, Y. Zhang, R. L. Ge, L. Auvil, B. Capitanu, G. Zhang, H. A. Lewin and J. Ma. 2013. Reference-assisted chromosome assembly. *Proc. Natl. Acad. Sci. (USA)* **110**:1785-90.

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Murphy, W. J., D. M. Larkin, A. Everts-van der Wind, G. Bourque, G. Tesler, L. Auvin, J. E. Beever, B. P. Chowdhary, F. Galibert, L. Gatzke, C. Hitte, S. N. Meyers, E. A. Ostrander, G. Pape, H. G. Parker, T. Raudsepp, M. B. Rogatcheva, L. B. Schook, L. C. Skow, M. Welge, J. E. Womack, S. J. O'Brien, P. A. Pevzner and H. A. Lewin. 2005. Dynamics of mammalian chromosome evolution inferred from multispecies comparative maps. *Science* **309**:613-617.

## **FIVE OTHER SIGNIFICANT PUBLICATIONS**

Biase, F. H., C. Rabel, M. Guillomot, I. Hue, K. Andropolis, C. Olmstead, R. Oliveira, R. Wallace, D. Le Bourhis, C. Richard, E. Champion, A. Chaulot-Talmon, C. Giraud-Delville, G. Taghouti, H. Jammes, J. P. Renard, O. Sandra, H. A. Lewin. 2016. Massive dysregulation of genes involved in cell signaling and placental development in cloned cattle conceptuses and maternal endometrium. *Proc. Natl. Acad. Sci. (USA)* **113**:14492-14501.

Yang, X., S. L. Smith, X. C. Tian, H. A. Lewin and T. Wakayama. 2007. Nuclear reprogramming in cloned embryos and its implications for therapeutic cloning. *Nat. Genet.* **39**:295-302.

Everts-van der Wind, A., D. M. Larkin, C. A. Green, J. S. Elliott, C. A. Olmstead, R. Chiu, J. E. Schein, M. A. Marra, J. E. Womack and H. A. Lewin. 2005. A high-resolution whole-genome cattle-human comparative map reveals details of mammalian chromosome evolution. *Proc. Natl. Acad. Sci. (USA)* **102**:18526-18531.

Band, M. R., J. H. Larson, M. Rebeiz, C. A. Green, D. W. Heyen, J. Donovan, R. Windish, C. Steining, P. Mahyuddin, J. E. Womack and H. A. Lewin. 2000. An ordered comparative map of the cattle and human genomes. *Genome Res.* **10**:1359-1368.

Bouzat, J. L., L. K. McNeil, H. M. Robertson, L. F. Solter, J. Nixon, J. E. Beever, H. R. Gaskins, G. Olsen, S. Subramaniam, M. K. Sogin and H. A. Lewin. 2000. Phylogenomic analysis of the alpha proteasome gene family from early diverging eukaryotes. *J. Mol. Evol.* **51**:532-543.

## **Synergistic Activities**

- Founding Co-editor: *Annual Reviews of Animal and Veterinary BioSciences*, 2010-present.
- Serving on Genome 10K Executive Committee, 2011-present
- Serving as Earth BioGenome Project Chairperson, 2015-present
- Foreign Member, Royal Swedish Academy of Agriculture and Forestry (elected 2007).
- Member, National Academy of Sciences, USA (elected 2012).

## Summary

Dr. Marques-Bonet is the Principal Investigator of the group "Comparative Genomics" as a part of the Institute of Evolutionary Biology (univ. Pompeu Fabra and CSIC) with a dual appointment at CRG/CNAG. He started his own laboratory in 2010 after a Marie Curie fellowship (2008) in Seattle, University of Washington. In 2011 he obtained the competitive **ERC Starting Grant 2010**. In 2011, he was selected as an **ICREA research investigator** at the Universitat Pompeu Fabra (UPF). In 2013, he was also selected for the **EMBO young Investigator award** and associate editor for BMC Genomics. In 2014, he was also appointed head of the comparative genomics group at CRG-CNAG (Centro Nacional de Analisis Genomico-CRG). Since 2015 he is part of a **NIH U01 grant** together with Nenad Sestan (Yale University) and Dr. Christopher Walsh (Harvard School of Medicine). He is part of the council member for the G10K (15 members) and the Dog G10K (12 members), two international efforts to sequence 10,000 vertebrates to study genome evolution and 10,000 dog genomes. He has been appointed part of **LABEX CeMEB Scientific Council - Montpellier, France** and he is now the **director of the Institute of Evolutionary Biology**. From 2017 he is a Howard Hughes Medical Institution (**HHMI**) **Early International Career Award**.

His group is now formed by 8 PhD students and 2 postdocs whose work is focused on characterizing human specific genomics features, in methods for estimating selection on duplicated sequences, the evolution of epigenetics in humans or the impact of CNVs in phenotypic traits. He has already trained 5 PhD students and 3 postdocs, all of them working actively in the academia in UK and USA. He is currently the coordinator a course within the Masters of Bioinformatics at UPF. He has been organizer a symposium at the American Society of Human genetics (Boston, 2013), SMBE (Houston, 2012), International Primate Genomics (Chicago, 2016) and organizer of the EMBO Young Investigator meeting in 2015 in Barcelona.

With a total of more than **100 peer-reviewed publications**, he has published 16 papers in Nature and Science (1 as a first author, two as a senior author and another with a lab member as co-first) and has published **17 manuscripts with senior authorship** in journals such as Nature, Science, Genome Research, Plos Genetics, NAR or Genome Biology.

### Most relevant publications (out of 100, h-index 43)

- Kuderna et al. **Tomas Marques-Bonet**. "A 3-way hybrid approach to generate a new high quality chimpanzee reference genome (Pan\_tro\_3.0)" *GigaScience* 2017
- Hernandez et al. **Tomas Marques-Bonet**. "The impact of endogenous content, replicates and pooling on genome capture from fecal samples" *Molecular Ecology Resources* 2017.
- Solis-Moruno et al. **Tomas Marques-Bonet**. "Potential damaging mutation in LRP5 from genome sequencing of the first reported chimpanzee with the Chiari malformation" *Scientific Reports* 2017.
- deManuel et al. **Tomas Marques-Bonet**. "Chimpanzee diversity reveals ancestral admixture with bonobos" *Science* 2016.
- Irene Hernando-Herraez et al. **Tomas Marques-Bonet**. "Evolutionary insights into human DNA methylation" *Plos Genetics* 2015.
- Tugce Bilgin Sonay et al. **Tomàs-Marques Bonet\***, **Andreas Wagner\***. "Human and great ape variation in tandem repeats population variation and its correspondence impact to on gene expression divergence" *Genome Research* 2015
- Irene Hernando-Herraez et al. **Tomas Marques-Bonet**. "A genome-wide comparative study of the DNA methylation landscape in great apes" *Nucleic Acid Research* 2015.
- Xue, Prado-Martinez et al.... **Tomàs-Marques Bonet**, **Chris Tyler Smith**, **Aylwyn Scally**. "Population sequencing of Mountain gorillas reveal the genomic impact of long-term population decline and inbreeding". *Science* 2015.
- Gibbon Consortium "The gibbon genome provides a novel perspective on the accelerated karyotype evolution of small apes". *Nature* 2014 Sep 11;513(7517):195-201. doi: 10.1038/nature13679.
- Oscar Ramirez, Iñigo Olalde, Jonas Berglund, Belen Lorente-Galdos, Matthew T. Webster, Robert K. Wayne, Carles Lalueza-Fox, Carles Vilà, **Tomas Marques-Bonet**. "Analysis of structural diversity in wolf-like canids reveals post-domestication variants." *BMC genomics* 2014.
- Iñigo Olalde, et al.... **Tomàs Marquèès-Bonet\***, **Carles Lalueza-Fox\***. "Genomic analysis of the blood attributed to Louis XVI (1754-1793), king of France". *Scientific Reports* 2014
- *Elephant Shark Consortium*. "The elephant shark genome provides unique insights into gnathostome evolution". *Nature*. 2014 Jan 9;505(7482):174-9. doi: 10.1038/nature12826.



- Iñigo Olalde et al...“Derived Immune and Ancestral Pigmentation Alleles in a 7,000-Year-old Mesolithic European” *Nature*. 2014 Jan 26. doi: 10.1038/nature12960.
- Javier Prado-Martinez et al. .... **Tomas Marques-Bonet** “Great ape genetic diversity and population history”. *Nature* 2013.
- Irene Hernando-Herraez, Javier Prado-Martinez, Paras Garg, Marcos Fernandez-Callejo, Holger Heyn, Christina Hvilsom, Arcadi Navarro, Manel Esteller, Andrew J. Sharp, **Tomas Marques-Bonet** “Dynamics of DNA Methylation in Recent Human and Great Apes Evolution”. *PLOS Genetics* 2013.
- Belen Lorente-Galdos, Jon Bleyhl, Gabriel Santpere, Laura Vives, Oscar Ramirez, Jessica Hernandez, Roger Anglada, Greg M. Copper, Arcadi Navarro, Evan Eichler, **Tomas Marques-Bonet** “Fast exon evolution in duplicated regions in hominids”. *Genome Biology*, 2013.
- Javier Prado-Martinez et al..... **Tomas Marques-Bonet**. “The genome sequencing of an albino Western lowland gorilla reveals inbreeding in the wild. “ *BMC Genomics* 2013.
- *Bonobo Genome Consortium*. The bonobo genome compared with the genomes of chimpanzee and human. *Nature*. 2012 Jun 28;486(7404):527-31. doi: 10.1038/nature11128.
- *Gorilla Genome Consortium*. Insights into hominid evolution from the gorilla genome sequence” *Nature*, 2012.
- *Orangutan Genome Consortium*. “Comparative and demographic analysis of orang-utan genomes” *Nature* 2011 (Cover)
- *Denisovan Genome Consortium*. “A Draft Genome Sequence and Dental Morphology of an Archaic Hominin group from Denisova Cave, Russia”. *Nature* 2010 Volume:468, Pages: 1053-1060(23 December 2010) DOI:doi:10.1038/nature09710
- *Neandertal Genome Consortium*. “A draft sequence and preliminary analysis of the Neandertal genome” *Science*, 2010.
- **Tomas Marques-Bonet**, Jeffrey M. Kidd, Mario Ventura, Tina A. Graves, Ze Cheng, LaDeanna W. Hillier, Zhaoshi Jiang, Carl Baker, Ray Malfavon-Borja, Lucinda A. Fulton, Can Alkan, Gozde Aksay, Priscillia Siswara, Lin Chen, Maria Francesca Cardone, Arcadi Navarro, Elaine R. Mardis, Richard K. Wilson, Evan E. Eichler. “A Burst of Segmental Duplications in the African Great Ape Genome Ancestor” *Nature*. 2009.

### *Projects/Grants*

- \* ERC Starting grant [REDACTED] This grant focuses on sequencing non-human genome primates and assess patterns of diversity and structural variation.
- \* MICINN Plan nacional [REDACTED]. This grant focuses on the effect of inversions over gene expression.
- \* NIH [REDACTED] This grant focuses on somatic mutations in autism spectrum disorders (ASD): single neuron analyses.
- \* MICINN Plan nacional [REDACTED]-P. “Evolucion de la diversidad estructural del cromosoma y humano” This grant focuses on the reconstruction and variability of human Y chromosomes.
- \* MICINN Excelencia [REDACTED]. “Structural variation and impact on gene expression of the human y chromosome” This grant focuses on the reconstruction and variability of human Y chromosomes.
- \* Beca PRIC. Barcelona Zoo. [REDACTED].PI: Tomas Marques-Bonet.
- \* EMBO Small Grant [REDACTED] Tomas Marques-Bonet.

### *Awards*

- \* Howard Hugues International investigator [REDACTED]
- \* EMBO Young Investigator Award [REDACTED]
- \* 2n place. Ciutat de Barcelona Award. [REDACTED]
- \* Best poster at “The Biology of the genomes” CSH, [REDACTED]
- \* Premi Josep M Sala i Trepal. Societat Catalana de Biologia. [REDACTED]
- \* AAAS Newcomb Cleveland Award (most outstanding paper published in Science [REDACTED])

### *Most relevant invited Talks (total 70 since 2010):*

- \* Dahlem Colloquia in Molecular Genetics. Berlin. Invited by Dra. Katja Nowick. [REDACTED]
- \* Max Planck Institute. Evolutionary genetics department. Invited by Dr. Svante Paabo. Leipzig [REDACTED]

- \* Plenary Speaker. Genetics and Genomics in Wildlife Studies: Implications for Ecology, Evolution and Conservation Biology. Sevilla October. [REDACTED] Invited by Jose A Godoy.
- \* Invited talk. University of Oxford. February [REDACTED] Invited by Chris Pontig.
- \* Invited talk. Meeting: A day with ancient DNA. Florence. March [REDACTED] Invited by David Caramelli.
- \* Plenary speaker. Max Planck Institute for Aging. Retreat [REDACTED] September [REDACTED]
- \* Florida. Workshop G10K vertebrate. Invited by Stephen O Brien. April [REDACTED]
- \* ASHG [REDACTED] Invited Speaker and co-chair, symposium organizer. Boston [REDACTED]
- \* Chicago [REDACTED] Invited by Yoav Gilad. University of Chicago.
- \* San Francisco [REDACTED] G10K Workshop. Invited by Beth Sapiro.

## Curriculum Vitae

19 Sept. 2017

### Robert W. MURPHY

*Sr. Curator, Centre for Biodiversity and Conservation Biology  
Royal Ontario Museum*

&

*Professor, Ecology and Evolutionary Biology  
University of Toronto*

&

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Chinese Academy of Sciences*

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Home page: <http://labs.eeb.utoronto.ca/murphy>

#### CITIZENSHIP:

[REDACTED]

#### EDUCATION:

Ph.D. — [REDACTED] University of [REDACTED]

PostDoc — [REDACTED], University of [REDACTED]

#### WORK EXPERIENCE (GENERAL):

[REDACTED] Visiting Senior International Professor, Chinese Academy of Sciences,  
stationed in the [REDACTED] Institute of Zoology

[REDACTED] Adjunct Professor, [REDACTED] [REDACTED] University, [REDACTED]

[REDACTED] Professor, Department of Ecology and Evolutionary Biology,  
University of [REDACTED] (Full Professor, [REDACTED])

[REDACTED] Curator of Herpetology, Department of Natural History (Sr. Curator,  
[REDACTED])

**UNIVERSITY TEACHING (recent):**

EEB384h: Biology of Amphibians. Undergraduate course, about 40 students ( )  
 EEB1310: Philosophy and Methods. Graduate course for entering students. Enrollment about 15 students ( )  
 EEB462/1462h: Advanced Topics in Phylogenetic Systematics. Undergraduate / graduate-level course centering on numerical phylogenetics. Enrollment about 15 students.  
 EEB497/498: Undergraduate research. Typically, 1–2 students/yr.  
 Graduate student supervision University of Toronto: Currently Sponsor 3 Ph.D.  
 Graduate student supervision Chinese Academy of Sciences: Co-Sponsor 1 Ph.D.

**UNIVERSITY & MUSEUM COMMITTEE SERVICE (representative):**

Curatorial Promotions Committee ( ), Chair  
 Professorial/Curatorial Search Committees (various)  
 ROM Animal Care Committee ( ), Chair  
 ROM Department of Natural History Advisory Committee  
 ROM Foundation Grant Review Committee (various times)  
 DNH Research Committee ( )t  
 Schad Foundation Grant Review Committee (Chair, )  
 Laboratory of Molecular Systematics Policy Committee ( )  
 Acting Head, Department of Natural History (various times)  
 ROMCA Mentorship Committee ( )  
 ROMCA Auditor ( )

**PROFESSIONAL SERVICES:****International Positions:**

Advisory Board, Institute of Tropical Biology, Vietnam Academy of Sciences  
 Co-Chair: Amphibians. Genome 10K Project. (With Andrew J. Crawford)  
 Co-Chair: Non-Avian Reptiles: Genome 10K Project. (With Barry Sinervo)  
 Co-Chair: International Barcode of Life initiative: *ColdCode*, The Global Initiative to DNA Barcode Amphibians and Nonavian Reptiles (with Wen-Zhi Wang)  
 Council Member (elected), Genome 10K  
 Co-sponsored symposia: World Congress of Herpetology  
 Organizing Committee, World Congress of Herpetology, Hangzhou, China  
 Executive Committee, World Congress Herpetology, Elected

**Graduate Student Committees:**

University of Toronto, EEB, Dept. Geography  
 Chinese Academy of Sciences  
 University of Arizona, Tucson, USA

University of Guelph, Canada  
Centro de Investigaciones Biológicas del Noroeste, La Paz, Mexico

#### Editorial Services:

Associate Editor, Herpetological Biology and Conservation (From foundation in 2006–present)  
Editorial Board, Russian Journal of Herpetology (1993–present).  
Editorial Board, Asian Herpetological Research (Asiatic Herpetological Research Society, and the Chinese Society for the Study of Amphibians and Reptiles; 1992–present).  
Editorial Board, Herpetological Conservation and Biology (foundation–present)  
Advisory Board, Amphibian and Reptile Conservation (2010–present).  
Board of Governors, American Society of Ichthyologists and Herpetologists, Class of 1993 (elected)  
Guest Editor: Biochemical Systematics and Ecology  
Guest Editor: Journal of Arid Environments

*Reviewer—Journals:* Nature, Scientific Reports, BMC Evolutionary Biology, PLoS ONE, Heredity, Journal of Heredity, Journal of Biogeography, Biochemical Genetics; Systematic Biology; Molecular Ecology; Molecular Ecology Resources, Biochemical Systematics and Ecology, Molecular Phylogenetics and Evolution, Genome/Génome, Canadian Journal of Zoology, Zootaxa, Comparative Biochemistry and Physiology, Current Zoology, Zoological Research, Journal of Arid Environments, Carnegie Museum of Natural History, Copeia, Herpetologica, Journal of Herpetology, Journal of Natural History (UK), Transactions of the San Diego Society of Natural History, Systematic Zoology, Canadian Museum of Nature, Prince of Wales Northern Heritage Centre, N.W.T., Southwestern Naturalist, Journal of Parasitology, Occasional Papers of the California Academy of Sciences, Asian Herpetological Research; et al.

*Reviewer—Grants:* NSERC; NSF Systematics Panel; NSF (other panels); National Geographic Society; Florida Game and Fresh Water Fish Commission; Society for the Study of Amphibians and Reptiles, Grants in Herpetology, Graduate Student Section; Ohio University; Morafka Award, Desert Tortoise Council.

#### Some PRIMARY INTERNATIONAL COLLABORATORS:

Prof. Zhang Ya-Ping, Vice-President, Chinese Academy of Sciences (Life Sciences and International Relations)  
Prof. Shi Hai-tao, Vice-President, Hainan Normal University  
Prof. Huang Da-Wei, Institute of Zoology, Chinese Academy of Sciences, Beijing  
Prof. Shi Peng, Professor, Kunming Institute of Zoology  
Prof. Hussam Zaher, Museum of Natural History, São Paulo, Brazil  
Prof. Liu Shao-Ying, Sichuan Academy of Forestry, Chengdu  
Prof. Fausto R. Méndez de la Cruz, Institute of Ecology, National Autonomous University of Mexico (UNAM), Mexico City

Prof. Sergio Ticul Álvarez-Castañeda, Centro de Investigaciones Biológicas del Noroeste, La Paz, Mexico

Prof. Natalia B. Ananjeva, Vice-Director, Zoological Institute, Russian Academy of Sciences, St. Petersburg, Russia

Prof. Nikolai Orlov, Zoological Institute, Russian Academy of Sciences, St. Petersburg, Russia

**GRANTS** (last 6 years; all funds in Canadian dollars):

██████████. Conservation genetics of the desert tortoise at 29 Palms, California. US DoD research contract (PI, PD)

██████████ (¥██████████ /mo. Chinese Academy of Sciences (CAS) President's International Fellowship Initiative (PIFI). Financial support for research collaboration and training. Includes international economy airfare, health insurance, housing, and stipend

██████████. Conservation genetics of the Chinese giant salamander. Kunming Institute of Zoology, Chinese Academy of Sciences (PI)

██████████. Conservation genetics of the desert tortoise at 29 Palms, California. US DoD research contract (PI, PD)

██████████. Evolutionary and Conservation Genetics of Reptiles. NSERC Discovery Grant (PI, PD)

██████████. DNA barcoding of Southeast Asian amphibians and reptiles. Kunming Institute of Zoology, Chinese Academy of Sciences (Co-PI)

██████████. Molecular systematics and conservation genetics of amphibians and reptiles. NSERC Discovery Grant (PI, PD)

██████████. Northern Research Supplement. NSERC Discovery Grant (PI, PD)

██████████. Conservation genetics of the desert tortoise at 29 Palms, California. US DoD research contract (PI, PD)

██████████. Molecular systematics and conservation genetics of amphibians and reptiles. NSERC Discovery Grant (PI, PD)

██████████. Building a future for the Chinese giant salamander: a consolidated approach to the conservation of *Andrias davidianus*. US Fish and Wildlife Service Wildlife Without Borders - Amphibians in Decline (with Helen Meredith, PD)

██████████. Conservation of the Chinese Giant Salamander. Ocean Park, Hong Kong Research Grants (with Helen Meredith, PD)

██████████ Conservation genetics of spotted turtles in Ontario. Species at Risk Stewardship Fund (PI, PD)

██████████ Molecular systematics and conservation genetics of amphibians and reptiles. NSERC Discovery Grant (PI, PD)

██████████ Barcoding Vietnamese amphibians and reptiles. Kunming Institute of Zoology, Chinese Academy of Sciences (PI, PD)

██████████ Acquisition of genetic resources from Vietnamese amphibians and reptiles. Kunming Institute of Zoology, Chinese Academy of Sciences (PI, PD)

██████████ Acquisition of genetic resources from Vietnamese amphibians and reptiles. Kunming Institute of Zoology, Chinese Academy of Sciences (PI, PD)

## **SCHOLARLY PRESENTATIONS**

Not tracked: typically >5 per yr. Given the extent of collaborations, my name often appears on papers presented at meetings.

## **PUBLICATIONS (2006–2017 only):**

In the vast majority of publications, I make critical and significant contributions, and usually far beyond writing and editing, which often appears in the ‘Contributions of Authors’ section of papers. I rarely take credit for project conception and design because doing so serves no purpose at this stage in my career. My coauthors take most credit because this promotes their careers and facilitates their acquisition of additional grants. I do not force my name on papers and often provide editorial and conceptual feedback on projects without authorship.

Many independent projects are underway, such as a Hi-C genome of Agassiz’s Desert Tortoise, a Tibetan frog, and a Tibetan lizard, and a genomic assessment of limb loss in squamate reptiles. Because I am not the corresponding author for most of my collaborative contributions, often I am not aware of the dates of submission and decisions from the editors. I only track my history of revisions and written feedback.

The following list of published papers reflects the extent of activity and diversity of current projects.

**In progress**

1. Hi-C genome of Agassiz's desert tortoise
2. Evolution of megophryid frogs

**In manuscript:**

1. Yan, Fang, Wei-wei Zhou, Andrew Cunningham, Sue Chen, Ya-ping Zhang, Jing Che, and Robert W. Murphy. Salamander pie: alarm for conservation of endangered species. *Nature*.
2. Yong Shao, Jing-Xiu Li, Ming-Shan Wang, Robert W. Murphy, and Dong-Dong Wu. The closest living relatives of primates and divergences based on genomic data. *Molecular Biology and Evolution Letters* (rec. 25v17; rtn. 30v17; rev. 2vi17).
3. Xiaobing Li, Xuejuan Shen, Xiao Chen, Dan Xiang, Robert W. Murphy, and Yongyi Shen. Detection of potentially erroneous sequences of fishes in GenBank. (Rec 1v17. Rtn.)
4. A large-scale molecular phylogeny of the Asian metacarpal-tubercled toads, genus *Leptolalax* (Anura: Megophryidae), sheds new light on its diversity, taxonomy and biogeography. *MPE/Zootaxa*. (rec. 21iv17; rtn. 25iv17).
5. Tang, Ming Kun, Wei Jin, Ying Tang, Chao Chao Yan, Robert W. Murphy, Zhi Yu Sun, Xiu Yue Zhang, Tao Zeng, Rui Liao, Quan Feng Hou, Bi Song Yue, and Shao Ying Liu. Reassessment of the taxonomic status of *Craseomys* and three controversial species of *Myodes* and *Alticola* (Rodentia: Arvicolinae). *Zootaxa* (rec. 14iv17; rtn. 18iv17; rec. 2v17; rtn. 3v17)
6. Nneji, Lotanna M., Adeniyi C. Adeola, Temidayo, E. Olagunju, Segun O. Oladipo, Oluyinka A. Iyiola, Olatunde Omotoso, Timothy Auta, Usman D. Abbas, Halima Abdullahi, Yan Fang, Adiaha A. A. Ugwumba, Robert W. Murphy, and Che Jing. Matrilineal relationships of Nigerian *Agama* lizards (*Agama agama*) within the West African radiation: inferences on the biogeography of Nigerian *Agama* lizards. *Journal of Biogeography*.
7. Nneji, Lotanna M., Adeniyi C. Adeola, Yan Fang, Adiaha A. A. Ugwumba, Robert W. Murphy, and Che Jing. The first record of *Agama parafricana* (Sauria: Agamidae) from Nigeria. *Zoological Research*.
8. Shen, Yong-yi et al. The evolution and pathogenicity of the infectious virus H7N9. *The Lancet*.



9. Zhou, Weiwei, Zhiyong Yuan, et al. Riverine refugia in Northeast Asia: evidence from an endemic frog, *Rana amurensis* (Ranidae). (rec. 7iv17)
10. Lin, Guoliang, Jing Chai, Feng Huang, Robert W. Murphy, and Jing Luo. An overview of pre-mRNA. (rec. 5iv17; rec. 8v17)
11. Yin, Fanqian, Robert. W. Murphy, Yaping Zhang, and Jing Luo. Chromatin architecture and function. (rec. 5iv17; rtn 20iv17)
12. Sun, Yan-Bo, Ting-Ting Fu, Xiao-Long Tu, Robert W. Murphy, Ya-Ping Zhang, and Jing Che. Elevation gradients reveal adaptations to high-elevation. *Molecular Biology and Evolution*. ("final" edit 30 Mar. 17).
13. Li, Jia-tang et al. Phases of geographical dispersion of the India genus *Polypedates* (Amphibia: Anura: Rhacophoridae) across Southeast Asia from the Oligocene onward.
14. Wang, Guo-dong, Bao-lin Zhang, Wei-wei Zhou, Yong-xin Li, Jie-qiong Jin, Yong Shao, He-chuan Yang, Yan-hu Liu, Fang Yan, Hong-man Chen, Li Jin, Feng Gao, Jun-xiao Yang, Yao-guang Zhang, Wei-wei Zhai, Hai-peng Li, Robert W. Murphy, David B. Wake, Ya-ping Zhang, and Jing Che. Population genomic perspectives on ecological adaptation and paleoclimatology along a speciation continuum in the Tibetan frog *Nanorana parkeri*. *PLoS Biology*
15. Nguyen, Luan Thanh, Nikolay A. Poyarkov Jr., D.T. Le, Ba Dinh Vo, H.T. Phan, Tang Van Duong, Robert W. Murphy, and Sang Ngoc Nguyen. A new species of *Leptolalax* (Anura: Megophryidae) from Son Tra Peninsula, central Vietnam.
16. Kong, Kevin Sungsik, Santiago J. Sánchez-Pacheco, and Robert W. Murphy. Median-joining mayhem. *Systematic Biology*.
17. Solovyeva, Evgeniya N., Nikolay A. Poyarkov Jr., Evgeniy A. Dunayev, Roman A. Nazarov, Anna A. Bannikova, Vladimir S. Lebedev, Robert W. Murphy, and Jing Che. Biogeographic consequences of Cenozoic Aridization in Central Eurasia: a case study of toad-headed agamas (*Phrynocephalus*).
18. Peng Shi et al. Predictable evolutionary pathways to adaptation. (rtn. 15ii17)

### Submitted

1. Kang, Yinfeng, Xuejuan Shen<sup>a</sup>, Runyu Yuan, Bin Xiang, Pei Gao, Robert W. Murphy, Ming Liao, Yongyi Shen, Tao Ren. Pathogenicity and transmissibility of three avian influenza A (H5N6) viruses isolated from wild birds in 2014-2015. *Veterinary Microbiology* (2vi17)
2. Zhou, Weiwei, Baolin Zhang, Dahu Zou, Jieqiong Jin, Hongman Chen, Theodore J. Papenfuss, Robert W. Murphy, Shuangquan Duan, Song Huang, and Jing Che. Deep

canyon drives speciation in two agamid rock lizards (*Laudakia*). *Journal of Biogeography*. ("final" edit 1iv17; sub. Evol. 14iv17; rej. 17iv17; sub 22iv17)

3. Zhou, Weiwei, Junxiao Yang, Baolin Zhang, Wei Gao, Jieqiong Jin, Hongman Chen, Yunyu Wang, Wenzhi Wang, Robert W. Murphy, and Jing Che. Sky-islands of Southwest China can drive population structure: an example from *Rana chaochiaoensis* (Ranidae). *BMC Evolutionary Biology*. (returned 8 April 17; sub 20iv17)
- 4.
5. Nguyen, Sang Ngoc, Jie-Qiong Jin, Ba Dinh Vo, Luan Thanh Nguyen, Wei-Wei Zhou, Jing Che, Robert W. Murphy, and Ya-Ping Zhang. *In review*. A new species of *Acanthosaura* Gray 1831 (Reptilia: Agamidae) from central Vietnam. *Zootaxa*.
6. Nguyen, Sang Ngoc, Luan Thanh Nguyen, Vu Dang Hoang Nguyen, and Robert W. Murphy. *In review*. Testing an alternative capture-analysis-release approach to document the reptile fauna of Hon Ba Nature Reserve, central Vietnam. *Zootaxa*.
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Plus >120 other publications. Available at <http://labs.eeb.utoronto.ca/murphy/publications>

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- [152] E. Myers, "What's Behind Blast," *Models and Algorithms for Genome Evolution (MAGE) Conference*, Computational Biology 19 (Spring-Verlag 2013), 3-15.
- [153] E. Myers, "Efficient Alignment Discovery amongst Noisy Long Reads," *Proc. Workshop on Algorithms for Bioinformatics (WABI)*, Wroclaw, Poland 2014), 52-67. Also published as Springer-Verlag LNCS #8791.
- [154] D. Kainmueller, F. Jug, C. Rother, E. Myers, "Active Graph Matching for Automatic Joint Segmentation and Annotation of *C. elegans*," *Conf. on Medical Image Computing and Computer-Assisted Intervention (MICCAI)*, Boston, MA 2014), 81-88. Also published as Springer-Verlag LNCS #8673.
- [155] F. Jug, T. Pietzsch, D. Kainmueller, J. Funke, M. Kaiser, E. van Nimwegen, C. Rother, E. Myers, "Optimal Joint Segmentation and Tracking of *Escherichia Coli* in the Mother Machine," *Conf. on Bayesian and Graphical Models for Biomedical Imaging (BAMBI)*, Boston, MA 2014), 25-36. Also published as Springer-Verlag LNCS #8677.
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*Computer-Assisted Intervention* (MICCAI, Munich, Germany 2015), 653-690. Also published as Springer-Verlag LNCS #9349.

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- [160] *Best Science Paper Award!*. D.L. Richmond, D. Kainmueller, M.Y. Yang, E.W. Myers, and C. Rother, “Mapping Auto-context to a Deep, Sparse ConvNet for Semantic Segmentation,” *British Machine Vision Conference (BMVC)*, (York, Britain 2016), accepted.
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#### Volumes and Proceedings

- [164] E. Myers (ed.) *Algorithmica: Special Issue on Computational Biology* 13, 1-2 (1995).
- [165] E. Myers and D. Hirschberg (eds.), *Proceedings of the 7th Annual Symposium on Combinatorial Pattern Matching*, Springer-Verlag Lecture Notes in Computer Science #1075 (Heidelberg, 1996).
- [166] E. Myers (ed.), *Journal of Computational Biology: Special RECOMB 2002 Issue* Volume 10, 3-4 (2003), 237-667.
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#### Book Chapters

- [169] E. Myers, “Advances in Sequence Assembly,” in *Automated DNA Sequencing and Analysis Techniques* (C. Ventner, ed.), Academic Press Limited (London, England 1994), 231-238.
- [170] E. Myers, “Algorithmic Advances for Searching Biosequence Databases,” in *Computational Methods in Genome Research* (S. Suhai, ed.), Plenum Press (New York, 1994), 121-135.
- [171] E. Myers, “Seeing Conserved Signals: Using algorithms to detect similarities between biosequences,” in *Calculating the Secrets of life: Applications of the Mathematical Sciences in Molecular Biology* (Lander & Waterman, eds.), National Academy Press (Washington, D.C. 1995), 56-89.
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#### Software

*BIGMAC*: A source-to-source translator for adding object-oriented extensions to FORTRAN (1978).

*egrep*: Developed the immediate precursor to the current version with Al Aho at Bell Labs in 1979.

*diff*: The GNU diff tool has my algorithm at its heart (see [6]) and was developed from a prototype I supplied to them in 1988.

*anrep*: A language and system for specifying high level protein and DNA sequence patterns.

*FAKI*: A library of algorithms for solving the shotgun DNA sequencing problem. Licensed and sold as part of Applied Biosystem's Inheret package from 1990-1996.

*BLAST*: The mostly widely used sequence similarity search tool for molecular biologists. The paper [16] below was a widely cited scientific paper for several years in the early 90's. See <http://www.ncbi.nlm.nih.gov/BLAST>.

*Mac-PC-Molecule2*: A Mac and Windows based program for visualizing molecular structures. The first version was developed in 1988 and continued refinement has lead to the current product. See <http://www.molvent.com>.

*FAKtory*: A complete environment in support of DNA sequencing including a new library of algorithms for shotgun assembly, a Tcl/Tk user interface, and a data management component. See <http://www.cs.arizona.edu/factory>.

*Celera Assembler*: A proprietary suite of programs totalling over 1/2 million lines of code used to assemble the Drosophila, Human, and Mouse genomes.

#### **Other Reports and Thesis (Not appearing elsewhere)**

- [173] E. Myers, "The BIGMAC Users Manual," Tech. Rep. CU-CS-145-78, Dept. of Computer Science, U. of Colorado, Boulder, CO (1978).
- [174] E. Myers, "A Precise and Efficient Algorithm for Determining Existential Summary Data Flow Information," Tech. Rep. CU-CS-175-80, Dept. of Computer Science, U. of Colorado, Boulder, CO (1980).
- [175] L. Osterweil and E. Myers, "BIGMAC II: A FORTRAN Language Augmentation Tool," Tech. Rep. CU-CS-179-80, Dept. of Computer Science, U. of Colorado, Boulder, CO (1980).
- [176] E. Myers, "A Depth-First Search Characterization of k-Connectivity and Its Application to Connectivity Testing," Ph.D. Thesis, University of Colorado (1981).
- [177] E. Myers, "AVL Dags," Tech. Rep. TR82-9, Dept. of Computer Science, U. of Arizona, Tucson, AZ (1982).
- [178] E. Myers, "Incremental Alignment Algorithms and Their Applications," Tech. Rep. TR86-22, Dept. of Computer Science, U. of Arizona, Tucson, AZ (1986).
- [179] J. Kececiloglu and E. Myers, "A Procedural Interface for a Fragment Assembly Tool," Tech. Rep. TR89-5, Dept. of Computer Science, U. of Arizona, Tucson, AZ (1989).
- [180] S. Miller and E. Myers, "A Fragment Assembly Project Environment," Tech. Rep. TR91-17, Dept. of Computer Science, U. of Arizona, Tucson, AZ (1991).
- [181] E. Myers, "Sequence Comparison Algorithms in Molecular Biology," Tech. Rep. TR91-29, Dept. of Computer Science, U. of Arizona, Tucson, AZ (1991).
- [182] S. Larson, M. Jain and E. Myers, "An Interface for a Fragment Assembly Kernel," Tech. Rep. TR93-20, Dept. of Computer Science, U. of Arizona, Tucson, AZ (1993).
- [183] S. Larson, M. Jain, E. Anson, and E. Myers, "An Interface for a Fragment Assembly Kernel (updated)," Tech. Rep. TR96-04, Dept. of Computer Science, U. of Arizona, Tucson, AZ (1996).
- [184] E. Myers, "A Suite of UNIX Filters for Fragment Assembly," Tech. Rep. TR96-07, Dept. of Computer Science, U. of Arizona, Tucson, AZ (1996).

#### **Grants**

- [1] *The Design and Analysis of a Practical and Precise Interprocedural Data Flow Analysis System*, Principal Investigator, 1982-1985 (\$50,000), NSF grant.

- [2] *A Programming Systems Laboratory*, Co-Principal Investigator with G. Andrews, T. Budd, P. Downey, C. Fraser, R. Griswold, D. Hanson, G. Levin, W. Miller, and R. Schlichting, 1984-1989 (\$3,634,000), NSF Coordinated Experimental Research Program.
- [3] *The Design and Analysis of Efficient Applicative Data Types and Their Applications*, Principal Investigator, 1985-1987 (\$100,000), NSF grant.
- [4] *A Workshop on Algorithms for Molecular Genetics*, Co-Principal Investigator with W. Miller, March 26-28, 1988 (\$30,000), NLM grant.
- [5] *Efficient Software for the Analysis of Biosequences*, Principal Investigator, 1988-1991 (\$423,000), NLM grant.
- [6] *A Laboratory for Programming Languages and Software Systems*, Co-Principal Investigator with G. Andrews, R. Griswold, and U. Manber, 1989-1994 (\$1,976,000), NSF Institutional Infrastructure Program.
- [7] *A Workshop on Recognizing Genes and Other Genomic Structure Components*, Co-Principal Investigator with M. Turner, C. Burks, and G. Stormo, May 28-June 18, 1990 (\$47,000), NSF grant.
- [8] *Problems in Discrete Pattern Matching*, Co-Principal Investigator with U. Manber, 1991-1993 (\$134,000), NSF grant.
- [9] *A Software Environment to Support Large-Scale Sequencing*, Subcontract to C. Lawrence at Baylor Medical College, 1991-1994 (\$291,000, subcontract only), DOE grant.
- [10] *Efficient Software for the Analysis of Biosequences*, Principal Investigator, 1992-1995 (\$554,000), NLM grant.
- [11] *Computer Upgrade for Sequence Analysis*, Co-Principal Investigator with A. Adams, G. Burd, J. Law, M. Wells, and S. Ward, 1994 (\$33,000), NSF grant.
- [12] *A Workshop on Identifying Features in Biological Sequences*, Co-Principal Investigator with T. Applequist, C. Burks, and G. Stormo, May 30-June 19, 1994 (\$8,000), NSF grant.
- [13] *A Flexible Sequence Reconstructor for Large Scale DNA Sequencing Projects*, Principal Investigator, 1994-1997 (\$403,000), DOE grant.
- [14] *A Laboratory for Scalable Systems*, Co-Principal Investigator with L. Peterson, 1995-2000 (\$1,000,000), NSF grant.
- [15] *Efficient Software for the Analysis of Biosequences*, Principal Investigator, 1996-1999 (\$639,000), NLM grant.
- [16] *A Flexible Sequence Reconstructor for Large Scale DNA Sequencing Projects*, Principal Investigator, 1997-1998 (\$192,000), DOE grant.
- [17] *Making the Most of Sequencing: Improved Assembly, Improved Protocols, and True Comparative Annotation Tools*, Principal Investigator, 2003-2005 (\$330,000), LDRD program grant, LBNL.
- [18] *A Computational Systems Biology Program for Drosophila*, Principal Investigator, 2004-2009 (EU 750,000), Max Planck and Alexander von Humboldt Societies.
- [19] *Collective Organization of Cells and Tissues: Systems Biology of Tissue Size and Shape* co-PI with Tony Hyman *et al.*, 2012-2015 (EU 6,000,000), German Federal Ministry of Education and Research (BMBF).

## Professional Activities

### Awards:

Elected to the European Molecular Biology Organization (EMBO, [REDACTED])  
 1st Volterra Lecture of the Norwegian Digital Life Program ([REDACTED])

ISCB Senior Scientist Award (International Society for Computational Biology, [REDACTED])  
Linnaeus Lecture (Uppsala Universitet, Sweden, [REDACTED])  
Fellow of the ISCB (International Society for Computational Biology, [REDACTED])  
Honorary Doctorate, ETH, Zurich ([REDACTED])  
Elected to Leopoldina, the German National Academy of Science, ([REDACTED])  
University of Colorado Distinguished Engineering Alumni Award ([REDACTED])  
International Max Planck Research Prize ([REDACTED])  
Elected to the National Academy of Engineering ([REDACTED])  
Fellow of the ACM (Association for Computing Machinery, [REDACTED])  
ACM Paris Kanellakis Theory and Practice Prize ([REDACTED])  
Genome Technology Magazine most influential in Bioinformatics ([REDACTED])  
Newcomb Cleveland Best Paper of the Year Award, Science ([REDACTED])  
IEEE 3rd Millenium Achievement Award ([REDACTED])  
Faculty of Science Distinguished Teaching Award (U. of Arizona, [REDACTED])  
University of Colorado Fellowship (U. of Colorado, [REDACTED])  
Honeywell Outstanding Junior Engineer (Caltech, [REDACTED])  
Tau Beta Pi (Caltech, [REDACTED])

#### *Boards*

IDbyDNA, Scientific Advisory Board, [REDACTED]  
Human Longevity, Inc., Scientific Advisory Board, [REDACTED]  
Burroughs-Wellcome Fund, Interfaces in Science Advisory Committee, [REDACTED]  
MPI for Computer Science, Saarbrücken, Science Advisory Board, [REDACTED]  
ARC Centre in Bioinformatics, U. of Queensland, Advisory Board and Honorary Professor, [REDACTED]  
Helicos, Science Advisory Board, [REDACTED]  
Membership Peer Committee (Section 5: Computer Science), NAE, [REDACTED]  
Allan Wilson Centre for Molecular Ecology and Evolution (New Zealand), Panel, [REDACTED]  
Hawaii IDeA Network for Biomedical Research Excellence, External Advisory Committee, [REDACTED]  
454 Corporation, Science Advisory Board, [REDACTED]  
Genomatica, Science Advisory Board, [REDACTED]  
Paracel, Science Advisory Board, [REDACTED]  
International Society for Computational Biology, Board Member, [REDACTED].  
Adhoc Review Committee for the National Center for Human Genome Research, Aug. & Dec., [REDACTED]  
Biomedical Library Review Committee, NLM, [REDACTED]

#### *Editor:*

Bioinformatics, ISMB 2003 Supplement, 2003.  
Lecture Notes in Bioinformatics, Editorial Board, 2003-present.

Journal of Bioinformatics and Computational Biology, Associate Editor, 2002-2004.

Journal of Computational Biology, RECOMB '02 Special Issue, Guest-Editor.

Kluwer "Computational Biology" book series, 1999-present.

Journal of Computational Biology, Associate Editor, 1997-present.

Bioinformatics, Editorial Board, 1994-2005.

RAIRO Informatique Theorique et Applications, Editorial Board, 1998-present.

GENECombis, Editorial Board, 1995-1998.

Journal of Computational Biology, Editorial Board, 1993-1997.

Algorithmica, Special Issue on Computational Biology, Vol. 13, Nos. 1-2.

#### *Meeting Organizer:*

"A Workshop on Algorithms for Molecular Genetics," with W. Miller (Washington, D.C., [REDACTED])

"A Workshop on Recognizing Genes and Other Genomic Structure Components," with C. Burks and G. Stormo (Aspen, Colorado, [REDACTED]) with C. Burks and C. Fields (Aspen, Colorado, [REDACTED])

"A Workshop on Identifying Signals in Biological Sequences," with C. Burks and G. Stormo (Aspen, Colorado, [REDACTED]) with C. Burks and W. Pearson (Aspen, Colorado, [REDACTED])

' IMA Summer Program: Molecular Biology,' with M. Waterman, T.P. Speed, J.P. Mesirov, K. Schulten, D.W. Sumners (Minneapolis, Minnesota, [REDACTED])

Co-chair, [REDACTED] Combinatorial Pattern Matching Conference (Laguna Beach, CA, [REDACTED])

Organizer, RECOMB satellite meeting on Assembly Algorithms (Los Angeles, CA, [REDACTED])

Program Chair, 6th Conference on Computational Molecular Biology, RECOMB 2002 (Washington, D.C., [REDACTED])

Organizer, RECOMB satellite meeting on Assembly Algorithms (Stanford, CA, [REDACTED])

Program Chair, [REDACTED] Conference on Intelligent Systems in Molecular Biology, ISMB [REDACTED] (Brisbane, Australia, [REDACTED])

Program Co-Chair, [REDACTED] Workshop on Algorithms in Bioinformatics, WABI [REDACTED] (Mallorca, Spain [REDACTED])

Conference Chair, [REDACTED] Conference on Intelligent Systems in Molecular Biology, ISMB [REDACTED] (Stockholm, Sweden, [REDACTED])

Program Co-Chair, [REDACTED] Asia Pacific Bioinformatics Conference, ABPC [REDACTED] (Bangalore, India, [REDACTED])

#### *Program Committees:*

[REDACTED] Combinatorial Pattern Matching Conference (Tucson, AZ, [REDACTED])

[REDACTED] Combinatorial Pattern Matching Conference (Padova, Italy, [REDACTED])

[REDACTED] Combinatorial Pattern Matching Conference (Asilomar, CA, [REDACTED])

Intelligent Systems for Molecular Biology [REDACTED] (Stanford, CA).

Latin American Conference on Theoretical Informatics [REDACTED] (Vina del Mar, Chile, [REDACTED])

Intelligent Systems for Molecular Biology [REDACTED] (St. Louis, MO).

[REDACTED] Conference on Computational Molecular Biology (Sante Fe, NM, [REDACTED])

[REDACTED] Workshop on Implementing Automata (London, Ontario, [REDACTED])

Latin American Conference on Theoretical Informatics [REDACTED] (Campinas, Brazil, [REDACTED])

■ Conference on Computational Molecular Biology (New York, NY, ■)  
 ■ Workshop on Implementing Automata (Rouen, France, ■)  
 ■ Combinatorial Pattern Matching Conference (Warwick, UK, ■)  
 Intelligent Systems for Molecular Biology (Heidelberg, Germany, ■)  
 Computational Genomics III (Baltimore, MD, ■)  
 Computational Genomics V (Reston, VA ■)  
 Workshop on Algorithms in Bioinformatics (Rome, Italy ■)  
 Genome Informatics Workshop ■ (Tokyo, Japan ■)  
 ■ Computing and Combinatorics Conference, COCOON ■ (Big Sky, MT).  
 European Conference on Computational Biology, ECCB ■ (Paris, France).  
 Intelligent Systems for Molecular Biology (Glasgow, Scotland, ■)  
 ■ Conference on Computational Molecular Biology (Boston, MA, ■)  
 ■ Conference on Computational Molecular Biology (Venice, Italy, ■)  
 ■ Workshop on Algorithms in Bioinformatics, WABI ■ (Zurich, Switzerland).  
 ■ Workshop on Algorithms in Bioinformatics, WABI ■ (Philadelphia, PA).  
 ■ Combinatorial Pattern Matching Conference (Pisa, Italy, ■)  
 ■ Combinatorial Pattern Matching Conference (Lille, France, ■)  
 Area Chair, Intelligent Systems for Molecular Biology (Boston, MA, ■)  
 Area Chair, Intelligent Systems for Molecular Biology (Vienna, Austria, ■)  
 11th Workshop on Algorithms in Bioinformatics, WABI 2011 (Saarbrücken, Germany ■)

*Panels:*

Working group on training, Office for Human Genome Research, NIH (■)  
 Biomedical Library Review Committee, NLM (■)  
 DOE Human Genome Computational Task Force (■)  
 Affiliate, Los Alamos National Laboratory (■).  
 Adhoc Review Committee for the National Center for Human Genome Research (August & December, ■)

*Member:*

National Academy of Engineering, Leopoldino, Association for Computing Machinery (SIGACT, SIGPLAN, and SIGGRAPH), Society for Industrial and Applied Mathematics, International Society for Computational Biology, and IEEE Computer Society (Senior member).

*Reviewer:*

Journal of the ACM, ACM Transactions on Programming Languages, SIAM Journal on Computing, Information Processing Letters, Software — Practice & Experience, Algorithmica, International Journal of Parallel Programming, Bulletin of Mathematical Biology, Journal of Theoretical Biology, Nucleic Acids Research, National Institutes of Health, National Science Foundation, Genomics, Genome Research, Science, Nature.

*Invited Conference, Plenary, and Distinguished Lecture Presentations:*

“An Incremental Alignment Algorithm and Its Application to Sequence Reconstruction.” *Symposium on Macromolecules, Genes, and Computers* (1986, Waterville, New Hampshire).

“An Approach to Pattern Matching for Biosequences.” *The Interface Between Computer Science and Molecular Biology* (1989, Sante Fe, New Mexico).

“A Rigorous Method for Fragment Assembly.” *The Wolf Trap Genome Sequencing Conference* (1989, Washington, D.C.).

“A Sublinear Algorithm for Similarity Searching.” *SIAM Annual Meeting* (1990, Chicago, Illinois); *Mathematical Approaches to DNA II* (1991, Sante Fe, New Mexico); and *'91 Symposium on the Interface: Computing Sciences and Statistics* (1991, Seattle, Washington).

“Practical and Theoretical Advances in Fragment Assembly.” *Genome Sequencing Conference II* (1990, Hilton Head, S. Carolina).

“Approximate Regular Expression Matching with Concave Gap Penalties.” *2nd International Conference on Industrial and Applied Mathematics (ICIAM)* (1991, Washington, D.C.).

“Approximate Matching of Network Expressions with Spacers.” *Latin American Symposium on Theoretical Computer Science (LATIN '92)* (1992, Sao Paulo, Brazil).

“Algorithmic Advances for Searching Biosequence Databases.” *International Symposium on Computational Methods in Genome Research* (1992, Heidelberg, Germany).

“Non-Numerical Problems in Genome Research.” *1993 SIAM Annual Meeting* (1993, Philadelphia, Pennsylvania).

“Towards Simplifying Fragment Assembly,” *Automation in Mapping and DNA Sequencing* (1994, Cambridge, England).

“An Alternative Formulation of Sequence Assembly,” *DIMACS workshop on Combinatorial Methods for DNA Mapping and Sequencing* (1994, Piscataway, New Jersey).

“Trends in Software and Algorithms for DNA Sequencing,” *7th Conference of the Jacques Cartier Center: Informatique et Biologie Moleculaire* (1994, Lyon, France).

“BLAST & Slam: Using Neighborhoods to Accelerate Data Base Searches,” *Dagstuhl Seminar on Molekular Bioinformatik* (1995, Dagstuhl, Germany).

“Rapid Overlap Detection for DNA Sequencing,” *9th Annual Meeting of the CIAR Program in Evolutionary Biology* (1995, Montreal, Canada).

“A Customizable Software System for Fragment Assembly,” *Annual DOE Contractors Workshop* (1996, Sante Fe, New Mexico).

“Is Whole Genome Shotgun Sequencing Feasible?” *2nd International Symposium on Computational Methods in Genome Research* (1996, Heidelberg, Germany). Also at *Bat Sheva de Rothschild Seminar on Computational Aspects of the Human Genome Project* (1996, Nahsholim, Israel).

“Approaches to Whole Genome Shotgun Sequencing.” *16th Congress of the Brazilian Computer Science Society* (1996, Recife, Brazil).

“A Customizable Environment for Fragment Assembly.” *8th Genome Sequencing Conference* (1996, Hilton Head, S. Carolina).

“On the Feasibility of Human Whole Genome Shotgun Sequencing.” *10th Genome Sequencing Conference* (1998, Miami, Florida).

“Progress Towards the Sequencing of Drosophila.” *3rd Conf. on Computational Molecular Biology* (1999, Lyon, France).

“A Whole Genome Assembler for Drosophila.” *11th Genome Sequence Conference* (1999, Miami); *3rd German Computational Biology Conference* (1999, Hanover, Germany); *Intersection of Structural Biology and Genomics* (1999, Cornell); Lecture Series, U. of Texas (1999, Austin, TX); Distinguished Lecturer Series, Princeton (1999, Princeton, NJ).

“The Whole Genome Assembly of Drosophila.” *Symp. on Discrete Algorithms* (2000, San Francisco); *Association for the Advancement of American Science Annual Meeting* (2000, Washington, D.C.); *41st Annual Drosophila Conference* (2000, Pittsburg); *Genomes 2000* (2000, Pasteur Institute,



Paris); *BioInformatics 2000* (2000, Helsingor, Denmark); *JOBIM 2000* (2000, Montpellier, France); *Genome Sequencing & Biology* (2000, Cold Spring Harbor, NY).

“On Assembling the Drosophila and Human Genomes.” *Frontiers of Genomics* (2000, Madison, WI); *Real World Algorithms* (2000, Carnegie-Mellon, Pittsburg, PA); *Math 2000* (2000, Hamilton, ON); Lecture Series, Caltech (2000, Pasadena, CA); *ISMB 2000* (2000, San Diego, CA); *Los Alamos Computer Science Institute Inauguration* (2000, Santa Fe, NM); Lecture Series, Sandia (2000, Albuquerque, NM); Student Lecture Series, Washington University (2000, St. Louis, MO); *Symposium on the Informatics Interface*, Pharmacia & Upjohn (2000, Kalamazoo, MI); DIMACs Distinguished Lecture Series (2000, Piscataway, NJ); Distinguished Lecture at Columbia (2000, New York, NY), Wadsworth Center (2000, Albany, NY), and Rensselaer Polytechnic Institute (2000, Troy, NY); *11th Genomics Informatics Workshop 2000* (2000, Tokyo, Japan); Keystone Genomics Conference (2001, Breckenridge, CO).

“Whole Genome Shotgun on Multiple Donors.” *Pharmacogenetics and Pharmacogenomics, an Insitute Pasteur Euroconference* (2000, Paris).

“The Assembly of the Human Genome and Its Implications.” *Brazilian International Genomics Conference* (2001, Rio de Janeiro, Brazil); *37th SRI Memorial Lecture* (2001, Shriram Institue, New Dehli, India); *1st CDFD Distinguished Lecture* (2001, Hyderabad, India); *1st RECOMB Satellite Workshop on DNA Assembly* (2001, Los Angeles, CA); *ACM Sigmod/Sigpod conference* (2001, Santa Barbara, CA); *Ernst Schering Foundation Workshop #38: Bioinformatics and Genome Analysis* (2001, Berlin); *11th Gene Congress* (2001, Stockholm, Sweden), .

“The Whole Genome Assembly of Mouse and Human.” *15th International Mouse Genome Conference* (2001, Edinburgh, Scotland).

“Reconstructing Genomes: Experience from Our Human and Mouse Projects.” *13th Genome Sequence Conference* (2001, San Diego, CA); *VII Program in Mathematics and Molecular Biology Workshop* (2002, Santa Fe, NM). *BiGIALS Symposium* (2002, Amherst, MA) *COCOON 2002* (2002, Singapore)

“String Graphs and the Limits of Assembly.” *2nd RECOMB Satellite Workshop on DNA Assembly* (2002, Palo Alto, Angeles, CA);

“Accelerating Smith-Waterman Searches.” *Maps, Sequences, and Genomes* (2002, Los Angeles, CA).

“Enabling Systems Biology.” *Theory of Computation and the Sciences* (2002, Berkeley, CA); *The New Biotechnology and Its Impact on the Future of San Diego* (2002, San Diego, CA); *Computer Research Association (CRA) Annual Meeting* (2002, Snowbird, UT); *AAAS Annual Meeting: BioInformatics Symposium* (2003, Denver, CO).

“Advances in Whole Genome Assembly.” *DNA and the Legacy of Molecular Biology* (2003, San Diego, CA); Public Lecture at the Institute for Mathematics and Its Applications (2003, Minneapolis, MN); *ACM Paris Kanellakis Memorial Workshop* (2003, San Diego, CA); *68th Symposium on Quantitative Biology: The Genome of Homo Sapiens* (2003, Cold Spring, NY); *12th Intl. Conf. on Genes, Gene Famillies, and Isozymes.* (2003, Berlin), *Distinguished Lecture Series (U. of Texas, Dallas, 2003).*

“Efficient Algorithms for Comparing Genomes.” *Distinguished Leccture Series* (2003, Stanford).

“On the Shotgun DNA Sequencing Assembly Problem.” *Combinatorail Pattern Matching Conference* (2004, Istanbul).

“On the Limits of Shotgun Sequencing and the Value of Comparative Genomics.” *Distinguished Lecture Series* (2004, UCLA and U. Utah). *3rd Conference on Systems Biology* (2004, Stanford),

“Super Computing and Bioinformatics.” *SIAM Conference on Parallel Processing for Scientific Computing* (2004, San Francisco).

“Whole Genome Sequencing, Comparative Genomics, and System Biology.” *IEEE International Conference on Data Mining* (Melbourne, FA 2003), *International Conference on Machine Learning* (Banff, CA 2004), *Computational Bio-Networks* (Recife, Brazil 2004), *Bologna Bioinformatics Winter School* (Bologna, Italy, 2005) *Distinguished Lecture Series* (2004, UC).

“Whole Genome Sequencing and Imaging-Based Systems Biology.” *Distinguished Alumni Award Lecture* (Boulder, CO 2005), *Pantelleria Summer School* (Pantelleria, Italy, 2005), *Distinguished Lecture Series* (Academica Sinica, Taipei, 2005).

“Computer-Assisted Forensic Analysis of Mass Disasters.” *Distinguished Lecture Series* (Duke, NC 2006). *Rocky Mountain Regional Bioinformatics Conference* (Aspen, CO 2005).

“Some Imaging Applications in Molecular Biology.” *Gulf-Coast Center for Cancer Research Distinguished Lecture Series* (Rice, TX 2006). *Biological Imaging Lecture Series* (U. Wisconsin, WI 2006). *Lipari Summer School on Proteomes and Proteins* (Lipari, Italy 2006). *German Computational Biology Conference* (Tuebingen, Germany 2006). *Distinguished Speakers Series, Biotech Club* (Caltech, CA 2006). *Honorary Doctorate Lecture* (ETH, Zurich 2006). *International Symposium on Computational Biology & Bioinformatics* (Bhubaneswar, India 2006). *International Conference on Bioinformatics* (New Dehli, India 2006). *International Conference on High Performance Computing* (Bangalore, India 2006).

“Whole Genome Sequencing and Image-Based Systems Biology.” *Kanellakis Lecture* (Brown, RI 2007).

“Imaging Bioinformatics.” *ISMB 2008 Keynote* (Boston, MA 2008); *Distinguished Lecture Series* (Brown, Providence, RI 2009). *Intl. Conf. on Systems Biology Plenary* (Stanford, CA 2009).

“Image-Based Modeling for Molecular Biology.” *7th ELSO Meeting, Plenary* (Nice, France 2008); *Swiss Institute of Bioinformatics Ph.D. School* (Jongny, Switzerland 2008);

“Machine-Vision and Molecular Biology.” *LMB Graduate Student Symposium* (MRC, Cambridge, England, 2009).

“Decoding the Genome with Bioimage Informatics.” *Distinguished Lecture Series* (UC Irvine, CA, 2010); *CSHL Meeting on Automated Imaging and High Throughput Phenotyping* (NY, 2010); *Distinguished Lecture at the Scientific Computing and Imaging Institute of the U. Utah* (Salt Lake City, UT 2012); *ECCB 2012 Keynote* (Basel, Switzerland 2012).

“Building Cellular Atlases with Light.” *10th Anniversary Symposium of the Center for Bioinformatics, Saarland* (Saarland, DE, 2011); *INSERM Workshop on Quantitative Fluorescence Microscopy* (Lisbon, Portugal 2011)

“Toward Perfect Single Cell Lineage Tracking.” *Riken CDB Symposium: Quantitate Developmental Biology* (Kobe, Japan 2012).

“Building Neuroanatomical Models with Light Microscopy.” *VIZBI Visualization in the Biosciences* (Heidelberg, DE 2012).

“Molecular Cell Biology via Bio-Image Informatics.” *The 2013 Linnaeus Lecture* (Uppsala, Sweden 2013).

“Discrete Methods for Image Analysis Applied to Molecular Biology.” *Combinatorial Pattern Matching 2013* (Karlsruhe, Germany 2013).

“A Blast from the Past” *Celebration for Andrzej Ehrenfeucht’s 80th Birthday* (Boulder, CO 2012). *Celebration for David Sankoff’s 50th Year of Research* (Montreal, CA 2013).

“Light-based Systems Biology.” *International Conference on Systems Biology* (Copenhagen, Denmark 2013). *German Conference on Bioinformatics* (Goettingen, Germany 2013).

“Extracting Quantitative Models in Molecular Biology.” *German Conference on Pattern Recognition* (Saarbruecken, Germany 2013).

## Educational Activities

### *Students:*

- Torben [REDACTED] "Combinatorial Bin Packing Problems," Ph.D 1985, committee.
- Gerhard [REDACTED] "A Rule-Based P.L. Applied to Image Recognition," M.S. 1986, advisor.
- Alan [REDACTED] "An Optimizing Code-Generator Generator," Ph.D. 1988, committee.
- Gerhard [REDACTED] "A Pattern Matching System for Biosequences," Ph.D. 1991, advisor.
- John [REDACTED] "Exact and Approximate Algorithms for DNA Sequence Reconstruction," Ph.D. 1991, advisor.
- Sun [REDACTED] "Algorithms for Approximate Pattern Matching," Ph.D. 1992, committee.
- Jim [REDACTED] "Discrete Pattern Matching Over Sequences and Interval Sets," Ph.D. 1993, advisor.
- Mudita [REDACTED] "Algorithms for Physical Mapping Using Unique Probes," Ph.D. 1996, advisor.
- Eric [REDACTED] "Algorithms for Whole-Genome Shotgun Sequencing," Ph.D. 1999, advisor.
- Steffen [REDACTED] "Time-Resolved Quantification of Centrosomes by Automated Image Analysis Suggests Limiting Component to Set Centrosome Size in *C. Elegans* Embryos," Ph.D. 2010, co-advisor with A.A. Human (MPI-CBG, Dresden), degree awarded by T.U. Dresden.
- Stephan [REDACTED] "Reconstruction of Multi-View Microscopic Acquisitions," Ph.D. 2011, committee member.

### *Courses taught:*

Data structures, Algorithms, Theory of computation, Computer graphics, First and second semester introductions to programming (PASCAL, C, Scheme, etc.), Computer architecture, Software tools, Theory seminar, and advanced courses on special topics in algorithm analysis (probabilistic algorithms and algorithms for molecular biology). University of Arizona, 1981-1998, U.C. Berkeley, 2003-2006, Technical University Dresden, 2013-present.

Member of the Applied Mathematics Program, 1982-95.

Organizer of departmental seminar, Foundations of Computation, 1984-1992.

Instructor for "Essential Computational Genomics," at Cold Spring Harbor

Instructor for "Mathematics in Molecular Biology," a SIMMS tutorial workshop, Stanford '91 & Rutgers '92.

## Curriculum Vitae

Adam [REDACTED] Phillippy, Ph.D.

**Office** Genome Informatics Section  
49 Convent Drive, Room 4A22  
Bethesda, Maryland 20892  
[REDACTED]

**E-Mail** adam.phillippy@nih.gov

**Web Sites** <https://genomeinformatics.github.io>  
<https://genome.gov/staff/phillippy>

### Education

[REDACTED] [REDACTED] University [REDACTED]  
B.S., Computer Science

[REDACTED] University of [REDACTED]  
M.S., Computer Science

[REDACTED] University of [REDACTED]  
Ph.D., Computer Science

### Predoctoral Experience

[REDACTED] Bioinformatics Software Engineer  
The Institute for Genomic Research

[REDACTED] Bioinformatics Software Engineer  
J. Craig Venter Institute

[REDACTED] Bioinformatics Software Engineer  
University of [REDACTED] School of Medicine

### Faculty Appointments

[REDACTED] Affiliate Faculty, [REDACTED] Pathogen Research Institute  
University of Maryland

[REDACTED] Principal Investigator, Genomics  
National Biodefense Analysis and Countermeasures Center

[REDACTED] Senior Principal Investigator, Genomics  
National Biodefense Analysis and Countermeasures Center

[REDACTED] – Investigator and Head, Genome Informatics Section  
Computational and Statistical Genomics Branch, National Human Genome  
Research Institute, National Institutes of Health

### ***Institutional Service Appointments***



Training Instructor, The Institute for Genomic Research  
Teaching Assistant, University of Maryland  
Peer Mentor, University of Maryland  
Orientation Committee, University of Maryland  
Industrial Advisory Board, Computer Science, Loyola University Maryland  
Information Technology Management Committee, NHGRI  
Data Storage and Backup Working Group, NHGRI  
Stadtman Investigator Search Committee, NIH  
Co-chair, Genomic Data Science, NHGRI Strategic Planning Committee

### ***External Service Appointments***



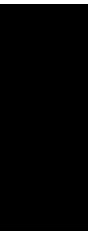
DHS Banbury Microbial Forensics Working Group  
Volunteer speaker, Frederick County Schools STEM Career Day  
FBI Microbial Forensics Working Group  
NCBI/FDA Whole-Genome SNP Typing Working Group  
Chair, Maize Genome Database  
ASM/AAM Applications of Clinical Microbial NGS Working Group  
External Reviewer, Heidelberg Institute for Theoretical Studies  
Non-voting member, Genome10K Executive Council  
Chair, Genome Assembly Working Group, Genome10K

### ***Review Panels***



Grant review panel, Department of Homeland Security  
Grant review panel, Department of Homeland Security  
Grant review panel, Department of Homeland Security  
Grant review panel, National Science Foundation  
Grant review panel, National Institutes of Health  
Grant review panel, Department of Homeland Security  
Grant review panel, National Cancer Institute

### ***Program Committees***



ACM Conference on Bioinformatics, Computational Biology and Biomedicine  
ACM Conference on Bioinformatics, Computational Biology and Biomedicine  
RECOMB Satellite Workshop on Massively Parallel Sequencing  
RECOMB Satellite Workshop on Massively Parallel Sequencing  
Workshop on Algorithms in Bioinformatics (WABI)  
ASM Conference on Rapid Applied Microbial NGS and Bioinformatic Pipelines

### ***Awards and Honors***



Federated Women's Club of Hershey Scholarship  
Presidential Scholarship, Loyola University Maryland  
Upsilon Pi Epsilon, Loyola University Maryland  
Hauber Research Fellowship, Loyola University Maryland  
Research Fellowship, The Institute for Genomic Research

Summa Cum Laude, Loyola University Maryland  
James D. Rozics Computer Science Medal, Loyola University Maryland  
Phi Beta Kappa, Loyola University Maryland  
Verizon Graduate Fellowship, University of Maryland  
Loyola University Maryland Notable Alumni  
NBACC Outstanding Performance Award  
NBACC Outstanding Performance Award

### ***Memberships in Professional Societies***

– International Society for Computational Biology

### ***Editorial and Evaluative Positions***

Guest Editor, Genome Research, May “Genome Assembly Issue”  
Guest Editor, PLOS Computational Biology

### ***Reviewer for Journals***

Bioinformatics, BMC Bioinformatics, BMC Biology, BMC Genomics, Briefings in Bioinformatics, Developmental Cell, Genome Biology, Genome Research, Journal of Clinical Microbiology, Molecular Biology and Evolution, Nature, Nature Biotechnology, Nature Communications, Nature Methods, Nature Protocols, Nature Reviews Genetics, Nucleic Acids Research, PLOS Computational Biology, PLOS Genetics, PLOS ONE

### ***Graduate Students***

Sergey Ph.D. co-advisor, University of Maryland  
Andrew Ph.D. committee, University of Notre Dame  
Karsten Ph.D. committee, University of Maryland School of Medicine  
Maria thesis examiner, Cold Spring Harbor Laboratory  
Brian Ph.D. advisor, University of Maryland  
Ole defense opponent, University of Oslo

### ***Invited Talks (since )***

1. University of Notre Dame. South Bend, IN. January
2. National Biodefense Analysis and Countermeasures Center. Frederick, MD. February
3. Lycoming College. Williamsport, PA. April
4. NCBI Computational Biology Branch. Bethesda, MD. April
5. University of Notre Dame. South Bend, IN. September
6. Panel discussion. CDC. Embracing next generation technologies in outbreak investigations. Atlanta, GA. September
7. Panel discussion. AGBT. The future of fighting infectious disease. Marco Island, FL. February
8. AGBT. Marco Island, FL. February
9. NGS Leaders Featured Webinar. August

10. NCBI. Disease Outbreak Detection in the Genomics Era. Bethesda, MD. September [REDACTED]
11. Pacific Biosciences User Group Meeting. Menlo Park, CA. October [REDACTED]
12. Northern Arizona University. Flagstaff, AZ. October [REDACTED]
13. University of Maryland. College Park, MD. October [REDACTED]
14. FDA. White Oak, MD. March [REDACTED]
15. Johns Hopkins University. Baltimore, MD. March [REDACTED]
16. Thomas Johnson Middle School. Frederick, MD. April [REDACTED]
17. Panel discussion. Genome Standards Consortium Meeting. Bethesda, MD. April [REDACTED]
18. Genome Standards Consortium Meeting. Bethesda, MD. April [REDACTED]
19. Pacific Biosciences User Group Meeting. Baltimore, MD. June [REDACTED]
20. CDC. Atlanta, GA. June [REDACTED]
21. Johns Hopkins University. Baltimore, MD. October [REDACTED]
22. NCI. Frederick MD. February [REDACTED]
23. Thomas Johnson Middle School. Frederick, MD. April [REDACTED]
24. University of Liverpool. Liverpool, UK. April [REDACTED]
25. Pacific Biosciences User Group Meeting. Baltimore, MD. July [REDACTED]
26. NIST. Gaithersburg, MD. October [REDACTED]
27. NCBI Annotation Workshop. Bethesda, MD. October [REDACTED]
28. Keynote. Michigan State Cyberinfrastructure Days. East Lansing, MI. October [REDACTED]
29. Loyola University Maryland. Baltimore, MD. November [REDACTED]
30. NCI. Frederick, MD. December [REDACTED]
31. MAD SSci Meeting. Baltimore, MD. June [REDACTED]
32. NHGRI. Bethesda, MD. February [REDACTED]
33. Applied Bioinformatics and Public Health Microbiology. Hinxton, UK. May [REDACTED]
34. Smithsonian National Museum of Natural History. Washington, D.C. November [REDACTED]
35. Genomics and Evolution of Pathogens and Hosts. Atlanta, GA. November [REDACTED]
36. NCI. Bethesda, MD. February [REDACTED]
37. University of Washington. Seattle, WA. February [REDACTED]
38. University of British Columbia. Vancouver, BC. February [REDACTED]
39. University of Texas at San Antonio. San Antonio, TX. March [REDACTED]
40. In-Q-Tel. Arlington, VA. September [REDACTED]
41. Microbial Genomics. Lake Arrowhead, CA. September [REDACTED]
42. International Congress of Entomology. Orlando, FL. September [REDACTED]
43. NCBI Annotation Workshop. Bethesda, MD. October [REDACTED]
44. Johns Hopkins University. Baltimore, MD. October [REDACTED]

45. Mid-Atlantic Microbiome Meet-up. College Park, MD. October [REDACTED]
46. Genome10k Executive Committee Meeting. Ashburn, VA. November [REDACTED]
47. University of California San Diego. San Diego, CA. November [REDACTED]
48. Duke University. Durham, NC. November [REDACTED]
49. DHS BioWatch advisory meeting. Washington, D.C. January [REDACTED]
50. University of Maryland. College Park, MD. May [REDACTED]
51. Biology of Genomes, Oxford Nanopore workshop. Cold Spring Harbor, NY. May [REDACTED]
52. NHGRI Division of Intramural Research Summer Seminar. Bethesda, MD. June [REDACTED]
53. Keynote. ISMB HiTSeq. Prague, Czech Republic. July [REDACTED]
54. Bioinformatics: from algorithms to applications. St. Petersburg, Russia. August [REDACTED]
55. University of Oslo. Oslo, Norway. August [REDACTED]
56. Keynote. Genome Science Conference. Norwich, UK. August [REDACTED]
57. Georgetown University. Washington, D.C. September [REDACTED]
58. Keynote. Genome to Phenome. USDA, Beltsville, MD. November [REDACTED]

### ***Selected Conference Talks (since 2010)***

1. Sequencing, Finishing, and Analysis in the Future. Santa Fe, NM. June [REDACTED]
2. Sequencing, Finishing, and Analysis in the Future. Santa Fe, NM. May [REDACTED]
3. ISMB. Boston, MA. July [REDACTED]
4. Genome Informatics. Cold Spring Harbor, NY. October [REDACTED]
5. International Meeting on Microbial Epidemiological Markers. Estoril, Portugal. March [REDACTED]
6. Genome Informatics. Cold Spring Harbor, NY. November [REDACTED]

### ***Peer-Reviewed Publications***

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

Google metrics as of September 2017: **h-index = 34, i-10 index = 44**

1. Delcher AL, Phillippy A, Carlton J, Salzberg SL. Fast algorithms for large-scale genome alignment and comparison. Nucleic Acids Res. 2002 Jun 1;30(11):2478-83. PubMed PMID: 12034836; PubMed Central PMCID: PMC117189.
2. Delcher AL, Salzberg SL, Phillippy AM. Using MUMmer to identify similar regions in large sequence sets. Curr Protoc Bioinformatics. 2003 Feb;Chapter 10:Unit 10.3. PubMed PMID: 18428693.
3. Kurtz S, Phillippy A, Delcher AL, Smoot M, Shumway M, Antonescu C, Salzberg SL. Versatile and open software for comparing large genomes. Genome Biol. 2004;5(2):R12. PubMed PMID: 14759262; PubMed Central PMCID: PMC395750.
4. Pop M, Phillippy A, Delcher AL, Salzberg SL. Comparative genome assembly. Brief Bioinform. 2004 Sep;5(3):237-48. PubMed PMID: 15383210.



5. Seshadri R, Adrian L, Fouts DE, Eisen JA, Phillippy AM, Methe BA, Ward NL, Nelson WC, Deboy RT, Khouri HM, Kolonay JF, Dodson RJ, Daugherty SC, Brinkac LM, Sullivan SA, Madupu R, Nelson KE, Kang KH, Impraim M, Tran K, Robinson JM, Forberger HA, Fraser CM, Zinder SH, Heidelberg JF. Genome sequence of the PCE-dechlorinating bacterium *Dehalococcoides ethenogenes*. *Science*. 2005 Jan 7;307(5706):105-8. PubMed PMID: 15637277.
6. Schatz MC, Phillippy AM, Shneiderman B, Salzberg SL. Hawkeye: an interactive visual analytics tool for genome assemblies. *Genome Biol*. 2007;8(3):R34. PubMed PMID: 17349036; PubMed Central PMCID: PMC1868940.
7. Phillippy AM, Mason JA, Ayanbule K, Sommer DD, Taviani E, Huq A, Colwell RR, Knight IT, Salzberg SL. Comprehensive DNA signature discovery and validation. *PLoS Comput Biol*. 2007 May;3(5):e98. PubMed PMID: 17511514; PubMed Central PMCID: PMC1868776.
8. Clark AG, Eisen MB, Smith DR, Bergman CM, Oliver B, Markow TA, Kaufman TC, Kellis M, Gelbart W, Iyer VN, Pollard DA, Sackton TB, Larracuent AM, Singh ND, Abad JP, Abt DN, Adryan B, Aguade M, Akashi H, Anderson WW, Aquadro CF, Ardell DH, Arguello R, Artieri CG, Barbash DA, Barker D, Barsanti P, Batterham P, Batzoglou S, Begun D, Bhutkar A, Blanco E, Bosak SA, Bradley RK, Brand AD, Brent MR, Brooks AN, Brown RH, Butlin RK, Caggese C, Calvi BR, Bernardo de Carvalho A, Caspi A, Castrezana S, Celniker SE, Chang JL, Chapple C, Chatterji S, Chinwalla A, Civetta A, Clifton SW, Comeron JM, Costello JC, Coyne JA, Daub J, David RG, Delcher AL, Delehaunty K, Do CB, Ebling H, Edwards K, Eickbush T, Evans JD, Filipinski A, Findeiss S, Freyhult E, Fulton L, Fulton R, Garcia AC, Gardiner A, Garfield DA, Garvin BE, Gibson G, Gilbert D, Gnerre S, Godfrey J, Good R, Gotea V, Gravely B, Greenberg AJ, Griffiths-Jones S, Gross S, Guigo R, Gustafson EA, Haerty W, Hahn MW, Halligan DL, Halpern AL, Halter GM, Han MV, Heger A, Hillier L, Hinrichs AS, Holmes I, Hoskins RA, Hubisz MJ, Hultmark D, Huntley MA, Jaffe DB, Jagadeeshan S, Jeck WR, Johnson J, Jones CD, Jordan WC, Karpen GH, Kataoka E, Keightley PD, Kheradpour P, Kirkness EF, Koerich LB, Kristiansen K, Kudrna D, Kulathinal RJ, Kumar S, Kwok R, Lander E, Langley CH, Lapoint R, Lazzaro BP, Lee SJ, Levesque L, Li R, Lin CF, Lin MF, Lindblad-Toh K, Llopart A, Long M, Low L, Lozovsky E, Lu J, Luo M, Machado CA, Makalowski W, Marzo M, Matsuda M, Matzkin L, McAllister B, McBride CS, McKernan B, McKernan K, Mendez-Lago M, Minx P, Mollenhauer MU, Montooth K, Mount SM, Mu X, Myers E, Negre B, Newfeld S, Nielsen R, Noor MA, O'Grady P, Pachter L, Papacit M, Parisi MJ, Parisi M, Parts L, Pedersen JS, Pesole G, Phillippy AM, Ponting CP, Pop M, Porcelli D, Powell JR, Prohaska S, Pruitt K, Puig M, Quesneville H, Ram KR, Rand D, Rasmussen MD, Reed LK, Reenan R, Reily A, Remington KA, Rieger TT, Ritchie MG, Robin C, Rogers YH, Rohde C, Rozas J, Rubenfield MJ, Ruiz A, Russo S, Salzberg SL, Sanchez-Gracia A, Saranga DJ, Sato H, Schaeffer SW, Schatz MC, Schlenke T, Schwartz R, Segarra C, Singh RS, Sirot L, Sirota M, Sisneros NB, Smith CD, Smith TF, Spieth J, Stage DE, Stark A, Stephan W, Strausberg RL, Strempel S, Sturgill D, Sutton G, Sutton GG, Tao W, Teichmann S, Tobar YN, Tomimura Y, Tsolas JM, Valente VL, Venter E, Venter JC, Vicario S, Vieira FG, Vilella AJ, Villasante A, Walenz B, Wang J, Wasserman M, Watts T, Wilson D, Wilson RK, Wing RA, Wolfner MF, Wong A, Wong GK, Wu CI, Wu G, Yamamoto D, Yang HP, Yang SP, Yorke JA, Yoshida K, Zdobnov E, Zhang P, Zhang Y, Zimin AV, Baldwin J, Abdouelleil A, Abdulkadir J, Abebe A, Abera B, Abreu J, Acer SC, Aftuck L, Alexander A, An P, Anderson E, Anderson S, Arachi H, Azer M, Bachantsang P, Barry A, Bayul T, Berlin A, Bessette D, Bloom T, Blye J, Boguslavskiy L, Bonnet C, Boukhgalter B, Bourzgui I, Brown A, Cahill P, Channer S, Cheshatsang Y, Chuda L, Citroen M, Collymore A, Cooke P, Costello M, D'Aco K, Daza R, De Haan G, DeGray S, DeMaso C, Dhargay N, Dooley K, Dooley E, Doricent M, Dorje P, Dorjee K, Dupes A, Elong R, Falk J, Farina A, Faro S, Ferguson D, Fisher S, Foley CD, Franke A, Friedrich D, Gadbois L, Gearin G, Gearin CR, Giannoukos G, Goode T, Graham J, Grandbois E, Grewal S, Gyaltsen K, Hafez N, Hagos B, Hall J, Henson C, Hollinger A, Honan T, Huard MD, Hughes L,

Hurhula B, Husby ME, Kamat A, Kanga B, Kashin S, Khazanovich D, Kisner P, Lance K, Lara M, Lee W, Lennon N, Letendre F, LeVine R, Lipovsky A, Liu X, Liu J, Liu S, Lokyitsang T, Lokyitsang Y, Lubonja R, Lui A, MacDonald P, Magnisalis V, Maru K, Matthews C, McCusker W, McDonough S, Mehta T, Meldrim J, Meneus L, Mihai O, Mihalev A, Mihova T, Mittelman R, Mlenga V, Montmayeur A, Mulrain L, Navidi A, Naylor J, Negash T, Nguyen T, Nguyen N, Nicol R, Norbu C, Norbu N, Novod N, O'Neill B, Osman S, Markiewicz E, Oyono OL, Patti C, Phunkhang P, Pierre F, Priest M, Raghuraman S, Rege F, Reyes R, Rise C, Rogov P, Ross K, Ryan E, Settipalli S, Shea T, Sherpa N, Shi L, Shih D, Sparrow T, Spaulding J, Stalker J, Stange-Thomann N, Stavropoulos S, Stone C, Strader C, Tesfaye S, Thomson T, Thoulutsang Y, Thoulutsang D, Topham K, Topping I, Tsamla T, Vassiliev H, Vo A, Wangchuk T, Wangdi T, Weiland M, Wilkinson J, Wilson A, Yadav S, Young G, Yu Q, Zembek L, Zhong D, Zimmer A, Zwirko Z, Jaffe DB, Alvarez P, Brockman W, Butler J, Chin C, Gnerre S, Grabherr M, Kleber M, Mauceli E, MacCallum I. Evolution of genes and genomes on the Drosophila phylogeny. *Nature*. 2007 Nov 8;450(7167):203-18. PubMed PMID: 17994087.

9. Samet H, Phillippy A, Sankaranarayanan. Knowledge discovery using the Sand spatial browser. *Proceedings of the 8th Annual International Conference on Digital Government Research: Bridging Disciplines & Domains*. Philadelphia, Pennsylvania. 2007.
10. Phillippy AM, Schatz MC, Pop M. Genome assembly forensics: finding the elusive mis-assembly. *Genome Biol*. 2008;9(3):R55. PubMed PMID: 18341692; PubMed Central PMCID: PMC2397507.
11. Salzberg SL, Sommer DD, Schatz MC, Phillippy AM, Rabinowicz PD, Tsuge S, Furutani A, Ochiai H, Delcher AL, Kelley D, Madupu R, Puiu D, Radune D, Shumway M, Trapnell C, Aparna G, Jha G, Pandey A, Patil PB, Ishihara H, Meyer DF, Szurek B, Verdier V, Koebnik R, Dow JM, Ryan RP, Hirata H, Tsuyumu S, Won Lee S, Seo YS, Sriariyanum M, Ronald PC, Sonti RV, Van Sluys MA, Leach JE, White FF, Bogdanove AJ. Genome sequence and rapid evolution of the rice pathogen *Xanthomonas oryzae* pv *oryzae* PXO99A. *BMC Genomics*. 2008 May 1;9:204. PubMed PMID: 18452608; PubMed Central PMCID: PMC2432079.
12. Phillippy AM, Ayanbule K, Edwards NJ, Salzberg SL. Insignia: a DNA signature search web server for diagnostic assay development. *Nucleic Acids Res*. 2009 Jul;37(Web Server issue):W229-34. PubMed PMID: 19417071; PubMed Central PMCID: PMC2703920.
13. Phillippy AM, Deng X, Zhang W, Salzberg SL. Efficient oligonucleotide probe selection for pan-genomic tiling arrays. *BMC Bioinformatics*. 2009 Sep 16;10:293. PubMed PMID: 19758451; PubMed Central PMCID: PMC2753849.
14. Schatz MC, Phillippy AM, Gajer P, DeSantis TZ, Andersen GL, Ravel J. Integrated microbial survey analysis of prokaryotic communities for the PhyloChip microarray. *Appl Environ Microbiol*. 2010 Aug;76(16):5636-8. PubMed PMID: 20581189; PubMed Central PMCID: PMC2918976.
15. Wang S, Phillippy AM, Deng K, Rui X, Li Z, Tortorello ML, Zhang W. Transcriptomic responses of *Salmonella enterica* serovars Enteritidis and Typhimurium to chlorine-based oxidative stress. *Appl Environ Microbiol*. 2010 Aug;76(15):5013-24. PubMed PMID: 20562293; PubMed Central PMCID: PMC2916494.
16. Deng X, Phillippy AM, Li Z, Salzberg SL, Zhang W. Probing the pan-genome of *Listeria monocytogenes*: new insights into intraspecific niche expansion and genomic diversification. *BMC Genomics*. 2010 Sep 16;11:500. PubMed PMID: 20846431; PubMed Central PMCID: PMC2996996.
17. Rasko DA, Worsham PL, Abshire TG, Stanley ST, Bannan JD, Wilson MR, Langham RJ, Decker RS, Jiang L, Read TD, Phillippy AM, Salzberg SL, Pop M, Van Ert MN, Kenefic LJ, Keim PS, Fraser-Liggett CM, Ravel J. *Bacillus anthracis* comparative genome analysis in support of the

Amerithrax investigation. *Proc Natl Acad Sci U S A*. 2011 Mar 22;108(12):5027-32. PubMed PMID: 21383169; PubMed Central PMCID: PMC3064363.

18. Sahl JW, Johnson JK, Harris AD, Phillippy AM, Hsiao WW, Thom KA, Rasko DA. Genomic comparison of multi-drug resistant invasive and colonizing *Acinetobacter baumannii* isolated from diverse human body sites reveals genomic plasticity. *BMC Genomics*. 2011 Jun 4;12:291. PubMed PMID: 21639920; PubMed Central PMCID: PMC3126785.
19. Ondov BD, Bergman NH, Phillippy AM. Interactive metagenomic visualization in a Web browser. *BMC Bioinformatics*. 2011 Sep 30;12:385. PubMed PMID: 21961884; PubMed Central PMCID: PMC3190407.
20. Bogdanove AJ, Koebnik R, Lu H, Furutani A, Angiuoli SV, Patil PB, Van Sluys MA, Ryan RP, Meyer DF, Han SW, Aparna G, Rajaram M, Delcher AL, Phillippy AM, Puiu D, Schatz MC, Shumway M, Sommer DD, Trapnell C, Benahmed F, Dimitrov G, Madupu R, Radune D, Sullivan S, Jha G, Ishihara H, Lee SW, Pandey A, Sharma V, Sriariyanun M, Szurek B, Vera-Cruz CM, Dorman KS, Ronald PC, Verdier V, Dow JM, Sonti RV, Tsuge S, Brendel VP, Rabinowicz PD, Leach JE, White FF, Salzberg SL. Two new complete genome sequences offer insight into host and tissue specificity of plant pathogenic *Xanthomonas* spp. *J Bacteriol*. 2011 Oct;193(19):5450-64. PubMed PMID: 21784931; PubMed Central PMCID: PMC3187462.
21. Earl D, Bradnam K, St John J, Darling A, Lin D, Fass J, Yu HO, Buffalo V, Zerbino DR, Diekhans M, Nguyen N, Ariyaratne PN, Sung WK, Ning Z, Haimel M, Simpson JT, Fonseca NA, Birol I, Docking TR, Ho IY, Rokhsar DS, Chikhi R, Lavenier D, Chapuis G, Naquin D, Maillet N, Schatz MC, Kelley DR, Phillippy AM, Koren S, Yang SP, Wu W, Chou WC, Srivastava A, Shaw TI, Ruby JG, Skewes-Cox P, Betegon M, Dimon MT, Solovyev V, Seledtsov I, Kosarev P, Vorobyev D, Ramirez-Gonzalez R, Leggett R, MacLean D, Xia F, Luo R, Li Z, Xie Y, Liu B, Gnerre S, MacCallum I, Przybylski D, Ribeiro FJ, Yin S, Sharpe T, Hall G, Kersey PJ, Durbin R, Jackman SD, Chapman JA, Huang X, DeRisi JL, Caccamo M, Li Y, Jaffe DB, Green RE, Haussler D, Korf I, Paten B. Assemblathon 1: a competitive assessment of de novo short read assembly methods. *Genome Res*. 2011 Dec;21(12):2224-41. PubMed PMID: 21926179; PubMed Central PMCID: PMC3227110.
22. Donia MS, Fricke WF, Partensky F, Cox J, Elshahawi SI, White JR, Phillippy AM, Schatz MC, Piel J, Haygood MG, Ravel J, Schmidt EW. Complex microbiome underlying secondary and primary metabolism in the tunicate-Prochloron symbiosis. *Proc Natl Acad Sci U S A*. 2011 Dec 20;108(51):E1423-32. PubMed PMID: 22123943; PubMed Central PMCID: PMC3251135.
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## **Preprints**

1. Jain M, Koren S, Quick J, Rand AC, Sasani TA, Tyson JR, Beggs AD, Dilthey AT, Fiddes IT, Malla S, Marriott H, Miga KH, Nieto T, O'Grady J, Olsen HE, Pedersen BS, Rhie A, Richardson H, Quinlan A, Snutch TP, Tee S, Paten B, Phillippy AM, Simpson JT, Loman NJ, Loose M. Nanopore sequencing and assembly of a human genome with ultra-long reads. *bioRxiv.* 2017. doi: 10.1101/128835.

2. Miller JR, Koren S, Dilley K, Puri Vinita, Brown DM, Harkins DM, Thibaud-Nissen F, Rosen B, Chen X-G, Tu Z, Sharakhov IV, Sharakhova MV, Sebra R, Stockwell TB, Bergman NH, Sutton GG, Phillippy AM, Piermarini PM, Shabman RS. Analysis of the *Aedes albopictus* C6/36 genome provides insight into cell line adaptations to in vitro viral propagation. *bioRxiv*. 2017. doi: 10.1101/157081
3. Jain C, Rodriguez-R LM, Phillippy AM, Konstantinidis KT, Aluru S. High-throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries. *bioRxiv*. 2017. doi: 10.1101/225342

### **Other Publications**

1. Delcher AL, Salzberg SL, Phillippy AM. Using MUMmer to identify similar regions in large sequence sets. *Curr Protoc Bioinformatics*. Chapter 10: Unit 10 13. 2003.
2. Phillippy AM. Whole-genome sequence analysis for pathogen detection and diagnostics. Ph.D. Dissertation. University of Maryland. 2010.
3. Ondov BD, Bergman NH, Phillippy AM. Krona: Interactive metagenomic visualization in a Web browser. *Encyclopedia of Metagenomics*. Springer. 2015 Jan 4.

## Beth Shapiro

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## Curriculum Vitae

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### Education:

DPhil (Zoology) [REDACTED] University, [REDACTED]  
MS (Ecology) University of [REDACTED]  
BS (Ecology) University of [REDACTED]

### Current Position:

Professor, Ecology and Evolutionary Biology, UC Santa Cruz, (2016- present)  
Director of Evolutionary Genomics, UCSC Genomics Institute, UC Santa Cruz (2015-present)

### Past Positions:

Associate Professor, Ecology and Evolutionary Biology, UC Santa Cruz, [REDACTED]  
Shaffer Associate Professor, Department of Biology, The Pennsylvania State University [REDACTED]  
Shaffer Assistant Professor, Department of Biology, The Pennsylvania State University [REDACTED]  
Director, Henry Wellcome Ancient Biomolecules Centre, Oxford University [REDACTED]  
Royal Society University Research Fellow, Oxford University [REDACTED]  
Wellcome Trust Research Fellow, Oxford University [REDACTED]

### Selected Honors and Awards:

Professor, Howard Hughes Medical Institute, [REDACTED]  
Member, New York Academy of Sciences, [REDACTED]  
National Finalist, Blavatnik Awards for Young Scientists, [REDACTED]  
Finalist, LA Times Book Award (for *How to Clone a Mammoth*), [REDACTED]  
AAAS/Subaru SB&F Prize for Excellence in Science Books (for *How to Clone a Mammoth*), [REDACTED]  
Packard Fellow, [REDACTED]  
PopTech Science and Public Leadership Fellow, [REDACTED]  
National Geographic Emerging Explorer, [REDACTED]  
MacArthur Fellow, [REDACTED]  
Searle Scholar, [REDACTED]  
Visiting Fellow, Isaac Newton Institute for Mathematical Sciences, University of Cambridge, [REDACTED]  
Smithsonian Young Innovator, [REDACTED]  
University Research Fellow, The Royal Society, [REDACTED]  
Research Fellow, Balliol College, University of Oxford [REDACTED]  
Rhodes Scholar, [REDACTED]

### Professional Activities:

Board of Reviewing Editors, *Science* [REDACTED]  
Associate Editor, *Journal of Heredity* [REDACTED]  
Board of Directors, Revive & Restore (not-for-profit conservation organization)  
American Genetics Association, Council [REDACTED]  
Member: Contamination Control and Planetary Protection Working Group; Mars 2020 Mission; NASA.  
[REDACTED]  
Organizing Committee: Advances in Genome Biology and Technology meeting [REDACTED]



Editorial Board, *STAR: Science and Technology of Archaeological Research*; <http://www.maneyonline.com/loi/sta> [REDACTED]  
Editorial Board, *PaleoAmerica*; <http://www.maneyonline.com/loi/pal> [REDACTED]  
Executive Committee Member: *Genome10K/Vertebrate Genome Project*. <https://genome10k.soe.ucsc.edu/> [REDACTED]  
Member: Public Interfaces of the Life Sciences Roundtable, The National Academies [REDACTED]  
Panelist: *Molecular Evolution and Genomics* funding panel, Genes and Genome Systems Cluster, Division of Molecular and Cellular Biosciences, The National Science Foundation. [REDACTED]  
Panelist: *Public Interfaces of Science*, The National Academies. [REDACTED]  
US Co-Chair: *Indonesian-American Kavli Frontiers of Science*, The National Academy of Science [REDACTED]  
US Session Chair: *German-American Kavli Frontiers of Science*, The National Academy of Science [REDACTED]  
Associate Editor, *Molecular Biology and Evolution*; <http://mbe.oxfordjournals.org/> [REDACTED]

### Research Interests:

Molecular evolution; Genome evolution; Viral evolution; The interface of genomics and climate change; Ancient DNA; Paleontology; Human evolution, Extinction and speciation; Reconstructing demographic changes through time; Science communication

### Selected Invited/plenary talks:

#### Upcoming Academic Speaking Events

[REDACTED] Anniversary Celebration plenary speaker, University of Georgia Institute of Ecology, Athens, GA 12 January [REDACTED]  
Plant and Animal Genomes, Illumina "Greatest Hits" symposium, 16 January [REDACTED]  
Plenary Speaker, Advances in Genome Biology and Technology, Orlando FL. February [REDACTED]  
Schrödinger at 75: What is life? The Future of Biology. Dublin, Ireland, September [REDACTED]

#### Past Public Speaking Events (selected)

Northern California Science Writers Association Annual Meeting, Plenary Speaker 6 December [REDACTED]  
Isaac Asimov [REDACTED] Lectures, American Museum of Natural History, New York. 29 March [REDACTED]  
Auckland Museum, Auckland, New Zealand. 12 October [REDACTED]  
Allan Wilson Lecture Series, University of Otago. Dunedin, New Zealand . 10 October [REDACTED]  
Friday Night Seminar, Woods Hole, Mass. 12 August [REDACTED]  
Hay Literary Festival, London. 23 May [REDACTED]  
The Royal Institution, London, 23 May [REDACTED]  
Seminars About Long-Term Thinking (SALT), The Long Now Foundation. April [REDACTED]  
*Ferguson Lecture*. Washington University, St Louis. 31 March [REDACTED]

## **Publication List**

### **Journal articles:**

- (1) Heintzman PD, Zazula GD, MacPhee RDE, Scott E, Cahill JA, McHorse BK, Stiller M, Orlando L, Southon JR, Froese DG, Shapiro B. 2017. A new genus of horse from Pleistocene North America. *eLife* 6:e29944.
- (2) Murray GGR, Soares AER, Novak BJ, Schaefer NK, Cahill JA, Baker AJ, Demboski JR, Doll A, Da Fonseca RR, Fulton TL, Gilbert MTP, Heintzman PD, Letts B, McIntosh G, O'Connell BL, Peck M, Pipes M-L, Rice ES, Santos KM, Sohrweide AG, Vohr SH, Corbett-Detig RB, Green RE, Shapiro B. 2017. Natural selection shaped the rise and fall of passenger pigeon genomic diversity. *Science* 358: 951-954.
- (3) Benazzo A, Trucchi E, Cahill JA, Daisano Delser P, Mona S, Fumagalli M, Bunnefeld L, Cornetti L, Ghirotto S, Giradi M, Ometto L, Panziera A, Rota-Stabelli O, Zanetti E, Karamanlidis A, Groffi C, Paule L, Gentile L, Vilá C, Vicario S, Boitani L, Orlando L, Fuselli S, Cernesi C, Shapiro B, Ciucci P, Bertorelle G. 2017. Survival and divergence in a small group: the extraordinary genomic history of the endangered Apennine brown bear stragglers. *Proceedings of the National Academy of Sciences USA* 114:E9589-E9597.
- (4) Kirillova IV, Chernova OF, Kukarsih VV, Shapiro B, van der Plischt J, Shidlovskiy FK, Heintzman PD, van Kolfschoten T, Zazina OG. 2017. Discovery of the skull of *Stephanorhinus kirchbergensis* (Jager, 1839) above the Arctic Circle. *Quaternary Research* 88:537-550.
- (5) Zazula GD, Hall E, Hare PG, Thomas C, Matthewes R, La Farge C, Martel AL, Heintzman PD, Shapiro B. 2017. A middle Holocene steppe bison and paleoenvironments from the Versleue Meadows, Whitehorse, Yukon, Canada. *Canadian Journal of Earth Sciences* 54:1138-1152.
- (6) Maschenko EN, Potapova OR, Vershinina A, Shapiro B, Streletskaia IR, Vasilev AA, Oblogov GE, Kharlamova AS, van der Plicht J, Tikhonov AN, Serdyuk NV, Tarasenko KK. The Zhenya Mammoth (*Mammuthus primigenius* (Blum.)): taphonomy, geology, age, morphology and ancient DNA of a 48,000 year old frozen mummy from Western Taymyr, Russia. *Quaternary International* 445: 104-134.
- (7) vonHoldt BM, Cahill JA, Gronau I, Shapiro B, Wall J, Wayne RK. 2017. Response to *Whole genome data do not support recent hybrid origins of red wolves and eastern wolves*. *Science Advances* 3: e1701233
- (8) Meyer M, Palkopoulou E, Baleka S, Stiller M, Penkman K, Alt KW, Ishida Y, Mania D, Mallick S, Meijer T, Meller T, Nagel S, Nickel B, Ostritz S, Roca AL, Rohland N, Schauer K, Schüler T, Reich D, Shapiro B, Hofreiter M. 2017. Nuclear and mitochondrial genome sequences of the Middle Pleistocene Eurasian straight-tusked elephant rewrite elephant evolutionary history. *eLife* 6: e23413.
- (9) Wang Y, Heintzman P, Newsom L, Bigelow N, Wooller M, Shapiro B, Williams J. 2017. The southern coastal Beringian land bridge: cryptic refugium or pseudo refugium for woody plants during the Last Glacial Maximum? *Journal of Biogeography* 44:1559-1571.
- (10) Froese DG, Stiller M, Heintzman PD, Reyes AV, Zazula GD, Soares AER, Meyer M, Hall E, Jensen BKL, Arnold L, MacPhee RDE, Shapiro B. 2017. New fossil and genomic evidence constrains the timing of bison arrival in North America. *Proc Natl Acad Sci USA*. 114:3457-3462.
- (11) Schaefer NK, Shapiro B, Green RE. AD-LIBS: 2017. Inferring ancestry across hybrid genomes using low-coverage sequence data. *BMC Bioinformatics*. 18:203.
- (12) Chang D\*, Knapp M\*, Enk J\*, Lippold S, Kircher M, Lister A, MacPhee RDE, Widga C, Czechowski P, Sommer R, Hodges E, Stümpel N, Barnes I, Dalén L, Derevianko A, Germonpré M, Hillebrand-Voiculescu A, Constantin S, Kuznetsova T, Mol D, Rathgeber R, Rosendahl W, Tikhonov AN, Willerslev E, Hannon G, Lalueza-Fox C, Jørgen U, Poinar H, Hofreiter M, Shapiro B. 2017. The evolutionary and phylogeographic history of woolly mammoths: a comprehensive mitogenomic analysis. *Scientific Reports* 7:44585
- (13) Węcek K, Hartmann S, Pajmians JLA, Taron U, Xenikoudakis G, Cahill JA, Heintzman PD, Shapiro B, Baryshnikov G, Bunevich AN, Crees JJ, Dobosz R, Manaserian N, Okarma H, Tokarska M,

- Turvey ST, Wójcik JM, Żyła W, Szymura JM, Hofreiter M, Barlow A. 2017. Complex admixture preceded and followed the extinction of wisent in the wild. *Molecular Biology and Evolution* 34: 598-612.
- (14) Rearden J, Ankeny RA, Bangham J, Darling K, Hilgartner S, Maxson Jones K, Shapiro B, Stevens H, and the Genomic Open workshop group. 2016. Bermuda 2.0: Reflections from Santa Cruz. *GigaScience* 5:1-4.
  - (15) Soares AER, Novak B, Haile J, Fjeldsø J, Gilbert MTP, Poinar H, Church G, Shapiro B. 2016. Complete mitochondrial genomes of living and extinct pigeons revise the timing of the columbiform radiation. *BMC Evolutionary Biology* 16: 1-9.
  - (16) Soubrier J, Gower G, Chen K, Richards S, Llamas B, Mitchell KJ, [35 authors], Shapiro B, Cooper A. 2016. Early cave art and ancient DNA record the origin of European bison. *Nature Communications* 7:13158.
  - (17) vonHoldt BM, Cahill JA, Fan Z, Gronau I, Robinson J, Pollinger JP, Shapiro B, Wall J, Wayne RK. 2016. Whole-genome sequence analysis shows that two endemic species of North American wolf are admixtures of the coyote and gray wolf. *Science Advances* 2: e150175.
  - (18) Shapiro B. 2016. Pathways to de-extinction: How close can we get to resurrection of an extinct species? *Functional Ecology*. 10.1111/1365-2435.12705 <http://onlinelibrary.wiley.com/doi/10.1111/1365-2435.12705/full>
  - (19) Heintzman PD, Froese DG, Ives JW, Soares AER, Zazula GD, Letts B, Andrews TD, Driver JC, Hall E, Hare G, Jass CN, MacKay G, Southon JR, Stiller M, Woywitka R, Suchard MA, Shapiro B. 2016. Bison phylogeography constrains dispersal and viability of the 'Ice Free Corridor' in western Canada. *Proc Natl Acad Sci USA*. Proc 113: 8057-8063. <http://www.pnas.org/content/113/29/8057.full?sid=7b4833d6-a9ea-4887-8123-7ef48f5c26f9>
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Selva Biological Station, Costa Rica. *Agr. For. Ent.* 2: 39-47.

### Book reviews:

- (1) Shapiro, B. Book review: Reading the story in DNA by Lindell Bromham. 2010. *Quart. Rev. Biol.* 85: 223.
- (2) Shapiro B. Book review: Return of the Crazy Bird: the Sad, Strange Tale of the Dodo by Clara Pinto-Correia. 2004. *Quart. Rev. Biol.* 79: 197-198.

### Book chapters:

- (1) Heintzman P, Soares AER, Shapiro B. Paleogenomics. Reviews in Cell Biology and Molecular Medicine 1: 243-267.
- (2) Shapiro B. 2013. Ancient DNA. Pp 475-481 in Princeton Guide to Evolution. Losos, J. Ed. Princeton University Press.
- (3) Pybus OG, Shapiro B. 2009. Natural selection and adaptation of molecular sequences. In Lemey P, Salemi N, Vandamme A-M. *The Phylogenetics Handbook*. Cambridge Univ. Press.
- (4) Shapiro B, Gilbert MTP, Barnes I. 2008. Using DNA to investigate the human past. Pp 207-242 in H Schutkowski, *Between Biology and Culture*. No. 56 in series: Cambridge Studies in Biological and Evolutionary Anthropology Cambridge University Press.
- (5) Barnett R, Shapiro B, Barnes I. 2003. Ancient DNA from vertebrate fossils. In Elias SA, Ed. *Encyclopedia of Quaternary Science*. Elsevier.

### Books:

- (1) Forthcoming (2019): Shapiro B. Wild(ish) Life. Basic Books, New York.
- (2) Shapiro B, Hofreiter M (Eds). 2012. Ancient DNA. Methods and Protocols. Methods in Molecular Biology vol 840. Springer, New York. DOI 10.1007/978-1-61779-516-9\_1
- (3) Shapiro, B. 2015. How to Clone a Mammoth: The Science of De-Extinction. Princeton University Press, Princeton, NJ. ISBN 978-0-691-15705-4.

### Newspaper and Magazine Articles:

- (1) Shapiro B, 2015. Long Live the Mammoth. *Popular Science*, May 2015 <http://www.popsoci.com/de-extinction-long-live-mammoth>.
- (2) Shapiro, B. 2015. Should we clone a mammoth? *The Chronicle of Higher Education*, April 27 2015. <http://chronicle.com/article/Should-We-Clone-a-Mammoth-/229575>
- (3) Shapiro, B. 2015. Could we "de-extinctify" a mammoth? *The Observer* 26 April 2015. <http://www.theguardian.com/science/2015/apr/26/woolly-mammoth-normal-for-norfolk-de-extinction>

### Current External Research Support

NSF [REDACTED]. Inferring admixture history in non-model organisms using local ancestry detection [REDACTED]

HHMI Professor (to B. Shapiro and R. Wayne, UCLA). \$ [REDACTED] (50% to UCSC).

IMLS [REDACTED]. Advancing collections stewardship through development and dissemination of genomic technologies for biological collections. [REDACTED]

The Original Horse (private donation). [REDACTED]

UC President's Research Catalyst Award [REDACTED] The UC Conservation Genomics Network.  
\$ [REDACTED] UCSC portion: [REDACTED]

NSF [REDACTED] Collaborative Research: Land bridges, ice-free corridors, and biome shifts: Impacts on the evolution and extinction of horses in ice-age Beringia. \$ [REDACTED] National Science Foundation, Co-PI Dan Mann (UAF, [REDACTED])  
New technology for probing the genomes of the past. Gordon and Betty Moore Foundation. Co-PIs: B Shapiro and RE Green. [REDACTED]  
NSF [REDACTED] An evaluation of the timing, development, and scale of anthropogenic burning in Central California. K. Lightfoot (UC Berkeley) PI, [REDACTED] subaward to UCSC) [REDACTED]  
Assessing DNA preservation in archival material. \$ [REDACTED] The Smithsonian Institution. [REDACTED]

## Videos and interviews available online:

### A short video take on what I do:

[http://poptech.org/popcasts/quick\\_takes\\_beth\\_shapiro](http://poptech.org/popcasts/quick_takes_beth_shapiro)

### And how I “live curious”:

<http://video.nationalgeographic.com/video/specials/in-the-field-specials/curiosity-beth-shapiro/>

### Longer talks/seminars

TEDxDeExtinction:

Ancient DNA: What it is, and what it could be  
National Geographic Society, Washington D.C.

<http://longnow.org/revive/tedxdeextinction/ancient-dna-what-it-is-and-what-it-could-be/>

Pop!Tech:

Understanding Extinction

Swedish Embassy, Washington D.C

[http://poptech.org/popcasts/beth\\_shapiro\\_species\\_extinction](http://poptech.org/popcasts/beth_shapiro_species_extinction)

Pop!Tech:

What goes extinct?

Pop!Tech annual meeting

[http://poptech.org/popcasts/beth\\_shapiro\\_what\\_goes\\_extinct](http://poptech.org/popcasts/beth_shapiro_what_goes_extinct)

World Science Festival:

Cool Jobs

[http://worldsciencefestival.com/participants/beth\\_shapiro](http://worldsciencefestival.com/participants/beth_shapiro)

### Radio, TV, and documentaries:

Dateline: On Assignment. The Clone Zone. May 2016. <http://www.nbcnews.com/dateline/video/the-de-extinction-download-688897603654>

*Die Trying: Hunt for the Superbear*. 90 Miles Productions for National Geographic TV. Release Date: 12 July 2014.

*Undoing Forever*. CBC Radio One IDEAS. Release date: 19 June 2014.

*Reawakening Extinct Species*. KQED QUEST. Release date: 23 April 2014.

*The Dodo's Guide to Surviving Extinction*. BBC. Release date: 4 November 2007.

*Extinct*. Wall to Wall TV. Release date: 25 September 2001.



## CURRICULUM VITAE

### **Professor Byrappa Venkatesh**

Research Director, Institute of Molecular and Cell Biology, A\*STAR, Singapore;

Adjunct Professor, Department of Paediatrics, Yong Loo Lin School of Medicine, National University of Singapore, Singapore  
and

Joint Scientist, KK Women's and Children's hospital, Singapore

Email: [mcbbv@imcb.a-star.edu.sg](mailto:mcbbv@imcb.a-star.edu.sg)

### **Education**

Ph.D. National University of [REDACTED]

M.Sc. University of Agricultural Sciences, [REDACTED]

B.Sc. University of Agricultural Sciences, [REDACTED]

### **Professional appointments**

2008 – Present Professor and Research Director, Institute of Molecular and Cell Biology, Singapore and

Adjunct Professor, Department of Paediatrics, National University of Singapore

2016 – Present Joint Scientist, KK Women's and Children's hospital, Singapore

Associate Professor, Institute of Molecular and Cell Biology, Singapore;  
Adjunct Associate Professor, Department of Paediatrics, National University of Singapore

Assistant Professor, Institute of Molecular and Cell Biology, Singapore;  
Adjunct Senior Fellow, Department of Paediatrics, National University of Singapore

Research Associate, Institute of Molecular and Cell Biology, National University of Singapore, Singapore

Research Fellow, Institute of Molecular and Cell Biology National University of Singapore, Singapore

Sydney Brenner's Molecular Genetics Unit, MRC, Cambridge, UK

Jr. Research Fellow, Institute of Molecular and Cell Biology, National University of Singapore, Singapore

Research Scholar, Department of Zoology, National University of Singapore, Singapore

### **Selected publications**

Aparicio, S., ...(37 authors)..., **Venkatesh, B.**, Rokhsar, D. and Brenner, S. Whole-genome shotgun assembly and analysis of the genome of *Fugu rubripes*. *Science* (2002) 297, 1301-1310. [cover image; *Accompanied by a "Perspective" article*]

Koh, E.G.L., Lam, K., Christoffels, A., Erdmann, M.V., Brenner, S. and **Venkatesh, B.** Hox gene clusters in the Indonesian coelacanth, *Latimeria menadoensis*. *Proc. Natl. Acad. Sci. USA* (2003) 100, 1084-1088.

Yu, W.P., Brenner, S. and **Venkatesh, B.** Duplication, degeneration and subfunctionalization of the nested synapsin-Timp genes in Fugu. *Trends Genet.* (2003) 19, 180-183.

**Venkatesh, B.** Evolution and diversity of fish genomes. *Curr. Opin. Genet. Dev.* (2003) 13, 588-592.

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Chou, C.F., Tohari, S., Brenner, S. and **Venkatesh, B.** Erythropoietin gene from a teleost fish, *Fugu rubripes*. *Blood* (2004) 104:1498-1503. [Accompanied by a "Commentary" article]

**Venkatesh, B.**, Tay, A., Dandona, N., Patil, J.G. and Brenner, S. A compact cartilaginous fish model genome. *Curr. Biol.* (2005) 15, R82-R83.

Kai, W., Kikuchi, K., Fujita, M., Suetake, H., Yoshiura, Y., Ototake, M., Fujiwara, A., **Venkatesh, B.**, Miyaki, K. and Suzuki, Y. A genetic linkage map for the tiger pufferfish, *Takifugu rubripes*. *Genetics* (2005) 171: 227-238.

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Lee, A. P., Koh, E.G.L., Tay, A., Brenner, S. and **Venkatesh, B.** Highly conserved syntenic blocks at the vertebrate Hox loci and conserved regulatory elements within and outside Hox gene clusters. *Proc. Natl. Acad. Sci. USA*. (2006) 103, 6994-6999.

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**Venkatesh, B.**, Kirkness, E.F., Loh, Y.H., Halpern, A.L., Lee, A.P., Johnson, J., Dandona, N., Viswanathan, L.D., Tay, A., Venter, J.C., Strausberg, R.L. and Brenner, S. Ancient noncoding elements conserved in the human genome. *Science* (2006) 314, 1892.

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Lee, A.P., Kerk, S.Y., Tan, Y.Y., Brenner, S. and **Venkatesh, B.** Ancient vertebrate conserved noncoding elements have been evolving rapidly in teleost fishes. *Mol. Biol. Evol.* (2011) 28: 1205-1215.

Kai, W., Kikuchi, K., Tohari, S., Chew AH, Tay, A., Fujiwara, A., Hosoya, S., Suetake, H., Naruse, K., Brenner, S., Suzuki, Y. and **Venkatesh, B.** Integration of the genetic map and genome assembly of fugu facilitates insights into distinct features of genome evolution in teleosts and mammals. *Genome Biol. Evol.* (2011) 3: 424-442.

Lane, D.P., Madhumala, A., Lee, A.P., Tay, B-H., Verma, C., Brenner, S. and **Venkatesh, B.** Conservation of all three p53 family members and Mdm2 and Mdm4 in the cartilaginous fish. *Cell Cycle* (2011) 10: 4272-4279.

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Kamiya, T., Kai, W., Tasumi, S., Oka, A., Matsunaga, T., Mizuno, N., Fujita, M., Suetake, H., Suzuki, S., Hosoya, S., Tohari, S., Brenner, S., Miyadai, T., **Venkatesh, B.**, Suzuki, Y., Kikuchi, K. A Trans-species missense SNP in *Amhr2* is associated with sex determination in the tiger pufferfish, *Takifugu rubripes* (fugu). ***PLoS Genetics*** (2012) 8(7): e1002798.

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**Venkatesh, B.**, et al. (32 authors). Elephant shark genome provides unique insights into gnathostome evolution. ***Nature*** (2014) 505: 174-179. [cover image]

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Genome 10K Community of Scientists. The Genome 10K Project: A way forward. ***Annu. Rev. Anim. Biosci.*** (2015) 3: 57-111.

Ravi, V., Yu, W., Pillai, N.E., Lian, M.M., Tay, B., Tohari, S., Brenner, S. and **Venkatesh, B.** Cyclostomes lack clustered protocadherins. ***Mol. Biol. Evol.*** (2015) 33:311-315.

Coffill C.R., Lee, A.P., Siau, J.W., Chee, S.M., Joseph, T.L., Tan, Y.S., Madhumalar, A., Tay, B., Brenner, S., Verma, C.S., Ghadessy, F.J., **Venkatesh, B.** and Lane, D.P. The p53-Mdm2 interaction and the E3 ligase activity of Mdm2/Mdm4 are conserved from lamprey to human. ***Genes Dev.*** (2016) 30: 281-292.

- Braasch, I. et al. The spotted gar genome illuminates vertebrate evolution and facilitates human-teleost comparisons. *Nature Genet.* (2016) 48:427-437. [Accompanied by a “News & Views” article]
- Bian, C., Hu, Y., Ravi, V.,..... O’Brien, S.J., Orbán, L. \*, **Venkatesh, B.** \* and Shi, Q\*. The Asian arowana (*Scleropages formosus*) genome provides new insights into the evolution of an early lineage of teleosts. *Sci. Rep.* (2016) 6: 24501.
- Sun, Y., Huang, Y., Li, X., Baldwin, C.C. Zhou, Z., Yan, Z., Crandall, K.A., Zhang, Y., Zhao, X., Wang, M., Fang, A., Zhang, X., Huang, H., Lopez, J.V., Kilfoyle, K., Zhang, Y., Ortí, G\*, **Venkatesh, B.**\* and Shi, Q\*. Fish-T1K (Transcriptomes of 1,000 Fishes) Project: large-scale transcriptome data for fish evolution studies. *GigaScience* (2016) 5:18.
- Pan, H., Yu, H., Ravi, V., Li, C., Lee, A.P., Lian, M.M., Tay, B-H., Brenner, S., Wang, J., Yang, H., Zhang, G. and **Venkatesh, B.** The genome of the largest bony fish, ocean sunfish (*Mola mola*), provides insights into its fast growth rate. *GigaScience* (2016) 5:36.
- Lin, Q., Fan, S., Zhang, Y., Xu, M., Zhang, H., Yang, Y., Lee, A.P., Woltering, J.M., Ravi, V., Gunter, H.M., Luo, W., Gao, Z., Lim, Z.W., Qin, G., Schneider, R.F., Wang, X., Xiong, P., Li, G., Wang, K., Min, J., Zhang, C., Qiu, Y., Bai, J., He, W., Bian, C., Zhang, X., Shan, D., Qu, H., Sun, Y., Gao, Q., Huang, L., Shi, Q., Meyer, A. and Venkatesh, B. The seahorse genome and the evolution of its specialized morphology. *Nature* (2016) 540: 395-399. [cover image; and Nature Editorial]
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- Ravi, V. and **Venkatesh, B.** The divergent genomes of teleosts. *Annu. Rev. Anim. Biosci.* (In Press).



# CURRICULUM VITAE

TANDY WARNOW  
FOUNDER PROFESSOR OF COMPUTER SCIENCE

## 1 Contact Information

*Department of Computer Science*  
*The University of Illinois at Urbana-Champaign*  
Email: [warnow@illinois.edu](mailto:warnow@illinois.edu)  
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## 2 Research Interests

Phylogenetic tree inference in biology and historical linguistics, multiple sequence alignment, metagenomic analysis, big data, statistical inference, probabilistic analysis of algorithms, machine learning, combinatorial and graph-theoretic algorithms, and experimental performance studies of algorithms.

## 3 Professional Appointments

- Associate Head for the Department of Computer Science, The University of Illinois at Urbana-Champaign, 2017-present.
- Founder Professor of Computer Science, the University of Illinois at Urbana-Champaign, 2014-present.
- Member, Carl R. Woese Institute for Genomic Biology. Affiliate of the National Center for Supercomputing Applications (NCSA). Affiliate faculty in the Departments of Mathematics, Electrical and Computer Engineering, Statistics, Animal Biology, Entomology, Plant Biology, and Bioengineering, 2014-present.
- National Science Foundation, Program Director for Big Data, [REDACTED]
- Member, Big Data Senior Steering Group of NITRD (The Networking and Information Technology Research and Development Program), subcommittee of the National Technology Council (coordinating federal agencies), [REDACTED]
- Departmental Scholar, Institute for Pure and Applied Mathematics, UCLA, [REDACTED]
- Visiting Researcher, University of Maryland, [REDACTED]
- Visiting Researcher, Smithsonian Institute, [REDACTED].
- Professeur Invité, Ecole Polytechnique Fédérale de Lausanne (EPFL), [REDACTED]
- Visiting Researcher, Microsoft New England, [REDACTED]

- Visiting Scholar, UC Berkeley, [REDACTED]; co-taught (with Johanna Nichols and Donald Ringe) the course *Computational Methods in Linguistic Reconstruction* at the [REDACTED] Linguistic Institute held at Berkeley.
- Visiting Scholar, Program for Evolutionary Dynamics at Harvard University, [REDACTED]
- Radcliffe Institute for Advanced Studies, Emeline Bigelow Conland Fellow, [REDACTED]
- Visiting Scholar, University of California at Berkeley, [REDACTED]
- University of Texas at Austin, [REDACTED]
  - Co-Director, Center for Computational Biology and Bioinformatics, [REDACTED]
  - Professor, Department of Computer Science, University of Texas at Austin (effective [REDACTED]. Assoc. Professor [REDACTED].
  - Member, Texas Institute for Computational and Applied Mathematics, and the Institute for Cellular and Molecular Biology.
  - Member, Graduate Programs in Computer Sciences, Molecular Biology, Computational and Applied Mathematics, and the Program in Ecology, Evolution, and Behavior.
- University of Pennsylvania, [REDACTED]
  - Associate Professor (tenured [REDACTED]), Department of Computer and Information Sciences.
  - Member, Institute for Research in Cognitive Sciences.
  - Co-PI, Graduate and Postdoctoral Research Training Program (RTG) in Computational Biology. (PI: Warren Ewens).
- University of Arizona, [REDACTED] Visiting Professor, Departments of Computer Science and Ecology and Evolutionary Biology.
- Yale University, [REDACTED] Visiting Researcher, Department of Computer Science.
- Princeton University, [REDACTED] Visiting Professor, Departments of Mathematics and Computer Sciences.
- DIMACS, [REDACTED] visitor.

## 4 Education

- Postdoctoral Fellowship [REDACTED], University of [REDACTED], with Michael Waterman and Simon Tavaré.
- Ph.D. Mathematics ([REDACTED] University of California, [REDACTED])  
 Dissertation: *Combinatorial Algorithms for Constructing Phylogenetic Trees*.  
 Committee: Eugene Lawler (advisor), Manuel Blum, David Gale, Dan Gusfield, and Richard Karp.
- B.A. Mathematics ([REDACTED] *magna cum laude*, University of [REDACTED] [REDACTED])

## 5 Honors

- Fellow of the International Society for Computational Biology (ISCB), [REDACTED]
- Fellow of the Association for Computing Machinery (ACM), [REDACTED] Citation: *For contributions to mathematical theory, algorithms, and software for large-scale molecular phylogenetics and historical linguistics.*
- Founder Professor of Engineering, the University of Illinois at Urbana-Champaign, [REDACTED] present
- David Bruton, Jr. Centennial Professorship in Computer Science, [REDACTED]
- John Simon Guggenheim Foundation Fellowship, [REDACTED] *New problems in evolutionary estimation.*
- Radcliffe Institute for Advanced Study, Emeline Bigelow Conland Fellow, [REDACTED]
- David and Lucile Packard Foundation Fellowship, [REDACTED], *Algorithms for reconstructing evolutionary trees in biology and linguistics.*
- NSF National Young Investigator Award, [REDACTED]. *Combinatorial Problems in Evolutionary Tree Construction.*

## 6 Current and Former Graduate Students

Current:

- Sarah [REDACTED] (second year CS PhD student at UIUC)
- Erin [REDACTED] (fifth year PhD student in Computer Science at UIUC, co-supervised with Bill Gropp, NSF graduate fellow)
- Michael [REDACTED] (sixth year PhD student in Statistics at UIUC)
- Ehsan [REDACTED] (second year CS PhD student at UIUC)
- Pranjal [REDACTED] (fourth year PhD student in Computer Science at UIUC, NSF graduate fellow)

Former:

- Md. Shamsuzzoha [REDACTED] (PhD Fall 2016). Assistant Professor, Department of Computer Science and Engineering (CSE), Bangladesh University of Engineering and Technology.
- Ganesh [REDACTED] (PhD August 2006), Apple Computers
- Ashu [REDACTED] (MS May 2016, Computer Science at the University of Illinois at Urbana-Champaign), now at Apple
- Kevin [REDACTED] (PhD May 2011), Assistant Professor of Computer Science, Michigan State University
- Siavash [REDACTED] (PhD August 2015), Assistant Professor of Electrical and Computer Engineering, UCSD
- Luay [REDACTED] (PhD May 2004), Professor and Chair of Computer Science at Rice University.

- Serita [REDACTED] (PhD December 2009), Assistant Professor of Computer Science at Calvin College.
- Nam-phuong [REDACTED] (PhD August 2014), postdoctoral researcher at UCSD with Vineet Bafna
- Usman [REDACTED] (PhD May 2004), Associate Professor of Computer Science at NJIT.
- Michelle [REDACTED] (PhD May 2009), visiting professor at Emory University, Department of Mathematics
- Li-San [REDACTED] (PhD May 2003), Associate Professor of Pathology and Laboratory Medicine at the University of Pennsylvania.
- Shibu [REDACTED] (PhD received 2000), Professor of Computer Science at Central Florida University

## 7 Former Postdoctoral advisees

- Kevin [REDACTED] (Chief Quant at Summer Road)
- François [REDACTED] (now self-employed)
- Ruth [REDACTED] (NSF Postdoctoral Fellow in Mathematics)
- Dannie [REDACTED] (Associate Professor of Biology and of Computer Science, Carnegie Mellon University)
- Daniel [REDACTED] (C4 Professor of Bioinformatics, Tübingen University, Germany)
- Nam-phuong [REDACTED] (now at UCSD CS, postdoc with Vineet Bafna)
- Ken [REDACTED] (now retired)
- Katherine [REDACTED] [REDACTED] Professor of Mathematics and Computer Science, Lehman College, CUNY)
- Elizabeth [REDACTED] (Associate Professor of Computer Science, Harvey Mudd College)
- Shel [REDACTED] (visiting faculty, Emory University, Mathematics & Computer Science)

## 8 Current Grant Support

- NSF grant [REDACTED] 9. This is a collaborative grant with the University of Maryland, for new methods for metagenomic dataset analysis, building on our TIPP method for taxon identification of reads in a metagenomic sample. (This grant ends [REDACTED].)
- NSF [REDACTED], AitF: Full: Collaborative Research: Graph-Theoretic Algorithms to Improve Phylogenomic Analyses. I am the overall PI, and this project is collaborative with Satish Rao (UC Berkeley PI) and Chandra Chekuri (UIUC). We are developing new theoretical computer science and discrete algorithms for improving the estimation of large species and gene trees, and specifically enabling statistical methods to scale to ultra-large datasets. (This grant ends [REDACTED].)
- NSF [REDACTED] ABI Innovation: New methods for multiple sequence alignment with improved accuracy and scalability. PI Warnow. [REDACTED]. Award Amount: [REDACTED] (No Co-PIs).

## 9 Recent Grant Support

- NSF [REDACTED] Collaborative Research: Novel Methodologies for Genome-scale Evolutionary Analysis of Multi-locus data. PI, [REDACTED]. Collaborative grant with Rice University and Stanford University. [REDACTED]
- NSF [REDACTED] (ATOL): Collaborative Research: Large-Scale Simultaneous Multiple Alignment and Phylogeny Estimation. Overall PI: Warnow. Collaborative grant with the University of Georgia, The University of Nebraska, and the University of Kansas. Total amount: \$ [REDACTED] Million for the entire project. [REDACTED]
- NSF [REDACTED] (Large): Building the Tree of Life – A National Resource for Phyloinformatics and Computational Phylogenetics. Overall PI: Warnow, [REDACTED] (extended to [REDACTED] Collaborative with four other institutions (UCSD, UNM, Florida State University, and UC Berkeley). Total amount: [REDACTED] for the entire project. Final report in abridged form available at <http://www.cs.utexas.edu/users/tandy/CIPRES-FINAL.pdf>.
- NSF [REDACTED] (small): Collaborative Research, Algorithms for Inferring Reticulate Evolution in Historical Linguistics. Overall PI: Warnow, (with Donald Ringe, at the University of Pennsylvania), [REDACTED].
- NSF [REDACTED] (medium): Collaborative Research, Reconstructing Complex Evolutionary Histories. Overall PI: Warnow, [REDACTED] (extended to [REDACTED] collaborative with the University of New Mexico. Total amount [REDACTED]
- NSF [REDACTED]: IGERT: Computational Phylogenetics and Applications to Biology. PI: David Hillis, Co-PIs Warnow, Jansen, and Gutell, [REDACTED] (extended to [REDACTED] Total amount: \$ [REDACTED]
- NSF [REDACTED]: Comparative Chloroplast Genomics: Integrating Computational Methods, Molecular Evolution, and Phylogeny. PI: Robert Jansen, Co-PIs Warnow and Raubeson, [REDACTED] Total amount: [REDACTED]
- NSF [REDACTED] (medium): Exploring the Tree of Life, PI: Tandy Warnow, [REDACTED] (extended to [REDACTED] Total amount: \$ [REDACTED]
- NSF [REDACTED]: Collaborative Research, Computing Optimal Phylogenetic Trees Under Genome Rearrangement Metrics. PI: Robert Jansen, [REDACTED] Participant: Warnow. Total amount: \$ [REDACTED]
- NSF [REDACTED] CISE Research Instrumentation. PI: Doug Burger. Co-PIs: Tandy Warnow, Harrick Vin, Steve Keckler, and Inderjit Dhillon, [REDACTED] Total amount: \$ [REDACTED]
- NSF [REDACTED] (Linguistics): Character-based Methods for Reconstructing the Evolutionary History of Natural Languages. PI: Tandy Warnow. Co-PI's: Donald Ringe and Ann Taylor. [REDACTED] Total amount: \$ [REDACTED]
- NSF [REDACTED] (Research Training, Computational Biology): Statistical and Computational Methods for Data Management and Analysis in Molecular Genetics. PI: Warren Ewens. Co-PI: Tandy Warnow, David Roos, and David Searls. [REDACTED] Total amount: \$ [REDACTED]
- NSF [REDACTED] (Theory of Computing): NSF Young Investigator: Computational Problems in Evolutionary Tree Reconstruction, [REDACTED] Total amount: \$ [REDACTED]

## 10 National and International Service

- Member, Faculty of 1000, 2017-present
- Genome 10K Executive Committee Member, 2015-present
- Paris Kanellakis Award Committee Member, 2015-present
- WABI (Workshop on Algorithms for Bioinformatics) Steering Committee 2013-present
- Co-organizer, IPAM (Institute for Pure and Applied Mathematics) workshop on Multiple Sequence Alignment, 2015
- Co-organizer, Programme on Mathematical, Statistical and Computational Aspects of the new science of Metagenomics, Sir Isaac Newton Institute of Mathematical Sciences, Cambridge University, 2012-2014
- Program Director for Big Data, National Science Foundation, July 2012 - July 2013
- Chair, NIH BDMA (Biodata Management and Analysis) Study Section, 2010-2012
- PLoS Currents: Tree of Life, Board of Reviewers, 2010-present.
- Faculty Recruiting Committee, ETH-Zurich, 2010-2011.
- Advisory Board, IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006-2012.
- Advisory Board, Springer, Computational Biology Book Series, 2005 - present.
- Participant, Institutes of Medicine Workshop on Interdisciplinary Programs and Academic Health Centers on Tuesday, September 26th, 2006.
- Member, Board of Directors, the International Society for Computational Biology (ISCB), 2001-2004.
- Committee member, National Academy of Sciences Committee on Interdisciplinarity (2003-2004).
- Program committee co-chair, National Academy of Sciences (USA), Japanese-American Frontiers of Science (2003).
- Committee member, National Academy of Sciences, Committee for Biological Cyberinfrastructure (BIOACCI). (2003).
- Committee member, National Research Council Committee on Interdisciplinarity. (2003).
- Program committee, National Academy of Sciences (USA), Japanese-American Frontiers of Science (2002).
- Panelist, Howard Hughes Medical Institute, Postdoctoral Fellowships in Biological Sciences, 2003.
- Program committee co-chair: Great Lakes Bioinformatics (GLBIO) 2017; Combinatorics and Computing (COCOON) 2003; European Conference on Computational Biology (ECCB) 2008; Track for Evolution and Phylogeny, Intelligent Systems for Molecular Biology (ISMB) 2006, 2007, 2008, 2011, 2013, and 2014; ACM-SIAM Symposium on Discrete Algorithms (SODA) 1999; Workshop on Algorithms for Bioinformatics (WABI) 2009; Great Lakes Bioinformatics (GLBIO) 2016.
- Conference co-chair, Intelligent Systems for Molecular Biology (ISMB) 2018.
- Program committee member: AAAI 2015; ALLENEX 2005; COCOON 1998 and 2003; EACL 2012 Joint Workshop of LINGVIS (Visualization of Linguistic Patterns) and UNCLH (Uncovering Language History from Multilingual Resources); FUN 2001; GLBIO 2016; ICALP 2005; ISMB 2006, 2007, 2008, 2009, 2012, 2013, 2014, and 2016; JOBIM 2000; RECOMB 1997, 2001, 2002, 2004, 2009, 2010, 2011, 2014, 2016, and 2018; RECOMB-CG 2015; SODA 2001; STOC 1998; FOCS 1996; WABI 2001, 2002 2004, 2005, 2006, 2009, 2010, and 2015; and WADS 2001.

- NSF Panelist, 1995, 1996, 2000, 2001, 2002, 2003, 2007, and 2016.
- Proposal reviewer for NSERC, 1999-2006.
- Reviewer for faculty candidates at the Royal Institute of Technology in Stockholm, Sweden, 1999.

## 11 Invited Lectures

### 2017

- NIPS Workshop on Advances in Modeling and Learning Interactions from Complex Data, Long Beach CA, December 8, 2017.
- Kew Royal Botanical Gardens, October 5, 2017.
- Keynote speaker, ACM-BCB and WABI, Cambridge, MA. August 20-23, 2017.
- STAMPS, Marine Biology Laboratory at Woods Hole, August 6, 2017.
- Keynote speaker. IPDPS (IEEE International Parallel and Distributed Processing) Symposium, Orlando FL. May 30, 2017.
- NeLLi: From New Lineages of Life to New Functions at the DOE Joint Genome Institute (JGI). April 5, 2017.
- Second Workshop on Statistical and Algorithmic Challenges in Microbiome Data Analysis at The Broad Institute of MIT and Harvard, in Cambridge, MA. February 16-17, 2017.
- Plant Biology, UIUC. January 27, 2017.

### 2016

- Simons Center, New York City. December 2016.
- National Institutes of Health, NLM. December 2016.
- NYU CS department, November 2016.
- CLIMB conference, Lausanne, Switzerland, November 2016.
- Statistics Department Colloquium, University of Chicago. October 2016.
- Georgia Tech, Math Department IMPACT Distinguished Lecture. October, 2016.
- Georgia Tech, CSE Department. Distinguished Lecture. October, 2016.
- Princeton CS Department. October, 2016.
- University of Pennsylvania, Math Department. October, 2016.
- CMU Computational Biology. September, 2016.
- Using Ensembles of HMMs for Grand Challenges in Bioinformatics, as part of the Schloss Dagstuhl seminar Next generation sequencing - Algorithms and Software for Biomedical Applications August, 2016.
- Oxford University Statistics Department. August 2016.

- University of Trento, Italy. August, 2016.
- SIAM Conference Discrete Math, Georgia State University, Atlanta, Georgia, USA. June, 2016.
- Blue Waters Symposium, Oregon. (PDF) (PPTX) June, 2016.
- Austin, Texas Phylogenomics Symposium, Advances in Multiple Sequence Alignment June, 2016.
- Austin, Texas. Evolution 2016 meeting. June, 2016.
- UCSD Bioinformatics seminar, May 2016
- MIT Computer Science conference on historical linguistics, May 2016
- Molecules as documents of evolutionary history: 50 years after Roscoff (Brittany), France, May 2016
- Co-evolution in proteins and RNA, theory and experiments, Cargese, Corsica, April 2016
- PhyloPizza, Smithsonian Institute, March 2016
- CEHG Symposium at Stanford University, March 2016
- Toyota Technology Institute of Chicago, February 2016
- ITA (Information Theory and Applications), Plenary Talk, February 2016
- University of Washington, Combi seminar, February 2016
- UC Davis, Genomics Institute, January 2016.
- UC San Francisco, January 2016
- UC Berkeley, Museum of Comparative Zoology, January 2016
- Pacific Symposium on Biocomputing, January 2016

## 2015

- HHMI (Howard Hughes Medical Institute), November 2015
- University of California at San Diego, Distinguished Lecture, November 2015
- American Mathematical Society, Chicago, October 2015
- Program for Evolutionary Dynamics, Harvard University, October 2015
- University of Maryland, September 2015
- Duke University, September 2015
- Annual meeting of the Society for Molecular Biology and Evolution, July 2015
- Great Lakes Bioinformatics Conference; Keynote speaker, May 2015
- Genome 10K, March 2015
- National Center for Supercomputing Applications, February 2015
- IPAM (Institute for Pure and Applied Mathematics at UCLA), January 2015



## 2014

- Department of Computer Science, Swarthmore College, December 2014
- Institute for Genomic Biology, University of Illinois at Urbana-Champaign, November 2014
- Institute for Biomedical Informatics, The University of Pennsylvania, October 2014
- Mathematics Colloquium, University of Illinois at Urbana-Champaign, October 2014
- Gotham Seminar on Genomics & Statistics, Columbia University, October 2014
- Department of Computer Science, Case Western University, September 2014 (Distinguished Lecture)
- Pacific Northwestern National Laboratories, September 2014
- Simons Institute for the Theory of Computing (Berkeley), April 2014
- Copenhagen University, March 2014
- Newton Institute for Mathematical Sciences at Cambridge University, March 2014
- Janelia Farm (HHMI), February 2014

## 2013

- MAGE (Models and Algorithms for Genome Evolution), *plenary speaker* August 2013; invited by Nadia El-Mabrouk (Univ Montreal, Computer Science)
- Evolution 2014 annual meeting, Symposium on Practical Phylogenomics, invited by David Posada (Biology, University of Vigo)
- IPAM (Institute for Pure and Applied Mathematics) *plenary speaker*, June 2013; invited by Eleazar Eskin (UCLA CS)
- 10K Genome, Hollywood; invited by David Haussler (UCSC, Computer Science)
- Janelia Farm (Howard Hughes Medical Institute), March 2013; invited by Sean Eddy
- Smithsonian Institution, Frontiers in Phylogenomics, invited by Charles Mitter (University of Maryland, Entomology)

## 2012

- Computational and Statistical Phylogenomics, Vigo, Spain, Sept 2012; invited by David Posada (University of Vigo Biology)
- M.I.T. Bioinformatics, May 2012; invited by Bonnie Berger (MIT CS)
- Smithsonian Institution, May 2012; invited by Mike Braun
- J Craig Venter Institute, May 2012; invited by Karen Nelson
- UCLA Computational Biosciences, April 2012; invited by Matteo Pelligrini (UCLA Biology)
- University of Southern California, Symposium for Mike Waterman and Simon Tavaré, March 2012; invited by Fengzhu Sun (USC Computational Biology)
- University of Pennsylvania, Bio-Mathematics Seminar, March 2012; invited by Robin Pemantle (Penn Mathematics) and Junhyong Kim (Penn Biology)

## 2011

- Janelia Farm, Dec 2011; invited by Sean Eddy
- Science Faculty Colloquium, Bristol University, *distinguished lecture*, Dec 2011
- Univ Wisconsin Biostatistics, Nov 2011; invited by Cecile Ané (Biostatistics)
- UCLA Institute for Pure and Applied Mathematics (IPAM), Nov 2011; invited by Eleazar Eskin (UCLA CS)
- Heilbronn Annual Conference, University of Bristol, England, September 2011; *plenary speaker*, invited by Trevor Wooley (Bristol Mathematics)
- J Craig Venter Institute, Oct 2011; invited by Shibu Yooseph
- Newton Institute, University of Cambridge, June 2011; invited by Vincent Moulton (University of East Anglia, UK)
- UC Berkeley, Lens on the Sciences, May 2011; invited by Mike Jordan and Dick Karp (Berkeley CS)
- Princeton University, Ecology and Evolutionary Biology, May 2011; invited by Laura Landweber (Princeton EEB)
- University of Maryland, April 2011
- Harvard University, invited by Stuart Shieber (Harvard CS) and Naomi Pierce (Harvard OEB)
- Bardonnechia, Italy; invited by Riccardo Zecchina (Physics, University of Turin), February 2011

## 2010

- Brown University, December 2010; *distinguished lecture*, invited by Ben Raphael (Brown CS)
- North Carolina State University, Department of Mathematics, December 2010; invited by Loek Helminck
- Microsoft Research, Computational Aspects of Biological Information, December 2010; invited by Jennifer Chayes (MSRE) and Riccardo Zecchina (Turin Physics)
- Washington Area Phylogenetics Consortium PHYLO-PIZZA, December 2010; invited by Mike Braun (Smithsonian Institute)
- Microsoft Research New England, November 2010; invited by Jennifer Chayes
- Johns Hopkins University, Department of Computer Science, November 2010; invited by Rao Kosaraju (JHU CS)
- Dartmouth College, Department of Computer Science, November 2010; invited by Peter Winkler (Dartmouth Math and CS)
- iEvolBio conference, Evolution Meeting, June 2010.
- RECOMB Bioinformatics Education Conference, May 2010; invited by Pavel Pevzner (UCSD CS)

- Illinois Language and Linguistics Society conference (ILLS 2), May 2010.
- University of Illinois at Chicago, April 2010; invited by Jerry Bona (UIC Mathematics)
- University of Chicago, April 2010; invited by Wen-Hsiung Li (Univ Chicago Biology)
- Princeton University, Computer Science Colloquium, Feb 2010; invited by Olga Troyanskaya (Princeton CS)
- NESCENT (National Evolutionary Synthesis Center), Feb 2010; invited by Allen Rodrigo (NESCENT)
- CMU-UPitt, Computational Biology Seminar, Feb 2010;
- Yale University Computer Science Colloquium, Jan 2010; invited by Joan Feigenbaum (Yale CS)

## 2009

- Workshop on Molecular Evolution and Phylogenetics, SAMSI, April 2009.
- Swadesh Centenary Conference, Leipzig, Germany, *plenary speaker*, January, 2009.

## 2008

- Harvard Symposium on The Science of The Human Past, Dec 5, 2008; invited by Stuart Shieber (Harvard, CS)
- European Conference on Complex Systems Science (ECCS08), Sept 11-17, 2008; *plenary speaker*, invited by Riccardo Zecchina (Turin, Physics)
- School of Computer and Communication Sciences at EPFL, June 12, 2008; *distinguished lecture*, invited by Bernard Moret (EPFL Computer Science)
- MIEP (Mathematics and Informatics in Evolution and Phylogeny), June 2008; invited by Olivier Gascuel (Montpellier Computer Science)
- Department of Computer Sciences, Northwestern University, May 2, 2008
- School of Informatics, Indiana University, April 11, 2008
- Department of EECS, UC Berkeley, Distinguished Lecture, Feb. 6, 2008; invited by Dick Karp (Berkeley CS)
- EECS Colloquium, UC Berkeley, Feb. 2008; invited by Satish Rao (Berkeley CS)

## Distinguished lectures and keynote talks before 2008

- The Sir Isaac Newton Institute for Mathematical Sciences, September 4, 2007
- Department of Computer Sciences, University of Nebraska, Distinguished Lecture, Oct. 30, 2007.
- College of Computing, Georgia Inst. of Technology, Distinguished Lecture, Nov. 1, 2007; invited by David Bader (GaTech CS)

- Department of Computer Science, UC Davis, Distinguished Lecture, Nov. 15, 2007; invited by Dan Gusfield (UCD CS)
- Plenary talk, Workshop on Graph Algorithms (WG'06), Bergen, Norway, June 2006.
- Mathematics Department, Distinguished Lecture, The University of South Carolina, March 28, 2006; invited by Laszlo Székely (USC Math)
- Symposium on Languages and Genes, The University of California at Santa Barbara, Sept. 2006.
- Symposium on Stochastic Processes and Applications, Plenary talk, June 27, 2005).
- Grace Hopper 2004, invited speaker.
- The McDonald Institute for Archaeological Research at Cambridge University, Summer 2004.
- Virginia Tech (East Coast Indo-European Conference), May 26, 2004
- University of Illinois at Chicago, Department of Computer Sciences, distinguished lecture, 2003.
- Annual meeting, Mathematics Association of America (2003), Invited Lecture.
- SMBE (Society for Molecular Biology and Evolution) invited lecture, 2003.
- Radcliffe Institute of Advanced Studies, Conference on Computational Biology: Function, Pathways, Phylogenies and Populations. May 19, 2003
- Invited talk, Mathfest 2003 (annual meeting of the Mathematics Association of America), Boulder, Colorado, July 31, 2003.
- University of Toronto, Department of Computer Science. Distinguished Lecture. April 2002; invited by Toni Pitassi (Toronto CS)
- Distinguished Lecture. Department of Computer Science, University of British Columbia, January 2001; invited by Anne Condon (UBC CS)
- SCOPH (Showcase on Competing Technologies for Phylogenetics: A RECOMB Phylogenetics Conference, April 2001, Montreal Canada; invited by David Sankoff
- Plenary talk at the Annual Meeting of the Canadian Applied and Industrial Mathematics Society (CAIMS), June, 2001, Victoria, British Columbia Canada.
- CRA Distinguished lecture, EECS Joint Colloquium, University of California at Berkeley, October, 2001, Berkeley, CA.
- Plenary talk, Deep Green. June 2, 2000, University of Maryland, College Park, MD.

**Publications** (see <http://www.cs.utexas.edu/users/tandy/papers.html>)

1. Kannan, S. and T. Warnow, 1992. "Triangulating Three-Colored Graphs," *SIAM J. on Discrete Mathematics*, Vol. 5 No. 2, pp. 249-258. (A preliminary version appeared in the Proceedings of the ACM/SIAM Symposium on Discrete Algorithms, 1991.)
2. Bodlaender, H., M. R. Fellows, and T. J. Warnow, 1992. "Two Strikes Against Perfect Phylogeny", Proc. 19th Int'l Colloq. on Automata, Languages, and Programming (ICALP92), Springer Verlag, pages 273-283, in *LNCS 623*.
3. Steel, M. and T. Warnow, 1993. "Kaikoura Tree Theorems: The Maximum Agreement Subtree Problem." *Information Processing Letters*, 48, pp. 77-82.
4. Warnow, T., 1993. "Constructing phylogenetic trees efficiently using compatibility criteria." *New Zealand Journal of Botany*, Vol. 31, pp. 239-248.
5. Kannan, S. and T. Warnow, 1994. "Inferring Evolutionary History from DNA Sequences." *SIAM J. on Computing*, Vol. 23, No. 4, pp. 713-737. (A preliminary version of this paper appeared at FOCS 1990.)
6. Warnow, T., 1994. "Tree Compatibility and Inferring Evolutionary History." *Journal of Algorithms*, 16, pp. 388-407. (A preliminary version of this paper appeared at SODA 1993.)
7. McMorris, F. R., T. Warnow, and T. Wimer, 1994. "Triangulating Vertex Colored Graphs." *SIAM J. on Discrete Mathematics*, Vol. 7, No. 2, pp. 296-306. (A preliminary version of this paper appeared at SODA 1993.)
8. Farach, M., S. Kannan, and T. Warnow, 1995. "A Robust Model for Finding Optimal Evolutionary Trees." *Algorithmica*, special issue on Computational Biology, Vol. 13, No. 1, pp. 155-179. (A preliminary version of this paper appeared at STOC 1993.)
9. Kannan, S., and T. Warnow, 1995. "Tree Reconstruction from Partial Orders." *SIAM J. on Computing*, Vol. 24 No. 3, pp. 511-520. (A preliminary version of this paper appeared at WADS.)
10. Kannan, S., T. Warnow, and S. Yoosheph, 1995. "Computing the local consensus of trees." *SIAM J. Computing*, Vol. 27, No. 6, pp. 1695-1724. (A preliminary version appeared in the Association for Computing Machinery and the Society of Industrial Applied Mathematics, Proceedings, ACM/SIAM Symposium on Discrete Algorithms, 1995, pp. 68-77.)
11. Taylor, A., D. Ringe, and T. Warnow. 1995. "Character-based reconstruction of a linguistic cladogram." Proceedings of the 12th International Conference on Historical Linguistics (Manchester, August 1995).
12. Warnow, T., D. Ringe, and A. Taylor, 1996. "Reconstructing the evolutionary history of natural languages." Proceedings of ACM-SIAM Symposium on Discrete Algorithms (SODA), 1996, pp. 314-322.
13. Phillips, C. A., and T. Warnow, 1996. "The Asymmetric Median Tree: a new model for building consensus trees." *Discrete Applied Mathematics*, Special Issue on Computational Molecular Biology, 71, pp. 311-335.
14. Goldberg, L. A., P.W. Goldberg, C.A. Phillips, E. Sweedyk, and T. Warnow, 1996. "Minimizing phylogenetic number to find good evolutionary trees." *Discrete Applied Mathematics*, Volume 71, Numbers 1-3, pp. 111-136. (A preliminary version of this paper appeared in *Combinatorial Pattern Matching* 1995)

15. Benham, C., S. Kannan, M. Paterson, and T. Warnow, 1996. "Hen's Teeth and Whale's Feet: Generalized Character Compatibility." *Journal of Computational Biology*. Vol 2. No 4. pp 527-536. (A preliminary version of this appeared in *Combinatorial Pattern Matching*, 1995.)
16. Kannan, S., E. Lawler, and T. Warnow, 1996. "Determining the Evolutionary Tree." *Journal of Algorithms*, 21(1): 26-50. (A preliminary version of this paper appeared at SODA 1990.)
17. Ringe, D., T. Warnow, A. Taylor, A. Michailov, and L. Levison, 1997. "Computational cladistics and the position of Tocharian." In V. Mair (Ed.), *The Bronze Age and Early Iron Age Peoples of Eastern Central Asia*, a special volume of the *Journal of Indoeuropean Studies*.
18. Erdős, P. L., M. Steel, L. Székely, and T. Warnow, 1997. "Local quartet splits of a binary tree infer all quartet splits via one dyadic inference rule." *Computers and Artificial Intelligence*, Number 2, Vol 16, pp. 217-227.
19. Warnow, T. 1997. "Mathematical approaches to comparative linguistics." *Proceedings of the National Academy of Sciences*, Vol. 94, pp. 6585-6590, 1997.
20. Kannan, S. and T. Warnow, 1997. "A fast algorithm for the computation and enumeration of perfect phylogenies when the number of character states is fixed." *SIAM J. Computing*, Vol. 26, No. 6, pp. 1749-1763. (A preliminary version appeared in the proceedings of the ACM/SIAM Symposium on Discrete Algorithms, 1995.)
21. Rice, K. and T. Warnow. 1997. "Parsimony is Hard to Beat!" *Proceedings, Third Annual International Conference of Computing and Combinatorics (COCOON)*, Shanghai, China, 1997, pp. 124-133. T. Jiang and D.T. Lee, Eds.
22. Erdős, P. L., M. Steel, L. Szekeley, and T. Warnow, 1997. "Inferring big trees from short sequences." *Springer-Verlag Lecture Notes in Computer Science*, 1256, P. Degano, R. Gorrieri, A. Marchetti-Spaccamela (Eds.), *Proceedings of the 24th International Congress on Automata, Languages, and Programming (ICALP)*, Bologna, Italy, pp. 827-837.
23. Huson, D., S. Nettles, L. Parida, T. Warnow, and S. Yooseph. 1998. "A Divide-and-Conquer Approach to Tree Reconstruction." *Algorithms and Experiments (ALEX) 1998*. Trento, Italy.
24. Bonet, M., M. Steel, T. Warnow, and S. Yooseph. 1998. "Faster algorithms for solving parsimony and compatibility." *The Journal of Computational Biology*, Vol. 5, No. 3, pp. 409-422. By invitation, for the special issue on selected papers from RECOMB 1998.
25. Huson, D., K. A. Smith and T. Warnow. 1999. "Correcting Large Distances for Phylogenetic Reconstruction." *Proceedings, 3rd Workshop on Algorithms Engineering (WAE)*, London, England, 1999, pp. 273-286.
26. Warnow, T.. 1999. "Some combinatorial problems in phylogenetics." Invited paper, *Proceedings of the International Colloquium on Combinatorics and Graph Theory*, Balatonlelle, Hungary, July 15-20, 1996, eds. A. Gyárfás, L. Lovász, L.A. Székely, Volume 7 of *Bolyai Society Mathematical Studies*, Budapest, pp. 363-413.
27. Erdős, P. L., M. Steel, L. Székely, and T. Warnow. 1999. "A few logs suffice to build almost all trees - I." *Random Structures and Algorithms*, 14, 153-184. (Also appears as DIMACS Technical Report 97-71.)
28. Erdős, P. L., M. Steel, L. Székely, and T. Warnow. 1999. "A few logs suffice to build almost all trees - II." *Theoretical Computer Science*, 221 (1-2) (1999) pp. 77-118, by invitation, in the issue of selected papers from ICALP 1997. (Also appears as DIMACS Technical Report 97-72.)

29. Bonet, M., C.A. Phillips, T. Warnow, and S. Yooseph, 1999. "Constructing evolutionary trees in the presence of polymorphic characters." *SIAM J. Computing*, Vol. 29. No. 1, pp. 103-131. (A preliminary version appeared in the ACM Symposium on the Theory of Computing, 1996.)
30. Henzinger, M., V. King, and T. Warnow. 1999. "Constructing a tree from homeomorphic subtrees, with applications to computational molecular biology." *Algorithmica*, 24(1): 1-13 (1999). (A preliminary version appeared in the Association for Computing Machinery and the Society of Industrial and Applied Mathematics, Proceedings, ACM/SIAM Symposium on Discrete Algorithms, 1996, pp. 333-340.)
31. Huson, D., S. Nettles, and T. Warnow. 1999. "Disk-Covering, a fast converging method for phylogenetic tree reconstruction." Special issue of the *Journal of Computational Biology* for selected papers from RECOMB 1999, Vol. 6, No. 3, 1999, pp. 369-386. (This appeared in a preliminary form in the Proceedings of RECOMB 1999, as "Obtaining highly accurate topology estimates of evolutionary trees from very short sequences." Lyon, France.)
32. Huson, D., S. Nettles, K. Rice, T. Warnow, and S. Yooseph. 1999. "The Hybrid tree reconstruction method." *The Journal of Experimental Algorithmics*, Volume 4, Article 5, 1999. Special issue for selected papers from The Workshop on Algorithms Engineering, Saarbrücken, Germany, 1998. <http://www.jea.acm.org/1999/HusonHybrid/>.
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Dziwulski, Kara &lt;kara\_dziwulski@fws.gov&gt;

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**ESA/CITES Import Permit PRT# 43635C**6 messages

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**Dziwulski, Kara** <kara\_dziwulski@fws.gov>

Wed, Mar 7, 2018 at 4:07 PM

To: Erich Jarvis &lt;ejarvis@mail.rockefeller.edu&gt;, Olivier Fedrigo &lt;ofedrigo@mail.rockefeller.edu&gt;

Cc: Sadye Paez &lt;spaez@mail.rockefeller.edu&gt;, Jackie Mountcastle [REDACTED]

Dr. Jarvis,

After final consultation with the CITES Division of Scientific Authority and CITES Division of Management Authority leadership I wanted to clarify how our office will be moving forward with your permit application and the future steps you will need to take to obtain additional permits for the authorizations you seek.

Due to legal obligations under CITES we will not be able to combine your import and export/re-export requests into one permit. Therefore, our office will be using the current application you submitted to create **one multi-use, CITES/ESA Import Permit** that will allow you to import CITES Appendix I listed species, certain "threatened" or "endangered" species under the U.S. Endangered Species Act, species protected under the Wild Bird Conservation Act (WBCA), and salamander samples considered "injurious" under the Lacey Act.

Please be aware that this permit will **NOT** cover you for the following:

- Marine Mammal Protection Act protected specimens
  - You will need to submit a separate application to our office (attached below) to allow import of MMPA-protected species under the USFWS's jurisdiction (e.g. polar bear, walrus, sea otters)
  - You will need to work with the National Marine Fisheries Service (NMFS) to obtain a permit for all cetacean and pinned species (except walrus) you are looking to import.
- Migratory Bird Treaty Act protected specimens
  - You will need to work with the regional USFWS Migratory Bird Treaty Office to obtain the permits required for the species that fall under this protection
- Bald and Golden Eagle Act protected specimens
  - You will need to work with the USFWS Migratory Bird Treaty Office

The import permit we would create will provide you **U.S. Endangered Species Act Authorization for activities conducted over a 5-year period** after it has been published in the federal register for required 30-day public comment. However, since CITES permits can only be issued for a one-year period **you will need to renew the permit with us on a yearly-basis to renew your CITES authorization.**

**Before we continue with your permit you need to clarify who should be given authorization for the permit.**

Basically, would you rather the permit be under you and Dr. Fedrigo: "Dr. Jarvis and Dr. Fedrigo c/o Rockefeller University", or would like it under "Rockefeller University" with the researchers not specified. I ask as we are unable to make the permit out to the "G10K Organization" as it is a global organization.

**If the permit is to be addressed under both of your names:**

- Please specify who would be considered the principal investigator (aka listed first)?
- Please be aware that you and Dr. Fedrigo will be held responsible for all activities conducted under the permit.
- Please be aware that **all CITES Export Permits issued by foreign countries to export scientific samples to you must be addressed exactly as written on your permit (e.g. "Dr. Jarvis and Dr. Fedrigo c/o Rockefeller University"). This is a CITES requirement regardless of what you decide to list on your permit.**

***Please also keep in mind that the easiest way for you to obtain the scientific samples you seek is to receive donations from other U.S. institutions (e.g. universities, zoos, museums). If no commercial transaction occurs, no permit is required for inter-state movement of ESA or CITES-listed specimens (this is not the case for MMPA specimens).***

**Your future regulatory steps should include:**

- Submit an application to our office to set-up a masterfile for export/re-export of these specimens: <https://www.fws.gov/international/pdf/permit-application-form-3-200-37-export-import-interstate-and-foreign-commerce-take-of->

[animals.pdf](#)

- Submit an application to our office for a USFWS MMPA Permit ([attached below](#))
- Submit an application to NMFS for a NMFS MMPA Permit (cetaceans and pinnipeds, except walrus) ([contact Jennifer Skidmore: jennifer.skidmore@noaa.gov](#))
- Submit an application to the USFWS Migratory Bird Office for MBTA and Bald and Golden Eagle Act Permit

If you could please provide me the additional clarification I seek regarding who this permit should be made-out for as soon as possible it would be greatly appreciated.

If you have any additional questions please feel free to contact me for additional clarification.

Kara

***If we do not receive the information requested above within 45 days from the date of this email, your incomplete application will be placed in our inactive files and we will not complete your request for a permit.***

--  
Kara Dziwulski  
Permits Biologist  
Division of Management Authority  
U.S. Fish and Wildlife Service  
Office of International Affairs  
5275 Leesburg Pike, MS:IA  
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**Dziwulski, Kara** <kara\_dziwulski@fws.gov>

Wed, Mar 7, 2018 at 4:11 PM

To: Erich Jarvis <ejarvis@mail.rockefeller.edu>, Olivier Fedrigo <ofedrigo@mail.rockefeller.edu>

Cc: Sadye Paez <spaez@mail.rockefeller.edu>, Jackie Mountcastle [REDACTED]

Whoops... after all that I forgot to attach the newest USFWS Marine Mammal Application... :)

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**Erich Jarvis** <ejarvis@mail.rockefeller.edu>

Wed, Mar 7, 2018 at 6:04 PM

To: "Dziwulski, Kara" <kara\_dziwulski@fws.gov>

Cc: Olivier Fedrigo <ofedrigo@mail.rockefeller.edu>, Sadye Paez <spaez@mail.rockefeller.edu>, Jackie Mountcastle [REDACTED], Melanie Couture <mcouture@mail.rockefeller.edu>

Dear Kara,

This is very good news. I am glad to hear that we will be able to receive a multi-use import permit. This is the type that we currently need the most. I am ccing Melanie Couture in our group at Rockefeller, whom we just hired to handle permits for our genomics project. We will get back to you shortly with our responses about the authorization name, and other items. I just wanted to acknowledge receiving your message.

Best

Erich

[Quoted text hidden]

Erich D. Jarvis, Ph.D.  
Investigator, Howard Hughes Medical Institute  
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[1230 York Avenue, New York, New York 10065](#)

<http://www.jarvislab.net/>  
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**Dziwulski, Kara** <kara\_dziwulski@fws.gov>  
To: Erich Jarvis <ejarvis@mail.rockefeller.edu>

Thu, Mar 8, 2018 at 9:11 AM

Erich,

Great to hear this will be helpful! Once you send me the information regarding the authorization name I can submit this permit application to the federal register and start the public comment process which is currently taking approximately 3-4 months to complete total.

In terms of the other permit applications you need to send into our office, you need to mail those to the general address on the first page of the application. Please do not forward those to me personally as we have certain teams of biologists that handle certain permit types.

That being said, those of us working on these suite of permits for you will be sure to communicate with one another. It also wouldn't hurt to reference the other permit #'s you have with us in your additional applications.

Thanks,

Kara

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**Erich Jarvis** <ejarvis@mail.rockefeller.edu>

Thu, Mar 8, 2018 at 11:35 AM

To: "Dziwulski, Kara" <kara\_dziwulski@fws.gov>

Cc: Olivier Fedrigo <ofedrigo@mail.rockefeller.edu>, Sadye Paez <spaez@mail.rockefeller.edu>, Jackie Mountcastle <[REDACTED]>, Melanie Couture <mcouture@mail.rockefeller.edu>

Hi Kara,

For the authorization names, we are going to go with "Dr. Erich D. Jarvis and Dr. Olivier Fedrigo c/o Rockefeller University". I will be the principle investigator.

Below you mentioned the public comment period is 30 days, but in another message mentioned 3-4 months. I am double checking if there are different, or is the longer estimate the real length. Do you foresee any potential issues in the public comment period that we should be aware of?

Best

Erich

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Erich D. Jarvis, Ph.D.  
Investigator, Howard Hughes Medical Institute  
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**Dziwulski, Kara** <kara\_dziwulski@fws.gov>

Thu, Mar 8, 2018 at 12:11 PM

To: Erich Jarvis <ejarvis@mail.rockefeller.edu>

Cc: Olivier Fedrigo <ofedrigo@mail.rockefeller.edu>, Sadye Paez <spaez@mail.rockefeller.edu>, Jackie Mountcastle <[REDACTED]>, Melanie Couture <mcouture@mail.rockefeller.edu>

Erich,

Thanks for the clarification. The public comment period itself lasts 30-days. However, with the new administration change it is taking 2-3 months to get to the notice published before it even enters the official public comment period. This is why the entire process (publishing + commenting) is taking 3-4 months. Unfortunately, there is no reliable way to determine how long it will take before a notice gets approved for publishing.

I don't foresee there being an issue in getting your notice published but depending on how many public comments we receive on the notice it will take us longer to issue the actual permit. Controversial permit requests obviously receive more public comments. Since your request is very broad in terms of it's request I am preparing for perhaps more comments than usual, but there is no way to really tell. The more comments you have the more it will take for me to issue the permit after the public comment period as our office needs to take all public comments into consideration before we can reach a final decision on whether the permit will be issued or not.

Hope this all makes sense?

Thanks!

Kara

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